Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1846.481	1847.062	-858.796	0.643	3551.496	0.648	29	0.831	K.YKEAAELAAESPQGLLR.T
R1/RRR1-3/2	1846.589	1847.062	-256.704	0.631	3044.218	0.652	28	0.667	K.YKEAAELAAESPQGLLR.T
R1/RRR1-1/2	1846.585	1847.062	-259.224	0.606	3010.708	0.621	27	0.641	K.YKEAAELAAESPQGLLR.T
R1/RRR1-1/2	1842.660	1843.120	-250.341	0.571	3140.593	0.528	26	0.623	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-3/2	1846.493	1847.062	-852.359	0.596	2940.262	0.608	27	0.614	K.YKEAAELAAESPQGLLR.T
R1/RRR1-2/2	1566.166	1565.711	291.314	0.599	2761.747	0.522	24	0.519	R.SQALEAHAASFASFK.V
R1/RRR1-2/2	1842.859	1843.120	-142.086	0.597	2658.080	0.542	24	0.499	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-3/2	1843.485	1843.120	198.941	0.628	2575.026	0.559	24	0.485	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-3/2	1565.285	1565.711	-272.957	0.558	2502.968	0.558	23	0.474	R.SQALEAHAASFASFK.V
R1/RRR1-2/2	1843.971	1843.120	-81.046	0.608	2435.413	0.507	24	0.432	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-2/2	1565.288	1565.711	-271.001	0.532	2287.367	0.558	23	0.428	R.SQALEAHAASFASFK.V
R1/RRR1-2/2	1565.666	1565.711	-28.982	0.565	2293.505	0.542	23	0.422	R.SQALEAHAASFASFK.V
R1/RRR1-3/2	1565.383	1565.711	-210.133	0.534	2317.310	0.520	23	0.419	R.SQALEAHAASFASFK.V
R1/RRR1-3/2	1842.452	1843.120	-907.656	0.565	2365.106	0.501	23	0.417	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-3/2	1566.234	1565.711	-305.937	0.554	2229.218	0.524	23	0.402	R.SQALEAHAASFASFK.V
R1/RRR1-2/2	1842.699	1843.120	-228.874	0.582	2305.089	0.497	23	0.402	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-2/3	1847.160	1847.062	53.112	0.611	2403.623	0.552	35	0.398	K.YKEAAELAAESPQGLLR.T
R1/RRR1-3/2	1438.104	1437.534	-299.310	0.554	2110.704	0.536	20	0.383	R.AAEEANVYDDLVK.Y
R1/RRR1-3/2	1843.533	1843.120	224.771	0.602	2177.034	0.496	23	0.376	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-3/2	1629.420	1628.849	-263.866	0.495	2021.000	0.539	25	0.370	R.QLIDQVVSTALPESK.S
R1/RRR1-1/3	1846.703	1847.062	-194.904	0.580	2382.948	0.500	35	0.363	K.YKEAAELAAESPQGLLR.T
R1/RRR1-3/2	1633.638	1632.740	-62.402	0.539	1799.760	0.581	19	0.351	K.EVCFACVDAEEFR.L
R1/RRR1-3/2	1141.320	1141.346	-23.130	0.525	1746.269	0.531	17	0.323	R.GNLQIVVQAAK.E
R1/RRR1-3/2	1361.315	1361.482	-123.003	0.475	1928.771	0.437	19	0.322	R.VEEDAVWSQVAK.A
R1/RRR1-2/2	1451.601	1450.619	-12.197	0.547	1658.954	0.568	20	0.321	R.EGLVSEAIESFIR.A
R1/RRR1-1/2	1565.747	1565.711	23.020	0.522	1747.797	0.507	20	0.312	R.SQALEAHAASFASFK.V
R1/RRR1-3/2	1140.900	1141.346	-392.090	0.460	1693.397	0.512	17	0.309	R.GNLQIVVQAAK.E
R1/RRR1-3/2	1226.187	1226.403	-176.898	0.461	1710.199	0.496	18	0.308	K.VDGELIFAYAK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1225.637	1226.403	-1445.060	0.477	1706.412	0.492	18	0.307	K.VDGELIFAYAK.I
R1/RRR1-2/2	1437.161	1437.534	-260.147	0.528	1638.762	0.529	20	0.306	R.AAEEANVYDDLVK.Y
R1/RRR1-3/2	1360.928	1361.482	-1145.315	0.437	1799.263	0.442	19	0.305	R.VEEDAVWSQVAK.A
R1/RRR1-3/2	1437.331	1437.534	-141.115	0.524	1676.354	0.505	20	0.304	R.AAEEANVYDDLVK.Y
R1/RRR1-3/2	1480.368	1480.648	-189.532	0.492	1597.487	0.532	20	0.304	R.GKLNAYESLELSR.L
R1/RRR1-2/2	1141.279	1141.346	-58.533	0.593	1679.596	0.501	17	0.303	R.GNLQIVVQAAK.E
R1/RRR1-3/2	1140.498	1141.346	-1624.861	0.467	1583.942	0.540	17	0.302	R.GNLQIVVQAAK.E
R1/RRR1-1/2	1450.218	1450.619	-277.139	0.487	1713.932	0.476	20	0.302	R.EGLVSEAIESFIR.A
R1/RRR1-3/2	1451.312	1450.619	-211.970	0.549	1556.379	0.550	19	0.301	R.EGLVSEAIESFIR.A
R1/RRR1-2/3	1846.265	1847.062	-976.050	0.548	2228.203	0.453	34	0.301	K.YKEAAELAAESPQGLLR.T
R1/RRR1-2/2	1226.181	1226.403	-181.392	0.567	1632.680	0.505	18	0.300	K.VDGELIFAYAK.I
R1/RRR1-2/2	1362.472	1361.482	-7.064	0.553	1505.910	0.555	19	0.298	R.VEEDAVWSQVAK.A
R1/RRR1-2/2	1438.053	1437.534	-335.250	0.582	1547.017	0.536	20	0.296	R.AAEEANVYDDLVK.Y
R1/RRR1-2/2	1362.021	1361.482	-339.672	0.577	1503.073	0.547	19	0.295	R.VEEDAVWSQVAK.A
R1/RRR1-2/2	1295.315	1295.424	-84.372	0.465	1651.177	0.466	18	0.295	K.LNAYESLELSR.L
R1/RRR1-2/2	1226.251	1226.403	-123.870	0.502	1650.061	0.473	18	0.294	K.VDGELIFAYAK.I
R1/RRR1-2/2	1361.957	1361.482	350.096	0.543	1569.745	0.503	19	0.291	R.VEEDAVWSQVAK.A
R1/RRR1-2/2	1450.273	1450.619	-239.307	0.517	1581.406	0.502	19	0.291	R.EGLVSEAIESFIR.A
R1/RRR1-2/2	1141.183	1141.346	-143.511	0.565	1490.345	0.532	17	0.289	R.GNLQIVVQAAK.E
R1/RRR1-2/2	1844.005	1843.120	-62.454	0.499	1674.105	0.468	20	0.289	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-2/2	1141.118	1141.346	-199.956	0.423	1508.391	0.519	16	0.285	R.GNLQIVVQAAK.E
R1/RRR1-3/2	1506.054	1506.591	-1023.651	0.459	1765.170	0.381	19	0.285	R.GQCDDELINVTNK.N
R1/RRR1-2/2	1450.295	1450.619	-223.600	0.505	1607.944	0.465	19	0.284	R.EGLVSEAIESFIR.A
R1/RRR1-1/2	1226.132	1226.403	-221.941	0.423	1676.473	0.423	17	0.283	K.VDGELIFAYAK.I
R1/RRR1-3/2	1628.416	1628.849	-266.510	0.455	1512.580	0.486	22	0.278	R.QLIDQVVSTALPESK.S
R1/RRR1-3/2	1450.149	1450.619	-325.108	0.507	1580.897	0.455	19	0.278	R.EGLVSEAIESFIR.A
R1/RRR1-2/2	1105.716	1105.269	405.206	0.505	1482.101	0.486	16	0.277	R.DPTLAVVAYR.R
R1/RRR1-1/2	1361.695	1361.482	157.206	0.481	1536.838	0.456	18	0.274	R.VEEDAVWSQVAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1105.167	1105.269	-92.020	0.463	1289.187	0.563	15	0.273	R.DPTLAVVAYR.R
R1/RRR1-2/2	1736.250	1736.941	-977.067	0.508	1241.190	0.575	22	0.269	K.VVGNENPSTLICFASK.T
R1/RRR1-3/2	1440.453	1439.579	-88.007	0.515	1554.365	0.420	18	0.267	K.GNM*QLFSVDQQR.S
R1/RRR1-3/2	1480.171	1480.648	-323.477	0.450	1399.701	0.484	19	0.266	R.GKLNAYESLELSR.L
R1/RRR1-1/2	1105.323	1105.269	49.003	0.357	1347.124	0.518	16	0.265	R.DPTLAVVAYR.R
R1/RRR1-2/2	1843.675	1843.120	-241.703	0.492	1383.279	0.509	20	0.265	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-3/2	1373.193	1373.496	-221.622	0.449	1499.555	0.437	18	0.265	R.ADDATHFLDVIR.A
R1/RRR1-2/2	1345.277	1344.448	-128.019	0.579	1219.071	0.539	18	0.263	R.LYDEELYEAAK.I
R1/RRR1-1/3	1673.858	1673.876	-11.025	0.524	2276.994	0.365	33	0.262	R.RPITADSALM*NPNTR.I
R1/RRR1-3/2	1736.247	1736.941	-978.550	0.485	1227.098	0.555	21	0.262	K.VVGNENPSTLICFASK.T
R1/RRR1-2/2	1345.086	1344.448	-270.036	0.566	1152.388	0.549	18	0.260	R.LYDEELYEAAK.I
R1/RRR1-1/3	1674.556	1673.876	-191.909	0.566	2135.617	0.411	31	0.257	R.RPITADSALM*NPNTR.I
R1/RRR1-2/2	1736.399	1736.941	-890.889	0.543	1231.633	0.527	21	0.255	K.VVGNENPSTLICFASK.T
R1/RRR1-2/2	1844.376	1843.120	139.631	0.472	1473.445	0.428	20	0.255	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-2/2	1344.091	1344.448	-266.592	0.545	1249.300	0.487	18	0.254	R.LYDEELYEAAK.I
R1/RRR1-3/2	1304.144	1304.480	-258.610	0.432	1393.925	0.433	17	0.252	K.LKQFQGAVDAAR.K
R1/RRR1-2/2	1436.776	1437.534	-1226.738	0.445	1354.329	0.447	19	0.252	R.AAEEANVYDDLVK.Y
R1/RRR1-2/2	1104.699	1105.269	-1425.373	0.400	1155.487	0.534	15	0.252	R.DPTLAVVAYR.R
R1/RRR1-3/2	1736.203	1736.941	-1003.750	0.502	1048.260	0.587	20	0.251	K.VVGNENPSTLICFASK.T
R1/RRR1-3/2	1304.407	1304.480	-55.906	0.425	1430.613	0.407	18	0.251	K.LKQFQGAVDAAR.K
R1/RRR1-3/2	1736.386	1736.941	-898.228	0.494	1038.806	0.587	20	0.251	K.VVGNENPSTLICFASK.T
R1/RRR1-2/2	1440.124	1439.579	-317.066	0.532	1370.988	0.432	17	0.249	K.GNM*QLFSVDQQR.S
R1/RRR1-1/2	1437.148	1437.534	-269.265	0.483	1252.952	0.471	19	0.248	R.AAEEANVYDDLVK.Y
R1/RRR1-3/3	1846.572	1847.062	-266.129	0.566	1896.934	0.486	32	0.246	K.YKEAAELAAESPQGLLR.T
R1/RRR1-1/2	1344.130	1344.448	-237.162	0.449	1244.530	0.449	18	0.245	R.LYDEELYEAAK.I
R1/RRR1-2/2	1737.575	1736.941	-211.012	0.549	1055.159	0.551	20	0.244	K.VVGNENPSTLICFASK.T
R1/RRR1-3/2	1537.555	1537.749	-126.582	0.531	1060.989	0.531	19	0.243	K.RANLPGAENLVVQR.F
R1/RRR1-2/2	1628.826	1628.849	-14.328	0.435	1289.426	0.427	21	0.241	R.QLIDQVVSTALPESK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1438.988	1439.579	-1109.118	0.426	1372.145	0.387	17	0.240	K.GNM*QLFSVDQQR.S
R1/RRR1-2/2	1373.151	1373.496	-252.123	0.432	1331.739	0.402	17	0.240	R.ADDATHFLDVIR.A
R1/RRR1-1/2	1373.375	1373.496	-88.580	0.415	1364.868	0.377	17	0.238	R.ADDATHFLDVIR.A
R1/RRR1-2/2	1099.311	1099.261	45.485	0.472	1068.495	0.477	14	0.237	K.VANVELYYK.A
R1/RRR1-1/2	1437.237	1437.534	-207.146	0.468	1142.296	0.466	18	0.237	R.AAEEANVYDDLVK.Y
R1/RRR1-3/2	1070.144	1070.306	-151.665	0.427	975.116	0.513	14	0.236	K.YGLIYVITK.L
R1/RRR1-3/2	1343.773	1344.448	-1250.413	0.438	1119.823	0.450	17	0.235	R.LYDEELYEAAK.I
R1/RRR1-1/2	1628.460	1628.849	-239.737	0.461	1177.491	0.446	20	0.235	R.QLIDQVVSTALPESK.S
R1/RRR1-3/2	1374.354	1373.496	-103.751	0.468	1114.517	0.453	17	0.233	R.ADDATHFLDVIR.A
R1/RRR1-3/2	1098.956	1099.261	-278.040	0.487	981.800	0.472	14	0.231	K.VANVELYYK.A
R1/RRR1-2/2	1098.973	1099.261	-262.773	0.531	902.308	0.494	14	0.231	K.VANVELYYK.A
R1/RRR1-2/2	1304.434	1304.480	-34.974	0.386	1284.337	0.380	17	0.231	K.LKQFQGAVDAAR.K
R1/RRR1-1/2	1226.174	1226.403	-187.184	0.379	1175.259	0.420	16	0.231	K.VDGELIFAYAK.I
R1/RRR1-3/2	1099.092	1099.261	-154.020	0.502	907.985	0.489	14	0.231	K.VANVELYYK.A
R1/RRR1-1/2	1099.030	1099.261	-210.733	0.470	901.116	0.494	14	0.231	K.VANVELYYK.A
R1/RRR1-3/2	1070.300	1070.306	-5.103	0.372	987.139	0.492	14	0.230	K.YGLIYVITK.L
R1/RRR1-3/2	1537.647	1537.749	-66.695	0.525	1016.899	0.465	22	0.230	K.RANLPGAENLVVQR.F
R1/RRR1-3/2	1070.283	1070.306	-21.576	0.407	970.590	0.482	14	0.229	K.YGLIYVITK.L
R1/RRR1-3/2	1439.097	1439.579	-336.350	0.426	1352.780	0.338	17	0.229	K.GNM*QLFSVDQQR.S
R1/RRR1-1/2	1736.352	1736.941	-917.990	0.440	985.796	0.494	20	0.228	K.VVGNENPSTLICFASK.T
R1/RRR1-3/2	1344.095	1344.448	-263.950	0.463	952.251	0.469	17	0.228	R.LYDEELYEAAK.I
R1/RRR1-3/2	1373.101	1373.496	-288.245	0.454	1159.927	0.407	17	0.228	R.ADDATHFLDVIR.A
R1/RRR1-2/2	1070.136	1070.306	-159.103	0.394	974.852	0.472	14	0.228	K.YGLIYVITK.L
R1/RRR1-3/2	1304.156	1304.480	-249.032	0.363	1349.445	0.330	17	0.227	K.LKQFQGAVDAAR.K
R1/RRR1-1/2	1343.994	1344.448	-338.944	0.372	1038.270	0.444	17	0.227	R.LYDEELYEAAK.I
R1/RRR1-2/3	1674.068	1673.876	114.919	0.515	2236.766	0.304	33	0.226	R.RPITADSALM*NPNTR.I
R1/RRR1-3/2	1099.037	1099.261	-204.159	0.467	946.217	0.452	14	0.226	K.VANVELYYK.A
R1/RRR1-3/2	1374.096	1373.496	-292.046	0.418	1073.617	0.428	17	0.226	R.ADDATHFLDVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	1847.162	1847.062	54.603	0.582	1796.966	0.482	32	0.226	K.YKEAAELAAESPQGLLR.T
R1/RRR1-3/3	1673.672	1673.876	-122.294	0.526	2159.615	0.324	31	0.224	R.RPITADSALM*NPNTR.I
R1/RRR1-1/2	1099.187	1099.261	-67.346	0.423	904.478	0.454	14	0.223	K.VANVELYYK.A
R1/RRR1-1/3	1846.457	1847.062	-871.612	0.524	1806.761	0.479	33	0.223	K.YKEAAELAAESPQGLLR.T
R1/RRR1-2/2	1070.238	1070.306	-63.219	0.332	1007.877	0.446	14	0.223	K.YGLIYVITK.L
R1/RRR1-1/2	1100.182	1099.261	-71.626	0.504	948.798	0.427	14	0.222	K.VANVELYYK.A
R1/RRR1-2/2	1325.868	1326.567	-1285.398	0.352	1270.957	0.338	16	0.222	K.IIYAFISNWAK.L
R1/RRR1-3/3	1847.291	1847.062	124.490	0.558	1789.656	0.480	33	0.221	K.YKEAAELAAESPQGLLR.T
R1/RRR1-3/2	1381.253	1381.563	-225.204	0.461	866.865	0.456	19	0.220	R.ANLPGAENLVVQR.F
R1/RRR1-2/2	1098.877	1099.261	-350.929	0.449	822.006	0.462	13	0.220	K.VANVELYYK.A
R1/RRR1-2/2	1381.268	1381.563	-213.678	0.384	820.379	0.481	19	0.220	R.ANLPGAENLVVQR.F
R1/RRR1-1/2	1374.268	1373.496	-166.211	0.450	1031.862	0.405	17	0.220	R.ADDATHFLDVIR.A
R1/RRR1-2/2	1105.998	1105.269	-245.827	0.376	1066.704	0.395	14	0.219	R.DPTLAVVAYR.R
R1/RRR1-2/2	1372.682	1373.496	-1325.226	0.361	1260.146	0.306	17	0.217	R.ADDATHFLDVIR.A
R1/RRR1-1/2	1343.531	1344.448	-1431.532	0.354	760.856	0.481	16	0.216	R.LYDEELYEAAK.I
R1/RRR1-3/2	1344.162	1344.448	-213.383	0.453	848.407	0.424	16	0.215	R.LYDEELYEAAK.I
R1/RRR1-3/2	1436.683	1437.534	-1292.098	0.353	892.887	0.447	16	0.214	R.AAEEANVYDDLVK.Y
R1/RRR1-3/2	1105.182	1105.269	-79.057	0.333	952.483	0.406	15	0.214	R.DPTLAVVAYR.R
R1/RRR1-1/2	1374.206	1373.496	-211.480	0.384	985.264	0.390	16	0.213	R.ADDATHFLDVIR.A
R1/RRR1-3/2	1111.761	1112.260	-449.832	0.422	966.892	0.366	14	0.213	R.FQELFAQTK.Y
R1/RRR1-2/2	862.934	862.996	-71.951	0.388	663.553	0.459	13	0.213	K.VVAAFAER.R
R1/RRR1-3/2	1016.167	1016.130	36.254	0.419	981.811	0.365	16	0.212	K.SPEQVSAAVK.A
R1/RRR1-3/2	1381.177	1381.563	-279.822	0.451	864.841	0.399	19	0.212	R.ANLPGAENLVVQR.F
R1/RRR1-3/2	1112.011	1112.260	-224.018	0.484	790.996	0.396	14	0.212	R.FQELFAQTK.Y
R1/RRR1-1/2	1104.760	1105.269	-1369.438	0.331	1004.311	0.375	14	0.212	R.DPTLAVVAYR.R
R1/RRR1-2/2	1381.360	1381.563	-146.922	0.400	783.404	0.422	19	0.212	R.ANLPGAENLVVQR.F
R1/RRR1-1/2	1382.459	1381.563	-75.422	0.439	750.942	0.418	19	0.211	R.ANLPGAENLVVQR.F
R1/RRR1-2/2	1111.658	1112.260	-1445.307	0.410	744.652	0.399	14	0.210	R.FQELFAQTK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1627.919	1628.849	-1189.274	0.342	880.633	0.428	18	0.210	R.QLIDQVVSTALPESK.S
R1/RRR1-3/2	1449.348	1450.619	-1571.492	0.319	1130.751	0.326	17	0.210	R.EGLVSEAIESFIR.A
R1/RRR1-3/2	1260.217	1261.455	-1781.009	0.380	845.338	0.410	16	0.209	K.RDPTLAVVAYR.R
R1/RRR1-2/2	1381.148	1381.563	-301.104	0.454	730.020	0.417	18	0.209	R.ANLPGAENLVVQR.F
R1/RRR1-2/2	1112.458	1112.260	178.339	0.367	969.796	0.338	14	0.209	R.FQELFAQTK.Y
R1/RRR1-3/3	1847.858	1847.062	-110.435	0.578	1641.863	0.506	31	0.209	K.YKEAAELAAESPQGLLR.T
R1/RRR1-2/2	1674.510	1673.876	-219.252	0.381	221.226	0.555	17	0.208	R.RPITADSALM*NPNTR.I
R1/RRR1-1/2	1436.620	1437.534	-1336.131	0.372	795.385	0.432	15	0.208	R.AAEEANVYDDLVK.Y
R1/RRR1-3/2	1554.622	1555.715	-1350.170	0.329	1443.285	0.184	20	0.207	K.EAAELAAESPQGLLR.T
R1/RRR1-1/2	1111.601	1112.260	-1496.708	0.433	647.954	0.395	13	0.207	R.FQELFAQTK.Y
R1/RRR1-1/2	1111.448	1112.260	-1635.165	0.327	821.551	0.376	14	0.207	R.FQELFAQTK.Y
R1/RRR1-3/2	1016.902	1016.130	-225.044	0.379	840.900	0.375	16	0.207	K.SPEQVSAAVK.A
R1/RRR1-1/2	1099.265	1099.261	3.385	0.360	695.075	0.400	13	0.207	K.VANVELYYK.A
R1/RRR1-3/2	1380.710	1381.563	-1345.808	0.356	779.203	0.388	19	0.206	R.ANLPGAENLVVQR.F
R1/RRR1-1/2	1436.577	1437.534	-1365.915	0.301	953.697	0.357	17	0.205	R.AAEEANVYDDLVK.Y
R1/RRR1-2/2	1112.122	1112.260	-123.811	0.400	933.152	0.319	14	0.205	R.FQELFAQTK.Y
R1/RRR1-1/2	863.105	862.996	126.520	0.383	661.538	0.388	13	0.205	K.VVAAFAER.R
R1/RRR1-3/2	1673.391	1673.876	-290.809	0.335	344.019	0.485	19	0.204	R.RPITADSALM*NPNTR.I
R1/RRR1-3/2	1111.458	1112.260	-1625.565	0.367	819.830	0.325	14	0.203	R.FQELFAQTK.Y
R1/RRR1-3/2	1673.465	1673.876	-246.460	0.340	293.555	0.480	18	0.203	R.RPITADSALM*NPNTR.I
R1/RRR1-3/2	862.529	862.996	-543.545	0.320	582.811	0.394	13	0.202	K.VVAAFAER.R
R1/RRR1-1/2	1382.224	1381.563	-245.862	0.395	353.062	0.432	14	0.201	R.ANLPGAENLVVQR.F
R1/RRR1-1/2	1380.664	1381.563	-1379.552	0.251	677.206	0.418	18	0.200	R.ANLPGAENLVVQR.F
R1/RRR1-3/2	1673.349	1673.876	-915.750	0.295	278.849	0.487	18	0.200	R.RPITADSALM*NPNTR.I
R1/RRR1-1/2	862.606	862.996	-453.365	0.274	593.392	0.429	12	0.200	K.VVAAFAER.R
R1/RRR1-3/2	1015.976	1016.130	-152.701	0.329	815.581	0.344	15	0.200	K.SPEQVSAAVK.A
R1/RRR1-2/2	1673.410	1673.876	-279.392	0.286	287.788	0.490	18	0.200	R.RPITADSALM*NPNTR.I
R1/RRR1-1/2	1140.561	1141.346	-1569.165	0.321	477.485	0.441	12	0.199	R.GNLQIVVQAAK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1627.742	1628.849	-1298.169	0.304	917.758	0.324	18	0.198	R.QLIDQVVSTALPESK.S
R1/RRR1-1/2	1628.143	1628.849	-1050.666	0.364	687.788	0.383	16	0.197	R.QLIDQVVSTALPESK.S
R1/RRR1-1/2	1844.362	1843.120	131.666	0.463	563.839	0.392	17	0.197	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-3/2	1844.662	1843.120	-248.675	0.384	286.646	0.409	14	0.196	K.FNLNVQAVNVLLDNIR.S
R1/RRR1-1/3	1673.638	1673.876	-142.927	0.553	1806.033	0.404	29	0.194	R.RPITADSALM*NPNTR.I
R1/RRR1-3/2	1261.196	1261.455	-205.965	0.411	603.317	0.310	15	0.193	K.RDPTLAVVAYR.R
R1/RRR1-2/2	1673.275	1673.876	-959.766	0.221	172.274	0.363	15	0.193	R.RPITADSALM*NPNTR.I
R1/RRR1-2/2	1261.251	1261.455	-162.466	0.375	584.751	0.253	15	0.189	K.RDPTLAVVAYR.R
R1/RRR1-3/2	1627.847	1628.849	-1233.703	0.293	691.175	0.237	17	0.186	R.QLIDQVVSTALPESK.S
R1/RRR1-1/2	1111.892	1112.260	-331.955	0.342	388.165	0.278	10	0.176	-.FQELFAQTK.-
R1/RRR1-3/3	1674.696	1673.876	-108.109	0.526	1799.285	0.339	31	0.165	R.RPITADSALM*NPNTR.I
R1/RRR1-2/3	1673.794	1673.876	-49.319	0.505	1585.054	0.367	29	0.147	R.RPITADSALM*NPNTR.I
R1/RRR1-2/3	1674.055	1673.876	106.691	0.531	1594.801	0.362	30	0.146	R.RPITADSALM*NPNTR.I
R1/RRR1-3/3	1673.593	1673.876	-169.926	0.484	1677.458	0.295	28	0.139	R.RPITADSALM*NPNTR.I
R1/RRR1-3/3	1778.897	1779.076	-100.847	0.439	1135.372	0.467	30	0.125	K.LHVIELGAQPGKPGFSK.K
R1/RRR1-3/3	1929.337	1930.109	-921.364	0.423	995.581	0.463	24	0.116	K.VDELVKDRIESQNEVR.A
R1/RRR1-3/3	1304.336	1304.480	-110.974	0.456	1393.279	0.346	26	0.115	K.LKQFQGAVDAAR.K
R1/RRR1-3/3	1780.351	1779.076	155.442	0.436	1082.354	0.414	29	0.110	K.LHVIELGAQPGKPGFSK.K
R1/RRR1-3/3	1480.744	1480.648	64.725	0.529	1358.297	0.330	27	0.110	R.GKLNAYESLELSR.L
R1/RRR1-3/3	1585.389	1584.801	-260.893	0.510	1276.764	0.358	27	0.110	R.ALQHYTELPDIKR.V
R1/RRR1-3/3	1780.116	1779.076	22.785	0.463	753.095	0.504	28	0.107	K.LHVIELGAQPGKPGFSK.K
R1/RRR1-3/3	1930.624	1930.109	-251.911	0.429	958.858	0.426	24	0.106	K.VDELVKDRIESQNEVR.A
R1/RRR1-2/3	1480.143	1480.648	-1020.114	0.472	1177.353	0.369	25	0.105	R.GKLNAYESLELSR.L
R1/RRR1-2/3	1584.363	1584.801	-277.252	0.449	1157.881	0.368	26	0.102	R.ALQHYTELPDIKR.V
R1/RRR1-3/3	1479.746	1480.648	-1288.842	0.417	1125.989	0.367	24	0.101	R.GKLNAYESLELSR.L
R1/RRR1-3/3	1930.405	1930.109	153.761	0.430	734.726	0.450	22	0.100	K.VDELVKDRIESQNEVR.A
R1/RRR1-2/3	1480.723	1480.648	51.082	0.515	1126.164	0.354	25	0.100	R.GKLNAYESLELSR.L
R1/RRR1-1/3	1480.469	1480.648	-120.969	0.478	1050.685	0.341	23	0.095	R.GKLNAYESLELSR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	1480.509	1480.648	-94.047	0.493	1151.660	0.319	25	0.094	R.GKLNAYESLELSR.L
R1/RRR1-3/3	1304.947	1304.480	358.860	0.501	969.030	0.356	24	0.090	K.LKQFQGAVDAAR.K
R1/RRR1-2/3	1930.545	1930.109	226.525	0.400	924.964	0.355	26	0.090	K.VDELVKDRIESQNEVR.A
R1/RRR1-7/2	1446.107	1446.542	-301.887	0.556	2415.552	0.484	20	0.429	K.SPEDATNLIDDKK.I
R1/RRR1-7/2	1489.311	1489.700	-261.478	0.504	1675.711	0.548	20	0.319	K.VVVADNVHDFVFK.S
R1/RRR1-7/2	1489.350	1489.700	-235.823	0.506	1656.007	0.549	20	0.316	K.VVVADNVHDFVFK.S
R1/RRR1-7/2	1446.129	1446.542	-286.473	0.553	1726.098	0.446	20	0.295	K.SPEDATNLIDDKK.I
R1/RRR1-7/2	1490.350	1489.700	-235.500	0.578	1475.230	0.533	20	0.288	K.VVVADNVHDFVFK.S
R1/RRR1-7/2	1523.210	1522.730	316.008	0.535	1380.545	0.570	20	0.285	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/2	1522.357	1522.730	-245.830	0.478	1399.798	0.561	20	0.285	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/2	1279.045	1279.464	-328.682	0.472	1546.817	0.461	17	0.278	R.TADEIVDFIKK.N
R1/RRR1-7/2	1876.912	1878.071	-1154.142	0.463	1473.112	0.503	19	0.274	K.SVYYGAAEEFKDKEIK.F
R1/RRR1-7/2	1278.805	1279.464	-1301.492	0.464	1532.903	0.447	17	0.273	R.TADEIVDFIKK.N
R1/RRR1-7/2	1878.489	1878.071	223.000	0.497	1421.853	0.516	20	0.272	K.SVYYGAAEEFKDKEIK.F
R1/RRR1-7/2	1877.367	1878.071	-910.471	0.489	1201.760	0.502	19	0.245	K.SVYYGAAEEFKDKEIK.F
R1/RRR1-7/2	1446.216	1446.542	-225.924	0.533	1337.835	0.417	19	0.243	K.SPEDATNLIDDKK.I
R1/RRR1-7/2	1279.278	1279.464	-145.821	0.457	1360.747	0.395	16	0.241	R.TADEIVDFIKK.N
R1/RRR1-7/2	1195.536	1196.377	-1544.222	0.271	1323.061	0.422	16	0.238	K.YEIQGFPTLK.I
R1/RRR1-7/2	1522.294	1522.730	-286.859	0.466	1051.619	0.492	18	0.236	K.AHVEPDQIVSWLK.Q
R1/RRR1-3/2	1523.463	1522.730	-175.651	0.394	1029.626	0.506	17	0.234	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/2	1150.375	1151.291	-1670.832	0.426	1048.543	0.439	15	0.226	R.TADEIVDFIK.K
R1/RRR1-6/2	1523.379	1522.730	-230.635	0.350	1115.420	0.420	18	0.226	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/1	1037.491	1038.133	-1587.263	0.143	615.573	0.212	11	0.224	K.DFDVTALEK.F
R1/RRR1-7/2	1151.112	1151.291	-156.207	0.460	1071.250	0.401	16	0.223	R.TADEIVDFIK.K
R1/RRR1-7/2	1151.282	1151.291	-7.616	0.506	1088.650	0.393	16	0.222	R.TADEIVDFIK.K
R1/RRR1-7/2	1195.601	1196.377	-1489.555	0.303	1051.377	0.424	14	0.218	K.YEIQGFPTLK.I
R1/RRR1-7/2	1453.140	1452.591	-311.716	0.376	422.446	0.531	17	0.210	K.SEPIPEVNNEPVK.V
R1/RRR1-7/2	1453.287	1452.591	-210.419	0.367	502.310	0.494	18	0.208	K.SEPIPEVNNEPVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	989.665	990.181	-1536.742	0.386	426.353	0.491	13	0.208	K.HDPPIVLAK.V
R1/RRR1-7/2	1506.427	1507.625	-1463.588	0.373	754.194	0.473	16	0.208	K.SVYYGAAEEFKDK.E
R1/RRR1-7/2	1717.812	1717.990	-104.247	0.467	492.631	0.532	17	0.207	K.AAQELSKHDPPIVLAK.V
R1/RRR1-7/2	1280.047	1279.464	-326.416	0.372	362.384	0.446	17	0.207	R.EAEGIVEYLKK.Q
R1/RRR1-7/2	1452.292	1452.591	-206.938	0.413	429.383	0.457	17	0.205	K.SEPIPEVNNEPVK.V
R1/RRR1-7/2	1453.148	1452.591	-306.154	0.338	501.450	0.441	19	0.204	K.SEPIPEVNNEPVK.V
R1/RRR1-7/2	1717.381	1717.990	-940.036	0.452	401.305	0.533	16	0.204	K.AAQELSKHDPPIVLAK.V
R1/RRR1-7/2	975.691	976.063	-382.122	0.403	1098.577	0.278	14	0.204	K.SDEDVVIAK.M
R1/RRR1-7/2	1280.391	1279.464	-56.955	0.360	314.541	0.442	14	0.202	R.EAEGIVEYLKK.Q
R1/RRR1-7/2	989.566	990.181	-1636.619	0.324	420.822	0.431	13	0.201	K.HDPPIVLAK.V
R1/RRR1-7/2	1537.290	1537.781	-320.378	0.411	630.627	0.416	18	0.201	R.LFKPFDELVVDSK.D
R1/RRR1-7/2	1717.473	1717.990	-886.448	0.455	468.938	0.469	17	0.200	K.AAQELSKHDPPIVLAK.V
R1/RRR1-7/2	1279.195	1279.464	-210.724	0.338	403.299	0.349	17	0.200	R.EAEGIVEYLKK.Q
R1/RRR1-7/2	1453.206	1452.591	-265.869	0.331	308.997	0.444	15	0.199	K.SEPIPEVNNEPVK.V
R1/RRR1-2/2	1524.009	1522.730	183.926	0.329	320.956	0.454	12	0.199	K.AHVEPDQIVSWLK.Q
R1/RRR1-5/2	1523.511	1522.730	-143.821	0.352	601.222	0.364	15	0.198	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/2	989.924	990.181	-259.809	0.333	372.456	0.359	12	0.197	K.HDPPIVLAK.V
R1/RRR1-4/2	1523.302	1522.730	-281.766	0.356	464.229	0.390	13	0.197	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/2	886.079	885.986	104.516	0.352	859.141	0.297	14	0.196	K.FFQSSAAK.A
R1/RRR1-2/2	1523.931	1522.730	132.597	0.268	430.355	0.356	14	0.195	K.AHVEPDQIVSWLK.Q
R1/RRR1-3/2	1522.467	1522.730	-173.193	0.271	649.385	0.301	17	0.195	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/2	975.225	976.063	-1890.248	0.395	847.924	0.266	13	0.192	K.SDEDVVIAK.M
R1/RRR1-6/2	1523.855	1522.730	82.387	0.358	411.634	0.378	12	0.189	-.AHVEPDQIVSWLK.-
R1/RRR1-7/2	1279.024	1279.464	-344.961	0.236	796.738	0.273	14	0.188	R.EAEGIVEYLKK.Q
R1/RRR1-7/2	1522.328	1522.730	-264.896	0.298	669.962	0.214	15	0.188	K.AHVEPDQIVSWLK.Q
R1/RRR1-1/2	1522.410	1522.730	-210.837	0.296	151.882	0.355	12	0.187	-.AHVEPDQIVSWLK.-
R1/RRR1-7/3	1880.813	1881.000	-99.646	0.482	1208.075	0.604	29	0.171	R.SDYDFGHTLHANHLPR.G
R1/RRR1-7/3	1881.805	1881.000	-103.823	0.522	1232.792	0.582	31	0.166	R.SDYDFGHTLHANHLPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/3	1880.887	1881.000	-60.195	0.480	1260.260	0.554	29	0.163	R.SDYDFGHTLHANHLPR.G
R1/RRR1-2/2	1523.936	1522.730	135.810	0.260	215.542	0.351	11	0.159	-.AHVEPDQIVSWLK.-
R1/RRR1-7/3	1538.409	1537.781	-242.478	0.490	1482.440	0.448	26	0.156	R.LFKPFDELVVDSK.D
R1/RRR1-7/3	1446.308	1446.542	-162.301	0.530	1298.616	0.498	26	0.148	K.SPEDATNLIDDKK.I
R1/RRR1-7/3	1522.804	1522.730	48.626	0.425	1855.381	0.257	27	0.148	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/3	1446.444	1446.542	-67.694	0.525	1304.303	0.482	27	0.142	K.SPEDATNLIDDKK.I
R1/RRR1-2/3	1446.846	1446.542	210.820	0.502	1225.447	0.480	24	0.138	K.SPEDATNLIDDKK.I
R1/RRR1-1/2	1524.163	1522.730	285.124	0.310	157.401	0.394	9	0.133	-.AHVEPDQIVSWLK.-
R1/RRR1-7/2	1628.204	1627.775	264.348	0.466	669.194	0.608	20	0.130	K.EKAESAPAEPLKDEL.-
R1/RRR1-7/2	1628.256	1627.775	296.523	0.514	637.171	0.581	20	0.127	K.EKAESAPAEPLKDEL.-
R1/RRR1-7/3	1522.945	1522.730	141.718	0.420	1663.772	0.262	26	0.125	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/3	1447.973	1446.542	298.257	0.518	1182.233	0.442	25	0.123	K.SPEDATNLIDDKK.I
R1/RRR1-7/2	1627.237	1627.775	-947.719	0.403	759.883	0.566	20	0.123	K.EKAESAPAEPLKDEL.-
R1/RRR1-7/3	1522.761	1522.730	20.767	0.475	1610.326	0.279	27	0.123	K.AHVEPDQIVSWLK.Q
R1/RRR1-7/2	1370.057	1370.487	-315.159	0.466	827.279	0.478	17	0.111	K.AESAPAEPLKDEL.-
R1/RRR1-7/2	1369.968	1370.487	-1112.466	0.434	970.640	0.402	18	0.109	K.AESAPAEPLKDEL.-
R1/RRR1-3/3	1446.458	1446.542	-57.916	0.450	984.669	0.427	24	0.106	K.SPEDATNLIDDKK.I
R1/RRR1-5/3	1447.202	1446.542	-235.340	0.395	1092.801	0.376	24	0.101	K.SPEDATNLIDDKK.I
R1/RRR1-7/2	1370.314	1370.487	-126.662	0.429	874.186	0.397	17	0.101	K.AESAPAEPLKDEL.-
R1/RRR1-3/3	1446.565	1446.542	16.105	0.417	863.906	0.400	22	0.097	K.SPEDATNLIDDKK.I
R1/RRR1-7/3	1537.859	1537.781	50.777	0.477	887.061	0.399	22	0.096	R.LFKPFDELVVDSK.D
R1/RRR1-2/3	1447.051	1446.542	-340.197	0.435	894.583	0.380	22	0.095	K.SPEDATNLIDDKK.I
R1/RRR1-5/3	1446.718	1446.542	122.103	0.417	825.191	0.387	22	0.094	K.SPEDATNLIDDKK.I
R1/RRR1-7/3	1537.600	1537.781	-117.748	0.446	992.694	0.350	24	0.089	-.LFKPFDELVVDSK.-
R1/RRR1-5/3	1926.666	1927.150	-252.333	0.532	2371.480	0.559	37	0.389	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/3	1926.774	1927.150	-195.796	0.541	2171.829	0.605	36	0.361	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/1	963.528	964.097	-1633.626	0.331	789.936	0.178	11	0.313	R.FQELGLEK.G
R1/RRR1-5/2	1268.103	1268.491	-306.415	0.444	1715.421	0.482	17	0.305	R.IKQQGLNITPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/3	1927.265	1927.150	59.735	0.523	1944.788	0.577	34	0.295	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/2	1234.548	1235.414	-1516.052	0.427	1556.147	0.525	18	0.295	K.NLTGLVELYGR.N
R1/RRR1-5/2	1234.684	1235.414	-1405.912	0.476	1448.358	0.518	18	0.281	K.NLTGLVELYGR.N
R1/RRR1-4/2	1016.113	1016.177	-63.092	0.428	2016.050	0.228	17	0.274	R.SLSALQGALR.K
R1/RRR1-5/2	1747.259	1747.949	-970.230	0.491	1169.033	0.617	26	0.273	R.TM*ASTVPLAVEGEPSNK.-
R1/RRR1-5/1	963.484	964.097	-1678.875	0.361	730.304	0.182	11	0.270	R.FQELGLEK.G
R1/RRR1-1/2	1234.947	1235.414	-379.680	0.516	1319.283	0.523	16	0.267	K.NLTGLVELYGR.N
R1/RRR1-5/2	1206.068	1205.349	-233.551	0.488	1454.219	0.458	18	0.267	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1268.215	1268.491	-218.148	0.492	1347.467	0.480	17	0.261	R.IKQQGLNITPR.I
R1/RRR1-5/2	1926.733	1927.150	-217.049	0.526	1066.172	0.599	24	0.257	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/2	1205.761	1205.349	342.849	0.463	1385.976	0.445	17	0.256	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1236.071	1235.414	-278.498	0.532	1221.522	0.500	17	0.253	K.NLTGLVELYGR.N
R1/RRR1-5/2	1747.359	1747.949	-912.858	0.505	1000.340	0.580	24	0.249	R.TM*ASTVPLAVEGEPSNK.-
R1/RRR1-5/2	1926.570	1927.150	-822.714	0.486	917.378	0.620	22	0.246	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/2	1747.387	1747.949	-896.447	0.458	937.958	0.596	23	0.244	R.TM*ASTVPLAVEGEPSNK.-
R1/RRR1-5/2	1268.266	1268.491	-178.173	0.440	1157.383	0.494	16	0.244	R.IKQQGLNITPR.I
R1/RRR1-1/2	1015.965	1016.177	-208.801	0.419	1640.549	0.268	17	0.242	R.SLSALQGALR.K
R1/RRR1-5/2	1926.754	1927.150	-206.117	0.518	942.096	0.577	22	0.240	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/2	1016.084	1016.177	-92.014	0.478	1764.086	0.214	16	0.238	R.SLSALQGALR.K
R1/RRR1-5/2	1205.116	1205.349	-193.808	0.474	1135.062	0.447	18	0.238	K.SIGNGVQFLNR.H
R1/RRR1-2/3	1927.540	1927.150	203.026	0.516	1630.281	0.571	29	0.237	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/2	1417.084	1416.712	263.123	0.553	891.576	0.535	18	0.237	R.LMTLTGVYGFWK.Y
R1/RRR1-1/2	1206.231	1205.349	-98.013	0.490	940.855	0.498	17	0.234	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1433.262	1432.712	-314.589	0.568	1050.810	0.458	19	0.232	R.LM*TLTGVYGFWK.Y
R1/RRR1-5/2	1416.143	1416.712	-1111.207	0.502	853.729	0.512	18	0.231	R.LMTLTGVYGFWK.Y
R1/RRR1-3/2	1206.332	1205.349	-13.764	0.466	1004.702	0.465	16	0.230	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1226.147	1226.406	-211.753	0.425	766.350	0.553	16	0.228	R.VVHGIDVFDPK.F
R1/RRR1-5/2	1205.114	1205.349	-195.027	0.467	758.871	0.511	16	0.226	K.SIGNGVQFLNR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1015.527	1016.177	-1629.382	0.393	1486.520	0.246	16	0.223	R.SLSALQGALR.K
R1/RRR1-1/2	1205.023	1205.349	-270.840	0.425	705.139	0.505	16	0.222	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1204.572	1205.349	-1479.377	0.376	919.380	0.441	17	0.222	K.SIGNGVQFLNR.H
R1/RRR1-1/2	1016.087	1016.177	-88.399	0.387	1493.616	0.228	16	0.221	R.SLSALQGALR.K
R1/RRR1-5/2	1863.696	1864.118	-227.018	0.541	803.154	0.535	17	0.220	K.MFDLIEQYNLNGHIR.W
R1/RRR1-5/2	1205.106	1205.349	-201.938	0.477	832.166	0.440	17	0.220	K.SIGNGVQFLNR.H
R1/RRR1-1/2	1205.368	1205.349	16.596	0.439	774.682	0.464	16	0.220	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1193.277	1193.444	-140.611	0.363	677.806	0.504	15	0.216	R.NKPIIFSM*AR.L
R1/RRR1-5/2	1432.110	1432.712	-1121.818	0.471	959.140	0.403	17	0.216	R.LM*TLTGVYGFWK.Y
R1/RRR1-1/2	1205.239	1205.349	-91.185	0.411	751.844	0.426	16	0.214	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1254.244	1254.456	-169.329	0.401	1173.843	0.326	16	0.213	K.ASALLVEFFEK.C
R1/RRR1-5/2	1016.042	1016.177	-132.748	0.451	1420.100	0.226	16	0.213	R.SLSALQGALR.K
R1/RRR1-4/3	1926.619	1927.150	-797.248	0.371	1578.354	0.546	29	0.213	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/2	1227.088	1226.406	-259.883	0.350	652.190	0.510	15	0.213	R.VVHGIDVFDPK.F
R1/RRR1-2/2	1205.958	1205.349	-324.439	0.433	949.505	0.353	17	0.212	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1144.343	1144.408	-57.520	0.466	847.649	0.383	14	0.211	R.YLEMLYALK.Y
R1/RRR1-5/2	1192.613	1193.444	-1539.772	0.283	824.480	0.443	16	0.211	R.NKPIIFSM*AR.L
R1/RRR1-3/2	1205.172	1205.349	-146.660	0.446	582.636	0.415	15	0.209	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1415.244	1415.574	-234.156	0.453	653.727	0.449	15	0.208	K.TKYPNSDLYWK.K
R1/RRR1-4/2	1416.460	1416.712	-178.202	0.384	852.557	0.384	16	0.208	R.LMTLTGVYGFWK.Y
R1/RRR1-5/2	1194.077	1193.444	-308.575	0.335	683.020	0.430	15	0.207	R.NKPIIFSM*AR.L
R1/RRR1-1/2	1206.467	1205.349	98.884	0.446	668.412	0.389	15	0.207	K.SIGNGVQFLNR.H
R1/RRR1-1/2	1016.427	1016.177	247.106	0.410	1427.275	0.183	16	0.207	R.SLSALQGALR.K
R1/RRR1-5/2	1415.987	1416.712	-1222.181	0.375	742.457	0.402	16	0.207	R.LMTLTGVYGFWK.Y
R1/RRR1-5/2	1144.024	1144.350	-285.602	0.358	1095.950	0.304	16	0.206	-.SLSALQGALRK.-
R1/RRR1-5/2	1226.162	1226.406	-199.468	0.311	716.828	0.434	16	0.206	R.VVHGIDVFDPK.F
R1/RRR1-1/2	1433.915	1432.712	142.285	0.438	713.756	0.390	16	0.206	R.LM*TLTGVYGFWK.Y
R1/RRR1-5/2	1160.102	1160.408	-264.567	0.339	881.760	0.352	14	0.205	R.YLEM*LYALK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1206.265	1205.349	-69.691	0.383	574.266	0.424	14	0.204	-.SIGNGVQFLNR.-
R1/RRR1-5/2	1415.253	1415.574	-227.926	0.421	662.837	0.412	15	0.204	K.TKYPNSDLYWK.K
R1/RRR1-5/2	1262.407	1263.425	-1602.956	0.416	721.274	0.394	16	0.204	K.LKDGAFEDVLR.S
R1/RRR1-4/2	1226.356	1226.406	-41.194	0.292	956.729	0.331	17	0.203	R.VVHGIDVFDPK.F
R1/RRR1-5/2	1432.244	1432.712	-327.550	0.360	556.812	0.428	14	0.203	R.LM*TLTGVYGFWK.Y
R1/RRR1-5/2	1138.879	1139.329	-395.745	0.486	1004.973	0.288	15	0.202	R.AM*ENEM*LLR.I
R1/RRR1-5/2	1390.118	1390.518	-288.856	0.314	441.166	0.484	20	0.202	R.LLPDATGTTCGQR.L
R1/RRR1-3/2	1204.915	1205.349	-360.894	0.332	432.277	0.305	14	0.200	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1160.120	1160.408	-248.837	0.353	630.145	0.353	13	0.200	R.YLEM*LYALK.Y
R1/RRR1-2/2	1206.233	1205.349	-95.982	0.358	496.031	0.348	13	0.199	K.SIGNGVQFLNR.H
R1/RRR1-4/2	1431.909	1432.712	-1262.633	0.418	810.099	0.333	15	0.199	R.LM*TLTGVYGFWK.Y
R1/RRR1-5/2	1389.623	1390.518	-1367.926	0.277	476.716	0.476	21	0.199	R.LLPDATGTTCGQR.L
R1/RRR1-5/2	1415.573	1416.712	-1515.835	0.310	666.665	0.366	15	0.199	R.LMTLTGVYGFWK.Y
R1/RRR1-2/2	1205.000	1205.349	-289.845	0.328	465.983	0.317	13	0.198	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1159.385	1160.408	-1750.061	0.287	778.494	0.332	13	0.198	R.YLEM*LYALK.Y
R1/RRR1-5/2	1177.091	1177.445	-301.502	0.299	573.189	0.350	14	0.197	R.NKPIIFSMAR.L
R1/RRR1-5/2	1144.129	1144.350	-193.438	0.396	896.879	0.321	15	0.197	-.SLSALQGALRK.-
R1/RRR1-5/2	1138.400	1139.329	-1699.758	0.365	967.993	0.263	14	0.197	R.AM*ENEM*LLR.I
R1/RRR1-1/2	1417.313	1416.712	-282.363	0.402	575.367	0.371	14	0.197	-.LMTLTGVYGFWK.-
R1/RRR1-5/2	1139.264	1139.329	-57.403	0.430	1006.724	0.243	15	0.197	R.AM*ENEM*LLR.I
R1/RRR1-3/2	1206.007	1205.349	-284.020	0.282	635.257	0.287	15	0.196	K.SIGNGVQFLNR.H
R1/RRR1-5/2	1177.068	1177.445	-321.168	0.254	555.518	0.336	14	0.194	R.NKPIIFSMAR.L
R1/RRR1-5/2	1263.328	1263.425	-77.107	0.373	542.289	0.346	14	0.193	K.LKDGAFEDVLR.S
R1/RRR1-5/2	1176.688	1177.445	-1497.369	0.228	351.602	0.315	12	0.193	R.NKPIIFSMAR.L
R1/RRR1-5/2	1414.400	1415.574	-1541.849	0.368	574.098	0.321	14	0.193	K.TKYPNSDLYWK.K
R1/RRR1-4/2	1432.390	1432.712	-225.115	0.311	381.604	0.317	12	0.192	-.LM*TLTGVYGFWK.-
R1/RRR1-1/2	1205.600	1205.349	209.551	0.387	504.366	0.248	13	0.191	-.SIGNGVQFLNR.-
R1/RRR1-5/2	1143.896	1144.408	-1325.689	0.321	672.174	0.176	14	0.189	R.YLEMLYALK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1192.420	1193.444	-1702.769	0.226	378.969	0.315	11	0.189	-.NKPIIFSM*AR.-
R1/RRR1-5/2	1416.276	1416.712	-309.024	0.192	425.586	0.315	12	0.189	R.LMTLTGVYGFWK.Y
R1/RRR1-5/2	963.930	964.097	-173.648	0.382	923.018	0.125	14	0.186	R.FQELGLEK.G
R1/RRR1-4/2	1227.487	1226.406	65.971	0.260	624.216	0.169	15	0.186	R.VVHGIDVFDPK.F
R1/RRR1-2/2	964.184	964.097	90.526	0.340	797.977	0.126	13	0.185	-.FQELGLEK.-
R1/RRR1-5/2	963.672	964.097	-442.092	0.310	780.916	0.147	13	0.184	-.FQELGLEK.-
R1/RRR1-3/2	964.078	964.097	-19.953	0.266	760.270	0.035	13	0.183	-.FQELGLEK.-
R1/RRR1-1/2	964.090	964.097	-7.126	0.394	808.305	0.108	13	0.183	-.FQELGLEK.-
R1/RRR1-3/2	963.871	964.097	-235.774	0.258	922.277	0.061	14	0.182	-.FQELGLEK.-
R1/RRR1-3/2	963.398	964.097	-1768.827	0.227	815.611	0.045	13	0.180	-.FQELGLEK.-
R1/RRR1-3/2	963.544	964.097	-1616.840	0.328	795.353	0.095	13	0.179	-.FQELGLEK.-
R1/RRR1-5/2	1143.509	1144.408	-1665.660	0.281	539.904	0.220	12	0.176	-.YLEMLYALK.-
R1/RRR1-1/3	1927.061	1927.150	-46.713	0.428	1492.459	0.447	27	0.170	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-1/3	1926.878	1927.150	-141.743	0.409	1072.360	0.540	27	0.145	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/3	1415.456	1415.574	-84.097	0.485	1067.927	0.491	23	0.119	K.TKYPNSDLYWK.K
R1/RRR1-5/3	1584.554	1584.816	-166.101	0.517	699.617	0.577	25	0.116	K.M*GVTHCTIAHALEK.T
R1/RRR1-5/3	1584.995	1584.816	112.963	0.481	677.026	0.580	25	0.114	K.M*GVTHCTIAHALEK.T
R1/RRR1-5/3	1880.097	1880.117	-10.564	0.500	817.399	0.501	26	0.111	K.M*FDLIEQYNLNGHIR.W
R1/RRR1-5/3	1415.249	1415.574	-230.488	0.452	788.665	0.495	20	0.104	K.TKYPNSDLYWK.K
R1/RRR1-1/3	1926.356	1927.150	-934.167	0.308	1009.261	0.380	26	0.101	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/3	1414.748	1415.574	-1295.092	0.430	1016.358	0.420	22	0.101	K.TKYPNSDLYWK.K
R1/RRR1-5/3	1263.595	1263.425	135.099	0.517	1446.974	0.253	24	0.097	-.LKDGAFEDVLR.-
R1/RRR1-5/3	1879.989	1880.117	-68.495	0.402	589.203	0.433	23	0.092	K.M*FDLIEQYNLNGHIR.W
R1/RRR1-5/3	1864.405	1864.118	154.837	0.357	427.195	0.445	22	0.091	K.MFDLIEQYNLNGHIR.W
R1/RRR1-5/3	1879.773	1880.117	-183.691	0.402	711.036	0.400	25	0.089	K.M*FDLIEQYNLNGHIR.W
R1/RRR1-4/3	1927.006	1927.150	-75.210	0.245	1015.321	0.310	25	0.088	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-4/3	1263.591	1263.425	132.338	0.384	1361.640	0.212	22	0.086	-.LKDGAFEDVLR.-
R1/RRR1-3/3	1927.376	1927.150	117.666	0.318	328.025	0.399	21	0.086	-.IGDSLSAHPNELVAVFTR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/3	1927.257	1927.150	55.447	0.291	588.905	0.319	23	0.085	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-5/3	1263.422	1263.425	-2.250	0.518	1194.010	0.254	22	0.081	-.LKDGAFEDVLR.-
R1/RRR1-2/3	1927.414	1927.150	137.197	0.261	876.936	0.267	27	0.078	R.IGDSLSAHPNELVAVFTR.L
R1/RRR1-1/3	1263.568	1263.425	113.591	0.469	1035.167	0.208	20	0.074	K.LKDGAFEDVLR.S
R1/RRR1-5/3	1264.408	1263.425	-13.191	0.528	1159.167	0.214	21	0.073	-.LKDGAFEDVLR.-
R1/RRR1-1/3	1263.762	1263.425	267.472	0.419	914.037	0.234	20	0.071	-.LKDGAFEDVLR.-
R1/RRR1-3/2	1568.551	1569.783	-1427.243	0.426	2597.403	0.332	22	0.406	K.YLLQSGLQEYLNK.Q
R1/RRR1-4/2	1571.293	1569.783	-312.822	0.663	2323.161	0.487	22	0.402	K.YLLQSGLQEYLNK.Q
R1/RRR1-5/2	1570.494	1569.783	-184.658	0.629	2365.375	0.450	22	0.397	K.YLLQSGLQEYLNK.Q
R1/RRR1-5/2	1570.778	1569.783	-3.321	0.632	2190.960	0.469	21	0.370	K.YLLQSGLQEYLNK.Q
R1/RRR1-4/3	1994.798	1994.066	-134.431	0.518	2121.177	0.544	37	0.329	K.SEGHDTIVLAGAEYGSGSSR.D
R1/RRR1-4/2	1570.306	1569.783	-304.754	0.581	1962.899	0.442	21	0.325	K.YLLQSGLQEYLNK.Q
R1/RRR1-4/2	1545.138	1545.656	-985.400	0.493	1695.604	0.542	20	0.320	K.M*FVDYNEPQTER.V
R1/RRR1-5/2	1570.916	1569.783	84.907	0.559	1838.515	0.457	20	0.311	K.YLLQSGLQEYLNK.Q
R1/RRR1-4/2	1498.830	1498.684	98.303	0.549	1759.985	0.489	20	0.311	R.SDETVAMIEAYLR.A
R1/RRR1-4/2	1545.164	1545.656	-319.304	0.511	1588.089	0.541	20	0.305	K.M*FVDYNEPQTER.V
R1/RRR1-4/2	1497.749	1498.684	-1295.822	0.425	1816.703	0.430	20	0.303	R.SDETVAMIEAYLR.A
R1/RRR1-4/2	1528.224	1528.563	-222.453	0.464	1648.332	0.494	21	0.298	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/2	1528.264	1528.563	-196.651	0.447	1493.498	0.531	21	0.287	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/2	1724.234	1724.761	-888.085	0.616	1585.909	0.442	23	0.275	R.NCDNFQVNQNDVEK.I
R1/RRR1-4/2	1724.239	1724.761	-885.526	0.610	1654.380	0.413	23	0.275	R.NCDNFQVNQNDVEK.I
R1/RRR1-4/2	1280.129	1280.431	-236.597	0.432	1501.911	0.468	18	0.274	K.FVEFYGEGM*GK.L
R1/RRR1-4/1	1039.608	1040.237	-1571.547	0.181	689.714	0.232	11	0.274	K.LYVFDAALK.Y
R1/RRR1-1/2	1569.551	1569.783	-148.652	0.537	1642.530	0.408	20	0.272	K.YLLQSGLQEYLNK.Q
R1/RRR1-4/3	1514.916	1514.683	153.979	0.539	2241.136	0.399	29	0.271	R.SDETVAM*IEAYLR.A
R1/RRR1-3/2	1568.447	1569.783	-1493.925	0.413	1735.922	0.334	19	0.266	K.YLLQSGLQEYLNK.Q
R1/RRR1-4/2	1528.346	1528.563	-142.646	0.461	1331.586	0.514	20	0.263	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/2	1265.222	1264.431	-166.311	0.474	1284.980	0.509	18	0.262	K.FVEFYGEGMGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1724.286	1724.761	-275.977	0.610	1539.192	0.392	23	0.256	R.NCDNFQVNQNDVEK.I
R1/RRR1-4/2	1264.118	1264.431	-248.590	0.342	1367.397	0.428	18	0.248	K.FVEFYGEGMGK.L
R1/RRR1-4/2	1514.543	1514.683	-92.457	0.448	1381.059	0.418	18	0.247	R.SDETVAM*IEAYLR.A
R1/RRR1-4/2	1544.204	1545.656	-1592.706	0.318	1232.430	0.491	18	0.246	K.M*FVDYNEPQTER.V
R1/RRR1-4/2	1529.371	1529.656	-186.901	0.511	1051.166	0.501	18	0.239	K.MFVDYNEPQTER.V
R1/RRR1-4/2	1294.357	1293.453	-73.745	0.407	905.432	0.556	17	0.238	K.FYSLPALNDPR.I
R1/RRR1-4/2	1530.060	1529.656	264.420	0.540	1054.322	0.489	18	0.237	K.MFVDYNEPQTER.V
R1/RRR1-4/2	1497.519	1498.684	-1449.975	0.337	1572.876	0.279	19	0.237	R.SDETVAMIEAYLR.A
R1/RRR1-4/2	1566.349	1565.896	290.102	0.505	886.411	0.553	20	0.237	R.SNLVGM*GIIPLCFK.A
R1/RRR1-4/2	1550.329	1549.897	279.759	0.517	1005.603	0.502	20	0.235	R.SNLVGMGIIPLCFK.A
R1/RRR1-4/2	1529.916	1529.656	170.011	0.562	954.053	0.518	17	0.234	K.MFVDYNEPQTER.V
R1/RRR1-4/2	1116.658	1117.278	-1454.953	0.423	880.160	0.524	20	0.232	K.TSLAPGSGVVTK.Y
R1/RRR1-4/3	1994.216	1994.066	75.718	0.507	1668.665	0.535	34	0.228	K.SEGHDTIVLAGAEYGSGSSR.D
R1/RRR1-4/2	1514.092	1514.683	-1054.128	0.425	1140.765	0.423	17	0.227	R.SDETVAM*IEAYLR.A
R1/RRR1-4/2	1117.033	1117.278	-219.723	0.408	828.282	0.508	20	0.226	K.TSLAPGSGVVTK.Y
R1/RRR1-4/2	1566.894	1565.896	-0.991	0.492	741.770	0.549	18	0.225	R.SNLVGM*GIIPLCFK.A
R1/RRR1-4/2	1279.843	1280.431	-1244.579	0.355	1105.381	0.402	16	0.222	K.FVEFYGEGM*GK.L
R1/RRR1-4/2	1203.272	1203.326	-45.037	0.529	753.057	0.438	16	0.216	K.IIDWENTSPK.L
R1/RRR1-4/2	1514.324	1514.683	-237.843	0.365	1098.055	0.371	17	0.215	R.SDETVAM*IEAYLR.A
R1/RRR1-4/2	1203.023	1203.326	-252.563	0.483	628.427	0.475	15	0.215	K.IIDWENTSPK.L
R1/RRR1-4/2	1646.386	1645.881	-301.529	0.489	559.755	0.556	18	0.214	K.NILTTLPKPGGGEYGK.F
R1/RRR1-4/2	1293.171	1293.453	-218.294	0.366	879.269	0.401	17	0.213	K.FYSLPALNDPR.I
R1/RRR1-4/3	1993.582	1994.066	-243.280	0.503	1591.209	0.533	34	0.213	K.SEGHDTIVLAGAEYGSGSSR.D
R1/RRR1-4/2	1766.519	1766.957	-248.501	0.515	468.253	0.544	18	0.212	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-5/2	1515.805	1514.683	80.474	0.460	930.732	0.410	16	0.212	R.SDETVAM*IEAYLR.A
R1/RRR1-4/2	1766.698	1766.957	-146.879	0.514	604.167	0.509	18	0.211	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-1/2	1292.431	1293.453	-1568.560	0.305	797.726	0.429	16	0.210	K.FYSLPALNDPR.I
R1/RRR1-5/2	1203.253	1203.326	-61.217	0.468	700.796	0.396	16	0.209	K.IIDWENTSPK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1117.087	1117.278	-170.938	0.415	792.408	0.388	19	0.208	K.TSLAPGSGVVTK.Y
R1/RRR1-4/2	1645.743	1645.881	-84.336	0.473	531.812	0.517	18	0.208	K.NILTTLPKPGGGEYGK.F
R1/RRR1-4/2	1766.544	1766.957	-234.567	0.554	510.760	0.503	18	0.208	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-8/2	1571.342	1569.783	-281.645	0.480	835.756	0.401	16	0.206	K.YLLQSGLQEYLNK.Q
R1/RRR1-4/2	1548.606	1549.897	-1483.496	0.316	969.257	0.361	18	0.206	R.SNLVGMGIIPLCFK.A
R1/RRR1-4/2	1288.450	1289.421	-1533.781	0.322	975.041	0.355	16	0.206	K.FDFHGQPAELK.H
R1/RRR1-5/2	1117.189	1117.278	-80.070	0.371	602.055	0.434	17	0.206	K.TSLAPGSGVVTK.Y
R1/RRR1-4/2	1386.823	1386.580	175.925	0.424	844.971	0.393	17	0.205	K.DM*TM*SPPGPHGVK.N
R1/RRR1-4/2	1279.455	1280.431	-1548.690	0.221	1435.234	0.154	17	0.204	K.FVEFYGEGM*GK.L
R1/RRR1-4/3	1725.621	1724.761	-81.469	0.495	1946.906	0.365	29	0.203	R.NCDNFQVNQNDVEK.I
R1/RRR1-1/2	1292.641	1293.453	-1405.675	0.307	618.633	0.427	14	0.203	K.FYSLPALNDPR.I
R1/RRR1-4/2	1386.785	1386.580	148.296	0.430	386.345	0.486	15	0.202	K.DM*TM*SPPGPHGVK.N
R1/RRR1-4/2	1564.892	1565.896	-1284.434	0.318	591.515	0.428	17	0.200	R.SNLVGM*GIIPLCFK.A
R1/RRR1-2/2	1293.482	1293.453	23.133	0.361	580.451	0.368	13	0.198	K.FYSLPALNDPR.I
R1/RRR1-3/2	1292.228	1293.453	-1726.848	0.297	597.698	0.369	14	0.198	K.FYSLPALNDPR.I
R1/RRR1-4/2	1202.383	1203.326	-1621.066	0.349	605.968	0.331	15	0.198	K.IIDWENTSPK.L
R1/RRR1-4/2	1645.327	1645.881	-947.643	0.403	414.235	0.474	16	0.198	K.NILTTLPKPGGGEYGK.F
R1/RRR1-5/2	1118.085	1117.278	-173.305	0.373	455.143	0.401	15	0.197	-.TSLAPGSGVVTK.-
R1/RRR1-4/2	1290.250	1290.317	-52.629	0.305	787.078	0.331	14	0.196	K.SDWHSCLDNR.V
R1/RRR1-2/2	1550.886	1549.897	-6.759	0.386	595.277	0.389	15	0.196	R.SNLVGMGIIPLCFK.A
R1/RRR1-4/2	1288.413	1289.421	-1563.094	0.290	942.002	0.297	15	0.196	K.FDFHGQPAELK.H
R1/RRR1-4/2	1292.511	1293.453	-1506.511	0.255	607.893	0.355	14	0.196	K.FYSLPALNDPR.I
R1/RRR1-1/2	1203.045	1203.326	-234.443	0.375	622.169	0.283	15	0.195	K.IIDWENTSPK.L
R1/RRR1-3/2	1293.010	1293.453	-343.502	0.351	584.209	0.341	13	0.194	-.FYSLPALNDPR.-
R1/RRR1-3/2	1294.037	1293.453	-322.225	0.242	446.030	0.282	12	0.191	K.FYSLPALNDPR.I
R1/RRR1-4/2	1290.080	1290.317	-184.176	0.313	798.858	0.257	14	0.190	K.SDWHSCLDNR.V
R1/RRR1-1/2	1292.278	1293.453	-1687.556	0.217	568.174	0.298	13	0.190	K.FYSLPALNDPR.I
R1/RRR1-2/2	1293.103	1293.453	-271.328	0.235	478.895	0.334	11	0.189	-.FYSLPALNDPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1515.680	1514.683	-2.076	0.421	966.662	0.231	15	0.187	R.SDETVAM*IEAYLR.A
R1/RRR1-4/2	1263.480	1264.431	-1549.170	0.213	720.872	0.115	13	0.181	K.FVEFYGEGMGK.L
R1/RRR1-4/2	1289.598	1290.317	-1337.026	0.181	674.826	0.124	13	0.180	-.SDWHSCLDNR.-
R1/RRR1-4/3	1514.659	1514.683	-15.990	0.525	1873.310	0.321	28	0.170	R.SDETVAM*IEAYLR.A
R1/RRR1-4/3	1750.874	1750.958	-48.266	0.575	1245.808	0.578	30	0.166	R.SPNAVQSNMELEFKR.N
R1/RRR1-4/3	1724.066	1724.761	-986.253	0.480	1728.018	0.296	28	0.145	R.NCDNFQVNQNDVEK.I
R1/RRR1-3/3	1528.651	1528.563	57.370	0.540	1165.359	0.512	29	0.140	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/3	1498.099	1498.684	-1061.174	0.403	1581.507	0.346	26	0.137	R.SDETVAMIEAYLR.A
R1/RRR1-4/3	1528.722	1528.563	104.100	0.496	1110.813	0.521	29	0.136	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/3	1498.704	1498.684	13.870	0.451	1642.844	0.242	26	0.117	R.SDETVAMIEAYLR.A
R1/RRR1-4/3	1528.894	1528.563	216.764	0.489	916.849	0.471	27	0.113	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/3	1750.925	1750.958	-18.896	0.522	792.040	0.501	26	0.113	R.SPNAVQSNMELEFKR.N
R1/RRR1-5/3	1528.893	1528.563	216.524	0.441	850.727	0.482	25	0.112	K.AGEDADSLGLTGHER.Y
R1/RRR1-2/3	1529.655	1528.563	59.934	0.468	806.315	0.461	25	0.107	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/3	1657.224	1657.972	-1057.615	0.434	1102.119	0.388	24	0.105	K.KACELGLEVKPWVK.T
R1/RRR1-1/3	1528.527	1528.563	-23.968	0.455	694.315	0.464	23	0.105	K.AGEDADSLGLTGHER.Y
R1/RRR1-4/3	1751.100	1750.958	81.476	0.460	680.174	0.471	25	0.103	R.SPNAVQSNMELEFKR.N
R1/RRR1-4/3	1766.720	1766.957	-134.722	0.479	701.768	0.466	26	0.103	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-4/3	1766.944	1766.957	-7.172	0.455	740.863	0.462	26	0.102	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-2/3	1528.174	1528.563	-255.439	0.403	777.907	0.444	24	0.102	K.AGEDADSLGLTGHER.Y
R1/RRR1-1/3	1767.275	1766.957	180.509	0.477	756.440	0.440	25	0.101	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-1/3	1529.496	1528.563	-44.165	0.436	705.732	0.434	24	0.100	K.AGEDADSLGLTGHER.Y
R1/RRR1-3/3	1528.444	1528.563	-77.920	0.419	884.489	0.407	26	0.099	K.AGEDADSLGLTGHER.Y
R1/RRR1-3/3	1527.530	1528.563	-1334.770	0.431	636.709	0.476	22	0.099	-.AGEDADSLGLTGHER.-
R1/RRR1-3/3	1766.524	1766.957	-245.667	0.455	480.618	0.419	22	0.097	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-4/3	1658.420	1657.972	271.409	0.452	1005.595	0.357	22	0.096	K.KACELGLEVKPWVK.T
R1/RRR1-5/3	1528.646	1528.563	54.367	0.428	681.185	0.391	23	0.095	K.AGEDADSLGLTGHER.Y
R1/RRR1-2/3	1767.097	1766.957	79.195	0.443	580.681	0.401	23	0.094	R.SPNAVQSNM*ELEFKR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	1528.486	1528.563	-50.643	0.429	492.174	0.396	20	0.093	-.AGEDADSLGLTGHER.-
R1/RRR1-4/3	1289.784	1289.421	282.342	0.442	1104.907	0.329	23	0.090	K.FDFHGQPAELK.H
R1/RRR1-3/3	1766.741	1766.957	-122.766	0.387	594.535	0.345	24	0.087	R.SPNAVQSNM*ELEFKR.N
R1/RRR1-5/3	1289.115	1289.421	-237.511	0.343	745.790	0.249	21	0.069	-.FDFHGQPAELK.-
R1/RRR1-4/3	1289.402	1289.421	-14.122	0.404	778.563	0.193	20	0.069	-.FDFHGQPAELK.-
R1/RRR1-4/3	1289.621	1289.421	155.491	0.428	784.553	0.188	20	0.065	-.FDFHGQPAELK.-
R1/RRR1-4/3	1656.854	1657.972	-1282.092	0.319	971.451	0.146	22	0.063	K.KACELGLEVKPWVK.T
R1/RRR1-4/2	1646.613	1646.869	-156.194	0.530	2846.727	0.550	23	0.563	K.LLVAGDLQSFGEQLR.N
R1/RRR1-4/2	1646.387	1646.869	-293.571	0.491	2640.547	0.586	23	0.526	K.LLVAGDLQSFGEQLR.N
R1/RRR1-4/2	1979.731	1980.162	-218.041	0.588	2144.173	0.579	24	0.408	K.VSEDDKLVEYDALLVDR.F
R1/RRR1-4/2	1980.816	1980.162	-174.901	0.596	2128.173	0.549	24	0.393	K.VSEDDKLVEYDALLVDR.F
R1/RRR1-4/2	1745.304	1745.956	-949.856	0.540	1958.544	0.600	23	0.383	R.ALM*DEM*AVVATNEYR.S
R1/RRR1-4/2	1979.727	1980.162	-220.206	0.600	2007.976	0.577	24	0.381	K.VSEDDKLVEYDALLVDR.F
R1/RRR1-4/2	1861.471	1860.958	-262.084	0.634	2119.868	0.517	25	0.379	K.DITADDKQELDEALQR.E
R1/RRR1-4/2	1860.421	1860.958	-828.208	0.600	1925.067	0.498	24	0.339	K.DITADDKQELDEALQR.E
R1/RRR1-4/2	1745.390	1745.956	-900.074	0.501	1701.220	0.570	21	0.328	R.ALM*DEM*AVVATNEYR.S
R1/RRR1-4/2	1267.554	1268.444	-1496.281	0.452	1678.201	0.513	21	0.308	K.LADLEAAPAAVAR.L
R1/RRR1-4/2	1860.344	1860.958	-869.969	0.590	1676.209	0.498	23	0.301	K.DITADDKQELDEALQR.E
R1/RRR1-4/2	1267.561	1268.444	-1489.993	0.463	1433.252	0.567	20	0.290	K.LADLEAAPAAVAR.L
R1/RRR1-3/2	1268.029	1268.444	-328.641	0.439	1322.338	0.485	19	0.257	K.LADLEAAPAAVAR.L
R1/RRR1-4/2	1268.082	1268.444	-286.530	0.414	1322.800	0.463	19	0.252	K.LADLEAAPAAVAR.L
R1/RRR1-4/2	1470.185	1470.677	-335.751	0.464	1413.663	0.406	16	0.248	R.AGMSYFHETIWK.G
R1/RRR1-4/2	1187.961	1188.293	-280.886	0.426	1034.566	0.542	16	0.245	R.TPPTPQDEM*R.A
R1/RRR1-4/2	1187.901	1188.293	-331.404	0.431	916.612	0.580	15	0.242	R.TPPTPQDEM*R.A
R1/RRR1-3/2	1268.154	1268.444	-230.034	0.436	1198.607	0.449	18	0.238	K.LADLEAAPAAVAR.L
R1/RRR1-4/2	1113.933	1114.299	-329.886	0.521	1240.974	0.391	14	0.232	R.LSAAWQM*YK.A
R1/RRR1-4/2	1120.068	1120.237	-151.135	0.456	549.040	0.616	17	0.230	K.GDPGIAALYDK.L
R1/RRR1-4/2	1120.141	1120.237	-86.199	0.468	604.800	0.585	17	0.228	K.GDPGIAALYDK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1913.598	1914.112	-793.548	0.456	825.159	0.541	19	0.222	K.NQTVDLVFTAHPTQSVR.R
R1/RRR1-2/2	1646.110	1646.869	-1071.851	0.356	1045.611	0.443	20	0.222	K.LLVAGDLQSFGEQLR.N
R1/RRR1-4/2	1187.965	1188.293	-277.484	0.372	687.443	0.572	14	0.222	R.TPPTPQDEM*R.A
R1/RRR1-4/2	1098.240	1098.300	-54.807	0.374	1020.918	0.406	14	0.219	R.LSAAWQMYK.A
R1/RRR1-4/2	1315.182	1316.491	-1760.478	0.388	1129.086	0.370	15	0.219	K.RQDWLLSELR.G
R1/RRR1-4/2	1067.971	1068.169	-185.679	0.419	933.540	0.425	15	0.219	R.HQSIDAQLR.L
R1/RRR1-2/2	1267.918	1268.444	-1207.798	0.305	1028.709	0.408	17	0.215	K.LADLEAAPAAVAR.L
R1/RRR1-4/2	1119.689	1120.237	-1387.155	0.350	452.167	0.575	16	0.214	K.GDPGIAALYDK.L
R1/RRR1-3/2	1268.040	1268.444	-320.141	0.369	1081.458	0.370	16	0.213	K.LADLEAAPAAVAR.L
R1/RRR1-4/2	1491.323	1490.733	-275.165	0.492	592.059	0.482	17	0.213	R.AIPWIFAWTQTR.F
R1/RRR1-4/2	1113.529	1114.299	-1594.582	0.419	1018.812	0.356	14	0.213	R.LSAAWQM*YK.A
R1/RRR1-4/2	1114.111	1114.299	-169.824	0.486	1000.856	0.358	14	0.212	R.LSAAWQM*YK.A
R1/RRR1-4/2	1023.032	1023.168	-133.576	0.427	832.008	0.387	11	0.210	K.HYIEFWK.K
R1/RRR1-4/2	976.022	976.154	-135.494	0.419	765.623	0.391	12	0.208	R.SIVFKEPR.F
R1/RRR1-4/2	1316.552	1316.491	46.628	0.445	1147.345	0.294	15	0.208	K.RQDWLLSELR.G
R1/RRR1-4/2	1490.367	1490.733	-245.766	0.461	608.773	0.427	17	0.207	R.AIPWIFAWTQTR.F
R1/RRR1-4/2	1316.216	1316.491	-209.634	0.367	1120.589	0.289	15	0.206	K.RQDWLLSELR.G
R1/RRR1-4/2	1022.463	1023.168	-1672.755	0.471	846.064	0.346	11	0.205	K.HYIEFWK.K
R1/RRR1-4/2	975.953	976.154	-207.012	0.424	800.928	0.351	12	0.205	R.SIVFKEPR.F
R1/RRR1-4/2	1068.534	1068.169	343.337	0.379	1103.985	0.274	15	0.205	R.HQSIDAQLR.L
R1/RRR1-4/2	1490.256	1490.733	-320.549	0.369	561.697	0.418	17	0.203	R.AIPWIFAWTQTR.F
R1/RRR1-4/2	1912.808	1914.112	-1208.141	0.412	634.841	0.486	17	0.202	K.NQTVDLVFTAHPTQSVR.R
R1/RRR1-4/2	975.533	976.154	-1667.379	0.405	692.040	0.327	11	0.198	R.SIVFKEPR.F
R1/RRR1-4/2	1067.279	1068.169	-1776.026	0.372	751.317	0.316	14	0.198	R.HQSIDAQLR.L
R1/RRR1-4/2	976.100	976.154	-55.581	0.335	738.218	0.271	12	0.195	R.SIVFKEPR.F
R1/RRR1-4/2	1490.314	1490.733	-281.841	0.333	653.258	0.283	18	0.193	R.AIPWIFAWTQTR.F
R1/RRR1-4/2	1713.444	1713.958	-885.960	0.331	897.324	0.316	16	0.193	R.ALMDEMAVVATNEYR.S
R1/RRR1-1/2	975.722	976.154	-443.847	0.342	918.557	0.214	12	0.192	R.SIVFKEPR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1114.149	1114.299	-135.312	0.344	384.782	0.313	11	0.189	-.LSAAWQM*YK.-
R1/RRR1-4/2	975.758	976.154	-407.693	0.292	736.662	0.201	12	0.189	R.SIVFKEPR.F
R1/RRR1-4/2	1023.903	1023.168	-259.259	0.198	775.016	0.228	10	0.184	K.HYIEFWK.K
R1/RRR1-1/2	1120.628	1120.237	349.556	0.316	283.530	0.398	12	0.178	-.GDPGIAALYDK.-
R1/RRR1-4/3	1743.885	1742.932	-26.955	0.480	1024.902	0.479	26	0.121	R.INGKQEVM*IGYSDSGK.D
R1/RRR1-4/3	1860.948	1860.958	-4.982	0.519	1287.490	0.381	31	0.118	K.DITADDKQELDEALQR.E
R1/RRR1-4/3	1831.848	1832.114	-145.633	0.486	882.510	0.474	25	0.112	R.IRDPSFEVM*PQPALSK.E
R1/RRR1-4/3	1860.529	1860.958	-230.834	0.523	1196.907	0.364	29	0.109	K.DITADDKQELDEALQR.E
R1/RRR1-4/3	1832.038	1832.114	-41.563	0.473	754.971	0.412	23	0.097	R.IRDPSFEVM*PQPALSK.E
R1/RRR1-4/3	1742.227	1742.932	-981.924	0.445	907.126	0.397	25	0.096	R.INGKQEVM*IGYSDSGK.D
R1/RRR1-4/3	1861.254	1860.958	159.605	0.533	897.509	0.374	27	0.095	K.DITADDKQELDEALQR.E
R1/RRR1-4/3	1831.983	1832.114	-71.739	0.473	739.705	0.375	22	0.092	R.IRDPSFEVM*PQPALSK.E
R1/RRR1-3/3	1861.062	1860.958	56.103	0.408	842.473	0.219	24	0.073	K.DITADDKQELDEALQR.E
R1/RRR1-4/3	1817.262	1816.115	81.542	0.386	556.721	0.331	22	0.067	-.IRDPSFEVMPQPALSK.-
R1/RRR1-5/2	1970.837	1971.200	-184.515	0.617	3041.755	0.660	26	0.676	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1971.444	1971.200	123.986	0.638	3015.662	0.622	25	0.646	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1968.633	1969.312	-855.139	0.615	2404.986	0.487	24	0.418	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/2	1970.049	1969.312	-134.031	0.624	2259.065	0.471	24	0.382	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/2	1969.811	1969.312	254.306	0.629	2044.497	0.483	23	0.347	K.LFQDKESLYPLLNFLK.A
R1/RRR1-1/3	1961.303	1961.210	47.867	0.550	2281.940	0.514	35	0.345	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-4/3	1960.856	1961.210	-181.122	0.543	2115.709	0.538	33	0.320	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-1/3	1971.217	1971.200	8.527	0.556	1983.553	0.582	35	0.299	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1968.899	1969.312	-210.349	0.491	1735.391	0.464	21	0.297	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/3	1960.800	1961.210	-209.788	0.559	1942.209	0.558	31	0.294	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1840.703	1841.009	-166.996	0.560	1476.292	0.546	22	0.287	R.DLANLVIVCGDHGNQSK.D
R1/RRR1-2/3	1971.394	1971.200	98.891	0.516	1938.906	0.561	33	0.283	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/3	1961.282	1961.210	36.818	0.556	1911.462	0.531	31	0.275	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/3	1972.191	1971.200	-4.639	0.569	1832.675	0.592	34	0.272	R.HQLLAEFDALIEADKEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/3	1970.799	1971.200	-204.126	0.560	1929.370	0.540	34	0.270	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1839.946	1841.009	-1124.760	0.506	1303.276	0.549	21	0.267	R.DLANLVIVCGDHGNQSK.D
R1/RRR1-5/2	1542.347	1541.768	-273.683	0.514	1649.807	0.389	19	0.267	K.LGVTQCTIAHALEK.T
R1/RRR1-5/2	1540.880	1541.768	-1229.197	0.495	1737.828	0.347	19	0.266	K.LGVTQCTIAHALEK.T
R1/RRR1-5/2	1541.283	1541.768	-315.418	0.506	1627.654	0.395	19	0.266	K.LGVTQCTIAHALEK.T
R1/RRR1-1/3	1971.334	1971.200	68.057	0.565	1912.524	0.543	35	0.266	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1840.367	1841.009	-895.179	0.524	1235.051	0.563	21	0.263	R.DLANLVIVCGDHGNQSK.D
R1/RRR1-5/3	1960.811	1961.210	-203.980	0.494	1793.100	0.518	30	0.245	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-2/3	1971.817	1971.200	-194.831	0.530	1720.145	0.574	34	0.241	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1960.588	1961.210	-829.734	0.530	956.478	0.572	21	0.239	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1967.928	1969.312	-1215.116	0.467	1354.987	0.396	22	0.239	K.LFQDKESLYPLLNFLK.A
R1/RRR1-3/3	1960.943	1961.210	-136.534	0.513	1825.396	0.484	30	0.238	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-1/2	1969.289	1969.312	-11.478	0.473	1251.335	0.447	19	0.238	K.LFQDKESLYPLLNFLK.A
R1/RRR1-4/2	1241.394	1241.462	-54.700	0.433	1266.125	0.400	17	0.236	R.IKQQGLDITPK.I
R1/RRR1-4/3	1972.714	1971.200	-246.908	0.540	1607.809	0.600	33	0.232	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1540.517	1541.768	-1465.376	0.419	1459.145	0.302	18	0.228	K.LGVTQCTIAHALEK.T
R1/RRR1-5/2	1241.296	1241.462	-134.600	0.467	1377.785	0.317	17	0.227	R.IKQQGLDITPK.I
R1/RRR1-5/2	1389.082	1388.546	-334.553	0.437	667.443	0.537	21	0.226	R.LLPDAVGTTCGQR.V
R1/RRR1-4/2	1961.279	1961.210	35.358	0.533	661.512	0.606	19	0.226	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1241.244	1241.462	-176.133	0.493	1252.411	0.354	17	0.225	R.IKQQGLDITPK.I
R1/RRR1-5/2	1968.509	1969.312	-918.385	0.392	1146.011	0.399	22	0.224	K.LFQDKESLYPLLNFLK.A
R1/RRR1-3/2	1241.249	1241.462	-172.483	0.433	1233.984	0.357	16	0.224	R.IKQQGLDITPK.I
R1/RRR1-5/2	1961.682	1961.210	241.504	0.500	754.142	0.566	18	0.222	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1241.258	1241.462	-165.182	0.427	1147.480	0.371	16	0.221	R.IKQQGLDITPK.I
R1/RRR1-3/2	1960.356	1961.210	-948.249	0.490	771.153	0.536	20	0.221	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1968.758	1969.312	-791.713	0.458	1253.747	0.346	21	0.220	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/2	1388.106	1388.546	-317.677	0.435	703.771	0.474	21	0.219	R.LLPDAVGTTCGQR.V
R1/RRR1-1/2	1388.329	1388.546	-156.150	0.415	605.969	0.497	20	0.218	R.LLPDAVGTTCGQR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1241.142	1241.462	-258.420	0.443	1156.495	0.340	17	0.217	R.IKQQGLDITPK.I
R1/RRR1-4/2	1388.057	1388.546	-353.147	0.397	770.170	0.454	21	0.217	R.LLPDAVGTTCGQR.V
R1/RRR1-4/2	1960.898	1961.210	-159.570	0.478	838.305	0.490	20	0.217	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1255.027	1254.418	-312.046	0.459	861.635	0.425	18	0.216	K.VIGTEHTDILR.V
R1/RRR1-5/3	1960.565	1961.210	-841.585	0.538	1510.483	0.575	30	0.216	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1960.422	1961.210	-914.554	0.473	705.343	0.541	18	0.216	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1960.546	1961.210	-851.297	0.484	742.725	0.511	19	0.215	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1254.098	1254.418	-255.848	0.455	896.909	0.411	17	0.215	K.VIGTEHTDILR.V
R1/RRR1-5/2	1960.357	1961.210	-948.061	0.396	764.509	0.519	18	0.214	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-2/2	1388.124	1388.546	-304.883	0.432	641.364	0.453	20	0.214	R.LLPDAVGTTCGQR.V
R1/RRR1-1/2	1389.258	1388.546	-207.338	0.368	690.716	0.455	21	0.214	R.LLPDAVGTTCGQR.V
R1/RRR1-5/2	1387.413	1388.546	-1541.571	0.291	677.693	0.492	21	0.212	R.LLPDAVGTTCGQR.V
R1/RRR1-5/2	1275.981	1275.477	-390.257	0.447	704.835	0.454	16	0.212	K.NM*TGLVEM*YGK.N
R1/RRR1-1/2	1388.002	1388.546	-1115.477	0.364	622.019	0.460	20	0.212	R.LLPDAVGTTCGQR.V
R1/RRR1-5/3	1961.249	1961.210	20.244	0.485	1562.522	0.531	29	0.209	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1962.969	1961.210	-122.851	0.473	652.278	0.511	17	0.208	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-3/2	1963.136	1961.210	-37.583	0.539	583.729	0.519	18	0.208	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-2/2	1388.122	1388.546	-305.765	0.335	472.211	0.450	18	0.206	R.LLPDAVGTTCGQR.V
R1/RRR1-5/2	1227.341	1228.332	-1627.606	0.390	1297.470	0.226	16	0.206	K.YPNSDIYLDK.F
R1/RRR1-2/3	1960.929	1961.210	-143.559	0.517	1625.482	0.496	30	0.206	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/3	1971.084	1971.200	-58.931	0.550	1680.701	0.488	32	0.205	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1275.041	1275.477	-343.204	0.409	819.066	0.373	16	0.205	K.NM*TGLVEM*YGK.N
R1/RRR1-3/2	1971.027	1969.312	-145.022	0.412	717.650	0.397	19	0.202	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/2	1254.230	1254.418	-150.197	0.450	723.418	0.357	16	0.201	K.VIGTEHTDILR.V
R1/RRR1-4/2	1241.220	1241.462	-195.371	0.363	883.802	0.320	15	0.201	R.IKQQGLDITPK.I
R1/RRR1-1/2	1241.242	1241.462	-178.007	0.442	988.316	0.297	15	0.200	R.IKQQGLDITPK.I
R1/RRR1-5/2	1540.233	1541.768	-2302.064	0.376	1270.330	0.213	17	0.198	K.LGVTQCTIAHALEK.T
R1/RRR1-5/2	1104.611	1105.291	-1525.064	0.402	898.900	0.282	14	0.197	R.ALENEM*LLR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1387.975	1388.546	-1135.171	0.287	510.095	0.272	18	0.195	R.LLPDAVGTTCGQR.V
R1/RRR1-4/3	1961.169	1961.210	-20.959	0.511	1453.487	0.532	28	0.195	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/1	1253.756	1254.418	-1329.584	0.286	551.621	0.263	14	0.192	K.VIGTEHTDILR.V
R1/RRR1-5/2	1389.427	1388.546	-85.795	0.195	219.650	0.422	16	0.192	-.LLPDAVGTTCGQR.-
R1/RRR1-5/2	1274.219	1275.477	-1777.531	0.277	414.537	0.330	13	0.190	K.NM*TGLVEM*YGK.N
R1/RRR1-2/3	1970.391	1971.200	-920.684	0.496	1479.300	0.526	30	0.189	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/2	1105.040	1105.291	-227.135	0.401	687.529	0.245	12	0.188	R.ALENEM*LLR.I
R1/RRR1-4/2	1969.802	1969.312	249.832	0.324	616.868	0.269	17	0.188	K.LFQDKESLYPLLNFLK.A
R1/RRR1-1/2	1959.642	1961.210	-1826.113	0.317	601.360	0.323	16	0.188	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-4/3	1971.254	1971.200	27.439	0.450	1350.723	0.569	30	0.182	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/3	1961.250	1961.210	20.619	0.501	1495.694	0.487	30	0.181	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/2	1105.151	1105.291	-127.072	0.394	719.599	0.224	12	0.177	-.ALENEM*LLR.-
R1/RRR1-5/3	1969.954	1971.200	-1143.703	0.464	1173.302	0.522	27	0.151	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-4/3	1971.180	1971.200	-10.107	0.508	1105.613	0.532	28	0.147	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-5/3	1969.668	1969.312	181.341	0.441	1527.708	0.372	30	0.142	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/3	1969.501	1969.312	96.313	0.410	1563.474	0.326	30	0.133	K.LFQDKESLYPLLNFLK.A
R1/RRR1-2/3	1960.351	1961.210	-951.100	0.395	928.849	0.490	23	0.126	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/3	1968.878	1969.312	-220.991	0.404	1518.277	0.324	31	0.125	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/3	1457.537	1457.610	-49.790	0.448	1342.509	0.383	24	0.121	K.TKYPNSDIYLDK.F
R1/RRR1-5/3	1970.338	1971.200	-947.833	0.475	918.325	0.467	24	0.120	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-3/3	1961.520	1961.210	158.437	0.418	966.635	0.448	24	0.119	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-4/3	1960.162	1961.210	-1047.978	0.399	904.284	0.465	26	0.116	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/3	1457.683	1457.610	50.504	0.509	1115.578	0.428	24	0.112	K.TKYPNSDIYLDK.F
R1/RRR1-1/3	1960.883	1961.210	-167.258	0.386	877.072	0.428	25	0.108	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/3	1969.185	1969.312	-64.739	0.418	1062.369	0.361	27	0.100	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/3	1241.789	1241.462	263.873	0.508	1354.182	0.306	25	0.099	R.IKQQGLDITPK.I
R1/RRR1-2/3	1970.790	1971.200	-208.787	0.467	880.048	0.362	25	0.098	R.HQLLAEFDALIEADKEK.Y
R1/RRR1-1/3	1970.258	1971.200	-988.606	0.450	918.344	0.347	25	0.096	R.HQLLAEFDALIEADKEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/3	1961.329	1961.210	60.788	0.394	804.258	0.343	23	0.094	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-5/3	1457.445	1457.610	-113.555	0.486	1084.985	0.332	23	0.092	K.TKYPNSDIYLDK.F
R1/RRR1-1/3	1969.149	1969.312	-82.741	0.393	1082.662	0.307	27	0.091	K.LFQDKESLYPLLNFLK.A
R1/RRR1-2/3	1961.135	1961.210	-38.472	0.298	958.897	0.298	24	0.088	R.LGATFSSHPNELIALFSR.Y
R1/RRR1-1/3	1968.716	1969.312	-813.131	0.404	1081.106	0.292	28	0.088	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/3	1241.780	1241.462	256.924	0.489	1273.838	0.248	24	0.085	R.IKQQGLDITPK.I
R1/RRR1-5/3	1241.950	1241.462	393.674	0.498	1175.247	0.254	22	0.083	R.IKQQGLDITPK.I
R1/RRR1-5/3	1968.756	1969.312	-792.778	0.366	777.189	0.311	25	0.083	K.LFQDKESLYPLLNFLK.A
R1/RRR1-5/3	1970.009	1969.312	-154.333	0.377	1179.280	0.221	26	0.081	K.LFQDKESLYPLLNFLK.A
R1/RRR1-2/3	1241.611	1241.462	119.988	0.477	755.732	0.263	21	0.080	R.IKQQGLDITPK.I
R1/RRR1-2/3	1241.767	1241.462	245.834	0.482	1299.629	0.206	24	0.079	R.IKQQGLDITPK.I
R1/RRR1-5/3	1241.492	1241.462	23.992	0.491	1018.615	0.262	22	0.078	-.IKQQGLDITPK.-
R1/RRR1-2/3	1242.382	1241.462	-64.917	0.520	1180.632	0.218	23	0.077	R.IKQQGLDITPK.I
R1/RRR1-3/3	1241.477	1241.462	12.158	0.469	1205.195	0.208	22	0.077	-.IKQQGLDITPK.-
R1/RRR1-3/3	1241.884	1241.462	341.048	0.519	777.363	0.276	19	0.077	-.IKQQGLDITPK.-
R1/RRR1-4/3	1241.377	1241.462	-68.767	0.465	881.043	0.230	21	0.076	R.IKQQGLDITPK.I
R1/RRR1-5/3	1968.700	1969.312	-821.160	0.303	1049.063	0.224	26	0.076	K.LFQDKESLYPLLNFLK.A
R1/RRR1-4/3	1241.559	1241.462	78.427	0.496	1017.379	0.229	22	0.074	-.IKQQGLDITPK.-
R1/RRR1-1/3	1241.714	1241.462	203.396	0.491	696.627	0.252	20	0.067	-.IKQQGLDITPK.-
R1/RRR1-5/2	1844.723	1844.098	-203.933	0.529	2064.814	0.526	23	0.369	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-4/2	1843.703	1844.098	-214.737	0.481	2118.979	0.441	24	0.350	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-4/2	1844.529	1844.098	234.341	0.537	1970.081	0.498	24	0.343	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-5/2	1844.477	1844.098	206.269	0.529	2040.532	0.457	24	0.341	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-5/2	1846.376	1846.969	-865.210	0.505	1741.390	0.568	22	0.336	K.YTQGFSGADITEICQR.A
R1/RRR1-5/2	1843.522	1844.098	-857.584	0.457	2163.473	0.371	24	0.335	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-5/2	1844.353	1844.098	138.969	0.514	1964.167	0.461	24	0.331	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-5/2	1843.416	1844.098	-915.019	0.479	2171.460	0.345	23	0.326	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-5/2	1843.071	1844.098	-1103.056	0.440	1883.565	0.450	23	0.316	K.NAPSIIFIDEIDSIAPK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1447.476	1447.766	-200.930	0.441	1619.974	0.532	19	0.304	R.IVSQLLTLM*DGLK.Q
R1/RRR1-4/2	1844.653	1844.098	-242.039	0.534	1769.563	0.462	23	0.300	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-4/2	1158.564	1159.360	-1554.399	0.373	1258.480	0.563	18	0.266	K.GILLYGPPGSGK.T
R1/RRR1-4/2	1188.034	1188.316	-237.921	0.479	1416.799	0.451	19	0.261	K.TALGTSNPSALR.E
R1/RRR1-5/2	1187.989	1188.316	-275.960	0.497	1245.561	0.502	19	0.256	K.TALGTSNPSALR.E
R1/RRR1-5/2	1565.270	1565.746	-305.030	0.499	1393.356	0.459	18	0.255	K.AIANECQANFISVK.G
R1/RRR1-3/2	1188.086	1188.316	-194.628	0.473	1281.798	0.483	19	0.255	K.TALGTSNPSALR.E
R1/RRR1-4/2	1565.411	1565.746	-214.979	0.489	1279.461	0.490	18	0.252	K.AIANECQANFISVK.G
R1/RRR1-4/2	1159.491	1159.360	113.450	0.399	1149.286	0.512	18	0.246	K.GILLYGPPGSGK.T
R1/RRR1-4/2	1843.545	1844.098	-844.689	0.450	1488.565	0.376	21	0.245	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-5/2	1565.323	1565.746	-271.543	0.484	1266.085	0.462	18	0.244	K.AIANECQANFISVK.G
R1/RRR1-4/2	1330.422	1329.521	-75.151	0.425	1356.560	0.409	17	0.244	K.LAEDVDLELIAK.D
R1/RRR1-4/2	1564.847	1565.746	-1217.569	0.418	1380.317	0.403	18	0.242	K.AIANECQANFISVK.G
R1/RRR1-4/2	1678.433	1677.969	277.446	0.471	1228.176	0.456	19	0.240	R.VLNQLLTEMDGMNAK.K
R1/RRR1-1/2	1188.086	1188.316	-194.422	0.416	1144.713	0.455	19	0.237	K.TALGTSNPSALR.E
R1/RRR1-4/2	1188.050	1188.316	-224.933	0.527	1039.205	0.471	19	0.235	K.TALGTSNPSALR.E
R1/RRR1-4/2	1565.217	1565.746	-979.717	0.455	1144.544	0.465	17	0.234	K.AIANECQANFISVK.G
R1/RRR1-4/2	1187.891	1188.316	-359.161	0.442	1090.032	0.424	19	0.229	K.TALGTSNPSALR.E
R1/RRR1-2/2	1187.937	1188.316	-320.291	0.413	1368.254	0.315	19	0.227	K.TALGTSNPSALR.E
R1/RRR1-4/2	1252.327	1252.437	-87.952	0.334	992.948	0.509	16	0.227	K.GVLFYGPPGCGK.T
R1/RRR1-5/2	1565.538	1565.746	-133.548	0.521	1062.741	0.453	18	0.226	K.AIANECQANFISVK.G
R1/RRR1-5/2	1159.796	1159.360	377.550	0.432	972.657	0.458	17	0.224	K.GILLYGPPGSGK.T
R1/RRR1-5/2	1953.676	1953.165	-251.042	0.540	921.783	0.504	19	0.221	K.GPELLTM*WFGESEANVR.E
R1/RRR1-5/2	1448.639	1447.766	-87.683	0.418	900.971	0.458	16	0.217	R.IVSQLLTLM*DGLK.Q
R1/RRR1-5/2	1800.585	1801.033	-249.459	0.458	802.191	0.476	20	0.217	R.LDQLIYIPLPDEQSR.L
R1/RRR1-5/2	1431.437	1431.767	-231.251	0.392	915.285	0.458	15	0.216	R.IVSQLLTLMDGLK.Q
R1/RRR1-5/2	1801.321	1801.033	160.097	0.483	768.633	0.476	20	0.216	R.LDQLIYIPLPDEQSR.L
R1/RRR1-5/2	1076.106	1076.143	-34.430	0.469	779.498	0.451	15	0.215	K.LAGESESNLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1159.979	1159.360	-329.066	0.409	852.008	0.450	16	0.215	K.GILLYGPPGSGK.T
R1/RRR1-5/2	1188.043	1188.316	-230.499	0.462	971.362	0.384	18	0.215	K.TALGTSNPSALR.E
R1/RRR1-1/2	1188.111	1188.316	-173.395	0.422	1040.242	0.345	19	0.213	K.TALGTSNPSALR.E
R1/RRR1-5/2	1076.089	1076.143	-50.132	0.506	798.850	0.423	15	0.212	K.LAGESESNLR.K
R1/RRR1-5/2	1300.514	1299.412	78.553	0.402	658.978	0.475	17	0.212	R.EIDIGVPDEVGR.L
R1/RRR1-3/2	1187.921	1188.316	-333.384	0.439	918.299	0.378	17	0.211	K.TALGTSNPSALR.E
R1/RRR1-4/2	1299.961	1299.412	-347.788	0.452	707.934	0.426	18	0.210	R.EIDIGVPDEVGR.L
R1/RRR1-5/2	1431.366	1431.767	-280.446	0.327	783.598	0.459	15	0.208	R.IVSQLLTLMDGLK.Q
R1/RRR1-2/2	1188.133	1188.316	-154.843	0.470	772.955	0.383	17	0.207	K.TALGTSNPSALR.E
R1/RRR1-4/2	1300.500	1299.412	67.916	0.429	636.933	0.416	17	0.206	R.EIDIGVPDEVGR.L
R1/RRR1-5/2	1800.799	1801.033	-130.583	0.445	669.574	0.434	19	0.206	R.LDQLIYIPLPDEQSR.L
R1/RRR1-4/2	1158.660	1159.360	-1471.531	0.362	591.105	0.473	14	0.205	K.GILLYGPPGSGK.T
R1/RRR1-5/2	1589.037	1587.953	53.349	0.399	1043.680	0.317	18	0.202	R.RIVSQLLTLMDGLK.Q
R1/RRR1-5/2	1300.411	1299.412	-0.999	0.476	491.079	0.443	15	0.201	-.EIDIGVPDEVGR.-
R1/RRR1-4/2	968.887	969.160	-282.889	0.304	711.803	0.369	12	0.201	R.ELVELPLR.H
R1/RRR1-5/2	968.899	969.160	-269.743	0.375	759.112	0.308	13	0.200	R.ELVELPLR.H
R1/RRR1-4/2	968.604	969.160	-1611.110	0.337	799.431	0.313	13	0.200	R.ELVELPLR.H
R1/RRR1-4/2	958.872	959.079	-216.509	0.361	857.087	0.318	14	0.199	K.DVDLNALAK.Y
R1/RRR1-5/2	969.004	969.160	-161.303	0.313	544.600	0.348	11	0.197	R.ELVELPLR.H
R1/RRR1-5/2	1300.016	1299.412	-305.674	0.382	386.613	0.407	13	0.197	R.EIDIGVPDEVGR.L
R1/RRR1-5/2	968.928	969.160	-240.293	0.286	459.043	0.359	10	0.196	R.ELVELPLR.H
R1/RRR1-5/2	1446.766	1447.766	-1386.494	0.305	508.176	0.403	13	0.193	R.IVSQLLTLM*DGLK.Q
R1/RRR1-4/2	958.939	959.079	-146.526	0.351	893.744	0.244	15	0.193	K.DVDLNALAK.Y
R1/RRR1-4/2	968.334	969.160	-1891.119	0.230	584.981	0.343	11	0.193	R.ELVELPLR.H
R1/RRR1-4/2	1843.503	1844.098	-867.688	0.338	340.287	0.340	14	0.190	K.NAPSIIFIDEIDSIAPK.R
R1/RRR1-4/2	1800.616	1801.033	-232.523	0.385	429.595	0.346	15	0.189	-.LDQLIYIPLPDEQSR.-
R1/RRR1-5/2	1588.788	1587.953	-104.082	0.418	829.930	0.291	16	0.188	R.RIVSQLLTLMDGLK.Q
R1/RRR1-3/2	1076.091	1076.143	-47.743	0.389	728.654	0.224	14	0.187	K.LAGESESNLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1447.182	1447.766	-1097.598	0.371	795.153	0.266	14	0.187	R.IVSQLLTLM*DGLK.Q
R1/RRR1-4/2	1799.921	1801.033	-1176.844	0.311	476.189	0.275	15	0.186	R.LDQLIYIPLPDEQSR.L
R1/RRR1-10/2	1916.854	1918.175	-1214.597	0.556	2999.475	0.558	26	0.603	K.SLVEEDKLELATSLIEK.A
R1/RRR1-10/2	1918.526	1918.175	183.629	0.635	2970.377	0.579	25	0.602	K.SLVEEDKLELATSLIEK.A
R1/RRR1-11/2	1917.565	1918.175	-841.965	0.614	2897.776	0.579	24	0.581	K.SLVEEDKLELATSLIEK.A
R1/RRR1-11/2	1918.721	1918.175	-237.545	0.617	2863.430	0.562	25	0.564	K.SLVEEDKLELATSLIEK.A
R1/RRR1-10/2	1917.849	1918.175	-170.557	0.621	2674.109	0.576	25	0.522	K.SLVEEDKLELATSLIEK.A
R1/RRR1-11/2	1574.202	1574.758	-991.469	0.468	2530.123	0.501	26	0.459	K.GVTTIIGGGDSVAAVEK.A
R1/RRR1-10/2	1574.371	1574.758	-246.651	0.485	2333.914	0.554	25	0.437	K.GVTTIIGGGDSVAAVEK.A
R1/RRR1-10/3	1918.550	1918.175	195.937	0.533	2475.201	0.505	33	0.401	K.SLVEEDKLELATSLIEK.A
R1/RRR1-11/2	1574.235	1574.758	-970.216	0.482	2184.179	0.529	25	0.396	K.GVTTIIGGGDSVAAVEK.A
R1/RRR1-10/2	1388.690	1389.578	-1363.731	0.396	2200.878	0.453	21	0.375	K.ELDYLVGAVANPK.K
R1/RRR1-10/2	1388.757	1389.578	-1315.352	0.397	2281.537	0.399	21	0.372	K.ELDYLVGAVANPK.K
R1/RRR1-11/2	1918.452	1918.175	144.642	0.625	1893.164	0.596	21	0.360	K.SLVEEDKLELATSLIEK.A
R1/RRR1-11/2	1920.420	1921.103	-878.711	0.529	1835.558	0.605	24	0.358	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-10/2	1803.568	1804.016	-249.210	0.527	1891.204	0.556	24	0.350	K.M*SHISTGGGASLELLEGK.T
R1/RRR1-11/3	1752.243	1752.048	111.434	0.535	2421.994	0.435	33	0.349	K.LAATLPDGGVLLLENVR.F
R1/RRR1-10/2	1803.335	1804.016	-934.773	0.498	1842.365	0.519	25	0.332	K.M*SHISTGGGASLELLEGK.T
R1/RRR1-10/2	1388.669	1389.578	-1379.447	0.385	2038.792	0.404	20	0.330	K.ELDYLVGAVANPK.K
R1/RRR1-11/2	1390.141	1389.578	-315.362	0.466	1737.733	0.485	20	0.309	K.ELDYLVGAVANPK.K
R1/RRR1-11/2	1574.265	1574.758	-313.942	0.437	1655.285	0.500	23	0.298	K.GVTTIIGGGDSVAAVEK.A
R1/RRR1-10/2	1573.579	1574.758	-1388.992	0.340	1724.734	0.461	22	0.295	K.GVTTIIGGGDSVAAVEK.A
R1/RRR1-10/2	1920.302	1921.103	-940.356	0.497	1427.003	0.575	21	0.286	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-10/2	1919.879	1921.103	-1161.410	0.485	1404.513	0.561	21	0.280	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-10/3	1918.391	1918.175	113.047	0.495	2111.190	0.447	32	0.276	K.SLVEEDKLELATSLIEK.A
R1/RRR1-10/2	1573.340	1574.758	-1541.262	0.356	1583.428	0.452	23	0.275	K.GVTTIIGGGDSVAAVEK.A
R1/RRR1-11/2	1755.927	1755.030	-58.474	0.453	1607.267	0.431	21	0.274	K.TVIWNGPMGVFEFEK.F
R1/RRR1-10/2	1043.134	1043.282	-142.798	0.531	1340.186	0.497	17	0.266	K.IGVIESLLAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/3	1752.011	1752.048	-21.260	0.549	2147.425	0.395	32	0.264	K.LAATLPDGGVLLLENVR.F
R1/RRR1-11/2	1043.179	1043.282	-99.248	0.536	1139.610	0.524	16	0.253	K.IGVIESLLAK.V
R1/RRR1-11/2	1043.146	1043.282	-130.590	0.545	1130.502	0.526	16	0.253	K.IGVIESLLAK.V
R1/RRR1-10/1	1042.824	1043.282	-440.869	0.138	651.611	0.227	12	0.252	K.IGVIESLLAK.V
R1/RRR1-11/2	1921.553	1921.103	235.206	0.523	1108.471	0.578	20	0.251	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-10/2	1774.313	1774.908	-901.800	0.501	989.122	0.574	21	0.248	R.FYKEEEKNDPEFAK.K
R1/RRR1-10/2	1774.391	1774.908	-857.530	0.515	924.174	0.585	20	0.245	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/2	1150.941	1150.261	-279.418	0.472	988.299	0.542	18	0.243	R.SVGTLTESDLK.G
R1/RRR1-10/2	1043.037	1043.282	-235.310	0.508	1124.541	0.484	16	0.243	K.IGVIESLLAK.V
R1/RRR1-10/2	1093.019	1093.258	-219.733	0.441	1327.023	0.399	17	0.241	K.FAAGTDAIAKK.L
R1/RRR1-11/2	1043.104	1043.282	-171.442	0.507	1084.977	0.483	16	0.240	K.IGVIESLLAK.V
R1/RRR1-11/2	1756.382	1755.030	201.418	0.448	1480.680	0.338	20	0.238	K.TVIWNGPMGVFEFEK.F
R1/RRR1-11/2	1092.911	1093.258	-318.900	0.408	1312.101	0.390	17	0.237	K.FAAGTDAIAKK.L
R1/RRR1-10/2	1042.571	1043.282	-1646.070	0.412	1143.812	0.446	16	0.235	K.IGVIESLLAK.V
R1/RRR1-11/2	1751.617	1752.048	-247.206	0.494	805.558	0.573	24	0.235	K.LAATLPDGGVLLLENVR.F
R1/RRR1-11/2	1149.966	1150.261	-257.935	0.464	924.239	0.522	17	0.234	R.SVGTLTESDLK.G
R1/RRR1-11/2	1774.236	1774.908	-944.900	0.485	897.996	0.530	20	0.232	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/2	1751.725	1752.048	-185.124	0.502	821.324	0.549	24	0.232	K.LAATLPDGGVLLLENVR.F
R1/RRR1-11/2	1774.417	1774.908	-277.495	0.535	859.619	0.520	20	0.229	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/2	1751.417	1752.048	-934.141	0.483	724.759	0.569	23	0.229	K.LAATLPDGGVLLLENVR.F
R1/RRR1-10/2	1751.866	1752.048	-104.317	0.519	662.277	0.567	22	0.225	K.LAATLPDGGVLLLENVR.F
R1/RRR1-10/2	1752.390	1752.048	195.519	0.534	660.979	0.564	22	0.225	K.LAATLPDGGVLLLENVR.F
R1/RRR1-10/2	1092.911	1093.258	-318.676	0.375	1242.448	0.349	17	0.223	K.FAAGTDAIAKK.L
R1/RRR1-10/2	1803.671	1804.016	-191.768	0.434	851.342	0.508	18	0.217	K.M*SHISTGGGASLELLEGK.T
R1/RRR1-10/2	964.958	965.085	-132.289	0.416	1052.985	0.365	17	0.217	K.FAAGTDAIAK.K
R1/RRR1-11/2	1804.281	1804.016	147.456	0.432	920.469	0.479	18	0.216	K.M*SHISTGGGASLELLEGK.T
R1/RRR1-11/2	1073.041	1073.313	-254.061	0.435	433.774	0.519	14	0.216	K.YSLKPLVPR.L
R1/RRR1-10/2	1751.467	1752.048	-905.454	0.479	585.876	0.532	21	0.216	K.LAATLPDGGVLLLENVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1075.075	1075.286	-196.638	0.396	661.797	0.470	18	0.215	K.KPFAAIVGGSK.V
R1/RRR1-11/2	1770.129	1771.029	-1076.809	0.405	988.558	0.414	18	0.214	K.TVIWNGPM*GVFEFEK.F
R1/RRR1-11/2	1150.000	1150.261	-228.329	0.352	653.481	0.518	16	0.213	R.SVGTLTESDLK.G
R1/RRR1-10/2	1073.081	1073.313	-216.514	0.412	344.017	0.517	13	0.212	K.YSLKPLVPR.L
R1/RRR1-10/2	1074.503	1075.286	-1664.382	0.344	671.685	0.460	18	0.211	K.KPFAAIVGGSK.V
R1/RRR1-11/2	1075.107	1075.286	-166.908	0.395	594.913	0.454	17	0.211	K.KPFAAIVGGSK.V
R1/RRR1-10/2	1074.673	1075.286	-1504.844	0.348	593.503	0.467	17	0.209	K.KPFAAIVGGSK.V
R1/RRR1-11/2	1770.725	1771.029	-172.100	0.432	922.834	0.411	17	0.209	K.TVIWNGPM*GVFEFEK.F
R1/RRR1-10/2	1074.625	1075.286	-1549.688	0.334	654.008	0.439	17	0.207	K.KPFAAIVGGSK.V
R1/RRR1-11/2	1756.312	1755.030	161.551	0.411	1072.656	0.325	19	0.206	K.TVIWNGPMGVFEFEK.F
R1/RRR1-10/2	1755.470	1755.030	251.391	0.462	700.219	0.475	15	0.206	K.TVIWNGPMGVFEFEK.F
R1/RRR1-10/2	1073.190	1073.313	-115.069	0.372	438.382	0.421	14	0.205	K.YSLKPLVPR.L
R1/RRR1-10/2	1072.696	1073.313	-1511.727	0.428	408.033	0.382	14	0.205	K.YSLKPLVPR.L
R1/RRR1-11/2	1075.228	1075.286	-53.816	0.315	583.783	0.397	18	0.203	K.KPFAAIVGGSK.V
R1/RRR1-10/2	964.492	965.085	-1656.952	0.377	1000.346	0.282	17	0.202	K.FAAGTDAIAK.K
R1/RRR1-11/2	1525.896	1526.800	-1251.297	0.328	671.860	0.449	18	0.200	-.GVSLLLPTDVVVADK.-
R1/RRR1-10/2	964.725	965.085	-374.091	0.320	968.595	0.270	17	0.198	K.FAAGTDAIAK.K
R1/RRR1-10/3	1918.926	1918.175	-130.399	0.464	1680.794	0.444	29	0.194	K.SLVEEDKLELATSLIEK.A
R1/RRR1-11/2	1803.994	1804.016	-12.150	0.357	706.591	0.371	17	0.192	K.M*SHISTGGGASLELLEGK.T
R1/RRR1-3/2	1752.770	1752.048	-159.378	0.349	259.504	0.379	14	0.191	K.LAATLPDGGVLLLENVR.F
R1/RRR1-10/2	1920.879	1921.103	-116.492	0.276	399.632	0.315	15	0.185	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-10/2	1525.684	1526.800	-1390.866	0.265	516.619	0.299	14	0.182	-.GVSLLLPTDVVVADK.-
R1/RRR1-11/2	964.631	965.085	-471.860	0.152	838.224	0.149	15	0.180	K.FAAGTDAIAK.K
R1/RRR1-7/2	1804.875	1804.016	-78.149	0.204	627.088	0.188	16	0.179	K.M*SHISTGGGASLELLEGK.T
R1/RRR1-10/3	1774.527	1774.908	-215.216	0.502	1296.114	0.514	27	0.154	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/3	1774.320	1774.908	-897.595	0.436	1199.627	0.480	23	0.138	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/3	1774.799	1774.908	-61.723	0.452	1277.880	0.449	24	0.137	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/3	1075.459	1075.286	161.693	0.414	1498.667	0.399	25	0.135	K.KPFAAIVGGSK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1774.417	1774.908	-277.641	0.439	1197.712	0.450	25	0.127	R.FYKEEEKNDPEFAK.K
R1/RRR1-10/3	1774.876	1774.908	-18.158	0.411	1031.425	0.474	24	0.118	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/3	1774.802	1774.908	-59.550	0.418	1087.579	0.449	25	0.116	R.FYKEEEKNDPEFAK.K
R1/RRR1-11/3	1751.563	1752.048	-277.838	0.376	1220.264	0.347	28	0.105	K.LAATLPDGGVLLLENVR.F
R1/RRR1-11/3	1920.636	1921.103	-243.499	0.415	793.521	0.490	32	0.105	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-11/3	1921.914	1921.103	-98.312	0.412	720.991	0.488	29	0.103	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-11/3	1075.391	1075.286	98.344	0.379	1353.245	0.320	24	0.103	K.KPFAAIVGGSK.V
R1/RRR1-10/3	1921.394	1921.103	152.028	0.381	969.679	0.408	30	0.101	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-11/3	1920.671	1921.103	-225.231	0.358	655.163	0.466	26	0.097	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-10/3	1921.450	1921.103	181.368	0.371	487.208	0.459	26	0.094	K.LASVADLYVNDAFGTAHR.A
R1/RRR1-11/3	1075.273	1075.286	-11.469	0.390	1038.224	0.361	21	0.093	K.KPFAAIVGGSK.V
R1/RRR1-10/3	1075.197	1075.286	-83.039	0.381	1190.070	0.306	23	0.090	K.KPFAAIVGGSK.V
R1/RRR1-10/3	1075.374	1075.286	82.719	0.350	874.748	0.324	20	0.082	K.KPFAAIVGGSK.V
R1/RRR1-10/3	1075.210	1075.286	-70.398	0.349	981.150	0.268	22	0.077	K.KPFAAIVGGSK.V
R1/RRR1-2/3	1917.647	1918.175	-799.542	0.364	623.913	0.263	22	0.075	-.SLVEEDKLELATSLIEK.-
R1/RRR1-5/2	1569.255	1569.746	-314.008	0.589	2096.001	0.560	22	0.399	R.KYQAFAQTLQQSR.G
R1/RRR1-5/2	1441.149	1441.574	-295.619	0.549	2046.626	0.505	19	0.365	K.YQAFAQTLQQSR.G
R1/RRR1-5/2	1441.217	1441.574	-248.371	0.545	1997.114	0.449	19	0.337	K.YQAFAQTLQQSR.G
R1/RRR1-4/2	1442.207	1441.574	-255.162	0.547	1845.022	0.509	19	0.333	K.YQAFAQTLQQSR.G
R1/RRR1-5/2	1352.821	1353.503	-1246.665	0.472	1480.856	0.474	19	0.275	K.LAEDVDLEHIAK.D
R1/RRR1-3/2	1559.429	1558.757	-211.250	0.561	1871.577	0.550	20	0.349	K.LVYELFTDTLTSR.L
R1/RRR1-3/2	1559.420	1558.757	-216.747	0.545	1942.573	0.503	20	0.345	K.LVYELFTDTLTSR.L
R1/RRR1-3/2	1558.263	1558.757	-318.031	0.446	1825.706	0.465	20	0.315	K.LVYELFTDTLTSR.L
R1/RRR1-3/2	1674.489	1674.788	-178.966	0.488	1433.019	0.495	23	0.272	K.AIENTAASISDVPEEK.L
R1/RRR1-3/2	1674.562	1674.788	-135.601	0.467	1484.115	0.461	23	0.269	K.AIENTAASISDVPEEK.L
R1/RRR1-3/2	1627.606	1626.750	-88.887	0.481	1435.719	0.470	19	0.269	R.IYDNKFESQYYR.I
R1/RRR1-3/2	1143.904	1144.343	-385.173	0.497	1327.994	0.481	16	0.258	K.GLALAEIESLK.T
R1/RRR1-3/2	1674.350	1674.788	-262.270	0.439	1368.764	0.464	22	0.256	K.AIENTAASISDVPEEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1096.072	1096.219	-134.114	0.492	1230.756	0.499	14	0.254	R.HDNVQLLEK.L
R1/RRR1-3/2	1835.655	1836.147	-268.768	0.525	1019.512	0.564	23	0.248	R.FINVPIGASWVEVTM*R.T
R1/RRR1-3/2	1095.687	1096.219	-1402.009	0.479	1183.686	0.469	14	0.244	R.HDNVQLLEK.L
R1/RRR1-3/2	1096.026	1096.219	-176.122	0.483	1193.076	0.464	14	0.243	R.HDNVQLLEK.L
R1/RRR1-3/2	1648.505	1648.774	-163.817	0.455	1454.262	0.334	19	0.236	K.VLNDM*IQDDSEQPK.K
R1/RRR1-2/2	1558.659	1558.757	-63.204	0.357	1331.400	0.375	19	0.234	K.LVYELFTDTLTSR.L
R1/RRR1-3/2	1227.608	1227.392	175.873	0.472	1068.869	0.466	18	0.234	K.IIGLDGSEAPVR.V
R1/RRR1-3/2	1226.645	1227.392	-1429.001	0.454	988.906	0.470	17	0.228	K.IIGLDGSEAPVR.V
R1/RRR1-3/2	1144.299	1144.343	-38.691	0.367	1008.667	0.446	16	0.223	K.GLALAEIESLK.T
R1/RRR1-3/2	1055.825	1056.153	-311.547	0.369	1339.700	0.300	14	0.222	R.AFEYAQQAK.E
R1/RRR1-3/2	1508.454	1508.761	-204.767	0.430	973.659	0.442	19	0.221	R.LTEPSFLESLM*PK.K
R1/RRR1-3/2	1422.719	1423.620	-1340.182	0.435	953.594	0.453	16	0.219	K.IPEYIM*VTNNGR.T
R1/RRR1-1/2	1228.177	1227.392	-176.113	0.420	1063.418	0.371	18	0.217	K.IIGLDGSEAPVR.V
R1/RRR1-3/2	1057.153	1056.153	-0.534	0.443	1189.839	0.331	13	0.216	R.AFEYAQQAK.E
R1/RRR1-3/2	1508.211	1508.761	-1031.131	0.424	849.596	0.453	18	0.215	R.LTEPSFLESLM*PK.K
R1/RRR1-3/2	1309.105	1309.495	-299.156	0.421	576.088	0.515	16	0.215	K.LADFVPLTNYR.L
R1/RRR1-3/2	1055.463	1056.153	-1606.360	0.318	1220.767	0.311	13	0.214	R.AFEYAQQAK.E
R1/RRR1-3/2	1144.282	1144.343	-53.351	0.398	966.464	0.405	14	0.212	K.GLALAEIESLK.T
R1/RRR1-25/2	908.956	909.065	-119.426	0.382	529.143	0.469	13	0.212	K.YGSLTVLR.E
R1/RRR1-3/2	825.982	825.979	3.764	0.411	434.374	0.476	11	0.211	R.VPLLNNR.I
R1/RRR1-1/2	1227.425	1227.392	26.672	0.394	1072.401	0.326	18	0.210	K.IIGLDGSEAPVR.V
R1/RRR1-3/2	1236.979	1237.409	-349.018	0.424	854.946	0.383	19	0.209	R.LGSM*ETGTGLVR.A
R1/RRR1-3/2	1309.273	1309.495	-169.693	0.384	656.928	0.457	16	0.209	K.LADFVPLTNYR.L
R1/RRR1-25/2	908.801	909.065	-291.219	0.369	447.070	0.458	12	0.209	K.YGSLTVLR.E
R1/RRR1-25/2	908.734	909.065	-364.805	0.352	456.268	0.461	12	0.208	K.YGSLTVLR.E
R1/RRR1-3/2	1237.081	1237.409	-265.753	0.434	780.279	0.408	17	0.207	R.LGSM*ETGTGLVR.A
R1/RRR1-3/2	1508.141	1508.761	-1077.534	0.359	745.511	0.441	17	0.207	R.LTEPSFLESLM*PK.K
R1/RRR1-3/2	825.945	825.979	-41.301	0.433	458.039	0.404	11	0.206	R.VPLLNNR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1837.438	1836.147	158.486	0.427	762.045	0.439	18	0.205	R.FINVPIGASWVEVTM*R.T
R1/RRR1-3/2	909.059	909.065	-5.739	0.335	595.248	0.398	13	0.204	K.YGSLTVLR.E
R1/RRR1-1/2	1227.396	1227.392	3.031	0.375	970.943	0.324	16	0.203	K.IIGLDGSEAPVR.V
R1/RRR1-3/2	826.252	825.979	331.543	0.379	358.545	0.366	10	0.201	R.VPLLNNR.I
R1/RRR1-3/2	909.122	909.065	63.754	0.296	567.646	0.389	13	0.201	K.YGSLTVLR.E
R1/RRR1-3/2	1310.120	1309.495	-287.243	0.372	424.880	0.429	14	0.200	K.LADFVPLTNYR.L
R1/RRR1-3/2	1309.973	1310.485	-1157.246	0.358	781.250	0.371	17	0.199	K.LTTGHGLLQVDR.A
R1/RRR1-3/2	1236.802	1237.409	-1303.275	0.424	624.458	0.364	16	0.198	R.LGSM*ETGTGLVR.A
R1/RRR1-3/2	908.502	909.065	-1724.971	0.313	353.135	0.384	11	0.197	-.YGSLTVLR.-
R1/RRR1-3/2	1003.257	1003.211	45.263	0.444	920.744	0.275	13	0.196	K.ILECIVQK.A
R1/RRR1-3/2	1820.375	1820.148	124.926	0.318	348.139	0.357	14	0.187	R.FINVPIGASWVEVTMR.T
R1/RRR1-2/2	1228.202	1227.392	-155.773	0.375	695.341	0.184	15	0.181	-.IIGLDGSEAPVR.-
R1/RRR1-2/2	1227.091	1227.392	-246.412	0.379	619.525	0.268	14	0.178	-.IIGLDGSEAPVR.-
R1/RRR1-9/2	1997.758	1997.392	183.824	0.630	3097.725	0.587	28	0.648	R.IGLAGLAVMGQNLALNIAEK.G
R1/RRR1-9/2	1667.426	1666.881	-273.566	0.599	3217.532	0.518	26	0.644	R.GLLYLGMGVSGGEEGAR.N
R1/RRR1-9/2	1997.616	1997.392	112.555	0.608	2884.256	0.585	28	0.586	R.IGLAGLAVMGQNLALNIAEK.G
R1/RRR1-9/2	1682.399	1682.880	-286.779	0.552	3072.421	0.477	26	0.582	R.GLLYLGM*GVSGGEEGAR.N
R1/RRR1-9/2	1667.175	1666.881	176.871	0.577	3006.466	0.505	26	0.577	R.GLLYLGMGVSGGEEGAR.N
R1/RRR1-9/2	1682.347	1682.880	-914.054	0.566	2979.337	0.478	26	0.557	R.GLLYLGM*GVSGGEEGAR.N
R1/RRR1-9/2	1682.370	1682.880	-900.578	0.534	2906.416	0.475	26	0.537	R.GLLYLGM*GVSGGEEGAR.N
R1/RRR1-8/2	1997.093	1997.392	-149.934	0.559	2363.286	0.547	25	0.439	R.IGLAGLAVMGQNLALNIAEK.G
R1/RRR1-9/2	1665.832	1666.881	-1233.721	0.451	2585.865	0.420	25	0.438	R.GLLYLGMGVSGGEEGAR.N
R1/RRR1-9/2	1109.899	1110.292	-355.055	0.515	1396.319	0.562	17	0.288	R.LPANLVQAQR.D
R1/RRR1-9/2	1415.113	1414.646	330.613	0.555	1530.120	0.491	20	0.285	K.ICSYAQGM*NIIK.A
R1/RRR1-9/3	1997.096	1997.392	-148.622	0.436	2024.161	0.497	37	0.284	R.IGLAGLAVMGQNLALNIAEK.G
R1/RRR1-9/2	1215.703	1216.371	-1376.399	0.494	1623.286	0.371	18	0.264	K.GWSLNLGELAR.I
R1/RRR1-9/2	1215.684	1216.371	-1391.829	0.450	1740.701	0.307	18	0.262	K.GWSLNLGELAR.I
R1/RRR1-9/2	1564.334	1563.780	-286.272	0.550	1324.436	0.443	21	0.249	R.FLSGLKDERVEAAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1111.237	1110.292	-49.208	0.532	1256.105	0.450	16	0.246	R.LPANLVQAQR.D
R1/RRR1-9/2	1415.239	1414.646	-288.503	0.518	1193.452	0.471	18	0.244	K.ICSYAQGM*NIIK.A
R1/RRR1-9/2	1111.210	1110.292	-73.890	0.481	1236.878	0.439	17	0.243	R.LPANLVQAQR.D
R1/RRR1-9/2	1554.168	1553.697	303.883	0.490	1183.900	0.444	20	0.236	K.VFQGDFSSNLPVDK.A
R1/RRR1-9/2	1824.879	1823.984	-57.338	0.547	1091.752	0.496	17	0.233	K.LTNSELQQVFSEWNK.G
R1/RRR1-9/2	1415.016	1414.646	262.279	0.508	1018.052	0.460	17	0.227	K.ICSYAQGM*NIIK.A
R1/RRR1-9/2	1260.018	1259.308	-231.422	0.432	751.646	0.537	14	0.223	R.DYFGAHTYER.V
R1/RRR1-9/2	1761.898	1762.978	-1184.452	0.484	791.578	0.514	23	0.222	K.VAAQVPDSGPCVTYIGK.G
R1/RRR1-9/2	1553.337	1553.697	-232.729	0.427	1007.449	0.409	19	0.217	K.VFQGDFSSNLPVDK.A
R1/RRR1-9/2	1553.332	1553.697	-235.804	0.459	959.244	0.413	19	0.215	K.VFQGDFSSNLPVDK.A
R1/RRR1-9/2	1054.178	1053.196	-17.028	0.447	427.915	0.492	14	0.214	K.GFPISVYNR.T
R1/RRR1-9/2	1572.203	1571.736	297.729	0.472	579.277	0.491	19	0.210	R.NGPSLM*PGGSFEAYK.Y
R1/RRR1-7/2	1111.289	1110.292	-2.271	0.415	954.382	0.348	17	0.210	R.LPANLVQAQR.D
R1/RRR1-9/2	1762.426	1762.978	-883.359	0.439	627.492	0.473	21	0.208	K.VAAQVPDSGPCVTYIGK.G
R1/RRR1-4/2	1763.748	1762.978	-130.757	0.515	566.581	0.493	20	0.208	K.VAAQVPDSGPCVTYIGK.G
R1/RRR1-9/2	1571.173	1571.736	-998.155	0.385	577.628	0.482	19	0.207	R.NGPSLM*PGGSFEAYK.Y
R1/RRR1-9/2	1762.391	1762.978	-903.454	0.475	631.467	0.462	21	0.207	K.VAAQVPDSGPCVTYIGK.G
R1/RRR1-9/2	1215.724	1216.371	-1359.355	0.376	1039.152	0.316	17	0.206	K.GWSLNLGELAR.I
R1/RRR1-9/2	1260.217	1259.308	-72.731	0.397	691.079	0.422	14	0.205	R.DYFGAHTYER.V
R1/RRR1-9/2	944.129	944.067	65.605	0.446	816.310	0.309	13	0.200	K.AQLIEDVR.Q
R1/RRR1-9/2	1597.550	1597.775	-141.673	0.434	657.459	0.395	16	0.198	R.VDM*PGSFHTEWFK.I
R1/RRR1-9/2	1571.275	1571.736	-294.456	0.379	453.557	0.406	17	0.197	R.NGPSLM*PGGSFEAYK.Y
R1/RRR1-9/2	943.424	944.067	-1746.968	0.407	802.121	0.299	12	0.197	K.AQLIEDVR.Q
R1/RRR1-9/2	943.707	944.067	-383.007	0.363	760.147	0.311	12	0.197	K.AQLIEDVR.Q
R1/RRR1-9/2	1597.096	1597.775	-1054.604	0.342	366.048	0.403	14	0.192	R.VDM*PGSFHTEWFK.I
R1/RRR1-9/2	1571.878	1571.736	90.521	0.304	302.081	0.351	15	0.192	R.NGPSLM*PGGSFEAYK.Y
R1/RRR1-8/2	1052.949	1053.196	-234.840	0.362	421.254	0.290	14	0.191	-.GFPISVYNR.-
R1/RRR1-8/2	1052.972	1053.196	-212.974	0.229	478.525	0.272	14	0.191	K.GFPISVYNR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1571.743	1571.736	4.295	0.234	415.674	0.353	18	0.190	R.NGPSLM*PGGSFEAYK.Y
R1/RRR1-9/2	1054.053	1053.196	-135.627	0.176	240.147	0.473	12	0.190	K.GFPISVYNR.T
R1/RRR1-3/2	1554.394	1553.697	-195.550	0.346	615.456	0.283	15	0.186	K.VFQGDFSSNLPVDK.A
R1/RRR1-8/3	1381.697	1381.566	95.328	0.482	1098.393	0.322	23	0.091	-.DRLPANLVQAQR.-
R1/RRR1-7/3	1382.705	1381.566	100.660	0.511	1107.534	0.261	23	0.080	-.DRLPANLVQAQR.-
R1/RRR1-6/3	1381.930	1381.566	264.092	0.380	1197.006	0.215	24	0.077	R.DRLPANLVQAQR.D
R1/RRR1-9/3	1381.824	1381.566	187.159	0.480	1018.950	0.224	22	0.074	-.DRLPANLVQAQR.-
R1/RRR1-9/3	1381.722	1381.566	113.270	0.517	805.497	0.324	20	0.074	-.DRLPANLVQAQR.-
R1/RRR1-8/3	1380.933	1381.566	-1186.053	0.326	838.185	0.133	19	0.065	-.DRLPANLVQAQR.-
R1/RRR1-6/2	1968.690	1969.179	-248.930	0.613	3515.058	0.559	27	0.778	K.KISEDEYVSAIKEEISK.V
R1/RRR1-6/2	1556.231	1556.618	-249.527	0.487	3400.122	0.523	24	0.718	K.DEAYFAANAAAQASR.R
R1/RRR1-6/2	1556.372	1556.618	-158.485	0.500	3185.311	0.497	24	0.637	K.DEAYFAANAAAQASR.R
R1/RRR1-1/2	1809.195	1808.137	32.015	0.590	2549.787	0.629	24	0.511	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1808.522	1808.137	213.665	0.591	2524.519	0.587	24	0.486	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-5/2	1807.774	1808.137	-201.214	0.576	2525.730	0.578	24	0.482	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-4/2	1807.276	1808.137	-1032.722	0.551	2405.263	0.598	24	0.464	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1807.518	1808.137	-898.463	0.567	2406.967	0.595	24	0.463	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-5/2	1807.573	1808.137	-867.820	0.556	2396.653	0.588	24	0.458	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1808.785	1808.137	-195.213	0.580	2254.830	0.615	22	0.437	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1807.322	1808.137	-1007.359	0.540	2241.289	0.606	23	0.432	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-5/2	1808.282	1808.137	80.511	0.583	2213.759	0.597	22	0.421	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1808.993	1808.137	-79.860	0.597	2120.632	0.624	22	0.413	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1809.442	1808.137	168.965	0.573	2169.483	0.569	21	0.401	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1807.901	1808.137	-131.242	0.566	2067.062	0.572	23	0.384	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-4/2	1808.506	1808.137	204.731	0.573	1995.499	0.586	22	0.375	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1791.333	1792.138	-1010.382	0.496	2056.052	0.515	22	0.363	K.GMLTGPVTILNWSFVR.N
R1/RRR1-4/2	1808.948	1808.137	-104.634	0.578	1733.674	0.610	21	0.339	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-5/1	1022.551	1022.181	362.741	0.297	764.339	0.327	12	0.335	K.SWLAFAAQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1807.481	1808.137	-919.210	0.489	1872.763	0.492	21	0.324	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1809.690	1808.137	-247.819	0.546	1659.250	0.573	20	0.316	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-6/2	1486.388	1486.653	-178.221	0.480	1846.110	0.349	21	0.286	R.IPSTEEIADRINK.M
R1/RRR1-6/2	1707.600	1707.951	-206.112	0.448	1576.310	0.441	20	0.273	K.LDSEIKSWLAFAAQK.V
R1/RRR1-6/1	1021.717	1022.181	-455.909	0.194	663.401	0.306	11	0.271	K.SWLAFAAQK.V
R1/RRR1-5/2	1659.493	1659.826	-201.684	0.489	1292.468	0.526	21	0.261	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/2	1659.504	1659.826	-194.895	0.485	1278.939	0.517	21	0.258	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/2	1739.332	1740.015	-970.100	0.516	1043.992	0.576	22	0.251	K.YTEVKPALTNM*VSAAK.L
R1/RRR1-3/3	1969.331	1969.179	77.328	0.554	1642.795	0.621	33	0.248	K.KISEDEYVSAIKEEISK.V
R1/RRR1-5/2	1659.368	1659.826	-276.886	0.514	1179.054	0.509	21	0.247	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-6/2	1840.640	1841.006	-199.396	0.512	1303.114	0.454	20	0.244	K.ISEDEYVSAIKEEISK.V
R1/RRR1-2/3	1970.838	1969.179	-173.557	0.551	1754.646	0.550	35	0.237	K.KISEDEYVSAIKEEISK.V
R1/RRR1-6/1	1021.484	1022.181	-1666.313	0.191	603.284	0.289	10	0.236	K.SWLAFAAQK.V
R1/RRR1-6/2	1021.645	1022.181	-1508.591	0.409	1276.598	0.381	15	0.234	K.SWLAFAAQK.V
R1/RRR1-6/2	1131.043	1131.218	-155.731	0.472	1086.545	0.437	17	0.233	R.IPSTEEIADR.I
R1/RRR1-6/2	1021.625	1022.181	-1527.795	0.437	1281.955	0.373	15	0.233	K.SWLAFAAQK.V
R1/RRR1-6/2	1659.409	1659.826	-252.236	0.421	1051.161	0.500	19	0.232	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-6/2	1660.263	1659.826	263.963	0.511	972.343	0.523	19	0.231	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-6/2	1660.406	1659.826	-253.707	0.407	909.478	0.546	18	0.229	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/2	1130.943	1131.218	-243.977	0.469	809.842	0.485	17	0.228	R.IPSTEEIADR.I
R1/RRR1-1/2	1132.231	1131.218	10.964	0.482	856.427	0.475	15	0.225	R.IPSTEEIADR.I
R1/RRR1-6/2	1194.182	1194.362	-151.598	0.501	1111.902	0.391	16	0.224	R.SDEKLLSVFR.E
R1/RRR1-6/2	1131.067	1131.218	-133.753	0.451	1052.599	0.394	17	0.224	R.IPSTEEIADR.I
R1/RRR1-5/2	1021.884	1022.181	-292.241	0.443	1142.993	0.378	14	0.223	K.SWLAFAAQK.V
R1/RRR1-5/2	1021.697	1022.181	-475.164	0.398	1301.603	0.309	15	0.222	K.SWLAFAAQK.V
R1/RRR1-6/2	1707.745	1707.951	-120.921	0.493	1014.030	0.446	19	0.221	K.LDSEIKSWLAFAAQK.V
R1/RRR1-6/1	1021.488	1022.181	-1662.831	0.225	546.152	0.368	10	0.221	-.SWLAFAAQK.-
R1/RRR1-6/2	1193.449	1194.362	-1607.963	0.493	1092.826	0.378	16	0.221	R.SDEKLLSVFR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1840.363	1841.006	-895.314	0.488	1181.288	0.390	19	0.220	K.ISEDEYVSAIKEEISK.V
R1/RRR1-5/1	942.640	943.123	-513.378	0.196	585.192	0.259	10	0.220	K.VVEVNALAK.A
R1/RRR1-6/2	1194.157	1194.362	-172.620	0.496	1084.913	0.371	16	0.219	R.SDEKLLSVFR.E
R1/RRR1-2/2	1130.848	1131.218	-328.123	0.462	692.263	0.449	16	0.218	R.IPSTEEIADR.I
R1/RRR1-5/2	1131.036	1131.218	-161.902	0.451	845.227	0.407	17	0.218	R.IPSTEEIADR.I
R1/RRR1-1/2	1659.760	1659.826	-40.175	0.403	1003.236	0.436	18	0.217	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/2	1194.042	1194.362	-269.434	0.498	965.727	0.402	15	0.217	R.SDEKLLSVFR.E
R1/RRR1-6/2	1841.307	1841.006	164.067	0.529	1133.139	0.398	19	0.217	K.ISEDEYVSAIKEEISK.V
R1/RRR1-1/2	1132.014	1131.218	-180.798	0.471	673.471	0.441	16	0.217	R.IPSTEEIADR.I
R1/RRR1-2/2	1130.539	1131.218	-1489.831	0.473	686.367	0.436	16	0.217	R.IPSTEEIADR.I
R1/RRR1-5/2	1022.026	1022.181	-152.755	0.452	1047.263	0.369	14	0.216	K.SWLAFAAQK.V
R1/RRR1-5/2	1840.527	1841.006	-260.875	0.521	1011.400	0.428	19	0.216	K.ISEDEYVSAIKEEISK.V
R1/RRR1-6/2	1486.126	1486.653	-1030.209	0.475	1249.924	0.320	18	0.216	R.IPSTEEIADRINK.M
R1/RRR1-3/2	1130.902	1131.218	-280.254	0.487	730.842	0.420	16	0.216	R.IPSTEEIADR.I
R1/RRR1-5/2	943.027	943.123	-101.999	0.452	658.421	0.415	15	0.214	K.VVEVNALAK.A
R1/RRR1-1/2	1131.037	1131.218	-161.036	0.420	693.828	0.413	16	0.213	R.IPSTEEIADR.I
R1/RRR1-5/2	1707.768	1707.951	-107.728	0.473	963.844	0.418	18	0.212	K.LDSEIKSWLAFAAQK.V
R1/RRR1-5/2	942.827	943.123	-314.343	0.381	457.153	0.471	13	0.212	K.VVEVNALAK.A
R1/RRR1-5/2	1840.474	1841.006	-834.789	0.531	990.025	0.426	18	0.212	K.ISEDEYVSAIKEEISK.V
R1/RRR1-5/2	942.603	943.123	-1616.454	0.419	532.324	0.426	14	0.212	K.VVEVNALAK.A
R1/RRR1-1/2	942.971	943.123	-161.342	0.403	527.678	0.420	14	0.211	K.VVEVNALAK.A
R1/RRR1-4/2	1131.214	1131.218	-3.421	0.449	719.029	0.383	16	0.211	R.IPSTEEIADR.I
R1/RRR1-5/2	1193.516	1194.362	-1551.554	0.479	961.780	0.359	15	0.210	R.SDEKLLSVFR.E
R1/RRR1-3/2	942.270	943.123	-1972.146	0.388	453.875	0.426	13	0.209	K.VVEVNALAK.A
R1/RRR1-1/2	943.000	943.123	-130.825	0.404	613.915	0.391	14	0.209	K.VVEVNALAK.A
R1/RRR1-6/3	1850.122	1850.028	51.108	0.490	1816.261	0.425	27	0.209	K.AEHAFYLDWAVHSFR.I
R1/RRR1-2/2	1131.140	1131.218	-69.665	0.399	559.583	0.395	15	0.208	R.IPSTEEIADR.I
R1/RRR1-6/2	1131.258	1131.218	35.434	0.444	865.505	0.330	17	0.208	R.IPSTEEIADR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	942.352	943.123	-1884.924	0.361	493.772	0.421	13	0.208	K.VVEVNALAK.A
R1/RRR1-4/3	1969.561	1969.179	194.809	0.475	1584.855	0.545	32	0.208	K.KISEDEYVSAIKEEISK.V
R1/RRR1-6/2	1723.278	1724.015	-1010.994	0.459	601.483	0.484	20	0.207	K.YTEVKPALTNMVSAAK.L
R1/RRR1-2/2	1659.854	1659.826	16.921	0.514	891.661	0.419	18	0.207	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-4/2	943.052	943.123	-74.602	0.399	436.516	0.383	13	0.207	K.VVEVNALAK.A
R1/RRR1-3/2	943.130	943.123	7.840	0.390	384.716	0.403	12	0.207	K.VVEVNALAK.A
R1/RRR1-5/2	1131.079	1131.218	-123.252	0.333	754.521	0.366	16	0.206	R.IPSTEEIADR.I
R1/RRR1-6/3	1968.972	1969.179	-105.383	0.536	1462.124	0.593	32	0.206	K.KISEDEYVSAIKEEISK.V
R1/RRR1-5/3	1739.918	1740.015	-55.898	0.466	1660.256	0.520	33	0.206	K.YTEVKPALTNM*VSAAK.L
R1/RRR1-1/2	943.032	943.123	-96.156	0.378	434.402	0.357	13	0.205	K.VVEVNALAK.A
R1/RRR1-3/2	943.005	943.123	-125.242	0.365	421.901	0.340	13	0.204	K.VVEVNALAK.A
R1/RRR1-2/2	942.492	943.123	-1735.380	0.354	445.626	0.354	13	0.204	K.VVEVNALAK.A
R1/RRR1-2/2	942.839	943.123	-302.132	0.301	296.766	0.403	11	0.203	K.VVEVNALAK.A
R1/RRR1-3/2	1132.295	1131.218	67.949	0.335	558.029	0.295	14	0.199	R.IPSTEEIADR.I
R1/RRR1-4/2	942.559	943.123	-1663.943	0.274	482.168	0.318	12	0.198	K.VVEVNALAK.A
R1/RRR1-3/2	1193.528	1194.362	-1541.691	0.425	567.137	0.385	11	0.197	R.SDEKLLSVFR.E
R1/RRR1-5/1	1021.530	1022.181	-1621.052	0.232	506.065	0.348	10	0.195	K.SWLAFAAQK.V
R1/RRR1-6/1	942.448	943.123	-1781.955	0.184	517.593	0.300	10	0.192	K.VVEVNALAK.A
R1/RRR1-6/1	942.545	943.123	-1679.022	0.188	486.475	0.365	10	0.190	K.VVEVNALAK.A
R1/RRR1-2/2	1807.176	1808.137	-1088.334	0.322	530.304	0.340	14	0.190	K.GM*LTGPVTILNWSFVR.N
R1/RRR1-2/2	1708.382	1707.951	253.088	0.310	314.069	0.359	13	0.188	K.LDSEIKSWLAFAAQK.V
R1/RRR1-25/2	1131.978	1131.218	-212.820	0.284	640.107	0.133	14	0.183	-.IPSTEEIADR.-
R1/RRR1-10/2	1194.581	1194.362	184.015	0.193	670.158	0.175	12	0.183	R.SDEKLLSVFR.E
R1/RRR1-6/3	1739.952	1740.015	-36.370	0.493	1484.162	0.516	34	0.174	K.YTEVKPALTNM*VSAAK.L
R1/RRR1-5/1	1021.486	1022.181	-1664.392	0.184	466.932	0.266	10	0.163	K.SWLAFAAQK.V
R1/RRR1-5/3	1969.274	1969.179	48.326	0.494	1286.182	0.470	29	0.146	K.KISEDEYVSAIKEEISK.V
R1/RRR1-2/3	1968.472	1969.179	-869.926	0.494	1163.387	0.519	29	0.146	K.KISEDEYVSAIKEEISK.V
R1/RRR1-3/3	1661.199	1659.826	225.001	0.440	1157.419	0.509	27	0.143	K.YGAGIGPGVYDIHSPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/3	1739.838	1740.015	-101.713	0.412	1288.095	0.485	32	0.141	K.YTEVKPALTNM*VSAAK.L
R1/RRR1-6/3	1739.833	1740.015	-104.985	0.488	1185.323	0.505	31	0.138	K.YTEVKPALTNM*VSAAK.L
R1/RRR1-5/3	1739.961	1740.015	-31.197	0.427	1284.430	0.474	32	0.138	K.YTEVKPALTNM*VSAAK.L
R1/RRR1-6/3	1660.027	1659.826	121.423	0.487	677.544	0.637	25	0.137	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-6/3	1660.635	1659.826	-115.439	0.458	847.998	0.611	29	0.137	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1659.838	1659.826	7.028	0.434	863.111	0.594	29	0.134	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-3/3	1969.878	1969.179	-153.286	0.487	931.826	0.562	30	0.133	K.KISEDEYVSAIKEEISK.V
R1/RRR1-2/3	1659.412	1659.826	-250.731	0.448	733.086	0.612	27	0.132	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1659.963	1659.826	82.372	0.418	797.072	0.604	29	0.131	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-1/3	1659.364	1659.826	-279.515	0.474	758.056	0.570	27	0.126	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1194.560	1194.362	166.378	0.451	1450.899	0.366	22	0.123	R.SDEKLLSVFR.E
R1/RRR1-2/3	1660.037	1659.826	127.064	0.479	555.082	0.578	25	0.121	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1868.158	1868.188	-15.982	0.514	861.420	0.527	30	0.121	R.KYTEVKPALTNM*VSAAK.L
R1/RRR1-5/3	1724.684	1724.015	-192.542	0.417	1051.134	0.471	28	0.119	K.YTEVKPALTNMVSAAK.L
R1/RRR1-4/3	1660.397	1659.826	-259.689	0.460	490.147	0.558	23	0.117	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-1/3	1659.556	1659.826	-163.395	0.443	622.575	0.538	24	0.117	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-4/3	1659.769	1659.826	-34.908	0.449	616.614	0.547	26	0.116	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-2/3	1660.401	1659.826	-256.813	0.426	547.832	0.554	25	0.115	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-4/3	1660.486	1659.826	-205.922	0.488	633.682	0.529	26	0.115	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1660.908	1659.826	49.116	0.408	613.635	0.520	25	0.111	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1194.743	1194.362	319.764	0.488	1350.141	0.349	21	0.111	R.SDEKLLSVFR.E
R1/RRR1-6/3	1869.149	1868.188	-20.821	0.488	738.955	0.507	28	0.111	R.KYTEVKPALTNM*VSAAK.L
R1/RRR1-6/3	1659.526	1659.826	-181.658	0.376	517.514	0.523	23	0.110	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1969.251	1969.179	36.949	0.407	817.602	0.466	26	0.107	K.KISEDEYVSAIKEEISK.V
R1/RRR1-6/3	1869.046	1868.188	-75.947	0.468	532.955	0.511	26	0.106	R.KYTEVKPALTNM*VSAAK.L
R1/RRR1-6/3	1867.902	1868.188	-153.438	0.487	701.007	0.481	28	0.105	R.KYTEVKPALTNM*VSAAK.L
R1/RRR1-6/3	1659.202	1659.826	-982.230	0.372	486.895	0.465	21	0.104	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-5/3	1868.506	1868.188	170.673	0.516	715.151	0.459	28	0.103	R.KYTEVKPALTNM*VSAAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/3	1724.693	1724.015	-187.643	0.463	820.729	0.441	26	0.103	K.YTEVKPALTNMVSAAK.L
R1/RRR1-6/3	1194.313	1194.362	-41.337	0.492	1248.120	0.348	21	0.103	R.SDEKLLSVFR.E
R1/RRR1-3/3	1659.119	1659.826	-1031.981	0.394	510.557	0.451	24	0.102	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-6/3	1852.019	1852.188	-91.775	0.457	687.429	0.456	27	0.101	R.KYTEVKPALTNMVSAAK.L
R1/RRR1-5/3	1868.190	1868.188	1.320	0.494	867.379	0.421	30	0.101	R.KYTEVKPALTNM*VSAAK.L
R1/RRR1-6/3	1661.123	1659.826	179.350	0.372	480.965	0.446	24	0.101	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-10/3	1659.653	1659.826	-104.957	0.390	456.066	0.405	21	0.100	K.YGAGIGPGVYDIHSPR.I
R1/RRR1-6/3	1194.479	1194.362	97.969	0.520	1088.606	0.345	20	0.094	R.SDEKLLSVFR.E
R1/RRR1-6/3	1194.161	1194.362	-169.145	0.454	1127.769	0.317	20	0.091	R.SDEKLLSVFR.E
R1/RRR1-5/3	1194.517	1194.362	129.946	0.451	1065.173	0.334	20	0.090	R.SDEKLLSVFR.E
R1/RRR1-5/3	1850.166	1850.028	74.930	0.368	977.465	0.345	23	0.089	K.AEHAFYLDWAVHSFR.I
R1/RRR1-3/3	1968.962	1969.179	-110.513	0.324	744.517	0.327	25	0.084	K.KISEDEYVSAIKEEISK.V
R1/RRR1-6/3	1849.559	1850.028	-254.114	0.371	964.676	0.237	24	0.074	K.AEHAFYLDWAVHSFR.I
R1/RRR1-8/2	1985.180	1983.204	-12.249	0.628	2688.548	0.569	26	0.518	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-8/2	1745.357	1745.940	-909.746	0.596	2527.554	0.636	26	0.513	R.HMDGFGVNTYTFVTR.D
R1/RRR1-8/2	1982.585	1983.204	-819.231	0.553	2704.244	0.531	26	0.507	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-7/2	1983.080	1983.204	-62.951	0.631	2613.859	0.583	26	0.506	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-7/2	1981.924	1983.204	-1153.716	0.517	2639.865	0.554	26	0.503	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-8/2	1982.405	1983.204	-910.280	0.571	2613.174	0.555	25	0.495	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-7/2	1745.533	1745.940	-233.618	0.591	2445.368	0.633	26	0.493	R.HMDGFGVNTYTFVTR.D
R1/RRR1-7/2	1747.203	1745.940	151.391	0.560	2484.845	0.593	26	0.485	R.HMDGFGVNTYTFVTR.D
R1/RRR1-8/2	1981.989	1983.204	-1120.937	0.510	2530.464	0.541	25	0.471	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-7/2	1745.297	1745.940	-944.152	0.538	2405.756	0.597	26	0.469	R.HMDGFGVNTYTFVTR.D
R1/RRR1-2/2	1982.374	1983.204	-925.859	0.518	2328.573	0.560	25	0.434	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-7/2	1983.434	1983.204	116.384	0.609	2304.104	0.570	25	0.430	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-3/2	1984.138	1983.204	-33.483	0.586	2333.298	0.554	23	0.429	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-8/2	1745.225	1745.940	-985.302	0.536	2078.055	0.572	24	0.391	R.HMDGFGVNTYTFVTR.D
R1/RRR1-2/2	1540.523	1540.785	-170.448	0.579	2009.573	0.529	20	0.360	R.GPILLEDYHLIEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1540.453	1540.785	-215.918	0.575	1967.395	0.541	20	0.357	R.GPILLEDYHLIEK.L
R1/RRR1-1/2	1540.171	1540.785	-1050.739	0.569	1938.132	0.545	20	0.354	R.GPILLEDYHLIEK.L
R1/RRR1-8/2	1540.407	1540.785	-246.208	0.582	1898.281	0.555	20	0.351	R.GPILLEDYHLIEK.L
R1/RRR1-8/2	1540.206	1540.785	-1027.900	0.558	1926.921	0.528	20	0.347	R.GPILLEDYHLIEK.L
R1/RRR1-4/2	1540.403	1540.785	-248.355	0.538	1939.153	0.516	20	0.345	R.GPILLEDYHLIEK.L
R1/RRR1-8/2	1540.404	1540.785	-247.957	0.582	1859.693	0.542	20	0.340	R.GPILLEDYHLIEK.L
R1/RRR1-7/2	1539.941	1540.785	-1200.847	0.578	1830.753	0.548	20	0.338	R.GPILLEDYHLIEK.L
R1/RRR1-7/2	1527.980	1527.856	81.523	0.591	1860.504	0.540	21	0.337	R.LGPNYLMLPVNAPK.C
R1/RRR1-7/2	1540.296	1540.785	-318.402	0.565	1819.326	0.538	20	0.333	R.GPILLEDYHLIEK.L
R1/RRR1-2/2	1539.667	1540.785	-1379.984	0.549	1871.633	0.510	20	0.332	R.GPILLEDYHLIEK.L
R1/RRR1-6/2	1540.203	1540.785	-1030.447	0.529	1874.255	0.505	20	0.332	R.GPILLEDYHLIEK.L
R1/RRR1-1/2	1540.527	1540.785	-167.983	0.560	1812.117	0.509	20	0.323	R.GPILLEDYHLIEK.L
R1/RRR1-2/2	1540.158	1540.785	-1059.572	0.572	1774.707	0.506	20	0.316	R.GPILLEDYHLIEK.L
R1/RRR1-1/2	1982.308	1983.204	-959.428	0.460	1824.123	0.472	22	0.312	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-3/2	1540.063	1540.785	-1121.171	0.532	1646.047	0.495	19	0.295	R.GPILLEDYHLIEK.L
R1/RRR1-3/2	1540.362	1540.785	-275.227	0.551	1586.921	0.511	19	0.292	R.GPILLEDYHLIEK.L
R1/RRR1-6/2	1543.543	1543.855	-203.253	0.562	1600.614	0.482	21	0.285	R.LGPNYLM*LPVNAPK.C
R1/RRR1-7/2	1527.331	1527.856	-1001.213	0.543	1434.102	0.553	19	0.283	R.LGPNYLMLPVNAPK.C
R1/RRR1-7/2	1543.328	1543.855	-992.801	0.543	1332.307	0.579	20	0.280	R.LGPNYLM*LPVNAPK.C
R1/RRR1-4/2	1540.668	1540.785	-76.022	0.506	1559.156	0.481	18	0.280	R.GPILLEDYHLIEK.L
R1/RRR1-1/2	1543.323	1543.855	-996.137	0.517	1467.114	0.493	20	0.273	R.LGPNYLM*LPVNAPK.C
R1/RRR1-1/2	1543.591	1543.855	-171.916	0.519	1345.481	0.532	20	0.270	R.LGPNYLM*LPVNAPK.C
R1/RRR1-4/2	1540.234	1540.785	-1009.917	0.528	1446.093	0.491	18	0.269	R.GPILLEDYHLIEK.L
R1/RRR1-8/2	1528.998	1527.856	92.840	0.596	1263.362	0.578	18	0.269	R.LGPNYLMLPVNAPK.C
R1/RRR1-7/2	1984.174	1983.204	-15.279	0.510	1562.485	0.438	21	0.266	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-7/2	1544.401	1543.855	-295.102	0.582	1233.871	0.561	20	0.266	R.LGPNYLM*LPVNAPK.C
R1/RRR1-7/2	1761.374	1761.939	-891.157	0.509	1156.599	0.579	24	0.265	R.HM*DGFGVNTYTFVTR.D
R1/RRR1-7/2	1544.277	1543.855	273.737	0.569	1280.915	0.530	20	0.263	R.LGPNYLM*LPVNAPK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1543.546	1543.855	-200.873	0.501	1320.205	0.514	19	0.262	R.LGPNYLM*LPVNAPK.C
R1/RRR1-6/2	1125.080	1125.303	-199.325	0.549	1235.902	0.521	18	0.261	R.SPGAQTPVIVR.F
R1/RRR1-2/2	1543.530	1543.855	-211.187	0.512	1366.561	0.491	19	0.261	R.LGPNYLM*LPVNAPK.C
R1/RRR1-2/2	1528.567	1527.856	-189.643	0.513	1358.235	0.491	19	0.260	R.LGPNYLMLPVNAPK.C
R1/RRR1-2/2	1125.257	1125.303	-41.522	0.536	1398.091	0.451	18	0.259	R.SPGAQTPVIVR.F
R1/RRR1-6/2	1529.223	1527.856	240.865	0.530	1304.475	0.508	19	0.259	R.LGPNYLMLPVNAPK.C
R1/RRR1-8/2	1125.113	1125.303	-169.175	0.508	1306.130	0.483	18	0.259	R.SPGAQTPVIVR.F
R1/RRR1-2/2	1124.634	1125.303	-1488.726	0.511	1186.603	0.514	18	0.256	R.SPGAQTPVIVR.F
R1/RRR1-8/2	1125.128	1125.303	-156.550	0.502	1299.335	0.470	18	0.255	R.SPGAQTPVIVR.F
R1/RRR1-8/2	1124.681	1125.303	-1447.078	0.494	1191.298	0.504	18	0.254	R.SPGAQTPVIVR.F
R1/RRR1-7/2	1761.372	1761.939	-892.201	0.540	965.730	0.590	24	0.253	R.HM*DGFGVNTYTFVTR.D
R1/RRR1-6/2	1543.681	1543.855	-113.451	0.563	1267.565	0.499	19	0.253	R.LGPNYLM*LPVNAPK.C
R1/RRR1-5/2	1124.934	1125.303	-329.413	0.514	1167.902	0.505	18	0.252	R.SPGAQTPVIVR.F
R1/RRR1-4/2	1124.640	1125.303	-1482.947	0.542	1072.568	0.544	17	0.252	R.SPGAQTPVIVR.F
R1/RRR1-8/2	1543.155	1543.855	-1104.943	0.478	1325.501	0.465	19	0.252	R.LGPNYLM*LPVNAPK.C
R1/RRR1-7/2	1125.080	1125.303	-198.998	0.495	1190.402	0.493	18	0.251	R.SPGAQTPVIVR.F
R1/RRR1-8/2	1529.370	1527.856	-318.515	0.495	1219.763	0.510	18	0.251	R.LGPNYLMLPVNAPK.C
R1/RRR1-3/2	1543.594	1543.855	-170.170	0.485	1237.219	0.482	19	0.248	R.LGPNYLM*LPVNAPK.C
R1/RRR1-1/2	1125.184	1125.303	-106.705	0.491	1146.784	0.490	18	0.248	R.SPGAQTPVIVR.F
R1/RRR1-7/2	1124.558	1125.303	-1556.547	0.509	1102.779	0.507	17	0.247	R.SPGAQTPVIVR.F
R1/RRR1-3/2	1544.302	1543.855	289.986	0.530	1122.148	0.520	19	0.246	R.LGPNYLM*LPVNAPK.C
R1/RRR1-3/2	1544.883	1543.855	17.881	0.539	1102.109	0.523	19	0.245	R.LGPNYLM*LPVNAPK.C
R1/RRR1-2/2	1125.046	1125.303	-229.476	0.548	1250.186	0.444	18	0.245	R.SPGAQTPVIVR.F
R1/RRR1-1/2	1543.472	1543.855	-249.430	0.523	1217.856	0.484	18	0.244	R.LGPNYLM*LPVNAPK.C
R1/RRR1-7/2	1125.399	1125.303	85.010	0.451	1255.030	0.436	18	0.244	R.SPGAQTPVIVR.F
R1/RRR1-7/2	969.999	970.107	-111.027	0.500	1222.338	0.452	14	0.244	R.FAGELAHPK.V
R1/RRR1-7/2	1124.716	1125.303	-1415.681	0.489	1177.859	0.461	18	0.244	R.SPGAQTPVIVR.F
R1/RRR1-8/2	1761.402	1761.939	-875.016	0.580	781.004	0.613	22	0.244	R.HM*DGFGVNTYTFVTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1125.061	1125.303	-215.869	0.503	1087.456	0.498	17	0.244	R.SPGAQTPVIVR.F
R1/RRR1-6/2	1124.581	1125.303	-1535.611	0.505	1141.967	0.471	18	0.244	R.SPGAQTPVIVR.F
R1/RRR1-7/2	1070.825	1071.168	-321.132	0.525	1151.008	0.463	15	0.243	R.VFAYADTQR.Y
R1/RRR1-2/2	1981.462	1983.204	-1894.179	0.354	1479.963	0.365	21	0.243	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-1/2	970.000	970.107	-110.396	0.506	1081.510	0.484	15	0.242	R.FAGELAHPK.V
R1/RRR1-7/2	1526.594	1527.856	-1486.521	0.451	1226.752	0.456	19	0.242	R.LGPNYLMLPVNAPK.C
R1/RRR1-8/2	1543.511	1543.855	-223.723	0.487	1200.038	0.467	19	0.242	R.LGPNYLM*LPVNAPK.C
R1/RRR1-3/2	1125.139	1125.303	-146.101	0.498	1021.763	0.508	17	0.242	R.SPGAQTPVIVR.F
R1/RRR1-5/2	1125.087	1125.303	-192.685	0.511	1081.689	0.488	17	0.242	R.SPGAQTPVIVR.F
R1/RRR1-4/2	1125.249	1125.303	-48.269	0.514	1132.561	0.469	17	0.241	R.SPGAQTPVIVR.F
R1/RRR1-6/2	1071.071	1071.168	-90.148	0.442	1059.208	0.486	15	0.240	R.VFAYADTQR.Y
R1/RRR1-2/2	1070.653	1071.168	-1419.010	0.467	1064.913	0.480	15	0.240	R.VFAYADTQR.Y
R1/RRR1-8/2	970.002	970.107	-108.376	0.557	1087.307	0.471	15	0.240	R.FAGELAHPK.V
R1/RRR1-3/2	1125.130	1125.303	-154.046	0.505	1019.770	0.500	17	0.240	R.SPGAQTPVIVR.F
R1/RRR1-7/2	1761.273	1761.939	-948.976	0.569	752.287	0.596	22	0.239	R.HM*DGFGVNTYTFVTR.D
R1/RRR1-6/2	1543.918	1543.855	40.810	0.497	1189.944	0.465	18	0.239	R.LGPNYLM*LPVNAPK.C
R1/RRR1-4/2	970.143	970.107	37.911	0.437	1012.670	0.493	15	0.238	R.FAGELAHPK.V
R1/RRR1-10/2	1124.943	1125.303	-321.356	0.466	976.573	0.505	17	0.238	R.SPGAQTPVIVR.F
R1/RRR1-5/2	1124.689	1125.303	-1439.774	0.486	959.318	0.503	17	0.237	R.SPGAQTPVIVR.F
R1/RRR1-5/2	1070.856	1071.168	-291.510	0.419	1162.604	0.431	15	0.237	R.VFAYADTQR.Y
R1/RRR1-4/2	1070.960	1071.168	-194.878	0.456	936.511	0.500	15	0.236	R.VFAYADTQR.Y
R1/RRR1-7/2	1071.046	1071.168	-113.813	0.518	926.474	0.493	15	0.236	R.VFAYADTQR.Y
R1/RRR1-8/2	969.476	970.107	-1686.699	0.501	941.224	0.500	14	0.235	R.FAGELAHPK.V
R1/RRR1-7/2	1604.440	1603.755	-196.776	0.551	1365.202	0.366	20	0.234	K.LFVQVIDPEEEER.F
R1/RRR1-7/2	969.958	970.107	-153.571	0.544	1061.105	0.444	15	0.233	R.FAGELAHPK.V
R1/RRR1-3/2	1124.640	1125.303	-1483.493	0.481	1008.925	0.466	17	0.233	R.SPGAQTPVIVR.F
R1/RRR1-1/2	1072.123	1071.168	-42.210	0.443	947.262	0.476	15	0.232	R.VFAYADTQR.Y
R1/RRR1-8/2	1761.382	1761.939	-886.357	0.536	808.527	0.537	22	0.231	R.HM*DGFGVNTYTFVTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1071.008	1071.168	-149.599	0.511	921.779	0.470	15	0.231	R.VFAYADTQR.Y
R1/RRR1-9/2	1124.992	1125.303	-277.591	0.421	1184.433	0.400	17	0.231	R.SPGAQTPVIVR.F
R1/RRR1-3/2	1071.956	1071.168	-198.238	0.490	908.132	0.474	15	0.231	R.VFAYADTQR.Y
R1/RRR1-7/2	969.994	970.107	-115.951	0.488	914.125	0.482	14	0.231	R.FAGELAHPK.V
R1/RRR1-3/2	1071.151	1071.168	-15.844	0.534	917.536	0.465	15	0.231	R.VFAYADTQR.Y
R1/RRR1-4/2	1543.532	1543.855	-210.235	0.517	1153.896	0.423	20	0.230	R.LGPNYLM*LPVNAPK.C
R1/RRR1-1/2	1125.138	1125.303	-147.408	0.491	966.428	0.457	17	0.229	R.SPGAQTPVIVR.F
R1/RRR1-1/2	1125.991	1125.303	-278.324	0.544	957.319	0.458	17	0.229	R.SPGAQTPVIVR.F
R1/RRR1-1/2	1070.857	1071.168	-290.824	0.511	921.371	0.449	15	0.228	R.VFAYADTQR.Y
R1/RRR1-4/2	1543.322	1543.855	-996.693	0.504	1086.114	0.443	18	0.227	R.LGPNYLM*LPVNAPK.C
R1/RRR1-5/2	969.951	970.107	-160.389	0.418	957.668	0.445	15	0.227	R.FAGELAHPK.V
R1/RRR1-8/2	1274.027	1273.287	-204.948	0.450	1328.490	0.329	15	0.226	R.DEEVDYYPSR.H
R1/RRR1-2/2	1543.344	1543.855	-982.319	0.490	1106.541	0.424	18	0.225	R.LGPNYLM*LPVNAPK.C
R1/RRR1-9/2	1071.395	1071.168	212.601	0.460	755.944	0.488	14	0.225	R.VFAYADTQR.Y
R1/RRR1-6/2	1071.302	1071.168	125.761	0.411	914.870	0.453	14	0.225	R.VFAYADTQR.Y
R1/RRR1-7/2	1126.337	1125.303	30.262	0.458	1142.969	0.378	17	0.225	R.SPGAQTPVIVR.F
R1/RRR1-3/2	1071.063	1071.168	-97.693	0.447	929.264	0.425	15	0.224	R.VFAYADTQR.Y
R1/RRR1-4/2	1071.050	1071.168	-110.383	0.479	900.253	0.429	15	0.224	R.VFAYADTQR.Y
R1/RRR1-5/2	1543.240	1543.855	-1050.060	0.405	960.189	0.459	18	0.224	R.LGPNYLM*LPVNAPK.C
R1/RRR1-6/2	1124.686	1125.303	-1442.172	0.460	893.708	0.441	17	0.224	R.SPGAQTPVIVR.F
R1/RRR1-2/2	969.870	970.107	-244.857	0.397	1057.856	0.395	15	0.224	R.FAGELAHPK.V
R1/RRR1-6/2	969.647	970.107	-475.544	0.450	872.955	0.444	14	0.222	R.FAGELAHPK.V
R1/RRR1-7/2	1125.352	1125.303	43.235	0.439	954.789	0.424	16	0.222	R.SPGAQTPVIVR.F
R1/RRR1-8/2	970.092	970.107	-14.970	0.417	1005.930	0.387	15	0.220	R.FAGELAHPK.V
R1/RRR1-22/2	970.449	970.107	353.563	0.331	962.510	0.426	14	0.220	R.FAGELAHPK.V
R1/RRR1-2/2	1070.504	1071.168	-1558.398	0.417	1006.738	0.378	15	0.220	R.VFAYADTQR.Y
R1/RRR1-4/2	969.813	970.107	-304.081	0.374	912.432	0.424	14	0.219	R.FAGELAHPK.V
R1/RRR1-7/2	1104.531	1105.188	-1504.404	0.398	817.957	0.486	11	0.219	-.SHVQEYWR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	969.744	970.107	-374.680	0.425	942.944	0.401	14	0.218	R.FAGELAHPK.V
R1/RRR1-2/2	1070.849	1071.168	-298.258	0.504	833.581	0.419	14	0.218	R.VFAYADTQR.Y
R1/RRR1-8/2	1125.381	1125.303	69.563	0.444	961.198	0.395	16	0.218	R.SPGAQTPVIVR.F
R1/RRR1-1/2	1070.602	1071.168	-1466.766	0.380	911.899	0.398	15	0.218	R.VFAYADTQR.Y
R1/RRR1-9/2	1528.400	1527.856	-299.411	0.456	1065.754	0.393	17	0.217	R.LGPNYLMLPVNAPK.C
R1/RRR1-1/2	969.512	970.107	-1649.508	0.417	990.188	0.368	15	0.217	R.FAGELAHPK.V
R1/RRR1-9/2	1124.940	1125.303	-323.969	0.381	990.971	0.373	17	0.217	R.SPGAQTPVIVR.F
R1/RRR1-7/2	1604.133	1603.755	236.639	0.522	1179.450	0.349	19	0.216	K.LFVQVIDPEEEER.F
R1/RRR1-7/2	1543.702	1543.855	-99.490	0.446	875.404	0.443	17	0.216	R.LGPNYLM*LPVNAPK.C
R1/RRR1-2/2	1272.995	1273.287	-229.929	0.359	1330.426	0.263	14	0.216	-.DEEVDYYPSR.-
R1/RRR1-8/2	1272.947	1273.287	-268.122	0.381	1244.817	0.300	15	0.216	R.DEEVDYYPSR.H
R1/RRR1-3/2	969.997	970.107	-113.805	0.360	1030.863	0.350	15	0.215	R.FAGELAHPK.V
R1/RRR1-5/2	1543.581	1543.855	-178.183	0.493	919.129	0.422	17	0.214	R.LGPNYLM*LPVNAPK.C
R1/RRR1-7/2	1105.089	1105.188	-89.810	0.406	744.400	0.457	12	0.214	-.SHVQEYWR.-
R1/RRR1-8/2	1542.613	1543.855	-1458.209	0.405	854.932	0.435	16	0.213	R.LGPNYLM*LPVNAPK.C
R1/RRR1-7/2	1104.942	1105.188	-222.792	0.453	803.845	0.425	12	0.213	-.SHVQEYWR.-
R1/RRR1-8/2	1272.403	1273.287	-1484.805	0.293	1353.961	0.234	15	0.212	R.DEEVDYYPSR.H
R1/RRR1-7/2	988.941	989.110	-171.423	0.431	635.193	0.439	11	0.211	R.FSTVIHER.G
R1/RRR1-9/2	1124.363	1125.303	-1730.830	0.388	720.554	0.400	16	0.211	R.SPGAQTPVIVR.F
R1/RRR1-7/2	988.908	989.110	-205.105	0.462	636.546	0.428	11	0.211	R.FSTVIHER.G
R1/RRR1-10/2	1071.025	1071.168	-133.707	0.420	674.348	0.366	14	0.209	R.VFAYADTQR.Y
R1/RRR1-5/2	1070.884	1071.168	-265.778	0.424	738.205	0.360	14	0.209	R.VFAYADTQR.Y
R1/RRR1-9/2	1070.984	1071.168	-172.352	0.384	853.157	0.347	14	0.209	R.VFAYADTQR.Y
R1/RRR1-7/2	1603.211	1603.755	-965.510	0.470	1131.348	0.314	19	0.209	K.LFVQVIDPEEEER.F
R1/RRR1-8/2	989.076	989.110	-34.489	0.435	463.071	0.442	10	0.208	R.FSTVIHER.G
R1/RRR1-2/2	1105.008	1105.188	-162.946	0.328	759.326	0.406	12	0.208	R.SHVQEYWR.V
R1/RRR1-2/2	1273.160	1273.287	-100.265	0.406	1240.438	0.253	15	0.208	R.DEEVDYYPSR.H
R1/RRR1-8/2	988.493	989.110	-1640.501	0.429	496.689	0.439	10	0.208	R.FSTVIHER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1104.907	1105.188	-255.045	0.423	637.988	0.440	11	0.208	-.SHVQEYWR.-
R1/RRR1-5/2	1071.212	1071.168	41.306	0.356	687.015	0.380	13	0.207	R.VFAYADTQR.Y
R1/RRR1-1/2	1106.000	1105.188	-169.774	0.372	715.123	0.401	11	0.207	R.SHVQEYWR.V
R1/RRR1-7/2	1273.022	1273.287	-208.668	0.365	1305.125	0.217	15	0.206	R.DEEVDYYPSR.H
R1/RRR1-8/2	988.501	989.110	-1632.437	0.359	563.348	0.410	11	0.206	R.FSTVIHER.G
R1/RRR1-3/2	1542.654	1543.855	-1431.502	0.363	917.163	0.352	17	0.206	R.LGPNYLM*LPVNAPK.C
R1/RRR1-4/2	1542.344	1543.855	-2283.494	0.369	1088.910	0.291	18	0.205	R.LGPNYLM*LPVNAPK.C
R1/RRR1-6/2	989.049	989.110	-61.353	0.358	664.138	0.381	11	0.204	R.FSTVIHER.G
R1/RRR1-8/2	1105.050	1105.188	-125.158	0.390	771.263	0.367	12	0.204	-.SHVQEYWR.-
R1/RRR1-2/2	1104.431	1105.188	-1595.001	0.274	625.647	0.422	11	0.202	R.SHVQEYWR.V
R1/RRR1-7/2	988.916	989.110	-196.560	0.401	525.936	0.368	10	0.202	R.FSTVIHER.G
R1/RRR1-4/2	988.445	989.110	-1689.137	0.377	522.520	0.347	10	0.200	R.FSTVIHER.G
R1/RRR1-5/2	989.033	989.110	-78.066	0.299	414.444	0.343	10	0.199	R.FSTVIHER.G
R1/RRR1-22/2	970.552	970.107	460.628	0.329	602.979	0.376	11	0.199	-.FAGELAHPK.-
R1/RRR1-11/2	1544.102	1543.855	160.300	0.332	529.026	0.363	14	0.197	R.LGPNYLM*LPVNAPK.C
R1/RRR1-3/2	988.227	989.110	-1910.662	0.344	395.894	0.338	10	0.197	-.FSTVIHER.-
R1/RRR1-22/2	970.941	970.107	-170.818	0.293	555.948	0.316	11	0.197	R.FAGELAHPK.V
R1/RRR1-8/2	1527.418	1527.856	-287.740	0.311	471.705	0.323	14	0.196	R.LGPNYLMLPVNAPK.C
R1/RRR1-1/2	988.971	989.110	-140.838	0.356	495.185	0.325	10	0.196	-.FSTVIHER.-
R1/RRR1-8/2	1528.263	1527.856	267.294	0.331	543.382	0.273	16	0.196	R.LGPNYLMLPVNAPK.C
R1/RRR1-1/2	988.151	989.110	-1988.498	0.297	509.563	0.342	10	0.195	-.FSTVIHER.-
R1/RRR1-9/2	1104.712	1105.188	-431.866	0.298	538.271	0.322	11	0.195	-.SHVQEYWR.-
R1/RRR1-11/2	1124.382	1125.303	-1713.595	0.234	546.455	0.254	13	0.194	R.SPGAQTPVIVR.F
R1/RRR1-9/2	1528.915	1527.856	38.790	0.283	779.971	0.280	16	0.194	R.LGPNYLMLPVNAPK.C
R1/RRR1-1/2	1272.832	1273.287	-358.278	0.266	1107.469	0.167	13	0.192	-.DEEVDYYPSR.-
R1/RRR1-1/2	1273.049	1273.287	-187.409	0.328	928.968	0.221	13	0.190	-.DEEVDYYPSR.-
R1/RRR1-7/2	1272.614	1273.287	-1318.695	0.273	1057.260	0.152	14	0.190	-.DEEVDYYPSR.-
R1/RRR1-8/2	1746.113	1745.940	99.807	0.309	423.752	0.292	14	0.188	-.HMDGFGVNTYTFVTR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1272.964	1273.287	-254.268	0.314	856.687	0.189	13	0.186	-.DEEVDYYPSR.-
R1/RRR1-11/2	1125.108	1125.303	-173.855	0.292	477.731	0.301	14	0.180	-.SPGAQTPVIVR.-
R1/RRR1-7/3	1982.714	1983.204	-247.979	0.507	1446.061	0.465	28	0.167	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-7/3	1951.118	1952.248	-1094.942	0.374	1459.728	0.474	31	0.163	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-7/3	1952.186	1952.248	-31.906	0.409	1389.403	0.496	30	0.163	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-7/2	1070.964	1071.168	-191.219	0.177	457.357	0.208	10	0.156	-.VFAYADTQR.-
R1/RRR1-7/2	1071.108	1071.168	-55.624	0.227	498.992	0.232	11	0.141	-.VFAYADTQR.-
R1/RRR1-8/3	1982.879	1983.204	-164.415	0.384	1373.620	0.427	30	0.139	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-5/3	1540.723	1540.785	-40.546	0.440	1042.622	0.518	25	0.129	R.GPILLEDYHLIEK.L
R1/RRR1-7/3	1952.128	1952.248	-61.636	0.422	985.066	0.505	27	0.127	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-6/3	1540.582	1540.785	-132.223	0.437	782.857	0.535	21	0.121	R.GPILLEDYHLIEK.L
R1/RRR1-7/3	1541.016	1540.785	150.266	0.459	824.516	0.509	23	0.116	R.GPILLEDYHLIEK.L
R1/RRR1-2/3	1540.633	1540.785	-99.198	0.455	994.813	0.472	25	0.116	R.GPILLEDYHLIEK.L
R1/RRR1-3/3	1540.814	1540.785	19.053	0.410	729.930	0.489	22	0.109	R.GPILLEDYHLIEK.L
R1/RRR1-1/3	1541.160	1540.785	244.036	0.470	693.870	0.480	22	0.108	R.GPILLEDYHLIEK.L
R1/RRR1-4/3	1541.013	1540.785	148.359	0.445	731.423	0.469	21	0.108	R.GPILLEDYHLIEK.L
R1/RRR1-3/3	1540.710	1540.785	-48.771	0.446	754.128	0.457	21	0.107	R.GPILLEDYHLIEK.L
R1/RRR1-5/3	1541.385	1540.785	-260.398	0.387	742.835	0.470	21	0.107	R.GPILLEDYHLIEK.L
R1/RRR1-8/3	1763.406	1761.939	265.694	0.469	947.516	0.452	26	0.107	R.HM*DGFGVNTYTFVTR.D
R1/RRR1-3/3	1952.930	1952.248	-163.300	0.401	858.924	0.431	25	0.106	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-7/3	1540.751	1540.785	-22.308	0.411	545.790	0.503	19	0.106	-.GPILLEDYHLIEK.-
R1/RRR1-6/3	1951.098	1952.248	-1105.402	0.361	641.562	0.504	24	0.106	-.DGIKFPDVIHAFKPNPR.-
R1/RRR1-5/3	1540.859	1540.785	48.016	0.436	1002.062	0.423	26	0.106	R.GPILLEDYHLIEK.L
R1/RRR1-3/3	1541.005	1540.785	143.473	0.411	929.491	0.417	23	0.104	R.GPILLEDYHLIEK.L
R1/RRR1-6/3	1126.462	1126.293	150.731	0.512	1021.763	0.426	21	0.104	R.RFAGELAHPK.V
R1/RRR1-5/3	1952.007	1952.248	-123.642	0.413	828.326	0.411	25	0.102	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-8/3	1982.571	1983.204	-826.346	0.383	1083.695	0.380	28	0.102	R.AIWVNYLSQCDESLGVK.I
R1/RRR1-4/3	1540.276	1540.785	-982.315	0.414	824.633	0.418	22	0.102	R.GPILLEDYHLIEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/3	1951.827	1952.248	-216.241	0.390	959.488	0.387	27	0.101	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-8/3	1126.288	1126.293	-3.992	0.525	1047.009	0.402	21	0.101	R.RFAGELAHPK.V
R1/RRR1-6/3	1539.786	1540.785	-1301.921	0.397	810.517	0.418	22	0.101	R.GPILLEDYHLIEK.L
R1/RRR1-7/3	1537.683	1538.777	-1365.848	0.388	979.293	0.425	26	0.098	K.FPDVIHAFKPNPR.S
R1/RRR1-2/3	1952.666	1952.248	214.710	0.368	855.658	0.388	26	0.097	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-1/3	1540.613	1540.785	-111.835	0.359	635.837	0.396	20	0.096	R.GPILLEDYHLIEK.L
R1/RRR1-7/3	1540.465	1540.785	-208.415	0.367	718.156	0.391	21	0.095	R.GPILLEDYHLIEK.L
R1/RRR1-2/3	1540.184	1540.785	-1042.472	0.301	443.951	0.356	17	0.095	R.GPILLEDYHLIEK.L
R1/RRR1-2/3	1540.600	1540.785	-120.181	0.380	743.656	0.375	21	0.094	R.GPILLEDYHLIEK.L
R1/RRR1-5/3	1952.185	1952.248	-32.282	0.330	624.912	0.414	23	0.094	-.DGIKFPDVIHAFKPNPR.-
R1/RRR1-7/3	1541.090	1540.785	198.642	0.399	842.376	0.362	23	0.093	R.GPILLEDYHLIEK.L
R1/RRR1-4/3	1539.788	1540.785	-1300.966	0.300	543.163	0.358	18	0.092	R.GPILLEDYHLIEK.L
R1/RRR1-1/3	1540.752	1540.785	-21.116	0.418	627.889	0.334	21	0.091	R.GPILLEDYHLIEK.L
R1/RRR1-6/3	1540.425	1540.785	-234.172	0.334	655.439	0.341	19	0.090	R.GPILLEDYHLIEK.L
R1/RRR1-5/3	1126.387	1126.293	83.891	0.490	1019.259	0.331	21	0.088	R.RFAGELAHPK.V
R1/RRR1-6/3	1950.954	1952.248	-1179.285	0.331	837.668	0.328	25	0.088	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-5/3	1952.254	1952.248	3.279	0.332	709.031	0.329	23	0.087	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-7/3	1542.780	1543.855	-1349.533	0.336	1257.866	0.250	26	0.085	R.LGPNYLM*LPVNAPK.C
R1/RRR1-9/3	1540.621	1540.785	-106.828	0.291	682.733	0.290	19	0.085	R.GPILLEDYHLIEK.L
R1/RRR1-1/3	1950.424	1952.248	-1966.262	0.304	694.744	0.312	23	0.085	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-6/3	1126.298	1126.293	4.650	0.413	679.033	0.300	18	0.083	R.RFAGELAHPK.V
R1/RRR1-8/3	1543.698	1543.855	-102.235	0.374	957.100	0.303	24	0.081	R.LGPNYLM*LPVNAPK.C
R1/RRR1-6/3	1126.706	1126.293	367.327	0.431	625.703	0.280	17	0.080	-.RFAGELAHPK.-
R1/RRR1-4/3	1951.955	1952.248	-150.272	0.308	659.503	0.243	23	0.080	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-7/3	1126.718	1126.293	378.407	0.464	1049.635	0.270	21	0.080	R.RFAGELAHPK.V
R1/RRR1-8/3	1951.632	1952.248	-830.600	0.261	641.955	0.244	21	0.079	R.DGIKFPDVIHAFKPNPR.S
R1/RRR1-3/3	1126.733	1126.293	392.094	0.470	1017.190	0.238	21	0.074	-.RFAGELAHPK.-
R1/RRR1-3/3	1126.183	1126.293	-98.088	0.444	892.996	0.225	20	0.070	-.RFAGELAHPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/3	1126.699	1126.293	361.624	0.424	901.628	0.155	20	0.065	-.RFAGELAHPK.-
R1/RRR1-4/3	1126.537	1126.293	217.072	0.431	873.110	0.129	19	0.061	-.RFAGELAHPK.-
R1/RRR1-1/2	1954.402	1954.172	117.988	0.609	3147.759	0.575	26	0.652	R.SPVYAQFSEALNGLSTIR.A
R1/RRR1-2/2	1954.749	1954.172	-217.258	0.612	3021.579	0.554	25	0.603	R.SPVYAQFSEALNGLSTIR.A
R1/RRR1-1/2	1953.510	1954.172	-853.360	0.533	2856.235	0.520	25	0.545	R.SPVYAQFSEALNGLSTIR.A
R1/RRR1-1/2	1955.036	1954.172	-70.180	0.586	2722.823	0.534	25	0.515	R.SPVYAQFSEALNGLSTIR.A
R1/RRR1-1/2	1485.652	1485.708	-37.878	0.508	2526.777	0.503	21	0.464	K.ILVLDEATAAVDVR.T
R1/RRR1-2/2	1953.985	1954.172	-96.221	0.552	2240.125	0.549	24	0.412	R.SPVYAQFSEALNGLSTIR.A
R1/RRR1-2/2	1953.205	1954.172	-1010.457	0.452	2362.245	0.459	24	0.405	R.SPVYAQFSEALNGLSTIR.A
R1/RRR1-1/2	1488.229	1487.641	-277.053	0.552	2257.042	0.490	22	0.396	R.LASLAENSLNAVER.V
R1/RRR1-2/2	1487.199	1487.641	-297.827	0.476	2140.684	0.484	20	0.372	R.LASLAENSLNAVER.V
R1/RRR1-2/2	1488.200	1487.641	-296.639	0.548	1866.254	0.477	21	0.323	R.LASLAENSLNAVER.V
R1/RRR1-1/2	1201.295	1201.352	-47.455	0.462	2037.629	0.336	17	0.313	R.LEDLLLAEER.L
R1/RRR1-1/2	1484.821	1485.708	-1274.451	0.366	1808.470	0.457	21	0.310	K.ILVLDEATAAVDVR.T
R1/RRR1-1/2	1487.219	1487.641	-283.992	0.504	1760.117	0.477	19	0.306	R.LASLAENSLNAVER.V
R1/RRR1-1/2	1486.859	1487.641	-1201.557	0.411	1757.109	0.449	20	0.299	R.LASLAENSLNAVER.V
R1/RRR1-1/2	1541.344	1541.708	-236.888	0.471	1613.881	0.467	21	0.289	K.M*VQSTGPSNAEYLK.T
R1/RRR1-2/2	1487.269	1487.641	-250.724	0.444	1670.830	0.426	20	0.282	R.LASLAENSLNAVER.V
R1/RRR1-2/2	1358.190	1357.538	-257.244	0.495	1359.089	0.456	17	0.256	K.RLEDLLLAEER.L
R1/RRR1-2/2	1356.968	1357.538	-1160.658	0.506	1395.948	0.417	18	0.252	K.RLEDLLLAEER.L
R1/RRR1-1/2	1401.177	1400.603	-304.752	0.392	1195.946	0.513	16	0.247	K.DAVITLQNVLEGK.H
R1/RRR1-1/2	1850.452	1851.007	-842.992	0.479	1060.523	0.544	23	0.244	R.HDLDLLPGGDLTEIGER.G
R1/RRR1-1/2	1642.336	1642.705	-224.963	0.426	1294.373	0.405	18	0.237	K.LDSWDETETLYNR.F
R1/RRR1-1/2	1642.219	1642.705	-296.404	0.449	905.028	0.481	15	0.218	K.LDSWDETETLYNR.F
R1/RRR1-1/2	1941.399	1941.343	28.877	0.478	345.708	0.602	20	0.215	R.LLLPNPPLDPELPAISIK.N
R1/RRR1-1/2	844.167	844.941	-2107.204	0.311	760.868	0.492	11	0.213	R.HANIFSR.I
R1/RRR1-2/2	1400.410	1400.603	-138.191	0.436	1018.204	0.394	16	0.212	K.DAVITLQNVLEGK.H
R1/RRR1-1/2	1503.414	1503.753	-226.318	0.425	791.040	0.452	18	0.211	R.APM*VFFHTNPLGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1941.294	1941.343	-25.077	0.410	309.463	0.593	19	0.209	R.LLLPNPPLDPELPAISIK.N
R1/RRR1-2/2	1754.952	1754.109	-89.971	0.445	476.735	0.516	20	0.209	K.VLGIIPQAPVLFSGSVR.F
R1/RRR1-1/2	844.409	844.941	-1819.798	0.353	833.393	0.383	12	0.208	R.HANIFSR.I
R1/RRR1-1/2	1940.768	1941.343	-813.856	0.361	407.428	0.576	18	0.206	R.LLLPNPPLDPELPAISIK.N
R1/RRR1-1/2	844.355	844.941	-1884.297	0.313	750.329	0.411	11	0.205	R.HANIFSR.I
R1/RRR1-2/2	1754.289	1754.109	102.971	0.414	447.016	0.478	20	0.205	K.VLGIIPQAPVLFSGSVR.F
R1/RRR1-1/2	1754.399	1754.109	165.914	0.386	498.432	0.479	20	0.204	K.VLGIIPQAPVLFSGSVR.F
R1/RRR1-2/2	1754.921	1754.109	-107.694	0.363	501.181	0.472	21	0.204	K.VLGIIPQAPVLFSGSVR.F
R1/RRR1-1/2	1489.239	1488.672	-291.417	0.360	760.060	0.419	16	0.202	R.DNILFGSPFQPPR.Y
R1/RRR1-2/2	1941.506	1941.343	83.961	0.393	324.636	0.514	18	0.201	R.LLLPNPPLDPELPAISIK.N
R1/RRR1-1/2	1753.773	1754.109	-192.029	0.372	505.793	0.445	20	0.201	K.VLGIIPQAPVLFSGSVR.F
R1/RRR1-1/2	1123.009	1123.198	-168.947	0.245	872.223	0.364	15	0.200	K.TLVFGDGEER.L
R1/RRR1-2/2	1940.716	1941.343	-840.943	0.311	361.001	0.505	19	0.198	R.LLLPNPPLDPELPAISIK.N
R1/RRR1-1/2	1753.680	1754.109	-245.379	0.386	461.997	0.412	19	0.198	K.VLGIIPQAPVLFSGSVR.F
R1/RRR1-1/2	1122.451	1123.198	-1560.887	0.230	764.323	0.367	14	0.195	K.TLVFGDGEER.L
R1/RRR1-2/2	1122.851	1123.198	-310.288	0.267	715.573	0.358	13	0.195	K.TLVFGDGEER.L
R1/RRR1-1/2	1123.046	1123.198	-135.581	0.249	716.900	0.356	14	0.195	K.TLVFGDGEER.L
R1/RRR1-2/2	1399.418	1400.603	-1565.793	0.330	745.361	0.333	14	0.191	K.DAVITLQNVLEGK.H
R1/RRR1-1/2	1488.206	1488.672	-313.997	0.267	640.430	0.319	14	0.186	R.DNILFGSPFQPPR.Y
R1/RRR1-2/3	1852.187	1851.007	97.455	0.417	1153.140	0.435	26	0.122	R.HDLDLLPGGDLTEIGER.G
R1/RRR1-1/3	1503.491	1503.753	-174.808	0.489	790.724	0.565	24	0.120	R.APM*VFFHTNPLGR.I
R1/RRR1-1/3	1942.157	1941.343	-96.058	0.424	974.483	0.481	28	0.116	R.LLLPNPPLDPELPAISIK.N
R1/RRR1-1/3	1755.593	1754.109	276.158	0.420	1010.104	0.434	25	0.110	-.VLGIIPQAPVLFSGSVR.-
R1/RRR1-1/3	1503.771	1503.753	11.717	0.430	756.252	0.495	23	0.105	R.APM*VFFHTNPLGR.I
R1/RRR1-2/3	1940.785	1941.343	-804.992	0.396	687.076	0.453	25	0.095	R.LLLPNPPLDPELPAISIK.N
R1/RRR1-1/3	1503.677	1503.753	-50.450	0.374	563.056	0.458	21	0.095	R.APM*VFFHTNPLGR.I
R1/RRR1-2/3	1503.458	1503.753	-196.677	0.410	789.213	0.407	22	0.093	R.APM*VFFHTNPLGR.I
R1/RRR1-2/3	1502.489	1503.753	-1511.223	0.369	576.120	0.410	21	0.090	R.APM*VFFHTNPLGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	1272.434	1272.478	-34.228	0.510	1043.851	0.325	19	0.089	K.RPITDKDIWK.L
R1/RRR1-2/3	1754.055	1754.109	-30.763	0.351	665.351	0.427	26	0.087	K.VLGIIPQAPVLFSGSVR.F
R1/RRR1-1/3	1852.106	1851.007	53.433	0.390	534.522	0.449	23	0.087	-.HDLDLLPGGDLTEIGER.-
R1/RRR1-2/3	1502.819	1503.753	-1291.042	0.351	824.451	0.238	22	0.074	R.APM*VFFHTNPLGR.I
R1/RRR1-1/3	1271.527	1272.478	-1539.039	0.420	840.555	0.253	19	0.074	K.RPITDKDIWK.L
R1/RRR1-6/2	1414.202	1413.562	-254.847	0.480	2226.660	0.612	21	0.440	K.SSVHDVVLVGGSTR.I
R1/RRR1-6/2	1414.259	1413.562	-214.667	0.477	2125.012	0.585	21	0.408	K.SSVHDVVLVGGSTR.I
R1/RRR1-6/2	1437.679	1437.625	37.590	0.557	2117.533	0.506	18	0.373	R.VQQLLQDFFNGK.E
R1/RRR1-6/2	1437.057	1437.625	-1094.184	0.565	2078.226	0.504	18	0.365	R.VQQLLQDFFNGK.E
R1/RRR1-6/2	1437.377	1437.625	-172.542	0.567	2072.483	0.475	18	0.354	R.VQQLLQDFFNGK.E
R1/RRR1-5/2	1676.085	1676.683	-955.892	0.472	1875.645	0.546	23	0.346	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/2	1676.278	1676.683	-241.955	0.474	1816.164	0.570	23	0.344	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/2	1676.304	1676.683	-226.613	0.494	1819.736	0.564	23	0.343	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/2	1308.972	1309.490	-1162.995	0.340	1875.444	0.515	19	0.336	R.EIAEAYLGTTIK.N
R1/RRR1-6/2	1437.289	1437.625	-234.057	0.534	2023.884	0.441	18	0.335	R.VQQLLQDFFNGK.E
R1/RRR1-6/2	1309.440	1309.490	-38.674	0.439	1853.893	0.511	19	0.335	R.EIAEAYLGTTIK.N
R1/RRR1-6/2	1967.615	1968.236	-826.211	0.553	1844.138	0.510	22	0.331	R.VQQLLQDFFNGKELCK.S
R1/RRR1-6/2	1232.175	1232.436	-211.941	0.532	1961.416	0.441	21	0.329	K.DAGVIAGLNVM*R.I
R1/RRR1-6/2	1413.369	1413.562	-136.838	0.485	1726.150	0.558	21	0.329	K.SSVHDVVLVGGSTR.I
R1/RRR1-6/2	1438.207	1437.625	-291.542	0.554	1798.317	0.520	18	0.326	R.VQQLLQDFFNGK.E
R1/RRR1-6/2	1676.184	1676.683	-298.286	0.466	1733.645	0.523	23	0.317	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/2	1231.456	1232.436	-1612.455	0.482	1679.440	0.469	19	0.296	K.DAGVIAGLNVM*R.I
R1/RRR1-6/2	1216.184	1216.436	-208.152	0.464	1663.901	0.453	20	0.291	K.DAGVIAGLNVMR.I
R1/RRR1-6/2	1215.666	1216.436	-1460.740	0.417	1715.072	0.430	19	0.290	K.DAGVIAGLNVMR.I
R1/RRR1-6/2	1233.066	1232.436	-300.558	0.524	1601.058	0.439	19	0.278	K.DAGVIAGLNVM*R.I
R1/RRR1-10/2	1437.031	1437.625	-1112.096	0.574	1576.286	0.467	17	0.278	R.VQQLLQDFFNGK.E
R1/RRR1-6/2	1375.120	1375.492	-271.281	0.411	1446.076	0.480	16	0.269	K.NALENYAYNM*R.N
R1/RRR1-6/2	1375.953	1375.492	335.659	0.514	1311.097	0.508	16	0.262	K.NALENYAYNM*R.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1676.318	1676.683	-218.212	0.502	1366.516	0.490	21	0.260	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/2	1443.641	1442.665	-16.420	0.486	1379.118	0.413	17	0.249	R.FEELNMDLFRK.C
R1/RRR1-6/2	1197.234	1197.277	-36.162	0.518	1196.246	0.483	17	0.248	R.FSDASVQSDIK.L
R1/RRR1-6/2	1375.088	1375.492	-295.150	0.450	1240.931	0.460	16	0.245	K.NALENYAYNM*R.N
R1/RRR1-6/2	1438.376	1437.625	-173.444	0.518	1231.068	0.478	15	0.244	-.VQQLLQDFFNGK.-
R1/RRR1-6/3	1557.824	1557.756	44.028	0.536	2266.069	0.314	26	0.242	R.ARFEELNM*DLFR.K
R1/RRR1-6/2	1309.124	1309.490	-280.634	0.281	1334.893	0.411	17	0.238	R.EIAEAYLGTTIK.N
R1/RRR1-6/2	1359.077	1359.493	-306.624	0.422	1261.234	0.411	16	0.236	K.NALENYAYNMR.N
R1/RRR1-10/2	1437.304	1437.625	-223.747	0.360	1162.096	0.438	17	0.232	R.VQQLLQDFFNGK.E
R1/RRR1-6/2	1967.611	1968.236	-827.954	0.533	1045.529	0.482	17	0.225	R.VQQLLQDFFNGKELCK.S
R1/RRR1-6/2	1567.331	1566.844	311.799	0.579	1075.064	0.419	22	0.224	K.QFAAEEISSMVLIK.M
R1/RRR1-6/2	1566.804	1566.844	-25.523	0.518	1116.562	0.391	22	0.223	K.QFAAEEISSMVLIK.M
R1/RRR1-6/2	1567.097	1566.844	161.524	0.545	1016.380	0.422	21	0.221	K.QFAAEEISSMVLIK.M
R1/RRR1-14/2	1676.162	1676.683	-910.268	0.372	1022.083	0.448	19	0.221	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/2	1540.938	1541.757	-1183.463	0.468	1006.989	0.416	18	0.220	R.ARFEELNMDLFR.K
R1/RRR1-6/2	1541.410	1541.757	-225.793	0.433	992.741	0.402	18	0.217	R.ARFEELNMDLFR.K
R1/RRR1-1/2	1438.298	1437.625	-227.934	0.463	845.478	0.470	15	0.216	-.VQQLLQDFFNGK.-
R1/RRR1-6/2	1682.205	1681.830	223.400	0.385	593.523	0.488	20	0.209	K.NAVVTVPAYFNDSQR.Q
R1/RRR1-6/2	1869.281	1869.109	92.445	0.484	738.173	0.474	18	0.209	R.FSDASVQSDIKLWPFK.V
R1/RRR1-6/2	1294.599	1295.492	-1466.831	0.437	604.994	0.432	14	0.206	R.M*VNHFVQEFK.R
R1/RRR1-6/2	1294.499	1295.492	-1543.838	0.391	733.711	0.394	15	0.205	R.M*VNHFVQEFK.R
R1/RRR1-2/2	1197.588	1197.277	260.741	0.274	667.948	0.423	16	0.203	R.FSDASVQSDIK.L
R1/RRR1-10/2	1197.922	1197.277	-297.282	0.297	512.346	0.477	13	0.202	R.FSDASVQSDIK.L
R1/RRR1-6/2	1556.711	1557.756	-1317.337	0.406	420.550	0.392	16	0.201	R.ARFEELNM*DLFR.K
R1/RRR1-4/2	1197.601	1197.277	271.984	0.311	449.801	0.384	14	0.199	R.FSDASVQSDIK.L
R1/RRR1-5/2	1197.182	1197.277	-79.424	0.289	624.918	0.386	14	0.199	R.FSDASVQSDIK.L
R1/RRR1-6/2	1295.065	1295.492	-330.678	0.420	530.750	0.357	14	0.198	R.M*VNHFVQEFK.R
R1/RRR1-14/2	1681.233	1681.830	-952.965	0.307	409.516	0.444	17	0.196	K.NAVVTVPAYFNDSQR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1197.740	1197.277	387.874	0.253	329.521	0.395	12	0.195	R.FSDASVQSDIK.L
R1/RRR1-6/2	1681.205	1681.830	-969.622	0.284	559.174	0.379	20	0.195	K.NAVVTVPAYFNDSQR.Q
R1/RRR1-2/2	1681.351	1681.830	-286.301	0.361	367.180	0.359	17	0.194	K.NAVVTVPAYFNDSQR.Q
R1/RRR1-6/2	1868.675	1869.109	-233.031	0.417	461.814	0.426	15	0.193	R.FSDASVQSDIKLWPFK.V
R1/RRR1-6/2	1868.399	1869.109	-918.052	0.387	451.244	0.396	16	0.192	R.FSDASVQSDIKLWPFK.V
R1/RRR1-5/2	1197.890	1197.277	-324.069	0.218	289.487	0.333	12	0.191	-.FSDASVQSDIK.-
R1/RRR1-5/2	1566.784	1566.844	-38.339	0.367	444.958	0.262	17	0.191	K.QFAAEEISSMVLIK.M
R1/RRR1-6/2	1540.454	1541.757	-1499.375	0.348	802.153	0.271	15	0.190	R.ARFEELNMDLFR.K
R1/RRR1-3/2	1197.841	1197.277	-365.274	0.209	300.651	0.372	12	0.187	-.FSDASVQSDIK.-
R1/RRR1-6/2	1582.170	1582.844	-1060.908	0.388	694.640	0.213	18	0.185	K.QFAAEEISSM*VLIK.M
R1/RRR1-6/3	1557.609	1557.756	-94.744	0.540	1836.064	0.374	25	0.185	R.ARFEELNM*DLFR.K
R1/RRR1-6/3	1557.344	1557.756	-265.520	0.503	1939.778	0.281	24	0.172	R.ARFEELNM*DLFR.K
R1/RRR1-3/2	1197.919	1197.277	-299.224	0.232	230.402	0.365	11	0.165	-.FSDASVQSDIK.-
R1/RRR1-6/3	1677.638	1676.683	-26.691	0.458	779.693	0.597	30	0.125	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/3	1677.674	1676.683	-5.453	0.453	698.094	0.603	29	0.123	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/3	1676.112	1676.683	-939.887	0.384	528.182	0.580	25	0.112	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-13/3	1678.030	1676.683	207.531	0.448	391.231	0.554	23	0.111	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/3	1868.533	1869.109	-846.211	0.453	743.798	0.527	27	0.110	R.FSDASVQSDIKLWPFK.V
R1/RRR1-14/3	1676.572	1676.683	-66.435	0.426	562.373	0.536	26	0.108	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-15/3	1675.704	1676.683	-1184.192	0.353	423.437	0.493	22	0.101	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-13/3	1676.586	1676.683	-57.781	0.370	551.493	0.446	24	0.096	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-7/3	1676.652	1676.683	-18.345	0.321	428.012	0.386	22	0.091	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/3	1868.457	1869.109	-886.643	0.394	608.848	0.440	25	0.091	R.FSDASVQSDIKLWPFK.V
R1/RRR1-8/3	1675.876	1676.683	-1081.387	0.320	741.736	0.318	24	0.083	K.ATAGDTHLGGEDFDNR.M
R1/RRR1-6/3	1869.436	1869.109	175.345	0.289	496.742	0.360	21	0.080	R.FSDASVQSDIKLWPFK.V
R1/RRR1-21/2	1930.486	1931.131	-854.532	0.626	3654.198	0.691	30	0.896	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1930.544	1931.131	-824.255	0.621	3349.176	0.676	29	0.778	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1913.207	1914.037	-959.543	0.584	3465.478	0.612	27	0.777	K.M*NVEYELEDGGSLSPEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1913.359	1914.037	-879.670	0.606	3435.885	0.608	27	0.764	K.M*NVEYELEDGGSLSPEK.E
R1/RRR1-21/2	1930.572	1931.131	-809.656	0.637	3099.003	0.696	29	0.707	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1914.408	1914.037	194.109	0.648	3047.659	0.613	27	0.642	K.M*NVEYELEDGGSLSPEK.E
R1/RRR1-21/3	1932.086	1931.131	-23.144	0.557	2893.115	0.657	40	0.626	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-22/2	1930.609	1931.131	-790.298	0.609	2819.564	0.677	28	0.614	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1898.335	1898.038	156.688	0.633	2905.838	0.559	26	0.574	K.MNVEYELEDGGSLSPEK.E
R1/RRR1-21/3	1931.275	1931.131	74.826	0.527	2707.785	0.662	37	0.569	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1897.430	1898.038	-849.867	0.596	2707.468	0.532	25	0.510	K.MNVEYELEDGGSLSPEK.E
R1/RRR1-21/2	1898.127	1898.038	46.855	0.620	2614.773	0.579	25	0.508	K.MNVEYELEDGGSLSPEK.E
R1/RRR1-22/3	1931.044	1931.131	-45.190	0.552	2591.476	0.624	38	0.502	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1339.070	1339.455	-288.071	0.508	2223.653	0.607	23	0.433	K.VEGDGGAGTVTTM*K.L
R1/RRR1-21/2	1339.051	1339.455	-302.247	0.512	2254.444	0.567	23	0.423	K.VEGDGGAGTVTTM*K.L
R1/RRR1-22/2	1668.485	1668.849	-218.902	0.537	1928.721	0.614	21	0.412	K.M*IEDYLVAHPTEYA.-
R1/RRR1-21/2	1668.459	1668.849	-234.462	0.477	1950.027	0.562	21	0.409	K.M*IEDYLVAHPTEYA.-
R1/RRR1-21/3	1951.251	1951.170	41.713	0.561	2460.314	0.515	35	0.407	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-22/3	1931.906	1931.131	-116.689	0.537	2135.040	0.683	35	0.402	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1652.459	1652.849	-236.626	0.485	1854.912	0.644	20	0.394	K.MIEDYLVAHPTEYA.-
R1/RRR1-22/2	1669.254	1668.849	243.805	0.577	1844.942	0.645	21	0.384	K.M*IEDYLVAHPTEYA.-
R1/RRR1-21/3	1950.580	1951.170	-817.835	0.520	2389.760	0.518	36	0.384	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-21/2	1652.470	1652.849	-229.956	0.488	1865.195	0.598	21	0.383	K.MIEDYLVAHPTEYA.-
R1/RRR1-20/3	1951.017	1951.170	-78.866	0.473	2487.130	0.465	36	0.381	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-22/2	1339.000	1339.455	-341.029	0.511	2020.880	0.574	22	0.381	K.VEGDGGAGTVTTM*K.L
R1/RRR1-21/2	1669.439	1668.849	-246.279	0.574	1843.867	0.625	21	0.377	K.M*IEDYLVAHPTEYA.-
R1/RRR1-20/2	1669.474	1668.849	-225.373	0.580	1800.033	0.652	21	0.368	K.M*IEDYLVAHPTEYA.-
R1/RRR1-21/1	1219.688	1220.313	-1336.706	0.235	780.749	0.348	15	0.368	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1668.299	1668.849	-931.690	0.489	1846.283	0.566	20	0.367	K.M*IEDYLVAHPTEYA.-
R1/RRR1-22/2	1670.193	1668.849	207.015	0.609	1812.922	0.634	21	0.365	K.M*IEDYLVAHPTEYA.-
R1/RRR1-21/2	1652.177	1652.849	-1015.152	0.419	1800.179	0.615	21	0.364	K.MIEDYLVAHPTEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/3	1930.598	1931.131	-796.176	0.551	2059.327	0.633	36	0.352	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-20/3	1951.011	1951.170	-82.067	0.556	2280.335	0.497	34	0.348	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-21/2	1323.056	1323.456	-302.757	0.429	1764.299	0.597	22	0.343	K.VEGDGGAGTVTTMK.L
R1/RRR1-21/2	1323.079	1323.456	-285.262	0.473	1649.627	0.614	22	0.332	K.VEGDGGAGTVTTMK.L
R1/RRR1-22/2	1338.860	1339.455	-1194.826	0.514	1748.227	0.559	21	0.330	K.VEGDGGAGTVTTM*K.L
R1/RRR1-21/2	1339.100	1339.455	-265.572	0.491	1686.568	0.587	20	0.328	K.VEGDGGAGTVTTM*K.L
R1/RRR1-21/2	1323.034	1323.456	-319.235	0.479	1688.040	0.577	22	0.327	K.VEGDGGAGTVTTMK.L
R1/RRR1-20/2	1669.323	1668.849	285.235	0.554	1676.456	0.604	20	0.309	K.M*IEDYLVAHPTEYA.-
R1/RRR1-21/1	1219.575	1220.313	-1429.593	0.157	745.868	0.190	15	0.308	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1950.643	1951.170	-785.257	0.561	1555.585	0.575	23	0.304	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-22/2	1339.102	1339.455	-264.383	0.489	1514.144	0.563	21	0.299	K.VEGDGGAGTVTTM*K.L
R1/RRR1-21/2	1950.500	1951.170	-858.632	0.571	1337.703	0.615	21	0.285	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-21/2	1950.489	1951.170	-864.600	0.550	1367.186	0.597	21	0.284	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-22/2	1148.037	1148.285	-216.988	0.467	1362.681	0.512	19	0.269	K.IEAAGAGSCLAK.M
R1/RRR1-21/1	1219.643	1220.313	-1374.100	0.207	648.042	0.290	14	0.263	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1147.863	1148.285	-368.912	0.442	1428.886	0.450	19	0.261	K.IEAAGAGSCLAK.M
R1/RRR1-20/3	1931.758	1931.131	-193.421	0.488	1674.896	0.618	33	0.260	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-20/3	1951.232	1951.170	31.925	0.521	1957.138	0.468	32	0.259	R.DNAAHVIKSEVLDVPAGSK.V
R1/RRR1-20/2	1668.122	1668.849	-1038.510	0.470	1550.028	0.519	18	0.252	K.M*IEDYLVAHPTEYA.-
R1/RRR1-22/2	1287.255	1286.565	-241.030	0.543	1138.069	0.499	18	0.248	K.LILDGYFGM*LK.M
R1/RRR1-20/2	1148.117	1148.285	-147.337	0.452	1229.588	0.458	18	0.244	K.IEAAGAGSCLAK.M
R1/RRR1-22/2	1147.904	1148.285	-332.847	0.469	1110.044	0.497	18	0.243	K.IEAAGAGSCLAK.M
R1/RRR1-22/2	1148.024	1148.285	-228.296	0.488	1145.667	0.483	18	0.243	K.IEAAGAGSCLAK.M
R1/RRR1-21/2	1148.007	1148.285	-243.444	0.461	1148.859	0.481	18	0.243	K.IEAAGAGSCLAK.M
R1/RRR1-21/2	1147.583	1148.285	-1487.868	0.438	1182.951	0.452	18	0.239	K.IEAAGAGSCLAK.M
R1/RRR1-21/2	1270.219	1270.565	-273.325	0.498	906.588	0.528	18	0.239	K.LILDGYFGMLK.M
R1/RRR1-20/2	1286.167	1286.565	-310.156	0.465	1071.974	0.470	18	0.238	K.LILDGYFGM*LK.M
R1/RRR1-20/2	1147.976	1148.285	-270.540	0.434	1139.560	0.456	18	0.237	K.IEAAGAGSCLAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1286.121	1286.565	-345.866	0.468	1166.879	0.425	18	0.236	K.LILDGYFGM*LK.M
R1/RRR1-22/2	1286.336	1286.565	-178.002	0.497	1112.554	0.442	18	0.235	K.LILDGYFGM*LK.M
R1/RRR1-21/2	1286.292	1286.565	-212.560	0.472	1086.865	0.442	18	0.234	K.LILDGYFGM*LK.M
R1/RRR1-21/2	1270.091	1270.565	-374.765	0.454	890.735	0.497	18	0.232	K.LILDGYFGMLK.M
R1/RRR1-22/2	1286.170	1286.565	-307.680	0.418	1004.617	0.465	17	0.231	K.LILDGYFGM*LK.M
R1/RRR1-21/2	1271.039	1270.565	373.790	0.507	893.265	0.479	18	0.230	K.LILDGYFGMLK.M
R1/RRR1-25/2	1339.356	1339.455	-74.465	0.478	823.767	0.541	18	0.229	K.VEGDGGAGTVTTM*K.L
R1/RRR1-20/2	1285.877	1286.565	-1316.758	0.409	1106.581	0.407	18	0.228	K.LILDGYFGM*LK.M
R1/RRR1-21/2	1270.080	1270.565	-383.251	0.473	862.248	0.470	18	0.227	K.LILDGYFGMLK.M
R1/RRR1-21/2	1270.039	1270.565	-1205.202	0.453	917.558	0.453	18	0.227	K.LILDGYFGMLK.M
R1/RRR1-20/2	1148.046	1148.285	-209.095	0.442	1017.516	0.447	17	0.226	K.IEAAGAGSCLAK.M
R1/RRR1-20/2	1285.969	1286.565	-1244.304	0.401	975.913	0.440	17	0.225	K.LILDGYFGM*LK.M
R1/RRR1-21/2	1147.476	1148.285	-1581.476	0.411	1050.958	0.417	17	0.223	K.IEAAGAGSCLAK.M
R1/RRR1-21/2	1285.966	1286.565	-1247.354	0.419	1123.432	0.362	18	0.222	K.LILDGYFGM*LK.M
R1/RRR1-19/2	1147.269	1148.285	-1762.652	0.318	1094.448	0.397	17	0.220	K.IEAAGAGSCLAK.M
R1/RRR1-21/2	1063.825	1063.252	-402.658	0.386	720.147	0.482	15	0.218	K.VFSDAPAMPK.V
R1/RRR1-21/2	1269.971	1270.565	-1258.870	0.431	880.701	0.402	18	0.217	K.LILDGYFGMLK.M
R1/RRR1-20/2	1101.503	1102.220	-1563.227	0.313	1135.710	0.345	16	0.215	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1093.523	1094.279	-1611.248	0.306	1146.704	0.345	16	0.215	K.VCAGFIDAIK.V
R1/RRR1-22/2	1079.924	1079.252	-303.909	0.382	725.561	0.453	15	0.215	K.VFSDAPAM*PK.V
R1/RRR1-21/2	1269.667	1270.565	-1499.287	0.385	883.041	0.376	18	0.213	K.LILDGYFGMLK.M
R1/RRR1-22/2	1078.834	1079.252	-388.539	0.321	635.396	0.475	14	0.210	K.VFSDAPAM*PK.V
R1/RRR1-21/2	1078.911	1079.252	-316.451	0.363	644.734	0.435	14	0.209	K.VFSDAPAM*PK.V
R1/RRR1-21/2	1220.887	1220.313	-350.758	0.332	663.210	0.443	17	0.208	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1062.815	1063.252	-412.487	0.303	744.828	0.422	15	0.208	K.VFSDAPAMPK.V
R1/RRR1-22/2	1078.979	1079.252	-253.112	0.392	749.773	0.382	15	0.208	K.VFSDAPAM*PK.V
R1/RRR1-20/2	1102.030	1102.220	-173.163	0.427	1120.218	0.296	16	0.208	K.SEVLDVPAGSK.V
R1/RRR1-21/3	1951.061	1951.170	-56.367	0.507	1656.045	0.487	32	0.207	R.DNAAHVIKSEVLDVPAGSK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1219.924	1220.313	-319.821	0.325	680.471	0.421	17	0.207	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1102.049	1102.220	-155.273	0.412	983.300	0.326	15	0.205	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1062.772	1063.252	-453.286	0.288	734.206	0.403	15	0.205	K.VFSDAPAMPK.V
R1/RRR1-21/2	1094.926	1094.279	-323.345	0.492	1136.281	0.272	16	0.204	K.VCAGFIDAIK.V
R1/RRR1-20/2	1101.974	1102.220	-224.170	0.375	1121.124	0.260	16	0.203	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1285.718	1286.565	-1440.336	0.355	619.903	0.372	14	0.203	K.LILDGYFGM*LK.M
R1/RRR1-21/2	1101.949	1102.220	-247.174	0.398	947.433	0.310	15	0.202	K.SEVLDVPAGSK.V
R1/RRR1-20/2	1078.839	1079.252	-383.544	0.382	686.730	0.347	14	0.202	K.VFSDAPAM*PK.V
R1/RRR1-25/2	1101.844	1102.220	-342.427	0.298	901.376	0.335	14	0.201	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1286.103	1286.565	-359.865	0.364	670.474	0.311	16	0.201	K.LILDGYFGM*LK.M
R1/RRR1-22/2	1219.966	1220.313	-285.286	0.264	827.166	0.340	18	0.200	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1093.524	1094.279	-1610.351	0.300	1131.496	0.245	16	0.200	K.VCAGFIDAIK.V
R1/RRR1-22/2	1269.841	1270.565	-1362.360	0.337	373.023	0.312	13	0.200	K.LILDGYFGMLK.M
R1/RRR1-22/2	1101.989	1102.220	-209.945	0.363	817.487	0.337	14	0.200	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1285.553	1286.565	-1569.953	0.311	797.252	0.304	16	0.200	K.LILDGYFGM*LK.M
R1/RRR1-22/2	1101.537	1102.220	-1532.724	0.308	1184.185	0.215	16	0.200	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1543.672	1543.852	-117.222	0.462	790.557	0.354	18	0.199	K.EKLILDGYFGM*LK.M
R1/RRR1-20/2	1220.920	1220.313	-323.471	0.281	695.806	0.346	17	0.199	K.LNPAVDDGGSFK.T
R1/RRR1-22/2	1101.904	1102.220	-287.519	0.375	854.885	0.318	14	0.199	-.SEVLDVPAGSK.-
R1/RRR1-20/2	1078.976	1079.252	-255.723	0.288	615.347	0.346	14	0.199	K.VFSDAPAM*PK.V
R1/RRR1-21/2	1101.883	1102.220	-307.081	0.385	911.734	0.286	15	0.198	K.SEVLDVPAGSK.V
R1/RRR1-22/2	1220.119	1220.313	-159.715	0.267	551.642	0.389	15	0.198	K.LNPAVDDGGSFK.T
R1/RRR1-20/3	1931.082	1931.131	-25.312	0.507	1260.706	0.626	29	0.197	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1219.972	1220.313	-280.467	0.294	436.457	0.364	14	0.197	K.LNPAVDDGGSFK.T
R1/RRR1-21/1	1101.583	1102.220	-1490.579	0.298	479.829	0.425	13	0.197	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1543.351	1543.852	-975.455	0.503	727.731	0.342	18	0.196	K.EKLILDGYFGM*LK.M
R1/RRR1-16/2	1220.288	1220.313	-20.931	0.307	364.984	0.321	12	0.194	K.LNPAVDDGGSFK.T
R1/RRR1-22/2	1063.095	1063.252	-148.179	0.299	521.958	0.239	13	0.194	K.VFSDAPAMPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1079.012	1079.252	-222.694	0.301	543.519	0.246	13	0.193	K.VFSDAPAM*PK.V
R1/RRR1-20/2	1219.876	1220.313	-360.081	0.241	602.798	0.304	16	0.193	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1220.004	1220.313	-254.467	0.212	581.906	0.334	16	0.193	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1219.882	1220.313	-354.358	0.222	524.115	0.320	15	0.192	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1285.552	1286.565	-1570.335	0.221	564.465	0.249	13	0.190	-.LILDGYFGM*LK.-
R1/RRR1-21/2	1078.869	1079.252	-355.956	0.262	502.788	0.235	12	0.190	-.VFSDAPAM*PK.-
R1/RRR1-21/2	1220.344	1220.313	25.422	0.190	451.358	0.290	14	0.190	K.LNPAVDDGGSFK.T
R1/RRR1-21/2	1219.937	1220.313	-309.681	0.190	557.909	0.267	15	0.189	K.LNPAVDDGGSFK.T
R1/RRR1-2/2	1340.052	1339.455	-301.291	0.324	322.277	0.399	11	0.187	-.VEGDGGAGTVTTM*K.-
R1/RRR1-21/1	1101.563	1102.220	-1508.611	0.266	477.156	0.382	13	0.186	K.SEVLDVPAGSK.V
R1/RRR1-22/3	1930.199	1931.131	-1003.954	0.426	1519.643	0.494	32	0.184	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-21/2	1667.915	1668.849	-1162.843	0.413	1238.391	0.534	19	0.182	K.M*IEDYLVAHPTEYA.-
R1/RRR1-22/2	1094.221	1094.279	-53.218	0.181	923.905	0.081	14	0.178	K.VCAGFIDAIK.V
R1/RRR1-18/2	1147.952	1148.285	-291.344	0.287	505.941	0.247	13	0.171	-.IEAAGAGSCLAK.-
R1/RRR1-21/1	1101.614	1102.220	-1462.752	0.239	436.714	0.365	12	0.169	K.SEVLDVPAGSK.V
R1/RRR1-21/2	1102.424	1102.220	185.738	0.284	521.683	0.302	10	0.163	-.SEVLDVPAGSK.-
R1/RRR1-18/2	1101.471	1102.220	-1592.284	0.238	531.672	0.215	11	0.160	-.SEVLDVPAGSK.-
R1/RRR1-21/2	1339.209	1339.455	-184.183	0.191	94.344	0.505	13	0.156	-.VEGDGGAGTVTTM*K.-
R1/RRR1-22/2	1651.774	1652.849	-1260.306	0.136	1034.172	0.143	17	0.122	K.MIEDYLVAHPTEYA.-
R1/RRR1-21/2	1669.070	1668.849	132.918	0.305	525.206	0.317	15	0.120	K.M*IEDYLVAHPTEYA.-
R1/RRR1-1/2	1667.442	1668.849	-1447.632	0.280	689.715	0.180	16	0.103	K.M*IEDYLVAHPTEYA.-
R1/RRR1-20/3	1930.346	1931.131	-927.479	0.315	738.918	0.386	23	0.092	K.SHVTETKIEAAGAGSCLAK.M
R1/RRR1-10/3	1451.091	1450.816	190.079	0.539	2930.348	0.411	29	0.464	K.FLKPAVAGFLMQK.E
R1/RRR1-11/3	1466.261	1466.816	-1063.600	0.533	2781.636	0.440	30	0.429	K.FLKPAVAGFLM*QK.E
R1/RRR1-11/2	1546.229	1546.705	-308.311	0.485	2193.159	0.541	24	0.402	K.GATTIIGGGDSVAAVEK.A
R1/RRR1-11/3	1450.795	1450.816	-15.083	0.527	2713.749	0.408	30	0.390	K.FLKPAVAGFLMQK.E
R1/RRR1-11/2	1546.252	1546.705	-293.896	0.498	2160.806	0.525	24	0.390	K.GATTIIGGGDSVAAVEK.A
R1/RRR1-10/2	1546.308	1546.705	-257.066	0.471	2132.099	0.522	24	0.383	K.GATTIIGGGDSVAAVEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1546.123	1546.705	-1025.788	0.453	2221.315	0.459	24	0.378	K.GATTIIGGGDSVAAVEK.A
R1/RRR1-11/2	1546.383	1546.705	-208.519	0.477	2105.510	0.496	24	0.369	K.GATTIIGGGDSVAAVEK.A
R1/RRR1-11/3	1450.801	1450.816	-10.525	0.560	2696.828	0.370	30	0.364	K.FLKPAVAGFLMQK.E
R1/RRR1-10/2	1546.186	1546.705	-985.283	0.489	1995.078	0.522	24	0.358	K.GATTIIGGGDSVAAVEK.A
R1/RRR1-10/3	1466.633	1466.816	-125.250	0.544	2430.808	0.472	28	0.352	K.FLKPAVAGFLM*QK.E
R1/RRR1-10/3	1735.849	1736.049	-115.445	0.569	2474.482	0.416	34	0.348	K.LAAALPEGGVLLLENVR.F
R1/RRR1-11/3	1466.461	1466.816	-242.862	0.557	2254.292	0.512	28	0.326	K.FLKPAVAGFLM*QK.E
R1/RRR1-11/3	1451.428	1450.816	-268.566	0.590	2490.488	0.375	29	0.315	K.FLKPAVAGFLMQK.E
R1/RRR1-11/3	1466.714	1466.816	-69.898	0.539	2198.620	0.477	27	0.298	K.FLKPAVAGFLM*QK.E
R1/RRR1-11/3	1735.776	1736.049	-157.560	0.512	2263.252	0.374	31	0.280	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/2	1735.417	1736.049	-943.248	0.562	1354.098	0.536	27	0.274	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/2	1735.341	1736.049	-987.457	0.550	1317.306	0.535	27	0.270	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/3	1450.624	1450.816	-132.826	0.519	2252.747	0.390	27	0.270	K.FLKPAVAGFLMQK.E
R1/RRR1-11/3	1736.024	1736.049	-14.297	0.551	2255.702	0.349	32	0.265	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/2	1735.459	1736.049	-919.168	0.534	1263.463	0.534	27	0.265	K.LAAALPEGGVLLLENVR.F
R1/RRR1-11/2	1736.555	1736.049	-285.308	0.580	1180.499	0.543	26	0.258	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/3	1466.350	1466.816	-318.279	0.530	2105.353	0.422	26	0.255	K.FLKPAVAGFLM*QK.E
R1/RRR1-10/3	1736.290	1736.049	138.972	0.561	2022.095	0.416	32	0.244	K.LAAALPEGGVLLLENVR.F
R1/RRR1-11/2	1735.870	1736.049	-103.656	0.548	1094.787	0.507	25	0.243	K.LAAALPEGGVLLLENVR.F
R1/RRR1-11/2	1736.533	1736.049	279.796	0.571	977.332	0.506	24	0.233	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/3	1467.790	1466.816	-17.587	0.554	1923.786	0.433	25	0.226	K.FLKPAVAGFLM*QK.E
R1/RRR1-3/2	1736.206	1736.049	90.575	0.475	726.649	0.559	21	0.225	K.LAAALPEGGVLLLENVR.F
R1/RRR1-2/2	1737.683	1736.049	-211.211	0.529	672.846	0.549	21	0.222	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/3	1736.186	1736.049	79.426	0.551	2052.740	0.342	32	0.219	K.LAAALPEGGVLLLENVR.F
R1/RRR1-2/2	1735.058	1736.049	-1150.908	0.437	810.844	0.485	21	0.218	K.LAAALPEGGVLLLENVR.F
R1/RRR1-11/3	1736.685	1736.049	-209.965	0.549	1958.947	0.364	31	0.212	K.LAAALPEGGVLLLENVR.F
R1/RRR1-11/2	1466.489	1466.816	-223.228	0.521	559.293	0.436	19	0.207	K.FLKPAVAGFLM*QK.E
R1/RRR1-10/2	1736.905	1736.049	-83.223	0.391	635.935	0.440	19	0.204	K.LAAALPEGGVLLLENVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1466.215	1466.816	-1095.064	0.472	447.021	0.433	17	0.203	K.FLKPAVAGFLM*QK.E
R1/RRR1-10/2	1466.178	1466.816	-1120.227	0.425	431.928	0.359	17	0.197	K.FLKPAVAGFLM*QK.E
R1/RRR1-9/2	1734.532	1736.049	-2033.602	0.224	350.218	0.334	14	0.187	K.LAAALPEGGVLLLENVR.F
R1/RRR1-10/3	1450.345	1450.816	-325.960	0.483	1550.622	0.357	24	0.141	K.FLKPAVAGFLMQK.E
R1/RRR1-7/2	1779.528	1779.974	-251.447	0.584	2412.291	0.580	26	0.464	K.SVGPVVDGDAVVTFNFR.A
R1/RRR1-7/2	1779.555	1779.974	-236.307	0.545	2232.211	0.595	25	0.432	K.SVGPVVDGDAVVTFNFR.A
R1/RRR1-7/2	1435.161	1434.578	-291.137	0.593	2054.459	0.569	21	0.389	R.GWDAQVLGEAPYK.F
R1/RRR1-7/2	1434.249	1434.578	-229.858	0.512	2185.007	0.481	21	0.383	R.GWDAQVLGEAPYK.F
R1/RRR1-7/2	1435.168	1434.578	-286.699	0.519	2138.182	0.497	21	0.380	R.GWDAQVLGEAPYK.F
R1/RRR1-7/2	1404.129	1404.570	-314.955	0.452	2164.170	0.437	20	0.368	R.YAGM*LQYDGELK.L
R1/RRR1-7/2	1779.423	1779.974	-874.027	0.546	1828.957	0.561	23	0.342	K.SVGPVVDGDAVVTFNFR.A
R1/RRR1-7/2	986.993	987.175	-185.469	0.534	1128.173	0.502	17	0.248	K.LVDLALASGK.I
R1/RRR1-7/2	1482.422	1482.629	-140.044	0.485	1201.902	0.479	17	0.245	K.FGHVTFFWNGNR.S
R1/RRR1-7/2	1482.283	1482.629	-233.891	0.403	1292.894	0.437	18	0.244	K.FGHVTFFWNGNR.S
R1/RRR1-7/2	1483.043	1482.629	279.820	0.429	1178.192	0.425	16	0.231	K.FGHVTFFWNGNR.S
R1/RRR1-7/2	986.566	987.175	-1636.197	0.465	990.245	0.460	17	0.230	K.LVDLALASGK.I
R1/RRR1-7/2	1070.239	1070.307	-64.134	0.522	1466.126	0.300	14	0.230	R.LDQVQLLLK.G
R1/RRR1-7/2	1069.546	1070.307	-1651.947	0.432	1414.168	0.301	14	0.228	R.LDQVQLLLK.G
R1/RRR1-7/2	1482.108	1482.629	-1029.285	0.463	1121.502	0.419	17	0.227	K.FGHVTFFWNGNR.S
R1/RRR1-7/2	986.523	987.175	-1679.582	0.434	970.419	0.449	17	0.226	K.LVDLALASGK.I
R1/RRR1-9/2	986.894	987.175	-285.854	0.505	904.044	0.459	16	0.225	K.LVDLALASGK.I
R1/RRR1-7/2	1069.767	1070.307	-1443.990	0.471	1385.595	0.296	14	0.224	R.LDQVQLLLK.G
R1/RRR1-7/2	1350.380	1349.518	-101.876	0.478	939.364	0.466	16	0.222	R.DAILSGKFDQVR.V
R1/RRR1-7/2	910.913	911.041	-140.272	0.312	981.361	0.450	12	0.219	R.VHILTDGR.D
R1/RRR1-7/2	1865.936	1866.060	-66.903	0.425	657.877	0.497	23	0.213	K.ASDQYLPPFVIVDESGK.S
R1/RRR1-7/2	1349.159	1349.518	-266.680	0.373	929.720	0.421	16	0.213	R.DAILSGKFDQVR.V
R1/RRR1-9/2	986.987	987.175	-191.052	0.475	805.963	0.412	15	0.212	K.LVDLALASGK.I
R1/RRR1-7/2	1483.953	1482.629	219.171	0.422	895.531	0.418	15	0.211	K.FGHVTFFWNGNR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1006.011	1006.137	-125.552	0.478	893.000	0.353	16	0.210	K.FQNAVEAVK.T
R1/RRR1-7/2	1319.894	1319.444	342.237	0.457	959.690	0.342	17	0.207	K.IYDGEGFNYIK.E
R1/RRR1-7/2	1349.221	1349.518	-220.205	0.414	792.328	0.409	16	0.206	R.DAILSGKFDQVR.V
R1/RRR1-7/2	1005.976	1006.137	-160.487	0.446	856.742	0.336	16	0.206	K.FQNAVEAVK.T
R1/RRR1-7/2	1865.373	1866.060	-907.333	0.440	462.810	0.494	19	0.204	K.ASDQYLPPFVIVDESGK.S
R1/RRR1-7/2	1319.433	1319.444	-8.223	0.410	831.992	0.352	16	0.202	K.IYDGEGFNYIK.E
R1/RRR1-7/2	1865.466	1866.060	-857.144	0.427	389.713	0.495	18	0.202	K.ASDQYLPPFVIVDESGK.S
R1/RRR1-7/2	1319.364	1319.444	-60.562	0.386	847.340	0.324	16	0.199	K.IYDGEGFNYIK.E
R1/RRR1-7/2	1006.029	1006.137	-107.659	0.467	734.001	0.289	15	0.195	-.FQNAVEAVK.-
R1/RRR1-15/2	1867.022	1866.060	-20.697	0.382	306.291	0.305	16	0.189	K.ASDQYLPPFVIVDESGK.S
R1/RRR1-7/2	910.904	911.041	-150.758	0.252	434.396	0.321	10	0.188	R.VHILTDGR.D
R1/RRR1-13/2	1781.276	1779.974	169.803	0.318	668.863	0.311	15	0.185	K.SVGPVVDGDAVVTFNFR.A
R1/RRR1-6/2	1780.677	1779.974	-167.125	0.319	197.491	0.357	12	0.173	-.SVGPVVDGDAVVTFNFR.-
R1/RRR1-15/2	1005.193	1006.137	-1939.803	0.339	760.384	0.083	14	0.172	-.FQNAVEAVK.-
R1/RRR1-7/3	1576.823	1576.782	25.995	0.420	951.301	0.427	24	0.102	K.ARDAILSGKFDQVR.V
R1/RRR1-7/3	1734.242	1732.965	159.998	0.413	875.439	0.450	29	0.102	K.GTLHLIGLLSDGGVHSR.L
R1/RRR1-7/3	1576.005	1576.782	-1130.842	0.372	746.428	0.409	21	0.090	K.ARDAILSGKFDQVR.V
R1/RRR1-7/3	1482.464	1482.629	-111.680	0.388	1154.042	0.307	23	0.089	K.FGHVTFFWNGNR.S
R1/RRR1-7/3	1482.134	1482.629	-334.871	0.471	951.533	0.341	20	0.088	-.FGHVTFFWNGNR.-
R1/RRR1-7/3	1482.259	1482.629	-250.589	0.395	1118.612	0.190	23	0.071	K.FGHVTFFWNGNR.S
R1/RRR1-7/3	1732.213	1732.965	-1014.339	0.234	838.534	0.262	24	0.070	K.GTLHLIGLLSDGGVHSR.L
R1/RRR1-7/3	1575.810	1576.782	-1255.220	0.327	527.484	0.324	19	0.062	-.ARDAILSGKFDQVR.-
R1/RRR1-7/3	1732.544	1732.965	-243.681	0.287	691.841	0.200	20	0.053	-.GTLHLIGLLSDGGVHSR.-
R1/RRR1-6/2	1879.368	1880.002	-872.498	0.534	2430.318	0.468	24	0.423	K.SWEDLTSDKDAIETIR.A
R1/RRR1-6/2	1856.420	1855.901	-259.961	0.609	2254.115	0.521	25	0.407	R.TAWWDGSAVYGNNEER.A
R1/RRR1-6/2	1879.828	1880.002	-93.308	0.535	2291.839	0.472	24	0.396	K.SWEDLTSDKDAIETIR.A
R1/RRR1-6/2	1854.897	1855.901	-1083.482	0.513	2166.489	0.504	24	0.385	R.TAWWDGSAVYGNNEER.A
R1/RRR1-6/2	1855.392	1855.901	-815.737	0.567	2218.219	0.480	24	0.385	R.TAWWDGSAVYGNNEER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1879.540	1880.002	-246.927	0.524	2203.803	0.479	24	0.382	K.SWEDLTSDKDAIETIR.A
R1/RRR1-1/2	1856.823	1855.901	-42.109	0.570	2056.152	0.527	23	0.371	R.TAWWDGSAVYGNNEER.A
R1/RRR1-6/2	1879.485	1880.002	-809.906	0.527	2160.185	0.473	23	0.371	K.SWEDLTSDKDAIETIR.A
R1/RRR1-7/2	1879.709	1880.002	-156.366	0.502	1935.639	0.458	22	0.327	K.SWEDLTSDKDAIETIR.A
R1/RRR1-6/2	1163.103	1163.348	-211.757	0.497	1873.062	0.440	16	0.315	R.IDLAALEVYR.D
R1/RRR1-7/2	1162.675	1163.348	-1443.598	0.445	1749.707	0.385	17	0.283	R.IDLAALEVYR.D
R1/RRR1-6/2	1632.890	1633.915	-1244.139	0.389	1561.202	0.458	21	0.276	R.NSWAGVSILQALFVK.E
R1/RRR1-6/2	1628.143	1628.720	-971.556	0.513	1296.407	0.550	21	0.273	R.FFTSNFNEETYTK.K
R1/RRR1-6/2	1751.587	1752.050	-264.965	0.452	1447.514	0.485	25	0.270	K.DTFGHIGGPILGGLVGLK.K
R1/RRR1-6/2	1633.302	1633.915	-990.751	0.439	1378.767	0.470	20	0.258	R.NSWAGVSILQALFVK.E
R1/RRR1-6/2	1751.127	1752.050	-1101.192	0.464	1311.978	0.501	23	0.257	K.DTFGHIGGPILGGLVGLK.K
R1/RRR1-6/2	1629.332	1628.720	-238.632	0.550	1126.381	0.544	20	0.254	R.FFTSNFNEETYTK.K
R1/RRR1-6/2	1752.049	1752.050	-0.811	0.483	1273.422	0.495	24	0.253	K.DTFGHIGGPILGGLVGLK.K
R1/RRR1-6/2	1628.225	1628.720	-304.441	0.489	1059.616	0.552	19	0.249	R.FFTSNFNEETYTK.K
R1/RRR1-7/2	1455.339	1455.770	-296.943	0.444	884.445	0.608	19	0.246	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1632.779	1633.915	-1312.011	0.362	1407.750	0.377	20	0.240	R.NSWAGVSILQALFVK.E
R1/RRR1-6/2	1022.065	1022.181	-114.655	0.454	1114.559	0.462	15	0.238	R.ANWYGLLGK.K
R1/RRR1-7/2	1455.560	1455.770	-144.648	0.442	707.553	0.626	17	0.236	K.VPVPIGLLYLNTR.R
R1/RRR1-7/2	1455.451	1455.770	-219.612	0.449	768.565	0.585	18	0.234	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1455.349	1455.770	-289.622	0.414	804.449	0.575	18	0.233	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1021.789	1022.181	-384.773	0.464	850.159	0.508	14	0.229	R.ANWYGLLGK.K
R1/RRR1-7/2	1455.439	1454.695	-176.879	0.414	510.784	0.639	18	0.229	K.VHTIDWTVELLK.T
R1/RRR1-6/2	1455.358	1454.695	-232.161	0.468	631.636	0.580	17	0.227	K.VHTIDWTVELLK.T
R1/RRR1-1/2	1455.430	1455.770	-234.252	0.410	795.976	0.549	16	0.226	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1022.020	1022.181	-158.866	0.403	816.759	0.503	14	0.224	R.ANWYGLLGK.K
R1/RRR1-6/2	1522.390	1521.700	-204.245	0.483	1073.051	0.411	20	0.224	R.SDRIDLAALEVYR.D
R1/RRR1-5/2	1454.739	1455.770	-1400.034	0.387	625.414	0.580	16	0.222	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1163.258	1163.348	-77.741	0.404	1361.483	0.280	16	0.221	R.IDLAALEVYR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1456.504	1455.770	-183.138	0.425	583.645	0.520	17	0.216	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1522.455	1521.700	-161.131	0.480	765.459	0.482	17	0.216	R.SDRIDLAALEVYR.D
R1/RRR1-6/2	1454.620	1455.770	-1482.384	0.348	685.881	0.529	16	0.216	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1454.454	1454.695	-166.223	0.465	482.744	0.494	18	0.215	K.VHTIDWTVELLK.T
R1/RRR1-6/2	1454.293	1454.695	-277.204	0.447	562.889	0.496	16	0.213	K.VHTIDWTVELLK.T
R1/RRR1-2/2	1455.837	1455.770	46.709	0.371	400.716	0.587	14	0.212	K.VPVPIGLLYLNTR.R
R1/RRR1-6/2	1455.741	1455.770	-19.564	0.371	511.858	0.499	16	0.209	K.VPVPIGLLYLNTR.R
R1/RRR1-7/2	1021.466	1022.181	-1683.975	0.323	819.036	0.419	14	0.209	R.ANWYGLLGK.K
R1/RRR1-7/2	1521.072	1521.700	-1073.431	0.448	882.316	0.400	17	0.209	R.SDRIDLAALEVYR.D
R1/RRR1-7/2	1022.145	1022.181	-35.948	0.440	765.713	0.387	13	0.207	R.ANWYGLLGK.K
R1/RRR1-7/2	1633.481	1633.915	-266.583	0.295	1089.325	0.335	18	0.206	R.NSWAGVSILQALFVK.E
R1/RRR1-6/2	1293.201	1293.537	-260.420	0.404	553.175	0.486	14	0.202	K.LVIGDDGLLLHK.E
R1/RRR1-6/2	1131.070	1131.222	-134.078	0.435	1020.630	0.285	18	0.202	K.ENGVALSGDIR.N
R1/RRR1-6/2	1455.450	1455.770	-219.948	0.342	545.924	0.431	15	0.202	K.VPVPIGLLYLNTR.R
R1/RRR1-2/2	1163.347	1163.348	-1.432	0.425	690.801	0.357	14	0.201	R.IDLAALEVYR.D
R1/RRR1-6/2	1130.990	1131.222	-205.428	0.427	879.044	0.280	17	0.196	K.ENGVALSGDIR.N
R1/RRR1-6/3	1993.429	1993.381	24.186	0.459	1633.804	0.469	34	0.195	K.IKDTFGHIGGPILGGLVGLK.K
R1/RRR1-7/2	1520.666	1521.700	-1341.672	0.356	682.508	0.341	15	0.194	R.SDRIDLAALEVYR.D
R1/RRR1-1/2	1454.923	1454.695	156.810	0.292	300.886	0.369	12	0.193	K.VHTIDWTVELLK.T
R1/RRR1-1/2	1455.580	1455.770	-130.430	0.307	451.309	0.378	13	0.193	-.VPVPIGLLYLNTR.-
R1/RRR1-7/2	1164.369	1163.348	17.917	0.328	756.737	0.260	14	0.192	R.IDLAALEVYR.D
R1/RRR1-6/2	1132.156	1131.222	-58.248	0.418	773.423	0.274	16	0.191	-.ENGVALSGDIR.-
R1/RRR1-1/2	1163.869	1163.348	-412.966	0.356	536.569	0.247	13	0.191	R.IDLAALEVYR.D
R1/RRR1-1/2	1454.003	1454.695	-1167.153	0.290	367.117	0.303	12	0.190	K.VHTIDWTVELLK.T
R1/RRR1-6/2	1521.155	1521.700	-1018.801	0.358	573.191	0.255	16	0.189	R.SDRIDLAALEVYR.D
R1/RRR1-7/3	1992.039	1993.381	-1179.518	0.418	1733.711	0.406	37	0.184	K.IKDTFGHIGGPILGGLVGLK.K
R1/RRR1-6/3	1993.017	1993.381	-183.421	0.486	1352.979	0.548	36	0.175	K.IKDTFGHIGGPILGGLVGLK.K
R1/RRR1-6/3	1454.671	1454.695	-16.431	0.469	1261.671	0.434	24	0.125	K.VHTIDWTVELLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/3	1522.830	1521.700	85.287	0.508	1212.759	0.409	24	0.119	R.SDRIDLAALEVYR.D
R1/RRR1-7/3	1521.643	1521.700	-37.594	0.523	1215.166	0.387	23	0.116	-.SDRIDLAALEVYR.-
R1/RRR1-6/3	1521.953	1521.700	166.709	0.499	1260.698	0.341	24	0.106	-.SDRIDLAALEVYR.-
R1/RRR1-6/3	1521.951	1521.700	165.261	0.496	1142.845	0.378	23	0.105	-.SDRIDLAALEVYR.-
R1/RRR1-7/3	1522.260	1521.700	-289.890	0.516	1120.267	0.355	22	0.103	-.SDRIDLAALEVYR.-
R1/RRR1-6/3	1455.678	1454.695	-12.046	0.559	923.139	0.437	23	0.101	-.VHTIDWTVELLK.-
R1/RRR1-7/3	1454.709	1454.695	9.576	0.463	1080.796	0.381	23	0.101	K.VHTIDWTVELLK.T
R1/RRR1-6/3	1521.733	1521.700	22.028	0.489	1146.178	0.341	23	0.100	-.SDRIDLAALEVYR.-
R1/RRR1-6/3	1991.975	1993.381	-1211.640	0.382	670.080	0.439	27	0.095	K.IKDTFGHIGGPILGGLVGLK.K
R1/RRR1-6/3	1455.120	1455.770	-1136.943	0.402	1143.572	0.271	23	0.084	K.VPVPIGLLYLNTR.R
R1/RRR1-6/3	1454.867	1454.695	118.263	0.547	634.520	0.425	20	0.078	-.VHTIDWTVELLK.-
R1/RRR1-7/3	1454.170	1454.695	-1052.227	0.335	951.950	0.231	22	0.073	K.VHTIDWTVELLK.T
R1/RRR1-6/3	1455.280	1455.770	-337.180	0.391	988.036	0.184	22	0.068	K.VPVPIGLLYLNTR.R
R1/RRR1-21/2	1923.350	1924.095	-909.966	0.634	3309.320	0.598	26	0.718	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-21/2	1923.677	1924.095	-217.903	0.628	3235.472	0.600	26	0.697	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-21/2	1924.417	1924.095	167.734	0.646	3089.821	0.614	26	0.659	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-20/2	1923.671	1924.095	-221.150	0.634	2844.258	0.622	25	0.591	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-21/2	1978.447	1979.086	-830.846	0.605	2500.981	0.691	27	0.536	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-19/2	1638.415	1638.823	-249.759	0.484	2175.113	0.563	21	0.518	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1978.354	1979.086	-878.168	0.590	2429.373	0.672	26	0.509	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/2	1979.408	1979.086	163.383	0.593	2448.688	0.650	27	0.505	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-20/2	1622.417	1622.823	-250.969	0.474	2086.882	0.567	22	0.473	K.MIEDYLVAHPAEYA.-
R1/RRR1-20/2	1639.121	1638.823	182.617	0.516	2070.408	0.581	21	0.468	K.M*IEDYLVAHPAEYA.-
R1/RRR1-18/2	1638.323	1638.823	-918.333	0.474	2083.976	0.504	21	0.454	K.M*IEDYLVAHPAEYA.-
R1/RRR1-18/2	1638.080	1638.823	-1067.134	0.468	2001.491	0.558	20	0.433	K.M*IEDYLVAHPAEYA.-
R1/RRR1-19/2	1638.292	1638.823	-936.809	0.516	1963.876	0.605	20	0.427	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1638.234	1638.823	-972.492	0.444	1953.047	0.580	20	0.419	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1638.290	1638.823	-938.155	0.483	1935.148	0.596	20	0.414	K.M*IEDYLVAHPAEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1623.763	1622.823	-37.069	0.545	1884.101	0.644	21	0.401	K.MIEDYLVAHPAEYA.-
R1/RRR1-20/2	1638.830	1638.823	4.393	0.511	1806.125	0.627	20	0.367	K.M*IEDYLVAHPAEYA.-
R1/RRR1-20/2	1638.166	1638.823	-1014.087	0.473	1870.335	0.512	20	0.362	K.M*IEDYLVAHPAEYA.-
R1/RRR1-20/2	1622.289	1622.823	-948.722	0.416	1839.736	0.506	20	0.352	K.MIEDYLVAHPAEYA.-
R1/RRR1-19/2	1639.190	1638.823	224.812	0.534	1772.270	0.599	20	0.344	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1637.706	1638.823	-1296.146	0.318	1828.001	0.419	20	0.334	K.M*IEDYLVAHPAEYA.-
R1/RRR1-17/2	1638.012	1638.823	-1108.738	0.307	1827.610	0.412	20	0.333	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1638.455	1638.823	-225.167	0.479	1711.326	0.583	19	0.321	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1622.290	1622.823	-947.967	0.433	1725.671	0.556	20	0.321	K.MIEDYLVAHPAEYA.-
R1/RRR1-22/2	1638.119	1638.823	-1043.341	0.462	1733.454	0.551	20	0.320	K.M*IEDYLVAHPAEYA.-
R1/RRR1-20/1	1177.545	1178.320	-1512.125	0.296	636.402	0.500	15	0.302	K.LNPAAGVGSTYK.T
R1/RRR1-21/1	1177.616	1178.320	-1450.794	0.298	594.610	0.557	15	0.292	K.LNPAAGVGSTYK.T
R1/RRR1-20/1	1177.562	1178.320	-1497.338	0.278	600.676	0.542	15	0.292	K.LNPAAGVGSTYK.T
R1/RRR1-20/2	1207.957	1208.295	-280.520	0.422	1675.905	0.448	20	0.290	K.LEATGDGSCVAK.L
R1/RRR1-21/2	1638.439	1638.823	-234.585	0.450	1633.326	0.558	19	0.289	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1207.538	1208.295	-1459.013	0.434	1612.945	0.461	20	0.286	K.LEATGDGSCVAK.L
R1/RRR1-19/2	1269.974	1270.454	-379.138	0.371	1671.930	0.428	18	0.282	R.VAVCDAASHVLK.S
R1/RRR1-21/2	1289.812	1290.467	-1287.134	0.390	1550.165	0.419	17	0.267	K.DIVDGYYGM*LK.M
R1/RRR1-21/2	1530.966	1531.755	-1171.979	0.508	1432.149	0.461	22	0.266	K.EKDIVDGYYGMLK.M
R1/RRR1-21/2	1270.062	1270.454	-309.799	0.449	1555.270	0.411	19	0.266	R.VAVCDAASHVLK.S
R1/RRR1-20/2	1270.245	1270.454	-164.593	0.440	1371.267	0.446	18	0.254	R.VAVCDAASHVLK.S
R1/RRR1-21/2	1289.879	1290.467	-1235.146	0.350	1428.962	0.415	17	0.252	K.DIVDGYYGM*LK.M
R1/RRR1-21/2	1207.284	1208.295	-1670.466	0.352	1392.789	0.431	19	0.251	K.LEATGDGSCVAK.L
R1/RRR1-21/2	1531.265	1531.755	-321.319	0.510	1287.004	0.457	22	0.251	K.EKDIVDGYYGMLK.M
R1/RRR1-21/2	1547.161	1547.755	-1033.375	0.473	1483.926	0.374	22	0.250	K.EKDIVDGYYGM*LK.M
R1/RRR1-20/2	1270.107	1270.454	-273.638	0.379	1319.803	0.456	18	0.250	R.VAVCDAASHVLK.S
R1/RRR1-17/2	1082.869	1083.240	-344.242	0.444	1186.504	0.495	16	0.250	K.AFM*DASSLPK.A
R1/RRR1-20/2	1208.158	1208.295	-113.767	0.451	1367.058	0.421	19	0.249	K.LEATGDGSCVAK.L

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1207.982	1208.295	-259.838	0.418	1257.490	0.467	19	0.248	K.LEATGDGSCVAK.L
R1/RRR1-20/2	1622.239	1622.823	-979.469	0.390	1537.385	0.496	19	0.248	K.MIEDYLVAHPAEYA.-
R1/RRR1-18/2	1084.110	1083.240	-120.683	0.426	1055.814	0.538	15	0.246	K.AFM*DASSLPK.A
R1/RRR1-21/2	1178.031	1178.320	-245.761	0.454	808.486	0.614	19	0.246	K.LNPAAGVGSTYK.T
R1/RRR1-21/2	1546.987	1547.755	-1146.115	0.448	1307.880	0.422	21	0.244	K.EKDIVDGYYGM*LK.M
R1/RRR1-21/2	1178.032	1178.320	-244.930	0.417	912.493	0.569	20	0.244	K.LNPAAGVGSTYK.T
R1/RRR1-18/2	1638.088	1638.823	-1061.897	0.429	1557.310	0.464	19	0.244	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/2	1269.421	1270.454	-1605.962	0.348	1429.906	0.365	19	0.242	R.VAVCDAASHVLK.S
R1/RRR1-17/2	1178.175	1178.320	-122.897	0.362	890.377	0.591	19	0.242	K.LNPAAGVGSTYK.T
R1/RRR1-21/2	1269.519	1270.454	-1528.491	0.425	1192.202	0.466	17	0.241	R.VAVCDAASHVLK.S
R1/RRR1-19/2	1177.949	1178.320	-315.419	0.403	755.749	0.627	18	0.241	K.LNPAAGVGSTYK.T
R1/RRR1-22/2	1637.541	1638.823	-1397.289	0.288	1552.981	0.397	19	0.239	K.M*IEDYLVAHPAEYA.-
R1/RRR1-20/2	1084.073	1083.240	-155.022	0.421	1166.588	0.451	15	0.238	K.AFM*DASSLPK.A
R1/RRR1-20/2	1269.411	1270.454	-1614.270	0.330	1483.641	0.324	19	0.238	R.VAVCDAASHVLK.S
R1/RRR1-21/3	1978.535	1979.086	-786.199	0.492	1779.837	0.523	35	0.237	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/2	1084.320	1083.240	73.555	0.411	1295.168	0.388	16	0.237	K.AFM*DASSLPK.A
R1/RRR1-20/2	1177.995	1178.320	-276.430	0.362	873.003	0.561	20	0.237	K.LNPAAGVGSTYK.T
R1/RRR1-19/2	1178.067	1178.320	-215.406	0.467	778.615	0.555	19	0.236	K.LNPAAGVGSTYK.T
R1/RRR1-20/2	1177.965	1178.320	-302.526	0.366	860.083	0.552	20	0.235	K.LNPAAGVGSTYK.T
R1/RRR1-18/2	1269.965	1270.454	-386.275	0.357	1149.583	0.452	17	0.233	R.VAVCDAASHVLK.S
R1/RRR1-20/2	1208.042	1208.295	-209.758	0.395	1203.128	0.412	18	0.232	K.LEATGDGSCVAK.L
R1/RRR1-17/2	1083.048	1083.240	-178.456	0.413	1060.955	0.450	15	0.231	K.AFM*DASSLPK.A
R1/RRR1-18/2	1178.125	1178.320	-165.720	0.390	731.016	0.565	18	0.230	K.LNPAAGVGSTYK.T
R1/RRR1-20/2	1083.045	1083.240	-180.491	0.469	1234.828	0.384	15	0.230	K.AFM*DASSLPK.A
R1/RRR1-20/2	1082.984	1083.240	-237.708	0.448	1251.501	0.375	15	0.230	K.AFM*DASSLPK.A
R1/RRR1-21/2	1177.556	1178.320	-1502.608	0.342	903.286	0.505	20	0.229	K.LNPAAGVGSTYK.T
R1/RRR1-19/2	1083.077	1083.240	-151.321	0.478	1112.346	0.409	16	0.229	K.AFM*DASSLPK.A
R1/RRR1-22/2	1177.708	1178.320	-1372.566	0.353	926.145	0.485	20	0.228	K.LNPAAGVGSTYK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1178.262	1178.320	-49.318	0.367	887.434	0.493	20	0.228	K.LNPAAGVGSTYK.T
R1/RRR1-21/1	1177.697	1178.320	-1382.080	0.314	458.940	0.570	14	0.227	K.LNPAAGVGSTYK.T
R1/RRR1-20/2	1178.061	1178.320	-220.604	0.393	866.691	0.481	20	0.227	K.LNPAAGVGSTYK.T
R1/RRR1-21/2	1531.306	1531.755	-294.126	0.457	1107.342	0.401	20	0.225	K.EKDIVDGYYGMLK.M
R1/RRR1-19/2	1083.094	1083.240	-135.605	0.411	1143.229	0.375	16	0.224	K.AFM*DASSLPK.A
R1/RRR1-20/2	1547.332	1547.755	-274.112	0.472	1029.733	0.424	20	0.224	K.EKDIVDGYYGM*LK.M
R1/RRR1-21/2	1289.641	1290.467	-1420.409	0.334	1082.796	0.433	15	0.223	K.DIVDGYYGM*LK.M
R1/RRR1-18/2	1178.001	1178.320	-271.544	0.397	678.499	0.514	18	0.223	K.LNPAAGVGSTYK.T
R1/RRR1-18/2	1177.519	1178.320	-1533.536	0.317	709.635	0.542	18	0.222	K.LNPAAGVGSTYK.T
R1/RRR1-3/2	1178.166	1178.320	-130.588	0.324	707.499	0.538	18	0.222	K.LNPAAGVGSTYK.T
R1/RRR1-17/2	1178.205	1178.320	-97.642	0.376	655.492	0.521	17	0.221	K.LNPAAGVGSTYK.T
R1/RRR1-22/2	1177.442	1178.320	-1599.563	0.305	675.254	0.548	18	0.220	K.LNPAAGVGSTYK.T
R1/RRR1-19/2	1177.369	1178.320	-1662.266	0.319	678.477	0.532	17	0.219	K.LNPAAGVGSTYK.T
R1/RRR1-21/3	1978.975	1979.086	-56.190	0.496	1519.990	0.590	34	0.218	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-17/2	1177.476	1178.320	-1571.027	0.363	747.172	0.450	18	0.216	K.LNPAAGVGSTYK.T
R1/RRR1-21/2	977.822	978.036	-219.764	0.423	1131.597	0.338	15	0.216	K.SDVLEAESK.V
R1/RRR1-22/3	1979.298	1979.086	107.589	0.476	1497.154	0.590	33	0.216	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/2	1066.882	1067.241	-337.238	0.404	671.811	0.468	14	0.215	K.AFMDASSLPK.A
R1/RRR1-22/2	1177.493	1178.320	-1555.718	0.304	605.808	0.512	17	0.214	K.LNPAAGVGSTYK.T
R1/RRR1-17/2	1082.764	1083.240	-441.183	0.372	874.153	0.424	14	0.214	-.AFM*DASSLPK.-
R1/RRR1-16/2	1177.917	1178.320	-342.972	0.346	562.875	0.497	16	0.213	K.LNPAAGVGSTYK.T
R1/RRR1-2/2	1177.865	1178.320	-387.269	0.345	511.294	0.521	15	0.213	K.LNPAAGVGSTYK.T
R1/RRR1-20/2	977.891	978.036	-148.757	0.380	1006.374	0.387	14	0.213	-.SDVLEAESK.-
R1/RRR1-23/2	1178.122	1178.320	-168.214	0.316	689.517	0.450	18	0.212	K.LNPAAGVGSTYK.T
R1/RRR1-18/2	1083.583	1083.240	317.668	0.360	886.332	0.385	14	0.211	K.AFM*DASSLPK.A
R1/RRR1-21/3	1979.711	1979.086	-189.973	0.470	1481.842	0.593	35	0.210	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/2	1547.091	1547.755	-1078.215	0.430	918.599	0.358	19	0.208	K.EKDIVDGYYGM*LK.M
R1/RRR1-20/3	1978.823	1979.086	-133.227	0.488	1586.806	0.529	34	0.207	K.SHSTETKLEATGDGSCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1274.222	1274.468	-193.098	0.310	719.014	0.445	14	0.204	K.DIVDGYYGMLK.M
R1/RRR1-22/3	1978.172	1979.086	-970.539	0.441	1483.995	0.564	33	0.203	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-3/2	1177.683	1178.320	-1393.803	0.284	429.742	0.401	15	0.203	K.LNPAAGVGSTYK.T
R1/RRR1-20/2	1067.084	1067.241	-147.854	0.314	528.104	0.389	13	0.202	K.AFMDASSLPK.A
R1/RRR1-19/2	1083.489	1083.240	230.006	0.353	636.061	0.360	13	0.202	K.AFM*DASSLPK.A
R1/RRR1-21/2	1682.339	1682.764	-253.310	0.346	1042.511	0.299	21	0.200	K.VEYELEDGSSLSPEK.E
R1/RRR1-16/2	1177.997	1178.320	-274.455	0.251	617.338	0.352	17	0.200	K.LNPAAGVGSTYK.T
R1/RRR1-20/2	1066.793	1067.241	-421.278	0.262	656.640	0.380	13	0.200	K.AFMDASSLPK.A
R1/RRR1-21/3	1923.916	1924.095	-93.245	0.452	1764.644	0.443	33	0.200	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-21/2	1177.934	1178.320	-328.623	0.233	569.947	0.347	15	0.197	K.LNPAAGVGSTYK.T
R1/RRR1-25/2	1083.816	1083.240	-392.856	0.238	395.393	0.322	11	0.195	K.AFM*DASSLPK.A
R1/RRR1-21/2	1066.354	1067.241	-1774.350	0.281	533.484	0.330	12	0.194	-.AFMDASSLPK.-
R1/RRR1-21/3	1979.194	1979.086	54.703	0.508	1329.338	0.593	34	0.189	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/3	1978.444	1979.086	-832.463	0.457	1442.674	0.552	35	0.189	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/2	1637.595	1638.823	-1364.272	0.391	1237.638	0.533	18	0.184	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/3	1978.798	1979.086	-145.851	0.472	1380.020	0.557	34	0.184	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/2	1621.527	1622.823	-1420.180	0.321	1271.668	0.470	18	0.182	K.MIEDYLVAHPAEYA.-
R1/RRR1-20/3	1979.098	1979.086	6.358	0.493	1335.447	0.551	33	0.178	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-22/3	1978.245	1979.086	-933.275	0.483	1235.477	0.583	33	0.174	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-20/3	1978.908	1979.086	-89.881	0.489	1246.309	0.576	33	0.174	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-21/3	1924.641	1924.095	-236.567	0.510	1516.255	0.456	30	0.171	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-21/1	1177.642	1178.320	-1429.034	0.195	472.159	0.280	14	0.166	K.LNPAAGVGSTYK.T
R1/RRR1-18/3	1978.474	1979.086	-817.320	0.472	1068.360	0.575	30	0.156	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-15/3	1978.906	1979.086	-91.180	0.490	1159.606	0.547	33	0.155	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-19/3	1978.988	1979.086	-49.601	0.472	1015.451	0.558	29	0.148	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-18/3	1979.066	1979.086	-10.160	0.427	1041.693	0.551	31	0.145	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-3/2	1639.170	1638.823	212.415	0.373	944.219	0.521	17	0.143	K.M*IEDYLVAHPAEYA.-
R1/RRR1-19/3	1978.696	1979.086	-197.464	0.394	1003.761	0.539	29	0.139	K.SHSTETKLEATGDGSCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1639.040	1638.823	133.175	0.318	1092.790	0.359	18	0.136	K.M*IEDYLVAHPAEYA.-
R1/RRR1-21/3	1924.129	1924.095	17.580	0.493	1387.791	0.399	31	0.135	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-19/3	1979.065	1979.086	-10.624	0.402	1072.470	0.486	29	0.133	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-16/3	1979.047	1979.086	-19.811	0.411	1133.985	0.459	30	0.131	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-19/3	1978.185	1979.086	-963.848	0.426	931.604	0.513	28	0.130	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-18/3	1978.136	1979.086	-988.661	0.401	874.289	0.525	28	0.127	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-20/3	1978.373	1979.086	-868.233	0.435	943.935	0.501	29	0.127	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-20/3	1924.607	1924.095	-254.225	0.422	1179.297	0.435	29	0.123	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-20/3	1923.835	1924.095	-135.730	0.477	1271.264	0.393	31	0.121	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-14/3	1980.314	1979.086	115.664	0.389	820.658	0.513	29	0.120	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-17/3	1978.138	1979.086	-987.453	0.385	969.676	0.455	28	0.119	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-20/3	1923.675	1924.095	-218.992	0.442	1321.216	0.358	30	0.118	K.LKVEYELEDGSSLSPEK.E
R1/RRR1-21/2	1637.530	1638.823	-1404.402	0.277	774.277	0.344	19	0.118	K.M*IEDYLVAHPAEYA.-
R1/RRR1-11/3	1980.260	1979.086	88.030	0.398	387.305	0.483	26	0.109	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-17/3	1978.432	1979.086	-838.223	0.358	635.275	0.429	24	0.103	K.SHSTETKLEATGDGSCVAK.L
R1/RRR1-14/3	1978.373	1979.086	-868.140	0.321	272.376	0.428	20	0.097	-.SHSTETKLEATGDGSCVAK.-
R1/RRR1-3/2	1560.464	1559.743	-179.333	0.500	2072.688	0.582	23	0.393	K.IDQSALTGESLPVTK.G
R1/RRR1-2/2	1633.499	1633.746	-151.377	0.518	1936.821	0.536	21	0.354	R.TALTYIDADGNWHR.A
R1/RRR1-3/2	1634.137	1633.746	240.386	0.561	1775.809	0.564	21	0.336	R.TALTYIDADGNWHR.A
R1/RRR1-3/2	1492.482	1492.742	-174.293	0.467	1931.924	0.482	19	0.334	K.LSVDKNLVEVFTK.G
R1/RRR1-1/2	1559.393	1559.743	-225.702	0.459	1743.680	0.512	21	0.314	K.IDQSALTGESLPVTK.G
R1/RRR1-2/2	1560.154	1559.743	263.949	0.498	1713.228	0.514	21	0.310	K.IDQSALTGESLPVTK.G
R1/RRR1-3/2	1559.273	1559.743	-302.513	0.450	1663.441	0.506	21	0.301	K.IDQSALTGESLPVTK.G
R1/RRR1-2/2	1633.165	1633.746	-970.968	0.439	1687.665	0.489	20	0.301	R.TALTYIDADGNWHR.A
R1/RRR1-5/2	1493.496	1492.742	-165.403	0.524	1505.403	0.566	18	0.297	K.LSVDKNLVEVFTK.G
R1/RRR1-1/2	1559.235	1559.743	-970.127	0.436	1739.694	0.453	21	0.297	K.IDQSALTGESLPVTK.G
R1/RRR1-2/2	1558.537	1559.743	-1419.759	0.362	1685.836	0.480	21	0.296	K.IDQSALTGESLPVTK.G
R1/RRR1-3/2	1407.183	1407.643	-327.987	0.520	1589.480	0.513	19	0.295	K.GVDKDHVLLLAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1493.445	1492.742	-199.678	0.529	1517.240	0.542	21	0.295	K.LSVDKNLVEVFTK.G
R1/RRR1-4/2	1559.169	1559.743	-1012.886	0.416	1647.803	0.469	21	0.289	K.IDQSALTGESLPVTK.G
R1/RRR1-1/2	1634.184	1633.746	268.850	0.521	1488.485	0.519	20	0.283	R.TALTYIDADGNWHR.A
R1/RRR1-2/2	1633.427	1633.746	-195.908	0.471	1458.795	0.530	19	0.282	R.TALTYIDADGNWHR.A
R1/RRR1-2/2	1914.683	1915.182	-261.058	0.590	1493.774	0.518	24	0.280	R.LGM*GTNM*YPSSALLGQNK.D
R1/RRR1-3/2	1559.353	1559.743	-251.383	0.454	1531.671	0.489	20	0.279	K.IDQSALTGESLPVTK.G
R1/RRR1-2/2	1397.956	1398.451	-354.763	0.541	1281.294	0.572	21	0.277	K.NPGDEVFSGSTCK.Q
R1/RRR1-2/2	1398.094	1398.451	-256.119	0.505	1332.066	0.533	21	0.272	K.NPGDEVFSGSTCK.Q
R1/RRR1-1/2	1643.372	1642.829	-279.060	0.485	1459.348	0.484	23	0.272	K.DASLEALPVDELIEK.A
R1/RRR1-1/2	1633.336	1633.746	-251.915	0.476	1384.869	0.513	19	0.269	R.TALTYIDADGNWHR.A
R1/RRR1-3/2	1406.440	1407.643	-1571.033	0.437	1472.170	0.444	19	0.263	K.GVDKDHVLLLAAR.A
R1/RRR1-3/2	1492.466	1492.742	-185.370	0.497	1293.582	0.519	19	0.263	K.LSVDKNLVEVFTK.G
R1/RRR1-2/2	1406.857	1407.643	-1273.365	0.511	1316.859	0.510	18	0.262	K.GVDKDHVLLLAAR.A
R1/RRR1-1/2	1940.530	1940.229	155.868	0.576	1321.767	0.509	25	0.260	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-1/2	1492.353	1492.742	-261.192	0.468	1306.791	0.496	19	0.259	K.LSVDKNLVEVFTK.G
R1/RRR1-1/2	1558.767	1559.743	-1272.039	0.338	1534.096	0.400	20	0.257	K.IDQSALTGESLPVTK.G
R1/RRR1-4/2	1397.955	1398.451	-355.639	0.517	1047.901	0.587	20	0.257	K.NPGDEVFSGSTCK.Q
R1/RRR1-2/2	1163.174	1163.370	-168.613	0.452	1639.057	0.338	18	0.257	K.M*ITGDQLAIGK.E
R1/RRR1-2/2	1938.934	1940.229	-1187.126	0.522	1301.940	0.486	24	0.253	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-3/2	1398.150	1398.451	-215.652	0.448	1178.532	0.516	20	0.252	K.NPGDEVFSGSTCK.Q
R1/RRR1-1/2	1491.696	1492.742	-1375.854	0.451	1272.167	0.469	18	0.248	K.LSVDKNLVEVFTK.G
R1/RRR1-2/2	1491.970	1492.742	-1190.876	0.448	1225.068	0.469	19	0.245	K.LSVDKNLVEVFTK.G
R1/RRR1-2/2	1940.567	1940.229	174.540	0.572	1245.402	0.482	24	0.245	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-3/2	1915.246	1915.182	33.788	0.551	1205.050	0.501	22	0.245	R.LGM*GTNM*YPSSALLGQNK.D
R1/RRR1-2/2	1492.749	1492.742	4.789	0.377	1309.379	0.443	17	0.244	K.LSVDKNLVEVFTK.G
R1/RRR1-7/2	1939.487	1940.229	-900.564	0.496	1232.219	0.462	24	0.242	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-1/2	1398.157	1398.451	-210.922	0.501	945.146	0.555	19	0.241	K.NPGDEVFSGSTCK.Q
R1/RRR1-3/2	1914.580	1915.182	-838.728	0.545	1174.101	0.488	22	0.239	R.LGM*GTNM*YPSSALLGQNK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1491.381	1492.742	-1587.542	0.358	1242.159	0.431	19	0.238	K.LSVDKNLVEVFTK.G
R1/RRR1-2/2	1492.330	1492.742	-276.948	0.483	1090.573	0.484	18	0.237	K.LSVDKNLVEVFTK.G
R1/RRR1-5/2	1939.960	1940.229	-139.266	0.543	1140.760	0.476	24	0.237	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-1/2	1162.830	1163.370	-1327.925	0.467	1070.532	0.470	17	0.236	K.M*ITGDQLAIGK.E
R1/RRR1-3/2	1163.124	1163.370	-211.989	0.420	1253.832	0.402	17	0.236	K.M*ITGDQLAIGK.E
R1/RRR1-3/2	1939.994	1940.229	-121.276	0.555	1103.560	0.453	23	0.228	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-2/2	1406.911	1407.643	-1235.374	0.459	1041.394	0.454	18	0.227	K.GVDKDHVLLLAAR.A
R1/RRR1-4/2	1633.449	1633.746	-182.338	0.429	1034.934	0.473	17	0.227	R.TALTYIDADGNWHR.A
R1/RRR1-3/2	1163.159	1163.370	-181.773	0.451	1234.413	0.357	18	0.227	K.M*ITGDQLAIGK.E
R1/RRR1-2/2	1940.632	1940.229	208.225	0.576	1088.973	0.458	23	0.227	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-2/2	1163.183	1163.370	-161.454	0.444	980.996	0.447	17	0.227	K.M*ITGDQLAIGK.E
R1/RRR1-4/2	1940.223	1940.229	-3.257	0.556	991.528	0.484	22	0.226	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-1/2	1940.499	1940.229	139.655	0.576	1088.787	0.441	24	0.225	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-1/2	1914.959	1915.182	-116.523	0.521	974.735	0.489	20	0.223	R.LGM*GTNM*YPSSALLGQNK.D
R1/RRR1-5/2	1940.684	1940.229	235.285	0.545	1017.969	0.440	23	0.220	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-1/2	1939.327	1940.229	-983.848	0.496	937.366	0.439	22	0.216	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-4/2	1941.529	1940.229	155.283	0.535	932.524	0.452	21	0.216	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-2/2	1162.840	1163.370	-1320.124	0.441	953.761	0.392	16	0.216	K.M*ITGDQLAIGK.E
R1/RRR1-5/2	1940.652	1940.229	218.885	0.588	1081.504	0.409	23	0.216	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-2/2	1643.130	1642.829	183.409	0.479	1064.040	0.366	22	0.215	K.DASLEALPVDELIEK.A
R1/RRR1-1/2	1026.802	1027.156	-345.751	0.408	756.823	0.419	16	0.214	K.LGDIVPADAR.L
R1/RRR1-2/2	1027.064	1027.156	-90.673	0.492	674.822	0.432	15	0.213	K.LGDIVPADAR.L
R1/RRR1-1/2	1026.451	1027.156	-1665.956	0.396	730.785	0.432	15	0.213	K.LGDIVPADAR.L
R1/RRR1-1/2	1026.961	1027.156	-190.709	0.464	793.743	0.381	16	0.211	K.LGDIVPADAR.L
R1/RRR1-3/2	1162.347	1163.370	-1745.396	0.372	1074.047	0.313	17	0.210	K.M*ITGDQLAIGK.E
R1/RRR1-2/2	1642.572	1642.829	-156.951	0.450	902.760	0.369	21	0.209	K.DASLEALPVDELIEK.A
R1/RRR1-5/2	1642.439	1642.829	-238.069	0.441	955.978	0.355	21	0.209	K.DASLEALPVDELIEK.A
R1/RRR1-4/2	1643.286	1642.829	278.909	0.434	963.740	0.352	21	0.209	K.DASLEALPVDELIEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1162.418	1163.370	-1684.198	0.329	891.778	0.360	16	0.208	K.M*ITGDQLAIGK.E
R1/RRR1-2/2	1026.646	1027.156	-1475.661	0.376	687.737	0.374	15	0.206	K.LGDIVPADAR.L
R1/RRR1-4/2	1163.157	1163.370	-183.668	0.426	827.268	0.358	15	0.206	K.M*ITGDQLAIGK.E
R1/RRR1-3/2	1939.629	1940.229	-827.401	0.521	769.314	0.426	20	0.204	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-2/2	1642.981	1642.829	92.510	0.459	824.660	0.364	20	0.204	K.DASLEALPVDELIEK.A
R1/RRR1-3/2	1642.704	1642.829	-76.666	0.432	774.620	0.386	18	0.204	K.DASLEALPVDELIEK.A
R1/RRR1-4/2	1642.383	1642.829	-272.295	0.401	867.029	0.340	20	0.203	K.DASLEALPVDELIEK.A
R1/RRR1-4/2	1163.277	1163.370	-80.608	0.429	823.766	0.324	16	0.203	K.M*ITGDQLAIGK.E
R1/RRR1-4/2	1026.848	1027.156	-301.619	0.409	476.272	0.413	13	0.202	-.LGDIVPADAR.-
R1/RRR1-4/2	1026.446	1027.156	-1671.333	0.401	517.801	0.408	13	0.202	-.LGDIVPADAR.-
R1/RRR1-3/2	1914.413	1915.182	-926.803	0.537	617.089	0.472	18	0.201	R.LGM*GTNM*YPSSALLGQNK.D
R1/RRR1-1/2	1162.507	1163.370	-1607.396	0.427	900.847	0.293	16	0.201	K.M*ITGDQLAIGK.E
R1/RRR1-4/2	1939.810	1940.229	-216.596	0.486	592.782	0.439	18	0.201	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-3/2	1026.490	1027.156	-1627.963	0.394	509.231	0.393	13	0.200	-.LGDIVPADAR.-
R1/RRR1-3/2	1940.318	1940.229	45.962	0.442	708.447	0.401	19	0.200	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-1/2	1147.092	1147.371	-243.744	0.331	617.813	0.340	14	0.199	K.MITGDQLAIGK.E
R1/RRR1-3/2	1642.147	1642.829	-1027.391	0.327	779.737	0.333	19	0.199	K.DASLEALPVDELIEK.A
R1/RRR1-1/2	1642.188	1642.829	-1002.464	0.353	698.730	0.339	18	0.198	K.DASLEALPVDELIEK.A
R1/RRR1-1/2	1643.534	1642.829	-179.953	0.491	634.279	0.356	18	0.197	K.DASLEALPVDELIEK.A
R1/RRR1-5/2	1643.333	1642.829	-302.759	0.493	769.620	0.333	19	0.197	K.DASLEALPVDELIEK.A
R1/RRR1-3/2	1147.206	1147.371	-143.825	0.283	538.742	0.310	14	0.196	K.MITGDQLAIGK.E
R1/RRR1-3/2	1642.216	1642.829	-985.299	0.373	552.590	0.323	17	0.195	K.DASLEALPVDELIEK.A
R1/RRR1-5/2	1027.094	1027.156	-60.630	0.438	474.407	0.366	13	0.195	-.LGDIVPADAR.-
R1/RRR1-4/2	1492.449	1492.742	-196.940	0.353	625.843	0.353	14	0.195	K.LSVDKNLVEVFTK.G
R1/RRR1-2/2	1406.597	1407.643	-1459.354	0.374	615.769	0.339	16	0.194	K.GVDKDHVLLLAAR.A
R1/RRR1-1/2	1940.326	1940.229	50.253	0.538	969.466	0.308	22	0.194	R.WGEQEAAILVPGDIISIK.L
R1/RRR1-2/2	1027.052	1027.156	-101.999	0.438	565.178	0.377	14	0.194	-.LGDIVPADAR.-
R1/RRR1-6/2	1939.216	1940.229	-1040.917	0.366	504.396	0.381	16	0.193	R.WGEQEAAILVPGDIISIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1147.099	1147.371	-237.659	0.230	634.312	0.324	14	0.193	-.MITGDQLAIGK.-
R1/RRR1-4/2	1026.979	1027.156	-173.180	0.417	504.922	0.382	13	0.193	-.LGDIVPADAR.-
R1/RRR1-2/2	1558.354	1559.743	-1538.171	0.287	1013.833	0.245	17	0.192	K.IDQSALTGESLPVTK.G
R1/RRR1-4/2	1641.886	1642.829	-1187.136	0.270	650.552	0.275	18	0.192	K.DASLEALPVDELIEK.A
R1/RRR1-5/2	1642.223	1642.829	-980.970	0.354	649.185	0.284	17	0.192	K.DASLEALPVDELIEK.A
R1/RRR1-1/2	1147.149	1147.371	-193.889	0.182	450.579	0.302	13	0.192	K.MITGDQLAIGK.E
R1/RRR1-2/3	1429.646	1429.649	-2.074	0.539	1952.365	0.368	28	0.191	R.KVHAVIDKYAER.G
R1/RRR1-7/2	1642.354	1642.829	-290.043	0.321	573.854	0.271	16	0.190	K.DASLEALPVDELIEK.A
R1/RRR1-1/2	1146.281	1147.371	-1828.579	0.177	699.529	0.244	15	0.189	K.MITGDQLAIGK.E
R1/RRR1-4/2	1147.230	1147.371	-123.011	0.183	640.533	0.242	14	0.189	K.MITGDQLAIGK.E
R1/RRR1-3/3	1429.018	1429.649	-1144.902	0.576	1534.229	0.533	26	0.186	R.KVHAVIDKYAER.G
R1/RRR1-3/2	1027.908	1027.156	-242.705	0.387	511.475	0.359	13	0.186	-.LGDIVPADAR.-
R1/RRR1-4/3	1407.977	1407.643	237.771	0.563	1828.007	0.387	27	0.185	K.GVDKDHVLLLAAR.A
R1/RRR1-1/3	1407.322	1407.643	-229.307	0.512	1525.626	0.417	26	0.152	K.GVDKDHVLLLAAR.A
R1/RRR1-1/3	1408.763	1407.643	84.936	0.514	1703.543	0.339	27	0.149	K.GVDKDHVLLLAAR.A
R1/RRR1-1/3	1429.708	1429.649	41.087	0.598	1634.161	0.334	26	0.137	R.KVHAVIDKYAER.G
R1/RRR1-1/3	1429.946	1429.649	208.431	0.558	1346.961	0.443	26	0.134	R.KVHAVIDKYAER.G
R1/RRR1-7/3	1429.700	1429.649	35.821	0.571	1528.195	0.371	27	0.133	R.KVHAVIDKYAER.G
R1/RRR1-2/3	1407.060	1407.643	-1128.571	0.530	1514.137	0.346	26	0.130	K.GVDKDHVLLLAAR.A
R1/RRR1-5/3	1429.690	1429.649	28.627	0.590	1425.173	0.392	26	0.129	R.KVHAVIDKYAER.G
R1/RRR1-3/3	1429.476	1429.649	-121.558	0.533	1630.394	0.316	27	0.129	R.KVHAVIDKYAER.G
R1/RRR1-3/3	1408.957	1407.643	222.963	0.558	1338.814	0.397	25	0.128	K.GVDKDHVLLLAAR.A
R1/RRR1-4/3	1406.698	1407.643	-1386.843	0.502	1329.430	0.398	25	0.126	K.GVDKDHVLLLAAR.A
R1/RRR1-2/3	1430.001	1429.649	247.080	0.568	1489.353	0.347	26	0.124	R.KVHAVIDKYAER.G
R1/RRR1-2/3	1407.861	1407.643	154.955	0.544	1283.095	0.402	25	0.124	K.GVDKDHVLLLAAR.A
R1/RRR1-5/3	1407.261	1407.643	-272.775	0.513	1401.116	0.346	25	0.120	K.GVDKDHVLLLAAR.A
R1/RRR1-3/3	1492.973	1492.742	155.511	0.473	1204.719	0.433	27	0.120	K.LSVDKNLVEVFTK.G
R1/RRR1-4/3	1407.488	1407.643	-111.061	0.532	1269.303	0.391	25	0.120	K.GVDKDHVLLLAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/3	1839.914	1840.094	-98.414	0.528	1112.403	0.426	31	0.118	K.KHIVGM*TGDGVNDAPALK.K
R1/RRR1-5/3	1407.729	1407.643	61.298	0.525	1205.147	0.391	23	0.117	K.GVDKDHVLLLAAR.A
R1/RRR1-5/3	1429.763	1429.649	79.749	0.562	1244.145	0.405	25	0.117	R.KVHAVIDKYAER.G
R1/RRR1-2/3	1407.122	1407.643	-1084.668	0.494	1488.458	0.306	26	0.117	K.GVDKDHVLLLAAR.A
R1/RRR1-2/3	1429.768	1429.649	83.731	0.573	1136.027	0.430	24	0.116	R.KVHAVIDKYAER.G
R1/RRR1-2/3	1598.980	1598.829	94.549	0.473	1293.733	0.341	25	0.109	R.EVHFLPFNPVDKR.T
R1/RRR1-1/3	1406.818	1407.643	-1301.347	0.463	1384.334	0.303	25	0.108	K.GVDKDHVLLLAAR.A
R1/RRR1-1/3	1492.858	1492.742	77.773	0.511	1048.414	0.409	25	0.107	K.LSVDKNLVEVFTK.G
R1/RRR1-3/3	1599.072	1598.829	152.084	0.454	1345.620	0.304	25	0.104	R.EVHFLPFNPVDKR.T
R1/RRR1-3/3	1840.509	1840.094	226.218	0.485	1013.967	0.384	30	0.102	K.KHIVGM*TGDGVNDAPALK.K
R1/RRR1-1/3	1599.207	1598.829	236.939	0.413	996.464	0.385	23	0.099	R.EVHFLPFNPVDKR.T
R1/RRR1-5/3	1493.071	1492.742	221.431	0.405	795.260	0.427	23	0.099	K.LSVDKNLVEVFTK.G
R1/RRR1-3/3	1407.646	1407.643	1.938	0.488	918.150	0.373	20	0.098	-.GVDKDHVLLLAAR.-
R1/RRR1-3/3	1839.924	1840.094	-92.823	0.462	1036.680	0.357	29	0.098	K.KHIVGM*TGDGVNDAPALK.K
R1/RRR1-3/3	1492.985	1492.742	163.383	0.476	730.297	0.409	23	0.097	K.LSVDKNLVEVFTK.G
R1/RRR1-3/3	1493.508	1492.742	-157.295	0.438	799.471	0.397	23	0.096	K.LSVDKNLVEVFTK.G
R1/RRR1-1/3	1492.931	1492.742	127.222	0.420	677.945	0.407	22	0.095	K.LSVDKNLVEVFTK.G
R1/RRR1-2/3	1493.785	1492.742	28.997	0.490	671.922	0.379	22	0.094	K.LSVDKNLVEVFTK.G
R1/RRR1-4/3	1493.001	1492.742	174.452	0.468	677.435	0.381	22	0.094	K.LSVDKNLVEVFTK.G
R1/RRR1-1/3	1492.736	1492.742	-3.668	0.408	685.163	0.393	22	0.094	K.LSVDKNLVEVFTK.G
R1/RRR1-3/3	1600.048	1598.829	136.802	0.443	991.789	0.354	25	0.093	R.EVHFLPFNPVDKR.T
R1/RRR1-5/3	1492.266	1492.742	-319.962	0.428	845.078	0.367	23	0.092	K.LSVDKNLVEVFTK.G
R1/RRR1-2/3	1492.754	1492.742	8.020	0.415	726.849	0.358	22	0.090	K.LSVDKNLVEVFTK.G
R1/RRR1-4/3	1492.956	1492.742	143.581	0.405	559.872	0.332	20	0.090	K.LSVDKNLVEVFTK.G
R1/RRR1-2/3	1492.997	1492.742	171.746	0.441	671.435	0.338	21	0.089	K.LSVDKNLVEVFTK.G
R1/RRR1-8/3	1407.910	1407.643	189.648	0.454	1038.407	0.300	23	0.089	K.GVDKDHVLLLAAR.A
R1/RRR1-5/3	1599.745	1598.829	-52.711	0.430	980.809	0.333	25	0.089	R.EVHFLPFNPVDKR.T
R1/RRR1-4/3	1492.745	1492.742	2.238	0.378	615.630	0.329	22	0.088	K.LSVDKNLVEVFTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/3	1598.374	1598.829	-285.622	0.362	828.537	0.288	20	0.082	R.EVHFLPFNPVDKR.T
R1/RRR1-2/3	1598.981	1598.829	95.008	0.400	645.352	0.268	20	0.077	-.EVHFLPFNPVDKR.-
R1/RRR1-2/3	1599.171	1598.829	214.205	0.339	563.420	0.288	19	0.077	-.EVHFLPFNPVDKR.-
R1/RRR1-3/3	1840.158	1840.094	34.838	0.377	741.507	0.266	29	0.076	K.KHIVGM*TGDGVNDAPALK.K
R1/RRR1-1/3	1598.492	1598.829	-211.840	0.351	735.726	0.199	19	0.075	R.EVHFLPFNPVDKR.T
R1/RRR1-5/3	1598.888	1598.829	36.548	0.345	605.653	0.247	18	0.068	-.EVHFLPFNPVDKR.-
R1/RRR1-3/2	1459.448	1459.670	-152.567	0.441	2422.080	0.586	26	0.472	K.LVAEAGIGTVASGVSK.G
R1/RRR1-3/2	1459.546	1459.670	-85.532	0.510	2125.179	0.630	25	0.426	K.LVAEAGIGTVASGVSK.G
R1/RRR1-3/2	1459.329	1459.670	-234.885	0.451	1939.814	0.560	24	0.364	K.LVAEAGIGTVASGVSK.G
R1/RRR1-3/2	1881.475	1879.998	254.403	0.505	1605.617	0.573	19	0.313	K.SASWADELYFCSLSSR.T
R1/RRR1-3/2	1906.727	1907.199	-248.415	0.514	1629.296	0.474	25	0.289	R.FGVTPTFLVNAEQIEIK.I
R1/RRR1-3/2	1907.748	1907.199	-237.179	0.524	1498.975	0.436	24	0.263	R.FGVTPTFLVNAEQIEIK.I
R1/RRR1-3/2	1905.842	1907.199	-1240.181	0.438	1376.410	0.477	23	0.259	R.FGVTPTFLVNAEQIEIK.I
R1/RRR1-3/2	1402.363	1401.654	-208.184	0.421	1376.054	0.413	20	0.247	K.GM*AGGELVVVPVEK.T
R1/RRR1-3/2	1521.262	1521.699	-288.180	0.380	1141.465	0.399	18	0.224	K.VFTDEGLEVLGWR.T
R1/RRR1-3/2	1521.572	1521.699	-83.494	0.432	1026.149	0.432	17	0.221	K.VFTDEGLEVLGWR.T
R1/RRR1-2/2	1676.110	1676.807	-1015.631	0.404	1337.913	0.285	20	0.215	K.ASDSANLDSTAELLLR.S
R1/RRR1-3/2	1676.149	1676.807	-992.013	0.447	1362.844	0.288	19	0.215	K.ASDSANLDSTAELLLR.S
R1/RRR1-1/2	1906.554	1907.199	-865.130	0.426	1119.705	0.371	21	0.215	R.FGVTPTFLVNAEQIEIK.I
R1/RRR1-10/2	1522.655	1521.699	-28.755	0.356	1000.299	0.393	17	0.213	K.VFTDEGLEVLGWR.T
R1/RRR1-3/2	1275.592	1276.379	-1404.785	0.306	1145.080	0.337	19	0.212	K.GLQNGDTATSAIK.Q
R1/RRR1-3/2	1022.074	1022.177	-100.519	0.318	850.510	0.447	13	0.212	K.GLIEAYVEK.T
R1/RRR1-3/2	1172.902	1173.368	-399.014	0.362	648.257	0.506	16	0.210	R.VNAPAGQM*QLK.G
R1/RRR1-3/2	1979.394	1980.190	-909.972	0.385	880.299	0.392	19	0.202	K.GQM*EAWDGPALLLFSDGR.T
R1/RRR1-2/2	1966.122	1964.191	-35.285	0.427	724.023	0.452	17	0.201	K.GQMEAWDGPALLLFSDGR.T
R1/RRR1-3/2	1277.054	1276.379	-254.700	0.371	471.662	0.459	15	0.199	K.GLQNGDTATSAIK.Q
R1/RRR1-3/2	1021.604	1022.177	-1543.526	0.189	601.662	0.345	12	0.187	K.GLIEAYVEK.T
R1/RRR1-3/2	1022.042	1022.177	-132.508	0.220	707.114	0.271	12	0.186	K.GLIEAYVEK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1520.996	1521.699	-1122.588	0.216	535.675	0.247	15	0.185	K.VFTDEGLEVLGWR.T
R1/RRR1-3/2	1978.800	1980.190	-1211.573	0.291	641.489	0.258	17	0.181	K.GQM*EAWDGPALLLFSDGR.T
R1/RRR1-2/2	1521.306	1521.699	-258.635	0.236	683.012	0.140	14	0.181	-.VFTDEGLEVLGWR.-
R1/RRR1-3/3	1636.991	1636.877	69.392	0.422	882.272	0.503	30	0.111	K.IAQGAKPGEGGQLPGKK.V
R1/RRR1-3/3	1713.697	1713.864	-97.682	0.523	930.539	0.434	27	0.104	R.ICHTNNCPVGVASQR.E
R1/RRR1-3/3	1508.320	1508.705	-255.432	0.350	1033.122	0.394	29	0.098	K.IAQGAKPGEGGQLPGK.K
R1/RRR1-3/3	1636.869	1636.877	-5.439	0.436	720.384	0.462	27	0.097	K.IAQGAKPGEGGQLPGKK.V
R1/RRR1-3/3	1713.602	1713.864	-153.311	0.468	716.662	0.419	23	0.093	R.ICHTNNCPVGVASQR.E
R1/RRR1-3/3	1372.669	1372.533	99.356	0.444	1163.376	0.270	22	0.086	R.ETHEAIAIAM*NR.I
R1/RRR1-3/3	1508.649	1508.705	-36.985	0.351	950.565	0.335	27	0.085	K.IAQGAKPGEGGQLPGK.K
R1/RRR1-3/3	1509.094	1508.705	258.876	0.333	895.781	0.304	26	0.079	K.IAQGAKPGEGGQLPGK.K
R1/RRR1-3/3	1372.780	1372.533	180.421	0.456	926.647	0.266	21	0.074	-.ETHEAIAIAM*NR.-
R1/RRR1-9/2	1762.135	1760.969	94.245	0.520	2832.106	0.458	22	0.511	R.FKDIFQEVYEAGWK.S
R1/RRR1-10/3	1778.023	1777.908	64.955	0.564	2939.840	0.448	36	0.511	R.DATDDKVTVEAAEATLK.Y
R1/RRR1-10/3	1777.008	1777.908	-1072.829	0.560	2664.594	0.498	36	0.449	R.DATDDKVTVEAAEATLK.Y
R1/RRR1-10/2	1760.084	1760.969	-1074.163	0.572	2475.680	0.453	23	0.425	R.FKDIFQEVYEAGWK.S
R1/RRR1-10/2	1760.313	1760.969	-943.401	0.579	2500.725	0.435	23	0.423	R.FKDIFQEVYEAGWK.S
R1/RRR1-10/2	1437.097	1436.569	-329.255	0.579	2144.772	0.599	20	0.417	R.AFAEASM*TTAYEK.K
R1/RRR1-10/2	1761.391	1760.969	240.189	0.624	2354.187	0.493	23	0.414	R.FKDIFQEVYEAGWK.S
R1/RRR1-10/2	1321.146	1321.453	-233.040	0.561	1964.366	0.610	22	0.389	K.LEAACVGTVESGK.M
R1/RRR1-10/2	1437.050	1436.569	335.634	0.580	2005.386	0.565	20	0.377	R.AFAEASM*TTAYEK.K
R1/RRR1-1/2	1762.311	1760.969	194.557	0.529	2187.865	0.463	21	0.372	R.FKDIFQEVYEAGWK.S
R1/RRR1-10/2	1321.002	1321.453	-342.526	0.516	1853.685	0.605	22	0.367	K.LEAACVGTVESGK.M
R1/RRR1-10/2	1778.418	1777.908	-276.320	0.581	1880.907	0.517	25	0.338	R.DATDDKVTVEAAEATLK.Y
R1/RRR1-10/2	1321.054	1321.453	-302.382	0.497	1631.811	0.602	20	0.328	K.LEAACVGTVESGK.M
R1/RRR1-10/2	1798.766	1798.934	-93.906	0.534	1890.787	0.493	23	0.328	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1436.041	1436.569	-1067.506	0.484	1730.048	0.557	19	0.328	R.AFAEASM*TTAYEK.K
R1/RRR1-10/3	1777.103	1777.908	-1019.135	0.542	2303.031	0.441	33	0.321	R.DATDDKVTVEAAEATLK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1798.414	1798.934	-847.982	0.508	1775.282	0.504	22	0.314	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1777.028	1777.908	-1061.027	0.538	1749.970	0.486	25	0.309	R.DATDDKVTVEAAEATLK.Y
R1/RRR1-10/2	1420.108	1420.570	-326.037	0.496	1774.112	0.465	19	0.307	R.AFAEASMTTAYEK.K
R1/RRR1-10/2	1798.460	1798.934	-264.254	0.513	1682.413	0.505	22	0.301	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1778.378	1777.908	264.882	0.572	1641.164	0.498	23	0.295	R.DATDDKVTVEAAEATLK.Y
R1/RRR1-10/2	1497.284	1496.694	-274.642	0.572	1544.312	0.488	22	0.284	K.DLALLIHGSSNVTR.S
R1/RRR1-10/2	1496.302	1496.694	-262.957	0.521	1535.711	0.487	22	0.283	K.DLALLIHGSSNVTR.S
R1/RRR1-1/2	1798.819	1798.934	-64.363	0.434	1642.236	0.449	23	0.282	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1798.440	1798.934	-275.354	0.524	1545.836	0.482	21	0.276	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1797.540	1798.934	-1335.813	0.394	1605.703	0.441	22	0.275	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1496.357	1496.694	-225.554	0.527	1432.320	0.490	22	0.272	K.DLALLIHGSSNVTR.S
R1/RRR1-10/2	1252.354	1252.505	-120.800	0.541	1113.074	0.489	18	0.244	R.LIDDMVAYALK.S
R1/RRR1-10/2	1135.214	1136.285	-1829.581	0.379	1317.160	0.416	15	0.243	K.YYDLGVLHR.D
R1/RRR1-10/2	1252.131	1252.505	-299.665	0.551	1047.376	0.503	18	0.242	R.LIDDMVAYALK.S
R1/RRR1-1/2	1760.315	1760.969	-942.565	0.443	1456.812	0.357	19	0.240	R.FKDIFQEVYEAGWK.S
R1/RRR1-10/2	1252.320	1252.505	-148.080	0.574	1060.684	0.477	18	0.237	R.LIDDMVAYALK.S
R1/RRR1-10/2	1269.259	1268.505	-194.212	0.515	1038.202	0.473	18	0.235	R.LIDDM*VAYALK.S
R1/RRR1-10/2	1135.326	1136.285	-1730.185	0.405	1306.389	0.377	15	0.235	K.YYDLGVLHR.D
R1/RRR1-10/2	1577.999	1577.888	70.249	0.474	1452.287	0.310	20	0.232	K.DKLIFPFLDLDIK.Y
R1/RRR1-1/2	1799.195	1798.934	145.383	0.478	1267.072	0.403	20	0.229	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1135.378	1136.285	-1684.599	0.463	1060.621	0.435	14	0.228	K.YYDLGVLHR.D
R1/RRR1-10/2	993.970	994.045	-75.892	0.346	892.174	0.530	13	0.228	R.HAFGDQYR.C
R1/RRR1-3/2	1799.522	1798.934	-229.807	0.503	1077.256	0.470	19	0.227	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1269.569	1268.505	51.081	0.473	917.966	0.469	17	0.226	R.LIDDM*VAYALK.S
R1/RRR1-10/2	993.851	994.045	-196.015	0.368	810.512	0.526	12	0.223	R.HAFGDQYR.C
R1/RRR1-2/2	1798.827	1798.934	-59.870	0.460	1101.424	0.436	19	0.223	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	993.560	994.045	-489.607	0.353	696.719	0.535	12	0.218	R.HAFGDQYR.C
R1/RRR1-10/2	1268.189	1268.505	-249.889	0.366	950.695	0.353	17	0.208	R.LIDDM*VAYALK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1800.162	1798.934	127.077	0.425	920.929	0.390	17	0.203	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1056.375	1057.226	-1757.037	0.328	1071.511	0.262	16	0.199	-.ATDAVLKGPGK.-
R1/RRR1-10/3	1798.854	1798.934	-44.971	0.482	1552.378	0.503	30	0.192	K.GGETSTNSIASIFAWTR.G
R1/RRR1-10/2	1134.011	1134.216	-181.020	0.404	912.933	0.220	17	0.192	K.CATITPDEAR.V
R1/RRR1-10/2	1577.438	1577.888	-286.378	0.456	966.740	0.262	17	0.191	-.DKLIFPFLDLDIK.-
R1/RRR1-10/2	1133.981	1134.216	-207.261	0.337	819.430	0.229	16	0.190	K.CATITPDEAR.V
R1/RRR1-10/2	1133.413	1134.216	-1594.941	0.289	630.328	0.251	15	0.188	-.CATITPDEAR.-
R1/RRR1-10/3	1799.026	1798.934	51.198	0.418	989.076	0.406	27	0.102	K.GGETSTNSIASIFAWTR.G
R1/RRR1-6/2	1427.355	1427.588	-163.718	0.473	2330.851	0.620	21	0.466	K.STVHDVVLVGGSTR.I
R1/RRR1-6/2	1427.046	1427.588	-1084.272	0.444	2118.453	0.574	21	0.402	K.STVHDVVLVGGSTR.I
R1/RRR1-6/2	1427.315	1427.588	-192.288	0.463	2024.624	0.587	20	0.389	K.STVHDVVLVGGSTR.I
R1/RRR1-6/2	1544.386	1544.752	-237.671	0.497	1704.285	0.459	22	0.297	K.M*KETAEAYLGSTVK.N
R1/RRR1-6/2	1247.910	1248.435	-1225.657	0.500	1301.581	0.511	19	0.264	K.DAGVISGLNVM*R.I
R1/RRR1-6/2	1247.601	1248.435	-1474.052	0.447	1396.760	0.466	19	0.262	K.DAGVISGLNVM*R.I
R1/RRR1-6/2	1544.531	1544.752	-143.713	0.546	1311.460	0.489	20	0.256	K.M*KETAEAYLGSTVK.N
R1/RRR1-6/2	1248.083	1248.435	-282.553	0.512	1352.572	0.458	19	0.256	K.DAGVISGLNVM*R.I
R1/RRR1-6/2	1544.299	1544.752	-294.372	0.510	1298.320	0.448	20	0.246	K.M*KETAEAYLGSTVK.N
R1/RRR1-6/2	1584.351	1583.788	-276.627	0.552	1181.612	0.456	23	0.241	K.QFSAEEISSMVLNK.M
R1/RRR1-6/2	1583.147	1583.788	-1039.771	0.501	993.856	0.405	21	0.216	-.QFSAEEISSMVLNK.-
R1/RRR1-6/2	1269.066	1269.383	-250.129	0.335	1135.640	0.346	16	0.212	K.ETAEAYLGSTVK.N
R1/RRR1-6/2	1583.622	1583.788	-105.426	0.520	926.559	0.343	20	0.201	-.QFSAEEISSMVLNK.-
R1/RRR1-14/2	1544.068	1544.752	-1094.104	0.355	867.789	0.236	16	0.186	K.M*KETAEAYLGSTVK.N
R1/RRR1-6/2	1599.362	1599.788	-267.021	0.463	521.640	0.223	18	0.186	K.QFSAEEISSM*VLNK.M
R1/RRR1-6/3	1544.558	1544.752	-125.923	0.481	1527.138	0.421	30	0.151	K.M*KETAEAYLGSTVK.N
R1/RRR1-6/3	1544.128	1544.752	-1054.900	0.404	1092.967	0.342	25	0.095	K.M*KETAEAYLGSTVK.N
R1/RRR1-6/3	1544.270	1544.752	-313.018	0.338	685.342	0.282	22	0.075	-.M*KETAEAYLGSTVK.-
R1/RRR1-6/3	1528.106	1528.753	-1080.838	0.318	835.663	0.208	24	0.069	K.MKETAEAYLGSTVK.N
R1/RRR1-5/2	1846.358	1847.057	-922.778	0.578	2391.253	0.590	24	0.467	R.KPEEITKEEYAAFYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1846.415	1847.057	-892.247	0.574	2442.366	0.551	24	0.462	R.KPEEITKEEYAAFYK.S
R1/RRR1-5/2	1846.544	1847.057	-821.967	0.618	1929.713	0.566	22	0.363	R.KPEEITKEEYAAFYK.S
R1/RRR1-5/2	1839.571	1838.052	-262.409	0.632	1332.956	0.574	22	0.280	K.HSEFISYPISLWTEK.T
R1/RRR1-5/2	1542.508	1542.675	-108.554	0.520	1315.257	0.471	19	0.254	K.SLTNDWEEHLAVK.H
R1/RRR1-5/2	1839.681	1838.052	-202.229	0.586	1255.429	0.503	21	0.253	K.HSEFISYPISLWTEK.T
R1/RRR1-5/2	1528.331	1528.689	-235.416	0.519	1331.154	0.441	22	0.249	K.GIVDSEDLPLNISR.Q
R1/RRR1-5/2	1584.348	1584.710	-228.792	0.522	1268.213	0.475	19	0.248	K.SGDELTSLKDYVTR.M
R1/RRR1-2/2	1529.315	1528.689	-245.752	0.537	1331.842	0.403	21	0.239	K.GIVDSEDLPLNISR.Q
R1/RRR1-5/2	1262.028	1262.437	-324.868	0.503	1243.200	0.418	17	0.237	K.KAVENSPFLEK.L
R1/RRR1-5/2	1542.362	1542.675	-203.585	0.528	1119.808	0.471	18	0.236	K.SLTNDWEEHLAVK.H
R1/RRR1-3/2	1529.188	1528.689	327.022	0.518	1161.738	0.440	21	0.235	K.GIVDSEDLPLNISR.Q
R1/RRR1-5/2	1584.400	1584.710	-196.406	0.506	1031.511	0.506	18	0.235	K.SGDELTSLKDYVTR.M
R1/RRR1-6/2	1528.633	1528.689	-37.053	0.515	1223.559	0.395	21	0.230	K.GIVDSEDLPLNISR.Q
R1/RRR1-4/2	1529.254	1528.689	-285.553	0.533	1278.867	0.379	21	0.230	K.GIVDSEDLPLNISR.Q
R1/RRR1-5/2	1528.334	1528.689	-233.172	0.493	1228.586	0.376	21	0.227	K.GIVDSEDLPLNISR.Q
R1/RRR1-5/2	1321.959	1321.463	376.711	0.523	799.196	0.523	16	0.227	K.HFSVEGQLEFK.A
R1/RRR1-5/2	1542.190	1542.675	-315.311	0.525	1162.744	0.420	17	0.227	K.SLTNDWEEHLAVK.H
R1/RRR1-5/2	1584.359	1584.710	-222.068	0.514	926.093	0.503	17	0.226	K.SGDELTSLKDYVTR.M
R1/RRR1-6/2	1528.247	1528.689	-290.709	0.445	1142.918	0.389	20	0.224	K.GIVDSEDLPLNISR.Q
R1/RRR1-5/2	1528.068	1528.689	-1064.109	0.393	1163.188	0.371	21	0.223	K.GIVDSEDLPLNISR.Q
R1/RRR1-3/2	1528.393	1528.689	-194.551	0.478	1246.503	0.346	21	0.223	K.GIVDSEDLPLNISR.Q
R1/RRR1-6/2	1273.575	1273.421	120.881	0.508	1074.370	0.400	18	0.221	K.SDLVNNLGTIAR.S
R1/RRR1-1/2	1529.213	1528.689	-312.783	0.529	1018.451	0.413	20	0.220	K.GIVDSEDLPLNISR.Q
R1/RRR1-3/2	1529.225	1528.689	-304.694	0.518	1069.759	0.398	19	0.218	K.GIVDSEDLPLNISR.Q
R1/RRR1-6/2	1584.398	1584.710	-197.720	0.496	881.978	0.466	17	0.217	K.SGDELTSLKDYVTR.M
R1/RRR1-6/2	1527.572	1528.689	-1390.349	0.361	1329.703	0.273	21	0.217	K.GIVDSEDLPLNISR.Q
R1/RRR1-1/2	1528.438	1528.689	-164.826	0.492	1132.732	0.354	20	0.216	K.GIVDSEDLPLNISR.Q
R1/RRR1-6/2	1542.276	1542.675	-259.247	0.495	822.703	0.432	18	0.212	K.SLTNDWEEHLAVK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1321.729	1321.463	202.487	0.471	827.838	0.416	16	0.211	K.HFSVEGQLEFK.A
R1/RRR1-5/2	1133.960	1134.264	-268.918	0.428	758.473	0.422	15	0.211	K.AVENSPFLEK.L
R1/RRR1-5/2	1134.024	1134.264	-211.788	0.470	672.737	0.422	14	0.207	K.AVENSPFLEK.L
R1/RRR1-1/2	1527.680	1528.689	-1319.563	0.337	1064.621	0.307	19	0.206	K.GIVDSEDLPLNISR.Q
R1/RRR1-1/2	1584.399	1584.710	-196.561	0.460	705.093	0.445	16	0.206	K.SGDELTSLKDYVTR.M
R1/RRR1-6/2	1542.510	1542.675	-107.205	0.477	550.463	0.449	16	0.205	K.SLTNDWEEHLAVK.H
R1/RRR1-5/2	1262.090	1262.437	-275.279	0.464	716.346	0.401	15	0.204	K.KAVENSPFLEK.L
R1/RRR1-5/3	1321.545	1321.463	62.377	0.596	1625.374	0.526	24	0.202	K.HFSVEGQLEFK.A
R1/RRR1-5/2	1357.126	1357.621	-366.068	0.456	1119.076	0.276	17	0.201	K.VIKEVLGDKVEK.V
R1/RRR1-5/2	1081.679	1082.191	-1401.829	0.403	750.012	0.342	14	0.201	R.APFDLFDTR.K
R1/RRR1-5/2	1262.110	1262.437	-259.850	0.509	774.148	0.355	15	0.199	K.KAVENSPFLEK.L
R1/RRR1-5/2	1133.483	1134.264	-1576.157	0.355	503.613	0.391	13	0.199	K.AVENSPFLEK.L
R1/RRR1-3/2	1273.276	1273.421	-114.680	0.371	668.025	0.388	15	0.198	K.SDLVNNLGTIAR.S
R1/RRR1-5/2	1357.439	1357.621	-134.809	0.425	873.890	0.341	15	0.198	K.VIKEVLGDKVEK.V
R1/RRR1-2/2	1584.403	1584.710	-193.933	0.496	804.630	0.373	16	0.198	K.SGDELTSLKDYVTR.M
R1/RRR1-5/2	1081.557	1082.191	-1515.191	0.375	730.937	0.329	13	0.198	R.APFDLFDTR.K
R1/RRR1-5/2	1274.159	1273.421	-205.984	0.391	635.631	0.411	13	0.196	-.SDLVNNLGTIAR.-
R1/RRR1-5/3	1320.965	1321.463	-377.628	0.597	1614.188	0.503	23	0.195	K.HFSVEGQLEFK.A
R1/RRR1-6/2	1134.089	1134.264	-154.557	0.319	493.194	0.339	13	0.194	K.AVENSPFLEK.L
R1/RRR1-1/2	1320.739	1321.463	-1308.838	0.274	435.516	0.383	13	0.192	K.HFSVEGQLEFK.A
R1/RRR1-4/2	1527.781	1528.689	-1252.799	0.333	917.928	0.207	19	0.191	K.GIVDSEDLPLNISR.Q
R1/RRR1-6/3	1846.819	1847.057	-129.457	0.546	1351.483	0.560	31	0.172	R.KPEEITKEEYAAFYK.S
R1/RRR1-2/3	1846.553	1847.057	-817.263	0.494	1284.610	0.564	28	0.169	R.KPEEITKEEYAAFYK.S
R1/RRR1-5/2	1081.846	1082.191	-319.672	0.288	442.882	0.393	10	0.169	-.APFDLFDTR.-
R1/RRR1-5/3	1528.858	1528.689	110.538	0.517	1580.754	0.382	29	0.149	K.GIVDSEDLPLNISR.Q
R1/RRR1-6/3	1846.642	1847.057	-225.641	0.522	1177.597	0.516	29	0.142	R.KPEEITKEEYAAFYK.S
R1/RRR1-6/3	1847.171	1847.057	61.662	0.545	1110.494	0.490	30	0.128	R.KPEEITKEEYAAFYK.S
R1/RRR1-4/3	1584.800	1584.710	57.153	0.528	1188.862	0.464	28	0.128	K.SGDELTSLKDYVTR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	1847.514	1847.057	248.236	0.516	904.321	0.536	27	0.126	R.KPEEITKEEYAAFYK.S
R1/RRR1-5/3	1585.818	1584.710	68.543	0.520	1060.741	0.467	26	0.120	K.SGDELTSLKDYVTR.M
R1/RRR1-2/3	1847.760	1847.057	-161.330	0.481	938.462	0.492	26	0.119	R.KPEEITKEEYAAFYK.S
R1/RRR1-5/3	1528.260	1528.689	-282.143	0.437	1217.991	0.418	26	0.119	K.GIVDSEDLPLNISR.Q
R1/RRR1-3/3	1585.355	1584.710	-224.756	0.468	1039.118	0.467	26	0.117	K.SGDELTSLKDYVTR.M
R1/RRR1-7/3	1847.261	1847.057	110.872	0.462	860.864	0.458	24	0.110	R.KPEEITKEEYAAFYK.S
R1/RRR1-1/3	1845.617	1847.057	-1325.967	0.428	929.267	0.444	24	0.110	R.KPEEITKEEYAAFYK.S
R1/RRR1-5/3	1585.254	1584.710	-288.720	0.472	985.304	0.443	25	0.110	K.SGDELTSLKDYVTR.M
R1/RRR1-5/3	1846.314	1847.057	-946.979	0.491	767.082	0.475	26	0.108	R.KPEEITKEEYAAFYK.S
R1/RRR1-4/3	1847.874	1847.057	-99.302	0.420	950.252	0.419	26	0.104	R.KPEEITKEEYAAFYK.S
R1/RRR1-4/3	1846.633	1847.057	-230.516	0.448	572.290	0.458	22	0.103	R.KPEEITKEEYAAFYK.S
R1/RRR1-3/3	1847.622	1847.057	-235.992	0.472	443.659	0.446	20	0.099	-.KPEEITKEEYAAFYK.-
R1/RRR1-5/3	1527.956	1528.689	-1137.797	0.459	1249.479	0.291	24	0.097	K.GIVDSEDLPLNISR.Q
R1/RRR1-4/3	1584.361	1584.710	-220.685	0.447	753.476	0.458	24	0.095	-.SGDELTSLKDYVTR.-
R1/RRR1-3/3	1585.225	1584.710	-306.567	0.363	690.389	0.368	22	0.087	K.SGDELTSLKDYVTR.M
R1/RRR1-5/3	1965.694	1966.225	-780.870	0.366	965.573	0.343	24	0.086	K.KHSEFISYPISLWTEK.T
R1/RRR1-5/3	1585.808	1584.710	62.174	0.474	931.666	0.325	25	0.086	-.SGDELTSLKDYVTR.-
R1/RRR1-6/2	1496.433	1496.694	-174.897	0.566	2860.765	0.572	23	0.577	K.SQIHEIVLVGGSTR.I
R1/RRR1-6/2	1496.314	1496.694	-254.773	0.525	2737.539	0.549	23	0.534	K.SQIHEIVLVGGSTR.I
R1/RRR1-6/2	1496.370	1496.694	-216.879	0.560	2659.904	0.572	22	0.524	K.SQIHEIVLVGGSTR.I
R1/RRR1-6/2	1537.117	1537.620	-980.661	0.481	1734.679	0.480	20	0.306	K.NGHVEIIANDQGNR.I
R1/RRR1-6/2	1538.238	1537.620	-248.943	0.529	1533.437	0.532	20	0.293	K.NGHVEIIANDQGNR.I
R1/RRR1-6/2	1537.393	1537.620	-147.779	0.479	1592.726	0.466	20	0.283	K.NGHVEIIANDQGNR.I
R1/RRR1-6/2	1507.245	1507.777	-1019.430	0.356	1553.833	0.445	21	0.272	K.VFSPEEVSAMILGK.M
R1/RRR1-6/2	1507.490	1507.777	-190.508	0.384	1437.042	0.437	21	0.258	K.VFSPEEVSAMILGK.M
R1/RRR1-6/2	1524.226	1524.663	-287.459	0.516	1214.521	0.464	18	0.244	R.ARFEELNNDLFR.K
R1/RRR1-6/2	1524.366	1524.663	-195.386	0.469	1252.479	0.413	19	0.237	R.ARFEELNNDLFR.K
R1/RRR1-6/2	1507.198	1507.777	-1050.737	0.288	1269.130	0.360	19	0.223	K.VFSPEEVSAMILGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1143.639	1144.305	-1461.524	0.373	736.227	0.461	17	0.208	-.FDLSGIPAAPR.-
R1/RRR1-6/2	1524.471	1524.663	-125.821	0.350	878.474	0.372	17	0.205	R.ARFEELNNDLFR.K
R1/RRR1-6/2	1402.901	1403.585	-1204.170	0.356	912.746	0.359	15	0.203	R.NQLETYVYNMK.N
R1/RRR1-6/3	1384.832	1385.612	-1288.692	0.518	1923.033	0.396	29	0.198	K.M*KETAEAYLGKK.I
R1/RRR1-6/2	1226.455	1227.305	-1512.579	0.345	729.059	0.362	13	0.197	-.DYFEGKEPNK.-
R1/RRR1-6/2	1402.974	1403.585	-1152.270	0.375	821.141	0.295	14	0.192	R.NQLETYVYNMK.N
R1/RRR1-6/2	1226.387	1227.305	-1568.071	0.337	711.188	0.207	13	0.185	R.DYFEGKEPNK.G
R1/RRR1-6/3	1653.258	1652.835	256.335	0.547	1763.211	0.400	26	0.185	R.ARFEELNNDLFRK.T
R1/RRR1-6/2	1227.089	1227.305	-176.568	0.360	586.857	0.293	12	0.184	-.DYFEGKEPNK.-
R1/RRR1-6/2	1297.152	1297.398	-190.534	0.332	868.411	0.207	13	0.183	R.FEELNNDLFR.K
R1/RRR1-6/3	1537.210	1537.620	-267.159	0.495	1716.060	0.384	28	0.171	K.NGHVEIIANDQGNR.I
R1/RRR1-6/3	1652.992	1652.835	94.830	0.566	1675.263	0.387	25	0.169	R.ARFEELNNDLFRK.T
R1/RRR1-6/3	1537.528	1537.620	-59.980	0.517	1362.849	0.444	26	0.144	K.NGHVEIIANDQGNR.I
R1/RRR1-6/2	1970.313	1970.856	-785.371	0.471	990.552	0.504	24	0.128	R.TGGAPGGGADGEGGGDDEHDEL.-
R1/RRR1-6/3	1652.263	1652.835	-954.565	0.539	1150.767	0.423	23	0.119	R.ARFEELNNDLFRK.T
R1/RRR1-6/2	1970.304	1970.856	-790.284	0.463	798.300	0.534	22	0.116	R.TGGAPGGGADGEGGGDDEHDEL.-
R1/RRR1-6/2	1970.243	1970.856	-821.442	0.439	774.620	0.484	24	0.108	R.TGGAPGGGADGEGGGDDEHDEL.-
R1/RRR1-6/3	1524.737	1524.663	48.925	0.576	1175.812	0.349	24	0.102	R.ARFEELNNDLFR.K
R1/RRR1-6/3	1524.667	1524.663	3.034	0.564	1108.288	0.342	23	0.097	R.ARFEELNNDLFR.K
R1/RRR1-6/3	1384.705	1385.612	-1380.856	0.429	1222.121	0.304	24	0.093	K.M*KETAEAYLGKK.I
R1/RRR1-6/3	1385.000	1385.612	-1166.806	0.459	1191.964	0.273	24	0.087	K.M*KETAEAYLGKK.I
R1/RRR1-6/3	1502.274	1502.783	-1007.694	0.356	1273.242	0.229	25	0.082	K.IVNKDGKPYIQVK.I
R1/RRR1-6/3	1524.269	1524.663	-259.145	0.522	973.038	0.262	24	0.078	R.ARFEELNNDLFR.K
R1/RRR1-6/3	1502.841	1502.783	38.436	0.355	701.779	0.274	21	0.075	K.IVNKDGKPYIQVK.I
R1/RRR1-6/3	1503.632	1502.783	-100.743	0.376	977.416	0.246	22	0.073	-.IVNKDGKPYIQVK.-
R1/RRR1-6/3	1538.505	1537.620	-74.904	0.418	766.027	0.197	21	0.062	-.NGHVEIIANDQGNR.-
R1/RRR1-4/2	1290.379	1291.478	-1631.496	0.471	2093.159	0.525	19	0.377	R.AIADGSLLDFLR.Q
R1/RRR1-4/2	1291.246	1291.478	-180.406	0.538	2046.753	0.524	19	0.368	R.AIADGSLLDFLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1291.189	1291.478	-224.792	0.509	1938.179	0.541	19	0.356	R.AIADGSLLDFLR.Q
R1/RRR1-3/2	1292.119	1291.478	-278.452	0.534	1812.672	0.565	18	0.343	R.AIADGSLLDFLR.Q
R1/RRR1-5/2	1291.235	1291.478	-188.657	0.501	1815.037	0.538	19	0.335	R.AIADGSLLDFLR.Q
R1/RRR1-4/2	1077.449	1077.212	220.156	0.514	1418.491	0.488	16	0.270	K.SPAEVFDALK.S
R1/RRR1-5/2	1290.742	1291.478	-1348.646	0.436	1277.531	0.567	16	0.269	R.AIADGSLLDFLR.Q
R1/RRR1-4/2	1077.195	1077.212	-16.096	0.493	1392.787	0.489	16	0.268	K.SPAEVFDALK.S
R1/RRR1-4/2	1886.511	1886.995	-257.437	0.542	1393.753	0.466	23	0.259	K.DITPDDKQELDEALQR.E
R1/RRR1-4/2	1887.390	1886.995	210.077	0.508	1391.276	0.434	24	0.253	K.DITPDDKQELDEALQR.E
R1/RRR1-4/2	1328.269	1328.497	-172.059	0.505	1296.868	0.471	19	0.252	K.LADLESAPAALTR.L
R1/RRR1-4/2	1328.227	1328.497	-203.683	0.496	1159.118	0.471	18	0.239	K.LADLESAPAALTR.L
R1/RRR1-1/2	1077.759	1077.212	-421.650	0.346	1121.178	0.484	14	0.236	K.SPAEVFDALK.S
R1/RRR1-3/2	1077.726	1077.212	-452.791	0.380	1291.984	0.394	15	0.236	K.SPAEVFDALK.S
R1/RRR1-3/2	1078.231	1077.212	17.418	0.410	1113.776	0.465	14	0.235	K.SPAEVFDALK.S
R1/RRR1-4/2	1853.432	1853.070	196.090	0.536	903.974	0.584	18	0.234	K.SQTVDLVLTAHPTQSVR.R
R1/RRR1-5/2	1329.233	1328.497	-199.292	0.447	1140.241	0.440	17	0.231	K.LADLESAPAALTR.L
R1/RRR1-2/2	1329.236	1328.497	-196.988	0.392	1294.016	0.372	18	0.230	K.LADLESAPAALTR.L
R1/RRR1-3/2	1291.455	1291.478	-17.502	0.408	877.369	0.522	16	0.228	R.AIADGSLLDFLR.Q
R1/RRR1-4/2	1886.565	1886.995	-228.550	0.541	1066.943	0.456	20	0.225	K.DITPDDKQELDEALQR.E
R1/RRR1-4/2	1327.751	1328.497	-1318.801	0.394	1125.213	0.396	18	0.223	K.LADLESAPAALTR.L
R1/RRR1-1/2	1328.530	1328.497	25.380	0.402	1150.412	0.386	17	0.222	K.LADLESAPAALTR.L
R1/RRR1-4/2	1077.164	1077.212	-44.626	0.398	873.181	0.471	13	0.220	K.SPAEVFDALK.S
R1/RRR1-5/2	1328.422	1328.497	-56.094	0.357	933.058	0.398	16	0.210	K.LADLESAPAALTR.L
R1/RRR1-2/2	1291.525	1291.478	36.251	0.425	819.721	0.408	15	0.208	R.AIADGSLLDFLR.Q
R1/RRR1-3/2	1328.077	1328.497	-317.101	0.318	1208.986	0.240	18	0.203	K.LADLESAPAALTR.L
R1/RRR1-4/2	1125.330	1125.293	32.247	0.355	1118.667	0.268	14	0.202	R.NCLVQLYSK.D
R1/RRR1-1/2	1291.783	1291.478	236.989	0.385	561.204	0.398	15	0.202	R.AIADGSLLDFLR.Q
R1/RRR1-1/2	1077.609	1077.212	368.964	0.372	513.896	0.418	11	0.198	-.SPAEVFDALK.-
R1/RRR1-3/2	1077.152	1077.212	-55.993	0.337	530.312	0.287	12	0.193	K.SPAEVFDALK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1328.371	1328.497	-94.900	0.326	1001.823	0.222	17	0.192	K.LADLESAPAALTR.L
R1/RRR1-1/2	1078.021	1077.212	-177.474	0.282	485.900	0.296	11	0.185	-.SPAEVFDALK.-
R1/RRR1-4/3	1473.779	1473.659	81.937	0.519	1580.468	0.313	24	0.131	R.RQEWLLSELNGK.R
R1/RRR1-4/3	1886.853	1886.995	-75.156	0.485	1222.434	0.386	28	0.116	K.DITPDDKQELDEALQR.E
R1/RRR1-4/3	1886.088	1886.995	-1014.288	0.496	1234.002	0.376	28	0.115	K.DITPDDKQELDEALQR.E
R1/RRR1-4/3	1887.041	1886.995	24.609	0.494	932.823	0.403	26	0.101	K.DITPDDKQELDEALQR.E
R1/RRR1-4/3	1473.846	1473.659	127.665	0.486	1365.946	0.262	23	0.098	R.RQEWLLSELNGK.R
R1/RRR1-4/3	1168.338	1168.373	-30.361	0.499	1228.922	0.337	23	0.097	K.RPLFGPDLPR.T
R1/RRR1-4/3	1168.167	1168.373	-176.420	0.423	1037.620	0.371	21	0.093	K.RPLFGPDLPR.T
R1/RRR1-4/3	1168.434	1168.373	52.004	0.429	1002.032	0.332	20	0.086	K.RPLFGPDLPR.T
R1/RRR1-5/2	1819.319	1819.945	-896.518	0.524	2217.085	0.541	24	0.407	K.NATLTNEKESDACPIR.A
R1/RRR1-3/2	1815.316	1815.062	140.787	0.573	2162.388	0.575	24	0.403	K.AYLPVIESFGFSSQLR.A
R1/RRR1-13/2	1815.079	1815.062	9.740	0.562	2138.858	0.572	25	0.398	K.AYLPVIESFGFSSQLR.A
R1/RRR1-1/2	1814.699	1815.062	-200.155	0.519	2165.865	0.539	25	0.392	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1814.410	1815.062	-912.912	0.514	2188.264	0.522	25	0.390	K.AYLPVIESFGFSSQLR.A
R1/RRR1-13/2	1815.547	1815.062	268.361	0.584	2063.324	0.579	25	0.387	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/2	1815.349	1815.062	158.860	0.593	2091.827	0.559	24	0.383	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/2	1814.708	1815.062	-195.161	0.533	2042.496	0.521	24	0.362	K.AYLPVIESFGFSSQLR.A
R1/RRR1-2/2	1815.846	1815.062	-118.914	0.578	1872.894	0.583	24	0.354	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/2	1819.231	1819.945	-945.018	0.536	1878.293	0.549	22	0.347	K.NATLTNEKESDACPIR.A
R1/RRR1-4/2	1819.531	1819.945	-228.491	0.554	1897.758	0.539	22	0.346	K.NATLTNEKESDACPIR.A
R1/RRR1-5/2	1819.557	1819.945	-213.819	0.558	1955.386	0.509	22	0.345	K.NATLTNEKESDACPIR.A
R1/RRR1-3/2	1814.207	1815.062	-1025.516	0.496	1897.979	0.538	23	0.344	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/2	1815.347	1815.062	157.646	0.581	1824.303	0.569	24	0.342	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1815.764	1815.062	-164.233	0.606	1745.306	0.597	24	0.339	K.AYLPVIESFGFSSQLR.A
R1/RRR1-13/2	1814.289	1815.062	-979.782	0.508	1937.715	0.493	24	0.336	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1814.505	1815.062	-860.435	0.543	1866.121	0.504	24	0.328	K.AYLPVIESFGFSSQLR.A
R1/RRR1-3/2	1814.708	1815.062	-195.431	0.507	1798.017	0.523	23	0.324	K.AYLPVIESFGFSSQLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1819.269	1819.945	-924.337	0.511	1685.020	0.529	22	0.311	K.NATLTNEKESDACPIR.A
R1/RRR1-2/2	1814.214	1815.062	-1021.395	0.490	1676.019	0.536	22	0.310	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1820.354	1819.945	225.077	0.550	1653.870	0.517	21	0.301	K.NATLTNEKESDACPIR.A
R1/RRR1-4/2	1347.244	1347.588	-256.153	0.464	1450.771	0.578	19	0.296	R.VIYASQLTAKPR.L
R1/RRR1-12/2	1814.297	1815.062	-975.459	0.507	1630.815	0.506	22	0.295	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1389.419	1388.586	-120.515	0.503	1615.712	0.494	17	0.294	R.GFVQFCYEPIK.Q
R1/RRR1-4/2	1815.557	1815.062	273.755	0.488	1445.376	0.554	21	0.284	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/2	1425.329	1425.569	-169.105	0.476	1455.979	0.505	20	0.279	R.LWGENFFDPATK.K
R1/RRR1-5/2	1816.115	1815.062	29.622	0.508	1318.577	0.580	21	0.277	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1425.275	1425.569	-207.424	0.475	1427.563	0.481	20	0.270	R.LWGENFFDPATK.K
R1/RRR1-4/2	1816.688	1815.062	-206.204	0.468	1410.861	0.507	21	0.269	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1424.897	1425.569	-1177.505	0.471	1371.711	0.502	19	0.268	R.LWGENFFDPATK.K
R1/RRR1-4/2	1815.862	1815.062	-110.081	0.457	1393.744	0.516	19	0.267	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/2	1426.204	1425.569	-256.909	0.488	1244.454	0.518	19	0.260	R.LWGENFFDPATK.K
R1/RRR1-4/2	1348.215	1347.588	-277.764	0.496	1185.124	0.547	18	0.259	R.VIYASQLTAKPR.L
R1/RRR1-4/2	1347.145	1347.588	-329.426	0.478	1225.012	0.518	18	0.257	R.VIYASQLTAKPR.L
R1/RRR1-2/2	1652.180	1651.841	205.525	0.499	1625.145	0.347	19	0.252	K.ILSEEFGWDKDLAK.K
R1/RRR1-5/2	1347.203	1347.588	-286.879	0.474	1065.262	0.564	17	0.251	R.VIYASQLTAKPR.L
R1/RRR1-2/2	1813.729	1815.062	-1289.867	0.379	1370.046	0.440	22	0.250	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1651.277	1651.841	-950.308	0.506	1554.169	0.357	19	0.247	K.ILSEEFGWDKDLAK.K
R1/RRR1-1/2	1652.339	1651.841	302.427	0.496	1406.449	0.405	18	0.244	K.ILSEEFGWDKDLAK.K
R1/RRR1-5/2	1425.220	1425.569	-245.661	0.521	1189.101	0.471	18	0.244	R.LWGENFFDPATK.K
R1/RRR1-4/2	1389.372	1388.586	-154.006	0.405	1148.544	0.480	15	0.239	R.GFVQFCYEPIK.Q
R1/RRR1-4/2	1640.258	1639.845	252.096	0.584	1073.792	0.504	20	0.239	R.NCDPEGPLM*LYVSK.M
R1/RRR1-4/2	1650.791	1651.841	-1245.704	0.494	1573.609	0.310	19	0.238	K.ILSEEFGWDKDLAK.K
R1/RRR1-1/2	1425.447	1425.569	-86.118	0.445	1180.098	0.415	18	0.232	R.LWGENFFDPATK.K
R1/RRR1-5/3	1820.031	1819.945	47.378	0.438	1784.918	0.515	30	0.232	K.NATLTNEKESDACPIR.A
R1/RRR1-4/2	1652.389	1651.841	-274.203	0.499	1378.103	0.359	18	0.231	K.ILSEEFGWDKDLAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1425.282	1425.569	-202.269	0.487	987.739	0.476	17	0.230	R.LWGENFFDPATK.K
R1/RRR1-3/2	1347.096	1347.588	-366.521	0.441	963.388	0.499	16	0.229	R.VIYASQLTAKPR.L
R1/RRR1-1/2	1816.142	1815.062	44.588	0.395	975.598	0.487	21	0.228	K.AYLPVIESFGFSSQLR.A
R1/RRR1-2/2	1426.429	1425.569	-98.418	0.435	951.388	0.480	17	0.228	R.LWGENFFDPATK.K
R1/RRR1-5/2	1553.501	1553.742	-155.862	0.431	1149.857	0.407	20	0.228	R.LWGENFFDPATKK.W
R1/RRR1-4/2	1388.171	1388.586	-299.669	0.416	1331.963	0.332	16	0.226	R.GFVQFCYEPIK.Q
R1/RRR1-1/2	1651.545	1651.841	-179.673	0.502	1385.279	0.330	18	0.225	K.ILSEEFGWDKDLAK.K
R1/RRR1-5/2	1639.381	1639.845	-284.005	0.448	1133.493	0.376	21	0.221	R.NCDPEGPLM*LYVSK.M
R1/RRR1-2/2	1425.469	1425.569	-70.312	0.446	891.858	0.460	16	0.221	R.LWGENFFDPATK.K
R1/RRR1-13/2	1651.125	1651.841	-1042.642	0.459	1374.305	0.308	17	0.220	K.ILSEEFGWDKDLAK.K
R1/RRR1-1/2	1425.802	1425.569	163.448	0.404	787.090	0.477	16	0.218	R.LWGENFFDPATK.K
R1/RRR1-5/2	1814.618	1815.062	-245.101	0.358	920.866	0.437	19	0.215	K.AYLPVIESFGFSSQLR.A
R1/RRR1-7/2	1814.867	1815.062	-107.645	0.413	897.801	0.457	17	0.215	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/2	1641.284	1639.845	267.753	0.541	973.215	0.397	20	0.213	R.NCDPEGPLM*LYVSK.M
R1/RRR1-1/2	1425.704	1425.569	94.929	0.383	934.357	0.389	17	0.213	R.LWGENFFDPATK.K
R1/RRR1-2/2	956.184	956.081	107.353	0.382	812.169	0.402	15	0.210	R.GGGQVIPTAR.R
R1/RRR1-5/2	1652.366	1651.841	-288.137	0.446	1240.431	0.283	19	0.209	K.ILSEEFGWDKDLAK.K
R1/RRR1-3/2	1387.974	1388.586	-1164.546	0.406	964.044	0.367	14	0.208	R.GFVQFCYEPIK.Q
R1/RRR1-4/2	1120.059	1120.219	-143.485	0.358	861.326	0.386	15	0.205	K.EGALAEENMR.G
R1/RRR1-13/2	955.499	956.081	-1660.757	0.379	658.490	0.393	14	0.204	R.GGGQVIPTAR.R
R1/RRR1-1/2	1651.345	1651.841	-301.290	0.420	1098.094	0.307	17	0.204	K.ILSEEFGWDKDLAK.K
R1/RRR1-5/2	1641.158	1639.845	190.708	0.497	775.353	0.361	18	0.199	R.NCDPEGPLM*LYVSK.M
R1/RRR1-5/2	1639.255	1639.845	-972.895	0.413	906.896	0.309	19	0.198	R.NCDPEGPLM*LYVSK.M
R1/RRR1-12/2	955.944	956.081	-144.423	0.408	668.699	0.316	14	0.197	R.GGGQVIPTAR.R
R1/RRR1-3/2	1425.943	1425.569	262.518	0.372	458.722	0.397	12	0.197	R.LWGENFFDPATK.K
R1/RRR1-5/2	1553.290	1553.742	-292.091	0.362	946.781	0.285	18	0.197	R.LWGENFFDPATKK.W
R1/RRR1-5/2	1553.295	1553.742	-289.095	0.348	759.915	0.339	17	0.197	R.LWGENFFDPATKK.W
R1/RRR1-12/2	956.042	956.081	-41.059	0.375	460.212	0.308	13	0.197	R.GGGQVIPTAR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1426.121	1425.569	-315.304	0.301	401.600	0.357	13	0.196	R.LWGENFFDPATK.K
R1/RRR1-1/2	955.646	956.081	-456.823	0.300	609.472	0.351	13	0.196	R.GGGQVIPTAR.R
R1/RRR1-13/2	955.882	956.081	-209.629	0.370	446.924	0.332	12	0.196	R.GGGQVIPTAR.R
R1/RRR1-12/2	955.530	956.081	-1628.157	0.332	546.635	0.349	13	0.195	-.GGGQVIPTAR.-
R1/RRR1-3/2	1424.889	1425.569	-1182.924	0.285	557.202	0.305	13	0.192	R.LWGENFFDPATK.K
R1/RRR1-4/2	1552.564	1553.742	-1407.241	0.276	817.035	0.282	17	0.191	-.LWGENFFDPATKK.-
R1/RRR1-1/2	1388.608	1388.586	16.082	0.314	564.763	0.271	12	0.188	R.GFVQFCYEPIK.Q
R1/RRR1-5/2	1387.960	1388.586	-1174.349	0.318	671.005	0.246	12	0.186	R.GFVQFCYEPIK.Q
R1/RRR1-3/2	1653.005	1651.841	99.207	0.428	644.566	0.273	14	0.185	K.ILSEEFGWDKDLAK.K
R1/RRR1-4/3	1820.785	1819.945	-88.037	0.443	1521.286	0.480	34	0.167	K.NATLTNEKESDACPIR.A
R1/RRR1-4/3	1504.927	1503.774	101.760	0.479	1633.544	0.413	27	0.163	R.RVIYASQLTAKPR.L
R1/RRR1-4/3	1814.784	1815.062	-153.231	0.436	999.404	0.540	23	0.138	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/3	1814.485	1815.062	-871.315	0.445	1298.589	0.435	27	0.137	K.AYLPVIESFGFSSQLR.A
R1/RRR1-4/3	1819.302	1819.945	-905.888	0.445	1268.103	0.442	31	0.131	K.NATLTNEKESDACPIR.A
R1/RRR1-4/3	1503.913	1503.774	92.344	0.489	1391.067	0.392	27	0.127	R.RVIYASQLTAKPR.L
R1/RRR1-5/3	1820.001	1819.945	30.628	0.404	1162.916	0.458	29	0.126	K.NATLTNEKESDACPIR.A
R1/RRR1-3/3	1820.078	1819.945	73.410	0.424	954.829	0.520	27	0.126	K.NATLTNEKESDACPIR.A
R1/RRR1-4/3	1819.813	1819.945	-72.711	0.424	1278.485	0.423	32	0.125	K.NATLTNEKESDACPIR.A
R1/RRR1-2/3	1820.777	1819.945	-92.375	0.440	1064.339	0.463	29	0.120	K.NATLTNEKESDACPIR.A
R1/RRR1-5/3	1815.048	1815.062	-7.199	0.388	986.341	0.466	22	0.119	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/3	1503.434	1503.774	-227.067	0.468	1181.206	0.392	24	0.112	-.RVIYASQLTAKPR.-
R1/RRR1-3/3	1819.115	1819.945	-1009.059	0.388	960.501	0.454	27	0.111	K.NATLTNEKESDACPIR.A
R1/RRR1-1/3	1814.859	1815.062	-111.835	0.410	899.676	0.461	26	0.109	K.AYLPVIESFGFSSQLR.A
R1/RRR1-3/3	1819.748	1819.945	-108.642	0.403	928.795	0.442	28	0.107	K.NATLTNEKESDACPIR.A
R1/RRR1-2/3	1819.071	1819.945	-1033.314	0.413	929.185	0.430	26	0.107	K.NATLTNEKESDACPIR.A
R1/RRR1-2/3	1820.560	1819.945	-212.330	0.367	1052.335	0.399	28	0.105	K.NATLTNEKESDACPIR.A
R1/RRR1-4/3	1502.937	1503.774	-1226.023	0.459	1015.144	0.397	22	0.104	R.RVIYASQLTAKPR.L
R1/RRR1-3/3	1504.666	1503.774	-72.031	0.472	1132.094	0.350	24	0.100	R.RVIYASQLTAKPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1569.444	1569.715	-173.527	0.326	663.078	0.333	14	0.094	K.EQM*TPLSDFEDKL.-
R1/RRR1-3/3	1505.221	1503.774	297.569	0.443	1026.916	0.338	25	0.091	R.RVIYASQLTAKPR.L
R1/RRR1-3/3	1815.223	1815.062	89.221	0.396	536.747	0.385	22	0.091	K.AYLPVIESFGFSSQLR.A
R1/RRR1-5/2	1569.110	1569.715	-1026.502	0.281	616.008	0.242	15	0.090	K.EQM*TPLSDFEDKL.-
R1/RRR1-4/2	1569.008	1569.715	-1091.337	0.359	735.650	0.264	16	0.085	K.EQM*TPLSDFEDKL.-
R1/RRR1-4/2	1569.410	1569.715	-195.063	0.427	907.429	0.262	16	0.085	K.EQM*TPLSDFEDKL.-
R1/RRR1-5/3	1814.819	1815.062	-133.899	0.277	939.372	0.304	23	0.082	K.AYLPVIESFGFSSQLR.A
R1/RRR1-1/3	1818.433	1819.945	-1937.223	0.296	798.173	0.296	25	0.081	K.NATLTNEKESDACPIR.A
R1/RRR1-5/3	1503.628	1503.774	-97.812	0.407	1061.438	0.252	23	0.080	R.RVIYASQLTAKPR.L
R1/RRR1-6/3	1503.256	1503.774	-1012.940	0.208	775.845	0.163	25	0.070	R.RVIYASQLTAKPR.L
R1/RRR1-4/3	1814.643	1815.062	-231.476	0.286	847.568	0.200	22	0.070	K.AYLPVIESFGFSSQLR.A
R1/RRR1-12/2	1569.289	1569.615	-208.284	0.592	2488.200	0.628	25	0.507	K.HGGSVDEQVDAALDR.L
R1/RRR1-12/2	1569.323	1569.615	-186.746	0.578	2489.214	0.626	25	0.506	K.HGGSVDEQVDAALDR.L
R1/RRR1-12/2	1569.044	1569.615	-1004.405	0.565	2208.408	0.631	24	0.444	K.HGGSVDEQVDAALDR.L
R1/RRR1-12/2	1406.377	1405.664	-204.640	0.547	2391.598	0.488	22	0.428	K.FAADAVTLKDILK.K
R1/RRR1-12/2	1725.244	1725.878	-950.087	0.485	2014.849	0.626	25	0.400	K.ATGTVVVSDSGDFATIGK.Y
R1/RRR1-12/2	1725.470	1725.878	-237.470	0.511	2011.612	0.609	25	0.394	K.ATGTVVVSDSGDFATIGK.Y
R1/RRR1-12/2	1725.473	1725.878	-235.412	0.508	1776.474	0.644	24	0.362	K.ATGTVVVSDSGDFATIGK.Y
R1/RRR1-12/2	1489.148	1489.589	-296.608	0.479	1853.913	0.456	20	0.320	R.FDFNEDQM*AVEK.L
R1/RRR1-12/2	1404.822	1405.664	-1315.214	0.466	1844.455	0.447	19	0.314	K.FAADAVTLKDILK.K
R1/RRR1-12/2	1488.490	1489.589	-1414.510	0.386	1683.464	0.395	19	0.278	R.FDFNEDQM*AVEK.L
R1/RRR1-12/2	1918.825	1919.168	-179.531	0.553	1125.904	0.629	25	0.271	K.YKPQDATTNPSLILAASK.K
R1/RRR1-12/2	1918.522	1919.168	-860.754	0.519	934.084	0.595	23	0.244	K.YKPQDATTNPSLILAASK.K
R1/RRR1-12/2	1918.627	1919.168	-805.444	0.533	876.676	0.590	23	0.239	K.YKPQDATTNPSLILAASK.K
R1/RRR1-12/2	1522.103	1522.639	-1011.892	0.442	1059.715	0.409	22	0.222	K.EYAKEEDPGVASVK.S
R1/RRR1-12/2	1522.194	1522.639	-293.232	0.436	925.815	0.386	21	0.210	K.EYAKEEDPGVASVK.S
R1/RRR1-12/2	935.992	936.087	-101.195	0.480	785.375	0.379	15	0.206	K.FAADAVTLK.D
R1/RRR1-12/3	1558.542	1558.759	-139.498	0.570	1628.342	0.517	33	0.203	K.KLDADGAAALDIEKK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	997.504	998.182	-1686.622	0.325	691.352	0.341	13	0.197	K.TIVM*GASFR.N
R1/RRR1-12/2	997.959	998.182	-224.161	0.350	833.358	0.291	14	0.196	K.TIVM*GASFR.N
R1/RRR1-12/2	999.035	998.182	-146.833	0.356	704.671	0.291	14	0.195	K.TIVM*GASFR.N
R1/RRR1-12/2	1289.202	1289.588	-300.736	0.456	972.767	0.222	15	0.186	R.LLVEFGKEILK.I
R1/RRR1-12/3	1229.517	1229.450	54.449	0.527	1758.472	0.267	22	0.136	K.ALHIIELYEK.E
R1/RRR1-12/3	1229.255	1229.450	-158.589	0.451	1771.131	0.234	22	0.127	K.ALHIIELYEK.E
R1/RRR1-4/2	1832.231	1831.958	149.310	0.588	2245.347	0.576	25	0.428	K.TEDLWAALEEGSGEPVK.T
R1/RRR1-5/2	1832.035	1831.958	42.130	0.554	1945.007	0.537	24	0.356	K.TEDLWAALEEGSGEPVK.T
R1/RRR1-4/2	1693.168	1693.893	-1022.000	0.460	1985.369	0.477	20	0.347	R.YGVLDDTYALCM*AGK.Q
R1/RRR1-4/2	1831.538	1831.958	-229.734	0.441	1723.542	0.481	23	0.304	K.TEDLWAALEEGSGEPVK.T
R1/RRR1-4/2	1516.320	1516.744	-280.157	0.444	1587.013	0.383	19	0.263	R.MLQSYLGAETFQK.S
R1/RRR1-4/2	1211.618	1212.339	-1424.795	0.440	1371.313	0.454	17	0.258	K.LNVNQTGFYR.V
R1/RRR1-4/2	1211.679	1212.339	-1374.098	0.475	1292.549	0.426	17	0.245	K.LNVNQTGFYR.V
R1/RRR1-4/2	1211.969	1212.339	-306.666	0.517	1210.825	0.460	16	0.245	K.LNVNQTGFYR.V
R1/RRR1-5/2	1212.084	1212.339	-211.785	0.480	1093.396	0.452	16	0.234	K.LNVNQTGFYR.V
R1/RRR1-4/2	1169.419	1169.223	167.873	0.486	1102.383	0.393	15	0.222	R.VSYDEELASR.L
R1/RRR1-4/2	1168.998	1169.223	-193.407	0.460	1107.787	0.351	15	0.215	R.VSYDEELASR.L
R1/RRR1-4/2	1168.472	1169.223	-1503.707	0.433	1158.061	0.317	15	0.213	R.VSYDEELASR.L
R1/RRR1-5/2	1211.993	1212.339	-286.658	0.441	870.877	0.397	15	0.212	K.LNVNQTGFYR.V
R1/RRR1-4/2	1107.161	1106.257	-86.878	0.481	993.074	0.340	14	0.209	R.NQDSIFLLR.G
R1/RRR1-4/2	1105.584	1106.257	-1517.922	0.421	787.461	0.383	14	0.208	R.NQDSIFLLR.G
R1/RRR1-4/2	1168.059	1168.285	-194.506	0.425	810.391	0.411	14	0.207	K.SGEGHLDALLR.G
R1/RRR1-5/2	1106.879	1106.257	-342.750	0.448	815.311	0.371	14	0.207	R.NQDSIFLLR.G
R1/RRR1-4/2	1833.893	1834.148	-139.309	0.523	572.828	0.486	20	0.205	R.FNEVLPVGEGTLVIAFK.G
R1/RRR1-5/2	1212.266	1212.339	-60.559	0.374	923.628	0.341	15	0.205	-.LNVNQTGFYR.-
R1/RRR1-4/2	1325.074	1324.548	-358.937	0.382	500.356	0.511	14	0.204	K.EYFAVPYPLPK.M
R1/RRR1-5/2	1168.962	1169.223	-223.997	0.431	799.601	0.324	14	0.199	R.VSYDEELASR.L
R1/RRR1-4/2	1167.569	1168.285	-1474.144	0.285	744.118	0.313	14	0.193	K.SGEGHLDALLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1169.235	1169.223	9.570	0.324	650.288	0.299	13	0.193	R.VSYDEELASR.L
R1/RRR1-5/2	1168.376	1168.285	78.321	0.335	696.256	0.289	14	0.192	K.SGEGHLDALLR.G
R1/RRR1-4/2	1832.668	1834.148	-1357.108	0.304	401.794	0.431	18	0.191	R.FNEVLPVGEGTLVIAFK.G
R1/RRR1-5/2	1167.848	1168.285	-375.284	0.295	1044.520	0.192	15	0.190	K.SGEGHLDALLR.G
R1/RRR1-5/2	1106.036	1106.257	-199.989	0.382	610.579	0.220	12	0.188	R.NQDSIFLLR.G
R1/RRR1-3/2	1030.195	1029.172	21.914	0.327	952.469	0.207	15	0.187	R.AEANLGNVLK.E
R1/RRR1-4/2	876.913	877.063	-170.494	0.349	910.276	0.184	14	0.186	K.FALEVAVK.T
R1/RRR1-5/2	1168.102	1168.285	-157.289	0.358	520.575	0.357	12	0.182	-.SGEGHLDALLR.-
R1/RRR1-4/3	1354.154	1354.488	-246.899	0.516	1277.520	0.302	25	0.094	K.IYKETDLSQEK.V
R1/RRR1-5/3	1354.722	1354.488	173.053	0.423	794.486	0.308	21	0.078	-.IYKETDLSQEK.-
R1/RRR1-4/3	1355.092	1354.488	-292.854	0.414	882.202	0.264	22	0.076	K.IYKETDLSQEK.V
R1/RRR1-4/3	1354.099	1354.488	-288.141	0.422	834.249	0.276	22	0.072	-.IYKETDLSQEK.-
R1/RRR1-5/3	1354.166	1354.488	-238.353	0.432	593.552	0.302	19	0.071	-.IYKETDLSQEK.-
R1/RRR1-13/2	1985.361	1986.176	-917.312	0.590	2276.934	0.599	24	0.445	K.THNSFILQQFENPANPK.I
R1/RRR1-13/2	1985.657	1986.176	-767.587	0.610	1946.037	0.615	22	0.383	K.THNSFILQQFENPANPK.I
R1/RRR1-13/2	1689.282	1688.864	247.832	0.557	1896.423	0.633	26	0.381	K.VDGLVSGIGTGGTITGAGR.Y
R1/RRR1-13/2	1688.458	1688.864	-241.225	0.515	1774.399	0.616	26	0.353	K.VDGLVSGIGTGGTITGAGR.Y
R1/RRR1-13/2	1688.459	1688.864	-241.008	0.500	1478.760	0.636	24	0.312	K.VDGLVSGIGTGGTITGAGR.Y
R1/RRR1-13/2	1689.502	1690.041	-913.153	0.471	1866.292	0.422	21	0.306	K.AFGAELILTDPLLGMK.G
R1/RRR1-13/2	1706.391	1706.040	206.552	0.543	1572.245	0.551	20	0.300	K.AFGAELILTDPLLGM*K.G
R1/RRR1-13/2	1818.761	1818.064	-166.722	0.535	1652.802	0.501	22	0.299	K.DVTELIGNTPLVYLNR.V
R1/RRR1-13/2	1817.342	1818.064	-950.312	0.412	1778.255	0.385	22	0.285	K.DVTELIGNTPLVYLNR.V
R1/RRR1-13/2	1214.530	1215.382	-1528.943	0.445	1697.930	0.402	18	0.281	K.GAVQKAEELAAK.T
R1/RRR1-13/2	1705.425	1706.040	-949.979	0.471	1363.024	0.555	18	0.273	K.AFGAELILTDPLLGM*K.G
R1/RRR1-13/2	1705.455	1706.040	-931.798	0.508	1445.344	0.503	20	0.271	K.AFGAELILTDPLLGM*K.G
R1/RRR1-13/2	1819.545	1818.064	265.551	0.524	1367.359	0.531	20	0.270	K.DVTELIGNTPLVYLNR.V
R1/RRR1-13/2	1216.197	1215.382	-152.176	0.518	1474.570	0.453	18	0.266	K.GAVQKAEELAAK.T
R1/RRR1-13/2	1372.583	1373.511	-1408.781	0.380	1435.426	0.469	18	0.265	R.IGYSM*ITDAEEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1372.906	1373.511	-1172.478	0.437	1369.578	0.471	18	0.260	R.IGYSM*ITDAEEK.G
R1/RRR1-13/2	1372.654	1373.511	-1357.063	0.417	1408.244	0.398	18	0.247	R.IGYSM*ITDAEEK.G
R1/RRR1-13/2	1474.202	1474.642	-299.207	0.510	853.576	0.528	17	0.230	K.IHYETTGPEIWK.S
R1/RRR1-13/2	1286.007	1285.513	384.958	0.444	1212.177	0.346	17	0.221	R.YLSSVLFQSIK.K
R1/RRR1-13/2	1215.048	1215.382	-275.558	0.440	1032.145	0.389	18	0.217	K.GAVQKAEELAAK.T
R1/RRR1-13/2	1474.354	1474.642	-195.703	0.490	707.433	0.497	16	0.216	K.IHYETTGPEIWK.S
R1/RRR1-13/2	1283.208	1283.425	-169.284	0.302	1350.333	0.244	17	0.212	K.LESM*EPCSSVK.D
R1/RRR1-13/2	1474.276	1474.642	-249.030	0.438	719.958	0.465	16	0.211	K.IHYETTGPEIWK.S
R1/RRR1-13/2	1413.660	1413.686	-18.847	0.340	884.669	0.396	16	0.205	R.YLSSVLFQSIKK.E
R1/RRR1-13/2	1397.978	1397.645	238.605	0.433	957.477	0.303	17	0.199	K.LFVVVFPSFGER.Y
R1/RRR1-13/2	1283.291	1283.425	-104.682	0.354	1112.050	0.235	16	0.197	K.LESM*EPCSSVK.D
R1/RRR1-13/2	1397.206	1397.645	-315.432	0.333	937.168	0.271	15	0.193	K.LFVVVFPSFGER.Y
R1/RRR1-13/2	1396.338	1397.645	-1657.633	0.320	1162.542	0.123	17	0.185	K.LFVVVFPSFGER.Y
R1/RRR1-13/2	1283.218	1283.425	-161.268	0.254	663.395	0.076	14	0.180	K.LESM*EPCSSVK.D
R1/RRR1-13/3	1817.847	1818.064	-119.633	0.457	1301.768	0.509	30	0.153	K.DVTELIGNTPLVYLNR.V
R1/RRR1-13/3	1818.312	1818.064	136.844	0.407	1234.058	0.402	28	0.118	K.DVTELIGNTPLVYLNR.V
R1/RRR1-13/3	1706.176	1706.040	79.804	0.454	1330.468	0.340	28	0.115	K.AFGAELILTDPLLGM*K.G
R1/RRR1-13/3	1985.865	1986.176	-157.015	0.428	902.641	0.431	28	0.099	K.THNSFILQQFENPANPK.I
R1/RRR1-11/2	1865.375	1864.133	129.975	0.609	3001.042	0.653	26	0.665	R.M*FVADGGELLM*AQSYAK.N
R1/RRR1-11/2	1531.232	1531.695	-303.255	0.481	1889.461	0.473	22	0.327	K.LIFGADSPAIQENR.V
R1/RRR1-11/2	1450.275	1449.629	-244.878	0.525	1536.445	0.621	22	0.321	R.VATVQCLSGTGSLR.V
R1/RRR1-11/2	1531.254	1531.695	-289.098	0.456	1787.725	0.452	22	0.306	K.LIFGADSPAIQENR.V
R1/RRR1-11/2	1531.371	1531.695	-212.242	0.492	1748.157	0.464	21	0.303	K.LIFGADSPAIQENR.V
R1/RRR1-11/2	1574.617	1574.798	-115.282	0.527	1553.156	0.539	22	0.297	R.VGALSIVCGSADVAVR.V
R1/RRR1-11/2	1450.213	1449.629	-287.777	0.554	1367.091	0.567	21	0.284	R.VATVQCLSGTGSLR.V
R1/RRR1-11/3	1708.833	1708.979	-85.493	0.507	2103.898	0.442	33	0.261	R.VKEYLPITGLADFNK.L
R1/RRR1-11/2	1708.270	1708.979	-1003.392	0.561	1262.961	0.475	23	0.250	R.VKEYLPITGLADFNK.L
R1/RRR1-11/2	1571.281	1570.748	-298.331	0.530	1390.975	0.420	19	0.249	K.DSAMFNEWTVELK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1449.181	1449.629	-310.118	0.517	1079.640	0.553	19	0.249	R.VATVQCLSGTGSLR.V
R1/RRR1-11/2	1481.482	1481.674	-130.298	0.464	1213.924	0.484	20	0.248	K.EYLPITGLADFNK.L
R1/RRR1-11/2	907.866	908.059	-212.990	0.372	1213.569	0.432	15	0.236	R.ISM*AGLSGR.T
R1/RRR1-11/2	1708.199	1708.979	-1045.005	0.508	1091.413	0.460	22	0.233	R.VKEYLPITGLADFNK.L
R1/RRR1-11/2	1573.739	1574.798	-1312.296	0.320	1367.552	0.360	20	0.232	R.VGALSIVCGSADVAVR.V
R1/RRR1-11/2	1709.522	1708.979	-268.119	0.537	954.970	0.479	21	0.226	R.VKEYLPITGLADFNK.L
R1/RRR1-11/2	1454.437	1454.697	-179.358	0.544	652.448	0.516	20	0.221	R.TEEGKPLVLNVVR.R
R1/RRR1-11/2	1076.596	1077.302	-1589.157	0.431	868.635	0.392	17	0.212	K.VFTLAGLTVR.S
R1/RRR1-11/2	1558.499	1558.807	-198.099	0.414	553.721	0.508	21	0.209	R.TIPHLADAIHAAVTK.L
R1/RRR1-11/2	1455.429	1454.697	-184.704	0.521	624.858	0.406	19	0.204	R.TEEGKPLVLNVVR.R
R1/RRR1-10/2	1531.411	1531.695	-185.693	0.387	1029.923	0.323	18	0.204	K.LIFGADSPAIQENR.V
R1/RRR1-11/2	1455.249	1454.697	-308.909	0.457	684.174	0.383	20	0.204	R.TEEGKPLVLNVVR.R
R1/RRR1-11/2	1077.006	1077.302	-275.067	0.421	743.027	0.352	16	0.202	K.VFTLAGLTVR.S
R1/RRR1-11/2	1480.670	1481.674	-1357.406	0.316	805.690	0.395	17	0.202	K.EYLPITGLADFNK.L
R1/RRR1-11/2	1076.773	1077.302	-1424.249	0.373	640.924	0.307	15	0.195	K.VFTLAGLTVR.S
R1/RRR1-11/2	1587.042	1586.748	186.268	0.425	978.637	0.263	16	0.191	K.DSAM*FNEWTVELK.G
R1/RRR1-2/2	1531.737	1531.695	27.608	0.332	679.921	0.167	16	0.181	K.LIFGADSPAIQENR.V
R1/RRR1-11/2	1481.705	1481.674	20.525	0.251	598.246	0.195	14	0.181	K.EYLPITGLADFNK.L
R1/RRR1-11/3	1709.707	1708.979	-159.282	0.507	1532.493	0.412	30	0.153	R.VKEYLPITGLADFNK.L
R1/RRR1-11/3	1531.453	1531.695	-158.394	0.475	1548.315	0.350	28	0.137	K.LIFGADSPAIQENR.V
R1/RRR1-11/3	1531.625	1531.695	-45.783	0.378	1615.606	0.272	27	0.123	K.LIFGADSPAIQENR.V
R1/RRR1-11/3	1531.118	1531.695	-1032.891	0.447	1047.566	0.295	26	0.084	K.LIFGADSPAIQENR.V
R1/RRR1-11/3	1708.556	1708.979	-248.464	0.430	1027.113	0.260	28	0.078	R.VKEYLPITGLADFNK.L
R1/RRR1-11/2	1474.259	1474.642	-260.411	0.442	1742.747	0.423	20	0.289	R.GAAAGSVEEVKNTLK.N
R1/RRR1-11/2	1926.444	1926.046	206.850	0.534	1265.205	0.562	23	0.267	K.ESGM*TLITAEDLDDAAEK.A
R1/RRR1-11/2	1909.806	1910.047	-126.527	0.534	1284.120	0.553	23	0.266	K.ESGMTLITAEDLDDAAEK.A
R1/RRR1-11/2	1318.350	1318.495	-110.295	0.449	1262.073	0.470	19	0.248	K.CDVIASGIVNAAK.Q
R1/RRR1-11/2	1924.946	1926.046	-1094.478	0.468	1129.278	0.500	23	0.240	K.ESGM*TLITAEDLDDAAEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1474.581	1474.642	-41.483	0.470	1195.681	0.450	20	0.237	R.GAAAGSVEEVKNTLK.N
R1/RRR1-10/2	1926.322	1926.046	143.685	0.553	900.336	0.535	21	0.227	K.ESGM*TLITAEDLDDAAEK.A
R1/RRR1-11/2	1095.099	1095.277	-163.526	0.444	1041.044	0.444	16	0.226	K.SGLQGGVHIVK.A
R1/RRR1-11/2	1474.339	1474.642	-206.002	0.472	1061.726	0.448	18	0.224	R.GAAAGSVEEVKNTLK.N
R1/RRR1-11/2	1094.962	1095.277	-288.782	0.452	934.815	0.455	15	0.220	K.SGLQGGVHIVK.A
R1/RRR1-11/2	818.926	818.943	-20.574	0.429	763.338	0.489	11	0.220	K.YGINVPR.G
R1/RRR1-11/2	1018.698	1019.284	-1561.473	0.497	1090.730	0.354	16	0.218	K.M*LGQILVTK.Q
R1/RRR1-10/2	817.882	817.995	-139.162	0.470	411.162	0.498	11	0.218	K.VPIDVFK.G
R1/RRR1-11/2	1002.537	1003.285	-1748.073	0.439	952.189	0.399	15	0.218	K.MLGQILVTK.Q
R1/RRR1-11/2	1003.163	1003.285	-121.393	0.416	903.545	0.410	15	0.217	K.MLGQILVTK.Q
R1/RRR1-10/2	1018.954	1019.284	-324.885	0.424	1108.833	0.329	16	0.215	K.M*LGQILVTK.Q
R1/RRR1-11/2	1018.952	1019.284	-326.928	0.467	1004.087	0.362	15	0.215	K.M*LGQILVTK.Q
R1/RRR1-10/2	817.948	817.995	-58.020	0.430	390.101	0.424	11	0.211	K.VPIDVFK.G
R1/RRR1-11/2	819.009	818.943	81.084	0.418	664.287	0.450	10	0.209	K.YGINVPR.G
R1/RRR1-10/2	1474.196	1474.642	-302.945	0.466	724.516	0.469	17	0.209	R.GAAAGSVEEVKNTLK.N
R1/RRR1-11/2	817.449	817.995	-1897.190	0.295	361.818	0.455	11	0.204	K.VPIDVFK.G
R1/RRR1-11/2	1531.290	1531.607	-207.696	0.421	600.272	0.430	18	0.203	R.DTTQEDPREVAAAK.A
R1/RRR1-11/2	1390.725	1389.622	74.867	0.447	939.265	0.328	17	0.202	K.NVFPSEKEIVVK.S
R1/RRR1-11/2	817.451	817.995	-1894.189	0.283	364.920	0.396	11	0.201	K.VPIDVFK.G
R1/RRR1-11/3	1620.765	1619.824	-36.313	0.523	1789.002	0.427	27	0.200	R.LNIHEYQGAELM*GK.Y
R1/RRR1-11/2	1389.300	1389.622	-232.095	0.422	848.450	0.344	16	0.200	K.NVFPSEKEIVVK.S
R1/RRR1-10/2	817.367	817.995	-1998.042	0.273	371.348	0.367	11	0.200	K.VPIDVFK.G
R1/RRR1-10/2	1473.699	1474.642	-1322.536	0.373	474.946	0.449	16	0.199	R.GAAAGSVEEVKNTLK.N
R1/RRR1-11/2	1046.175	1047.188	-1929.587	0.299	677.975	0.372	12	0.196	K.ILTSDDRVK.A
R1/RRR1-11/2	1531.038	1531.607	-1028.138	0.442	545.820	0.369	18	0.196	R.DTTQEDPREVAAAK.A
R1/RRR1-11/2	1047.237	1047.188	47.162	0.315	725.888	0.313	13	0.194	K.ILTSDDRVK.A
R1/RRR1-11/2	1531.193	1531.607	-271.518	0.429	493.867	0.338	17	0.192	R.DTTQEDPREVAAAK.A
R1/RRR1-11/2	1047.035	1047.188	-146.593	0.324	704.844	0.285	13	0.192	K.ILTSDDRVK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1390.587	1389.622	-24.707	0.338	904.217	0.260	16	0.192	K.NVFPSEKEIVVK.S
R1/RRR1-11/2	817.547	817.995	-549.264	0.177	354.552	0.423	11	0.192	K.VPIDVFK.G
R1/RRR1-10/2	1317.926	1318.495	-1194.298	0.225	615.467	0.180	15	0.180	K.CDVIASGIVNAAK.Q
R1/RRR1-11/3	1604.649	1603.825	-110.005	0.446	1116.095	0.473	24	0.126	R.LNIHEYQGAELMGK.Y
R1/RRR1-11/3	1619.607	1619.824	-134.275	0.501	1132.050	0.384	26	0.107	R.LNIHEYQGAELM*GK.Y
R1/RRR1-11/3	1619.504	1619.824	-198.242	0.489	924.292	0.337	24	0.089	R.LNIHEYQGAELM*GK.Y
R1/RRR1-8/2	1985.393	1985.085	155.244	0.573	2638.990	0.629	26	0.543	R.GNPTVEVDVCCSDGTFAR.A
R1/RRR1-8/2	1984.413	1985.085	-845.501	0.582	2440.786	0.637	26	0.498	R.GNPTVEVDVCCSDGTFAR.A
R1/RRR1-8/2	1984.617	1985.085	-236.691	0.551	2412.560	0.633	26	0.490	R.GNPTVEVDVCCSDGTFAR.A
R1/RRR1-8/2	1493.325	1492.656	-222.077	0.611	2217.451	0.607	24	0.429	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1493.335	1492.656	-215.188	0.595	2053.573	0.576	23	0.385	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1491.947	1492.656	-1148.467	0.451	2079.023	0.498	23	0.364	R.IEEELGAAAVYAGAK.F
R1/RRR1-2/2	1492.431	1492.656	-151.001	0.492	2086.374	0.479	23	0.358	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1902.486	1902.953	-246.201	0.564	1895.235	0.559	23	0.357	K.TYDLNFKEENNDGSQK.I
R1/RRR1-8/2	1872.686	1872.241	237.913	0.619	1867.077	0.584	26	0.354	K.LAM*QEFMILPTGAASFK.E
R1/RRR1-8/2	1902.494	1902.953	-242.081	0.588	1822.597	0.579	23	0.351	K.TYDLNFKEENNDGSQK.I
R1/RRR1-1/2	1493.377	1492.656	-186.815	0.569	1829.625	0.578	22	0.347	R.IEEELGAAAVYAGAK.F
R1/RRR1-10/2	1492.322	1492.656	-224.113	0.478	1875.240	0.538	22	0.342	R.IEEELGAAAVYAGAK.F
R1/RRR1-9/2	1492.094	1492.656	-1049.557	0.457	2077.860	0.421	22	0.337	R.IEEELGAAAVYAGAK.F
R1/RRR1-9/2	1492.452	1492.656	-136.560	0.524	1871.851	0.519	23	0.336	R.IEEELGAAAVYAGAK.F
R1/RRR1-1/2	1581.440	1581.839	-252.904	0.500	1715.630	0.521	24	0.314	K.AVDNVNSVIAPALIGK.D
R1/RRR1-2/2	1492.275	1492.656	-255.708	0.467	1761.136	0.496	22	0.312	R.IEEELGAAAVYAGAK.F
R1/RRR1-2/2	1492.137	1492.656	-1020.726	0.467	1802.640	0.474	22	0.312	R.IEEELGAAAVYAGAK.F
R1/RRR1-3/2	1492.295	1492.656	-242.331	0.462	1726.050	0.513	21	0.311	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1552.450	1552.802	-227.736	0.441	1792.184	0.451	20	0.309	K.IPLYQHIANLAGNK.Q
R1/RRR1-1/2	1492.136	1492.656	-1021.629	0.415	1742.349	0.492	22	0.308	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1889.552	1888.241	165.155	0.612	1628.794	0.544	26	0.306	K.LAM*QEFM*ILPTGAASFK.E
R1/RRR1-7/2	1574.274	1574.758	-308.652	0.555	1520.897	0.584	23	0.305	K.VNQIGSVTESIEAVK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1492.266	1492.656	-261.781	0.425	1741.932	0.480	22	0.305	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1872.681	1872.241	235.363	0.597	1557.357	0.575	24	0.304	K.LAM*QEFMILPTGAASFK.E
R1/RRR1-8/2	1581.400	1581.839	-278.305	0.478	1593.184	0.547	22	0.302	K.AVDNVNSVIAPALIGK.D
R1/RRR1-8/3	1574.972	1574.758	136.337	0.546	2068.299	0.529	30	0.301	K.VNQIGSVTESIEAVK.M
R1/RRR1-1/2	1582.246	1581.839	258.330	0.493	1624.185	0.525	23	0.301	K.AVDNVNSVIAPALIGK.D
R1/RRR1-3/2	1492.134	1492.656	-1022.779	0.394	1771.743	0.440	22	0.297	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1887.572	1888.241	-886.645	0.567	1405.175	0.580	25	0.289	K.LAM*QEFM*ILPTGAASFK.E
R1/RRR1-8/2	1872.441	1872.241	106.839	0.593	1400.558	0.570	25	0.285	K.LAMQEFM*ILPTGAASFK.E
R1/RRR1-8/2	1581.422	1581.839	-264.520	0.443	1596.998	0.471	22	0.283	K.AVDNVNSVIAPALIGK.D
R1/RRR1-8/2	1887.610	1888.241	-866.649	0.547	1454.010	0.532	25	0.282	K.LAM*QEFM*ILPTGAASFK.E
R1/RRR1-19/2	1574.500	1574.758	-164.203	0.499	1514.068	0.503	22	0.282	K.VNQIGSVTESIEAVK.M
R1/RRR1-6/2	1574.280	1574.758	-304.762	0.484	1367.411	0.554	22	0.278	K.VNQIGSVTESIEAVK.M
R1/RRR1-4/2	1575.208	1574.758	286.455	0.558	1410.242	0.536	22	0.278	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1574.348	1574.758	-261.276	0.521	1424.212	0.526	22	0.277	K.VNQIGSVTESIEAVK.M
R1/RRR1-2/2	1574.531	1574.758	-144.449	0.525	1348.517	0.556	22	0.277	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1871.662	1872.241	-846.619	0.540	1239.132	0.593	24	0.274	K.LAMQEFM*ILPTGAASFK.E
R1/RRR1-8/2	1855.608	1856.242	-883.208	0.520	1291.626	0.541	24	0.266	K.LAMQEFMILPTGAASFK.E
R1/RRR1-7/2	1581.523	1581.839	-200.092	0.455	1391.455	0.499	22	0.266	K.AVDNVNSVIAPALIGK.D
R1/RRR1-1/2	1889.532	1888.241	154.401	0.573	1303.544	0.537	23	0.265	K.LAM*QEFM*ILPTGAASFK.E
R1/RRR1-8/2	1190.123	1190.397	-231.228	0.528	1460.548	0.423	16	0.258	K.MGVEVYHNLK.S
R1/RRR1-8/2	1855.485	1856.242	-949.781	0.499	1255.654	0.510	24	0.256	K.LAMQEFMILPTGAASFK.E
R1/RRR1-7/2	1575.291	1574.758	-297.183	0.536	1244.614	0.515	21	0.256	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1574.311	1574.758	-284.536	0.505	1198.955	0.529	21	0.255	K.VNQIGSVTESIEAVK.M
R1/RRR1-3/2	1575.301	1574.758	-291.041	0.492	1177.569	0.531	20	0.253	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1856.445	1856.242	109.968	0.584	1133.232	0.555	22	0.252	K.LAMQEFMILPTGAASFK.E
R1/RRR1-8/2	1871.373	1872.241	-1001.613	0.513	1162.012	0.511	23	0.247	K.LAMQEFM*ILPTGAASFK.E
R1/RRR1-8/2	1574.363	1574.758	-251.863	0.496	1177.876	0.499	21	0.247	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1190.072	1190.397	-274.139	0.534	1344.719	0.416	16	0.246	K.MGVEVYHNLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1792.433	1791.983	251.876	0.524	959.555	0.584	23	0.245	R.AAVPSGASTGVYEALELR.D
R1/RRR1-5/2	1574.184	1574.758	-1003.148	0.460	1215.176	0.472	21	0.244	K.VNQIGSVTESIEAVK.M
R1/RRR1-1/2	1574.434	1574.758	-206.126	0.467	1251.420	0.457	21	0.244	K.VNQIGSVTESIEAVK.M
R1/RRR1-6/2	1574.260	1574.758	-317.365	0.473	1220.770	0.467	21	0.244	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1580.811	1581.839	-1286.210	0.409	1253.467	0.464	20	0.243	K.AVDNVNSVIAPALIGK.D
R1/RRR1-3/2	1574.193	1574.758	-997.153	0.500	1117.664	0.489	20	0.239	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1870.801	1872.241	-1308.403	0.481	1022.096	0.529	21	0.238	K.LAM*QEFMILPTGAASFK.E
R1/RRR1-1/2	1574.300	1574.758	-291.537	0.481	1095.210	0.472	20	0.234	K.VNQIGSVTESIEAVK.M
R1/RRR1-3/2	1888.335	1888.241	50.109	0.559	974.585	0.528	21	0.234	K.LAM*QEFM*ILPTGAASFK.E
R1/RRR1-8/2	1190.035	1190.397	-305.631	0.467	1293.460	0.358	16	0.230	K.MGVEVYHNLK.S
R1/RRR1-7/2	1573.638	1574.758	-1351.205	0.360	1136.913	0.408	20	0.225	K.VNQIGSVTESIEAVK.M
R1/RRR1-6/2	1857.887	1856.242	-191.680	0.510	904.127	0.508	19	0.224	K.LAMQEFMILPTGAASFK.E
R1/RRR1-2/2	1581.415	1581.839	-268.392	0.379	887.447	0.507	20	0.224	K.AVDNVNSVIAPALIGK.D
R1/RRR1-8/3	1492.671	1492.656	10.645	0.504	1900.752	0.438	31	0.222	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/2	1791.484	1791.983	-279.567	0.475	633.374	0.552	23	0.221	R.AAVPSGASTGVYEALELR.D
R1/RRR1-2/2	1888.187	1888.241	-28.737	0.448	812.339	0.500	19	0.218	K.LAM*QEFM*ILPTGAASFK.E
R1/RRR1-8/2	1790.848	1791.983	-1195.728	0.429	571.010	0.560	22	0.218	R.AAVPSGASTGVYEALELR.D
R1/RRR1-8/2	1205.476	1206.397	-1598.005	0.518	901.355	0.424	15	0.217	K.M*GVEVYHNLK.S
R1/RRR1-8/2	1681.363	1680.975	231.668	0.565	729.946	0.488	21	0.216	K.KIPLYQHIANLAGNK.Q
R1/RRR1-8/2	1680.506	1680.975	-280.107	0.481	755.356	0.468	22	0.216	K.KIPLYQHIANLAGNK.Q
R1/RRR1-8/2	1206.050	1206.397	-287.857	0.492	985.066	0.371	16	0.214	K.M*GVEVYHNLK.S
R1/RRR1-1/2	1888.121	1888.241	-63.819	0.550	797.154	0.467	20	0.213	K.LAM*QEFM*ILPTGAASFK.E
R1/RRR1-7/2	1791.322	1791.983	-930.214	0.430	586.359	0.517	21	0.212	R.AAVPSGASTGVYEALELR.D
R1/RRR1-8/2	1681.513	1680.975	-275.861	0.525	626.069	0.479	20	0.210	K.KIPLYQHIANLAGNK.Q
R1/RRR1-6/2	1791.318	1791.983	-932.198	0.446	553.920	0.484	20	0.207	R.AAVPSGASTGVYEALELR.D
R1/RRR1-8/1	1493.841	1492.656	124.744	0.509	432.919	0.530	15	0.206	R.IEEELGAAAVYAGAK.F
R1/RRR1-10/2	1574.296	1574.758	-294.493	0.399	592.581	0.412	19	0.206	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	1207.050	1206.397	-287.822	0.539	797.377	0.369	15	0.205	K.M*GVEVYHNLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1580.673	1581.839	-1374.471	0.298	511.655	0.430	21	0.202	K.AVDNVNSVIAPALIGK.D
R1/RRR1-3/2	1792.310	1791.983	182.898	0.429	353.391	0.450	19	0.201	R.AAVPSGASTGVYEALELR.D
R1/RRR1-3/2	1791.248	1791.983	-971.538	0.414	547.481	0.414	21	0.201	R.AAVPSGASTGVYEALELR.D
R1/RRR1-10/2	1573.641	1574.758	-1349.335	0.314	542.858	0.387	18	0.200	K.VNQIGSVTESIEAVK.M
R1/RRR1-10/2	1573.681	1574.758	-1323.626	0.311	595.457	0.369	18	0.199	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	918.831	919.094	-287.507	0.464	724.578	0.329	13	0.198	-.SCNALLLK.-
R1/RRR1-5/2	1791.075	1791.983	-1068.360	0.332	393.896	0.373	19	0.195	R.AAVPSGASTGVYEALELR.D
R1/RRR1-4/2	1580.831	1581.839	-1273.647	0.292	413.214	0.330	18	0.194	K.AVDNVNSVIAPALIGK.D
R1/RRR1-8/2	918.391	919.094	-1859.977	0.404	797.436	0.263	13	0.193	-.SCNALLLK.-
R1/RRR1-3/2	1573.364	1574.758	-1526.454	0.274	1089.974	0.205	18	0.193	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/2	918.811	919.094	-309.367	0.462	771.194	0.294	13	0.192	-.SCNALLLK.-
R1/RRR1-3/2	1791.343	1791.983	-918.516	0.310	132.345	0.452	17	0.189	-.AAVPSGASTGVYEALELR.-
R1/RRR1-7/2	1581.013	1581.839	-1158.112	0.324	863.648	0.212	18	0.186	K.AVDNVNSVIAPALIGK.D
R1/RRR1-7/2	1580.689	1581.839	-1363.922	0.343	816.422	0.236	16	0.184	K.AVDNVNSVIAPALIGK.D
R1/RRR1-8/3	1574.502	1574.758	-163.162	0.482	1470.162	0.476	26	0.171	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/3	1493.190	1492.656	-312.876	0.490	1538.745	0.422	27	0.162	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/3	1574.653	1574.758	-66.925	0.482	1321.407	0.482	26	0.152	K.VNQIGSVTESIEAVK.M
R1/RRR1-8/3	1491.770	1492.656	-1267.538	0.408	1695.117	0.326	28	0.151	R.IEEELGAAAVYAGAK.F
R1/RRR1-8/3	1902.661	1902.953	-153.682	0.424	596.506	0.592	29	0.110	K.TYDLNFKEENNDGSQK.I
R1/RRR1-8/3	1792.839	1791.983	-80.907	0.468	829.934	0.496	30	0.110	R.AAVPSGASTGVYEALELR.D
R1/RRR1-8/3	1792.224	1791.983	135.010	0.456	889.618	0.482	32	0.109	R.AAVPSGASTGVYEALELR.D
R1/RRR1-8/3	1902.487	1902.953	-245.500	0.376	445.814	0.577	25	0.103	K.TYDLNFKEENNDGSQK.I
R1/RRR1-8/3	1792.064	1791.983	45.043	0.421	900.931	0.419	32	0.098	R.AAVPSGASTGVYEALELR.D
R1/RRR1-8/3	1902.515	1902.953	-230.631	0.375	438.308	0.491	25	0.094	K.TYDLNFKEENNDGSQK.I
R1/RRR1-8/3	1856.048	1856.242	-104.802	0.424	994.453	0.302	27	0.081	-.LAMQEFMILPTGAASFK.-
R1/RRR1-8/3	1857.435	1856.242	104.266	0.417	657.590	0.247	24	0.068	-.LAMQEFMILPTGAASFK.-
R1/RRR1-4/2	1657.527	1656.768	-146.080	0.553	1758.257	0.565	21	0.335	K.SDWLSCLDNDVGFK.G
R1/RRR1-4/2	1515.211	1515.630	-277.065	0.522	1609.561	0.527	20	0.305	K.M*FVDYNQPEAER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1558.183	1558.589	-261.708	0.499	1619.180	0.513	22	0.300	K.SGEDADTLGLTGHER.F
R1/RRR1-4/2	1515.714	1515.630	55.994	0.517	1438.115	0.557	19	0.291	K.M*FVDYNQPEAER.V
R1/RRR1-4/2	1515.003	1515.630	-1076.859	0.498	1419.946	0.565	19	0.290	K.M*FVDYNQPEAER.V
R1/RRR1-5/2	1501.980	1500.656	215.888	0.558	1651.535	0.430	19	0.278	R.SDDTVAMIESYLR.A
R1/RRR1-4/2	1517.601	1516.656	-36.508	0.561	1343.868	0.524	20	0.270	R.SDDTVAM*IESYLR.A
R1/RRR1-4/2	1517.328	1516.656	-216.942	0.532	1467.115	0.469	19	0.268	R.SDDTVAM*IESYLR.A
R1/RRR1-4/2	1656.573	1656.768	-118.226	0.503	1361.701	0.515	19	0.267	K.SDWLSCLDNDVGFK.G
R1/RRR1-4/2	1283.214	1282.426	-165.888	0.408	1286.361	0.525	18	0.263	K.YYSLPALSDPR.I
R1/RRR1-4/2	1538.602	1537.843	-156.977	0.529	1052.949	0.593	21	0.258	R.SNLAGM*GIIPLCFK.S
R1/RRR1-4/2	1557.571	1558.589	-1299.427	0.492	1217.279	0.519	22	0.255	K.SGEDADTLGLTGHER.F
R1/RRR1-3/2	1516.675	1516.656	13.036	0.405	1589.131	0.335	20	0.251	R.SDDTVAM*IESYLR.A
R1/RRR1-4/2	1557.727	1558.589	-1199.162	0.491	1086.710	0.536	21	0.246	K.SGEDADTLGLTGHER.F
R1/RRR1-4/2	1655.703	1656.768	-1250.882	0.387	1426.095	0.391	20	0.246	K.SDWLSCLDNDVGFK.G
R1/RRR1-4/2	1283.439	1282.426	9.768	0.427	1040.338	0.522	17	0.241	K.YYSLPALSDPR.I
R1/RRR1-4/2	1616.767	1616.793	-16.555	0.515	797.852	0.530	21	0.229	R.DIWPSTEEIAEVVK.S
R1/RRR1-4/2	1290.985	1291.437	-351.154	0.439	1038.970	0.461	18	0.229	K.VAEFSFHGTPAK.L
R1/RRR1-4/2	1617.566	1616.793	-141.211	0.489	705.760	0.519	20	0.222	R.DIWPSTEEIAEVVK.S
R1/RRR1-5/2	1173.217	1173.300	-71.341	0.415	776.570	0.443	16	0.216	K.ILDWENSAPK.Q
R1/RRR1-4/2	1281.491	1282.426	-1514.881	0.294	1155.017	0.352	16	0.215	K.YYSLPALSDPR.I
R1/RRR1-5/2	1173.257	1173.300	-37.006	0.509	818.319	0.413	16	0.215	K.ILDWENSAPK.Q
R1/RRR1-4/2	1172.457	1173.300	-1576.498	0.405	842.407	0.393	16	0.212	K.ILDWENSAPK.Q
R1/RRR1-4/2	1173.098	1173.300	-173.005	0.515	822.483	0.389	16	0.211	K.ILDWENSAPK.Q
R1/RRR1-4/2	951.390	952.086	-1787.999	0.282	816.827	0.453	14	0.211	K.LSVFDAATK.Y
R1/RRR1-4/2	1198.206	1198.258	-43.286	0.312	1091.793	0.342	16	0.211	R.NCDEFQVTGK.D
R1/RRR1-4/2	1173.144	1173.300	-133.235	0.512	787.651	0.378	16	0.209	K.ILDWENSAPK.Q
R1/RRR1-5/2	1173.246	1173.300	-46.607	0.530	675.475	0.403	15	0.208	K.ILDWENSAPK.Q
R1/RRR1-5/2	1283.257	1282.426	-132.011	0.418	1020.490	0.322	16	0.206	K.YYSLPALSDPR.I
R1/RRR1-5/2	1616.394	1616.793	-247.662	0.331	697.543	0.434	20	0.206	R.DIWPSTEEIAEVVK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1144.133	1144.346	-187.123	0.377	515.834	0.489	15	0.205	K.TSLAPGSGVVKK.Y
R1/RRR1-4/2	952.041	952.086	-47.662	0.328	578.274	0.417	13	0.204	K.LSVFDAATK.Y
R1/RRR1-4/2	951.662	952.086	-447.156	0.305	744.375	0.382	14	0.204	K.LSVFDAATK.Y
R1/RRR1-4/2	1616.140	1616.793	-1026.424	0.341	615.353	0.415	19	0.202	R.DIWPSTEEIAEVVK.S
R1/RRR1-5/2	952.059	952.086	-28.628	0.325	750.440	0.346	14	0.201	K.LSVFDAATK.Y
R1/RRR1-2/2	1517.016	1516.656	238.211	0.364	1072.594	0.261	17	0.198	R.SDDTVAM*IESYLR.A
R1/RRR1-4/2	1197.593	1198.258	-1394.657	0.314	1010.326	0.275	15	0.198	R.NCDEFQVTGK.D
R1/RRR1-5/2	952.211	952.086	131.460	0.288	474.771	0.326	12	0.196	K.LSVFDAATK.Y
R1/RRR1-3/2	952.244	952.086	165.786	0.305	539.880	0.324	12	0.196	K.LSVFDAATK.Y
R1/RRR1-4/2	1143.821	1144.346	-1337.712	0.368	451.645	0.397	14	0.196	K.TSLAPGSGVVKK.Y
R1/RRR1-4/2	1143.551	1144.346	-1575.128	0.329	537.539	0.381	15	0.195	K.TSLAPGSGVVKK.Y
R1/RRR1-5/2	1656.219	1656.768	-937.936	0.382	513.537	0.409	14	0.194	K.SDWLSCLDNDVGFK.G
R1/RRR1-5/2	1537.939	1537.843	62.761	0.376	479.304	0.416	15	0.194	R.SNLAGM*GIIPLCFK.S
R1/RRR1-3/2	1617.233	1616.793	272.349	0.302	439.671	0.373	16	0.193	R.DIWPSTEEIAEVVK.S
R1/RRR1-3/2	1173.444	1173.300	123.057	0.345	746.770	0.240	15	0.193	K.ILDWENSAPK.Q
R1/RRR1-5/2	1502.082	1500.656	284.017	0.329	510.986	0.332	13	0.190	R.SDDTVAMIESYLR.A
R1/RRR1-1/2	1283.348	1282.426	-61.117	0.254	518.509	0.277	12	0.187	K.YYSLPALSDPR.I
R1/RRR1-2/2	952.226	952.086	146.759	0.180	305.418	0.329	9	0.184	-.LSVFDAATK.-
R1/RRR1-4/3	1558.807	1558.589	139.832	0.519	815.983	0.511	26	0.115	K.SGEDADTLGLTGHER.F
R1/RRR1-5/3	1557.615	1558.589	-1271.337	0.418	839.536	0.442	24	0.103	K.SGEDADTLGLTGHER.F
R1/RRR1-4/3	1558.344	1558.589	-157.940	0.485	618.181	0.465	23	0.102	K.SGEDADTLGLTGHER.F
R1/RRR1-4/3	1558.648	1558.589	37.570	0.475	677.585	0.457	24	0.101	K.SGEDADTLGLTGHER.F
R1/RRR1-5/3	1559.859	1558.589	173.254	0.456	587.490	0.448	23	0.098	K.SGEDADTLGLTGHER.F
R1/RRR1-5/3	1558.463	1558.589	-81.447	0.437	524.237	0.378	21	0.085	-.SGEDADTLGLTGHER.-
R1/RRR1-3/3	1557.982	1558.589	-1034.571	0.320	736.205	0.283	23	0.078	K.SGEDADTLGLTGHER.F
R1/RRR1-7/2	1322.034	1321.461	-324.014	0.547	2103.126	0.527	20	0.384	R.NVVIEQSYGSPK.V
R1/RRR1-7/2	1434.391	1434.684	-205.046	0.431	2329.254	0.346	21	0.364	R.GISM*AVDAVVTNLK.G
R1/RRR1-7/2	1321.236	1321.461	-170.381	0.477	1749.572	0.548	19	0.330	R.NVVIEQSYGSPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1320.998	1321.461	-351.703	0.430	1785.685	0.498	19	0.320	R.NVVIEQSYGSPK.V
R1/RRR1-7/2	1902.502	1902.181	169.473	0.483	1481.796	0.596	28	0.303	K.AAVEEGIVPGGGVALLYASK.E
R1/RRR1-7/2	1434.709	1434.684	17.393	0.474	1963.826	0.340	20	0.299	R.GISM*AVDAVVTNLK.G
R1/RRR1-7/2	1146.911	1147.218	-268.229	0.452	1510.174	0.481	19	0.278	K.IGGASEAEVGEK.K
R1/RRR1-7/2	1387.279	1386.576	-214.959	0.561	1415.388	0.515	19	0.277	R.GYISPYFVTNPK.T
R1/RRR1-7/2	1147.110	1147.218	-94.312	0.448	1505.642	0.451	19	0.271	K.IGGASEAEVGEK.K
R1/RRR1-7/2	1387.333	1386.576	-176.119	0.531	1194.248	0.586	18	0.270	R.GYISPYFVTNPK.T
R1/RRR1-7/2	1901.770	1902.181	-216.615	0.473	1185.752	0.607	26	0.269	K.AAVEEGIVPGGGVALLYASK.E
R1/RRR1-7/2	1387.172	1386.576	-292.559	0.486	1151.131	0.581	18	0.264	R.GYISPYFVTNPK.T
R1/RRR1-7/2	1901.638	1902.181	-813.734	0.475	1142.109	0.569	26	0.256	K.AAVEEGIVPGGGVALLYASK.E
R1/RRR1-7/2	1268.082	1268.447	-288.489	0.442	1383.387	0.416	19	0.250	K.SVAAGM*NAM*DLR.R
R1/RRR1-7/2	1586.261	1586.679	-264.253	0.502	1145.581	0.473	19	0.238	R.SAIELSTSDYDKEK.L
R1/RRR1-7/2	1585.867	1586.679	-1145.998	0.477	1134.519	0.470	18	0.235	R.SAIELSTSDYDKEK.L
R1/RRR1-7/2	1030.819	1031.142	-314.116	0.427	1244.927	0.385	16	0.231	R.GVEELADAVK.V
R1/RRR1-7/2	1587.155	1586.679	300.576	0.591	969.945	0.489	17	0.223	R.SAIELSTSDYDKEK.L
R1/RRR1-7/2	1030.970	1031.142	-166.809	0.468	1065.399	0.392	16	0.221	R.GVEELADAVK.V
R1/RRR1-7/2	967.312	967.147	171.177	0.427	715.050	0.419	14	0.207	K.VSNLHAVVK.V
R1/RRR1-7/2	1547.597	1546.665	-44.194	0.434	734.775	0.459	17	0.205	K.IGGASEAEVGEKKDR.V
R1/RRR1-7/2	1146.387	1147.218	-1601.348	0.339	976.992	0.339	16	0.203	K.IGGASEAEVGEK.K
R1/RRR1-7/3	1862.101	1862.072	15.766	0.509	1383.723	0.480	29	0.164	K.VTVSKDDTVILDGAGDKK.S
R1/RRR1-7/3	1861.740	1862.072	-178.861	0.495	1234.657	0.481	29	0.145	K.VTVSKDDTVILDGAGDKK.S
R1/RRR1-7/3	1902.059	1902.181	-64.385	0.331	1476.020	0.363	29	0.138	K.AAVEEGIVPGGGVALLYASK.E
R1/RRR1-7/3	1862.182	1862.072	59.653	0.495	1118.022	0.480	28	0.133	K.VTVSKDDTVILDGAGDKK.S
R1/RRR1-7/3	1901.675	1902.181	-794.249	0.325	925.301	0.384	27	0.092	K.AAVEEGIVPGGGVALLYASK.E
R1/RRR1-9/2	1504.227	1504.744	-1011.626	0.412	1544.013	0.496	20	0.284	K.ECILSGLLSVDGLK.V
R1/RRR1-9/2	1504.286	1504.744	-305.432	0.440	1409.032	0.483	19	0.265	K.ECILSGLLSVDGLK.V
R1/RRR1-9/2	1504.168	1504.744	-1051.389	0.316	1539.704	0.415	20	0.262	K.ECILSGLLSVDGLK.V
R1/RRR1-9/2	1072.670	1073.180	-1412.289	0.432	658.732	0.512	16	0.218	K.AVDGSYVFSK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1864.551	1864.003	-243.396	0.498	995.183	0.444	17	0.217	-.NFFIYVQDYNEADPK.-
R1/RRR1-9/2	1072.371	1073.180	-1692.009	0.374	793.068	0.484	16	0.217	K.AVDGSYVFSK.G
R1/RRR1-9/2	1171.940	1172.404	-396.484	0.395	866.663	0.418	15	0.211	K.FM*M*ANGTLVR.T
R1/RRR1-9/2	1292.188	1292.456	-207.847	0.360	1106.686	0.342	15	0.210	K.VVCDPSYLPNK.V
R1/RRR1-9/2	1419.052	1419.608	-1099.525	0.421	994.605	0.367	18	0.210	R.YLNEPAIDTVKR.M
R1/RRR1-9/2	1263.274	1263.421	-117.139	0.422	706.092	0.375	15	0.198	R.YLNEPAIDTVK.R
R1/RRR1-9/2	1096.457	1097.224	-1616.104	0.336	815.011	0.280	13	0.191	R.DYNVDM*VPK.F
R1/RRR1-9/3	1626.887	1626.798	55.185	0.478	1498.039	0.430	30	0.154	R.FRGEDKPPAHLGSSK.D
R1/RRR1-9/3	1805.689	1805.970	-155.765	0.465	1501.819	0.328	28	0.127	R.DDRYLNEPAIDTVKR.M
R1/RRR1-9/3	1625.907	1626.798	-1166.657	0.448	1292.834	0.394	29	0.120	R.FRGEDKPPAHLGSSK.D
R1/RRR1-9/3	1806.148	1805.970	98.991	0.418	1352.970	0.289	27	0.103	R.DDRYLNEPAIDTVKR.M
R1/RRR1-9/3	1470.040	1469.732	210.506	0.524	982.913	0.393	24	0.099	K.IHKVPATDM*EALK.S
R1/RRR1-9/3	1806.962	1805.970	-4.453	0.410	933.797	0.369	24	0.092	R.DDRYLNEPAIDTVKR.M
R1/RRR1-9/3	1470.744	1469.732	8.695	0.503	745.070	0.372	24	0.088	K.IHKVPATDM*EALK.S
R1/RRR1-9/3	1469.895	1469.732	111.321	0.477	853.024	0.294	22	0.081	K.IHKVPATDM*EALK.S
R1/RRR1-21/2	1263.691	1264.456	-1400.963	0.491	2056.466	0.572	20	0.383	R.LQAALSTGLFSR.I
R1/RRR1-2/2	1264.307	1264.456	-117.817	0.487	1988.269	0.504	19	0.348	R.LQAALSTGLFSR.I
R1/RRR1-14/2	1608.732	1609.806	-1293.113	0.441	1859.640	0.551	22	0.341	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/2	1264.754	1264.456	236.585	0.546	1777.139	0.577	20	0.340	R.LQAALSTGLFSR.I
R1/RRR1-21/2	1265.197	1264.456	-204.830	0.555	1786.412	0.552	20	0.333	R.LQAALSTGLFSR.I
R1/RRR1-24/2	1312.091	1312.497	-310.886	0.431	1879.647	0.507	21	0.332	R.VLVGVVASPEADR.D
R1/RRR1-22/2	1312.071	1312.497	-325.448	0.442	1808.262	0.531	21	0.329	R.VLVGVVASPEADR.D
R1/RRR1-19/2	1265.276	1264.456	-142.306	0.538	1739.043	0.551	19	0.325	R.LQAALSTGLFSR.I
R1/RRR1-4/2	1264.558	1264.456	80.884	0.491	1723.660	0.544	19	0.321	R.LQAALSTGLFSR.I
R1/RRR1-21/2	1264.190	1264.456	-210.804	0.536	1555.124	0.618	19	0.320	R.LQAALSTGLFSR.I
R1/RRR1-13/2	1263.652	1264.456	-1431.721	0.460	1688.219	0.555	19	0.319	R.LQAALSTGLFSR.I
R1/RRR1-20/2	1264.438	1264.456	-13.906	0.475	1682.543	0.556	19	0.318	R.LQAALSTGLFSR.I
R1/RRR1-11/2	1264.418	1264.456	-29.787	0.474	1703.102	0.545	19	0.318	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1263.820	1264.456	-1298.226	0.516	1548.987	0.615	19	0.318	R.LQAALSTGLFSR.I
R1/RRR1-24/2	1264.200	1264.456	-203.055	0.535	1652.154	0.559	20	0.317	R.LQAALSTGLFSR.I
R1/RRR1-22/2	1264.197	1264.456	-205.573	0.516	1584.204	0.589	19	0.315	R.LQAALSTGLFSR.I
R1/RRR1-24/2	1609.309	1609.806	-309.236	0.447	1859.460	0.460	21	0.312	K.LDISGHTVSAVGPDIK.H
R1/RRR1-14/2	1609.266	1609.806	-959.900	0.442	1721.674	0.527	21	0.312	K.LDISGHTVSAVGPDIK.H
R1/RRR1-15/2	1263.989	1264.456	-370.278	0.490	1616.326	0.561	19	0.311	R.LQAALSTGLFSR.I
R1/RRR1-24/2	1263.996	1264.456	-364.948	0.512	1473.105	0.627	18	0.310	R.LQAALSTGLFSR.I
R1/RRR1-1/2	1263.610	1264.456	-1464.906	0.480	1660.417	0.538	19	0.310	R.LQAALSTGLFSR.I
R1/RRR1-24/2	1608.718	1609.806	-1301.724	0.417	1706.496	0.528	21	0.310	K.LDISGHTVSAVGPDIK.H
R1/RRR1-25/2	1264.177	1264.456	-220.879	0.464	1645.842	0.539	19	0.308	R.LQAALSTGLFSR.I
R1/RRR1-22/2	1264.160	1264.456	-234.829	0.506	1650.462	0.528	19	0.306	R.LQAALSTGLFSR.I
R1/RRR1-14/2	1264.108	1264.456	-275.808	0.530	1623.758	0.539	19	0.306	R.LQAALSTGLFSR.I
R1/RRR1-15/2	1608.849	1609.806	-1219.808	0.428	1693.576	0.516	21	0.305	K.LDISGHTVSAVGPDIK.H
R1/RRR1-1/2	1312.241	1312.497	-195.901	0.450	1490.164	0.599	20	0.304	R.VLVGVVASPEADR.D
R1/RRR1-14/2	1609.368	1609.806	-272.632	0.413	1783.726	0.466	21	0.304	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/2	1264.127	1264.456	-260.889	0.543	1571.945	0.554	19	0.304	R.LQAALSTGLFSR.I
R1/RRR1-5/2	1264.144	1264.456	-247.422	0.426	1603.285	0.541	19	0.303	R.LQAALSTGLFSR.I
R1/RRR1-3/2	1263.395	1264.456	-1636.300	0.428	1734.080	0.473	19	0.301	R.LQAALSTGLFSR.I
R1/RRR1-7/2	1264.404	1264.456	-41.116	0.501	1613.763	0.527	19	0.301	R.LQAALSTGLFSR.I
R1/RRR1-9/2	1264.202	1264.456	-201.214	0.436	1538.214	0.560	19	0.300	R.LQAALSTGLFSR.I
R1/RRR1-3/2	1263.660	1264.456	-1425.220	0.471	1621.337	0.512	19	0.298	R.LQAALSTGLFSR.I
R1/RRR1-18/2	1265.162	1264.456	-232.707	0.361	1564.462	0.546	19	0.297	R.LQAALSTGLFSR.I
R1/RRR1-14/2	1264.311	1264.456	-114.525	0.464	1589.560	0.521	19	0.296	R.LQAALSTGLFSR.I
R1/RRR1-15/2	1263.959	1264.456	-394.019	0.567	1447.483	0.584	18	0.295	R.LQAALSTGLFSR.I
R1/RRR1-19/2	1264.214	1264.456	-191.818	0.460	1460.338	0.576	19	0.295	R.LQAALSTGLFSR.I
R1/RRR1-22/2	1312.108	1312.497	-297.258	0.442	1607.867	0.508	20	0.294	R.VLVGVVASPEADR.D
R1/RRR1-22/2	1609.992	1609.806	115.927	0.534	1669.234	0.480	23	0.292	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/2	1264.246	1264.456	-166.730	0.501	1460.001	0.566	18	0.292	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1610.296	1609.806	305.228	0.505	1500.565	0.555	22	0.292	K.LDISGHTVSAVGPDIK.H
R1/RRR1-13/2	1263.682	1264.456	-1407.852	0.490	1466.386	0.557	18	0.291	R.LQAALSTGLFSR.I
R1/RRR1-1/2	1263.382	1264.456	-1646.007	0.399	1695.275	0.451	19	0.290	R.LQAALSTGLFSR.I
R1/RRR1-19/2	1313.093	1312.497	-308.784	0.539	1428.635	0.570	19	0.289	R.VLVGVVASPEADR.D
R1/RRR1-24/2	1263.712	1264.456	-1383.888	0.493	1378.109	0.587	18	0.288	R.LQAALSTGLFSR.I
R1/RRR1-21/2	1311.614	1312.497	-1439.856	0.381	1594.094	0.496	20	0.288	R.VLVGVVASPEADR.D
R1/RRR1-17/2	1609.670	1609.806	-84.248	0.518	1533.642	0.530	21	0.288	K.LDISGHTVSAVGPDIK.H
R1/RRR1-14/2	1263.690	1264.456	-1401.254	0.486	1319.068	0.611	18	0.288	R.LQAALSTGLFSR.I
R1/RRR1-22/2	1312.372	1312.497	-96.057	0.494	1400.470	0.564	20	0.285	R.VLVGVVASPEADR.D
R1/RRR1-24/2	1608.917	1609.806	-1177.446	0.406	1569.260	0.503	21	0.285	K.LDISGHTVSAVGPDIK.H
R1/RRR1-3/2	1265.195	1264.456	-206.379	0.491	1377.507	0.567	19	0.284	R.LQAALSTGLFSR.I
R1/RRR1-24/2	1312.085	1312.497	-315.367	0.465	1473.942	0.528	20	0.284	R.VLVGVVASPEADR.D
R1/RRR1-25/2	1312.139	1312.497	-273.550	0.479	1327.032	0.590	20	0.284	R.VLVGVVASPEADR.D
R1/RRR1-25/2	1263.551	1264.456	-1512.067	0.406	1510.600	0.512	19	0.284	R.LQAALSTGLFSR.I
R1/RRR1-25/2	1263.681	1264.456	-1408.337	0.427	1372.415	0.575	18	0.283	R.LQAALSTGLFSR.I
R1/RRR1-13/2	1263.704	1264.456	-1390.194	0.414	1467.532	0.532	18	0.283	R.LQAALSTGLFSR.I
R1/RRR1-15/2	1610.366	1609.806	-273.755	0.493	1423.454	0.553	21	0.281	K.LDISGHTVSAVGPDIK.H
R1/RRR1-25/2	1312.061	1312.497	-333.476	0.422	1381.400	0.565	19	0.281	R.VLVGVVASPEADR.D
R1/RRR1-19/2	1264.271	1264.456	-146.971	0.431	1397.007	0.553	18	0.281	R.LQAALSTGLFSR.I
R1/RRR1-16/2	1265.198	1264.456	-204.540	0.467	1341.972	0.570	18	0.280	R.LQAALSTGLFSR.I
R1/RRR1-4/2	1263.846	1264.456	-1277.953	0.427	1514.292	0.492	18	0.279	R.LQAALSTGLFSR.I
R1/RRR1-14/2	1312.086	1312.497	-314.060	0.451	1424.368	0.529	20	0.279	R.VLVGVVASPEADR.D
R1/RRR1-7/2	1312.204	1312.497	-223.898	0.451	1327.663	0.574	19	0.278	R.VLVGVVASPEADR.D
R1/RRR1-12/2	1264.406	1264.456	-39.567	0.500	1361.566	0.547	18	0.277	R.LQAALSTGLFSR.I
R1/RRR1-9/2	1312.193	1312.497	-232.764	0.451	1499.745	0.491	19	0.277	R.VLVGVVASPEADR.D
R1/RRR1-22/2	1263.990	1264.456	-369.696	0.405	1447.442	0.515	18	0.277	R.LQAALSTGLFSR.I
R1/RRR1-23/2	1311.525	1312.497	-1508.383	0.389	1584.665	0.446	20	0.275	R.VLVGVVASPEADR.D
R1/RRR1-15/2	1311.655	1312.497	-1409.008	0.371	1386.375	0.544	19	0.275	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1312.192	1312.497	-233.417	0.467	1243.049	0.593	19	0.275	R.VLVGVVASPEADR.D
R1/RRR1-21/2	1609.615	1609.806	-118.937	0.491	1529.175	0.478	21	0.274	K.LDISGHTVSAVGPDIK.H
R1/RRR1-22/2	1609.282	1609.806	-949.924	0.440	1605.627	0.437	22	0.274	K.LDISGHTVSAVGPDIK.H
R1/RRR1-2/2	1312.268	1312.497	-175.370	0.471	1335.700	0.549	19	0.274	R.VLVGVVASPEADR.D
R1/RRR1-13/2	1311.807	1312.497	-1292.457	0.392	1403.203	0.523	19	0.273	R.VLVGVVASPEADR.D
R1/RRR1-23/2	1311.581	1312.497	-1465.003	0.377	1481.873	0.484	20	0.273	R.VLVGVVASPEADR.D
R1/RRR1-15/2	1312.180	1312.497	-242.377	0.461	1254.431	0.580	19	0.272	R.VLVGVVASPEADR.D
R1/RRR1-1/2	1264.189	1264.456	-211.967	0.514	1356.757	0.531	18	0.272	R.LQAALSTGLFSR.I
R1/RRR1-11/2	1312.383	1312.497	-87.100	0.465	1251.506	0.576	19	0.271	R.VLVGVVASPEADR.D
R1/RRR1-24/2	1312.100	1312.497	-303.885	0.425	1484.325	0.473	20	0.271	R.VLVGVVASPEADR.D
R1/RRR1-2/2	1311.960	1312.497	-1174.904	0.394	1475.704	0.476	19	0.270	R.VLVGVVASPEADR.D
R1/RRR1-4/2	1312.271	1312.497	-173.131	0.488	1540.622	0.442	20	0.270	R.VLVGVVASPEADR.D
R1/RRR1-5/2	1312.014	1312.497	-369.696	0.382	1488.364	0.466	20	0.269	R.VLVGVVASPEADR.D
R1/RRR1-25/2	1312.172	1312.497	-248.724	0.438	1391.010	0.508	19	0.269	R.VLVGVVASPEADR.D
R1/RRR1-21/2	1609.381	1609.806	-264.413	0.439	1467.568	0.481	22	0.269	K.LDISGHTVSAVGPDIK.H
R1/RRR1-15/2	1263.502	1264.456	-1551.081	0.434	1322.529	0.529	18	0.268	R.LQAALSTGLFSR.I
R1/RRR1-19/2	1312.361	1312.497	-104.081	0.465	1277.127	0.546	19	0.267	R.VLVGVVASPEADR.D
R1/RRR1-1/2	1312.378	1312.497	-91.205	0.474	1286.112	0.541	19	0.267	R.VLVGVVASPEADR.D
R1/RRR1-22/2	1609.378	1609.806	-266.239	0.463	1506.411	0.454	22	0.267	K.LDISGHTVSAVGPDIK.H
R1/RRR1-12/2	1264.133	1264.456	-256.045	0.502	1349.282	0.509	18	0.267	R.LQAALSTGLFSR.I
R1/RRR1-20/2	1312.200	1312.497	-226.884	0.463	1302.267	0.531	19	0.266	R.VLVGVVASPEADR.D
R1/RRR1-24/2	1264.014	1264.456	-350.898	0.433	1227.805	0.563	17	0.265	R.LQAALSTGLFSR.I
R1/RRR1-21/2	1313.162	1312.497	-255.902	0.503	1201.325	0.561	19	0.264	R.VLVGVVASPEADR.D
R1/RRR1-14/2	1312.263	1312.497	-179.103	0.481	1348.498	0.502	19	0.264	R.VLVGVVASPEADR.D
R1/RRR1-2/2	1312.197	1312.497	-229.498	0.432	1410.472	0.470	20	0.263	R.VLVGVVASPEADR.D
R1/RRR1-23/2	1312.147	1312.497	-268.044	0.396	1516.533	0.421	20	0.262	R.VLVGVVASPEADR.D
R1/RRR1-20/2	1264.175	1264.456	-222.622	0.437	1351.912	0.490	18	0.262	R.LQAALSTGLFSR.I
R1/RRR1-4/2	1312.352	1312.497	-110.892	0.469	1240.171	0.536	19	0.262	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1264.370	1264.456	-68.232	0.488	1288.223	0.511	18	0.261	R.LQAALSTGLFSR.I
R1/RRR1-7/2	1312.084	1312.497	-316.020	0.391	1306.933	0.515	18	0.261	R.VLVGVVASPEADR.D
R1/RRR1-10/2	1312.461	1312.497	-27.297	0.446	1472.053	0.435	19	0.260	R.VLVGVVASPEADR.D
R1/RRR1-15/2	1312.195	1312.497	-231.178	0.458	1215.691	0.538	19	0.260	R.VLVGVVASPEADR.D
R1/RRR1-5/2	1313.235	1312.497	-200.321	0.499	1145.986	0.557	18	0.257	R.VLVGVVASPEADR.D
R1/RRR1-17/2	1312.168	1312.497	-251.337	0.442	1246.097	0.514	19	0.257	R.VLVGVVASPEADR.D
R1/RRR1-10/2	1313.299	1312.497	-151.553	0.490	1250.897	0.517	18	0.257	R.VLVGVVASPEADR.D
R1/RRR1-14/2	1049.047	1049.270	-213.783	0.506	1455.740	0.418	16	0.257	R.LGVM*LTATAR.C
R1/RRR1-22/2	1049.022	1049.270	-237.130	0.460	1508.375	0.389	17	0.256	R.LGVM*LTATAR.C
R1/RRR1-23/2	1265.310	1264.456	-115.499	0.469	1535.366	0.393	17	0.256	R.LQAALSTGLFSR.I
R1/RRR1-24/2	1754.186	1754.945	-1005.596	0.449	1189.082	0.527	21	0.254	R.EELEKWM*AAYPQSR.V
R1/RRR1-15/2	1048.969	1049.270	-288.033	0.497	1522.936	0.380	16	0.254	R.LGVM*LTATAR.C
R1/RRR1-26/2	1311.650	1312.497	-1412.653	0.350	1356.044	0.460	19	0.254	R.VLVGVVASPEADR.D
R1/RRR1-17/2	1311.668	1312.497	-1398.819	0.374	1378.800	0.445	19	0.253	R.VLVGVVASPEADR.D
R1/RRR1-20/2	1264.141	1264.456	-249.748	0.413	1304.365	0.467	17	0.252	R.LQAALSTGLFSR.I
R1/RRR1-13/2	1311.566	1312.497	-1476.596	0.370	1097.947	0.561	18	0.251	R.VLVGVVASPEADR.D
R1/RRR1-12/2	1263.607	1264.456	-1467.817	0.448	1059.154	0.565	16	0.251	R.LQAALSTGLFSR.I
R1/RRR1-2/2	1049.159	1049.270	-106.513	0.439	1417.072	0.404	16	0.250	R.LGVM*LTATAR.C
R1/RRR1-13/2	1311.508	1312.497	-1521.379	0.370	1216.513	0.507	18	0.250	R.VLVGVVASPEADR.D
R1/RRR1-3/2	1048.662	1049.270	-1538.330	0.400	1424.092	0.400	16	0.250	R.LGVM*LTATAR.C
R1/RRR1-13/2	1048.991	1049.270	-266.901	0.503	1412.599	0.405	16	0.250	R.LGVM*LTATAR.C
R1/RRR1-3/2	1312.307	1312.497	-145.696	0.432	1133.009	0.528	18	0.249	R.VLVGVVASPEADR.D
R1/RRR1-26/2	1311.980	1312.497	-1160.142	0.379	1253.289	0.477	19	0.249	R.VLVGVVASPEADR.D
R1/RRR1-2/2	1049.104	1049.270	-158.802	0.486	1494.822	0.366	16	0.248	R.LGVM*LTATAR.C
R1/RRR1-17/2	1311.656	1312.497	-1408.167	0.392	1172.265	0.510	18	0.248	R.VLVGVVASPEADR.D
R1/RRR1-24/2	1049.294	1049.270	22.438	0.452	1450.871	0.379	16	0.248	R.LGVM*LTATAR.C
R1/RRR1-14/2	1049.025	1049.270	-234.796	0.465	1431.803	0.385	16	0.248	R.LGVM*LTATAR.C
R1/RRR1-25/2	1049.140	1049.270	-124.020	0.462	1388.364	0.399	16	0.247	R.LGVM*LTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/2	1048.426	1049.270	-1764.063	0.425	1437.635	0.376	16	0.246	R.LGVM*LTATAR.C
R1/RRR1-16/2	1311.498	1312.497	-1528.765	0.415	1075.699	0.535	17	0.245	R.VLVGVVASPEADR.D
R1/RRR1-19/2	1312.024	1312.497	-361.667	0.417	1311.931	0.427	19	0.245	R.VLVGVVASPEADR.D
R1/RRR1-23/2	1609.535	1609.806	-168.616	0.448	1308.731	0.441	21	0.244	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/2	1110.177	1110.271	-84.987	0.438	1195.439	0.461	14	0.244	K.WMAAYPQSR.V
R1/RRR1-16/2	1312.098	1312.497	-305.099	0.452	1031.806	0.544	17	0.244	R.VLVGVVASPEADR.D
R1/RRR1-7/2	1312.397	1312.497	-76.370	0.455	1142.364	0.495	18	0.244	R.VLVGVVASPEADR.D
R1/RRR1-9/2	1313.203	1312.497	-224.753	0.515	1113.451	0.505	18	0.244	R.VLVGVVASPEADR.D
R1/RRR1-3/2	1312.233	1312.497	-202.153	0.425	1135.165	0.499	18	0.244	R.VLVGVVASPEADR.D
R1/RRR1-18/2	1311.992	1312.497	-1151.080	0.387	1266.187	0.448	18	0.244	R.VLVGVVASPEADR.D
R1/RRR1-23/2	1049.087	1049.270	-175.261	0.508	1359.619	0.397	16	0.244	R.LGVM*LTATAR.C
R1/RRR1-3/2	1312.400	1312.497	-74.597	0.459	1057.466	0.530	17	0.243	R.VLVGVVASPEADR.D
R1/RRR1-24/2	1125.991	1126.270	-248.431	0.430	1184.752	0.455	15	0.243	K.WM*AAYPQSR.V
R1/RRR1-12/2	1312.130	1312.497	-280.457	0.442	1004.246	0.542	18	0.243	R.VLVGVVASPEADR.D
R1/RRR1-1/2	1609.458	1609.806	-216.855	0.457	1233.591	0.465	21	0.243	K.LDISGHTVSAVGPDIK.H
R1/RRR1-15/2	1048.607	1049.270	-1590.719	0.441	1395.554	0.374	16	0.242	R.LGVM*LTATAR.C
R1/RRR1-11/2	1312.252	1312.497	-187.689	0.406	995.152	0.549	17	0.241	R.VLVGVVASPEADR.D
R1/RRR1-1/2	1312.419	1312.497	-59.670	0.454	1007.095	0.537	17	0.241	R.VLVGVVASPEADR.D
R1/RRR1-4/2	1311.754	1312.497	-1332.737	0.431	946.369	0.562	17	0.241	R.VLVGVVASPEADR.D
R1/RRR1-16/2	1264.420	1264.456	-28.044	0.387	1252.640	0.435	17	0.241	R.LQAALSTGLFSR.I
R1/RRR1-20/2	1312.249	1312.497	-189.555	0.412	967.423	0.546	18	0.241	R.VLVGVVASPEADR.D
R1/RRR1-13/2	1609.026	1609.806	-1109.338	0.469	1245.082	0.443	22	0.240	K.LDISGHTVSAVGPDIK.H
R1/RRR1-17/2	1264.327	1264.456	-102.321	0.436	1029.303	0.507	17	0.239	R.LQAALSTGLFSR.I
R1/RRR1-14/2	1109.812	1110.271	-414.326	0.464	1112.130	0.453	15	0.239	K.WMAAYPQSR.V
R1/RRR1-12/2	1312.135	1312.497	-276.817	0.431	1201.061	0.435	19	0.238	R.VLVGVVASPEADR.D
R1/RRR1-26/2	1311.963	1312.497	-1172.569	0.385	1151.228	0.463	18	0.238	R.VLVGVVASPEADR.D
R1/RRR1-18/2	1264.182	1264.456	-217.004	0.404	934.792	0.554	15	0.237	R.LQAALSTGLFSR.I
R1/RRR1-25/2	1049.960	1049.270	-296.274	0.529	1341.488	0.376	16	0.237	R.LGVM*LTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1311.564	1312.497	-1478.372	0.382	1201.656	0.437	18	0.237	R.VLVGVVASPEADR.D
R1/RRR1-27/2	1049.521	1049.270	239.536	0.463	1242.203	0.402	16	0.237	R.LGVM*LTATAR.C
R1/RRR1-24/2	1032.948	1033.271	-313.706	0.486	1157.741	0.428	16	0.236	R.LGVMLTATAR.C
R1/RRR1-14/2	1109.458	1110.271	-1638.759	0.344	1273.716	0.389	16	0.236	K.WMAAYPQSR.V
R1/RRR1-22/2	1048.941	1049.270	-315.121	0.487	1285.352	0.383	16	0.236	R.LGVM*LTATAR.C
R1/RRR1-15/2	1109.792	1110.271	-432.426	0.403	1025.530	0.471	15	0.235	K.WMAAYPQSR.V
R1/RRR1-12/2	1311.632	1312.497	-1426.301	0.363	1041.086	0.500	17	0.235	R.VLVGVVASPEADR.D
R1/RRR1-23/2	1754.353	1754.945	-909.817	0.488	958.137	0.518	20	0.235	R.EELEKWM*AAYPQSR.V
R1/RRR1-15/2	1531.389	1531.733	-225.671	0.427	1465.942	0.311	18	0.233	K.DLYYDVLQFINK.L
R1/RRR1-13/2	1050.142	1049.270	-122.852	0.496	1383.911	0.337	16	0.233	R.LGVM*LTATAR.C
R1/RRR1-15/2	1127.005	1126.270	-235.822	0.381	932.084	0.492	15	0.232	K.WM*AAYPQSR.V
R1/RRR1-23/2	1264.211	1264.456	-194.433	0.379	979.546	0.500	16	0.232	R.LQAALSTGLFSR.I
R1/RRR1-18/2	1312.462	1312.497	-27.110	0.447	988.057	0.490	17	0.232	R.VLVGVVASPEADR.D
R1/RRR1-7/2	1264.099	1264.456	-283.462	0.374	923.855	0.528	15	0.232	R.LQAALSTGLFSR.I
R1/RRR1-14/2	1125.907	1126.270	-323.483	0.374	868.290	0.509	15	0.231	K.WM*AAYPQSR.V
R1/RRR1-14/2	1125.944	1126.270	-290.089	0.467	903.261	0.468	15	0.231	K.WM*AAYPQSR.V
R1/RRR1-23/2	1125.974	1126.270	-263.440	0.369	853.379	0.519	14	0.231	K.WM*AAYPQSR.V
R1/RRR1-23/2	1109.882	1110.271	-350.869	0.395	1160.654	0.396	15	0.230	K.WMAAYPQSR.V
R1/RRR1-24/2	1049.016	1049.270	-242.968	0.330	1360.013	0.331	15	0.230	R.LGVM*LTATAR.C
R1/RRR1-24/2	1110.939	1110.271	-299.177	0.382	1058.986	0.437	14	0.230	K.WMAAYPQSR.V
R1/RRR1-21/2	1049.234	1049.270	-34.390	0.404	1255.294	0.367	15	0.230	R.LGVM*LTATAR.C
R1/RRR1-24/2	1110.418	1110.271	133.349	0.362	1119.846	0.413	14	0.229	K.WMAAYPQSR.V
R1/RRR1-19/2	1049.159	1049.270	-105.812	0.417	1207.593	0.377	15	0.228	R.LGVM*LTATAR.C
R1/RRR1-14/2	1048.555	1049.270	-1640.541	0.446	1172.703	0.387	15	0.228	R.LGVM*LTATAR.C
R1/RRR1-20/2	1311.656	1312.497	-1408.167	0.359	1066.600	0.430	19	0.227	R.VLVGVVASPEADR.D
R1/RRR1-25/2	1126.070	1126.270	-178.500	0.388	954.203	0.454	14	0.227	K.WM*AAYPQSR.V
R1/RRR1-23/2	1109.972	1110.271	-269.545	0.441	1043.325	0.417	14	0.227	K.WMAAYPQSR.V
R1/RRR1-24/2	1033.118	1033.271	-148.449	0.523	1050.355	0.422	15	0.227	R.LGVMLTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1048.929	1049.270	-325.863	0.486	1145.886	0.390	15	0.226	R.LGVM*LTATAR.C
R1/RRR1-23/2	1126.003	1126.270	-238.207	0.392	975.353	0.441	14	0.226	K.WM*AAYPQSR.V
R1/RRR1-3/2	1048.650	1049.270	-1549.556	0.384	1328.579	0.316	16	0.226	R.LGVM*LTATAR.C
R1/RRR1-24/2	1532.188	1531.733	297.375	0.499	1403.576	0.312	18	0.226	K.DLYYDVLQFINK.L
R1/RRR1-15/2	1125.719	1126.270	-1382.018	0.397	923.027	0.453	14	0.226	K.WM*AAYPQSR.V
R1/RRR1-24/2	1110.004	1110.271	-240.527	0.423	803.187	0.488	13	0.225	K.WMAAYPQSR.V
R1/RRR1-24/2	1109.892	1110.271	-342.371	0.421	1041.825	0.404	14	0.225	K.WMAAYPQSR.V
R1/RRR1-25/2	1125.899	1126.270	-330.663	0.445	913.254	0.422	15	0.224	K.WM*AAYPQSR.V
R1/RRR1-23/2	1033.116	1033.271	-150.582	0.460	955.428	0.442	15	0.224	-.LGVMLTATAR.-
R1/RRR1-15/2	1109.825	1110.271	-402.627	0.441	885.376	0.435	14	0.223	K.WMAAYPQSR.V
R1/RRR1-24/2	1127.063	1126.270	-184.535	0.423	746.419	0.471	14	0.223	K.WM*AAYPQSR.V
R1/RRR1-13/2	1049.202	1049.270	-65.315	0.440	1127.964	0.372	15	0.223	R.LGVM*LTATAR.C
R1/RRR1-22/2	1125.862	1126.270	-363.189	0.413	739.645	0.475	14	0.223	K.WM*AAYPQSR.V
R1/RRR1-16/2	1311.512	1312.497	-1518.480	0.354	885.211	0.487	16	0.223	R.VLVGVVASPEADR.D
R1/RRR1-25/2	1125.927	1126.270	-305.208	0.455	778.627	0.456	14	0.223	K.WM*AAYPQSR.V
R1/RRR1-22/2	1126.040	1126.270	-205.036	0.369	934.141	0.430	14	0.222	K.WM*AAYPQSR.V
R1/RRR1-23/2	1032.867	1033.271	-391.730	0.510	974.055	0.415	15	0.222	R.LGVMLTATAR.C
R1/RRR1-2/2	1609.204	1609.806	-998.055	0.471	885.574	0.480	19	0.221	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/2	1125.954	1126.270	-281.605	0.382	893.897	0.429	14	0.221	K.WM*AAYPQSR.V
R1/RRR1-25/2	1609.348	1609.806	-285.036	0.442	1009.054	0.430	20	0.221	K.LDISGHTVSAVGPDIK.H
R1/RRR1-15/2	1125.644	1126.270	-1448.677	0.430	789.841	0.436	14	0.220	K.WM*AAYPQSR.V
R1/RRR1-24/2	1754.348	1754.945	-913.031	0.493	743.778	0.511	18	0.219	R.EELEKWM*AAYPQSR.V
R1/RRR1-27/2	1050.023	1049.270	-235.622	0.440	1022.892	0.389	14	0.219	R.LGVM*LTATAR.C
R1/RRR1-21/2	1311.245	1312.497	-1723.093	0.354	770.267	0.493	16	0.219	R.VLVGVVASPEADR.D
R1/RRR1-15/2	1531.235	1531.733	-326.523	0.365	1518.432	0.210	18	0.219	K.DLYYDVLQFINK.L
R1/RRR1-5/2	1263.568	1264.456	-1498.287	0.380	694.836	0.494	15	0.218	R.LQAALSTGLFSR.I
R1/RRR1-15/2	1754.249	1754.945	-969.336	0.394	807.454	0.494	18	0.218	R.EELEKWM*AAYPQSR.V
R1/RRR1-21/2	1132.915	1133.194	-246.903	0.437	752.394	0.416	16	0.218	R.NTDQLEGSLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1048.443	1049.270	-1747.919	0.379	1199.495	0.316	15	0.218	R.LGVM*LTATAR.C
R1/RRR1-14/2	1109.918	1110.271	-318.757	0.405	1012.636	0.358	15	0.218	K.WMAAYPQSR.V
R1/RRR1-23/2	1033.097	1033.271	-169.073	0.478	971.165	0.383	15	0.217	R.LGVMLTATAR.C
R1/RRR1-15/2	1109.742	1110.271	-1381.826	0.414	851.537	0.405	14	0.217	K.WMAAYPQSR.V
R1/RRR1-12/2	1133.929	1133.194	-234.265	0.479	711.346	0.413	16	0.217	R.NTDQLEGSLR.E
R1/RRR1-24/2	1126.150	1126.270	-107.275	0.349	792.955	0.436	14	0.217	K.WM*AAYPQSR.V
R1/RRR1-22/2	1125.607	1126.270	-1481.792	0.323	945.444	0.392	15	0.217	K.WM*AAYPQSR.V
R1/RRR1-3/2	1133.003	1133.194	-168.969	0.456	749.587	0.403	16	0.217	R.NTDQLEGSLR.E
R1/RRR1-14/2	1125.982	1126.270	-256.262	0.360	861.559	0.418	13	0.216	K.WM*AAYPQSR.V
R1/RRR1-24/2	1754.248	1754.945	-970.384	0.493	933.113	0.429	19	0.216	R.EELEKWM*AAYPQSR.V
R1/RRR1-12/2	1134.197	1133.194	2.849	0.531	703.250	0.409	16	0.216	R.NTDQLEGSLR.E
R1/RRR1-23/2	1754.487	1754.945	-261.866	0.451	761.584	0.478	19	0.216	R.EELEKWM*AAYPQSR.V
R1/RRR1-24/2	1033.210	1033.271	-59.323	0.470	912.762	0.387	15	0.216	R.LGVMLTATAR.C
R1/RRR1-17/2	1132.898	1133.194	-262.145	0.480	792.296	0.390	16	0.216	R.NTDQLEGSLR.E
R1/RRR1-23/2	1133.971	1133.194	-197.114	0.465	1079.526	0.332	16	0.215	R.NTDQLEGSLR.E
R1/RRR1-24/2	1109.473	1110.271	-1624.721	0.332	835.822	0.422	13	0.215	K.WMAAYPQSR.V
R1/RRR1-24/2	1127.080	1126.270	-168.781	0.433	598.636	0.436	13	0.215	K.WM*AAYPQSR.V
R1/RRR1-3/2	1132.501	1133.194	-1499.574	0.416	692.981	0.397	16	0.215	R.NTDQLEGSLR.E
R1/RRR1-23/2	1048.517	1049.270	-1677.267	0.366	1117.508	0.322	15	0.214	R.LGVM*LTATAR.C
R1/RRR1-20/2	1125.967	1126.270	-270.293	0.450	717.883	0.400	14	0.214	K.WM*AAYPQSR.V
R1/RRR1-18/2	1132.877	1133.194	-280.631	0.434	823.653	0.375	16	0.214	R.NTDQLEGSLR.E
R1/RRR1-15/2	1032.464	1033.271	-1755.512	0.409	846.522	0.408	15	0.214	-.LGVMLTATAR.-
R1/RRR1-27/2	1132.791	1133.194	-357.283	0.410	806.643	0.377	16	0.214	R.NTDQLEGSLR.E
R1/RRR1-18/2	1132.411	1133.194	-1579.486	0.367	788.373	0.385	16	0.213	R.NTDQLEGSLR.E
R1/RRR1-26/2	1132.980	1133.194	-190.046	0.449	721.691	0.380	16	0.213	R.NTDQLEGSLR.E
R1/RRR1-6/2	1265.129	1264.456	-259.230	0.346	560.307	0.490	15	0.213	R.LQAALSTGLFSR.I
R1/RRR1-1/2	1132.541	1133.194	-1463.954	0.378	754.624	0.385	16	0.213	R.NTDQLEGSLR.E
R1/RRR1-14/2	1610.400	1609.806	-252.766	0.422	1079.256	0.350	21	0.213	K.LDISGHTVSAVGPDIK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1132.990	1133.194	-180.534	0.440	794.787	0.361	16	0.212	R.NTDQLEGSLR.E
R1/RRR1-21/2	1133.107	1133.194	-76.784	0.482	786.908	0.363	16	0.212	R.NTDQLEGSLR.E
R1/RRR1-23/2	1609.196	1609.806	-1003.310	0.349	1253.265	0.282	21	0.212	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/2	1126.296	1126.270	22.970	0.427	701.323	0.378	14	0.212	K.WM*AAYPQSR.V
R1/RRR1-4/2	1132.520	1133.194	-1482.576	0.434	793.746	0.357	16	0.212	R.NTDQLEGSLR.E
R1/RRR1-18/2	1263.322	1264.456	-1694.351	0.315	601.386	0.494	14	0.211	R.LQAALSTGLFSR.I
R1/RRR1-20/2	1132.549	1133.194	-1457.133	0.429	793.588	0.353	16	0.211	R.NTDQLEGSLR.E
R1/RRR1-23/2	1609.372	1609.806	-270.044	0.437	1213.971	0.295	22	0.211	K.LDISGHTVSAVGPDIK.H
R1/RRR1-26/2	1133.035	1133.194	-141.301	0.411	681.434	0.360	16	0.211	R.NTDQLEGSLR.E
R1/RRR1-1/2	1132.412	1133.194	-1578.945	0.387	853.120	0.345	16	0.211	R.NTDQLEGSLR.E
R1/RRR1-25/2	1133.023	1133.194	-151.785	0.448	728.838	0.355	16	0.211	R.NTDQLEGSLR.E
R1/RRR1-19/2	1132.956	1133.194	-210.907	0.447	775.800	0.344	16	0.210	R.NTDQLEGSLR.E
R1/RRR1-18/2	1125.955	1126.270	-280.408	0.254	773.094	0.426	14	0.210	K.WM*AAYPQSR.V
R1/RRR1-24/2	1132.485	1133.194	-1513.758	0.379	729.214	0.351	16	0.210	R.NTDQLEGSLR.E
R1/RRR1-14/2	1609.050	1609.806	-1094.255	0.377	1244.186	0.274	21	0.210	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/2	1133.011	1133.194	-162.160	0.445	723.214	0.344	16	0.210	R.NTDQLEGSLR.E
R1/RRR1-15/2	1033.103	1033.271	-163.147	0.421	867.441	0.345	15	0.210	R.LGVMLTATAR.C
R1/RRR1-24/2	1132.937	1133.194	-227.337	0.398	792.793	0.335	16	0.209	R.NTDQLEGSLR.E
R1/RRR1-3/2	1133.016	1133.194	-158.161	0.454	627.503	0.352	15	0.209	R.NTDQLEGSLR.E
R1/RRR1-26/2	1132.316	1133.194	-1663.418	0.417	784.244	0.331	16	0.209	R.NTDQLEGSLR.E
R1/RRR1-14/2	1133.030	1133.194	-145.732	0.396	632.147	0.353	15	0.209	R.NTDQLEGSLR.E
R1/RRR1-27/2	1133.113	1133.194	-72.246	0.464	712.320	0.349	15	0.208	R.NTDQLEGSLR.E
R1/RRR1-18/2	1133.043	1133.194	-134.168	0.473	720.675	0.333	16	0.208	R.NTDQLEGSLR.E
R1/RRR1-1/2	1049.605	1049.270	320.355	0.305	1105.724	0.283	15	0.208	R.LGVM*LTATAR.C
R1/RRR1-23/2	1133.287	1133.194	82.474	0.446	787.571	0.339	15	0.208	R.NTDQLEGSLR.E
R1/RRR1-24/2	921.899	922.014	-124.523	0.423	640.051	0.358	11	0.208	R.CVFPDQR.L
R1/RRR1-24/2	921.857	922.014	-170.616	0.371	740.688	0.346	12	0.207	R.CVFPDQR.L
R1/RRR1-4/2	1132.546	1133.194	-1460.056	0.379	645.561	0.341	15	0.207	R.NTDQLEGSLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-25/2	1132.947	1133.194	-218.690	0.409	694.419	0.335	15	0.207	R.NTDQLEGSLR.E
R1/RRR1-2/2	1132.904	1133.194	-256.523	0.401	790.246	0.314	16	0.207	R.NTDQLEGSLR.E
R1/RRR1-22/2	1132.953	1133.194	-213.501	0.463	665.323	0.336	15	0.207	R.NTDQLEGSLR.E
R1/RRR1-5/2	1132.971	1133.194	-197.396	0.399	640.576	0.332	15	0.207	R.NTDQLEGSLR.E
R1/RRR1-23/2	1133.141	1133.194	-47.500	0.472	781.229	0.317	16	0.207	R.NTDQLEGSLR.E
R1/RRR1-14/2	1033.448	1033.271	172.307	0.234	793.224	0.398	15	0.207	R.LGVMLTATAR.C
R1/RRR1-23/2	1264.213	1264.456	-192.884	0.312	855.916	0.340	17	0.206	R.LQAALSTGLFSR.I
R1/RRR1-22/2	1132.991	1133.194	-180.210	0.493	703.877	0.313	16	0.206	R.NTDQLEGSLR.E
R1/RRR1-11/2	1132.923	1133.194	-239.876	0.366	677.637	0.304	16	0.206	R.NTDQLEGSLR.E
R1/RRR1-19/2	1132.999	1133.194	-172.644	0.452	747.961	0.302	16	0.205	R.NTDQLEGSLR.E
R1/RRR1-23/2	921.462	922.014	-1689.017	0.408	489.527	0.337	10	0.205	R.CVFPDQR.L
R1/RRR1-2/2	1132.963	1133.194	-204.638	0.429	557.019	0.320	14	0.205	R.NTDQLEGSLR.E
R1/RRR1-19/2	1132.997	1133.194	-174.590	0.388	642.814	0.306	15	0.205	R.NTDQLEGSLR.E
R1/RRR1-16/2	1132.203	1133.194	-1763.830	0.374	774.957	0.294	16	0.205	R.NTDQLEGSLR.E
R1/RRR1-24/2	1132.848	1133.194	-306.469	0.360	692.197	0.293	16	0.204	R.NTDQLEGSLR.E
R1/RRR1-7/2	1133.064	1133.194	-115.040	0.341	741.013	0.297	16	0.204	R.NTDQLEGSLR.E
R1/RRR1-27/2	1132.966	1133.194	-201.827	0.447	781.916	0.292	16	0.204	R.NTDQLEGSLR.E
R1/RRR1-24/2	1264.214	1264.456	-191.721	0.355	581.250	0.427	14	0.204	-.LQAALSTGLFSR.-
R1/RRR1-22/2	1133.078	1133.194	-102.828	0.503	755.783	0.303	16	0.204	R.NTDQLEGSLR.E
R1/RRR1-23/2	1132.523	1133.194	-1480.085	0.382	762.766	0.282	16	0.204	R.NTDQLEGSLR.E
R1/RRR1-23/2	921.411	922.014	-1745.187	0.342	479.316	0.338	10	0.204	R.CVFPDQR.L
R1/RRR1-24/2	921.946	922.014	-73.919	0.367	506.960	0.327	10	0.203	R.CVFPDQR.L
R1/RRR1-9/2	1132.530	1133.194	-1473.698	0.356	602.806	0.281	15	0.203	R.NTDQLEGSLR.E
R1/RRR1-5/2	1132.652	1133.194	-1365.333	0.360	668.082	0.312	14	0.203	R.NTDQLEGSLR.E
R1/RRR1-17/2	1133.029	1133.194	-145.840	0.491	717.930	0.288	16	0.203	R.NTDQLEGSLR.E
R1/RRR1-1/2	922.044	922.014	32.319	0.338	403.888	0.342	9	0.203	R.CVFPDQR.L
R1/RRR1-24/2	1048.687	1049.270	-1513.891	0.310	656.852	0.350	13	0.203	R.LGVM*LTATAR.C
R1/RRR1-20/2	921.976	922.014	-40.850	0.439	484.641	0.295	10	0.202	R.CVFPDQR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1311.588	1312.497	-1459.768	0.299	509.580	0.437	13	0.202	R.VLVGVVASPEADR.D
R1/RRR1-20/2	1133.169	1133.194	-22.108	0.455	669.279	0.287	15	0.202	R.NTDQLEGSLR.E
R1/RRR1-22/2	1264.355	1264.456	-79.950	0.310	406.568	0.317	14	0.202	R.LQAALSTGLFSR.I
R1/RRR1-25/2	921.923	922.014	-98.756	0.383	392.156	0.291	9	0.202	R.CVFPDQR.L
R1/RRR1-23/2	1133.132	1133.194	-55.280	0.364	501.215	0.232	14	0.202	R.NTDQLEGSLR.E
R1/RRR1-25/2	1132.885	1133.194	-273.604	0.443	664.341	0.276	15	0.202	R.NTDQLEGSLR.E
R1/RRR1-25/2	921.990	922.014	-26.242	0.311	421.947	0.336	9	0.201	R.CVFPDQR.L
R1/RRR1-14/2	921.924	922.014	-97.693	0.392	512.599	0.281	10	0.201	R.CVFPDQR.L
R1/RRR1-9/2	1133.007	1133.194	-165.619	0.371	512.615	0.218	14	0.201	R.NTDQLEGSLR.E
R1/RRR1-1/2	1132.979	1133.194	-190.803	0.500	686.485	0.286	15	0.201	R.NTDQLEGSLR.E
R1/RRR1-14/2	922.015	922.014	1.114	0.415	528.238	0.280	10	0.201	R.CVFPDQR.L
R1/RRR1-2/2	1132.498	1133.194	-1501.848	0.370	734.878	0.257	15	0.200	R.NTDQLEGSLR.E
R1/RRR1-20/2	921.802	922.014	-230.662	0.342	517.595	0.277	10	0.200	R.CVFPDQR.L
R1/RRR1-15/2	1530.802	1531.733	-1265.763	0.354	1282.528	0.193	17	0.199	K.DLYYDVLQFINK.L
R1/RRR1-10/2	1049.915	1049.270	-339.551	0.255	996.956	0.254	14	0.199	R.LGVM*LTATAR.C
R1/RRR1-23/2	921.828	922.014	-202.631	0.327	626.911	0.264	11	0.199	R.CVFPDQR.L
R1/RRR1-24/2	1264.143	1264.456	-247.810	0.254	528.996	0.405	12	0.199	R.LQAALSTGLFSR.I
R1/RRR1-9/2	1132.555	1133.194	-1452.044	0.345	705.597	0.201	15	0.197	R.NTDQLEGSLR.E
R1/RRR1-17/2	1132.548	1133.194	-1458.107	0.383	663.748	0.182	15	0.196	R.NTDQLEGSLR.E
R1/RRR1-6/2	1610.658	1609.806	-91.722	0.324	339.131	0.357	14	0.196	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/2	1049.306	1049.270	33.989	0.247	675.990	0.250	13	0.195	R.LGVM*LTATAR.C
R1/RRR1-4/2	1132.446	1133.194	-1548.516	0.329	780.854	0.188	15	0.195	R.NTDQLEGSLR.E
R1/RRR1-1/2	921.347	922.014	-1814.276	0.351	511.626	0.254	10	0.192	-.CVFPDQR.-
R1/RRR1-3/2	1049.047	1049.270	-212.965	0.232	771.505	0.206	13	0.192	R.LGVM*LTATAR.C
R1/RRR1-23/2	1608.274	1609.806	-2202.768	0.336	1207.290	0.164	20	0.192	K.LDISGHTVSAVGPDIK.H
R1/RRR1-25/2	1048.846	1049.270	-405.501	0.243	827.536	0.132	15	0.190	R.LGVM*LTATAR.C
R1/RRR1-23/2	1609.358	1609.806	-279.176	0.348	594.327	0.215	18	0.190	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/2	1608.416	1609.806	-1489.914	0.298	986.969	0.185	20	0.190	K.LDISGHTVSAVGPDIK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1531.027	1531.733	-1117.952	0.343	1045.852	0.195	16	0.189	-.DLYYDVLQFINK.-
R1/RRR1-21/2	921.994	922.014	-21.727	0.360	416.840	0.325	9	0.185	-.CVFPDQR.-
R1/RRR1-24/3	1910.099	1911.131	-1067.046	0.495	1034.547	0.590	25	0.154	R.REELEKWM*AAYPQSR.V
R1/RRR1-24/3	1910.795	1911.131	-176.319	0.504	1058.945	0.561	27	0.145	R.REELEKWM*AAYPQSR.V
R1/RRR1-15/2	1610.388	1609.806	-260.294	0.419	451.768	0.279	15	0.141	-.LDISGHTVSAVGPDIK.-
R1/RRR1-15/3	1910.712	1911.131	-220.060	0.470	928.260	0.576	25	0.139	R.REELEKWM*AAYPQSR.V
R1/RRR1-1/3	1609.645	1609.806	-100.117	0.453	1149.638	0.504	29	0.139	K.LDISGHTVSAVGPDIK.H
R1/RRR1-22/3	1609.368	1609.806	-272.906	0.462	1026.474	0.535	28	0.137	K.LDISGHTVSAVGPDIK.H
R1/RRR1-15/3	1610.948	1609.806	88.830	0.531	906.356	0.561	29	0.134	K.LDISGHTVSAVGPDIK.H
R1/RRR1-15/3	1608.952	1609.806	-1155.360	0.471	918.564	0.546	28	0.131	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/3	1910.088	1911.131	-1073.110	0.422	919.986	0.551	25	0.131	R.REELEKWM*AAYPQSR.V
R1/RRR1-26/3	1610.647	1609.806	-99.067	0.454	781.591	0.575	26	0.130	K.LDISGHTVSAVGPDIK.H
R1/RRR1-18/2	921.226	922.014	-1946.890	0.301	349.852	0.320	8	0.129	-.CVFPDQR.-
R1/RRR1-23/3	1610.703	1609.806	-63.831	0.508	822.957	0.543	27	0.127	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/3	1910.441	1911.131	-887.184	0.463	923.778	0.519	25	0.126	R.REELEKWM*AAYPQSR.V
R1/RRR1-23/3	1910.919	1911.131	-111.242	0.482	804.266	0.528	23	0.124	R.REELEKWM*AAYPQSR.V
R1/RRR1-24/3	1894.657	1895.132	-251.362	0.395	842.321	0.524	22	0.123	R.REELEKWMAAYPQSR.V
R1/RRR1-23/3	1610.903	1609.806	60.445	0.490	939.437	0.503	29	0.123	K.LDISGHTVSAVGPDIK.H
R1/RRR1-14/3	1610.715	1609.806	-56.305	0.476	1032.687	0.480	30	0.123	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/3	1910.198	1911.131	-1015.266	0.439	621.335	0.550	20	0.120	R.REELEKWM*AAYPQSR.V
R1/RRR1-17/3	1609.898	1609.806	57.327	0.428	932.232	0.485	27	0.120	K.LDISGHTVSAVGPDIK.H
R1/RRR1-20/3	1609.840	1609.806	21.393	0.481	810.576	0.515	28	0.119	K.LDISGHTVSAVGPDIK.H
R1/RRR1-3/3	1610.518	1609.806	-179.355	0.444	836.442	0.510	28	0.118	K.LDISGHTVSAVGPDIK.H
R1/RRR1-22/3	1609.215	1609.806	-991.285	0.435	895.418	0.484	27	0.117	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/3	1910.860	1911.131	-142.578	0.455	708.287	0.536	25	0.117	R.REELEKWM*AAYPQSR.V
R1/RRR1-21/3	1609.394	1609.806	-256.584	0.432	615.624	0.530	24	0.116	K.LDISGHTVSAVGPDIK.H
R1/RRR1-23/3	1609.852	1609.806	28.580	0.457	855.571	0.492	28	0.116	K.LDISGHTVSAVGPDIK.H
R1/RRR1-21/3	1609.776	1609.806	-18.423	0.456	662.539	0.510	25	0.114	K.LDISGHTVSAVGPDIK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1609.874	1609.806	42.383	0.447	662.654	0.509	25	0.114	K.LDISGHTVSAVGPDIK.H
R1/RRR1-14/3	1313.703	1312.497	157.393	0.447	976.448	0.477	24	0.114	R.VLVGVVASPEADR.D
R1/RRR1-23/3	1911.179	1911.131	24.844	0.405	853.370	0.489	25	0.114	R.REELEKWM*AAYPQSR.V
R1/RRR1-25/3	1609.629	1609.806	-110.045	0.428	934.382	0.453	27	0.113	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/3	1910.889	1911.131	-126.910	0.417	558.273	0.546	24	0.113	R.REELEKWM*AAYPQSR.V
R1/RRR1-17/3	1610.423	1609.806	-238.439	0.433	838.746	0.474	27	0.113	K.LDISGHTVSAVGPDIK.H
R1/RRR1-21/3	1609.064	1609.806	-1085.656	0.397	721.238	0.497	25	0.112	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/3	1911.986	1911.131	-76.152	0.452	715.340	0.507	25	0.112	R.REELEKWM*AAYPQSR.V
R1/RRR1-25/3	1609.973	1609.806	104.322	0.374	1021.452	0.431	28	0.112	K.LDISGHTVSAVGPDIK.H
R1/RRR1-15/3	1910.672	1911.131	-241.019	0.426	778.289	0.472	22	0.111	R.REELEKWM*AAYPQSR.V
R1/RRR1-18/3	1609.739	1609.806	-41.812	0.407	729.743	0.488	26	0.111	K.LDISGHTVSAVGPDIK.H
R1/RRR1-14/3	1911.192	1911.131	31.762	0.428	674.847	0.494	23	0.110	R.REELEKWM*AAYPQSR.V
R1/RRR1-24/3	1895.142	1895.132	5.606	0.410	1012.730	0.405	23	0.110	R.REELEKWMAAYPQSR.V
R1/RRR1-15/3	1912.184	1911.131	27.776	0.472	829.627	0.454	25	0.109	R.REELEKWM*AAYPQSR.V
R1/RRR1-1/3	1609.093	1609.806	-1067.260	0.383	990.509	0.415	27	0.108	K.LDISGHTVSAVGPDIK.H
R1/RRR1-19/3	1609.763	1609.806	-26.751	0.418	479.800	0.468	22	0.107	K.LDISGHTVSAVGPDIK.H
R1/RRR1-20/3	1609.646	1609.806	-99.547	0.456	624.806	0.454	24	0.106	K.LDISGHTVSAVGPDIK.H
R1/RRR1-14/3	1912.063	1911.131	-35.520	0.426	897.371	0.426	25	0.106	R.REELEKWM*AAYPQSR.V
R1/RRR1-22/3	1912.524	1911.131	206.094	0.416	766.795	0.452	25	0.104	R.REELEKWM*AAYPQSR.V
R1/RRR1-20/3	1609.612	1609.806	-120.657	0.431	602.218	0.442	24	0.104	K.LDISGHTVSAVGPDIK.H
R1/RRR1-19/3	1609.499	1609.806	-191.070	0.377	756.426	0.425	26	0.101	K.LDISGHTVSAVGPDIK.H
R1/RRR1-14/3	1313.475	1312.497	-17.079	0.461	914.781	0.422	24	0.101	R.VLVGVVASPEADR.D
R1/RRR1-25/3	1609.913	1609.806	66.909	0.474	634.736	0.418	24	0.099	-.LDISGHTVSAVGPDIK.-
R1/RRR1-24/3	1312.722	1312.497	171.408	0.422	810.587	0.428	23	0.097	R.VLVGVVASPEADR.D
R1/RRR1-15/3	1312.277	1312.497	-168.615	0.351	577.200	0.437	20	0.087	-.VLVGVVASPEADR.-
R1/RRR1-15/3	1311.939	1312.497	-1191.593	0.382	716.250	0.357	22	0.086	R.VLVGVVASPEADR.D
R1/RRR1-1/3	1609.704	1609.806	-63.490	0.341	853.882	0.279	26	0.084	K.LDISGHTVSAVGPDIK.H
R1/RRR1-24/3	1312.333	1312.497	-125.505	0.424	571.540	0.362	20	0.082	-.VLVGVVASPEADR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/3	1312.661	1312.497	125.106	0.416	370.272	0.367	17	0.081	-.VLVGVVASPEADR.-
R1/RRR1-8/2	1910.577	1911.020	-232.534	0.591	2852.457	0.480	27	0.528	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/2	1910.448	1911.020	-825.106	0.610	2777.222	0.523	26	0.527	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/3	1911.154	1911.020	70.617	0.552	2757.810	0.477	35	0.473	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/3	1911.018	1911.020	-0.975	0.481	2676.352	0.451	33	0.435	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/2	1910.497	1911.020	-799.579	0.550	2385.126	0.466	24	0.412	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/2	1480.570	1481.550	-1340.793	0.415	2259.400	0.516	24	0.408	K.YGVDSGANLVTGGDR.L
R1/RRR1-8/2	1481.155	1481.550	-267.465	0.503	2060.212	0.577	24	0.393	K.YGVDSGANLVTGGDR.L
R1/RRR1-8/2	1481.148	1481.550	-271.765	0.499	2027.004	0.552	24	0.377	K.YGVDSGANLVTGGDR.L
R1/RRR1-8/2	1818.395	1818.879	-267.081	0.567	1673.238	0.568	23	0.322	K.NGVEQGPQIDDEQFNK.I
R1/RRR1-8/3	1911.018	1911.020	-0.687	0.463	2405.367	0.373	34	0.312	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/2	1817.892	1818.879	-1096.310	0.586	1577.113	0.550	22	0.302	K.NGVEQGPQIDDEQFNK.I
R1/RRR1-8/2	1818.251	1818.879	-897.919	0.545	1505.832	0.563	22	0.297	K.NGVEQGPQIDDEQFNK.I
R1/RRR1-8/2	1399.271	1399.655	-274.892	0.502	1426.449	0.532	19	0.278	K.VGPALACGNTVVLK.T
R1/RRR1-8/2	1399.270	1399.655	-275.592	0.518	1336.765	0.552	21	0.276	K.VGPALACGNTVVLK.T
R1/RRR1-8/2	1464.467	1464.645	-122.030	0.469	1304.943	0.524	21	0.265	K.TAEQTPLSALFASK.L
R1/RRR1-2/2	1481.290	1481.550	-175.776	0.417	1468.569	0.433	21	0.259	K.YGVDSGANLVTGGDR.L
R1/RRR1-8/2	1672.675	1672.947	-162.691	0.573	1322.698	0.508	20	0.259	K.IAQEEIFGPVQSILK.F
R1/RRR1-8/2	1398.808	1399.655	-1324.195	0.485	1229.361	0.531	20	0.258	K.VGPALACGNTVVLK.T
R1/RRR1-9/2	1465.234	1464.645	-281.735	0.443	1182.050	0.537	20	0.255	K.TAEQTPLSALFASK.L
R1/RRR1-2/3	1911.976	1911.020	-22.811	0.519	1933.775	0.479	33	0.253	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/2	1464.401	1464.645	-167.185	0.443	1082.137	0.545	19	0.247	K.TAEQTPLSALFASK.L
R1/RRR1-9/2	1464.491	1464.645	-105.475	0.428	1151.301	0.483	19	0.240	K.TAEQTPLSALFASK.L
R1/RRR1-8/2	1671.904	1672.947	-1225.286	0.419	1480.670	0.342	20	0.239	K.IAQEEIFGPVQSILK.F
R1/RRR1-8/2	1464.216	1464.645	-294.223	0.448	924.463	0.564	18	0.238	K.TAEQTPLSALFASK.L
R1/RRR1-2/2	1674.575	1672.947	-222.753	0.513	1326.824	0.406	19	0.236	K.IAQEEIFGPVQSILK.F
R1/RRR1-8/2	1819.360	1818.879	265.107	0.558	1153.049	0.464	20	0.233	K.NGVEQGPQIDDEQFNK.I
R1/RRR1-8/3	1819.009	1818.879	71.838	0.522	1784.023	0.487	28	0.231	K.NGVEQGPQIDDEQFNK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1674.474	1672.947	-283.163	0.538	1352.826	0.366	20	0.229	K.IAQEEIFGPVQSILK.F
R1/RRR1-3/2	1464.460	1464.645	-127.215	0.385	1138.658	0.417	20	0.227	K.TAEQTPLSALFASK.L
R1/RRR1-8/1	903.451	904.043	-1767.803	0.236	565.105	0.346	11	0.219	K.SVTLELGGK.S
R1/RRR1-8/2	1377.605	1378.599	-1451.405	0.478	1403.682	0.276	17	0.218	K.GIDSLKNYLQVK.A
R1/RRR1-8/2	1672.393	1672.947	-931.647	0.476	1049.189	0.410	18	0.217	K.IAQEEIFGPVQSILK.F
R1/RRR1-8/1	903.543	904.043	-554.969	0.238	535.991	0.367	10	0.214	K.SVTLELGGK.S
R1/RRR1-8/2	1097.234	1098.188	-1786.345	0.287	980.752	0.418	18	0.214	K.IAFTGSTDTGK.I
R1/RRR1-8/2	1097.816	1098.188	-340.003	0.384	829.111	0.395	16	0.207	K.IAFTGSTDTGK.I
R1/RRR1-8/2	1176.081	1175.318	-201.924	0.424	728.342	0.405	14	0.205	R.KAFDEGPWPK.M
R1/RRR1-8/2	1174.480	1175.318	-1568.987	0.379	693.487	0.409	13	0.202	R.KAFDEGPWPK.M
R1/RRR1-8/2	1091.896	1092.227	-303.946	0.443	1136.543	0.254	14	0.202	K.FNDLNEVIK.R
R1/RRR1-1/2	1399.928	1399.655	195.593	0.397	817.297	0.389	15	0.201	-.VGPALACGNTVVLK.-
R1/RRR1-8/2	1093.101	1092.227	-115.101	0.453	1160.946	0.243	14	0.201	K.FNDLNEVIK.R
R1/RRR1-8/2	1464.322	1464.645	-221.626	0.356	764.303	0.380	16	0.200	K.TAEQTPLSALFASK.L
R1/RRR1-8/2	1174.925	1175.318	-335.301	0.383	621.614	0.369	13	0.197	R.KAFDEGPWPK.M
R1/RRR1-2/2	1465.789	1464.645	98.013	0.328	467.407	0.433	14	0.196	K.TAEQTPLSALFASK.L
R1/RRR1-8/2	1091.414	1092.227	-1666.302	0.358	1120.749	0.215	14	0.196	K.FNDLNEVIK.R
R1/RRR1-8/2	1379.466	1378.599	-96.532	0.488	1132.431	0.255	15	0.194	K.GIDSLKNYLQVK.A
R1/RRR1-7/2	1674.515	1672.947	-258.223	0.519	963.808	0.301	18	0.193	K.IAQEEIFGPVQSILK.F
R1/RRR1-7/2	1398.931	1399.655	-1235.769	0.332	534.874	0.357	14	0.191	K.VGPALACGNTVVLK.T
R1/RRR1-8/2	1097.188	1098.188	-1828.154	0.258	805.961	0.285	16	0.191	K.IAFTGSTDTGK.I
R1/RRR1-2/2	1674.387	1672.947	263.638	0.511	857.689	0.313	17	0.191	K.IAQEEIFGPVQSILK.F
R1/RRR1-1/2	1673.826	1672.947	-72.388	0.373	460.395	0.308	15	0.191	K.IAQEEIFGPVQSILK.F
R1/RRR1-9/2	1673.607	1672.947	-203.715	0.450	936.438	0.267	17	0.189	K.IAQEEIFGPVQSILK.F
R1/RRR1-1/2	1673.836	1672.947	-66.023	0.413	767.020	0.252	17	0.187	K.IAQEEIFGPVQSILK.F
R1/RRR1-2/2	1399.734	1399.655	56.803	0.312	589.928	0.268	14	0.186	K.VGPALACGNTVVLK.T
R1/RRR1-8/2	1378.279	1378.599	-232.352	0.422	941.629	0.210	16	0.186	K.GIDSLKNYLQVK.A
R1/RRR1-2/2	1399.846	1399.655	137.003	0.333	477.792	0.389	12	0.184	-.VGPALACGNTVVLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1674.061	1672.947	68.339	0.465	539.566	0.324	14	0.182	-.IAQEEIFGPVQSILK.-
R1/RRR1-8/3	1672.746	1672.947	-120.422	0.443	1698.616	0.365	28	0.165	K.IAQEEIFGPVQSILK.F
R1/RRR1-8/1	903.395	904.043	-1830.460	0.153	372.560	0.364	9	0.149	-.SVTLELGGK.-
R1/RRR1-2/3	1910.851	1911.020	-88.533	0.463	1403.102	0.336	31	0.122	R.TGELIAHVAEGDAEDINR.A
R1/RRR1-8/3	1175.666	1175.318	297.355	0.530	1061.705	0.454	21	0.112	R.KAFDEGPWPK.M
R1/RRR1-8/3	1378.591	1378.599	-5.659	0.538	1004.341	0.427	29	0.099	K.GIDSLKNYLQVK.A
R1/RRR1-8/3	1174.694	1175.318	-1386.105	0.455	1124.910	0.346	19	0.096	R.KAFDEGPWPK.M
R1/RRR1-8/3	1175.409	1175.318	78.049	0.542	817.391	0.406	18	0.095	R.KAFDEGPWPK.M
R1/RRR1-8/3	1378.808	1378.599	152.315	0.500	922.426	0.408	28	0.093	K.GIDSLKNYLQVK.A
R1/RRR1-8/3	1378.589	1378.599	-6.858	0.462	602.967	0.441	23	0.092	K.GIDSLKNYLQVK.A
R1/RRR1-8/3	1818.304	1818.879	-868.711	0.354	448.598	0.351	21	0.075	-.NGVEQGPQIDDEQFNK.-
R1/RRR1-8/3	1673.129	1672.947	109.349	0.311	713.855	0.287	21	0.072	-.IAQEEIFGPVQSILK.-
R1/RRR1-6/2	1582.584	1582.844	-164.602	0.511	919.773	0.297	20	0.194	K.QFSAEEISSMVLIK.M
R1/RRR1-6/2	1598.620	1598.843	-139.835	0.358	486.362	0.243	17	0.185	-.QFSAEEISSM*VLIK.-
R1/RRR1-8/2	1865.498	1866.064	-841.837	0.549	2574.526	0.509	24	0.477	R.DAEGQDVLLFIDNIFR.F
R1/RRR1-8/2	1708.142	1709.007	-1095.071	0.483	2408.888	0.575	23	0.462	R.LVLEVAQHLGENMVR.T
R1/RRR1-8/2	1493.374	1493.647	-183.372	0.514	2527.348	0.488	22	0.451	R.FTQANSEVSALLGR.I
R1/RRR1-8/2	1493.357	1493.647	-194.688	0.539	2533.766	0.477	22	0.447	R.FTQANSEVSALLGR.I
R1/RRR1-8/2	1865.495	1866.064	-843.282	0.550	2315.506	0.559	23	0.438	R.DAEGQDVLLFIDNIFR.F
R1/RRR1-8/2	1493.303	1493.647	-231.181	0.521	2431.612	0.489	22	0.431	R.FTQANSEVSALLGR.I
R1/RRR1-8/2	1709.497	1709.007	287.731	0.576	2094.449	0.633	22	0.417	R.LVLEVAQHLGENMVR.T
R1/RRR1-8/2	1492.960	1493.647	-1133.254	0.470	2391.634	0.467	22	0.414	R.FTQANSEVSALLGR.I
R1/RRR1-9/2	1458.328	1458.792	-319.423	0.497	2400.266	0.455	20	0.408	K.TVLIMELINNVAK.A
R1/RRR1-8/2	1474.553	1474.791	-162.156	0.537	2378.542	0.464	20	0.405	K.TVLIM*ELINNVAK.A
R1/RRR1-8/2	1458.206	1458.792	-1091.077	0.500	2378.796	0.428	20	0.393	K.TVLIMELINNVAK.A
R1/RRR1-8/2	1474.532	1474.791	-176.523	0.547	2265.542	0.478	20	0.389	K.TVLIM*ELINNVAK.A
R1/RRR1-10/2	1459.453	1458.792	-232.684	0.574	2390.249	0.418	20	0.388	K.TVLIMELINNVAK.A
R1/RRR1-8/2	1708.641	1709.007	-215.159	0.583	1933.167	0.627	21	0.383	R.LVLEVAQHLGENMVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1474.399	1474.791	-266.888	0.445	2296.004	0.394	20	0.367	K.TVLIM*ELINNVAK.A
R1/RRR1-8/2	1458.279	1458.792	-1040.899	0.557	2263.023	0.409	20	0.362	K.TVLIMELINNVAK.A
R1/RRR1-8/2	1458.444	1458.792	-239.477	0.531	2261.189	0.395	20	0.357	K.TVLIMELINNVAK.A
R1/RRR1-9/2	1457.605	1458.792	-1505.051	0.410	2202.859	0.412	20	0.356	K.TVLIMELINNVAK.A
R1/RRR1-9/2	1493.366	1493.647	-188.456	0.520	1985.200	0.465	21	0.337	R.FTQANSEVSALLGR.I
R1/RRR1-9/2	1493.201	1493.647	-299.664	0.527	1975.566	0.403	22	0.316	R.FTQANSEVSALLGR.I
R1/RRR1-8/1	975.637	976.154	-1559.576	0.301	724.223	0.333	14	0.313	K.IGLFGGAGVGK.T
R1/RRR1-8/2	1724.429	1725.007	-917.762	0.530	1485.765	0.591	21	0.302	R.LVLEVAQHLGENM*VR.T
R1/RRR1-8/1	975.452	976.154	-1749.968	0.156	722.535	0.223	14	0.295	K.IGLFGGAGVGK.T
R1/RRR1-9/2	1474.234	1474.791	-1059.889	0.398	1844.308	0.372	18	0.288	K.TVLIM*ELINNVAK.A
R1/RRR1-8/2	1724.434	1725.007	-914.351	0.541	1419.486	0.573	20	0.288	R.LVLEVAQHLGENM*VR.T
R1/RRR1-9/2	1474.420	1474.791	-252.685	0.432	1797.251	0.368	18	0.280	K.TVLIM*ELINNVAK.A
R1/RRR1-8/2	1410.286	1410.644	-254.513	0.452	1464.431	0.491	22	0.275	R.VLNTGSPITVPVGR.A
R1/RRR1-8/2	1279.108	1279.446	-265.077	0.421	1377.880	0.484	19	0.264	R.TIAM*DGTEGLVR.G
R1/RRR1-8/2	1724.387	1725.007	-941.996	0.516	1101.925	0.600	21	0.262	R.LVLEVAQHLGENM*VR.T
R1/RRR1-8/2	1279.092	1279.446	-277.237	0.431	1329.208	0.490	19	0.260	R.TIAM*DGTEGLVR.G
R1/RRR1-8/2	1391.048	1391.516	-337.425	0.482	1090.948	0.571	23	0.257	K.AHGGFSVFAGVGER.T
R1/RRR1-8/2	1390.541	1391.516	-1424.872	0.454	1117.768	0.564	23	0.257	K.AHGGFSVFAGVGER.T
R1/RRR1-8/2	1856.532	1857.040	-814.816	0.516	1050.994	0.591	23	0.256	R.M*LSPHVLGEDHYNTAR.G
R1/RRR1-8/2	1857.496	1857.040	246.176	0.569	1047.865	0.589	23	0.256	R.M*LSPHVLGEDHYNTAR.G
R1/RRR1-8/2	1410.409	1410.644	-167.074	0.428	1291.850	0.474	21	0.252	R.VLNTGSPITVPVGR.A
R1/RRR1-8/1	975.652	976.154	-1544.744	0.239	610.155	0.379	14	0.251	K.IGLFGGAGVGK.T
R1/RRR1-11/2	1474.752	1474.791	-26.559	0.465	1480.320	0.396	18	0.251	K.TVLIM*ELINNVAK.A
R1/RRR1-2/2	1493.232	1493.647	-278.257	0.466	1403.273	0.410	20	0.248	R.FTQANSEVSALLGR.I
R1/RRR1-8/2	1856.425	1857.040	-872.836	0.532	956.789	0.575	23	0.245	R.M*LSPHVLGEDHYNTAR.G
R1/RRR1-2/2	1410.300	1410.644	-244.613	0.367	1239.115	0.466	20	0.243	R.VLNTGSPITVPVGR.A
R1/RRR1-8/2	1390.526	1391.516	-1435.629	0.426	1118.054	0.500	23	0.243	K.AHGGFSVFAGVGER.T
R1/RRR1-8/2	1410.339	1410.644	-217.174	0.420	1039.274	0.544	19	0.243	R.VLNTGSPITVPVGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1399.711	1400.608	-1359.380	0.426	1005.904	0.518	16	0.233	R.VGLTGLTVAEHFR.D
R1/RRR1-8/2	1278.976	1279.446	-368.110	0.370	1063.673	0.483	18	0.233	R.TIAM*DGTEGLVR.G
R1/RRR1-7/2	1493.396	1493.647	-168.448	0.383	1328.664	0.378	18	0.233	R.FTQANSEVSALLGR.I
R1/RRR1-8/2	976.021	976.154	-136.999	0.444	1138.860	0.421	17	0.230	K.IGLFGGAGVGK.T
R1/RRR1-8/2	1175.220	1174.374	-131.437	0.531	1115.609	0.419	17	0.230	K.VVDLLAPYQR.G
R1/RRR1-8/2	1174.074	1174.374	-256.392	0.484	938.817	0.457	16	0.225	K.VVDLLAPYQR.G
R1/RRR1-8/2	975.724	976.154	-441.838	0.450	1118.594	0.386	17	0.222	K.IGLFGGAGVGK.T
R1/RRR1-8/2	975.900	976.154	-261.222	0.451	1130.169	0.375	17	0.221	K.IGLFGGAGVGK.T
R1/RRR1-9/2	1410.292	1410.644	-250.084	0.336	1163.210	0.355	20	0.218	R.VLNTGSPITVPVGR.A
R1/RRR1-8/2	1400.261	1400.608	-248.203	0.433	823.575	0.489	16	0.218	R.VGLTGLTVAEHFR.D
R1/RRR1-9/2	975.749	976.154	-416.355	0.427	804.375	0.447	15	0.213	K.IGLFGGAGVGK.T
R1/RRR1-9/2	1279.030	1279.446	-326.262	0.355	1132.645	0.321	18	0.211	R.TIAM*DGTEGLVR.G
R1/RRR1-11/2	1474.974	1474.791	123.857	0.413	882.142	0.428	14	0.210	K.TVLIM*ELINNVAK.A
R1/RRR1-8/2	1400.419	1400.608	-135.393	0.417	959.177	0.375	16	0.207	R.VGLTGLTVAEHFR.D
R1/RRR1-9/2	1410.327	1410.644	-225.683	0.394	751.288	0.420	17	0.206	R.VLNTGSPITVPVGR.A
R1/RRR1-11/2	1475.146	1474.791	241.038	0.348	550.406	0.294	14	0.192	K.TVLIM*ELINNVAK.A
R1/RRR1-8/2	1459.532	1458.792	-178.480	0.419	519.477	0.299	14	0.192	K.TVLIMELINNVAK.A
R1/RRR1-10/2	1458.332	1458.792	-316.651	0.297	757.852	0.254	16	0.192	K.TVLIMELINNVAK.A
R1/RRR1-2/2	1401.864	1400.608	183.532	0.264	230.288	0.396	12	0.191	R.VGLTGLTVAEHFR.D
R1/RRR1-1/2	1410.411	1410.644	-165.858	0.274	744.470	0.284	15	0.189	R.VLNTGSPITVPVGR.A
R1/RRR1-7/2	1175.398	1174.374	20.145	0.329	399.345	0.362	10	0.186	-.VVDLLAPYQR.-
R1/RRR1-8/2	1410.453	1410.644	-135.818	0.159	604.105	0.264	15	0.183	R.VLNTGSPITVPVGR.A
R1/RRR1-9/1	975.376	976.154	-1828.119	0.123	541.319	0.171	13	0.182	K.IGLFGGAGVGK.T
R1/RRR1-10/2	1458.117	1458.792	-1152.525	0.325	533.115	0.273	13	0.181	-.TVLIMELINNVAK.-
R1/RRR1-2/2	1401.824	1400.608	155.064	0.263	189.777	0.358	12	0.167	-.VGLTGLTVAEHFR.-
R1/RRR1-8/3	1856.389	1857.040	-892.251	0.486	1521.462	0.449	30	0.166	R.M*LSPHVLGEDHYNTAR.G
R1/RRR1-8/3	1708.566	1709.007	-258.674	0.466	1099.552	0.552	30	0.138	R.LVLEVAQHLGENMVR.T
R1/RRR1-8/3	1856.451	1857.040	-858.486	0.522	1233.584	0.466	30	0.136	R.M*LSPHVLGEDHYNTAR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/3	1474.936	1474.791	98.533	0.499	1514.567	0.368	27	0.135	K.TVLIM*ELINNVAK.A
R1/RRR1-8/3	1840.855	1841.041	-101.543	0.480	1071.493	0.518	28	0.134	R.MLSPHVLGEDHYNTAR.G
R1/RRR1-8/3	1856.760	1857.040	-151.193	0.486	1130.034	0.474	29	0.128	R.M*LSPHVLGEDHYNTAR.G
R1/RRR1-8/3	1840.377	1841.041	-906.824	0.535	919.810	0.489	26	0.119	R.MLSPHVLGEDHYNTAR.G
R1/RRR1-8/3	1400.999	1400.608	280.335	0.487	1023.544	0.500	27	0.119	R.VGLTGLTVAEHFR.D
R1/RRR1-8/3	1708.379	1709.007	-956.106	0.380	954.453	0.517	32	0.113	R.LVLEVAQHLGENMVR.T
R1/RRR1-8/3	1708.298	1709.007	-1003.670	0.464	676.045	0.574	30	0.111	R.LVLEVAQHLGENMVR.T
R1/RRR1-8/3	1400.730	1400.608	87.652	0.476	1015.742	0.452	27	0.108	R.VGLTGLTVAEHFR.D
R1/RRR1-8/3	1410.373	1410.644	-193.044	0.399	1140.077	0.401	27	0.107	R.VLNTGSPITVPVGR.A
R1/RRR1-8/3	1410.385	1410.644	-184.318	0.376	1242.701	0.359	27	0.105	R.VLNTGSPITVPVGR.A
R1/RRR1-8/3	1401.610	1400.608	1.859	0.496	727.872	0.501	24	0.105	R.VGLTGLTVAEHFR.D
R1/RRR1-8/3	1840.261	1841.041	-970.053	0.469	794.753	0.440	25	0.102	R.MLSPHVLGEDHYNTAR.G
R1/RRR1-8/3	1725.976	1725.007	-17.459	0.476	854.296	0.459	30	0.102	R.LVLEVAQHLGENM*VR.T
R1/RRR1-8/3	1493.752	1493.647	70.595	0.421	1104.598	0.359	23	0.100	-.FTQANSEVSALLGR.-
R1/RRR1-8/3	1493.346	1493.647	-201.668	0.354	1141.110	0.311	23	0.091	R.FTQANSEVSALLGR.I
R1/RRR1-9/3	1400.517	1400.608	-65.236	0.361	687.162	0.295	22	0.079	R.VGLTGLTVAEHFR.D
R1/RRR1-8/3	1474.250	1474.791	-1048.924	0.430	1042.438	0.241	25	0.077	K.TVLIM*ELINNVAK.A
R1/RRR1-8/3	1409.587	1410.644	-1464.043	0.299	1039.926	0.252	24	0.075	R.VLNTGSPITVPVGR.A
R1/RRR1-8/3	1458.499	1458.792	-201.281	0.439	835.715	0.239	26	0.075	K.TVLIMELINNVAK.A
R1/RRR1-8/3	1457.797	1458.792	-1372.918	0.412	882.942	0.239	25	0.074	K.TVLIMELINNVAK.A
R1/RRR1-8/3	1458.610	1458.792	-124.838	0.442	889.176	0.213	25	0.072	K.TVLIMELINNVAK.A
R1/RRR1-9/3	1400.100	1400.608	-1079.788	0.373	1087.786	0.138	24	0.065	-.VGLTGLTVAEHFR.-
R1/RRR1-5/2	1240.579	1241.379	-1455.190	0.554	2007.924	0.546	19	0.370	K.IDNPIGATNIGR.A
R1/RRR1-5/2	1240.956	1241.379	-342.322	0.527	2015.660	0.510	21	0.361	K.IDNPIGATNIGR.A
R1/RRR1-5/2	1950.778	1951.170	-201.444	0.558	1854.118	0.577	22	0.352	R.LEGPIAWDVLYNFEQR.W
R1/RRR1-5/2	1859.433	1860.057	-876.453	0.555	1811.446	0.538	25	0.336	R.AYLPVQELLNGEEIDR.W
R1/RRR1-5/2	1240.424	1241.379	-1580.530	0.504	1775.325	0.525	21	0.327	K.IDNPIGATNIGR.A
R1/RRR1-5/2	1952.517	1951.170	178.175	0.572	1570.389	0.562	21	0.303	R.LEGPIAWDVLYNFEQR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1950.069	1951.170	-1080.769	0.518	1543.502	0.511	21	0.286	R.LEGPIAWDVLYNFEQR.W
R1/RRR1-5/2	1509.302	1508.695	-260.773	0.489	1429.800	0.535	20	0.283	R.IVSFVGGLDLCDGR.Y
R1/RRR1-1/2	1951.769	1951.170	-206.173	0.460	1561.633	0.473	21	0.279	R.LEGPIAWDVLYNFEQR.W
R1/RRR1-5/2	1819.393	1820.000	-885.647	0.496	1347.339	0.555	20	0.275	K.IVVVDHELPNQGSQQR.R
R1/RRR1-5/2	1372.308	1372.553	-178.761	0.488	1351.282	0.472	19	0.258	K.AGLVSGKDQIIDR.S
R1/RRR1-5/2	1371.908	1372.553	-1202.012	0.494	1346.973	0.468	20	0.257	K.AGLVSGKDQIIDR.S
R1/RRR1-1/2	1241.220	1241.379	-128.492	0.460	1374.443	0.449	19	0.256	K.IDNPIGATNIGR.A
R1/RRR1-1/2	1859.292	1860.057	-952.643	0.452	1260.506	0.484	22	0.250	R.AYLPVQELLNGEEIDR.W
R1/RRR1-5/2	1406.815	1406.561	181.145	0.498	960.773	0.529	16	0.237	R.DYLTFFCLGNR.E
R1/RRR1-5/2	1371.781	1372.553	-1295.393	0.453	1130.230	0.471	18	0.236	K.AGLVSGKDQIIDR.S
R1/RRR1-5/2	1880.095	1880.989	-1010.220	0.461	763.622	0.625	21	0.231	R.SIDGGAAFGFPDTPEEAAK.A
R1/RRR1-5/2	1406.463	1406.561	-70.044	0.447	998.742	0.493	15	0.231	R.DYLTFFCLGNR.E
R1/RRR1-5/2	1287.300	1287.449	-116.474	0.401	1262.582	0.374	16	0.229	R.SIQDAYIHAIR.R
R1/RRR1-2/2	1860.116	1860.057	31.357	0.515	950.396	0.487	19	0.223	R.AYLPVQELLNGEEIDR.W
R1/RRR1-2/2	1859.768	1860.057	-156.397	0.420	1085.672	0.432	19	0.222	R.AYLPVQELLNGEEIDR.W
R1/RRR1-4/2	1241.346	1241.379	-26.494	0.402	1050.269	0.384	17	0.217	K.IDNPIGATNIGR.A
R1/RRR1-5/2	1200.948	1201.378	-359.074	0.473	957.912	0.398	15	0.214	-.M*ITNEPINPR.-
R1/RRR1-5/2	1406.880	1406.561	227.435	0.411	704.276	0.484	15	0.213	R.DYLTFFCLGNR.E
R1/RRR1-5/2	1200.592	1201.378	-1492.486	0.411	1039.454	0.351	15	0.212	-.M*ITNEPINPR.-
R1/RRR1-3/2	1241.217	1241.379	-131.255	0.403	821.167	0.428	16	0.211	K.IDNPIGATNIGR.A
R1/RRR1-5/2	1200.540	1201.378	-1535.485	0.438	1022.508	0.335	15	0.208	-.M*ITNEPINPR.-
R1/RRR1-3/2	1241.231	1241.379	-120.008	0.392	733.563	0.408	17	0.207	K.IDNPIGATNIGR.A
R1/RRR1-5/2	1858.594	1858.086	-265.652	0.462	565.007	0.489	16	0.201	K.VTLYQDAHVPDNFIPK.I
R1/RRR1-5/2	1950.900	1951.170	-138.924	0.292	686.109	0.319	17	0.190	R.LEGPIAWDVLYNFEQR.W
R1/RRR1-6/2	1952.804	1951.170	-188.069	0.327	301.084	0.316	14	0.189	R.LEGPIAWDVLYNFEQR.W
R1/RRR1-5/2	1287.702	1287.449	196.380	0.358	429.791	0.266	13	0.188	R.SIQDAYIHAIR.R
R1/RRR1-5/2	1856.781	1858.086	-1245.123	0.359	442.389	0.362	14	0.184	-.VTLYQDAHVPDNFIPK.-
R1/RRR1-5/3	1820.324	1820.000	178.529	0.482	1020.175	0.523	30	0.127	K.IVVVDHELPNQGSQQR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/3	1951.391	1951.170	113.457	0.452	1094.479	0.428	28	0.113	R.LEGPIAWDVLYNFEQR.W
R1/RRR1-5/3	1819.558	1820.000	-243.602	0.364	711.981	0.470	25	0.096	K.IVVVDHELPNQGSQQR.R
R1/RRR1-5/3	1819.749	1820.000	-138.111	0.366	743.220	0.411	26	0.089	K.IVVVDHELPNQGSQQR.R
R1/RRR1-7/2	1620.232	1619.792	272.374	0.568	2084.634	0.554	23	0.389	K.IGDTAGTIDNIIQCK.L
R1/RRR1-7/2	1618.815	1619.792	-1225.384	0.491	1979.128	0.508	22	0.354	K.IGDTAGTIDNIIQCK.L
R1/RRR1-7/2	1619.330	1619.792	-286.454	0.501	1884.814	0.535	22	0.347	K.IGDTAGTIDNIIQCK.L
R1/RRR1-7/2	1529.398	1528.729	-217.399	0.547	1542.201	0.609	24	0.319	R.VVAIIAEGVPESDTK.Q
R1/RRR1-7/2	1817.332	1817.977	-908.075	0.491	1683.465	0.542	26	0.316	R.ETPSVAGIINPGSDGFQK.L
R1/RRR1-7/2	1599.353	1599.899	-969.141	0.418	1907.896	0.432	24	0.316	K.VILGPATVGGIQAGAFK.I
R1/RRR1-7/2	1817.469	1817.977	-832.489	0.531	1501.873	0.612	24	0.310	R.ETPSVAGIINPGSDGFQK.L
R1/RRR1-7/2	1817.573	1817.977	-223.214	0.509	1505.453	0.588	25	0.304	R.ETPSVAGIINPGSDGFQK.L
R1/RRR1-7/2	1528.336	1528.729	-258.086	0.451	1411.417	0.596	23	0.295	R.VVAIIAEGVPESDTK.Q
R1/RRR1-7/2	1528.229	1528.729	-984.602	0.416	1184.903	0.593	22	0.266	R.VVAIIAEGVPESDTK.Q
R1/RRR1-1/2	1599.660	1599.899	-149.604	0.406	1319.198	0.510	21	0.258	K.VILGPATVGGIQAGAFK.I
R1/RRR1-1/2	1817.767	1817.977	-116.095	0.424	1230.170	0.492	22	0.246	R.ETPSVAGIINPGSDGFQK.L
R1/RRR1-7/2	1248.817	1249.396	-1268.625	0.405	1352.801	0.416	15	0.246	K.TTQALFYNYK.Q
R1/RRR1-1/2	1600.451	1599.899	-280.577	0.447	1088.916	0.534	21	0.243	K.VILGPATVGGIQAGAFK.I
R1/RRR1-7/2	1290.959	1290.464	384.472	0.476	1306.372	0.405	15	0.240	R.M*LDFDFLCGR.E
R1/RRR1-7/2	1563.120	1563.696	-1011.067	0.490	1224.086	0.456	18	0.239	K.SGGM*SNEM*YNTIAR.V
R1/RRR1-7/2	1248.655	1249.396	-1399.007	0.416	1144.845	0.460	15	0.237	K.TTQALFYNYK.Q
R1/RRR1-6/2	1599.636	1599.899	-164.532	0.449	1200.285	0.421	22	0.230	K.VILGPATVGGIQAGAFK.I
R1/RRR1-7/2	1563.163	1563.696	-983.704	0.465	1121.886	0.432	18	0.227	K.SGGM*SNEM*YNTIAR.V
R1/RRR1-7/2	1248.428	1249.396	-1581.774	0.334	1035.247	0.414	15	0.218	K.TTQALFYNYK.Q
R1/RRR1-7/2	1563.102	1563.696	-1022.672	0.444	976.745	0.408	17	0.212	K.SGGM*SNEM*YNTIAR.V
R1/RRR1-7/2	1836.251	1836.033	119.245	0.480	525.717	0.506	20	0.203	K.DAGAVVPTSYEALETAIK.E
R1/RRR1-7/2	1311.349	1310.526	-135.252	0.436	728.128	0.357	15	0.196	K.LYRPGSVGFVSK.S
R1/RRR1-6/2	1599.185	1599.899	-1074.822	0.318	559.942	0.376	19	0.194	K.VILGPATVGGIQAGAFK.I
R1/RRR1-7/2	1309.691	1310.526	-1405.324	0.429	639.930	0.325	14	0.190	K.LYRPGSVGFVSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1289.964	1290.464	-1166.328	0.374	671.300	0.294	12	0.188	R.M*LDFDFLCGR.E
R1/RRR1-6/2	1598.881	1599.899	-1265.854	0.264	453.943	0.306	17	0.187	-.VILGPATVGGIQAGAFK.-
R1/RRR1-7/3	1311.698	1310.526	131.545	0.482	891.340	0.477	22	0.108	K.LYRPGSVGFVSK.S
R1/RRR1-7/3	1658.694	1658.920	-136.759	0.430	1094.401	0.381	27	0.102	K.VQKPVVAWVSGTCAR.L
R1/RRR1-7/3	1658.433	1658.920	-294.141	0.364	1348.325	0.291	28	0.101	K.VQKPVVAWVSGTCAR.L
R1/RRR1-7/3	1310.602	1310.526	58.414	0.432	885.988	0.400	23	0.092	K.LYRPGSVGFVSK.S
R1/RRR1-7/3	1311.662	1310.526	103.965	0.443	578.685	0.403	22	0.088	K.LYRPGSVGFVSK.S
R1/RRR1-7/3	1883.346	1884.210	-992.914	0.344	690.413	0.362	24	0.083	R.AGKDLVSSLVSGLLTIGPR.F
R1/RRR1-7/3	1884.076	1884.210	-71.140	0.346	1049.872	0.256	28	0.079	R.AGKDLVSSLVSGLLTIGPR.F
R1/RRR1-7/3	1882.802	1884.210	-1282.514	0.270	720.989	0.175	23	0.062	-.AGKDLVSSLVSGLLTIGPR.-
R1/RRR1-14/2	1819.544	1820.040	-273.439	0.561	1977.743	0.556	24	0.366	K.SAQDIALADLPTTHPIR.L
R1/RRR1-14/2	1819.452	1820.040	-875.322	0.554	1760.702	0.618	23	0.350	K.SAQDIALADLPTTHPIR.L
R1/RRR1-15/2	1819.665	1820.040	-206.674	0.570	1858.607	0.560	23	0.346	K.SAQDIALADLPTTHPIR.L
R1/RRR1-14/2	1338.374	1337.504	-97.118	0.572	1685.452	0.573	20	0.330	R.KEAAENTLVAYK.S
R1/RRR1-15/2	1819.451	1820.040	-875.726	0.523	1787.651	0.535	23	0.328	K.SAQDIALADLPTTHPIR.L
R1/RRR1-14/2	1819.572	1820.040	-257.824	0.545	1697.570	0.565	23	0.323	K.SAQDIALADLPTTHPIR.L
R1/RRR1-14/2	1337.214	1337.504	-216.964	0.579	1562.763	0.570	19	0.310	R.KEAAENTLVAYK.S
R1/RRR1-14/2	1336.903	1337.504	-1200.607	0.546	1574.925	0.549	19	0.306	R.KEAAENTLVAYK.S
R1/RRR1-14/2	1318.723	1319.400	-1275.837	0.461	1689.612	0.439	18	0.288	K.TADVGELTVEER.N
R1/RRR1-15/2	1319.028	1319.400	-283.075	0.462	1647.297	0.411	18	0.276	K.TADVGELTVEER.N
R1/RRR1-14/1	770.459	770.895	-568.276	0.282	737.411	0.159	8	0.275	-.YLAEFK.-
R1/RRR1-14/1	770.340	770.895	-2025.272	0.311	721.540	0.202	8	0.271	-.YLAEFK.-
R1/RRR1-15/2	1319.289	1319.400	-84.602	0.525	1499.761	0.458	18	0.270	K.TADVGELTVEER.N
R1/RRR1-14/2	1640.338	1639.832	-301.819	0.498	1489.652	0.457	25	0.269	K.LLDSHLVPSATAAESK.V
R1/RRR1-15/2	1419.183	1419.563	-268.360	0.466	1485.923	0.452	19	0.268	R.IISSIEQKEESR.G
R1/RRR1-14/2	1639.591	1639.832	-147.454	0.471	1376.500	0.507	23	0.268	K.LLDSHLVPSATAAESK.V
R1/RRR1-14/2	1419.234	1419.563	-232.463	0.492	1409.201	0.479	18	0.266	R.IISSIEQKEESR.G
R1/RRR1-14/2	1639.520	1639.832	-190.774	0.462	1313.064	0.503	24	0.261	K.LLDSHLVPSATAAESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1319.179	1319.400	-168.419	0.493	1448.047	0.431	18	0.258	K.TADVGELTVEER.N
R1/RRR1-16/2	1419.300	1419.563	-185.696	0.506	1194.164	0.513	18	0.253	R.IISSIEQKEESR.G
R1/RRR1-15/2	1638.888	1639.832	-1189.756	0.453	1194.421	0.517	23	0.252	K.LLDSHLVPSATAAESK.V
R1/RRR1-13/2	1419.251	1419.563	-220.641	0.479	1285.493	0.464	18	0.250	R.IISSIEQKEESR.G
R1/RRR1-15/2	1820.378	1820.040	186.669	0.494	1258.131	0.500	20	0.249	K.SAQDIALADLPTTHPIR.L
R1/RRR1-14/2	1419.164	1419.563	-282.081	0.484	1311.387	0.445	19	0.249	R.IISSIEQKEESR.G
R1/RRR1-14/2	1319.081	1319.400	-242.408	0.527	1499.277	0.371	18	0.247	K.TADVGELTVEER.N
R1/RRR1-14/2	1419.207	1419.563	-251.619	0.470	1204.057	0.484	18	0.247	R.IISSIEQKEESR.G
R1/RRR1-14/2	1319.009	1319.400	-297.188	0.423	1412.901	0.383	18	0.244	K.TADVGELTVEER.N
R1/RRR1-15/2	1419.242	1419.563	-226.767	0.475	1181.064	0.472	18	0.243	R.IISSIEQKEESR.G
R1/RRR1-15/2	1639.507	1639.832	-198.766	0.429	1053.399	0.506	22	0.237	K.LLDSHLVPSATAAESK.V
R1/RRR1-15/2	1418.643	1419.563	-1357.637	0.491	1157.787	0.439	18	0.235	R.IISSIEQKEESR.G
R1/RRR1-14/1	770.469	770.895	-555.079	0.340	673.942	0.166	8	0.232	-.YLAEFK.-
R1/RRR1-15/2	1208.866	1209.331	-385.846	0.380	974.586	0.457	16	0.223	K.EAAENTLVAYK.S
R1/RRR1-14/2	1052.014	1052.163	-141.593	0.412	803.356	0.520	14	0.223	R.GNEAYVASIK.E
R1/RRR1-14/2	1210.070	1209.331	-216.286	0.405	882.940	0.449	16	0.218	K.EAAENTLVAYK.S
R1/RRR1-15/2	1639.341	1639.832	-300.061	0.418	850.407	0.462	20	0.215	K.LLDSHLVPSATAAESK.V
R1/RRR1-14/2	1190.056	1190.439	-322.601	0.380	1555.898	0.166	16	0.214	K.DSTLIMQLLR.D
R1/RRR1-15/2	1051.390	1052.163	-1690.955	0.382	758.690	0.451	15	0.212	R.GNEAYVASIK.E
R1/RRR1-15/2	1209.200	1209.331	-108.302	0.431	801.388	0.433	15	0.212	K.EAAENTLVAYK.S
R1/RRR1-14/2	1190.055	1190.439	-323.219	0.432	1460.389	0.180	15	0.207	K.DSTLIMQLLR.D
R1/RRR1-14/2	1209.099	1209.331	-192.562	0.394	648.607	0.423	14	0.204	K.EAAENTLVAYK.S
R1/RRR1-14/2	1209.084	1209.331	-204.412	0.266	637.767	0.353	14	0.193	K.EAAENTLVAYK.S
R1/RRR1-14/2	1052.100	1052.163	-59.538	0.309	586.041	0.320	13	0.192	R.GNEAYVASIK.E
R1/RRR1-14/3	1818.658	1820.040	-1313.678	0.372	1621.151	0.431	32	0.171	K.SAQDIALADLPTTHPIR.L
R1/RRR1-15/3	1821.337	1820.040	163.775	0.473	1410.612	0.468	31	0.157	K.SAQDIALADLPTTHPIR.L
R1/RRR1-14/3	1818.499	1820.040	-1953.008	0.393	1532.431	0.379	31	0.145	K.SAQDIALADLPTTHPIR.L
R1/RRR1-14/3	1640.075	1639.832	148.580	0.350	1308.717	0.376	30	0.115	K.LLDSHLVPSATAAESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1640.800	1639.832	-19.306	0.381	1054.334	0.451	29	0.111	K.LLDSHLVPSATAAESK.V
R1/RRR1-11/2	1025.429	1025.054	366.367	0.285	1072.227	0.109	14	0.098	-.EAAKPEGEGH.-
R1/RRR1-15/3	1640.680	1639.832	-92.851	0.398	947.517	0.373	26	0.093	K.LLDSHLVPSATAAESK.V
R1/RRR1-14/3	1818.699	1820.040	-1290.725	0.310	1090.411	0.181	28	0.069	K.SAQDIALADLPTTHPIR.L
R1/RRR1-11/2	1499.566	1499.734	-112.806	0.548	2518.705	0.614	22	0.498	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/2	1500.335	1499.734	-267.228	0.585	2264.846	0.666	22	0.463	R.VPTVDVSVVDLTVR.I
R1/RRR1-13/2	1499.831	1499.734	64.522	0.504	2196.044	0.661	22	0.445	R.VPTVDVSVVDLTVR.I
R1/RRR1-3/2	1499.175	1499.734	-1043.538	0.494	2182.099	0.598	21	0.418	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/2	1499.411	1499.734	-216.194	0.533	2051.434	0.645	22	0.411	R.VPTVDVSVVDLTVR.I
R1/RRR1-3/2	1499.720	1499.734	-9.520	0.518	2049.371	0.594	21	0.391	R.VPTVDVSVVDLTVR.I
R1/RRR1-10/2	1500.076	1499.734	228.568	0.537	1895.928	0.647	20	0.381	R.VPTVDVSVVDLTVR.I
R1/RRR1-12/2	1499.417	1499.734	-212.519	0.519	1941.161	0.618	21	0.380	R.VPTVDVSVVDLTVR.I
R1/RRR1-14/2	1500.736	1499.734	1.092	0.545	1854.785	0.637	20	0.370	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/1	1436.836	1435.607	159.603	0.393	717.151	0.464	17	0.352	R.AASFNIIPSSTGAAK.A
R1/RRR1-7/2	1499.374	1499.734	-241.106	0.497	1847.581	0.576	21	0.350	R.VPTVDVSVVDLTVR.I
R1/RRR1-16/2	1499.308	1499.734	-285.377	0.492	1775.653	0.612	20	0.349	R.VPTVDVSVVDLTVR.I
R1/RRR1-13/2	1500.725	1499.734	-6.087	0.530	1671.649	0.627	19	0.337	R.VPTVDVSVVDLTVR.I
R1/RRR1-15/2	1499.558	1499.734	-117.787	0.493	1688.873	0.592	19	0.328	R.VPTVDVSVVDLTVR.I
R1/RRR1-7/2	1499.153	1499.734	-1057.764	0.426	1690.475	0.558	20	0.319	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/2	1762.365	1762.859	-281.269	0.522	1670.088	0.555	20	0.317	K.LVSWYDNEWGYSSR.V
R1/RRR1-11/2	1756.520	1757.017	-283.877	0.531	1628.564	0.561	21	0.314	K.TLLFGEKEVTVFGCR.N
R1/RRR1-11/2	1762.387	1762.859	-268.760	0.506	1542.569	0.574	19	0.304	K.LVSWYDNEWGYSSR.V
R1/RRR1-11/2	1756.658	1757.017	-205.026	0.527	1533.711	0.572	20	0.303	K.TLLFGEKEVTVFGCR.N
R1/RRR1-11/2	1762.609	1762.859	-142.234	0.509	1576.312	0.548	19	0.301	K.LVSWYDNEWGYSSR.V
R1/RRR1-11/2	1757.603	1757.017	-236.333	0.549	1456.883	0.584	20	0.296	K.TLLFGEKEVTVFGCR.N
R1/RRR1-11/2	1762.448	1762.859	-234.016	0.536	1473.903	0.559	19	0.291	K.LVSWYDNEWGYSSR.V
R1/RRR1-11/1	1436.887	1435.607	195.045	0.403	598.976	0.499	17	0.281	R.AASFNIIPSSTGAAK.A
R1/RRR1-11/2	1762.573	1762.859	-162.868	0.496	1429.557	0.540	19	0.281	K.LVSWYDNEWGYSSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1499.595	1499.734	-93.208	0.475	1276.614	0.589	20	0.277	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/2	1163.154	1162.320	-143.327	0.487	1506.412	0.460	17	0.271	K.AGIALNDNFVK.-
R1/RRR1-17/2	1499.818	1499.734	55.788	0.472	1217.924	0.577	20	0.268	R.VPTVDVSVVDLTVR.I
R1/RRR1-3/2	1162.107	1162.320	-183.807	0.400	1500.587	0.438	16	0.264	K.AGIALNDNFVK.-
R1/RRR1-11/2	1762.368	1762.859	-279.462	0.471	1289.459	0.535	18	0.263	K.LVSWYDNEWGYSSR.V
R1/RRR1-11/2	1499.863	1499.734	86.153	0.434	1202.553	0.540	18	0.255	R.VPTVDVSVVDLTVR.I
R1/RRR1-3/2	1162.115	1162.320	-177.063	0.442	1372.233	0.421	17	0.249	K.AGIALNDNFVK.-
R1/RRR1-9/2	1162.272	1162.320	-41.780	0.433	1251.620	0.426	17	0.241	K.AGIALNDNFVK.-
R1/RRR1-11/2	1162.120	1162.320	-172.638	0.492	1122.691	0.454	17	0.238	K.AGIALNDNFVK.-
R1/RRR1-2/2	1162.137	1162.320	-158.307	0.410	1183.199	0.435	15	0.235	K.AGIALNDNFVK.-
R1/RRR1-11/2	1162.905	1162.320	-357.928	0.499	1104.070	0.454	16	0.235	K.AGIALNDNFVK.-
R1/RRR1-11/2	1163.111	1162.320	-180.912	0.456	1324.702	0.375	16	0.235	K.AGIALNDNFVK.-
R1/RRR1-9/2	1162.081	1162.320	-206.253	0.416	1238.660	0.395	17	0.234	K.AGIALNDNFVK.-
R1/RRR1-10/2	1162.331	1162.320	9.205	0.444	1353.019	0.349	17	0.233	K.AGIALNDNFVK.-
R1/RRR1-11/2	1134.053	1134.226	-152.619	0.452	1042.869	0.461	14	0.232	K.YDTVHGQWK.H
R1/RRR1-11/2	1307.158	1306.513	-272.532	0.371	1249.041	0.396	18	0.232	K.DAPMFVVGVNEK.E
R1/RRR1-11/2	1161.985	1162.320	-289.195	0.400	1199.318	0.401	16	0.231	K.AGIALNDNFVK.-
R1/RRR1-10/2	1162.182	1162.320	-119.110	0.437	1260.890	0.367	16	0.229	K.AGIALNDNFVK.-
R1/RRR1-3/2	1161.467	1162.320	-1600.798	0.354	1123.542	0.420	16	0.229	K.AGIALNDNFVK.-
R1/RRR1-11/2	1163.042	1162.320	-239.875	0.482	1138.209	0.409	16	0.228	K.AGIALNDNFVK.-
R1/RRR1-15/2	1161.699	1162.320	-1399.490	0.373	1188.953	0.367	16	0.224	K.AGIALNDNFVK.-
R1/RRR1-11/2	1163.002	1162.320	-274.835	0.449	1046.303	0.407	16	0.223	K.AGIALNDNFVK.-
R1/RRR1-11/2	1161.558	1162.320	-1522.039	0.388	1016.407	0.420	16	0.223	K.AGIALNDNFVK.-
R1/RRR1-11/1	1436.843	1435.607	164.374	0.339	499.501	0.468	16	0.222	R.AASFNIIPSSTGAAK.A
R1/RRR1-11/2	1133.989	1134.226	-209.311	0.446	834.584	0.471	13	0.222	K.YDTVHGQWK.H
R1/RRR1-12/2	1133.441	1134.226	-1579.131	0.384	834.550	0.470	13	0.220	K.YDTVHGQWK.H
R1/RRR1-4/2	1162.353	1162.320	27.955	0.360	1188.099	0.336	16	0.219	K.AGIALNDNFVK.-
R1/RRR1-11/1	1434.833	1435.607	-1240.550	0.151	576.352	0.246	16	0.219	R.AASFNIIPSSTGAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1498.443	1499.734	-1534.058	0.346	937.174	0.475	15	0.219	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/2	1162.993	1162.320	-281.996	0.458	1059.249	0.370	16	0.218	K.AGIALNDNFVK.-
R1/RRR1-11/2	1435.155	1435.607	-315.964	0.446	979.958	0.406	21	0.218	R.AASFNIIPSSTGAAK.A
R1/RRR1-13/2	1436.252	1435.607	-247.695	0.458	667.200	0.500	19	0.217	R.AASFNIIPSSTGAAK.A
R1/RRR1-12/2	833.933	833.958	-29.453	0.372	1010.238	0.356	13	0.216	K.IGINGFGR.I
R1/RRR1-11/2	1435.304	1435.607	-212.117	0.418	728.060	0.454	21	0.215	R.AASFNIIPSSTGAAK.A
R1/RRR1-11/2	1134.004	1134.226	-195.704	0.415	769.664	0.445	13	0.215	K.YDTVHGQWK.H
R1/RRR1-12/2	1436.324	1435.607	-197.560	0.453	733.943	0.454	20	0.215	R.AASFNIIPSSTGAAK.A
R1/RRR1-12/2	1134.001	1134.226	-198.728	0.384	826.516	0.431	13	0.214	K.YDTVHGQWK.H
R1/RRR1-13/2	1162.235	1162.320	-74.017	0.400	1083.860	0.336	16	0.214	K.AGIALNDNFVK.-
R1/RRR1-13/2	1162.223	1162.320	-84.131	0.377	922.757	0.398	14	0.213	K.AGIALNDNFVK.-
R1/RRR1-12/2	1293.115	1292.463	-270.000	0.488	700.832	0.410	18	0.212	R.LEKPASYDQIK.A
R1/RRR1-11/2	833.890	833.958	-81.431	0.450	795.337	0.374	12	0.212	K.IGINGFGR.I
R1/RRR1-2/2	1162.099	1162.320	-191.184	0.388	924.053	0.372	15	0.212	K.AGIALNDNFVK.-
R1/RRR1-26/2	1134.366	1134.226	123.734	0.397	786.752	0.417	13	0.212	K.YDTVHGQWK.H
R1/RRR1-11/2	833.432	833.958	-1835.979	0.378	762.780	0.383	12	0.211	K.IGINGFGR.I
R1/RRR1-10/2	1161.455	1162.320	-1610.617	0.338	1015.038	0.348	15	0.211	K.AGIALNDNFVK.-
R1/RRR1-25/2	833.626	833.958	-398.995	0.405	791.912	0.372	12	0.211	K.IGINGFGR.I
R1/RRR1-11/2	1436.197	1435.607	-286.494	0.456	602.228	0.453	19	0.210	R.AASFNIIPSSTGAAK.A
R1/RRR1-11/2	833.880	833.958	-93.178	0.438	752.873	0.364	12	0.210	K.IGINGFGR.I
R1/RRR1-1/2	1134.132	1134.226	-83.192	0.405	802.062	0.396	13	0.210	K.YDTVHGQWK.H
R1/RRR1-10/2	1435.365	1435.607	-169.372	0.431	622.497	0.444	19	0.210	R.AASFNIIPSSTGAAK.A
R1/RRR1-11/2	1435.239	1435.607	-257.339	0.467	640.146	0.440	19	0.209	R.AASFNIIPSSTGAAK.A
R1/RRR1-12/2	1133.873	1134.226	-311.914	0.369	763.288	0.407	13	0.209	K.YDTVHGQWK.H
R1/RRR1-9/2	1435.170	1435.607	-305.297	0.442	574.129	0.455	18	0.209	R.AASFNIIPSSTGAAK.A
R1/RRR1-3/2	833.759	833.958	-239.747	0.367	909.259	0.332	12	0.209	K.IGINGFGR.I
R1/RRR1-11/2	928.859	929.139	-302.198	0.393	800.612	0.394	14	0.208	K.KVVISAPSK.D
R1/RRR1-4/2	1162.077	1162.320	-209.942	0.371	1037.727	0.318	15	0.208	K.AGIALNDNFVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1435.369	1435.607	-166.557	0.472	539.734	0.455	18	0.208	R.AASFNIIPSSTGAAK.A
R1/RRR1-26/2	833.986	833.958	33.383	0.381	694.181	0.379	11	0.208	K.IGINGFGR.I
R1/RRR1-25/2	833.844	833.958	-136.939	0.365	791.371	0.349	12	0.208	K.IGINGFGR.I
R1/RRR1-3/2	834.212	833.958	305.337	0.411	821.340	0.337	12	0.208	K.IGINGFGR.I
R1/RRR1-4/2	1162.030	1162.320	-250.621	0.364	1174.912	0.271	15	0.207	K.AGIALNDNFVK.-
R1/RRR1-26/2	833.531	833.958	-513.173	0.322	817.062	0.351	12	0.207	K.IGINGFGR.I
R1/RRR1-2/2	1161.365	1162.320	-1688.757	0.327	859.505	0.384	13	0.207	K.AGIALNDNFVK.-
R1/RRR1-1/2	1293.060	1292.463	-312.337	0.434	462.623	0.429	15	0.207	R.LEKPASYDQIK.A
R1/RRR1-12/2	834.026	833.958	81.679	0.381	842.504	0.323	12	0.206	K.IGINGFGR.I
R1/RRR1-2/2	833.788	833.958	-203.762	0.347	879.272	0.320	12	0.206	K.IGINGFGR.I
R1/RRR1-11/2	929.114	929.139	-27.490	0.384	732.179	0.398	13	0.206	K.KVVISAPSK.D
R1/RRR1-26/2	1134.274	1134.226	42.787	0.364	880.511	0.344	13	0.205	K.YDTVHGQWK.H
R1/RRR1-25/2	833.934	833.958	-28.719	0.355	703.134	0.344	11	0.205	K.IGINGFGR.I
R1/RRR1-10/2	1435.219	1435.607	-271.504	0.406	544.323	0.396	19	0.204	R.AASFNIIPSSTGAAK.A
R1/RRR1-10/2	833.927	833.958	-37.088	0.324	636.995	0.352	11	0.204	K.IGINGFGR.I
R1/RRR1-12/2	833.657	833.958	-362.557	0.326	669.009	0.346	11	0.204	K.IGINGFGR.I
R1/RRR1-10/2	833.919	833.958	-46.485	0.327	600.963	0.344	11	0.204	K.IGINGFGR.I
R1/RRR1-15/2	1435.226	1435.607	-266.470	0.397	384.279	0.444	16	0.204	R.AASFNIIPSSTGAAK.A
R1/RRR1-6/2	834.003	833.958	54.082	0.354	811.150	0.318	11	0.203	K.IGINGFGR.I
R1/RRR1-11/2	1293.058	1292.463	-314.231	0.488	541.773	0.369	16	0.203	R.LEKPASYDQIK.A
R1/RRR1-9/2	1435.192	1435.607	-290.192	0.428	396.054	0.458	15	0.203	R.AASFNIIPSSTGAAK.A
R1/RRR1-12/2	1762.171	1762.859	-960.680	0.449	636.896	0.431	16	0.203	K.LVSWYDNEWGYSSR.V
R1/RRR1-4/2	1435.408	1435.607	-138.831	0.394	470.077	0.417	17	0.203	R.AASFNIIPSSTGAAK.A
R1/RRR1-7/2	1162.173	1162.320	-127.434	0.374	789.826	0.356	13	0.203	K.AGIALNDNFVK.-
R1/RRR1-15/2	1162.255	1162.320	-56.107	0.342	758.303	0.362	13	0.203	K.AGIALNDNFVK.-
R1/RRR1-7/2	1435.176	1435.607	-301.456	0.404	454.627	0.423	16	0.202	R.AASFNIIPSSTGAAK.A
R1/RRR1-13/2	833.663	833.958	-354.183	0.337	443.818	0.350	9	0.202	K.IGINGFGR.I
R1/RRR1-10/2	1435.228	1435.607	-265.104	0.393	541.663	0.382	18	0.202	R.AASFNIIPSSTGAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	833.609	833.958	-419.859	0.390	615.523	0.292	11	0.201	K.IGINGFGR.I
R1/RRR1-11/2	1434.648	1435.607	-1369.715	0.348	462.012	0.421	16	0.201	R.AASFNIIPSSTGAAK.A
R1/RRR1-2/2	1161.173	1162.320	-1854.474	0.312	581.739	0.386	12	0.201	K.AGIALNDNFVK.-
R1/RRR1-2/2	833.919	833.958	-47.072	0.351	693.040	0.289	11	0.200	K.IGINGFGR.I
R1/RRR1-7/2	834.087	833.958	155.509	0.349	714.683	0.287	11	0.200	K.IGINGFGR.I
R1/RRR1-8/2	1162.024	1162.320	-255.890	0.333	637.487	0.392	12	0.200	-.AGIALNDNFVK.-
R1/RRR1-9/2	833.997	833.958	46.889	0.399	593.441	0.307	10	0.200	K.IGINGFGR.I
R1/RRR1-3/2	834.035	833.958	92.541	0.326	652.961	0.280	11	0.200	K.IGINGFGR.I
R1/RRR1-11/2	834.378	833.958	505.282	0.389	675.930	0.248	12	0.199	K.IGINGFGR.I
R1/RRR1-1/2	1292.203	1292.463	-201.971	0.410	452.982	0.317	15	0.199	R.LEKPASYDQIK.A
R1/RRR1-12/2	929.024	929.139	-124.095	0.397	723.977	0.332	13	0.199	K.KVVISAPSK.D
R1/RRR1-8/2	1435.087	1435.607	-1062.412	0.384	385.594	0.384	15	0.199	R.AASFNIIPSSTGAAK.A
R1/RRR1-24/2	833.989	833.958	37.640	0.301	738.689	0.271	11	0.198	K.IGINGFGR.I
R1/RRR1-11/2	1292.171	1292.463	-226.706	0.473	716.373	0.283	18	0.198	R.LEKPASYDQIK.A
R1/RRR1-5/2	834.169	833.958	254.128	0.368	620.841	0.274	10	0.198	K.IGINGFGR.I
R1/RRR1-9/2	1161.994	1162.320	-281.290	0.313	695.433	0.309	13	0.197	K.AGIALNDNFVK.-
R1/RRR1-6/2	833.984	833.958	31.328	0.302	714.362	0.252	11	0.197	K.IGINGFGR.I
R1/RRR1-12/2	1292.142	1292.463	-249.073	0.433	633.457	0.281	17	0.197	R.LEKPASYDQIK.A
R1/RRR1-11/2	1292.166	1292.463	-230.592	0.434	617.535	0.279	17	0.197	R.LEKPASYDQIK.A
R1/RRR1-2/2	833.533	833.958	-510.968	0.335	690.882	0.274	11	0.197	-.IGINGFGR.-
R1/RRR1-12/2	1291.966	1292.463	-385.383	0.461	688.503	0.266	18	0.196	R.LEKPASYDQIK.A
R1/RRR1-1/2	833.413	833.958	-1859.527	0.259	857.937	0.232	12	0.196	K.IGINGFGR.I
R1/RRR1-11/1	1499.950	1499.734	144.317	0.335	344.553	0.603	15	0.195	R.VPTVDVSVVDLTVR.I
R1/RRR1-1/2	833.889	833.958	-82.753	0.309	722.480	0.222	11	0.195	K.IGINGFGR.I
R1/RRR1-11/1	1161.726	1162.320	-1376.524	0.237	536.664	0.286	13	0.195	K.AGIALNDNFVK.-
R1/RRR1-11/2	1322.107	1322.512	-307.165	0.315	719.733	0.303	18	0.195	K.DAPM*FVVGVNEK.E
R1/RRR1-9/2	1435.189	1435.607	-292.581	0.391	328.870	0.316	15	0.194	-.AASFNIIPSSTGAAK.-
R1/RRR1-23/2	1764.315	1762.859	259.083	0.330	207.455	0.338	13	0.193	-.LVSWYDNEWGYSSR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1322.135	1322.512	-286.508	0.327	626.722	0.305	16	0.192	K.DAPM*FVVGVNEK.E
R1/RRR1-11/2	834.272	833.958	378.107	0.327	778.478	0.150	12	0.192	K.IGINGFGR.I
R1/RRR1-16/2	1162.102	1162.320	-188.023	0.173	509.322	0.278	12	0.192	K.AGIALNDNFVK.-
R1/RRR1-23/2	1161.963	1162.320	-308.167	0.363	446.739	0.312	11	0.190	-.AGIALNDNFVK.-
R1/RRR1-12/2	834.778	833.958	-215.694	0.264	826.716	0.125	12	0.190	K.IGINGFGR.I
R1/RRR1-1/2	1436.163	1435.607	-310.201	0.341	285.120	0.402	14	0.189	-.AASFNIIPSSTGAAK.-
R1/RRR1-12/2	929.218	929.139	85.170	0.289	546.031	0.260	11	0.189	K.KVVISAPSK.D
R1/RRR1-11/2	1322.050	1322.512	-350.428	0.276	611.552	0.237	17	0.189	K.DAPM*FVVGVNEK.E
R1/RRR1-1/2	1161.381	1162.320	-1674.923	0.287	659.498	0.264	12	0.182	-.AGIALNDNFVK.-
R1/RRR1-17/2	1435.349	1435.607	-180.463	0.337	292.707	0.348	13	0.176	-.AASFNIIPSSTGAAK.-
R1/RRR1-11/1	1434.881	1435.607	-1206.291	0.148	473.208	0.278	15	0.175	R.AASFNIIPSSTGAAK.A
R1/RRR1-5/2	1435.414	1435.607	-134.736	0.334	277.514	0.400	14	0.172	-.AASFNIIPSSTGAAK.-
R1/RRR1-11/3	1499.387	1499.734	-232.048	0.417	1730.129	0.370	27	0.168	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/3	1499.208	1499.734	-1021.392	0.417	1829.745	0.298	29	0.156	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/1	1499.033	1499.734	-1138.496	0.216	220.181	0.508	15	0.140	R.VPTVDVSVVDLTVR.I
R1/RRR1-11/3	1756.416	1757.017	-914.168	0.440	1119.925	0.522	26	0.137	K.TLLFGEKEVTVFGCR.N
R1/RRR1-10/3	1292.615	1292.463	118.474	0.490	827.396	0.485	22	0.108	R.LEKPASYDQIK.A
R1/RRR1-13/3	1292.074	1292.463	-301.499	0.501	726.937	0.484	21	0.106	R.LEKPASYDQIK.A
R1/RRR1-12/3	1292.426	1292.463	-28.583	0.530	738.201	0.473	21	0.106	R.LEKPASYDQIK.A
R1/RRR1-11/3	1293.482	1292.463	15.124	0.505	1105.452	0.399	23	0.105	R.LEKPASYDQIK.A
R1/RRR1-11/3	1756.499	1757.017	-866.656	0.378	1019.224	0.424	24	0.105	K.TLLFGEKEVTVFGCR.N
R1/RRR1-10/3	1292.410	1292.463	-41.231	0.480	764.295	0.470	22	0.104	R.LEKPASYDQIK.A
R1/RRR1-3/3	1292.494	1292.463	23.851	0.470	679.245	0.457	19	0.100	-.LEKPASYDQIK.-
R1/RRR1-2/3	1292.246	1292.463	-167.865	0.512	616.634	0.473	20	0.099	-.LEKPASYDQIK.-
R1/RRR1-2/3	1292.673	1292.463	163.506	0.429	543.032	0.428	19	0.099	R.LEKPASYDQIK.A
R1/RRR1-12/3	1292.248	1292.463	-166.444	0.498	926.450	0.411	24	0.098	R.LEKPASYDQIK.A
R1/RRR1-23/3	1291.971	1292.463	-382.123	0.416	879.292	0.393	21	0.096	R.LEKPASYDQIK.A
R1/RRR1-11/3	1292.694	1292.463	179.415	0.517	670.346	0.408	22	0.096	R.LEKPASYDQIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1292.509	1292.463	36.213	0.484	816.928	0.396	23	0.094	R.LEKPASYDQIK.A
R1/RRR1-4/3	1292.347	1292.463	-89.692	0.466	528.800	0.388	19	0.092	-.LEKPASYDQIK.-
R1/RRR1-4/3	1292.342	1292.463	-94.098	0.400	571.269	0.355	20	0.092	R.LEKPASYDQIK.A
R1/RRR1-13/3	1292.222	1292.463	-186.771	0.447	607.232	0.430	19	0.091	-.LEKPASYDQIK.-
R1/RRR1-11/3	1292.852	1292.463	302.270	0.508	776.674	0.413	23	0.091	-.LEKPASYDQIK.-
R1/RRR1-13/3	1292.830	1292.463	285.086	0.432	581.215	0.329	19	0.091	R.LEKPASYDQIK.A
R1/RRR1-11/3	1292.490	1292.463	20.867	0.527	692.445	0.437	22	0.090	-.LEKPASYDQIK.-
R1/RRR1-2/3	1292.806	1292.463	266.624	0.474	848.703	0.389	23	0.090	-.LEKPASYDQIK.-
R1/RRR1-11/3	1293.578	1292.463	89.234	0.472	707.373	0.308	21	0.086	R.LEKPASYDQIK.A
R1/RRR1-11/3	1499.197	1499.734	-1028.505	0.448	1088.675	0.266	23	0.083	-.VPTVDVSVVDLTVR.-
R1/RRR1-12/3	1499.431	1499.734	-203.013	0.304	1050.669	0.199	22	0.070	R.VPTVDVSVVDLTVR.I
R1/RRR1-6/2	1652.282	1651.906	228.450	0.543	1862.097	0.623	24	0.371	R.ASDLDIASILGM*GFPK.F
R1/RRR1-6/2	1249.228	1249.443	-172.753	0.571	2081.520	0.482	17	0.363	R.LWALEIANYR.K
R1/RRR1-6/2	1635.457	1635.906	-275.544	0.453	1831.704	0.513	22	0.328	R.ASDLDIASILGMGFPK.F
R1/RRR1-6/2	1635.578	1635.906	-201.265	0.392	1786.910	0.462	22	0.306	R.ASDLDIASILGMGFPK.F
R1/RRR1-6/2	1931.852	1933.198	-1218.223	0.463	1653.035	0.499	21	0.297	R.GGLVFWADTIGAPYIHSK.L
R1/RRR1-6/2	1250.284	1249.443	-127.169	0.543	1469.479	0.521	16	0.285	R.LWALEIANYR.K
R1/RRR1-6/2	1308.679	1309.540	-1425.964	0.423	1397.680	0.524	20	0.276	K.VPGVTDVQLKPR.K
R1/RRR1-6/2	1652.786	1651.906	-72.528	0.569	1386.473	0.537	21	0.273	R.ASDLDIASILGM*GFPK.F
R1/RRR1-6/2	1531.134	1530.739	259.116	0.543	1475.439	0.480	20	0.272	R.GLVDALCSPDELIK.M
R1/RRR1-6/2	1248.474	1249.443	-1581.912	0.447	1558.281	0.422	16	0.270	R.LWALEIANYR.K
R1/RRR1-6/2	1628.346	1628.769	-260.807	0.442	1121.090	0.614	25	0.266	R.SLPLSAPNATQQASSR.S
R1/RRR1-6/2	1309.101	1309.540	-336.287	0.466	1133.171	0.579	19	0.262	K.VPGVTDVQLKPR.K
R1/RRR1-6/2	1932.375	1933.198	-946.457	0.455	1493.011	0.432	20	0.258	R.GGLVFWADTIGAPYIHSK.L
R1/RRR1-1/2	1249.464	1249.443	16.991	0.454	1225.238	0.510	15	0.255	R.LWALEIANYR.K
R1/RRR1-6/2	1159.940	1160.353	-357.049	0.354	1175.680	0.501	16	0.245	K.ALVHAFFAQR.L
R1/RRR1-6/2	1628.366	1628.769	-248.022	0.490	995.012	0.544	24	0.242	R.SLPLSAPNATQQASSR.S
R1/RRR1-6/2	1628.331	1628.769	-269.532	0.452	1132.889	0.480	25	0.240	R.SLPLSAPNATQQASSR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1530.408	1530.739	-216.456	0.463	1275.745	0.409	19	0.235	R.GLVDALCSPDELIK.M
R1/RRR1-6/2	1650.630	1651.906	-1382.787	0.321	1243.826	0.423	20	0.232	R.ASDLDIASILGM*GFPK.F
R1/RRR1-6/2	886.916	887.059	-161.393	0.321	1116.162	0.456	16	0.229	K.AIVLTGAGGK.F
R1/RRR1-6/2	1159.354	1159.425	-61.317	0.457	1020.819	0.447	17	0.228	K.MIAANLEGLVK.R
R1/RRR1-6/2	1174.675	1175.424	-1493.572	0.349	1053.715	0.429	17	0.223	K.M*IAANLEGLVK.R
R1/RRR1-6/2	1456.602	1456.709	-73.685	0.460	756.907	0.510	19	0.221	K.TSPQAILDLITVGK.M
R1/RRR1-6/2	1456.523	1456.709	-128.664	0.423	750.546	0.506	19	0.219	K.TSPQAILDLITVGK.M
R1/RRR1-6/2	1530.266	1530.739	-309.607	0.458	1111.377	0.368	18	0.214	R.GLVDALCSPDELIK.M
R1/RRR1-5/2	1455.880	1456.709	-1260.512	0.462	747.626	0.464	18	0.213	K.TSPQAILDLITVGK.M
R1/RRR1-6/2	1160.038	1160.353	-271.949	0.389	792.315	0.461	14	0.213	K.ALVHAFFAQR.L
R1/RRR1-6/2	1091.424	1091.264	147.352	0.468	860.186	0.372	15	0.210	R.VM*DENVVIR.A
R1/RRR1-4/2	1456.975	1456.709	182.556	0.381	432.935	0.526	17	0.209	K.TSPQAILDLITVGK.M
R1/RRR1-2/2	1176.482	1175.424	49.167	0.384	720.791	0.429	15	0.208	K.M*IAANLEGLVK.R
R1/RRR1-6/2	1091.047	1091.264	-199.355	0.508	753.054	0.389	14	0.207	R.VM*DENVVIR.A
R1/RRR1-6/2	1174.435	1175.424	-1698.731	0.377	790.045	0.386	16	0.206	K.M*IAANLEGLVK.R
R1/RRR1-4/2	1457.052	1456.709	235.906	0.437	354.465	0.460	16	0.204	K.TSPQAILDLITVGK.M
R1/RRR1-6/2	1090.560	1091.264	-1566.885	0.408	705.362	0.359	14	0.202	R.VM*DENVVIR.A
R1/RRR1-6/2	1174.807	1175.424	-1380.222	0.407	667.022	0.337	15	0.198	K.M*IAANLEGLVK.R
R1/RRR1-5/2	1456.425	1456.709	-195.590	0.305	436.274	0.349	16	0.194	K.TSPQAILDLITVGK.M
R1/RRR1-3/2	1309.347	1309.540	-147.896	0.308	252.942	0.353	13	0.193	K.VPGVTDVQLKPR.K
R1/RRR1-2/2	1457.081	1456.709	255.984	0.277	384.377	0.395	13	0.191	K.TSPQAILDLITVGK.M
R1/RRR1-5/2	1653.141	1651.906	142.714	0.359	691.377	0.350	15	0.190	R.ASDLDIASILGM*GFPK.F
R1/RRR1-6/3	1456.893	1456.709	126.041	0.561	1288.142	0.467	26	0.143	K.TSPQAILDLITVGK.M
R1/RRR1-6/3	1456.219	1456.709	-337.635	0.490	1276.245	0.363	27	0.112	K.TSPQAILDLITVGK.M
R1/RRR1-6/3	1456.231	1456.709	-329.309	0.514	1205.872	0.381	27	0.111	K.TSPQAILDLITVGK.M
R1/RRR1-8/2	1968.626	1968.196	219.133	0.650	3367.820	0.576	27	0.723	K.EYVFVANSDNLGAIVDIK.I
R1/RRR1-8/2	1968.533	1968.196	171.936	0.631	3423.329	0.529	27	0.715	K.EYVFVANSDNLGAIVDIK.I
R1/RRR1-8/2	1968.274	1968.196	40.022	0.622	3219.449	0.545	26	0.660	K.EYVFVANSDNLGAIVDIK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1314.265	1313.528	-200.816	0.499	2582.701	0.512	22	0.475	K.VLQLETAAGAAIR.F
R1/RRR1-8/2	1313.930	1313.528	306.517	0.518	2411.051	0.551	21	0.452	K.VLQLETAAGAAIR.F
R1/RRR1-1/2	1312.477	1313.528	-1567.271	0.438	2262.559	0.464	21	0.388	K.VLQLETAAGAAIR.F
R1/RRR1-8/2	1313.737	1313.528	159.217	0.491	2159.038	0.428	21	0.356	K.VLQLETAAGAAIR.F
R1/RRR1-8/2	1452.012	1452.636	-1121.787	0.511	1991.155	0.458	23	0.340	K.VSGDVWFGSGVTLK.G
R1/RRR1-8/2	1451.940	1452.636	-1171.763	0.549	1953.565	0.477	23	0.340	K.VSGDVWFGSGVTLK.G
R1/RRR1-8/2	1476.325	1476.704	-257.393	0.529	1941.549	0.344	19	0.294	K.IFNTNNLWVNLK.A
R1/RRR1-8/2	1359.417	1359.592	-129.389	0.459	1968.113	0.315	20	0.291	R.IVTEDFLPLPSK.G
R1/RRR1-8/2	1359.310	1359.592	-208.032	0.472	1876.176	0.355	20	0.290	R.IVTEDFLPLPSK.G
R1/RRR1-9/2	1360.501	1359.592	-67.460	0.452	1679.068	0.443	20	0.289	R.IVTEDFLPLPSK.G
R1/RRR1-8/2	1452.313	1452.636	-223.121	0.525	1641.076	0.451	21	0.285	K.VSGDVWFGSGVTLK.G
R1/RRR1-9/2	1313.631	1313.528	78.049	0.457	1534.338	0.411	19	0.262	K.VLQLETAAGAAIR.F
R1/RRR1-9/2	1476.319	1476.704	-261.623	0.435	1789.849	0.283	18	0.260	K.IFNTNNLWVNLK.A
R1/RRR1-8/2	1359.059	1359.592	-1131.936	0.384	1503.228	0.320	18	0.239	R.IVTEDFLPLPSK.G
R1/RRR1-8/2	1475.854	1476.704	-1257.555	0.404	1677.786	0.244	18	0.239	K.IFNTNNLWVNLK.A
R1/RRR1-3/2	1968.813	1968.196	-194.997	0.483	1342.463	0.410	20	0.236	K.EYVFVANSDNLGAIVDIK.I
R1/RRR1-1/2	1360.222	1359.592	-273.062	0.379	1151.322	0.409	17	0.227	R.IVTEDFLPLPSK.G
R1/RRR1-8/2	1758.559	1758.953	-224.786	0.501	591.408	0.587	20	0.222	R.TNPSNPSIELGPEFKK.V
R1/RRR1-8/2	1758.494	1758.953	-261.835	0.491	564.848	0.584	19	0.219	R.TNPSNPSIELGPEFKK.V
R1/RRR1-8/2	1630.503	1630.780	-170.278	0.460	588.179	0.560	19	0.218	R.TNPSNPSIELGPEFK.K
R1/RRR1-8/2	1758.520	1758.953	-246.932	0.477	540.883	0.580	19	0.217	R.TNPSNPSIELGPEFKK.V
R1/RRR1-9/2	1476.329	1476.704	-255.070	0.452	1375.754	0.270	17	0.216	K.IFNTNNLWVNLK.A
R1/RRR1-1/2	1359.280	1359.592	-230.105	0.375	1139.295	0.320	17	0.212	R.IVTEDFLPLPSK.G
R1/RRR1-8/2	1630.334	1630.780	-274.683	0.403	544.252	0.532	18	0.210	R.TNPSNPSIELGPEFK.K
R1/RRR1-3/2	1360.519	1359.592	-54.050	0.375	943.679	0.377	15	0.208	R.IVTEDFLPLPSK.G
R1/RRR1-9/2	1312.732	1313.528	-1372.316	0.426	943.870	0.359	16	0.205	K.VLQLETAAGAAIR.F
R1/RRR1-8/2	1315.237	1315.538	-229.433	0.316	275.065	0.512	15	0.201	K.SIPSIVELDTLK.V
R1/RRR1-8/2	1629.655	1630.780	-1308.216	0.303	693.286	0.422	19	0.200	R.TNPSNPSIELGPEFK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1314.654	1315.538	-1437.085	0.259	302.948	0.517	17	0.198	K.SIPSIVELDTLK.V
R1/RRR1-1/2	1312.471	1313.528	-1571.850	0.362	863.333	0.314	16	0.197	K.VLQLETAAGAAIR.F
R1/RRR1-8/2	1315.073	1315.538	-354.870	0.261	232.731	0.439	15	0.195	K.SIPSIVELDTLK.V
R1/RRR1-8/2	959.071	958.157	-89.962	0.409	1114.501	0.195	13	0.192	K.M*EIIPNPK.E
R1/RRR1-16/2	1360.161	1359.592	-317.722	0.273	556.182	0.327	14	0.192	R.IVTEDFLPLPSK.G
R1/RRR1-8/2	1572.333	1570.769	-278.353	0.331	865.566	0.302	17	0.190	K.SGKLEIPDGAVLENK.D
R1/RRR1-8/2	1314.444	1313.528	-64.142	0.311	216.387	0.335	16	0.184	-.VLQLETAAGAAIR.-
R1/RRR1-10/2	1476.004	1476.704	-1155.065	0.278	698.303	0.098	14	0.179	K.IFNTNNLWVNLK.A
R1/RRR1-8/3	1570.467	1570.769	-192.895	0.362	969.408	0.366	25	0.089	K.SGKLEIPDGAVLENK.D
R1/RRR1-8/2	1877.197	1878.159	-1048.239	0.535	1761.549	0.567	22	0.335	R.VYVQEGIYDKFVAAFK.A
R1/RRR1-8/2	1663.499	1663.898	-240.576	0.483	1463.357	0.594	25	0.300	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-8/2	1821.541	1821.131	225.536	0.567	1343.955	0.614	24	0.291	K.TAEQTPLSGLVMAQFVK.E
R1/RRR1-8/2	1877.517	1878.159	-877.401	0.548	1353.911	0.610	21	0.290	R.VYVQEGIYDKFVAAFK.A
R1/RRR1-8/2	1108.227	1108.273	-41.276	0.482	1456.049	0.531	18	0.286	K.VAFTGSTLVGR.T
R1/RRR1-8/2	1821.618	1821.131	268.341	0.542	1312.934	0.608	24	0.286	K.TAEQTPLSGLVMAQFVK.E
R1/RRR1-8/2	1876.677	1878.159	-1326.718	0.493	1515.468	0.512	21	0.284	R.VYVQEGIYDKFVAAFK.A
R1/RRR1-8/2	1664.250	1663.898	212.127	0.450	1396.592	0.562	25	0.283	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-8/2	1522.327	1522.642	-207.390	0.475	1512.401	0.500	21	0.283	R.ELGEAALANYTQNK.S
R1/RRR1-8/2	1837.405	1837.130	149.805	0.554	1329.203	0.583	23	0.280	K.TAEQTPLSGLVM*AQFVK.E
R1/RRR1-8/2	1664.470	1663.898	-257.942	0.519	1279.405	0.587	24	0.276	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-8/2	1821.890	1821.131	-132.565	0.566	1211.348	0.617	22	0.275	K.TAEQTPLSGLVMAQFVK.E
R1/RRR1-8/2	1663.371	1663.898	-921.022	0.468	1269.181	0.585	23	0.273	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-8/2	1109.158	1108.273	-103.279	0.563	1326.287	0.533	18	0.273	K.VAFTGSTLVGR.T
R1/RRR1-8/2	1836.588	1837.130	-842.174	0.509	1197.533	0.587	23	0.267	K.TAEQTPLSGLVM*AQFVK.E
R1/RRR1-8/2	1522.215	1522.642	-281.002	0.529	1354.420	0.515	19	0.267	R.ELGEAALANYTQNK.S
R1/RRR1-8/2	1663.458	1663.898	-265.460	0.446	1191.702	0.592	23	0.266	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-8/2	1557.287	1556.789	320.414	0.473	1079.237	0.539	21	0.249	K.GYFIQPTIFTNVR.N
R1/RRR1-8/2	1522.358	1522.642	-187.199	0.483	1363.776	0.435	19	0.249	R.ELGEAALANYTQNK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1213.967	1214.349	-315.238	0.486	1259.635	0.458	16	0.248	R.VYVQEGIYDK.F
R1/RRR1-8/2	1556.162	1556.789	-1049.148	0.440	906.592	0.549	18	0.234	K.GYFIQPTIFTNVR.N
R1/RRR1-8/2	1664.283	1663.898	232.059	0.421	875.060	0.560	20	0.230	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-8/2	1556.269	1556.789	-979.685	0.411	766.303	0.550	18	0.225	K.GYFIQPTIFTNVR.N
R1/RRR1-8/2	1663.570	1663.898	-197.731	0.379	782.400	0.562	20	0.224	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-8/2	1354.299	1354.620	-237.642	0.462	950.486	0.474	18	0.224	K.IGPALATGNTVVLK.T
R1/RRR1-8/2	1353.781	1354.620	-1362.449	0.436	941.672	0.456	17	0.219	K.IGPALATGNTVVLK.T
R1/RRR1-8/2	1353.721	1354.620	-1407.461	0.350	854.684	0.445	17	0.211	K.IGPALATGNTVVLK.T
R1/RRR1-3/2	1354.234	1354.620	-286.475	0.350	526.183	0.450	15	0.199	K.IGPALATGNTVVLK.T
R1/RRR1-8/2	1107.236	1108.273	-1844.738	0.345	575.587	0.416	14	0.199	K.VAFTGSTLVGR.T
R1/RRR1-2/2	1354.238	1354.620	-282.948	0.325	420.584	0.469	14	0.197	K.IGPALATGNTVVLK.T
R1/RRR1-9/2	1663.949	1663.898	30.639	0.322	566.561	0.342	16	0.189	K.EAGFPAGVLNVISGFGK.I
R1/RRR1-3/2	1877.809	1878.159	-186.908	0.304	282.397	0.349	13	0.187	R.VYVQEGIYDKFVAAFK.A
R1/RRR1-1/2	1354.385	1354.620	-174.256	0.303	232.574	0.396	10	0.148	-.IGPALATGNTVVLK.-
R1/RRR1-8/3	1477.689	1477.516	116.976	0.497	1300.901	0.457	28	0.140	K.AGKDEGATVETGGER.H
R1/RRR1-8/3	1993.888	1994.242	-177.876	0.443	1008.275	0.393	26	0.102	R.HGDKGYFIQPTIFTNVR.N
R1/RRR1-8/3	1477.374	1477.516	-96.567	0.517	852.463	0.440	26	0.102	K.AGKDEGATVETGGER.H
R1/RRR1-8/3	1993.551	1994.242	-850.722	0.439	738.717	0.323	25	0.081	R.HGDKGYFIQPTIFTNVR.N
R1/RRR1-2/2	1592.320	1592.644	-204.041	0.582	2754.559	0.554	23	0.540	R.TQDLENELSTANEK.F
R1/RRR1-2/2	1592.293	1592.644	-221.269	0.570	2585.718	0.539	23	0.491	R.TQDLENELSTANEK.F
R1/RRR1-2/2	1592.567	1592.644	-48.635	0.552	2586.116	0.523	23	0.484	R.TQDLENELSTANEK.F
R1/RRR1-2/2	1838.715	1839.040	-177.298	0.543	2089.330	0.590	24	0.408	R.HKLEEVESDLEALGIR.E
R1/RRR1-2/2	1612.550	1611.732	-113.102	0.594	2044.428	0.586	20	0.391	K.VSQLSDELEAYQTK.A
R1/RRR1-2/2	1612.499	1611.732	-144.768	0.554	2093.010	0.551	21	0.389	K.VSQLSDELEAYQTK.A
R1/RRR1-2/2	1611.460	1611.732	-169.631	0.491	1959.222	0.492	20	0.345	K.VSQLSDELEAYQTK.A
R1/RRR1-2/2	1507.349	1507.625	-184.190	0.515	1834.035	0.526	22	0.337	K.INELQASLDSTTSK.N
R1/RRR1-2/2	1202.447	1203.328	-1569.050	0.412	2112.184	0.328	18	0.321	K.TAALEEQALTR.E
R1/RRR1-2/2	1507.289	1507.625	-223.756	0.489	1471.877	0.491	20	0.275	K.INELQASLDSTTSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1203.216	1203.328	-93.069	0.404	1650.828	0.351	19	0.264	K.TAALEEQALTR.E
R1/RRR1-2/2	1506.464	1507.625	-1438.845	0.374	1044.777	0.406	17	0.215	K.INELQASLDSTTSK.N
R1/RRR1-2/2	1075.092	1074.253	-150.283	0.457	931.258	0.371	15	0.209	K.LALVNTEVSK.L
R1/RRR1-2/2	1297.225	1297.393	-129.835	0.365	1075.228	0.329	15	0.205	R.DFSLDSSTLPSK.Q
R1/RRR1-2/2	1010.843	1010.123	-277.022	0.428	984.527	0.282	13	0.198	-.YNITLEEK.-
R1/RRR1-2/2	1058.732	1059.155	-401.126	0.357	1020.136	0.254	15	0.198	K.LQLEEAEAR.V
R1/RRR1-2/2	1010.092	1010.123	-30.438	0.358	910.108	0.199	12	0.184	-.YNITLEEK.-
R1/RRR1-2/2	1058.806	1059.155	-331.253	0.347	860.107	0.118	14	0.180	K.LQLEEAEAR.V
R1/RRR1-2/2	1073.232	1074.253	-1888.812	0.294	550.605	0.278	12	0.179	-.LALVNTEVSK.-
R1/RRR1-2/3	1832.301	1834.018	-2034.820	0.420	1502.181	0.356	31	0.135	R.SLADKDKELADATQSLK.E
R1/RRR1-2/3	1527.297	1527.660	-238.310	0.469	1370.803	0.312	23	0.109	-.FKEVEADLEQYR.-
R1/RRR1-2/3	1526.619	1527.660	-1340.779	0.423	1525.608	0.215	24	0.098	K.FKEVEADLEQYR.S
R1/RRR1-23/3	1317.655	1318.502	-1405.993	0.351	1498.265	0.248	27	0.098	K.RTSLEASLLEAK.Q
R1/RRR1-2/3	1833.353	1834.018	-910.966	0.486	756.209	0.422	25	0.097	R.SLADKDKELADATQSLK.E
R1/RRR1-2/3	1834.681	1834.018	-184.369	0.463	673.528	0.404	23	0.090	-.SLADKDKELADATQSLK.-
R1/RRR1-8/3	1317.379	1318.502	-1615.959	0.381	728.726	0.349	23	0.085	K.RTSLEASLLEAK.Q
R1/RRR1-7/3	1317.892	1318.502	-1225.415	0.381	746.065	0.350	24	0.085	K.RTSLEASLLEAK.Q
R1/RRR1-9/3	1317.882	1318.502	-1232.810	0.317	574.761	0.297	21	0.083	K.RTSLEASLLEAK.Q
R1/RRR1-8/3	1318.201	1318.502	-228.648	0.345	636.816	0.315	22	0.083	K.RTSLEASLLEAK.Q
R1/RRR1-1/3	1317.956	1318.502	-1176.305	0.310	583.762	0.295	21	0.083	K.RTSLEASLLEAK.Q
R1/RRR1-2/3	1527.820	1527.660	104.723	0.471	1324.523	0.198	25	0.080	K.FKEVEADLEQYR.S
R1/RRR1-4/3	1317.786	1318.502	-1306.067	0.397	634.086	0.287	23	0.079	-.RTSLEASLLEAK.-
R1/RRR1-9/3	1317.284	1318.502	-1688.713	0.272	665.222	0.264	23	0.079	K.RTSLEASLLEAK.Q
R1/RRR1-6/3	1318.097	1318.502	-308.086	0.324	710.416	0.277	23	0.077	-.RTSLEASLLEAK.-
R1/RRR1-9/3	1638.792	1638.812	-11.970	0.550	1651.575	0.522	31	0.208	R.FRGEDKPPAHLGASR.D
R1/RRR1-9/3	1639.129	1638.812	193.857	0.531	1506.165	0.505	31	0.177	R.FRGEDKPPAHLGASR.D
R1/RRR1-9/3	1638.597	1638.812	-131.450	0.540	1405.496	0.505	30	0.165	R.FRGEDKPPAHLGASR.D
R1/RRR1-8/3	1638.796	1638.812	-9.953	0.497	605.840	0.443	24	0.096	R.FRGEDKPPAHLGASR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1913.707	1915.135	-1272.448	0.608	2560.617	0.599	26	0.507	K.VKDELVLDGNDIELVSR.S
R1/RRR1-18/2	1914.606	1915.135	-800.932	0.627	2626.196	0.563	26	0.505	K.VKDELVLDGNDIELVSR.S
R1/RRR1-23/2	1582.454	1582.827	-236.417	0.517	2548.775	0.573	23	0.487	R.TAISHVQNLITGVTK.G
R1/RRR1-17/2	1914.638	1915.135	-260.306	0.615	2544.712	0.549	26	0.480	K.VKDELVLDGNDIELVSR.S
R1/RRR1-18/2	1915.684	1915.135	-235.749	0.650	2526.957	0.543	26	0.471	K.VKDELVLDGNDIELVSR.S
R1/RRR1-18/2	1844.395	1844.996	-871.119	0.472	2014.809	0.531	25	0.442	K.FLDGIYVSDKGTITEDA.-
R1/RRR1-18/3	1915.887	1915.135	-129.743	0.597	2746.272	0.449	36	0.440	K.VKDELVLDGNDIELVSR.S
R1/RRR1-22/2	1581.953	1582.827	-1187.841	0.508	2223.012	0.603	22	0.427	R.TAISHVQNLITGVTK.G
R1/RRR1-17/2	1914.558	1915.135	-825.893	0.603	2289.350	0.541	25	0.420	K.VKDELVLDGNDIELVSR.S
R1/RRR1-18/2	1375.490	1374.675	-134.731	0.551	2287.428	0.516	20	0.410	R.KVDMLEGVTILR.S
R1/RRR1-18/2	1583.127	1582.827	190.205	0.557	2140.681	0.576	22	0.400	R.TAISHVQNLITGVTK.G
R1/RRR1-23/2	1582.396	1582.827	-272.946	0.495	2096.736	0.595	22	0.400	R.TAISHVQNLITGVTK.G
R1/RRR1-18/2	1583.319	1582.827	312.207	0.547	1902.905	0.638	21	0.378	R.TAISHVQNLITGVTK.G
R1/RRR1-17/2	1581.699	1582.827	-1349.195	0.507	1949.129	0.599	21	0.373	R.TAISHVQNLITGVTK.G
R1/RRR1-18/2	1583.293	1582.827	295.277	0.565	1871.497	0.628	20	0.368	R.TAISHVQNLITGVTK.G
R1/RRR1-17/2	1582.445	1582.827	-242.143	0.540	1878.074	0.597	21	0.360	R.TAISHVQNLITGVTK.G
R1/RRR1-17/2	1582.391	1582.827	-275.964	0.516	1872.740	0.597	21	0.359	R.TAISHVQNLITGVTK.G
R1/RRR1-22/2	1582.352	1582.827	-300.964	0.493	1794.937	0.618	21	0.353	R.TAISHVQNLITGVTK.G
R1/RRR1-19/2	1582.448	1582.827	-239.667	0.513	1908.390	0.559	21	0.353	R.TAISHVQNLITGVTK.G
R1/RRR1-20/2	1582.102	1582.827	-1093.160	0.492	1818.186	0.582	21	0.345	R.TAISHVQNLITGVTK.G
R1/RRR1-23/2	1583.385	1582.827	-279.657	0.528	1704.902	0.609	20	0.335	R.TAISHVQNLITGVTK.G
R1/RRR1-22/2	1582.103	1582.827	-1092.540	0.500	1700.063	0.575	21	0.325	R.TAISHVQNLITGVTK.G
R1/RRR1-19/3	1915.494	1915.135	188.483	0.537	2246.499	0.468	32	0.318	K.VKDELVLDGNDIELVSR.S
R1/RRR1-19/2	1582.068	1582.827	-1114.620	0.520	1541.126	0.605	20	0.311	R.TAISHVQNLITGVTK.G
R1/RRR1-18/2	1512.487	1512.695	-137.908	0.500	1526.714	0.559	21	0.302	K.HLNLDFQLLEGGR.K
R1/RRR1-18/2	1511.678	1512.695	-1338.310	0.480	1583.056	0.527	21	0.300	K.HLNLDFQLLEGGR.K
R1/RRR1-17/2	1374.282	1374.675	-286.839	0.494	1718.241	0.465	19	0.299	R.KVDMLEGVTILR.S
R1/RRR1-19/2	1581.943	1582.827	-1194.040	0.513	1487.192	0.571	19	0.293	R.TAISHVQNLITGVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1582.513	1582.827	-198.961	0.512	1451.438	0.562	19	0.286	R.TAISHVQNLITGVTK.G
R1/RRR1-20/2	1582.234	1582.827	-1009.729	0.496	1345.827	0.603	19	0.285	R.TAISHVQNLITGVTK.G
R1/RRR1-21/2	1582.407	1582.827	-265.903	0.445	1266.216	0.521	19	0.257	R.TAISHVQNLITGVTK.G
R1/RRR1-18/2	1845.161	1844.996	89.473	0.514	1475.202	0.581	22	0.245	K.FLDGIYVSDKGTITEDA.-
R1/RRR1-18/2	1320.612	1321.509	-1440.429	0.461	1304.094	0.418	17	0.243	R.KLQVDAWFGTR.R
R1/RRR1-17/2	1374.198	1374.675	-348.155	0.548	1136.453	0.478	17	0.239	R.KVDMLEGVTILR.S
R1/RRR1-17/2	1375.746	1374.675	51.564	0.483	1261.342	0.393	18	0.233	R.KVDMLEGVTILR.S
R1/RRR1-18/2	1390.351	1390.675	-233.382	0.502	1071.117	0.451	19	0.233	R.KVDM*LEGVTILR.S
R1/RRR1-18/2	1321.312	1321.509	-149.244	0.446	1150.084	0.415	16	0.228	R.KLQVDAWFGTR.R
R1/RRR1-18/2	1320.546	1321.509	-1491.311	0.382	1261.757	0.343	16	0.223	R.KLQVDAWFGTR.R
R1/RRR1-20/2	1389.639	1390.675	-1469.375	0.427	901.913	0.457	17	0.222	R.KVDM*LEGVTILR.S
R1/RRR1-18/2	1844.188	1844.996	-983.748	0.444	1424.524	0.540	22	0.221	K.FLDGIYVSDKGTITEDA.-
R1/RRR1-17/2	1157.252	1157.297	-39.739	0.481	1046.714	0.394	16	0.221	K.FLDGIYVSDK.G
R1/RRR1-18/2	1389.560	1390.675	-1525.937	0.444	885.441	0.443	18	0.220	R.KVDM*LEGVTILR.S
R1/RRR1-19/2	856.963	856.990	-31.091	0.391	492.480	0.523	12	0.220	K.VVTVEGPR.G
R1/RRR1-22/2	856.827	856.990	-190.995	0.395	493.104	0.514	12	0.220	K.VVTVEGPR.G
R1/RRR1-23/2	856.972	856.990	-20.946	0.386	541.408	0.509	12	0.219	K.VVTVEGPR.G
R1/RRR1-17/2	1390.125	1390.675	-1118.319	0.406	985.259	0.403	18	0.218	R.KVDM*LEGVTILR.S
R1/RRR1-22/2	856.691	856.990	-350.236	0.375	440.785	0.512	12	0.218	K.VVTVEGPR.G
R1/RRR1-17/2	1390.270	1390.675	-291.784	0.445	766.787	0.456	17	0.216	R.KVDM*LEGVTILR.S
R1/RRR1-23/2	857.020	856.990	35.914	0.434	321.139	0.508	10	0.216	K.VVTVEGPR.G
R1/RRR1-17/2	856.532	856.990	-535.700	0.365	539.453	0.484	12	0.216	K.VVTVEGPR.G
R1/RRR1-24/2	856.834	856.990	-181.848	0.360	463.001	0.516	11	0.216	K.VVTVEGPR.G
R1/RRR1-18/2	856.746	856.990	-285.047	0.388	450.683	0.492	11	0.215	K.VVTVEGPR.G
R1/RRR1-18/2	856.939	856.990	-58.952	0.333	456.632	0.502	12	0.214	K.VVTVEGPR.G
R1/RRR1-17/2	856.393	856.990	-1870.677	0.316	591.417	0.474	13	0.214	K.VVTVEGPR.G
R1/RRR1-24/2	857.001	856.990	13.057	0.378	354.199	0.453	11	0.213	K.VVTVEGPR.G
R1/RRR1-17/2	1157.087	1157.297	-182.277	0.387	1082.404	0.334	16	0.212	K.FLDGIYVSDK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1156.971	1157.297	-282.829	0.440	1137.832	0.317	15	0.211	K.FLDGIYVSDK.G
R1/RRR1-19/2	856.955	856.990	-41.235	0.349	457.192	0.433	12	0.211	K.VVTVEGPR.G
R1/RRR1-17/3	1914.357	1915.135	-931.388	0.561	1828.288	0.432	32	0.211	K.VKDELVLDGNDIELVSR.S
R1/RRR1-18/2	1390.472	1390.675	-145.748	0.485	873.597	0.381	18	0.211	R.KVDM*LEGVTILR.S
R1/RRR1-17/2	856.462	856.990	-1789.041	0.322	422.661	0.481	11	0.211	K.VVTVEGPR.G
R1/RRR1-23/2	856.943	856.990	-54.523	0.368	340.864	0.461	10	0.211	K.VVTVEGPR.G
R1/RRR1-18/2	856.586	856.990	-473.061	0.297	581.643	0.450	13	0.210	K.VVTVEGPR.G
R1/RRR1-18/2	1193.117	1193.336	-184.572	0.368	915.722	0.384	16	0.210	K.LQVDAWFGTR.R
R1/RRR1-18/2	1193.240	1193.336	-80.815	0.359	720.499	0.442	14	0.207	K.LQVDAWFGTR.R
R1/RRR1-20/2	856.208	856.990	-2087.438	0.291	526.105	0.424	12	0.207	K.VVTVEGPR.G
R1/RRR1-20/2	856.383	856.990	-1881.707	0.302	593.809	0.383	13	0.206	K.VVTVEGPR.G
R1/RRR1-18/2	1511.950	1512.695	-1157.485	0.320	866.263	0.394	17	0.204	K.HLNLDFQLLEGGR.K
R1/RRR1-21/2	856.989	856.990	-0.516	0.264	355.451	0.369	10	0.202	K.VVTVEGPR.G
R1/RRR1-25/2	856.786	856.990	-239.020	0.249	336.059	0.393	10	0.202	K.VVTVEGPR.G
R1/RRR1-19/2	856.363	856.990	-1905.771	0.311	383.887	0.361	11	0.201	-.VVTVEGPR.-
R1/RRR1-24/2	856.960	856.990	-34.377	0.231	463.137	0.379	11	0.200	K.VVTVEGPR.G
R1/RRR1-19/2	1389.964	1390.675	-1234.017	0.328	577.992	0.296	16	0.196	R.KVDM*LEGVTILR.S
R1/RRR1-25/2	856.420	856.990	-1838.880	0.165	274.282	0.415	9	0.192	-.VVTVEGPR.-
R1/RRR1-25/2	1375.976	1374.675	219.107	0.261	477.027	0.284	12	0.190	R.KVDMLEGVTILR.S
R1/RRR1-18/2	1192.490	1193.336	-1553.198	0.280	399.762	0.286	11	0.188	K.LQVDAWFGTR.R
R1/RRR1-18/2	1156.469	1157.297	-1586.013	0.196	448.391	0.279	12	0.186	K.FLDGIYVSDK.G
R1/RRR1-18/3	1915.865	1915.135	-140.960	0.527	1619.200	0.442	29	0.184	K.VKDELVLDGNDIELVSR.S
R1/RRR1-19/3	1915.201	1915.135	34.795	0.563	1501.267	0.436	28	0.167	K.VKDELVLDGNDIELVSR.S
R1/RRR1-17/3	1913.628	1915.135	-1837.654	0.440	1379.476	0.421	28	0.143	K.VKDELVLDGNDIELVSR.S
R1/RRR1-25/3	1582.740	1582.827	-54.593	0.464	964.608	0.483	27	0.119	R.TAISHVQNLITGVTK.G
R1/RRR1-17/3	1391.010	1390.675	241.718	0.511	1518.885	0.303	25	0.118	R.KVDM*LEGVTILR.S
R1/RRR1-20/3	1583.143	1582.827	200.519	0.480	1098.261	0.430	27	0.117	R.TAISHVQNLITGVTK.G
R1/RRR1-24/3	1583.093	1582.827	168.855	0.575	1123.307	0.436	31	0.116	R.TAISHVQNLITGVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/3	1582.627	1582.827	-126.660	0.520	1062.933	0.452	30	0.116	R.TAISHVQNLITGVTK.G
R1/RRR1-23/3	1583.121	1582.827	186.485	0.472	978.058	0.465	30	0.113	R.TAISHVQNLITGVTK.G
R1/RRR1-18/3	1391.097	1390.675	304.809	0.447	1571.839	0.248	26	0.107	R.KVDM*LEGVTILR.S
R1/RRR1-17/3	1914.376	1915.135	-921.497	0.435	1120.761	0.366	27	0.106	K.VKDELVLDGNDIELVSR.S
R1/RRR1-24/3	1584.015	1582.827	119.558	0.511	1133.888	0.365	28	0.105	R.TAISHVQNLITGVTK.G
R1/RRR1-20/3	1583.371	1582.827	-288.561	0.496	943.717	0.421	28	0.105	R.TAISHVQNLITGVTK.G
R1/RRR1-20/3	1582.806	1582.827	-12.935	0.400	699.441	0.444	24	0.102	R.TAISHVQNLITGVTK.G
R1/RRR1-19/3	1582.533	1582.827	-185.738	0.410	938.181	0.392	28	0.099	R.TAISHVQNLITGVTK.G
R1/RRR1-22/3	1584.097	1582.827	171.260	0.502	634.030	0.397	26	0.097	R.TAISHVQNLITGVTK.G
R1/RRR1-17/3	1582.319	1582.827	-955.789	0.432	862.377	0.381	27	0.096	R.TAISHVQNLITGVTK.G
R1/RRR1-18/3	1582.730	1582.827	-61.207	0.443	864.608	0.382	28	0.095	R.TAISHVQNLITGVTK.G
R1/RRR1-22/3	1583.046	1582.827	138.813	0.485	943.497	0.372	30	0.095	R.TAISHVQNLITGVTK.G
R1/RRR1-18/3	1914.263	1915.135	-980.747	0.468	984.388	0.338	26	0.095	K.VKDELVLDGNDIELVSR.S
R1/RRR1-18/3	1512.666	1512.695	-19.363	0.472	1247.833	0.276	23	0.094	-.HLNLDFQLLEGGR.-
R1/RRR1-24/3	1583.331	1582.827	-313.971	0.507	783.730	0.390	27	0.093	-.TAISHVQNLITGVTK.-
R1/RRR1-23/3	1582.444	1582.827	-242.500	0.464	612.775	0.388	24	0.093	-.TAISHVQNLITGVTK.-
R1/RRR1-19/3	1582.830	1582.827	1.917	0.468	750.359	0.343	26	0.091	R.TAISHVQNLITGVTK.G
R1/RRR1-22/3	1583.299	1582.827	299.443	0.465	701.173	0.316	27	0.088	R.TAISHVQNLITGVTK.G
R1/RRR1-18/3	1582.890	1582.827	39.973	0.430	702.509	0.334	27	0.086	-.TAISHVQNLITGVTK.-
R1/RRR1-21/3	1582.300	1582.827	-967.872	0.394	672.703	0.337	22	0.084	-.TAISHVQNLITGVTK.-
R1/RRR1-18/3	1512.397	1512.695	-197.873	0.447	1130.272	0.248	22	0.081	-.HLNLDFQLLEGGR.-
R1/RRR1-18/3	1512.825	1512.695	86.256	0.480	828.944	0.344	21	0.076	-.HLNLDFQLLEGGR.-
R1/RRR1-17/3	1390.076	1390.675	-1153.335	0.363	1041.080	0.212	22	0.072	R.KVDM*LEGVTILR.S
R1/RRR1-17/3	1390.694	1390.675	14.102	0.457	950.380	0.206	21	0.071	-.KVDM*LEGVTILR.-
R1/RRR1-18/3	1390.553	1390.675	-87.329	0.387	831.346	0.167	20	0.068	-.KVDM*LEGVTILR.-
R1/RRR1-10/2	1390.197	1390.568	-267.526	0.518	1877.450	0.606	22	0.369	R.VATLQSLSGTGSLR.L
R1/RRR1-10/2	1700.130	1700.912	-1051.333	0.499	1860.564	0.563	23	0.353	R.IGAINVVCSTPEVANR.V
R1/RRR1-10/2	1391.314	1390.568	-183.095	0.555	1708.626	0.596	22	0.338	R.VATLQSLSGTGSLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1560.312	1559.788	-305.921	0.525	1843.866	0.474	21	0.317	K.ATAELLFGADNPVLK.Q
R1/RRR1-10/2	1700.452	1700.912	-271.205	0.553	1531.946	0.608	21	0.314	R.IGAINVVCSTPEVANR.V
R1/RRR1-10/3	1697.057	1696.958	58.337	0.529	2392.262	0.353	34	0.289	R.LARPM*YSNPPIHGAR.I
R1/RRR1-10/2	1389.762	1390.568	-1303.213	0.395	1497.915	0.524	22	0.285	R.VATLQSLSGTGSLR.L
R1/RRR1-11/2	1560.526	1559.788	-168.341	0.524	1537.906	0.461	20	0.271	K.ATAELLFGADNPVLK.Q
R1/RRR1-11/2	1560.321	1559.788	-300.583	0.523	1511.602	0.472	19	0.270	K.ATAELLFGADNPVLK.Q
R1/RRR1-10/2	973.024	973.192	-172.528	0.480	1328.192	0.458	17	0.255	R.ISLAGLSLAK.C
R1/RRR1-11/2	1558.994	1559.788	-1154.286	0.340	1391.162	0.394	18	0.240	K.ATAELLFGADNPVLK.Q
R1/RRR1-10/2	1558.865	1559.788	-1237.321	0.333	1512.752	0.332	19	0.240	K.ATAELLFGADNPVLK.Q
R1/RRR1-11/2	1389.584	1390.568	-1431.932	0.372	1132.093	0.480	22	0.238	R.VATLQSLSGTGSLR.L
R1/RRR1-10/2	972.672	973.192	-1567.680	0.430	1292.993	0.377	17	0.235	R.ISLAGLSLAK.C
R1/RRR1-10/2	1559.177	1559.788	-1036.753	0.366	1367.710	0.340	18	0.227	K.ATAELLFGADNPVLK.Q
R1/RRR1-10/2	972.945	973.192	-254.465	0.444	1095.693	0.407	16	0.226	R.ISLAGLSLAK.C
R1/RRR1-10/2	889.968	890.065	-109.043	0.521	902.306	0.435	13	0.221	R.LAAAFIQR.Y
R1/RRR1-11/2	1389.770	1390.568	-1297.479	0.377	981.591	0.438	20	0.220	R.VATLQSLSGTGSLR.L
R1/RRR1-10/2	890.031	890.065	-37.777	0.525	863.384	0.436	13	0.219	R.LAAAFIQR.Y
R1/RRR1-10/2	889.936	890.065	-144.817	0.450	881.765	0.426	13	0.218	R.LAAAFIQR.Y
R1/RRR1-10/2	1465.458	1465.675	-148.349	0.388	982.645	0.422	18	0.216	K.EYLPIEGLAAFNK.A
R1/RRR1-10/2	1532.553	1532.763	-137.461	0.491	929.829	0.389	20	0.213	R.TEELQPYVLNVVK.K
R1/RRR1-10/2	1532.072	1532.763	-1106.960	0.375	942.960	0.319	19	0.202	R.TEELQPYVLNVVK.K
R1/RRR1-10/2	1532.101	1532.763	-1087.600	0.388	685.987	0.360	17	0.198	R.TEELQPYVLNVVK.K
R1/RRR1-8/2	1561.177	1559.788	249.503	0.365	682.016	0.392	14	0.195	K.ATAELLFGADNPVLK.Q
R1/RRR1-10/3	1696.544	1696.958	-245.077	0.447	1922.439	0.348	31	0.192	R.LARPM*YSNPPIHGAR.I
R1/RRR1-3/2	1561.045	1559.788	164.739	0.339	575.563	0.326	16	0.192	K.ATAELLFGADNPVLK.Q
R1/RRR1-11/2	1532.002	1532.763	-1152.965	0.326	565.765	0.234	16	0.187	R.TEELQPYVLNVVK.K
R1/RRR1-3/2	1559.884	1559.788	61.567	0.290	661.517	0.199	15	0.182	K.ATAELLFGADNPVLK.Q
R1/RRR1-10/2	1855.778	1854.988	-113.651	0.528	1047.783	0.642	21	0.167	K.CEYLADAIIDSFHNVS.-
R1/RRR1-16/2	973.923	973.192	-276.461	0.292	350.413	0.291	10	0.159	-.ISLAGLSLAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1854.408	1854.988	-854.663	0.450	881.748	0.566	19	0.129	K.CEYLADAIIDSFHNVS.-
R1/RRR1-10/3	1893.960	1894.117	-83.181	0.442	1343.595	0.358	26	0.124	K.GENKEYLPIEGLAAFNK.A
R1/RRR1-10/2	1853.909	1854.988	-1124.940	0.384	586.318	0.455	18	0.104	K.CEYLADAIIDSFHNVS.-
R1/RRR1-8/2	1842.368	1842.085	153.938	0.653	2759.244	0.635	26	0.585	K.HVAEADIIFVSVNTPTK.T
R1/RRR1-9/2	1477.249	1476.699	-305.966	0.562	1960.378	0.503	22	0.345	R.IITTNLWSAELSK.L
R1/RRR1-8/2	1682.279	1682.979	-1014.018	0.485	1700.544	0.560	22	0.328	K.CPAIEVVVVDISKPR.I
R1/RRR1-9/2	1477.277	1476.699	-286.981	0.584	1851.330	0.493	22	0.325	R.IITTNLWSAELSK.L
R1/RRR1-9/2	1355.155	1354.450	-217.886	0.523	1675.765	0.557	18	0.320	K.AADLTYWESAAR.M
R1/RRR1-8/3	1683.146	1682.979	99.169	0.559	2104.437	0.549	31	0.317	K.CPAIEVVVVDISKPR.I
R1/RRR1-8/2	1355.161	1354.450	-213.910	0.544	1739.140	0.505	18	0.314	K.AADLTYWESAAR.M
R1/RRR1-9/2	1354.360	1354.450	-66.320	0.547	1629.736	0.542	18	0.309	K.AADLTYWESAAR.M
R1/RRR1-8/2	1355.274	1354.450	-129.694	0.599	1649.873	0.536	18	0.309	K.AADLTYWESAAR.M
R1/RRR1-8/2	1355.356	1354.450	-69.162	0.546	1766.876	0.477	18	0.309	K.AADLTYWESAAR.M
R1/RRR1-8/2	1075.028	1075.246	-202.910	0.546	1681.146	0.471	17	0.297	K.LAANAFLAQR.I
R1/RRR1-8/2	1074.538	1075.246	-1593.909	0.501	1573.663	0.498	17	0.291	K.LAANAFLAQR.I
R1/RRR1-8/2	1476.245	1476.699	-308.745	0.475	1589.381	0.473	20	0.284	R.IITTNLWSAELSK.L
R1/RRR1-9/2	1074.530	1075.246	-1601.328	0.417	1643.157	0.427	17	0.280	K.LAANAFLAQR.I
R1/RRR1-2/2	1075.339	1075.246	86.918	0.505	1526.978	0.476	17	0.280	K.LAANAFLAQR.I
R1/RRR1-7/2	1075.152	1075.246	-88.097	0.474	1559.828	0.455	17	0.278	K.LAANAFLAQR.I
R1/RRR1-10/2	1076.301	1075.246	51.462	0.436	1466.096	0.480	17	0.273	K.LAANAFLAQR.I
R1/RRR1-2/2	1075.055	1075.246	-178.191	0.452	1507.098	0.439	17	0.268	K.LAANAFLAQR.I
R1/RRR1-8/2	1074.675	1075.246	-1466.449	0.495	1530.222	0.427	17	0.268	K.LAANAFLAQR.I
R1/RRR1-7/2	1074.997	1075.246	-232.643	0.506	1471.544	0.445	17	0.266	K.LAANAFLAQR.I
R1/RRR1-8/3	1683.882	1682.979	-57.858	0.607	1928.983	0.515	30	0.265	K.CPAIEVVVVDISKPR.I
R1/RRR1-8/2	1475.682	1476.699	-1371.204	0.424	1515.577	0.422	20	0.263	R.IITTNLWSAELSK.L
R1/RRR1-8/2	1272.214	1272.453	-188.958	0.436	1225.342	0.537	20	0.261	R.VVSSM*FNTVSGK.K
R1/RRR1-8/3	1682.062	1682.979	-1143.431	0.538	1903.923	0.524	30	0.261	K.CPAIEVVVVDISKPR.I
R1/RRR1-2/2	1475.919	1476.699	-1209.634	0.327	1625.722	0.361	19	0.259	R.IITTNLWSAELSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1074.984	1075.246	-244.491	0.468	1484.550	0.410	17	0.259	K.LAANAFLAQR.I
R1/RRR1-6/2	1476.517	1476.699	-124.103	0.477	1375.823	0.452	19	0.255	R.IITTNLWSAELSK.L
R1/RRR1-7/2	1476.203	1476.699	-337.036	0.384	1510.540	0.388	20	0.254	R.IITTNLWSAELSK.L
R1/RRR1-6/2	1074.759	1075.246	-454.382	0.386	1349.263	0.438	16	0.250	K.LAANAFLAQR.I
R1/RRR1-8/2	1271.946	1272.453	-1188.361	0.349	1198.403	0.519	20	0.250	R.VVSSM*FNTVSGK.K
R1/RRR1-10/2	1476.961	1476.699	178.013	0.473	1122.432	0.507	18	0.244	R.IITTNLWSAELSK.L
R1/RRR1-8/2	1475.343	1476.699	-1601.978	0.386	1379.519	0.389	19	0.242	R.IITTNLWSAELSK.L
R1/RRR1-8/2	1271.967	1272.453	-383.242	0.375	1144.143	0.474	19	0.238	R.VVSSM*FNTVSGK.K
R1/RRR1-6/2	1076.122	1075.246	-116.007	0.483	1219.230	0.410	16	0.236	K.LAANAFLAQR.I
R1/RRR1-3/2	1476.413	1476.699	-194.103	0.310	1274.406	0.383	18	0.230	R.IITTNLWSAELSK.L
R1/RRR1-5/2	1075.056	1075.246	-176.824	0.420	1021.020	0.434	16	0.227	K.LAANAFLAQR.I
R1/RRR1-6/2	1075.301	1075.246	51.169	0.420	1050.663	0.426	15	0.226	K.LAANAFLAQR.I
R1/RRR1-10/2	1076.194	1075.246	-48.762	0.408	917.414	0.462	15	0.225	K.LAANAFLAQR.I
R1/RRR1-3/2	1476.439	1476.699	-177.100	0.366	1088.943	0.420	17	0.224	R.IITTNLWSAELSK.L
R1/RRR1-6/2	1476.158	1476.699	-1047.119	0.313	1128.637	0.361	18	0.217	R.IITTNLWSAELSK.L
R1/RRR1-8/2	1626.150	1625.799	216.796	0.440	490.220	0.537	21	0.213	R.ETPAIDVCHGLLGDK.A
R1/RRR1-2/2	1475.984	1476.699	-1165.284	0.295	934.663	0.394	18	0.211	R.IITTNLWSAELSK.L
R1/RRR1-8/2	1069.463	1070.224	-1652.420	0.387	972.563	0.342	14	0.207	R.NVVDPEKLR.E
R1/RRR1-8/2	1626.422	1625.799	-232.284	0.499	293.693	0.529	18	0.207	R.ETPAIDVCHGLLGDK.A
R1/RRR1-8/2	1069.450	1070.224	-1664.231	0.363	706.662	0.440	12	0.206	R.NVVDPEKLR.E
R1/RRR1-5/2	1475.937	1476.699	-1197.674	0.338	753.248	0.402	15	0.204	R.IITTNLWSAELSK.L
R1/RRR1-1/2	1620.015	1619.796	135.540	0.414	829.567	0.408	17	0.202	K.FLNASVGFGGSCFQK.D
R1/RRR1-4/2	1476.011	1476.699	-1147.428	0.278	720.095	0.380	15	0.199	R.IITTNLWSAELSK.L
R1/RRR1-7/2	1475.862	1476.699	-1248.256	0.302	763.164	0.324	16	0.197	R.IITTNLWSAELSK.L
R1/RRR1-8/2	1070.040	1070.224	-172.962	0.378	789.577	0.325	12	0.197	R.NVVDPEKLR.E
R1/RRR1-8/2	1477.659	1476.699	-27.477	0.304	676.516	0.303	14	0.192	R.IITTNLWSAELSK.L
R1/RRR1-3/2	1475.461	1476.699	-1521.606	0.224	604.813	0.162	16	0.189	R.IITTNLWSAELSK.L
R1/RRR1-8/3	1801.470	1802.046	-877.768	0.458	1045.940	0.534	26	0.133	R.IFDNM*QKPAFVFDGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/3	1802.856	1802.046	-105.946	0.488	836.549	0.540	25	0.119	R.IFDNM*QKPAFVFDGR.N
R1/RRR1-8/3	1801.037	1802.046	-1118.836	0.431	755.996	0.474	23	0.102	R.IFDNM*QKPAFVFDGR.N
R1/RRR1-7/2	1121.179	1121.268	-80.113	0.500	1400.894	0.435	16	0.254	R.GAINFATIDAK.A
R1/RRR1-7/2	1101.270	1101.237	30.395	0.481	1059.653	0.565	16	0.253	K.HGVEGYPTLK.V
R1/RRR1-7/2	1101.054	1101.237	-167.089	0.462	1113.796	0.531	16	0.250	K.HGVEGYPTLK.V
R1/RRR1-7/2	1120.776	1121.268	-440.205	0.428	1306.854	0.423	16	0.243	R.GAINFATIDAK.A
R1/RRR1-7/2	1494.545	1493.640	-64.031	0.473	656.380	0.659	20	0.239	K.ALAPEYEEAATSLK.E
R1/RRR1-7/2	1494.148	1493.640	-330.694	0.496	754.849	0.610	20	0.237	K.ALAPEYEEAATSLK.E
R1/RRR1-7/2	1101.041	1101.237	-178.211	0.447	1085.245	0.431	15	0.228	K.HGVEGYPTLK.V
R1/RRR1-7/2	1198.932	1199.334	-336.143	0.459	1117.250	0.369	16	0.220	K.YEELGELFAK.S
R1/RRR1-7/2	1193.285	1193.414	-108.310	0.491	900.564	0.426	16	0.219	R.TIEDLITFIK.E
R1/RRR1-7/2	1193.111	1193.414	-255.380	0.513	690.114	0.483	15	0.218	R.TIEDLITFIK.E
R1/RRR1-7/2	1198.965	1199.334	-309.277	0.456	1127.919	0.346	16	0.216	K.YEELGELFAK.S
R1/RRR1-8/2	1120.708	1121.268	-1395.944	0.374	1017.245	0.404	15	0.216	R.GAINFATIDAK.A
R1/RRR1-7/2	1192.840	1193.414	-1323.437	0.433	761.022	0.443	16	0.215	R.TIEDLITFIK.E
R1/RRR1-7/2	1199.299	1199.334	-29.362	0.477	1068.770	0.349	16	0.214	K.YEELGELFAK.S
R1/RRR1-8/2	1193.455	1193.414	34.100	0.431	598.229	0.469	14	0.211	R.TIEDLITFIK.E
R1/RRR1-7/2	1369.918	1369.459	335.638	0.379	541.446	0.458	19	0.207	K.SEPIPESNDGPVK.V
R1/RRR1-7/2	1369.268	1369.459	-139.814	0.353	598.893	0.424	20	0.205	K.SEPIPESNDGPVK.V
R1/RRR1-7/2	1324.936	1324.418	-365.166	0.345	687.955	0.453	15	0.204	K.NYDQIVLDDTK.D
R1/RRR1-8/2	1193.095	1193.414	-268.724	0.296	780.992	0.383	14	0.202	R.TIEDLITFIK.E
R1/RRR1-7/2	1313.460	1314.513	-1567.870	0.399	647.914	0.408	14	0.196	K.TLSDALRPIAEK.H
R1/RRR1-7/2	1492.706	1493.640	-1299.790	0.316	472.185	0.383	18	0.195	K.ALAPEYEEAATSLK.E
R1/RRR1-7/2	1369.122	1369.459	-247.052	0.317	494.335	0.318	18	0.194	K.SEPIPESNDGPVK.V
R1/RRR1-8/2	1369.036	1369.459	-310.118	0.262	503.636	0.294	18	0.191	K.SEPIPESNDGPVK.V
R1/RRR1-7/2	1621.494	1621.856	-224.155	0.400	787.422	0.302	15	0.186	R.TIEDLITFIKENGK.Y
R1/RRR1-7/3	1609.653	1608.819	-103.502	0.485	1558.388	0.334	26	0.137	K.VDKFPAFAIQETNK.N
R1/RRR1-7/3	1609.079	1608.819	161.753	0.404	972.229	0.232	23	0.072	-.VDKFPAFAIQETNK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/3	1608.273	1608.819	-964.612	0.417	1059.839	0.126	23	0.064	-.VDKFPAFAIQETNK.-
R1/RRR1-8/2	1967.633	1968.071	-223.240	0.547	2062.238	0.618	25	0.411	R.ADEHVDVTNPATQEVVSR.I
R1/RRR1-8/2	1444.533	1444.573	-27.683	0.532	2494.958	0.392	20	0.411	K.AESLDDAIQIVNR.N
R1/RRR1-8/2	1444.304	1444.573	-186.720	0.474	2411.427	0.358	20	0.383	K.AESLDDAIQIVNR.N
R1/RRR1-8/2	1951.230	1949.303	-37.346	0.555	1862.226	0.470	24	0.318	K.DPGAAM*M*LAELAMEAGLPK.G
R1/RRR1-8/2	1163.096	1163.305	-180.704	0.411	1667.724	0.484	17	0.299	R.IPLTTADEFR.A
R1/RRR1-8/2	1163.075	1163.305	-198.287	0.468	1652.370	0.413	17	0.279	R.IPLTTADEFR.A
R1/RRR1-8/2	1289.946	1290.405	-357.037	0.451	1281.360	0.530	18	0.264	K.ASFAGDLNFYGK.A
R1/RRR1-8/2	1204.081	1204.312	-192.551	0.566	1249.940	0.521	18	0.262	K.LAENITTEQGK.T
R1/RRR1-8/2	1220.950	1220.400	-369.793	0.452	1369.887	0.468	18	0.261	R.LLIGGEFVESR.A
R1/RRR1-8/2	1203.428	1204.312	-1570.212	0.532	1207.403	0.518	18	0.257	K.LAENITTEQGK.T
R1/RRR1-8/2	1204.033	1204.312	-233.133	0.588	1231.568	0.507	18	0.257	K.LAENITTEQGK.T
R1/RRR1-8/2	1289.935	1290.405	-365.583	0.425	1146.905	0.545	18	0.253	K.ASFAGDLNFYGK.A
R1/RRR1-8/2	1162.749	1163.305	-1341.997	0.389	1392.505	0.394	16	0.245	R.IPLTTADEFR.A
R1/RRR1-8/3	1967.399	1968.071	-852.352	0.464	1863.044	0.472	31	0.239	R.ADEHVDVTNPATQEVVSR.I
R1/RRR1-8/2	1220.028	1220.400	-306.045	0.404	1383.493	0.360	18	0.238	R.LLIGGEFVESR.A
R1/RRR1-8/2	1932.033	1933.303	-1178.532	0.425	1276.607	0.390	22	0.231	-.DPGAAMM*LAELAMEAGLPK.-
R1/RRR1-8/2	1220.233	1220.400	-136.923	0.392	1162.487	0.384	17	0.224	R.LLIGGEFVESR.A
R1/RRR1-8/2	1139.165	1139.328	-143.550	0.406	1148.966	0.381	15	0.222	K.AGVQFFTQIK.T
R1/RRR1-8/2	1093.954	1094.265	-285.159	0.431	767.530	0.394	14	0.205	R.VSLSM*PTSQK.-
R1/RRR1-8/2	1093.808	1094.265	-418.513	0.387	802.164	0.368	15	0.204	R.VSLSM*PTSQK.-
R1/RRR1-8/2	1093.978	1094.265	-262.433	0.380	682.885	0.319	13	0.194	R.VSLSM*PTSQK.-
R1/RRR1-12/2	1101.376	1102.183	-1645.671	0.269	971.482	0.243	16	0.193	-.LIQSGADNGAR.-
R1/RRR1-3/2	1164.392	1163.305	74.488	0.353	380.330	0.302	11	0.192	R.IPLTTADEFR.A
R1/RRR1-12/2	1102.119	1102.183	-58.502	0.353	1010.747	0.144	16	0.185	-.LIQSGADNGAR.-
R1/RRR1-12/2	1102.015	1102.183	-153.611	0.368	817.395	0.181	15	0.180	-.LIQSGADNGAR.-
R1/RRR1-8/3	1968.861	1968.071	-106.974	0.449	1211.978	0.476	27	0.141	R.ADEHVDVTNPATQEVVSR.I
R1/RRR1-8/3	1968.033	1968.071	-19.269	0.417	1052.720	0.470	26	0.123	R.ADEHVDVTNPATQEVVSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/3	1916.609	1917.304	-886.982	0.422	1325.043	0.342	31	0.116	K.DPGAAMMLAELAMEAGLPK.G
R1/RRR1-7/1	1030.559	1031.142	-1540.200	0.182	1184.155	0.216	13	0.758	K.AIDDAEGLVK.V
R1/RRR1-7/2	1836.637	1836.033	-216.164	0.574	2513.946	0.612	28	0.505	R.VPYTAGIGLESVGVETDK.A
R1/RRR1-7/2	1835.603	1836.033	-234.561	0.575	2572.031	0.526	29	0.481	R.VPYTAGIGLESVGVETDK.A
R1/RRR1-7/2	1835.633	1836.033	-218.550	0.558	2051.168	0.570	27	0.388	R.VPYTAGIGLESVGVETDK.A
R1/RRR1-7/2	1947.239	1948.118	-967.841	0.502	1846.120	0.563	26	0.347	K.LASPSEVSVDLSDGGSTVVK.G
R1/RRR1-7/2	1948.056	1948.118	-32.218	0.553	1673.527	0.608	26	0.333	K.LASPSEVSVDLSDGGSTVVK.G
R1/RRR1-7/2	1947.500	1948.118	-833.424	0.516	1447.061	0.571	24	0.289	K.LASPSEVSVDLSDGGSTVVK.G
R1/RRR1-8/2	1130.445	1131.305	-1650.251	0.367	1387.856	0.461	17	0.258	K.NIIIATGSDVK.S
R1/RRR1-8/2	1131.028	1131.305	-245.691	0.409	1433.855	0.416	18	0.254	K.NIIIATGSDVK.S
R1/RRR1-7/2	1726.202	1726.996	-1042.588	0.545	1133.090	0.502	21	0.243	K.FSNLEVDLPAM*M*AQK.D
R1/RRR1-7/2	1131.024	1131.305	-248.506	0.413	1128.321	0.472	17	0.239	K.NIIIATGSDVK.S
R1/RRR1-7/2	1726.263	1726.996	-1007.301	0.518	1113.004	0.497	19	0.238	K.FSNLEVDLPAM*M*AQK.D
R1/RRR1-7/2	1130.538	1131.305	-1567.266	0.344	1159.097	0.449	17	0.234	K.NIIIATGSDVK.S
R1/RRR1-7/2	1130.915	1131.305	-345.534	0.399	1075.264	0.441	16	0.228	K.NIIIATGSDVK.S
R1/RRR1-8/2	1130.684	1131.305	-1437.771	0.376	1051.021	0.444	16	0.226	K.NIIIATGSDVK.S
R1/RRR1-7/2	1031.080	1031.142	-60.395	0.495	892.246	0.448	17	0.224	K.AIDDAEGLVK.V
R1/RRR1-7/2	917.965	918.075	-120.255	0.473	1067.277	0.363	14	0.217	-.FPLLANSR.-
R1/RRR1-8/2	1031.005	1031.142	-132.840	0.484	998.812	0.342	17	0.211	K.AIDDAEGLVK.V
R1/RRR1-7/2	1030.421	1031.142	-1674.866	0.379	734.217	0.425	16	0.210	K.AIDDAEGLVK.V
R1/RRR1-8/2	1030.939	1031.142	-197.218	0.444	619.783	0.404	15	0.207	K.AIDDAEGLVK.V
R1/RRR1-8/2	1132.976	1133.234	-228.410	0.320	508.711	0.519	16	0.205	K.VVGVDTSGDGVK.L
R1/RRR1-7/2	1187.355	1187.368	-11.509	0.351	253.030	0.451	16	0.204	K.SLPGVTIDEKK.I
R1/RRR1-7/2	1187.051	1187.368	-268.236	0.334	217.730	0.505	14	0.203	K.SLPGVTIDEKK.I
R1/RRR1-7/2	1133.150	1133.234	-74.296	0.389	501.558	0.428	16	0.202	K.VVGVDTSGDGVK.L
R1/RRR1-8/2	1133.067	1133.234	-147.673	0.339	582.983	0.427	15	0.199	K.VVGVDTSGDGVK.L
R1/RRR1-7/2	1187.016	1187.368	-297.641	0.300	202.928	0.366	14	0.198	K.SLPGVTIDEKK.I
R1/RRR1-7/2	1030.283	1031.142	-1809.853	0.314	625.800	0.317	15	0.196	K.AIDDAEGLVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	918.007	918.075	-74.503	0.324	811.025	0.256	12	0.190	-.FPLLANSR.-
R1/RRR1-8/2	918.263	918.075	205.254	0.360	919.278	0.204	13	0.189	-.FPLLANSR.-
R1/RRR1-7/2	917.575	918.075	-546.497	0.312	844.863	0.207	12	0.183	-.FPLLANSR.-
R1/RRR1-21/2	1130.993	1131.305	-276.118	0.273	541.869	0.153	11	0.175	-.NIIIATGSDVK.-
R1/RRR1-8/2	917.864	918.075	-230.584	0.357	678.686	0.268	11	0.161	-.FPLLANSR.-
R1/RRR1-8/3	1540.556	1540.729	-112.372	0.455	891.543	0.447	24	0.102	K.ALLHSSHM*YHEAK.S
R1/RRR1-8/3	1451.445	1451.603	-109.216	0.431	1240.669	0.332	25	0.102	R.TCHAHPTVSEALK.E
R1/RRR1-7/3	1540.794	1540.729	42.361	0.440	773.827	0.403	23	0.091	K.ALLHSSHM*YHEAK.S
R1/RRR1-8/3	1540.946	1540.729	141.755	0.468	799.818	0.385	24	0.090	K.ALLHSSHM*YHEAK.S
R1/RRR1-7/3	1540.470	1540.729	-168.173	0.444	698.874	0.393	22	0.089	K.ALLHSSHM*YHEAK.S
R1/RRR1-7/3	1451.810	1451.603	142.548	0.483	728.658	0.361	21	0.089	R.TCHAHPTVSEALK.E
R1/RRR1-8/3	1451.433	1451.603	-117.948	0.482	663.974	0.379	21	0.087	-.TCHAHPTVSEALK.-
R1/RRR1-7/3	1451.773	1451.603	117.377	0.436	711.375	0.347	22	0.086	R.TCHAHPTVSEALK.E
R1/RRR1-7/3	1451.810	1451.603	142.674	0.434	1056.253	0.293	25	0.084	R.TCHAHPTVSEALK.E
R1/RRR1-8/3	1451.702	1451.603	68.423	0.446	988.072	0.296	24	0.084	R.TCHAHPTVSEALK.E
R1/RRR1-15/2	1281.200	1281.503	-237.407	0.477	1515.673	0.485	17	0.280	K.NM*GLLLAEFEK.I
R1/RRR1-15/2	1071.947	1072.194	-230.677	0.469	1006.402	0.488	15	0.233	R.TPVNGDDLLK.G
R1/RRR1-15/2	1369.827	1370.490	-1218.229	0.428	950.665	0.512	18	0.229	K.ITIDPDDPAAVSR.Y
R1/RRR1-15/2	1071.531	1072.194	-1556.677	0.423	1000.204	0.445	15	0.224	R.TPVNGDDLLK.G
R1/RRR1-15/2	1626.741	1627.778	-1255.615	0.432	979.079	0.475	19	0.223	K.EKITIDPDDPAAVSR.Y
R1/RRR1-15/2	1073.096	1072.194	-91.917	0.423	992.962	0.425	15	0.221	R.TPVNGDDLLK.G
R1/RRR1-15/2	1280.509	1281.503	-1562.289	0.381	1138.005	0.316	15	0.209	K.NM*GLLLAEFEK.I
R1/RRR1-15/2	1512.270	1512.621	-232.414	0.462	583.828	0.430	16	0.201	R.EEFKDEEM*PDVK.K
R1/RRR1-15/2	968.582	968.174	423.010	0.436	776.468	0.342	13	0.200	K.GIFFEVKK.K
R1/RRR1-15/2	1281.678	1281.503	136.674	0.394	343.994	0.388	12	0.192	-.NM*GLLLAEFEK.-
R1/RRR1-15/2	1263.099	1262.352	-200.905	0.220	132.942	0.493	15	0.189	R.QKADLLSDSER.I
R1/RRR1-15/3	1627.591	1627.778	-115.375	0.426	1474.356	0.389	26	0.144	K.EKITIDPDDPAAVSR.Y
R1/RRR1-15/3	1234.663	1234.513	121.754	0.568	1319.267	0.404	23	0.125	K.KFETALGVLKK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1230.743	1230.435	251.667	0.489	898.708	0.424	20	0.097	R.IKYTIDTFTK.G
R1/RRR1-15/3	1230.203	1230.435	-188.772	0.417	1042.908	0.374	20	0.094	R.IKYTIDTFTK.G
R1/RRR1-15/3	1234.934	1234.513	342.273	0.495	941.342	0.314	21	0.083	K.KFETALGVLKK.E
R1/RRR1-15/3	1230.524	1230.435	72.613	0.387	833.419	0.320	19	0.080	R.IKYTIDTFTK.G
R1/RRR1-7/2	1295.798	1296.501	-1318.440	0.483	1818.484	0.620	21	0.363	K.VVAAGANPVQITR.G
R1/RRR1-7/2	1296.238	1296.501	-203.136	0.537	1844.914	0.569	21	0.351	K.VVAAGANPVQITR.G
R1/RRR1-7/2	1295.539	1296.501	-1518.773	0.431	1896.293	0.527	21	0.345	K.VVAAGANPVQITR.G
R1/RRR1-7/2	1284.568	1285.472	-1486.852	0.463	1923.040	0.471	18	0.331	R.DLINVLEEAIR.G
R1/RRR1-8/2	1296.056	1296.501	-344.679	0.491	1663.760	0.544	20	0.315	K.VVAAGANPVQITR.G
R1/RRR1-7/2	1286.370	1285.472	-79.343	0.558	1595.311	0.462	17	0.281	R.DLINVLEEAIR.G
R1/RRR1-11/2	1284.819	1285.472	-1290.063	0.379	1704.706	0.363	17	0.270	R.DLINVLEEAIR.G
R1/RRR1-7/2	1285.321	1285.472	-117.892	0.461	1497.665	0.434	17	0.265	R.DLINVLEEAIR.G
R1/RRR1-7/2	1506.097	1506.638	-1025.897	0.376	1306.500	0.459	20	0.249	R.GYISPYFVTDSEK.M
R1/RRR1-7/2	1175.106	1175.274	-143.744	0.411	1228.042	0.475	17	0.245	K.NAGVNGSVVTEK.V
R1/RRR1-7/2	1088.198	1088.240	-38.323	0.451	1091.067	0.513	15	0.243	R.KGVVTLEEGR.S
R1/RRR1-9/2	1284.502	1285.472	-1538.496	0.395	1094.176	0.441	16	0.230	R.DLINVLEEAIR.G
R1/RRR1-6/2	1284.814	1285.472	-1294.452	0.320	1313.930	0.357	16	0.229	R.DLINVLEEAIR.G
R1/RRR1-7/2	1506.132	1506.638	-1002.787	0.356	1034.764	0.436	19	0.222	R.GYISPYFVTDSEK.M
R1/RRR1-7/2	1246.096	1246.383	-230.569	0.506	692.995	0.501	17	0.221	R.CCLEHAASVAK.T
R1/RRR1-9/2	1285.174	1285.472	-232.608	0.394	1330.081	0.288	17	0.220	R.DLINVLEEAIR.G
R1/RRR1-7/2	1044.046	1044.187	-135.403	0.470	928.493	0.429	16	0.219	K.IVNDGVTVAR.E
R1/RRR1-7/2	1542.305	1542.670	-237.014	0.498	1184.747	0.351	20	0.217	R.EVELEDPVENIGAK.L
R1/RRR1-7/2	1541.828	1542.670	-1197.868	0.408	1109.012	0.344	19	0.212	R.EVELEDPVENIGAK.L
R1/RRR1-7/2	1043.969	1044.187	-209.064	0.431	819.224	0.412	16	0.211	K.IVNDGVTVAR.E
R1/RRR1-7/2	1176.133	1175.274	-120.821	0.425	730.729	0.454	16	0.211	K.NAGVNGSVVTEK.V
R1/RRR1-7/2	1174.981	1175.274	-250.672	0.408	764.672	0.458	15	0.211	K.NAGVNGSVVTEK.V
R1/RRR1-7/2	1542.398	1542.670	-176.909	0.511	1160.674	0.325	20	0.210	R.EVELEDPVENIGAK.L
R1/RRR1-7/2	1174.923	1175.274	-300.079	0.400	639.642	0.469	15	0.208	K.NAGVNGSVVTEK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1285.239	1285.472	-181.345	0.353	695.523	0.359	16	0.203	R.DLINVLEEAIR.G
R1/RRR1-13/2	1322.426	1321.504	-59.311	0.390	833.797	0.384	16	0.202	R.NVVLESKYGSPK.I
R1/RRR1-16/2	1285.736	1285.472	206.108	0.368	496.548	0.373	14	0.201	R.DLINVLEEAIR.G
R1/RRR1-7/2	1505.961	1506.638	-1116.722	0.289	925.545	0.338	18	0.200	R.GYISPYFVTDSEK.M
R1/RRR1-8/2	1245.957	1246.383	-342.619	0.432	326.900	0.401	15	0.199	-.CCLEHAASVAK.-
R1/RRR1-8/2	1246.056	1246.383	-262.609	0.403	346.070	0.362	14	0.199	R.CCLEHAASVAK.T
R1/RRR1-8/2	1246.361	1246.383	-17.251	0.402	269.905	0.400	14	0.198	-.CCLEHAASVAK.-
R1/RRR1-8/2	1295.402	1296.501	-1625.549	0.286	542.875	0.446	13	0.195	K.VVAAGANPVQITR.G
R1/RRR1-7/2	960.061	960.067	-6.135	0.439	928.208	0.265	13	0.192	K.GVVTLEEGR.S
R1/RRR1-10/2	1284.469	1285.472	-1563.985	0.290	531.637	0.224	13	0.190	R.DLINVLEEAIR.G
R1/RRR1-10/2	1284.251	1285.472	-1734.332	0.259	656.875	0.191	15	0.189	R.DLINVLEEAIR.G
R1/RRR1-9/3	1247.375	1246.383	-6.058	0.342	755.144	0.348	20	0.079	R.CCLEHAASVAK.T
R1/RRR1-8/3	1247.163	1246.383	-176.437	0.336	1166.397	0.204	23	0.073	R.CCLEHAASVAK.T
R1/RRR1-7/2	1705.626	1705.010	-226.039	0.571	2215.702	0.588	23	0.425	K.SALGILM*NLGLIEESK.I
R1/RRR1-7/2	1704.403	1705.010	-946.136	0.521	2220.051	0.575	23	0.422	K.SALGILM*NLGLIEESK.I
R1/RRR1-7/2	1705.325	1705.010	184.885	0.551	2035.579	0.623	22	0.402	K.SALGILM*NLGLIEESK.I
R1/RRR1-7/2	1604.148	1603.761	241.751	0.480	1695.326	0.430	22	0.286	K.GFLTINSQPAVNGER.S
R1/RRR1-7/2	1846.201	1845.946	138.631	0.540	1110.384	0.614	21	0.261	R.SDSTSVGWGGPGGYVYQK.A
R1/RRR1-7/2	1845.369	1845.946	-857.456	0.474	1022.547	0.590	21	0.247	R.SDSTSVGWGGPGGYVYQK.A
R1/RRR1-7/2	1603.787	1603.761	16.062	0.470	1132.835	0.512	20	0.244	K.GFLTINSQPAVNGER.S
R1/RRR1-7/2	1845.525	1845.946	-228.988	0.511	1060.527	0.535	21	0.239	R.SDSTSVGWGGPGGYVYQK.A
R1/RRR1-7/2	1889.356	1889.052	161.385	0.496	1096.903	0.507	20	0.237	K.LTSSPWSELDGLQPETK.I
R1/RRR1-16/2	1890.454	1889.052	212.845	0.547	1125.946	0.493	20	0.235	K.LTSSPWSELDGLQPETK.I
R1/RRR1-7/2	1889.344	1889.052	154.841	0.517	1021.672	0.520	20	0.234	K.LTSSPWSELDGLQPETK.I
R1/RRR1-7/2	1604.369	1603.761	-244.940	0.546	1103.678	0.466	21	0.233	K.GFLTINSQPAVNGER.S
R1/RRR1-7/2	1198.955	1199.381	-355.948	0.442	1279.090	0.379	15	0.232	K.LQEEWAVPVK.S
R1/RRR1-16/2	1888.481	1889.052	-834.769	0.453	1099.566	0.480	20	0.232	K.LTSSPWSELDGLQPETK.I
R1/RRR1-7/2	990.204	990.133	72.320	0.463	1005.316	0.423	15	0.225	K.IDDALTTIK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-25/2	990.045	990.133	-89.302	0.420	906.035	0.413	15	0.218	K.IDDALTTIK.S
R1/RRR1-16/2	1888.059	1889.052	-1058.875	0.433	1060.741	0.425	19	0.218	K.LTSSPWSELDGLQPETK.I
R1/RRR1-25/2	990.113	990.133	-19.675	0.422	921.482	0.416	14	0.218	K.IDDALTTIK.S
R1/RRR1-16/2	1200.141	1199.381	-199.916	0.399	1005.308	0.391	15	0.216	K.LQEEWAVPVK.S
R1/RRR1-7/2	1198.672	1199.381	-1429.662	0.406	968.926	0.411	14	0.216	K.LQEEWAVPVK.S
R1/RRR1-7/2	990.124	990.133	-9.412	0.463	796.914	0.421	14	0.215	K.IDDALTTIK.S
R1/RRR1-16/2	1200.188	1199.381	-160.837	0.414	1000.019	0.377	15	0.214	K.LQEEWAVPVK.S
R1/RRR1-7/2	989.953	990.133	-182.440	0.446	782.363	0.417	14	0.214	K.IDDALTTIK.S
R1/RRR1-7/2	1604.261	1603.761	312.253	0.461	924.522	0.410	20	0.213	K.GFLTINSQPAVNGER.S
R1/RRR1-7/2	1325.006	1324.550	345.721	0.468	700.085	0.445	19	0.212	K.AFPSLTYIAVNK.D
R1/RRR1-24/2	990.241	990.133	109.781	0.404	804.812	0.388	14	0.210	K.IDDALTTIK.S
R1/RRR1-7/2	1199.217	1199.381	-136.872	0.439	976.231	0.365	14	0.210	-.LQEEWAVPVK.-
R1/RRR1-25/2	1186.302	1185.359	-48.158	0.422	777.377	0.426	16	0.209	K.SNGIQNVLALR.G
R1/RRR1-25/2	989.471	990.133	-1684.354	0.331	823.773	0.395	14	0.209	K.IDDALTTIK.S
R1/RRR1-7/2	1165.163	1165.313	-129.419	0.398	1281.948	0.243	14	0.208	K.AYLEFFCSK.E
R1/RRR1-7/2	1324.204	1324.550	-261.997	0.422	639.501	0.432	18	0.206	K.AFPSLTYIAVNK.D
R1/RRR1-1/2	989.888	990.133	-248.501	0.331	617.992	0.356	12	0.199	K.IDDALTTIK.S
R1/RRR1-7/2	1602.586	1603.761	-1361.330	0.340	1039.089	0.247	20	0.195	K.GFLTINSQPAVNGER.S
R1/RRR1-9/2	1704.837	1705.010	-101.900	0.366	486.604	0.398	13	0.188	K.SALGILM*NLGLIEESK.I
R1/RRR1-7/2	1164.792	1165.313	-1309.475	0.309	874.519	0.212	12	0.187	-.AYLEFFCSK.-
R1/RRR1-7/2	1602.590	1603.761	-1358.729	0.266	1078.198	0.116	20	0.183	K.GFLTINSQPAVNGER.S
R1/RRR1-6/2	1186.041	1185.359	-268.464	0.341	565.163	0.200	14	0.181	-.SNGIQNVLALR.-
R1/RRR1-7/3	1327.579	1327.553	18.932	0.527	1165.995	0.305	22	0.087	-.KLQEEWAVPVK.-
R1/RRR1-7/3	1704.651	1705.010	-211.344	0.332	1089.551	0.309	23	0.087	K.SALGILM*NLGLIEESK.I
R1/RRR1-7/3	1327.414	1327.553	-105.309	0.465	1121.044	0.239	22	0.076	-.KLQEEWAVPVK.-
R1/RRR1-14/2	1794.585	1795.025	-246.268	0.511	2766.462	0.569	27	0.550	K.LTVSTVSSSGVGLTSTAVK.K
R1/RRR1-14/2	1794.406	1795.025	-904.939	0.489	2713.840	0.548	26	0.526	K.LTVSTVSSSGVGLTSTAVK.K
R1/RRR1-14/2	1531.507	1530.747	-156.901	0.567	2281.146	0.573	22	0.436	K.KGGLYTLDVSSVYK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1794.416	1795.025	-899.270	0.468	2214.274	0.592	25	0.427	K.LTVSTVSSSGVGLTSTAVK.K
R1/RRR1-14/2	1530.330	1530.747	-273.592	0.504	2237.981	0.547	22	0.417	K.KGGLYTLDVSSVYK.Y
R1/RRR1-14/2	1530.342	1530.747	-265.669	0.515	2065.953	0.540	22	0.381	K.KGGLYTLDVSSVYK.Y
R1/RRR1-14/2	1766.603	1766.977	-211.981	0.552	1506.579	0.540	23	0.294	R.RLSTNENTLTVGGLYK.V
R1/RRR1-14/2	1298.038	1297.436	-308.027	0.493	1374.901	0.568	18	0.285	K.SVLTISGEFDTK.A
R1/RRR1-14/2	1297.353	1297.436	-64.138	0.512	1408.817	0.550	18	0.284	K.SVLTISGEFDTK.A
R1/RRR1-14/2	1347.395	1347.631	-175.433	0.476	1472.763	0.460	18	0.270	K.LAALLQHEVKPK.S
R1/RRR1-14/2	1610.413	1610.790	-235.049	0.498	1184.784	0.542	20	0.255	R.LSTNENTLTVGGLYK.V
R1/RRR1-14/2	1610.321	1610.790	-292.619	0.464	1155.761	0.538	20	0.251	R.LSTNENTLTVGGLYK.V
R1/RRR1-14/2	1610.350	1610.790	-274.062	0.492	1155.438	0.515	20	0.247	R.LSTNENTLTVGGLYK.V
R1/RRR1-14/2	961.542	962.083	-1607.409	0.408	1642.905	0.279	15	0.245	K.SSVVAELTR.R
R1/RRR1-14/2	1297.088	1297.436	-269.079	0.357	1145.535	0.494	17	0.240	K.SVLTISGEFDTK.A
R1/RRR1-14/2	961.566	962.083	-1582.157	0.400	1585.181	0.265	15	0.236	K.SSVVAELTR.R
R1/RRR1-14/2	1147.278	1147.309	-27.385	0.479	993.320	0.475	16	0.229	K.GPGLFSDIGKR.A
R1/RRR1-14/2	990.991	991.123	-132.768	0.427	682.657	0.535	15	0.221	K.GPGLFSDIGK.K
R1/RRR1-14/2	1147.218	1147.309	-79.255	0.446	997.219	0.410	16	0.218	K.GPGLFSDIGKR.A
R1/RRR1-14/2	1147.029	1147.309	-244.612	0.472	765.180	0.489	14	0.216	K.GPGLFSDIGKR.A
R1/RRR1-14/2	961.487	962.083	-1664.294	0.397	1478.810	0.205	15	0.216	K.SSVVAELTR.R
R1/RRR1-14/2	991.158	991.123	35.995	0.355	521.681	0.549	13	0.209	K.GPGLFSDIGK.K
R1/RRR1-16/2	961.756	962.083	-340.492	0.352	1516.458	0.153	15	0.209	K.SSVVAELTR.R
R1/RRR1-15/2	962.001	962.083	-85.605	0.388	1185.597	0.191	14	0.196	K.SSVVAELTR.R
R1/RRR1-15/2	961.853	962.083	-239.387	0.312	854.641	0.187	14	0.189	K.SSVVAELTR.R
R1/RRR1-16/2	961.383	962.083	-1773.235	0.279	777.327	0.151	12	0.185	K.SSVVAELTR.R
R1/RRR1-14/3	1530.712	1530.747	-23.094	0.469	1625.128	0.346	27	0.147	K.KGGLYTLDVSSVYK.Y
R1/RRR1-14/3	1795.016	1795.025	-5.165	0.428	1038.270	0.454	31	0.115	K.LTVSTVSSSGVGLTSTAVK.K
R1/RRR1-14/3	1530.465	1530.747	-184.977	0.445	1305.333	0.320	25	0.106	K.KGGLYTLDVSSVYK.Y
R1/RRR1-14/3	1531.131	1530.747	251.831	0.483	1188.914	0.323	25	0.099	K.KGGLYTLDVSSVYK.Y
R1/RRR1-14/3	1347.240	1347.631	-291.289	0.265	1231.784	0.286	26	0.086	K.LAALLQHEVKPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/3	1794.383	1795.025	-918.059	0.303	860.701	0.211	27	0.067	-.LTVSTVSSSGVGLTSTAVK.-
R1/RRR1-13/2	1699.420	1699.843	-249.467	0.531	2375.875	0.595	24	0.466	K.GNAYAQVAIGTEDVYK.S
R1/RRR1-13/2	1699.430	1699.843	-243.270	0.531	1967.798	0.575	23	0.374	K.GNAYAQVAIGTEDVYK.S
R1/RRR1-13/3	1604.238	1603.841	248.445	0.458	1498.662	0.389	29	0.363	K.VVLVDNADFLKELQ.-
R1/RRR1-13/2	1699.290	1699.843	-916.468	0.519	1831.005	0.608	24	0.362	K.GNAYAQVAIGTEDVYK.S
R1/RRR1-13/2	1046.971	1047.184	-204.957	0.466	1864.031	0.492	16	0.331	K.SAEAVELVTK.E
R1/RRR1-13/2	1046.998	1047.184	-178.523	0.500	1729.793	0.525	16	0.321	K.SAEAVELVTK.E
R1/RRR1-13/2	1047.046	1047.184	-132.208	0.475	1707.977	0.463	16	0.300	K.SAEAVELVTK.E
R1/RRR1-13/2	1233.040	1233.438	-324.462	0.456	1384.441	0.478	18	0.265	K.VVLVDNADFLK.E
R1/RRR1-13/2	1232.594	1233.438	-1500.575	0.400	1275.584	0.506	17	0.257	K.VVLVDNADFLK.E
R1/RRR1-13/2	1184.520	1184.366	130.382	0.496	1252.686	0.474	16	0.251	K.SPEVVLEWPK.K
R1/RRR1-13/2	1249.123	1249.396	-219.620	0.494	1212.705	0.437	18	0.240	K.IASFLDPDGWK.V
R1/RRR1-13/2	1233.137	1233.438	-245.602	0.389	1210.069	0.385	17	0.228	K.VVLVDNADFLK.E
R1/RRR1-13/2	1248.534	1249.396	-1496.324	0.394	1017.730	0.373	17	0.214	K.IASFLDPDGWK.V
R1/RRR1-13/2	1513.858	1514.766	-1264.295	0.367	580.740	0.561	17	0.213	R.GPTPEPLCQVM*LR.V
R1/RRR1-13/2	1249.293	1249.396	-82.776	0.475	1038.585	0.353	17	0.212	K.IASFLDPDGWK.V
R1/RRR1-13/2	1514.289	1514.766	-315.677	0.418	513.085	0.504	17	0.208	R.GPTPEPLCQVM*LR.V
R1/RRR1-13/2	1556.663	1555.800	-87.825	0.411	178.474	0.478	15	0.196	-.SPEVVLEWPKKDK.-
R1/RRR1-13/2	1183.704	1184.366	-1408.435	0.247	583.440	0.340	13	0.190	K.SPEVVLEWPK.K
R1/RRR1-13/2	1183.385	1184.366	-1678.646	0.233	764.047	0.211	14	0.185	K.SPEVVLEWPK.K
R1/RRR1-13/3	1603.590	1603.841	-156.766	0.449	1025.267	0.462	24	0.159	K.VVLVDNADFLKELQ.-
R1/RRR1-13/2	1604.342	1603.841	-311.873	0.525	1148.902	0.432	21	0.135	K.VVLVDNADFLKELQ.-
R1/RRR1-13/2	1603.391	1603.841	-281.284	0.431	1100.293	0.426	21	0.133	K.VVLVDNADFLKELQ.-
R1/RRR1-13/3	1504.905	1504.802	68.486	0.499	1060.215	0.413	26	0.107	K.ILRQPGPLPGLNTK.I
R1/RRR1-13/2	1605.123	1603.841	176.310	0.459	1029.760	0.299	18	0.101	K.VVLVDNADFLKELQ.-
R1/RRR1-13/2	1603.500	1603.841	-213.614	0.494	910.637	0.318	19	0.092	K.VVLVDNADFLKELQ.-
R1/RRR1-13/2	1604.278	1603.841	273.022	0.392	864.184	0.261	17	0.091	K.VVLVDNADFLKELQ.-
R1/RRR1-13/2	1605.333	1603.841	307.316	0.434	655.865	0.268	15	0.088	K.VVLVDNADFLKELQ.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/3	1505.355	1504.802	-297.700	0.479	891.875	0.312	24	0.084	K.ILRQPGPLPGLNTK.I
R1/RRR1-13/3	1504.734	1504.802	-45.747	0.442	863.332	0.281	24	0.077	-.ILRQPGPLPGLNTK.-
R1/RRR1-4/3	1975.248	1974.290	-21.368	0.594	3664.986	0.572	42	0.916	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-4/2	1570.388	1570.728	-217.416	0.600	2457.464	0.495	24	0.439	R.YDAQISVFGSNLQK.K
R1/RRR1-4/2	1571.444	1570.728	-181.430	0.618	2386.386	0.524	24	0.435	R.YDAQISVFGSNLQK.K
R1/RRR1-1/2	1973.890	1974.290	-203.366	0.488	2365.761	0.492	27	0.418	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-4/2	1973.692	1974.290	-812.004	0.509	2262.340	0.520	27	0.407	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-3/2	1973.512	1974.290	-903.401	0.495	2244.515	0.496	27	0.394	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-3/2	1570.518	1570.728	-133.826	0.590	2167.630	0.498	23	0.382	R.YDAQISVFGSNLQK.K
R1/RRR1-4/2	1973.771	1974.290	-771.899	0.550	1941.732	0.543	27	0.354	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-3/2	1973.545	1974.290	-887.008	0.534	1844.053	0.527	26	0.332	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-3/2	1570.826	1570.728	62.308	0.456	1602.253	0.445	23	0.280	R.YDAQISVFGSNLQK.K
R1/RRR1-3/2	1570.010	1570.728	-1097.836	0.460	1524.601	0.454	21	0.272	R.YDAQISVFGSNLQK.K
R1/RRR1-4/2	1448.245	1448.566	-222.649	0.439	1554.019	0.309	19	0.242	R.RFPIAGSSDDVQR.L
R1/RRR1-3/2	1248.199	1248.362	-131.011	0.458	1002.083	0.468	17	0.230	K.LTVTDDDVIEK.S
R1/RRR1-4/2	1248.147	1248.362	-173.001	0.450	1148.101	0.380	18	0.225	K.LTVTDDDVIEK.S
R1/RRR1-3/2	1248.110	1248.362	-202.435	0.454	1049.577	0.391	17	0.220	K.LTVTDDDVIEK.S
R1/RRR1-3/2	1248.096	1248.362	-213.719	0.395	932.638	0.411	17	0.216	K.LTVTDDDVIEK.S
R1/RRR1-4/2	1291.443	1292.380	-1503.965	0.433	1093.569	0.374	17	0.216	R.FPIAGSSDDVQR.L
R1/RRR1-4/2	1318.917	1319.447	-1163.230	0.447	840.884	0.425	15	0.214	R.LKFEDYFSNR.V
R1/RRR1-4/2	1248.055	1248.362	-246.786	0.437	966.202	0.369	17	0.212	K.LTVTDDDVIEK.S
R1/RRR1-4/2	1080.061	1080.223	-150.045	0.423	839.799	0.400	14	0.211	K.LHVEALQNR.A
R1/RRR1-3/2	1282.060	1282.342	-220.472	0.437	872.196	0.393	16	0.209	R.APEIDEDLHSR.Q
R1/RRR1-4/2	1079.478	1080.223	-1621.210	0.319	867.247	0.364	14	0.204	K.LHVEALQNR.A
R1/RRR1-3/2	1080.140	1080.223	-76.695	0.445	707.642	0.373	13	0.203	K.LHVEALQNR.A
R1/RRR1-4/2	1319.039	1319.447	-309.712	0.425	712.754	0.386	14	0.203	R.LKFEDYFSNR.V
R1/RRR1-3/2	1319.781	1319.447	253.763	0.417	626.582	0.390	14	0.202	R.LKFEDYFSNR.V
R1/RRR1-4/2	957.925	958.053	-133.324	0.439	873.663	0.318	11	0.198	-.DWNIGQPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1282.217	1282.342	-97.265	0.412	844.809	0.318	15	0.197	R.APEIDEDLHSR.Q
R1/RRR1-4/2	1079.728	1080.223	-459.435	0.317	585.571	0.327	12	0.194	K.LHVEALQNR.A
R1/RRR1-4/2	1247.195	1248.362	-1742.372	0.282	495.397	0.330	13	0.191	-.LTVTDDDVIEK.-
R1/RRR1-4/2	1974.192	1974.290	-49.715	0.388	681.046	0.371	17	0.189	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-4/2	957.438	958.053	-1691.218	0.372	940.898	0.255	11	0.185	-.DWNIGQPK.-
R1/RRR1-4/3	1805.246	1804.100	80.959	0.441	1432.469	0.277	32	0.107	K.M*AEAVDKVIVPDFQPK.Q
R1/RRR1-4/3	1974.931	1974.290	-182.249	0.396	779.199	0.380	28	0.088	R.LFASNVLVSGLNGLGAEIAK.N
R1/RRR1-4/2	1287.376	1286.503	-99.158	0.429	1897.781	0.551	19	0.352	R.VASIQQQLASLK.L
R1/RRR1-4/2	1287.064	1286.503	-341.855	0.446	1746.719	0.488	18	0.310	R.VASIQQQLASLK.L
R1/RRR1-4/2	1212.267	1213.324	-1702.080	0.371	1805.074	0.442	17	0.306	K.FYVQTVGDQR.V
R1/RRR1-4/2	1213.395	1213.324	58.463	0.482	1701.002	0.424	17	0.288	K.FYVQTVGDQR.V
R1/RRR1-4/2	1212.978	1213.324	-286.324	0.462	1580.647	0.428	17	0.275	K.FYVQTVGDQR.V
R1/RRR1-3/2	1287.326	1286.503	-138.157	0.468	1247.348	0.533	18	0.262	R.VASIQQQLASLK.L
R1/RRR1-4/2	1274.716	1274.359	280.888	0.392	1384.479	0.477	15	0.261	R.DVEIEVEAVDR.T
R1/RRR1-5/2	1286.309	1286.503	-150.925	0.397	1379.099	0.447	18	0.254	R.VASIQQQLASLK.L
R1/RRR1-5/2	1286.293	1286.503	-163.872	0.403	1197.091	0.500	18	0.248	R.VASIQQQLASLK.L
R1/RRR1-5/2	1286.425	1286.503	-60.780	0.416	1150.487	0.487	17	0.242	R.VASIQQQLASLK.L
R1/RRR1-4/2	1647.184	1647.726	-938.918	0.457	949.849	0.459	23	0.222	R.ISTVDGQPTTNTADAR.V
R1/RRR1-4/2	1058.145	1058.254	-103.167	0.418	787.563	0.468	15	0.216	K.VVVTEVLGGGK.F
R1/RRR1-4/2	1325.993	1326.479	-367.552	0.426	849.314	0.440	17	0.213	R.TGTFLGSLWESK.T
R1/RRR1-4/2	1647.256	1647.726	-285.983	0.477	698.579	0.488	21	0.213	R.ISTVDGQPTTNTADAR.V
R1/RRR1-3/2	1059.029	1058.254	-212.565	0.276	795.509	0.469	15	0.209	K.VVVTEVLGGGK.F
R1/RRR1-4/2	1418.607	1419.565	-1383.908	0.430	1026.481	0.345	16	0.207	K.AALQNLEQFQEK.A
R1/RRR1-4/2	1057.523	1058.254	-1641.205	0.345	719.906	0.427	15	0.206	K.VVVTEVLGGGK.F
R1/RRR1-5/2	1418.777	1419.565	-1264.048	0.380	1065.800	0.309	17	0.205	K.AALQNLEQFQEK.A
R1/RRR1-3/2	1286.351	1286.503	-118.178	0.316	840.913	0.381	15	0.203	R.VASIQQQLASLK.L
R1/RRR1-4/2	1434.109	1434.684	-1101.776	0.446	723.091	0.435	15	0.202	K.TNM*ASVLLEAGLAK.L
R1/RRR1-4/2	1418.609	1419.565	-1382.525	0.392	965.696	0.304	17	0.201	K.AALQNLEQFQEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1434.131	1434.684	-1085.964	0.361	669.145	0.408	16	0.198	K.TNM*ASVLLEAGLAK.L
R1/RRR1-4/2	1418.552	1419.565	-1422.801	0.359	1082.422	0.246	17	0.197	K.AALQNLEQFQEK.A
R1/RRR1-3/2	1058.053	1058.254	-189.733	0.284	580.197	0.373	14	0.195	K.VVVTEVLGGGK.F
R1/RRR1-4/2	1325.879	1326.479	-1210.867	0.376	630.642	0.350	15	0.193	R.TGTFLGSLWESK.T
R1/RRR1-3/2	1058.134	1058.254	-113.119	0.273	385.284	0.482	13	0.192	-.VVVTEVLGGGK.-
R1/RRR1-3/2	1433.986	1434.684	-1187.593	0.385	771.993	0.318	16	0.191	K.TNM*ASVLLEAGLAK.L
R1/RRR1-5/2	1523.249	1522.687	-288.126	0.266	608.325	0.284	16	0.186	R.SHYFDLLLAAESR.A
R1/RRR1-5/2	1523.113	1522.687	281.060	0.241	823.592	0.217	16	0.183	R.SHYFDLLLAAESR.A
R1/RRR1-5/3	1502.450	1502.659	-139.164	0.501	1353.563	0.391	26	0.125	R.HSAIVEYVFSGHR.F
R1/RRR1-4/3	1502.190	1502.659	-312.550	0.481	1149.063	0.328	24	0.096	R.HSAIVEYVFSGHR.F
R1/RRR1-5/3	1502.571	1502.659	-58.728	0.474	1045.431	0.344	24	0.093	R.HSAIVEYVFSGHR.F
R1/RRR1-5/3	1502.628	1502.659	-20.592	0.481	998.699	0.332	24	0.088	-.HSAIVEYVFSGHR.-
R1/RRR1-19/2	1548.282	1548.681	-258.162	0.489	3053.337	0.507	25	0.580	R.AWSAADAVASWVGEK.K
R1/RRR1-22/1	1549.942	1548.681	169.048	0.440	842.956	0.537	17	0.481	R.AWSAADAVASWVGEK.K
R1/RRR1-19/2	1548.068	1548.681	-1044.984	0.407	2612.289	0.461	24	0.452	R.AWSAADAVASWVGEK.K
R1/RRR1-24/2	1548.399	1548.681	-182.786	0.490	2466.608	0.525	24	0.445	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.197	1548.681	-313.614	0.466	2389.028	0.529	23	0.430	R.AWSAADAVASWVGEK.K
R1/RRR1-23/2	1547.831	1548.681	-1198.443	0.418	2346.198	0.532	24	0.422	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.286	1548.681	-255.789	0.486	2381.678	0.488	24	0.413	R.AWSAADAVASWVGEK.K
R1/RRR1-23/2	1548.233	1548.681	-289.961	0.447	2325.099	0.498	24	0.406	R.AWSAADAVASWVGEK.K
R1/RRR1-20/2	1548.395	1548.681	-185.475	0.503	2256.983	0.512	22	0.396	R.AWSAADAVASWVGEK.K
R1/RRR1-17/2	1549.262	1548.681	-271.196	0.519	2198.951	0.534	23	0.394	R.AWSAADAVASWVGEK.K
R1/RRR1-12/2	1547.891	1548.681	-1159.955	0.377	2307.453	0.458	23	0.387	R.AWSAADAVASWVGEK.K
R1/RRR1-17/2	1548.302	1548.681	-245.664	0.494	2184.628	0.512	23	0.383	R.AWSAADAVASWVGEK.K
R1/RRR1-3/2	1548.418	1548.681	-170.053	0.481	2157.775	0.521	23	0.382	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.313	1548.681	-238.071	0.497	2078.987	0.559	23	0.381	R.AWSAADAVASWVGEK.K
R1/RRR1-17/2	1548.366	1548.681	-203.745	0.498	2166.019	0.511	23	0.379	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.178	1548.681	-973.892	0.485	2158.681	0.509	23	0.378	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1548.440	1548.681	-155.897	0.490	2095.609	0.535	23	0.376	R.AWSAADAVASWVGEK.K
R1/RRR1-5/2	1549.454	1548.681	-147.024	0.580	2042.174	0.560	23	0.373	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.414	1548.681	-172.979	0.512	2081.415	0.528	23	0.370	R.AWSAADAVASWVGEK.K
R1/RRR1-21/2	1548.731	1548.681	32.207	0.531	1994.747	0.556	23	0.365	R.AWSAADAVASWVGEK.K
R1/RRR1-4/2	1549.383	1548.681	-192.706	0.560	1971.233	0.570	22	0.364	R.AWSAADAVASWVGEK.K
R1/RRR1-21/2	1549.216	1548.681	-300.920	0.550	1963.542	0.572	22	0.364	R.AWSAADAVASWVGEK.K
R1/RRR1-13/2	1548.286	1548.681	-255.868	0.439	2113.259	0.487	23	0.363	R.AWSAADAVASWVGEK.K
R1/RRR1-21/2	1676.401	1676.854	-271.079	0.515	1975.694	0.552	23	0.360	R.AWSAADAVASWVGEKK.N
R1/RRR1-4/2	1549.951	1548.681	175.002	0.583	1915.407	0.578	22	0.357	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.146	1548.681	-994.395	0.451	2036.589	0.513	22	0.357	R.AWSAADAVASWVGEK.K
R1/RRR1-2/2	1548.468	1548.681	-138.024	0.497	1981.742	0.537	23	0.357	R.AWSAADAVASWVGEK.K
R1/RRR1-19/2	1549.271	1548.681	-265.347	0.559	1939.879	0.560	23	0.357	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1549.241	1548.681	-284.951	0.508	2008.278	0.518	23	0.355	R.AWSAADAVASWVGEK.K
R1/RRR1-2/2	1548.556	1548.681	-81.169	0.512	2018.886	0.511	23	0.354	R.AWSAADAVASWVGEK.K
R1/RRR1-24/2	1547.501	1548.681	-1412.636	0.389	2098.576	0.466	23	0.353	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.211	1548.681	-304.595	0.474	1987.626	0.521	23	0.352	R.AWSAADAVASWVGEK.K
R1/RRR1-6/2	1549.240	1548.681	-285.663	0.513	2045.491	0.494	23	0.352	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1676.329	1676.854	-912.295	0.542	1912.988	0.560	23	0.352	R.AWSAADAVASWVGEKK.N
R1/RRR1-21/2	1547.517	1548.681	-1402.574	0.340	2233.941	0.390	24	0.351	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1549.110	1548.681	278.003	0.470	1972.152	0.521	22	0.349	R.AWSAADAVASWVGEK.K
R1/RRR1-12/2	1549.245	1548.681	-282.106	0.525	1913.741	0.518	22	0.338	R.AWSAADAVASWVGEK.K
R1/RRR1-15/2	1549.541	1548.681	-90.757	0.547	1817.090	0.567	21	0.338	R.AWSAADAVASWVGEK.K
R1/RRR1-24/2	1547.967	1548.681	-1110.622	0.368	2179.277	0.373	23	0.337	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1549.519	1548.681	-104.665	0.515	1789.037	0.560	22	0.333	R.AWSAADAVASWVGEK.K
R1/RRR1-3/2	1549.379	1548.681	-195.156	0.558	1814.022	0.545	22	0.331	R.AWSAADAVASWVGEK.K
R1/RRR1-4/2	1549.206	1548.681	-307.324	0.516	1806.542	0.543	22	0.330	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.284	1548.681	-257.213	0.482	1853.405	0.518	22	0.330	R.AWSAADAVASWVGEK.K
R1/RRR1-21/2	1549.149	1548.681	302.892	0.543	1827.802	0.529	22	0.328	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1549.151	1548.681	304.472	0.546	1782.845	0.549	21	0.327	R.AWSAADAVASWVGEK.K
R1/RRR1-5/2	1549.494	1548.681	-121.102	0.542	1758.732	0.549	22	0.325	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1676.382	1676.854	-282.110	0.558	1695.665	0.579	23	0.324	R.AWSAADAVASWVGEKK.N
R1/RRR1-20/2	1547.425	1548.681	-1462.316	0.344	1998.998	0.425	22	0.323	R.AWSAADAVASWVGEK.K
R1/RRR1-23/2	1675.701	1676.854	-1288.268	0.494	1880.457	0.485	23	0.323	R.AWSAADAVASWVGEKK.N
R1/RRR1-18/2	1548.192	1548.681	-316.778	0.456	1853.671	0.498	21	0.323	R.AWSAADAVASWVGEK.K
R1/RRR1-21/2	1676.406	1676.854	-267.791	0.553	1678.920	0.573	22	0.319	R.AWSAADAVASWVGEKK.N
R1/RRR1-3/2	1548.081	1548.681	-1036.750	0.411	1788.089	0.512	22	0.318	R.AWSAADAVASWVGEK.K
R1/RRR1-16/2	1548.294	1548.681	-250.410	0.490	1687.372	0.543	21	0.312	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.324	1548.681	-231.427	0.429	1797.875	0.482	22	0.311	R.AWSAADAVASWVGEK.K
R1/RRR1-14/2	1548.096	1548.681	-1026.775	0.415	1828.693	0.466	22	0.311	R.AWSAADAVASWVGEK.K
R1/RRR1-23/2	1676.775	1676.854	-46.959	0.555	1626.692	0.558	23	0.309	R.AWSAADAVASWVGEKK.N
R1/RRR1-16/2	1548.232	1548.681	-290.594	0.473	1771.181	0.490	21	0.309	R.AWSAADAVASWVGEK.K
R1/RRR1-9/2	1548.445	1548.681	-152.655	0.406	1787.051	0.477	22	0.308	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.731	1548.681	32.523	0.474	1702.375	0.518	21	0.307	R.AWSAADAVASWVGEK.K
R1/RRR1-20/2	1549.419	1548.681	-169.864	0.573	1559.477	0.574	21	0.304	R.AWSAADAVASWVGEK.K
R1/RRR1-18/2	1548.105	1548.681	-1020.916	0.386	1899.859	0.398	22	0.302	R.AWSAADAVASWVGEK.K
R1/RRR1-21/2	1676.341	1676.854	-905.423	0.493	1696.585	0.499	22	0.301	R.AWSAADAVASWVGEKK.N
R1/RRR1-16/2	1547.560	1548.681	-1374.607	0.363	1805.920	0.434	22	0.298	R.AWSAADAVASWVGEK.K
R1/RRR1-5/2	1548.228	1548.681	-293.125	0.359	1843.293	0.415	22	0.298	R.AWSAADAVASWVGEK.K
R1/RRR1-13/2	1547.917	1548.681	-1143.009	0.372	1852.151	0.403	22	0.296	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1550.218	1548.681	-299.383	0.534	1491.183	0.574	21	0.296	R.AWSAADAVASWVGEK.K
R1/RRR1-14/2	1547.818	1548.681	-1206.996	0.370	1777.292	0.434	22	0.295	R.AWSAADAVASWVGEK.K
R1/RRR1-15/2	1548.400	1548.681	-182.232	0.484	1659.892	0.492	21	0.294	R.AWSAADAVASWVGEK.K
R1/RRR1-1/2	1549.218	1548.681	-299.734	0.539	1518.773	0.554	21	0.294	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1678.221	1676.854	219.262	0.570	1578.157	0.519	23	0.291	R.AWSAADAVASWVGEKK.N
R1/RRR1-18/2	1676.195	1676.854	-992.863	0.504	1603.406	0.507	21	0.290	R.AWSAADAVASWVGEKK.N
R1/RRR1-21/3	1384.574	1384.522	38.049	0.563	1908.852	0.613	28	0.289	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-25/2	1548.047	1548.681	-1058.602	0.377	1773.344	0.413	21	0.288	R.AWSAADAVASWVGEK.K
R1/RRR1-1/2	1676.282	1676.854	-940.514	0.509	1594.827	0.496	21	0.286	R.AWSAADAVASWVGEKK.N
R1/RRR1-23/2	1547.659	1548.681	-1310.123	0.336	1774.649	0.397	22	0.285	R.AWSAADAVASWVGEK.K
R1/RRR1-18/2	1677.328	1676.854	283.760	0.559	1544.834	0.507	23	0.284	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1405.180	1405.579	-284.888	0.511	1629.336	0.449	18	0.284	K.VCGHYTQVVWR.K
R1/RRR1-18/2	1548.466	1548.681	-139.369	0.441	1637.833	0.453	21	0.282	R.AWSAADAVASWVGEK.K
R1/RRR1-14/2	1548.125	1548.681	-1007.933	0.371	1745.215	0.399	22	0.282	R.AWSAADAVASWVGEK.K
R1/RRR1-1/2	1548.232	1548.681	-290.673	0.446	1567.859	0.481	20	0.280	R.AWSAADAVASWVGEK.K
R1/RRR1-2/2	1676.538	1676.854	-189.118	0.534	1493.084	0.506	22	0.277	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/3	1385.641	1384.522	86.486	0.605	1921.596	0.570	27	0.276	R.RADGVGPVSWDPK.V
R1/RRR1-14/2	1676.142	1676.854	-1024.158	0.482	1457.176	0.505	22	0.274	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/3	1383.711	1384.522	-1312.859	0.511	1843.959	0.604	27	0.273	R.RADGVGPVSWDPK.V
R1/RRR1-12/2	1547.941	1548.681	-1127.409	0.338	1673.119	0.397	21	0.272	R.AWSAADAVASWVGEK.K
R1/RRR1-9/2	1547.945	1548.681	-1124.479	0.368	1537.825	0.460	21	0.272	R.AWSAADAVASWVGEK.K
R1/RRR1-20/2	1677.490	1676.854	-217.403	0.583	1291.372	0.573	21	0.271	R.AWSAADAVASWVGEKK.N
R1/RRR1-16/2	1677.117	1676.854	157.644	0.534	1492.585	0.493	20	0.271	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1676.338	1676.854	-907.178	0.542	1329.431	0.554	21	0.271	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1406.128	1405.579	-322.312	0.526	1593.558	0.417	18	0.270	K.VCGHYTQVVWR.K
R1/RRR1-22/3	1384.738	1384.522	156.481	0.551	1854.641	0.590	27	0.270	R.RADGVGPVSWDPK.V
R1/RRR1-12/2	1676.530	1676.854	-193.865	0.526	1337.809	0.520	21	0.264	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1549.056	1548.681	243.077	0.469	1495.368	0.449	20	0.263	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1676.408	1676.854	-266.915	0.456	1429.206	0.475	21	0.263	R.AWSAADAVASWVGEKK.N
R1/RRR1-1/2	1676.293	1676.854	-934.081	0.514	1306.936	0.522	21	0.261	R.AWSAADAVASWVGEKK.N
R1/RRR1-3/2	1142.955	1143.274	-280.192	0.488	989.072	0.603	18	0.259	K.VASFAQSYAAK.R
R1/RRR1-14/2	1143.131	1143.274	-125.701	0.507	995.820	0.594	18	0.258	K.VASFAQSYAAK.R
R1/RRR1-22/2	1405.169	1405.579	-292.907	0.522	1415.103	0.444	17	0.258	K.VCGHYTQVVWR.K
R1/RRR1-20/2	1676.355	1676.854	-298.402	0.509	1327.116	0.498	21	0.258	R.AWSAADAVASWVGEKK.N
R1/RRR1-1/2	1142.996	1143.274	-243.868	0.482	1022.658	0.584	18	0.258	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1676.554	1676.854	-179.549	0.506	1246.608	0.527	21	0.257	R.AWSAADAVASWVGEKK.N
R1/RRR1-21/2	1675.342	1676.854	-2102.307	0.488	1296.117	0.504	21	0.256	R.AWSAADAVASWVGEKK.N
R1/RRR1-3/3	1385.609	1384.522	63.293	0.581	1721.926	0.620	27	0.256	R.RADGVGPVSWDPK.V
R1/RRR1-16/3	1385.509	1384.522	-9.475	0.568	1836.188	0.565	27	0.256	R.RADGVGPVSWDPK.V
R1/RRR1-4/2	1144.024	1143.274	-219.462	0.528	917.031	0.599	18	0.255	K.VASFAQSYAAK.R
R1/RRR1-9/2	1143.989	1143.274	-249.543	0.530	1003.076	0.570	18	0.255	K.VASFAQSYAAK.R
R1/RRR1-22/2	1142.924	1143.274	-307.516	0.495	1036.267	0.559	18	0.254	K.VASFAQSYAAK.R
R1/RRR1-22/2	1143.006	1143.274	-235.511	0.493	1027.200	0.561	18	0.254	K.VASFAQSYAAK.R
R1/RRR1-28/2	1142.981	1143.274	-257.154	0.532	1015.594	0.561	18	0.254	K.VASFAQSYAAK.R
R1/RRR1-6/2	1143.045	1143.274	-201.012	0.456	980.208	0.579	18	0.253	K.VASFAQSYAAK.R
R1/RRR1-2/2	1142.987	1143.274	-252.118	0.488	1028.382	0.553	18	0.252	K.VASFAQSYAAK.R
R1/RRR1-22/2	1227.941	1228.336	-322.020	0.452	1409.834	0.417	19	0.252	R.ADGVGPVSWDPK.V
R1/RRR1-21/2	1143.039	1143.274	-206.369	0.492	1066.719	0.537	18	0.252	K.VASFAQSYAAK.R
R1/RRR1-22/2	1405.125	1405.579	-324.459	0.512	1449.259	0.410	16	0.252	K.VCGHYTQVVWR.K
R1/RRR1-18/2	1143.000	1143.274	-240.011	0.489	1004.682	0.558	18	0.252	K.VASFAQSYAAK.R
R1/RRR1-13/2	1143.184	1143.274	-79.320	0.517	1016.869	0.550	18	0.252	K.VASFAQSYAAK.R
R1/RRR1-21/2	1405.962	1405.579	272.693	0.508	1388.816	0.424	17	0.251	K.VCGHYTQVVWR.K
R1/RRR1-6/2	1142.846	1143.274	-375.138	0.492	995.634	0.557	18	0.251	K.VASFAQSYAAK.R
R1/RRR1-22/2	1143.909	1143.274	-320.309	0.448	1182.841	0.493	18	0.251	K.VASFAQSYAAK.R
R1/RRR1-22/2	1405.229	1405.579	-250.201	0.536	1446.846	0.403	17	0.250	K.VCGHYTQVVWR.K
R1/RRR1-19/2	1143.033	1143.274	-211.083	0.478	977.994	0.558	18	0.250	K.VASFAQSYAAK.R
R1/RRR1-9/2	1142.973	1143.274	-264.012	0.461	903.094	0.586	18	0.250	K.VASFAQSYAAK.R
R1/RRR1-16/2	1143.115	1143.274	-139.091	0.484	997.187	0.548	18	0.249	K.VASFAQSYAAK.R
R1/RRR1-25/2	1144.075	1143.274	-174.612	0.553	911.106	0.565	18	0.248	K.VASFAQSYAAK.R
R1/RRR1-20/2	1142.900	1143.274	-327.770	0.437	935.667	0.574	18	0.248	K.VASFAQSYAAK.R
R1/RRR1-14/2	1143.070	1143.274	-179.157	0.516	965.589	0.550	18	0.248	K.VASFAQSYAAK.R
R1/RRR1-23/2	1143.068	1143.274	-181.085	0.454	984.372	0.552	18	0.248	K.VASFAQSYAAK.R
R1/RRR1-28/2	1142.665	1143.274	-1412.517	0.466	919.937	0.570	18	0.248	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1142.508	1143.274	-1550.310	0.426	958.892	0.565	18	0.248	K.VASFAQSYAAK.R
R1/RRR1-24/2	1142.933	1143.274	-299.372	0.445	959.848	0.557	18	0.247	K.VASFAQSYAAK.R
R1/RRR1-9/2	1142.889	1143.274	-337.950	0.529	876.981	0.570	18	0.247	K.VASFAQSYAAK.R
R1/RRR1-19/2	1143.978	1143.274	-259.071	0.506	907.325	0.563	18	0.247	K.VASFAQSYAAK.R
R1/RRR1-8/2	1143.111	1143.274	-143.376	0.481	1028.730	0.526	18	0.247	K.VASFAQSYAAK.R
R1/RRR1-21/2	1227.610	1228.336	-1409.725	0.410	1363.697	0.413	19	0.247	R.ADGVGPVSWDPK.V
R1/RRR1-22/2	1548.435	1548.681	-159.535	0.427	1379.284	0.421	20	0.247	R.AWSAADAVASWVGEK.K
R1/RRR1-1/2	1143.076	1143.274	-174.014	0.473	968.633	0.543	18	0.246	K.VASFAQSYAAK.R
R1/RRR1-12/2	1142.931	1143.274	-300.980	0.451	920.998	0.561	18	0.246	K.VASFAQSYAAK.R
R1/RRR1-22/2	1143.045	1143.274	-201.012	0.462	946.139	0.550	18	0.246	K.VASFAQSYAAK.R
R1/RRR1-13/2	1547.193	1548.681	-1612.732	0.347	1454.984	0.384	20	0.246	R.AWSAADAVASWVGEK.K
R1/RRR1-16/2	1143.099	1143.274	-153.232	0.469	992.265	0.531	18	0.246	K.VASFAQSYAAK.R
R1/RRR1-22/2	1676.585	1676.854	-160.997	0.504	1197.013	0.498	20	0.245	R.AWSAADAVASWVGEKK.N
R1/RRR1-2/2	1143.093	1143.274	-159.016	0.474	962.968	0.536	18	0.245	K.VASFAQSYAAK.R
R1/RRR1-22/2	1675.310	1676.854	-2121.715	0.385	1529.319	0.352	20	0.245	R.AWSAADAVASWVGEKK.N
R1/RRR1-7/2	1142.538	1143.274	-1523.478	0.408	967.050	0.547	18	0.244	K.VASFAQSYAAK.R
R1/RRR1-6/2	1142.930	1143.274	-301.944	0.508	851.545	0.572	17	0.244	K.VASFAQSYAAK.R
R1/RRR1-21/1	1142.557	1143.274	-1507.099	0.120	685.527	0.058	14	0.244	K.VASFAQSYAAK.R
R1/RRR1-1/2	1142.749	1143.274	-1338.806	0.427	994.927	0.529	18	0.244	K.VASFAQSYAAK.R
R1/RRR1-24/2	1142.997	1143.274	-242.582	0.462	934.027	0.542	18	0.244	K.VASFAQSYAAK.R
R1/RRR1-3/2	1676.314	1676.854	-921.068	0.456	1294.896	0.450	20	0.244	R.AWSAADAVASWVGEKK.N
R1/RRR1-27/2	1143.046	1143.274	-199.726	0.474	966.325	0.528	18	0.244	K.VASFAQSYAAK.R
R1/RRR1-22/3	1383.763	1384.522	-1274.984	0.535	1699.828	0.611	28	0.244	R.RADGVGPVSWDPK.V
R1/RRR1-19/2	1676.288	1676.854	-936.859	0.474	1378.779	0.412	21	0.243	R.AWSAADAVASWVGEKK.N
R1/RRR1-4/2	1143.054	1143.274	-192.655	0.502	955.534	0.524	18	0.243	K.VASFAQSYAAK.R
R1/RRR1-21/2	1142.535	1143.274	-1526.376	0.417	1020.822	0.511	18	0.242	K.VASFAQSYAAK.R
R1/RRR1-22/2	1228.202	1228.336	-109.318	0.459	1094.947	0.504	17	0.242	R.ADGVGPVSWDPK.V
R1/RRR1-22/3	1384.941	1384.522	303.786	0.546	1813.194	0.545	27	0.242	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1142.501	1143.274	-1556.320	0.419	1001.643	0.515	18	0.242	K.VASFAQSYAAK.R
R1/RRR1-13/2	1142.946	1143.274	-288.014	0.475	964.322	0.517	18	0.242	K.VASFAQSYAAK.R
R1/RRR1-12/2	1142.517	1143.274	-1542.797	0.439	957.072	0.520	18	0.241	K.VASFAQSYAAK.R
R1/RRR1-13/2	1142.968	1143.274	-268.298	0.454	930.893	0.526	18	0.241	K.VASFAQSYAAK.R
R1/RRR1-22/2	1405.031	1405.579	-1105.269	0.473	1258.312	0.431	16	0.241	K.VCGHYTQVVWR.K
R1/RRR1-22/2	1143.713	1143.274	385.214	0.430	1111.312	0.466	18	0.240	K.VASFAQSYAAK.R
R1/RRR1-4/2	1142.542	1143.274	-1520.795	0.378	1035.973	0.504	18	0.240	K.VASFAQSYAAK.R
R1/RRR1-8/2	1143.715	1143.274	386.926	0.487	869.773	0.529	18	0.239	K.VASFAQSYAAK.R
R1/RRR1-23/2	1406.283	1405.579	-211.357	0.474	1321.974	0.393	17	0.239	K.VCGHYTQVVWR.K
R1/RRR1-21/2	1676.225	1676.854	-974.658	0.501	1111.886	0.495	20	0.238	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1227.982	1228.336	-289.007	0.429	1162.520	0.454	18	0.238	R.ADGVGPVSWDPK.V
R1/RRR1-21/2	1142.521	1143.274	-1538.933	0.414	1007.424	0.488	18	0.237	K.VASFAQSYAAK.R
R1/RRR1-22/2	1142.994	1143.274	-245.797	0.420	930.025	0.508	18	0.237	K.VASFAQSYAAK.R
R1/RRR1-22/2	1143.945	1143.274	-288.297	0.471	967.708	0.488	18	0.237	K.VASFAQSYAAK.R
R1/RRR1-4/2	1676.416	1676.854	-262.166	0.474	1142.309	0.472	20	0.236	R.AWSAADAVASWVGEKK.N
R1/RRR1-24/2	1142.425	1143.274	-1623.622	0.380	954.434	0.509	18	0.236	K.VASFAQSYAAK.R
R1/RRR1-17/2	1142.887	1143.274	-339.665	0.439	908.406	0.508	18	0.236	K.VASFAQSYAAK.R
R1/RRR1-21/3	1384.486	1384.522	-26.019	0.546	1634.017	0.606	26	0.236	R.RADGVGPVSWDPK.V
R1/RRR1-23/2	1143.201	1143.274	-63.683	0.443	986.118	0.477	18	0.235	K.VASFAQSYAAK.R
R1/RRR1-10/2	1143.139	1143.274	-118.524	0.476	1022.402	0.463	18	0.235	K.VASFAQSYAAK.R
R1/RRR1-1/2	1675.833	1676.854	-1209.335	0.488	1047.097	0.497	20	0.235	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1676.249	1676.854	-960.401	0.472	1142.073	0.469	19	0.234	R.AWSAADAVASWVGEKK.N
R1/RRR1-19/2	1228.091	1228.336	-199.454	0.406	1134.614	0.445	18	0.234	R.ADGVGPVSWDPK.V
R1/RRR1-22/2	1585.144	1585.607	-292.478	0.424	1108.363	0.471	17	0.234	K.NYHYDTNTCDPGK.V
R1/RRR1-2/2	1143.134	1143.274	-122.380	0.506	867.461	0.489	18	0.233	K.VASFAQSYAAK.R
R1/RRR1-26/2	1143.091	1143.274	-160.409	0.438	741.384	0.540	17	0.233	K.VASFAQSYAAK.R
R1/RRR1-3/2	1142.476	1143.274	-1578.217	0.372	864.316	0.516	18	0.232	K.VASFAQSYAAK.R
R1/RRR1-22/2	1548.090	1548.681	-1030.733	0.373	1306.416	0.381	19	0.232	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1142.955	1143.274	-279.441	0.417	800.611	0.515	18	0.232	K.VASFAQSYAAK.R
R1/RRR1-17/2	1142.503	1143.274	-1554.281	0.417	846.951	0.500	18	0.232	K.VASFAQSYAAK.R
R1/RRR1-19/2	1142.548	1143.274	-1515.107	0.380	980.426	0.468	18	0.232	K.VASFAQSYAAK.R
R1/RRR1-22/2	1142.548	1143.274	-1515.536	0.395	817.717	0.523	17	0.231	K.VASFAQSYAAK.R
R1/RRR1-1/3	1384.504	1384.522	-13.152	0.542	1654.560	0.594	27	0.231	R.RADGVGPVSWDPK.V
R1/RRR1-21/2	1676.354	1676.854	-298.914	0.481	1021.247	0.483	20	0.230	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1675.548	1676.854	-1380.385	0.462	1050.583	0.476	19	0.230	R.AWSAADAVASWVGEKK.N
R1/RRR1-26/2	1144.247	1143.274	-23.606	0.470	654.566	0.527	17	0.229	K.VASFAQSYAAK.R
R1/RRR1-22/2	1585.174	1585.607	-273.781	0.416	1086.118	0.453	17	0.229	K.NYHYDTNTCDPGK.V
R1/RRR1-22/2	1676.459	1676.854	-236.233	0.438	1042.426	0.472	19	0.229	R.AWSAADAVASWVGEKK.N
R1/RRR1-6/2	1548.404	1548.681	-179.306	0.428	1186.316	0.416	18	0.229	R.AWSAADAVASWVGEK.K
R1/RRR1-5/2	1142.454	1143.274	-1597.860	0.386	825.901	0.491	18	0.228	K.VASFAQSYAAK.R
R1/RRR1-7/2	1142.386	1143.274	-1657.866	0.361	923.620	0.469	18	0.228	K.VASFAQSYAAK.R
R1/RRR1-28/2	1142.533	1143.274	-1528.093	0.446	739.194	0.494	17	0.227	K.VASFAQSYAAK.R
R1/RRR1-22/2	1385.175	1384.522	-251.437	0.499	709.924	0.490	21	0.227	R.RADGVGPVSWDPK.V
R1/RRR1-21/3	1548.551	1548.681	-84.301	0.478	1839.261	0.478	29	0.227	R.AWSAADAVASWVGEK.K
R1/RRR1-18/2	1675.813	1676.854	-1221.624	0.484	949.201	0.490	19	0.226	R.AWSAADAVASWVGEKK.N
R1/RRR1-20/2	1228.173	1228.336	-132.648	0.359	1282.988	0.340	19	0.226	R.ADGVGPVSWDPK.V
R1/RRR1-6/2	1547.830	1548.681	-1199.077	0.307	1337.553	0.333	19	0.226	R.AWSAADAVASWVGEK.K
R1/RRR1-16/2	1676.263	1676.854	-952.066	0.485	972.629	0.479	19	0.226	R.AWSAADAVASWVGEKK.N
R1/RRR1-12/2	1142.585	1143.274	-1482.160	0.441	684.387	0.508	16	0.225	K.VASFAQSYAAK.R
R1/RRR1-26/2	1142.370	1143.274	-1671.823	0.337	867.875	0.470	18	0.225	K.VASFAQSYAAK.R
R1/RRR1-22/1	1548.873	1548.681	124.265	0.348	487.419	0.501	16	0.225	R.AWSAADAVASWVGEK.K
R1/RRR1-18/2	1142.467	1143.274	-1586.160	0.377	588.459	0.544	16	0.224	K.VASFAQSYAAK.R
R1/RRR1-22/2	1585.961	1585.607	223.988	0.463	1119.190	0.407	18	0.224	K.NYHYDTNTCDPGK.V
R1/RRR1-15/2	1548.220	1548.681	-298.425	0.408	1180.847	0.379	19	0.223	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1229.010	1228.336	-265.753	0.430	1174.803	0.364	18	0.223	R.ADGVGPVSWDPK.V
R1/RRR1-21/2	1228.054	1228.336	-229.769	0.414	985.595	0.433	17	0.222	R.ADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1142.332	1143.274	-1705.104	0.358	719.688	0.486	17	0.222	K.VASFAQSYAAK.R
R1/RRR1-22/2	1675.414	1676.854	-1460.735	0.392	1080.363	0.412	19	0.221	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1384.260	1384.522	-189.866	0.453	571.149	0.478	20	0.221	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1384.270	1384.522	-182.788	0.443	659.548	0.458	21	0.221	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1142.396	1143.274	-1649.171	0.340	833.361	0.438	18	0.220	K.VASFAQSYAAK.R
R1/RRR1-22/3	1548.647	1548.681	-21.917	0.501	1665.489	0.536	28	0.220	R.AWSAADAVASWVGEK.K
R1/RRR1-20/2	1228.108	1228.336	-186.192	0.374	1027.798	0.405	17	0.219	R.ADGVGPVSWDPK.V
R1/RRR1-21/2	1228.045	1228.336	-237.248	0.370	927.441	0.441	17	0.219	R.ADGVGPVSWDPK.V
R1/RRR1-25/2	1142.454	1143.274	-1598.182	0.445	609.504	0.465	16	0.219	K.VASFAQSYAAK.R
R1/RRR1-21/2	1585.038	1585.607	-992.338	0.384	1021.552	0.423	17	0.219	K.NYHYDTNTCDPGK.V
R1/RRR1-21/2	1405.073	1405.579	-1075.260	0.440	1163.544	0.350	16	0.219	K.VCGHYTQVVWR.K
R1/RRR1-20/2	1383.662	1384.522	-1348.512	0.479	452.425	0.489	18	0.219	R.RADGVGPVSWDPK.V
R1/RRR1-16/2	1142.505	1143.274	-1552.886	0.362	675.061	0.464	17	0.219	K.VASFAQSYAAK.R
R1/RRR1-22/2	1383.876	1384.522	-1193.210	0.409	592.887	0.466	20	0.219	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1675.297	1676.854	-2129.185	0.418	1040.600	0.419	18	0.218	R.AWSAADAVASWVGEKK.N
R1/RRR1-21/2	1405.268	1405.579	-222.139	0.436	1298.646	0.298	16	0.218	K.VCGHYTQVVWR.K
R1/RRR1-21/2	1585.106	1585.607	-949.349	0.428	1121.342	0.376	17	0.218	K.NYHYDTNTCDPGK.V
R1/RRR1-22/2	1384.199	1384.522	-234.278	0.450	543.467	0.448	20	0.218	R.RADGVGPVSWDPK.V
R1/RRR1-20/2	1384.201	1384.522	-232.685	0.410	670.013	0.430	21	0.217	R.RADGVGPVSWDPK.V
R1/RRR1-21/2	1404.304	1405.579	-1625.125	0.380	1058.842	0.382	15	0.217	K.VCGHYTQVVWR.K
R1/RRR1-22/2	1142.991	1143.274	-248.582	0.349	904.683	0.388	18	0.217	K.VASFAQSYAAK.R
R1/RRR1-22/2	1227.757	1228.336	-1289.688	0.364	1271.402	0.289	18	0.216	R.ADGVGPVSWDPK.V
R1/RRR1-21/2	1384.195	1384.522	-236.666	0.439	585.250	0.430	20	0.216	R.RADGVGPVSWDPK.V
R1/RRR1-10/2	1142.440	1143.274	-1610.204	0.356	593.430	0.460	16	0.216	K.VASFAQSYAAK.R
R1/RRR1-15/2	1676.557	1676.854	-177.504	0.503	1004.927	0.420	19	0.216	-.AWSAADAVASWVGEKK.-
R1/RRR1-24/2	1385.229	1384.522	-211.830	0.423	616.667	0.427	20	0.215	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1228.040	1228.336	-241.636	0.334	1071.999	0.373	16	0.215	R.ADGVGPVSWDPK.V
R1/RRR1-18/2	1384.236	1384.522	-207.294	0.455	434.813	0.469	17	0.215	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1142.488	1143.274	-1567.698	0.328	697.144	0.438	17	0.215	K.VASFAQSYAAK.R
R1/RRR1-21/2	1585.019	1585.607	-1004.401	0.389	958.067	0.425	16	0.215	K.NYHYDTNTCDPGK.V
R1/RRR1-20/2	1144.223	1143.274	-45.007	0.308	323.965	0.483	16	0.215	K.VASFAQSYAAK.R
R1/RRR1-22/1	1548.779	1548.681	63.480	0.352	416.807	0.577	16	0.215	R.AWSAADAVASWVGEK.K
R1/RRR1-21/1	1142.576	1143.274	-1490.572	0.159	600.815	0.185	13	0.214	K.VASFAQSYAAK.R
R1/RRR1-21/2	1384.162	1384.522	-261.174	0.422	602.636	0.410	20	0.214	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1678.344	1676.854	292.999	0.471	717.605	0.477	18	0.214	R.AWSAADAVASWVGEKK.N
R1/RRR1-22/2	1548.843	1548.681	105.089	0.357	1110.901	0.350	18	0.214	R.AWSAADAVASWVGEK.K
R1/RRR1-23/2	1384.135	1384.522	-280.640	0.409	594.702	0.410	20	0.213	R.RADGVGPVSWDPK.V
R1/RRR1-19/2	1676.300	1676.854	-929.621	0.452	1040.264	0.357	22	0.213	R.AWSAADAVASWVGEKK.N
R1/RRR1-27/2	1142.230	1143.274	-1794.868	0.339	504.476	0.455	15	0.213	K.VASFAQSYAAK.R
R1/RRR1-22/2	1143.001	1143.274	-239.154	0.291	740.114	0.421	17	0.212	K.VASFAQSYAAK.R
R1/RRR1-21/2	1384.021	1384.522	-1087.989	0.405	571.658	0.403	19	0.211	R.RADGVGPVSWDPK.V
R1/RRR1-19/2	1228.272	1228.336	-52.294	0.408	1116.240	0.318	17	0.211	R.ADGVGPVSWDPK.V
R1/RRR1-22/2	1143.026	1143.274	-217.297	0.336	594.392	0.403	16	0.210	K.VASFAQSYAAK.R
R1/RRR1-22/2	1384.107	1384.522	-300.372	0.367	571.860	0.382	20	0.210	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1384.194	1384.522	-237.551	0.391	529.475	0.385	19	0.210	R.RADGVGPVSWDPK.V
R1/RRR1-19/3	1384.507	1384.522	-11.162	0.565	1623.139	0.551	27	0.210	R.RADGVGPVSWDPK.V
R1/RRR1-23/2	1384.036	1384.522	-352.050	0.417	418.791	0.400	17	0.210	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1142.382	1143.274	-1661.302	0.306	568.818	0.431	15	0.210	K.VASFAQSYAAK.R
R1/RRR1-22/2	1384.064	1384.522	-332.050	0.389	452.782	0.372	18	0.209	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1142.307	1143.274	-1727.007	0.319	667.382	0.365	17	0.208	K.VASFAQSYAAK.R
R1/RRR1-16/2	1384.412	1384.522	-79.473	0.388	502.626	0.349	19	0.208	R.RADGVGPVSWDPK.V
R1/RRR1-17/2	1384.306	1384.522	-156.781	0.399	411.901	0.368	17	0.208	R.RADGVGPVSWDPK.V
R1/RRR1-15/2	1385.358	1384.522	-119.012	0.438	489.974	0.355	18	0.207	R.RADGVGPVSWDPK.V
R1/RRR1-25/2	1675.868	1676.854	-1188.708	0.408	641.438	0.445	17	0.207	R.AWSAADAVASWVGEKK.N
R1/RRR1-17/2	1675.407	1676.854	-1464.687	0.435	419.605	0.476	16	0.207	R.AWSAADAVASWVGEKK.N
R1/RRR1-24/2	1384.037	1384.522	-351.165	0.363	431.919	0.366	17	0.207	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1384.121	1384.522	-290.461	0.376	450.771	0.336	18	0.207	R.RADGVGPVSWDPK.V
R1/RRR1-12/2	1385.330	1384.522	-138.988	0.372	357.316	0.339	16	0.206	R.RADGVGPVSWDPK.V
R1/RRR1-4/2	1385.550	1384.522	20.182	0.403	400.773	0.325	17	0.206	R.RADGVGPVSWDPK.V
R1/RRR1-19/2	1383.785	1384.522	-1259.117	0.380	457.359	0.323	18	0.206	R.RADGVGPVSWDPK.V
R1/RRR1-18/2	1383.604	1384.522	-1390.425	0.370	483.084	0.335	18	0.206	R.RADGVGPVSWDPK.V
R1/RRR1-12/2	1384.080	1384.522	-320.104	0.326	287.432	0.310	15	0.206	R.RADGVGPVSWDPK.V
R1/RRR1-2/2	1384.126	1384.522	-286.834	0.353	470.468	0.333	18	0.206	R.RADGVGPVSWDPK.V
R1/RRR1-16/2	1384.299	1384.522	-161.557	0.416	464.166	0.312	18	0.205	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1383.237	1384.522	-1656.514	0.304	464.196	0.345	18	0.205	R.RADGVGPVSWDPK.V
R1/RRR1-23/2	1383.672	1384.522	-1341.070	0.360	432.942	0.388	18	0.205	-.RADGVGPVSWDPK.-
R1/RRR1-22/2	1300.208	1299.460	-194.229	0.388	919.962	0.365	16	0.205	K.VASFAQSYAAKR.A
R1/RRR1-13/2	1384.348	1384.522	-126.351	0.366	550.136	0.310	19	0.204	R.RADGVGPVSWDPK.V
R1/RRR1-10/2	1550.197	1548.681	-313.209	0.361	756.633	0.381	17	0.204	R.AWSAADAVASWVGEK.K
R1/RRR1-2/2	1384.283	1384.522	-173.234	0.372	374.732	0.297	16	0.204	R.RADGVGPVSWDPK.V
R1/RRR1-14/2	1383.716	1384.522	-1309.173	0.358	453.186	0.309	17	0.204	R.RADGVGPVSWDPK.V
R1/RRR1-18/3	1384.972	1384.522	325.925	0.563	1574.865	0.555	27	0.203	R.RADGVGPVSWDPK.V
R1/RRR1-9/2	1383.932	1384.522	-1152.553	0.345	465.822	0.279	18	0.203	R.RADGVGPVSWDPK.V
R1/RRR1-3/2	1384.973	1384.522	326.686	0.400	527.303	0.348	19	0.203	-.RADGVGPVSWDPK.-
R1/RRR1-22/2	1142.224	1143.274	-1800.022	0.257	859.384	0.301	18	0.203	K.VASFAQSYAAK.R
R1/RRR1-22/2	1549.307	1548.681	-242.344	0.358	622.673	0.384	17	0.203	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1678.275	1676.854	251.500	0.381	584.541	0.408	17	0.203	R.AWSAADAVASWVGEKK.N
R1/RRR1-14/2	1384.414	1384.522	-78.500	0.358	499.555	0.279	18	0.203	R.RADGVGPVSWDPK.V
R1/RRR1-19/2	1385.008	1384.522	351.872	0.439	400.462	0.350	17	0.202	-.RADGVGPVSWDPK.-
R1/RRR1-4/2	1384.142	1384.522	-275.685	0.406	389.601	0.337	17	0.202	-.RADGVGPVSWDPK.-
R1/RRR1-22/2	1144.212	1143.274	-54.424	0.268	511.686	0.310	15	0.202	K.VASFAQSYAAK.R
R1/RRR1-2/2	1385.465	1384.522	-41.589	0.379	493.911	0.268	18	0.202	R.RADGVGPVSWDPK.V
R1/RRR1-19/2	1384.101	1384.522	-304.973	0.374	337.561	0.333	16	0.202	-.RADGVGPVSWDPK.-
R1/RRR1-16/2	1383.605	1384.522	-1389.716	0.364	497.227	0.232	19	0.202	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1384.133	1384.522	-281.879	0.341	595.372	0.258	20	0.202	R.RADGVGPVSWDPK.V
R1/RRR1-20/2	1384.077	1384.522	-322.759	0.340	358.877	0.316	16	0.201	-.RADGVGPVSWDPK.-
R1/RRR1-22/1	1548.761	1548.681	52.018	0.313	418.950	0.524	16	0.201	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1383.153	1384.522	-1717.871	0.316	339.847	0.270	16	0.201	-.RADGVGPVSWDPK.-
R1/RRR1-12/2	1384.153	1384.522	-267.191	0.375	636.374	0.247	20	0.200	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1143.780	1143.274	-433.172	0.251	459.120	0.318	13	0.200	K.VASFAQSYAAK.R
R1/RRR1-14/2	1384.379	1384.522	-103.796	0.394	448.764	0.308	17	0.200	-.RADGVGPVSWDPK.-
R1/RRR1-15/2	1384.193	1384.522	-238.524	0.359	487.415	0.279	18	0.199	-.RADGVGPVSWDPK.-
R1/RRR1-24/2	1384.128	1384.522	-285.595	0.403	448.262	0.266	18	0.199	-.RADGVGPVSWDPK.-
R1/RRR1-22/2	1142.226	1143.274	-1797.875	0.205	799.505	0.296	17	0.199	K.VASFAQSYAAK.R
R1/RRR1-21/2	1548.081	1548.681	-1036.275	0.326	792.936	0.329	16	0.198	R.AWSAADAVASWVGEK.K
R1/RRR1-17/2	1384.284	1384.522	-172.704	0.381	295.519	0.336	15	0.198	-.RADGVGPVSWDPK.-
R1/RRR1-22/2	1383.214	1384.522	-1673.891	0.282	645.925	0.192	20	0.197	R.RADGVGPVSWDPK.V
R1/RRR1-3/2	1675.702	1676.854	-1288.049	0.415	816.794	0.316	18	0.197	R.AWSAADAVASWVGEKK.N
R1/RRR1-8/2	1548.383	1548.681	-193.226	0.326	754.886	0.332	15	0.197	R.AWSAADAVASWVGEK.K
R1/RRR1-5/2	1384.119	1384.522	-292.231	0.321	285.039	0.321	14	0.197	-.RADGVGPVSWDPK.-
R1/RRR1-22/2	1384.252	1384.522	-195.351	0.372	370.151	0.286	16	0.196	-.RADGVGPVSWDPK.-
R1/RRR1-24/2	1406.074	1405.579	352.521	0.426	937.265	0.251	16	0.196	K.VCGHYTQVVWR.K
R1/RRR1-1/2	1405.096	1405.579	-345.205	0.377	867.383	0.266	15	0.196	K.VCGHYTQVVWR.K
R1/RRR1-21/3	1384.692	1384.522	123.328	0.559	1451.652	0.570	25	0.195	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1383.463	1384.522	-1493.050	0.354	352.220	0.331	16	0.194	-.RADGVGPVSWDPK.-
R1/RRR1-11/2	1547.415	1548.681	-1468.576	0.298	866.677	0.223	17	0.191	R.AWSAADAVASWVGEK.K
R1/RRR1-22/2	1548.028	1548.681	-1070.636	0.274	685.530	0.241	15	0.190	R.AWSAADAVASWVGEK.K
R1/RRR1-12/3	1385.585	1384.522	45.798	0.544	1439.209	0.553	24	0.190	R.RADGVGPVSWDPK.V
R1/RRR1-11/2	1547.455	1548.681	-1442.428	0.264	891.491	0.188	17	0.189	R.AWSAADAVASWVGEK.K
R1/RRR1-9/3	1384.122	1384.522	-289.542	0.522	1468.487	0.548	25	0.189	R.RADGVGPVSWDPK.V
R1/RRR1-2/3	1384.518	1384.522	-2.805	0.501	1474.293	0.552	26	0.188	R.RADGVGPVSWDPK.V
R1/RRR1-21/2	1298.501	1299.460	-1513.140	0.316	709.720	0.252	16	0.187	K.VASFAQSYAAKR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1584.226	1585.607	-1507.177	0.215	815.949	0.238	14	0.185	K.NYHYDTNTCDPGK.V
R1/RRR1-20/3	1384.594	1384.522	52.374	0.541	1434.727	0.543	25	0.183	R.RADGVGPVSWDPK.V
R1/RRR1-22/2	1675.185	1676.854	-2196.789	0.308	952.516	0.137	17	0.182	R.AWSAADAVASWVGEKK.N
R1/RRR1-2/2	1228.059	1228.336	-226.378	0.327	900.221	0.102	16	0.182	R.ADGVGPVSWDPK.V
R1/RRR1-18/2	1228.140	1228.336	-159.569	0.250	827.767	0.084	14	0.182	-.ADGVGPVSWDPK.-
R1/RRR1-1/3	1384.454	1384.522	-49.500	0.542	1296.493	0.571	24	0.176	R.RADGVGPVSWDPK.V
R1/RRR1-7/3	1384.336	1384.522	-135.074	0.535	1418.204	0.535	26	0.175	R.RADGVGPVSWDPK.V
R1/RRR1-15/3	1384.161	1384.522	-261.272	0.460	1335.800	0.559	24	0.175	R.RADGVGPVSWDPK.V
R1/RRR1-21/3	1384.387	1384.522	-97.924	0.443	1705.753	0.405	26	0.172	R.RADGVGPVSWDPK.V
R1/RRR1-22/3	1384.515	1384.522	-4.795	0.533	1321.489	0.548	24	0.172	R.RADGVGPVSWDPK.V
R1/RRR1-3/3	1383.874	1384.522	-1194.592	0.491	1352.027	0.533	25	0.167	R.RADGVGPVSWDPK.V
R1/RRR1-2/3	1384.518	1384.522	-3.070	0.512	1332.352	0.535	25	0.166	R.RADGVGPVSWDPK.V
R1/RRR1-22/3	1385.408	1384.522	-82.253	0.505	1272.698	0.546	24	0.164	R.RADGVGPVSWDPK.V
R1/RRR1-20/3	1384.333	1384.522	-136.799	0.548	1202.296	0.570	24	0.164	R.RADGVGPVSWDPK.V
R1/RRR1-3/3	1384.849	1384.522	236.702	0.522	1120.979	0.604	24	0.163	R.RADGVGPVSWDPK.V
R1/RRR1-23/3	1384.679	1384.522	113.382	0.518	1339.186	0.522	25	0.163	R.RADGVGPVSWDPK.V
R1/RRR1-1/3	1383.754	1384.522	-1281.496	0.480	1153.617	0.563	23	0.157	R.RADGVGPVSWDPK.V
R1/RRR1-9/3	1383.953	1384.522	-1136.931	0.488	1206.493	0.540	24	0.154	R.RADGVGPVSWDPK.V
R1/RRR1-15/3	1383.921	1384.522	-1160.579	0.531	1249.670	0.525	25	0.154	R.RADGVGPVSWDPK.V
R1/RRR1-7/3	1384.318	1384.522	-147.546	0.457	1189.803	0.543	24	0.152	R.RADGVGPVSWDPK.V
R1/RRR1-23/1	1142.624	1143.274	-1448.720	0.134	439.703	0.251	12	0.152	K.VASFAQSYAAK.R
R1/RRR1-11/3	1384.601	1384.522	57.414	0.542	999.298	0.580	22	0.150	R.RADGVGPVSWDPK.V
R1/RRR1-12/3	1384.052	1384.522	-340.644	0.458	1196.453	0.533	25	0.148	R.RADGVGPVSWDPK.V
R1/RRR1-12/3	1384.403	1384.522	-86.248	0.509	1060.848	0.542	21	0.147	R.RADGVGPVSWDPK.V
R1/RRR1-16/3	1384.302	1384.522	-159.621	0.464	1187.251	0.512	23	0.146	R.RADGVGPVSWDPK.V
R1/RRR1-18/3	1384.308	1384.522	-155.110	0.536	1030.495	0.564	23	0.146	R.RADGVGPVSWDPK.V
R1/RRR1-15/3	1384.364	1384.522	-114.641	0.497	1050.502	0.543	22	0.144	R.RADGVGPVSWDPK.V
R1/RRR1-19/3	1384.689	1384.522	120.941	0.524	1050.775	0.539	22	0.144	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	1384.357	1384.522	-119.285	0.538	1067.080	0.539	22	0.143	-.RADGVGPVSWDPK.-
R1/RRR1-22/3	1384.568	1384.522	33.142	0.499	1067.193	0.524	23	0.139	R.RADGVGPVSWDPK.V
R1/RRR1-17/3	1384.799	1384.522	200.770	0.527	926.592	0.579	24	0.139	R.RADGVGPVSWDPK.V
R1/RRR1-20/3	1383.834	1384.522	-1223.426	0.502	1025.733	0.551	25	0.138	R.RADGVGPVSWDPK.V
R1/RRR1-22/1	1142.570	1143.274	-1495.724	0.115	432.012	0.156	12	0.137	K.VASFAQSYAAK.R
R1/RRR1-4/1	1144.220	1143.274	-47.189	0.264	372.523	0.308	12	0.136	K.VASFAQSYAAK.R
R1/RRR1-19/3	1384.649	1384.522	92.295	0.562	1029.272	0.510	22	0.135	R.RADGVGPVSWDPK.V
R1/RRR1-7/3	1384.323	1384.522	-144.495	0.462	1080.904	0.511	25	0.132	R.RADGVGPVSWDPK.V
R1/RRR1-4/3	1383.939	1384.522	-1147.293	0.485	1083.670	0.485	23	0.130	R.RADGVGPVSWDPK.V
R1/RRR1-18/3	1384.582	1384.522	43.753	0.527	957.690	0.501	21	0.129	R.RADGVGPVSWDPK.V
R1/RRR1-17/3	1385.564	1384.522	30.423	0.541	873.403	0.538	23	0.128	R.RADGVGPVSWDPK.V
R1/RRR1-21/3	1548.709	1548.681	18.284	0.499	1050.435	0.480	24	0.128	R.AWSAADAVASWVGEK.K
R1/RRR1-22/3	1548.176	1548.681	-974.653	0.490	991.188	0.498	26	0.124	R.AWSAADAVASWVGEK.K
R1/RRR1-16/3	1384.144	1384.522	-273.615	0.465	999.399	0.478	23	0.122	R.RADGVGPVSWDPK.V
R1/RRR1-21/3	1548.394	1548.681	-185.721	0.465	1116.272	0.459	28	0.122	R.AWSAADAVASWVGEK.K
R1/RRR1-22/3	1384.397	1384.522	-90.892	0.504	551.341	0.546	22	0.117	R.RADGVGPVSWDPK.V
R1/RRR1-9/3	1384.291	1384.522	-167.184	0.439	846.814	0.492	22	0.114	-.RADGVGPVSWDPK.-
R1/RRR1-26/3	1384.426	1384.522	-69.532	0.455	540.505	0.512	20	0.113	R.RADGVGPVSWDPK.V
R1/RRR1-23/3	1405.928	1405.579	248.698	0.570	1233.598	0.391	24	0.111	K.VCGHYTQVVWR.K
R1/RRR1-26/3	1384.630	1384.522	78.237	0.462	757.429	0.488	24	0.110	R.RADGVGPVSWDPK.V
R1/RRR1-23/3	1384.232	1384.522	-209.913	0.467	1043.974	0.405	23	0.110	R.RADGVGPVSWDPK.V
R1/RRR1-26/3	1384.750	1384.522	164.968	0.466	503.242	0.520	20	0.109	-.RADGVGPVSWDPK.-
R1/RRR1-11/3	1384.048	1384.522	-343.431	0.448	516.747	0.516	20	0.109	-.RADGVGPVSWDPK.-
R1/RRR1-17/3	1384.181	1384.522	-247.072	0.421	483.767	0.517	21	0.107	-.RADGVGPVSWDPK.-
R1/RRR1-4/3	1404.411	1405.579	-1548.510	0.394	301.736	0.292	17	0.105	K.VCGHYTQVVWR.K
R1/RRR1-13/3	1385.814	1384.522	211.181	0.464	739.015	0.445	23	0.105	R.RADGVGPVSWDPK.V
R1/RRR1-22/3	1384.429	1384.522	-67.675	0.476	665.216	0.452	23	0.105	R.RADGVGPVSWDPK.V
R1/RRR1-22/3	1384.004	1384.522	-1100.132	0.407	492.577	0.448	21	0.104	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/3	1384.255	1384.522	-193.326	0.415	589.380	0.440	24	0.101	R.RADGVGPVSWDPK.V
R1/RRR1-14/3	1384.822	1384.522	217.212	0.355	434.759	0.406	22	0.101	R.RADGVGPVSWDPK.V
R1/RRR1-22/3	1406.865	1405.579	203.583	0.582	998.527	0.385	22	0.100	K.VCGHYTQVVWR.K
R1/RRR1-14/3	1384.766	1384.522	176.770	0.405	432.635	0.436	20	0.100	-.RADGVGPVSWDPK.-
R1/RRR1-21/3	1405.963	1405.579	273.380	0.527	828.564	0.412	21	0.100	K.VCGHYTQVVWR.K
R1/RRR1-23/3	1406.775	1405.579	139.757	0.567	1085.602	0.361	22	0.100	K.VCGHYTQVVWR.K
R1/RRR1-13/3	1384.393	1384.522	-93.147	0.407	432.394	0.513	21	0.098	-.RADGVGPVSWDPK.-
R1/RRR1-22/3	1406.829	1405.579	178.131	0.569	1198.950	0.340	24	0.098	K.VCGHYTQVVWR.K
R1/RRR1-16/3	1405.568	1405.579	-8.512	0.532	945.659	0.386	22	0.098	K.VCGHYTQVVWR.K
R1/RRR1-4/3	1405.266	1405.579	-223.892	0.372	436.717	0.305	20	0.097	K.VCGHYTQVVWR.K
R1/RRR1-22/3	1585.596	1585.607	-7.044	0.328	595.025	0.478	24	0.096	K.NYHYDTNTCDPGK.V
R1/RRR1-23/3	1585.673	1585.607	42.065	0.486	776.672	0.435	28	0.095	K.NYHYDTNTCDPGK.V
R1/RRR1-19/3	1404.853	1405.579	-1232.967	0.528	784.888	0.374	21	0.094	K.VCGHYTQVVWR.K
R1/RRR1-21/3	1406.571	1405.579	-5.938	0.564	833.048	0.368	21	0.094	K.VCGHYTQVVWR.K
R1/RRR1-21/3	1405.721	1405.579	100.841	0.548	961.313	0.364	21	0.094	-.VCGHYTQVVWR.-
R1/RRR1-3/3	1405.135	1405.579	-316.973	0.508	716.687	0.372	21	0.094	K.VCGHYTQVVWR.K
R1/RRR1-22/3	1405.785	1405.579	146.300	0.513	791.416	0.351	20	0.092	K.VCGHYTQVVWR.K
R1/RRR1-20/3	1405.463	1405.579	-82.996	0.524	714.979	0.340	19	0.092	K.VCGHYTQVVWR.K
R1/RRR1-18/3	1548.761	1548.681	51.961	0.387	547.524	0.431	22	0.092	-.AWSAADAVASWVGEK.-
R1/RRR1-20/3	1405.770	1405.579	135.981	0.513	662.010	0.323	18	0.092	K.VCGHYTQVVWR.K
R1/RRR1-18/3	1405.290	1405.579	-206.899	0.482	495.761	0.325	18	0.092	-.VCGHYTQVVWR.-
R1/RRR1-22/3	1585.816	1585.607	132.509	0.320	879.069	0.414	29	0.092	K.NYHYDTNTCDPGK.V
R1/RRR1-22/3	1404.737	1405.579	-1315.434	0.533	959.239	0.338	22	0.091	K.VCGHYTQVVWR.K
R1/RRR1-2/3	1405.485	1405.579	-67.706	0.480	575.417	0.341	18	0.090	-.VCGHYTQVVWR.-
R1/RRR1-22/3	1406.210	1405.579	-263.488	0.525	852.846	0.337	21	0.090	K.VCGHYTQVVWR.K
R1/RRR1-11/3	1384.086	1384.522	-316.088	0.344	474.562	0.444	20	0.090	-.RADGVGPVSWDPK.-
R1/RRR1-22/3	1585.386	1585.607	-139.916	0.378	511.260	0.374	23	0.090	K.NYHYDTNTCDPGK.V
R1/RRR1-22/3	1405.734	1405.579	109.986	0.566	1031.741	0.314	22	0.090	K.VCGHYTQVVWR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/3	1405.726	1405.579	104.760	0.533	901.517	0.325	21	0.089	K.VCGHYTQVVWR.K
R1/RRR1-16/3	1406.038	1405.579	327.442	0.524	695.780	0.349	19	0.089	-.VCGHYTQVVWR.-
R1/RRR1-22/3	1586.564	1585.607	-26.988	0.428	818.108	0.385	28	0.089	K.NYHYDTNTCDPGK.V
R1/RRR1-17/3	1405.712	1405.579	94.309	0.471	684.470	0.312	20	0.089	K.VCGHYTQVVWR.K
R1/RRR1-21/3	1405.730	1405.579	107.634	0.514	902.441	0.311	21	0.087	K.VCGHYTQVVWR.K
R1/RRR1-4/3	1405.276	1405.579	-216.441	0.387	555.294	0.360	19	0.087	-.VCGHYTQVVWR.-
R1/RRR1-23/3	1585.725	1585.607	75.071	0.401	475.481	0.420	21	0.087	-.NYHYDTNTCDPGK.-
R1/RRR1-22/3	1405.820	1405.579	171.640	0.531	1009.024	0.312	22	0.086	-.VCGHYTQVVWR.-
R1/RRR1-16/3	1406.436	1405.579	-102.569	0.483	1067.879	0.293	23	0.086	K.VCGHYTQVVWR.K
R1/RRR1-24/3	1405.585	1405.579	4.293	0.442	795.235	0.303	21	0.086	K.VCGHYTQVVWR.K
R1/RRR1-23/3	1405.751	1405.579	122.134	0.467	942.626	0.303	22	0.086	K.VCGHYTQVVWR.K
R1/RRR1-22/3	1585.461	1585.607	-92.185	0.308	440.584	0.345	22	0.085	-.NYHYDTNTCDPGK.-
R1/RRR1-22/3	1405.129	1405.579	-321.287	0.462	985.596	0.289	22	0.085	K.VCGHYTQVVWR.K
R1/RRR1-19/3	1404.808	1405.579	-1264.905	0.463	632.117	0.328	19	0.084	-.VCGHYTQVVWR.-
R1/RRR1-2/3	1405.414	1405.579	-118.412	0.519	476.420	0.336	17	0.084	-.VCGHYTQVVWR.-
R1/RRR1-18/3	1405.625	1405.579	32.253	0.523	652.371	0.270	19	0.084	-.VCGHYTQVVWR.-
R1/RRR1-19/3	1585.827	1585.607	139.110	0.348	494.803	0.307	22	0.083	-.NYHYDTNTCDPGK.-
R1/RRR1-21/3	1384.162	1384.522	-260.609	0.350	264.699	0.383	17	0.082	-.RADGVGPVSWDPK.-
R1/RRR1-20/3	1404.951	1405.579	-1162.684	0.508	696.175	0.260	19	0.082	-.VCGHYTQVVWR.-
R1/RRR1-20/3	1548.023	1548.681	-1073.931	0.324	634.637	0.300	22	0.082	R.AWSAADAVASWVGEK.K
R1/RRR1-22/3	1586.674	1585.607	42.694	0.351	624.494	0.263	26	0.081	K.NYHYDTNTCDPGK.V
R1/RRR1-18/3	1548.827	1548.681	94.883	0.310	618.574	0.294	22	0.081	R.AWSAADAVASWVGEK.K
R1/RRR1-21/3	1405.559	1405.579	-14.915	0.323	595.421	0.267	18	0.080	-.VCGHYTQVVWR.-
R1/RRR1-21/3	1405.068	1405.579	-1078.933	0.516	798.825	0.302	21	0.079	-.VCGHYTQVVWR.-
R1/RRR1-22/3	1405.264	1405.579	-224.938	0.486	526.580	0.316	17	0.079	-.VCGHYTQVVWR.-
R1/RRR1-24/3	1405.601	1405.579	15.137	0.495	952.247	0.235	22	0.078	K.VCGHYTQVVWR.K
R1/RRR1-1/3	1406.048	1405.579	334.232	0.442	591.357	0.272	18	0.078	-.VCGHYTQVVWR.-
R1/RRR1-24/3	1383.987	1384.522	-1112.752	0.391	517.101	0.333	19	0.076	-.RADGVGPVSWDPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/3	1547.744	1548.681	-1254.962	0.332	462.559	0.323	20	0.068	-.AWSAADAVASWVGEK.-
R1/RRR1-20/3	1384.478	1384.522	-31.989	0.376	760.719	0.127	21	0.064	-.RADGVGPVSWDPK.-
R1/RRR1-4/2	1885.398	1885.881	-256.615	0.586	1926.843	0.641	26	0.386	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-4/2	1469.233	1469.645	-281.348	0.504	1952.518	0.521	22	0.353	R.FIGTAGAASSTM*NPK.N
R1/RRR1-4/2	1469.259	1469.645	-264.010	0.502	1899.696	0.499	22	0.337	R.FIGTAGAASSTM*NPK.N
R1/RRR1-4/2	1469.176	1469.645	-320.777	0.488	1880.984	0.501	22	0.335	R.FIGTAGAASSTM*NPK.N
R1/RRR1-4/2	1567.551	1567.796	-156.730	0.464	1978.783	0.446	22	0.334	R.GCALECAILSPTFK.V
R1/RRR1-4/2	1885.453	1885.881	-227.386	0.607	1542.561	0.630	25	0.318	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-4/2	1885.395	1885.881	-258.629	0.561	1581.243	0.612	24	0.318	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-4/3	1422.117	1422.655	-1084.466	0.497	2361.261	0.324	30	0.259	K.HANPVLLSSDLKK.K
R1/RRR1-8/2	1568.258	1567.796	295.532	0.471	1360.387	0.440	19	0.249	R.GCALECAILSPTFK.V
R1/RRR1-4/3	1422.507	1422.655	-104.466	0.525	2250.057	0.320	29	0.236	K.HANPVLLSSDLKK.K
R1/RRR1-8/2	1568.089	1567.796	187.423	0.395	1326.653	0.330	19	0.224	R.GCALECAILSPTFK.V
R1/RRR1-4/2	1743.653	1741.919	-152.908	0.416	844.343	0.534	16	0.220	R.GPSIDQLAYCINSFR.D
R1/RRR1-4/2	1041.025	1041.183	-152.379	0.424	1002.227	0.385	14	0.215	K.IQQQDALPK.H
R1/RRR1-4/2	1541.284	1541.811	-993.818	0.224	1442.623	0.222	18	0.212	R.AVLDAATIAGLCPLR.L
R1/RRR1-8/2	1568.315	1567.796	-307.483	0.409	1141.511	0.324	18	0.209	R.GCALECAILSPTFK.V
R1/RRR1-4/2	936.769	937.077	-329.642	0.333	512.756	0.523	10	0.209	R.DIAAFPFR.V
R1/RRR1-4/2	936.938	937.077	-148.464	0.333	541.091	0.452	10	0.203	R.DIAAFPFR.V
R1/RRR1-8/2	936.997	937.077	-84.949	0.350	606.230	0.395	11	0.202	R.DIAAFPFR.V
R1/RRR1-8/2	1360.052	1359.511	-338.543	0.372	1073.928	0.295	17	0.202	R.GIDVVLNEESKR.E
R1/RRR1-8/2	936.872	937.077	-218.653	0.263	710.773	0.385	11	0.199	R.DIAAFPFR.V
R1/RRR1-8/2	936.464	937.077	-1727.135	0.300	488.501	0.437	9	0.198	R.DIAAFPFR.V
R1/RRR1-4/2	1041.037	1041.183	-140.734	0.381	1037.758	0.255	14	0.198	K.IQQQDALPK.H
R1/RRR1-4/2	1886.981	1885.881	53.101	0.331	323.869	0.519	17	0.195	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-7/2	1542.893	1541.811	53.437	0.293	511.769	0.331	13	0.184	-.AVLDAATIAGLCPLR.-
R1/RRR1-4/2	936.315	937.077	-1887.466	0.110	540.091	0.197	10	0.181	-.DIAAFPFR.-
R1/RRR1-4/2	1541.000	1541.811	-1178.569	0.133	678.137	0.033	13	0.173	R.AVLDAATIAGLCPLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1422.813	1422.655	111.247	0.473	1941.003	0.249	27	0.156	K.HANPVLLSSDLKK.K
R1/RRR1-4/3	1422.945	1422.655	204.810	0.496	1698.837	0.321	26	0.147	K.HANPVLLSSDLKK.K
R1/RRR1-4/3	1885.089	1885.881	-953.578	0.468	1265.323	0.440	34	0.135	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-4/3	1886.521	1885.881	-191.374	0.516	950.603	0.519	32	0.127	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-10/3	1422.269	1422.655	-271.963	0.482	1613.936	0.275	26	0.122	K.HANPVLLSSDLKK.K
R1/RRR1-10/3	1885.852	1885.881	-15.434	0.442	1022.983	0.421	30	0.111	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-4/3	1481.537	1481.638	-67.867	0.396	919.600	0.459	24	0.106	R.VSEGPDGFPLVHAR.Y
R1/RRR1-9/3	1422.400	1422.655	-179.490	0.458	1553.163	0.230	25	0.106	K.HANPVLLSSDLKK.K
R1/RRR1-4/3	1885.889	1885.881	4.433	0.477	696.688	0.439	28	0.099	K.APADAAADGAENGAPNSEEK.S
R1/RRR1-8/3	1481.580	1481.638	-39.230	0.376	948.951	0.411	25	0.098	R.VSEGPDGFPLVHAR.Y
R1/RRR1-4/3	1481.779	1481.638	95.376	0.366	663.854	0.452	22	0.095	R.VSEGPDGFPLVHAR.Y
R1/RRR1-8/3	1481.879	1481.638	163.533	0.358	686.099	0.431	24	0.091	R.VSEGPDGFPLVHAR.Y
R1/RRR1-4/3	1481.399	1481.638	-161.350	0.342	659.034	0.421	22	0.090	R.VSEGPDGFPLVHAR.Y
R1/RRR1-3/2	1648.333	1648.802	-285.574	0.545	2637.969	0.501	24	0.486	K.YLAAEQGGGQTIVANR.V
R1/RRR1-3/2	1624.452	1623.746	-181.389	0.586	2398.023	0.581	24	0.463	R.LAGESNTELLDFASR.F
R1/RRR1-3/2	1623.318	1623.746	-264.330	0.559	2378.283	0.585	23	0.461	R.LAGESNTELLDFASR.F
R1/RRR1-3/2	1648.264	1648.802	-936.074	0.519	2532.606	0.488	24	0.457	K.YLAAEQGGGQTIVANR.V
R1/RRR1-3/2	1624.210	1623.746	286.406	0.591	2175.275	0.588	22	0.417	R.LAGESNTELLDFASR.F
R1/RRR1-3/2	1648.004	1648.802	-1094.096	0.510	2293.760	0.452	23	0.391	K.YLAAEQGGGQTIVANR.V
R1/RRR1-3/2	1596.421	1596.767	-217.245	0.419	2117.519	0.475	18	0.368	R.VVASDWESFTLWR.V
R1/RRR1-8/2	1268.147	1268.403	-202.712	0.500	1856.634	0.499	18	0.334	R.FAQAQLDVYGR.A
R1/RRR1-3/2	1447.306	1447.618	-216.195	0.509	1742.040	0.511	19	0.318	K.NLNVEQNIEFVK.N
R1/RRR1-3/2	1622.023	1621.817	127.371	0.484	1663.317	0.504	20	0.302	K.SPLTFVGEWAAEWK.V
R1/RRR1-3/2	1262.958	1263.340	-303.495	0.444	1544.308	0.472	16	0.281	K.YYQDAYNAVR.K
R1/RRR1-3/2	1622.129	1621.817	193.029	0.529	1369.642	0.548	20	0.277	K.SPLTFVGEWAAEWK.V
R1/RRR1-3/2	1447.130	1447.618	-338.393	0.433	1375.648	0.449	17	0.254	K.NLNVEQNIEFVK.N
R1/RRR1-3/2	1262.975	1263.340	-290.209	0.424	1376.212	0.438	16	0.254	K.YYQDAYNAVR.K
R1/RRR1-3/2	1262.981	1263.340	-284.876	0.437	1217.053	0.498	15	0.251	K.YYQDAYNAVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1268.086	1268.403	-250.998	0.435	1202.653	0.445	17	0.239	R.FAQAQLDVYGR.A
R1/RRR1-1/2	1622.177	1621.817	222.610	0.387	886.146	0.493	16	0.219	K.SPLTFVGEWAAEWK.V
R1/RRR1-3/2	1595.995	1596.767	-1113.947	0.315	1286.170	0.299	18	0.215	R.VVASDWESFTLWR.V
R1/RRR1-3/2	1107.522	1108.229	-1546.441	0.416	1081.835	0.320	14	0.210	R.INETTFNLR.V
R1/RRR1-3/2	1622.768	1621.817	-30.075	0.445	372.144	0.491	17	0.207	K.SPLTFVGEWAAEWK.V
R1/RRR1-3/2	1178.156	1178.323	-142.021	0.436	902.721	0.370	16	0.207	K.FISSNGLNAVR.I
R1/RRR1-3/2	1447.022	1447.618	-1106.025	0.403	851.138	0.406	15	0.207	K.NLNVEQNIEFVK.N
R1/RRR1-3/2	1177.637	1178.323	-1435.653	0.431	859.981	0.359	17	0.206	K.FISSNGLNAVR.I
R1/RRR1-3/2	1133.972	1134.267	-261.033	0.334	710.940	0.457	13	0.204	K.NGYISLNQPK.L
R1/RRR1-3/2	1179.193	1178.323	-110.747	0.466	769.082	0.352	16	0.201	K.FISSNGLNAVR.I
R1/RRR1-3/2	1108.193	1108.229	-32.881	0.474	716.030	0.348	13	0.198	-.INETTFNLR.-
R1/RRR1-3/2	1108.324	1108.229	85.657	0.425	614.337	0.307	12	0.193	R.INETTFNLR.V
R1/RRR1-1/2	1622.531	1621.817	-176.774	0.436	258.655	0.464	13	0.192	-.SPLTFVGEWAAEWK.-
R1/RRR1-1/2	1622.179	1621.817	223.742	0.311	317.228	0.344	13	0.191	K.SPLTFVGEWAAEWK.V
R1/RRR1-1/2	1623.760	1623.746	8.625	0.317	172.525	0.389	11	0.184	-.LAGESNTELLDFASR.-
R1/RRR1-12/2	1330.123	1330.456	-251.350	0.510	1880.792	0.519	20	0.343	K.FSNACGAICTTK.K
R1/RRR1-12/2	1452.324	1452.588	-182.232	0.497	1911.026	0.496	20	0.339	K.SAGILCSYDPNVR.L
R1/RRR1-12/2	1329.965	1330.456	-370.874	0.477	1643.514	0.484	19	0.296	K.FSNACGAICTTK.K
R1/RRR1-12/2	1330.084	1330.456	-280.722	0.484	1418.258	0.534	19	0.282	K.FSNACGAICTTK.K
R1/RRR1-12/2	1452.094	1452.588	-341.030	0.497	1256.062	0.512	17	0.255	K.SAGILCSYDPNVR.L
R1/RRR1-12/2	1452.402	1452.588	-128.608	0.505	1240.328	0.503	17	0.252	K.SAGILCSYDPNVR.L
R1/RRR1-12/2	1907.658	1907.287	195.458	0.517	800.107	0.617	22	0.236	K.KGAIPALPTVAVAQELISK.A
R1/RRR1-12/2	1906.695	1907.287	-837.133	0.504	767.296	0.594	21	0.228	K.KGAIPALPTVAVAQELISK.A
R1/RRR1-12/2	1778.555	1779.114	-879.204	0.427	734.648	0.559	23	0.225	K.GAIPALPTVAVAQELISK.A
R1/RRR1-11/2	1778.286	1779.114	-1031.153	0.452	664.481	0.601	20	0.225	K.GAIPALPTVAVAQELISK.A
R1/RRR1-12/2	1255.852	1255.404	358.031	0.518	784.066	0.491	17	0.224	R.LPLWPSEDAAR.A
R1/RRR1-12/2	1907.867	1907.287	-220.735	0.447	745.473	0.577	21	0.223	K.KGAIPALPTVAVAQELISK.A
R1/RRR1-12/2	1255.166	1255.404	-190.665	0.434	550.808	0.519	16	0.218	R.LPLWPSEDAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1255.073	1255.404	-264.722	0.401	526.632	0.461	15	0.209	R.LPLWPSEDAAR.A
R1/RRR1-12/2	987.468	988.160	-1718.768	0.429	609.798	0.437	14	0.208	K.LLIVTDGEK.G
R1/RRR1-11/2	1778.766	1779.114	-196.076	0.424	519.690	0.526	18	0.208	K.GAIPALPTVAVAQELISK.A
R1/RRR1-12/2	1503.246	1503.599	-235.027	0.385	994.934	0.344	18	0.206	K.DDSIFHNEEKLR.E
R1/RRR1-12/2	1233.906	1234.254	-283.055	0.431	909.985	0.347	15	0.205	K.DDSIFHNEEK.L
R1/RRR1-12/2	1778.449	1779.114	-939.082	0.395	582.353	0.441	21	0.204	K.GAIPALPTVAVAQELISK.A
R1/RRR1-11/2	1778.407	1779.114	-962.787	0.415	456.664	0.493	18	0.203	K.GAIPALPTVAVAQELISK.A
R1/RRR1-11/2	1255.154	1255.404	-199.738	0.353	399.609	0.416	13	0.201	R.LPLWPSEDAAR.A
R1/RRR1-9/2	1780.768	1779.114	-194.893	0.368	310.386	0.515	16	0.200	K.GAIPALPTVAVAQELISK.A
R1/RRR1-12/2	1234.257	1234.254	2.519	0.398	980.363	0.276	15	0.198	K.DDSIFHNEEK.L
R1/RRR1-1/2	1778.423	1779.114	-953.553	0.292	447.391	0.432	17	0.194	K.GAIPALPTVAVAQELISK.A
R1/RRR1-12/2	1254.899	1255.404	-1202.961	0.308	477.298	0.321	13	0.194	R.LPLWPSEDAAR.A
R1/RRR1-12/2	1254.881	1255.404	-1217.809	0.301	623.588	0.318	13	0.193	R.LPLWPSEDAAR.A
R1/RRR1-10/2	1778.531	1779.114	-892.639	0.310	385.456	0.310	18	0.192	K.GAIPALPTVAVAQELISK.A
R1/RRR1-10/2	1779.227	1779.114	63.887	0.298	221.722	0.314	14	0.191	K.GAIPALPTVAVAQELISK.A
R1/RRR1-9/2	1778.444	1779.114	-941.700	0.255	288.213	0.425	15	0.191	K.GAIPALPTVAVAQELISK.A
R1/RRR1-16/2	1256.584	1255.404	143.853	0.254	385.623	0.337	12	0.190	-.LPLWPSEDAAR.-
R1/RRR1-12/2	1233.937	1234.254	-257.250	0.385	793.472	0.254	14	0.190	K.DDSIFHNEEK.L
R1/RRR1-12/2	987.528	988.160	-1657.416	0.282	546.805	0.283	14	0.190	K.LLIVTDGEK.G
R1/RRR1-1/2	1255.592	1255.404	150.208	0.279	282.142	0.316	11	0.186	-.LPLWPSEDAAR.-
R1/RRR1-12/3	1906.755	1907.287	-805.457	0.338	1424.896	0.332	28	0.123	K.KGAIPALPTVAVAQELISK.A
R1/RRR1-12/3	1907.875	1907.287	-216.442	0.392	1057.932	0.398	28	0.105	K.KGAIPALPTVAVAQELISK.A
R1/RRR1-8/2	1663.521	1663.805	-171.461	0.567	3338.750	0.548	25	0.709	K.ATDSESTEVILDAALK.S
R1/RRR1-8/2	1761.615	1761.914	-169.976	0.553	1934.136	0.480	23	0.334	K.VENQEGVVNFDEILR.E
R1/RRR1-8/2	1760.687	1761.914	-1268.435	0.504	1714.547	0.507	23	0.311	K.VENQEGVVNFDEILR.E
R1/RRR1-8/2	1663.383	1663.805	-254.357	0.445	1804.917	0.401	21	0.293	K.ATDSESTEVILDAALK.S
R1/RRR1-2/2	1762.317	1761.914	229.502	0.541	1535.853	0.477	21	0.277	K.VENQEGVVNFDEILR.E
R1/RRR1-8/2	1762.320	1761.914	231.030	0.582	1459.715	0.513	21	0.277	K.VENQEGVVNFDEILR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	955.946	956.208	-274.807	0.440	1197.740	0.420	15	0.235	K.AALIVVLTR.G
R1/RRR1-7/2	1761.369	1761.914	-879.719	0.516	1249.461	0.424	20	0.235	K.VENQEGVVNFDEILR.E
R1/RRR1-8/2	1155.170	1155.369	-173.146	0.388	715.673	0.611	18	0.232	R.GLVPLLAEGSAK.A
R1/RRR1-8/2	1813.594	1814.097	-831.365	0.418	771.381	0.594	23	0.231	R.SAPLPMSPLESLASSAVR.T
R1/RRR1-8/2	1186.602	1187.285	-1422.950	0.438	1236.718	0.343	18	0.224	K.ILAGLENDDAR.V
R1/RRR1-8/2	1813.535	1814.097	-863.663	0.456	656.160	0.546	22	0.219	R.SAPLPMSPLESLASSAVR.T
R1/RRR1-8/2	1187.015	1187.285	-228.223	0.431	1102.064	0.370	17	0.219	K.ILAGLENDDAR.V
R1/RRR1-8/2	1186.555	1187.285	-1462.526	0.462	1086.855	0.367	17	0.218	K.ILAGLENDDAR.V
R1/RRR1-8/2	1205.401	1204.376	20.925	0.491	888.777	0.426	16	0.215	R.GDLGM*EIPVEK.I
R1/RRR1-8/2	1155.224	1155.369	-125.763	0.322	640.614	0.513	18	0.212	R.GLVPLLAEGSAK.A
R1/RRR1-8/2	787.008	786.983	32.342	0.398	826.944	0.384	13	0.209	R.IGVASVIK.I
R1/RRR1-8/2	1829.515	1830.096	-867.069	0.413	324.411	0.557	19	0.208	R.SAPLPM*SPLESLASSAVR.T
R1/RRR1-3/2	1761.373	1761.914	-877.562	0.450	967.400	0.395	17	0.208	K.VENQEGVVNFDEILR.E
R1/RRR1-8/2	1205.275	1204.376	-84.212	0.497	859.315	0.379	16	0.207	R.GDLGM*EIPVEK.I
R1/RRR1-8/2	786.930	786.983	-67.387	0.371	822.019	0.351	13	0.204	R.IGVASVIK.I
R1/RRR1-7/2	1186.470	1187.285	-1534.557	0.362	872.398	0.347	16	0.203	K.ILAGLENDDAR.V
R1/RRR1-8/2	1828.658	1830.096	-1337.428	0.396	358.632	0.482	19	0.202	R.SAPLPM*SPLESLASSAVR.T
R1/RRR1-7/2	1156.497	1155.369	110.780	0.272	686.011	0.442	16	0.202	R.GLVPLLAEGSAK.A
R1/RRR1-8/2	786.479	786.983	-1917.176	0.401	681.142	0.343	12	0.200	R.IGVASVIK.I
R1/RRR1-7/2	1829.092	1830.096	-1098.943	0.392	281.650	0.437	18	0.199	R.SAPLPM*SPLESLASSAVR.T
R1/RRR1-8/2	1204.046	1204.376	-274.860	0.384	745.161	0.351	15	0.198	R.GDLGM*EIPVEK.I
R1/RRR1-7/2	1829.852	1830.096	-133.837	0.380	214.952	0.461	16	0.198	R.SAPLPM*SPLESLASSAVR.T
R1/RRR1-8/2	1154.961	1155.369	-354.454	0.254	450.026	0.510	14	0.198	R.GLVPLLAEGSAK.A
R1/RRR1-7/2	1187.139	1187.285	-123.723	0.365	813.547	0.306	16	0.198	K.ILAGLENDDAR.V
R1/RRR1-8/2	1828.529	1830.096	-1956.826	0.323	222.281	0.481	16	0.197	R.SAPLPM*SPLESLASSAVR.T
R1/RRR1-1/2	1154.928	1155.369	-382.875	0.245	354.367	0.433	12	0.191	R.GLVPLLAEGSAK.A
R1/RRR1-8/2	1056.031	1056.175	-136.717	0.179	930.210	0.180	15	0.180	R.ETDAFM*VAR.G
R1/RRR1-8/2	1815.309	1814.097	117.451	0.367	208.057	0.499	11	0.175	-.SAPLPMSPLESLASSAVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1184.176	1183.426	-211.193	0.584	2451.938	0.504	22	0.445	R.LAVQLVAGGGGIK.S
R1/RRR1-7/2	1183.111	1183.426	-266.645	0.556	2376.953	0.513	22	0.433	R.LAVQLVAGGGGIK.S
R1/RRR1-7/2	1182.436	1183.426	-1687.448	0.460	2103.942	0.518	21	0.381	R.LAVQLVAGGGGIK.S
R1/RRR1-7/2	1720.486	1719.960	-276.231	0.550	1684.042	0.589	20	0.327	R.ALDSGIVAQAALDVFTK.E
R1/RRR1-7/2	1652.272	1651.796	288.952	0.557	1418.795	0.571	23	0.290	K.FPSAISESGEITVEGK.V
R1/RRR1-7/2	1650.784	1651.796	-1222.420	0.530	1532.022	0.498	24	0.285	K.FPSAISESGEITVEGK.V
R1/RRR1-7/2	1718.757	1719.960	-1285.773	0.336	1739.729	0.374	21	0.276	R.ALDSGIVAQAALDVFTK.E
R1/RRR1-7/2	1651.528	1651.796	-162.846	0.521	1178.401	0.538	21	0.253	K.FPSAISESGEITVEGK.V
R1/RRR1-7/2	919.947	920.131	-199.717	0.423	745.027	0.442	15	0.214	K.TLAILGFGK.V
R1/RRR1-7/2	1086.081	1085.213	-121.458	0.431	896.537	0.388	14	0.211	K.M*LNDETFAK.M
R1/RRR1-7/3	1539.953	1540.767	-1181.468	0.473	1812.710	0.469	32	0.209	K.HAVM*AIGVDEEPKK.S
R1/RRR1-7/2	920.057	920.131	-79.926	0.398	654.327	0.414	14	0.207	K.TLAILGFGK.V
R1/RRR1-7/2	1719.477	1719.960	-281.804	0.392	1053.075	0.357	19	0.206	R.ALDSGIVAQAALDVFTK.E
R1/RRR1-7/2	919.607	920.131	-1661.802	0.406	695.414	0.384	14	0.204	K.TLAILGFGK.V
R1/RRR1-18/2	1145.275	1144.260	12.870	0.396	945.371	0.287	13	0.192	-.GGVIDEDALVR.-
R1/RRR1-7/2	1084.933	1085.213	-258.476	0.381	504.166	0.285	12	0.191	K.M*LNDETFAK.M
R1/RRR1-7/3	1540.166	1540.767	-1042.624	0.436	1729.121	0.444	29	0.190	K.HAVM*AIGVDEEPKK.S
R1/RRR1-6/2	1145.122	1144.260	-121.420	0.383	728.353	0.203	13	0.180	-.GGVIDEDALVR.-
R1/RRR1-7/3	1540.102	1540.767	-1084.285	0.410	1575.226	0.483	30	0.175	K.HAVM*AIGVDEEPKK.S
R1/RRR1-6/2	1144.979	1144.260	-245.905	0.273	441.728	0.264	13	0.175	-.GGVIDEDALVR.-
R1/RRR1-7/3	1164.309	1164.379	-60.910	0.499	1913.948	0.258	25	0.152	R.NKYVGVSLVGK.T
R1/RRR1-7/3	1719.517	1719.960	-258.736	0.454	1243.009	0.492	30	0.144	R.ALDSGIVAQAALDVFTK.E
R1/RRR1-7/3	1826.769	1827.014	-134.416	0.521	818.329	0.475	28	0.108	K.GLGM*HVIAHDPYASADR.A
R1/RRR1-7/3	1827.007	1827.014	-3.820	0.489	1080.102	0.398	30	0.107	K.GLGM*HVIAHDPYASADR.A
R1/RRR1-7/3	1164.884	1164.379	-426.229	0.449	1486.107	0.222	21	0.098	R.NKYVGVSLVGK.T
R1/RRR1-7/3	1827.760	1827.014	-139.501	0.445	859.523	0.416	27	0.098	K.GLGM*HVIAHDPYASADR.A
R1/RRR1-7/3	1163.969	1164.379	-353.773	0.410	1475.208	0.177	21	0.087	R.NKYVGVSLVGK.T
R1/RRR1-9/2	1503.438	1503.768	-220.257	0.517	2297.559	0.413	20	0.375	K.TVFIQELINNIAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1437.449	1436.595	-102.264	0.580	1958.715	0.576	21	0.372	R.FTQAGSEVSALLGR.I
R1/RRR1-9/2	1437.473	1436.595	-85.568	0.515	1945.866	0.573	21	0.369	R.FTQAGSEVSALLGR.I
R1/RRR1-9/2	1350.151	1350.585	-322.889	0.460	2092.050	0.452	20	0.356	K.LVDLKDTIASFK.A
R1/RRR1-9/2	1503.310	1503.768	-305.304	0.481	2121.272	0.444	20	0.355	K.TVFIQELINNIAK.A
R1/RRR1-8/2	1503.610	1503.768	-105.581	0.518	2274.363	0.371	20	0.355	K.TVFIQELINNIAK.A
R1/RRR1-9/2	1503.221	1503.768	-1031.933	0.435	2291.574	0.339	20	0.350	K.TVFIQELINNIAK.A
R1/RRR1-9/2	1351.360	1350.585	-167.398	0.524	1953.554	0.493	19	0.345	K.LVDLKDTIASFK.A
R1/RRR1-8/2	1503.223	1503.768	-1030.628	0.422	2308.270	0.311	20	0.344	K.TVFIQELINNIAK.A
R1/RRR1-9/2	1435.593	1436.595	-1399.090	0.373	2033.884	0.396	21	0.327	R.FTQAGSEVSALLGR.I
R1/RRR1-9/2	1775.478	1774.992	274.073	0.534	1418.391	0.590	22	0.292	R.GISELGIYPAVDPLDSK.S
R1/RRR1-9/2	1774.365	1774.992	-919.783	0.434	1297.665	0.597	21	0.277	R.GISELGIYPAVDPLDSK.S
R1/RRR1-9/2	1774.291	1774.992	-961.846	0.451	1276.539	0.552	21	0.264	R.GISELGIYPAVDPLDSK.S
R1/RRR1-8/2	1503.199	1503.768	-1046.853	0.405	1724.089	0.293	19	0.255	K.TVFIQELINNIAK.A
R1/RRR1-9/2	1377.084	1376.518	-316.301	0.387	1165.671	0.388	17	0.223	R.IM*NVTGDPIDER.G
R1/RRR1-9/2	1149.013	1149.322	-269.017	0.548	1092.649	0.393	14	0.221	R.VQQILQEYK.S
R1/RRR1-9/2	1148.975	1149.322	-302.273	0.507	1111.373	0.340	14	0.214	R.VQQILQEYK.S
R1/RRR1-9/2	1349.746	1350.585	-1366.795	0.424	934.065	0.377	14	0.205	K.LVDLKDTIASFK.A
R1/RRR1-9/2	1405.926	1406.609	-1200.621	0.331	818.673	0.395	18	0.203	R.VALTGLTVAEEFR.S
R1/RRR1-14/2	1503.826	1503.768	38.705	0.387	193.675	0.381	15	0.203	K.TVFIQELINNIAK.A
R1/RRR1-8/2	1406.027	1406.609	-1128.520	0.324	839.360	0.395	15	0.201	R.VALTGLTVAEEFR.S
R1/RRR1-9/2	1148.545	1149.322	-1551.115	0.375	794.873	0.342	13	0.200	R.VQQILQEYK.S
R1/RRR1-9/2	1376.278	1376.518	-175.482	0.336	1201.565	0.151	17	0.189	R.IM*NVTGDPIDER.G
R1/RRR1-8/2	1773.560	1774.992	-1375.344	0.242	546.092	0.374	14	0.184	R.GISELGIYPAVDPLDSK.S
R1/RRR1-8/2	1435.289	1436.595	-1611.538	0.239	592.688	0.196	14	0.180	-.FTQAGSEVSALLGR.-
R1/RRR1-9/3	1876.226	1876.150	41.032	0.512	1074.617	0.637	30	0.170	K.AKDTGAPITIPVGHATLGR.I
R1/RRR1-9/3	1876.063	1876.150	-46.579	0.462	937.383	0.546	29	0.130	K.AKDTGAPITIPVGHATLGR.I
R1/RRR1-9/3	1436.744	1436.595	103.862	0.346	1171.613	0.336	25	0.096	R.FTQAGSEVSALLGR.I
R1/RRR1-9/3	1436.435	1436.595	-111.551	0.339	937.697	0.338	23	0.084	-.FTQAGSEVSALLGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/3	1436.581	1436.595	-9.905	0.322	772.051	0.250	22	0.072	R.FTQAGSEVSALLGR.I
R1/RRR1-8/2	1999.278	1999.112	83.311	0.542	2068.871	0.615	25	0.405	R.GNPTVEVDICCSDGTFAR.A
R1/RRR1-8/2	1515.357	1514.829	-312.492	0.541	2028.597	0.585	21	0.389	K.LGANAILAVSLALCK.A
R1/RRR1-8/2	1514.344	1514.829	-320.786	0.437	2159.313	0.487	21	0.379	K.LGANAILAVSLALCK.A
R1/RRR1-8/2	1998.810	1999.112	-151.582	0.574	1849.787	0.592	24	0.355	R.GNPTVEVDICCSDGTFAR.A
R1/RRR1-8/2	1998.343	1999.112	-887.764	0.488	1857.136	0.558	24	0.346	R.GNPTVEVDICCSDGTFAR.A
R1/RRR1-8/2	1904.553	1904.240	164.797	0.581	1633.747	0.618	25	0.333	K.LAM*QEFM*ILPTGASSFK.E
R1/RRR1-8/2	1903.448	1904.240	-944.173	0.597	1480.950	0.601	24	0.305	K.LAM*QEFM*ILPTGASSFK.E
R1/RRR1-8/2	1581.289	1581.839	-983.077	0.413	1591.733	0.508	22	0.295	K.AVDNVNSIIGPALIGK.D
R1/RRR1-8/2	1997.593	1999.112	-1767.087	0.408	1298.534	0.515	21	0.256	R.GNPTVEVDICCSDGTFAR.A
R1/RRR1-8/2	1903.622	1904.240	-852.499	0.549	1036.771	0.601	22	0.254	K.LAM*QEFM*ILPTGASSFK.E
R1/RRR1-8/2	1998.921	1999.112	-95.957	0.335	380.472	0.476	14	0.192	R.GNPTVEVDICCSDGTFAR.A
R1/RRR1-8/2	1513.457	1514.829	-1571.990	0.296	609.345	0.366	16	0.190	K.LGANAILAVSLALCK.A
R1/RRR1-7/2	1788.774	1789.066	-163.562	0.502	2068.677	0.536	23	0.382	K.ALLQDIAIVTGAEFQAK.D
R1/RRR1-7/2	1637.234	1637.688	-277.938	0.506	2104.499	0.510	24	0.376	K.TNDSAGDGTTTASVLAR.E
R1/RRR1-7/2	1637.257	1637.688	-263.875	0.530	1952.726	0.531	25	0.356	K.TNDSAGDGTTTASVLAR.E
R1/RRR1-7/2	1915.432	1915.178	133.045	0.553	1764.279	0.518	24	0.319	K.DLGLLVESTTVEQLGIAR.K
R1/RRR1-7/2	1637.233	1637.688	-278.461	0.489	1693.988	0.535	24	0.316	K.TNDSAGDGTTTASVLAR.E
R1/RRR1-7/3	1788.891	1789.066	-97.785	0.475	2313.145	0.418	32	0.315	K.ALLQDIAIVTGAEFQAK.D
R1/RRR1-7/2	1915.036	1915.178	-74.075	0.536	1680.001	0.506	25	0.304	K.DLGLLVESTTVEQLGIAR.K
R1/RRR1-7/2	1480.171	1480.646	-322.402	0.483	1454.214	0.522	20	0.282	R.GYISPQFVTNPEK.S
R1/RRR1-7/2	1914.715	1915.178	-242.455	0.518	1471.581	0.518	25	0.281	K.DLGLLVESTTVEQLGIAR.K
R1/RRR1-7/2	1291.187	1291.347	-124.183	0.550	1302.275	0.481	19	0.257	K.VGAATETELEDR.K
R1/RRR1-7/2	1479.545	1480.646	-1424.392	0.376	1194.223	0.458	19	0.238	R.GYISPQFVTNPEK.S
R1/RRR1-7/2	1064.181	1065.161	-1867.025	0.403	1258.894	0.403	14	0.235	K.SLVEFENAR.I
R1/RRR1-7/2	1291.047	1291.347	-233.068	0.524	1148.713	0.449	18	0.235	K.VGAATETELEDR.K
R1/RRR1-7/2	1290.926	1291.347	-326.890	0.438	1153.423	0.425	18	0.231	K.VGAATETELEDR.K
R1/RRR1-7/2	1480.232	1480.646	-280.783	0.444	1067.522	0.430	18	0.224	R.GYISPQFVTNPEK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	898.543	899.113	-1752.265	0.413	945.731	0.421	14	0.218	R.GILNVAAIK.A
R1/RRR1-7/2	898.950	899.113	-181.773	0.504	838.854	0.443	14	0.218	R.GILNVAAIK.A
R1/RRR1-7/2	1473.216	1473.478	-178.567	0.411	692.456	0.503	17	0.214	R.ELSQTDSAYDSEK.L
R1/RRR1-7/2	898.683	899.113	-479.784	0.408	750.400	0.456	13	0.213	R.GILNVAAIK.A
R1/RRR1-7/2	1473.060	1473.478	-284.478	0.385	779.835	0.458	17	0.211	R.ELSQTDSAYDSEK.L
R1/RRR1-7/2	1064.964	1065.161	-186.088	0.337	1149.810	0.253	15	0.203	K.SLVEFENAR.I
R1/RRR1-7/2	1064.929	1065.161	-218.976	0.288	1020.254	0.265	14	0.198	-.SLVEFENAR.-
R1/RRR1-7/2	1472.843	1473.478	-1113.153	0.284	707.435	0.389	17	0.197	R.ELSQTDSAYDSEK.L
R1/RRR1-7/2	858.044	858.018	30.449	0.490	987.448	0.191	13	0.187	R.LGADIIQK.A
R1/RRR1-7/2	857.915	858.018	-120.395	0.537	1031.972	0.177	13	0.184	R.LGADIIQK.A
R1/RRR1-7/2	857.930	858.018	-102.554	0.537	949.374	0.184	13	0.183	R.LGADIIQK.A
R1/RRR1-7/3	1788.554	1789.066	-847.735	0.357	754.385	0.205	24	0.066	-.ALLQDIAIVTGAEFQAK.-
R1/RRR1-8/2	1850.631	1851.159	-827.892	0.516	2356.923	0.521	26	0.427	K.AVGEEMGIGFLGIGFQPK.W
R1/RRR1-8/2	1851.918	1851.159	-130.218	0.573	2184.641	0.492	25	0.379	K.AVGEEMGIGFLGIGFQPK.W
R1/RRR1-8/2	1530.432	1530.662	-151.011	0.432	1930.050	0.506	23	0.345	R.EVDAVISSGVTPAER.L
R1/RRR1-8/2	1850.774	1851.159	-208.625	0.507	1894.297	0.507	24	0.335	K.AVGEEMGIGFLGIGFQPK.W
R1/RRR1-8/2	1867.528	1868.058	-821.729	0.512	1670.165	0.560	25	0.322	R.SGM*LPFVFDDSFGFER.Y
R1/RRR1-8/2	1866.470	1867.158	-907.389	0.505	1640.526	0.579	22	0.316	K.AVGEEM*GIGFLGIGFQPK.W
R1/RRR1-8/2	1865.809	1867.158	-1263.115	0.419	1682.981	0.460	23	0.290	K.AVGEEM*GIGFLGIGFQPK.W
R1/RRR1-8/2	1930.773	1931.267	-256.735	0.556	1216.111	0.665	26	0.289	R.AGLALQPIATAIFANSPFK.E
R1/RRR1-8/2	1259.367	1259.431	-50.906	0.536	1745.376	0.402	17	0.285	R.DLAEEILQLSK.N
R1/RRR1-8/2	1530.201	1530.662	-302.259	0.356	1701.500	0.423	22	0.285	R.EVDAVISSGVTPAER.L
R1/RRR1-8/2	1258.602	1259.431	-1457.505	0.452	1721.427	0.382	17	0.279	R.DLAEEILQLSK.N
R1/RRR1-8/2	1530.141	1530.662	-997.375	0.327	1630.351	0.380	21	0.265	R.EVDAVISSGVTPAER.L
R1/RRR1-8/2	1931.472	1931.267	106.774	0.596	995.301	0.628	25	0.257	R.AGLALQPIATAIFANSPFK.E
R1/RRR1-8/2	1930.369	1931.267	-985.940	0.496	1059.069	0.605	25	0.257	R.AGLALQPIATAIFANSPFK.E
R1/RRR1-8/2	1866.824	1867.158	-179.743	0.476	1363.281	0.465	22	0.253	K.AVGEEM*GIGFLGIGFQPK.W
R1/RRR1-8/2	1259.219	1259.431	-168.854	0.418	1490.257	0.358	16	0.246	R.DLAEEILQLSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1932.888	1931.267	-196.721	0.515	911.084	0.591	24	0.241	R.AGLALQPIATAIFANSPFK.E
R1/RRR1-8/2	1931.561	1931.199	188.098	0.491	872.232	0.560	20	0.234	R.YVDYALDVPM*YFVYR.N
R1/RRR1-8/2	1931.289	1931.199	46.434	0.541	720.654	0.606	18	0.230	R.YVDYALDVPM*YFVYR.N
R1/RRR1-8/2	1287.340	1287.553	-165.655	0.465	1077.339	0.435	16	0.227	K.WALSDIPIM*PK.G
R1/RRR1-8/2	1271.242	1271.553	-245.848	0.321	948.471	0.434	15	0.215	K.WALSDIPIMPK.G
R1/RRR1-8/2	994.102	994.166	-65.290	0.541	612.710	0.395	13	0.203	-.LLNLYETK.-
R1/RRR1-8/2	1287.238	1287.553	-245.089	0.330	1044.467	0.293	15	0.201	K.WALSDIPIM*PK.G
R1/RRR1-8/2	993.487	994.166	-1695.168	0.394	640.023	0.319	13	0.198	R.LLNLYETK.W
R1/RRR1-8/2	993.637	994.166	-1543.721	0.432	583.502	0.305	13	0.195	-.LLNLYETK.-
R1/RRR1-1/2	1867.844	1867.158	-168.894	0.284	767.308	0.351	19	0.193	K.AVGEEM*GIGFLGIGFQPK.W
R1/RRR1-2/2	1868.394	1868.058	180.021	0.180	135.949	0.276	16	0.191	R.SGM*LPFVFDDSFGFER.Y
R1/RRR1-8/2	1286.931	1287.553	-1263.699	0.303	637.197	0.264	13	0.187	K.WALSDIPIM*PK.G
R1/RRR1-8/2	1850.943	1852.059	-1146.719	0.304	233.313	0.370	13	0.181	-.SGMLPFVFDDSFGFER.-
R1/RRR1-8/2	1309.960	1310.477	-1161.464	0.280	938.488	0.547	14	0.127	R.SVDPVFQELLY.-
R1/RRR1-8/2	1310.155	1310.477	-246.490	0.219	748.716	0.417	14	0.098	R.SVDPVFQELLY.-
R1/RRR1-8/2	1309.741	1310.477	-1328.802	0.176	560.944	0.318	12	0.092	R.SVDPVFQELLY.-
R1/RRR1-7/2	1321.228	1321.504	-209.395	0.512	1748.182	0.479	19	0.308	K.LGDLSQTQIFAK.I
R1/RRR1-7/2	1321.192	1321.504	-236.924	0.500	1674.798	0.474	19	0.296	K.LGDLSQTQIFAK.I
R1/RRR1-7/2	1322.335	1321.504	-128.203	0.555	1510.432	0.524	19	0.290	K.LGDLSQTQIFAK.I
R1/RRR1-7/2	1216.250	1215.380	-106.970	0.515	1558.565	0.457	17	0.280	K.IDFLSLSYTR.H
R1/RRR1-7/2	1171.762	1172.274	-1293.640	0.412	1583.660	0.419	17	0.272	R.WSFTGAFEAR.Q
R1/RRR1-7/2	1215.151	1215.380	-188.782	0.441	1505.358	0.378	17	0.254	K.IDFLSLSYTR.H
R1/RRR1-7/2	1171.717	1172.274	-1332.876	0.380	1405.896	0.362	16	0.240	R.WSFTGAFEAR.Q
R1/RRR1-3/2	1322.037	1321.504	-354.668	0.475	857.942	0.515	17	0.228	K.LGDLSQTQIFAK.I
R1/RRR1-7/2	1377.269	1376.623	-257.325	0.503	819.459	0.519	20	0.227	R.GLYPVETISIVGK.I
R1/RRR1-7/2	1299.401	1298.464	-48.960	0.428	893.622	0.499	15	0.222	K.ASVIICFTSSGR.A
R1/RRR1-1/2	1320.627	1321.504	-1425.394	0.329	986.910	0.388	17	0.212	K.LGDLSQTQIFAK.I
R1/RRR1-7/2	1376.272	1376.623	-255.910	0.454	824.252	0.425	20	0.212	R.GLYPVETISIVGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1215.159	1215.380	-182.332	0.478	903.823	0.382	14	0.209	K.IDFLSLSYTR.H
R1/RRR1-7/2	1214.688	1215.380	-1397.003	0.326	992.410	0.345	14	0.206	K.IDFLSLSYTR.H
R1/RRR1-7/2	1133.815	1133.346	415.329	0.339	635.596	0.429	13	0.198	-.GLFPM*LADPR.-
R1/RRR1-2/2	1320.742	1321.504	-1337.851	0.305	478.127	0.274	13	0.189	K.LGDLSQTQIFAK.I
R1/RRR1-7/2	1298.194	1298.464	-208.867	0.320	488.662	0.349	12	0.187	K.ASVIICFTSSGR.A
R1/RRR1-1/2	1171.578	1172.274	-1451.752	0.193	737.960	0.272	13	0.185	R.WSFTGAFEAR.Q
R1/RRR1-1/2	1321.111	1321.504	-298.662	0.317	436.831	0.319	13	0.185	-.LGDLSQTQIFAK.-
R1/RRR1-7/3	1645.940	1645.006	-40.207	0.494	1366.337	0.399	25	0.134	K.YRPTM*PVLSVVIPR.L
R1/RRR1-7/3	1320.749	1320.538	160.554	0.424	1569.279	0.284	26	0.117	K.CNM*AGKPAVVTR.V
R1/RRR1-7/3	1320.124	1320.538	-314.741	0.418	1096.042	0.350	23	0.094	K.CNM*AGKPAVVTR.V
R1/RRR1-7/3	1645.457	1645.006	274.568	0.462	911.467	0.304	22	0.083	K.YRPTM*PVLSVVIPR.L
R1/RRR1-7/3	1937.677	1938.155	-247.303	0.291	1001.267	0.302	28	0.078	K.HVGEPM*THLESIASSAVR.A
R1/RRR1-7/3	1304.648	1304.538	84.535	0.290	769.276	0.230	19	0.069	K.CNMAGKPAVVTR.V
R1/RRR1-12/2	1918.596	1919.128	-800.798	0.581	3767.881	0.576	30	0.857	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-12/2	1918.500	1919.128	-851.383	0.588	3391.986	0.593	29	0.736	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-11/2	1918.625	1919.128	-785.790	0.570	3278.221	0.553	29	0.679	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-11/2	1918.546	1919.128	-827.367	0.526	3277.543	0.478	29	0.640	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-11/2	1919.384	1919.128	133.919	0.583	3163.246	0.508	28	0.618	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-12/2	1918.519	1919.128	-841.419	0.572	2881.490	0.557	28	0.565	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-12/2	1578.316	1578.622	-194.526	0.559	2136.299	0.579	25	0.409	R.DNGVDDAGVVFDAGAR.T
R1/RRR1-12/2	1578.348	1578.622	-174.120	0.577	2039.854	0.585	25	0.392	R.DNGVDDAGVVFDAGAR.T
R1/RRR1-12/2	1579.054	1578.622	274.282	0.581	1932.101	0.588	24	0.373	R.DNGVDDAGVVFDAGAR.T
R1/RRR1-12/2	991.874	992.197	-326.758	0.463	1661.455	0.480	15	0.298	R.TALAFVTLR.A
R1/RRR1-12/2	991.518	992.197	-1698.164	0.434	1687.583	0.460	15	0.295	R.TALAFVTLR.A
R1/RRR1-12/2	992.163	992.197	-34.073	0.516	1709.471	0.438	15	0.292	R.TALAFVTLR.A
R1/RRR1-11/2	992.144	992.197	-53.695	0.528	1610.225	0.451	15	0.284	R.TALAFVTLR.A
R1/RRR1-11/2	991.954	992.197	-245.515	0.469	1622.071	0.440	15	0.282	R.TALAFVTLR.A
R1/RRR1-12/2	1358.170	1358.480	-228.941	0.518	1427.124	0.511	20	0.278	R.IVQDPSSLQDQK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1401.520	1401.632	-80.599	0.545	1382.393	0.528	20	0.278	K.ILSIWDQADIVK.V
R1/RRR1-12/2	1358.129	1358.480	-258.788	0.491	1358.032	0.430	20	0.251	R.IVQDPSSLQDQK.K
R1/RRR1-12/2	1402.609	1401.632	-16.464	0.548	1111.344	0.524	18	0.248	K.ILSIWDQADIVK.V
R1/RRR1-12/2	1357.559	1358.480	-1419.175	0.408	1367.349	0.418	19	0.248	R.IVQDPSSLQDQK.K
R1/RRR1-11/2	1401.708	1401.632	54.452	0.467	1106.494	0.454	18	0.233	K.ILSIWDQADIVK.V
R1/RRR1-12/2	1420.262	1419.565	-213.932	0.501	908.239	0.514	17	0.228	K.EAGALLSYDPNLR.E
R1/RRR1-11/2	1358.140	1358.480	-250.763	0.459	1128.005	0.400	18	0.225	R.IVQDPSSLQDQK.K
R1/RRR1-12/2	1400.922	1401.632	-1224.749	0.455	1082.670	0.412	17	0.223	K.ILSIWDQADIVK.V
R1/RRR1-12/2	1317.304	1317.550	-187.340	0.302	735.282	0.410	15	0.200	K.LLLVTLGDQGCK.Y
R1/RRR1-3/2	1918.943	1919.128	-96.830	0.385	453.175	0.471	18	0.200	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-12/2	1316.674	1317.550	-1429.581	0.354	840.418	0.350	15	0.199	K.LLLVTLGDQGCK.Y
R1/RRR1-12/2	1419.242	1419.565	-227.975	0.401	871.992	0.302	17	0.195	K.EAGALLSYDPNLR.E
R1/RRR1-1/2	1918.460	1919.128	-872.078	0.402	745.895	0.277	21	0.188	K.VQQVDTTGAGDAFVGALLR.R
R1/RRR1-3/2	1919.006	1919.128	-64.096	0.321	365.578	0.335	15	0.186	-.VQQVDTTGAGDAFVGALLR.-
R1/RRR1-12/2	1317.346	1317.550	-155.455	0.241	503.493	0.291	14	0.186	K.LLLVTLGDQGCK.Y
R1/RRR1-1/2	1919.338	1919.128	109.554	0.345	461.209	0.272	17	0.183	-.VQQVDTTGAGDAFVGALLR.-
R1/RRR1-11/2	1418.735	1419.565	-1293.341	0.237	531.379	0.240	13	0.182	K.EAGALLSYDPNLR.E
R1/RRR1-12/3	1514.637	1514.666	-19.055	0.494	1035.978	0.391	27	0.098	R.RIVQDPSSLQDQK.K
R1/RRR1-12/3	1513.787	1514.666	-1245.180	0.382	472.649	0.355	20	0.082	R.RIVQDPSSLQDQK.K
R1/RRR1-6/2	1940.629	1940.214	214.724	0.590	3068.140	0.553	27	0.622	K.GVNPDEAVAMGAAIQGGILR.G
R1/RRR1-6/2	1940.679	1940.214	240.143	0.587	2933.159	0.576	27	0.596	K.GVNPDEAVAMGAAIQGGILR.G
R1/RRR1-6/2	1777.556	1777.956	-225.828	0.546	1923.494	0.577	26	0.368	R.IINEPTAAALSYGTNNK.E
R1/RRR1-6/2	1938.614	1940.214	-1862.657	0.409	2153.425	0.425	24	0.355	K.GVNPDEAVAMGAAIQGGILR.G
R1/RRR1-6/2	1778.464	1777.956	-277.552	0.588	1608.538	0.578	24	0.316	R.IINEPTAAALSYGTNNK.E
R1/RRR1-6/2	1461.230	1461.515	-195.701	0.468	1421.506	0.630	19	0.305	K.APNGDAWVETTDGK.Q
R1/RRR1-6/2	1777.259	1777.956	-958.104	0.542	1553.663	0.555	24	0.302	R.IINEPTAAALSYGTNNK.E
R1/RRR1-6/2	1355.027	1355.433	-300.132	0.447	1611.431	0.423	19	0.276	R.NNADTTIYSVEK.S
R1/RRR1-7/2	1522.780	1522.728	34.524	0.479	1317.705	0.472	18	0.253	R.SKFESLVNSLIER.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1355.292	1355.433	-104.036	0.452	1323.497	0.462	18	0.253	R.NNADTTIYSVEK.S
R1/RRR1-6/2	1523.426	1522.728	-199.043	0.354	1456.756	0.367	19	0.244	R.SKFESLVNSLIER.T
R1/RRR1-6/2	1523.337	1522.728	-257.487	0.455	1293.629	0.437	18	0.243	R.SKFESLVNSLIER.T
R1/RRR1-6/2	1355.122	1355.433	-229.546	0.468	1164.201	0.456	17	0.237	R.NNADTTIYSVEK.S
R1/RRR1-6/2	1205.450	1206.285	-1527.053	0.422	1358.521	0.309	19	0.225	R.SSGGLSEAEIQK.M
R1/RRR1-6/2	1205.601	1206.285	-1400.728	0.480	1190.541	0.380	17	0.224	R.SSGGLSEAEIQK.M
R1/RRR1-6/2	1540.682	1539.757	-48.842	0.469	540.566	0.544	19	0.215	K.QYSPSQIGAFVLTK.M
R1/RRR1-6/2	1553.319	1553.701	-246.526	0.478	589.809	0.534	18	0.215	R.QAVTNPQNTFFGTK.R
R1/RRR1-6/2	1539.344	1539.757	-269.046	0.423	570.130	0.496	18	0.208	K.QYSPSQIGAFVLTK.M
R1/RRR1-6/2	1553.284	1553.701	-269.312	0.436	475.560	0.532	16	0.207	R.QAVTNPQNTFFGTK.R
R1/RRR1-6/2	1205.496	1206.285	-1488.297	0.398	1055.281	0.323	17	0.207	R.SSGGLSEAEIQK.M
R1/RRR1-7/2	993.893	994.276	-386.985	0.391	1595.096	0.050	14	0.195	K.M*VPYKIVK.A
R1/RRR1-7/2	1523.900	1522.728	113.236	0.352	462.262	0.377	14	0.193	R.SKFESLVNSLIER.T
R1/RRR1-7/2	993.933	994.276	-346.565	0.426	1279.550	0.058	14	0.180	K.M*VPYKIVK.A
R1/RRR1-1/2	993.502	994.276	-1790.562	0.436	926.637	0.048	12	0.168	-.M*VPYKIVK.-
R1/RRR1-6/3	1523.504	1522.728	-147.287	0.575	1274.247	0.375	25	0.117	R.SKFESLVNSLIER.T
R1/RRR1-6/3	1522.689	1522.728	-25.869	0.533	1157.847	0.370	25	0.105	R.SKFESLVNSLIER.T
R1/RRR1-6/3	1522.375	1522.728	-232.405	0.453	991.699	0.309	25	0.084	R.SKFESLVNSLIER.T
R1/RRR1-13/2	1783.401	1782.884	-271.360	0.577	1748.193	0.545	23	0.327	K.ASEISVSAEEEFNIEK.L
R1/RRR1-13/2	1782.712	1782.884	-96.262	0.516	1732.471	0.514	23	0.315	K.ASEISVSAEEEFNIEK.L
R1/RRR1-13/2	1781.828	1782.884	-1157.255	0.399	1776.002	0.445	22	0.301	K.ASEISVSAEEEFNIEK.L
R1/RRR1-13/2	1190.994	1191.310	-266.628	0.512	1158.960	0.443	17	0.237	-.IVCENTLDAR.-
R1/RRR1-13/2	1191.167	1191.310	-120.426	0.450	1169.332	0.413	17	0.233	K.IVCENTLDAR.L
R1/RRR1-13/2	1191.054	1191.310	-215.936	0.439	1135.786	0.416	17	0.231	K.IVCENTLDAR.L
R1/RRR1-14/2	1190.988	1191.310	-271.256	0.471	1161.915	0.401	17	0.230	K.IVCENTLDAR.L
R1/RRR1-13/3	1584.954	1584.823	82.981	0.547	1942.856	0.453	29	0.228	R.KKIEYSM*QLNASR.I
R1/RRR1-13/2	1153.073	1153.307	-203.511	0.428	1068.686	0.435	18	0.228	R.FCSGGVVLASR.D
R1/RRR1-14/2	1192.072	1191.310	-200.140	0.484	1089.134	0.406	17	0.227	K.IVCENTLDAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1027.145	1027.243	-95.553	0.396	1257.702	0.334	15	0.224	K.ELVVQGLLR.L
R1/RRR1-14/2	1191.066	1191.310	-206.065	0.423	1039.926	0.411	16	0.223	K.IVCENTLDAR.L
R1/RRR1-14/2	1026.699	1027.243	-1507.664	0.378	1220.711	0.311	15	0.217	K.ELVVQGLLR.L
R1/RRR1-13/2	1027.114	1027.243	-125.237	0.411	1024.549	0.365	14	0.215	K.ELVVQGLLR.L
R1/RRR1-14/2	1027.017	1027.243	-220.622	0.368	1164.149	0.287	14	0.209	K.ELVVQGLLR.L
R1/RRR1-13/3	1584.979	1584.823	99.086	0.562	1987.764	0.389	30	0.209	R.KKIEYSM*QLNASR.I
R1/RRR1-13/2	1027.144	1027.243	-96.268	0.432	885.228	0.349	13	0.206	K.ELVVQGLLR.L
R1/RRR1-13/2	1038.346	1039.297	-1884.117	0.240	890.116	0.312	14	0.194	R.LKEPAVLLR.C
R1/RRR1-13/2	1152.379	1153.307	-1677.913	0.241	620.937	0.376	14	0.190	R.FCSGGVVLASR.D
R1/RRR1-13/2	1038.502	1039.297	-1732.807	0.212	727.424	0.300	14	0.187	R.LKEPAVLLR.C
R1/RRR1-14/2	1026.892	1027.243	-342.621	0.288	897.456	0.109	13	0.183	-.ELVVQGLLR.-
R1/RRR1-13/3	1584.079	1584.823	-1104.332	0.501	1652.259	0.373	29	0.151	R.KKIEYSM*QLNASR.I
R1/RRR1-13/3	1457.001	1456.650	241.908	0.562	1407.882	0.425	27	0.136	K.KIEYSM*QLNASR.I
R1/RRR1-13/2	976.947	977.182	-241.454	0.367	661.778	0.562	12	0.120	R.KLLFGQVTA.-
R1/RRR1-13/2	976.486	977.182	-1742.173	0.361	868.120	0.470	13	0.114	R.KLLFGQVTA.-
R1/RRR1-13/2	977.219	977.182	38.137	0.386	722.685	0.511	12	0.114	R.KLLFGQVTA.-
R1/RRR1-13/3	1456.271	1456.650	-261.036	0.534	1001.558	0.397	24	0.099	K.KIEYSM*QLNASR.I
R1/RRR1-13/3	1456.433	1456.650	-149.662	0.504	887.075	0.339	22	0.087	K.KIEYSM*QLNASR.I
R1/RRR1-13/3	1568.656	1568.823	-107.007	0.436	949.251	0.262	22	0.079	R.KKIEYSMQLNASR.I
R1/RRR1-13/3	1568.833	1568.823	5.914	0.448	824.448	0.277	22	0.077	-.KKIEYSMQLNASR.-
R1/RRR1-13/2	1709.580	1708.932	-206.733	0.556	1909.451	0.579	25	0.364	R.GWVPTLLGYSAQGACK.F
R1/RRR1-13/2	1505.272	1505.610	-224.869	0.507	1921.777	0.538	21	0.355	K.YYSDIAGPEYAQK.Y
R1/RRR1-13/2	1708.174	1708.932	-1032.692	0.499	1884.491	0.523	26	0.342	R.GWVPTLLGYSAQGACK.F
R1/RRR1-14/2	1708.274	1708.932	-973.717	0.495	1595.032	0.519	25	0.298	R.GWVPTLLGYSAQGACK.F
R1/RRR1-14/2	1709.226	1708.932	172.018	0.519	1437.057	0.574	24	0.293	R.GWVPTLLGYSAQGACK.F
R1/RRR1-14/2	1708.100	1708.932	-1075.816	0.455	1545.317	0.498	25	0.286	R.GWVPTLLGYSAQGACK.F
R1/RRR1-13/2	1505.162	1505.610	-298.502	0.525	1364.614	0.563	20	0.283	K.YYSDIAGPEYAQK.Y
R1/RRR1-13/2	1708.249	1708.932	-988.568	0.489	1480.579	0.508	24	0.280	R.GWVPTLLGYSAQGACK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1505.130	1505.610	-319.740	0.482	1373.487	0.539	20	0.277	K.YYSDIAGPEYAQK.Y
R1/RRR1-13/1	937.444	938.060	-1728.842	0.310	584.587	0.439	11	0.251	K.SEGALGLYK.G
R1/RRR1-13/1	937.466	938.060	-1705.162	0.318	566.987	0.437	11	0.240	K.SEGALGLYK.G
R1/RRR1-13/2	1213.268	1213.407	-115.508	0.389	1327.763	0.391	14	0.239	K.FGFYEFFKK.C
R1/RRR1-14/2	1214.418	1213.407	8.609	0.380	1041.280	0.464	14	0.229	K.FGFYEFFKK.C
R1/RRR1-13/2	1213.114	1213.407	-242.287	0.405	1077.474	0.415	14	0.224	K.FGFYEFFKK.C
R1/RRR1-14/2	937.452	938.060	-1719.698	0.404	827.210	0.476	15	0.223	K.SEGALGLYK.G
R1/RRR1-13/2	747.847	747.908	-81.386	0.459	763.026	0.484	11	0.220	K.HAVPVPK.S
R1/RRR1-14/2	1062.949	1063.277	-309.344	0.485	745.326	0.479	13	0.220	K.LGLWGLFTR.G
R1/RRR1-13/2	938.055	938.060	-4.713	0.484	541.092	0.515	13	0.220	K.SEGALGLYK.G
R1/RRR1-13/2	747.527	747.908	-511.203	0.464	775.676	0.465	11	0.216	-.HAVPVPK.-
R1/RRR1-13/2	1063.290	1063.277	12.251	0.467	730.148	0.448	13	0.215	K.LGLWGLFTR.G
R1/RRR1-13/2	1062.933	1063.277	-324.553	0.414	812.725	0.418	14	0.214	K.LGLWGLFTR.G
R1/RRR1-13/2	1063.214	1063.277	-59.376	0.458	708.588	0.447	13	0.214	K.LGLWGLFTR.G
R1/RRR1-13/2	1063.077	1063.277	-188.491	0.483	704.499	0.435	13	0.213	K.LGLWGLFTR.G
R1/RRR1-13/2	1063.110	1063.277	-157.045	0.421	618.171	0.464	12	0.212	K.LGLWGLFTR.G
R1/RRR1-13/2	1063.066	1063.277	-198.513	0.412	713.169	0.421	13	0.210	K.LGLWGLFTR.G
R1/RRR1-13/2	1085.157	1085.234	-71.489	0.333	885.704	0.427	12	0.210	K.FGFYEFFK.K
R1/RRR1-14/2	1062.822	1063.277	-429.419	0.439	697.763	0.408	13	0.209	K.LGLWGLFTR.G
R1/RRR1-14/2	937.423	938.060	-1751.098	0.342	766.637	0.353	15	0.205	K.SEGALGLYK.G
R1/RRR1-1/2	937.888	938.060	-183.430	0.373	666.845	0.356	14	0.204	K.SEGALGLYK.G
R1/RRR1-13/2	938.014	938.060	-48.571	0.367	512.276	0.396	13	0.202	-.SEGALGLYK.-
R1/RRR1-13/2	937.698	938.060	-386.375	0.397	630.530	0.335	14	0.200	-.SEGALGLYK.-
R1/RRR1-14/2	937.833	938.060	-242.451	0.389	654.004	0.289	14	0.199	K.SEGALGLYK.G
R1/RRR1-2/2	937.943	938.060	-124.939	0.332	678.878	0.323	14	0.198	-.SEGALGLYK.-
R1/RRR1-12/2	937.893	938.060	-178.730	0.311	509.036	0.285	13	0.197	K.SEGALGLYK.G
R1/RRR1-2/2	1576.407	1575.786	-241.440	0.404	655.584	0.426	14	0.197	K.FASFETIVEQIYK.H
R1/RRR1-1/2	938.049	938.060	-11.761	0.314	447.081	0.258	12	0.196	K.SEGALGLYK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1710.577	1708.932	-208.473	0.345	437.185	0.445	15	0.196	R.GWVPTLLGYSAQGACK.F
R1/RRR1-3/2	1709.980	1708.932	27.881	0.354	316.287	0.396	14	0.193	R.GWVPTLLGYSAQGACK.F
R1/RRR1-14/2	1063.022	1063.277	-240.792	0.251	390.110	0.292	10	0.193	K.LGLWGLFTR.G
R1/RRR1-13/1	937.562	938.060	-532.613	0.238	436.458	0.370	9	0.172	K.SEGALGLYK.G
R1/RRR1-16/2	1375.174	1375.547	-271.874	0.501	1955.855	0.490	19	0.344	K.VIACVGETLEQR.E
R1/RRR1-15/2	1375.026	1375.547	-1109.620	0.398	1891.379	0.450	19	0.320	K.VIACVGETLEQR.E
R1/RRR1-16/2	1376.167	1375.547	-276.482	0.553	1765.115	0.511	19	0.320	K.VIACVGETLEQR.E
R1/RRR1-16/2	1340.113	1340.501	-290.041	0.466	1688.698	0.536	22	0.318	R.IIYGGSVTGANCK.E
R1/RRR1-16/2	1340.182	1340.501	-238.683	0.488	1663.255	0.543	22	0.317	R.IIYGGSVTGANCK.E
R1/RRR1-15/2	1376.171	1375.547	-274.079	0.535	1737.231	0.500	19	0.313	K.VIACVGETLEQR.E
R1/RRR1-16/2	1339.987	1340.501	-1133.427	0.520	1546.175	0.551	21	0.303	R.IIYGGSVTGANCK.E
R1/RRR1-16/2	1374.429	1375.547	-1545.355	0.362	1673.832	0.396	19	0.275	K.VIACVGETLEQR.E
R1/RRR1-16/2	1605.420	1604.746	-203.520	0.473	1198.127	0.623	19	0.274	K.WLAANVSAEVAESTR.I
R1/RRR1-16/2	1395.052	1395.497	-319.605	0.467	1330.604	0.547	19	0.273	R.SLLGESNEFVGDK.V
R1/RRR1-18/2	1606.143	1604.746	247.778	0.473	1296.167	0.573	19	0.272	K.WLAANVSAEVAESTR.I
R1/RRR1-16/2	1636.291	1636.748	-280.118	0.479	1295.444	0.532	22	0.266	K.VATPDQAQEVHDGLR.K
R1/RRR1-16/2	1395.123	1395.497	-268.600	0.458	1247.095	0.542	19	0.263	R.SLLGESNEFVGDK.V
R1/RRR1-16/2	1637.160	1636.748	252.282	0.532	1101.255	0.564	21	0.254	K.VATPDQAQEVHDGLR.K
R1/RRR1-16/2	1424.161	1424.560	-281.092	0.438	1424.115	0.395	19	0.246	R.ESGSTMDVVAAQTK.A
R1/RRR1-16/1	954.474	955.094	-1701.972	0.319	625.082	0.370	11	0.245	K.FFVGGNWK.C
R1/RRR1-16/2	1424.101	1424.560	-323.145	0.469	1214.727	0.452	18	0.238	R.ESGSTMDVVAAQTK.A
R1/RRR1-16/2	1394.489	1395.497	-1444.369	0.317	1200.308	0.459	19	0.236	R.SLLGESNEFVGDK.V
R1/RRR1-16/2	1636.220	1636.748	-936.904	0.478	1170.068	0.453	21	0.236	K.VATPDQAQEVHDGLR.K
R1/RRR1-16/2	1439.655	1440.559	-1326.394	0.343	1234.922	0.403	20	0.231	R.ESGSTM*DVVAAQTK.A
R1/RRR1-16/2	1440.256	1440.559	-211.357	0.399	1027.779	0.460	18	0.226	R.ESGSTM*DVVAAQTK.A
R1/RRR1-16/2	1440.151	1440.559	-284.146	0.446	1054.275	0.445	18	0.226	R.ESGSTM*DVVAAQTK.A
R1/RRR1-16/2	1765.433	1764.921	-277.451	0.492	900.632	0.492	19	0.221	K.VATPDQAQEVHDGLRK.W
R1/RRR1-16/2	1440.092	1440.559	-325.478	0.422	1041.318	0.418	18	0.220	R.ESGSTM*DVVAAQTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1440.215	1440.559	-239.757	0.389	1026.047	0.420	18	0.219	R.ESGSTM*DVVAAQTK.A
R1/RRR1-16/2	1440.044	1440.559	-1055.324	0.413	1106.022	0.375	19	0.218	R.ESGSTM*DVVAAQTK.A
R1/RRR1-16/2	1440.061	1440.559	-347.335	0.428	987.097	0.418	18	0.217	R.ESGSTM*DVVAAQTK.A
R1/RRR1-15/2	1441.203	1440.559	-247.918	0.402	971.658	0.400	18	0.214	R.ESGSTM*DVVAAQTK.A
R1/RRR1-16/2	1604.433	1604.746	-195.480	0.379	723.270	0.482	18	0.210	K.WLAANVSAEVAESTR.I
R1/RRR1-15/2	1440.029	1440.559	-1065.708	0.404	874.525	0.385	17	0.206	R.ESGSTM*DVVAAQTK.A
R1/RRR1-16/2	1423.500	1424.560	-1451.228	0.327	1045.209	0.326	17	0.205	R.ESGSTMDVVAAQTK.A
R1/RRR1-16/2	1764.320	1764.921	-910.030	0.428	615.724	0.495	16	0.204	K.VATPDQAQEVHDGLRK.W
R1/RRR1-16/2	1764.402	1764.921	-863.426	0.444	665.728	0.467	17	0.204	K.VATPDQAQEVHDGLRK.W
R1/RRR1-18/2	1604.127	1604.746	-1012.511	0.251	829.443	0.320	19	0.193	K.WLAANVSAEVAESTR.I
R1/RRR1-16/1	954.487	955.094	-1687.709	0.331	435.083	0.290	10	0.147	K.FFVGGNWK.C
R1/RRR1-16/3	1375.768	1375.547	161.462	0.518	908.065	0.381	25	0.091	K.VIACVGETLEQR.E
R1/RRR1-16/3	1375.298	1375.547	-181.275	0.468	1135.932	0.301	26	0.087	K.VIACVGETLEQR.E
R1/RRR1-16/3	1375.505	1375.547	-30.773	0.485	761.834	0.341	24	0.083	K.VIACVGETLEQR.E
R1/RRR1-15/2	1419.090	1419.517	-301.854	0.506	2138.102	0.561	19	0.401	K.TVDVEELTVEER.N
R1/RRR1-15/2	1419.745	1419.517	161.041	0.546	2111.177	0.565	20	0.398	K.TVDVEELTVEER.N
R1/RRR1-14/2	1419.343	1419.517	-122.373	0.526	2026.774	0.549	19	0.376	K.TVDVEELTVEER.N
R1/RRR1-14/2	1419.078	1419.517	-309.794	0.495	1994.316	0.547	19	0.369	K.TVDVEELTVEER.N
R1/RRR1-14/2	1418.732	1419.517	-1261.758	0.394	2043.788	0.455	19	0.347	K.TVDVEELTVEER.N
R1/RRR1-15/2	1774.459	1774.014	251.392	0.586	1598.848	0.603	23	0.319	K.AAQDIALADLAPTHPIR.L
R1/RRR1-14/2	1774.386	1774.014	210.346	0.574	1503.949	0.599	22	0.304	K.AAQDIALADLAPTHPIR.L
R1/RRR1-14/2	1655.153	1655.831	-1016.951	0.477	1631.197	0.497	24	0.296	K.LLDSHLVPSSTAAESK.V
R1/RRR1-14/2	1774.351	1774.014	190.477	0.542	1452.317	0.582	22	0.293	K.AAQDIALADLAPTHPIR.L
R1/RRR1-14/2	1774.332	1774.014	179.714	0.562	1466.932	0.576	22	0.293	K.AAQDIALADLAPTHPIR.L
R1/RRR1-15/2	1773.399	1774.014	-913.311	0.555	1397.804	0.589	22	0.288	K.AAQDIALADLAPTHPIR.L
R1/RRR1-15/2	1772.981	1774.014	-1149.908	0.499	1438.278	0.559	22	0.285	K.AAQDIALADLAPTHPIR.L
R1/RRR1-15/2	1654.816	1655.831	-1221.143	0.465	1468.542	0.484	24	0.273	K.LLDSHLVPSSTAAESK.V
R1/RRR1-14/2	1655.550	1655.831	-170.068	0.471	1407.202	0.475	24	0.264	K.LLDSHLVPSSTAAESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1216.053	1216.343	-239.618	0.479	1232.867	0.500	17	0.254	K.EAAESTM*VAYK.A
R1/RRR1-14/2	1655.325	1655.831	-912.406	0.485	1348.827	0.432	24	0.248	K.LLDSHLVPSSTAAESK.V
R1/RRR1-15/2	1375.066	1375.510	-324.073	0.451	1290.333	0.416	19	0.241	R.IVSSIEQKEEGR.G
R1/RRR1-15/2	1655.357	1655.831	-287.543	0.439	1201.198	0.461	22	0.240	K.LLDSHLVPSSTAAESK.V
R1/RRR1-15/2	1376.063	1375.510	-325.617	0.486	1054.733	0.494	18	0.238	R.IVSSIEQKEEGR.G
R1/RRR1-15/2	1656.231	1655.831	242.059	0.502	1031.722	0.501	21	0.234	K.LLDSHLVPSSTAAESK.V
R1/RRR1-14/2	1216.114	1216.343	-188.964	0.415	1158.803	0.431	17	0.233	K.EAAESTM*VAYK.A
R1/RRR1-15/2	1374.536	1375.510	-1440.483	0.437	1077.701	0.454	17	0.230	R.IVSSIEQKEEGR.G
R1/RRR1-14/2	1215.576	1216.343	-1458.259	0.385	1086.153	0.441	16	0.228	K.EAAESTM*VAYK.A
R1/RRR1-15/2	1215.807	1216.343	-1267.854	0.441	978.935	0.411	16	0.218	K.EAAESTM*VAYK.A
R1/RRR1-14/3	1774.239	1774.014	126.925	0.465	1552.978	0.559	30	0.211	K.AAQDIALADLAPTHPIR.L
R1/RRR1-15/2	1773.880	1774.014	-75.966	0.294	1035.739	0.378	18	0.208	K.AAQDIALADLAPTHPIR.L
R1/RRR1-15/2	1139.503	1140.271	-1556.762	0.454	789.726	0.342	13	0.199	R.GNEEHVTLIK.E
R1/RRR1-14/2	1215.395	1216.343	-1607.568	0.340	739.370	0.295	14	0.193	K.EAAESTM*VAYK.A
R1/RRR1-15/2	1140.076	1140.271	-171.680	0.469	611.505	0.368	12	0.192	-.GNEEHVTLIK.-
R1/RRR1-15/2	1140.296	1140.271	21.194	0.431	543.621	0.355	12	0.191	-.GNEEHVTLIK.-
R1/RRR1-14/2	1140.072	1140.271	-175.762	0.490	540.798	0.399	12	0.190	-.GNEEHVTLIK.-
R1/RRR1-14/2	1140.032	1140.271	-210.887	0.399	653.034	0.296	12	0.188	-.GNEEHVTLIK.-
R1/RRR1-14/2	1139.754	1140.271	-1335.556	0.475	495.154	0.339	12	0.182	-.GNEEHVTLIK.-
R1/RRR1-15/3	1774.717	1774.014	-167.970	0.421	1445.895	0.522	30	0.179	K.AAQDIALADLAPTHPIR.L
R1/RRR1-15/3	1774.132	1774.014	66.478	0.435	1424.720	0.529	30	0.179	K.AAQDIALADLAPTHPIR.L
R1/RRR1-14/3	1774.425	1774.014	232.069	0.368	1493.360	0.504	31	0.177	K.AAQDIALADLAPTHPIR.L
R1/RRR1-14/2	1199.999	1200.344	-287.992	0.198	515.666	0.150	13	0.166	-.EAAESTMVAYK.-
R1/RRR1-14/3	1773.762	1774.014	-142.866	0.345	1447.782	0.480	30	0.163	K.AAQDIALADLAPTHPIR.L
R1/RRR1-14/3	1656.564	1655.831	-161.694	0.363	1270.525	0.505	30	0.145	K.LLDSHLVPSSTAAESK.V
R1/RRR1-15/3	1773.525	1774.014	-276.469	0.424	1065.239	0.536	26	0.140	K.AAQDIALADLAPTHPIR.L
R1/RRR1-14/3	1655.365	1655.831	-282.594	0.377	1209.210	0.428	31	0.119	K.LLDSHLVPSSTAAESK.V
R1/RRR1-14/3	1655.823	1655.831	-4.786	0.328	808.903	0.492	26	0.105	K.LLDSHLVPSSTAAESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1655.942	1655.831	67.304	0.270	1049.325	0.220	27	0.073	K.LLDSHLVPSSTAAESK.V
R1/RRR1-15/3	1656.157	1655.831	197.261	0.269	912.089	0.229	26	0.072	-.LLDSHLVPSSTAAESK.-
R1/RRR1-15/3	1655.810	1655.831	-13.104	0.248	998.893	0.160	26	0.065	K.LLDSHLVPSSTAAESK.V
R1/RRR1-14/2	1803.615	1804.124	-839.299	0.581	4005.784	0.572	28	0.947	K.NFMIDFLM*GGVSAAVSK.T
R1/RRR1-15/2	1818.851	1820.123	-1252.927	0.502	3696.002	0.573	27	0.835	K.NFM*IDFLM*GGVSAAVSK.T
R1/RRR1-14/2	1803.407	1804.124	-954.675	0.559	3587.586	0.605	28	0.814	K.NFMIDFLM*GGVSAAVSK.T
R1/RRR1-15/2	1804.045	1804.124	-44.095	0.606	3601.397	0.591	27	0.808	K.NFMIDFLM*GGVSAAVSK.T
R1/RRR1-15/2	1819.209	1820.123	-1055.486	0.559	3592.809	0.568	27	0.793	K.NFM*IDFLM*GGVSAAVSK.T
R1/RRR1-15/2	1805.278	1804.124	85.745	0.601	3013.910	0.606	25	0.628	K.NFM*IDFLMGGVSAAVSK.T
R1/RRR1-14/2	1802.640	1804.124	-1381.895	0.409	2745.785	0.559	25	0.534	K.NFMIDFLM*GGVSAAVSK.T
R1/RRR1-15/2	1499.716	1498.745	-19.235	0.540	2067.369	0.576	20	0.393	R.GFNISCVGIIVYR.G
R1/RRR1-15/2	1818.471	1820.123	-2014.685	0.397	2087.461	0.515	22	0.370	K.NFM*IDFLM*GGVSAAVSK.T
R1/RRR1-15/2	1498.423	1498.745	-215.520	0.454	2103.575	0.464	20	0.361	R.GFNISCVGIIVYR.G
R1/RRR1-15/2	1498.224	1498.745	-1018.050	0.419	2020.252	0.466	20	0.347	R.GFNISCVGIIVYR.G
R1/RRR1-15/2	1227.042	1227.413	-302.699	0.461	1552.953	0.415	17	0.266	K.SSMDAFSQILK.N
R1/RRR1-14/2	1243.189	1243.412	-179.614	0.451	1285.890	0.472	17	0.253	K.SSM*DAFSQILK.N
R1/RRR1-14/2	1243.144	1243.412	-215.865	0.446	1369.003	0.413	17	0.247	K.SSM*DAFSQILK.N
R1/RRR1-14/2	1244.257	1243.412	-125.143	0.486	1287.206	0.433	16	0.243	K.SSM*DAFSQILK.N
R1/RRR1-14/2	1362.153	1361.590	-321.981	0.519	1379.899	0.395	17	0.243	K.LLIQNQDEM*IK.S
R1/RRR1-15/2	1243.136	1243.412	-222.465	0.423	1308.245	0.421	16	0.243	K.SSM*DAFSQILK.N
R1/RRR1-15/2	1242.654	1243.412	-1419.276	0.419	1352.951	0.402	16	0.242	K.SSM*DAFSQILK.N
R1/RRR1-15/2	1243.280	1243.412	-106.530	0.443	1268.196	0.416	16	0.238	K.SSM*DAFSQILK.N
R1/RRR1-15/2	1345.006	1345.591	-1181.996	0.491	1377.177	0.360	17	0.236	K.LLIQNQDEMIK.S
R1/RRR1-15/2	1346.189	1345.591	-299.465	0.545	1282.440	0.392	18	0.236	K.LLIQNQDEMIK.S
R1/RRR1-14/2	1227.073	1227.413	-277.847	0.431	1269.707	0.393	16	0.234	K.SSMDAFSQILK.N
R1/RRR1-14/2	1361.162	1361.590	-315.649	0.505	1295.828	0.370	17	0.232	K.LLIQNQDEM*IK.S
R1/RRR1-15/2	1447.014	1447.661	-1142.077	0.468	914.604	0.496	20	0.232	R.YFPTQALNFAFK.D
R1/RRR1-1/2	1361.274	1361.590	-232.606	0.506	1247.980	0.383	17	0.231	K.LLIQNQDEM*IK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1344.681	1345.591	-1424.116	0.460	1268.920	0.371	17	0.231	K.LLIQNQDEMIK.S
R1/RRR1-13/2	1362.158	1361.590	-318.025	0.521	1225.031	0.388	17	0.230	K.LLIQNQDEM*IK.S
R1/RRR1-14/2	1361.152	1361.590	-322.578	0.499	1263.504	0.372	17	0.230	K.LLIQNQDEM*IK.S
R1/RRR1-15/2	1227.048	1227.413	-298.208	0.421	1208.775	0.391	16	0.229	K.SSMDAFSQILK.N
R1/RRR1-14/2	1447.193	1447.661	-324.419	0.428	726.051	0.544	19	0.227	R.YFPTQALNFAFK.D
R1/RRR1-3/2	1361.214	1361.590	-276.960	0.489	1318.819	0.334	17	0.226	K.LLIQNQDEM*IK.S
R1/RRR1-14/2	1344.615	1345.591	-1473.539	0.386	1305.952	0.322	18	0.226	K.LLIQNQDEMIK.S
R1/RRR1-14/2	1447.318	1447.661	-237.934	0.477	742.514	0.510	19	0.225	R.YFPTQALNFAFK.D
R1/RRR1-2/2	1243.088	1243.412	-261.773	0.352	1274.614	0.342	16	0.225	K.SSM*DAFSQILK.N
R1/RRR1-15/2	1424.223	1423.598	-263.886	0.502	916.585	0.460	18	0.224	R.TIKDEGFASLWR.G
R1/RRR1-14/2	1423.346	1423.598	-177.684	0.439	890.418	0.467	18	0.223	R.TIKDEGFASLWR.G
R1/RRR1-15/2	1345.075	1345.591	-1130.232	0.499	1153.347	0.367	17	0.222	K.LLIQNQDEMIK.S
R1/RRR1-14/2	1424.154	1423.598	-312.644	0.455	947.418	0.449	17	0.222	R.TIKDEGFASLWR.G
R1/RRR1-15/2	1447.177	1447.661	-335.505	0.401	868.879	0.460	20	0.221	R.YFPTQALNFAFK.D
R1/RRR1-13/2	1362.600	1361.590	7.623	0.529	1189.353	0.351	17	0.221	K.LLIQNQDEM*IK.S
R1/RRR1-15/2	1447.419	1447.661	-168.131	0.387	814.919	0.474	20	0.220	R.YFPTQALNFAFK.D
R1/RRR1-3/2	1362.105	1361.590	-357.229	0.497	1263.119	0.318	17	0.219	K.LLIQNQDEM*IK.S
R1/RRR1-15/2	1226.552	1227.413	-1521.744	0.390	1103.022	0.362	15	0.216	K.SSMDAFSQILK.N
R1/RRR1-14/2	1344.468	1345.591	-1583.436	0.392	1241.224	0.295	17	0.216	K.LLIQNQDEMIK.S
R1/RRR1-1/2	1361.261	1361.590	-242.682	0.492	1285.745	0.288	17	0.215	K.LLIQNQDEM*IK.S
R1/RRR1-4/2	1361.181	1361.590	-301.343	0.424	1007.880	0.355	17	0.215	K.LLIQNQDEM*IK.S
R1/RRR1-1/2	1362.018	1361.590	314.972	0.533	1121.014	0.340	17	0.215	K.LLIQNQDEM*IK.S
R1/RRR1-14/2	881.720	881.950	-260.796	0.412	625.518	0.487	12	0.215	K.GIGDCFGR.T
R1/RRR1-14/2	1423.288	1423.598	-218.897	0.443	971.436	0.383	18	0.214	R.TIKDEGFASLWR.G
R1/RRR1-15/3	1804.376	1804.124	139.929	0.531	1716.130	0.501	34	0.214	K.NFMIDFLM*GGVSAAVSK.T
R1/RRR1-12/2	1361.315	1361.590	-202.379	0.455	1300.671	0.262	17	0.212	K.LLIQNQDEM*IK.S
R1/RRR1-14/2	1361.214	1361.590	-277.050	0.490	1101.024	0.322	17	0.212	K.LLIQNQDEM*IK.S
R1/RRR1-2/2	1360.675	1361.590	-1411.655	0.445	1157.208	0.294	17	0.211	K.LLIQNQDEM*IK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1362.187	1361.590	-296.626	0.515	1177.141	0.301	17	0.211	K.LLIQNQDEM*IK.S
R1/RRR1-15/2	1423.453	1423.598	-102.237	0.450	787.194	0.414	17	0.211	R.TIKDEGFASLWR.G
R1/RRR1-14/2	1447.180	1447.661	-333.220	0.426	613.755	0.444	18	0.210	R.YFPTQALNFAFK.D
R1/RRR1-1/2	1243.128	1243.412	-229.460	0.378	928.742	0.361	16	0.210	K.SSM*DAFSQILK.N
R1/RRR1-14/2	1362.256	1361.590	-245.651	0.462	1259.672	0.250	17	0.208	K.LLIQNQDEM*IK.S
R1/RRR1-10/2	1361.650	1361.590	44.045	0.405	1259.961	0.238	17	0.208	K.LLIQNQDEM*IK.S
R1/RRR1-14/2	881.924	881.950	-29.031	0.299	712.885	0.463	12	0.208	K.GIGDCFGR.T
R1/RRR1-15/2	1423.216	1423.598	-269.320	0.461	812.392	0.374	17	0.206	R.TIKDEGFASLWR.G
R1/RRR1-14/2	1226.505	1227.413	-1560.335	0.368	959.480	0.344	14	0.206	K.SSMDAFSQILK.N
R1/RRR1-2/2	1360.773	1361.590	-1339.393	0.418	1197.670	0.230	17	0.203	K.LLIQNQDEM*IK.S
R1/RRR1-14/2	881.458	881.950	-559.514	0.286	637.057	0.443	12	0.203	K.GIGDCFGR.T
R1/RRR1-2/2	1362.202	1361.590	-285.658	0.513	1187.167	0.243	17	0.201	K.LLIQNQDEM*IK.S
R1/RRR1-13/2	772.081	771.888	250.856	0.463	1068.720	0.248	13	0.200	K.GAGANILR.A
R1/RRR1-1/2	1242.840	1243.412	-1268.830	0.280	887.275	0.290	15	0.197	K.SSM*DAFSQILK.N
R1/RRR1-4/2	1362.263	1361.590	-240.706	0.368	1090.677	0.214	16	0.197	K.LLIQNQDEM*IK.S
R1/RRR1-2/2	1423.721	1423.598	86.547	0.390	369.302	0.377	13	0.197	R.TIKDEGFASLWR.G
R1/RRR1-1/2	1423.307	1423.598	-204.958	0.316	695.503	0.276	16	0.193	R.TIKDEGFASLWR.G
R1/RRR1-1/2	881.973	881.950	26.083	0.211	403.570	0.358	11	0.191	K.GIGDCFGR.T
R1/RRR1-13/2	771.814	771.888	-96.150	0.425	869.093	0.199	12	0.189	K.GAGANILR.A
R1/RRR1-1/2	771.990	771.888	131.778	0.406	606.130	0.184	11	0.188	K.GAGANILR.A
R1/RRR1-14/2	771.879	771.888	-11.597	0.398	724.181	0.169	12	0.188	K.GAGANILR.A
R1/RRR1-14/2	771.855	771.888	-42.529	0.399	751.760	0.164	12	0.187	K.GAGANILR.A
R1/RRR1-14/2	771.929	771.888	53.752	0.396	833.677	0.164	12	0.186	K.GAGANILR.A
R1/RRR1-10/2	1361.414	1361.590	-129.429	0.423	890.403	0.163	15	0.186	K.LLIQNQDEM*IK.S
R1/RRR1-14/2	1499.062	1498.745	212.551	0.242	532.863	0.234	13	0.183	R.GFNISCVGIIVYR.G
R1/RRR1-15/2	771.296	771.888	-2070.321	0.299	558.327	0.206	10	0.181	-.GAGANILR.-
R1/RRR1-14/3	1821.046	1820.123	-42.520	0.461	825.586	0.466	28	0.105	K.NFM*IDFLM*GGVSAAVSK.T
R1/RRR1-14/3	1804.741	1804.124	-212.740	0.405	1016.153	0.340	27	0.092	-.NFM*IDFLMGGVSAAVSK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1804.088	1804.124	-19.874	0.360	737.513	0.378	23	0.088	K.NFM*IDFLMGGVSAAVSK.T
R1/RRR1-5/2	1761.806	1762.000	-110.748	0.537	3138.487	0.580	25	0.657	R.FLVLNAAELAVDGSSVR.F
R1/RRR1-5/2	1755.336	1754.916	239.552	0.570	2448.256	0.491	25	0.438	R.ETALLYDELLSSASNK.Q
R1/RRR1-5/2	1761.304	1762.000	-965.949	0.432	2307.708	0.522	23	0.419	R.FLVLNAAELAVDGSSVR.F
R1/RRR1-5/2	1755.583	1754.916	-190.576	0.573	2020.408	0.574	23	0.383	R.ETALLYDELLSSASNK.Q
R1/RRR1-5/2	1754.439	1754.916	-272.699	0.532	2061.314	0.540	23	0.379	R.ETALLYDELLSSASNK.Q
R1/RRR1-5/2	1760.960	1762.000	-1161.860	0.383	1550.514	0.458	20	0.272	R.FLVLNAAELAVDGSSVR.F
R1/RRR1-5/2	1156.263	1156.269	-5.147	0.413	1384.618	0.441	16	0.254	K.AAEVSEFFAGK.T
R1/RRR1-8/2	1763.472	1762.000	268.232	0.435	1033.981	0.524	20	0.235	R.FLVLNAAELAVDGSSVR.F
R1/RRR1-7/2	1763.725	1762.000	-156.305	0.432	1180.894	0.424	20	0.228	R.FLVLNAAELAVDGSSVR.F
R1/RRR1-5/2	1213.993	1213.324	-273.780	0.514	1201.217	0.354	16	0.222	K.LNVDQTGFYR.V
R1/RRR1-5/2	1467.645	1467.648	-1.553	0.486	516.361	0.525	18	0.214	K.TWPSSSLISDFVK.S
R1/RRR1-5/2	1188.116	1188.313	-166.078	0.303	965.551	0.392	16	0.210	K.ISVDATPELSR.D
R1/RRR1-5/2	1468.424	1467.648	-153.052	0.398	503.671	0.488	18	0.207	K.TWPSSSLISDFVK.S
R1/RRR1-5/2	1188.409	1188.313	81.224	0.369	693.781	0.331	15	0.194	-.ISVDATPELSR.-
R1/RRR1-5/2	1156.182	1156.269	-75.993	0.300	583.071	0.261	12	0.184	-.AAEVSEFFAGK.-
R1/RRR1-11/2	1189.467	1188.313	129.737	0.281	678.949	0.166	13	0.181	K.ISVDATPELSR.D
R1/RRR1-5/2	1929.572	1930.111	-799.733	0.505	840.546	0.483	19	0.111	R.SEPNLAQTVHELLQHNV.-
R1/RRR1-5/2	1929.839	1930.111	-141.582	0.473	615.065	0.492	17	0.107	R.SEPNLAQTVHELLQHNV.-
R1/RRR1-5/2	1928.938	1930.111	-1130.122	0.373	744.426	0.458	18	0.103	R.SEPNLAQTVHELLQHNV.-
R1/RRR1-5/3	1452.529	1451.603	-51.395	0.494	1420.317	0.222	26	0.093	-.VKYDDELAAGLEK.-
R1/RRR1-5/3	1338.599	1338.448	112.803	0.484	1075.887	0.331	22	0.087	-.IYRETAEAQEK.-
R1/RRR1-5/3	1451.251	1451.603	-243.626	0.476	1142.879	0.198	23	0.075	R.VKYDDELAAGLEK.A
R1/RRR1-5/3	1451.668	1451.603	44.894	0.459	1238.062	0.085	24	0.063	-.VKYDDELAAGLEK.-
R1/RRR1-23/3	1775.898	1775.858	22.736	0.548	2660.323	0.503	33	0.440	K.FEANRDVDNPDVIDR.L
R1/RRR1-23/3	1775.438	1775.858	-236.897	0.562	2439.810	0.407	32	0.327	K.FEANRDVDNPDVIDR.L
R1/RRR1-23/3	1622.154	1622.763	-995.002	0.491	2172.293	0.495	28	0.302	R.HLFYQDASDLREK.F
R1/RRR1-23/2	1424.187	1424.632	-313.583	0.464	1616.027	0.457	18	0.287	R.ALKDTLNWAVHR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/3	1775.241	1775.858	-913.130	0.519	2075.750	0.421	31	0.249	K.FEANRDVDNPDVIDR.L
R1/RRR1-23/2	1365.143	1365.476	-244.364	0.423	1277.518	0.426	17	0.241	R.HLFYQDASDLR.E
R1/RRR1-23/2	1194.245	1194.276	-25.898	0.521	1150.831	0.428	17	0.235	R.LIDDAEAQYR.N
R1/RRR1-23/2	1193.691	1194.276	-1331.622	0.433	1174.776	0.373	17	0.226	R.LIDDAEAQYR.N
R1/RRR1-23/2	1193.801	1194.276	-398.919	0.476	964.741	0.421	16	0.221	R.LIDDAEAQYR.N
R1/RRR1-24/2	1194.231	1194.276	-38.201	0.492	1108.215	0.346	17	0.217	R.LIDDAEAQYR.N
R1/RRR1-23/2	1157.819	1158.201	-330.843	0.386	918.660	0.398	15	0.212	R.DVDNPDVIDR.L
R1/RRR1-24/3	1774.995	1775.858	-1052.731	0.414	1795.026	0.443	28	0.206	K.FEANRDVDNPDVIDR.L
R1/RRR1-23/3	1424.393	1424.632	-168.624	0.524	1855.714	0.431	26	0.205	R.ALKDTLNWAVHR.H
R1/RRR1-24/2	1193.508	1194.276	-1485.910	0.347	909.471	0.307	16	0.202	R.LIDDAEAQYR.N
R1/RRR1-24/2	1194.129	1194.276	-123.511	0.468	708.539	0.326	16	0.201	R.LIDDAEAQYR.N
R1/RRR1-23/2	1413.477	1414.542	-1464.724	0.373	1424.540	0.431	17	0.198	K.GIEIIYNYGKED.-
R1/RRR1-24/2	1157.402	1158.201	-1558.287	0.285	746.448	0.338	14	0.196	R.DVDNPDVIDR.L
R1/RRR1-23/2	1157.390	1158.201	-1569.200	0.265	742.570	0.334	14	0.194	R.DVDNPDVIDR.L
R1/RRR1-23/2	1157.480	1158.201	-1490.801	0.296	659.820	0.320	13	0.193	R.DVDNPDVIDR.L
R1/RRR1-23/2	1414.161	1414.542	-270.006	0.421	1323.729	0.490	17	0.184	K.GIEIIYNYGKED.-
R1/RRR1-23/3	1622.840	1622.763	47.741	0.463	1674.713	0.443	26	0.183	R.HLFYQDASDLREK.F
R1/RRR1-24/3	1776.049	1775.858	108.044	0.527	1541.467	0.445	29	0.166	K.FEANRDVDNPDVIDR.L
R1/RRR1-23/3	1424.558	1424.632	-52.318	0.539	1570.402	0.407	26	0.152	R.ALKDTLNWAVHR.H
R1/RRR1-24/3	1423.934	1424.632	-1196.668	0.496	1449.187	0.449	25	0.150	R.ALKDTLNWAVHR.H
R1/RRR1-23/3	1424.362	1424.632	-190.547	0.496	1448.409	0.379	24	0.132	R.ALKDTLNWAVHR.H
R1/RRR1-24/3	1775.655	1775.858	-114.408	0.419	1161.570	0.344	25	0.102	K.FEANRDVDNPDVIDR.L
R1/RRR1-23/3	1622.678	1622.763	-52.645	0.387	1046.088	0.371	23	0.096	R.HLFYQDASDLREK.F
R1/RRR1-24/2	1414.276	1414.542	-188.347	0.258	592.314	0.214	14	0.085	K.GIEIIYNYGKED.-
R1/RRR1-13/2	1595.213	1594.754	288.159	0.571	2676.578	0.622	26	0.551	R.VADHAGVALAGLTADGR.V
R1/RRR1-13/2	1594.336	1594.754	-263.222	0.535	2600.529	0.560	25	0.503	R.VADHAGVALAGLTADGR.V
R1/RRR1-13/2	1594.293	1594.754	-289.955	0.522	2490.618	0.608	25	0.498	R.VADHAGVALAGLTADGR.V
R1/RRR1-13/2	1711.371	1711.770	-233.989	0.516	2026.598	0.562	23	0.381	R.NQYDTDVTTWSPAGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1711.340	1711.770	-252.094	0.537	2002.825	0.561	23	0.377	R.NQYDTDVTTWSPAGR.L
R1/RRR1-13/2	1710.906	1711.770	-1092.801	0.491	1973.542	0.507	22	0.352	R.NQYDTDVTTWSPAGR.L
R1/RRR1-13/2	1444.217	1444.678	-319.499	0.556	2085.913	0.427	19	0.344	R.LFQVEYAM*EAVK.Q
R1/RRR1-13/2	1444.214	1444.678	-321.704	0.478	1865.551	0.389	19	0.300	R.LFQVEYAM*EAVK.Q
R1/RRR1-13/2	1444.246	1444.678	-299.655	0.513	1867.438	0.372	19	0.294	R.LFQVEYAM*EAVK.Q
R1/RRR1-13/2	1503.441	1503.680	-159.586	0.459	1580.597	0.455	20	0.279	K.DALSAIKETLQGEK.L
R1/RRR1-13/2	1503.343	1503.680	-224.832	0.426	1264.879	0.474	19	0.248	K.DALSAIKETLQGEK.L
R1/RRR1-13/2	1503.210	1503.680	-313.307	0.449	1313.469	0.444	19	0.246	K.DALSAIKETLQGEK.L
R1/RRR1-13/2	1377.970	1378.551	-1150.343	0.429	1242.604	0.429	18	0.237	K.LTSSNCTVAIVGR.K
R1/RRR1-13/2	1873.522	1874.043	-813.921	0.520	643.944	0.477	16	0.202	R.RFEGYNDYTPEQLIK.D
R1/RRR1-13/2	1377.919	1378.551	-1188.061	0.350	780.760	0.386	16	0.200	K.LTSSNCTVAIVGR.K
R1/RRR1-13/2	1377.409	1378.551	-1559.256	0.278	1055.536	0.228	17	0.192	K.LTSSNCTVAIVGR.K
R1/RRR1-13/3	1895.179	1896.112	-1022.732	0.447	1034.201	0.476	29	0.117	R.KDDGTVEPFEM*IDVKR.I
R1/RRR1-13/3	1239.126	1239.410	-229.406	0.470	1074.996	0.351	22	0.095	R.SRTHAVLAAANK.A
R1/RRR1-13/3	1896.422	1896.112	164.392	0.450	792.278	0.338	26	0.083	R.KDDGTVEPFEM*IDVKR.I
R1/RRR1-13/3	1239.516	1239.410	86.409	0.452	876.120	0.249	20	0.073	-.SRTHAVLAAANK.-
R1/RRR1-11/2	1497.194	1497.546	-235.487	0.498	2228.939	0.589	22	0.430	R.SALDEVTDTGAFDR.S
R1/RRR1-12/2	1497.001	1497.546	-1034.830	0.481	2010.028	0.541	22	0.371	R.SALDEVTDTGAFDR.S
R1/RRR1-12/2	1539.266	1539.666	-260.470	0.522	2098.181	0.479	21	0.364	R.YICGNQLTEADVR.L
R1/RRR1-12/2	1497.209	1497.546	-225.426	0.533	1716.917	0.609	21	0.343	R.SALDEVTDTGAFDR.S
R1/RRR1-12/2	1739.488	1739.942	-261.318	0.583	1919.273	0.507	23	0.342	R.LYEALDKCEEILSR.Q
R1/RRR1-11/2	1739.965	1739.942	13.256	0.490	1802.813	0.519	22	0.328	R.LYEALDKCEEILSR.Q
R1/RRR1-12/2	1361.199	1361.484	-209.543	0.464	1875.272	0.475	19	0.326	K.TVVNNESSEIIR.M
R1/RRR1-11/2	1361.783	1361.484	220.941	0.494	1796.339	0.486	19	0.317	K.TVVNNESSEIIR.M
R1/RRR1-12/2	1497.169	1497.546	-252.746	0.556	1692.162	0.527	21	0.314	R.SALDEVTDTGAFDR.S
R1/RRR1-12/2	1539.263	1539.666	-262.220	0.550	1789.518	0.478	21	0.314	R.YICGNQLTEADVR.L
R1/RRR1-12/2	1361.187	1361.484	-218.719	0.497	1743.042	0.493	19	0.312	K.TVVNNESSEIIR.M
R1/RRR1-11/2	1740.216	1739.942	158.401	0.543	1648.396	0.526	21	0.307	R.LYEALDKCEEILSR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1739.330	1739.942	-929.300	0.605	1607.095	0.531	21	0.301	R.LYEALDKCEEILSR.Q
R1/RRR1-12/2	1739.695	1739.942	-142.418	0.589	1573.128	0.519	22	0.295	R.LYEALDKCEEILSR.Q
R1/RRR1-11/2	1361.117	1361.484	-270.004	0.451	1618.795	0.476	19	0.290	K.TVVNNESSEIIR.M
R1/RRR1-11/2	1361.134	1361.484	-257.857	0.435	1578.827	0.438	19	0.275	K.TVVNNESSEIIR.M
R1/RRR1-12/2	1361.138	1361.484	-254.438	0.450	1524.461	0.446	19	0.271	K.TVVNNESSEIIR.M
R1/RRR1-11/2	1538.468	1539.666	-1432.549	0.361	1602.971	0.365	21	0.260	R.YICGNQLTEADVR.L
R1/RRR1-12/2	1539.312	1539.666	-230.555	0.509	1422.942	0.445	19	0.258	R.YICGNQLTEADVR.L
R1/RRR1-11/2	1739.716	1739.942	-130.311	0.509	1349.930	0.473	20	0.257	R.LYEALDKCEEILSR.Q
R1/RRR1-12/3	1888.088	1888.159	-37.723	0.523	1873.484	0.509	33	0.249	K.GLDHAIGFTSVKPIFER.T
R1/RRR1-11/2	1538.521	1539.666	-1398.122	0.391	1343.783	0.371	20	0.236	R.YICGNQLTEADVR.L
R1/RRR1-11/2	1336.082	1336.432	-263.425	0.522	1017.173	0.404	17	0.220	K.KQEPYDEAVTR.L
R1/RRR1-11/2	1335.995	1336.432	-328.510	0.491	1029.930	0.396	17	0.219	K.KQEPYDEAVTR.L
R1/RRR1-12/2	1336.067	1336.432	-274.150	0.490	1031.064	0.363	17	0.214	K.KQEPYDEAVTR.L
R1/RRR1-12/2	1336.045	1336.432	-290.833	0.496	993.458	0.365	17	0.212	K.KQEPYDEAVTR.L
R1/RRR1-11/2	1335.563	1336.432	-1404.228	0.475	914.372	0.343	16	0.205	K.KQEPYDEAVTR.L
R1/RRR1-12/2	1336.098	1336.432	-251.051	0.475	954.529	0.330	16	0.204	K.KQEPYDEAVTR.L
R1/RRR1-11/2	1325.977	1326.501	-1152.723	0.386	927.154	0.323	15	0.201	R.M*LNTEFNEIAK.N
R1/RRR1-11/2	1326.346	1326.501	-117.132	0.386	755.090	0.279	16	0.193	R.M*LNTEFNEIAK.N
R1/RRR1-12/2	1310.087	1310.502	-317.343	0.299	416.951	0.327	13	0.191	R.MLNTEFNEIAK.N
R1/RRR1-12/3	1887.924	1888.159	-124.790	0.500	1402.940	0.548	30	0.184	K.GLDHAIGFTSVKPIFER.T
R1/RRR1-12/3	1255.815	1255.403	329.368	0.457	1639.482	0.474	24	0.174	R.FDEVYAVHFK.C
R1/RRR1-12/3	1888.774	1888.159	-204.110	0.399	1591.082	0.444	31	0.173	K.GLDHAIGFTSVKPIFER.T
R1/RRR1-12/3	1336.256	1336.432	-132.833	0.484	1757.360	0.392	26	0.167	K.KQEPYDEAVTR.L
R1/RRR1-12/3	1336.455	1336.432	16.562	0.539	1676.712	0.382	25	0.155	K.KQEPYDEAVTR.L
R1/RRR1-11/3	1887.344	1888.159	-964.635	0.393	1462.437	0.404	28	0.147	K.GLDHAIGFTSVKPIFER.T
R1/RRR1-12/3	1739.030	1739.942	-1102.453	0.542	1318.372	0.473	28	0.144	R.LYEALDKCEEILSR.Q
R1/RRR1-11/3	1336.525	1336.432	69.327	0.538	1655.264	0.335	26	0.136	K.KQEPYDEAVTR.L
R1/RRR1-11/3	1336.337	1336.432	-71.805	0.531	1516.914	0.357	24	0.130	K.KQEPYDEAVTR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/3	1255.773	1255.403	296.034	0.377	1171.636	0.488	21	0.124	R.FDEVYAVHFK.C
R1/RRR1-12/3	1739.505	1739.942	-251.469	0.541	1119.471	0.473	28	0.124	R.LYEALDKCEEILSR.Q
R1/RRR1-12/3	1255.402	1255.403	-0.558	0.449	1249.209	0.437	21	0.122	R.FDEVYAVHFK.C
R1/RRR1-12/3	1739.705	1739.942	-136.161	0.571	976.102	0.502	27	0.120	R.LYEALDKCEEILSR.Q
R1/RRR1-11/3	1336.486	1336.432	40.197	0.515	1458.084	0.344	24	0.120	K.KQEPYDEAVTR.L
R1/RRR1-12/3	1255.679	1255.403	220.879	0.415	1173.677	0.393	21	0.105	R.FDEVYAVHFK.C
R1/RRR1-11/3	1887.192	1888.159	-1045.095	0.339	721.273	0.262	23	0.076	K.GLDHAIGFTSVKPIFER.T
R1/RRR1-10/3	1749.670	1748.915	-140.704	0.557	2815.132	0.468	34	0.479	K.SYELPDGQVITIGAER.F
R1/RRR1-10/2	1460.062	1460.531	-322.062	0.424	2090.851	0.488	20	0.367	K.AEYDESGPSIVHR.K
R1/RRR1-10/2	1460.221	1460.531	-212.606	0.404	2077.890	0.482	20	0.363	K.AEYDESGPSIVHR.K
R1/RRR1-12/2	1748.296	1748.915	-928.946	0.528	1817.156	0.581	27	0.349	K.SYELPDGQVITIGAER.F
R1/RRR1-10/2	1748.341	1748.915	-903.081	0.552	1898.922	0.540	27	0.348	K.SYELPDGQVITIGAER.F
R1/RRR1-12/2	1749.375	1748.915	263.815	0.554	1650.548	0.580	26	0.323	K.SYELPDGQVITIGAER.F
R1/RRR1-12/2	1749.229	1748.915	179.983	0.589	1530.260	0.613	25	0.316	K.SYELPDGQVITIGAER.F
R1/RRR1-10/1	998.559	999.163	-1611.567	0.336	803.948	0.136	11	0.315	R.DLTDYLMK.I
R1/RRR1-10/2	1748.319	1748.915	-915.628	0.537	1604.945	0.545	26	0.307	K.SYELPDGQVITIGAER.F
R1/RRR1-9/2	1748.285	1748.915	-935.255	0.530	1553.001	0.551	25	0.301	K.SYELPDGQVITIGAER.F
R1/RRR1-11/2	1747.941	1748.915	-1132.619	0.509	1630.206	0.501	26	0.297	K.SYELPDGQVITIGAER.F
R1/RRR1-10/2	1748.474	1748.915	-252.762	0.534	1439.004	0.588	25	0.297	K.SYELPDGQVITIGAER.F
R1/RRR1-9/2	1748.322	1748.915	-913.665	0.511	1469.576	0.537	25	0.287	K.SYELPDGQVITIGAER.F
R1/RRR1-15/2	1748.493	1748.915	-241.906	0.496	1395.568	0.554	24	0.282	K.SYELPDGQVITIGAER.F
R1/RRR1-9/2	1749.629	1748.915	-164.142	0.549	1369.805	0.561	24	0.281	K.SYELPDGQVITIGAER.F
R1/RRR1-10/2	1459.669	1460.531	-1279.216	0.408	1345.011	0.494	17	0.259	K.AEYDESGPSIVHR.K
R1/RRR1-7/2	977.112	977.013	101.420	0.500	1213.297	0.490	16	0.252	K.AGFAGDDAPR.A
R1/RRR1-10/2	976.327	977.013	-1732.300	0.408	1253.262	0.464	16	0.248	K.AGFAGDDAPR.A
R1/RRR1-10/2	976.571	977.013	-454.056	0.473	1255.870	0.447	16	0.246	K.AGFAGDDAPR.A
R1/RRR1-10/2	976.297	977.013	-1762.450	0.387	1267.380	0.441	16	0.245	K.AGFAGDDAPR.A
R1/RRR1-7/2	977.026	977.013	13.708	0.477	1225.071	0.450	16	0.244	K.AGFAGDDAPR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	976.965	977.013	-49.078	0.429	1319.565	0.413	16	0.244	K.AGFAGDDAPR.A
R1/RRR1-1/2	977.062	977.013	50.299	0.426	1255.603	0.432	16	0.243	K.AGFAGDDAPR.A
R1/RRR1-1/2	976.672	977.013	-350.460	0.471	1264.837	0.415	16	0.240	K.AGFAGDDAPR.A
R1/RRR1-21/2	1748.042	1748.915	-1074.769	0.475	1287.238	0.419	23	0.239	K.SYELPDGQVITIGAER.F
R1/RRR1-10/2	976.845	977.013	-172.292	0.482	1207.323	0.426	16	0.238	K.AGFAGDDAPR.A
R1/RRR1-10/2	976.774	977.013	-245.633	0.468	1153.712	0.443	16	0.238	K.AGFAGDDAPR.A
R1/RRR1-12/2	1134.069	1133.193	-109.647	0.485	881.751	0.525	17	0.238	R.GYSFTTTAER.E
R1/RRR1-8/2	977.891	977.013	-125.281	0.492	1258.408	0.400	16	0.237	K.AGFAGDDAPR.A
R1/RRR1-12/2	1132.974	1133.193	-193.721	0.465	898.113	0.524	16	0.236	R.GYSFTTTAER.E
R1/RRR1-2/2	976.140	977.013	-1924.664	0.346	1254.710	0.407	16	0.236	K.AGFAGDDAPR.A
R1/RRR1-8/2	976.895	977.013	-120.646	0.435	1214.593	0.409	16	0.235	K.AGFAGDDAPR.A
R1/RRR1-13/2	1748.651	1748.915	-151.701	0.503	1104.551	0.473	22	0.235	K.SYELPDGQVITIGAER.F
R1/RRR1-9/2	976.784	977.013	-235.101	0.426	1234.795	0.399	16	0.235	K.AGFAGDDAPR.A
R1/RRR1-2/2	977.078	977.013	67.340	0.488	1226.872	0.400	16	0.234	K.AGFAGDDAPR.A
R1/RRR1-10/2	976.817	977.013	-200.624	0.478	1152.733	0.422	16	0.234	K.AGFAGDDAPR.A
R1/RRR1-10/2	1132.952	1133.193	-213.285	0.462	879.982	0.500	16	0.232	R.GYSFTTTAER.E
R1/RRR1-9/2	1133.997	1133.193	-172.924	0.457	799.067	0.523	16	0.231	R.GYSFTTTAER.E
R1/RRR1-10/2	1132.993	1133.193	-177.076	0.449	873.801	0.492	16	0.230	R.GYSFTTTAER.E
R1/RRR1-9/2	1133.027	1133.193	-147.138	0.475	864.662	0.488	16	0.229	R.GYSFTTTAER.E
R1/RRR1-9/2	976.888	977.013	-127.791	0.470	1201.776	0.379	16	0.229	K.AGFAGDDAPR.A
R1/RRR1-1/2	976.521	977.013	-505.610	0.386	1156.086	0.397	16	0.229	K.AGFAGDDAPR.A
R1/RRR1-10/2	1516.345	1516.687	-226.457	0.453	1082.334	0.435	17	0.229	K.IWHHTFYNELR.V
R1/RRR1-11/2	1132.877	1133.193	-279.226	0.419	807.985	0.512	16	0.229	R.GYSFTTTAER.E
R1/RRR1-8/2	976.848	977.013	-169.534	0.416	1218.071	0.361	16	0.227	K.AGFAGDDAPR.A
R1/RRR1-9/2	1132.999	1133.193	-171.564	0.398	857.306	0.483	16	0.226	R.GYSFTTTAER.E
R1/RRR1-2/2	1133.191	1133.193	-1.254	0.393	789.414	0.493	16	0.224	R.GYSFTTTAER.E
R1/RRR1-10/1	998.450	999.163	-1721.187	0.330	631.670	0.217	10	0.224	R.DLTDYLMK.I
R1/RRR1-9/2	976.617	977.013	-406.018	0.384	1214.503	0.342	16	0.223	K.AGFAGDDAPR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1132.735	1133.193	-405.293	0.364	784.206	0.489	16	0.222	R.GYSFTTTAER.E
R1/RRR1-10/2	1164.026	1164.355	-283.579	0.380	819.275	0.475	16	0.220	K.EITALAPSSM*K.I
R1/RRR1-10/2	1516.424	1516.687	-174.287	0.442	1045.102	0.403	16	0.219	K.IWHHTFYNELR.V
R1/RRR1-7/2	1132.995	1133.193	-175.130	0.373	740.094	0.447	16	0.216	R.GYSFTTTAER.E
R1/RRR1-10/2	1164.010	1164.355	-296.941	0.325	814.483	0.469	16	0.216	K.EITALAPSSM*K.I
R1/RRR1-11/2	1132.348	1133.193	-1633.636	0.300	786.014	0.467	16	0.215	R.GYSFTTTAER.E
R1/RRR1-12/2	1165.175	1164.355	-154.997	0.411	864.679	0.418	16	0.215	K.EITALAPSSM*K.I
R1/RRR1-10/2	1132.144	1133.193	-1814.859	0.334	799.661	0.432	16	0.214	R.GYSFTTTAER.E
R1/RRR1-14/2	976.360	977.013	-1697.881	0.389	1010.720	0.362	14	0.214	K.AGFAGDDAPR.A
R1/RRR1-2/2	976.911	977.013	-104.978	0.410	791.702	0.395	14	0.211	K.AGFAGDDAPR.A
R1/RRR1-10/2	1516.174	1516.687	-1000.910	0.427	963.065	0.371	16	0.210	K.IWHHTFYNELR.V
R1/RRR1-10/2	1748.791	1748.915	-70.965	0.378	676.574	0.464	16	0.205	K.SYELPDGQVITIGAER.F
R1/RRR1-10/2	1145.139	1145.381	-212.298	0.384	224.822	0.532	15	0.205	R.HTGVMVGMGQK.D
R1/RRR1-11/2	1132.938	1133.193	-225.176	0.321	562.757	0.398	14	0.204	R.GYSFTTTAER.E
R1/RRR1-11/2	1164.014	1164.355	-293.575	0.290	681.912	0.420	15	0.204	K.EITALAPSSM*K.I
R1/RRR1-10/2	1148.206	1148.355	-130.690	0.361	619.987	0.402	13	0.202	K.EITALAPSSMK.I
R1/RRR1-25/2	1163.995	1164.355	-309.778	0.284	505.940	0.432	14	0.201	K.EITALAPSSM*K.I
R1/RRR1-15/2	1132.849	1133.193	-304.090	0.304	471.421	0.337	14	0.201	R.GYSFTTTAER.E
R1/RRR1-11/2	1163.984	1164.355	-319.669	0.271	585.112	0.411	14	0.200	K.EITALAPSSM*K.I
R1/RRR1-10/2	1163.903	1164.355	-388.909	0.273	684.376	0.394	14	0.199	-.EITALAPSSM*K.-
R1/RRR1-10/2	1132.859	1133.193	-295.874	0.306	307.566	0.297	12	0.198	-.GYSFTTTAER.-
R1/RRR1-14/2	976.229	977.013	-1833.184	0.298	794.652	0.273	14	0.197	K.AGFAGDDAPR.A
R1/RRR1-12/2	1164.035	1164.355	-275.373	0.387	492.727	0.323	13	0.196	K.EITALAPSSM*K.I
R1/RRR1-12/2	1163.900	1164.355	-391.750	0.287	734.987	0.304	15	0.196	K.EITALAPSSM*K.I
R1/RRR1-10/2	1148.201	1148.355	-134.850	0.301	473.211	0.294	12	0.193	K.EITALAPSSMK.I
R1/RRR1-13/2	976.360	977.013	-1697.629	0.271	913.443	0.179	14	0.191	K.AGFAGDDAPR.A
R1/RRR1-15/2	1164.402	1164.355	41.004	0.271	551.422	0.257	12	0.190	K.EITALAPSSM*K.I
R1/RRR1-10/3	1516.753	1516.687	43.774	0.513	1225.160	0.459	24	0.125	K.IWHHTFYNELR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1516.172	1516.687	-1001.969	0.503	1350.163	0.406	25	0.122	K.IWHHTFYNELR.V
R1/RRR1-10/3	1516.622	1516.687	-42.683	0.468	1151.609	0.364	22	0.101	K.IWHHTFYNELR.V
R1/RRR1-10/3	1516.662	1516.687	-16.405	0.482	991.921	0.395	22	0.098	K.IWHHTFYNELR.V
R1/RRR1-10/3	1146.000	1145.381	-334.053	0.451	1071.040	0.366	21	0.096	R.HTGVMVGMGQK.D
R1/RRR1-12/3	1750.394	1748.915	274.216	0.399	567.448	0.440	25	0.091	K.SYELPDGQVITIGAER.F
R1/RRR1-10/3	1517.055	1516.687	243.152	0.500	889.174	0.330	21	0.087	K.IWHHTFYNELR.V
R1/RRR1-10/3	1145.071	1145.381	-272.201	0.421	804.873	0.375	19	0.086	R.HTGVMVGMGQK.D
R1/RRR1-12/3	1517.377	1516.687	-204.647	0.415	564.521	0.265	23	0.085	K.IWHHTFYNELR.V
R1/RRR1-10/3	1517.546	1516.687	-93.164	0.401	634.644	0.282	19	0.083	K.IWHHTFYNELR.V
R1/RRR1-12/3	1516.713	1516.687	17.257	0.408	466.732	0.289	21	0.081	-.IWHHTFYNELR.-
R1/RRR1-12/3	1517.130	1516.687	292.651	0.420	638.101	0.261	20	0.078	-.IWHHTFYNELR.-
R1/RRR1-12/3	1749.327	1748.915	235.993	0.349	730.932	0.278	27	0.075	K.SYELPDGQVITIGAER.F
R1/RRR1-11/2	1685.437	1684.961	283.339	0.478	2246.873	0.554	24	0.426	R.ILVTGGAGFIGSHLVDK.L
R1/RRR1-11/2	1446.283	1445.753	-326.062	0.573	2183.148	0.531	23	0.396	K.TNVIGTLNMLGLAK.R
R1/RRR1-11/2	1462.207	1461.753	311.906	0.551	1999.725	0.586	23	0.383	K.TNVIGTLNM*LGLAK.R
R1/RRR1-11/2	1203.584	1204.404	-1516.297	0.482	2176.766	0.466	19	0.376	R.VVSNFIAQAVR.G
R1/RRR1-11/2	1445.369	1445.753	-266.802	0.565	2092.493	0.514	23	0.373	K.TNVIGTLNMLGLAK.R
R1/RRR1-11/2	1445.315	1445.753	-304.170	0.553	1979.519	0.532	23	0.360	K.TNVIGTLNMLGLAK.R
R1/RRR1-11/2	1203.530	1204.404	-1561.330	0.455	2091.432	0.460	19	0.358	R.VVSNFIAQAVR.G
R1/RRR1-11/2	1460.577	1461.753	-1493.893	0.415	2075.280	0.468	23	0.355	K.TNVIGTLNM*LGLAK.R
R1/RRR1-11/2	1203.739	1204.404	-1386.824	0.492	2188.320	0.381	19	0.348	R.VVSNFIAQAVR.G
R1/RRR1-11/2	1461.236	1461.753	-1040.838	0.466	2010.914	0.439	23	0.335	K.TNVIGTLNM*LGLAK.R
R1/RRR1-11/2	1616.706	1617.885	-1351.637	0.413	1670.427	0.422	21	0.284	R.SFCYVADMVNGLIK.L
R1/RRR1-11/2	1512.357	1512.693	-222.763	0.474	948.738	0.575	21	0.244	R.GEPLTVQKPGTQTR.S
R1/RRR1-11/2	1512.356	1512.693	-223.735	0.436	947.109	0.559	21	0.240	R.GEPLTVQKPGTQTR.S
R1/RRR1-11/2	1156.422	1157.344	-1666.435	0.468	1231.316	0.403	15	0.233	K.AKEVLGWEPK.I
R1/RRR1-11/2	1512.415	1512.693	-184.382	0.386	887.988	0.507	20	0.224	R.GEPLTVQKPGTQTR.S
R1/RRR1-11/2	1157.261	1157.344	-72.008	0.471	1011.133	0.399	14	0.216	K.AKEVLGWEPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1461.523	1461.753	-157.329	0.367	1098.297	0.356	20	0.215	K.TNVIGTLNM*LGLAK.R
R1/RRR1-11/2	967.790	968.091	-311.928	0.436	649.148	0.397	12	0.208	R.IFNTYGPR.M
R1/RRR1-10/2	968.445	968.091	366.811	0.417	729.582	0.373	12	0.207	R.IFNTYGPR.M
R1/RRR1-11/2	967.876	968.091	-222.844	0.435	808.396	0.334	13	0.206	R.IFNTYGPR.M
R1/RRR1-12/2	967.990	968.091	-104.175	0.422	597.004	0.356	11	0.202	R.IFNTYGPR.M
R1/RRR1-10/2	968.209	968.091	122.459	0.391	610.615	0.380	11	0.201	-.IFNTYGPR.-
R1/RRR1-12/2	967.972	968.091	-123.276	0.435	643.819	0.334	12	0.199	-.IFNTYGPR.-
R1/RRR1-11/2	967.943	968.091	-152.879	0.438	675.261	0.353	12	0.198	-.IFNTYGPR.-
R1/RRR1-10/2	968.067	968.091	-24.613	0.369	676.654	0.248	11	0.193	R.IFNTYGPR.M
R1/RRR1-11/2	1205.228	1204.404	-145.942	0.445	807.119	0.261	14	0.188	R.VVSNFIAQAVR.G
R1/RRR1-12/2	968.082	968.091	-8.804	0.439	696.775	0.323	12	0.186	-.IFNTYGPR.-
R1/RRR1-12/2	1462.463	1461.753	-198.837	0.183	580.501	0.068	15	0.182	-.TNVIGTLNM*LGLAK.-
R1/RRR1-11/3	1445.970	1445.753	150.405	0.429	1442.844	0.367	25	0.133	K.TNVIGTLNMLGLAK.R
R1/RRR1-11/3	1382.559	1382.570	-7.768	0.451	822.665	0.533	24	0.108	R.VAETLMFDYHR.Q
R1/RRR1-11/3	1382.524	1382.570	-33.141	0.462	699.134	0.489	21	0.100	R.VAETLMFDYHR.Q
R1/RRR1-11/3	1398.489	1398.569	-57.548	0.440	597.789	0.498	23	0.097	R.VAETLM*FDYHR.Q
R1/RRR1-11/3	1398.472	1398.569	-69.761	0.352	431.044	0.518	20	0.095	R.VAETLM*FDYHR.Q
R1/RRR1-10/2	1826.170	1827.024	-1018.194	0.473	1982.580	0.477	22	0.343	K.LAYVALDYEQELEAAK.S
R1/RRR1-10/2	1826.363	1827.024	-912.501	0.480	1894.855	0.442	21	0.317	K.LAYVALDYEQELEAAK.S
R1/RRR1-10/2	1826.357	1827.024	-915.655	0.486	1818.963	0.421	21	0.299	K.LAYVALDYEQELEAAK.S
R1/RRR1-10/2	1430.085	1430.504	-294.225	0.439	1624.731	0.481	18	0.293	K.GEYDESGPAIVHR.K
R1/RRR1-6/2	1740.461	1740.944	-278.196	0.558	2691.595	0.553	24	0.523	R.NIIHFNTLANQAVER.A
R1/RRR1-6/2	1740.374	1740.944	-905.034	0.551	2551.044	0.597	24	0.509	R.NIIHFNTLANQAVER.A
R1/RRR1-6/2	1740.544	1740.944	-230.700	0.560	2577.990	0.578	24	0.506	R.NIIHFNTLANQAVER.A
R1/RRR1-6/2	1562.338	1562.774	-279.881	0.519	2515.414	0.450	22	0.434	R.TTLVANTSNM*PVAAR.E
R1/RRR1-6/2	1519.094	1519.635	-1017.201	0.528	2160.355	0.586	24	0.418	K.FEDPAEGEDVLVAK.F
R1/RRR1-6/2	1561.622	1562.774	-1381.969	0.369	2506.361	0.376	22	0.407	R.TTLVANTSNM*PVAAR.E
R1/RRR1-6/2	1546.364	1546.775	-266.637	0.505	2184.179	0.530	23	0.398	R.TTLVANTSNMPVAAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1518.644	1519.635	-1314.514	0.406	2089.386	0.540	23	0.384	K.FEDPAEGEDVLVAK.F
R1/RRR1-6/2	1562.314	1562.774	-295.088	0.488	2291.908	0.435	22	0.383	R.TTLVANTSNM*PVAAR.E
R1/RRR1-7/2	1562.115	1562.774	-1064.961	0.460	2207.112	0.460	22	0.377	R.TTLVANTSNM*PVAAR.E
R1/RRR1-6/2	1518.439	1519.635	-1450.317	0.379	2041.237	0.543	23	0.375	K.FEDPAEGEDVLVAK.F
R1/RRR1-6/2	1605.415	1605.769	-220.833	0.542	1814.287	0.553	22	0.341	K.DALAESDKITLETAK.L
R1/RRR1-6/2	1812.295	1813.024	-956.859	0.518	1645.795	0.623	24	0.334	R.LAEM*PADSGYPAYLAAR.L
R1/RRR1-6/2	1812.427	1813.024	-883.831	0.524	1603.126	0.605	24	0.322	R.LAEM*PADSGYPAYLAAR.L
R1/RRR1-6/2	1606.336	1605.769	-270.555	0.565	1601.085	0.582	22	0.318	K.DALAESDKITLETAK.L
R1/RRR1-6/3	1741.944	1740.944	-0.332	0.596	2101.832	0.517	29	0.305	R.NIIHFNTLANQAVER.A
R1/RRR1-7/3	1741.681	1740.944	-151.543	0.513	2082.703	0.487	29	0.284	R.NIIHFNTLANQAVER.A
R1/RRR1-6/3	1741.054	1740.944	63.416	0.571	2180.360	0.443	31	0.283	R.NIIHFNTLANQAVER.A
R1/RRR1-6/2	1605.191	1605.769	-985.753	0.501	1302.680	0.539	20	0.267	K.DALAESDKITLETAK.L
R1/RRR1-6/2	1473.412	1472.623	-143.643	0.508	1314.261	0.515	19	0.264	R.EDDLNEIVQLVGK.D
R1/RRR1-6/2	1796.354	1797.025	-932.720	0.468	1221.990	0.534	23	0.257	R.LAEMPADSGYPAYLAAR.L
R1/RRR1-6/2	1796.460	1797.025	-873.780	0.487	1132.405	0.559	22	0.253	R.LAEMPADSGYPAYLAAR.L
R1/RRR1-6/2	1201.331	1201.310	17.773	0.588	1171.247	0.499	17	0.251	K.LYDDLTTGFR.N
R1/RRR1-7/2	1812.459	1813.024	-866.455	0.521	1035.742	0.593	20	0.250	R.LAEM*PADSGYPAYLAAR.L
R1/RRR1-6/2	1471.856	1472.623	-1203.906	0.363	1517.642	0.356	20	0.249	R.EDDLNEIVQLVGK.D
R1/RRR1-6/2	1201.114	1201.310	-163.465	0.544	1148.860	0.469	17	0.243	K.LYDDLTTGFR.N
R1/RRR1-6/2	1472.265	1472.623	-243.632	0.381	1341.283	0.389	19	0.238	R.EDDLNEIVQLVGK.D
R1/RRR1-7/2	1201.034	1201.310	-230.554	0.424	1141.196	0.406	17	0.229	K.LYDDLTTGFR.N
R1/RRR1-6/2	1812.272	1813.024	-970.046	0.516	770.842	0.552	20	0.224	R.LAEM*PADSGYPAYLAAR.L
R1/RRR1-6/3	1741.141	1740.944	113.621	0.535	1904.520	0.387	28	0.208	R.NIIHFNTLANQAVER.A
R1/RRR1-6/2	1578.153	1578.795	-1043.294	0.433	386.155	0.481	17	0.205	K.HFPSVNWLISYSK.Y
R1/RRR1-6/2	1579.579	1578.795	-137.399	0.472	476.490	0.447	18	0.205	K.HFPSVNWLISYSK.Y
R1/RRR1-7/3	1741.843	1740.944	-58.533	0.466	1601.008	0.455	27	0.181	R.NIIHFNTLANQAVER.A
R1/RRR1-6/3	1814.190	1813.024	91.483	0.423	1223.532	0.481	29	0.138	R.LAEM*PADSGYPAYLAAR.L
R1/RRR1-6/3	1606.004	1605.769	147.006	0.508	1177.863	0.462	28	0.128	K.DALAESDKITLETAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/3	1563.037	1562.774	168.494	0.492	1242.130	0.395	28	0.118	R.TTLVANTSNM*PVAAR.E
R1/RRR1-6/3	1607.091	1605.769	201.036	0.495	638.201	0.544	23	0.111	K.DALAESDKITLETAK.L
R1/RRR1-6/3	1562.553	1562.774	-141.982	0.375	1235.442	0.372	26	0.110	R.TTLVANTSNM*PVAAR.E
R1/RRR1-6/3	1741.538	1740.944	-234.232	0.482	958.612	0.430	24	0.109	R.NIIHFNTLANQAVER.A
R1/RRR1-6/3	1605.535	1605.769	-146.015	0.473	907.760	0.456	27	0.106	K.DALAESDKITLETAK.L
R1/RRR1-12/2	1747.688	1748.146	-262.754	0.519	2391.750	0.538	27	0.445	K.VAVLGAAGGIGQPLGLLIK.M
R1/RRR1-12/2	1746.899	1748.146	-1290.011	0.444	2184.657	0.535	27	0.401	K.VAVLGAAGGIGQPLGLLIK.M
R1/RRR1-12/2	1468.979	1469.649	-1140.085	0.398	1897.699	0.445	24	0.321	K.AGAGSATLSMAYAAAR.F
R1/RRR1-12/2	1747.051	1748.146	-1202.787	0.451	1767.584	0.503	25	0.316	K.VAVLGAAGGIGQPLGLLIK.M
R1/RRR1-12/2	1347.872	1348.616	-1297.752	0.540	1742.262	0.474	20	0.307	K.KLFGVTTLDVVR.A
R1/RRR1-12/2	1347.995	1348.616	-1206.351	0.503	1768.693	0.443	20	0.302	K.KLFGVTTLDVVR.A
R1/RRR1-12/2	1277.468	1278.526	-1615.398	0.370	1664.621	0.481	19	0.295	K.GVDVVVIPAGVPR.K
R1/RRR1-12/2	1349.314	1348.616	-224.364	0.548	1647.658	0.472	20	0.294	K.KLFGVTTLDVVR.A
R1/RRR1-11/2	1348.609	1348.616	-4.867	0.436	1595.408	0.384	19	0.264	K.KLFGVTTLDVVR.A
R1/RRR1-12/2	1485.754	1485.648	71.533	0.426	1304.283	0.491	21	0.254	K.AGAGSATLSM*AYAAAR.F
R1/RRR1-12/2	1486.071	1485.648	285.236	0.489	1359.456	0.465	21	0.254	K.AGAGSATLSM*AYAAAR.F
R1/RRR1-12/2	1220.487	1220.443	36.053	0.509	1257.755	0.466	19	0.251	K.LFGVTTLDVVR.A
R1/RRR1-12/2	1259.150	1259.391	-191.909	0.509	1151.237	0.475	20	0.243	R.IQNAGTEVVEAK.A
R1/RRR1-12/2	1278.265	1278.526	-204.364	0.389	1179.309	0.486	18	0.242	K.GVDVVVIPAGVPR.K
R1/RRR1-12/2	1220.177	1220.443	-218.308	0.503	1488.184	0.336	19	0.242	K.LFGVTTLDVVR.A
R1/RRR1-12/2	1259.123	1259.391	-213.986	0.526	1086.510	0.488	19	0.240	R.IQNAGTEVVEAK.A
R1/RRR1-12/2	1220.328	1220.443	-94.673	0.504	1465.463	0.302	19	0.232	K.LFGVTTLDVVR.A
R1/RRR1-12/2	1259.133	1259.391	-205.817	0.506	851.565	0.498	18	0.226	R.IQNAGTEVVEAK.A
R1/RRR1-11/2	1221.307	1220.443	-112.041	0.463	1047.757	0.369	18	0.218	K.LFGVTTLDVVR.A
R1/RRR1-12/2	1415.206	1415.578	-263.404	0.477	1043.075	0.396	19	0.218	K.RIQNAGTEVVEAK.A
R1/RRR1-11/2	1221.465	1220.443	18.383	0.471	1034.409	0.371	17	0.217	K.LFGVTTLDVVR.A
R1/RRR1-10/2	1221.466	1220.443	19.084	0.355	1088.250	0.349	17	0.215	K.LFGVTTLDVVR.A
R1/RRR1-12/2	1277.618	1278.526	-1497.527	0.335	890.688	0.449	16	0.212	K.GVDVVVIPAGVPR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1220.187	1220.443	-210.680	0.410	1059.884	0.334	17	0.212	K.LFGVTTLDVVR.A
R1/RRR1-12/2	1415.334	1415.578	-172.635	0.469	894.221	0.377	17	0.205	K.RIQNAGTEVVEAK.A
R1/RRR1-11/2	1220.368	1220.443	-61.361	0.344	692.695	0.338	15	0.200	K.LFGVTTLDVVR.A
R1/RRR1-12/2	1415.136	1415.578	-313.253	0.425	686.762	0.360	17	0.197	K.RIQNAGTEVVEAK.A
R1/RRR1-13/2	1219.740	1220.443	-1400.049	0.319	487.923	0.281	13	0.194	K.LFGVTTLDVVR.A
R1/RRR1-13/2	1278.239	1278.526	-224.675	0.244	1041.081	0.237	17	0.192	K.GVDVVVIPAGVPR.K
R1/RRR1-8/2	1220.955	1220.443	-400.577	0.208	673.286	0.323	14	0.192	K.LFGVTTLDVVR.A
R1/RRR1-14/2	1219.685	1220.443	-1445.486	0.279	695.197	0.246	15	0.191	-.LFGVTTLDVVR.-
R1/RRR1-13/2	1220.348	1220.443	-78.418	0.228	504.148	0.299	13	0.190	-.LFGVTTLDVVR.-
R1/RRR1-12/3	1747.834	1748.146	-179.169	0.472	1232.487	0.407	31	0.124	K.VAVLGAAGGIGQPLGLLIK.M
R1/RRR1-12/3	1747.408	1748.146	-997.777	0.459	1087.853	0.396	31	0.108	K.VAVLGAAGGIGQPLGLLIK.M
R1/RRR1-12/3	1485.336	1485.648	-210.532	0.447	932.778	0.427	26	0.102	K.AGAGSATLSM*AYAAAR.F
R1/RRR1-12/3	1982.621	1983.123	-759.568	0.506	983.994	0.375	28	0.098	K.TRPSVTFTNEETEELTK.R
R1/RRR1-12/3	1982.560	1983.123	-790.717	0.321	307.516	0.398	20	0.081	-.TRPSVTFTNEETEELTK.-
R1/RRR1-12/3	1348.900	1348.616	211.333	0.511	1026.102	0.300	27	0.077	-.KLFGVTTLDVVR.-
R1/RRR1-12/3	1484.837	1485.648	-1223.144	0.376	569.597	0.318	22	0.076	-.AGAGSATLSM*AYAAAR.-
R1/RRR1-12/3	1348.958	1348.616	254.482	0.510	960.550	0.341	26	0.076	-.KLFGVTTLDVVR.-
R1/RRR1-12/3	1347.974	1348.616	-1221.593	0.423	835.155	0.250	25	0.059	-.KLFGVTTLDVVR.-
R1/RRR1-4/2	1343.102	1343.599	-370.984	0.422	1714.201	0.435	18	0.293	R.IIWSNLLQSLR.S
R1/RRR1-4/2	1343.423	1343.599	-131.567	0.406	1535.971	0.357	16	0.251	R.IIWSNLLQSLR.S
R1/RRR1-4/2	1698.433	1697.998	257.310	0.472	1253.896	0.474	20	0.245	K.QLLIGTIGDQVLALDK.R
R1/RRR1-4/2	1352.257	1352.561	-225.415	0.440	1078.672	0.491	17	0.235	K.YVVTLSSGGSILR.A
R1/RRR1-4/2	1280.354	1281.397	-1600.186	0.345	911.966	0.475	16	0.220	K.FTSDVTNEVIR.E
R1/RRR1-4/2	1580.167	1579.735	274.244	0.400	1009.927	0.401	18	0.215	K.ELWSIVFPSDTER.I
R1/RRR1-4/2	1078.092	1077.259	-154.635	0.486	985.777	0.364	14	0.212	K.LNLYQLNAK.T
R1/RRR1-4/2	1212.179	1212.398	-181.332	0.476	767.554	0.422	16	0.212	K.IIADQDVM*YK.Y
R1/RRR1-4/2	1697.649	1697.998	-205.734	0.437	674.690	0.515	16	0.209	K.QLLIGTIGDQVLALDK.R
R1/RRR1-4/2	1212.079	1212.398	-263.774	0.501	843.758	0.379	16	0.208	K.IIADQDVM*YK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1280.988	1281.397	-319.868	0.406	584.160	0.419	14	0.201	K.FTSDVTNEVIR.E
R1/RRR1-1/2	1958.801	1958.163	-185.055	0.487	762.823	0.454	15	0.199	K.DGVSVANVEHNLFEWLK.G
R1/RRR1-3/2	1699.283	1697.998	168.269	0.431	611.435	0.431	17	0.198	K.QLLIGTIGDQVLALDK.R
R1/RRR1-4/2	1554.584	1553.785	-130.078	0.403	753.430	0.387	18	0.197	K.VHISDLVQGLSGTVK.L
R1/RRR1-4/2	1077.378	1077.259	111.074	0.445	918.649	0.266	14	0.196	K.LNLYQLNAK.T
R1/RRR1-4/2	1280.552	1281.397	-1444.664	0.336	483.213	0.373	13	0.194	K.FTSDVTNEVIR.E
R1/RRR1-4/2	1351.700	1352.561	-1381.123	0.287	741.279	0.281	15	0.186	K.YVVTLSSGGSILR.A
R1/RRR1-4/2	1076.713	1077.259	-1439.679	0.250	689.942	0.115	12	0.181	-.LNLYQLNAK.-
R1/RRR1-4/2	1579.121	1579.735	-1025.288	0.171	798.552	0.080	16	0.175	K.ELWSIVFPSDTER.I
R1/RRR1-6/2	1707.365	1707.826	-270.752	0.531	1502.278	0.558	22	0.296	R.EVNSVNDNPVIDVHR.G
R1/RRR1-2/2	1708.628	1707.826	-116.416	0.559	1475.551	0.560	23	0.294	R.EVNSVNDNPVIDVHR.G
R1/RRR1-2/2	1707.405	1707.826	-247.584	0.517	1436.643	0.580	22	0.294	R.EVNSVNDNPVIDVHR.G
R1/RRR1-6/2	1376.515	1377.528	-1466.697	0.360	1504.609	0.478	20	0.274	R.VAFETGTAPITNR.I
R1/RRR1-6/2	1709.267	1707.826	258.616	0.548	1207.354	0.598	22	0.273	R.EVNSVNDNPVIDVHR.G
R1/RRR1-1/2	1707.391	1707.826	-255.689	0.507	1306.474	0.549	20	0.269	R.EVNSVNDNPVIDVHR.G
R1/RRR1-6/2	1709.198	1707.826	218.368	0.568	1173.753	0.593	21	0.267	R.EVNSVNDNPVIDVHR.G
R1/RRR1-6/2	1376.722	1377.528	-1315.824	0.339	1525.304	0.317	20	0.241	R.VAFETGTAPITNR.I
R1/RRR1-6/2	1624.473	1624.865	-242.285	0.492	885.043	0.477	19	0.225	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1376.562	1377.528	-1432.226	0.324	1123.718	0.419	18	0.224	R.VAFETGTAPITNR.I
R1/RRR1-2/2	1624.438	1624.865	-263.621	0.513	840.933	0.476	19	0.222	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1625.526	1624.865	-209.062	0.525	819.398	0.480	19	0.222	R.TSPQWLGPQIEVIR.A
R1/RRR1-1/2	1625.486	1624.865	-234.075	0.525	796.580	0.477	19	0.221	R.TSPQWLGPQIEVIR.A
R1/RRR1-4/2	1624.285	1624.865	-975.522	0.488	685.594	0.507	18	0.220	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1624.338	1624.865	-943.229	0.503	797.190	0.461	19	0.219	R.TSPQWLGPQIEVIR.A
R1/RRR1-3/2	1624.398	1624.865	-288.350	0.484	812.237	0.467	18	0.219	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1625.700	1624.865	-102.020	0.482	822.740	0.444	19	0.217	R.TSPQWLGPQIEVIR.A
R1/RRR1-5/2	1624.564	1624.865	-186.124	0.478	716.984	0.476	18	0.217	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1625.482	1624.865	-236.109	0.509	646.049	0.481	18	0.216	R.TSPQWLGPQIEVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1624.777	1624.865	-54.152	0.508	745.142	0.463	18	0.216	R.TSPQWLGPQIEVIR.A
R1/RRR1-1/2	1624.666	1624.865	-123.111	0.502	709.602	0.469	18	0.216	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1624.458	1624.865	-251.558	0.464	875.458	0.420	19	0.216	R.TSPQWLGPQIEVIR.A
R1/RRR1-2/2	1624.375	1624.865	-302.750	0.451	798.061	0.447	18	0.215	R.TSPQWLGPQIEVIR.A
R1/RRR1-3/2	1624.488	1624.865	-232.862	0.448	808.489	0.418	19	0.213	R.TSPQWLGPQIEVIR.A
R1/RRR1-5/2	1624.367	1624.865	-307.726	0.449	795.806	0.420	19	0.213	R.TSPQWLGPQIEVIR.A
R1/RRR1-5/2	1625.493	1624.865	-229.554	0.499	593.308	0.457	18	0.212	R.TSPQWLGPQIEVIR.A
R1/RRR1-2/2	1625.287	1624.865	260.152	0.535	740.552	0.440	18	0.212	R.TSPQWLGPQIEVIR.A
R1/RRR1-7/2	1625.035	1624.865	105.134	0.407	698.201	0.414	19	0.210	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1040.891	1041.138	-238.383	0.396	455.539	0.485	13	0.210	R.NPSLDYGFK.G
R1/RRR1-6/1	799.610	799.981	-465.562	0.267	521.439	0.415	10	0.209	R.LAIANIGK.L
R1/RRR1-1/2	1624.623	1624.865	-149.491	0.477	667.716	0.426	17	0.208	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1040.915	1041.138	-215.088	0.412	449.879	0.441	13	0.207	R.NPSLDYGFK.G
R1/RRR1-7/2	1624.429	1624.865	-269.350	0.458	526.613	0.436	16	0.206	R.TSPQWLGPQIEVIR.A
R1/RRR1-8/2	1624.438	1624.865	-263.696	0.409	566.709	0.432	16	0.206	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	872.412	873.032	-1862.430	0.298	841.748	0.407	12	0.206	K.ALLTAIDR.E
R1/RRR1-4/2	1624.439	1624.865	-263.093	0.475	563.275	0.431	16	0.206	R.TSPQWLGPQIEVIR.A
R1/RRR1-8/2	1624.339	1624.865	-942.626	0.408	581.059	0.396	17	0.204	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	935.127	935.102	26.957	0.510	821.932	0.340	13	0.201	K.VFLAISER.K
R1/RRR1-7/2	1624.200	1624.865	-1028.567	0.414	560.082	0.373	16	0.201	R.TSPQWLGPQIEVIR.A
R1/RRR1-4/2	1624.317	1624.865	-956.206	0.313	548.246	0.384	15	0.199	R.TSPQWLGPQIEVIR.A
R1/RRR1-5/2	1040.895	1041.138	-234.383	0.303	357.339	0.393	12	0.198	R.NPSLDYGFK.G
R1/RRR1-6/3	1464.749	1465.683	-1324.399	0.537	1541.442	0.535	29	0.197	K.KVLTTGPAGGLHSAR.F
R1/RRR1-2/2	1625.434	1624.865	-265.869	0.330	674.180	0.321	16	0.197	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1625.826	1624.865	-23.918	0.375	461.357	0.300	15	0.196	R.TSPQWLGPQIEVIR.A
R1/RRR1-6/2	1040.483	1041.138	-1595.361	0.278	459.569	0.360	13	0.196	R.NPSLDYGFK.G
R1/RRR1-6/1	799.410	799.981	-1971.227	0.278	494.959	0.402	10	0.193	R.LAIANIGK.L
R1/RRR1-6/2	872.619	873.032	-475.032	0.310	566.627	0.302	11	0.192	K.ALLTAIDR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1625.320	1624.865	280.712	0.375	250.792	0.325	12	0.191	-.TSPQWLGPQIEVIR.-
R1/RRR1-1/2	1378.555	1377.528	19.663	0.347	751.794	0.275	16	0.190	R.VAFETGTAPITNR.I
R1/RRR1-6/2	872.601	873.032	-495.247	0.266	709.467	0.267	12	0.190	K.ALLTAIDR.E
R1/RRR1-6/2	1625.245	1624.865	234.319	0.307	327.423	0.341	12	0.187	-.TSPQWLGPQIEVIR.-
R1/RRR1-1/2	1377.076	1377.528	-328.845	0.300	709.130	0.171	16	0.183	R.VAFETGTAPITNR.I
R1/RRR1-6/1	799.480	799.981	-1883.993	0.263	467.930	0.390	10	0.179	R.LAIANIGK.L
R1/RRR1-6/3	1465.647	1465.683	-24.495	0.536	1423.682	0.536	29	0.179	K.KVLTTGPAGGLHSAR.F
R1/RRR1-6/3	1464.686	1465.683	-1367.338	0.510	1383.388	0.545	28	0.177	K.KVLTTGPAGGLHSAR.F
R1/RRR1-2/3	1464.862	1465.683	-1246.690	0.381	732.230	0.418	25	0.092	K.KVLTTGPAGGLHSAR.F
R1/RRR1-3/3	1466.861	1465.683	121.845	0.334	718.979	0.336	24	0.081	K.KVLTTGPAGGLHSAR.F
R1/RRR1-16/1	1114.493	1115.219	-1553.729	0.296	1373.668	0.249	13	1.000	R.FWAAYVDDK.V
R1/RRR1-16/2	1459.403	1458.775	-255.763	0.518	1645.192	0.513	20	0.304	K.VRPAWLAILFGSK.T
R1/RRR1-16/2	1294.198	1294.482	-219.918	0.488	1426.149	0.467	17	0.264	K.SDLLLASNPVHK.S
R1/RRR1-16/2	1458.419	1458.775	-245.106	0.466	1185.614	0.558	18	0.259	K.VRPAWLAILFGSK.T
R1/RRR1-16/2	1458.216	1458.775	-1072.598	0.509	1197.698	0.532	18	0.255	K.VRPAWLAILFGSK.T
R1/RRR1-16/2	1293.673	1294.482	-1402.850	0.486	1232.186	0.507	17	0.254	K.SDLLLASNPVHK.S
R1/RRR1-16/2	1295.213	1294.482	-208.024	0.535	1187.039	0.508	17	0.250	K.SDLLLASNPVHK.S
R1/RRR1-16/2	1362.328	1362.601	-200.921	0.500	1142.796	0.499	19	0.247	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1363.191	1362.601	-301.837	0.541	991.597	0.510	18	0.238	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1363.034	1362.601	318.649	0.506	1053.225	0.484	18	0.237	K.LLGVWSSPYAIR.V
R1/RRR1-15/2	1361.880	1362.601	-1267.861	0.441	1200.331	0.423	19	0.236	K.LLGVWSSPYAIR.V
R1/RRR1-15/2	1362.244	1362.601	-263.219	0.488	1137.467	0.435	19	0.234	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1362.101	1362.601	-367.876	0.464	1105.177	0.442	19	0.234	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1657.487	1656.771	-171.864	0.568	962.113	0.492	21	0.230	K.SLPYEYVEENLGDK.S
R1/RRR1-16/2	1362.299	1362.601	-222.136	0.422	871.262	0.469	17	0.222	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1657.354	1656.771	-252.327	0.550	661.685	0.501	21	0.218	K.SLPYEYVEENLGDK.S
R1/RRR1-15/2	1361.938	1362.601	-1224.836	0.408	766.812	0.457	16	0.215	K.LLGVWSSPYAIR.V
R1/RRR1-15/2	1361.864	1362.601	-1279.564	0.396	908.808	0.409	17	0.215	K.LLGVWSSPYAIR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1361.989	1362.601	-1187.393	0.342	813.342	0.433	17	0.213	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1656.220	1656.771	-939.340	0.499	646.555	0.460	20	0.211	K.SLPYEYVEENLGDK.S
R1/RRR1-16/2	1363.520	1362.601	-59.858	0.344	746.833	0.445	15	0.209	K.LLGVWSSPYAIR.V
R1/RRR1-15/2	1361.811	1362.601	-1318.723	0.399	888.389	0.374	16	0.208	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1115.964	1115.219	-229.149	0.406	794.309	0.368	14	0.206	R.FWAAYVDDK.V
R1/RRR1-16/1	685.380	685.878	-729.031	0.314	584.778	0.297	8	0.205	-.VVLNLK.-
R1/RRR1-16/2	1362.333	1362.601	-197.595	0.425	689.816	0.397	15	0.204	K.LLGVWSSPYAIR.V
R1/RRR1-16/3	1459.313	1458.775	-317.371	0.502	1852.595	0.398	26	0.199	K.VRPAWLAILFGSK.T
R1/RRR1-6/2	1362.523	1362.601	-57.565	0.327	782.554	0.317	15	0.197	K.LLGVWSSPYAIR.V
R1/RRR1-16/2	1458.883	1458.775	74.222	0.361	390.834	0.427	13	0.195	K.VRPAWLAILFGSK.T
R1/RRR1-16/2	1115.020	1115.219	-178.612	0.416	787.374	0.267	14	0.195	R.FWAAYVDDK.V
R1/RRR1-16/3	1458.754	1458.775	-14.665	0.524	1881.123	0.368	27	0.191	K.VRPAWLAILFGSK.T
R1/RRR1-16/2	941.094	941.196	-108.713	0.441	862.889	0.224	12	0.189	R.VRVVLNLK.S
R1/RRR1-16/2	1114.576	1115.219	-1478.432	0.321	655.551	0.220	13	0.189	R.FWAAYVDDK.V
R1/RRR1-20/2	1115.631	1115.219	370.437	0.204	705.872	0.123	13	0.182	R.FWAAYVDDK.V
R1/RRR1-16/2	941.208	941.196	12.799	0.448	980.385	0.129	13	0.181	-.VRVVLNLK.-
R1/RRR1-16/2	941.156	941.196	-42.619	0.435	824.905	0.144	12	0.180	-.VRVVLNLK.-
R1/RRR1-16/1	685.416	685.878	-676.029	0.315	567.153	0.207	8	0.180	-.VVLNLK.-
R1/RRR1-16/1	685.438	685.878	-644.480	0.297	522.623	0.253	8	0.167	-.VVLNLK.-
R1/RRR1-16/3	1457.659	1458.775	-1455.825	0.495	1572.313	0.399	25	0.156	K.VRPAWLAILFGSK.T
R1/RRR1-9/2	1969.486	1969.163	164.642	0.546	1850.873	0.470	21	0.317	R.TMLELLNQLDGFSSDER.I
R1/RRR1-9/2	1968.554	1969.163	-819.784	0.467	1556.801	0.480	21	0.280	R.TMLELLNQLDGFSSDER.I
R1/RRR1-9/2	1662.535	1661.947	-248.551	0.501	1324.639	0.516	20	0.261	K.LAGPQLVQM*FIGDGAK.L
R1/RRR1-9/2	1195.843	1196.249	-340.391	0.484	1439.951	0.432	18	0.260	R.STDDFNGAQLK.A
R1/RRR1-9/2	1661.718	1661.947	-138.521	0.458	1266.488	0.481	20	0.248	K.LAGPQLVQM*FIGDGAK.L
R1/RRR1-10/2	1158.517	1159.360	-1594.939	0.348	1164.479	0.509	18	0.245	K.GVLLYGPPGTGK.T
R1/RRR1-9/2	1661.529	1661.947	-252.534	0.454	1268.123	0.470	19	0.244	K.LAGPQLVQM*FIGDGAK.L
R1/RRR1-9/2	1645.427	1645.948	-927.196	0.441	1264.336	0.467	19	0.244	K.LAGPQLVQMFIGDGAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1645.956	1645.948	5.162	0.412	1324.547	0.416	20	0.239	K.LAGPQLVQMFIGDGAK.L
R1/RRR1-9/2	1669.603	1669.986	-229.796	0.469	1207.795	0.410	22	0.231	R.QTIFLPVIGLVDPEK.L
R1/RRR1-9/2	1646.515	1645.948	-263.506	0.492	1128.032	0.458	19	0.230	K.LAGPQLVQMFIGDGAK.L
R1/RRR1-9/2	1195.914	1196.249	-280.479	0.503	896.689	0.506	16	0.228	R.STDDFNGAQLK.A
R1/RRR1-10/2	1159.027	1159.360	-287.609	0.384	997.107	0.423	17	0.220	K.GVLLYGPPGTGK.T
R1/RRR1-9/2	1158.644	1159.360	-1485.394	0.386	805.220	0.495	15	0.218	K.GVLLYGPPGTGK.T
R1/RRR1-9/2	1669.505	1669.986	-288.993	0.413	841.760	0.454	20	0.214	R.QTIFLPVIGLVDPEK.L
R1/RRR1-9/2	1669.532	1669.986	-272.854	0.434	930.723	0.403	21	0.212	R.QTIFLPVIGLVDPEK.L
R1/RRR1-9/2	1159.095	1159.360	-229.073	0.428	681.514	0.495	14	0.212	K.GVLLYGPPGTGK.T
R1/RRR1-10/2	1159.097	1159.360	-227.594	0.433	703.657	0.464	14	0.209	K.GVLLYGPPGTGK.T
R1/RRR1-9/2	1158.744	1159.360	-1398.516	0.349	808.164	0.429	15	0.208	K.GVLLYGPPGTGK.T
R1/RRR1-9/2	1887.475	1888.021	-821.786	0.450	790.350	0.384	20	0.201	K.DSYLILDTLPSEYDSR.V
R1/RRR1-9/2	1887.493	1888.021	-812.048	0.422	641.863	0.438	18	0.201	K.DSYLILDTLPSEYDSR.V
R1/RRR1-8/2	1663.570	1661.947	-227.716	0.422	535.906	0.471	14	0.197	-.LAGPQLVQM*FIGDGAK.-
R1/RRR1-9/2	1887.501	1888.021	-807.828	0.398	532.109	0.355	17	0.190	K.DSYLILDTLPSEYDSR.V
R1/RRR1-1/2	1671.349	1669.986	218.258	0.366	427.298	0.324	16	0.190	R.QTIFLPVIGLVDPEK.L
R1/RRR1-8/2	1159.280	1159.360	-68.502	0.181	291.360	0.381	12	0.186	-.GVLLYGPPGTGK.-
R1/RRR1-9/3	1439.650	1440.586	-1348.849	0.503	1667.440	0.437	28	0.171	R.KIEFPHPSEEAR.A
R1/RRR1-9/3	1680.708	1680.761	-31.596	0.479	1567.245	0.359	26	0.145	K.RFDSEVSGDREVQR.T
R1/RRR1-9/3	1440.877	1440.586	202.898	0.522	1316.935	0.396	24	0.123	R.KIEFPHPSEEAR.A
R1/RRR1-9/3	1440.891	1440.586	212.711	0.469	1267.544	0.384	25	0.113	R.KIEFPHPSEEAR.A
R1/RRR1-9/3	1681.090	1680.761	196.192	0.444	1217.738	0.305	24	0.097	K.RFDSEVSGDREVQR.T
R1/RRR1-9/3	1680.953	1680.761	114.594	0.377	697.235	0.240	23	0.074	K.RFDSEVSGDREVQR.T
R1/RRR1-7/2	1133.966	1134.219	-223.784	0.527	2329.121	0.471	20	0.409	K.GIDACIASGGGR.M
R1/RRR1-7/2	1133.597	1134.219	-1435.373	0.432	1600.003	0.447	19	0.281	K.GIDACIASGGGR.M
R1/RRR1-7/2	974.279	975.121	-1897.174	0.433	885.118	0.549	16	0.236	K.LVDTALASGK.I
R1/RRR1-7/2	974.991	975.121	-134.067	0.416	759.045	0.559	16	0.229	K.LVDTALASGK.I
R1/RRR1-7/2	974.574	975.121	-1593.076	0.368	716.835	0.485	15	0.214	K.LVDTALASGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1489.901	1490.598	-1142.730	0.435	2237.125	0.550	24	0.411	K.TDALDAAGNTTAAIGK.G
R1/RRR1-6/2	1490.219	1490.598	-254.828	0.449	2076.631	0.564	25	0.386	K.TDALDAAGNTTAAIGK.G
R1/RRR1-1/2	1596.556	1596.852	-185.631	0.543	1977.930	0.573	23	0.377	R.TGAATNVIFGLALGYK.S
R1/RRR1-6/2	1489.618	1490.598	-1332.978	0.388	2172.917	0.466	24	0.369	K.TDALDAAGNTTAAIGK.G
R1/RRR1-2/2	1490.188	1490.598	-275.785	0.440	2026.595	0.522	24	0.362	K.TDALDAAGNTTAAIGK.G
R1/RRR1-5/2	1489.557	1490.598	-1374.460	0.413	2058.830	0.479	23	0.353	K.TDALDAAGNTTAAIGK.G
R1/RRR1-4/2	1490.212	1490.598	-259.924	0.442	1961.642	0.488	24	0.340	K.TDALDAAGNTTAAIGK.G
R1/RRR1-2/2	1490.507	1490.598	-61.248	0.503	1798.091	0.570	23	0.339	K.TDALDAAGNTTAAIGK.G
R1/RRR1-2/2	1489.634	1490.598	-1322.114	0.357	2052.324	0.425	23	0.334	K.TDALDAAGNTTAAIGK.G
R1/RRR1-1/2	1490.258	1490.598	-228.860	0.480	1761.342	0.565	23	0.332	K.TDALDAAGNTTAAIGK.G
R1/RRR1-3/2	1489.949	1490.598	-1110.152	0.402	1924.224	0.453	23	0.323	K.TDALDAAGNTTAAIGK.G
R1/RRR1-2/2	1400.546	1400.563	-12.380	0.472	1724.407	0.504	22	0.311	K.AADVGADLVGKVER.N
R1/RRR1-6/2	1490.210	1490.598	-261.239	0.433	1609.946	0.557	23	0.307	K.TDALDAAGNTTAAIGK.G
R1/RRR1-1/2	1489.728	1490.598	-1258.746	0.360	1821.084	0.440	22	0.303	K.TDALDAAGNTTAAIGK.G
R1/RRR1-3/2	1490.076	1490.598	-1024.603	0.403	1668.566	0.473	23	0.292	K.TDALDAAGNTTAAIGK.G
R1/RRR1-3/2	1490.132	1490.598	-314.002	0.386	1616.644	0.472	22	0.284	K.TDALDAAGNTTAAIGK.G
R1/RRR1-6/2	1400.098	1400.563	-333.232	0.470	1532.522	0.496	21	0.284	K.AADVGADLVGKVER.N
R1/RRR1-1/2	1400.268	1400.563	-210.954	0.456	1373.330	0.504	20	0.266	K.AADVGADLVGKVER.N
R1/RRR1-5/2	1490.037	1490.598	-1050.759	0.417	1407.889	0.474	21	0.261	K.TDALDAAGNTTAAIGK.G
R1/RRR1-1/2	1400.386	1400.563	-127.003	0.505	1364.810	0.439	21	0.251	K.AADVGADLVGKVER.N
R1/RRR1-6/2	1015.863	1016.130	-264.324	0.408	1304.994	0.418	18	0.243	K.AADVGADLVGK.V
R1/RRR1-3/2	1016.088	1016.130	-41.465	0.376	1313.126	0.416	17	0.242	K.AADVGADLVGK.V
R1/RRR1-6/2	1015.743	1016.130	-382.965	0.425	1208.768	0.446	17	0.241	K.AADVGADLVGK.V
R1/RRR1-2/2	1597.351	1596.852	313.757	0.472	1109.445	0.507	18	0.237	R.TGAATNVIFGLALGYK.S
R1/RRR1-2/2	1016.049	1016.130	-80.750	0.443	1220.308	0.415	18	0.237	K.AADVGADLVGK.V
R1/RRR1-1/2	1399.653	1400.563	-1368.358	0.468	1133.963	0.450	20	0.234	K.AADVGADLVGKVER.N
R1/RRR1-6/2	1270.076	1270.457	-300.637	0.330	1307.480	0.383	17	0.231	K.AAVIGDTIGDPLK.D
R1/RRR1-1/3	1331.541	1332.447	-1435.467	0.505	1624.814	0.613	26	0.229	K.KYIEAGASEHAR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1015.354	1016.130	-1754.525	0.381	1075.556	0.439	17	0.229	K.AADVGADLVGK.V
R1/RRR1-6/2	1270.138	1270.457	-252.135	0.271	1505.662	0.264	18	0.227	K.AAVIGDTIGDPLK.D
R1/RRR1-6/2	1015.389	1016.130	-1720.100	0.359	1151.952	0.396	17	0.226	K.AADVGADLVGK.V
R1/RRR1-5/2	1015.953	1016.130	-174.758	0.417	1081.088	0.413	17	0.226	K.AADVGADLVGK.V
R1/RRR1-2/2	1015.355	1016.130	-1753.921	0.387	1151.591	0.380	18	0.225	K.AADVGADLVGK.V
R1/RRR1-2/2	1016.152	1016.130	21.434	0.439	1121.599	0.390	17	0.225	K.AADVGADLVGK.V
R1/RRR1-6/2	1232.049	1231.381	-270.066	0.364	904.429	0.466	15	0.219	K.FTIFNFGEQK.E
R1/RRR1-2/2	1401.246	1400.563	-226.796	0.435	942.431	0.442	17	0.217	K.AADVGADLVGKVER.N
R1/RRR1-1/2	794.950	794.918	39.335	0.413	867.161	0.402	13	0.211	R.VGGGIYTK.A
R1/RRR1-3/2	1015.388	1016.130	-1720.824	0.328	953.474	0.349	17	0.209	K.AADVGADLVGK.V
R1/RRR1-2/2	1015.467	1016.130	-1642.560	0.351	956.432	0.344	16	0.208	K.AADVGADLVGK.V
R1/RRR1-5/2	1015.933	1016.130	-195.370	0.380	862.776	0.355	15	0.205	K.AADVGADLVGK.V
R1/RRR1-5/2	1015.289	1016.130	-1818.914	0.342	983.494	0.277	17	0.202	K.AADVGADLVGK.V
R1/RRR1-1/3	1332.434	1332.447	-9.944	0.552	1494.494	0.584	25	0.200	K.KYIEAGASEHAR.T
R1/RRR1-4/2	1400.048	1400.563	-1085.591	0.321	725.108	0.286	16	0.190	K.AADVGADLVGKVER.N
R1/RRR1-2/2	1230.382	1231.381	-1629.553	0.361	519.378	0.292	11	0.186	-.FTIFNFGEQK.-
R1/RRR1-3/3	1332.475	1332.447	21.206	0.543	1421.755	0.551	24	0.180	K.KYIEAGASEHAR.T
R1/RRR1-5/3	1331.292	1332.447	-1623.350	0.524	1228.517	0.587	25	0.162	K.KYIEAGASEHAR.T
R1/RRR1-6/3	1332.030	1332.447	-314.239	0.528	1037.843	0.605	23	0.150	K.KYIEAGASEHAR.T
R1/RRR1-4/3	1332.317	1332.447	-98.029	0.529	1092.375	0.590	24	0.150	K.KYIEAGASEHAR.T
R1/RRR1-1/3	1332.990	1332.447	-343.956	0.565	1001.893	0.608	25	0.144	K.KYIEAGASEHAR.T
R1/RRR1-3/3	1332.873	1332.447	320.614	0.532	992.280	0.554	23	0.133	K.KYIEAGASEHAR.T
R1/RRR1-20/2	1017.553	1018.146	-1570.488	0.440	1625.423	0.424	19	0.278	K.STLVEGGGIGK.A
R1/RRR1-21/2	1017.897	1018.146	-245.392	0.414	1538.853	0.423	19	0.268	K.STLVEGGGIGK.A
R1/RRR1-21/2	1017.526	1018.146	-1597.002	0.412	1569.693	0.410	18	0.267	K.STLVEGGGIGK.A
R1/RRR1-21/2	1556.443	1556.726	-182.785	0.518	1400.874	0.481	18	0.267	R.LEFLDVDKCECK.S
R1/RRR1-21/2	1017.921	1018.146	-222.293	0.447	1416.966	0.473	18	0.266	K.STLVEGGGIGK.A
R1/RRR1-20/2	1018.056	1018.146	-88.889	0.467	1479.566	0.441	18	0.265	K.STLVEGGGIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1018.006	1018.146	-138.084	0.454	1363.970	0.431	17	0.251	K.STLVEGGGIGK.A
R1/RRR1-21/2	1070.888	1071.209	-300.534	0.391	1480.169	0.365	16	0.247	K.AIETATSHIK.V
R1/RRR1-20/2	1071.100	1071.209	-102.719	0.360	1166.302	0.443	15	0.234	K.AIETATSHIK.V
R1/RRR1-21/2	1071.088	1071.209	-113.351	0.405	1248.097	0.381	15	0.230	K.AIETATSHIK.V
R1/RRR1-20/2	1441.380	1441.695	-219.037	0.410	765.647	0.514	20	0.223	K.LLPGVEVKDEITK.A
R1/RRR1-21/2	1356.213	1356.575	-267.715	0.406	1267.606	0.333	18	0.222	R.AAVM*DWHTLAPK.I
R1/RRR1-21/2	1440.679	1441.695	-1403.669	0.401	718.686	0.502	19	0.218	K.LLPGVEVKDEITK.A
R1/RRR1-21/2	1441.351	1441.695	-239.004	0.386	689.508	0.490	19	0.215	K.LLPGVEVKDEITK.A
R1/RRR1-20/2	1441.217	1441.695	-332.560	0.362	781.588	0.464	20	0.215	K.LLPGVEVKDEITK.A
R1/RRR1-21/2	1441.247	1441.695	-311.825	0.379	693.669	0.489	19	0.215	K.LLPGVEVKDEITK.A
R1/RRR1-21/2	1093.552	1094.286	-1590.716	0.453	890.513	0.410	15	0.214	K.AKESLTGIFK.T
R1/RRR1-20/2	1441.262	1441.695	-301.373	0.367	793.088	0.434	20	0.212	K.LLPGVEVKDEITK.A
R1/RRR1-21/2	1093.636	1094.286	-1512.785	0.447	812.483	0.414	15	0.211	K.AKESLTGIFK.T
R1/RRR1-20/2	1356.262	1356.575	-231.234	0.409	1073.569	0.327	17	0.209	R.AAVM*DWHTLAPK.I
R1/RRR1-21/2	1356.141	1356.575	-321.447	0.427	970.663	0.363	16	0.208	R.AAVM*DWHTLAPK.I
R1/RRR1-20/2	1094.044	1094.286	-221.766	0.461	759.827	0.396	15	0.207	K.AKESLTGIFK.T
R1/RRR1-20/2	1355.458	1356.575	-1566.879	0.371	841.669	0.354	15	0.201	R.AAVM*DWHTLAPK.I
R1/RRR1-20/2	1356.278	1356.575	-220.128	0.367	877.652	0.322	15	0.198	R.AAVM*DWHTLAPK.I
R1/RRR1-21/2	1356.271	1356.575	-225.184	0.396	787.697	0.299	15	0.193	R.AAVM*DWHTLAPK.I
R1/RRR1-21/2	1071.055	1071.209	-143.991	0.297	628.109	0.269	12	0.185	-.AIETATSHIK.-
R1/RRR1-20/3	1843.150	1842.027	66.579	0.490	827.254	0.561	25	0.122	K.ERLEFLDVDKCECK.S
R1/RRR1-21/3	1356.245	1356.575	-244.201	0.348	765.153	0.555	23	0.109	R.AAVM*DWHTLAPK.I
R1/RRR1-20/3	1356.231	1356.575	-254.225	0.387	552.847	0.568	20	0.107	R.AAVM*DWHTLAPK.I
R1/RRR1-20/3	1841.882	1842.027	-78.919	0.422	682.559	0.435	23	0.095	K.ERLEFLDVDKCECK.S
R1/RRR1-21/3	1842.942	1842.027	-46.619	0.362	464.173	0.397	23	0.089	K.ERLEFLDVDKCECK.S
R1/RRR1-21/3	1356.614	1356.575	28.786	0.329	432.914	0.448	18	0.087	-.AAVM*DWHTLAPK.-
R1/RRR1-20/3	1356.584	1356.575	6.584	0.294	353.775	0.435	16	0.087	-.AAVM*DWHTLAPK.-
R1/RRR1-21/3	1841.460	1842.027	-853.498	0.362	577.860	0.382	25	0.086	K.ERLEFLDVDKCECK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/3	1356.381	1356.575	-143.303	0.247	372.020	0.386	17	0.082	-.AAVM*DWHTLAPK.-
R1/RRR1-20/3	1841.387	1842.027	-893.727	0.277	514.119	0.345	23	0.082	K.ERLEFLDVDKCECK.S
R1/RRR1-16/2	1628.370	1628.852	-297.045	0.527	2283.128	0.606	25	0.445	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-16/2	1628.381	1628.852	-290.426	0.477	2244.322	0.604	24	0.435	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-15/2	1628.355	1628.852	-306.296	0.524	2167.261	0.564	25	0.405	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-15/2	1628.421	1628.852	-265.758	0.494	2046.356	0.552	24	0.377	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-15/2	1627.876	1628.852	-1217.886	0.426	1988.824	0.582	24	0.376	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-16/2	1628.434	1628.852	-257.259	0.525	1995.790	0.568	25	0.374	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-18/2	1629.434	1628.852	-257.703	0.499	1870.703	0.573	24	0.354	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-15/2	1698.383	1698.866	-284.944	0.480	1877.185	0.547	24	0.348	R.VDFAPGGTNPPHVHPR.A
R1/RRR1-18/2	1628.633	1628.852	-134.764	0.506	1858.467	0.544	24	0.342	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-15/2	1698.612	1698.866	-149.683	0.492	1629.129	0.583	23	0.320	R.VDFAPGGTNPPHVHPR.A
R1/RRR1-15/2	1698.195	1698.866	-986.922	0.479	1428.456	0.591	23	0.295	R.VDFAPGGTNPPHVHPR.A
R1/RRR1-18/2	1627.992	1628.852	-1146.127	0.384	1570.963	0.513	23	0.290	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-16/2	1698.285	1698.866	-933.664	0.475	1295.310	0.576	22	0.275	R.VDFAPGGTNPPHVHPR.A
R1/RRR1-16/2	1698.447	1698.866	-247.592	0.514	1192.846	0.574	21	0.263	R.VDFAPGGTNPPHVHPR.A
R1/RRR1-16/2	1698.330	1698.866	-907.109	0.447	1244.811	0.528	23	0.259	R.VDFAPGGTNPPHVHPR.A
R1/RRR1-16/2	1278.184	1278.508	-253.613	0.435	1367.441	0.395	16	0.242	R.GLMHFQFNVGK.T
R1/RRR1-15/2	1277.557	1278.508	-1531.525	0.478	1375.645	0.368	16	0.237	R.GLMHFQFNVGK.T
R1/RRR1-16/2	957.787	958.137	-367.150	0.519	1342.666	0.367	15	0.236	R.ATEVGIVLR.G
R1/RRR1-18/2	958.133	958.137	-4.870	0.485	1357.457	0.321	15	0.228	R.ATEVGIVLR.G
R1/RRR1-14/2	958.108	958.137	-30.684	0.373	1316.261	0.330	14	0.228	-.ATEVGIVLR.-
R1/RRR1-15/2	1277.702	1278.508	-1417.318	0.452	1175.685	0.381	16	0.225	R.GLMHFQFNVGK.T
R1/RRR1-17/2	959.030	958.137	-111.978	0.485	1246.527	0.346	14	0.224	R.ATEVGIVLR.G
R1/RRR1-16/2	957.845	958.137	-306.539	0.441	1150.043	0.373	14	0.224	R.ATEVGIVLR.G
R1/RRR1-16/2	1278.439	1278.508	-54.169	0.454	1283.374	0.321	16	0.221	R.GLMHFQFNVGK.T
R1/RRR1-1/2	989.829	990.138	-312.899	0.471	853.806	0.411	14	0.220	R.AGETFVIPR.G
R1/RRR1-15/2	1277.879	1278.508	-1278.290	0.431	1322.028	0.293	16	0.218	R.GLMHFQFNVGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1278.358	1278.508	-117.576	0.419	1185.081	0.336	16	0.218	R.GLMHFQFNVGK.T
R1/RRR1-15/2	989.918	990.138	-222.706	0.437	819.305	0.403	14	0.217	R.AGETFVIPR.G
R1/RRR1-15/2	989.600	990.138	-1558.245	0.405	851.789	0.398	14	0.217	R.AGETFVIPR.G
R1/RRR1-13/2	990.027	990.138	-112.615	0.480	791.823	0.395	14	0.216	R.AGETFVIPR.G
R1/RRR1-16/2	989.933	990.138	-207.737	0.463	818.757	0.390	14	0.216	R.AGETFVIPR.G
R1/RRR1-17/2	958.237	958.137	104.760	0.510	1239.385	0.306	14	0.215	R.ATEVGIVLR.G
R1/RRR1-24/2	989.895	990.138	-246.088	0.517	801.780	0.388	14	0.215	R.AGETFVIPR.G
R1/RRR1-6/2	990.278	990.138	142.480	0.486	790.132	0.386	14	0.215	R.AGETFVIPR.G
R1/RRR1-6/2	990.036	990.138	-103.092	0.480	769.226	0.388	14	0.215	R.AGETFVIPR.G
R1/RRR1-15/2	1295.036	1294.507	-364.515	0.509	684.492	0.444	16	0.214	R.GLM*HFQFNVGK.T
R1/RRR1-14/2	989.936	990.138	-204.397	0.465	808.794	0.371	14	0.213	R.AGETFVIPR.G
R1/RRR1-13/2	957.572	958.137	-1639.197	0.378	1235.890	0.275	15	0.213	R.ATEVGIVLR.G
R1/RRR1-13/2	990.113	990.138	-25.055	0.466	773.581	0.366	14	0.212	R.AGETFVIPR.G
R1/RRR1-12/2	989.851	990.138	-290.504	0.467	783.728	0.365	14	0.212	R.AGETFVIPR.G
R1/RRR1-12/2	989.262	990.138	-1901.360	0.409	848.682	0.350	14	0.211	R.AGETFVIPR.G
R1/RRR1-15/2	990.020	990.138	-118.923	0.497	773.576	0.362	14	0.211	R.AGETFVIPR.G
R1/RRR1-7/2	990.051	990.138	-88.374	0.393	853.699	0.344	14	0.211	R.AGETFVIPR.G
R1/RRR1-23/2	989.620	990.138	-1538.295	0.411	924.900	0.328	14	0.210	R.AGETFVIPR.G
R1/RRR1-11/2	990.094	990.138	-44.470	0.457	731.183	0.349	14	0.210	R.AGETFVIPR.G
R1/RRR1-2/2	989.419	990.138	-1742.789	0.420	876.752	0.328	14	0.209	R.AGETFVIPR.G
R1/RRR1-15/2	989.916	990.138	-224.561	0.448	771.856	0.341	14	0.209	R.AGETFVIPR.G
R1/RRR1-23/2	989.947	990.138	-193.016	0.442	743.749	0.361	13	0.209	R.AGETFVIPR.G
R1/RRR1-17/2	991.027	990.138	-112.501	0.440	785.952	0.339	14	0.209	R.AGETFVIPR.G
R1/RRR1-14/2	989.943	990.138	-197.222	0.440	817.818	0.334	14	0.209	R.AGETFVIPR.G
R1/RRR1-18/2	989.495	990.138	-1665.444	0.448	808.608	0.335	14	0.209	R.AGETFVIPR.G
R1/RRR1-19/2	991.108	990.138	-30.218	0.440	745.510	0.340	14	0.209	R.AGETFVIPR.G
R1/RRR1-15/2	1294.204	1294.507	-234.669	0.490	714.528	0.400	16	0.209	R.GLM*HFQFNVGK.T
R1/RRR1-13/2	989.555	990.138	-1603.972	0.420	866.843	0.325	14	0.209	R.AGETFVIPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	989.654	990.138	-490.240	0.384	856.772	0.321	14	0.208	R.AGETFVIPR.G
R1/RRR1-16/2	989.902	990.138	-239.160	0.471	764.048	0.332	14	0.208	R.AGETFVIPR.G
R1/RRR1-16/2	990.010	990.138	-129.684	0.488	690.479	0.357	13	0.208	R.AGETFVIPR.G
R1/RRR1-26/2	989.753	990.138	-390.362	0.411	829.057	0.322	14	0.208	R.AGETFVIPR.G
R1/RRR1-18/2	989.391	990.138	-1770.929	0.406	849.686	0.308	14	0.207	R.AGETFVIPR.G
R1/RRR1-15/2	1294.136	1294.507	-287.473	0.454	701.210	0.381	16	0.207	R.GLM*HFQFNVGK.T
R1/RRR1-15/2	989.942	990.138	-198.088	0.491	777.826	0.322	14	0.207	R.AGETFVIPR.G
R1/RRR1-18/2	989.947	990.138	-193.263	0.411	804.981	0.312	14	0.207	R.AGETFVIPR.G
R1/RRR1-10/2	989.609	990.138	-1549.324	0.409	842.980	0.305	14	0.206	R.AGETFVIPR.G
R1/RRR1-16/2	1294.051	1294.507	-353.344	0.440	679.269	0.373	16	0.205	R.GLM*HFQFNVGK.T
R1/RRR1-16/2	1293.642	1294.507	-1446.035	0.463	579.261	0.395	15	0.205	R.GLM*HFQFNVGK.T
R1/RRR1-7/2	990.155	990.138	17.854	0.368	790.151	0.302	14	0.205	R.AGETFVIPR.G
R1/RRR1-16/2	989.520	990.138	-1639.788	0.386	763.605	0.300	14	0.205	R.AGETFVIPR.G
R1/RRR1-3/2	990.074	990.138	-64.257	0.420	734.708	0.300	14	0.205	R.AGETFVIPR.G
R1/RRR1-1/2	989.914	990.138	-227.036	0.424	783.248	0.316	13	0.205	R.AGETFVIPR.G
R1/RRR1-7/2	989.832	990.138	-309.930	0.307	807.631	0.311	14	0.205	R.AGETFVIPR.G
R1/RRR1-24/2	989.376	990.138	-1785.806	0.412	902.389	0.283	14	0.204	R.AGETFVIPR.G
R1/RRR1-16/2	989.796	990.138	-346.432	0.427	817.324	0.289	14	0.204	R.AGETFVIPR.G
R1/RRR1-16/2	1294.064	1294.507	-343.122	0.448	727.750	0.355	16	0.204	R.GLM*HFQFNVGK.T
R1/RRR1-14/2	989.854	990.138	-287.782	0.458	794.822	0.291	14	0.204	R.AGETFVIPR.G
R1/RRR1-16/2	989.484	990.138	-1676.723	0.405	695.196	0.282	14	0.204	R.AGETFVIPR.G
R1/RRR1-15/2	989.836	990.138	-305.475	0.402	760.174	0.299	13	0.203	R.AGETFVIPR.G
R1/RRR1-10/2	990.016	990.138	-123.870	0.415	722.107	0.277	14	0.203	R.AGETFVIPR.G
R1/RRR1-1/2	989.685	990.138	-459.297	0.344	836.814	0.276	14	0.203	R.AGETFVIPR.G
R1/RRR1-18/2	957.711	958.137	-446.313	0.360	956.662	0.299	14	0.203	-.ATEVGIVLR.-
R1/RRR1-10/2	989.973	990.138	-166.792	0.388	686.871	0.284	13	0.202	R.AGETFVIPR.G
R1/RRR1-25/2	989.789	990.138	-353.609	0.364	723.694	0.264	14	0.202	R.AGETFVIPR.G
R1/RRR1-15/2	989.927	990.138	-213.799	0.450	719.238	0.308	14	0.202	-.AGETFVIPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	989.516	990.138	-1644.002	0.358	855.990	0.252	14	0.201	R.AGETFVIPR.G
R1/RRR1-15/2	989.882	990.138	-259.697	0.406	738.530	0.251	14	0.201	R.AGETFVIPR.G
R1/RRR1-6/2	989.974	990.138	-166.420	0.378	635.936	0.254	13	0.201	R.AGETFVIPR.G
R1/RRR1-11/2	989.902	990.138	-238.788	0.434	794.463	0.257	14	0.201	R.AGETFVIPR.G
R1/RRR1-3/2	989.387	990.138	-1774.772	0.331	637.246	0.252	13	0.200	R.AGETFVIPR.G
R1/RRR1-25/2	989.577	990.138	-1581.790	0.355	712.414	0.236	14	0.200	R.AGETFVIPR.G
R1/RRR1-2/2	989.159	990.138	-2006.524	0.317	666.835	0.246	13	0.200	R.AGETFVIPR.G
R1/RRR1-12/2	989.906	990.138	-234.582	0.412	794.218	0.224	14	0.198	R.AGETFVIPR.G
R1/RRR1-11/2	989.502	990.138	-1658.627	0.332	813.160	0.214	14	0.198	R.AGETFVIPR.G
R1/RRR1-19/2	989.238	990.138	-1926.161	0.381	694.611	0.214	13	0.197	R.AGETFVIPR.G
R1/RRR1-19/2	989.335	990.138	-1827.586	0.360	685.482	0.201	13	0.197	R.AGETFVIPR.G
R1/RRR1-1/2	958.037	958.137	-104.810	0.289	847.941	0.265	14	0.197	R.ATEVGIVLR.G
R1/RRR1-7/2	989.312	990.138	-1850.895	0.242	573.706	0.243	13	0.196	-.AGETFVIPR.-
R1/RRR1-15/2	989.865	990.138	-276.894	0.374	751.049	0.245	13	0.196	-.AGETFVIPR.-
R1/RRR1-20/2	989.847	990.138	-294.340	0.244	748.631	0.221	13	0.196	R.AGETFVIPR.G
R1/RRR1-23/2	989.555	990.138	-1604.096	0.288	908.654	0.183	14	0.195	R.AGETFVIPR.G
R1/RRR1-3/2	957.750	958.137	-405.259	0.292	646.612	0.243	13	0.192	-.ATEVGIVLR.-
R1/RRR1-20/2	989.360	990.138	-1802.542	0.255	686.914	0.074	13	0.191	-.AGETFVIPR.-
R1/RRR1-9/2	990.045	990.138	-94.187	0.329	829.036	0.139	14	0.191	-.AGETFVIPR.-
R1/RRR1-9/2	989.919	990.138	-222.087	0.315	805.165	0.142	13	0.190	-.AGETFVIPR.-
R1/RRR1-2/2	1629.576	1628.852	-170.074	0.404	925.958	0.242	19	0.189	R.GELLVGIIGTLDTGNR.Y
R1/RRR1-3/2	957.986	958.137	-158.877	0.265	685.769	0.182	13	0.189	-.ATEVGIVLR.-
R1/RRR1-3/2	957.892	958.137	-257.313	0.316	798.187	0.239	13	0.185	-.ATEVGIVLR.-
R1/RRR1-15/2	759.935	759.829	139.991	0.438	833.365	0.592	11	0.136	K.SKFTGGY.-
R1/RRR1-15/2	759.980	759.829	198.141	0.391	857.733	0.501	11	0.119	K.SKFTGGY.-
R1/RRR1-16/3	1413.702	1413.688	10.287	0.517	1029.151	0.351	27	0.092	K.ALRVDTGVVELLK.S
R1/RRR1-16/2	760.167	759.829	445.006	0.250	726.713	0.312	10	0.090	K.SKFTGGY.-
R1/RRR1-16/3	1413.634	1413.688	-37.911	0.502	944.057	0.268	25	0.074	-.ALRVDTGVVELLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/3	1413.739	1413.688	36.009	0.483	891.841	0.236	24	0.068	-.ALRVDTGVVELLK.-
R1/RRR1-23/3	1456.755	1456.668	59.865	0.485	2286.725	0.457	30	1.000	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/3	1456.690	1456.668	15.111	0.480	2226.965	0.495	28	0.961	R.SGTLIDAIGIYVHP.-
R1/RRR1-21/3	1457.172	1456.668	-341.616	0.465	1859.013	0.438	28	0.621	R.SGTLIDAIGIYVHP.-
R1/RRR1-22/3	1456.662	1456.668	-4.305	0.481	1869.061	0.407	28	0.613	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/3	1456.577	1456.668	-63.062	0.473	1871.421	0.384	28	0.608	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/3	1456.362	1456.668	-210.866	0.410	1742.380	0.357	27	0.517	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1536.400	1536.798	-259.680	0.545	2223.965	0.565	24	0.417	K.KLLGVTIYSSDAIR.S
R1/RRR1-22/2	1536.492	1536.798	-199.502	0.555	2245.848	0.527	24	0.407	K.KLLGVTIYSSDAIR.S
R1/RRR1-23/2	1536.685	1536.798	-73.350	0.561	2119.406	0.550	23	0.390	K.KLLGVTIYSSDAIR.S
R1/RRR1-22/2	1537.276	1536.798	312.160	0.598	1977.078	0.547	23	0.363	K.KLLGVTIYSSDAIR.S
R1/RRR1-23/2	1536.398	1536.798	-260.796	0.548	1843.771	0.563	23	0.348	K.KLLGVTIYSSDAIR.S
R1/RRR1-24/2	1535.785	1536.798	-1314.512	0.516	1829.500	0.561	22	0.344	K.KLLGVTIYSSDAIR.S
R1/RRR1-23/2	1408.203	1408.625	-300.623	0.563	1739.191	0.560	21	0.328	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1457.135	1456.668	321.682	0.507	1763.445	0.552	22	0.326	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/2	1536.484	1536.798	-205.001	0.531	1760.971	0.518	22	0.320	K.KLLGVTIYSSDAIR.S
R1/RRR1-12/2	1409.415	1408.625	-149.557	0.518	1645.435	0.575	21	0.320	K.LLGVTIYSSDAIR.S
R1/RRR1-13/2	1409.538	1408.625	-61.639	0.560	1722.154	0.532	21	0.317	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1536.334	1536.798	-303.125	0.518	1772.141	0.497	22	0.315	K.KLLGVTIYSSDAIR.S
R1/RRR1-23/2	1837.583	1838.014	-234.775	0.503	1598.175	0.591	25	0.313	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-22/2	1535.809	1536.798	-1299.026	0.533	1688.953	0.530	21	0.312	K.KLLGVTIYSSDAIR.S
R1/RRR1-24/2	1837.599	1838.014	-226.178	0.521	1612.548	0.577	26	0.311	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1837.526	1838.014	-266.366	0.523	1575.934	0.591	26	0.311	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1837.725	1838.014	-157.606	0.493	1620.666	0.569	25	0.309	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1409.289	1408.625	-239.055	0.586	1627.078	0.550	21	0.309	K.LLGVTIYSSDAIR.S
R1/RRR1-20/2	1409.197	1408.625	-304.320	0.539	1583.800	0.563	21	0.308	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1408.311	1408.625	-223.224	0.558	1619.057	0.547	21	0.308	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1409.250	1408.625	-266.516	0.543	1566.122	0.564	21	0.306	K.LLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1408.286	1408.625	-241.138	0.515	1689.059	0.502	21	0.304	K.LLGVTIYSSDAIR.S
R1/RRR1-21/2	1409.258	1408.625	-261.128	0.577	1510.373	0.578	21	0.303	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1838.202	1838.014	102.933	0.518	1493.460	0.604	25	0.303	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1536.462	1536.798	-219.348	0.529	1588.099	0.543	21	0.303	K.KLLGVTIYSSDAIR.S
R1/RRR1-20/2	1456.266	1456.668	-277.249	0.478	1703.637	0.529	21	0.302	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/2	1837.673	1838.014	-186.127	0.500	1477.886	0.600	25	0.300	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1457.337	1456.668	-227.813	0.511	1605.864	0.642	21	0.299	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/2	1837.749	1838.014	-144.280	0.502	1477.931	0.595	25	0.298	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-26/2	1456.341	1456.668	-225.615	0.467	1736.465	0.474	22	0.298	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1991.471	1993.210	-1883.306	0.469	1519.928	0.581	22	0.298	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1837.893	1838.014	-65.926	0.511	1459.120	0.600	25	0.297	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1838.710	1838.014	-165.845	0.498	1682.151	0.496	25	0.297	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-13/2	1408.391	1408.625	-166.792	0.499	1639.621	0.495	21	0.296	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1839.726	1838.014	-156.636	0.569	1479.848	0.586	25	0.295	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1839.251	1838.014	129.302	0.527	1533.905	0.555	25	0.294	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-2/2	1409.373	1408.625	-179.272	0.492	1544.907	0.524	21	0.292	K.LLGVTIYSSDAIR.S
R1/RRR1-19/2	1455.618	1456.668	-1412.394	0.335	1662.198	0.510	21	0.292	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/2	1408.225	1408.625	-284.620	0.549	1519.689	0.534	21	0.292	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1991.631	1993.210	-1802.869	0.464	1459.804	0.583	22	0.291	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-26/2	1408.334	1408.625	-207.398	0.492	1591.612	0.498	21	0.291	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1838.188	1838.014	94.941	0.485	1485.268	0.559	25	0.290	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1839.252	1838.014	129.768	0.558	1532.864	0.542	25	0.289	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-14/2	1409.920	1408.625	209.838	0.525	1543.438	0.509	21	0.288	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1838.434	1838.014	229.257	0.566	1470.875	0.561	25	0.287	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-22/2	1408.257	1408.625	-262.096	0.507	1554.243	0.500	21	0.287	K.LLGVTIYSSDAIR.S
R1/RRR1-19/2	1992.551	1993.210	-835.350	0.489	1295.591	0.635	23	0.287	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1409.039	1408.625	294.777	0.519	1640.588	0.462	21	0.287	K.LLGVTIYSSDAIR.S
R1/RRR1-13/2	1992.739	1993.210	-237.140	0.511	1255.222	0.651	23	0.286	K.EFSIPLQDSGHVVGFFGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1838.459	1838.014	243.040	0.499	1356.317	0.598	25	0.285	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-21/2	1407.585	1408.625	-1453.371	0.398	1581.345	0.484	21	0.285	K.LLGVTIYSSDAIR.S
R1/RRR1-19/2	1408.365	1408.625	-185.312	0.518	1413.156	0.556	20	0.285	K.LLGVTIYSSDAIR.S
R1/RRR1-26/2	1457.326	1456.668	-235.124	0.503	1569.731	0.631	21	0.285	R.SGTLIDAIGIYVHP.-
R1/RRR1-22/2	1407.841	1408.625	-1270.823	0.519	1576.100	0.477	21	0.283	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1837.799	1838.014	-117.094	0.529	1433.710	0.553	25	0.282	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1838.143	1838.014	70.365	0.519	1355.627	0.590	24	0.282	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/3	1456.446	1456.668	-153.101	0.399	1311.165	0.434	24	0.281	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1992.712	1993.210	-250.967	0.493	1355.641	0.591	22	0.281	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1992.572	1993.210	-824.772	0.495	1238.747	0.641	22	0.281	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1838.371	1838.014	195.032	0.557	1442.449	0.548	25	0.281	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1408.298	1408.625	-233.138	0.525	1593.698	0.460	21	0.281	K.LLGVTIYSSDAIR.S
R1/RRR1-22/2	1407.734	1408.625	-1347.109	0.471	1572.058	0.466	21	0.280	K.LLGVTIYSSDAIR.S
R1/RRR1-18/2	1408.275	1408.625	-249.138	0.524	1532.695	0.482	21	0.280	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1838.557	1838.014	-249.235	0.548	1428.879	0.553	24	0.280	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-18/2	1408.324	1408.625	-214.442	0.508	1545.252	0.476	21	0.280	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1838.544	1838.014	-256.229	0.508	1422.753	0.542	25	0.278	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-18/2	1457.183	1456.668	-334.042	0.499	1585.451	0.581	21	0.276	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1838.127	1838.014	61.906	0.503	1386.815	0.552	24	0.276	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1837.733	1838.014	-153.342	0.525	1451.260	0.522	25	0.276	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1837.476	1838.014	-839.550	0.504	1292.241	0.584	25	0.275	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1839.472	1838.014	250.028	0.564	1280.193	0.594	24	0.274	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1839.303	1838.014	157.723	0.499	1431.269	0.527	24	0.274	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1408.028	1408.625	-1137.177	0.463	1408.700	0.509	20	0.273	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1837.505	1838.014	-823.545	0.484	1275.563	0.586	24	0.272	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1838.428	1838.014	226.328	0.566	1456.211	0.510	25	0.272	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-13/2	1992.640	1993.210	-790.335	0.517	1167.979	0.630	22	0.272	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-19/2	1408.181	1408.625	-316.104	0.487	1557.740	0.434	21	0.271	K.LLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1838.378	1838.014	198.894	0.519	1400.523	0.527	24	0.270	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1838.494	1838.014	261.948	0.549	1279.039	0.578	24	0.270	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-1/2	1735.236	1735.876	-948.497	0.506	1272.317	0.561	25	0.270	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-1/2	1407.986	1408.625	-1167.473	0.488	1645.175	0.396	21	0.270	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1838.455	1838.014	240.909	0.518	1287.889	0.567	25	0.270	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1839.361	1838.014	189.403	0.517	1300.865	0.562	24	0.269	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1456.367	1456.668	-207.367	0.469	1635.241	0.488	21	0.269	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/2	1735.395	1735.876	-278.302	0.490	1241.411	0.565	25	0.268	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1837.570	1838.014	-242.373	0.525	1225.682	0.587	24	0.268	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1407.805	1408.625	-1296.860	0.461	1532.438	0.427	21	0.266	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1837.692	1838.014	-175.531	0.560	1228.036	0.587	23	0.266	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1736.344	1735.876	269.955	0.546	1250.696	0.556	24	0.266	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1837.707	1838.014	-167.468	0.522	1253.207	0.568	23	0.265	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1735.365	1735.876	-873.569	0.541	1136.317	0.592	24	0.264	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1992.448	1993.210	-887.134	0.483	1060.023	0.631	23	0.263	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-5/2	1992.774	1993.210	-219.686	0.497	1035.149	0.639	23	0.263	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-17/2	1456.368	1456.668	-206.947	0.490	1526.821	0.594	21	0.262	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1993.572	1993.210	181.876	0.525	1053.973	0.638	21	0.262	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1993.452	1993.210	121.573	0.519	971.603	0.657	23	0.262	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1838.415	1838.014	219.070	0.495	1286.365	0.536	24	0.262	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1837.753	1838.014	-142.414	0.508	1277.069	0.539	24	0.261	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-15/2	1736.307	1735.876	248.736	0.524	1054.844	0.615	23	0.261	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1966.921	1966.187	-135.240	0.468	1504.503	0.443	24	0.261	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-20/2	1408.187	1408.625	-311.755	0.435	1406.178	0.461	20	0.261	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1992.744	1993.210	-234.927	0.507	1152.528	0.584	23	0.261	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1992.578	1993.210	-821.574	0.483	1044.238	0.625	23	0.260	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-14/2	1993.048	1993.210	-81.742	0.533	931.997	0.670	22	0.260	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1992.872	1993.210	-170.219	0.568	1035.304	0.632	22	0.260	K.EFSIPLQDSGHVVGFFGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1993.093	1993.210	-58.949	0.530	994.230	0.646	22	0.260	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1456.065	1456.668	-1104.369	0.441	1608.920	0.477	21	0.260	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1735.402	1735.876	-274.350	0.496	1067.431	0.602	23	0.259	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-13/2	1735.318	1735.876	-900.757	0.494	1138.973	0.569	24	0.259	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-19/2	1736.269	1735.876	226.951	0.523	1241.292	0.523	25	0.259	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-1/2	1992.162	1993.210	-1031.322	0.449	1032.417	0.627	23	0.259	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-21/2	1992.719	1993.210	-247.218	0.501	989.100	0.637	23	0.259	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-3/2	1735.397	1735.876	-276.961	0.502	1084.092	0.589	23	0.258	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1735.419	1735.876	-264.470	0.507	1217.289	0.532	24	0.258	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1408.038	1408.625	-1130.212	0.476	1357.426	0.466	20	0.258	K.LLGVTIYSSDAIR.S
R1/RRR1-24/2	1836.544	1838.014	-1348.977	0.448	1092.006	0.604	23	0.258	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1839.300	1838.014	156.458	0.493	1311.300	0.506	24	0.257	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1992.620	1993.210	-800.481	0.524	962.630	0.644	22	0.257	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1837.512	1838.014	-819.410	0.469	1149.348	0.571	24	0.257	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-15/2	1736.372	1735.876	285.957	0.479	1211.585	0.526	25	0.257	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-22/2	1992.191	1993.210	-1016.679	0.461	1065.141	0.602	23	0.257	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-12/2	1408.293	1408.625	-236.268	0.444	1263.909	0.500	20	0.257	K.LLGVTIYSSDAIR.S
R1/RRR1-25/2	1735.401	1735.876	-274.633	0.513	1030.603	0.601	23	0.256	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1837.585	1838.014	-233.909	0.499	1273.132	0.514	25	0.256	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1837.550	1838.014	-253.103	0.476	1300.442	0.504	24	0.256	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-21/2	1993.303	1993.210	46.645	0.517	932.764	0.646	22	0.255	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1838.549	1838.014	-253.298	0.512	1353.624	0.483	24	0.255	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1993.643	1993.210	217.857	0.526	897.994	0.661	21	0.254	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-3/2	1992.571	1993.210	-825.326	0.485	1004.116	0.616	22	0.254	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-19/2	1992.489	1993.210	-866.715	0.499	978.748	0.624	22	0.254	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1737.251	1735.876	216.251	0.491	1210.781	0.513	25	0.254	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-19/2	1992.402	1993.210	-910.383	0.481	998.387	0.629	20	0.254	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1735.819	1735.876	-33.336	0.498	1146.934	0.539	24	0.253	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1407.691	1408.625	-1377.679	0.368	1477.563	0.396	21	0.253	K.LLGVTIYSSDAIR.S
R1/RRR1-21/2	1735.345	1735.876	-885.080	0.477	1102.228	0.561	23	0.253	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-22/2	1735.247	1735.876	-942.000	0.460	1073.194	0.567	24	0.253	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-20/2	1994.317	1993.210	53.804	0.522	849.301	0.670	21	0.253	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-14/2	1992.432	1993.210	-895.253	0.488	964.461	0.624	22	0.253	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1837.463	1838.014	-846.152	0.511	1194.167	0.533	24	0.253	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/2	1838.634	1838.014	-206.872	0.498	1136.489	0.564	22	0.252	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1837.479	1838.014	-837.416	0.484	1128.192	0.561	23	0.252	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-17/2	1736.232	1735.876	205.448	0.538	1034.655	0.578	23	0.252	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-22/2	1993.053	1993.210	-79.284	0.492	947.998	0.638	20	0.252	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1735.371	1735.876	-870.391	0.455	1124.631	0.540	24	0.252	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1993.372	1993.210	81.101	0.526	930.755	0.635	21	0.252	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-25/2	1735.366	1735.876	-872.934	0.505	1017.719	0.581	23	0.251	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-22/2	1992.556	1993.210	-832.767	0.487	939.991	0.626	22	0.251	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-11/2	1993.892	1993.210	-160.429	0.514	987.341	0.601	23	0.251	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-19/2	1456.184	1456.668	-333.430	0.437	1595.254	0.455	21	0.251	R.SGTLIDAIGIYVHP.-
R1/RRR1-15/2	1993.767	1993.210	-223.200	0.514	908.991	0.639	21	0.251	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-15/2	1993.503	1993.210	147.242	0.508	922.781	0.634	21	0.251	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1837.373	1838.014	-895.438	0.456	1137.701	0.549	23	0.250	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/2	1838.430	1838.014	227.127	0.477	1195.970	0.531	22	0.250	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-10/2	1735.565	1735.876	-180.146	0.487	1123.375	0.531	24	0.250	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1966.709	1966.187	-243.515	0.459	1365.846	0.459	23	0.250	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-13/2	1735.352	1735.876	-881.196	0.464	1169.160	0.513	24	0.250	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-7/2	1992.491	1993.210	-865.669	0.492	944.956	0.619	21	0.249	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-18/2	1992.411	1993.210	-905.832	0.472	910.059	0.627	22	0.249	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1994.180	1993.210	-15.448	0.523	987.867	0.594	22	0.249	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-12/2	1736.298	1735.876	243.660	0.521	1051.278	0.555	23	0.249	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-15/2	1408.522	1408.625	-73.244	0.477	1215.777	0.483	19	0.248	K.LLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1991.390	1993.210	-1924.454	0.454	1163.286	0.536	20	0.248	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-3/2	1994.004	1993.210	-103.623	0.525	856.630	0.640	21	0.248	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-18/2	1736.451	1735.876	-245.769	0.491	1107.619	0.530	23	0.248	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1456.103	1456.668	-1077.938	0.406	1570.022	0.462	21	0.247	R.SGTLIDAIGIYVHP.-
R1/RRR1-17/2	1456.310	1456.668	-246.806	0.433	1519.077	0.530	21	0.247	R.SGTLIDAIGIYVHP.-
R1/RRR1-12/2	1992.900	1993.210	-156.454	0.490	963.665	0.609	20	0.247	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-15/2	1992.686	1993.210	-767.460	0.471	997.961	0.587	21	0.247	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-16/2	1735.503	1735.876	-215.568	0.498	1020.670	0.559	22	0.246	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-20/2	1456.544	1456.668	-85.708	0.433	1541.486	0.499	21	0.246	R.SGTLIDAIGIYVHP.-
R1/RRR1-20/2	1736.241	1735.876	210.665	0.438	1104.132	0.519	24	0.246	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-14/2	1408.356	1408.625	-191.746	0.468	1178.813	0.483	19	0.246	K.LLGVTIYSSDAIR.S
R1/RRR1-21/2	1407.926	1408.625	-1210.482	0.436	1059.712	0.537	18	0.246	K.LLGVTIYSSDAIR.S
R1/RRR1-22/2	1735.230	1735.876	-951.464	0.485	1074.713	0.532	23	0.246	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-20/2	1735.295	1735.876	-914.316	0.485	1014.889	0.553	23	0.246	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1407.661	1408.625	-1399.105	0.406	1335.668	0.419	20	0.246	K.LLGVTIYSSDAIR.S
R1/RRR1-21/2	1992.561	1993.210	-830.245	0.480	933.272	0.596	22	0.245	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-15/2	1736.560	1735.876	-182.934	0.488	1172.666	0.489	24	0.245	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-18/2	1992.506	1993.210	-858.228	0.489	922.477	0.598	22	0.245	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1966.735	1966.187	-230.065	0.449	1260.707	0.480	23	0.245	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/2	1992.514	1993.210	-854.046	0.482	916.952	0.607	21	0.245	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-3/2	1992.619	1993.210	-801.158	0.461	879.808	0.622	21	0.245	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1457.322	1456.668	-238.065	0.504	1417.719	0.638	20	0.244	R.SGTLIDAIGIYVHP.-
R1/RRR1-18/2	1408.497	1408.625	-90.718	0.451	1242.329	0.453	19	0.244	K.LLGVTIYSSDAIR.S
R1/RRR1-15/2	1735.522	1735.876	-204.913	0.455	1044.581	0.537	23	0.244	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-14/2	1736.262	1735.876	222.651	0.522	1022.956	0.543	23	0.244	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-1/2	1993.766	1993.210	-223.814	0.523	856.878	0.621	21	0.244	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-25/2	1736.258	1735.876	220.254	0.471	1090.145	0.514	23	0.243	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1993.550	1993.210	170.700	0.545	816.171	0.635	20	0.243	K.EFSIPLQDSGHVVGFFGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1736.332	1735.876	263.187	0.508	1024.372	0.533	23	0.242	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-16/2	1735.291	1735.876	-916.434	0.455	1002.559	0.548	22	0.242	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-22/2	1735.288	1735.876	-917.988	0.431	995.956	0.543	23	0.242	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1966.236	1966.187	25.243	0.465	1190.890	0.499	22	0.242	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-26/2	1736.316	1735.876	254.093	0.467	974.555	0.553	22	0.242	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1737.263	1735.876	223.016	0.543	1016.482	0.532	23	0.241	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-26/2	1409.258	1408.625	-261.128	0.466	1253.587	0.440	18	0.241	K.LLGVTIYSSDAIR.S
R1/RRR1-6/2	1994.512	1993.210	151.772	0.481	780.441	0.641	20	0.241	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-14/2	1735.494	1735.876	-221.142	0.458	1008.489	0.532	23	0.241	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-16/2	1736.383	1735.876	-284.772	0.476	1042.204	0.519	23	0.241	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-1/2	1735.494	1735.876	-221.072	0.488	951.575	0.555	22	0.241	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-1/2	1992.924	1993.210	-144.165	0.468	860.038	0.604	21	0.240	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-21/2	1457.337	1456.668	-227.897	0.491	1447.738	0.590	20	0.240	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1993.441	1993.210	116.046	0.484	805.402	0.617	21	0.240	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-22/2	1837.970	1838.014	-23.689	0.494	1093.461	0.514	23	0.240	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-11/2	1992.490	1993.210	-866.223	0.490	801.747	0.618	21	0.240	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1965.543	1966.187	-838.855	0.404	1395.301	0.389	25	0.240	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-11/2	1735.580	1735.876	-171.538	0.486	915.359	0.569	21	0.240	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-22/2	1735.726	1735.876	-87.229	0.452	1095.052	0.488	24	0.240	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-16/2	1735.393	1735.876	-279.643	0.504	870.130	0.574	22	0.239	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-27/2	1735.599	1735.876	-160.320	0.524	889.904	0.574	21	0.239	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-18/2	1535.593	1536.798	-1440.175	0.396	1257.681	0.430	20	0.239	K.KLLGVTIYSSDAIR.S
R1/RRR1-22/2	1735.936	1735.876	34.446	0.464	1120.063	0.476	24	0.239	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1992.426	1993.210	-898.328	0.452	1053.566	0.518	22	0.238	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1837.878	1838.014	-74.187	0.510	959.994	0.565	21	0.238	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-19/2	1735.460	1735.876	-240.618	0.490	914.511	0.553	22	0.238	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-15/2	1735.294	1735.876	-914.739	0.489	836.934	0.584	21	0.238	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-14/2	1736.278	1735.876	232.239	0.495	1118.003	0.472	24	0.238	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1991.811	1993.210	-1208.414	0.421	984.426	0.555	20	0.238	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-25/2	1736.305	1735.876	247.819	0.459	1058.858	0.497	23	0.238	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-4/2	1992.640	1993.210	-790.335	0.524	795.946	0.613	20	0.238	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1735.748	1735.876	-74.108	0.406	1279.397	0.404	25	0.237	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1965.617	1966.187	-800.764	0.447	1214.758	0.463	23	0.237	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-25/2	1456.368	1456.668	-206.863	0.431	1498.027	0.509	20	0.237	R.SGTLIDAIGIYVHP.-
R1/RRR1-13/2	1735.248	1735.876	-941.011	0.445	940.304	0.540	22	0.237	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-12/2	1992.528	1993.210	-847.158	0.474	739.738	0.629	20	0.237	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-13/2	1993.477	1993.210	133.978	0.511	770.159	0.614	20	0.236	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-2/2	1992.694	1993.210	-763.525	0.476	743.537	0.623	20	0.236	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1991.544	1993.210	-1846.350	0.420	1003.329	0.523	22	0.236	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-25/2	1736.241	1735.876	210.313	0.464	987.379	0.515	22	0.235	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-25/2	1736.270	1735.876	227.586	0.520	864.320	0.561	21	0.235	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-25/2	1735.345	1735.876	-885.362	0.474	952.983	0.525	22	0.235	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1737.607	1735.876	-155.413	0.508	950.678	0.523	22	0.235	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-3/2	1736.419	1735.876	-264.318	0.529	883.123	0.550	21	0.234	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-20/2	1735.541	1735.876	-193.835	0.435	915.430	0.535	22	0.234	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-18/2	1456.375	1456.668	-201.566	0.429	1470.105	0.527	20	0.234	R.SGTLIDAIGIYVHP.-
R1/RRR1-18/2	1737.276	1735.876	230.907	0.508	934.606	0.523	22	0.234	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-21/2	1735.379	1735.876	-287.688	0.480	842.586	0.555	21	0.233	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-14/2	1992.447	1993.210	-887.626	0.443	780.201	0.597	20	0.233	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-21/2	1735.390	1735.876	-281.125	0.436	922.329	0.524	22	0.233	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-20/2	1456.265	1456.668	-277.753	0.466	1497.165	0.503	20	0.233	R.SGTLIDAIGIYVHP.-
R1/RRR1-18/2	1735.365	1735.876	-873.710	0.458	959.958	0.508	22	0.233	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-2/2	1992.302	1993.210	-960.822	0.444	700.621	0.628	19	0.233	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-14/2	1736.149	1735.876	157.644	0.453	987.115	0.498	22	0.233	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-25/2	1407.775	1408.625	-1318.022	0.389	1135.191	0.439	18	0.233	K.LLGVTIYSSDAIR.S
R1/RRR1-1/2	1735.511	1735.876	-211.404	0.459	855.147	0.547	21	0.232	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1408.210	1408.625	-295.404	0.469	945.759	0.505	17	0.232	K.LLGVTIYSSDAIR.S
R1/RRR1-21/2	1839.426	1838.014	224.874	0.468	1173.118	0.444	23	0.232	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-20/2	1735.339	1735.876	-888.610	0.444	995.971	0.492	22	0.232	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-25/2	1408.062	1408.625	-1113.411	0.449	1049.745	0.462	18	0.232	K.LLGVTIYSSDAIR.S
R1/RRR1-4/2	1993.105	1993.210	-53.297	0.504	683.560	0.611	20	0.232	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-18/2	1991.894	1993.210	-1166.320	0.427	814.040	0.578	20	0.232	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-2/2	1993.695	1993.210	243.890	0.504	691.006	0.617	19	0.231	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-17/2	1735.321	1735.876	-898.779	0.462	933.862	0.507	22	0.231	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-19/2	1735.290	1735.876	-916.717	0.440	853.649	0.532	22	0.231	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-12/2	1992.049	1993.210	-1088.048	0.423	786.988	0.580	20	0.230	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1735.407	1735.876	-271.386	0.425	977.198	0.483	23	0.230	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-17/2	1735.307	1735.876	-906.901	0.447	849.617	0.536	21	0.230	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-19/2	1736.128	1735.876	145.516	0.492	857.843	0.532	21	0.230	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1455.779	1456.668	-1301.726	0.342	1532.432	0.402	20	0.230	R.SGTLIDAIGIYVHP.-
R1/RRR1-3/2	1736.616	1735.876	-150.426	0.526	1004.169	0.482	22	0.230	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1991.452	1993.210	-1892.915	0.397	1025.570	0.487	21	0.230	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-17/2	1736.617	1735.876	-149.721	0.428	1035.695	0.459	23	0.230	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-14/2	1407.414	1408.625	-1575.688	0.397	1293.446	0.362	18	0.229	K.LLGVTIYSSDAIR.S
R1/RRR1-3/2	1735.428	1735.876	-259.460	0.463	889.248	0.518	21	0.229	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-18/2	1734.762	1735.876	-1222.388	0.380	984.797	0.486	22	0.229	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-14/2	1456.308	1456.668	-248.320	0.412	1485.003	0.484	20	0.229	R.SGTLIDAIGIYVHP.-
R1/RRR1-2/2	1735.331	1735.876	-893.130	0.480	773.248	0.556	20	0.229	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1736.535	1735.876	-197.249	0.474	962.771	0.483	22	0.229	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1456.193	1456.668	-327.374	0.422	1511.298	0.457	21	0.228	R.SGTLIDAIGIYVHP.-
R1/RRR1-26/2	1735.336	1735.876	-890.376	0.430	879.541	0.516	21	0.228	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1737.334	1735.876	263.952	0.493	933.320	0.488	22	0.228	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-26/2	1735.426	1735.876	-260.589	0.472	817.235	0.528	21	0.228	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-19/2	1737.266	1735.876	224.777	0.511	949.982	0.483	22	0.228	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1736.317	1735.876	254.587	0.510	881.310	0.510	21	0.227	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1966.666	1966.187	244.752	0.443	1169.391	0.436	22	0.227	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/2	1457.133	1456.668	319.834	0.477	1413.826	0.570	20	0.227	R.SGTLIDAIGIYVHP.-
R1/RRR1-7/2	1992.457	1993.210	-882.706	0.447	616.107	0.612	19	0.227	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-14/2	1736.282	1735.876	234.354	0.449	826.059	0.520	21	0.227	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-26/2	1736.260	1735.876	221.805	0.438	834.691	0.517	21	0.227	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-26/2	1735.562	1735.876	-181.557	0.456	852.978	0.510	21	0.226	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-26/2	1736.157	1735.876	162.157	0.451	761.110	0.546	20	0.226	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/2	1456.382	1456.668	-197.193	0.479	1482.740	0.495	20	0.226	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1966.562	1966.187	191.533	0.440	1072.818	0.471	21	0.226	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/2	1838.179	1838.014	90.213	0.464	945.904	0.500	21	0.226	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-12/2	1408.241	1408.625	-273.141	0.402	1075.390	0.417	18	0.225	K.LLGVTIYSSDAIR.S
R1/RRR1-22/2	1837.482	1838.014	-836.216	0.513	847.920	0.538	20	0.225	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-18/2	1735.259	1735.876	-934.937	0.461	802.706	0.515	21	0.225	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-9/2	1993.717	1993.210	-248.323	0.516	649.815	0.584	19	0.225	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-4/2	1735.422	1735.876	-262.494	0.462	746.890	0.537	20	0.225	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1966.445	1966.187	132.084	0.431	1097.344	0.445	22	0.224	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-25/2	1735.410	1735.876	-269.834	0.416	973.932	0.451	22	0.224	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-1/2	1408.182	1408.625	-315.669	0.433	1158.654	0.373	19	0.224	K.LLGVTIYSSDAIR.S
R1/RRR1-20/2	1737.213	1735.876	194.337	0.479	808.683	0.505	21	0.224	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-11/2	1735.352	1735.876	-880.984	0.448	835.302	0.497	21	0.224	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-6/2	1993.523	1993.210	157.252	0.472	630.673	0.590	18	0.223	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-9/2	1735.287	1735.876	-918.906	0.467	733.893	0.529	20	0.223	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-2/2	1736.355	1735.876	276.652	0.505	861.461	0.488	21	0.223	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-16/2	1408.444	1408.625	-128.797	0.456	1028.792	0.414	18	0.223	K.LLGVTIYSSDAIR.S
R1/RRR1-4/2	1457.177	1456.668	-338.076	0.468	1396.706	0.564	20	0.222	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/2	1737.497	1735.876	-219.266	0.476	886.410	0.464	22	0.222	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-19/2	1736.363	1735.876	281.305	0.496	792.800	0.493	21	0.221	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1992.939	1993.210	-136.854	0.466	544.434	0.589	18	0.220	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-22/2	1994.877	1993.210	-167.470	0.433	586.332	0.596	17	0.220	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-24/2	1837.727	1838.014	-156.274	0.400	960.840	0.470	20	0.220	-.IGPWGGNGGSAQDISVPPK.-
R1/RRR1-23/2	1408.149	1408.625	-338.892	0.370	792.677	0.476	17	0.219	K.LLGVTIYSSDAIR.S
R1/RRR1-10/2	1993.046	1993.210	-82.602	0.476	642.869	0.557	18	0.219	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-10/2	1993.881	1993.210	-165.773	0.474	625.766	0.557	17	0.217	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-16/2	1408.248	1408.625	-268.357	0.457	817.302	0.453	16	0.217	K.LLGVTIYSSDAIR.S
R1/RRR1-22/2	1735.639	1735.876	-137.319	0.379	770.563	0.476	20	0.216	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-13/2	1455.999	1456.668	-1150.081	0.417	1442.021	0.472	20	0.215	R.SGTLIDAIGIYVHP.-
R1/RRR1-7/2	1408.295	1408.625	-234.877	0.394	906.654	0.417	16	0.215	K.LLGVTIYSSDAIR.S
R1/RRR1-21/2	1456.903	1456.668	161.472	0.461	1461.734	0.464	20	0.215	R.SGTLIDAIGIYVHP.-
R1/RRR1-7/2	1991.489	1993.210	-1874.190	0.365	539.687	0.560	18	0.214	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-23/2	1965.434	1966.187	-894.531	0.409	1084.188	0.384	23	0.214	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-17/2	1736.527	1735.876	-202.115	0.458	762.537	0.455	20	0.214	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-22/2	1456.208	1456.668	-317.029	0.428	1483.576	0.421	20	0.213	R.SGTLIDAIGIYVHP.-
R1/RRR1-9/2	1457.240	1456.668	-294.792	0.440	1351.041	0.563	19	0.213	R.SGTLIDAIGIYVHP.-
R1/RRR1-17/2	1736.393	1735.876	-279.482	0.482	775.094	0.447	20	0.213	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-13/2	1456.267	1456.668	-276.240	0.457	1450.668	0.465	20	0.212	R.SGTLIDAIGIYVHP.-
R1/RRR1-19/2	1456.199	1456.668	-323.001	0.433	1453.516	0.451	20	0.212	R.SGTLIDAIGIYVHP.-
R1/RRR1-18/2	1456.204	1456.668	-319.805	0.416	1404.869	0.495	20	0.211	R.SGTLIDAIGIYVHP.-
R1/RRR1-28/2	1735.476	1735.876	-231.727	0.335	729.255	0.455	19	0.210	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/2	1408.106	1408.625	-1081.813	0.421	848.424	0.380	17	0.210	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1408.362	1408.625	-187.399	0.461	1137.645	0.297	19	0.209	K.LLGVTIYSSDAIR.S
R1/RRR1-3/2	1408.206	1408.625	-298.361	0.328	798.895	0.400	16	0.208	K.LLGVTIYSSDAIR.S
R1/RRR1-1/2	1994.698	1993.210	245.118	0.379	521.573	0.501	17	0.208	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-16/2	1456.284	1456.668	-264.802	0.423	1404.400	0.471	20	0.205	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1456.300	1456.668	-253.702	0.438	1412.092	0.463	20	0.204	R.SGTLIDAIGIYVHP.-
R1/RRR1-27/2	1736.298	1735.876	243.730	0.334	617.295	0.408	18	0.203	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1837.393	1838.014	-884.634	0.371	485.311	0.501	15	0.202	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-25/2	1456.292	1456.668	-258.747	0.459	1360.045	0.512	19	0.202	R.SGTLIDAIGIYVHP.-
R1/RRR1-4/2	1992.305	1993.210	-959.346	0.383	495.315	0.433	16	0.200	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-2/2	1408.260	1408.625	-259.922	0.325	588.129	0.397	13	0.200	K.LLGVTIYSSDAIR.S
R1/RRR1-17/2	1407.520	1408.625	-1499.977	0.358	649.465	0.355	14	0.200	K.LLGVTIYSSDAIR.S
R1/RRR1-26/2	1407.859	1408.625	-1257.936	0.334	410.692	0.279	14	0.199	K.LLGVTIYSSDAIR.S
R1/RRR1-10/2	1992.975	1993.210	-118.359	0.380	456.055	0.389	16	0.198	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-22/2	1839.097	1838.014	45.629	0.386	612.011	0.385	17	0.196	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-12/2	1456.198	1456.668	-323.842	0.427	1320.261	0.513	19	0.196	R.SGTLIDAIGIYVHP.-
R1/RRR1-3/2	1408.941	1408.625	225.365	0.392	840.708	0.266	16	0.195	K.LLGVTIYSSDAIR.S
R1/RRR1-20/2	1407.584	1408.625	-1454.155	0.296	485.390	0.278	13	0.195	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1966.665	1966.187	243.881	0.458	633.341	0.430	17	0.195	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/2	1408.935	1408.625	220.934	0.244	371.113	0.325	11	0.195	K.LLGVTIYSSDAIR.S
R1/RRR1-23/2	1408.269	1408.625	-253.139	0.349	589.316	0.309	14	0.194	-.LLGVTIYSSDAIR.-
R1/RRR1-25/2	1456.264	1456.668	-278.090	0.447	1326.767	0.503	19	0.194	R.SGTLIDAIGIYVHP.-
R1/RRR1-25/2	1992.641	1993.210	-789.966	0.270	353.200	0.390	13	0.194	K.EFSIPLQDSGHVVGFFGR.S
R1/RRR1-19/3	1457.747	1456.668	53.987	0.432	1186.012	0.329	23	0.193	R.SGTLIDAIGIYVHP.-
R1/RRR1-15/2	1457.360	1456.668	-212.267	0.419	1303.216	0.488	19	0.187	R.SGTLIDAIGIYVHP.-
R1/RRR1-7/2	1457.330	1456.668	-232.939	0.366	1161.314	0.590	19	0.184	R.SGTLIDAIGIYVHP.-
R1/RRR1-16/2	1456.528	1456.668	-96.217	0.422	1288.397	0.488	20	0.184	R.SGTLIDAIGIYVHP.-
R1/RRR1-27/2	1407.887	1408.625	-1238.083	0.294	372.714	0.363	10	0.181	-.LLGVTIYSSDAIR.-
R1/RRR1-3/2	1456.008	1456.668	-1143.262	0.309	1312.114	0.378	19	0.176	R.SGTLIDAIGIYVHP.-
R1/RRR1-22/2	1456.215	1456.668	-312.151	0.419	1268.946	0.465	19	0.176	R.SGTLIDAIGIYVHP.-
R1/RRR1-6/2	1457.100	1456.668	297.490	0.416	1182.085	0.536	18	0.175	R.SGTLIDAIGIYVHP.-
R1/RRR1-16/2	1457.460	1456.668	-143.115	0.433	1177.805	0.540	18	0.175	R.SGTLIDAIGIYVHP.-
R1/RRR1-17/2	1456.164	1456.668	-1036.273	0.392	1227.354	0.448	18	0.167	R.SGTLIDAIGIYVHP.-
R1/RRR1-6/2	1456.404	1456.668	-181.974	0.427	1166.166	0.510	18	0.167	R.SGTLIDAIGIYVHP.-
R1/RRR1-22/3	1456.822	1456.668	106.129	0.404	1114.175	0.316	23	0.165	R.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1456.240	1456.668	-294.574	0.360	1107.891	0.505	18	0.161	R.SGTLIDAIGIYVHP.-
R1/RRR1-7/2	1456.388	1456.668	-192.989	0.405	1149.121	0.469	18	0.158	R.SGTLIDAIGIYVHP.-
R1/RRR1-21/2	1456.213	1456.668	-313.749	0.411	1029.506	0.553	18	0.158	R.SGTLIDAIGIYVHP.-
R1/RRR1-14/2	1456.017	1456.668	-1137.116	0.352	1128.690	0.464	17	0.157	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/2	1455.788	1456.668	-1295.410	0.356	1024.251	0.457	18	0.143	R.SGTLIDAIGIYVHP.-
R1/RRR1-22/3	1735.766	1735.876	-63.711	0.402	1175.835	0.505	28	0.143	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/3	1736.586	1735.876	-167.992	0.481	1181.525	0.497	29	0.142	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-12/2	1456.129	1456.668	-1059.924	0.314	963.479	0.465	16	0.140	R.SGTLIDAIGIYVHP.-
R1/RRR1-11/2	1456.352	1456.668	-217.794	0.364	1091.893	0.359	16	0.135	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/3	1966.531	1966.187	175.467	0.349	1235.208	0.460	36	0.135	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.628	1966.187	225.139	0.460	1097.546	0.509	38	0.135	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-5/2	1456.387	1456.668	-193.241	0.332	808.025	0.486	16	0.134	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/3	1737.611	1735.876	-153.342	0.519	908.682	0.544	27	0.133	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-7/2	1456.437	1456.668	-159.188	0.185	518.611	0.343	12	0.131	R.SGTLIDAIGIYVHP.-
R1/RRR1-27/2	1456.390	1456.668	-191.307	0.368	677.475	0.462	15	0.128	R.SGTLIDAIGIYVHP.-
R1/RRR1-9/2	1456.644	1456.668	-16.442	0.347	742.736	0.454	16	0.128	R.SGTLIDAIGIYVHP.-
R1/RRR1-12/2	1456.415	1456.668	-173.986	0.325	735.264	0.448	15	0.127	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/3	1966.426	1966.187	121.960	0.441	1159.430	0.457	38	0.127	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-11/2	1456.322	1456.668	-238.060	0.336	542.692	0.386	14	0.127	R.SGTLIDAIGIYVHP.-
R1/RRR1-5/2	1455.575	1456.668	-1442.465	0.329	585.966	0.415	13	0.127	R.SGTLIDAIGIYVHP.-
R1/RRR1-19/3	1737.149	1735.876	157.475	0.480	870.495	0.527	26	0.126	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/3	1966.306	1966.187	61.070	0.429	1118.585	0.469	39	0.125	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-9/2	1455.535	1456.668	-1470.012	0.265	982.938	0.302	16	0.125	R.SGTLIDAIGIYVHP.-
R1/RRR1-22/3	1966.563	1966.187	191.993	0.339	1127.761	0.432	31	0.124	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-15/2	1456.289	1456.668	-260.934	0.373	913.411	0.390	16	0.123	-.SGTLIDAIGIYVHP.-
R1/RRR1-24/3	1966.641	1966.187	231.675	0.398	1065.616	0.472	38	0.122	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1736.873	1735.876	-2.271	0.512	1018.344	0.459	28	0.121	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/3	1967.962	1966.187	-114.302	0.412	1254.906	0.406	40	0.121	K.IGPWGGNGGSAQDISVPPKK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/3	1966.317	1966.187	66.394	0.463	1132.753	0.436	38	0.121	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1967.213	1966.187	13.585	0.460	986.517	0.475	36	0.121	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-10/2	1456.233	1456.668	-299.956	0.302	624.240	0.339	14	0.120	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/3	1967.097	1966.187	-45.606	0.418	1072.379	0.439	37	0.117	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1967.994	1966.187	-97.969	0.463	1087.664	0.423	36	0.117	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.990	1966.187	-100.136	0.455	1058.721	0.447	39	0.117	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1966.297	1966.187	56.401	0.427	1016.242	0.457	38	0.116	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1838.413	1838.014	217.997	0.403	1005.676	0.453	28	0.116	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-2/2	1455.961	1456.668	-1175.927	0.335	732.777	0.338	14	0.115	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/3	1967.955	1966.187	-117.849	0.440	1046.065	0.432	38	0.113	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-10/2	1455.801	1456.668	-1286.568	0.237	665.686	0.199	13	0.113	-.SGTLIDAIGIYVHP.-
R1/RRR1-23/3	1967.737	1966.187	-228.928	0.445	1160.881	0.395	39	0.113	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-15/2	1457.304	1456.668	-250.502	0.394	785.437	0.364	16	0.112	-.SGTLIDAIGIYVHP.-
R1/RRR1-23/3	1966.169	1966.187	-8.887	0.435	847.838	0.478	37	0.112	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1536.583	1536.798	-140.017	0.451	1012.531	0.456	26	0.111	K.KLLGVTIYSSDAIR.S
R1/RRR1-22/3	1735.765	1735.876	-64.557	0.403	781.081	0.482	25	0.111	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/3	1967.764	1966.187	-215.392	0.404	979.449	0.429	36	0.110	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.750	1966.187	-222.662	0.432	898.585	0.442	35	0.110	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/2	1456.411	1456.668	-176.929	0.294	802.399	0.244	16	0.110	R.SGTLIDAIGIYVHP.-
R1/RRR1-23/3	1966.392	1966.187	105.058	0.437	1076.060	0.412	40	0.109	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1967.958	1966.187	-116.542	0.468	953.796	0.428	37	0.109	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1966.094	1966.187	-47.373	0.391	311.867	0.427	24	0.109	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.902	1966.187	-145.146	0.385	909.805	0.439	35	0.109	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1965.954	1966.187	-118.561	0.419	775.507	0.443	31	0.108	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1966.837	1966.187	-178.019	0.413	938.244	0.428	36	0.108	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1967.111	1966.187	-38.604	0.397	1101.557	0.390	39	0.107	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.871	1966.187	-160.928	0.431	776.820	0.442	33	0.107	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-21/3	1967.089	1966.187	-49.901	0.402	528.974	0.458	29	0.106	K.IGPWGGNGGSAQDISVPPKK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/3	1967.954	1966.187	-118.316	0.418	1014.576	0.402	37	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1966.247	1966.187	30.623	0.417	822.607	0.440	35	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-21/3	1456.891	1456.668	153.774	0.400	887.190	0.398	25	0.106	R.SGTLIDAIGIYVHP.-
R1/RRR1-24/3	1967.864	1966.187	-164.331	0.447	1062.861	0.378	36	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1736.550	1735.876	-188.724	0.461	583.417	0.466	23	0.106	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/3	1966.346	1966.187	81.337	0.376	479.937	0.445	27	0.105	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.167	1966.187	-9.822	0.449	640.458	0.441	32	0.105	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1537.737	1536.798	-39.868	0.475	963.918	0.426	25	0.104	K.KLLGVTIYSSDAIR.S
R1/RRR1-24/3	1965.529	1966.187	-845.844	0.401	652.470	0.447	33	0.104	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1839.641	1838.014	-203.006	0.348	961.161	0.416	28	0.103	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/3	1967.167	1966.187	-9.754	0.415	540.721	0.425	29	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1967.790	1966.187	-202.043	0.430	949.350	0.391	35	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1966.450	1966.187	134.194	0.409	831.994	0.416	35	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1735.980	1735.876	59.652	0.406	421.770	0.488	20	0.103	-.IVTSANNTYEAGVPNGK.-
R1/RRR1-23/3	1966.457	1966.187	137.929	0.428	792.873	0.414	34	0.102	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1967.839	1966.187	-177.026	0.465	902.053	0.401	37	0.102	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1965.979	1966.187	-105.855	0.413	711.912	0.423	33	0.102	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-21/3	1968.092	1966.187	-48.134	0.387	1140.893	0.325	33	0.102	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-15/3	1968.154	1966.187	-16.592	0.421	756.892	0.393	30	0.101	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1838.210	1838.014	106.922	0.359	1047.664	0.376	30	0.100	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-22/3	1967.834	1966.187	-179.826	0.375	482.889	0.393	29	0.100	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.888	1966.187	-152.337	0.425	830.261	0.390	34	0.100	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1965.916	1966.187	-138.275	0.404	677.593	0.392	31	0.099	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1965.521	1966.187	-850.146	0.352	670.102	0.406	32	0.098	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-19/3	1736.311	1735.876	251.090	0.408	663.769	0.423	25	0.098	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-23/3	1966.490	1966.187	154.737	0.386	855.772	0.385	35	0.098	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-18/3	1967.889	1966.187	-151.730	0.334	549.737	0.384	27	0.098	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1736.106	1735.876	132.851	0.406	569.012	0.415	23	0.097	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/3	1736.392	1735.876	-280.125	0.422	426.454	0.423	20	0.097	-.IVTSANNTYEAGVPNGK.-
R1/RRR1-22/3	1968.099	1966.187	-44.681	0.443	681.364	0.372	32	0.097	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1966.936	1966.187	-127.590	0.449	872.328	0.374	37	0.097	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-21/3	1735.970	1735.876	54.045	0.388	667.467	0.414	25	0.096	K.IVTSANNTYEAGVPNGK.E
R1/RRR1-24/3	1967.362	1966.187	89.385	0.367	687.685	0.374	31	0.096	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1966.040	1966.187	-74.838	0.361	752.110	0.358	30	0.095	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1408.583	1408.625	-29.616	0.385	1020.351	0.381	26	0.095	K.LLGVTIYSSDAIR.S
R1/RRR1-24/3	1967.331	1966.187	73.423	0.365	909.868	0.348	35	0.094	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1966.466	1966.187	142.411	0.365	582.161	0.298	26	0.092	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1408.716	1408.625	65.036	0.404	924.736	0.380	25	0.091	K.LLGVTIYSSDAIR.S
R1/RRR1-23/3	1967.688	1966.187	-254.135	0.413	789.191	0.332	35	0.091	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1965.171	1966.187	-1028.703	0.286	693.702	0.346	31	0.091	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-24/3	1967.126	1966.187	-30.761	0.373	661.118	0.290	30	0.089	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-22/3	1536.470	1536.798	-213.897	0.344	825.926	0.369	24	0.086	K.KLLGVTIYSSDAIR.S
R1/RRR1-23/3	1967.716	1966.187	-239.758	0.230	647.466	0.286	27	0.086	K.IGPWGGNGGSAQDISVPPKK.L
R1/RRR1-23/3	1838.795	1838.014	-118.969	0.295	701.060	0.371	26	0.085	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-23/3	1838.639	1838.014	-204.582	0.349	795.139	0.308	27	0.082	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-24/3	1408.506	1408.625	-84.512	0.355	661.016	0.321	23	0.081	K.LLGVTIYSSDAIR.S
R1/RRR1-23/3	1536.244	1536.798	-1014.461	0.303	660.861	0.282	28	0.077	K.KLLGVTIYSSDAIR.S
R1/RRR1-24/3	1408.252	1408.625	-265.541	0.346	682.613	0.256	22	0.074	-.LLGVTIYSSDAIR.-
R1/RRR1-23/3	1408.198	1408.625	-304.155	0.240	710.827	0.199	21	0.070	K.LLGVTIYSSDAIR.S
R1/RRR1-23/3	1837.694	1838.014	-174.273	0.176	836.455	0.082	26	0.059	K.IGPWGGNGGSAQDISVPPK.K
R1/RRR1-7/2	1816.007	1815.103	-53.101	0.593	2594.645	0.579	25	0.506	R.TLKEWIVSSLGPDAVAK.H
R1/RRR1-7/2	1814.657	1815.103	-246.377	0.590	2418.062	0.576	24	0.462	R.TLKEWIVSSLGPDAVAK.H
R1/RRR1-7/2	1179.971	1180.339	-312.595	0.435	1211.950	0.460	15	0.241	K.GLQAHVGEIQK.T
R1/RRR1-7/2	1372.938	1372.530	297.988	0.528	1002.978	0.483	18	0.231	K.TFTTAETM*LNAR.T
R1/RRR1-7/2	1896.581	1896.130	238.432	0.548	721.584	0.525	22	0.218	R.YLAVEPSTPYNTTTLPK.-
R1/RRR1-7/2	949.704	950.031	-344.426	0.378	438.701	0.527	14	0.206	R.SGSWVGATGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1316.399	1316.488	-67.395	0.456	928.300	0.344	17	0.203	-.FLANVDPVDVAR.-
R1/RRR1-7/2	1316.520	1316.488	24.960	0.436	719.059	0.341	16	0.190	-.FLANVDPVDVAR.-
R1/RRR1-11/2	1814.539	1815.103	-864.602	0.372	1075.327	0.189	17	0.182	R.TLKEWIVSSLGPDAVAK.H
R1/RRR1-11/2	1814.391	1815.103	-946.257	0.373	1058.880	0.150	17	0.177	R.TLKEWIVSSLGPDAVAK.H
R1/RRR1-11/2	1814.398	1815.103	-942.744	0.389	994.433	0.134	17	0.173	R.TLKEWIVSSLGPDAVAK.H
R1/RRR1-7/3	1845.001	1844.139	-75.501	0.476	1319.085	0.463	29	0.147	R.SIKDLDPETTLVVVVSK.T
R1/RRR1-7/3	1702.974	1703.901	-1134.728	0.485	1380.652	0.451	31	0.143	K.FAPHIQQLSM*ESNGK.G
R1/RRR1-7/3	1703.044	1703.901	-1093.486	0.455	877.218	0.439	27	0.100	K.FAPHIQQLSM*ESNGK.G
R1/RRR1-7/3	1843.551	1844.139	-864.352	0.419	1052.354	0.373	26	0.100	R.SIKDLDPETTLVVVVSK.T
R1/RRR1-7/3	1703.656	1703.901	-144.522	0.392	742.613	0.386	27	0.086	K.FAPHIQQLSM*ESNGK.G
R1/RRR1-7/2	1272.011	1272.473	-364.285	0.332	1422.426	0.406	16	0.248	R.DLITILEDAIR.G
R1/RRR1-8/2	1272.328	1272.473	-114.669	0.455	1404.853	0.398	17	0.247	R.DLITILEDAIR.G
R1/RRR1-8/2	1272.668	1272.473	153.292	0.369	1011.895	0.413	16	0.219	R.DLITILEDAIR.G
R1/RRR1-9/2	1273.064	1272.473	-322.340	0.401	970.883	0.402	15	0.215	R.DLITILEDAIR.G
R1/RRR1-7/2	1017.181	1016.174	7.690	0.460	673.367	0.456	16	0.211	K.IVNDGVTVAK.E
R1/RRR1-7/2	1272.195	1272.473	-219.391	0.320	1096.848	0.329	16	0.211	R.DLITILEDAIR.G
R1/RRR1-5/2	1272.298	1272.473	-137.864	0.336	404.438	0.319	13	0.196	R.DLITILEDAIR.G
R1/RRR1-9/2	1272.489	1272.473	12.257	0.373	660.552	0.291	14	0.194	R.DLITILEDAIR.G
R1/RRR1-7/2	1272.108	1272.473	-287.933	0.188	714.013	0.257	14	0.187	R.DLITILEDAIR.G
R1/RRR1-10/2	1272.651	1272.473	140.306	0.224	212.648	0.348	11	0.176	-.DLITILEDAIR.-
R1/RRR1-14/2	1606.151	1606.584	-270.357	0.564	2548.606	0.513	24	0.472	K.DAAEGQEGEAATEEAK.K
R1/RRR1-14/2	1719.444	1719.920	-277.680	0.528	2545.469	0.502	24	0.464	R.ILDVVYNASNNELVR.T
R1/RRR1-14/2	1719.411	1719.920	-880.179	0.546	2454.647	0.516	24	0.450	R.ILDVVYNASNNELVR.T
R1/RRR1-15/2	1719.621	1719.920	-174.696	0.505	2180.235	0.495	23	0.385	R.ILDVVYNASNNELVR.T
R1/RRR1-14/2	1657.136	1656.735	243.182	0.585	1926.631	0.546	23	0.356	R.LDTGNYSWGSEAVTR.K
R1/RRR1-14/2	1656.480	1656.735	-154.377	0.535	1891.337	0.520	23	0.343	R.LDTGNYSWGSEAVTR.K
R1/RRR1-14/2	1720.391	1719.920	274.522	0.572	1829.898	0.545	22	0.339	R.ILDVVYNASNNELVR.T
R1/RRR1-14/2	1657.334	1656.735	-242.283	0.534	1835.039	0.532	22	0.337	R.LDTGNYSWGSEAVTR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1658.364	1656.735	-224.414	0.363	1038.333	0.367	19	0.210	R.LDTGNYSWGSEAVTR.K
R1/RRR1-14/2	966.045	966.070	-26.122	0.411	778.120	0.399	15	0.208	R.ADGYILEGK.E
R1/RRR1-14/2	1245.618	1246.437	-1464.834	0.219	1170.819	0.211	15	0.193	K.SAIVQVDAAPFK.Q
R1/RRR1-14/2	965.832	966.070	-247.085	0.326	591.325	0.296	13	0.191	R.ADGYILEGK.E
R1/RRR1-15/2	1246.105	1246.437	-267.216	0.243	613.401	0.254	14	0.183	K.SAIVQVDAAPFK.Q
R1/RRR1-21/2	1607.390	1606.584	-121.006	0.166	446.904	0.384	13	0.177	K.DAAEGQEGEAATEEAK.K
R1/RRR1-14/3	1862.902	1862.930	-15.361	0.582	1213.107	0.580	34	0.168	K.KDAAEGQEGEAATEEAKK.S
R1/RRR1-14/3	1734.339	1734.757	-242.193	0.481	1340.760	0.426	28	0.141	K.KDAAEGQEGEAATEEAK.K
R1/RRR1-6/2	1258.864	1259.434	-1251.498	0.519	2349.817	0.588	20	0.458	R.VNLVQVLGSDSK.V
R1/RRR1-6/2	1258.825	1259.434	-1281.979	0.493	2385.942	0.552	20	0.452	R.VNLVQVLGSDSK.V
R1/RRR1-6/2	1258.252	1259.434	-1739.614	0.427	1717.661	0.560	19	0.328	R.VNLVQVLGSDSK.V
R1/RRR1-6/2	1087.985	1088.240	-235.042	0.434	1042.197	0.540	15	0.242	K.GPITTSASVVR.G
R1/RRR1-6/2	1190.642	1191.402	-1482.288	0.324	1232.176	0.464	16	0.241	R.LSFQLSTPLGK.T
R1/RRR1-6/2	1128.007	1128.258	-223.229	0.414	900.487	0.522	16	0.229	R.ALSYLSSTSAK.Q
R1/RRR1-6/2	1246.153	1246.520	-295.994	0.323	1077.099	0.419	17	0.220	K.IVLDFLGLVEK.F
R1/RRR1-6/2	1299.562	1299.626	-49.614	0.418	744.668	0.448	16	0.210	R.VFVPLVLSLPSK.V
R1/RRR1-6/2	1191.144	1191.402	-216.742	0.377	784.565	0.419	14	0.206	R.LSFQLSTPLGK.T
R1/RRR1-6/2	1299.336	1299.626	-224.419	0.379	855.683	0.354	18	0.203	R.VFVPLVLSLPSK.V
R1/RRR1-6/2	1190.343	1191.402	-1734.457	0.309	731.613	0.369	14	0.197	R.LSFQLSTPLGK.T
R1/RRR1-6/2	1299.256	1299.626	-285.875	0.380	649.263	0.349	15	0.195	R.VFVPLVLSLPSK.V
R1/RRR1-6/2	1035.101	1035.219	-113.862	0.234	980.468	0.264	13	0.191	R.TFQILGVEK.D
R1/RRR1-6/2	1127.201	1128.258	-1830.313	0.253	551.184	0.213	14	0.184	R.ALSYLSSTSAK.Q
R1/RRR1-6/3	1453.109	1453.667	-1075.365	0.435	1329.538	0.343	25	0.114	K.APKPPAQAVDPFSK.F
R1/RRR1-6/3	1453.832	1453.667	113.421	0.460	1114.455	0.312	23	0.093	K.APKPPAQAVDPFSK.F
R1/RRR1-6/3	1453.477	1453.667	-131.428	0.420	1236.198	0.281	25	0.092	K.APKPPAQAVDPFSK.F
R1/RRR1-15/3	1807.586	1807.001	-230.347	0.597	2936.530	0.534	38	0.560	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-16/2	1806.484	1807.001	-842.024	0.566	2561.656	0.657	27	0.533	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-15/3	1807.068	1807.001	37.013	0.611	2687.336	0.576	37	0.502	K.TPAELSHAANAGLDIAVR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1806.562	1807.001	-243.686	0.562	2411.455	0.624	27	0.482	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-16/2	1806.511	1807.001	-271.820	0.579	2323.965	0.668	27	0.481	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-15/2	1807.533	1807.001	-259.744	0.525	2364.921	0.602	25	0.462	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-16/3	1807.059	1807.001	31.931	0.603	2563.609	0.537	35	0.444	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-15/2	1808.122	1807.001	67.403	0.581	2190.750	0.632	26	0.436	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-15/3	1806.874	1807.001	-70.317	0.566	2579.222	0.513	36	0.431	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-16/3	1806.934	1807.001	-37.384	0.574	2343.398	0.550	35	0.385	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-15/2	1806.437	1807.001	-868.141	0.523	1826.743	0.613	25	0.360	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-16/3	1806.997	1807.001	-2.217	0.568	2263.433	0.536	35	0.355	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-18/3	1807.236	1807.001	130.705	0.546	2313.890	0.509	37	0.348	K.TPAELSHAANAGLDIAVR.M
R1/RRR1-16/2	1498.261	1498.663	-269.151	0.488	1734.198	0.491	19	0.311	K.AFFEDYKEAHLK.L
R1/RRR1-16/2	1498.947	1498.663	189.533	0.540	1615.127	0.529	18	0.305	K.AFFEDYKEAHLK.L
R1/RRR1-16/2	1506.238	1506.644	-270.245	0.474	1586.094	0.492	21	0.290	R.LAWHSAGTFDVSSK.T
R1/RRR1-16/2	1497.763	1498.663	-1272.921	0.470	1521.188	0.503	19	0.286	K.AFFEDYKEAHLK.L
R1/RRR1-16/2	1506.249	1506.644	-262.765	0.509	1559.608	0.485	21	0.285	R.LAWHSAGTFDVSSK.T
R1/RRR1-16/2	1506.148	1506.644	-330.254	0.496	1320.221	0.492	21	0.260	R.LAWHSAGTFDVSSK.T
R1/RRR1-16/2	1557.390	1556.831	-283.618	0.497	892.920	0.486	20	0.225	K.ALLSDPAFRPLVEK.Y
R1/RRR1-15/2	1099.588	1100.247	-1513.393	0.435	1089.747	0.391	16	0.223	K.EGLLQLPSDK.A
R1/RRR1-16/2	1557.355	1556.831	-306.581	0.479	788.302	0.459	19	0.215	K.ALLSDPAFRPLVEK.Y
R1/RRR1-16/2	1008.823	1009.096	-271.690	0.429	1000.343	0.356	14	0.213	R.SGFEGPWTK.N
R1/RRR1-16/2	1556.447	1556.831	-247.289	0.449	636.789	0.487	18	0.212	K.ALLSDPAFRPLVEK.Y
R1/RRR1-16/2	911.784	912.046	-288.135	0.379	536.671	0.458	13	0.209	K.TGGPFGTM*K.T
R1/RRR1-16/2	1100.101	1100.247	-132.955	0.445	1050.217	0.315	16	0.208	K.EGLLQLPSDK.A
R1/RRR1-16/2	1099.799	1100.247	-409.303	0.410	1116.132	0.292	16	0.208	K.EGLLQLPSDK.A
R1/RRR1-16/2	1009.090	1009.096	-6.383	0.396	848.917	0.356	14	0.207	R.SGFEGPWTK.N
R1/RRR1-15/2	1099.776	1100.247	-429.908	0.412	849.899	0.349	15	0.205	K.EGLLQLPSDK.A
R1/RRR1-15/2	1009.012	1009.096	-84.286	0.397	741.280	0.367	13	0.204	R.SGFEGPWTK.N
R1/RRR1-15/2	1556.338	1556.831	-317.244	0.384	645.761	0.440	16	0.203	K.ALLSDPAFRPLVEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1008.746	1009.096	-348.542	0.364	775.842	0.343	14	0.203	R.SGFEGPWTK.N
R1/RRR1-15/2	1556.169	1556.831	-1071.173	0.393	855.914	0.370	17	0.203	K.ALLSDPAFRPLVEK.Y
R1/RRR1-16/2	1008.979	1009.096	-116.810	0.376	754.325	0.317	13	0.199	R.SGFEGPWTK.N
R1/RRR1-15/2	911.904	912.046	-155.847	0.332	475.018	0.387	12	0.197	-.TGGPFGTM*K.-
R1/RRR1-16/2	911.922	912.046	-135.839	0.374	406.619	0.504	11	0.197	-.TGGPFGTM*K.-
R1/RRR1-15/2	1008.153	1009.096	-1933.987	0.281	738.674	0.313	13	0.196	R.SGFEGPWTK.N
R1/RRR1-16/2	1008.917	1009.096	-178.586	0.376	982.228	0.224	14	0.195	R.SGFEGPWTK.N
R1/RRR1-15/2	1557.691	1556.831	-89.732	0.356	490.154	0.354	15	0.193	K.ALLSDPAFRPLVEK.Y
R1/RRR1-15/2	1099.929	1100.247	-290.373	0.416	729.947	0.269	14	0.193	K.EGLLQLPSDK.A
R1/RRR1-15/2	896.230	896.046	205.656	0.273	677.816	0.277	13	0.193	K.TGGPFGTMK.T
R1/RRR1-14/2	1557.562	1556.831	-172.907	0.272	359.427	0.335	15	0.192	K.ALLSDPAFRPLVEK.Y
R1/RRR1-16/2	1099.961	1100.247	-260.644	0.351	661.301	0.275	13	0.192	K.EGLLQLPSDK.A
R1/RRR1-16/2	911.569	912.046	-524.865	0.309	357.143	0.406	11	0.184	-.TGGPFGTM*K.-
R1/RRR1-15/2	912.005	912.046	-45.208	0.332	342.944	0.401	11	0.182	-.TGGPFGTM*K.-
R1/RRR1-15/2	911.419	912.046	-1789.591	0.282	293.801	0.382	10	0.141	-.TGGPFGTM*K.-
R1/RRR1-16/3	1808.197	1807.001	108.663	0.332	626.551	0.259	25	0.078	-.TPAELSHAANAGLDIAVR.-
R1/RRR1-14/2	1688.207	1687.833	222.026	0.534	2974.453	0.549	26	0.593	K.VVTAAAAGGGGELTVEER.N
R1/RRR1-15/2	1688.507	1687.833	-193.868	0.559	2941.335	0.531	26	0.574	K.VVTAAAAGGGGELTVEER.N
R1/RRR1-15/2	1687.658	1687.833	-104.223	0.509	2822.097	0.590	26	0.571	K.VVTAAAAGGGGELTVEER.N
R1/RRR1-14/2	1687.277	1687.833	-925.388	0.461	2920.755	0.478	26	0.546	K.VVTAAAAGGGGELTVEER.N
R1/RRR1-14/2	1954.385	1955.136	-898.406	0.515	2601.801	0.597	26	0.526	K.DAADATLAAYQAAQDIAM*K.E
R1/RRR1-14/2	1687.290	1687.833	-917.398	0.435	2506.742	0.464	24	0.439	K.VVTAAAAGGGGELTVEER.N
R1/RRR1-14/2	1546.238	1545.757	312.014	0.574	2400.336	0.478	23	0.429	R.VEAELSNICAGILR.L
R1/RRR1-15/2	1772.729	1773.021	-165.250	0.519	2288.589	0.528	23	0.418	R.ARVEAELSNICAGILR.L
R1/RRR1-14/2	1772.553	1773.021	-265.077	0.479	1779.725	0.506	21	0.318	R.ARVEAELSNICAGILR.L
R1/RRR1-14/2	1772.432	1773.021	-899.441	0.449	1731.619	0.477	22	0.304	R.ARVEAELSNICAGILR.L
R1/RRR1-14/3	1774.163	1773.021	80.348	0.535	2215.990	0.381	32	0.271	R.ARVEAELSNICAGILR.L
R1/RRR1-14/2	1772.245	1773.021	-1005.168	0.494	1492.176	0.466	21	0.268	R.ARVEAELSNICAGILR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/3	1772.954	1773.021	-37.963	0.460	1838.617	0.315	30	0.172	R.ARVEAELSNICAGILR.L
R1/RRR1-4/2	1731.133	1731.758	-941.834	0.526	2057.397	0.541	23	0.380	K.FNSGEYESSVAEQQR.A
R1/RRR1-4/2	1731.407	1731.758	-203.773	0.559	1896.537	0.532	22	0.347	K.FNSGEYESSVAEQQR.A
R1/RRR1-4/2	1387.081	1387.518	-316.058	0.552	1811.134	0.540	22	0.337	K.VVNADEDVGDLLK.V
R1/RRR1-5/2	1387.394	1387.518	-89.274	0.541	1871.509	0.482	22	0.328	K.VVNADEDVGDLLK.V
R1/RRR1-5/2	1571.527	1570.682	-98.681	0.590	1781.970	0.522	22	0.325	K.VFDAILDDQFGDSK.N
R1/RRR1-4/2	1732.216	1731.758	264.732	0.591	1672.073	0.550	21	0.316	K.FNSGEYESSVAEQQR.A
R1/RRR1-5/2	1387.260	1387.518	-186.454	0.530	1727.063	0.512	21	0.316	K.VVNADEDVGDLLK.V
R1/RRR1-4/2	1570.327	1570.682	-226.391	0.505	1659.286	0.538	22	0.313	K.VFDAILDDQFGDSK.N
R1/RRR1-4/2	1386.629	1387.518	-1365.935	0.437	1571.019	0.527	20	0.297	K.VVNADEDVGDLLK.V
R1/RRR1-4/2	1569.647	1570.682	-1300.039	0.436	1671.104	0.469	21	0.294	K.VFDAILDDQFGDSK.N
R1/RRR1-4/2	1386.392	1387.518	-1538.203	0.396	1333.385	0.452	19	0.250	K.VVNADEDVGDLLK.V
R1/RRR1-4/2	1117.702	1118.263	-1400.136	0.341	1048.625	0.394	15	0.217	R.VSIIEEAQTK.M
R1/RRR1-4/2	1791.386	1791.940	-869.899	0.440	799.820	0.499	20	0.216	R.AETISAVLYPNDNLDR.G
R1/RRR1-5/2	1313.170	1313.480	-237.066	0.350	1108.417	0.360	17	0.215	K.VVFLEDYNVSK.A
R1/RRR1-4/2	1026.160	1026.168	-7.828	0.455	463.282	0.501	13	0.213	K.HTVDAELLK.V
R1/RRR1-4/2	1117.551	1118.263	-1536.068	0.374	1055.898	0.346	15	0.211	R.VSIIEEAQTK.M
R1/RRR1-4/2	1778.815	1777.996	-102.530	0.488	735.907	0.483	20	0.210	R.TTGVTVSPDALFDVQVK.R
R1/RRR1-5/2	1026.036	1026.168	-129.665	0.340	331.629	0.507	12	0.204	K.HTVDAELLK.V
R1/RRR1-5/2	1313.185	1313.480	-225.689	0.387	773.108	0.363	16	0.201	K.VVFLEDYNVSK.A
R1/RRR1-4/2	1777.401	1777.996	-900.302	0.389	520.656	0.458	17	0.196	R.TTGVTVSPDALFDVQVK.R
R1/RRR1-3/2	1119.289	1118.263	23.561	0.292	405.008	0.381	13	0.195	R.VSIIEEAQTK.M
R1/RRR1-6/2	1571.315	1570.682	-233.807	0.300	422.522	0.324	14	0.187	-.VFDAILDDQFGDSK.-
R1/RRR1-5/2	1025.833	1026.168	-328.175	0.229	217.699	0.325	10	0.174	-.HTVDAELLK.-
R1/RRR1-15/2	1435.343	1435.650	-214.926	0.557	2637.114	0.535	23	0.502	K.YIGLLATGLTADAR.S
R1/RRR1-15/2	1434.806	1435.650	-1289.009	0.495	2565.741	0.467	22	0.456	K.YIGLLATGLTADAR.S
R1/RRR1-15/2	1849.726	1850.063	-182.465	0.590	2087.644	0.511	23	0.372	K.ATSAGLKEQEAINFLEK.K
R1/RRR1-15/2	1849.284	1850.063	-964.883	0.566	2088.667	0.507	23	0.371	K.ATSAGLKEQEAINFLEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1434.685	1435.650	-1373.861	0.439	1484.063	0.417	19	0.257	K.YIGLLATGLTADAR.S
R1/RRR1-15/2	1073.248	1073.225	21.149	0.509	1515.947	0.383	16	0.255	K.ATEIEVGVVR.K
R1/RRR1-15/2	1072.535	1073.225	-1580.219	0.403	1381.722	0.372	16	0.240	K.ATEIEVGVVR.K
R1/RRR1-15/2	1072.505	1073.225	-1609.033	0.450	1365.563	0.363	17	0.238	K.ATEIEVGVVR.K
R1/RRR1-15/2	946.744	947.071	-346.408	0.463	1078.986	0.465	17	0.236	K.SAGVTSIGVR.G
R1/RRR1-15/2	946.867	947.071	-216.927	0.460	1073.671	0.436	17	0.230	K.SAGVTSIGVR.G
R1/RRR1-15/2	947.014	947.071	-60.456	0.485	961.618	0.457	16	0.226	K.SAGVTSIGVR.G
R1/RRR1-15/2	1713.641	1713.999	-209.530	0.448	936.681	0.415	20	0.213	K.LLDQTSVTHLFPITK.Y
R1/RRR1-15/2	1160.665	1161.331	-1439.135	0.382	1040.355	0.347	14	0.211	R.LYQVEYAFK.A
R1/RRR1-15/2	1161.129	1161.331	-174.472	0.408	826.329	0.403	14	0.209	R.LYQVEYAFK.A
R1/RRR1-15/2	1713.789	1713.999	-122.924	0.455	897.497	0.383	19	0.205	K.LLDQTSVTHLFPITK.Y
R1/RRR1-15/3	1849.001	1850.063	-1118.431	0.405	1243.764	0.397	31	0.117	K.ATSAGLKEQEAINFLEK.K
R1/RRR1-15/3	1221.867	1221.380	399.994	0.465	1334.720	0.331	20	0.112	-.GKDSVCVVTQK.-
R1/RRR1-15/3	1221.478	1221.380	80.468	0.511	954.400	0.357	19	0.065	-.GKDSVCVVTQK.-
R1/RRR1-14/2	1939.303	1940.234	-998.381	0.565	4252.884	0.479	29	1.000	R.SSVQAALQQEIALAAGLLR.I
R1/RRR1-14/2	1278.353	1277.451	-77.255	0.578	1572.864	0.482	18	0.286	R.VQDLIDLFASR.G
R1/RRR1-14/2	1539.311	1539.676	-237.714	0.490	1356.781	0.548	22	0.275	R.DAADLVALSGGHTVGR.T
R1/RRR1-14/2	1277.182	1277.451	-211.823	0.523	1480.076	0.471	18	0.273	R.VQDLIDLFASR.G
R1/RRR1-14/2	1540.175	1539.676	325.325	0.500	1393.563	0.514	22	0.271	R.DAADLVALSGGHTVGR.T
R1/RRR1-14/2	1276.710	1277.451	-1368.169	0.486	1345.617	0.478	17	0.260	R.VQDLIDLFASR.G
R1/RRR1-14/2	1745.409	1744.970	252.419	0.499	1049.568	0.579	23	0.250	R.DAVVVSGGPSYAVPLGQK.D
R1/RRR1-14/2	1538.718	1539.676	-1275.881	0.441	1111.055	0.529	21	0.245	R.DAADLVALSGGHTVGR.T
R1/RRR1-14/2	1859.505	1859.999	-266.458	0.487	1230.657	0.488	19	0.242	R.GGSNSEQGM*GPNLTLQPR.A
R1/RRR1-14/2	1745.481	1744.970	-280.833	0.541	976.285	0.563	23	0.241	R.DAVVVSGGPSYAVPLGQK.D
R1/RRR1-14/2	1859.317	1859.999	-907.670	0.493	1344.161	0.426	20	0.240	R.GGSNSEQGM*GPNLTLQPR.A
R1/RRR1-14/2	1859.482	1859.999	-818.238	0.506	1332.624	0.433	19	0.238	R.GGSNSEQGM*GPNLTLQPR.A
R1/RRR1-13/2	1256.117	1256.477	-286.920	0.360	1337.880	0.358	16	0.232	R.ALQLVEDIRAK.V
R1/RRR1-14/2	1056.674	1057.226	-1472.891	0.441	1111.652	0.357	13	0.217	R.ALQLVEDIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1057.065	1057.226	-152.383	0.468	1102.103	0.339	13	0.211	-.ALQLVEDIR.-
R1/RRR1-14/2	1743.734	1744.970	-1285.752	0.313	850.153	0.460	21	0.209	R.DAVVVSGGPSYAVPLGQK.D
R1/RRR1-13/2	1277.029	1277.451	-331.310	0.311	1122.044	0.313	16	0.209	R.VQDLIDLFASR.G
R1/RRR1-13/2	1057.014	1057.226	-200.461	0.437	1032.695	0.309	13	0.206	R.ALQLVEDIR.A
R1/RRR1-14/2	1057.212	1057.226	-12.926	0.457	1041.676	0.319	13	0.205	-.ALQLVEDIR.-
R1/RRR1-13/2	1276.654	1277.451	-1411.961	0.285	811.377	0.423	14	0.205	R.VQDLIDLFASR.G
R1/RRR1-13/2	1057.143	1057.226	-78.596	0.457	1066.906	0.288	13	0.203	-.ALQLVEDIR.-
R1/RRR1-11/2	1056.350	1057.226	-1780.723	0.332	891.227	0.312	12	0.199	-.ALQLVEDIR.-
R1/RRR1-14/2	1056.824	1057.226	-381.112	0.350	931.129	0.193	13	0.190	R.ALQLVEDIR.A
R1/RRR1-13/2	1938.623	1940.234	-1867.827	0.323	718.353	0.227	23	0.183	R.SSVQAALQQEIALAAGLLR.I
R1/RRR1-1/2	1057.217	1057.226	-8.525	0.329	538.147	0.266	12	0.178	-.ALQLVEDIR.-
R1/RRR1-14/3	1939.369	1940.234	-964.421	0.401	1426.866	0.360	31	0.130	R.SSVQAALQQEIALAAGLLR.I
R1/RRR1-13/3	1939.976	1940.234	-133.086	0.394	1172.702	0.339	28	0.102	R.SSVQAALQQEIALAAGLLR.I
R1/RRR1-15/2	1740.518	1740.890	-214.384	0.627	1904.391	0.573	23	0.366	K.KTEGELFETEKEATK.N
R1/RRR1-15/2	1132.087	1132.377	-256.817	0.466	1264.008	0.486	15	0.251	K.SGLLLVTGPFK.I
R1/RRR1-15/2	1059.988	1060.183	-184.651	0.456	1131.006	0.510	16	0.248	K.VDISGVNVEK.F
R1/RRR1-18/2	1311.130	1311.466	-257.045	0.417	920.111	0.537	17	0.231	R.VNQSYVIATSTK.V
R1/RRR1-18/2	1059.935	1060.183	-235.024	0.362	1119.265	0.428	15	0.228	K.VDISGVNVEK.F
R1/RRR1-15/2	1499.289	1498.793	332.237	0.448	898.761	0.484	21	0.223	R.SSITPGTVLILLAGR.F
R1/RRR1-15/2	1060.022	1060.183	-152.998	0.379	1046.484	0.407	15	0.220	K.VDISGVNVEK.F
R1/RRR1-15/2	1059.562	1060.183	-1535.089	0.346	865.275	0.480	14	0.218	K.VDISGVNVEK.F
R1/RRR1-15/2	1132.206	1132.377	-151.570	0.416	867.182	0.465	14	0.216	K.SGLLLVTGPFK.I
R1/RRR1-18/2	1498.497	1498.793	-197.942	0.399	782.881	0.409	20	0.206	R.SSITPGTVLILLAGR.F
R1/RRR1-15/2	1498.274	1498.793	-1016.463	0.353	735.902	0.404	19	0.202	R.SSITPGTVLILLAGR.F
R1/RRR1-16/2	955.934	956.118	-193.672	0.371	806.068	0.345	14	0.202	K.AIEAVPDLK.T
R1/RRR1-15/2	1498.383	1498.793	-274.113	0.300	800.990	0.351	20	0.198	R.SSITPGTVLILLAGR.F
R1/RRR1-16/2	955.628	956.118	-514.678	0.329	553.721	0.378	12	0.197	K.AIEAVPDLK.T
R1/RRR1-15/2	1131.712	1132.377	-1476.278	0.325	624.455	0.343	13	0.192	K.SGLLLVTGPFK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	956.196	956.118	81.807	0.322	518.557	0.340	11	0.183	-.AIEAVPDLK.-
R1/RRR1-15/3	1211.260	1211.350	-74.570	0.482	1541.860	0.450	25	0.166	K.AEKPDAAAAAAPK.F
R1/RRR1-15/3	1211.719	1211.350	305.887	0.512	1541.485	0.414	25	0.156	K.AEKPDAAAAAAPK.F
R1/RRR1-15/3	1211.560	1211.350	174.351	0.495	1638.704	0.383	27	0.155	K.AEKPDAAAAAAPK.F
R1/RRR1-19/3	1211.227	1211.350	-101.713	0.501	1580.996	0.397	28	0.150	K.AEKPDAAAAAAPK.F
R1/RRR1-15/3	1740.659	1740.890	-132.939	0.550	1166.724	0.451	27	0.128	K.KTEGELFETEKEATK.N
R1/RRR1-15/3	1210.698	1211.350	-1367.992	0.473	1245.276	0.412	23	0.124	K.AEKPDAAAAAAPK.F
R1/RRR1-15/3	1740.395	1740.890	-284.862	0.467	913.856	0.448	27	0.107	K.KTEGELFETEKEATK.N
R1/RRR1-18/3	1740.018	1740.890	-1079.205	0.456	855.527	0.453	26	0.105	K.KTEGELFETEKEATK.N
R1/RRR1-16/3	1740.739	1740.890	-86.775	0.482	906.605	0.389	27	0.097	K.KTEGELFETEKEATK.N
R1/RRR1-16/3	1741.059	1740.890	97.733	0.475	682.509	0.408	25	0.095	K.KTEGELFETEKEATK.N
R1/RRR1-16/3	1741.078	1740.890	108.175	0.470	637.311	0.391	24	0.093	K.KTEGELFETEKEATK.N
R1/RRR1-1/3	1210.923	1211.350	-353.200	0.441	804.166	0.374	22	0.090	K.AEKPDAAAAAAPK.F
R1/RRR1-18/3	1741.771	1740.890	-68.306	0.480	828.286	0.340	26	0.088	K.KTEGELFETEKEATK.N
R1/RRR1-17/3	1740.906	1740.890	9.127	0.413	581.237	0.304	22	0.085	K.KTEGELFETEKEATK.N
R1/RRR1-21/2	1339.180	1339.436	-192.051	0.441	1437.255	0.392	20	0.249	R.NIIHGSDGPETAK.A
R1/RRR1-21/2	987.829	988.163	-339.189	0.495	1264.300	0.419	14	0.240	R.GLISEILSR.F
R1/RRR1-21/2	1299.038	1299.366	-252.935	0.395	1196.048	0.417	17	0.232	R.ELVSYTSNEEK.W
R1/RRR1-21/2	1217.711	1218.386	-1379.056	0.354	1287.986	0.335	15	0.224	K.AEIGLWFEPR.E
R1/RRR1-22/2	988.030	988.163	-134.900	0.480	1067.287	0.397	13	0.221	R.GLISEILSR.F
R1/RRR1-21/2	1339.067	1339.436	-277.010	0.431	977.217	0.439	17	0.219	R.NIIHGSDGPETAK.A
R1/RRR1-21/2	1300.098	1299.366	-206.960	0.400	999.161	0.414	15	0.216	R.ELVSYTSNEEK.W
R1/RRR1-21/2	988.004	988.163	-162.105	0.466	1024.238	0.379	13	0.216	R.GLISEILSR.F
R1/RRR1-22/2	987.661	988.163	-1525.975	0.422	1049.514	0.364	13	0.215	R.GLISEILSR.F
R1/RRR1-22/2	988.003	988.163	-163.035	0.509	1034.907	0.371	13	0.214	R.GLISEILSR.F
R1/RRR1-21/2	885.430	886.031	-1814.170	0.397	1041.727	0.366	14	0.214	R.GDLAVVVGR.N
R1/RRR1-21/2	1071.002	1071.252	-234.082	0.415	802.562	0.428	16	0.213	R.KLIGATDPQK.S
R1/RRR1-21/2	1217.435	1218.386	-1607.158	0.464	854.904	0.416	15	0.212	K.AEIGLWFEPR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1344.616	1345.572	-1458.969	0.401	624.785	0.454	15	0.205	R.TFIAIKPDGVQR.G
R1/RRR1-21/2	1339.153	1339.436	-212.627	0.434	921.712	0.375	16	0.205	R.NIIHGSDGPETAK.A
R1/RRR1-21/2	987.992	988.163	-174.066	0.353	833.661	0.349	13	0.203	R.GLISEILSR.F
R1/RRR1-21/2	1345.284	1345.572	-214.479	0.440	540.740	0.423	14	0.199	R.TFIAIKPDGVQR.G
R1/RRR1-21/2	1070.868	1071.252	-359.993	0.338	674.721	0.297	15	0.194	R.KLIGATDPQK.S
R1/RRR1-21/2	1346.140	1345.572	-321.577	0.403	537.743	0.402	14	0.190	-.TFIAIKPDGVQR.-
R1/RRR1-21/2	1071.115	1071.252	-128.323	0.329	811.742	0.224	16	0.189	-.KLIGATDPQK.-
R1/RRR1-21/2	885.336	886.031	-1920.156	0.239	858.703	0.219	14	0.186	R.GDLAVVVGR.N
R1/RRR1-20/2	987.967	988.163	-199.723	0.105	511.638	0.206	11	0.180	-.GLISEILSR.-
R1/RRR1-14/2	1368.228	1367.556	-240.387	0.507	1864.400	0.567	21	0.355	K.FDVGNVVM*VTGGR.N
R1/RRR1-14/2	1366.686	1367.556	-1372.852	0.456	1485.015	0.471	19	0.272	K.FDVGNVVM*VTGGR.N
R1/RRR1-14/2	1366.678	1367.556	-1378.683	0.423	1458.051	0.476	19	0.269	K.FDVGNVVM*VTGGR.N
R1/RRR1-14/3	1483.499	1483.818	-215.675	0.580	2267.392	0.352	27	0.256	K.SRECLPLILIIR.N
R1/RRR1-13/2	949.837	949.129	-307.769	0.457	1073.090	0.554	15	0.252	R.LGNVFTIGK.G
R1/RRR1-14/2	948.994	949.129	-142.643	0.502	1042.911	0.555	15	0.252	R.LGNVFTIGK.G
R1/RRR1-14/2	948.559	949.129	-1659.871	0.454	1053.524	0.550	15	0.250	R.LGNVFTIGK.G
R1/RRR1-14/2	949.110	949.129	-20.203	0.485	876.270	0.567	14	0.241	R.LGNVFTIGK.G
R1/RRR1-14/2	1483.677	1483.818	-95.281	0.540	1329.042	0.358	17	0.228	K.SRECLPLILIIR.N
R1/RRR1-14/3	1484.934	1483.818	78.724	0.640	2101.080	0.355	27	0.223	K.SRECLPLILIIR.N
R1/RRR1-14/2	1540.662	1539.820	-103.201	0.531	367.146	0.613	16	0.219	K.TYPAGFMDVISIPK.T
R1/RRR1-14/2	1539.342	1539.820	-311.918	0.432	474.945	0.523	18	0.212	K.TYPAGFMDVISIPK.T
R1/RRR1-14/2	1105.006	1105.334	-297.877	0.374	1006.336	0.362	14	0.211	R.EVISILM*QR.H
R1/RRR1-14/2	1485.076	1483.818	174.238	0.533	1191.040	0.313	17	0.210	-.SRECLPLILIIR.-
R1/RRR1-14/2	1555.437	1555.820	-247.075	0.412	245.995	0.438	17	0.204	K.TYPAGFM*DVISIPK.T
R1/RRR1-14/2	988.978	988.120	-144.242	0.541	1079.862	0.266	13	0.199	K.LSIIEEQR.K
R1/RRR1-14/2	987.550	988.120	-1594.645	0.518	994.984	0.250	13	0.195	K.LSIIEEQR.K
R1/RRR1-14/2	1555.238	1555.820	-1019.952	0.319	200.604	0.363	15	0.194	-.TYPAGFM*DVISIPK.-
R1/RRR1-14/2	987.983	988.120	-138.934	0.490	965.787	0.238	13	0.193	K.LSIIEEQR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1539.374	1539.820	-290.596	0.248	322.350	0.334	15	0.191	K.TYPAGFMDVISIPK.T
R1/RRR1-14/2	1106.015	1105.334	-288.970	0.386	833.264	0.246	13	0.190	R.EVISILM*QR.H
R1/RRR1-14/2	1351.184	1351.557	-277.244	0.332	578.958	0.379	13	0.187	-.FDVGNVVMVTGGR.-
R1/RRR1-14/3	1484.340	1483.818	-323.238	0.596	1763.810	0.376	26	0.172	K.SRECLPLILIIR.N
R1/RRR1-14/3	1216.387	1216.454	-55.735	0.485	1128.483	0.269	21	0.082	R.TIRYPDPIIK.A
R1/RRR1-14/3	1216.411	1216.454	-35.956	0.416	1246.085	0.231	23	0.079	R.TIRYPDPIIK.A
R1/RRR1-14/3	1215.997	1216.454	-377.150	0.405	1057.505	0.248	21	0.076	R.TIRYPDPIIK.A
R1/RRR1-16/2	1241.259	1241.401	-114.508	0.501	1781.573	0.547	18	0.334	K.AFM*DATGGLWR.T
R1/RRR1-16/2	1240.841	1241.401	-1261.414	0.418	1736.107	0.486	18	0.308	K.AFM*DATGGLWR.T
R1/RRR1-17/2	1241.025	1241.401	-304.149	0.466	1539.099	0.506	18	0.288	K.AFM*DATGGLWR.T
R1/RRR1-17/1	769.336	769.911	-2052.980	0.334	710.602	0.337	10	0.285	K.YFAGIAK.K
R1/RRR1-16/2	1240.574	1241.401	-1477.231	0.407	1376.848	0.529	16	0.272	K.AFM*DATGGLWR.T
R1/RRR1-16/1	769.459	769.911	-589.223	0.283	700.010	0.275	10	0.265	K.YFAGIAK.K
R1/RRR1-16/2	1744.985	1744.966	10.903	0.545	1045.805	0.593	24	0.259	K.LWQVPETLSDDVLTK.M
R1/RRR1-17/1	769.388	769.911	-1984.571	0.294	693.191	0.263	10	0.258	K.YFAGIAK.K
R1/RRR1-17/2	1744.422	1744.966	-888.125	0.537	998.625	0.595	24	0.256	K.LWQVPETLSDDVLTK.M
R1/RRR1-17/2	1744.305	1744.966	-955.499	0.503	1040.313	0.564	24	0.252	K.LWQVPETLSDDVLTK.M
R1/RRR1-17/3	1874.971	1875.067	-51.504	0.556	1952.590	0.456	33	0.252	K.LAEEIEKGASSVEGVEVK.L
R1/RRR1-17/2	1225.521	1225.402	97.947	0.379	1479.045	0.382	17	0.250	K.AFMDATGGLWR.T
R1/RRR1-17/2	1699.790	1699.889	-58.172	0.494	1128.417	0.540	19	0.248	R.VATELELQQAFHQGK.Y
R1/RRR1-17/2	1700.386	1699.889	293.233	0.546	1144.336	0.539	18	0.248	R.VATELELQQAFHQGK.Y
R1/RRR1-17/2	1700.491	1699.889	-234.478	0.521	1143.018	0.536	18	0.248	R.VATELELQQAFHQGK.Y
R1/RRR1-16/2	1744.525	1744.966	-253.685	0.525	898.787	0.590	23	0.246	K.LWQVPETLSDDVLTK.M
R1/RRR1-17/2	1472.985	1473.486	-1021.945	0.432	1071.167	0.532	22	0.243	K.GGSPYGSGTFAGDGSR.V
R1/RRR1-17/2	1744.606	1744.966	-207.144	0.492	940.821	0.552	23	0.241	K.LWQVPETLSDDVLTK.M
R1/RRR1-17/2	1062.937	1063.276	-319.934	0.473	1138.684	0.471	14	0.241	R.FGM*M*AAQFK.A
R1/RRR1-17/2	1473.060	1473.486	-289.963	0.440	833.039	0.563	20	0.229	K.GGSPYGSGTFAGDGSR.V
R1/RRR1-17/2	1062.862	1063.276	-390.110	0.511	960.476	0.454	14	0.226	R.FGM*M*AAQFK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1744.695	1744.966	-155.764	0.532	756.370	0.532	21	0.226	K.LWQVPETLSDDVLTK.M
R1/RRR1-17/2	1472.686	1473.486	-1226.007	0.332	810.256	0.471	20	0.210	K.GGSPYGSGTFAGDGSR.V
R1/RRR1-17/2	1224.911	1225.402	-401.682	0.358	583.233	0.505	13	0.209	K.AFMDATGGLWR.T
R1/RRR1-17/2	1062.452	1063.276	-1721.277	0.375	1063.326	0.289	14	0.204	R.FGM*M*AAQFK.A
R1/RRR1-17/2	1226.024	1225.402	-309.242	0.274	371.978	0.468	11	0.196	K.AFMDATGGLWR.T
R1/RRR1-17/3	1875.842	1875.067	-120.536	0.528	1521.528	0.506	31	0.191	K.LAEEIEKGASSVEGVEVK.L
R1/RRR1-17/2	1241.056	1241.401	-279.182	0.279	675.825	0.253	13	0.188	K.AFM*DATGGLWR.T
R1/RRR1-16/2	1047.809	1047.276	-446.768	0.315	959.944	0.146	14	0.185	R.FGMM*AAQFK.A
R1/RRR1-16/1	769.339	769.911	-2048.355	0.275	517.539	0.257	9	0.171	K.YFAGIAK.K
R1/RRR1-16/1	769.403	769.911	-1965.278	0.292	504.973	0.242	9	0.163	K.YFAGIAK.K
R1/RRR1-11/2	1644.583	1643.995	-250.936	0.495	989.390	0.496	20	0.231	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/2	1643.540	1643.995	-277.318	0.494	796.864	0.536	20	0.227	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/3	1643.612	1643.995	-233.513	0.489	1793.729	0.526	34	0.224	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/3	1643.952	1643.995	-26.009	0.505	1648.476	0.557	32	0.215	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/2	1643.541	1643.995	-276.573	0.479	669.213	0.498	19	0.215	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/2	1643.575	1643.995	-256.156	0.480	644.990	0.498	18	0.212	K.TLLLGEKPVTVFGIR.N
R1/RRR1-1/2	1643.629	1643.995	-223.073	0.450	684.248	0.479	18	0.211	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/2	1642.634	1643.995	-1441.511	0.416	592.117	0.481	18	0.208	K.TLLLGEKPVTVFGIR.N
R1/RRR1-9/2	1643.830	1643.995	-100.746	0.413	472.086	0.456	16	0.201	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/3	1643.972	1643.995	-14.055	0.460	1499.239	0.549	31	0.188	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/3	1643.586	1643.995	-249.160	0.490	1443.679	0.540	31	0.178	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/3	1643.917	1643.995	-47.348	0.463	1352.375	0.562	30	0.173	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/3	1644.378	1643.995	233.557	0.489	1483.607	0.507	32	0.171	K.TLLLGEKPVTVFGIR.N
R1/RRR1-11/3	1643.444	1643.995	-946.203	0.494	1315.240	0.532	31	0.158	K.TLLLGEKPVTVFGIR.N
R1/RRR1-13/3	1644.693	1643.995	-184.152	0.468	1295.389	0.506	30	0.149	K.TLLLGEKPVTVFGIR.N
R1/RRR1-10/3	1643.953	1643.995	-25.674	0.484	1231.142	0.515	28	0.148	K.TLLLGEKPVTVFGIR.N
R1/RRR1-10/3	1644.242	1643.995	151.033	0.493	864.275	0.528	27	0.122	K.TLLLGEKPVTVFGIR.N
R1/RRR1-13/3	1643.535	1643.995	-280.456	0.339	703.838	0.466	23	0.103	K.TLLLGEKPVTVFGIR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/3	1644.877	1643.995	-71.921	0.390	697.110	0.458	25	0.102	K.TLLLGEKPVTVFGIR.N
R1/RRR1-10/3	1643.826	1643.995	-102.653	0.374	1054.221	0.345	27	0.096	K.TLLLGEKPVTVFGIR.N
R1/RRR1-9/3	1643.699	1643.995	-180.316	0.321	654.486	0.346	21	0.089	K.TLLLGEKPVTVFGIR.N
R1/RRR1-7/3	1643.568	1643.995	-260.337	0.338	600.548	0.281	21	0.083	-.TLLLGEKPVTVFGIR.-
R1/RRR1-8/2	1359.097	1359.471	-275.900	0.456	1428.294	0.453	16	0.262	K.SVYAHWVPEDR.I
R1/RRR1-5/2	1160.223	1160.260	-31.406	0.563	1613.348	0.503	18	0.299	K.AIDLIDEAGSR.V
R1/RRR1-5/2	1159.969	1160.260	-251.488	0.491	1568.267	0.473	18	0.285	K.AIDLIDEAGSR.V
R1/RRR1-5/2	1610.426	1610.834	-253.902	0.496	1186.998	0.536	20	0.256	K.VPEPTVDETIQILR.G
R1/RRR1-5/2	1040.179	1039.231	-50.216	0.417	1282.444	0.393	13	0.236	R.LDEM*IVFR.Q
R1/RRR1-5/2	1398.160	1398.547	-277.912	0.487	1216.508	0.408	20	0.233	R.VLESLGADPNNIR.T
R1/RRR1-5/2	1476.753	1477.689	-1314.577	0.295	1352.640	0.326	19	0.225	R.GSGFVAVEIPFTPR.A
R1/RRR1-5/2	1478.134	1477.689	302.120	0.444	967.862	0.439	17	0.217	R.GSGFVAVEIPFTPR.A
R1/RRR1-5/2	1421.095	1421.446	-248.183	0.351	952.482	0.314	19	0.198	K.EGDSAIVDVDSEGK.V
R1/RRR1-5/2	1476.664	1477.689	-1375.350	0.232	853.305	0.205	16	0.182	R.GSGFVAVEIPFTPR.A
R1/RRR1-5/3	1208.362	1208.349	11.022	0.542	1141.533	0.403	21	0.108	K.HIEKDPALER.R
R1/RRR1-5/3	1208.467	1208.349	97.798	0.521	962.759	0.353	19	0.090	K.HIEKDPALER.R
R1/RRR1-5/3	1086.033	1086.139	-98.304	0.467	1137.434	0.288	17	0.085	K.YRGEFEER.L
R1/RRR1-5/3	1085.794	1086.139	-319.311	0.378	856.514	0.240	15	0.072	K.YRGEFEER.L
R1/RRR1-11/2	1347.233	1347.648	-308.775	0.517	2791.029	0.375	20	0.463	K.MELVDAAFPLLK.G
R1/RRR1-11/2	1348.055	1347.648	302.572	0.510	2623.190	0.369	20	0.424	K.MELVDAAFPLLK.G
R1/RRR1-12/2	1650.769	1650.987	-132.289	0.519	2299.649	0.477	25	0.397	K.VLVVANPANTNALILK.E
R1/RRR1-11/2	1650.580	1650.987	-247.651	0.521	2198.098	0.527	25	0.397	K.VLVVANPANTNALILK.E
R1/RRR1-11/2	1555.333	1555.668	-216.372	0.555	1877.993	0.613	24	0.372	K.SQASALEAHAAPNCK.V
R1/RRR1-11/2	1352.184	1352.451	-197.901	0.546	2035.499	0.498	20	0.362	K.MDATAQELSEEK.T
R1/RRR1-12/2	1555.203	1555.668	-300.077	0.539	1807.337	0.604	24	0.357	K.SQASALEAHAAPNCK.V
R1/RRR1-11/2	1346.625	1347.648	-1506.890	0.391	2287.883	0.341	20	0.351	K.MELVDAAFPLLK.G
R1/RRR1-11/2	1650.473	1650.987	-920.059	0.563	1736.343	0.575	25	0.334	K.VLVVANPANTNALILK.E
R1/RRR1-11/2	1556.157	1555.668	315.060	0.570	1622.541	0.612	23	0.330	K.SQASALEAHAAPNCK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1555.244	1555.668	-273.696	0.524	1628.498	0.609	23	0.330	K.SQASALEAHAAPNCK.V
R1/RRR1-12/2	1651.564	1650.987	-257.215	0.570	1593.873	0.607	24	0.322	K.VLVVANPANTNALILK.E
R1/RRR1-11/2	1555.086	1555.668	-1020.900	0.519	1604.914	0.572	23	0.315	K.SQASALEAHAAPNCK.V
R1/RRR1-11/2	1352.067	1352.451	-284.851	0.549	1725.643	0.496	20	0.312	K.MDATAQELSEEK.T
R1/RRR1-11/2	1650.247	1650.987	-1057.961	0.413	1762.290	0.439	24	0.297	K.VLVVANPANTNALILK.E
R1/RRR1-11/2	1351.554	1352.451	-1407.181	0.459	1559.607	0.497	19	0.289	K.MDATAQELSEEK.T
R1/RRR1-12/2	1650.515	1650.987	-287.199	0.509	1372.077	0.516	23	0.269	K.VLVVANPANTNALILK.E
R1/RRR1-12/2	1017.062	1016.174	-110.284	0.584	1566.472	0.376	15	0.256	K.LNVQVTDVK.N
R1/RRR1-11/2	1364.396	1363.648	-185.231	0.544	1386.135	0.408	18	0.245	K.M*ELVDAAFPLLK.G
R1/RRR1-11/2	1363.178	1363.648	-345.270	0.499	1370.630	0.399	18	0.243	K.M*ELVDAAFPLLK.G
R1/RRR1-10/2	1650.495	1650.987	-298.997	0.484	1167.184	0.471	21	0.238	K.VLVVANPANTNALILK.E
R1/RRR1-12/2	1347.168	1347.648	-357.413	0.360	1496.936	0.269	18	0.228	K.MELVDAAFPLLK.G
R1/RRR1-3/2	1016.641	1016.174	460.882	0.375	977.407	0.345	14	0.210	K.LNVQVTDVK.N
R1/RRR1-12/2	1363.271	1363.648	-277.260	0.321	925.240	0.387	15	0.208	-.M*ELVDAAFPLLK.-
R1/RRR1-11/2	1363.129	1363.648	-1117.647	0.386	1116.644	0.270	17	0.203	K.M*ELVDAAFPLLK.G
R1/RRR1-2/2	1016.033	1016.174	-138.232	0.398	560.347	0.349	12	0.200	K.LNVQVTDVK.N
R1/RRR1-1/2	1016.044	1016.174	-128.108	0.345	426.747	0.236	13	0.198	K.LNVQVTDVK.N
R1/RRR1-11/2	1652.373	1650.987	234.473	0.363	418.430	0.444	15	0.197	K.VLVVANPANTNALILK.E
R1/RRR1-11/2	1651.773	1650.987	-129.985	0.431	693.617	0.397	16	0.197	K.VLVVANPANTNALILK.E
R1/RRR1-2/2	1016.137	1016.174	-36.522	0.364	494.661	0.245	13	0.196	K.LNVQVTDVK.N
R1/RRR1-10/2	1015.190	1016.174	-1959.837	0.284	341.070	0.314	11	0.194	-.LNVQVTDVK.-
R1/RRR1-10/2	1015.563	1016.174	-1590.323	0.429	634.865	0.286	13	0.194	-.LNVQVTDVK.-
R1/RRR1-11/2	1650.613	1650.987	-227.173	0.407	699.908	0.347	16	0.193	K.VLVVANPANTNALILK.E
R1/RRR1-10/2	1651.957	1650.987	-18.500	0.340	237.228	0.457	12	0.192	-.VLVVANPANTNALILK.-
R1/RRR1-11/3	1624.037	1624.796	-1086.490	0.470	1678.731	0.440	28	0.183	R.KKM*DATAQELSEEK.T
R1/RRR1-12/2	1016.160	1016.174	-12.906	0.367	425.214	0.284	12	0.182	-.LNVQVTDVK.-
R1/RRR1-11/3	1651.757	1650.987	-139.853	0.497	1279.103	0.484	28	0.148	K.VLVVANPANTNALILK.E
R1/RRR1-12/3	1662.621	1661.749	-77.192	0.456	1133.379	0.536	29	0.142	K.QSSALSAASSACDHIR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/3	1662.102	1661.749	212.761	0.449	1131.695	0.511	28	0.136	K.QSSALSAASSACDHIR.D
R1/RRR1-12/3	1661.311	1661.749	-264.926	0.441	1091.453	0.528	28	0.136	K.QSSALSAASSACDHIR.D
R1/RRR1-12/3	1624.785	1624.796	-6.371	0.459	1362.024	0.408	27	0.131	R.KKM*DATAQELSEEK.T
R1/RRR1-11/3	1661.605	1661.749	-87.039	0.381	1109.811	0.451	29	0.117	K.QSSALSAASSACDHIR.D
R1/RRR1-12/3	1623.679	1624.796	-1307.520	0.456	955.686	0.405	23	0.100	R.KKM*DATAQELSEEK.T
R1/RRR1-13/2	1565.224	1565.732	-965.927	0.488	2043.998	0.539	23	0.377	R.LAIAGM*GTDENSLTR.I
R1/RRR1-13/2	1565.227	1565.732	-963.813	0.480	1826.359	0.511	22	0.330	R.LAIAGM*GTDENSLTR.I
R1/RRR1-13/2	1565.183	1565.732	-992.471	0.474	1628.680	0.517	22	0.302	R.LAIAGM*GTDENSLTR.I
R1/RRR1-13/2	1384.643	1384.605	27.181	0.438	1674.097	0.421	18	0.283	R.AVILWTLDPAER.D
R1/RRR1-13/2	1369.188	1369.416	-167.007	0.462	1508.532	0.406	18	0.259	R.SITDEISGDFER.A
R1/RRR1-13/2	958.629	959.127	-520.666	0.550	1135.048	0.554	14	0.259	R.GPAQLFAVR.Q
R1/RRR1-13/2	1369.076	1369.416	-249.117	0.443	1365.563	0.453	19	0.256	R.SITDEISGDFER.A
R1/RRR1-13/2	958.987	959.127	-146.263	0.548	1185.719	0.502	14	0.251	R.GPAQLFAVR.Q
R1/RRR1-13/2	958.498	959.127	-1704.485	0.487	1106.497	0.515	14	0.247	R.GPAQLFAVR.Q
R1/RRR1-13/2	1369.068	1369.416	-254.753	0.385	1447.680	0.378	18	0.246	R.SITDEISGDFER.A
R1/RRR1-13/2	1350.995	1350.418	-314.078	0.529	1206.119	0.435	17	0.238	R.YNDEYGHPINK.D
R1/RRR1-13/2	1384.228	1384.605	-273.280	0.417	1173.042	0.461	15	0.236	R.AVILWTLDPAER.D
R1/RRR1-13/2	1350.234	1350.418	-136.254	0.521	1163.081	0.416	17	0.230	R.YNDEYGHPINK.D
R1/RRR1-13/2	1057.834	1058.171	-318.942	0.406	1182.569	0.373	16	0.224	R.DAVLANEVAR.K
R1/RRR1-13/2	1145.241	1145.419	-156.366	0.426	494.383	0.596	14	0.218	K.LLVPLISAYR.Y
R1/RRR1-13/2	1057.696	1058.171	-449.789	0.455	1154.028	0.342	15	0.217	-.DAVLANEVAR.-
R1/RRR1-14/2	1237.219	1237.387	-136.033	0.580	1738.944	0.627	20	0.354	K.TLASDGLAGLYR.G
R1/RRR1-15/2	1236.989	1237.387	-322.733	0.491	1632.991	0.570	19	0.318	K.TLASDGLAGLYR.G
R1/RRR1-14/2	1237.011	1237.387	-305.011	0.534	1574.687	0.574	20	0.313	K.TLASDGLAGLYR.G
R1/RRR1-15/2	1236.968	1237.387	-339.863	0.438	1599.130	0.534	19	0.302	K.TLASDGLAGLYR.G
R1/RRR1-14/2	1237.295	1237.387	-74.969	0.534	1577.363	0.527	19	0.298	K.TLASDGLAGLYR.G
R1/RRR1-15/2	1237.128	1237.387	-209.873	0.398	1726.687	0.441	19	0.294	K.TLASDGLAGLYR.G
R1/RRR1-14/2	1237.050	1237.387	-273.725	0.498	1339.190	0.577	18	0.282	K.TLASDGLAGLYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1323.184	1322.537	-267.196	0.529	1297.680	0.579	20	0.279	R.GFGPSVAGIVVYR.G
R1/RRR1-14/2	1322.312	1322.537	-170.335	0.514	1082.064	0.634	19	0.269	R.GFGPSVAGIVVYR.G
R1/RRR1-14/2	1362.103	1361.590	-358.308	0.587	1352.339	0.481	17	0.260	K.LLVQNQEEM*LK.A
R1/RRR1-14/2	1322.108	1322.537	-325.570	0.490	1101.510	0.589	19	0.260	R.GFGPSVAGIVVYR.G
R1/RRR1-14/2	1322.270	1322.537	-202.656	0.509	1068.005	0.551	19	0.250	R.GFGPSVAGIVVYR.G
R1/RRR1-14/2	1361.017	1361.590	-1159.054	0.519	1385.981	0.400	17	0.245	K.LLVQNQEEM*LK.A
R1/RRR1-14/2	1365.414	1364.552	-101.920	0.417	1309.717	0.420	16	0.241	R.TTAEEGVMALWR.G
R1/RRR1-14/2	1361.228	1361.590	-266.704	0.502	1182.747	0.396	17	0.228	K.LLVQNQEEM*LK.A
R1/RRR1-14/2	1381.136	1380.552	-301.834	0.426	1143.270	0.357	16	0.216	R.TTAEEGVM*ALWR.G
R1/RRR1-14/2	1475.294	1475.675	-258.900	0.466	632.186	0.500	17	0.216	R.YFPTQALNFAFR.D
R1/RRR1-14/2	1365.172	1364.552	-279.516	0.395	1023.178	0.401	15	0.215	R.TTAEEGVMALWR.G
R1/RRR1-14/2	1475.214	1475.675	-312.945	0.390	669.837	0.495	18	0.215	R.YFPTQALNFAFR.D
R1/RRR1-14/2	1475.210	1475.675	-315.933	0.360	610.860	0.414	17	0.203	R.YFPTQALNFAFR.D
R1/RRR1-14/2	1300.877	1301.426	-1194.515	0.396	782.080	0.359	14	0.199	R.RYDGIVDCFR.R
R1/RRR1-14/2	1474.730	1475.675	-1322.358	0.294	611.011	0.384	18	0.198	R.YFPTQALNFAFR.D
R1/RRR1-13/2	1323.712	1322.537	132.396	0.260	472.649	0.397	13	0.190	R.GFGPSVAGIVVYR.G
R1/RRR1-14/2	1379.633	1380.552	-1395.155	0.268	945.401	0.151	15	0.183	R.TTAEEGVM*ALWR.G
R1/RRR1-1/2	1237.241	1237.387	-118.812	0.242	514.142	0.227	12	0.181	-.TLASDGLAGLYR.-
R1/RRR1-14/2	1364.302	1364.552	-184.477	0.231	955.785	0.091	15	0.179	R.TTAEEGVMALWR.G
R1/RRR1-9/2	1807.704	1807.939	-130.626	0.564	2698.532	0.633	28	0.561	K.GTVAVGFDADANGDVTAVK.L
R1/RRR1-10/2	1916.111	1916.121	-5.151	0.591	2637.914	0.613	24	0.531	R.LFTSGLAAFYEGYYANK.G
R1/RRR1-10/2	1914.805	1916.121	-1213.467	0.454	2749.565	0.534	24	0.526	R.LFTSGLAAFYEGYYANK.G
R1/RRR1-10/2	1916.113	1916.121	-4.384	0.583	2657.334	0.591	24	0.526	R.LFTSGLAAFYEGYYANK.G
R1/RRR1-9/2	1915.975	1916.121	-76.659	0.580	2404.207	0.619	23	0.476	R.LFTSGLAAFYEGYYANK.G
R1/RRR1-9/2	1915.582	1916.121	-805.829	0.534	2517.680	0.549	24	0.474	R.LFTSGLAAFYEGYYANK.G
R1/RRR1-9/2	1915.795	1916.121	-170.868	0.512	2462.317	0.547	24	0.461	R.LFTSGLAAFYEGYYANK.G
R1/RRR1-9/2	1995.425	1995.225	100.591	0.608	2316.941	0.571	25	0.436	K.LTDFGVQGAEANNILYLR.D
R1/RRR1-10/2	1994.798	1995.225	-214.737	0.576	2289.882	0.556	25	0.425	K.LTDFGVQGAEANNILYLR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1995.610	1995.225	193.592	0.604	2271.491	0.565	25	0.424	K.LTDFGVQGAEANNILYLR.D
R1/RRR1-10/2	1995.580	1995.225	178.380	0.592	2192.343	0.587	24	0.416	K.LTDFGVQGAEANNILYLR.D
R1/RRR1-9/2	1808.540	1807.939	-221.282	0.599	2093.248	0.608	25	0.407	K.GTVAVGFDADANGDVTAVK.L
R1/RRR1-10/2	1994.807	1995.225	-210.195	0.610	2170.261	0.571	24	0.404	K.LTDFGVQGAEANNILYLR.D
R1/RRR1-9/2	1995.510	1995.225	143.413	0.613	1990.407	0.579	23	0.372	K.LTDFGVQGAEANNILYLR.D
R1/RRR1-10/2	1807.577	1807.939	-201.350	0.498	1717.856	0.583	22	0.330	K.GTVAVGFDADANGDVTAVK.L
R1/RRR1-9/2	1448.439	1447.618	-124.226	0.451	480.070	0.529	18	0.215	K.ESVAPYERPALSK.G
R1/RRR1-9/2	1136.964	1137.273	-272.622	0.402	677.744	0.445	16	0.213	K.GYLFPQNAAR.L
R1/RRR1-10/2	1448.344	1447.618	-189.580	0.472	498.996	0.491	18	0.212	K.ESVAPYERPALSK.G
R1/RRR1-10/2	1448.287	1447.618	-229.406	0.441	445.745	0.492	17	0.209	K.ESVAPYERPALSK.G
R1/RRR1-10/2	1447.051	1447.618	-1086.373	0.421	528.305	0.472	18	0.209	K.ESVAPYERPALSK.G
R1/RRR1-9/2	1447.290	1447.618	-227.195	0.405	539.344	0.468	18	0.208	K.ESVAPYERPALSK.G
R1/RRR1-10/2	1475.343	1474.597	-172.501	0.418	370.720	0.528	15	0.203	R.LPGFHTCVGSGGER.L
R1/RRR1-9/2	1136.826	1137.273	-394.357	0.349	779.465	0.320	16	0.201	K.GYLFPQNAAR.L
R1/RRR1-10/2	1136.505	1137.273	-1560.331	0.336	679.780	0.339	15	0.200	K.GYLFPQNAAR.L
R1/RRR1-2/2	1137.197	1137.273	-66.280	0.309	479.639	0.374	12	0.196	K.GYLFPQNAAR.L
R1/RRR1-1/2	1137.251	1137.273	-19.445	0.354	623.769	0.304	13	0.194	K.GYLFPQNAAR.L
R1/RRR1-3/2	1137.540	1137.273	235.865	0.251	428.856	0.319	12	0.192	K.GYLFPQNAAR.L
R1/RRR1-1/2	1137.180	1137.273	-81.785	0.263	472.353	0.325	12	0.191	-.GYLFPQNAAR.-
R1/RRR1-9/2	1473.934	1474.597	-1131.850	0.387	364.571	0.274	15	0.187	R.LPGFHTCVGSGGER.L
R1/RRR1-9/3	1621.724	1620.807	-51.113	0.412	1308.551	0.293	26	0.101	R.DIDDADKLVAAM*QAK.K
R1/RRR1-10/3	1621.141	1620.807	206.408	0.400	991.523	0.346	23	0.092	R.DIDDADKLVAAM*QAK.K
R1/RRR1-9/3	1621.031	1620.807	138.332	0.327	1220.758	0.258	23	0.087	R.DIDDADKLVAAM*QAK.K
R1/RRR1-16/2	1609.285	1608.861	264.564	0.594	2726.840	0.476	22	0.495	K.ALLTELQALEEHLK.A
R1/RRR1-16/2	1608.477	1608.861	-239.595	0.539	2620.727	0.459	21	0.464	K.ALLTELQALEEHLK.A
R1/RRR1-16/2	1608.534	1608.861	-203.659	0.555	2212.358	0.449	20	0.373	K.ALLTELQALEEHLK.A
R1/RRR1-16/2	1893.537	1894.114	-835.450	0.576	1514.145	0.640	25	0.322	K.YPTPSLVTPPEYASVGSK.I
R1/RRR1-16/2	1893.320	1894.114	-950.395	0.456	919.560	0.564	21	0.234	K.YPTPSLVTPPEYASVGSK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	989.903	990.095	-194.695	0.391	672.798	0.521	14	0.216	K.VPVFNGGDGK.W
R1/RRR1-16/2	989.939	990.095	-157.459	0.322	682.268	0.502	14	0.210	K.VPVFNGGDGK.W
R1/RRR1-16/2	989.352	990.095	-1766.977	0.336	578.382	0.455	13	0.203	K.VPVFNGGDGK.W
R1/RRR1-16/2	1616.502	1616.885	-237.572	0.462	973.597	0.339	16	0.201	K.LIDVQNKPDWFLK.I
R1/RRR1-16/2	1264.120	1264.488	-291.496	0.378	938.265	0.298	16	0.201	K.IFSCFTTFLK.S
R1/RRR1-16/2	1616.439	1616.885	-276.590	0.425	947.626	0.280	16	0.192	K.LIDVQNKPDWFLK.I
R1/RRR1-16/2	1263.695	1264.488	-1422.758	0.283	721.545	0.175	14	0.184	K.IFSCFTTFLK.S
R1/RRR1-16/2	1264.269	1264.488	-173.312	0.229	736.723	0.077	15	0.180	K.IFSCFTTFLK.S
R1/RRR1-16/3	1829.013	1828.957	30.812	0.527	1516.874	0.482	32	0.177	K.AAVGHPDTLGDCPFSQR.V
R1/RRR1-16/3	1828.703	1828.957	-139.511	0.537	1422.051	0.458	31	0.158	K.AAVGHPDTLGDCPFSQR.V
R1/RRR1-16/3	1829.829	1828.957	-70.205	0.542	1284.825	0.452	32	0.138	K.AAVGHPDTLGDCPFSQR.V
R1/RRR1-16/3	1498.848	1498.753	63.780	0.512	1440.245	0.373	28	0.123	K.LYHLQVALEHFK.G
R1/RRR1-16/3	1498.606	1498.753	-98.467	0.565	1135.153	0.454	25	0.119	K.LYHLQVALEHFK.G
R1/RRR1-16/3	1498.815	1498.753	41.602	0.531	1143.111	0.387	26	0.104	K.LYHLQVALEHFK.G
R1/RRR1-8/2	1972.901	1974.161	-1148.939	0.583	3340.091	0.575	29	0.724	K.GHYTEGAELIDSVLDVVR.K
R1/RRR1-9/2	1343.292	1343.427	-100.681	0.560	1831.726	0.502	20	0.327	R.INVYYNEASGGR.Y
R1/RRR1-9/2	1343.372	1343.427	-40.522	0.463	1381.474	0.475	18	0.262	R.INVYYNEASGGR.Y
R1/RRR1-8/2	1343.867	1343.427	328.296	0.489	1234.038	0.498	17	0.252	R.INVYYNEASGGR.Y
R1/RRR1-8/2	1639.534	1639.945	-251.314	0.396	1382.978	0.434	19	0.250	R.LHFFM*VGFAPLTSR.G
R1/RRR1-8/2	1140.235	1140.403	-147.603	0.587	1103.422	0.504	17	0.248	K.LAVNLIPFPR.L
R1/RRR1-9/2	1698.274	1697.871	237.652	0.513	1004.619	0.500	20	0.234	K.NSSYFVEWIPNNVK.S
R1/RRR1-12/2	1141.521	1140.403	103.652	0.524	966.427	0.469	17	0.233	K.LAVNLIPFPR.L
R1/RRR1-8/2	1140.117	1140.403	-251.572	0.497	963.621	0.472	16	0.232	K.LAVNLIPFPR.L
R1/RRR1-8/2	1140.533	1140.403	114.477	0.477	766.865	0.536	15	0.231	K.LAVNLIPFPR.L
R1/RRR1-9/2	1139.711	1140.403	-1488.799	0.486	935.402	0.452	17	0.228	K.LAVNLIPFPR.L
R1/RRR1-12/2	1141.501	1140.403	86.064	0.503	987.567	0.435	16	0.227	K.LAVNLIPFPR.L
R1/RRR1-9/2	1140.120	1140.403	-248.242	0.544	939.862	0.431	16	0.223	K.LAVNLIPFPR.L
R1/RRR1-13/2	1141.452	1140.403	43.269	0.433	985.192	0.390	16	0.219	K.LAVNLIPFPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1697.335	1697.871	-907.785	0.436	935.185	0.446	19	0.219	K.NSSYFVEWIPNNVK.S
R1/RRR1-9/2	1344.020	1343.427	-303.318	0.370	714.452	0.497	17	0.216	R.INVYYNEASGGR.Y
R1/RRR1-10/2	1139.501	1140.403	-1673.452	0.474	784.685	0.427	14	0.214	K.LAVNLIPFPR.L
R1/RRR1-9/2	1732.463	1731.994	271.196	0.435	733.436	0.508	19	0.214	R.ALTVPELTQQMWDAK.N
R1/RRR1-9/2	1697.479	1697.871	-231.721	0.437	788.901	0.468	17	0.213	K.NSSYFVEWIPNNVK.S
R1/RRR1-8/2	1625.005	1623.946	36.723	0.430	831.320	0.463	16	0.212	R.LHFFMVGFAPLTSR.G
R1/RRR1-8/2	1697.318	1697.871	-918.038	0.406	758.903	0.457	17	0.210	K.NSSYFVEWIPNNVK.S
R1/RRR1-5/2	1140.203	1140.403	-175.527	0.460	801.667	0.385	14	0.209	K.LAVNLIPFPR.L
R1/RRR1-11/2	1141.417	1140.403	12.485	0.330	913.780	0.356	15	0.209	K.LAVNLIPFPR.L
R1/RRR1-14/2	1140.068	1140.403	-294.110	0.323	670.285	0.447	13	0.209	K.LAVNLIPFPR.L
R1/RRR1-5/2	1140.961	1140.403	-387.776	0.379	802.486	0.396	13	0.208	K.LAVNLIPFPR.L
R1/RRR1-15/2	1139.519	1140.403	-1658.277	0.316	558.840	0.396	13	0.203	K.LAVNLIPFPR.L
R1/RRR1-8/2	1342.138	1343.427	-1710.159	0.369	1041.990	0.290	17	0.203	R.INVYYNEASGGR.Y
R1/RRR1-7/2	1140.358	1140.403	-39.362	0.424	536.412	0.382	12	0.202	K.LAVNLIPFPR.L
R1/RRR1-10/2	1975.878	1974.161	-143.488	0.507	578.065	0.485	19	0.202	K.GHYTEGAELIDSVLDVVR.K
R1/RRR1-8/2	1624.572	1623.946	-230.815	0.412	863.087	0.371	17	0.202	R.LHFFMVGFAPLTSR.G
R1/RRR1-14/2	1141.216	1140.403	-163.891	0.416	555.472	0.349	12	0.199	K.LAVNLIPFPR.L
R1/RRR1-10/2	1139.659	1140.403	-1534.525	0.283	413.872	0.306	12	0.195	-.LAVNLIPFPR.-
R1/RRR1-8/2	1641.533	1639.945	-251.456	0.387	623.619	0.400	14	0.194	R.LHFFM*VGFAPLTSR.G
R1/RRR1-1/2	1139.985	1140.403	-367.380	0.314	475.175	0.319	10	0.194	K.LAVNLIPFPR.L
R1/RRR1-8/2	1696.748	1697.871	-1254.970	0.312	612.034	0.366	16	0.194	K.NSSYFVEWIPNNVK.S
R1/RRR1-10/2	1343.698	1343.427	202.229	0.281	502.134	0.271	16	0.193	R.INVYYNEASGGR.Y
R1/RRR1-20/2	1343.993	1343.427	-323.822	0.219	433.509	0.335	16	0.193	R.INVYYNEASGGR.Y
R1/RRR1-9/2	1384.822	1385.720	-1374.791	0.437	608.498	0.345	14	0.192	R.MMLTFSVFPSPK.V
R1/RRR1-12/2	1343.822	1343.427	295.325	0.228	508.703	0.257	16	0.191	R.INVYYNEASGGR.Y
R1/RRR1-9/2	1418.547	1417.719	-121.086	0.323	557.099	0.343	13	0.190	R.M*M*LTFSVFPSPK.V
R1/RRR1-8/2	1400.521	1401.719	-1574.019	0.315	753.907	0.306	13	0.189	R.M*MLTFSVFPSPK.V
R1/RRR1-22/3	1721.491	1721.810	-185.965	0.601	2794.000	0.533	32	0.497	K.HGYIGEFEFVDDHR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/3	1721.569	1721.810	-140.085	0.574	2505.647	0.538	32	0.408	K.HGYIGEFEFVDDHR.S
R1/RRR1-22/3	1722.241	1721.810	251.008	0.607	2544.540	0.492	31	0.398	K.HGYIGEFEFVDDHR.S
R1/RRR1-23/3	1721.145	1721.810	-970.320	0.546	2020.310	0.514	29	0.277	K.HGYIGEFEFVDDHR.S
R1/RRR1-23/3	1721.879	1721.810	40.195	0.590	2074.015	0.482	29	0.276	K.HGYIGEFEFVDDHR.S
R1/RRR1-23/3	1637.198	1637.818	-992.141	0.515	2026.724	0.465	32	0.251	R.FDVGVKEIESWTAR.L
R1/RRR1-23/3	1721.743	1721.810	-39.163	0.576	1872.511	0.451	28	0.223	K.HGYIGEFEFVDDHR.S
R1/RRR1-23/2	1637.371	1637.818	-273.577	0.480	766.180	0.522	19	0.222	R.FDVGVKEIESWTAR.L
R1/RRR1-23/2	1636.944	1637.818	-1148.236	0.423	809.123	0.450	20	0.213	R.FDVGVKEIESWTAR.L
R1/RRR1-23/2	900.212	900.058	172.172	0.371	866.348	0.375	13	0.209	K.IVVELNGR.L
R1/RRR1-23/2	788.868	788.909	-51.700	0.348	670.130	0.430	11	0.208	K.CGVISPR.F
R1/RRR1-23/2	958.552	959.122	-1642.503	0.383	961.646	0.335	15	0.207	R.VSVLNDALK.T
R1/RRR1-23/2	958.534	959.122	-1661.694	0.430	925.696	0.330	15	0.206	R.VSVLNDALK.T
R1/RRR1-23/2	788.796	788.909	-143.129	0.343	674.084	0.357	11	0.202	K.CGVISPR.F
R1/RRR1-22/2	959.124	959.122	1.645	0.352	646.553	0.352	13	0.199	R.VSVLNDALK.T
R1/RRR1-23/2	958.522	959.122	-1674.745	0.358	787.519	0.311	14	0.198	R.VSVLNDALK.T
R1/RRR1-23/2	991.845	992.067	-225.359	0.305	672.438	0.317	12	0.195	K.EIESWTAR.L
R1/RRR1-23/2	899.532	900.058	-1701.680	0.395	743.287	0.264	12	0.194	K.IVVELNGR.L
R1/RRR1-23/2	788.812	788.909	-123.104	0.302	471.562	0.328	9	0.193	-.CGVISPR.-
R1/RRR1-23/2	991.919	992.067	-149.677	0.286	502.125	0.313	10	0.192	K.EIESWTAR.L
R1/RRR1-23/2	991.903	992.067	-166.344	0.294	815.008	0.251	12	0.192	K.EIESWTAR.L
R1/RRR1-22/2	789.008	788.909	125.832	0.248	579.697	0.235	10	0.190	K.CGVISPR.F
R1/RRR1-22/2	991.871	992.067	-198.320	0.222	389.454	0.428	9	0.189	-.EIESWTAR.-
R1/RRR1-23/2	899.389	900.058	-1861.089	0.255	640.636	0.129	12	0.184	-.IVVELNGR.-
R1/RRR1-22/2	900.751	900.058	-341.736	0.245	702.828	0.121	13	0.184	K.IVVELNGR.L
R1/RRR1-23/3	1637.424	1637.818	-240.826	0.516	1623.037	0.443	29	0.175	R.FDVGVKEIESWTAR.L
R1/RRR1-22/2	789.266	788.909	453.730	0.166	600.055	0.186	10	0.174	-.CGVISPR.-
R1/RRR1-23/3	1637.776	1637.818	-25.247	0.501	1305.972	0.438	29	0.131	R.FDVGVKEIESWTAR.L
R1/RRR1-8/2	1742.731	1741.879	-85.684	0.552	1918.225	0.626	26	0.384	R.EVAAFAQFGSDLDAATK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1740.663	1741.879	-1277.259	0.386	2135.435	0.503	24	0.379	R.EVAAFAQFGSDLDAATK.Q
R1/RRR1-8/2	1274.136	1274.448	-244.905	0.461	1515.773	0.560	18	0.300	K.HALVVYDDLTK.Q
R1/RRR1-8/2	1741.759	1741.879	-69.143	0.506	1421.023	0.596	22	0.294	R.EVAAFAQFGSDLDAATK.Q
R1/RRR1-8/2	1273.781	1274.448	-1312.104	0.436	1383.123	0.486	17	0.265	K.HALVVYDDLTK.Q
R1/RRR1-8/2	1274.181	1274.448	-209.439	0.463	1242.326	0.535	17	0.262	K.HALVVYDDLTK.Q
R1/RRR1-8/2	1439.437	1439.689	-175.528	0.453	630.106	0.520	18	0.215	R.GIRPAINVGLSVSR.V
R1/RRR1-8/2	1439.428	1439.689	-181.313	0.471	646.837	0.506	18	0.214	R.GIRPAINVGLSVSR.V
R1/RRR1-8/2	1257.342	1257.462	-95.489	0.388	1066.494	0.348	18	0.211	K.TAVALDAILNQK.R
R1/RRR1-8/2	1053.284	1053.237	44.799	0.420	910.256	0.358	16	0.208	R.GLLDSVPVPR.I
R1/RRR1-8/2	1053.025	1053.237	-202.034	0.450	791.761	0.374	15	0.205	R.GLLDSVPVPR.I
R1/RRR1-8/2	1439.344	1439.689	-240.358	0.387	465.882	0.430	16	0.199	R.GIRPAINVGLSVSR.V
R1/RRR1-8/2	1052.703	1053.237	-1462.048	0.398	551.358	0.378	13	0.196	-.GLLDSVPVPR.-
R1/RRR1-7/2	1439.531	1439.689	-109.940	0.360	690.507	0.306	18	0.192	R.GIRPAINVGLSVSR.V
R1/RRR1-8/2	1002.242	1002.193	48.668	0.208	883.310	0.086	14	0.177	-.RSTVAQLVK.-
R1/RRR1-8/3	1907.093	1906.081	5.989	0.416	1157.394	0.539	31	0.145	K.TNESDLLATIDKEGALSK.D
R1/RRR1-8/3	1906.165	1906.081	43.888	0.382	976.975	0.475	29	0.113	K.TNESDLLATIDKEGALSK.D
R1/RRR1-1/3	1440.908	1439.689	152.718	0.400	1148.110	0.350	22	0.103	R.GIRPAINVGLSVSR.V
R1/RRR1-1/3	1439.778	1439.689	62.187	0.389	1020.702	0.349	23	0.094	R.GIRPAINVGLSVSR.V
R1/RRR1-9/3	1439.574	1439.689	-79.669	0.429	1277.765	0.244	23	0.091	R.GIRPAINVGLSVSR.V
R1/RRR1-7/3	1439.494	1439.689	-135.809	0.417	1361.505	0.209	25	0.087	R.GIRPAINVGLSVSR.V
R1/RRR1-7/3	1439.589	1439.689	-69.207	0.415	1216.915	0.251	24	0.087	R.GIRPAINVGLSVSR.V
R1/RRR1-2/3	1439.293	1439.689	-275.551	0.399	983.352	0.307	22	0.087	R.GIRPAINVGLSVSR.V
R1/RRR1-8/3	1905.176	1906.081	-1003.098	0.306	733.482	0.398	26	0.086	K.TNESDLLATIDKEGALSK.D
R1/RRR1-7/2	1414.100	1414.577	-337.985	0.449	2091.541	0.539	18	0.387	K.SVTDYITDIVCK.R
R1/RRR1-7/2	1414.453	1414.577	-87.566	0.485	1881.104	0.505	18	0.338	K.SVTDYITDIVCK.R
R1/RRR1-7/2	1651.979	1652.828	-1122.295	0.211	1593.479	0.364	20	0.252	K.YVELTADYVYPYR.N
R1/RRR1-7/2	1651.949	1652.828	-1140.697	0.279	1396.782	0.320	19	0.228	K.YVELTADYVYPYR.N
R1/RRR1-7/2	1406.978	1407.722	-1243.669	0.430	1119.246	0.419	15	0.223	K.MLIAMVETELEK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1570.193	1570.763	-1002.812	0.364	1040.897	0.438	16	0.220	K.SVTDYITDIVCKR.A
R1/RRR1-7/2	1570.638	1570.763	-79.872	0.418	910.031	0.464	16	0.217	K.SVTDYITDIVCKR.A
R1/RRR1-7/2	1244.004	1243.435	-347.192	0.500	1061.258	0.296	15	0.202	K.TIQEQLLLER.D
R1/RRR1-7/2	1235.052	1235.368	-256.324	0.430	855.917	0.352	14	0.202	R.DKIETPEQFK.Q
R1/RRR1-7/2	1652.136	1652.828	-1026.960	0.260	1255.235	0.190	18	0.197	K.YVELTADYVYPYR.N
R1/RRR1-7/2	1235.189	1235.368	-145.376	0.444	874.755	0.262	14	0.191	R.DKIETPEQFK.Q
R1/RRR1-7/2	1352.212	1352.520	-228.230	0.369	785.793	0.287	14	0.189	K.FASLRDEWSLK.N
R1/RRR1-7/2	1244.047	1243.435	-312.734	0.458	888.508	0.258	13	0.189	-.TIQEQLLLER.-
R1/RRR1-12/2	1424.360	1424.628	-188.389	0.488	1717.468	0.497	21	0.311	R.IHNAILQTISEGK.F
R1/RRR1-12/2	1424.091	1424.628	-1082.309	0.519	1682.396	0.512	21	0.310	R.IHNAILQTISEGK.F
R1/RRR1-12/2	1802.523	1802.018	-275.614	0.517	1484.203	0.554	26	0.292	R.ATLFPGDGIGPEIAESVK.Q
R1/RRR1-12/2	1424.397	1424.628	-162.683	0.514	1612.122	0.473	21	0.290	R.IHNAILQTISEGK.F
R1/RRR1-12/2	1802.499	1802.018	267.655	0.489	1403.931	0.510	25	0.270	R.ATLFPGDGIGPEIAESVK.Q
R1/RRR1-11/2	1801.446	1802.018	-875.304	0.497	1224.690	0.555	25	0.263	R.ATLFPGDGIGPEIAESVK.Q
R1/RRR1-11/2	1801.428	1802.018	-885.167	0.438	1357.718	0.494	25	0.261	R.ATLFPGDGIGPEIAESVK.Q
R1/RRR1-11/2	1685.326	1684.828	296.652	0.497	1361.669	0.431	20	0.249	R.TESFLTWESLESVR.R
R1/RRR1-12/2	1801.418	1802.018	-890.746	0.442	1127.899	0.491	23	0.238	R.ATLFPGDGIGPEIAESVK.Q
R1/RRR1-12/2	1464.924	1465.637	-1172.410	0.476	1314.214	0.363	19	0.232	K.TRYDDVNLVTIR.E
R1/RRR1-12/2	1242.924	1243.314	-314.790	0.451	982.747	0.436	16	0.223	R.HLQFNNQADR.I
R1/RRR1-12/2	1199.197	1199.339	-118.497	0.467	1290.941	0.322	15	0.221	R.VAEYAFHYAK.T
R1/RRR1-12/2	1243.056	1243.314	-207.789	0.420	1039.059	0.378	16	0.217	R.HLQFNNQADR.I
R1/RRR1-12/2	888.254	888.067	211.100	0.423	775.161	0.472	13	0.216	K.GPM*ATPIGK.G
R1/RRR1-12/2	1243.855	1243.314	-369.873	0.410	985.808	0.369	16	0.213	R.HLQFNNQADR.I
R1/RRR1-11/2	1801.633	1802.018	-214.043	0.392	846.802	0.426	21	0.208	R.ATLFPGDGIGPEIAESVK.Q
R1/RRR1-10/2	1802.821	1802.018	-109.722	0.422	732.776	0.457	20	0.207	R.ATLFPGDGIGPEIAESVK.Q
R1/RRR1-12/2	888.943	888.067	-139.869	0.377	599.559	0.366	12	0.198	K.GPM*ATPIGK.G
R1/RRR1-12/2	1465.703	1465.637	45.726	0.401	744.776	0.309	15	0.191	K.TRYDDVNLVTIR.E
R1/RRR1-11/2	888.915	888.067	-171.966	0.342	513.716	0.333	12	0.189	-.GPM*ATPIGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1438.384	1438.656	-189.616	0.550	2965.526	0.593	24	0.625	K.YVILGGGVAAGYAAR.E
R1/RRR1-10/2	1533.199	1533.665	-304.383	0.529	2212.500	0.360	23	0.344	K.VLGAFLEGGSPDENK.A
R1/RRR1-10/2	1587.431	1586.769	-213.617	0.525	1461.613	0.423	22	0.256	R.EVDDADKLVAAIQAK.K
R1/RRR1-10/2	1586.948	1586.769	112.981	0.493	1449.389	0.415	23	0.255	R.EVDDADKLVAAIQAK.K
R1/RRR1-10/2	1984.025	1985.143	-1070.788	0.488	1464.761	0.415	22	0.251	K.LSDFGTQGADSNNILYLR.E
R1/RRR1-10/2	1985.190	1985.143	23.707	0.568	1058.847	0.525	19	0.233	K.LSDFGTQGADSNNILYLR.E
R1/RRR1-10/2	1984.457	1985.143	-852.516	0.537	1051.711	0.503	19	0.229	K.LSDFGTQGADSNNILYLR.E
R1/RRR1-1/2	1984.368	1985.143	-897.533	0.494	906.808	0.448	21	0.213	K.LSDFGTQGADSNNILYLR.E
R1/RRR1-10/2	1532.633	1533.665	-1329.678	0.451	1315.481	0.269	21	0.211	K.VLGAFLEGGSPDENK.A
R1/RRR1-10/2	1431.238	1431.619	-266.528	0.432	674.233	0.423	19	0.207	K.EAVAPYERPALSK.G
R1/RRR1-10/2	1431.360	1431.619	-180.881	0.431	452.357	0.473	16	0.204	K.EAVAPYERPALSK.G
R1/RRR1-10/2	1430.699	1431.619	-1345.597	0.405	583.915	0.420	17	0.202	K.EAVAPYERPALSK.G
R1/RRR1-10/2	1587.337	1586.769	-273.099	0.512	775.182	0.371	21	0.201	R.EVDDADKLVAAIQAK.K
R1/RRR1-9/2	1985.053	1985.143	-45.495	0.330	280.867	0.394	15	0.190	K.LSDFGTQGADSNNILYLR.E
R1/RRR1-10/3	1472.783	1472.624	108.096	0.525	1194.479	0.385	30	0.108	R.LPGFHVCVGSGGER.L
R1/RRR1-10/3	1985.214	1985.143	35.881	0.357	995.994	0.399	27	0.099	K.LSDFGTQGADSNNILYLR.E
R1/RRR1-10/3	1473.567	1472.624	-38.696	0.468	675.296	0.370	24	0.086	R.LPGFHVCVGSGGER.L
R1/RRR1-10/3	1472.429	1472.624	-132.980	0.477	754.769	0.306	25	0.081	R.LPGFHVCVGSGGER.L
R1/RRR1-10/3	1986.611	1985.143	236.248	0.376	690.919	0.342	25	0.080	K.LSDFGTQGADSNNILYLR.E
R1/RRR1-10/2	1650.280	1650.767	-295.698	0.526	2666.625	0.559	25	0.520	K.SVIGETGSDVTTDQLK.E
R1/RRR1-10/2	1650.270	1650.767	-301.858	0.570	2288.886	0.603	25	0.450	K.SVIGETGSDVTTDQLK.E
R1/RRR1-10/2	1650.197	1650.767	-953.823	0.497	2017.121	0.534	23	0.369	K.SVIGETGSDVTTDQLK.E
R1/RRR1-10/2	1554.367	1553.781	-266.761	0.582	1736.383	0.535	21	0.324	K.YLTEDPLFQLVSK.L
R1/RRR1-10/2	1554.505	1553.781	-177.657	0.581	1624.105	0.555	21	0.314	K.YLTEDPLFQLVSK.L
R1/RRR1-10/2	1553.399	1553.781	-246.435	0.537	1714.707	0.509	21	0.313	K.YLTEDPLFQLVSK.L
R1/RRR1-10/2	1737.574	1736.051	-275.169	0.528	1385.746	0.532	21	0.273	K.VQLGNITVDM*VLGGM*R.G
R1/RRR1-10/2	1345.408	1345.529	-89.876	0.455	1121.353	0.477	17	0.238	R.SIGIGSQLIWDR.A
R1/RRR1-10/2	1093.544	1094.332	-1639.879	0.415	618.748	0.529	15	0.218	R.ALGLPLERPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1094.243	1094.332	-81.973	0.406	541.905	0.499	15	0.212	R.ALGLPLERPK.S
R1/RRR1-10/2	1344.455	1345.529	-1546.841	0.302	962.886	0.420	15	0.211	R.SIGIGSQLIWDR.A
R1/RRR1-10/2	1344.767	1345.529	-1314.405	0.376	865.981	0.427	16	0.211	R.SIGIGSQLIWDR.A
R1/RRR1-10/2	1094.047	1094.332	-261.718	0.375	511.771	0.471	14	0.206	R.ALGLPLERPK.S
R1/RRR1-10/2	1553.746	1553.781	-22.112	0.442	558.799	0.427	17	0.203	K.YLTEDPLFQLVSK.L
R1/RRR1-10/2	1735.433	1736.051	-935.302	0.441	826.441	0.408	17	0.202	K.VQLGNITVDM*VLGGM*R.G
R1/RRR1-10/2	1139.071	1139.328	-226.435	0.324	926.407	0.341	15	0.201	R.LPAVASYVYR.R
R1/RRR1-10/2	1735.251	1736.051	-1040.532	0.329	564.814	0.238	17	0.183	K.VQLGNITVDM*VLGGM*R.G
R1/RRR1-12/3	1201.839	1202.343	-1255.012	0.239	1351.357	0.119	23	0.067	R.VAQEATTLGGVR.W
R1/RRR1-10/3	1769.121	1769.891	-1003.490	0.538	2423.152	0.486	32	0.367	R.HYAHVDCPGHADYVK.N
R1/RRR1-10/3	1770.068	1769.891	99.902	0.564	2339.762	0.515	30	0.366	R.HYAHVDCPGHADYVK.N
R1/RRR1-10/3	1769.913	1769.891	12.333	0.595	2141.499	0.539	31	0.323	R.HYAHVDCPGHADYVK.N
R1/RRR1-10/2	1692.163	1692.898	-1028.499	0.475	1574.945	0.525	22	0.298	K.ILDHGEAGDNVGLLLR.G
R1/RRR1-10/2	1756.179	1756.016	93.113	0.501	1079.857	0.554	20	0.249	K.SFLM*PIEDVFSIQGR.G
R1/RRR1-10/2	1649.173	1649.847	-1018.327	0.437	1244.666	0.423	20	0.237	K.LM*DAVDEYIPDPVR.Q
R1/RRR1-10/2	1562.004	1561.676	210.492	0.459	1171.319	0.468	19	0.235	R.GSALSALQGTNDEIGK.N
R1/RRR1-10/2	1157.571	1157.344	196.880	0.422	1131.589	0.440	17	0.233	K.FPGDEIPIIR.G
R1/RRR1-10/2	1755.232	1756.016	-1019.293	0.405	738.538	0.497	19	0.214	K.SFLM*PIEDVFSIQGR.G
R1/RRR1-10/2	1739.458	1740.016	-898.824	0.408	672.173	0.462	18	0.206	K.SFLMPIEDVFSIQGR.G
R1/RRR1-16/2	1726.775	1726.949	-101.437	0.410	743.012	0.425	18	0.199	K.TGEDVEILGLTPSGPLK.T
R1/RRR1-10/2	1561.071	1561.676	-1031.652	0.356	894.749	0.286	18	0.190	R.GSALSALQGTNDEIGK.N
R1/RRR1-8/2	1530.905	1531.821	-1255.601	0.379	2216.536	0.480	23	0.389	K.ALGVDILTGFGAIVGK.Q
R1/RRR1-8/2	1531.337	1531.821	-316.986	0.451	1859.901	0.577	23	0.357	K.ALGVDILTGFGAIVGK.Q
R1/RRR1-8/2	1414.176	1413.605	-304.201	0.512	1839.273	0.532	20	0.340	K.GLGLENINVVTQR.G
R1/RRR1-8/2	1412.621	1413.605	-1408.754	0.415	1670.912	0.420	19	0.282	K.GLGLENINVVTQR.G
R1/RRR1-8/2	1187.918	1188.270	-297.415	0.475	1417.231	0.457	18	0.262	K.ALAENEGDGLAK.L
R1/RRR1-8/2	1379.144	1379.500	-259.106	0.425	780.587	0.527	17	0.221	K.SLGLQVSSPGYDR.Q
R1/RRR1-8/2	1458.100	1456.754	237.836	0.472	979.456	0.401	19	0.212	R.NIIIATGSVPFVPK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/3	1426.804	1426.640	114.797	0.475	1885.713	0.363	25	0.193	K.DGKPVQIELIDAK.T
R1/RRR1-8/3	1426.976	1426.640	236.149	0.545	1840.885	0.375	25	0.191	K.DGKPVQIELIDAK.T
R1/RRR1-8/2	1379.167	1379.500	-242.501	0.325	436.911	0.348	14	0.189	K.SLGLQVSSPGYDR.Q
R1/RRR1-8/3	1426.675	1426.640	24.311	0.473	1200.391	0.348	22	0.106	K.DGKPVQIELIDAK.T
R1/RRR1-8/2	1467.144	1467.566	-288.462	0.320	738.745	0.471	18	0.105	K.VNSGVSHSVNEPVAA.-
R1/RRR1-8/2	1467.179	1467.566	-264.588	0.299	687.903	0.397	18	0.096	K.VNSGVSHSVNEPVAA.-
R1/RRR1-8/2	1467.099	1467.566	-319.099	0.306	834.006	0.350	19	0.095	K.VNSGVSHSVNEPVAA.-
R1/RRR1-10/2	1731.102	1730.933	97.985	0.525	1581.919	0.459	20	0.280	R.FFYASSACIYPEFK.Q
R1/RRR1-10/2	1557.313	1557.779	-300.063	0.489	1467.436	0.475	21	0.268	R.ISITGAGGFIGSHIAR.R
R1/RRR1-10/2	1455.293	1455.685	-269.778	0.528	1271.797	0.494	21	0.255	K.VVSTQAPVQLGSLR.A
R1/RRR1-9/2	1455.393	1455.685	-200.944	0.551	1292.104	0.481	21	0.254	K.VVSTQAPVQLGSLR.A
R1/RRR1-10/2	1455.318	1455.685	-252.779	0.540	1195.828	0.508	21	0.252	K.VVSTQAPVQLGSLR.A
R1/RRR1-10/2	1456.378	1455.685	-210.981	0.523	1129.293	0.532	21	0.251	K.VVSTQAPVQLGSLR.A
R1/RRR1-11/2	1557.101	1557.779	-1081.068	0.444	1338.735	0.460	19	0.249	R.ISITGAGGFIGSHIAR.R
R1/RRR1-10/2	1557.219	1557.779	-1004.798	0.481	1347.470	0.447	20	0.248	R.ISITGAGGFIGSHIAR.R
R1/RRR1-9/2	1455.210	1455.685	-327.343	0.517	1167.166	0.453	20	0.236	K.VVSTQAPVQLGSLR.A
R1/RRR1-9/2	1455.480	1455.685	-141.375	0.489	1016.689	0.468	19	0.228	K.VVSTQAPVQLGSLR.A
R1/RRR1-10/2	1906.479	1906.983	-791.117	0.422	640.899	0.506	22	0.212	K.ESDAWPAEPQDAYGLEK.L
R1/RRR1-10/2	1906.408	1906.983	-828.524	0.448	595.934	0.502	21	0.210	K.ESDAWPAEPQDAYGLEK.L
R1/RRR1-11/2	1731.560	1730.933	-216.129	0.446	932.687	0.395	18	0.209	R.FFYASSACIYPEFK.Q
R1/RRR1-10/2	1468.497	1467.654	-107.188	0.433	574.742	0.447	14	0.204	R.FHNIYGPFGTWK.G
R1/RRR1-10/2	1468.282	1467.654	-254.467	0.423	774.849	0.381	16	0.204	R.FHNIYGPFGTWK.G
R1/RRR1-9/2	1557.294	1557.779	-312.489	0.398	906.281	0.383	17	0.202	R.ISITGAGGFIGSHIAR.R
R1/RRR1-10/2	1906.141	1906.983	-969.503	0.393	546.460	0.463	20	0.202	K.ESDAWPAEPQDAYGLEK.L
R1/RRR1-10/2	1556.598	1557.779	-1405.167	0.330	979.197	0.325	18	0.199	R.ISITGAGGFIGSHIAR.R
R1/RRR1-10/2	1468.400	1467.654	-173.817	0.396	741.749	0.322	16	0.196	-.FHNIYGPFGTWK.-
R1/RRR1-11/2	1467.835	1467.654	123.234	0.379	717.053	0.312	14	0.193	R.FHNIYGPFGTWK.G
R1/RRR1-10/2	1672.413	1672.854	-264.551	0.373	819.849	0.316	16	0.190	R.SFTFIDECVEGVLR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1468.368	1467.654	-195.417	0.325	503.065	0.298	13	0.189	-.FHNIYGPFGTWK.-
R1/RRR1-11/2	1467.601	1467.654	-36.425	0.264	654.937	0.143	15	0.184	R.FHNIYGPFGTWK.G
R1/RRR1-10/2	1467.548	1467.654	-72.968	0.232	694.643	0.174	14	0.183	R.FHNIYGPFGTWK.G
R1/RRR1-10/3	1534.620	1534.697	-50.879	0.420	987.516	0.463	25	0.107	K.SEGHYIIASDWKK.N
R1/RRR1-10/2	1386.146	1386.619	-342.681	0.472	1516.829	0.470	24	0.276	K.IVIIGGGDTATVAAK.Y
R1/RRR1-10/2	1386.223	1386.619	-286.753	0.463	1478.021	0.447	24	0.266	K.IVIIGGGDTATVAAK.Y
R1/RRR1-10/2	1511.066	1511.657	-1056.393	0.329	1792.633	0.250	19	0.255	K.ELDYFAQALESPK.R
R1/RRR1-9/2	1386.400	1386.619	-158.398	0.446	1182.790	0.418	22	0.231	K.IVIIGGGDTATVAAK.Y
R1/RRR1-10/2	1399.294	1399.575	-201.301	0.415	1317.039	0.364	16	0.229	K.AADGDIVLLENLR.F
R1/RRR1-10/2	1232.084	1232.367	-230.607	0.549	800.937	0.505	17	0.225	R.VDFNVPLDANK.N
R1/RRR1-10/2	1143.127	1143.406	-245.340	0.468	997.444	0.418	18	0.222	K.RPFLAILGGAK.V
R1/RRR1-10/2	1232.119	1232.367	-202.081	0.455	946.787	0.418	18	0.218	R.VDFNVPLDANK.N
R1/RRR1-10/2	1144.460	1143.406	46.579	0.466	690.774	0.402	16	0.206	K.RPFLAILGGAK.V
R1/RRR1-10/2	1143.347	1143.406	-52.430	0.466	928.252	0.322	17	0.203	K.RPFLAILGGAK.V
R1/RRR1-10/2	1385.659	1386.619	-1418.847	0.339	1084.336	0.276	21	0.201	K.IVIIGGGDTATVAAK.Y
R1/RRR1-9/2	1142.598	1143.406	-1587.907	0.433	712.614	0.296	15	0.193	K.RPFLAILGGAK.V
R1/RRR1-10/2	1510.467	1511.657	-1454.486	0.244	755.305	0.014	14	0.171	K.ELDYFAQALESPK.R
R1/RRR1-10/3	1384.911	1385.572	-1202.560	0.475	1587.764	0.407	26	0.158	R.AHSSM*VGVDLPQK.A
R1/RRR1-10/3	1650.022	1649.788	141.823	0.482	960.562	0.548	28	0.128	K.LGDVYINDAFGTAHR.A
R1/RRR1-9/3	1649.853	1649.788	39.427	0.429	847.739	0.542	25	0.120	K.LGDVYINDAFGTAHR.A
R1/RRR1-10/3	1650.542	1649.788	-149.896	0.473	946.384	0.493	27	0.116	K.LGDVYINDAFGTAHR.A
R1/RRR1-10/3	1650.145	1649.788	216.826	0.442	888.830	0.511	26	0.116	K.LGDVYINDAFGTAHR.A
R1/RRR1-10/3	1385.357	1385.572	-155.633	0.446	1362.557	0.305	25	0.107	-.AHSSM*VGVDLPQK.-
R1/RRR1-10/3	1385.611	1385.572	28.765	0.508	1246.822	0.321	24	0.102	R.AHSSM*VGVDLPQK.A
R1/RRR1-9/3	1649.459	1649.788	-200.618	0.357	638.037	0.490	23	0.099	K.LGDVYINDAFGTAHR.A
R1/RRR1-6/2	1690.381	1689.801	-249.498	0.538	1782.303	0.591	21	0.351	K.YSNSQAVVYVGCGER.G
R1/RRR1-6/2	1256.129	1256.434	-243.153	0.475	1110.032	0.530	19	0.250	K.LAADTPLLTGQR.V
R1/RRR1-6/2	1256.080	1256.434	-282.152	0.478	1121.320	0.515	19	0.248	K.LAADTPLLTGQR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1256.189	1256.434	-195.090	0.439	1124.610	0.476	19	0.240	K.LAADTPLLTGQR.V
R1/RRR1-7/2	1256.044	1256.434	-311.501	0.483	843.136	0.528	17	0.230	K.LAADTPLLTGQR.V
R1/RRR1-7/2	1256.138	1256.434	-235.841	0.423	867.454	0.477	18	0.223	K.LAADTPLLTGQR.V
R1/RRR1-1/2	1256.206	1256.434	-181.637	0.365	900.529	0.425	17	0.214	K.LAADTPLLTGQR.V
R1/RRR1-21/2	1992.464	1993.113	-829.979	0.626	3349.537	0.673	28	0.770	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/2	1992.488	1993.113	-817.925	0.631	3172.459	0.683	27	0.717	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1993.290	1993.113	89.519	0.598	3061.039	0.694	27	0.690	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/2	1992.632	1993.113	-242.006	0.615	3000.513	0.700	27	0.674	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/2	1992.378	1993.113	-873.400	0.593	2430.987	0.670	28	0.506	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1992.359	1993.113	-882.810	0.608	2350.262	0.694	27	0.496	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/3	1993.277	1993.113	82.818	0.544	2173.578	0.639	37	0.382	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/3	1992.355	1993.113	-884.970	0.467	2076.976	0.571	37	0.319	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1223.084	1222.321	-194.765	0.520	1587.147	0.541	20	0.304	K.LEATGDASCVAK.L
R1/RRR1-22/3	1993.963	1993.113	-75.018	0.536	1900.693	0.623	37	0.304	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1222.011	1222.321	-254.751	0.457	1631.643	0.499	20	0.298	K.LEATGDASCVAK.L
R1/RRR1-20/2	1222.018	1222.321	-249.139	0.491	1579.421	0.518	20	0.297	K.LEATGDASCVAK.L
R1/RRR1-20/2	1221.502	1222.321	-1494.156	0.455	1616.668	0.492	20	0.294	K.LEATGDASCVAK.L
R1/RRR1-20/3	1993.672	1993.113	-221.866	0.530	1830.052	0.618	35	0.290	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/2	1222.024	1222.321	-243.527	0.463	1541.803	0.476	20	0.281	K.LEATGDASCVAK.L
R1/RRR1-20/3	1993.792	1993.113	-161.427	0.531	1827.157	0.579	35	0.272	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1222.041	1222.321	-229.797	0.465	1387.773	0.483	19	0.265	K.LEATGDASCVAK.L
R1/RRR1-21/3	1992.570	1993.113	-776.575	0.472	1804.309	0.550	34	0.255	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-22/2	1221.479	1222.321	-1512.827	0.399	1405.261	0.429	19	0.254	K.LEATGDASCVAK.L
R1/RRR1-22/2	1221.501	1222.321	-1494.357	0.437	1272.881	0.477	19	0.252	K.LEATGDASCVAK.L
R1/RRR1-20/2	1221.926	1222.329	-331.421	0.364	1024.998	0.571	20	0.247	K.LNPSADAGSVYK.T
R1/RRR1-19/3	1993.206	1993.113	47.254	0.514	1533.584	0.593	32	0.226	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1222.029	1222.329	-246.832	0.351	921.153	0.460	20	0.222	K.LNPSADAGSVYK.T
R1/RRR1-22/2	1221.574	1222.329	-1441.247	0.363	757.877	0.523	18	0.222	K.LNPSADAGSVYK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1160.964	1161.201	-204.659	0.386	1280.462	0.310	17	0.220	K.DGASLSPEQEK.M
R1/RRR1-20/3	1992.477	1993.113	-823.159	0.509	1547.607	0.585	35	0.219	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-22/2	1222.037	1222.329	-239.917	0.330	968.757	0.427	20	0.219	K.LNPSADAGSVYK.T
R1/RRR1-22/3	1992.649	1993.113	-233.378	0.529	1490.401	0.584	33	0.213	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-22/3	1993.455	1993.113	172.544	0.518	1457.362	0.589	33	0.209	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1221.936	1222.321	-315.988	0.411	920.192	0.376	16	0.209	K.LEATGDASCVAK.L
R1/RRR1-21/2	1160.959	1161.201	-209.089	0.380	1124.822	0.298	16	0.207	K.DGASLSPEQEK.M
R1/RRR1-21/2	1221.490	1222.321	-1503.893	0.363	939.936	0.359	16	0.207	K.LEATGDASCVAK.L
R1/RRR1-21/2	1221.947	1222.321	-307.168	0.398	920.938	0.360	16	0.207	K.LEATGDASCVAK.L
R1/RRR1-20/2	1222.112	1222.329	-178.389	0.382	481.364	0.450	15	0.205	K.LNPSADAGSVYK.T
R1/RRR1-21/3	1992.862	1993.113	-126.176	0.500	1618.736	0.511	35	0.204	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/2	1222.125	1222.329	-167.668	0.287	787.996	0.367	19	0.203	K.LNPSADAGSVYK.T
R1/RRR1-1/2	1994.518	1993.113	203.950	0.397	573.089	0.519	16	0.203	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/2	1168.062	1168.361	-257.503	0.487	771.647	0.351	14	0.201	K.VCLDVHSLPK.V
R1/RRR1-21/2	1168.064	1168.361	-255.091	0.442	763.712	0.347	14	0.201	K.VCLDVHSLPK.V
R1/RRR1-21/2	1222.014	1222.329	-258.658	0.340	651.292	0.349	18	0.201	K.LNPSADAGSVYK.T
R1/RRR1-22/2	1221.515	1222.329	-1489.829	0.298	606.972	0.385	17	0.200	K.LNPSADAGSVYK.T
R1/RRR1-20/2	1221.854	1222.329	-390.662	0.352	600.955	0.366	16	0.200	K.LNPSADAGSVYK.T
R1/RRR1-20/2	1167.531	1168.361	-1572.768	0.474	742.171	0.337	14	0.199	K.VCLDVHSLPK.V
R1/RRR1-21/2	1167.681	1168.361	-1443.175	0.497	683.515	0.344	14	0.199	K.VCLDVHSLPK.V
R1/RRR1-21/2	1168.155	1168.361	-176.986	0.470	808.165	0.305	14	0.197	K.VCLDVHSLPK.V
R1/RRR1-20/2	1168.094	1168.361	-229.719	0.458	689.758	0.307	14	0.196	K.VCLDVHSLPK.V
R1/RRR1-22/2	1160.991	1161.201	-181.664	0.455	712.260	0.366	14	0.195	-.DGASLSPEQEK.-
R1/RRR1-21/2	1160.597	1161.201	-1386.367	0.358	921.182	0.250	16	0.194	-.DGASLSPEQEK.-
R1/RRR1-20/3	1993.090	1993.113	-11.255	0.516	1440.680	0.549	33	0.193	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/3	1993.406	1993.113	147.857	0.516	1406.812	0.549	33	0.187	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/3	1993.663	1993.113	-226.105	0.499	1376.615	0.540	33	0.180	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-21/3	1994.218	1993.113	53.186	0.539	1212.629	0.561	32	0.167	K.SHSTETKLEATGDASCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/3	1992.951	1993.113	-81.476	0.528	1251.910	0.501	32	0.154	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/3	1992.853	1993.113	-130.784	0.475	1140.984	0.521	32	0.146	K.SHSTETKLEATGDASCVAK.L
R1/RRR1-20/3	1571.269	1571.837	-1001.121	0.432	1283.243	0.442	28	0.130	K.TKIVVCDSATHVLK.A
R1/RRR1-6/2	1995.912	1997.232	-1166.180	0.622	2646.441	0.583	25	0.525	K.KISEEEYISAIKEEISK.V
R1/RRR1-6/2	1996.882	1997.232	-175.824	0.632	2403.638	0.622	24	0.483	K.KISEEEYISAIKEEISK.V
R1/RRR1-5/2	1869.435	1869.059	201.485	0.584	1880.661	0.487	23	0.326	K.ISEEEYISAIKEEISK.V
R1/RRR1-6/2	1868.464	1869.059	-856.490	0.571	1797.995	0.512	23	0.322	K.ISEEEYISAIKEEISK.V
R1/RRR1-6/2	1868.566	1869.059	-264.627	0.571	1709.907	0.514	22	0.309	K.ISEEEYISAIKEEISK.V
R1/RRR1-6/2	1869.107	1869.059	25.704	0.579	1616.817	0.552	22	0.307	K.ISEEEYISAIKEEISK.V
R1/RRR1-5/2	1869.591	1869.059	-251.384	0.567	1614.194	0.534	22	0.302	K.ISEEEYISAIKEEISK.V
R1/RRR1-6/3	1997.250	1997.232	9.059	0.616	1993.694	0.525	36	0.274	K.KISEEEYISAIKEEISK.V
R1/RRR1-5/2	1868.525	1869.059	-823.699	0.577	1425.782	0.493	21	0.266	K.ISEEEYISAIKEEISK.V
R1/RRR1-6/3	1996.397	1997.232	-922.214	0.531	1763.922	0.515	34	0.226	K.KISEEEYISAIKEEISK.V
R1/RRR1-2/3	1997.821	1997.232	-206.636	0.580	1668.932	0.555	34	0.225	K.KISEEEYISAIKEEISK.V
R1/RRR1-6/3	1997.027	1997.232	-103.044	0.526	1543.126	0.561	34	0.204	K.KISEEEYISAIKEEISK.V
R1/RRR1-5/3	1997.362	1997.232	65.056	0.574	1647.702	0.507	34	0.203	K.KISEEEYISAIKEEISK.V
R1/RRR1-4/3	1996.402	1997.232	-919.360	0.519	1411.099	0.538	30	0.183	K.KISEEEYISAIKEEISK.V
R1/RRR1-3/3	1997.230	1997.232	-0.964	0.529	1304.787	0.522	31	0.162	K.KISEEEYISAIKEEISK.V
R1/RRR1-2/3	1996.776	1997.232	-229.064	0.530	1164.211	0.502	29	0.143	K.KISEEEYISAIKEEISK.V
R1/RRR1-1/3	1996.551	1997.232	-844.783	0.504	1042.266	0.512	28	0.135	K.KISEEEYISAIKEEISK.V
R1/RRR1-5/3	1997.034	1997.232	-99.825	0.578	1218.606	0.455	32	0.133	K.KISEEEYISAIKEEISK.V
R1/RRR1-2/3	1998.166	1997.232	-33.163	0.493	1143.234	0.464	30	0.129	K.KISEEEYISAIKEEISK.V
R1/RRR1-1/3	1997.129	1997.232	-52.093	0.541	1208.954	0.433	32	0.126	K.KISEEEYISAIKEEISK.V
R1/RRR1-4/3	1995.747	1997.232	-1249.104	0.341	866.110	0.305	25	0.086	K.KISEEEYISAIKEEISK.V
R1/RRR1-8/2	1104.522	1105.224	-1545.986	0.377	1020.146	0.537	19	0.240	K.VVGVDTSGSGVK.L
R1/RRR1-8/2	1104.920	1105.224	-275.653	0.471	867.259	0.565	18	0.238	K.VVGVDTSGSGVK.L
R1/RRR1-8/2	1105.100	1105.224	-112.522	0.444	735.170	0.509	18	0.221	K.VVGVDTSGSGVK.L
R1/RRR1-7/2	1104.341	1105.224	-1710.102	0.337	625.023	0.450	16	0.204	K.VVGVDTSGSGVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1203.194	1202.419	-188.114	0.544	1888.832	0.504	20	0.339	R.LLAVEGCAALGK.L
R1/RRR1-7/2	1202.366	1202.419	-44.358	0.475	1873.553	0.414	20	0.309	R.LLAVEGCAALGK.L
R1/RRR1-7/2	1202.429	1202.419	7.677	0.534	1614.630	0.496	19	0.296	R.LLAVEGCAALGK.L
R1/RRR1-7/2	1534.023	1533.749	178.894	0.469	1717.671	0.408	20	0.285	K.ESDIVDWFVPVVK.R
R1/RRR1-7/2	1122.145	1122.258	-101.211	0.448	1412.174	0.517	17	0.277	R.LAAGEWFTAR.V
R1/RRR1-7/2	1121.943	1122.258	-281.838	0.435	1490.518	0.472	17	0.275	R.LAAGEWFTAR.V
R1/RRR1-7/2	1767.820	1766.115	-167.371	0.576	1126.381	0.607	25	0.269	K.VLQALIPILDQSVVEK.N
R1/RRR1-7/2	1284.178	1284.442	-206.665	0.512	1451.185	0.464	18	0.268	K.FAATVEQNYLK.T
R1/RRR1-7/2	1285.147	1284.442	-230.613	0.506	1311.268	0.471	18	0.256	K.FAATVEQNYLK.T
R1/RRR1-7/2	1122.153	1122.258	-93.573	0.447	1315.298	0.458	17	0.253	R.LAAGEWFTAR.V
R1/RRR1-7/2	1285.140	1284.442	-235.949	0.530	1362.080	0.437	18	0.253	K.FAATVEQNYLK.T
R1/RRR1-7/2	1766.668	1766.115	-253.971	0.544	1017.305	0.559	24	0.248	K.VLQALIPILDQSVVEK.N
R1/RRR1-7/2	1766.412	1766.115	168.529	0.503	880.942	0.504	23	0.228	K.VLQALIPILDQSVVEK.N
R1/RRR1-7/2	1533.241	1533.749	-986.734	0.342	1338.681	0.337	18	0.227	K.ESDIVDWFVPVVK.R
R1/RRR1-7/2	1765.557	1766.115	-885.191	0.477	923.255	0.444	23	0.220	K.VLQALIPILDQSVVEK.N
R1/RRR1-6/2	1765.677	1766.115	-248.982	0.458	780.553	0.440	22	0.212	K.VLQALIPILDQSVVEK.N
R1/RRR1-6/2	1765.904	1766.115	-119.643	0.464	684.202	0.427	20	0.205	K.VLQALIPILDQSVVEK.N
R1/RRR1-7/2	1190.043	1190.335	-246.264	0.415	863.067	0.340	14	0.204	K.INNPHYLYR.M
R1/RRR1-7/2	1215.126	1215.342	-178.407	0.450	694.443	0.368	15	0.201	R.LLRDNEAEVR.I
R1/RRR1-2/2	1285.289	1284.442	-119.514	0.366	709.106	0.350	15	0.199	K.FAATVEQNYLK.T
R1/RRR1-7/2	1189.600	1190.335	-1463.311	0.362	679.339	0.323	14	0.197	K.INNPHYLYR.M
R1/RRR1-7/2	1190.144	1190.335	-161.680	0.377	692.649	0.327	13	0.197	K.INNPHYLYR.M
R1/RRR1-7/2	1533.305	1533.749	-290.868	0.373	856.129	0.342	15	0.197	K.ESDIVDWFVPVVK.R
R1/RRR1-6/2	1283.977	1284.442	-363.178	0.363	725.098	0.276	16	0.194	K.FAATVEQNYLK.T
R1/RRR1-7/2	1767.306	1766.115	108.517	0.337	266.584	0.372	13	0.191	K.VLQALIPILDQSVVEK.N
R1/RRR1-7/2	1214.617	1215.342	-1424.099	0.408	679.097	0.275	13	0.188	-.LLRDNEAEVR.-
R1/RRR1-7/3	1765.934	1766.115	-102.939	0.421	1179.574	0.382	27	0.110	K.VLQALIPILDQSVVEK.N
R1/RRR1-7/3	1766.017	1766.115	-55.825	0.356	533.926	0.365	24	0.081	K.VLQALIPILDQSVVEK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1907.802	1908.144	-179.477	0.534	2272.616	0.511	23	0.413	R.GDFQELDQIAATKPFVK.I
R1/RRR1-7/2	1628.661	1629.877	-1364.343	0.318	1318.670	0.411	21	0.237	R.SLAIGQCDVALVVGAR.L
R1/RRR1-7/2	1453.110	1451.696	285.247	0.395	844.047	0.515	14	0.219	R.LNWLLHFGEPPK.W
R1/RRR1-7/2	1493.327	1492.662	-224.946	0.419	584.432	0.540	22	0.217	K.GVVPDTHPLSATAAR.S
R1/RRR1-7/3	1971.143	1971.246	-52.531	0.455	1964.159	0.345	31	0.215	R.KPAVINVIIDPYAGAESGR.M
R1/RRR1-7/2	1451.484	1451.696	-146.741	0.460	789.822	0.441	15	0.209	R.LNWLLHFGEPPK.W
R1/RRR1-7/2	1492.295	1492.662	-246.598	0.351	536.622	0.530	19	0.208	K.GVVPDTHPLSATAAR.S
R1/RRR1-7/2	1492.125	1492.662	-1033.124	0.302	469.032	0.491	19	0.200	K.GVVPDTHPLSATAAR.S
R1/RRR1-7/2	1025.857	1026.172	-307.997	0.313	623.103	0.370	11	0.194	-.AVLVQNEPR.-
R1/RRR1-7/2	1026.047	1026.172	-121.668	0.361	758.662	0.317	12	0.192	-.AVLVQNEPR.-
R1/RRR1-7/2	1025.845	1026.172	-319.458	0.288	484.622	0.274	12	0.189	-.AVLVQNEPR.-
R1/RRR1-7/3	1121.439	1121.315	111.392	0.486	998.853	0.446	22	0.107	R.KPHVGIVGDAK.R
R1/RRR1-7/3	1121.400	1121.315	76.840	0.429	1054.936	0.435	23	0.106	R.KPHVGIVGDAK.R
R1/RRR1-7/3	1121.537	1121.315	199.318	0.462	985.108	0.455	22	0.104	-.KPHVGIVGDAK.-
R1/RRR1-6/3	1120.871	1121.315	-397.142	0.371	701.274	0.368	18	0.075	-.KPHVGIVGDAK.-
R1/RRR1-5/2	1324.170	1324.468	-225.573	0.479	2141.552	0.540	21	0.394	K.ILVAGSHADDLGR.Q
R1/RRR1-6/2	1324.384	1324.468	-63.938	0.484	1875.559	0.523	21	0.342	K.ILVAGSHADDLGR.Q
R1/RRR1-5/2	1323.481	1324.468	-1505.858	0.422	1893.024	0.496	20	0.334	K.ILVAGSHADDLGR.Q
R1/RRR1-6/2	1324.281	1324.468	-141.420	0.463	1651.978	0.556	19	0.316	K.ILVAGSHADDLGR.Q
R1/RRR1-5/2	1059.148	1059.198	-47.697	0.551	1618.619	0.445	17	0.282	R.IGEATALEVR.A
R1/RRR1-6/2	1058.889	1059.198	-292.723	0.559	1649.796	0.431	17	0.281	R.IGEATALEVR.A
R1/RRR1-5/2	1058.828	1059.198	-351.251	0.507	1534.439	0.462	17	0.277	R.IGEATALEVR.A
R1/RRR1-6/2	1059.120	1059.198	-74.634	0.531	1568.709	0.429	17	0.272	R.IGEATALEVR.A
R1/RRR1-4/2	1060.053	1059.198	-137.285	0.512	1555.459	0.413	17	0.267	R.IGEATALEVR.A
R1/RRR1-5/2	1058.976	1059.198	-211.073	0.553	1497.701	0.411	17	0.260	R.IGEATALEVR.A
R1/RRR1-6/2	1324.144	1324.468	-245.458	0.449	1259.595	0.499	18	0.253	K.ILVAGSHADDLGR.Q
R1/RRR1-4/2	1059.205	1059.198	5.709	0.452	1361.388	0.391	17	0.244	R.IGEATALEVR.A
R1/RRR1-2/2	1058.288	1059.198	-1810.550	0.401	1262.438	0.402	16	0.236	R.IGEATALEVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1782.136	1782.063	40.973	0.420	1018.398	0.493	20	0.229	R.ATGIPYVFAPCVAVCR.D
R1/RRR1-3/2	1059.025	1059.198	-164.240	0.414	1092.728	0.400	16	0.225	R.IGEATALEVR.A
R1/RRR1-5/2	1189.063	1188.398	-282.507	0.464	961.325	0.450	17	0.225	K.SSYSPVLPLPK.K
R1/RRR1-3/2	1058.927	1059.198	-256.754	0.411	1166.762	0.356	16	0.222	R.IGEATALEVR.A
R1/RRR1-1/2	1059.029	1059.198	-160.193	0.463	999.811	0.412	15	0.221	R.IGEATALEVR.A
R1/RRR1-6/2	1278.216	1278.297	-63.086	0.390	837.683	0.477	13	0.215	R.CYESYSEDPK.V
R1/RRR1-6/2	1188.091	1188.398	-258.932	0.443	749.917	0.449	16	0.214	K.SSYSPVLPLPK.K
R1/RRR1-5/2	1189.329	1188.398	-57.815	0.476	826.104	0.420	16	0.213	K.SSYSPVLPLPK.K
R1/RRR1-6/2	1187.668	1188.398	-1460.640	0.391	694.206	0.454	15	0.210	K.SSYSPVLPLPK.K
R1/RRR1-5/2	1188.062	1188.398	-283.466	0.409	711.280	0.379	15	0.203	K.SSYSPVLPLPK.K
R1/RRR1-6/2	1780.522	1782.063	-1995.035	0.323	817.785	0.409	19	0.203	R.ATGIPYVFAPCVAVCR.D
R1/RRR1-5/2	1781.628	1782.063	-245.172	0.408	676.658	0.445	17	0.202	R.ATGIPYVFAPCVAVCR.D
R1/RRR1-6/2	1188.279	1188.398	-100.421	0.396	671.197	0.356	15	0.200	K.SSYSPVLPLPK.K
R1/RRR1-15/2	1783.326	1782.063	147.912	0.201	552.399	0.258	14	0.179	R.ATGIPYVFAPCVAVCR.D
R1/RRR1-5/3	1454.794	1454.659	93.105	0.402	1113.735	0.491	28	0.124	K.ATIFPHNVGLGATR.D
R1/RRR1-6/3	1454.752	1454.659	64.324	0.440	1007.624	0.485	26	0.117	K.ATIFPHNVGLGATR.D
R1/RRR1-6/3	1454.753	1454.659	65.082	0.385	1190.973	0.440	29	0.117	K.ATIFPHNVGLGATR.D
R1/RRR1-5/3	1454.463	1454.659	-135.043	0.403	1179.321	0.434	28	0.117	K.ATIFPHNVGLGATR.D
R1/RRR1-4/3	1454.814	1454.659	106.990	0.454	942.941	0.493	25	0.116	K.ATIFPHNVGLGATR.D
R1/RRR1-6/3	1454.710	1454.659	35.415	0.396	1039.016	0.464	27	0.113	K.ATIFPHNVGLGATR.D
R1/RRR1-5/3	1593.821	1593.835	-8.802	0.421	1325.449	0.309	22	0.106	K.M*HANHHLITDFLK.N
R1/RRR1-6/3	1594.353	1593.835	-302.690	0.348	929.712	0.278	20	0.077	K.M*HANHHLITDFLK.N
R1/RRR1-5/3	1595.028	1593.835	121.507	0.351	707.733	0.259	20	0.072	-.M*HANHHLITDFLK.-
R1/RRR1-7/2	1474.231	1474.730	-339.564	0.525	2148.875	0.583	21	0.410	R.LGANSLLDIVVFGR.A
R1/RRR1-7/2	1474.243	1474.730	-330.924	0.476	2092.843	0.535	21	0.382	R.LGANSLLDIVVFGR.A
R1/RRR1-7/2	1473.915	1474.730	-1234.621	0.425	1688.434	0.534	20	0.314	R.LGANSLLDIVVFGR.A
R1/RRR1-7/2	1296.253	1295.427	-134.466	0.495	1451.382	0.579	20	0.297	R.ATNTILATGGYGR.A
R1/RRR1-7/2	1296.066	1295.427	-278.927	0.512	1501.607	0.537	20	0.292	R.ATNTILATGGYGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1295.233	1295.427	-149.791	0.472	1526.115	0.511	20	0.288	R.ATNTILATGGYGR.A
R1/RRR1-7/2	1609.265	1608.819	277.958	0.494	1284.416	0.532	22	0.266	K.AVIELENYGLPFSR.T
R1/RRR1-7/2	1609.351	1608.819	-292.035	0.533	1182.342	0.535	21	0.257	K.AVIELENYGLPFSR.T
R1/RRR1-7/2	1127.886	1127.231	-307.165	0.501	1095.672	0.544	18	0.253	R.AFGGQSLDFGK.G
R1/RRR1-7/2	1474.216	1474.730	-1030.227	0.388	1328.353	0.472	19	0.253	R.LGANSLLDIVVFGR.A
R1/RRR1-7/2	1166.047	1166.336	-248.710	0.530	1289.342	0.430	17	0.246	R.VM*QNNAAVFR.T
R1/RRR1-7/2	1165.621	1166.336	-1475.560	0.488	1219.911	0.426	17	0.239	R.VM*QNNAAVFR.T
R1/RRR1-7/2	1165.838	1166.336	-428.129	0.440	1212.966	0.415	17	0.236	R.VM*QNNAAVFR.T
R1/RRR1-7/2	1608.181	1608.819	-1021.835	0.340	1119.526	0.461	20	0.231	K.AVIELENYGLPFSR.T
R1/RRR1-7/2	1127.113	1127.231	-105.110	0.463	1082.562	0.426	18	0.229	R.AFGGQSLDFGK.G
R1/RRR1-6/2	1609.668	1608.819	-94.213	0.485	900.173	0.471	19	0.221	K.AVIELENYGLPFSR.T
R1/RRR1-7/2	1126.457	1127.231	-1579.465	0.393	899.808	0.418	17	0.215	R.AFGGQSLDFGK.G
R1/RRR1-7/2	1263.158	1263.340	-144.289	0.430	479.686	0.489	16	0.209	K.HSLGYWENEK.V
R1/RRR1-1/2	1127.829	1127.231	-358.204	0.209	266.797	0.327	13	0.192	R.AFGGQSLDFGK.G
R1/RRR1-2/2	1127.506	1127.231	244.371	0.212	535.753	0.233	14	0.187	R.AFGGQSLDFGK.G
R1/RRR1-4/2	1475.158	1474.730	291.442	0.268	608.892	0.230	15	0.184	R.LGANSLLDIVVFGR.A
R1/RRR1-7/3	1790.323	1790.992	-935.118	0.384	902.670	0.507	27	0.114	R.AAIGLSEHGFNTACITK.L
R1/RRR1-7/3	1790.495	1790.992	-278.533	0.390	812.528	0.492	27	0.106	R.AAIGLSEHGFNTACITK.L
R1/RRR1-7/3	1791.217	1790.992	125.961	0.427	612.694	0.507	24	0.103	R.AAIGLSEHGFNTACITK.L
R1/RRR1-6/2	1788.729	1787.948	-122.839	0.554	2410.333	0.476	24	0.429	K.CGVNTAEDWLNPAAIR.E
R1/RRR1-6/3	1993.001	1993.209	-104.634	0.492	1782.712	0.541	32	0.251	R.KQFGPQTGGPETQVLNYK.T
R1/RRR1-6/2	1128.846	1129.249	-358.207	0.456	556.167	0.599	17	0.227	R.QGALANEQLGK.L
R1/RRR1-6/2	1128.933	1129.249	-280.635	0.414	534.539	0.608	16	0.223	R.QGALANEQLGK.L
R1/RRR1-6/2	1662.378	1662.822	-267.989	0.457	904.274	0.487	19	0.221	K.TDEFVIHSPTLTSSK.W
R1/RRR1-6/2	1128.611	1129.249	-1455.926	0.421	564.546	0.561	16	0.219	R.QGALANEQLGK.L
R1/RRR1-6/2	1187.970	1188.313	-289.569	0.522	942.168	0.394	16	0.215	R.LTEEEANLLR.L
R1/RRR1-6/2	1369.248	1369.635	-283.333	0.355	764.665	0.479	14	0.210	R.LFPLLASAYAFR.F
R1/RRR1-6/2	1188.004	1188.313	-261.219	0.475	963.754	0.313	16	0.203	R.LTEEEANLLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1187.977	1188.313	-283.692	0.488	972.515	0.306	16	0.203	R.LTEEEANLLR.L
R1/RRR1-6/3	1993.119	1993.209	-45.011	0.497	1463.767	0.551	31	0.196	R.KQFGPQTGGPETQVLNYK.T
R1/RRR1-6/2	1369.144	1369.635	-359.993	0.224	531.838	0.379	13	0.187	R.LFPLLASAYAFR.F
R1/RRR1-6/2	1369.131	1369.635	-1102.057	0.191	516.522	0.328	13	0.183	R.LFPLLASAYAFR.F
R1/RRR1-6/3	1892.947	1893.087	-74.461	0.467	1521.897	0.444	29	0.174	R.SLEDHSPLPGVTLGDIGGK.F
R1/RRR1-6/3	1893.096	1893.087	4.319	0.497	1265.261	0.495	29	0.154	R.SLEDHSPLPGVTLGDIGGK.F
R1/RRR1-6/3	1894.354	1893.087	141.272	0.448	833.870	0.397	25	0.097	R.SLEDHSPLPGVTLGDIGGK.F
R1/RRR1-6/2	1212.914	1212.424	404.926	0.549	1750.984	0.433	20	0.296	K.DAGIIAGLNVLR.I
R1/RRR1-6/2	1266.159	1266.299	-111.360	0.426	1662.046	0.465	21	0.293	K.LYSGGAGGSDEPR.S
R1/RRR1-6/2	1646.643	1646.866	-135.521	0.532	1430.864	0.578	23	0.293	R.IVNEPTAAAIAYGLDK.T
R1/RRR1-6/2	1212.110	1212.424	-260.266	0.541	1724.076	0.428	20	0.291	K.DAGIIAGLNVLR.I
R1/RRR1-6/2	1265.925	1266.299	-296.207	0.411	1636.739	0.434	21	0.282	K.LYSGGAGGSDEPR.S
R1/RRR1-6/2	1212.199	1212.424	-185.908	0.463	1634.896	0.423	20	0.279	K.DAGIIAGLNVLR.I
R1/RRR1-6/2	1167.099	1167.340	-207.255	0.535	1185.268	0.548	18	0.262	K.LSNVAHPITSK.L
R1/RRR1-6/2	1646.684	1646.866	-110.832	0.531	1099.046	0.578	21	0.255	R.IVNEPTAAAIAYGLDK.T
R1/RRR1-6/2	1265.605	1266.299	-1342.734	0.427	1479.029	0.398	20	0.254	K.LYSGGAGGSDEPR.S
R1/RRR1-6/2	1286.287	1286.415	-100.194	0.451	1134.107	0.466	16	0.237	R.NSLENYAFSLK.S
R1/RRR1-6/2	1647.352	1646.866	295.835	0.513	1056.474	0.504	21	0.236	R.IVNEPTAAAIAYGLDK.T
R1/RRR1-6/2	1285.879	1286.415	-1198.354	0.356	922.984	0.441	14	0.214	R.NSLENYAFSLK.S
R1/RRR1-6/2	1286.064	1286.415	-273.861	0.323	643.613	0.440	13	0.200	R.NSLENYAFSLK.S
R1/RRR1-6/3	1442.023	1442.603	-1098.661	0.508	1734.840	0.384	26	0.175	K.GKVEILVNDQGNR.I
R1/RRR1-6/3	1441.993	1442.603	-1120.208	0.449	1235.197	0.385	22	0.116	K.GKVEILVNDQGNR.I
R1/RRR1-6/3	1395.981	1396.613	-1172.216	0.520	1162.046	0.310	25	0.091	K.FEELNIDLFKK.T
R1/RRR1-14/2	1109.031	1108.293	-236.612	0.468	1261.874	0.476	15	0.251	K.M*EGLLWGASK.L
R1/RRR1-14/2	1145.900	1146.276	-329.155	0.489	1223.886	0.472	20	0.249	R.LSGVTADGQGIK.V
R1/RRR1-14/2	1146.965	1146.276	-272.273	0.509	1218.818	0.471	20	0.248	R.LSGVTADGQGIK.V
R1/RRR1-14/2	1108.345	1108.293	47.034	0.384	1347.310	0.414	15	0.244	K.M*EGLLWGASK.L
R1/RRR1-14/2	1272.335	1272.480	-113.899	0.465	1105.962	0.480	16	0.240	R.WFTHIDALLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1108.252	1108.293	-36.593	0.388	1237.485	0.412	15	0.235	K.M*EGLLWGASK.L
R1/RRR1-14/2	1151.107	1151.338	-200.561	0.499	1146.537	0.414	15	0.232	K.KLDEYLLTR.S
R1/RRR1-14/2	1146.007	1146.276	-235.856	0.463	995.176	0.464	19	0.229	R.LSGVTADGQGIK.V
R1/RRR1-13/2	1151.126	1151.338	-184.604	0.469	999.382	0.394	15	0.220	K.KLDEYLLTR.S
R1/RRR1-14/2	1271.469	1272.480	-1586.236	0.425	927.835	0.432	16	0.219	R.WFTHIDALLR.L
R1/RRR1-22/2	1745.786	1745.866	-46.330	0.488	534.855	0.567	22	0.218	K.VESTAVPSASTPDVADAK.A
R1/RRR1-14/2	1151.044	1151.338	-256.098	0.478	1073.996	0.349	15	0.216	K.KLDEYLLTR.S
R1/RRR1-14/2	1746.204	1745.866	193.898	0.481	540.764	0.540	22	0.214	K.VESTAVPSASTPDVADAK.A
R1/RRR1-22/2	1745.398	1745.866	-268.921	0.487	579.741	0.531	22	0.214	K.VESTAVPSASTPDVADAK.A
R1/RRR1-14/2	1746.253	1745.866	222.288	0.441	496.258	0.567	21	0.214	K.VESTAVPSASTPDVADAK.A
R1/RRR1-14/2	1745.474	1745.866	-225.559	0.458	556.522	0.518	22	0.212	K.VESTAVPSASTPDVADAK.A
R1/RRR1-14/2	1271.709	1272.480	-1396.752	0.454	766.337	0.411	16	0.211	R.WFTHIDALLR.L
R1/RRR1-14/2	1151.151	1151.338	-162.264	0.450	952.935	0.347	14	0.209	K.KLDEYLLTR.S
R1/RRR1-14/2	1022.457	1023.165	-1675.219	0.372	1077.059	0.299	13	0.205	K.LDEYLLTR.S
R1/RRR1-13/2	1107.631	1108.293	-1504.905	0.348	858.358	0.222	15	0.190	K.M*EGLLWGASK.L
R1/RRR1-20/2	1152.315	1151.338	-19.722	0.336	465.962	0.242	12	0.187	-.KLDEYLLTR.-
R1/RRR1-14/3	1272.649	1272.480	133.417	0.346	1017.881	0.387	19	0.094	R.WFTHIDALLR.L
R1/RRR1-14/3	1272.801	1272.480	253.451	0.367	861.539	0.393	19	0.086	-.WFTHIDALLR.-
R1/RRR1-14/3	1272.535	1272.480	43.372	0.273	684.038	0.312	16	0.075	R.WFTHIDALLR.L
R1/RRR1-12/3	1940.827	1940.190	-187.943	0.573	3344.943	0.590	37	0.778	K.VLIAVADNVGSNQLQEIR.K
R1/RRR1-12/3	1940.857	1940.190	-172.422	0.554	2956.731	0.620	35	0.644	K.VLIAVADNVGSNQLQEIR.K
R1/RRR1-12/3	1940.921	1940.190	-139.109	0.578	2745.553	0.607	35	0.556	K.VLIAVADNVGSNQLQEIR.K
R1/RRR1-12/2	1744.441	1743.942	286.880	0.620	2524.432	0.643	32	0.521	K.FAVAAPVAADSGAAAPSAAK.E
R1/RRR1-12/2	1744.264	1743.942	185.550	0.621	2427.462	0.656	32	0.504	K.FAVAAPVAADSGAAAPSAAK.E
R1/RRR1-12/2	1939.635	1940.190	-804.358	0.540	2345.385	0.531	27	0.433	K.VLIAVADNVGSNQLQEIR.K
R1/RRR1-12/2	1940.727	1940.190	-239.710	0.609	2145.240	0.571	26	0.405	K.VLIAVADNVGSNQLQEIR.K
R1/RRR1-12/2	1743.337	1743.942	-922.950	0.535	1852.896	0.626	29	0.371	K.FAVAAPVAADSGAAAPSAAK.E
R1/RRR1-12/2	1939.197	1940.190	-1031.078	0.493	2077.585	0.476	27	0.360	K.VLIAVADNVGSNQLQEIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1413.251	1412.697	-316.443	0.482	1242.056	0.482	18	0.248	K.GTVEIITPVELIK.K
R1/RRR1-12/2	1411.216	1411.619	-286.273	0.483	1192.184	0.476	16	0.244	K.KLCQLLDEYTK.V
R1/RRR1-12/2	1284.189	1283.446	-201.133	0.550	1309.091	0.415	16	0.242	K.LCQLLDEYTK.V
R1/RRR1-12/1	1411.827	1412.697	-1328.582	0.145	599.256	0.265	13	0.242	-.GTVEIITPVELIK.-
R1/RRR1-14/2	1412.303	1412.697	-279.464	0.420	1103.396	0.439	17	0.228	K.GTVEIITPVELIK.K
R1/RRR1-12/2	1283.202	1283.446	-190.602	0.471	1238.012	0.331	16	0.221	K.LCQLLDEYTK.V
R1/RRR1-12/2	1411.694	1412.697	-1422.862	0.389	949.629	0.427	16	0.215	K.GTVEIITPVELIK.K
R1/RRR1-12/2	1061.983	1062.199	-203.673	0.425	737.357	0.460	17	0.215	K.VGSSESALLAK.L
R1/RRR1-14/2	1061.995	1062.199	-192.488	0.468	782.389	0.440	17	0.215	K.VGSSESALLAK.L
R1/RRR1-12/2	1283.208	1283.446	-185.925	0.448	1180.358	0.300	16	0.212	K.LCQLLDEYTK.V
R1/RRR1-12/2	1412.212	1412.697	-344.506	0.386	982.005	0.371	16	0.208	K.GTVEIITPVELIK.K
R1/RRR1-12/2	1062.048	1062.199	-142.445	0.433	735.625	0.370	17	0.204	K.VGSSESALLAK.L
R1/RRR1-14/2	1412.573	1412.697	-87.943	0.410	766.048	0.406	15	0.204	K.GTVEIITPVELIK.K
R1/RRR1-15/2	1413.428	1412.697	-190.712	0.379	826.752	0.391	15	0.203	K.GTVEIITPVELIK.K
R1/RRR1-12/2	1412.281	1412.697	-295.247	0.324	798.008	0.335	15	0.196	K.GTVEIITPVELIK.K
R1/RRR1-14/2	1412.217	1412.697	-340.603	0.314	439.572	0.392	12	0.192	K.GTVEIITPVELIK.K
R1/RRR1-14/2	1061.220	1062.199	-1870.966	0.274	635.219	0.262	15	0.189	K.VGSSESALLAK.L
R1/RRR1-12/1	1411.883	1412.697	-1288.639	0.128	408.847	0.214	12	0.140	K.GTVEIITPVELIK.K
R1/RRR1-16/2	1406.176	1406.551	-267.159	0.561	3125.012	0.560	25	0.641	K.AM*AQVSQAGSGGLGR.V
R1/RRR1-16/2	1405.738	1406.551	-1293.602	0.565	2468.581	0.557	25	0.468	K.AM*AQVSQAGSGGLGR.V
R1/RRR1-25/2	1406.003	1406.551	-1104.043	0.559	2380.672	0.540	25	0.442	K.AM*AQVSQAGSGGLGR.V
R1/RRR1-25/2	1405.601	1406.551	-1391.635	0.533	2422.802	0.511	25	0.439	K.AM*AQVSQAGSGGLGR.V
R1/RRR1-16/2	1531.273	1531.776	-984.884	0.519	2244.083	0.586	24	0.433	K.AVASINSVLTDLVTK.G
R1/RRR1-16/2	1406.093	1406.551	-326.909	0.551	2322.239	0.509	25	0.417	K.AM*AQVSQAGSGGLGR.V
R1/RRR1-16/2	1531.570	1531.776	-134.831	0.548	2105.481	0.583	23	0.403	K.AVASINSVLTDLVTK.G
R1/RRR1-16/2	1531.253	1531.776	-998.090	0.539	1743.917	0.615	22	0.349	K.AVASINSVLTDLVTK.G
R1/RRR1-16/2	1879.315	1880.077	-940.408	0.516	1413.036	0.603	24	0.297	R.DLSPLTCAQCLSTAVSR.F
R1/RRR1-16/2	1490.086	1490.547	-310.314	0.506	1771.183	0.424	18	0.295	R.FDQYCGAQQGCR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1879.416	1880.077	-886.743	0.550	1280.793	0.642	24	0.291	R.DLSPLTCAQCLSTAVSR.F
R1/RRR1-16/2	1878.748	1880.077	-1243.207	0.471	1322.177	0.562	23	0.274	R.DLSPLTCAQCLSTAVSR.F
R1/RRR1-16/2	1393.065	1393.567	-1081.453	0.477	1395.822	0.488	17	0.266	K.GNNVIYGLVQCR.G
R1/RRR1-16/2	1489.985	1490.547	-1051.125	0.499	1706.623	0.337	18	0.262	R.FDQYCGAQQGCR.I
R1/RRR1-16/2	1241.067	1241.333	-214.929	0.472	1234.661	0.536	21	0.261	K.GSTGVGFATSTAGK.G
R1/RRR1-16/2	1393.037	1393.567	-1101.426	0.487	1307.663	0.437	17	0.245	K.GNNVIYGLVQCR.G
R1/RRR1-16/2	1490.016	1490.547	-1030.231	0.483	1549.223	0.315	18	0.241	R.FDQYCGAQQGCR.I
R1/RRR1-16/2	1240.927	1241.333	-328.320	0.426	1060.297	0.508	20	0.238	K.GSTGVGFATSTAGK.G
R1/RRR1-16/2	1393.074	1393.567	-354.863	0.495	1154.047	0.443	17	0.233	K.GNNVIYGLVQCR.G
R1/RRR1-16/2	1240.479	1241.333	-1499.033	0.339	881.516	0.477	19	0.217	K.GSTGVGFATSTAGK.G
R1/RRR1-25/2	1489.529	1490.547	-1358.539	0.343	1044.827	0.401	14	0.214	R.FDQYCGAQQGCR.I
R1/RRR1-15/2	1531.026	1531.776	-1146.982	0.345	660.692	0.465	16	0.202	K.AVASINSVLTDLVTK.G
R1/RRR1-25/2	1405.520	1406.551	-1449.034	0.371	836.667	0.338	18	0.198	K.AM*AQVSQAGSGGLGR.V
R1/RRR1-16/3	1406.603	1406.551	37.219	0.411	959.002	0.435	26	0.103	K.AM*AQVSQAGSGGLGR.V
R1/RRR1-16/3	1531.524	1531.776	-165.422	0.411	916.317	0.443	25	0.102	K.AVASINSVLTDLVTK.G
R1/RRR1-16/3	1531.872	1531.776	62.405	0.397	652.396	0.400	23	0.084	-.AVASINSVLTDLVTK.-
R1/RRR1-16/3	1406.382	1406.551	-120.394	0.332	940.913	0.253	24	0.073	-.AM*AQVSQAGSGGLGR.-
R1/RRR1-11/2	1818.372	1818.927	-857.595	0.637	3166.228	0.726	28	0.745	R.HETADINTFSWGVANR.G
R1/RRR1-11/2	1818.365	1818.927	-861.638	0.620	2806.044	0.727	27	0.636	R.HETADINTFSWGVANR.G
R1/RRR1-11/2	1819.296	1818.927	203.269	0.630	2729.500	0.662	27	0.581	R.HETADINTFSWGVANR.G
R1/RRR1-11/2	1812.042	1811.095	-29.319	0.615	2272.093	0.590	25	0.440	K.IIAEYIWIGGSGM*DLR.S
R1/RRR1-11/2	1810.478	1811.095	-895.506	0.547	2167.893	0.495	24	0.383	K.IIAEYIWIGGSGM*DLR.S
R1/RRR1-11/2	1627.162	1627.700	-947.762	0.492	1971.514	0.583	22	0.383	R.HKEHISAYGEGNER.R
R1/RRR1-11/1	1101.551	1102.220	-1519.966	0.150	583.483	0.418	12	0.259	R.TLSGPVTDPSK.L
R1/RRR1-11/3	1627.584	1627.700	-71.519	0.529	1942.790	0.519	30	0.258	R.HKEHISAYGEGNER.R
R1/RRR1-11/3	1627.720	1627.700	12.207	0.539	1845.681	0.536	29	0.248	R.HKEHISAYGEGNER.R
R1/RRR1-10/2	1818.658	1818.927	-148.554	0.474	1138.639	0.500	20	0.241	R.HETADINTFSWGVANR.G
R1/RRR1-11/2	1809.691	1811.095	-1331.939	0.301	1500.311	0.298	21	0.232	K.IIAEYIWIGGSGM*DLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1627.657	1627.700	-26.044	0.498	1822.504	0.469	28	0.218	R.HKEHISAYGEGNER.R
R1/RRR1-10/2	1819.249	1818.927	177.363	0.407	934.116	0.405	19	0.209	R.HETADINTFSWGVANR.G
R1/RRR1-11/2	1440.152	1440.667	-1055.190	0.397	898.275	0.373	17	0.204	-.TLSGPVTDPSKLPK.-
R1/RRR1-11/3	1627.750	1627.700	31.274	0.537	1620.010	0.497	28	0.194	R.HKEHISAYGEGNER.R
R1/RRR1-10/2	1440.319	1440.667	-242.576	0.316	638.016	0.348	15	0.191	-.TLSGPVTDPSKLPK.-
R1/RRR1-11/2	1440.223	1440.667	-308.901	0.354	654.579	0.315	16	0.190	-.TLSGPVTDPSKLPK.-
R1/RRR1-11/2	1441.213	1440.667	-315.995	0.403	709.952	0.268	16	0.186	-.TLSGPVTDPSKLPK.-
R1/RRR1-11/3	1400.192	1399.555	-260.106	0.534	1598.294	0.431	25	0.166	K.SM*RNDGGYEIIK.S
R1/RRR1-11/3	1628.168	1627.700	288.559	0.489	1283.266	0.403	24	0.127	R.HKEHISAYGEGNER.R
R1/RRR1-10/3	1627.705	1627.700	3.293	0.453	1128.017	0.471	25	0.127	R.HKEHISAYGEGNER.R
R1/RRR1-11/3	1818.855	1818.927	-39.697	0.493	1179.750	0.386	24	0.117	-.HETADINTFSWGVANR.-
R1/RRR1-11/3	1818.754	1818.927	-95.641	0.470	976.513	0.415	24	0.105	R.HETADINTFSWGVANR.G
R1/RRR1-11/3	1399.070	1399.555	-347.697	0.519	1018.215	0.372	23	0.097	K.SM*RNDGGYEIIK.S
R1/RRR1-11/3	1400.776	1399.555	158.241	0.465	939.984	0.330	24	0.085	K.SM*RNDGGYEIIK.S
R1/RRR1-11/3	1626.386	1627.700	-1427.012	0.386	763.800	0.287	21	0.081	R.HKEHISAYGEGNER.R
R1/RRR1-11/3	1626.839	1627.700	-1147.098	0.387	869.951	0.269	24	0.079	R.HKEHISAYGEGNER.R
R1/RRR1-11/3	1398.654	1399.555	-1363.250	0.349	689.943	0.239	22	0.075	K.SM*RNDGGYEIIK.S
R1/RRR1-15/2	1800.286	1801.010	-960.537	0.522	1918.753	0.466	23	0.332	R.DGPQLYM*IEPSGVSYK.Y
R1/RRR1-15/2	1083.693	1084.248	-1439.219	0.454	824.113	0.589	16	0.240	K.VPADLLEQAK.V
R1/RRR1-15/2	1084.135	1084.248	-104.082	0.423	878.826	0.565	16	0.238	K.VPADLLEQAK.V
R1/RRR1-15/2	1159.906	1160.303	-343.126	0.435	1052.717	0.495	18	0.236	K.AVDNSGTVVGIK.C
R1/RRR1-15/2	1086.078	1085.234	-144.705	0.520	1054.083	0.433	14	0.227	R.VFQVEYATK.A
R1/RRR1-15/2	1084.838	1084.248	-378.945	0.471	787.896	0.511	16	0.226	K.VPADLLEQAK.V
R1/RRR1-15/2	1085.133	1085.234	-93.718	0.444	1034.080	0.425	14	0.224	R.VFQVEYATK.A
R1/RRR1-15/2	1159.353	1160.303	-1686.935	0.355	837.040	0.469	17	0.215	K.AVDNSGTVVGIK.C
R1/RRR1-15/2	1159.442	1160.303	-1609.824	0.348	859.491	0.442	17	0.212	K.AVDNSGTVVGIK.C
R1/RRR1-15/2	826.898	826.962	-78.270	0.384	356.335	0.471	11	0.204	K.YFGAALGK.G
R1/RRR1-15/2	826.996	826.962	40.771	0.306	396.688	0.361	12	0.196	K.YFGAALGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1086.281	1085.234	42.762	0.290	763.286	0.306	13	0.193	R.VFQVEYATK.A
R1/RRR1-16/2	1083.804	1084.248	-410.599	0.298	583.625	0.335	13	0.193	K.VPADLLEQAK.V
R1/RRR1-15/2	1349.970	1350.435	-345.086	0.360	1276.984	0.436	18	0.164	K.VAAQAALEEM*DAD.-
R1/RRR1-15/2	1349.885	1350.435	-1151.534	0.298	935.807	0.431	17	0.112	K.VAAQAALEEM*DAD.-
R1/RRR1-15/2	1349.957	1350.435	-355.066	0.269	1060.243	0.302	17	0.110	K.VAAQAALEEM*DAD.-
R1/RRR1-14/2	1074.094	1074.255	-150.195	0.454	1738.830	0.530	17	0.314	R.TFLLSLVGSH.-
R1/RRR1-13/2	1075.200	1074.255	-50.629	0.558	1641.923	0.598	17	0.296	R.TFLLSLVGSH.-
R1/RRR1-14/2	1115.346	1115.393	-42.659	0.459	1541.814	0.502	16	0.289	K.LLLAYVGIPR.Y
R1/RRR1-14/2	1074.187	1074.255	-62.987	0.475	1606.466	0.545	17	0.271	R.TFLLSLVGSH.-
R1/RRR1-14/2	1372.354	1372.661	-224.606	0.521	1439.990	0.425	16	0.254	K.AM*LLWILDPAGR.D
R1/RRR1-14/2	1608.047	1608.692	-1025.727	0.500	992.155	0.576	21	0.247	K.SLAEAIHSETSGSYR.T
R1/RRR1-14/2	1189.946	1190.286	-286.104	0.445	1529.373	0.332	17	0.244	R.EALSGDTIDLR.A
R1/RRR1-14/2	1608.152	1608.692	-960.108	0.482	1118.838	0.495	22	0.241	K.SLAEAIHSETSGSYR.T
R1/RRR1-13/2	1189.480	1190.286	-1522.954	0.334	1662.955	0.218	18	0.234	R.EALSGDTIDLR.A
R1/RRR1-14/2	1189.402	1190.286	-1588.317	0.344	1115.890	0.365	15	0.217	-.EALSGDTIDLR.-
R1/RRR1-14/2	1114.908	1115.393	-436.702	0.480	927.522	0.432	14	0.217	K.LLLAYVGIPR.Y
R1/RRR1-14/2	1372.360	1372.661	-219.877	0.462	1235.120	0.300	17	0.214	-.AM*LLWILDPAGR.-
R1/RRR1-13/2	1021.090	1021.152	-60.806	0.369	1076.978	0.323	13	0.210	R.ALIQQEYR.T
R1/RRR1-13/2	1189.453	1190.286	-1545.841	0.354	1016.528	0.310	16	0.204	R.EALSGDTIDLR.A
R1/RRR1-14/2	1020.481	1021.152	-1641.928	0.347	809.376	0.364	12	0.204	R.ALIQQEYR.T
R1/RRR1-14/2	1189.517	1190.286	-1491.719	0.333	950.211	0.329	15	0.202	R.EALSGDTIDLR.A
R1/RRR1-13/2	1020.312	1021.152	-1808.279	0.282	787.984	0.372	12	0.201	R.ALIQQEYR.T
R1/RRR1-13/2	1021.335	1021.152	180.285	0.365	966.499	0.273	12	0.198	R.ALIQQEYR.T
R1/RRR1-13/2	1074.139	1074.255	-107.786	0.441	1206.774	0.533	16	0.168	R.TFLLSLVGSH.-
R1/RRR1-5/3	1880.917	1880.066	-79.125	0.502	1332.058	0.532	25	0.174	R.M*KEGQSEIYYITGESK.K
R1/RRR1-5/3	1879.336	1880.066	-923.032	0.461	1376.165	0.436	26	0.147	R.M*KEGQSEIYYITGESK.K
R1/RRR1-5/3	1879.728	1880.066	-180.167	0.452	1062.146	0.444	23	0.119	R.M*KEGQSEIYYITGESK.K
R1/RRR1-15/2	1819.935	1820.945	-1107.660	0.546	2152.753	0.576	27	0.410	K.NPGEQSHAANAGLDIAVR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1819.800	1820.945	-1181.750	0.535	1950.169	0.611	27	0.384	K.NPGEQSHAANAGLDIAVR.L
R1/RRR1-15/3	1822.058	1820.945	62.310	0.581	2105.860	0.579	33	0.345	K.NPGEQSHAANAGLDIAVR.L
R1/RRR1-15/2	1821.446	1820.945	-274.565	0.564	1682.950	0.576	26	0.327	K.NPGEQSHAANAGLDIAVR.L
R1/RRR1-15/3	1822.191	1820.945	135.881	0.579	1966.263	0.542	32	0.294	K.NPGEQSHAANAGLDIAVR.L
R1/RRR1-15/2	1310.091	1310.398	-234.913	0.491	1551.410	0.454	20	0.278	R.LPDATQGSDHLR.Q
R1/RRR1-15/2	1534.314	1534.657	-224.842	0.472	1342.542	0.548	20	0.274	R.LAWHSAGTFDVSSR.T
R1/RRR1-15/2	1310.056	1310.398	-262.210	0.462	1608.778	0.413	20	0.274	R.LPDATQGSDHLR.Q
R1/RRR1-15/2	1535.123	1534.657	303.984	0.557	1333.327	0.528	21	0.270	R.LAWHSAGTFDVSSR.T
R1/RRR1-15/2	1534.080	1534.657	-1031.367	0.460	1359.015	0.512	20	0.267	R.LAWHSAGTFDVSSR.T
R1/RRR1-15/2	1310.008	1310.398	-299.137	0.496	1500.787	0.404	19	0.258	R.LPDATQGSDHLR.Q
R1/RRR1-15/2	1600.304	1600.751	-280.297	0.454	786.250	0.559	22	0.230	K.SYPTVSDEYLAAVGK.A
R1/RRR1-15/2	1601.258	1600.751	-308.574	0.438	574.010	0.539	22	0.218	K.SYPTVSDEYLAAVGK.A
R1/RRR1-15/2	1600.348	1600.751	-252.594	0.375	523.552	0.528	21	0.211	K.SYPTVSDEYLAAVGK.A
R1/RRR1-15/3	1820.900	1820.945	-24.456	0.530	1539.809	0.513	31	0.197	K.NPGEQSHAANAGLDIAVR.L
R1/RRR1-15/3	1534.557	1534.657	-65.841	0.487	1334.907	0.467	27	0.145	R.LAWHSAGTFDVSSR.T
R1/RRR1-15/3	1534.833	1534.657	114.734	0.509	1234.154	0.440	27	0.127	R.LAWHSAGTFDVSSR.T
R1/RRR1-15/3	1534.387	1534.657	-176.804	0.468	1099.542	0.418	25	0.111	R.LAWHSAGTFDVSSR.T
R1/RRR1-14/2	1460.341	1460.637	-203.323	0.550	2111.868	0.469	20	0.363	K.NM*LANEGIGSFYK.G
R1/RRR1-14/2	1460.186	1460.637	-309.666	0.522	2157.433	0.438	20	0.361	K.NM*LANEGIGSFYK.G
R1/RRR1-14/2	1461.118	1460.637	329.899	0.577	2020.536	0.459	20	0.343	K.NM*LANEGIGSFYK.G
R1/RRR1-14/2	1328.338	1328.581	-183.480	0.530	1621.281	0.468	18	0.286	R.IIADEGVLALWK.G
R1/RRR1-14/2	1302.151	1302.459	-237.098	0.505	1551.792	0.455	22	0.278	K.IQLGEGSAAQVTK.N
R1/RRR1-14/2	1328.223	1328.581	-270.330	0.515	1464.672	0.475	20	0.273	R.IIADEGVLALWK.G
R1/RRR1-14/2	1302.153	1302.459	-235.969	0.497	1437.951	0.477	21	0.270	K.IQLGEGSAAQVTK.N
R1/RRR1-14/2	1329.204	1328.581	-284.961	0.435	1239.536	0.535	19	0.262	R.IIADEGVLALWK.G
R1/RRR1-14/2	1301.953	1302.459	-1160.143	0.465	1189.245	0.495	20	0.249	K.IQLGEGSAAQVTK.N
R1/RRR1-14/2	1347.354	1347.523	-126.469	0.458	1162.626	0.429	19	0.234	R.M*QADSTLPIAQR.R
R1/RRR1-15/2	1329.195	1328.581	-291.226	0.480	1009.014	0.473	17	0.230	R.IIADEGVLALWK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1327.934	1328.581	-1244.675	0.372	1360.116	0.335	18	0.230	R.IIADEGVLALWK.G
R1/RRR1-14/2	1347.246	1347.523	-206.361	0.471	1209.100	0.380	19	0.227	R.M*QADSTLPIAQR.R
R1/RRR1-12/2	1328.680	1328.581	74.124	0.378	1199.326	0.372	18	0.225	R.IIADEGVLALWK.G
R1/RRR1-14/2	1347.276	1347.523	-184.365	0.452	859.253	0.421	17	0.212	R.M*QADSTLPIAQR.R
R1/RRR1-14/2	992.037	992.115	-79.557	0.361	993.667	0.329	13	0.207	K.NAFHALYR.I
R1/RRR1-15/2	1329.667	1328.581	64.308	0.412	677.190	0.382	16	0.202	R.IIADEGVLALWK.G
R1/RRR1-14/2	991.997	992.115	-119.673	0.374	949.418	0.287	13	0.200	K.NAFHALYR.I
R1/RRR1-14/2	991.351	992.115	-1784.718	0.337	780.260	0.281	13	0.195	K.NAFHALYR.I
R1/RRR1-14/3	1529.421	1529.764	-224.850	0.465	1671.002	0.432	28	0.186	K.VKIQLGEGSAAQVTK.N
R1/RRR1-14/2	1301.701	1302.459	-1354.693	0.190	148.115	0.460	12	0.185	-.IQLGEGSAAQVTK.-
R1/RRR1-4/2	1197.124	1197.416	-244.808	0.488	1568.216	0.436	17	0.274	R.GRLNVLGNVVR.K
R1/RRR1-4/2	1699.497	1698.943	-262.928	0.542	1367.275	0.470	20	0.259	R.LIWSTQFENFLATK.W
R1/RRR1-4/2	1503.470	1503.680	-140.201	0.484	1231.897	0.399	19	0.229	K.LLGTGEVSKEDVQK.I
R1/RRR1-4/2	1196.541	1197.416	-1571.166	0.487	1073.621	0.410	16	0.222	R.GRLNVLGNVVR.K
R1/RRR1-4/2	983.712	984.178	-475.217	0.431	968.102	0.411	14	0.218	R.LNVLGNVVR.K
R1/RRR1-4/2	1780.167	1779.023	81.116	0.536	931.214	0.428	20	0.217	R.VEQLCPFPYDLIQR.E
R1/RRR1-4/2	1373.563	1374.524	-1431.698	0.382	1223.648	0.315	16	0.216	R.DWLSAYWTGFK.S
R1/RRR1-4/2	983.688	984.178	-499.125	0.459	842.336	0.371	13	0.206	R.LNVLGNVVR.K
R1/RRR1-4/2	1778.463	1779.023	-879.386	0.465	811.957	0.388	19	0.206	R.VEQLCPFPYDLIQR.E
R1/RRR1-4/2	1374.197	1374.524	-238.388	0.258	1242.619	0.223	16	0.201	R.DWLSAYWTGFK.S
R1/RRR1-4/2	1466.349	1466.583	-160.032	0.369	752.782	0.366	16	0.199	K.YHLGTSYDRPTR.G
R1/RRR1-4/2	1779.861	1779.023	-91.120	0.466	584.796	0.369	17	0.197	R.VEQLCPFPYDLIQR.E
R1/RRR1-4/2	1778.657	1779.023	-205.932	0.474	706.573	0.344	18	0.196	R.VEQLCPFPYDLIQR.E
R1/RRR1-3/2	1780.714	1779.023	-173.860	0.430	569.070	0.354	16	0.194	R.VEQLCPFPYDLIQR.E
R1/RRR1-4/2	984.216	984.178	38.924	0.448	794.455	0.276	13	0.193	R.LNVLGNVVR.K
R1/RRR1-3/2	1196.742	1197.416	-1402.810	0.346	626.369	0.313	13	0.190	R.GRLNVLGNVVR.K
R1/RRR1-4/2	1374.052	1374.524	-344.539	0.294	1044.889	0.202	14	0.189	R.DWLSAYWTGFK.S
R1/RRR1-4/2	1465.597	1466.583	-1359.337	0.315	458.136	0.314	13	0.187	-.YHLGTSYDRPTR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1779.900	1779.023	-69.174	0.446	410.323	0.367	12	0.186	-.VEQLCPFPYDLIQR.-
R1/RRR1-4/2	1466.340	1466.583	-166.045	0.354	446.115	0.275	13	0.186	-.YHLGTSYDRPTR.-
R1/RRR1-6/2	1857.602	1858.166	-844.493	0.575	2466.266	0.557	25	0.469	K.QIVVSCGTLSSPLVLQR.S
R1/RRR1-6/2	1857.669	1858.166	-268.289	0.566	2254.024	0.551	25	0.420	K.QIVVSCGTLSSPLVLQR.S
R1/RRR1-6/2	1858.553	1858.166	208.659	0.569	1812.859	0.536	22	0.331	K.QIVVSCGTLSSPLVLQR.S
R1/RRR1-6/2	1317.886	1318.328	-336.275	0.493	1550.458	0.532	18	0.297	R.ASASDYDDFQAK.G
R1/RRR1-6/2	1317.947	1318.328	-289.345	0.487	1411.482	0.520	18	0.276	R.ASASDYDDFQAK.G
R1/RRR1-6/2	1317.640	1318.328	-1284.877	0.456	1277.968	0.533	17	0.264	R.ASASDYDDFQAK.G
R1/RRR1-6/2	1950.647	1950.184	238.288	0.596	889.103	0.640	20	0.250	K.VSFGNYTYPIAWDFLR.A
R1/RRR1-6/2	1949.518	1950.184	-857.306	0.549	838.222	0.614	20	0.241	K.VSFGNYTYPIAWDFLR.A
R1/RRR1-1/2	1950.773	1950.184	-211.487	0.490	610.633	0.572	17	0.216	K.VSFGNYTYPIAWDFLR.A
R1/RRR1-6/2	1113.141	1113.248	-96.530	0.368	577.480	0.531	14	0.213	R.DLHGFEGPIK.V
R1/RRR1-6/2	1113.194	1113.248	-48.681	0.325	637.771	0.483	14	0.207	R.DLHGFEGPIK.V
R1/RRR1-6/2	1257.171	1257.377	-164.455	0.379	851.736	0.389	16	0.207	K.TASFYEARPSK.W
R1/RRR1-6/2	1037.234	1038.182	-1883.894	0.375	773.626	0.413	13	0.206	R.LANLDHNLK.V
R1/RRR1-6/2	1257.260	1257.377	-93.548	0.388	747.591	0.396	15	0.204	K.TASFYEARPSK.W
R1/RRR1-6/2	1038.095	1038.182	-84.519	0.419	634.046	0.402	13	0.203	R.LANLDHNLK.V
R1/RRR1-6/2	1113.141	1113.248	-95.980	0.372	722.600	0.381	15	0.203	R.DLHGFEGPIK.V
R1/RRR1-6/2	1257.945	1257.377	-344.415	0.411	452.583	0.367	12	0.193	K.TASFYEARPSK.W
R1/RRR1-6/3	1949.773	1950.184	-211.351	0.404	879.736	0.421	21	0.098	K.VSFGNYTYPIAWDFLR.A
R1/RRR1-6/3	1113.724	1113.248	429.159	0.472	1316.216	0.177	22	0.075	-.DLHGFEGPIK.-
R1/RRR1-6/3	1113.261	1113.248	11.799	0.506	988.880	0.230	20	0.072	-.DLHGFEGPIK.-
R1/RRR1-5/3	1113.406	1113.248	142.766	0.438	857.723	0.185	18	0.056	-.DLHGFEGPIK.-
R1/RRR1-6/2	1442.146	1441.632	-338.327	0.564	2202.748	0.608	22	0.431	K.AAM*LVAEDLGYSGK.A
R1/RRR1-6/2	1441.338	1441.632	-204.387	0.528	2002.688	0.567	21	0.376	K.AAM*LVAEDLGYSGK.A
R1/RRR1-6/2	1441.130	1441.632	-1045.507	0.533	1951.755	0.569	21	0.368	K.AAM*LVAEDLGYSGK.A
R1/RRR1-6/2	1425.034	1425.633	-1125.411	0.466	1904.899	0.556	20	0.354	K.AAMLVAEDLGYSGK.A
R1/RRR1-6/2	1614.228	1614.734	-936.015	0.487	2048.506	0.460	20	0.348	K.AVFDELQYSADDIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1424.875	1425.633	-1237.415	0.449	1852.485	0.512	19	0.331	K.AAMLVAEDLGYSGK.A
R1/RRR1-6/2	1614.252	1614.734	-299.946	0.523	1889.683	0.458	20	0.320	K.AVFDELQYSADDIK.A
R1/RRR1-6/2	1613.801	1614.734	-1201.802	0.408	2062.252	0.331	21	0.311	K.AVFDELQYSADDIK.A
R1/RRR1-6/2	1424.602	1425.633	-1429.651	0.376	1671.835	0.500	19	0.300	K.AAMLVAEDLGYSGK.A
R1/RRR1-1/2	1614.388	1614.734	-214.979	0.441	1680.992	0.335	19	0.259	K.AVFDELQYSADDIK.A
R1/RRR1-1/2	1614.193	1614.734	-957.500	0.444	1521.058	0.364	18	0.247	K.AVFDELQYSADDIK.A
R1/RRR1-6/2	1901.537	1901.115	222.873	0.526	622.500	0.651	21	0.231	K.YALPGNLTAGLQHGSWSK.F
R1/RRR1-6/2	1900.712	1901.115	-212.355	0.500	702.489	0.620	21	0.230	K.YALPGNLTAGLQHGSWSK.F
R1/RRR1-6/2	1250.889	1251.391	-1204.375	0.554	877.962	0.488	18	0.228	K.VPEYNAPGEM*K.L
R1/RRR1-6/2	1250.868	1251.391	-1221.525	0.515	877.019	0.452	18	0.221	K.VPEYNAPGEM*K.L
R1/RRR1-6/2	1545.235	1545.728	-320.078	0.437	700.460	0.404	19	0.201	K.HGVVDDRLNVHGVK.G
R1/RRR1-6/2	1031.049	1031.190	-137.347	0.407	838.296	0.251	13	0.193	K.AIEEWVKR.H
R1/RRR1-6/2	1030.943	1031.190	-240.090	0.398	843.151	0.225	12	0.188	-.AIEEWVKR.-
R1/RRR1-14/2	1407.070	1407.463	-279.720	0.497	1867.682	0.435	19	0.314	K.TVDSEELTVEER.N
R1/RRR1-14/2	1407.139	1407.463	-230.632	0.435	1761.869	0.416	19	0.293	K.TVDSEELTVEER.N
R1/RRR1-14/2	1814.605	1814.078	-261.363	0.556	1132.527	0.522	23	0.246	K.AAQDIALAELPPTHPIR.L
R1/RRR1-14/2	1406.624	1407.463	-1310.744	0.368	1591.829	0.305	18	0.245	K.TVDSEELTVEER.N
R1/RRR1-14/2	1813.520	1814.078	-861.577	0.523	1084.427	0.499	23	0.238	K.AAQDIALAELPPTHPIR.L
R1/RRR1-14/2	1681.549	1681.869	-190.520	0.432	917.024	0.537	21	0.231	K.LLDSHLVPSSTAPESK.V
R1/RRR1-14/2	1229.005	1229.342	-275.542	0.425	1109.488	0.414	17	0.226	K.DAAENTM*VAYK.A
R1/RRR1-14/2	1228.521	1229.342	-1486.839	0.375	1163.657	0.387	16	0.224	K.DAAENTM*VAYK.A
R1/RRR1-14/2	1814.540	1814.078	255.285	0.540	917.608	0.490	21	0.222	K.AAQDIALAELPPTHPIR.L
R1/RRR1-14/2	1228.964	1229.342	-308.826	0.446	965.194	0.436	16	0.220	K.DAAENTM*VAYK.A
R1/RRR1-14/2	1681.309	1681.869	-930.274	0.410	692.601	0.506	19	0.212	K.LLDSHLVPSSTAPESK.V
R1/RRR1-14/2	1681.427	1681.869	-263.351	0.411	522.552	0.548	17	0.208	K.LLDSHLVPSSTAPESK.V
R1/RRR1-14/3	1813.432	1814.078	-910.407	0.395	1345.112	0.398	32	0.126	K.AAQDIALAELPPTHPIR.L
R1/RRR1-14/3	1813.146	1814.078	-1068.766	0.253	1304.548	0.381	29	0.117	K.AAQDIALAELPPTHPIR.L
R1/RRR1-14/3	1813.552	1814.078	-843.915	0.420	976.364	0.481	29	0.116	K.AAQDIALAELPPTHPIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/3	1813.587	1814.078	-271.712	0.298	1252.428	0.375	29	0.112	K.AAQDIALAELPPTHPIR.L
R1/RRR1-14/3	1813.767	1814.078	-172.049	0.333	1197.628	0.342	30	0.101	K.AAQDIALAELPPTHPIR.L
R1/RRR1-14/3	1813.888	1814.078	-105.112	0.342	1081.368	0.281	31	0.083	K.AAQDIALAELPPTHPIR.L
R1/RRR1-16/2	1226.167	1226.449	-231.121	0.462	1456.926	0.530	17	0.285	K.LLANILYSYR.G
R1/RRR1-16/2	1226.284	1226.449	-134.850	0.566	1401.168	0.533	17	0.281	K.LLANILYSYR.G
R1/RRR1-17/2	1384.126	1384.476	-253.574	0.381	1588.143	0.443	20	0.277	K.GPGLYYVDSEGAR.L
R1/RRR1-16/2	1226.281	1226.449	-137.646	0.560	1380.661	0.520	17	0.276	K.LLANILYSYR.G
R1/RRR1-16/2	1333.193	1333.429	-177.210	0.493	1377.842	0.488	19	0.266	K.LSGDDVGELHYK.Y
R1/RRR1-16/2	1333.053	1333.429	-282.485	0.522	1281.399	0.477	18	0.253	K.LSGDDVGELHYK.Y
R1/RRR1-16/2	1332.575	1333.429	-1394.881	0.455	1170.823	0.513	18	0.250	K.LSGDDVGELHYK.Y
R1/RRR1-16/2	1373.297	1373.518	-161.118	0.470	1250.894	0.478	19	0.249	R.ASM*GGYISSQTVR.K
R1/RRR1-16/2	1372.436	1373.518	-1521.331	0.361	1211.740	0.477	19	0.243	R.ASM*GGYISSQTVR.K
R1/RRR1-16/2	1372.966	1373.518	-1133.360	0.496	1046.029	0.499	20	0.239	R.ASM*GGYISSQTVR.K
R1/RRR1-17/2	1374.038	1373.518	-350.027	0.518	961.125	0.524	19	0.237	R.ASM*GGYISSQTVR.K
R1/RRR1-17/2	1494.744	1494.695	32.982	0.503	978.729	0.477	21	0.232	R.YVM*PVEEAAELAR.R
R1/RRR1-17/2	1373.065	1373.518	-330.479	0.458	1005.611	0.470	20	0.230	R.ASM*GGYISSQTVR.K
R1/RRR1-17/2	1373.022	1373.518	-361.968	0.475	903.185	0.507	19	0.230	R.ASM*GGYISSQTVR.K
R1/RRR1-17/2	1384.093	1384.476	-277.375	0.415	1207.621	0.400	18	0.229	K.GPGLYYVDSEGAR.L
R1/RRR1-17/2	1493.947	1494.695	-1173.215	0.450	1007.677	0.401	21	0.220	R.YVM*PVEEAAELAR.R
R1/RRR1-16/2	1494.713	1494.695	12.013	0.418	819.729	0.413	19	0.211	R.YVM*PVEEAAELAR.R
R1/RRR1-16/2	969.934	970.107	-178.948	0.370	777.240	0.409	13	0.209	R.AIYQATFR.D
R1/RRR1-17/2	1226.114	1226.449	-274.070	0.430	642.838	0.448	13	0.208	K.LLANILYSYR.G
R1/RRR1-17/2	1493.958	1494.695	-1166.241	0.394	765.509	0.404	19	0.208	R.YVM*PVEEAAELAR.R
R1/RRR1-17/2	1226.299	1226.449	-123.266	0.354	728.080	0.412	13	0.205	K.LLANILYSYR.G
R1/RRR1-16/2	969.562	970.107	-1597.648	0.322	829.242	0.361	13	0.203	R.AIYQATFR.D
R1/RRR1-17/2	1226.170	1226.449	-228.524	0.363	648.155	0.382	12	0.199	K.LLANILYSYR.G
R1/RRR1-16/2	969.593	970.107	-1565.649	0.273	830.795	0.343	13	0.198	R.AIYQATFR.D
R1/RRR1-16/2	1493.997	1494.695	-1140.068	0.336	585.129	0.373	17	0.198	R.YVM*PVEEAAELAR.R

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1493.548	1494.695	-1442.086	0.310	817.755	0.298	19	0.196	R.YVM*PVEEAAELAR.R
R1/RRR1-12/2	1603.593	1603.887	-184.282	0.542	2238.995	0.612	23	0.444	K.HIVQDLKPEIPVSK.N
R1/RRR1-12/2	1603.481	1603.887	-254.162	0.524	1965.132	0.582	22	0.378	K.HIVQDLKPEIPVSK.N
R1/RRR1-12/2	1603.330	1603.887	-974.297	0.530	1934.719	0.593	22	0.376	K.HIVQDLKPEIPVSK.N
R1/RRR1-12/2	1249.035	1249.398	-291.194	0.539	2097.830	0.467	19	0.361	R.LWDLSTGVTTR.R
R1/RRR1-12/3	1940.138	1940.104	17.151	0.455	2346.308	0.501	34	0.358	R.FSPNTFQPTIVSGSWDR.T
R1/RRR1-12/2	1417.156	1417.589	-305.981	0.495	1803.929	0.537	19	0.334	K.DGVTLLWDLAEGK.R
R1/RRR1-12/2	1940.418	1940.104	162.186	0.510	1370.787	0.604	25	0.293	R.FSPNTFQPTIVSGSWDR.T
R1/RRR1-12/2	1417.307	1417.589	-199.433	0.397	1617.839	0.488	18	0.291	K.DGVTLLWDLAEGK.R
R1/RRR1-12/2	1417.221	1417.589	-259.920	0.506	1634.966	0.470	19	0.290	K.DGVTLLWDLAEGK.R
R1/RRR1-12/2	1248.761	1249.398	-1315.157	0.469	1545.285	0.488	18	0.285	R.LWDLSTGVTTR.R
R1/RRR1-12/2	1249.164	1249.398	-187.660	0.521	1542.690	0.487	18	0.285	R.LWDLSTGVTTR.R
R1/RRR1-12/2	1939.589	1940.104	-783.735	0.520	1372.999	0.539	25	0.276	R.FSPNTFQPTIVSGSWDR.T
R1/RRR1-12/2	1939.601	1940.104	-777.418	0.507	1304.265	0.548	24	0.270	R.FSPNTFQPTIVSGSWDR.T
R1/RRR1-12/2	1574.481	1573.775	-187.145	0.506	1123.655	0.520	19	0.246	K.DGVTLLWDLAEGKR.L
R1/RRR1-12/2	1573.418	1573.775	-227.580	0.484	1102.429	0.514	19	0.243	K.DGVTLLWDLAEGKR.L
R1/RRR1-12/2	1322.204	1322.449	-185.905	0.331	893.730	0.522	16	0.221	K.DVLSVAFSVDNR.Q
R1/RRR1-12/2	1573.591	1573.775	-117.536	0.491	698.399	0.449	16	0.205	K.DGVTLLWDLAEGKR.L
R1/RRR1-12/3	1941.966	1940.104	-71.352	0.491	1643.141	0.474	31	0.196	R.FSPNTFQPTIVSGSWDR.T
R1/RRR1-1/2	1574.247	1573.775	301.018	0.344	605.265	0.372	13	0.190	K.DGVTLLWDLAEGKR.L
R1/RRR1-11/2	1249.108	1249.398	-232.659	0.373	698.768	0.296	13	0.190	-.LWDLSTGVTTR.-
R1/RRR1-12/3	1940.919	1940.104	-95.583	0.504	1510.261	0.494	30	0.183	R.FSPNTFQPTIVSGSWDR.T
R1/RRR1-9/2	1574.358	1573.775	-265.940	0.329	456.452	0.331	12	0.176	-.DGVTLLWDLAEGKR.-
R1/RRR1-14/2	1400.934	1401.636	-1218.621	0.427	995.152	0.400	17	0.215	R.TIKDEGVIALWR.G
R1/RRR1-15/2	1401.175	1401.636	-329.656	0.324	833.727	0.359	15	0.198	R.TIKDEGVIALWR.G
R1/RRR1-14/2	895.908	895.976	-76.204	0.252	783.131	0.394	12	0.197	K.GIADCFGR.T
R1/RRR1-14/3	1401.929	1401.636	209.932	0.542	1345.099	0.313	23	0.108	-.TIKDEGVIALWR.-
R1/RRR1-14/3	1401.704	1401.636	48.808	0.480	1043.725	0.280	22	0.080	-.TIKDEGVIALWR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1401.783	1401.636	105.404	0.433	775.840	0.313	20	0.072	-.TIKDEGVIALWR.-
R1/RRR1-10/2	1572.598	1571.806	-132.247	0.504	1605.721	0.564	21	0.309	R.ISITGAGGFIASHIAR.R
R1/RRR1-10/2	1572.893	1571.806	55.843	0.452	1492.952	0.510	20	0.279	R.ISITGAGGFIASHIAR.R
R1/RRR1-11/2	1571.733	1571.806	-46.242	0.385	1177.421	0.514	19	0.244	R.ISITGAGGFIASHIAR.R
R1/RRR1-2/2	1571.507	1571.806	-190.460	0.322	754.904	0.441	17	0.203	R.ISITGAGGFIASHIAR.R
R1/RRR1-2/2	1571.535	1571.806	-172.927	0.387	744.351	0.389	16	0.197	R.ISITGAGGFIASHIAR.R
R1/RRR1-3/2	1571.831	1571.806	16.232	0.213	527.770	0.221	15	0.182	R.ISITGAGGFIASHIAR.R
R1/RRR1-13/2	1200.616	1200.477	116.091	0.279	881.647	0.074	15	0.175	-.AGMAVINVLSPK.-
R1/RRR1-5/2	1681.857	1682.769	-1140.213	0.488	2528.150	0.457	23	0.450	R.NQAFEDGVDPDFLSK.W
R1/RRR1-5/2	1220.351	1220.317	28.131	0.485	1081.989	0.425	17	0.227	R.DVVASNPTNFR.L
R1/RRR1-5/2	1253.855	1254.461	-1284.620	0.296	1033.613	0.421	17	0.217	K.GNIDTPLALAIR.N
R1/RRR1-5/2	1184.541	1185.359	-1539.330	0.417	400.071	0.527	15	0.211	R.QALLNAQISAR.N
R1/RRR1-5/2	1110.971	1111.315	-310.630	0.420	768.364	0.426	14	0.211	R.YINVVDLFK.L
R1/RRR1-5/2	1111.062	1111.315	-228.066	0.462	694.239	0.429	14	0.210	R.YINVVDLFK.L
R1/RRR1-5/2	1255.266	1254.461	-156.023	0.387	844.234	0.391	17	0.207	K.GNIDTPLALAIR.N
R1/RRR1-5/2	1254.063	1254.461	-317.949	0.247	1120.497	0.319	17	0.206	K.GNIDTPLALAIR.N
R1/RRR1-5/2	1219.579	1220.317	-1429.349	0.322	1009.282	0.333	16	0.205	R.DVVASNPTNFR.L
R1/RRR1-5/2	1184.521	1185.359	-1556.412	0.328	553.613	0.442	17	0.203	R.QALLNAQISAR.N
R1/RRR1-5/2	1219.118	1220.317	-1809.316	0.291	793.545	0.372	16	0.200	R.DVVASNPTNFR.L
R1/RRR1-5/2	1184.677	1185.359	-1424.022	0.325	421.813	0.412	15	0.198	R.QALLNAQISAR.N
R1/RRR1-5/3	1243.386	1243.403	-13.512	0.513	1317.658	0.444	23	0.133	K.RPGAAEHLHVR.G
R1/RRR1-5/3	1243.692	1243.403	232.951	0.535	1261.562	0.438	23	0.127	K.RPGAAEHLHVR.G
R1/RRR1-9/2	1296.154	1295.420	-206.361	0.533	2212.524	0.561	20	0.418	K.ADIEDYLASVAK.G
R1/RRR1-9/2	1296.148	1295.420	-210.613	0.556	2193.581	0.563	20	0.415	K.ADIEDYLASVAK.G
R1/RRR1-9/2	1528.323	1528.733	-268.824	0.550	1985.286	0.445	23	0.338	R.KLAEDNNVPLSSIK.G
R1/RRR1-9/2	1295.045	1295.420	-290.964	0.460	1877.372	0.393	19	0.303	K.ADIEDYLASVAK.G
R1/RRR1-9/2	1651.171	1649.910	158.713	0.473	1456.091	0.494	21	0.275	R.ILKADIEDYLASVAK.G
R1/RRR1-9/2	1016.970	1017.158	-185.720	0.407	695.846	0.486	15	0.215	K.GLATIADEVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1017.114	1017.158	-44.011	0.441	715.528	0.464	15	0.214	K.GLATIADEVK.Q
R1/RRR1-9/2	1143.068	1143.402	-293.124	0.387	1059.122	0.347	15	0.211	K.KISINDLVIK.A
R1/RRR1-9/2	1143.319	1143.402	-72.243	0.414	842.991	0.360	15	0.205	K.KISINDLVIK.A
R1/RRR1-9/2	1144.126	1143.402	-241.487	0.418	1033.467	0.289	16	0.203	K.KISINDLVIK.A
R1/RRR1-9/2	1015.208	1015.229	-20.636	0.429	898.687	0.271	15	0.198	K.ISINDLVIK.A
R1/RRR1-9/2	1015.140	1015.229	-87.697	0.449	881.801	0.272	15	0.198	K.ISINDLVIK.A
R1/RRR1-9/2	1015.143	1015.229	-84.320	0.451	842.961	0.252	15	0.195	K.ISINDLVIK.A
R1/RRR1-9/2	1016.956	1017.158	-199.207	0.292	498.720	0.296	14	0.192	K.GLATIADEVK.Q
R1/RRR1-13/2	1016.020	1015.229	-205.596	0.345	739.811	0.234	13	0.190	K.ISINDLVIK.A
R1/RRR1-9/3	1143.449	1143.402	41.683	0.446	873.122	0.315	19	0.081	K.KISINDLVIK.A
R1/RRR1-9/3	1143.211	1143.402	-167.633	0.465	1130.140	0.237	21	0.076	-.KISINDLVIK.-
R1/RRR1-12/2	1825.384	1826.237	-1018.281	0.462	2391.117	0.555	26	0.448	K.VAILGASGGIGQPLALLM*K.M
R1/RRR1-13/2	1826.980	1826.237	-141.294	0.560	2278.750	0.553	26	0.422	K.VAILGASGGIGQPLALLM*K.M
R1/RRR1-12/2	1824.990	1826.237	-1235.064	0.345	1955.111	0.476	23	0.334	K.VAILGASGGIGQPLALLM*K.M
R1/RRR1-12/2	1825.968	1826.237	-147.810	0.420	1496.521	0.479	22	0.270	K.VAILGASGGIGQPLALLM*K.M
R1/RRR1-13/2	1458.481	1457.635	-105.594	0.517	1219.144	0.588	21	0.269	K.AGAGSATLSM*AYAAAK.F
R1/RRR1-12/2	1186.196	1186.427	-194.628	0.450	1361.095	0.473	19	0.261	R.LLGVTTLDVVR.A
R1/RRR1-12/2	1186.284	1186.427	-120.200	0.486	1341.996	0.467	19	0.259	R.LLGVTTLDVVR.A
R1/RRR1-12/2	1186.285	1186.427	-119.683	0.466	1335.979	0.466	19	0.258	R.LLGVTTLDVVR.A
R1/RRR1-12/2	1457.164	1457.635	-323.816	0.455	1166.589	0.531	20	0.249	K.AGAGSATLSM*AYAAAK.F
R1/RRR1-13/2	1186.367	1186.427	-50.220	0.436	1041.721	0.408	17	0.222	R.LLGVTTLDVVR.A
R1/RRR1-13/2	1825.178	1826.237	-1131.564	0.396	985.180	0.446	22	0.218	K.VAILGASGGIGQPLALLM*K.M
R1/RRR1-13/2	1244.591	1245.365	-1429.152	0.421	789.731	0.450	19	0.218	R.IQNGGTEVVEAK.A
R1/RRR1-12/2	1245.121	1245.365	-195.841	0.452	831.360	0.418	19	0.215	R.IQNGGTEVVEAK.A
R1/RRR1-12/2	1244.526	1245.365	-1481.466	0.447	718.002	0.434	18	0.213	R.IQNGGTEVVEAK.A
R1/RRR1-13/2	1245.287	1245.365	-62.591	0.445	707.385	0.414	18	0.210	R.IQNGGTEVVEAK.A
R1/RRR1-12/2	1244.899	1245.365	-375.268	0.463	613.669	0.421	17	0.208	R.IQNGGTEVVEAK.A
R1/RRR1-13/2	1503.781	1502.697	55.885	0.436	878.763	0.414	16	0.207	R.ANTFVAEVLGLDPR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1456.389	1457.635	-1546.681	0.320	779.051	0.475	18	0.207	K.AGAGSATLSM*AYAAAK.F
R1/RRR1-12/2	1245.977	1245.365	-311.660	0.367	549.223	0.399	18	0.205	R.IQNGGTEVVEAK.A
R1/RRR1-13/2	1503.283	1502.697	-276.152	0.392	823.584	0.420	15	0.204	R.ANTFVAEVLGLDPR.D
R1/RRR1-12/2	1245.489	1245.365	100.112	0.408	329.278	0.399	14	0.202	R.IQNGGTEVVEAK.A
R1/RRR1-13/2	1244.992	1245.365	-300.204	0.446	702.661	0.337	18	0.202	R.IQNGGTEVVEAK.A
R1/RRR1-12/2	1502.684	1502.697	-8.198	0.307	1117.102	0.280	17	0.201	R.ANTFVAEVLGLDPR.D
R1/RRR1-13/2	1503.228	1502.697	-312.651	0.375	944.166	0.355	15	0.200	R.ANTFVAEVLGLDPR.D
R1/RRR1-13/2	1246.079	1245.365	-229.589	0.357	382.884	0.310	15	0.198	R.IQNGGTEVVEAK.A
R1/RRR1-13/2	1978.869	1977.198	-166.783	0.408	541.558	0.469	16	0.195	R.CGIEEILSLGPLNEFER.A
R1/RRR1-13/2	1186.094	1186.427	-281.149	0.342	618.728	0.325	14	0.194	R.LLGVTTLDVVR.A
R1/RRR1-13/2	1825.028	1826.237	-1214.107	0.362	711.400	0.368	19	0.193	K.VAILGASGGIGQPLALLM*K.M
R1/RRR1-12/2	1646.293	1645.838	277.284	0.624	2632.898	0.526	24	0.494	K.IKDEEGNPAFALVNK.A
R1/RRR1-12/2	1645.331	1645.838	-918.395	0.585	2442.537	0.538	23	0.456	K.IKDEEGNPAFALVNK.A
R1/RRR1-12/2	1646.277	1645.838	267.470	0.629	2130.266	0.549	22	0.393	K.IKDEEGNPAFALVNK.A
R1/RRR1-12/2	1722.562	1722.922	-209.937	0.567	1899.017	0.494	23	0.335	K.IRDEEGYPAFALVNK.V
R1/RRR1-12/2	1846.081	1845.993	48.043	0.593	1453.964	0.690	29	0.331	K.ILPWGDEAYAGGSANAPR.G
R1/RRR1-12/2	1845.478	1845.993	-823.105	0.557	1410.025	0.690	28	0.324	K.ILPWGDEAYAGGSANAPR.G
R1/RRR1-12/2	1845.567	1845.993	-231.039	0.551	1265.624	0.664	27	0.297	K.ILPWGDEAYAGGSANAPR.G
R1/RRR1-12/2	1722.502	1722.922	-244.987	0.559	1547.728	0.472	21	0.277	K.IRDEEGYPAFALVNK.V
R1/RRR1-12/2	1080.381	1081.161	-1652.947	0.432	1514.662	0.460	16	0.274	K.ADEGFSVTVR.G
R1/RRR1-12/2	1080.538	1081.161	-1506.648	0.430	1515.091	0.430	17	0.267	K.ADEGFSVTVR.G
R1/RRR1-12/2	1081.059	1081.161	-94.864	0.511	1501.197	0.425	17	0.265	K.ADEGFSVTVR.G
R1/RRR1-12/2	1722.396	1722.922	-888.819	0.555	1419.296	0.429	20	0.250	K.IRDEEGYPAFALVNK.V
R1/RRR1-12/2	1229.041	1229.362	-261.462	0.399	767.060	0.443	17	0.211	R.GGSVCLAPTNPR.D
R1/RRR1-12/2	1228.892	1229.362	-383.643	0.367	674.707	0.424	16	0.203	R.GGSVCLAPTNPR.D
R1/RRR1-12/2	1119.111	1119.211	-89.123	0.453	755.161	0.364	11	0.198	-.DEYQHWIK.-
R1/RRR1-12/2	1228.611	1229.362	-1429.005	0.310	738.921	0.303	17	0.193	R.GGSVCLAPTNPR.D
R1/RRR1-13/2	1081.478	1081.161	293.717	0.304	538.006	0.271	13	0.190	K.ADEGFSVTVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/3	1645.301	1645.838	-937.136	0.409	892.532	0.400	27	0.093	K.IKDEEGNPAFALVNK.A
R1/RRR1-12/3	1646.558	1645.838	-170.708	0.417	999.359	0.365	27	0.093	K.IKDEEGNPAFALVNK.A
R1/RRR1-12/3	1645.339	1645.838	-304.408	0.439	733.808	0.370	24	0.084	-.IKDEEGNPAFALVNK.-
R1/RRR1-11/2	1441.829	1442.643	-1261.756	0.448	1787.253	0.562	22	0.338	R.VPTANVSVVDLTAR.I
R1/RRR1-11/2	1277.193	1277.538	-270.682	0.454	1842.641	0.503	18	0.331	R.RVLDLLSYVAK.V
R1/RRR1-11/2	1675.614	1675.781	-100.077	0.464	1630.802	0.540	19	0.309	K.LVSWYDNEWGYSR.R
R1/RRR1-11/2	1442.315	1442.643	-227.894	0.522	1322.262	0.598	20	0.285	R.VPTANVSVVDLTAR.I
R1/RRR1-11/2	1442.305	1442.643	-234.771	0.485	1303.363	0.597	20	0.282	R.VPTANVSVVDLTAR.I
R1/RRR1-11/2	1675.186	1675.781	-954.943	0.450	1456.224	0.519	18	0.279	K.LVSWYDNEWGYSR.R
R1/RRR1-2/2	1442.863	1442.643	152.775	0.480	1296.904	0.557	19	0.270	R.VPTANVSVVDLTAR.I
R1/RRR1-12/2	1442.391	1442.643	-175.508	0.418	1403.603	0.507	19	0.269	R.VPTANVSVVDLTAR.I
R1/RRR1-11/2	1276.930	1277.538	-1262.940	0.475	1299.575	0.452	16	0.248	R.RVLDLLSYVAK.V
R1/RRR1-11/2	1276.899	1277.538	-1287.326	0.424	1203.923	0.460	15	0.240	R.RVLDLLSYVAK.V
R1/RRR1-11/2	1675.247	1675.781	-918.292	0.458	1057.137	0.488	16	0.232	K.LVSWYDNEWGYSR.R
R1/RRR1-11/2	1387.449	1386.536	-62.973	0.521	690.385	0.484	19	0.213	R.GAAQNIIPSSTGAAK.A
R1/RRR1-12/2	1386.229	1386.536	-222.187	0.395	560.626	0.437	18	0.202	R.GAAQNIIPSSTGAAK.A
R1/RRR1-12/2	1178.279	1178.320	-34.978	0.325	815.916	0.389	14	0.202	K.AGISLNDNFVK.L
R1/RRR1-11/2	1386.351	1386.536	-134.382	0.430	564.782	0.370	19	0.198	R.GAAQNIIPSSTGAAK.A
R1/RRR1-11/2	1386.162	1386.536	-270.602	0.390	563.459	0.338	17	0.193	R.GAAQNIIPSSTGAAK.A
R1/RRR1-12/2	1386.261	1386.536	-199.219	0.359	534.825	0.302	17	0.190	R.GAAQNIIPSSTGAAK.A
R1/RRR1-12/2	1386.975	1386.536	316.945	0.476	402.033	0.369	15	0.189	-.GAAQNIIPSSTGAAK.-
R1/RRR1-11/2	1179.259	1178.320	-51.872	0.311	691.292	0.269	14	0.188	K.AGISLNDNFVK.L
R1/RRR1-11/2	1177.520	1178.320	-1532.703	0.285	632.505	0.286	13	0.187	K.AGISLNDNFVK.L
R1/RRR1-11/3	1765.348	1764.958	221.679	0.517	1406.964	0.462	32	0.157	R.FKGEVSVDGTDLVVNGK.K
R1/RRR1-10/2	1260.879	1260.378	-396.632	0.585	1794.224	0.614	17	0.359	K.HGEIDYEAVVK.L
R1/RRR1-10/2	1260.224	1260.378	-122.668	0.573	1680.725	0.597	17	0.336	K.HGEIDYEAVVK.L
R1/RRR1-10/2	1163.163	1163.265	-88.589	0.519	2106.725	0.332	19	0.319	K.LAEGFNGADLR.N
R1/RRR1-10/2	1261.036	1260.378	-272.111	0.581	1512.049	0.584	17	0.308	K.HGEIDYEAVVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1277.272	1277.451	-140.490	0.497	1671.366	0.494	19	0.303	R.AIASNIDANFLK.I
R1/RRR1-10/2	1277.132	1277.451	-251.042	0.507	1601.928	0.524	19	0.302	R.AIASNIDANFLK.I
R1/RRR1-10/2	1722.370	1722.964	-928.285	0.542	1423.285	0.593	20	0.295	K.IVSSAIIDKYIGESAR.L
R1/RRR1-10/2	1164.335	1163.265	59.980	0.531	1787.928	0.368	19	0.284	K.LAEGFNGADLR.N
R1/RRR1-10/2	1276.480	1277.451	-1548.643	0.404	1552.008	0.461	19	0.278	R.AIASNIDANFLK.I
R1/RRR1-10/3	1723.774	1722.964	-110.429	0.481	1445.169	0.482	29	0.167	K.IVSSAIIDKYIGESAR.L
R1/RRR1-10/3	1651.769	1652.751	-1203.390	0.445	1223.850	0.419	25	0.122	R.RFSEGTSADREIQR.T
R1/RRR1-10/3	1652.457	1652.751	-178.026	0.428	1079.689	0.368	23	0.101	R.RFSEGTSADREIQR.T
R1/RRR1-10/3	1652.183	1652.751	-951.647	0.429	1045.576	0.341	23	0.093	R.RFSEGTSADREIQR.T
R1/RRR1-10/3	1722.326	1722.964	-953.660	0.373	844.402	0.350	28	0.083	K.IVSSAIIDKYIGESAR.L
R1/RRR1-10/2	1689.838	1688.818	11.621	0.570	1542.452	0.496	20	0.287	K.FLQSLEFFEENER.K
R1/RRR1-10/2	1250.057	1250.340	-226.704	0.433	1026.592	0.452	16	0.226	R.TSEALSEHFTK.E
R1/RRR1-10/2	1639.792	1639.960	-102.637	0.399	705.340	0.545	21	0.220	K.LSGLPPETVFQPLLK.D
R1/RRR1-10/2	1375.320	1374.650	-240.864	0.504	715.073	0.483	18	0.217	R.EAILPSVLYIQK.T
R1/RRR1-10/2	1558.574	1557.749	-113.144	0.469	965.026	0.443	15	0.216	K.M*EDNLLEFFPSAK.R
R1/RRR1-10/2	1374.410	1374.650	-175.459	0.437	697.444	0.428	17	0.207	R.EAILPSVLYIQK.T
R1/RRR1-10/2	1639.883	1639.960	-46.709	0.434	558.069	0.460	19	0.204	K.LSGLPPETVFQPLLK.D
R1/RRR1-10/2	1557.845	1557.749	61.674	0.420	1018.281	0.340	15	0.202	K.M*EDNLLEFFPSAK.R
R1/RRR1-10/3	1406.680	1406.526	109.868	0.499	1143.370	0.378	23	0.105	K.RTSEALSEHFTK.E
R1/RRR1-22/2	1369.227	1369.592	-267.153	0.544	2121.976	0.478	19	0.371	R.LVVIVDVVDQNR.A
R1/RRR1-21/2	1369.314	1369.592	-203.473	0.494	1256.555	0.508	17	0.256	R.LVVIVDVVDQNR.A
R1/RRR1-22/2	1354.985	1355.524	-1139.044	0.447	1230.791	0.457	18	0.243	R.VALVNYGKDYGR.L
R1/RRR1-22/1	863.402	864.024	-1883.907	0.285	591.227	0.354	10	0.231	R.VALVNYGK.D
R1/RRR1-22/2	1355.273	1355.524	-185.254	0.447	925.621	0.475	16	0.222	R.VALVNYGKDYGR.L
R1/RRR1-21/2	864.285	864.024	302.929	0.401	586.222	0.417	13	0.208	R.VALVNYGK.D
R1/RRR1-21/2	863.388	864.024	-1900.758	0.321	604.189	0.432	12	0.204	R.VALVNYGK.D
R1/RRR1-23/2	863.945	864.024	-91.636	0.341	436.340	0.448	11	0.203	R.VALVNYGK.D
R1/RRR1-22/2	1103.019	1103.275	-232.080	0.399	678.948	0.373	14	0.201	R.ALVDAPDM*VR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	863.939	864.024	-98.723	0.359	327.009	0.406	10	0.201	R.VALVNYGK.D
R1/RRR1-22/2	1259.892	1259.517	298.575	0.391	804.804	0.329	17	0.200	R.LSLTDIKIDIK.R
R1/RRR1-22/2	1102.264	1103.275	-1829.308	0.287	758.434	0.338	14	0.196	R.ALVDAPDM*VR.C
R1/RRR1-22/2	1102.720	1103.275	-1413.960	0.391	610.629	0.308	13	0.192	-.ALVDAPDM*VR.-
R1/RRR1-22/2	1259.038	1259.517	-381.847	0.320	723.969	0.218	16	0.187	R.LSLTDIKIDIK.R
R1/RRR1-22/2	1259.039	1259.517	-381.167	0.344	825.356	0.207	15	0.186	R.LSLTDIKIDIK.R
R1/RRR1-22/2	1086.806	1087.275	-433.236	0.239	539.367	0.206	11	0.174	-.ALVDAPDMVR.-
R1/RRR1-22/1	863.554	864.024	-546.074	0.265	341.850	0.421	9	0.144	-.VALVNYGK.-
R1/RRR1-22/3	1369.546	1369.592	-33.544	0.389	1577.523	0.253	25	0.111	R.LVVIVDVVDQNR.A
R1/RRR1-22/3	1370.393	1369.592	-145.472	0.494	1012.303	0.447	23	0.109	R.LVVIVDVVDQNR.A
R1/RRR1-9/2	1870.291	1870.114	94.948	0.602	2568.848	0.581	24	0.505	R.AVCMISNNTAVAEVFSR.I
R1/RRR1-9/2	1870.469	1870.114	190.180	0.598	2341.461	0.628	24	0.472	R.AVCMISNNTAVAEVFSR.I
R1/RRR1-9/2	1809.258	1810.107	-1024.644	0.532	2304.525	0.606	24	0.453	R.IHFM*LSSYAPVISAEK.A
R1/RRR1-9/2	1809.461	1810.107	-911.935	0.584	1741.086	0.608	21	0.343	R.IHFM*LSSYAPVISAEK.A
R1/RRR1-9/2	1809.322	1810.107	-989.217	0.513	1286.661	0.608	21	0.281	R.IHFM*LSSYAPVISAEK.A
R1/RRR1-9/2	1716.287	1716.956	-975.306	0.499	1596.355	0.449	23	0.278	R.AIFVDLEPTVIDEVR.T
R1/RRR1-9/2	1001.966	1002.147	-180.558	0.460	1195.731	0.554	16	0.263	K.DVNAAVATIK.T
R1/RRR1-9/2	1001.980	1002.147	-166.992	0.484	1285.054	0.505	17	0.262	K.DVNAAVATIK.T
R1/RRR1-9/2	1001.959	1002.147	-188.380	0.467	1184.595	0.498	16	0.250	K.DVNAAVATIK.T
R1/RRR1-9/2	1716.661	1716.956	-172.501	0.541	1083.316	0.457	22	0.232	R.AIFVDLEPTVIDEVR.T
R1/RRR1-3/2	1811.575	1810.107	259.104	0.447	1004.532	0.515	19	0.232	R.IHFM*LSSYAPVISAEK.A
R1/RRR1-9/2	1872.428	1873.093	-891.556	0.463	850.686	0.512	23	0.223	K.CGINYQPPSVVPGGDLAK.V
R1/RRR1-9/2	1873.088	1873.093	-2.524	0.443	808.150	0.505	23	0.219	K.CGINYQPPSVVPGGDLAK.V
R1/RRR1-9/2	1532.211	1532.807	-1045.331	0.404	876.728	0.448	19	0.214	R.LISQIISSLTTSLR.F
R1/RRR1-1/2	1717.269	1716.956	182.691	0.513	925.796	0.421	20	0.214	R.AIFVDLEPTVIDEVR.T
R1/RRR1-9/2	1715.677	1716.956	-1332.184	0.380	1073.427	0.335	21	0.210	R.AIFVDLEPTVIDEVR.T
R1/RRR1-9/2	1872.406	1873.093	-903.402	0.422	687.336	0.491	21	0.209	K.CGINYQPPSVVPGGDLAK.V
R1/RRR1-9/2	1532.973	1532.807	108.014	0.372	773.520	0.450	18	0.208	R.LISQIISSLTTSLR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1716.570	1716.956	-225.506	0.403	677.900	0.316	18	0.194	R.AIFVDLEPTVIDEVR.T
R1/RRR1-18/2	1715.631	1716.956	-1359.481	0.305	618.967	0.323	18	0.193	R.AIFVDLEPTVIDEVR.T
R1/RRR1-7/2	1716.624	1716.956	-193.902	0.401	621.350	0.303	17	0.191	R.AIFVDLEPTVIDEVR.T
R1/RRR1-10/2	1716.358	1716.956	-933.748	0.342	631.725	0.240	17	0.187	R.AIFVDLEPTVIDEVR.T
R1/RRR1-13/2	1715.829	1716.956	-1243.726	0.295	673.578	0.233	17	0.187	R.AIFVDLEPTVIDEVR.T
R1/RRR1-9/3	1795.675	1794.107	-241.455	0.370	1218.791	0.341	30	0.100	R.IHFMLSSYAPVISAEK.A
R1/RRR1-8/2	1258.285	1257.423	-109.916	0.579	2012.717	0.379	17	0.319	-.GWNLNLAELAR.-
R1/RRR1-8/2	1124.004	1124.318	-280.994	0.607	1554.796	0.548	17	0.303	R.LPANLIQAQR.D
R1/RRR1-8/2	1123.876	1124.318	-394.652	0.549	1653.410	0.493	17	0.301	R.LPANLIQAQR.D
R1/RRR1-8/2	1124.076	1124.318	-216.276	0.594	1538.598	0.494	17	0.286	R.LPANLIQAQR.D
R1/RRR1-9/2	1124.062	1124.318	-228.479	0.513	1365.256	0.539	17	0.279	R.LPANLIQAQR.D
R1/RRR1-8/2	1258.552	1257.423	102.867	0.515	1747.196	0.329	17	0.266	K.GWNLNLAELAR.I
R1/RRR1-9/2	1123.512	1124.318	-1613.030	0.420	1015.011	0.562	15	0.246	R.LPANLIQAQR.D
R1/RRR1-8/2	1256.375	1257.423	-1635.112	0.340	1140.731	0.321	16	0.211	K.GWNLNLAELAR.I
R1/RRR1-8/2	1210.027	1209.292	-220.443	0.370	692.586	0.402	15	0.201	R.DLFGAHTYER.I
R1/RRR1-9/2	1123.985	1124.318	-297.992	0.346	371.087	0.332	13	0.198	R.LPANLIQAQR.D
R1/RRR1-8/2	1055.573	1056.284	-1626.259	0.362	498.067	0.402	12	0.196	R.TVVLLVQAGR.A
R1/RRR1-8/2	1055.922	1056.284	-344.217	0.364	1029.784	0.224	14	0.192	R.TVVLLVQAGR.A
R1/RRR1-8/3	1760.852	1759.944	-52.478	0.478	1308.461	0.436	27	0.136	K.AYDRNPELANLIVDR.E
R1/RRR1-4/2	1496.103	1495.616	326.398	0.505	895.700	0.448	17	0.215	K.VSTILNDEFQNSK.E
R1/RRR1-4/2	1494.855	1495.616	-1181.779	0.370	941.823	0.338	17	0.201	K.VSTILNDEFQNSK.E
R1/RRR1-4/3	1681.414	1681.939	-909.670	0.382	1082.895	0.459	30	0.115	R.AADLGVESIVIGM*PHR.G
R1/RRR1-4/3	1680.950	1681.939	-1186.230	0.327	763.072	0.450	25	0.094	R.AADLGVESIVIGM*PHR.G
R1/RRR1-4/3	1681.606	1681.939	-198.328	0.358	782.279	0.386	27	0.086	R.AADLGVESIVIGM*PHR.G
R1/RRR1-10/3	1492.856	1491.714	95.201	0.581	3138.521	0.408	30	0.533	K.KVSPEVIAEYTVR.T
R1/RRR1-11/3	1491.778	1491.714	42.866	0.576	3011.775	0.365	29	0.466	K.KVSPEVIAEYTVR.T
R1/RRR1-11/3	1491.966	1491.714	169.649	0.585	2720.618	0.387	30	0.383	K.KVSPEVIAEYTVR.T
R1/RRR1-11/3	1491.347	1491.714	-247.010	0.581	2599.602	0.425	28	0.377	K.KVSPEVIAEYTVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1569.223	1569.698	-304.028	0.541	1948.729	0.532	24	0.357	K.GDAVLGEGASESLHVK.D
R1/RRR1-11/2	1491.437	1491.714	-186.401	0.595	1719.944	0.583	21	0.336	K.KVSPEVIAEYTVR.T
R1/RRR1-11/2	1569.345	1569.698	-225.909	0.491	1865.630	0.502	24	0.333	K.GDAVLGEGASESLHVK.D
R1/RRR1-11/2	1491.373	1491.714	-228.935	0.555	1622.710	0.547	20	0.310	K.KVSPEVIAEYTVR.T
R1/RRR1-10/2	1491.553	1491.714	-107.994	0.550	1634.245	0.540	20	0.310	K.KVSPEVIAEYTVR.T
R1/RRR1-11/2	1491.476	1491.714	-159.717	0.573	1658.252	0.523	20	0.308	K.KVSPEVIAEYTVR.T
R1/RRR1-10/3	1491.249	1491.714	-312.914	0.518	2290.026	0.396	25	0.290	K.KVSPEVIAEYTVR.T
R1/RRR1-10/2	1490.690	1491.714	-1362.081	0.509	1666.010	0.445	20	0.287	K.KVSPEVIAEYTVR.T
R1/RRR1-11/2	1569.139	1569.698	-997.010	0.514	1565.786	0.485	23	0.284	K.GDAVLGEGASESLHVK.D
R1/RRR1-10/3	1491.792	1491.714	52.714	0.550	2251.088	0.376	27	0.265	K.KVSPEVIAEYTVR.T
R1/RRR1-11/2	1312.224	1312.501	-211.299	0.378	1096.556	0.512	18	0.241	K.KPWSLSFSFGR.A
R1/RRR1-10/2	1364.341	1363.541	-147.229	0.477	817.410	0.445	18	0.216	K.VSPEVIAEYTVR.T
R1/RRR1-11/2	1154.613	1155.240	-1413.276	0.383	369.285	0.504	15	0.203	K.ANSEATLGTYK.G
R1/RRR1-10/2	1312.329	1312.501	-131.233	0.330	598.700	0.436	16	0.202	K.KPWSLSFSFGR.A
R1/RRR1-10/2	1363.173	1363.541	-270.674	0.387	595.125	0.400	16	0.200	K.VSPEVIAEYTVR.T
R1/RRR1-10/2	1362.886	1363.541	-1218.234	0.226	574.251	0.217	16	0.185	K.VSPEVIAEYTVR.T
R1/RRR1-11/3	1312.757	1312.501	195.513	0.513	1597.936	0.425	24	0.161	K.KPWSLSFSFGR.A
R1/RRR1-12/3	1491.801	1491.714	58.623	0.502	1655.577	0.348	27	0.146	K.KVSPEVIAEYTVR.T
R1/RRR1-11/3	1312.304	1312.501	-150.512	0.483	1324.847	0.442	22	0.134	K.KPWSLSFSFGR.A
R1/RRR1-11/3	1312.004	1312.501	-379.834	0.423	1504.570	0.347	23	0.126	K.KPWSLSFSFGR.A
R1/RRR1-12/3	1491.263	1491.714	-303.182	0.379	1135.316	0.263	27	0.081	K.KVSPEVIAEYTVR.T
R1/RRR1-7/2	1158.352	1158.327	21.604	0.452	1533.406	0.488	17	0.283	K.ALEDALAVLDK.I
R1/RRR1-7/2	1158.182	1158.327	-125.019	0.437	1487.312	0.499	17	0.280	K.ALEDALAVLDK.I
R1/RRR1-7/2	1158.281	1158.327	-39.810	0.481	1463.695	0.494	17	0.277	K.ALEDALAVLDK.I
R1/RRR1-7/2	1359.213	1359.551	-249.123	0.453	1372.571	0.424	18	0.250	R.TLAQNCGLNVIR.I
R1/RRR1-7/2	1120.712	1121.250	-1376.141	0.345	1379.771	0.346	17	0.234	R.NLQDAM*SVAR.N
R1/RRR1-7/2	1121.086	1121.250	-146.824	0.358	1293.501	0.344	16	0.226	R.NLQDAM*SVAR.N
R1/RRR1-7/2	1316.831	1317.516	-1283.155	0.391	1096.355	0.440	16	0.226	K.GLSDLAIHYLSK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	959.404	960.107	-1779.636	0.375	890.824	0.336	14	0.201	R.IDDIVSGIK.K
R1/RRR1-7/2	1057.878	1058.127	-236.523	0.334	732.201	0.369	15	0.200	K.VPGGQLEDSR.V
R1/RRR1-7/2	1057.990	1058.127	-129.915	0.298	444.553	0.348	13	0.188	-.VPGGQLEDSR.-
R1/RRR1-7/2	1057.841	1058.127	-271.948	0.307	529.977	0.301	14	0.188	-.VPGGQLEDSR.-
R1/RRR1-8/2	1360.218	1359.581	-267.416	0.519	1768.798	0.390	19	0.286	K.VGLM*VQQQVNAR.F
R1/RRR1-8/2	1359.051	1359.581	-1128.543	0.498	1850.612	0.333	19	0.282	K.VGLM*VQQQVNAR.F
R1/RRR1-8/2	1355.256	1355.560	-225.097	0.544	1545.431	0.467	18	0.280	R.TFLDQLVEVYK.Q
R1/RRR1-8/2	1355.301	1355.560	-191.845	0.516	1392.146	0.505	17	0.272	R.TFLDQLVEVYK.Q
R1/RRR1-8/2	1354.661	1355.560	-1406.666	0.439	1320.267	0.449	17	0.250	R.TFLDQLVEVYK.Q
R1/RRR1-8/2	1609.552	1609.854	-187.860	0.481	1214.512	0.468	19	0.243	R.KEHQFLAELGLAPR.N
R1/RRR1-8/2	1151.188	1150.349	-140.668	0.440	801.533	0.444	16	0.214	R.IPLVSFTGSTK.V
R1/RRR1-8/2	1426.791	1425.717	51.778	0.376	1159.363	0.341	17	0.214	R.EELFGPVLYVMK.V
R1/RRR1-8/2	1151.215	1150.349	-116.948	0.390	644.377	0.472	14	0.208	R.IPLVSFTGSTK.V
R1/RRR1-7/2	1150.503	1150.349	133.705	0.303	646.971	0.477	15	0.206	R.IPLVSFTGSTK.V
R1/RRR1-8/2	888.368	889.077	-1929.384	0.399	822.493	0.343	11	0.202	K.RPDIIFK.W
R1/RRR1-8/2	889.004	889.077	-81.823	0.465	655.667	0.350	11	0.201	K.RPDIIFK.W
R1/RRR1-7/2	1150.122	1150.349	-198.498	0.273	467.922	0.381	13	0.191	-.IPLVSFTGSTK.-
R1/RRR1-2/2	1282.201	1281.483	-221.021	0.517	1807.911	0.532	18	0.335	K.IIEEGPVTVAPR.E
R1/RRR1-2/2	1646.730	1646.909	-109.267	0.438	1916.925	0.450	23	0.327	R.LDQPIILTGYSALNK.L
R1/RRR1-2/2	1646.302	1646.909	-978.837	0.478	1943.099	0.412	23	0.319	R.LDQPIILTGYSALNK.L
R1/RRR1-2/2	1906.276	1905.095	95.211	0.563	1042.774	0.613	22	0.256	K.TVTANTATVSDYVGYLTK.G
R1/RRR1-2/2	1546.978	1546.679	193.915	0.461	1283.411	0.434	19	0.243	R.SLSELEM*FTEESK.G
R1/RRR1-1/2	1546.903	1546.679	145.801	0.479	1308.347	0.427	18	0.243	R.SLSELEM*FTEESK.G
R1/RRR1-1/2	1905.546	1905.095	237.310	0.471	765.679	0.546	23	0.223	K.TVTANTATVSDYVGYLTK.G
R1/RRR1-2/2	1281.009	1281.483	-370.997	0.327	1235.773	0.351	16	0.220	K.IIEEGPVTVAPR.E
R1/RRR1-2/2	1430.520	1429.691	-119.363	0.401	1074.913	0.365	15	0.212	R.EGLPLFILANWR.-
R1/RRR1-2/2	1430.837	1429.691	102.717	0.407	857.191	0.442	14	0.210	R.EGLPLFILANWR.-
R1/RRR1-2/2	994.932	994.123	-192.480	0.418	836.545	0.391	14	0.207	K.ATELVFADK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1430.832	1429.691	99.209	0.376	743.008	0.393	15	0.201	R.EGLPLFILANWR.-
R1/RRR1-2/3	1803.411	1803.135	153.522	0.415	1747.775	0.325	28	0.161	R.HVEPPLSALLELDKLK.V
R1/RRR1-2/3	1802.812	1803.135	-179.954	0.451	1538.130	0.414	31	0.155	R.HVEPPLSALLELDKLK.V
R1/RRR1-2/3	1802.543	1803.135	-886.292	0.505	1150.381	0.396	28	0.113	R.HVEPPLSALLELDKLK.V
R1/RRR1-7/2	1043.396	1044.187	-1721.512	0.411	1150.590	0.485	17	0.243	K.VVNDGVTIAR.A
R1/RRR1-7/2	1557.433	1556.829	-254.916	0.501	1211.502	0.429	20	0.231	K.LGLLSVTSGANPVSLK.K
R1/RRR1-7/2	1557.454	1556.829	-241.548	0.514	1165.509	0.433	20	0.228	K.LGLLSVTSGANPVSLK.K
R1/RRR1-7/2	1496.290	1496.689	-267.542	0.396	909.401	0.350	17	0.200	R.GYISPQFVTNLEK.S
R1/RRR1-6/2	1458.261	1458.513	-173.178	0.513	2208.058	0.555	23	0.415	R.VYGSSSNDVSSVTR.Q
R1/RRR1-6/2	1458.100	1458.513	-284.373	0.524	2111.789	0.555	23	0.396	R.VYGSSSNDVSSVTR.Q
R1/RRR1-6/2	1367.287	1366.591	-223.475	0.436	1857.450	0.492	19	0.331	R.TAILAEAIASHLR.Q
R1/RRR1-6/2	1459.126	1458.513	-266.300	0.551	1586.502	0.553	21	0.307	R.VYGSSSNDVSSVTR.Q
R1/RRR1-6/2	1045.766	1045.260	-473.419	0.431	780.685	0.316	13	0.199	R.LEWLSLKR.W
R1/RRR1-6/2	1045.608	1045.260	333.886	0.410	752.547	0.249	13	0.192	R.LEWLSLKR.W
R1/RRR1-6/2	1596.960	1597.798	-1154.674	0.257	713.357	0.307	15	0.185	R.AYFLAAANIFEPNR.A
R1/RRR1-6/2	1597.698	1597.798	-62.886	0.294	857.035	0.229	16	0.184	R.AYFLAAANIFEPNR.A
R1/RRR1-6/2	1349.129	1349.519	-290.100	0.364	993.740	0.174	14	0.183	R.GLAYIQDNLWR.L
R1/RRR1-6/2	1349.170	1349.519	-259.508	0.382	792.720	0.165	14	0.180	-.GLAYIQDNLWR.-
R1/RRR1-6/3	1666.625	1666.821	-117.889	0.441	1269.564	0.391	27	0.119	R.NNLQAHGVTEQSVLR.A
R1/RRR1-6/3	1666.869	1666.821	29.438	0.519	1001.515	0.437	25	0.111	R.NNLQAHGVTEQSVLR.A
R1/RRR1-6/3	1366.845	1366.591	186.254	0.421	1151.452	0.425	27	0.111	R.TAILAEAIASHLR.Q
R1/RRR1-6/3	1366.421	1366.591	-124.838	0.360	1023.251	0.435	28	0.101	R.TAILAEAIASHLR.Q
R1/RRR1-6/3	1366.404	1366.591	-137.743	0.339	943.011	0.404	27	0.092	R.TAILAEAIASHLR.Q
R1/RRR1-6/2	1725.154	1725.815	-966.217	0.566	2724.645	0.599	26	0.556	K.YNM*ENGGPAPESVTDK.I
R1/RRR1-6/2	1725.294	1725.815	-884.812	0.573	2545.057	0.587	26	0.504	K.YNM*ENGGPAPESVTDK.I
R1/RRR1-6/2	1743.669	1743.940	-155.575	0.531	1635.721	0.489	24	0.297	K.DNLGGDKLVTVEDIVR.Q
R1/RRR1-6/2	1555.632	1555.755	-79.462	0.454	1182.809	0.452	22	0.238	R.DSQDALAPLVDVALK.L
R1/RRR1-6/2	1556.359	1555.755	-255.013	0.427	1054.295	0.464	21	0.229	R.DSQDALAPLVDVALK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1031.421	1032.133	-1664.933	0.353	1017.037	0.465	16	0.224	K.GATIVVSGDGR.Y
R1/RRR1-6/2	1305.959	1306.511	-1192.029	0.433	760.764	0.510	20	0.222	R.SM*PTSAALDVVAK.N
R1/RRR1-6/2	1306.012	1306.511	-383.682	0.430	608.922	0.529	19	0.217	R.SM*PTSAALDVVAK.N
R1/RRR1-6/2	1555.175	1555.755	-1018.715	0.342	1147.117	0.362	20	0.216	R.DSQDALAPLVDVALK.L
R1/RRR1-6/2	1305.645	1306.511	-1433.692	0.333	676.843	0.468	19	0.208	R.SM*PTSAALDVVAK.N
R1/RRR1-6/2	1557.232	1555.755	307.295	0.459	901.522	0.336	18	0.197	R.DSQDALAPLVDVALK.L
R1/RRR1-6/3	1761.571	1761.960	-221.351	0.452	1149.662	0.384	28	0.110	K.KATTPFDGQKPGTSGLR.K
R1/RRR1-6/3	1761.955	1761.960	-3.247	0.410	885.059	0.331	26	0.086	K.KATTPFDGQKPGTSGLR.K
R1/RRR1-6/3	1761.932	1761.960	-16.172	0.432	796.574	0.326	24	0.085	K.KATTPFDGQKPGTSGLR.K
R1/RRR1-6/3	1761.990	1761.960	17.183	0.399	756.801	0.247	25	0.075	K.KATTPFDGQKPGTSGLR.K
R1/RRR1-6/2	1761.963	1760.968	-2.822	0.607	2637.115	0.608	23	0.526	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-6/2	1760.488	1760.968	-273.223	0.493	2565.928	0.562	22	0.490	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-6/2	1759.848	1760.968	-1208.164	0.438	2435.482	0.584	23	0.469	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-4/2	1760.627	1760.968	-194.133	0.524	2231.845	0.570	23	0.420	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-1/2	1760.744	1760.968	-127.295	0.496	1857.061	0.540	23	0.341	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-4/2	1726.956	1726.951	3.147	0.500	1343.561	0.438	18	0.247	R.TYNELVEYNIVLQK.A
R1/RRR1-1/2	1761.017	1760.968	27.907	0.454	1038.063	0.515	22	0.238	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-4/2	1744.359	1744.835	-273.643	0.408	916.247	0.547	20	0.230	R.QEPVDETVTDPLSGEK.V
R1/RRR1-1/2	1696.188	1695.854	197.522	0.507	1096.477	0.417	17	0.220	K.NISSEFEQWNTLVK.K
R1/RRR1-2/2	1760.731	1760.968	-134.945	0.400	902.604	0.478	19	0.219	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-4/2	970.889	971.176	-295.925	0.448	827.262	0.429	16	0.216	K.LGSLSGLVPK.E
R1/RRR1-4/2	971.113	971.176	-65.386	0.424	700.534	0.453	16	0.214	K.LGSLSGLVPK.E
R1/RRR1-4/2	971.142	971.176	-34.874	0.434	613.616	0.445	15	0.210	K.LGSLSGLVPK.E
R1/RRR1-4/2	1175.978	1176.262	-242.442	0.357	1133.855	0.314	15	0.209	K.AGEFFYSAQR.S
R1/RRR1-1/2	1760.977	1760.968	5.450	0.364	417.066	0.437	16	0.197	K.FTSAFQEIVDAYGIAK.Y
R1/RRR1-2/2	971.142	971.176	-35.252	0.286	404.939	0.282	13	0.193	K.LGSLSGLVPK.E
R1/RRR1-15/2	1617.384	1616.797	-256.065	0.549	2259.184	0.508	23	0.407	K.FPTLVTHQESLESK.V
R1/RRR1-15/2	1616.432	1616.797	-226.524	0.538	1983.589	0.517	22	0.358	K.FPTLVTHQESLESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1615.991	1616.797	-1120.468	0.516	2037.004	0.469	22	0.351	K.FPTLVTHQESLESK.V
R1/RRR1-15/2	1363.516	1363.586	-51.328	0.412	1613.152	0.455	19	0.284	K.YHAFLASEAIIK.Q
R1/RRR1-15/2	1247.453	1248.325	-1505.374	0.397	1100.990	0.349	18	0.215	R.EAISQITNESR.E
R1/RRR1-15/2	1248.108	1248.325	-174.379	0.494	1055.621	0.357	17	0.213	R.EAISQITNESR.E
R1/RRR1-15/3	1492.601	1491.759	-106.246	0.551	1850.328	0.399	29	0.193	K.KYHAFLASEAIIK.Q
R1/RRR1-15/2	1363.148	1363.586	-321.876	0.303	763.183	0.329	15	0.192	K.YHAFLASEAIIK.Q
R1/RRR1-15/3	1492.205	1491.759	299.672	0.518	1716.311	0.366	28	0.161	K.KYHAFLASEAIIK.Q
R1/RRR1-15/3	1873.066	1873.099	-17.958	0.470	1014.577	0.579	30	0.141	K.AGKFPTLVTHQESLESK.V
R1/RRR1-15/3	1617.042	1616.797	152.362	0.449	1227.506	0.440	28	0.123	K.FPTLVTHQESLESK.V
R1/RRR1-15/3	1872.811	1873.099	-154.269	0.496	734.239	0.577	27	0.122	K.AGKFPTLVTHQESLESK.V
R1/RRR1-15/3	1872.720	1873.099	-202.918	0.471	817.671	0.549	28	0.120	K.AGKFPTLVTHQESLESK.V
R1/RRR1-15/3	1616.119	1616.797	-1041.370	0.436	949.410	0.428	23	0.104	K.FPTLVTHQESLESK.V
R1/RRR1-15/3	1491.397	1491.759	-243.225	0.502	1162.465	0.348	25	0.100	K.KYHAFLASEAIIK.Q
R1/RRR1-15/3	1616.259	1616.797	-954.354	0.254	868.543	0.176	22	0.064	K.FPTLVTHQESLESK.V
R1/RRR1-7/2	1264.349	1264.453	-81.887	0.542	1427.312	0.559	20	0.292	R.ILAFSQDVVSGK.I
R1/RRR1-7/2	1817.550	1816.951	-221.061	0.542	1349.948	0.608	24	0.291	K.QGVAVTQENSLLDNTAR.I
R1/RRR1-7/2	1265.247	1264.453	-163.115	0.528	1357.663	0.531	20	0.276	R.ILAFSQDVVSGK.I
R1/RRR1-7/2	1816.532	1816.951	-231.430	0.496	1220.798	0.615	22	0.275	K.QGVAVTQENSLLDNTAR.I
R1/RRR1-7/2	1817.481	1816.951	-259.400	0.512	868.764	0.624	19	0.241	K.QGVAVTQENSLLDNTAR.I
R1/RRR1-7/2	1217.219	1218.336	-1744.141	0.324	1413.367	0.283	19	0.224	R.ALIAEGSCGSPR.S
R1/RRR1-7/2	1162.141	1162.364	-191.914	0.454	920.157	0.435	14	0.215	R.AVGALVALYER.A
R1/RRR1-7/2	1187.172	1187.330	-133.620	0.427	691.894	0.455	15	0.209	R.DPGLAPNSFLR.T
R1/RRR1-7/2	1187.228	1187.330	-86.072	0.428	673.650	0.362	15	0.198	R.DPGLAPNSFLR.T
R1/RRR1-7/2	1228.016	1228.404	-317.233	0.294	594.878	0.436	12	0.195	R.FPM*FDWVGGR.T
R1/RRR1-7/2	1162.196	1162.364	-144.920	0.252	535.359	0.305	12	0.186	-.AVGALVALYER.-
R1/RRR1-7/2	1162.197	1162.364	-143.550	0.210	422.011	0.341	11	0.184	R.AVGALVALYER.A
R1/RRR1-6/2	1819.733	1820.101	-203.135	0.521	2057.932	0.595	24	0.395	K.SAIGIGTLLM*DGLGDTIR.V
R1/RRR1-6/2	1803.846	1804.102	-142.172	0.518	1950.112	0.578	23	0.368	K.SAIGIGTLLMDGLGDTIR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1644.849	1644.958	-66.666	0.523	2353.536	0.347	25	0.362	R.GIAMEGATDALIQLIK.D
R1/RRR1-6/2	1820.558	1820.101	251.447	0.556	1737.630	0.613	22	0.342	K.SAIGIGTLLM*DGLGDTIR.V
R1/RRR1-6/2	1644.387	1644.958	-958.385	0.458	2211.716	0.341	24	0.337	R.GIAMEGATDALIQLIK.D
R1/RRR1-6/2	1520.426	1520.712	-188.967	0.514	1982.759	0.426	20	0.328	R.TLFDLQEVSAQIR.E
R1/RRR1-6/2	1520.201	1520.712	-997.211	0.434	2008.344	0.399	20	0.324	R.TLFDLQEVSAQIR.E
R1/RRR1-6/2	1519.760	1520.712	-1288.414	0.387	1993.882	0.383	20	0.318	R.TLFDLQEVSAQIR.E
R1/RRR1-6/2	1819.329	1820.101	-977.237	0.442	1556.197	0.537	22	0.293	K.SAIGIGTLLM*DGLGDTIR.V
R1/RRR1-6/2	1644.084	1644.958	-1143.249	0.386	2055.205	0.273	22	0.292	R.GIAMEGATDALIQLIK.D
R1/RRR1-6/2	1661.321	1660.958	219.362	0.495	1755.290	0.339	21	0.265	R.GIAM*EGATDALIQLIK.D
R1/RRR1-6/2	1316.351	1316.386	-27.123	0.434	1479.164	0.413	17	0.258	K.TEYVSCPSCGR.T
R1/RRR1-6/2	1316.017	1316.386	-281.397	0.462	1491.365	0.372	17	0.250	K.TEYVSCPSCGR.T
R1/RRR1-6/2	861.946	862.008	-72.033	0.401	658.794	0.427	11	0.209	K.APELLYR.S
R1/RRR1-6/2	861.879	862.008	-150.313	0.424	620.241	0.411	11	0.207	K.APELLYR.S
R1/RRR1-6/2	1660.140	1660.958	-1098.334	0.359	1358.815	0.210	18	0.202	R.GIAM*EGATDALIQLIK.D
R1/RRR1-6/2	861.723	862.008	-331.496	0.396	675.828	0.351	11	0.199	-.APELLYR.-
R1/RRR1-6/2	1215.946	1216.409	-382.290	0.256	882.278	0.293	15	0.192	K.DLATVDSILLR.E
R1/RRR1-3/2	1821.449	1820.101	191.499	0.352	283.140	0.325	15	0.188	K.SAIGIGTLLM*DGLGDTIR.V
R1/RRR1-6/2	1216.353	1216.409	-46.767	0.302	570.446	0.138	13	0.177	-.DLATVDSILLR.-
R1/RRR1-5/2	1612.664	1611.818	-95.708	0.520	938.666	0.497	19	0.227	R.VPEPTVDETIEILR.G
R1/RRR1-18/2	1633.285	1632.831	278.743	0.601	2772.182	0.530	22	0.522	K.TIAECLADELINAAK.G
R1/RRR1-19/2	1632.414	1632.831	-256.107	0.520	2786.839	0.440	23	0.488	K.TIAECLADELINAAK.G
R1/RRR1-17/2	1420.348	1420.639	-205.213	0.474	2466.206	0.505	21	0.444	R.VNQAIYLLTTGAR.E
R1/RRR1-17/2	1633.070	1632.831	146.452	0.574	2443.552	0.527	21	0.444	K.TIAECLADELINAAK.G
R1/RRR1-18/2	1632.117	1632.831	-1053.172	0.484	2605.294	0.409	22	0.434	K.TIAECLADELINAAK.G
R1/RRR1-19/2	1421.355	1420.639	-200.416	0.548	2263.313	0.583	21	0.432	R.VNQAIYLLTTGAR.E
R1/RRR1-19/2	1421.315	1420.639	-228.504	0.539	2124.918	0.591	21	0.407	R.VNQAIYLLTTGAR.E
R1/RRR1-19/2	1631.911	1632.831	-1180.287	0.369	2521.708	0.374	22	0.406	K.TIAECLADELINAAK.G
R1/RRR1-18/2	1420.264	1420.639	-265.053	0.468	2185.374	0.516	21	0.391	R.VNQAIYLLTTGAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1420.251	1420.639	-273.848	0.499	2034.349	0.557	20	0.377	R.VNQAIYLLTTGAR.E
R1/RRR1-18/2	1420.240	1420.639	-281.523	0.488	2136.284	0.501	21	0.377	R.VNQAIYLLTTGAR.E
R1/RRR1-17/2	1632.188	1632.831	-1009.430	0.464	2310.385	0.392	21	0.368	K.TIAECLADELINAAK.G
R1/RRR1-17/2	1631.996	1632.831	-1127.785	0.449	2293.197	0.374	21	0.359	K.TIAECLADELINAAK.G
R1/RRR1-18/3	1632.716	1632.831	-70.619	0.554	2513.638	0.423	33	0.353	K.TIAECLADELINAAK.G
R1/RRR1-18/3	1632.291	1632.831	-946.368	0.532	2614.113	0.364	34	0.347	K.TIAECLADELINAAK.G
R1/RRR1-19/2	1632.236	1632.831	-979.846	0.484	2117.242	0.408	20	0.338	K.TIAECLADELINAAK.G
R1/RRR1-18/3	1633.765	1632.831	-40.822	0.573	2388.217	0.433	31	0.331	K.TIAECLADELINAAK.G
R1/RRR1-18/2	1419.565	1420.639	-1465.429	0.410	1762.361	0.525	20	0.321	R.VNQAIYLLTTGAR.E
R1/RRR1-19/2	1419.503	1420.639	-1509.482	0.410	1620.751	0.499	21	0.295	R.VNQAIYLLTTGAR.E
R1/RRR1-17/2	1420.183	1420.639	-322.054	0.458	894.382	0.528	17	0.231	R.VNQAIYLLTTGAR.E
R1/RRR1-18/2	1225.059	1224.354	-240.824	0.430	644.442	0.581	18	0.229	K.HATYLPHTAGR.Y
R1/RRR1-18/2	1225.077	1224.354	-226.729	0.363	552.457	0.578	17	0.219	K.HATYLPHTAGR.Y
R1/RRR1-18/2	1576.476	1576.825	-222.091	0.571	482.357	0.524	18	0.212	R.RVNQAIYLLTTGAR.E
R1/RRR1-17/2	1224.234	1224.354	-97.972	0.375	453.716	0.514	16	0.211	K.HATYLPHTAGR.Y
R1/RRR1-21/2	1420.472	1420.639	-118.053	0.397	604.974	0.455	15	0.206	R.VNQAIYLLTTGAR.E
R1/RRR1-18/2	1575.490	1576.825	-1486.858	0.481	600.698	0.446	18	0.205	R.RVNQAIYLLTTGAR.E
R1/RRR1-18/2	1223.856	1224.354	-408.031	0.293	255.659	0.496	12	0.198	K.HATYLPHTAGR.Y
R1/RRR1-18/2	1101.125	1101.275	-136.501	0.454	774.749	0.327	14	0.198	R.KAQCPLVER.L
R1/RRR1-19/3	1632.776	1632.831	-33.723	0.529	1905.797	0.362	30	0.195	K.TIAECLADELINAAK.G
R1/RRR1-18/2	1576.183	1576.825	-1044.831	0.480	480.507	0.381	18	0.194	-.RVNQAIYLLTTGAR.-
R1/RRR1-18/2	1223.992	1224.354	-296.051	0.198	307.578	0.427	13	0.190	K.HATYLPHTAGR.Y
R1/RRR1-18/2	1632.264	1632.831	-963.178	0.401	762.856	0.201	15	0.176	-.TIAECLADELINAAK.-
R1/RRR1-18/2	1632.298	1632.831	-942.155	0.319	797.837	0.123	15	0.172	-.TIAECLADELINAAK.-
R1/RRR1-18/2	1632.228	1632.831	-985.252	0.340	719.985	0.138	14	0.171	-.TIAECLADELINAAK.-
R1/RRR1-17/3	1633.139	1632.831	189.395	0.461	1297.809	0.296	27	0.101	K.TIAECLADELINAAK.G
R1/RRR1-20/2	1087.269	1087.297	-25.856	0.435	873.478	0.530	16	0.232	K.AFEPILLAGR.S
R1/RRR1-21/2	1086.999	1087.297	-274.453	0.501	884.456	0.499	16	0.230	K.AFEPILLAGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	951.995	952.090	-99.687	0.469	962.146	0.450	13	0.227	K.TSQIYAIR.Q
R1/RRR1-21/2	1087.165	1087.297	-121.586	0.468	878.644	0.486	16	0.227	K.AFEPILLAGR.S
R1/RRR1-21/2	1086.851	1087.297	-411.251	0.361	919.842	0.477	16	0.223	K.AFEPILLAGR.S
R1/RRR1-20/2	951.820	952.090	-283.524	0.454	886.131	0.444	13	0.222	K.TSQIYAIR.Q
R1/RRR1-21/2	951.472	952.090	-1705.039	0.430	937.839	0.432	13	0.222	K.TSQIYAIR.Q
R1/RRR1-20/2	951.952	952.090	-145.351	0.460	972.415	0.405	13	0.220	K.TSQIYAIR.Q
R1/RRR1-21/2	952.010	952.090	-83.738	0.391	996.734	0.388	13	0.217	K.TSQIYAIR.Q
R1/RRR1-21/2	956.018	956.120	-107.208	0.386	859.499	0.408	13	0.213	K.ALVAYYQK.Y
R1/RRR1-20/2	951.200	952.090	-1992.439	0.356	731.365	0.397	13	0.208	K.TSQIYAIR.Q
R1/RRR1-21/2	885.059	885.043	17.484	0.371	883.540	0.385	11	0.208	R.TLLVADPR.R
R1/RRR1-21/2	1308.650	1309.490	-1409.997	0.378	788.542	0.414	16	0.206	K.TAVAVSYCKPGR.G
R1/RRR1-21/2	884.777	885.043	-301.340	0.336	829.038	0.387	11	0.205	R.TLLVADPR.R
R1/RRR1-19/2	885.073	885.043	33.393	0.334	1011.395	0.268	12	0.199	R.TLLVADPR.R
R1/RRR1-21/2	955.398	956.120	-1807.732	0.293	800.984	0.328	13	0.198	K.ALVAYYQK.Y
R1/RRR1-20/2	956.007	956.120	-117.967	0.325	495.423	0.374	11	0.198	K.ALVAYYQK.Y
R1/RRR1-21/2	1308.341	1309.490	-1647.372	0.339	638.573	0.390	15	0.197	K.TAVAVSYCKPGR.G
R1/RRR1-20/2	956.952	956.120	-175.554	0.342	752.489	0.293	13	0.197	K.ALVAYYQK.Y
R1/RRR1-19/2	951.884	952.090	-216.619	0.304	712.520	0.282	13	0.196	K.TSQIYAIR.Q
R1/RRR1-21/2	1309.007	1309.490	-370.451	0.316	717.046	0.319	16	0.193	K.TAVAVSYCKPGR.G
R1/RRR1-19/2	885.180	885.043	155.109	0.301	559.727	0.194	10	0.179	-.TLLVADPR.-
R1/RRR1-18/2	1133.632	1134.272	-1450.988	0.372	1093.449	0.470	15	0.234	R.FHQYQVVGR.G
R1/RRR1-18/2	1018.531	1019.256	-1698.265	0.521	835.054	0.317	14	0.202	R.FPCIQIIK.T
R1/RRR1-18/2	1134.211	1134.272	-54.256	0.374	728.206	0.365	13	0.201	R.FHQYQVVGR.G
R1/RRR1-18/2	1191.916	1192.303	-325.795	0.271	335.394	0.561	14	0.200	R.GLPTPTDEHPK.I
R1/RRR1-18/2	1133.896	1134.272	-332.856	0.386	946.637	0.290	14	0.200	R.FHQYQVVGR.G
R1/RRR1-18/2	1191.994	1192.303	-260.447	0.261	317.734	0.530	14	0.198	R.GLPTPTDEHPK.I
R1/RRR1-18/2	1019.039	1019.256	-212.857	0.480	802.316	0.265	14	0.193	-.FPCIQIIK.-
R1/RRR1-18/2	1193.204	1192.303	-83.588	0.263	383.489	0.389	14	0.193	R.GLPTPTDEHPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1018.515	1019.256	-1714.400	0.453	831.221	0.214	14	0.191	R.FPCIQIIK.T
R1/RRR1-18/3	1274.217	1274.574	-280.982	0.476	2421.771	0.080	25	0.177	R.VRFPCIQIIK.T
R1/RRR1-18/3	1238.424	1238.460	-29.484	0.444	966.428	0.400	21	0.094	K.SDIKFPLVYR.K
R1/RRR1-18/3	1238.355	1238.460	-84.803	0.429	683.945	0.442	19	0.091	K.SDIKFPLVYR.K
R1/RRR1-15/2	1146.997	1147.261	-230.315	0.425	1418.293	0.412	17	0.252	K.EAISQVVGESK.E
R1/RRR1-15/2	1146.780	1147.261	-420.828	0.346	1376.125	0.359	17	0.235	K.EAISQVVGESK.E
R1/RRR1-15/2	1146.425	1147.261	-1606.422	0.306	1101.208	0.366	15	0.213	K.EAISQVVGESK.E
R1/RRR1-13/2	1746.704	1746.001	-170.586	0.556	2164.371	0.465	23	0.371	K.GVDVILDNIGGLYLQR.N
R1/RRR1-13/2	1745.266	1746.001	-997.065	0.476	2109.165	0.456	22	0.360	K.GVDVILDNIGGLYLQR.N
R1/RRR1-13/2	987.665	988.160	-503.190	0.358	923.758	0.391	14	0.211	K.ALIVSEVEK.N
R1/RRR1-13/2	942.197	943.126	-2053.191	0.355	924.918	0.394	13	0.208	R.LTIQAAGLR.N
R1/RRR1-13/2	1099.165	1099.312	-134.628	0.495	697.289	0.394	15	0.206	R.RLTIQAAGLR.N
R1/RRR1-13/2	987.984	988.160	-178.590	0.304	1069.702	0.276	14	0.201	K.ALIVSEVEK.N
R1/RRR1-13/2	1066.780	1067.174	-370.899	0.311	965.755	0.303	16	0.200	K.VFVTAGSEEK.L
R1/RRR1-13/2	1067.087	1067.174	-81.764	0.369	830.300	0.306	15	0.196	K.VFVTAGSEEK.L
R1/RRR1-13/2	1099.080	1099.312	-211.726	0.459	797.594	0.259	15	0.191	R.RLTIQAAGLR.N
R1/RRR1-13/2	987.502	988.160	-1684.365	0.210	533.380	0.269	11	0.184	-.ALIVSEVEK.-
R1/RRR1-13/2	1099.359	1099.312	42.587	0.394	679.877	0.142	14	0.179	-.RLTIQAAGLR.-
R1/RRR1-11/2	1654.220	1652.751	284.245	0.502	2899.493	0.528	27	1.000	K.AAAVVAGNGATNGATNGVH.-
R1/RRR1-11/2	1653.251	1652.751	303.297	0.602	2855.842	0.534	27	0.958	K.AAAVVAGNGATNGATNGVH.-
R1/RRR1-11/2	1653.387	1652.751	-220.868	0.614	2818.965	0.559	27	0.938	K.AAAVVAGNGATNGATNGVH.-
R1/RRR1-11/2	1653.453	1652.751	-180.577	0.602	2832.272	0.528	27	0.937	K.AAAVVAGNGATNGATNGVH.-
R1/RRR1-11/2	1653.088	1652.751	204.820	0.556	2762.986	0.589	27	0.913	K.AAAVVAGNGATNGATNGVH.-
R1/RRR1-11/2	1169.412	1169.442	-25.925	0.578	1976.372	0.462	19	0.338	R.ALVDVLAALKR.A
R1/RRR1-12/2	1169.520	1169.442	66.519	0.473	1803.811	0.465	19	0.313	R.ALVDVLAALKR.A
R1/RRR1-13/2	1150.115	1150.310	-169.330	0.493	1516.611	0.594	18	0.310	K.SPLTTVYAAAR.A
R1/RRR1-11/2	1168.648	1169.442	-1540.044	0.532	1756.197	0.470	18	0.307	R.ALVDVLAALKR.A
R1/RRR1-11/2	1170.211	1169.442	-198.438	0.541	1674.672	0.475	18	0.298	R.ALVDVLAALKR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1150.008	1150.310	-263.035	0.534	1500.298	0.549	18	0.296	K.SPLTTVYAAAR.A
R1/RRR1-15/2	1150.297	1150.310	-11.347	0.423	1341.047	0.492	17	0.261	K.SPLTTVYAAAR.A
R1/RRR1-11/2	1012.940	1013.256	-312.710	0.535	1219.467	0.526	17	0.261	R.ALVDVLAALK.R
R1/RRR1-11/2	1013.072	1013.256	-182.386	0.537	1245.638	0.509	17	0.260	R.ALVDVLAALK.R
R1/RRR1-12/2	1012.682	1013.256	-1558.819	0.503	1242.174	0.491	17	0.255	R.ALVDVLAALK.R
R1/RRR1-12/2	1012.960	1013.256	-292.761	0.519	1191.556	0.510	17	0.255	R.ALVDVLAALK.R
R1/RRR1-11/2	1013.151	1013.256	-104.063	0.553	1226.679	0.492	17	0.254	R.ALVDVLAALK.R
R1/RRR1-12/2	1012.733	1013.256	-1508.326	0.497	1067.135	0.460	16	0.234	R.ALVDVLAALK.R
R1/RRR1-13/2	1150.222	1150.310	-76.174	0.427	900.687	0.441	16	0.219	K.SPLTTVYAAAR.A
R1/RRR1-14/2	1150.465	1150.310	135.093	0.374	523.764	0.456	17	0.210	K.SPLTTVYAAAR.A
R1/RRR1-3/2	1170.510	1169.442	57.676	0.318	840.697	0.331	15	0.199	R.ALVDVLAALKR.A
R1/RRR1-11/2	1151.420	1150.310	95.850	0.282	473.066	0.318	15	0.196	K.SPLTTVYAAAR.A
R1/RRR1-12/2	1151.079	1150.310	-201.098	0.221	601.317	0.348	14	0.192	K.SPLTTVYAAAR.A
R1/RRR1-15/2	1150.404	1150.310	82.524	0.217	334.154	0.324	14	0.188	-.SPLTTVYAAAR.-
R1/RRR1-12/3	1523.278	1523.718	-289.254	0.360	1299.330	0.355	25	0.110	R.EVVGDRDFFIVAR.T
R1/RRR1-11/3	1523.312	1523.718	-267.064	0.336	1208.524	0.344	24	0.101	-.EVVGDRDFFIVAR.-
R1/RRR1-11/3	1523.784	1523.718	43.733	0.410	1080.950	0.369	23	0.100	R.EVVGDRDFFIVAR.T
R1/RRR1-11/3	1523.850	1523.718	86.998	0.369	978.178	0.367	23	0.093	R.EVVGDRDFFIVAR.T
R1/RRR1-12/3	1523.352	1523.718	-241.017	0.360	900.074	0.344	22	0.087	R.EVVGDRDFFIVAR.T
R1/RRR1-12/3	1523.409	1523.718	-203.153	0.365	523.923	0.341	17	0.076	-.EVVGDRDFFIVAR.-
R1/RRR1-6/2	976.780	977.144	-373.360	0.503	1061.366	0.510	13	0.244	K.ANVLAFWR.Q
R1/RRR1-6/2	976.596	977.144	-1590.154	0.465	1049.134	0.510	13	0.242	K.ANVLAFWR.Q
R1/RRR1-6/2	1250.956	1251.328	-297.891	0.390	1146.805	0.371	15	0.221	K.SEEEQLNVFR.F
R1/RRR1-6/2	1115.686	1116.290	-1441.735	0.354	1171.232	0.369	16	0.220	R.VGIDEVASVVK.Q
R1/RRR1-6/2	1251.015	1251.328	-250.998	0.405	1136.625	0.361	16	0.219	K.SEEEQLNVFR.F
R1/RRR1-6/2	1251.099	1251.328	-183.064	0.437	1139.575	0.349	15	0.217	K.SEEEQLNVFR.F
R1/RRR1-6/2	1607.157	1606.847	193.532	0.430	772.243	0.505	18	0.215	R.VFTPSVIEPSFGIGR.I
R1/RRR1-5/2	1389.931	1390.615	-1214.790	0.393	849.361	0.453	16	0.212	K.LPFAAAQIGQAFR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1229.161	1229.325	-133.737	0.439	532.711	0.481	18	0.208	R.QAAVDAQAEAVR.A
R1/RRR1-6/2	1606.162	1606.847	-1051.934	0.327	886.416	0.383	18	0.202	R.VFTPSVIEPSFGIGR.I
R1/RRR1-1/2	1390.071	1390.615	-1113.376	0.281	685.215	0.360	15	0.191	K.LPFAAAQIGQAFR.N
R1/RRR1-6/2	1115.474	1116.290	-1632.995	0.324	717.928	0.306	14	0.190	R.VGIDEVASVVK.Q
R1/RRR1-17/2	1849.417	1850.066	-893.976	0.502	3116.744	0.500	25	0.623	R.NVQAILDSYTTIVNAAR.S
R1/RRR1-17/2	1375.235	1375.515	-204.199	0.479	2385.202	0.490	21	0.427	K.VWSQLSSAGLGNR.V
R1/RRR1-17/2	1375.996	1375.515	350.350	0.549	2188.653	0.506	21	0.392	K.VWSQLSSAGLGNR.V
R1/RRR1-17/2	1375.884	1375.515	268.955	0.521	1777.808	0.521	20	0.326	K.VWSQLSSAGLGNR.V
R1/RRR1-17/2	1381.150	1381.578	-311.201	0.514	1372.551	0.523	21	0.274	R.VDLVGSM*TSLQSK.C
R1/RRR1-17/3	1743.328	1741.805	-274.340	0.554	1861.824	0.567	29	0.273	R.NHEGHSGWQAYDIAR.N
R1/RRR1-17/2	1381.189	1381.578	-282.648	0.483	1185.332	0.519	20	0.254	R.VDLVGSM*TSLQSK.C
R1/RRR1-17/2	1380.878	1381.578	-1235.159	0.474	1179.378	0.429	20	0.234	R.VDLVGSM*TSLQSK.C
R1/RRR1-17/2	1090.647	1091.152	-1384.240	0.410	900.946	0.362	16	0.208	K.CGNPPAGFDR.N
R1/RRR1-17/2	1365.156	1365.579	-310.640	0.327	607.531	0.415	16	0.199	R.VDLVGSMTSLQSK.C
R1/RRR1-17/2	1090.747	1091.152	-372.627	0.315	810.781	0.258	16	0.192	K.CGNPPAGFDR.N
R1/RRR1-17/2	1090.760	1091.152	-360.724	0.319	733.477	0.273	15	0.192	K.CGNPPAGFDR.N
R1/RRR1-17/3	1741.528	1741.805	-159.500	0.469	761.015	0.407	24	0.093	R.NHEGHSGWQAYDIAR.N
R1/RRR1-17/3	1740.876	1741.805	-1111.166	0.396	373.183	0.425	20	0.091	R.NHEGHSGWQAYDIAR.N
R1/RRR1-16/2	1662.452	1662.908	-275.194	0.581	2259.720	0.525	23	0.411	K.LQQVLNVYDEILSK.N
R1/RRR1-16/2	1662.355	1662.908	-937.494	0.579	2157.461	0.483	22	0.375	K.LQQVLNVYDEILSK.N
R1/RRR1-16/2	1662.366	1662.908	-930.711	0.580	1847.757	0.527	21	0.336	K.LQQVLNVYDEILSK.N
R1/RRR1-16/2	1344.101	1343.460	-267.865	0.529	1432.705	0.529	17	0.282	R.YVCTQFPEGNK.T
R1/RRR1-16/2	1791.201	1791.081	66.741	0.555	1370.987	0.531	19	0.271	K.KLQQVLNVYDEILSK.N
R1/RRR1-16/2	1343.220	1343.460	-179.533	0.515	1426.911	0.462	17	0.265	R.YVCTQFPEGNK.T
R1/RRR1-16/2	1789.351	1791.081	-2091.250	0.410	1338.237	0.479	18	0.254	K.KLQQVLNVYDEILSK.N
R1/RRR1-16/2	1276.096	1275.439	-269.763	0.408	1066.234	0.438	15	0.225	K.LRDPNGQVTFK.H
R1/RRR1-16/2	1274.514	1275.439	-1514.527	0.445	986.180	0.432	16	0.221	K.LRDPNGQVTFK.H
R1/RRR1-16/2	1275.203	1275.439	-185.748	0.404	1072.116	0.388	16	0.219	K.LRDPNGQVTFK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1097.001	1097.203	-184.783	0.378	964.292	0.402	17	0.217	K.TLYGTGSLER.A
R1/RRR1-16/2	1096.422	1097.203	-1629.656	0.291	1047.907	0.399	17	0.216	K.TLYGTGSLER.A
R1/RRR1-16/2	1275.126	1275.439	-245.868	0.442	855.315	0.418	15	0.211	K.LRDPNGQVTFK.H
R1/RRR1-16/2	1096.905	1097.203	-272.979	0.303	832.121	0.436	16	0.211	K.TLYGTGSLER.A
R1/RRR1-16/2	1342.220	1343.460	-1673.841	0.315	1088.640	0.320	15	0.206	R.YVCTQFPEGNK.T
R1/RRR1-16/2	1096.361	1097.203	-1685.473	0.286	524.473	0.432	14	0.197	-.TLYGTGSLER.-
R1/RRR1-16/2	1097.064	1097.203	-127.520	0.228	694.761	0.291	15	0.190	K.TLYGTGSLER.A
R1/RRR1-16/2	1663.008	1662.908	60.326	0.327	293.705	0.349	11	0.180	-.LQQVLNVYDEILSK.-
R1/RRR1-16/3	1275.280	1275.439	-125.023	0.437	1245.085	0.282	25	0.088	K.LRDPNGQVTFK.H
R1/RRR1-16/3	1275.570	1275.439	102.924	0.413	694.542	0.379	22	0.087	K.LRDPNGQVTFK.H
R1/RRR1-16/3	1275.622	1275.439	143.808	0.403	736.934	0.376	23	0.086	K.LRDPNGQVTFK.H
R1/RRR1-16/3	1276.487	1275.439	38.202	0.441	1176.820	0.274	23	0.085	K.LRDPNGQVTFK.H
R1/RRR1-15/3	1275.010	1275.439	-337.223	0.314	615.039	0.331	20	0.082	K.LRDPNGQVTFK.H
R1/RRR1-16/3	1275.789	1275.439	275.219	0.359	654.930	0.304	23	0.081	K.LRDPNGQVTFK.H
R1/RRR1-15/2	1662.710	1663.767	-1240.971	0.330	2465.183	0.207	26	0.344	K.DLASAGADVGSATDWVK.N
R1/RRR1-16/2	1248.070	1248.478	-327.622	0.491	1850.865	0.494	19	0.328	K.LLNANSITM*VR.I
R1/RRR1-17/2	1663.038	1663.767	-1042.830	0.433	1736.750	0.470	24	0.304	K.DLASAGADVGSATDWVK.N
R1/RRR1-16/2	1249.198	1248.478	-224.904	0.555	1707.406	0.481	19	0.303	K.LLNANSITM*VR.I
R1/RRR1-16/2	1249.210	1248.478	-215.198	0.525	1667.812	0.496	18	0.302	K.LLNANSITM*VR.I
R1/RRR1-15/2	1247.851	1248.478	-1308.074	0.490	1653.460	0.484	18	0.297	K.LLNANSITM*VR.I
R1/RRR1-17/2	1535.345	1534.736	-255.393	0.543	1365.747	0.589	21	0.289	R.IYDTDPTVLNALAK.T
R1/RRR1-15/2	1248.196	1248.478	-226.948	0.497	1350.866	0.528	18	0.273	K.LLNANSITM*VR.I
R1/RRR1-17/2	1248.004	1248.478	-380.813	0.432	1580.568	0.425	18	0.272	K.LLNANSITM*VR.I
R1/RRR1-16/2	1534.397	1534.736	-221.638	0.442	1374.604	0.471	21	0.260	R.IYDTDPTVLNALAK.T
R1/RRR1-17/2	1247.561	1248.478	-1541.560	0.366	1344.511	0.477	17	0.257	K.LLNANSITM*VR.I
R1/RRR1-16/2	1534.243	1534.736	-321.813	0.446	1218.736	0.494	21	0.250	R.IYDTDPTVLNALAK.T
R1/RRR1-17/2	1534.132	1534.736	-1048.571	0.462	976.729	0.532	20	0.238	R.IYDTDPTVLNALAK.T
R1/RRR1-16/2	1232.149	1232.479	-268.156	0.375	969.668	0.428	16	0.220	K.LLNANSITMVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1533.958	1534.736	-1162.509	0.328	895.785	0.439	19	0.213	R.IYDTDPTVLNALAK.T
R1/RRR1-16/2	1533.607	1534.736	-1392.063	0.335	747.071	0.391	17	0.201	R.IYDTDPTVLNALAK.T
R1/RRR1-16/2	964.037	964.229	-199.343	0.462	620.022	0.379	12	0.200	-.VM*VM*LPNK.-
R1/RRR1-16/2	964.163	964.229	-68.139	0.439	745.467	0.350	12	0.200	-.VM*VM*LPNK.-
R1/RRR1-16/2	963.982	964.229	-256.637	0.420	629.605	0.345	12	0.200	K.VM*VM*LPNK.D
R1/RRR1-16/2	1398.322	1397.556	-167.555	0.506	811.955	0.361	16	0.197	-.DASNLIDPPEVVK.-
R1/RRR1-16/2	1398.149	1397.556	-292.013	0.475	797.116	0.330	16	0.194	-.DASNLIDPPEVVK.-
R1/RRR1-17/2	1248.323	1248.478	-124.332	0.274	437.135	0.291	12	0.192	K.LLNANSITM*VR.I
R1/RRR1-17/2	1398.290	1397.556	-190.587	0.310	650.327	0.325	15	0.191	R.DASNLIDPPEVVK.L
R1/RRR1-16/2	1397.236	1397.556	-229.287	0.418	612.844	0.287	14	0.186	-.DASNLIDPPEVVK.-
R1/RRR1-17/2	1398.091	1397.556	-333.536	0.357	648.282	0.231	14	0.183	R.DASNLIDPPEVVK.L
R1/RRR1-5/2	1102.073	1102.223	-136.383	0.511	1205.617	0.471	17	0.248	K.LGIIEDATNR.N
R1/RRR1-5/2	1101.364	1102.223	-1693.269	0.425	1352.748	0.370	17	0.238	K.LGIIEDATNR.N
R1/RRR1-5/2	1101.840	1102.223	-349.096	0.479	1169.269	0.405	17	0.231	K.LGIIEDATNR.N
R1/RRR1-5/2	1164.128	1164.245	-100.506	0.485	973.538	0.457	18	0.227	K.ALDTESVDSVK.I
R1/RRR1-5/2	1163.251	1164.245	-1719.279	0.321	892.166	0.415	18	0.210	K.ALDTESVDSVK.I
R1/RRR1-5/2	1552.450	1552.749	-193.350	0.356	1114.776	0.317	18	0.207	R.VFISDEFDELLPK.Y
R1/RRR1-4/3	1751.973	1751.922	29.092	0.529	1697.003	0.470	31	0.206	K.IGGVPHGLSTDSEVVQR.E
R1/RRR1-5/2	1166.607	1167.294	-1450.066	0.331	560.780	0.468	14	0.203	K.LASLDEYISR.M
R1/RRR1-4/3	1751.895	1751.922	-15.775	0.496	1573.152	0.514	30	0.200	K.IGGVPHGLSTDSEVVQR.E
R1/RRR1-5/2	1166.963	1167.294	-284.185	0.338	870.902	0.267	16	0.194	K.LASLDEYISR.M
R1/RRR1-5/2	1578.279	1578.702	-268.538	0.366	1038.524	0.250	16	0.192	K.ETTTEWELLNDVK.A
R1/RRR1-13/2	1317.962	1318.416	-344.802	0.456	2291.388	0.437	21	0.380	R.LANDTQGTVEAAK.W
R1/RRR1-9/2	1318.027	1318.416	-295.366	0.492	2158.724	0.468	21	0.366	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1318.228	1318.416	-142.813	0.522	1891.479	0.544	21	0.347	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1460.173	1460.527	-243.302	0.498	1737.253	0.559	20	0.332	K.AISTSNAYDDQFK.Q
R1/RRR1-10/2	1318.940	1318.416	-361.535	0.519	1699.881	0.574	21	0.328	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1460.131	1460.527	-272.406	0.493	1697.499	0.557	20	0.325	K.AISTSNAYDDQFK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1318.233	1318.416	-139.097	0.482	1780.003	0.490	21	0.314	R.LANDTQGTVEAAK.W
R1/RRR1-9/2	1318.054	1318.416	-274.831	0.491	1797.465	0.475	21	0.312	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1318.099	1318.416	-240.638	0.461	1767.981	0.475	21	0.308	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1318.359	1318.416	-42.684	0.454	1656.695	0.503	20	0.300	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1319.014	1318.416	-305.077	0.527	1479.101	0.577	20	0.298	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1317.899	1318.416	-1154.002	0.440	1690.400	0.473	21	0.297	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1286.248	1286.493	-191.293	0.436	1518.278	0.548	20	0.297	K.IPATAECVPSIK.E
R1/RRR1-9/2	1318.053	1318.416	-275.574	0.499	1607.469	0.496	20	0.292	R.LANDTQGTVEAAK.W
R1/RRR1-12/2	1317.644	1318.416	-1348.337	0.388	1643.814	0.473	21	0.290	R.LANDTQGTVEAAK.W
R1/RRR1-12/2	1318.023	1318.416	-298.432	0.486	1558.693	0.483	20	0.283	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1286.133	1286.493	-280.510	0.459	1385.844	0.554	19	0.282	K.IPATAECVPSIK.E
R1/RRR1-10/2	1318.484	1318.416	52.410	0.421	1493.331	0.493	20	0.277	R.LANDTQGTVEAAK.W
R1/RRR1-1/2	1318.283	1318.416	-100.734	0.451	1491.407	0.486	21	0.277	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1285.702	1286.493	-1397.549	0.412	1468.368	0.492	20	0.276	K.IPATAECVPSIK.E
R1/RRR1-10/2	1460.107	1460.527	-288.511	0.467	1192.684	0.566	18	0.262	K.AISTSNAYDDQFK.Q
R1/RRR1-1/2	1318.097	1318.416	-242.125	0.465	1330.356	0.496	20	0.262	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1319.085	1318.416	-251.133	0.566	1165.324	0.565	19	0.262	R.LANDTQGTVEAAK.W
R1/RRR1-1/2	1317.527	1318.416	-1438.041	0.384	1399.509	0.389	20	0.244	R.LANDTQGTVEAAK.W
R1/RRR1-11/2	1319.267	1318.416	-113.002	0.432	880.757	0.530	18	0.232	R.LANDTQGTVEAAK.W
R1/RRR1-14/2	1319.251	1318.416	-124.790	0.437	750.751	0.566	18	0.232	R.LANDTQGTVEAAK.W
R1/RRR1-16/2	1317.646	1318.416	-1346.848	0.404	686.340	0.506	16	0.217	R.LANDTQGTVEAAK.W
R1/RRR1-16/2	1319.700	1318.416	216.390	0.379	675.637	0.499	16	0.215	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1178.037	1178.320	-241.083	0.491	828.344	0.407	16	0.211	R.GVTSNPSIFQK.A
R1/RRR1-17/2	1319.095	1318.416	-243.984	0.326	596.804	0.488	15	0.209	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1178.087	1178.320	-198.566	0.466	666.123	0.412	15	0.206	R.GVTSNPSIFQK.A
R1/RRR1-17/2	1319.291	1318.416	-94.903	0.336	523.470	0.437	15	0.204	R.LANDTQGTVEAAK.W
R1/RRR1-18/2	1319.093	1318.416	-245.191	0.280	381.105	0.461	14	0.202	R.LANDTQGTVEAAK.W
R1/RRR1-10/2	1177.722	1178.320	-1360.594	0.400	589.282	0.363	14	0.198	R.GVTSNPSIFQK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1179.446	1178.320	107.482	0.419	539.340	0.361	14	0.198	R.GVTSNPSIFQK.A
R1/RRR1-10/2	1203.059	1203.416	-297.742	0.383	813.704	0.295	14	0.195	K.VVDRPNVYIK.I
R1/RRR1-9/2	1177.768	1178.320	-1321.661	0.351	827.050	0.265	15	0.193	R.GVTSNPSIFQK.A
R1/RRR1-10/2	1202.446	1203.416	-1643.280	0.329	758.467	0.283	14	0.192	K.VVDRPNVYIK.I
R1/RRR1-12/2	1178.876	1178.320	-377.590	0.248	451.634	0.349	12	0.189	-.GVTSNPSIFQK.-
R1/RRR1-10/2	1203.158	1203.416	-214.781	0.350	498.716	0.280	12	0.185	-.VVDRPNVYIK.-
R1/RRR1-5/2	1824.530	1824.025	-272.021	0.585	1394.183	0.583	23	0.291	R.LLSSGNVYTQEEILTR.I
R1/RRR1-5/2	1650.154	1650.813	-1008.160	0.456	1682.736	0.403	18	0.275	K.GILQNDPFEVFDQK.G
R1/RRR1-5/2	1345.329	1344.495	-123.463	0.540	1262.084	0.542	18	0.266	K.VFANAETTISYK.I
R1/RRR1-5/2	1651.151	1650.813	204.986	0.507	1665.256	0.375	18	0.264	K.GILQNDPFEVFDQK.G
R1/RRR1-5/2	1650.499	1650.813	-190.766	0.500	1307.656	0.416	17	0.236	K.GILQNDPFEVFDQK.G
R1/RRR1-5/2	1344.335	1344.495	-118.910	0.428	915.166	0.465	18	0.222	K.VFANAETTISYK.I
R1/RRR1-5/2	1566.336	1566.804	-299.709	0.439	541.416	0.528	17	0.208	R.LGISYPELTAM*QAR.A
R1/RRR1-5/2	1089.040	1089.291	-231.109	0.356	790.646	0.385	15	0.202	R.AM*DGLPVTIR.L
R1/RRR1-5/2	1279.455	1279.491	-28.090	0.405	717.220	0.386	15	0.201	K.LSEVNPM*LGFR.G
R1/RRR1-5/2	1279.167	1279.491	-253.459	0.431	841.265	0.338	16	0.200	K.LSEVNPM*LGFR.G
R1/RRR1-2/2	1652.107	1650.813	178.484	0.378	746.718	0.315	15	0.190	K.GILQNDPFEVFDQK.G
R1/RRR1-14/2	1534.189	1533.580	-255.426	0.598	2713.444	0.618	24	0.554	R.AAGGASGGEELTVEER.N
R1/RRR1-14/2	1533.241	1533.580	-221.725	0.515	2748.002	0.544	25	0.531	R.AAGGASGGEELTVEER.N
R1/RRR1-14/2	1533.216	1533.580	-237.780	0.498	2566.662	0.546	24	0.487	R.AAGGASGGEELTVEER.N
R1/RRR1-15/2	1533.564	1533.580	-10.507	0.518	2281.710	0.543	24	0.422	R.AAGGASGGEELTVEER.N
R1/RRR1-15/2	1532.874	1533.580	-1116.366	0.480	1837.031	0.527	21	0.333	R.AAGGASGGEELTVEER.N
R1/RRR1-14/2	1389.135	1389.537	-290.383	0.458	1483.396	0.528	20	0.288	R.IISSIEQKEEGR.G
R1/RRR1-14/2	1389.032	1389.537	-1086.620	0.446	1168.576	0.518	18	0.251	R.IISSIEQKEEGR.G
R1/RRR1-14/2	1390.109	1389.537	-308.763	0.477	990.338	0.574	17	0.247	R.IISSIEQKEEGR.G
R1/RRR1-15/2	1390.356	1389.537	-130.561	0.357	302.483	0.322	15	0.197	R.IISSIEQKEEGR.G
R1/RRR1-6/3	1885.278	1885.107	90.939	0.578	3612.017	0.470	38	0.790	K.IYQEYGITAENVIATAK.S
R1/RRR1-6/2	1404.047	1403.608	313.440	0.526	2892.568	0.559	24	0.580	K.AIGIDKFGASAPAGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1885.670	1885.107	-232.164	0.615	2672.397	0.635	27	0.552	K.IYQEYGITAENVIATAK.S
R1/RRR1-6/2	1885.424	1885.107	168.670	0.631	2685.749	0.594	26	0.534	K.IYQEYGITAENVIATAK.S
R1/RRR1-5/2	1886.477	1885.107	196.874	0.624	2441.542	0.657	26	0.504	K.IYQEYGITAENVIATAK.S
R1/RRR1-6/2	1884.697	1885.107	-217.992	0.555	2349.286	0.603	26	0.461	K.IYQEYGITAENVIATAK.S
R1/RRR1-6/2	1403.590	1403.608	-12.963	0.571	2193.920	0.563	22	0.413	K.AIGIDKFGASAPAGK.I
R1/RRR1-2/2	1885.072	1885.107	-18.745	0.553	2153.937	0.560	25	0.402	K.IYQEYGITAENVIATAK.S
R1/RRR1-6/2	1404.186	1403.608	-301.919	0.512	2305.001	0.443	22	0.390	K.AIGIDKFGASAPAGK.I
R1/RRR1-6/3	1884.923	1885.107	-97.870	0.542	2145.785	0.474	31	0.303	K.IYQEYGITAENVIATAK.S
R1/RRR1-6/2	1375.860	1376.540	-1224.811	0.471	1636.454	0.389	18	0.267	R.VSLEAGSTLGWQK.Y
R1/RRR1-6/3	1884.809	1885.107	-158.483	0.529	2093.109	0.418	31	0.264	K.IYQEYGITAENVIATAK.S
R1/RRR1-6/2	1375.533	1376.540	-1463.115	0.318	1567.537	0.265	19	0.233	R.VSLEAGSTLGWQK.Y
R1/RRR1-1/2	1376.304	1376.540	-172.015	0.398	1255.473	0.387	17	0.229	R.VSLEAGSTLGWQK.Y
R1/RRR1-2/2	1443.204	1442.640	-302.749	0.486	722.871	0.526	21	0.227	K.LAQLPGTSIEGVEK.G
R1/RRR1-1/2	1442.279	1442.640	-250.650	0.454	661.389	0.527	20	0.223	K.LAQLPGTSIEGVEK.G
R1/RRR1-6/2	1442.320	1442.640	-222.460	0.481	701.674	0.497	21	0.222	K.LAQLPGTSIEGVEK.G
R1/RRR1-5/2	1443.376	1442.640	-183.532	0.469	565.653	0.542	19	0.222	K.LAQLPGTSIEGVEK.G
R1/RRR1-3/2	1442.665	1442.640	17.601	0.418	738.050	0.493	21	0.221	K.LAQLPGTSIEGVEK.G
R1/RRR1-6/2	1442.333	1442.640	-212.950	0.468	718.004	0.487	21	0.221	K.LAQLPGTSIEGVEK.G
R1/RRR1-5/2	1442.188	1442.640	-313.829	0.444	543.939	0.521	19	0.218	K.LAQLPGTSIEGVEK.G
R1/RRR1-6/2	1616.300	1616.734	-269.483	0.470	735.534	0.491	18	0.215	K.M*FGDFQKDTPEER.N
R1/RRR1-2/2	1442.152	1442.640	-339.136	0.423	553.333	0.493	19	0.215	K.LAQLPGTSIEGVEK.G
R1/RRR1-6/2	1441.913	1442.640	-1201.310	0.437	633.066	0.464	20	0.215	K.LAQLPGTSIEGVEK.G
R1/RRR1-2/2	1442.382	1442.640	-178.989	0.421	624.487	0.453	20	0.213	K.LAQLPGTSIEGVEK.G
R1/RRR1-6/2	1375.668	1376.540	-1364.447	0.382	1223.058	0.306	17	0.212	R.VSLEAGSTLGWQK.Y
R1/RRR1-5/2	1442.233	1442.640	-283.088	0.431	451.525	0.487	18	0.212	K.LAQLPGTSIEGVEK.G
R1/RRR1-3/2	1442.514	1442.640	-87.475	0.416	487.167	0.453	18	0.209	K.LAQLPGTSIEGVEK.G
R1/RRR1-6/2	1443.516	1442.640	-86.227	0.441	448.090	0.449	17	0.207	K.LAQLPGTSIEGVEK.G
R1/RRR1-3/2	1442.453	1442.640	-129.495	0.372	496.698	0.447	18	0.207	K.LAQLPGTSIEGVEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1442.413	1442.640	-157.934	0.359	407.898	0.440	17	0.205	K.LAQLPGTSIEGVEK.G
R1/RRR1-4/2	1441.917	1442.640	-1198.505	0.386	364.920	0.428	16	0.204	K.LAQLPGTSIEGVEK.G
R1/RRR1-1/2	1441.736	1442.640	-1324.086	0.320	398.887	0.375	17	0.201	K.LAQLPGTSIEGVEK.G
R1/RRR1-1/2	1376.336	1376.540	-148.704	0.258	620.559	0.233	16	0.187	R.VSLEAGSTLGWQK.Y
R1/RRR1-3/2	1376.394	1376.540	-106.444	0.273	817.251	0.207	16	0.185	R.VSLEAGSTLGWQK.Y
R1/RRR1-3/2	1142.240	1142.331	-79.493	0.453	1508.117	0.545	18	0.295	K.VPIITTVDGAR.A
R1/RRR1-3/2	1745.236	1746.041	-1037.140	0.531	1080.542	0.623	20	0.262	K.LPLNGTVFLSLNDLTK.R
R1/RRR1-3/2	1142.384	1142.331	46.771	0.462	1217.415	0.485	17	0.249	K.VPIITTVDGAR.A
R1/RRR1-3/2	1143.287	1142.331	-38.618	0.480	1190.981	0.455	16	0.240	K.VPIITTVDGAR.A
R1/RRR1-3/2	1927.688	1926.093	-210.772	0.483	937.166	0.573	20	0.235	R.STGEVM*GIDYEFSGAFAK.A
R1/RRR1-3/2	1534.697	1534.865	-109.825	0.463	979.319	0.501	19	0.231	K.VLQLEGIPVEPVLK.I
R1/RRR1-3/2	1777.784	1777.996	-119.876	0.529	813.658	0.519	20	0.221	K.LSVGYTLDQIPNDITK.K
R1/RRR1-3/2	1534.190	1534.865	-1094.818	0.300	829.204	0.449	18	0.208	K.VLQLEGIPVEPVLK.I
R1/RRR1-3/2	1777.425	1777.996	-886.789	0.425	726.691	0.395	19	0.199	K.LSVGYTLDQIPNDITK.K
R1/RRR1-3/2	1207.544	1206.419	103.663	0.483	903.346	0.335	13	0.197	-.LRDYSVAIIR.-
R1/RRR1-3/2	1206.290	1206.419	-107.650	0.451	1049.686	0.188	15	0.187	R.LRDYSVAIIR.E
R1/RRR1-3/2	1533.760	1534.865	-1376.677	0.288	691.639	0.270	16	0.186	K.VLQLEGIPVEPVLK.I
R1/RRR1-3/2	1747.389	1746.041	199.862	0.263	678.302	0.199	15	0.177	K.LPLNGTVFLSLNDLTK.R
R1/RRR1-3/2	1206.393	1206.419	-21.882	0.436	632.862	0.229	12	0.171	-.LRDYSVAIIR.-
R1/RRR1-17/2	1712.662	1712.926	-154.531	0.591	2206.927	0.562	27	0.416	R.NQDTGLAELPATVAALK.N
R1/RRR1-17/2	1713.407	1712.926	281.358	0.639	2045.948	0.545	26	0.376	R.NQDTGLAELPATVAALK.N
R1/RRR1-17/2	1712.099	1712.926	-1070.229	0.542	1742.356	0.571	25	0.335	R.NQDTGLAELPATVAALK.N
R1/RRR1-17/2	1775.274	1775.896	-916.071	0.486	1863.155	0.395	22	0.300	R.TEDDIALANSVDVGSLR.H
R1/RRR1-17/2	1324.069	1324.380	-235.577	0.424	800.376	0.477	15	0.218	K.VVYDEYNHER.H
R1/RRR1-17/2	1324.305	1324.380	-56.915	0.433	740.314	0.487	15	0.217	K.VVYDEYNHER.H
R1/RRR1-17/2	1187.816	1188.359	-1303.059	0.433	661.156	0.413	14	0.202	R.AFAYFVLSGGR.F
R1/RRR1-17/2	1188.162	1188.359	-166.896	0.229	750.194	0.245	14	0.184	R.AFAYFVLSGGR.F
R1/RRR1-17/3	1932.687	1932.082	-204.921	0.475	1159.664	0.473	26	0.136	R.RTEDDIALANSVDVGSLR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/1	1318.755	1319.488	-1317.899	0.312	806.313	0.162	15	0.339	R.DDLFNINAGIVK.G
R1/RRR1-12/2	1318.646	1319.488	-1401.259	0.468	2149.993	0.327	19	0.324	R.DDLFNINAGIVK.G
R1/RRR1-12/2	1318.612	1319.488	-1427.480	0.452	2065.346	0.363	19	0.322	R.DDLFNINAGIVK.G
R1/RRR1-12/2	1319.233	1319.488	-194.027	0.532	1936.594	0.392	19	0.310	R.DDLFNINAGIVK.G
R1/RRR1-12/1	1318.787	1319.488	-1294.194	0.251	677.299	0.160	14	0.254	R.DDLFNINAGIVK.G
R1/RRR1-12/2	1233.546	1234.295	-1422.196	0.492	1046.559	0.490	19	0.238	R.TQDGGTEVVEAK.A
R1/RRR1-12/2	1234.070	1234.295	-183.308	0.540	913.101	0.456	18	0.222	R.TQDGGTEVVEAK.A
R1/RRR1-12/2	1390.143	1390.482	-244.549	0.433	1227.301	0.353	18	0.221	K.RTQDGGTEVVEAK.A
R1/RRR1-12/2	1233.438	1234.295	-1510.071	0.412	838.304	0.384	18	0.209	R.TQDGGTEVVEAK.A
R1/RRR1-11/2	1234.114	1234.295	-147.288	0.479	683.079	0.397	16	0.204	R.TQDGGTEVVEAK.A
R1/RRR1-11/2	1234.101	1234.295	-157.806	0.386	699.659	0.324	16	0.196	R.TQDGGTEVVEAK.A
R1/RRR1-11/2	1234.074	1234.295	-179.835	0.337	539.726	0.215	15	0.187	-.TQDGGTEVVEAK.-
R1/RRR1-14/3	1560.735	1560.650	54.700	0.435	1460.130	0.517	30	0.169	R.TLDAHIEEQFGSGR.L
R1/RRR1-14/3	1560.911	1560.650	167.529	0.459	1208.021	0.484	29	0.131	R.TLDAHIEEQFGSGR.L
R1/RRR1-14/3	1560.512	1560.650	-88.755	0.481	1073.494	0.488	28	0.121	R.TLDAHIEEQFGSGR.L
R1/RRR1-19/2	977.831	978.149	-326.241	0.419	1164.390	0.438	16	0.235	K.GLLSM*ANAGK.D
R1/RRR1-19/2	1240.199	1240.263	-52.186	0.425	652.588	0.417	14	0.203	K.GEGYEGSTFHR.V
R1/RRR1-19/2	977.707	978.149	-452.888	0.368	826.287	0.346	16	0.203	K.GLLSM*ANAGK.D
R1/RRR1-19/2	1239.975	1240.263	-233.287	0.384	623.225	0.399	14	0.200	K.GEGYEGSTFHR.V
R1/RRR1-19/2	1282.903	1283.330	-333.706	0.436	573.345	0.450	15	0.199	K.GDGTGGKSIYGDR.F
R1/RRR1-19/2	1239.823	1240.263	-356.164	0.388	680.212	0.379	14	0.199	K.GEGYEGSTFHR.V
R1/RRR1-19/2	977.628	978.149	-1560.157	0.323	679.482	0.370	13	0.197	K.GLLSM*ANAGK.D
R1/RRR1-18/2	1638.679	1637.770	-55.411	0.458	758.250	0.531	20	0.123	K.SGELEVPEEGIHVEL.-
R1/RRR1-19/2	1638.277	1637.770	-301.825	0.477	643.770	0.507	19	0.118	K.SGELEVPEEGIHVEL.-
R1/RRR1-18/2	1637.672	1637.770	-59.482	0.427	788.494	0.473	19	0.114	K.SGELEVPEEGIHVEL.-
R1/RRR1-19/2	1637.302	1637.770	-286.152	0.443	815.086	0.463	19	0.113	K.SGELEVPEEGIHVEL.-
R1/RRR1-19/2	1636.250	1637.770	-2157.698	0.324	671.379	0.425	19	0.109	K.SGELEVPEEGIHVEL.-
R1/RRR1-19/3	1106.840	1106.322	-436.402	0.462	888.130	0.429	20	0.099	K.KGLLSM*ANAGK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/3	1106.230	1106.322	-83.466	0.470	801.363	0.347	19	0.083	-.KGLLSM*ANAGK.-
R1/RRR1-19/3	1105.967	1106.322	-321.779	0.430	840.447	0.231	20	0.073	K.KGLLSM*ANAGK.D
R1/RRR1-7/2	1371.645	1372.553	-1394.871	0.439	3755.656	0.492	25	0.814	R.NVNSALAASGIGGIK.V
R1/RRR1-7/2	1373.140	1372.553	-301.612	0.592	3588.785	0.560	25	0.790	R.NVNSALAASGIGGIK.V
R1/RRR1-9/2	1372.178	1372.553	-273.627	0.498	2477.954	0.510	24	0.452	R.NVNSALAASGIGGIK.V
R1/RRR1-9/2	1371.953	1372.553	-1169.578	0.429	2276.822	0.418	21	0.375	R.NVNSALAASGIGGIK.V
R1/RRR1-7/2	1611.417	1611.845	-266.175	0.520	1577.492	0.450	20	0.276	R.SEVVQM*YVSLGINR.M
R1/RRR1-7/3	1372.546	1372.553	-4.747	0.469	2168.740	0.382	32	0.254	R.NVNSALAASGIGGIK.V
R1/RRR1-7/2	1799.377	1797.989	216.338	0.532	977.216	0.537	21	0.237	R.EISLNYATFQPGTTVR.D
R1/RRR1-7/2	1756.342	1755.949	224.148	0.508	897.257	0.550	19	0.231	R.DISLNYATFQPGTTVK.D
R1/RRR1-7/2	1611.290	1611.845	-967.856	0.425	1346.233	0.350	19	0.229	R.SEVVQM*YVSLGINR.M
R1/RRR1-7/2	1611.341	1611.845	-936.292	0.460	1221.344	0.388	20	0.228	R.SEVVQM*YVSLGINR.M
R1/RRR1-7/2	1799.529	1797.989	-256.613	0.536	852.537	0.529	20	0.226	R.EISLNYATFQPGTTVR.D
R1/RRR1-7/2	1756.432	1755.949	275.860	0.524	860.368	0.527	19	0.225	R.DISLNYATFQPGTTVK.D
R1/RRR1-7/2	1756.524	1755.949	-242.891	0.534	836.921	0.530	18	0.222	R.DISLNYATFQPGTTVK.D
R1/RRR1-7/2	1798.575	1797.989	-231.290	0.487	751.007	0.534	19	0.220	R.EISLNYATFQPGTTVR.D
R1/RRR1-13/2	1075.370	1075.201	157.392	0.438	885.403	0.411	13	0.214	R.HFGLFNPDK.T
R1/RRR1-14/2	1075.070	1075.201	-122.042	0.416	803.405	0.408	14	0.212	R.HFGLFNPDK.T
R1/RRR1-14/2	1076.105	1075.201	-90.067	0.434	734.279	0.421	13	0.210	R.HFGLFNPDK.T
R1/RRR1-14/2	1076.110	1075.201	-84.947	0.415	779.304	0.377	14	0.208	R.HFGLFNPDK.T
R1/RRR1-13/2	1074.732	1075.201	-437.533	0.368	640.954	0.430	12	0.206	R.HFGLFNPDK.T
R1/RRR1-9/2	1756.408	1755.949	261.992	0.475	619.660	0.451	18	0.203	R.DISLNYATFQPGTTVK.D
R1/RRR1-9/2	1371.622	1372.553	-1412.123	0.361	698.862	0.365	19	0.198	R.NVNSALAASGIGGIK.V
R1/RRR1-9/2	1076.180	1075.201	-19.638	0.249	608.016	0.302	11	0.189	-.HFGLFNPDK.-
R1/RRR1-7/3	1373.241	1372.553	-227.330	0.301	940.278	0.399	28	0.090	R.NVNSALAASGIGGIK.V
R1/RRR1-19/2	1566.142	1566.739	-1022.917	0.491	1258.217	0.513	18	0.256	K.VYFDVEIDGKPAGR.V
R1/RRR1-19/2	1941.609	1941.197	212.645	0.535	728.328	0.593	27	0.236	R.IIPSFM*IQGGDFTLGDGR.G
R1/RRR1-19/2	1940.761	1941.197	-225.275	0.490	674.362	0.596	26	0.232	R.IIPSFM*IQGGDFTLGDGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1940.481	1941.197	-887.121	0.510	691.847	0.564	26	0.228	R.IIPSFM*IQGGDFTLGDGR.G
R1/RRR1-20/2	1940.313	1941.197	-974.151	0.478	671.393	0.557	26	0.226	R.IIPSFM*IQGGDFTLGDGR.G
R1/RRR1-20/2	1940.485	1941.197	-884.974	0.469	674.961	0.541	26	0.223	R.IIPSFM*IQGGDFTLGDGR.G
R1/RRR1-19/2	1939.803	1941.197	-1238.115	0.453	604.076	0.576	24	0.223	R.IIPSFM*IQGGDFTLGDGR.G
R1/RRR1-19/2	1398.253	1398.574	-229.703	0.409	429.879	0.493	20	0.207	K.HTGPGLLSM*ANAGR.D
R1/RRR1-19/2	1398.326	1398.574	-177.681	0.347	358.240	0.556	19	0.206	K.HTGPGLLSM*ANAGR.D
R1/RRR1-19/2	1013.838	1014.115	-273.970	0.413	769.994	0.315	13	0.195	K.ADLTEVTHK.V
R1/RRR1-20/3	1229.355	1229.365	-8.039	0.465	1059.122	0.350	21	0.094	K.SKADLTEVTHK.V
R1/RRR1-20/3	1229.352	1229.365	-10.579	0.493	766.844	0.364	19	0.089	K.SKADLTEVTHK.V
R1/RRR1-20/3	1229.197	1229.365	-137.280	0.458	1057.566	0.326	21	0.089	-.SKADLTEVTHK.-
R1/RRR1-19/3	1229.705	1229.365	277.070	0.471	679.868	0.314	18	0.081	-.SKADLTEVTHK.-
R1/RRR1-19/3	1229.708	1229.365	279.608	0.466	625.483	0.285	17	0.080	-.SKADLTEVTHK.-
R1/RRR1-19/3	1229.133	1229.365	-189.584	0.453	831.286	0.260	19	0.078	K.SKADLTEVTHK.V
R1/RRR1-9/2	1089.135	1089.309	-160.599	0.407	857.310	0.447	14	0.215	K.VVDLLAPYAK.G
R1/RRR1-9/2	1089.213	1089.309	-88.984	0.231	395.242	0.285	10	0.177	-.VVDLLAPYAK.-
R1/RRR1-9/3	1407.734	1407.516	155.752	0.424	1024.058	0.377	23	0.098	-.AHGGYSVFAGVGER.-
R1/RRR1-9/3	1407.757	1407.516	172.317	0.450	1158.395	0.320	25	0.095	K.AHGGYSVFAGVGER.T
R1/RRR1-9/3	1406.998	1407.516	-1081.630	0.403	892.081	0.291	23	0.079	K.AHGGYSVFAGVGER.T
R1/RRR1-18/2	1610.335	1610.741	-252.396	0.508	1586.498	0.490	20	0.289	K.DGTNVEEAFQCIVK.N
R1/RRR1-18/2	1610.145	1610.741	-993.822	0.491	1411.825	0.496	20	0.270	K.DGTNVEEAFQCIVK.N
R1/RRR1-18/2	1610.457	1610.741	-176.503	0.497	1220.120	0.443	18	0.236	K.DGTNVEEAFQCIVK.N
R1/RRR1-17/2	1058.894	1058.254	-340.707	0.447	1183.605	0.398	18	0.230	K.VIILGDSGVGK.T
R1/RRR1-18/2	1036.521	1037.191	-1616.698	0.355	940.557	0.512	16	0.230	K.ATIGADFLTK.E
R1/RRR1-18/2	1036.977	1037.191	-207.404	0.422	921.154	0.418	16	0.218	K.ATIGADFLTK.E
R1/RRR1-17/2	1057.502	1058.254	-1661.036	0.372	1096.715	0.371	17	0.218	K.VIILGDSGVGK.T
R1/RRR1-17/2	1226.956	1227.348	-320.184	0.447	482.735	0.519	17	0.217	K.GNIPYFETSAK.D
R1/RRR1-18/2	1036.799	1037.191	-379.498	0.349	960.425	0.419	15	0.217	K.ATIGADFLTK.E
R1/RRR1-17/2	1037.104	1037.191	-84.482	0.347	859.883	0.441	15	0.215	K.ATIGADFLTK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1226.851	1227.348	-406.037	0.395	505.104	0.503	17	0.213	K.GNIPYFETSAK.D
R1/RRR1-18/2	1188.055	1188.359	-256.982	0.427	841.480	0.380	16	0.210	R.FQSLGVAFYR.G
R1/RRR1-18/2	1188.025	1188.359	-282.547	0.365	877.013	0.368	15	0.207	R.FQSLGVAFYR.G
R1/RRR1-17/2	1037.119	1037.191	-70.078	0.417	673.225	0.411	14	0.207	K.ATIGADFLTK.E
R1/RRR1-18/2	1057.328	1058.254	-1826.437	0.320	753.247	0.407	15	0.203	K.VIILGDSGVGK.T
R1/RRR1-17/2	1188.063	1188.359	-250.591	0.384	919.808	0.296	16	0.201	R.FQSLGVAFYR.G
R1/RRR1-17/2	1036.867	1037.191	-314.055	0.336	574.592	0.400	13	0.200	K.ATIGADFLTK.E
R1/RRR1-18/2	1227.004	1227.348	-280.856	0.315	419.709	0.392	16	0.200	K.GNIPYFETSAK.D
R1/RRR1-18/2	1057.433	1058.254	-1726.448	0.280	1090.087	0.263	17	0.200	K.VIILGDSGVGK.T
R1/RRR1-18/2	1226.835	1227.348	-1236.267	0.300	407.745	0.371	16	0.198	K.GNIPYFETSAK.D
R1/RRR1-17/2	1226.673	1227.348	-1369.280	0.227	428.295	0.431	16	0.195	K.GNIPYFETSAK.D
R1/RRR1-17/2	1187.416	1188.359	-1641.292	0.374	567.777	0.266	13	0.191	R.FQSLGVAFYR.G
R1/RRR1-17/2	1187.920	1188.359	-371.108	0.332	550.698	0.240	13	0.183	-.FQSLGVAFYR.-
R1/RRR1-10/2	1503.379	1502.729	-232.971	0.480	2568.492	0.355	21	0.412	K.CDVIVINTPLTEK.T
R1/RRR1-10/2	1501.536	1502.729	-1464.687	0.317	2898.169	0.083	21	0.384	K.CDVIVINTPLTEK.T
R1/RRR1-10/2	1502.365	1502.729	-242.907	0.426	2724.330	0.166	21	0.373	K.CDVIVINTPLTEK.T
R1/RRR1-10/2	1848.359	1848.090	145.888	0.551	1923.160	0.544	23	0.358	R.YFKGEDFPVQNYIVK.E
R1/RRR1-10/2	1848.378	1848.090	156.551	0.538	1331.098	0.538	21	0.271	R.YFKGEDFPVQNYIVK.E
R1/RRR1-10/2	1084.327	1084.297	27.369	0.560	1419.982	0.456	17	0.264	K.KGVIIVNNAR.G
R1/RRR1-10/2	1084.164	1084.297	-123.503	0.539	1317.558	0.474	17	0.258	K.KGVIIVNNAR.G
R1/RRR1-10/2	1083.468	1084.297	-1693.438	0.515	1242.678	0.482	16	0.252	K.KGVIIVNNAR.G
R1/RRR1-10/2	957.003	956.125	-126.928	0.474	871.774	0.303	14	0.198	-.GVIIVNNAR.-
R1/RRR1-14/2	1084.679	1084.297	352.901	0.374	613.556	0.324	14	0.196	K.KGVIIVNNAR.G
R1/RRR1-11/2	956.084	956.125	-42.146	0.404	936.463	0.243	13	0.193	K.GVIIVNNAR.G
R1/RRR1-11/2	956.959	956.125	-173.889	0.417	856.211	0.244	13	0.186	-.GVIIVNNAR.-
R1/RRR1-11/2	955.771	956.125	-370.614	0.344	627.189	0.182	12	0.185	-.GVIIVNNAR.-
R1/RRR1-10/3	1084.853	1085.276	-390.944	0.474	1581.793	0.188	22	0.091	R.LKIDPELEK.E
R1/RRR1-10/3	1086.137	1085.276	-128.364	0.476	1527.360	0.157	22	0.081	R.LKIDPELEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1085.513	1085.276	219.636	0.464	1216.220	0.154	20	0.068	R.LKIDPELEK.E
R1/RRR1-21/2	1721.704	1721.929	-131.604	0.526	2440.327	0.488	25	0.436	R.AAEACEQFGGVLVTLR.M
R1/RRR1-21/2	1722.669	1721.929	-151.644	0.552	2297.948	0.505	25	0.413	R.AAEACEQFGGVLVTLR.M
R1/RRR1-21/2	1748.252	1748.918	-955.932	0.532	2064.083	0.541	24	0.379	K.ATDDKAGQEALLNVFR.A
R1/RRR1-22/2	1748.934	1748.918	9.128	0.465	2048.169	0.492	24	0.360	K.ATDDKAGQEALLNVFR.A
R1/RRR1-21/2	1747.973	1748.918	-1116.208	0.539	1917.833	0.497	23	0.338	K.ATDDKAGQEALLNVFR.A
R1/RRR1-21/2	1766.024	1767.017	-1131.698	0.415	1800.732	0.542	25	0.337	K.ITLIGTSGISGSYVELR.-
R1/RRR1-21/2	1720.879	1721.929	-1194.826	0.414	2107.592	0.382	23	0.335	R.AAEACEQFGGVLVTLR.M
R1/RRR1-21/2	1748.620	1748.918	-171.099	0.509	1836.380	0.522	23	0.333	K.ATDDKAGQEALLNVFR.A
R1/RRR1-21/2	1218.421	1218.387	27.874	0.439	1268.671	0.407	16	0.236	K.AGQEALLNVFR.A
R1/RRR1-21/2	1617.307	1617.740	-268.492	0.501	1103.211	0.409	20	0.225	K.YLESFGPEENYLR.K
R1/RRR1-21/2	1617.605	1617.740	-83.684	0.493	1023.798	0.434	19	0.223	K.YLESFGPEENYLR.K
R1/RRR1-21/2	1218.324	1218.387	-52.118	0.378	862.283	0.426	14	0.209	K.AGQEALLNVFR.A
R1/RRR1-21/2	1616.462	1617.740	-1413.496	0.383	736.883	0.372	17	0.199	K.YLESFGPEENYLR.K
R1/RRR1-21/3	1749.999	1748.918	46.336	0.515	1430.137	0.332	26	0.130	-.ATDDKAGQEALLNVFR.-
R1/RRR1-6/2	1558.566	1558.759	-123.854	0.458	1821.287	0.404	22	0.296	K.TFGSSADIFAGIFPK.N
R1/RRR1-9/2	1559.637	1558.759	-78.237	0.513	1369.022	0.485	20	0.260	K.TFGSSADIFAGIFPK.N
R1/RRR1-6/2	1364.665	1364.574	66.965	0.459	1478.317	0.384	17	0.252	R.FIKEEFGQIPR.I
R1/RRR1-6/2	1643.202	1643.819	-986.868	0.464	1009.127	0.573	19	0.244	R.VNALYSTPSIYTDAK.H
R1/RRR1-6/2	1557.380	1558.759	-1532.057	0.330	1312.213	0.411	19	0.236	K.TFGSSADIFAGIFPK.N
R1/RRR1-6/2	1190.385	1191.363	-1667.233	0.359	780.656	0.489	14	0.214	K.HAENVPWPLK.T
R1/RRR1-9/2	1559.996	1558.759	152.527	0.407	1069.815	0.343	19	0.208	K.TFGSSADIFAGIFPK.N
R1/RRR1-6/2	1191.024	1191.363	-285.742	0.297	585.409	0.448	13	0.199	K.HAENVPWPLK.T
R1/RRR1-6/3	1967.958	1967.219	-132.998	0.458	1376.532	0.407	29	0.138	K.LNVHVVPHTHDDVGWLK.T
R1/RRR1-6/3	1723.705	1723.909	-118.566	0.469	595.452	0.586	25	0.113	R.IPVISDSIVVHDSEGR.E
R1/RRR1-6/3	1724.830	1723.909	-45.694	0.442	718.088	0.547	28	0.109	R.IPVISDSIVVHDSEGR.E
R1/RRR1-20/2	1344.136	1344.496	-268.952	0.469	2013.011	0.445	21	0.336	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/2	1343.912	1344.496	-1182.320	0.418	1871.483	0.447	21	0.315	R.VTGGEVGAASSLAPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1639.197	1639.792	-976.134	0.575	1329.729	0.592	24	0.287	K.HSGNISLDDVIEIAR.I
R1/RRR1-20/2	1344.204	1344.496	-218.113	0.430	1620.723	0.417	20	0.272	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/2	1344.141	1344.496	-264.760	0.437	1475.408	0.484	20	0.271	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/1	1343.695	1344.496	-1344.465	0.060	664.236	0.166	15	0.269	R.VTGGEVGAASSLAPK.I
R1/RRR1-20/2	1639.219	1639.792	-962.153	0.586	1048.515	0.635	22	0.267	K.HSGNISLDDVIEIAR.I
R1/RRR1-20/2	1343.671	1344.496	-1362.678	0.373	1496.820	0.409	20	0.256	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/2	1639.424	1639.792	-224.766	0.570	1009.717	0.597	22	0.255	K.HSGNISLDDVIEIAR.I
R1/RRR1-19/2	1640.431	1639.792	-220.747	0.597	1010.153	0.585	22	0.253	K.HSGNISLDDVIEIAR.I
R1/RRR1-20/2	1254.198	1254.544	-276.621	0.473	1069.006	0.551	22	0.252	K.VSVVPSAAALVIK.A
R1/RRR1-20/2	1639.384	1639.792	-249.716	0.574	956.984	0.602	21	0.251	K.HSGNISLDDVIEIAR.I
R1/RRR1-19/2	1640.354	1639.792	-267.556	0.586	927.349	0.596	22	0.249	K.HSGNISLDDVIEIAR.I
R1/RRR1-19/2	1344.053	1344.496	-330.913	0.378	1381.427	0.423	20	0.247	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/2	1254.253	1254.544	-232.974	0.473	1008.143	0.527	21	0.242	K.VSVVPSAAALVIK.A
R1/RRR1-19/2	1254.219	1254.544	-260.216	0.478	858.296	0.560	22	0.240	K.VSVVPSAAALVIK.A
R1/RRR1-20/2	1254.361	1254.544	-146.570	0.515	890.608	0.495	22	0.231	K.VSVVPSAAALVIK.A
R1/RRR1-19/2	1255.148	1254.544	-316.308	0.468	793.741	0.505	21	0.226	K.VSVVPSAAALVIK.A
R1/RRR1-20/3	1639.861	1639.792	42.205	0.532	1931.377	0.408	29	0.220	K.HSGNISLDDVIEIAR.I
R1/RRR1-20/2	1254.265	1254.544	-222.722	0.472	966.210	0.401	21	0.218	K.VSVVPSAAALVIK.A
R1/RRR1-20/2	881.513	882.082	-1785.144	0.417	381.888	0.480	13	0.211	K.IGPLGLSPK.K
R1/RRR1-20/2	881.975	882.082	-122.386	0.422	391.142	0.466	13	0.210	K.IGPLGLSPK.K
R1/RRR1-19/2	881.996	882.082	-98.090	0.430	368.655	0.459	13	0.210	K.IGPLGLSPK.K
R1/RRR1-20/2	881.511	882.082	-1788.066	0.371	369.945	0.490	13	0.210	K.IGPLGLSPK.K
R1/RRR1-19/3	1344.413	1344.496	-62.358	0.419	1880.360	0.424	31	0.209	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/3	1640.400	1639.792	-239.530	0.562	1887.187	0.396	29	0.208	K.HSGNISLDDVIEIAR.I
R1/RRR1-19/2	882.016	882.082	-75.600	0.417	333.130	0.447	12	0.207	K.IGPLGLSPK.K
R1/RRR1-23/2	1344.076	1344.496	-313.417	0.338	790.332	0.352	22	0.202	R.VTGGEVGAASSLAPK.I
R1/RRR1-18/2	882.211	882.082	146.332	0.334	427.220	0.412	12	0.201	K.IGPLGLSPK.K
R1/RRR1-23/2	1253.945	1254.544	-1279.256	0.332	700.002	0.385	17	0.201	K.VSVVPSAAALVIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/3	1639.221	1639.792	-961.451	0.530	1809.872	0.388	29	0.190	K.HSGNISLDDVIEIAR.I
R1/RRR1-19/1	1344.759	1344.496	195.843	0.186	452.896	0.266	15	0.162	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/3	1639.321	1639.792	-287.824	0.536	1597.836	0.370	28	0.153	K.HSGNISLDDVIEIAR.I
R1/RRR1-20/3	1344.211	1344.496	-213.066	0.439	1391.056	0.376	32	0.122	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/2	1731.075	1731.793	-995.831	0.331	1164.884	0.273	22	0.117	K.DLQEEISDGEVEIPSA.-
R1/RRR1-20/3	1344.092	1344.496	-301.490	0.427	1190.807	0.379	29	0.107	R.VTGGEVGAASSLAPK.I
R1/RRR1-20/3	1344.573	1344.496	57.439	0.381	900.418	0.300	28	0.080	R.VTGGEVGAASSLAPK.I
R1/RRR1-19/3	1344.056	1344.496	-328.143	0.377	524.691	0.303	22	0.075	-.VTGGEVGAASSLAPK.-
R1/RRR1-13/2	1307.855	1308.457	-1228.396	0.418	2211.641	0.437	20	0.368	K.VSCADITTLATR.D
R1/RRR1-12/2	1307.837	1308.457	-1242.456	0.411	2245.137	0.404	20	0.363	K.VSCADITTLATR.D
R1/RRR1-13/2	1308.198	1308.457	-199.033	0.472	2184.314	0.401	20	0.350	K.VSCADITTLATR.D
R1/RRR1-13/2	1308.012	1308.457	-341.247	0.457	1931.613	0.459	20	0.328	K.VSCADITTLATR.D
R1/RRR1-12/2	1308.215	1308.457	-185.460	0.491	2053.284	0.385	19	0.323	K.VSCADITTLATR.D
R1/RRR1-12/2	1307.709	1308.457	-1340.604	0.425	1825.446	0.406	18	0.296	K.VSCADITTLATR.D
R1/RRR1-16/2	1308.219	1308.457	-182.839	0.430	1820.089	0.392	19	0.292	K.VSCADITTLATR.D
R1/RRR1-16/2	1308.003	1308.457	-348.458	0.427	1691.674	0.450	20	0.292	K.VSCADITTLATR.D
R1/RRR1-10/2	1735.363	1734.933	248.518	0.567	1386.987	0.589	24	0.288	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-17/2	1734.593	1734.933	-196.835	0.504	1456.229	0.557	24	0.288	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-2/2	1734.383	1734.933	-896.654	0.498	1406.081	0.562	23	0.282	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-14/2	1308.052	1308.457	-310.910	0.380	1732.097	0.388	18	0.279	K.VSCADITTLATR.D
R1/RRR1-1/2	1734.629	1734.933	-175.796	0.520	1335.312	0.575	23	0.278	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-16/2	1736.190	1734.933	148.402	0.575	1317.710	0.572	24	0.276	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-14/2	1734.341	1734.933	-920.536	0.474	1396.544	0.525	23	0.272	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	1735.249	1734.933	182.774	0.552	1298.645	0.564	23	0.271	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-16/2	1307.960	1308.457	-381.513	0.410	1500.166	0.443	19	0.267	K.VSCADITTLATR.D
R1/RRR1-12/2	1734.330	1734.933	-927.320	0.494	1344.168	0.521	23	0.266	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-17/2	1734.298	1734.933	-945.551	0.435	1269.952	0.554	23	0.266	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-2/2	984.550	985.163	-1642.781	0.460	1591.271	0.389	17	0.265	R.DIGIAAGLVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1734.373	1734.933	-902.165	0.502	1295.909	0.525	23	0.262	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	985.073	985.163	-91.741	0.479	1377.575	0.460	17	0.260	R.DIGIAAGLVR.I
R1/RRR1-17/2	1734.440	1734.933	-285.232	0.500	1252.964	0.531	23	0.259	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-1/2	984.955	985.163	-210.962	0.496	1493.510	0.403	17	0.258	R.DIGIAAGLVR.I
R1/RRR1-13/2	1735.287	1734.933	204.431	0.522	1240.143	0.534	22	0.257	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	985.182	985.163	19.871	0.506	1382.866	0.439	17	0.256	R.DIGIAAGLVR.I
R1/RRR1-11/2	1735.061	1734.933	73.769	0.484	1259.668	0.510	23	0.255	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-17/2	985.997	985.163	-168.892	0.518	1384.337	0.433	17	0.255	R.DIGIAAGLVR.I
R1/RRR1-13/2	985.210	985.163	48.205	0.532	1428.335	0.404	17	0.252	R.DIGIAAGLVR.I
R1/RRR1-11/2	985.011	985.163	-154.518	0.450	1436.661	0.396	17	0.251	R.DIGIAAGLVR.I
R1/RRR1-13/2	1734.421	1734.933	-874.327	0.457	1281.703	0.476	22	0.249	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-13/2	984.861	985.163	-306.832	0.498	1249.418	0.456	16	0.248	R.DIGIAAGLVR.I
R1/RRR1-11/2	985.020	985.163	-144.821	0.514	1240.786	0.454	16	0.246	R.DIGIAAGLVR.I
R1/RRR1-17/2	985.054	985.163	-110.138	0.516	1235.981	0.455	16	0.246	R.DIGIAAGLVR.I
R1/RRR1-12/2	1734.529	1734.933	-233.830	0.465	1106.775	0.535	21	0.246	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-1/2	984.612	985.163	-1579.134	0.417	1420.920	0.375	16	0.245	R.DIGIAAGLVR.I
R1/RRR1-14/2	985.005	985.163	-160.361	0.328	1752.185	0.229	17	0.244	R.DIGIAAGLVR.I
R1/RRR1-16/2	1734.345	1734.933	-918.629	0.413	1135.668	0.508	22	0.243	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-17/2	984.503	985.163	-1690.490	0.461	1492.392	0.336	17	0.243	R.DIGIAAGLVR.I
R1/RRR1-9/2	1734.385	1734.933	-895.099	0.408	1182.001	0.485	22	0.242	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	984.948	985.163	-218.671	0.465	1258.821	0.427	16	0.242	R.DIGIAAGLVR.I
R1/RRR1-12/2	1141.348	1141.349	-1.138	0.550	1362.473	0.389	18	0.241	R.RDIGIAAGLVR.I
R1/RRR1-12/2	1572.336	1571.714	-241.442	0.549	865.273	0.553	22	0.241	K.DVPVNSVTQELDVR.T
R1/RRR1-10/2	1734.467	1734.933	-269.627	0.470	1046.562	0.530	21	0.240	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-11/2	984.766	985.163	-404.088	0.440	1205.927	0.438	16	0.240	R.DIGIAAGLVR.I
R1/RRR1-11/2	1734.012	1734.933	-1111.214	0.383	1101.536	0.515	21	0.240	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-13/2	984.927	985.163	-240.181	0.481	1206.995	0.424	16	0.238	R.DIGIAAGLVR.I
R1/RRR1-2/2	1734.358	1734.933	-911.209	0.493	1107.714	0.477	22	0.235	R.DAIVASGGPYFDVPLGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1734.333	1734.933	-925.271	0.457	1131.210	0.464	22	0.235	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-1/2	1734.263	1734.933	-965.902	0.421	1133.695	0.456	22	0.234	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-2/2	1734.515	1734.933	-242.020	0.453	1123.772	0.453	22	0.232	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-13/2	1734.174	1734.933	-1017.421	0.432	1002.595	0.479	21	0.228	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-14/2	1734.341	1734.933	-920.678	0.450	1065.586	0.450	21	0.227	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	1571.227	1571.714	-311.121	0.456	812.878	0.488	22	0.227	K.DVPVNSVTQELDVR.T
R1/RRR1-12/2	1572.510	1571.714	-130.542	0.556	759.488	0.498	21	0.225	K.DVPVNSVTQELDVR.T
R1/RRR1-13/2	1571.397	1571.714	-202.784	0.479	743.758	0.487	22	0.224	K.DVPVNSVTQELDVR.T
R1/RRR1-14/2	1572.332	1571.714	-244.012	0.510	810.356	0.461	22	0.223	K.DVPVNSVTQELDVR.T
R1/RRR1-6/2	1734.543	1734.933	-225.710	0.415	1017.733	0.436	21	0.222	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-1/2	1307.975	1308.457	-369.995	0.310	1267.885	0.334	18	0.222	K.VSCADITTLATR.D
R1/RRR1-11/2	1571.412	1571.714	-192.809	0.461	814.726	0.453	22	0.222	K.DVPVNSVTQELDVR.T
R1/RRR1-14/2	1733.902	1734.933	-1175.119	0.331	1023.628	0.430	21	0.220	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	1573.256	1571.714	-292.275	0.558	590.675	0.496	20	0.219	K.DVPVNSVTQELDVR.T
R1/RRR1-3/2	1734.113	1734.933	-1052.759	0.344	1117.226	0.377	22	0.219	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	1571.262	1571.714	-288.984	0.415	801.946	0.438	22	0.219	K.DVPVNSVTQELDVR.T
R1/RRR1-11/2	1571.327	1571.714	-246.973	0.437	667.805	0.452	21	0.216	K.DVPVNSVTQELDVR.T
R1/RRR1-2/2	1571.327	1571.714	-247.363	0.422	746.162	0.436	21	0.216	K.DVPVNSVTQELDVR.T
R1/RRR1-11/2	1571.296	1571.714	-267.316	0.432	660.203	0.448	21	0.216	K.DVPVNSVTQELDVR.T
R1/RRR1-6/2	985.298	985.163	137.794	0.376	1036.431	0.359	15	0.215	R.DIGIAAGLVR.I
R1/RRR1-9/2	1570.777	1571.714	-1237.370	0.394	696.315	0.427	21	0.213	K.DVPVNSVTQELDVR.T
R1/RRR1-14/2	1571.178	1571.714	-980.519	0.337	735.152	0.408	22	0.211	K.DVPVNSVTQELDVR.T
R1/RRR1-10/2	1571.126	1571.714	-1014.140	0.379	540.860	0.426	20	0.210	K.DVPVNSVTQELDVR.T
R1/RRR1-12/2	1572.375	1571.714	-216.441	0.476	203.868	0.489	17	0.209	-.DVPVNSVTQELDVR.-
R1/RRR1-2/2	1571.244	1571.714	-300.130	0.416	595.007	0.407	20	0.209	K.DVPVNSVTQELDVR.T
R1/RRR1-7/2	1734.158	1734.933	-1026.538	0.356	866.817	0.420	18	0.209	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-3/2	1734.219	1734.933	-991.343	0.421	817.880	0.419	19	0.209	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-10/2	1570.619	1571.714	-1337.899	0.348	427.152	0.449	18	0.208	K.DVPVNSVTQELDVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1572.080	1571.714	232.975	0.406	177.474	0.461	17	0.208	-.DVPVNSVTQELDVR.-
R1/RRR1-10/2	1570.317	1571.714	-1531.521	0.370	492.374	0.418	19	0.208	K.DVPVNSVTQELDVR.T
R1/RRR1-14/2	1570.612	1571.714	-1342.583	0.330	683.532	0.385	22	0.208	K.DVPVNSVTQELDVR.T
R1/RRR1-4/2	985.219	985.163	57.028	0.408	1059.768	0.287	15	0.206	R.DIGIAAGLVR.I
R1/RRR1-21/2	1735.668	1734.933	-153.471	0.376	785.779	0.412	18	0.206	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-11/2	1733.742	1734.933	-1267.881	0.326	758.198	0.419	18	0.205	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-12/2	1736.043	1734.933	63.501	0.386	612.542	0.450	17	0.205	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-19/2	1572.428	1571.714	-182.796	0.469	287.986	0.369	16	0.204	K.DVPVNSVTQELDVR.T
R1/RRR1-12/2	1736.429	1734.933	286.300	0.454	569.506	0.447	17	0.204	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-2/2	1571.242	1571.714	-301.533	0.377	747.861	0.331	20	0.203	K.DVPVNSVTQELDVR.T
R1/RRR1-1/2	985.187	985.163	24.718	0.390	910.527	0.306	14	0.203	R.DIGIAAGLVR.I
R1/RRR1-1/2	1570.460	1571.714	-1439.854	0.351	565.510	0.327	20	0.202	K.DVPVNSVTQELDVR.T
R1/RRR1-12/2	1571.179	1571.714	-979.895	0.342	669.831	0.321	21	0.202	K.DVPVNSVTQELDVR.T
R1/RRR1-1/2	1571.542	1571.714	-109.743	0.395	490.548	0.339	18	0.202	K.DVPVNSVTQELDVR.T
R1/RRR1-12/2	1733.902	1734.933	-1175.119	0.274	1027.824	0.255	20	0.197	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-10/2	1308.091	1308.457	-280.762	0.273	665.989	0.302	16	0.194	K.VSCADITTLATR.D
R1/RRR1-6/2	984.936	985.163	-230.856	0.249	719.959	0.246	14	0.194	R.DIGIAAGLVR.I
R1/RRR1-4/2	1734.754	1734.933	-103.864	0.361	596.418	0.319	16	0.192	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-18/2	1734.422	1734.933	-873.762	0.306	669.337	0.290	16	0.191	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-5/2	985.146	985.163	-16.792	0.253	814.157	0.126	15	0.188	R.DIGIAAGLVR.I
R1/RRR1-12/2	1734.738	1734.933	-112.758	0.344	438.918	0.345	14	0.188	-.DAIVASGGPYFDVPLGR.-
R1/RRR1-12/2	1140.576	1141.349	-1559.270	0.380	712.134	0.219	15	0.185	R.RDIGIAAGLVR.I
R1/RRR1-5/2	985.330	985.163	170.594	0.236	653.290	0.169	13	0.185	-.DIGIAAGLVR.-
R1/RRR1-12/3	1735.646	1734.933	-166.037	0.487	1353.875	0.542	30	0.175	R.DAIVASGGPYFDVPLGR.R
R1/RRR1-3/2	1847.005	1847.105	-54.464	0.530	3202.385	0.555	27	0.677	R.FNLALESGNIQIAVASAK.E
R1/RRR1-3/2	1497.320	1497.637	-212.081	0.463	911.905	0.438	18	0.216	R.QGNVGIVEYAYQR.T
R1/RRR1-2/2	1497.740	1497.637	68.863	0.410	728.262	0.457	17	0.209	R.QGNVGIVEYAYQR.T
R1/RRR1-3/2	771.834	771.928	-121.687	0.415	1158.414	0.233	12	0.202	R.LGIEALR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	771.399	771.928	-1987.668	0.332	1202.250	0.218	12	0.201	R.LGIEALR.Q
R1/RRR1-6/2	1191.978	1191.402	-356.491	0.302	770.032	0.340	16	0.198	K.TLDVPIYITR.V
R1/RRR1-3/2	1191.128	1191.402	-230.724	0.281	460.364	0.310	12	0.190	K.TLDVPIYITR.V
R1/RRR1-3/2	772.052	771.928	161.106	0.408	903.804	0.180	11	0.187	R.LGIEALR.Q
R1/RRR1-3/2	1191.403	1191.402	1.171	0.277	421.804	0.377	11	0.175	-.TLDVPIYITR.-
R1/RRR1-3/3	1298.669	1298.434	181.842	0.425	1380.497	0.379	25	0.121	R.RPGSVSLNQSPR.T
R1/RRR1-3/3	1298.956	1298.434	-368.662	0.468	1308.758	0.368	24	0.114	-.RPGSVSLNQSPR.-
R1/RRR1-3/3	1298.200	1298.434	-180.818	0.464	960.618	0.405	23	0.098	R.RPGSVSLNQSPR.T
R1/RRR1-2/3	1298.735	1298.434	232.741	0.396	698.368	0.355	21	0.074	-.RPGSVSLNQSPR.-
R1/RRR1-6/3	1298.515	1298.434	62.776	0.398	826.386	0.299	20	0.064	-.RPGSVSLNQSPR.-
R1/RRR1-13/2	1612.383	1612.674	-180.924	0.558	2891.425	0.563	25	0.579	K.VGDLDSYEIEGGETK.S
R1/RRR1-13/2	1612.282	1612.674	-243.737	0.543	2807.500	0.564	25	0.557	K.VGDLDSYEIEGGETK.S
R1/RRR1-13/2	1902.465	1902.181	149.783	0.632	2533.341	0.598	25	0.501	K.NPINYTQIAVLADDILK.N
R1/RRR1-13/2	1612.158	1612.674	-943.065	0.537	2547.732	0.562	24	0.491	K.VGDLDSYEIEGGETK.S
R1/RRR1-13/2	1901.532	1902.181	-869.411	0.563	2547.227	0.558	25	0.489	K.NPINYTQIAVLADDILK.N
R1/RRR1-12/2	1612.202	1612.674	-293.265	0.509	2361.938	0.510	23	0.427	K.VGDLDSYEIEGGETK.S
R1/RRR1-13/2	1901.566	1902.181	-851.496	0.575	2179.796	0.591	24	0.420	K.NPINYTQIAVLADDILK.N
R1/RRR1-13/3	1902.771	1902.181	-215.736	0.537	2584.498	0.482	36	0.417	K.NPINYTQIAVLADDILK.N
R1/RRR1-13/2	1194.057	1193.326	-226.262	0.569	1099.900	0.532	19	0.251	K.GLCGGINSTSVK.V
R1/RRR1-13/3	1902.003	1902.181	-93.644	0.478	2114.764	0.388	34	0.250	K.NPINYTQIAVLADDILK.N
R1/RRR1-13/2	1192.524	1193.326	-1515.575	0.441	1135.786	0.507	19	0.246	K.GLCGGINSTSVK.V
R1/RRR1-13/2	1192.431	1193.326	-1594.037	0.397	1189.204	0.484	20	0.245	K.GLCGGINSTSVK.V
R1/RRR1-13/2	1753.314	1753.910	-913.168	0.498	1117.792	0.430	20	0.226	R.DSKDNIEM*TVSELQK.N
R1/RRR1-13/2	1060.075	1060.226	-142.941	0.413	975.008	0.415	16	0.218	K.NVIVAITSDK.G
R1/RRR1-13/2	1755.526	1753.910	-219.325	0.552	980.780	0.440	20	0.218	R.DSKDNIEM*TVSELQK.N
R1/RRR1-13/2	1059.858	1060.226	-348.484	0.310	919.929	0.402	14	0.208	K.NVIVAITSDK.G
R1/RRR1-13/2	1753.224	1753.910	-964.753	0.443	539.363	0.350	17	0.191	R.DSKDNIEM*TVSELQK.N
R1/RRR1-13/3	1754.163	1753.910	144.387	0.497	1178.078	0.391	26	0.114	R.DSKDNIEM*TVSELQK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/3	1754.048	1753.910	78.643	0.425	1099.553	0.309	26	0.089	R.DSKDNIEM*TVSELQK.N
R1/RRR1-15/2	1142.266	1141.303	-32.222	0.477	1565.389	0.600	20	0.320	R.VPSPVTAGSAVR.L
R1/RRR1-15/2	1030.939	1031.145	-200.899	0.414	1510.478	0.538	20	0.294	K.VAAATAAAGEAK.G
R1/RRR1-15/2	1142.093	1141.303	-184.134	0.500	1474.977	0.508	20	0.283	R.VPSPVTAGSAVR.L
R1/RRR1-15/2	1211.265	1211.308	-35.743	0.465	1463.983	0.382	19	0.251	R.VSFGENFSPAR.A
R1/RRR1-15/2	1643.347	1643.829	-293.891	0.539	1239.980	0.459	22	0.242	R.SPAAEALGPTHVLHSR.Y
R1/RRR1-15/2	1454.403	1454.694	-200.324	0.445	1016.627	0.419	18	0.219	K.VKEGVEVPQLVEK.V
R1/RRR1-15/2	1211.168	1211.308	-116.315	0.470	1133.437	0.357	18	0.219	R.VSFGENFSPAR.A
R1/RRR1-15/3	1644.034	1643.829	125.322	0.484	1557.532	0.544	30	0.204	R.SPAAEALGPTHVLHSR.Y
R1/RRR1-15/2	1454.484	1454.694	-144.586	0.364	715.126	0.368	17	0.198	K.VKEGVEVPQLVEK.V
R1/RRR1-15/2	1454.295	1454.694	-274.846	0.344	721.073	0.345	16	0.194	K.VKEGVEVPQLVEK.V
R1/RRR1-15/3	1643.660	1643.829	-102.701	0.433	972.717	0.542	26	0.129	R.SPAAEALGPTHVLHSR.Y
R1/RRR1-15/3	1644.956	1643.829	77.541	0.494	1011.997	0.492	26	0.124	R.SPAAEALGPTHVLHSR.Y
R1/RRR1-9/2	1998.466	1999.212	-876.315	0.599	2998.962	0.602	28	0.629	K.TQDIQIVGDDLTVTNPIR.I
R1/RRR1-9/2	1998.657	1999.212	-780.237	0.582	2582.233	0.586	27	0.509	K.TQDIQIVGDDLTVTNPIR.I
R1/RRR1-9/2	1998.679	1999.212	-768.957	0.606	2399.812	0.558	27	0.453	K.TQDIQIVGDDLTVTNPIR.I
R1/RRR1-9/2	1777.411	1776.924	275.221	0.539	2208.375	0.514	25	0.398	R.SGETEDVTISDVVVGIR.A
R1/RRR1-9/3	1999.935	1999.212	-138.677	0.442	2538.353	0.399	35	0.363	K.TQDIQIVGDDLTVTNPIR.I
R1/RRR1-9/2	1574.509	1573.773	-168.402	0.557	1827.894	0.605	23	0.361	K.VNQIGTLTESIQAAK.D
R1/RRR1-9/2	1898.330	1899.007	-886.163	0.507	1972.265	0.517	24	0.355	R.IEEELGSNAVYAGENFR.K
R1/RRR1-9/2	1573.049	1573.773	-1099.140	0.471	1773.755	0.562	23	0.338	K.VNQIGTLTESIQAAK.D
R1/RRR1-9/2	1776.336	1776.924	-896.430	0.483	1919.335	0.490	23	0.337	R.SGETEDVTISDVVVGIR.A
R1/RRR1-9/2	1574.398	1573.773	-239.026	0.568	1706.960	0.592	22	0.336	K.VNQIGTLTESIQAAK.D
R1/RRR1-9/2	1899.365	1899.007	188.705	0.608	1674.842	0.558	24	0.319	R.IEEELGSNAVYAGENFR.K
R1/RRR1-9/2	1776.484	1776.924	-248.157	0.480	1695.122	0.471	22	0.296	R.SGETEDVTISDVVVGIR.A
R1/RRR1-9/2	1898.293	1899.007	-906.046	0.510	1490.388	0.543	24	0.291	R.IEEELGSNAVYAGENFR.K
R1/RRR1-9/3	1776.209	1776.924	-968.260	0.436	1364.349	0.356	27	0.124	R.SGETEDVTISDVVVGIR.A
R1/RRR1-9/3	1783.393	1783.916	-856.676	0.489	838.656	0.502	26	0.111	K.KYDLDFKNPDSDPTK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/3	1783.618	1783.916	-167.887	0.512	1038.990	0.437	28	0.111	K.KYDLDFKNPDSDPTK.W
R1/RRR1-9/3	1999.205	1999.212	-3.106	0.328	1393.976	0.270	27	0.104	K.TQDIQIVGDDLTVTNPIR.I
R1/RRR1-9/3	1784.311	1783.916	221.760	0.496	916.119	0.427	27	0.102	K.KYDLDFKNPDSDPTK.W
R1/RRR1-9/3	1898.238	1899.007	-934.717	0.319	1118.327	0.222	27	0.073	R.IEEELGSNAVYAGENFR.K
R1/RRR1-24/2	1963.896	1964.232	-171.660	0.447	1136.428	0.562	19	0.248	K.ANNM*VFVSGVLGLNPETGK.F
R1/RRR1-23/2	1405.345	1404.596	-179.612	0.514	1020.979	0.554	19	0.247	R.STYQVAALPLNAR.I
R1/RRR1-23/2	1405.152	1404.596	-317.482	0.527	1063.317	0.532	19	0.245	R.STYQVAALPLNAR.I
R1/RRR1-24/2	1405.269	1404.596	-233.466	0.469	1037.513	0.524	19	0.241	R.STYQVAALPLNAR.I
R1/RRR1-23/2	1055.920	1056.151	-219.453	0.469	866.307	0.540	17	0.234	K.ASGASYSSVVK.T
R1/RRR1-23/2	1055.959	1056.151	-182.341	0.415	1112.750	0.437	18	0.231	K.ASGASYSSVVK.T
R1/RRR1-23/2	1288.249	1287.489	-187.384	0.501	689.972	0.598	17	0.231	K.APAALGPYSQAIK.A
R1/RRR1-23/2	1055.500	1056.151	-1568.835	0.389	840.498	0.543	17	0.229	K.ASGASYSSVVK.T
R1/RRR1-24/2	1287.421	1287.489	-52.935	0.468	847.193	0.528	17	0.227	K.APAALGPYSQAIK.A
R1/RRR1-23/2	1287.135	1287.489	-276.201	0.475	623.265	0.565	16	0.221	K.APAALGPYSQAIK.A
R1/RRR1-24/2	1287.192	1287.489	-231.483	0.441	733.402	0.525	17	0.221	K.APAALGPYSQAIK.A
R1/RRR1-23/2	1287.213	1287.489	-215.214	0.455	717.522	0.513	17	0.219	K.APAALGPYSQAIK.A
R1/RRR1-24/2	1056.965	1056.151	-176.723	0.464	776.936	0.473	16	0.218	K.ASGASYSSVVK.T
R1/RRR1-24/2	1404.222	1404.596	-267.296	0.456	1047.147	0.372	18	0.213	R.STYQVAALPLNAR.I
R1/RRR1-24/2	1287.110	1287.489	-295.802	0.414	594.124	0.509	16	0.212	K.APAALGPYSQAIK.A
R1/RRR1-23/2	1540.273	1540.807	-998.499	0.482	691.563	0.431	18	0.205	K.TTIM*LADLQDFKK.V
R1/RRR1-23/2	1964.148	1964.232	-43.289	0.404	502.330	0.504	22	0.205	K.ANNM*VFVSGVLGLNPETGK.F
R1/RRR1-24/2	1964.378	1964.232	74.392	0.301	204.561	0.351	14	0.186	K.ANNM*VFVSGVLGLNPETGK.F
R1/RRR1-9/2	1931.906	1932.162	-132.621	0.573	1444.427	0.407	20	0.244	K.TLTETNKNLDEIVELAK.K
R1/RRR1-9/2	1847.937	1848.048	-60.333	0.504	1077.456	0.531	20	0.242	R.ELDHLANFLQAAVDYK.K
R1/RRR1-9/2	1069.844	1070.223	-354.844	0.417	958.416	0.486	16	0.229	K.VYAYGAAQVK.K
R1/RRR1-9/2	1847.717	1848.048	-180.013	0.427	1018.182	0.493	20	0.229	R.ELDHLANFLQAAVDYK.K
R1/RRR1-9/2	1069.924	1070.223	-280.664	0.465	1031.784	0.426	16	0.225	K.VYAYGAAQVK.K
R1/RRR1-9/2	1069.625	1070.223	-1498.325	0.394	940.492	0.461	16	0.223	K.VYAYGAAQVK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1143.978	1144.300	-282.617	0.307	805.124	0.291	14	0.193	K.NLDEIVELAK.K
R1/RRR1-9/2	1144.242	1144.300	-51.105	0.275	731.007	0.254	15	0.189	K.NLDEIVELAK.K
R1/RRR1-9/3	1848.701	1848.048	-188.401	0.438	1632.927	0.438	25	0.187	R.ELDHLANFLQAAVDYK.K
R1/RRR1-9/2	1144.208	1144.300	-80.319	0.196	581.149	0.253	14	0.185	K.NLDEIVELAK.K
R1/RRR1-9/3	1933.091	1932.162	-37.003	0.466	1397.761	0.415	30	0.141	K.TLTETNKNLDEIVELAK.K
R1/RRR1-9/3	1932.052	1932.162	-56.953	0.432	1064.924	0.419	27	0.111	K.TLTETNKNLDEIVELAK.K
R1/RRR1-9/3	1847.915	1848.048	-72.267	0.455	1434.924	0.278	27	0.111	R.ELDHLANFLQAAVDYK.K
R1/RRR1-9/3	1306.890	1307.458	-1203.520	0.470	1130.490	0.309	24	0.090	R.YM*HGAATSPEVK.V
R1/RRR1-9/3	1307.448	1307.458	-7.857	0.468	857.361	0.352	24	0.085	R.YM*HGAATSPEVK.V
R1/RRR1-9/3	1847.782	1848.048	-144.630	0.331	775.145	0.366	21	0.085	R.ELDHLANFLQAAVDYK.K
R1/RRR1-9/3	1291.511	1291.458	41.123	0.413	650.956	0.345	21	0.082	R.YMHGAATSPEVK.V
R1/RRR1-9/3	1931.311	1932.162	-961.439	0.334	868.438	0.264	25	0.074	K.TLTETNKNLDEIVELAK.K
R1/RRR1-3/3	1270.218	1270.420	-159.692	0.506	1958.401	0.459	28	0.226	R.RPGSVSLNQSPK.T
R1/RRR1-6/3	1270.492	1270.420	56.885	0.533	1699.019	0.388	25	0.164	R.RPGSVSLNQSPK.T
R1/RRR1-1/3	1270.733	1270.420	246.349	0.519	1447.675	0.479	26	0.156	R.RPGSVSLNQSPK.T
R1/RRR1-3/3	1270.679	1270.420	204.155	0.529	1443.886	0.443	25	0.147	R.RPGSVSLNQSPK.T
R1/RRR1-5/3	1270.478	1270.420	45.466	0.550	1482.872	0.412	26	0.141	R.RPGSVSLNQSPK.T
R1/RRR1-3/3	1270.652	1270.420	183.057	0.560	1484.602	0.398	25	0.139	R.RPGSVSLNQSPK.T
R1/RRR1-1/3	1270.290	1270.420	-102.864	0.517	1126.949	0.461	23	0.121	-.RPGSVSLNQSPK.-
R1/RRR1-1/3	1270.403	1270.420	-13.803	0.517	1078.155	0.471	24	0.120	R.RPGSVSLNQSPK.T
R1/RRR1-5/3	1269.922	1270.420	-393.578	0.533	1156.756	0.407	22	0.115	R.RPGSVSLNQSPK.T
R1/RRR1-6/3	1270.943	1270.420	-376.692	0.529	1090.803	0.431	23	0.114	R.RPGSVSLNQSPK.T
R1/RRR1-5/3	1270.804	1270.420	302.697	0.528	1032.969	0.417	22	0.109	R.RPGSVSLNQSPK.T
R1/RRR1-13/2	1492.218	1491.671	-304.456	0.525	1933.700	0.477	20	0.336	K.VAEIAAQLEQYQK.A
R1/RRR1-13/2	1900.263	1900.935	-882.749	0.554	1501.832	0.579	24	0.302	K.SADLFDSEGQSSQSNSIK.Q
R1/RRR1-13/2	1490.705	1491.671	-1322.972	0.343	1655.222	0.374	19	0.267	K.VAEIAAQLEQYQK.A
R1/RRR1-13/2	1400.264	1400.475	-151.409	0.455	1258.349	0.397	18	0.234	R.YQDIDPTFSGTR.E
R1/RRR1-13/2	1134.102	1134.267	-146.134	0.491	1144.168	0.439	15	0.233	K.ANEIFEAIAR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1401.176	1400.475	-213.963	0.520	1116.180	0.429	17	0.228	R.YQDIDPTFSGTR.E
R1/RRR1-13/2	1399.958	1400.475	-1086.797	0.429	1127.149	0.406	18	0.225	R.YQDIDPTFSGTR.E
R1/RRR1-13/2	1308.085	1308.444	-275.143	0.387	934.308	0.408	16	0.211	R.GDVVAITNSM*ER.Y
R1/RRR1-13/2	1490.408	1491.671	-1522.694	0.276	717.928	0.364	15	0.193	K.VAEIAAQLEQYQK.A
R1/RRR1-13/2	1308.084	1308.444	-276.266	0.348	686.474	0.316	15	0.191	R.GDVVAITNSM*ER.Y
R1/RRR1-4/2	1261.172	1261.514	-271.402	0.399	2211.382	0.526	19	0.403	R.ALLDEMAVVATK.E
R1/RRR1-4/2	1261.096	1261.514	-332.098	0.430	1978.920	0.517	19	0.357	R.ALLDEMAVVATK.E
R1/RRR1-4/2	1131.200	1131.261	-54.184	0.264	1173.343	0.255	16	0.201	K.SQEELINVAK.E
R1/RRR1-4/2	1260.858	1261.514	-1317.396	0.292	819.028	0.375	15	0.199	R.ALLDEMAVVATK.E
R1/RRR1-4/2	1513.004	1513.760	-1163.638	0.315	908.952	0.298	15	0.192	K.LLVSEELWPLGEK.L
R1/RRR1-4/2	1514.028	1513.760	177.699	0.299	808.093	0.165	13	0.176	K.LLVSEELWPLGEK.L
R1/RRR1-8/2	1594.367	1594.702	-210.537	0.546	2397.364	0.530	24	0.450	R.IEEELGDAAVYAGEK.F
R1/RRR1-8/2	1224.838	1225.373	-1256.775	0.445	1058.115	0.396	16	0.218	K.ISGDSLKDVYK.S
R1/RRR1-11/2	1593.367	1593.752	-242.558	0.412	1699.299	0.441	21	0.292	K.YVFTIDDDCFVAK.D
R1/RRR1-11/2	1240.065	1239.397	-267.827	0.459	1519.572	0.498	17	0.285	K.CYLSLAEQVR.E
R1/RRR1-11/2	1240.178	1239.397	-176.482	0.556	1468.959	0.454	17	0.268	K.CYLSLAEQVR.E
R1/RRR1-11/2	1502.390	1502.609	-146.414	0.519	1143.153	0.566	19	0.262	R.VPEGFDYELYNR.N
R1/RRR1-11/2	1503.207	1502.609	-268.265	0.560	1069.382	0.586	19	0.260	R.VPEGFDYELYNR.N
R1/RRR1-11/2	1239.092	1239.397	-246.595	0.461	1348.642	0.467	16	0.258	K.CYLSLAEQVR.E
R1/RRR1-11/2	1501.675	1502.609	-1291.537	0.497	1101.085	0.527	19	0.250	R.VPEGFDYELYNR.N
R1/RRR1-11/2	1138.986	1139.347	-317.397	0.554	924.317	0.560	16	0.246	R.YVDAVM*TVPK.G
R1/RRR1-11/2	1502.115	1502.609	-329.592	0.470	1040.830	0.526	19	0.244	R.VPEGFDYELYNR.N
R1/RRR1-11/2	1138.494	1139.347	-1632.134	0.445	804.482	0.577	16	0.238	R.YVDAVM*TVPK.G
R1/RRR1-10/2	1503.652	1502.609	28.694	0.473	897.513	0.519	18	0.233	R.VPEGFDYELYNR.N
R1/RRR1-10/2	1139.078	1139.347	-236.971	0.456	827.601	0.520	16	0.231	R.YVDAVM*TVPK.G
R1/RRR1-11/2	1592.634	1593.752	-1333.936	0.236	1564.779	0.242	20	0.228	K.YVFTIDDDCFVAK.D
R1/RRR1-11/2	1138.310	1139.347	-1794.814	0.418	976.746	0.446	16	0.226	R.YVDAVM*TVPK.G
R1/RRR1-11/2	1592.734	1593.752	-1270.894	0.276	1465.856	0.259	20	0.223	K.YVFTIDDDCFVAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1138.892	1139.347	-400.525	0.419	827.378	0.461	16	0.221	R.YVDAVM*TVPK.G
R1/RRR1-10/2	1139.062	1139.347	-250.840	0.449	846.054	0.397	16	0.214	R.YVDAVM*TVPK.G
R1/RRR1-11/2	1241.244	1241.456	-170.609	0.451	811.048	0.428	16	0.212	K.VICDHLSLGVK.T
R1/RRR1-11/2	1241.205	1241.456	-202.674	0.430	843.495	0.396	16	0.209	K.VICDHLSLGVK.T
R1/RRR1-11/2	1242.306	1241.456	-120.692	0.482	718.417	0.427	15	0.207	K.VICDHLSLGVK.T
R1/RRR1-1/2	1501.446	1502.609	-1445.122	0.304	916.395	0.367	18	0.207	R.VPEGFDYELYNR.N
R1/RRR1-1/2	1138.460	1139.347	-1662.296	0.297	634.795	0.440	14	0.205	R.YVDAVM*TVPK.G
R1/RRR1-3/2	1139.189	1139.347	-138.929	0.308	688.929	0.404	14	0.204	R.YVDAVM*TVPK.G
R1/RRR1-3/2	1502.272	1502.609	-225.074	0.404	814.552	0.364	16	0.204	R.VPEGFDYELYNR.N
R1/RRR1-10/2	1502.459	1502.609	-100.202	0.306	633.461	0.426	17	0.202	-.VPEGFDYELYNR.-
R1/RRR1-1/2	1138.521	1139.347	-1608.221	0.303	603.793	0.353	14	0.199	R.YVDAVM*TVPK.G
R1/RRR1-1/2	1139.170	1139.347	-155.805	0.334	537.288	0.376	13	0.198	-.YVDAVM*TVPK.-
R1/RRR1-11/2	1123.362	1123.348	13.339	0.299	964.060	0.203	15	0.192	R.YVDAVMTVPK.G
R1/RRR1-11/2	1502.345	1502.609	-176.409	0.222	350.721	0.435	11	0.190	R.VPEGFDYELYNR.N
R1/RRR1-8/2	1767.446	1768.025	-895.832	0.449	1790.586	0.424	24	0.296	K.AGM*VVTFAPSNVTTEVK.S
R1/RRR1-8/2	1766.807	1768.025	-1259.001	0.374	1741.464	0.391	24	0.281	K.AGM*VVTFAPSNVTTEVK.S
R1/RRR1-8/2	1327.508	1327.557	-36.487	0.553	1306.397	0.567	19	0.279	R.EHALLAFTLGVR.Q
R1/RRR1-8/2	1767.398	1768.025	-923.012	0.447	1568.481	0.445	23	0.273	K.AGM*VVTFAPSNVTTEVK.S
R1/RRR1-13/2	1027.097	1026.215	-114.868	0.516	1288.322	0.505	19	0.263	K.IGGIGTVPVGR.V
R1/RRR1-11/2	1025.634	1026.215	-1545.519	0.408	1333.630	0.465	18	0.256	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1261.818	1261.411	323.736	0.461	1221.102	0.502	17	0.253	K.ANISPNAPWYK.G
R1/RRR1-3/2	1025.622	1026.215	-1557.954	0.467	1276.798	0.457	18	0.251	K.IGGIGTVPVGR.V
R1/RRR1-3/2	1025.987	1026.215	-222.514	0.496	1243.805	0.451	19	0.248	K.IGGIGTVPVGR.V
R1/RRR1-12/2	1026.128	1026.215	-84.909	0.488	1189.214	0.470	19	0.248	K.IGGIGTVPVGR.V
R1/RRR1-9/2	1026.117	1026.215	-95.410	0.439	1193.636	0.472	19	0.248	K.IGGIGTVPVGR.V
R1/RRR1-2/2	1026.159	1026.215	-54.600	0.506	1222.321	0.462	18	0.247	K.IGGIGTVPVGR.V
R1/RRR1-4/2	1025.882	1026.215	-325.534	0.503	1120.599	0.493	18	0.247	K.IGGIGTVPVGR.V
R1/RRR1-2/2	1025.602	1026.215	-1577.443	0.471	1133.316	0.487	17	0.245	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1026.019	1026.215	-191.839	0.500	1200.859	0.446	19	0.244	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1026.096	1026.215	-116.293	0.477	1151.501	0.454	19	0.242	K.IGGIGTVPVGR.V
R1/RRR1-9/2	1026.057	1026.215	-154.244	0.478	1080.087	0.477	18	0.241	K.IGGIGTVPVGR.V
R1/RRR1-6/2	1026.146	1026.215	-67.487	0.535	1033.774	0.488	18	0.240	K.IGGIGTVPVGR.V
R1/RRR1-14/2	1026.049	1026.215	-162.001	0.463	1090.343	0.463	18	0.239	K.IGGIGTVPVGR.V
R1/RRR1-3/2	1026.105	1026.215	-107.820	0.540	1071.842	0.468	18	0.239	K.IGGIGTVPVGR.V
R1/RRR1-9/2	1026.066	1026.215	-145.651	0.435	1080.953	0.463	18	0.238	K.IGGIGTVPVGR.V
R1/RRR1-1/2	1026.098	1026.215	-114.026	0.502	970.681	0.492	17	0.236	K.IGGIGTVPVGR.V
R1/RRR1-7/2	1026.064	1026.215	-147.918	0.475	1045.221	0.458	18	0.235	K.IGGIGTVPVGR.V
R1/RRR1-13/2	1025.528	1026.215	-1649.787	0.457	1057.752	0.453	18	0.235	K.IGGIGTVPVGR.V
R1/RRR1-10/2	1025.472	1026.215	-1705.038	0.432	1142.898	0.422	18	0.234	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1026.121	1026.215	-92.188	0.484	937.393	0.483	17	0.233	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1027.038	1026.215	-172.336	0.505	965.135	0.472	17	0.232	K.IGGIGTVPVGR.V
R1/RRR1-12/2	1025.993	1026.215	-216.546	0.494	943.065	0.475	17	0.232	K.IGGIGTVPVGR.V
R1/RRR1-4/2	1026.090	1026.215	-121.783	0.497	918.309	0.480	17	0.231	K.IGGIGTVPVGR.V
R1/RRR1-9/2	1025.298	1026.215	-1875.614	0.362	1018.943	0.467	17	0.231	K.IGGIGTVPVGR.V
R1/RRR1-11/2	1025.992	1026.215	-217.620	0.428	917.246	0.477	17	0.230	K.IGGIGTVPVGR.V
R1/RRR1-7/2	1025.394	1026.215	-1780.989	0.437	919.885	0.472	17	0.229	K.IGGIGTVPVGR.V
R1/RRR1-13/2	1025.454	1026.215	-1722.261	0.415	912.824	0.471	17	0.228	K.IGGIGTVPVGR.V
R1/RRR1-14/2	1025.571	1026.215	-1608.053	0.453	957.243	0.451	17	0.228	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1752.327	1752.026	172.678	0.535	1002.507	0.469	22	0.225	K.AGMVVTFAPSNVTTEVK.S
R1/RRR1-1/2	1025.688	1026.215	-1492.796	0.426	796.869	0.484	16	0.225	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1751.255	1752.026	-1014.279	0.472	1081.964	0.440	21	0.224	K.AGMVVTFAPSNVTTEVK.S
R1/RRR1-8/2	1026.870	1026.215	-336.786	0.413	1053.047	0.409	15	0.223	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1109.033	1109.254	-200.001	0.303	1414.131	0.278	14	0.223	R.FDEIVKETK.N
R1/RRR1-2/2	1026.154	1026.215	-59.492	0.493	891.535	0.430	17	0.222	K.IGGIGTVPVGR.V
R1/RRR1-6/2	1025.520	1026.215	-1657.680	0.413	943.017	0.418	17	0.222	K.IGGIGTVPVGR.V
R1/RRR1-1/2	1025.645	1026.215	-1535.357	0.471	816.246	0.444	17	0.222	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1025.968	1026.215	-241.254	0.414	781.545	0.468	16	0.222	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1026.474	1026.215	253.037	0.324	889.158	0.462	16	0.221	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1261.233	1261.411	-141.500	0.443	907.246	0.456	16	0.220	K.ANISPNAPWYK.G
R1/RRR1-4/2	1025.980	1026.215	-229.676	0.441	827.708	0.447	15	0.219	K.IGGIGTVPVGR.V
R1/RRR1-5/2	1027.137	1026.215	-75.766	0.476	815.121	0.435	16	0.219	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1260.625	1261.411	-1420.979	0.448	749.100	0.516	14	0.219	K.ANISPNAPWYK.G
R1/RRR1-10/2	1026.028	1026.215	-182.291	0.453	784.835	0.428	16	0.217	K.IGGIGTVPVGR.V
R1/RRR1-15/2	1025.529	1026.215	-1648.950	0.435	757.801	0.427	16	0.216	K.IGGIGTVPVGR.V
R1/RRR1-11/2	1025.681	1026.215	-1499.969	0.361	779.624	0.435	16	0.216	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1751.520	1752.026	-862.017	0.509	895.205	0.440	21	0.213	K.AGMVVTFAPSNVTTEVK.S
R1/RRR1-8/2	1109.057	1109.254	-178.138	0.415	1229.183	0.287	14	0.212	R.FDEIVKETK.N
R1/RRR1-10/2	1025.948	1026.215	-261.069	0.458	676.714	0.409	15	0.211	K.IGGIGTVPVGR.V
R1/RRR1-9/2	1025.303	1026.215	-1870.111	0.298	638.220	0.423	16	0.209	K.IGGIGTVPVGR.V
R1/RRR1-1/2	1026.337	1026.215	119.222	0.338	809.226	0.393	14	0.209	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1109.097	1109.254	-142.143	0.301	1262.583	0.240	14	0.206	R.FDEIVKETK.N
R1/RRR1-8/2	1026.186	1026.215	-28.230	0.314	784.332	0.276	15	0.199	K.IGGIGTVPVGR.V
R1/RRR1-19/2	1025.932	1026.215	-276.707	0.248	571.884	0.270	13	0.196	K.IGGIGTVPVGR.V
R1/RRR1-8/2	1026.887	1026.215	-319.969	0.313	335.023	0.313	12	0.195	-.IGGIGTVPVGR.-
R1/RRR1-8/2	1327.567	1327.557	7.967	0.200	577.450	0.245	14	0.181	R.EHALLAFTLGVR.Q
R1/RRR1-10/2	1103.110	1103.299	-172.106	0.501	1158.322	0.503	19	0.250	K.RPFAAIVGGSK.V
R1/RRR1-10/2	1102.986	1103.299	-284.461	0.564	880.644	0.524	17	0.233	K.RPFAAIVGGSK.V
R1/RRR1-10/2	1000.299	1000.219	80.526	0.421	698.733	0.450	14	0.211	K.FSLAPLVPR.L
R1/RRR1-10/2	1000.539	1000.219	321.087	0.477	559.488	0.441	13	0.204	-.FSLAPLVPR.-
R1/RRR1-10/3	1103.155	1103.299	-131.434	0.463	1086.716	0.445	20	0.113	-.RPFAAIVGGSK.-
R1/RRR1-10/3	1936.587	1935.129	236.945	0.391	891.089	0.495	28	0.109	K.LASLADLYVNDAFGTAHR.A
R1/RRR1-10/3	1103.334	1103.299	31.380	0.401	740.572	0.263	18	0.072	-.RPFAAIVGGSK.-
R1/RRR1-7/2	1132.533	1133.320	-1582.883	0.450	1809.785	0.545	19	0.337	K.ALVSAGLSSSIK.V
R1/RRR1-7/2	1132.861	1133.320	-406.544	0.434	1737.132	0.540	19	0.324	K.ALVSAGLSSSIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1133.077	1133.320	-215.207	0.449	1741.089	0.501	19	0.313	K.ALVSAGLSSSIK.V
R1/RRR1-7/2	1783.569	1783.963	-221.222	0.569	1600.998	0.550	25	0.309	R.DISLNYATFQPGTTVR.D
R1/RRR1-13/2	1132.846	1133.320	-420.168	0.413	1585.913	0.498	18	0.290	K.ALVSAGLSSSIK.V
R1/RRR1-7/2	1132.590	1133.320	-1532.211	0.464	1446.819	0.553	18	0.288	K.ALVSAGLSSSIK.V
R1/RRR1-7/2	1563.450	1562.751	-192.616	0.575	1574.690	0.475	21	0.283	R.DNVEAYWPSVIIR.Y
R1/RRR1-7/2	1784.483	1783.963	-269.617	0.580	1267.116	0.510	22	0.255	R.DISLNYATFQPGTTVR.D
R1/RRR1-7/2	1782.604	1783.963	-1327.156	0.413	1386.138	0.446	22	0.254	R.DISLNYATFQPGTTVR.D
R1/RRR1-7/1	915.552	916.097	-1692.483	0.295	635.256	0.326	10	0.250	R.SEVVQLLK.S
R1/RRR1-7/2	1562.448	1562.751	-194.150	0.483	1352.918	0.395	20	0.241	R.DNVEAYWPSVIIR.Y
R1/RRR1-14/2	1562.607	1562.751	-92.192	0.481	1026.322	0.489	17	0.232	R.DNVEAYWPSVIIR.Y
R1/RRR1-7/2	1566.810	1567.767	-1252.615	0.431	882.537	0.483	19	0.224	R.IYYPDKEALDALR.G
R1/RRR1-7/2	1567.435	1567.767	-212.436	0.441	803.232	0.486	18	0.220	R.IYYPDKEALDALR.G
R1/RRR1-7/2	1562.080	1562.751	-1072.920	0.403	1282.092	0.312	19	0.219	R.DNVEAYWPSVIIR.Y
R1/RRR1-9/2	1132.673	1133.320	-1458.811	0.269	1076.652	0.393	17	0.215	K.ALVSAGLSSSIK.V
R1/RRR1-7/2	1567.203	1567.767	-1001.132	0.412	730.449	0.472	17	0.213	R.IYYPDKEALDALR.G
R1/RRR1-7/2	1561.821	1562.751	-1239.448	0.379	1246.653	0.287	18	0.212	R.DNVEAYWPSVIIR.Y
R1/RRR1-7/2	916.098	916.097	1.188	0.424	730.724	0.402	13	0.211	R.SEVVQLLK.S
R1/RRR1-14/2	916.078	916.097	-21.266	0.429	760.637	0.369	13	0.208	R.SEVVQLLK.S
R1/RRR1-7/2	915.883	916.097	-234.893	0.458	689.125	0.375	13	0.207	R.SEVVQLLK.S
R1/RRR1-7/2	915.944	916.097	-168.041	0.509	719.766	0.356	13	0.206	R.SEVVQLLK.S
R1/RRR1-14/2	915.936	916.097	-176.731	0.378	719.198	0.286	13	0.198	R.SEVVQLLK.S
R1/RRR1-13/2	1567.137	1567.767	-1043.441	0.310	695.746	0.347	17	0.197	R.IYYPDKEALDALR.G
R1/RRR1-13/2	1567.877	1567.767	70.312	0.361	693.419	0.266	16	0.190	R.IYYPDKEALDALR.G
R1/RRR1-13/2	1567.193	1567.767	-1007.779	0.339	456.698	0.297	14	0.189	-.IYYPDKEALDALR.-
R1/RRR1-14/2	1562.171	1562.751	-1014.545	0.317	660.926	0.265	14	0.187	R.DNVEAYWPSVIIR.Y
R1/RRR1-13/2	1562.190	1562.751	-1001.914	0.309	741.616	0.262	14	0.187	R.DNVEAYWPSVIIR.Y
R1/RRR1-13/2	1566.319	1567.767	-1567.557	0.224	615.160	0.196	17	0.186	R.IYYPDKEALDALR.G
R1/RRR1-7/1	915.588	916.097	-1652.700	0.277	488.273	0.312	9	0.177	-.SEVVQLLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	915.517	916.097	-1731.079	0.282	719.575	0.188	11	0.171	-.SEVVQLLK.-
R1/RRR1-7/1	915.479	916.097	-1773.265	0.257	427.923	0.286	9	0.148	-.SEVVQLLK.-
R1/RRR1-7/3	1568.692	1567.767	-47.979	0.404	753.078	0.511	29	0.103	R.IYYPDKEALDALR.G
R1/RRR1-9/3	1568.424	1567.767	-219.766	0.351	499.804	0.465	23	0.097	R.IYYPDKEALDALR.G
R1/RRR1-7/3	1568.699	1567.767	-43.530	0.403	768.597	0.453	28	0.097	R.IYYPDKEALDALR.G
R1/RRR1-13/3	1566.662	1567.767	-1347.852	0.358	413.344	0.428	21	0.097	R.IYYPDKEALDALR.G
R1/RRR1-13/3	1567.505	1567.767	-167.600	0.287	410.228	0.440	20	0.095	R.IYYPDKEALDALR.G
R1/RRR1-9/3	1567.095	1567.767	-1069.963	0.313	526.927	0.443	22	0.094	R.IYYPDKEALDALR.G
R1/RRR1-7/3	1567.885	1567.767	75.145	0.443	617.814	0.410	25	0.094	R.IYYPDKEALDALR.G
R1/RRR1-14/3	1567.658	1567.767	-69.762	0.298	430.174	0.413	22	0.093	R.IYYPDKEALDALR.G
R1/RRR1-14/3	1568.073	1567.767	195.771	0.353	560.330	0.392	24	0.091	R.IYYPDKEALDALR.G
R1/RRR1-13/3	1567.862	1567.767	60.621	0.323	511.800	0.388	24	0.091	R.IYYPDKEALDALR.G
R1/RRR1-13/3	1566.253	1567.767	-2250.422	0.338	541.107	0.306	23	0.087	R.IYYPDKEALDALR.G
R1/RRR1-14/3	1566.537	1567.767	-1428.032	0.339	597.184	0.332	25	0.086	R.IYYPDKEALDALR.G
R1/RRR1-10/2	1164.837	1165.366	-1316.362	0.404	573.022	0.467	16	0.209	R.LPPVASYVYR.R
R1/RRR1-10/2	1165.052	1165.366	-269.833	0.225	243.823	0.326	14	0.189	-.LPPVASYVYR.-
R1/RRR1-2/2	1593.582	1593.932	-220.245	0.527	1361.778	0.600	21	0.289	R.IVLNPISSLADLPLK.N
R1/RRR1-2/2	1594.486	1593.932	-280.475	0.499	1320.057	0.575	21	0.278	R.IVLNPISSLADLPLK.N
R1/RRR1-3/2	1594.813	1593.932	-74.976	0.453	1263.380	0.547	20	0.263	R.IVLNPISSLADLPLK.N
R1/RRR1-1/2	1593.653	1593.932	-175.982	0.475	1207.585	0.564	20	0.262	R.IVLNPISSLADLPLK.N
R1/RRR1-2/2	1592.723	1593.932	-1391.284	0.359	1297.169	0.504	20	0.255	R.IVLNPISSLADLPLK.N
R1/RRR1-3/2	1740.396	1740.935	-886.591	0.494	990.222	0.590	19	0.245	K.VYSIAAETGLPVDNYK.A
R1/RRR1-2/2	1544.420	1543.794	-242.635	0.499	1138.769	0.486	20	0.241	K.VSPGVWYLQLAPGR.S
R1/RRR1-1/2	1593.529	1593.932	-253.598	0.362	950.098	0.365	18	0.205	R.IVLNPISSLADLPLK.N
R1/RRR1-1/2	1593.065	1593.932	-1175.943	0.306	739.255	0.402	17	0.199	R.IVLNPISSLADLPLK.N
R1/RRR1-3/2	1549.775	1548.726	31.869	0.396	949.162	0.332	18	0.199	K.LGLEFGSNAVITNGR.V
R1/RRR1-3/2	1545.287	1543.794	319.891	0.381	664.333	0.330	16	0.190	K.VSPGVWYLQLAPGR.S
R1/RRR1-2/2	1549.704	1548.726	-13.795	0.334	728.140	0.313	16	0.188	K.LGLEFGSNAVITNGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1275.209	1275.479	-212.343	0.301	911.112	0.204	14	0.183	K.VIFVDADQIVR.A
R1/RRR1-2/2	1550.222	1548.726	321.400	0.287	522.682	0.248	14	0.181	-.LGLEFGSNAVITNGR.-
R1/RRR1-2/3	1886.903	1887.038	-71.845	0.482	956.976	0.486	30	0.116	K.GVALEDPKTEDLSQEVR.G
R1/RRR1-3/3	1887.022	1887.038	-8.384	0.453	910.626	0.482	27	0.113	K.GVALEDPKTEDLSQEVR.G
R1/RRR1-3/3	1886.081	1887.038	-1040.875	0.416	629.895	0.401	23	0.089	K.GVALEDPKTEDLSQEVR.G
R1/RRR1-8/2	1494.299	1494.716	-279.943	0.516	2678.448	0.515	22	0.504	K.VADFFDAAVNLALK.V
R1/RRR1-8/2	1493.811	1494.716	-1279.321	0.401	2695.358	0.496	22	0.500	K.VADFFDAAVNLALK.V
R1/RRR1-8/2	1493.968	1494.716	-1173.630	0.428	2361.102	0.480	21	0.417	K.VADFFDAAVNLALK.V
R1/RRR1-8/2	1092.012	1092.273	-239.557	0.580	2026.424	0.541	19	0.377	K.LIVAGASAYAR.L
R1/RRR1-8/2	1092.060	1092.273	-195.765	0.528	1793.078	0.609	19	0.360	K.LIVAGASAYAR.L
R1/RRR1-8/2	1208.109	1208.392	-235.386	0.551	1698.659	0.471	18	0.301	K.VLENVHIAANK.N
R1/RRR1-8/2	1208.141	1208.392	-208.321	0.530	1671.347	0.482	18	0.301	K.VLENVHIAANK.N
R1/RRR1-8/2	1000.074	1000.046	27.961	0.412	653.390	0.454	12	0.208	K.YSEGYPGAR.Y
R1/RRR1-8/2	999.912	1000.046	-135.134	0.302	682.086	0.414	12	0.200	K.YSEGYPGAR.Y
R1/RRR1-8/2	999.792	1000.046	-254.796	0.300	747.279	0.377	13	0.200	K.YSEGYPGAR.Y
R1/RRR1-8/3	1260.679	1260.381	236.999	0.520	1390.261	0.396	22	0.125	K.LRHDVEEYAK.Q
R1/RRR1-9/3	1260.225	1260.381	-124.185	0.471	1265.151	0.355	21	0.105	K.LRHDVEEYAK.Q
R1/RRR1-8/3	1260.029	1260.381	-280.016	0.432	1150.638	0.380	20	0.103	K.LRHDVEEYAK.Q
R1/RRR1-9/3	1259.985	1260.381	-315.153	0.413	1229.350	0.329	20	0.098	K.LRHDVEEYAK.Q
R1/RRR1-9/3	1260.265	1260.381	-92.121	0.419	1282.504	0.315	21	0.098	K.LRHDVEEYAK.Q
R1/RRR1-8/3	1260.673	1260.381	232.193	0.490	993.384	0.369	19	0.095	K.LRHDVEEYAK.Q
R1/RRR1-10/2	1694.927	1694.909	10.719	0.526	2165.808	0.548	22	0.401	R.IVTFNSDWQLLTEK.E
R1/RRR1-10/2	1694.420	1694.909	-289.729	0.552	2112.117	0.526	22	0.383	R.IVTFNSDWQLLTEK.E
R1/RRR1-10/2	1742.547	1742.950	-232.051	0.447	1612.463	0.435	22	0.276	R.DEDPAAVAATIPSFLPK.L
R1/RRR1-10/2	1742.642	1742.950	-177.517	0.451	1484.271	0.428	21	0.258	R.DEDPAAVAATIPSFLPK.L
R1/RRR1-10/2	1607.281	1607.786	-939.451	0.475	1147.892	0.473	22	0.241	R.DLPDSTFTISELIR.N
R1/RRR1-11/2	1694.301	1694.909	-952.047	0.442	1133.407	0.486	16	0.235	R.IVTFNSDWQLLTEK.E
R1/RRR1-10/2	1608.349	1607.786	-272.804	0.549	928.738	0.507	20	0.231	R.DLPDSTFTISELIR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1607.808	1607.786	13.356	0.496	966.829	0.438	20	0.221	R.DLPDSTFTISELIR.N
R1/RRR1-2/2	1607.729	1607.786	-36.068	0.429	935.827	0.399	20	0.213	R.DLPDSTFTISELIR.N
R1/RRR1-10/2	1693.549	1694.909	-1397.667	0.335	1101.657	0.341	17	0.209	R.IVTFNSDWQLLTEK.E
R1/RRR1-10/2	1454.968	1455.683	-1182.284	0.379	546.986	0.494	17	0.207	R.LTAPPEQILPGYR.S
R1/RRR1-10/2	1116.916	1117.231	-283.106	0.300	583.251	0.437	15	0.201	K.SCPGVENVVR.Y
R1/RRR1-10/2	1116.340	1117.231	-1699.508	0.367	536.427	0.388	15	0.201	K.SCPGVENVVR.Y
R1/RRR1-9/2	1607.971	1607.786	115.387	0.396	674.702	0.344	18	0.196	R.DLPDSTFTISELIR.N
R1/RRR1-10/2	1455.341	1455.683	-235.529	0.296	401.789	0.441	16	0.196	R.LTAPPEQILPGYR.S
R1/RRR1-10/2	1454.567	1455.683	-1458.952	0.296	344.212	0.434	14	0.193	R.LTAPPEQILPGYR.S
R1/RRR1-4/2	1696.399	1694.909	289.952	0.317	393.429	0.359	13	0.189	R.IVTFNSDWQLLTEK.E
R1/RRR1-10/2	1116.514	1117.231	-1543.088	0.182	431.152	0.289	14	0.185	-.SCPGVENVVR.-
R1/RRR1-1/2	1743.586	1742.950	-209.512	0.323	589.868	0.193	15	0.176	R.DEDPAAVAATIPSFLPK.L
R1/RRR1-6/2	1786.520	1786.919	-224.078	0.549	1564.435	0.522	24	0.295	-.AVFASGSPFDPVEYDGK.-
R1/RRR1-7/2	1787.483	1786.919	-244.575	0.590	1538.373	0.512	24	0.285	R.AVFASGSPFDPVEYDGK.I
R1/RRR1-7/2	1787.117	1786.919	111.151	0.589	1371.496	0.566	23	0.280	R.AVFASGSPFDPVEYDGK.I
R1/RRR1-7/2	1787.203	1786.919	159.580	0.572	1358.014	0.511	23	0.264	R.AVFASGSPFDPVEYDGK.I
R1/RRR1-7/2	980.195	980.100	97.042	0.561	1433.146	0.444	15	0.262	K.AYELGLASR.L
R1/RRR1-6/2	1787.642	1786.919	-155.447	0.536	1177.292	0.554	22	0.256	R.AVFASGSPFDPVEYDGK.I
R1/RRR1-6/2	1786.398	1786.919	-853.891	0.531	1331.798	0.475	23	0.253	R.AVFASGSPFDPVEYDGK.I
R1/RRR1-3/2	979.706	980.100	-402.801	0.462	1369.386	0.383	14	0.241	K.AYELGLASR.L
R1/RRR1-7/2	979.858	980.100	-247.296	0.491	1311.460	0.402	14	0.240	K.AYELGLASR.L
R1/RRR1-7/2	1166.142	1166.355	-183.697	0.432	1063.497	0.480	18	0.234	K.ISAHIAANVAAK.A
R1/RRR1-6/2	979.865	980.100	-240.172	0.502	1227.557	0.404	14	0.234	K.AYELGLASR.L
R1/RRR1-7/2	1165.454	1166.355	-1636.713	0.428	1042.635	0.492	17	0.234	K.ISAHIAANVAAK.A
R1/RRR1-7/2	979.621	980.100	-490.074	0.488	1463.369	0.273	15	0.226	K.AYELGLASR.L
R1/RRR1-7/2	1166.054	1166.355	-259.521	0.444	837.424	0.433	16	0.212	K.ISAHIAANVAAK.A
R1/RRR1-6/2	1315.445	1315.584	-106.164	0.418	634.273	0.475	18	0.210	K.TIKPTVLIGTSGK.G
R1/RRR1-6/2	1315.373	1315.584	-161.274	0.402	518.773	0.474	18	0.207	K.TIKPTVLIGTSGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1314.911	1315.584	-1276.370	0.343	766.528	0.393	19	0.203	K.TIKPTVLIGTSGK.G
R1/RRR1-7/3	1294.845	1294.528	244.976	0.500	785.574	0.457	21	0.105	R.KISAHIAANVAAK.A
R1/RRR1-7/3	1294.276	1294.528	-195.650	0.452	1249.167	0.332	25	0.102	R.KISAHIAANVAAK.A
R1/RRR1-6/3	1294.913	1294.528	297.723	0.457	777.507	0.441	21	0.100	R.KISAHIAANVAAK.A
R1/RRR1-7/3	1294.621	1294.528	72.091	0.430	941.949	0.334	23	0.088	R.KISAHIAANVAAK.A
R1/RRR1-6/3	1293.908	1294.528	-1256.315	0.408	737.838	0.352	20	0.087	R.KISAHIAANVAAK.A
R1/RRR1-6/3	1294.221	1294.528	-237.946	0.380	653.475	0.295	19	0.079	-.KISAHIAANVAAK.-
R1/RRR1-10/2	1480.127	1480.711	-1073.562	0.442	1548.362	0.459	21	0.277	R.ASIYNAM*PLAGVEK.L
R1/RRR1-10/2	1068.201	1068.250	-46.376	0.476	1382.845	0.387	16	0.243	R.FGLIYAGAQK.N
R1/RRR1-11/2	1068.055	1068.250	-183.486	0.464	1094.858	0.462	16	0.236	R.FGLIYAGAQK.N
R1/RRR1-11/2	1282.747	1283.502	-1372.897	0.361	989.714	0.532	18	0.234	K.NVGPSGVTIAIVR.K
R1/RRR1-10/2	1480.253	1480.711	-310.524	0.464	1089.937	0.450	19	0.229	R.ASIYNAM*PLAGVEK.L
R1/RRR1-10/2	1068.500	1068.250	234.261	0.485	1107.833	0.400	16	0.226	R.FGLIYAGAQK.N
R1/RRR1-11/2	1067.964	1068.250	-268.683	0.451	1133.458	0.390	16	0.225	R.FGLIYAGAQK.N
R1/RRR1-10/2	1283.337	1283.502	-129.332	0.444	854.278	0.507	17	0.224	K.NVGPSGVTIAIVR.K
R1/RRR1-10/2	1949.292	1949.109	94.115	0.460	753.802	0.545	22	0.223	K.YTSLPPFDAIEQNPEAR.F
R1/RRR1-10/2	1068.226	1068.250	-22.879	0.482	1161.067	0.362	16	0.222	R.FGLIYAGAQK.N
R1/RRR1-11/2	1067.669	1068.250	-1485.360	0.412	928.855	0.404	15	0.215	R.FGLIYAGAQK.N
R1/RRR1-10/2	1948.397	1949.109	-881.741	0.509	530.473	0.556	19	0.213	K.YTSLPPFDAIEQNPEAR.F
R1/RRR1-11/2	1283.252	1283.502	-195.937	0.382	686.553	0.474	15	0.208	K.NVGPSGVTIAIVR.K
R1/RRR1-10/2	1111.028	1111.232	-184.324	0.349	930.724	0.386	15	0.207	K.FSAASVAWSGK.D
R1/RRR1-10/2	1948.692	1949.109	-214.980	0.441	559.374	0.478	20	0.205	K.YTSLPPFDAIEQNPEAR.F
R1/RRR1-11/2	1480.316	1480.711	-267.832	0.402	772.267	0.387	20	0.204	R.ASIYNAM*PLAGVEK.L
R1/RRR1-10/2	1282.566	1283.502	-1514.566	0.317	616.324	0.479	15	0.204	K.NVGPSGVTIAIVR.K
R1/RRR1-10/2	1110.862	1111.232	-333.696	0.338	574.004	0.471	14	0.202	K.FSAASVAWSGK.D
R1/RRR1-10/2	1282.461	1283.502	-1596.603	0.292	557.317	0.471	14	0.199	K.NVGPSGVTIAIVR.K
R1/RRR1-11/2	1282.516	1283.502	-1553.192	0.242	422.592	0.350	13	0.183	-.NVGPSGVTIAIVR.-
R1/RRR1-12/2	1297.103	1297.569	-360.447	0.426	1114.826	0.516	19	0.246	K.LIVTVLPSLGER.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1216.077	1216.373	-243.610	0.478	1350.075	0.388	18	0.241	K.IRDSASQLIGR.T
R1/RRR1-12/2	1216.150	1216.373	-183.996	0.460	1294.688	0.405	17	0.239	K.IRDSASQLIGR.T
R1/RRR1-12/2	1186.630	1187.368	-1469.554	0.457	1211.131	0.428	16	0.237	-.VLEVKGEDAVK.-
R1/RRR1-12/2	1216.149	1216.373	-184.298	0.500	1297.076	0.390	17	0.236	K.IRDSASQLIGR.T
R1/RRR1-12/2	1298.110	1297.569	-354.886	0.474	909.335	0.523	18	0.233	K.LIVTVLPSLGER.Y
R1/RRR1-12/2	1298.182	1297.569	-299.221	0.478	1011.402	0.460	19	0.229	K.LIVTVLPSLGER.Y
R1/RRR1-12/2	1328.083	1328.495	-310.922	0.429	987.042	0.416	16	0.218	R.YLSSALFEELR.A
R1/RRR1-12/2	1328.137	1328.495	-270.809	0.439	709.313	0.433	14	0.205	-.YLSSALFEELR.-
R1/RRR1-12/2	981.792	982.179	-395.859	0.491	773.615	0.328	13	0.202	R.TPM*VYLNK.V
R1/RRR1-12/2	965.870	966.180	-321.865	0.353	787.127	0.312	12	0.198	R.TPMVYLNK.V
R1/RRR1-12/2	982.042	982.179	-139.924	0.356	562.922	0.374	11	0.194	-.TPM*VYLNK.-
R1/RRR1-12/2	1328.233	1328.495	-197.782	0.305	719.474	0.335	13	0.192	R.YLSSALFEELR.A
R1/RRR1-12/2	981.585	982.179	-1628.434	0.395	587.917	0.358	11	0.191	-.TPM*VYLNK.-
R1/RRR1-11/2	1216.031	1216.373	-282.283	0.321	569.716	0.238	15	0.188	-.IRDSASQLIGR.-
R1/RRR1-7/2	1470.848	1471.678	-1248.017	0.358	3005.578	0.323	21	0.504	K.ESIVDVEGVVSLPK.E
R1/RRR1-7/2	1472.252	1471.678	-290.122	0.531	2701.677	0.477	21	0.491	K.ESIVDVEGVVSLPK.E
R1/RRR1-7/2	1471.203	1471.678	-323.951	0.338	2726.968	0.437	21	0.482	K.ESIVDVEGVVSLPK.E
R1/RRR1-7/2	1532.477	1531.652	-114.697	0.567	2211.432	0.576	25	0.424	R.VWTEVGGLDEAAAGR.S
R1/RRR1-7/2	1531.145	1531.652	-987.125	0.539	2219.802	0.549	25	0.415	R.VWTEVGGLDEAAAGR.S
R1/RRR1-7/2	1531.193	1531.652	-300.784	0.488	2163.156	0.487	25	0.381	R.VWTEVGGLDEAAAGR.S
R1/RRR1-7/2	1307.252	1307.477	-173.234	0.405	1275.321	0.429	21	0.241	K.LIAGSSEGGAAVFK.L
R1/RRR1-7/2	1306.514	1307.477	-1507.609	0.330	1075.683	0.409	18	0.217	K.LIAGSSEGGAAVFK.L
R1/RRR1-8/2	1018.185	1018.151	33.356	0.420	713.591	0.398	13	0.206	R.TPANQAIFR.I
R1/RRR1-7/2	1049.689	1050.235	-1477.385	0.422	734.163	0.401	12	0.203	R.VFEVGPVFR.A
R1/RRR1-8/2	1017.952	1018.151	-196.246	0.469	816.295	0.352	13	0.203	R.TPANQAIFR.I
R1/RRR1-1/2	1017.932	1018.151	-215.614	0.366	458.869	0.351	13	0.199	R.TPANQAIFR.I
R1/RRR1-1/2	1018.155	1018.151	3.895	0.335	440.613	0.303	12	0.195	R.TPANQAIFR.I
R1/RRR1-8/2	1049.205	1050.235	-1940.235	0.390	780.988	0.301	12	0.193	-.VFEVGPVFR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1726.545	1726.953	-236.471	0.555	2630.149	0.558	26	0.506	R.LNLEAAGVEVDNIGAIK.V
R1/RRR1-8/2	1858.842	1859.065	-120.182	0.481	2606.785	0.530	24	0.491	K.ELAITSDEALSLEELPK.R
R1/RRR1-8/2	1859.409	1859.065	185.912	0.588	2491.414	0.510	25	0.452	K.ELAITSDEALSLEELPK.R
R1/RRR1-8/2	1725.949	1726.953	-1164.218	0.518	2254.565	0.538	25	0.414	R.LNLEAAGVEVDNIGAIK.V
R1/RRR1-8/2	1725.914	1726.953	-1184.388	0.481	1872.449	0.532	24	0.342	R.LNLEAAGVEVDNIGAIK.V
R1/RRR1-8/2	1857.925	1859.065	-1155.195	0.388	1922.074	0.411	22	0.312	K.ELAITSDEALSLEELPK.R
R1/RRR1-9/2	1860.019	1859.065	-24.461	0.508	1568.512	0.479	21	0.279	K.ELAITSDEALSLEELPK.R
R1/RRR1-3/2	1726.651	1726.953	-175.120	0.470	1656.923	0.407	21	0.272	R.LNLEAAGVEVDNIGAIK.V
R1/RRR1-1/2	1726.497	1726.953	-264.490	0.487	1407.772	0.467	20	0.257	R.LNLEAAGVEVDNIGAIK.V
R1/RRR1-8/2	1629.416	1629.799	-235.464	0.497	1249.891	0.512	22	0.257	R.TSVPNIWAVGDVTNR.M
R1/RRR1-9/2	1630.266	1629.799	287.520	0.541	1141.214	0.540	21	0.252	R.TSVPNIWAVGDVTNR.M
R1/RRR1-9/2	1630.165	1629.799	225.200	0.494	1122.906	0.519	22	0.247	R.TSVPNIWAVGDVTNR.M
R1/RRR1-9/2	1630.262	1629.799	285.193	0.479	1126.237	0.520	19	0.244	R.TSVPNIWAVGDVTNR.M
R1/RRR1-8/2	1045.962	1046.160	-189.352	0.356	1120.420	0.482	16	0.238	R.TVVASNLEGR.G
R1/RRR1-7/2	1629.616	1629.799	-112.669	0.475	817.328	0.471	19	0.216	R.TSVPNIWAVGDVTNR.M
R1/RRR1-8/2	1045.542	1046.160	-1551.926	0.318	853.544	0.442	15	0.213	R.TVVASNLEGR.G
R1/RRR1-8/2	1042.001	1042.213	-203.819	0.417	866.594	0.349	15	0.206	K.ILVYGSSFR.G
R1/RRR1-8/2	1046.161	1046.160	1.450	0.325	718.864	0.404	14	0.203	R.TVVASNLEGR.G
R1/RRR1-9/2	1045.936	1046.160	-214.290	0.363	713.130	0.311	15	0.197	R.TVVASNLEGR.G
R1/RRR1-8/2	1042.067	1042.213	-140.359	0.275	589.292	0.355	12	0.193	K.ILVYGSSFR.G
R1/RRR1-8/2	1041.932	1042.213	-270.578	0.296	633.030	0.306	12	0.191	K.ILVYGSSFR.G
R1/RRR1-9/2	1045.864	1046.160	-283.374	0.216	678.443	0.244	16	0.188	R.TVVASNLEGR.G
R1/RRR1-6/2	1335.176	1334.632	-342.833	0.468	1474.533	0.621	21	0.312	K.KPAAPVKPVAEVK.K
R1/RRR1-6/2	1851.562	1852.034	-255.816	0.532	1417.329	0.527	24	0.277	K.ANFLSADDFEPSLIPSK.T
R1/RRR1-6/2	1851.629	1852.034	-219.042	0.530	1279.320	0.504	23	0.255	K.ANFLSADDFEPSLIPSK.T
R1/RRR1-6/2	1851.547	1852.034	-263.687	0.534	1214.894	0.521	23	0.253	K.ANFLSADDFEPSLIPSK.T
R1/RRR1-6/2	1333.862	1334.632	-1331.117	0.420	643.684	0.507	18	0.213	K.KPAAPVKPVAEVK.K
R1/RRR1-6/2	1469.156	1468.641	-330.736	0.477	847.834	0.436	16	0.213	K.WHAPLIDNPNYK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1306.217	1306.531	-240.953	0.399	567.917	0.462	15	0.207	K.LADIPFLEPYK.T
R1/RRR1-6/2	1306.315	1306.531	-166.141	0.329	820.584	0.377	17	0.204	K.LADIPFLEPYK.T
R1/RRR1-6/2	1026.263	1026.253	9.949	0.406	691.151	0.376	13	0.202	K.KIFDVLYK.L
R1/RRR1-6/2	1468.093	1468.641	-1057.125	0.400	769.070	0.365	15	0.199	K.WHAPLIDNPNYK.G
R1/RRR1-6/2	1468.301	1468.641	-231.699	0.452	749.009	0.364	15	0.198	K.WHAPLIDNPNYK.G
R1/RRR1-2/2	1851.509	1852.034	-826.045	0.457	755.549	0.388	18	0.197	K.ANFLSADDFEPSLIPSK.T
R1/RRR1-6/2	1306.182	1306.531	-268.143	0.335	838.109	0.291	17	0.196	K.LADIPFLEPYK.T
R1/RRR1-1/2	1851.337	1852.034	-919.304	0.392	624.619	0.363	17	0.191	K.ANFLSADDFEPSLIPSK.T
R1/RRR1-6/3	1468.360	1468.641	-191.383	0.509	1512.183	0.223	26	0.098	K.WHAPLIDNPNYK.G
R1/RRR1-6/3	1468.176	1468.641	-317.123	0.472	1221.544	0.270	24	0.088	K.WHAPLIDNPNYK.G
R1/RRR1-6/3	1468.092	1468.641	-1058.261	0.503	911.401	0.253	21	0.077	K.WHAPLIDNPNYK.G
R1/RRR1-9/2	1349.402	1349.557	-115.469	0.475	1314.837	0.502	18	0.260	R.KGPLIVYGTEGSK.I
R1/RRR1-10/2	1349.197	1349.557	-268.033	0.421	1262.931	0.484	19	0.251	R.KGPLIVYGTEGSK.I
R1/RRR1-10/2	1349.076	1349.557	-358.087	0.447	1161.106	0.512	18	0.247	R.KGPLIVYGTEGSK.I
R1/RRR1-13/2	1796.721	1797.132	-229.484	0.352	1374.585	0.431	23	0.246	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-9/2	1446.416	1446.680	-182.468	0.533	1177.713	0.488	21	0.246	R.LNLLDLAPGGHLGR.F
R1/RRR1-9/2	1349.357	1349.557	-148.864	0.410	1175.829	0.488	18	0.243	R.KGPLIVYGTEGSK.I
R1/RRR1-9/2	1797.715	1797.132	-232.694	0.459	1272.954	0.456	23	0.242	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-9/2	1348.542	1349.557	-1499.391	0.445	1085.841	0.498	19	0.240	R.KGPLIVYGTEGSK.I
R1/RRR1-9/2	1886.310	1886.970	-882.874	0.497	963.120	0.535	22	0.236	K.TM*ISDSDYAEFDNFSK.W
R1/RRR1-10/2	1797.544	1797.132	229.432	0.460	1212.851	0.447	23	0.235	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-10/2	1349.103	1349.557	-338.114	0.430	909.081	0.531	17	0.231	R.KGPLIVYGTEGSK.I
R1/RRR1-9/2	1283.201	1283.416	-167.988	0.402	515.115	0.555	19	0.221	R.NLPGVDVANVER.L
R1/RRR1-10/2	1446.404	1446.680	-190.935	0.469	867.151	0.460	20	0.219	R.LNLLDLAPGGHLGR.F
R1/RRR1-10/2	1797.391	1797.132	144.439	0.405	1037.481	0.427	22	0.218	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-9/2	1283.131	1283.416	-222.673	0.394	423.794	0.512	18	0.215	R.NLPGVDVANVER.L
R1/RRR1-9/2	1283.241	1283.416	-136.688	0.395	403.092	0.503	18	0.214	R.NLPGVDVANVER.L
R1/RRR1-10/2	1282.807	1283.416	-1258.395	0.305	434.666	0.543	19	0.212	R.NLPGVDVANVER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1283.007	1283.416	-319.460	0.330	331.832	0.487	17	0.208	R.NLPGVDVANVER.L
R1/RRR1-9/2	1446.452	1446.680	-157.578	0.460	630.132	0.468	17	0.208	R.LNLLDLAPGGHLGR.F
R1/RRR1-2/2	1283.340	1283.416	-59.209	0.308	464.343	0.407	18	0.203	R.NLPGVDVANVER.L
R1/RRR1-9/2	1446.969	1446.680	200.742	0.402	588.283	0.410	17	0.200	R.LNLLDLAPGGHLGR.F
R1/RRR1-10/2	1282.748	1283.416	-1303.981	0.241	310.716	0.374	16	0.198	R.NLPGVDVANVER.L
R1/RRR1-13/2	1283.210	1283.416	-160.736	0.262	433.783	0.345	17	0.198	R.NLPGVDVANVER.L
R1/RRR1-13/2	1282.632	1283.416	-1395.453	0.227	349.324	0.316	16	0.196	R.NLPGVDVANVER.L
R1/RRR1-13/2	1445.384	1446.680	-1593.252	0.359	353.923	0.436	13	0.194	R.LNLLDLAPGGHLGR.F
R1/RRR1-2/2	1283.102	1283.416	-245.580	0.240	296.815	0.330	14	0.193	-.NLPGVDVANVER.-
R1/RRR1-3/2	1797.241	1797.132	60.453	0.289	608.372	0.301	17	0.184	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-9/2	1796.628	1797.132	-839.624	0.181	772.110	0.091	18	0.175	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-14/3	1446.917	1446.680	164.311	0.465	1681.614	0.405	29	0.167	R.LNLLDLAPGGHLGR.F
R1/RRR1-9/3	1446.601	1446.680	-54.398	0.376	1467.982	0.400	28	0.138	R.LNLLDLAPGGHLGR.F
R1/RRR1-9/3	1446.910	1446.680	159.489	0.396	1450.595	0.395	27	0.137	R.LNLLDLAPGGHLGR.F
R1/RRR1-1/3	1446.333	1446.680	-240.052	0.467	1316.046	0.432	26	0.135	R.LNLLDLAPGGHLGR.F
R1/RRR1-10/3	1446.781	1446.680	70.518	0.435	1384.110	0.397	26	0.133	R.LNLLDLAPGGHLGR.F
R1/RRR1-13/3	1446.770	1446.680	62.521	0.464	1401.141	0.378	25	0.132	R.LNLLDLAPGGHLGR.F
R1/RRR1-9/3	1446.352	1446.680	-226.843	0.416	1265.448	0.421	26	0.126	R.LNLLDLAPGGHLGR.F
R1/RRR1-10/3	1448.093	1446.680	286.395	0.481	1372.827	0.373	26	0.126	R.LNLLDLAPGGHLGR.F
R1/RRR1-10/3	1446.595	1446.680	-58.461	0.394	1274.361	0.393	26	0.120	R.LNLLDLAPGGHLGR.F
R1/RRR1-13/3	1446.675	1446.680	-3.235	0.375	1244.651	0.378	25	0.115	R.LNLLDLAPGGHLGR.F
R1/RRR1-13/3	1446.608	1446.680	-49.574	0.403	1181.268	0.394	25	0.114	R.LNLLDLAPGGHLGR.F
R1/RRR1-6/3	1446.676	1446.680	-2.727	0.398	1262.161	0.361	26	0.112	R.LNLLDLAPGGHLGR.F
R1/RRR1-9/3	1796.962	1797.132	-95.132	0.350	1354.700	0.303	33	0.105	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-6/3	1446.665	1446.680	-10.217	0.373	1072.430	0.377	23	0.105	R.LNLLDLAPGGHLGR.F
R1/RRR1-12/3	1446.659	1446.680	-14.406	0.392	1108.031	0.353	24	0.102	R.LNLLDLAPGGHLGR.F
R1/RRR1-6/3	1446.409	1446.680	-187.473	0.387	1001.154	0.377	24	0.100	R.LNLLDLAPGGHLGR.F
R1/RRR1-7/3	1446.319	1446.680	-249.832	0.399	832.046	0.395	22	0.098	R.LNLLDLAPGGHLGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/3	1447.008	1446.680	227.634	0.409	1044.554	0.320	25	0.092	R.LNLLDLAPGGHLGR.F
R1/RRR1-13/3	1796.288	1797.132	-1029.687	0.335	943.783	0.303	33	0.080	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-10/3	1797.442	1797.132	172.594	0.247	636.905	0.308	26	0.073	R.VAVASALAATSVPSLVLAR.G
R1/RRR1-9/2	1585.277	1585.824	-979.059	0.473	2484.469	0.344	21	0.393	R.FELTFYALNPELK.V
R1/RRR1-9/2	1585.494	1585.824	-208.703	0.508	2364.675	0.319	21	0.359	R.FELTFYALNPELK.V
R1/RRR1-9/2	959.587	960.110	-1592.311	0.480	1184.165	0.428	17	0.237	K.ASGASQLVVK.D
R1/RRR1-9/2	1041.591	1042.170	-1519.609	0.410	1035.926	0.491	13	0.233	K.YAELVYAGR.W
R1/RRR1-9/2	1041.963	1042.170	-198.656	0.378	1197.762	0.395	14	0.228	K.YAELVYAGR.W
R1/RRR1-9/2	959.870	960.110	-251.107	0.500	1074.885	0.416	17	0.227	K.ASGASQLVVK.D
R1/RRR1-9/2	959.333	960.110	-1858.068	0.450	982.568	0.419	17	0.222	K.ASGASQLVVK.D
R1/RRR1-9/2	1796.267	1796.915	-920.497	0.461	616.074	0.483	18	0.205	R.EWDITGREDAIEYAK.K
R1/RRR1-9/2	1004.919	1005.196	-275.609	0.422	730.435	0.393	12	0.203	K.HNVPIPVTK.K
R1/RRR1-9/2	1005.098	1005.196	-97.709	0.383	777.587	0.378	12	0.202	K.HNVPIPVTK.K
R1/RRR1-9/2	1005.102	1005.196	-93.446	0.278	504.420	0.432	10	0.193	-.HNVPIPVTK.-
R1/RRR1-7/2	1385.275	1385.595	-231.532	0.476	1818.982	0.438	21	0.309	K.SQGATILTGGVRPK.H
R1/RRR1-7/2	1462.217	1462.626	-280.558	0.504	1485.318	0.557	20	0.295	K.SPIVVFDDVDVEK.A
R1/RRR1-7/2	1462.554	1462.626	-49.861	0.516	1415.172	0.561	20	0.288	K.SPIVVFDDVDVEK.A
R1/RRR1-7/2	1462.439	1462.626	-128.311	0.516	1473.363	0.519	20	0.284	K.SPIVVFDDVDVEK.A
R1/RRR1-7/2	1306.056	1306.446	-299.761	0.501	1302.657	0.567	19	0.277	R.LGPVVSEGQYEK.I
R1/RRR1-7/2	1307.219	1306.446	-174.174	0.522	1237.924	0.578	19	0.273	R.LGPVVSEGQYEK.I
R1/RRR1-7/2	1306.054	1306.446	-301.167	0.475	1076.180	0.531	18	0.246	R.LGPVVSEGQYEK.I
R1/RRR1-1/2	1463.157	1462.626	-321.548	0.478	1035.815	0.488	17	0.232	K.SPIVVFDDVDVEK.A
R1/RRR1-7/2	1494.204	1494.628	-284.631	0.384	1261.520	0.316	18	0.216	R.ELGEGGIDNYLSVK.Q
R1/RRR1-7/2	1494.265	1494.628	-243.978	0.346	1032.156	0.398	17	0.212	R.ELGEGGIDNYLSVK.Q
R1/RRR1-7/2	1288.078	1288.431	-275.048	0.342	637.887	0.476	15	0.203	K.VAFTGSYETGKK.I
R1/RRR1-3/2	1462.276	1462.626	-240.189	0.294	790.865	0.324	16	0.194	K.SPIVVFDDVDVEK.A
R1/RRR1-8/2	1240.160	1240.477	-256.354	0.558	2278.182	0.440	18	0.381	R.ALNILADILQR.S
R1/RRR1-7/2	1239.930	1240.477	-1251.649	0.507	2254.657	0.446	18	0.381	R.ALNILADILQR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1240.481	1240.477	2.802	0.576	2185.841	0.440	18	0.364	R.ALNILADILQR.S
R1/RRR1-8/2	1241.221	1240.477	-207.110	0.564	2071.052	0.416	17	0.335	R.ALNILADILQR.S
R1/RRR1-8/2	1239.782	1240.477	-1371.788	0.483	1954.620	0.443	18	0.329	R.ALNILADILQR.S
R1/RRR1-7/2	1239.943	1240.477	-1241.071	0.511	1864.332	0.432	17	0.310	R.ALNILADILQR.S
R1/RRR1-8/2	1251.087	1251.372	-228.866	0.419	1247.870	0.474	16	0.249	K.YIETHYTAPR.M
R1/RRR1-8/2	1188.887	1189.344	-385.945	0.504	1226.904	0.470	18	0.248	R.IDAVDATTVKR.V
R1/RRR1-7/2	1211.663	1212.469	-1494.667	0.463	1324.711	0.419	16	0.245	R.RIPIPELFAR.I
R1/RRR1-8/2	1189.005	1189.344	-286.227	0.487	1152.007	0.445	17	0.236	R.IDAVDATTVKR.V
R1/RRR1-8/2	1212.214	1212.469	-210.854	0.457	1283.676	0.362	16	0.230	R.RIPIPELFAR.I
R1/RRR1-8/2	1213.336	1212.469	-109.851	0.473	1168.342	0.382	16	0.226	R.RIPIPELFAR.I
R1/RRR1-7/2	1188.936	1189.344	-344.634	0.497	1081.106	0.404	16	0.222	R.IDAVDATTVKR.V
R1/RRR1-7/2	1211.645	1212.469	-1509.847	0.446	1039.123	0.396	15	0.220	R.RIPIPELFAR.I
R1/RRR1-7/2	1213.207	1212.469	-216.433	0.467	1055.353	0.386	15	0.219	R.RIPIPELFAR.I
R1/RRR1-8/2	1212.420	1212.469	-40.355	0.442	962.824	0.401	15	0.217	R.RIPIPELFAR.I
R1/RRR1-7/2	1055.662	1056.282	-1539.251	0.389	509.835	0.518	14	0.216	R.IPIPELFAR.I
R1/RRR1-8/2	1055.944	1056.282	-321.484	0.300	644.433	0.449	15	0.207	R.IPIPELFAR.I
R1/RRR1-7/2	1056.382	1056.282	94.969	0.278	343.981	0.512	12	0.199	-.IPIPELFAR.-
R1/RRR1-8/2	1055.867	1056.282	-395.025	0.210	593.090	0.426	15	0.196	R.IPIPELFAR.I
R1/RRR1-7/2	1056.285	1056.282	2.711	0.221	429.907	0.351	13	0.193	R.IPIPELFAR.I
R1/RRR1-8/2	1056.190	1056.282	-88.288	0.169	392.865	0.452	13	0.190	R.IPIPELFAR.I
R1/RRR1-2/2	1212.636	1212.469	137.961	0.313	901.500	0.223	13	0.190	R.RIPIPELFAR.I
R1/RRR1-10/2	1654.442	1654.910	-283.653	0.487	1743.449	0.594	25	0.341	R.TPM*GGFLGALSSLSATK.L
R1/RRR1-10/2	1539.364	1539.543	-116.411	0.540	1785.344	0.502	21	0.323	R.EDQDAYAIQSNER.G
R1/RRR1-10/2	1540.001	1539.543	298.172	0.543	1658.384	0.531	20	0.312	R.EDQDAYAIQSNER.G
R1/RRR1-10/2	1654.421	1654.910	-296.460	0.464	1524.822	0.553	23	0.296	R.TPM*GGFLGALSSLSATK.L
R1/RRR1-10/2	1638.372	1638.910	-941.726	0.480	1422.936	0.547	24	0.283	R.TPMGGFLGALSSLSATK.L
R1/RRR1-10/2	1638.439	1638.910	-288.718	0.477	1264.446	0.559	22	0.266	R.TPMGGFLGALSSLSATK.L
R1/RRR1-10/2	1941.739	1942.207	-241.413	0.511	1214.725	0.568	24	0.264	R.NSGAFAWEIVPIEVPVGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1637.731	1638.910	-1334.583	0.466	1304.894	0.527	23	0.263	R.TPMGGFLGALSSLSATK.L
R1/RRR1-10/2	1088.976	1089.185	-191.991	0.429	1180.168	0.554	17	0.259	K.ALANAGLESSR.V
R1/RRR1-10/2	1197.681	1198.397	-1437.695	0.482	1315.004	0.481	16	0.257	K.AQELGLQVIAR.I
R1/RRR1-10/2	1941.314	1942.207	-977.859	0.472	1122.291	0.549	22	0.249	R.NSGAFAWEIVPIEVPVGR.G
R1/RRR1-10/2	1941.568	1942.207	-846.249	0.466	986.584	0.527	21	0.232	R.NSGAFAWEIVPIEVPVGR.G
R1/RRR1-10/2	1088.327	1089.185	-1711.865	0.418	1124.604	0.357	17	0.217	K.ALANAGLESSR.V
R1/RRR1-10/2	1173.283	1173.385	-86.573	0.541	1628.720	0.555	20	0.316	K.VIAISDVTGAVK.N
R1/RRR1-10/2	1173.157	1173.385	-194.809	0.523	1259.729	0.536	19	0.266	K.VIAISDVTGAVK.N
R1/RRR1-10/2	1082.070	1082.259	-175.368	0.449	1286.172	0.516	17	0.263	R.M*GAFTLGVNR.V
R1/RRR1-10/2	1162.229	1162.320	-78.758	0.426	1364.307	0.432	20	0.252	K.TAVANIPYGGAK.G
R1/RRR1-10/2	1173.151	1173.385	-199.402	0.482	1043.292	0.549	18	0.247	K.VIAISDVTGAVK.N
R1/RRR1-10/2	1162.252	1162.320	-59.057	0.492	1171.670	0.464	18	0.240	K.TAVANIPYGGAK.G
R1/RRR1-10/2	1301.023	1301.387	-280.028	0.395	1137.180	0.462	16	0.233	K.DDGTLASYVGFR.V
R1/RRR1-10/2	1748.366	1747.879	279.513	0.500	1217.941	0.414	21	0.230	-.GGIGCSPGDLSISELER.-
R1/RRR1-10/2	1747.642	1747.879	-136.096	0.504	1204.476	0.408	22	0.227	K.GGIGCSPGDLSISELER.L
R1/RRR1-10/2	1162.109	1162.320	-182.121	0.434	1102.188	0.401	18	0.223	K.TAVANIPYGGAK.G
R1/RRR1-9/2	1082.999	1082.259	-240.110	0.298	408.997	0.378	12	0.190	-.M*GAFTLGVNR.-
R1/RRR1-9/2	1135.986	1136.323	-297.539	0.371	1086.288	0.428	15	0.223	K.ALIAAEYTGVK.V
R1/RRR1-9/2	1094.112	1094.286	-159.757	0.391	729.492	0.541	15	0.223	K.NPLDLLPPSK.M
R1/RRR1-9/2	1335.864	1336.434	-1179.178	0.375	906.439	0.384	16	0.208	K.SFTSEFPHVER.Y
R1/RRR1-9/2	1094.119	1094.286	-152.594	0.339	759.964	0.407	14	0.204	K.NPLDLLPPSK.M
R1/RRR1-9/2	1336.273	1336.434	-120.910	0.403	843.586	0.336	15	0.199	K.SFTSEFPHVER.Y
R1/RRR1-9/2	1093.732	1094.286	-1425.225	0.265	510.407	0.357	12	0.190	K.NPLDLLPPSK.M
R1/RRR1-8/2	776.885	776.906	-27.991	0.420	921.420	0.197	11	0.190	K.VGGFLQR.M
R1/RRR1-9/2	1191.486	1190.480	5.178	0.419	799.748	0.311	13	0.189	-.MLVIGSTPPFK.-
R1/RRR1-8/2	776.500	776.906	-524.847	0.420	882.781	0.220	11	0.188	-.VGGFLQR.-
R1/RRR1-8/2	777.023	776.906	149.912	0.465	891.168	0.199	11	0.187	-.VGGFLQR.-
R1/RRR1-1/2	777.415	776.906	-633.843	0.461	712.005	0.179	11	0.182	-.VGGFLQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	777.120	776.906	275.777	0.347	565.156	0.168	11	0.177	-.VGGFLQR.-
R1/RRR1-11/2	1215.527	1216.323	-1482.261	0.413	1425.973	0.393	17	0.249	R.LLLEEENEAR.I
R1/RRR1-11/2	1216.014	1216.323	-254.698	0.530	1430.902	0.375	17	0.246	R.LLLEEENEAR.I
R1/RRR1-11/2	1099.056	1099.266	-191.456	0.453	1304.995	0.377	15	0.234	K.VLQDVLAGQR.G
R1/RRR1-11/2	1098.469	1099.266	-1640.440	0.376	1281.225	0.339	16	0.225	K.VLQDVLAGQR.G
R1/RRR1-11/2	1526.560	1525.820	-170.643	0.433	926.633	0.473	17	0.219	K.TVFNILGPLLNPAR.V
R1/RRR1-11/2	1098.375	1099.266	-1726.301	0.364	1056.445	0.382	13	0.215	-.VLQDVLAGQR.-
R1/RRR1-11/2	1447.646	1448.603	-1355.555	0.349	855.882	0.303	16	0.193	R.SGEAINTLESWIK.I
R1/RRR1-11/2	1447.752	1448.603	-1282.134	0.323	850.297	0.166	15	0.179	R.SGEAINTLESWIK.I
R1/RRR1-9/2	1526.500	1525.820	-210.353	0.301	622.025	0.163	14	0.176	K.TVFNILGPLLNPAR.V
R1/RRR1-11/3	1752.642	1752.910	-153.704	0.464	1768.955	0.257	28	0.149	-.VNTLHDGVALAQETQR.-
R1/RRR1-11/3	1752.514	1752.910	-226.652	0.456	1120.562	0.213	26	0.076	-.VNTLHDGVALAQETQR.-
R1/RRR1-8/2	1156.988	1157.302	-272.137	0.500	1724.583	0.531	19	0.324	R.DPAAATSGVVIR.R
R1/RRR1-8/2	1164.204	1164.290	-73.681	0.491	1282.270	0.494	18	0.259	K.LAGYDIPAESK.I
R1/RRR1-8/2	1164.070	1164.290	-189.177	0.477	1059.285	0.453	16	0.229	K.LAGYDIPAESK.I
R1/RRR1-8/2	1164.122	1164.290	-144.785	0.475	986.581	0.461	16	0.226	K.LAGYDIPAESK.I
R1/RRR1-8/2	1103.382	1103.342	36.440	0.437	1073.145	0.302	16	0.208	R.RFGDILLLR.M
R1/RRR1-8/2	1103.311	1103.342	-28.144	0.458	882.997	0.243	15	0.192	R.RFGDILLLR.M
R1/RRR1-8/3	1891.795	1892.018	-118.290	0.527	1098.807	0.438	33	0.114	R.FLEEEKAVEAHGNDFR.F
R1/RRR1-8/3	1469.637	1469.675	-25.511	0.476	1236.037	0.336	29	0.101	R.RDPAAATSGVVIRR.R
R1/RRR1-8/3	1469.761	1469.675	58.961	0.462	620.950	0.431	23	0.093	R.RDPAAATSGVVIRR.R
R1/RRR1-8/3	1469.208	1469.675	-318.400	0.423	583.359	0.376	22	0.083	-.RDPAAATSGVVIRR.-
R1/RRR1-9/2	1677.511	1677.902	-233.858	0.466	1745.961	0.432	21	0.295	K.IM*VNQADDVAGIISSK.A
R1/RRR1-9/2	1791.843	1792.023	-100.623	0.486	1492.906	0.511	25	0.284	K.TEAIFPATLETISNVGK.V
R1/RRR1-9/2	1373.192	1373.494	-220.998	0.414	1450.033	0.387	20	0.249	R.VLQDPSSSAEALR.T
R1/RRR1-9/2	1446.334	1446.665	-229.546	0.486	896.138	0.596	19	0.245	K.IPGTSELQISLCK.E
R1/RRR1-9/2	1373.121	1373.494	-272.815	0.493	1105.571	0.502	20	0.243	R.VLQDPSSSAEALR.T
R1/RRR1-9/2	1446.261	1446.665	-280.352	0.449	880.393	0.601	19	0.243	K.IPGTSELQISLCK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1446.063	1446.665	-1111.331	0.445	855.582	0.567	19	0.235	K.IPGTSELQISLCK.E
R1/RRR1-9/2	1372.645	1373.494	-1351.486	0.425	1145.747	0.420	20	0.230	R.VLQDPSSSAEALR.T
R1/RRR1-9/2	1323.093	1323.437	-260.736	0.465	892.537	0.387	15	0.206	K.SQLEEDPIVHR.H
R1/RRR1-9/2	1118.047	1118.311	-236.826	0.515	1934.036	0.536	19	0.358	K.APTIAAAAYLR.L
R1/RRR1-9/2	1597.939	1598.730	-1124.391	0.388	2158.582	0.393	21	0.348	R.SSICYIDGDEGILR.Y
R1/RRR1-9/2	1479.264	1479.662	-269.628	0.464	1900.852	0.484	20	0.334	K.IYDPGYLNTAPVR.S
R1/RRR1-9/2	1480.303	1479.662	-242.971	0.497	1742.240	0.553	21	0.331	K.IYDPGYLNTAPVR.S
R1/RRR1-9/2	1118.190	1118.311	-108.358	0.510	1820.130	0.512	18	0.331	K.APTIAAAAYLR.L
R1/RRR1-9/2	1118.488	1118.311	159.316	0.501	1824.025	0.484	18	0.323	K.APTIAAAAYLR.L
R1/RRR1-9/2	1598.137	1598.730	-999.757	0.417	2069.901	0.349	22	0.319	R.SSICYIDGDEGILR.Y
R1/RRR1-9/2	1478.540	1479.662	-1439.023	0.357	1459.478	0.454	21	0.264	K.IYDPGYLNTAPVR.S
R1/RRR1-9/2	914.984	915.029	-49.191	0.469	1094.710	0.476	15	0.237	R.GGALAVVDGR.T
R1/RRR1-9/2	915.287	915.029	282.705	0.469	1062.614	0.440	15	0.228	R.GGALAVVDGR.T
R1/RRR1-9/2	914.952	915.029	-85.056	0.435	1013.686	0.421	15	0.221	R.GGALAVVDGR.T
R1/RRR1-9/2	1598.309	1598.730	-264.483	0.398	1289.684	0.244	19	0.206	R.SSICYIDGDEGILR.Y
R1/RRR1-9/3	1928.872	1929.081	-108.907	0.371	938.291	0.370	29	0.091	R.VPASQGEQLGQIATSNATR.R
R1/RRR1-9/3	1929.013	1929.081	-35.780	0.390	681.087	0.409	26	0.088	R.VPASQGEQLGQIATSNATR.R
R1/RRR1-8/2	1516.233	1515.802	285.262	0.538	1247.292	0.464	21	0.246	R.LGPNYLM*LPANAPK.C
R1/RRR1-8/2	1680.323	1680.796	-282.177	0.431	1394.761	0.371	21	0.239	K.DLTDSIAAGNYPEWK.L
R1/RRR1-8/2	1515.338	1515.802	-307.143	0.443	980.818	0.473	18	0.225	R.LGPNYLM*LPANAPK.C
R1/RRR1-8/2	1970.237	1970.240	-1.405	0.513	1050.549	0.453	20	0.222	R.EGNFDLVGNNMPVFFIR.D
R1/RRR1-8/2	1680.642	1680.796	-91.982	0.453	1106.911	0.413	18	0.220	K.DLTDSIAAGNYPEWK.L
R1/RRR1-8/2	1515.218	1515.802	-1048.306	0.443	941.693	0.465	17	0.220	R.LGPNYLM*LPANAPK.C
R1/RRR1-8/2	1680.027	1680.796	-1056.480	0.356	1152.717	0.345	19	0.213	K.DLTDSIAAGNYPEWK.L
R1/RRR1-2/2	1151.337	1151.384	-40.794	0.345	743.405	0.511	14	0.213	R.APGVQTPIIVR.F
R1/RRR1-8/2	1986.283	1986.240	22.085	0.506	858.761	0.428	18	0.205	R.EGNFDLVGNNM*PVFFIR.D
R1/RRR1-3/2	1516.481	1515.802	-212.045	0.362	697.008	0.388	17	0.199	R.LGPNYLM*LPANAPK.C
R1/RRR1-8/2	1986.340	1986.240	50.808	0.453	490.142	0.440	15	0.193	R.EGNFDLVGNNM*PVFFIR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1985.817	1986.240	-213.249	0.398	511.546	0.384	15	0.189	R.EGNFDLVGNNM*PVFFIR.D
R1/RRR1-6/2	1151.102	1151.384	-245.129	0.256	471.568	0.311	13	0.186	-.APGVQTPIIVR.-
R1/RRR1-5/2	1156.075	1156.273	-171.422	0.481	1472.173	0.461	17	0.271	K.LDGNFIYASR.T
R1/RRR1-5/2	1155.949	1156.273	-280.855	0.401	1423.978	0.435	17	0.258	K.LDGNFIYASR.T
R1/RRR1-5/2	1155.897	1156.273	-325.991	0.387	1382.649	0.340	17	0.234	K.LDGNFIYASR.T
R1/RRR1-5/2	1240.246	1240.474	-184.271	0.320	652.533	0.404	16	0.199	K.SLLPVAGDQVLK.L
R1/RRR1-5/2	1240.136	1240.474	-273.538	0.342	471.815	0.436	15	0.199	K.SLLPVAGDQVLK.L
R1/RRR1-5/2	1534.144	1534.609	-304.435	0.441	681.920	0.391	18	0.198	K.STLDPNVYGDHTSK.I
R1/RRR1-5/2	1024.281	1025.097	-1778.741	0.276	712.881	0.376	15	0.196	K.STAAGESVFR.V
R1/RRR1-5/2	1240.174	1240.474	-242.727	0.301	579.282	0.397	15	0.195	K.SLLPVAGDQVLK.L
R1/RRR1-5/2	1025.122	1025.097	23.575	0.292	767.310	0.294	14	0.191	K.STAAGESVFR.V
R1/RRR1-5/3	1782.152	1782.079	40.897	0.439	1109.836	0.412	32	0.107	K.LVRPVLGGSQELPYPR.R
R1/RRR1-5/3	1781.861	1782.079	-122.770	0.490	904.305	0.384	28	0.094	K.LVRPVLGGSQELPYPR.R
R1/RRR1-4/2	1503.234	1502.740	329.492	0.514	1372.636	0.540	22	0.278	K.FSVSPVVQQGVQVK.N
R1/RRR1-4/2	1502.220	1502.740	-1014.608	0.511	1299.226	0.529	21	0.266	K.FSVSPVVQQGVQVK.N
R1/RRR1-4/2	1460.328	1460.572	-167.819	0.480	1121.441	0.477	18	0.235	K.SGTLTTSETAHNLK.V
R1/RRR1-7/2	1482.494	1481.722	-154.821	0.430	1255.057	0.408	16	0.234	R.AFNQFILDPIFR.I
R1/RRR1-5/2	1502.030	1502.740	-1141.572	0.436	1103.941	0.449	20	0.231	K.FSVSPVVQQGVQVK.N
R1/RRR1-4/2	1503.648	1502.740	-61.282	0.520	1028.845	0.481	19	0.231	K.FSVSPVVQQGVQVK.N
R1/RRR1-5/2	1459.851	1460.572	-1182.607	0.452	1019.518	0.453	19	0.224	K.SGTLTTSETAHNLK.V
R1/RRR1-4/2	1481.328	1481.722	-267.186	0.381	1088.919	0.371	16	0.215	R.AFNQFILDPIFR.I
R1/RRR1-7/2	1481.930	1481.722	140.568	0.419	826.646	0.455	15	0.213	R.AFNQFILDPIFR.I
R1/RRR1-4/2	1481.672	1481.722	-34.178	0.356	1149.048	0.335	16	0.213	R.AFNQFILDPIFR.I
R1/RRR1-4/2	1047.955	1048.199	-233.756	0.463	600.311	0.498	13	0.211	R.GAGQLM*PTTR.D
R1/RRR1-4/2	1146.874	1147.284	-359.210	0.453	1068.368	0.336	15	0.209	R.EGVIAEEPM*R.G
R1/RRR1-13/2	1047.487	1048.199	-1639.180	0.329	541.858	0.369	12	0.191	-.GAGQLM*PTTR.-
R1/RRR1-4/3	1502.800	1502.740	40.189	0.361	1318.804	0.222	26	0.085	K.FSVSPVVQQGVQVK.N
R1/RRR1-9/2	1514.446	1514.706	-172.332	0.555	1633.557	0.516	21	0.305	R.KLAEDNNVPLSSVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1987.180	1987.203	-11.313	0.481	1136.450	0.530	23	0.246	K.EALAAPGLSYTDVPNAQIR.K
R1/RRR1-9/2	1233.268	1233.438	-138.454	0.416	1368.626	0.387	18	0.241	R.VIDGAIGAEFLK.A
R1/RRR1-9/2	1232.859	1233.438	-1285.046	0.394	978.981	0.445	17	0.221	R.VIDGAIGAEFLK.A
R1/RRR1-9/2	1233.140	1233.438	-242.821	0.305	583.833	0.327	14	0.190	R.VIDGAIGAEFLK.A
R1/RRR1-18/2	1630.176	1630.999	-1121.608	0.568	2475.292	0.553	23	0.471	R.IKQVLLSLQAFTLR.L
R1/RRR1-19/2	1464.602	1464.562	27.034	0.584	1487.227	0.450	22	0.267	K.FDSDGNLIDAQIR.E
R1/RRR1-18/2	1464.106	1464.562	-312.392	0.568	1460.638	0.422	21	0.257	K.FDSDGNLIDAQIR.E
R1/RRR1-19/2	1465.359	1464.562	-138.918	0.596	1265.494	0.500	20	0.256	K.FDSDGNLIDAQIR.E
R1/RRR1-19/2	1629.700	1630.999	-1414.936	0.429	1231.729	0.464	18	0.242	R.IKQVLLSLQAFTLR.L
R1/RRR1-17/2	1464.224	1464.562	-231.591	0.535	1356.978	0.392	21	0.241	K.FDSDGNLIDAQIR.E
R1/RRR1-17/2	1463.511	1464.562	-1405.697	0.441	1338.313	0.392	21	0.241	K.FDSDGNLIDAQIR.E
R1/RRR1-18/2	1464.596	1464.562	22.938	0.545	1415.586	0.371	21	0.240	K.FDSDGNLIDAQIR.E
R1/RRR1-19/2	1463.997	1464.562	-1072.125	0.494	1273.591	0.378	21	0.232	K.FDSDGNLIDAQIR.E
R1/RRR1-18/2	1389.554	1389.668	-82.439	0.453	963.675	0.431	19	0.222	K.QVLLSLQAFTLR.L
R1/RRR1-17/2	932.831	933.003	-185.278	0.408	858.241	0.381	13	0.212	K.NALDWASR.G
R1/RRR1-18/2	932.841	933.003	-174.250	0.409	837.946	0.351	13	0.208	K.NALDWASR.G
R1/RRR1-18/2	1389.230	1389.668	-316.097	0.502	837.588	0.373	18	0.206	K.QVLLSLQAFTLR.L
R1/RRR1-18/2	932.793	933.003	-225.581	0.395	852.482	0.331	13	0.206	K.NALDWASR.G
R1/RRR1-19/2	933.032	933.003	31.151	0.398	892.542	0.303	13	0.203	K.NALDWASR.G
R1/RRR1-19/2	932.925	933.003	-83.811	0.397	884.224	0.274	13	0.200	K.NALDWASR.G
R1/RRR1-18/2	932.909	933.003	-101.005	0.457	838.025	0.276	13	0.199	K.NALDWASR.G
R1/RRR1-18/2	1389.336	1389.668	-239.756	0.434	649.525	0.331	17	0.197	K.QVLLSLQAFTLR.L
R1/RRR1-17/2	932.454	933.003	-1666.349	0.373	735.056	0.272	12	0.197	K.NALDWASR.G
R1/RRR1-18/2	1630.003	1630.999	-1228.240	0.292	662.825	0.374	16	0.193	R.IKQVLLSLQAFTLR.L
R1/RRR1-19/2	933.003	933.003	-0.605	0.363	729.965	0.224	12	0.193	K.NALDWASR.G
R1/RRR1-19/2	932.197	933.003	-1943.415	0.330	753.456	0.200	12	0.191	K.NALDWASR.G
R1/RRR1-19/2	1389.092	1389.668	-1137.783	0.331	819.270	0.072	17	0.178	K.QVLLSLQAFTLR.L
R1/RRR1-18/3	1630.917	1630.999	-50.352	0.467	1570.848	0.422	26	0.164	R.IKQVLLSLQAFTLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/3	1630.471	1630.999	-939.915	0.343	739.043	0.335	20	0.074	-.IKQVLLSLQAFTLR.-
R1/RRR1-18/3	1630.874	1630.999	-77.043	0.270	656.715	0.265	22	0.072	R.IKQVLLSLQAFTLR.L
R1/RRR1-6/2	1506.473	1505.742	-179.502	0.565	1898.512	0.496	21	0.335	K.IAGIQGGFFELQPK.E
R1/RRR1-6/2	1335.230	1335.534	-228.657	0.542	1277.117	0.481	19	0.254	R.INTLLQGYSGIR.F
R1/RRR1-6/2	1335.298	1335.534	-177.297	0.492	946.396	0.466	17	0.225	R.INTLLQGYSGIR.F
R1/RRR1-2/2	1335.514	1335.534	-14.816	0.450	802.550	0.449	16	0.213	R.INTLLQGYSGIR.F
R1/RRR1-7/2	1507.119	1505.742	250.735	0.365	456.160	0.508	17	0.204	K.IAGIQGGFFELQPK.E
R1/RRR1-6/2	1481.670	1481.759	-60.291	0.442	623.233	0.440	15	0.199	K.LLNANVTPCLPLR.G
R1/RRR1-6/2	1334.672	1335.534	-1399.294	0.340	952.526	0.284	18	0.199	R.INTLLQGYSGIR.F
R1/RRR1-17/2	1335.342	1335.534	-144.375	0.358	478.828	0.385	13	0.195	R.INTLLQGYSGIR.F
R1/RRR1-3/2	1506.769	1505.742	17.665	0.259	440.308	0.310	13	0.184	K.IAGIQGGFFELQPK.E
R1/RRR1-8/2	1720.647	1721.913	-1320.745	0.513	1622.428	0.538	21	0.306	R.DNGM*HALIIYDDLSK.Q
R1/RRR1-8/2	1706.285	1705.914	218.526	0.575	1508.840	0.553	20	0.293	R.DNGMHALIIYDDLSK.Q
R1/RRR1-9/2	1302.279	1301.514	-181.510	0.427	1348.258	0.391	18	0.240	K.TAIAIDTILNQK.Q
R1/RRR1-8/2	1301.889	1301.514	288.568	0.480	1203.832	0.407	18	0.232	K.TAIAIDTILNQK.Q
R1/RRR1-8/1	1300.798	1301.514	-1323.480	0.303	584.589	0.300	15	0.218	K.TAIAIDTILNQK.Q
R1/RRR1-8/2	1312.235	1312.580	-263.733	0.379	1112.599	0.360	16	0.216	-.AILSTINPELLK.-
R1/RRR1-8/2	1313.050	1312.580	358.567	0.448	1104.301	0.367	16	0.216	K.AILSTINPELLK.S
R1/RRR1-8/2	1705.413	1705.914	-882.881	0.397	1111.291	0.331	20	0.209	R.DNGMHALIIYDDLSK.Q
R1/RRR1-8/2	1312.252	1312.580	-251.228	0.360	1139.987	0.295	16	0.209	-.AILSTINPELLK.-
R1/RRR1-2/2	1312.364	1312.580	-165.095	0.334	1103.352	0.286	17	0.206	-.AILSTINPELLK.-
R1/RRR1-8/2	1077.125	1077.298	-161.594	0.429	910.467	0.341	14	0.205	R.KIELDAFLK.Q
R1/RRR1-8/2	1302.093	1301.514	-324.275	0.350	1261.872	0.194	18	0.200	K.TAIAIDTILNQK.Q
R1/RRR1-8/1	1300.807	1301.514	-1316.317	0.297	562.484	0.260	15	0.199	K.TAIAIDTILNQK.Q
R1/RRR1-8/2	1076.907	1077.298	-364.227	0.451	925.929	0.277	14	0.197	R.KIELDAFLK.Q
R1/RRR1-1/2	1312.635	1312.580	41.917	0.405	1068.438	0.241	16	0.197	-.AILSTINPELLK.-
R1/RRR1-8/2	1077.212	1077.298	-80.314	0.476	705.975	0.306	13	0.195	R.KIELDAFLK.Q
R1/RRR1-8/2	1313.161	1312.580	-320.050	0.377	757.609	0.311	14	0.195	K.AILSTINPELLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1312.065	1312.580	-1158.013	0.356	1042.559	0.228	16	0.194	-.AILSTINPELLK.-
R1/RRR1-1/2	1312.193	1312.580	-295.839	0.293	1163.125	0.175	16	0.193	K.AILSTINPELLK.S
R1/RRR1-1/2	1312.137	1312.580	-338.868	0.346	1111.131	0.195	16	0.193	K.AILSTINPELLK.S
R1/RRR1-2/2	1301.492	1301.514	-17.555	0.290	1186.070	0.158	17	0.192	K.TAIAIDTILNQK.Q
R1/RRR1-6/2	1313.006	1312.580	324.823	0.278	694.188	0.279	14	0.191	K.AILSTINPELLK.S
R1/RRR1-16/2	1302.583	1301.514	52.956	0.378	870.052	0.236	16	0.190	K.TAIAIDTILNQK.Q
R1/RRR1-6/2	1312.243	1312.580	-257.947	0.332	675.247	0.180	14	0.186	K.AILSTINPELLK.S
R1/RRR1-7/2	1312.458	1312.580	-93.625	0.379	888.699	0.199	14	0.185	K.AILSTINPELLK.S
R1/RRR1-8/2	1704.694	1705.914	-1305.933	0.368	779.140	0.245	17	0.185	R.DNGMHALIIYDDLSK.Q
R1/RRR1-1/2	1300.527	1301.514	-1533.001	0.263	653.868	0.224	13	0.185	K.TAIAIDTILNQK.Q
R1/RRR1-6/2	1312.287	1312.580	-224.164	0.354	739.911	0.222	13	0.184	-.AILSTINPELLK.-
R1/RRR1-8/2	1301.392	1301.514	-94.609	0.134	699.004	0.037	14	0.179	K.TAIAIDTILNQK.Q
R1/RRR1-8/1	1300.712	1301.514	-1389.647	0.257	441.939	0.179	14	0.138	K.TAIAIDTILNQK.Q
R1/RRR1-8/3	1077.138	1077.298	-149.556	0.450	1218.386	0.322	22	0.091	R.KIELDAFLK.Q
R1/RRR1-8/3	1077.278	1077.298	-18.948	0.473	1249.725	0.306	22	0.090	R.KIELDAFLK.Q
R1/RRR1-8/3	1076.996	1077.298	-281.477	0.455	1105.080	0.315	21	0.086	R.KIELDAFLK.Q
R1/RRR1-7/2	1577.226	1577.721	-314.362	0.516	2018.932	0.426	26	0.335	K.FAGAISDGGDIVLEGR.V
R1/RRR1-7/2	1030.143	1029.215	-70.791	0.552	2108.051	0.362	17	0.328	K.LSEAGLAVLR.G
R1/RRR1-7/2	1029.227	1029.215	10.991	0.506	1939.595	0.367	17	0.305	K.LSEAGLAVLR.G
R1/RRR1-7/2	1577.256	1577.721	-295.571	0.517	1590.664	0.459	24	0.282	K.FAGAISDGGDIVLEGR.V
R1/RRR1-6/2	1548.447	1548.722	-178.590	0.450	1443.628	0.493	21	0.271	R.AIGAELVSFDEAIGR.A
R1/RRR1-7/2	1548.329	1548.722	-254.912	0.439	1509.247	0.434	22	0.265	R.AIGAELVSFDEAIGR.A
R1/RRR1-7/2	1548.451	1548.722	-175.426	0.430	1344.785	0.455	21	0.252	R.AIGAELVSFDEAIGR.A
R1/RRR1-7/2	1341.400	1342.567	-1620.282	0.397	1131.513	0.550	18	0.249	K.LAVQLVAGESGGIK.G
R1/RRR1-7/2	1547.958	1548.722	-1143.136	0.385	1194.699	0.403	20	0.227	R.AIGAELVSFDEAIGR.A
R1/RRR1-7/2	1548.557	1548.722	-107.339	0.382	1097.171	0.293	20	0.204	R.AIGAELVSFDEAIGR.A
R1/RRR1-6/2	1548.530	1548.722	-124.261	0.363	1070.000	0.235	18	0.193	R.AIGAELVSFDEAIGR.A
R1/RRR1-5/2	1908.738	1909.090	-185.162	0.507	1636.921	0.541	20	0.306	K.IEGPAAWDVLYNFEQR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1910.757	1909.090	-175.163	0.513	1643.782	0.467	21	0.287	K.IEGPAAWDVLYNFEQR.W
R1/RRR1-3/2	1910.883	1909.090	-108.900	0.314	185.651	0.359	14	0.192	K.IEGPAAWDVLYNFEQR.W
R1/RRR1-5/2	1908.335	1909.090	-922.450	0.370	365.152	0.392	12	0.186	K.IEGPAAWDVLYNFEQR.W
R1/RRR1-8/2	1316.306	1315.498	-146.556	0.414	1054.228	0.111	15	0.176	-.QGGDKDLLLDLK.-
R1/RRR1-24/2	1798.346	1798.924	-880.148	0.574	2861.889	0.627	25	0.594	K.CANGGLDLDWDTVFSK.I
R1/RRR1-23/2	1798.022	1798.924	-1061.509	0.544	2729.915	0.609	25	0.551	K.CANGGLDLDWDTVFSK.I
R1/RRR1-23/2	1799.135	1798.924	117.282	0.553	2477.646	0.570	23	0.470	K.CANGGLDLDWDTVFSK.I
R1/RRR1-24/2	1800.332	1798.924	227.036	0.589	2371.960	0.591	23	0.455	K.CANGGLDLDWDTVFSK.I
R1/RRR1-23/2	1799.297	1798.924	207.706	0.584	2367.101	0.589	24	0.454	K.CANGGLDLDWDTVFSK.I
R1/RRR1-24/2	1798.605	1798.924	-178.393	0.591	2153.350	0.612	23	0.417	K.CANGGLDLDWDTVFSK.I
R1/RRR1-23/2	1797.859	1798.924	-1152.043	0.542	2096.576	0.628	23	0.413	K.CANGGLDLDWDTVFSK.I
R1/RRR1-23/2	1800.365	1798.924	245.258	0.582	2160.805	0.583	22	0.407	K.CANGGLDLDWDTVFSK.I
R1/RRR1-24/2	1799.234	1798.924	172.804	0.576	2129.451	0.572	23	0.397	K.CANGGLDLDWDTVFSK.I
R1/RRR1-24/2	1800.536	1798.924	-216.622	0.561	2039.413	0.576	22	0.381	K.CANGGLDLDWDTVFSK.I
R1/RRR1-23/2	1799.668	1798.924	-142.979	0.578	1816.183	0.572	21	0.340	K.CANGGLDLDWDTVFSK.I
R1/RRR1-23/2	1626.482	1626.790	-189.668	0.490	1835.840	0.551	22	0.340	K.YGWTAFCGPVGPTGR.D
R1/RRR1-23/2	1627.204	1626.790	255.030	0.513	1682.149	0.511	21	0.305	K.YGWTAFCGPVGPTGR.D
R1/RRR1-24/2	1625.970	1626.790	-1122.552	0.436	1566.754	0.482	21	0.282	K.YGWTAFCGPVGPTGR.D
R1/RRR1-24/2	1626.418	1626.790	-229.273	0.455	1480.058	0.444	20	0.262	K.YGWTAFCGPVGPTGR.D
R1/RRR1-24/2	1626.493	1626.790	-182.968	0.403	1355.849	0.493	19	0.259	K.YGWTAFCGPVGPTGR.D
R1/RRR1-23/2	1626.410	1626.790	-234.393	0.465	1215.687	0.508	19	0.249	K.YGWTAFCGPVGPTGR.D
R1/RRR1-23/2	1627.394	1626.790	-243.731	0.452	1149.737	0.533	18	0.247	K.YGWTAFCGPVGPTGR.D
R1/RRR1-23/2	1626.048	1626.790	-1074.760	0.440	1073.877	0.521	18	0.239	K.YGWTAFCGPVGPTGR.D
R1/RRR1-24/2	1627.196	1626.790	250.140	0.454	982.301	0.513	18	0.231	K.YGWTAFCGPVGPTGR.D
R1/RRR1-23/2	1136.882	1137.185	-266.934	0.501	835.203	0.414	17	0.220	K.IDTDGQGFQR.G
R1/RRR1-22/2	1136.872	1137.185	-275.336	0.538	707.774	0.443	16	0.219	K.IDTDGQGFQR.G
R1/RRR1-23/2	1136.915	1137.185	-238.065	0.512	708.276	0.428	16	0.217	K.IDTDGQGFQR.G
R1/RRR1-22/2	1137.063	1137.185	-106.882	0.537	775.423	0.419	16	0.217	K.IDTDGQGFQR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1137.030	1137.185	-136.498	0.510	846.288	0.387	17	0.216	K.IDTDGQGFQR.G
R1/RRR1-23/2	1136.952	1137.185	-205.320	0.495	877.208	0.372	17	0.215	K.IDTDGQGFQR.G
R1/RRR1-24/2	1136.946	1137.185	-210.813	0.511	870.448	0.369	17	0.214	K.IDTDGQGFQR.G
R1/RRR1-24/2	1625.500	1626.790	-1413.094	0.302	1074.039	0.377	18	0.213	K.YGWTAFCGPVGPTGR.D
R1/RRR1-25/2	1137.391	1137.185	181.857	0.429	613.096	0.395	16	0.212	K.IDTDGQGFQR.G
R1/RRR1-24/2	1138.033	1137.185	-133.903	0.424	661.437	0.386	16	0.211	K.IDTDGQGFQR.G
R1/RRR1-24/2	1137.098	1137.185	-76.299	0.461	604.683	0.398	15	0.211	K.IDTDGQGFQR.G
R1/RRR1-19/2	1136.530	1137.185	-1459.785	0.395	727.302	0.368	17	0.211	K.IDTDGQGFQR.G
R1/RRR1-25/2	1136.831	1137.185	-311.749	0.414	596.115	0.385	15	0.209	K.IDTDGQGFQR.G
R1/RRR1-22/2	1136.242	1137.185	-1714.566	0.369	722.601	0.368	16	0.209	K.IDTDGQGFQR.G
R1/RRR1-24/2	1137.989	1137.185	-172.318	0.471	685.254	0.355	16	0.208	K.IDTDGQGFQR.G
R1/RRR1-18/2	1136.849	1137.185	-296.343	0.429	508.399	0.391	14	0.208	K.IDTDGQGFQR.G
R1/RRR1-25/2	1137.261	1137.185	67.437	0.340	677.609	0.375	16	0.208	K.IDTDGQGFQR.G
R1/RRR1-24/2	1136.873	1137.185	-274.906	0.465	634.198	0.367	15	0.208	K.IDTDGQGFQR.G
R1/RRR1-24/2	1136.376	1137.185	-1596.494	0.378	584.942	0.361	15	0.206	K.IDTDGQGFQR.G
R1/RRR1-24/2	1137.836	1137.185	-306.954	0.440	557.414	0.337	15	0.205	K.IDTDGQGFQR.G
R1/RRR1-24/2	1137.444	1137.185	228.781	0.270	356.256	0.319	14	0.203	K.IDTDGQGFQR.G
R1/RRR1-21/2	1136.948	1137.185	-208.443	0.372	655.081	0.284	16	0.202	K.IDTDGQGFQR.G
R1/RRR1-24/2	1136.614	1137.185	-1385.565	0.311	483.794	0.240	15	0.201	K.IDTDGQGFQR.G
R1/RRR1-18/2	1137.320	1137.185	119.107	0.334	567.914	0.232	16	0.200	K.IDTDGQGFQR.G
R1/RRR1-23/2	1625.543	1626.790	-1386.318	0.272	725.869	0.296	15	0.189	K.YGWTAFCGPVGPTGR.D
R1/RRR1-12/2	1800.309	1798.924	214.322	0.271	272.500	0.369	12	0.188	-.CANGGLDLDWDTVFSK.-
R1/RRR1-23/3	1842.009	1842.041	-16.898	0.502	1087.064	0.557	27	0.150	R.SKYGWTAFCGPVGPTGR.D
R1/RRR1-23/3	1841.593	1842.041	-243.778	0.485	831.063	0.459	27	0.107	R.SKYGWTAFCGPVGPTGR.D
R1/RRR1-24/3	1841.959	1842.041	-44.517	0.493	760.994	0.462	25	0.106	R.SKYGWTAFCGPVGPTGR.D
R1/RRR1-24/3	1841.901	1842.041	-76.126	0.509	601.796	0.487	24	0.106	R.SKYGWTAFCGPVGPTGR.D
R1/RRR1-24/3	1842.243	1842.041	110.111	0.401	534.745	0.452	22	0.096	R.SKYGWTAFCGPVGPTGR.D
R1/RRR1-2/2	1064.019	1064.257	-223.766	0.358	942.034	0.393	14	0.212	-.FEILEAITK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1063.626	1064.257	-1537.280	0.425	870.325	0.368	14	0.207	-.FEILEAITK.-
R1/RRR1-6/2	1064.092	1064.257	-155.059	0.470	833.271	0.363	14	0.205	-.FEILEAITK.-
R1/RRR1-6/2	1064.051	1064.257	-193.382	0.430	820.033	0.360	14	0.199	-.FEILEAITK.-
R1/RRR1-17/2	1063.887	1064.257	-348.315	0.319	767.605	0.262	13	0.190	-.FEILEAITK.-
R1/RRR1-17/2	1064.103	1064.257	-144.471	0.244	575.064	0.265	12	0.177	-.FEILEAITK.-
R1/RRR1-4/2	1402.318	1402.619	-215.098	0.546	2442.185	0.441	20	0.416	R.IIDSTLLTQIER.Y
R1/RRR1-4/2	1433.307	1433.508	-140.828	0.513	2491.378	0.408	20	0.416	R.WSNEVQEAVQSR.A
R1/RRR1-4/2	1434.572	1433.508	44.499	0.547	2400.254	0.408	20	0.396	R.WSNEVQEAVQSR.A
R1/RRR1-4/2	1244.799	1245.534	-1398.128	0.411	1787.035	0.496	19	0.319	R.SIATLAITTLLK.T
R1/RRR1-4/2	1246.230	1245.534	-244.790	0.539	1885.028	0.418	19	0.310	R.SIATLAITTLLK.T
R1/RRR1-4/2	1245.165	1245.534	-296.917	0.471	1773.610	0.455	19	0.306	R.SIATLAITTLLK.T
R1/RRR1-4/2	1402.541	1402.619	-55.748	0.526	1772.511	0.419	18	0.293	R.IIDSTLLTQIER.Y
R1/RRR1-4/2	1171.046	1171.408	-310.168	0.553	1504.214	0.463	16	0.273	R.SPLAQCLLIR.Y
R1/RRR1-4/2	1433.123	1433.508	-269.680	0.486	1599.703	0.399	19	0.268	R.WSNEVQEAVQSR.A
R1/RRR1-4/2	1171.054	1171.408	-303.893	0.602	1411.772	0.464	16	0.262	R.SPLAQCLLIR.Y
R1/RRR1-4/2	1161.994	1161.291	-256.108	0.392	1444.633	0.436	18	0.260	R.AITELNGVTSR.E
R1/RRR1-4/2	1170.888	1171.408	-1302.135	0.515	1495.363	0.399	16	0.257	R.SPLAQCLLIR.Y
R1/RRR1-4/2	1160.337	1161.291	-1688.775	0.366	1320.213	0.394	18	0.238	R.AITELNGVTSR.E
R1/RRR1-4/2	1160.406	1161.291	-1628.850	0.369	990.869	0.430	18	0.221	R.AITELNGVTSR.E
R1/RRR1-2/2	1402.245	1402.619	-267.411	0.485	1076.075	0.405	16	0.219	R.IIDSTLLTQIER.Y
R1/RRR1-4/2	1401.664	1402.619	-1398.540	0.426	1057.135	0.391	16	0.216	R.IIDSTLLTQIER.Y
R1/RRR1-1/2	1171.619	1171.408	180.307	0.417	1012.265	0.337	15	0.208	R.SPLAQCLLIR.Y
R1/RRR1-4/2	1161.181	1161.291	-94.540	0.365	571.356	0.423	15	0.203	R.AITELNGVTSR.E
R1/RRR1-19/2	1175.028	1174.286	-220.236	0.437	1418.750	0.472	16	0.266	R.DNFFFAGIDK.V
R1/RRR1-19/2	1429.539	1429.604	-45.531	0.490	981.599	0.533	16	0.236	R.DNFFFAGIDKVR.F
R1/RRR1-19/2	1174.012	1174.286	-234.818	0.355	1250.347	0.373	15	0.227	R.DNFFFAGIDK.V
R1/RRR1-19/2	893.964	894.007	-48.499	0.382	1033.845	0.356	13	0.211	-.GGEYAVGIK.-
R1/RRR1-19/2	893.926	894.007	-90.412	0.407	999.303	0.365	13	0.211	-.GGEYAVGIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1007.074	1007.210	-135.389	0.419	798.811	0.297	12	0.200	R.FPFLLVDR.V
R1/RRR1-20/2	893.626	894.007	-427.078	0.352	749.871	0.352	13	0.199	K.GGEYAVGIK.N
R1/RRR1-18/2	1007.122	1007.210	-87.970	0.414	614.910	0.322	11	0.199	R.FPFLLVDR.V
R1/RRR1-18/2	1007.227	1007.210	16.701	0.468	659.526	0.303	11	0.194	-.FPFLLVDR.-
R1/RRR1-19/2	1006.986	1007.210	-222.700	0.422	630.906	0.291	11	0.194	-.FPFLLVDR.-
R1/RRR1-20/2	1007.128	1007.210	-81.404	0.446	621.971	0.296	11	0.194	-.FPFLLVDR.-
R1/RRR1-19/2	1007.038	1007.210	-171.382	0.417	779.407	0.304	11	0.194	-.FPFLLVDR.-
R1/RRR1-19/2	1006.334	1007.210	-1870.080	0.376	611.944	0.257	11	0.192	-.FPFLLVDR.-
R1/RRR1-19/2	1006.790	1007.210	-418.780	0.394	653.442	0.212	11	0.191	R.FPFLLVDR.V
R1/RRR1-19/2	1006.476	1007.210	-1728.460	0.422	612.357	0.243	11	0.187	-.FPFLLVDR.-
R1/RRR1-18/2	1007.094	1007.210	-115.813	0.411	620.782	0.238	11	0.187	-.FPFLLVDR.-
R1/RRR1-4/2	1698.202	1698.861	-979.924	0.483	1437.320	0.578	21	0.290	K.GAGVDGIITDFPATAHR.Y
R1/RRR1-4/2	1698.530	1698.861	-195.535	0.505	1416.117	0.528	21	0.275	K.GAGVDGIITDFPATAHR.Y
R1/RRR1-4/2	1163.049	1163.351	-260.612	0.487	1339.931	0.412	17	0.246	K.VNLVQSLFSR.V
R1/RRR1-4/2	1163.130	1163.351	-190.699	0.417	1361.166	0.400	17	0.245	K.VNLVQSLFSR.V
R1/RRR1-4/2	1011.815	1012.183	-365.636	0.455	1203.198	0.456	15	0.243	R.LSDFLAFAK.G
R1/RRR1-4/2	1118.489	1118.351	123.958	0.497	1315.616	0.411	18	0.243	K.LGFGVVDAVIK.A
R1/RRR1-4/2	1164.272	1163.351	-68.524	0.546	1297.425	0.406	17	0.241	K.VNLVQSLFSR.V
R1/RRR1-4/2	1011.513	1012.183	-1655.820	0.416	1166.133	0.436	15	0.235	R.LSDFLAFAK.G
R1/RRR1-4/2	1011.664	1012.183	-1506.592	0.469	944.212	0.491	15	0.232	R.LSDFLAFAK.G
R1/RRR1-4/2	1212.053	1212.421	-304.422	0.373	609.769	0.499	16	0.209	K.TLSGNPPTIIAK.G
R1/RRR1-4/2	1212.129	1212.421	-241.676	0.379	467.985	0.535	14	0.207	K.TLSGNPPTIIAK.G
R1/RRR1-7/2	1164.326	1163.351	-21.832	0.315	627.755	0.428	12	0.200	K.VNLVQSLFSR.V
R1/RRR1-4/2	1211.596	1212.421	-1510.818	0.314	571.300	0.437	15	0.199	K.TLSGNPPTIIAK.G
R1/RRR1-2/2	1698.881	1698.861	12.064	0.381	365.276	0.387	13	0.182	-.GAGVDGIITDFPATAHR.-
R1/RRR1-3/2	1118.078	1118.351	-244.704	0.394	713.046	0.252	13	0.177	-.LGFGVVDAVIK.-
R1/RRR1-15/2	1007.597	1008.107	-1502.769	0.476	1963.659	0.350	16	0.303	R.FGELDVAEK.V
R1/RRR1-15/2	1007.502	1008.107	-1597.457	0.490	1907.870	0.339	16	0.291	R.FGELDVAEK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1096.804	1097.295	-448.487	0.552	1302.954	0.495	16	0.261	K.APLLAAWAQR.F
R1/RRR1-15/2	1008.136	1008.107	29.377	0.442	1393.679	0.334	14	0.233	R.FGELDVAEK.V
R1/RRR1-15/2	1098.249	1097.295	-41.763	0.523	1229.747	0.387	15	0.229	K.APLLAAWAQR.F
R1/RRR1-16/2	1007.859	1008.107	-246.743	0.446	1313.360	0.322	14	0.224	R.FGELDVAEK.V
R1/RRR1-15/2	1844.691	1845.091	-217.609	0.446	1010.420	0.454	20	0.222	K.VFDEEKAPLLAAWAQR.F
R1/RRR1-15/2	1388.042	1388.590	-1118.973	0.268	471.749	0.492	18	0.199	K.VLPDVDGVVEFAK.M
R1/RRR1-15/2	1845.518	1845.091	232.159	0.343	657.358	0.348	17	0.189	K.VFDEEKAPLLAAWAQR.F
R1/RRR1-15/2	1387.766	1388.590	-1318.674	0.192	168.456	0.374	14	0.187	-.VLPDVDGVVEFAK.-
R1/RRR1-16/2	1389.454	1388.590	-98.394	0.174	287.285	0.383	14	0.185	K.VLPDVDGVVEFAK.M
R1/RRR1-15/3	1845.181	1845.091	49.254	0.411	1519.875	0.312	30	0.124	K.VFDEEKAPLLAAWAQR.F
R1/RRR1-16/3	1846.023	1845.091	-36.957	0.380	1123.975	0.286	23	0.090	-.VFDEEKAPLLAAWAQR.-
R1/RRR1-15/3	1844.624	1845.091	-253.599	0.391	1149.361	0.260	24	0.086	K.VFDEEKAPLLAAWAQR.F
R1/RRR1-6/2	1789.321	1789.966	-921.606	0.516	2064.285	0.491	22	0.359	R.ASSGDLDNTNIISQILK.L
R1/RRR1-6/2	1789.752	1789.966	-119.759	0.549	2094.101	0.459	23	0.353	R.ASSGDLDNTNIISQILK.L
R1/RRR1-6/2	1790.315	1789.966	195.822	0.547	1981.084	0.479	22	0.340	R.ASSGDLDNTNIISQILK.L
R1/RRR1-6/2	1789.633	1789.966	-186.402	0.537	1979.506	0.460	22	0.333	R.ASSGDLDNTNIISQILK.L
R1/RRR1-6/2	1811.751	1811.071	-177.436	0.497	1285.648	0.444	19	0.241	R.IVDSLEVVWGTVDHLK.A
R1/RRR1-6/2	1118.251	1117.232	17.014	0.529	791.952	0.462	16	0.219	R.LEGELADLEK.G
R1/RRR1-6/2	1747.943	1748.958	-1156.644	0.481	1172.945	0.351	18	0.214	K.FNQIEQELEKLTQK.F
R1/RRR1-6/2	1116.908	1117.232	-290.562	0.439	816.357	0.379	16	0.207	R.LEGELADLEK.G
R1/RRR1-6/3	1707.447	1706.969	280.539	0.441	800.462	0.485	23	0.104	R.LGQSKPIYQAFNAIR.N
R1/RRR1-22/2	1681.193	1681.849	-987.726	0.528	2873.112	0.572	25	0.573	K.GQTWSEDMIAAGSTVK.I
R1/RRR1-21/2	1681.251	1681.849	-953.538	0.544	2889.429	0.561	24	0.571	K.GQTWSEDMIAAGSTVK.I
R1/RRR1-21/2	1681.132	1681.849	-1024.614	0.528	2791.669	0.569	24	0.549	K.GQTWSEDMIAAGSTVK.I
R1/RRR1-21/2	1698.266	1697.848	246.786	0.591	2698.366	0.589	25	0.533	K.GQTWSEDM*IAAGSTVK.I
R1/RRR1-21/2	1698.406	1697.848	-261.246	0.590	2579.240	0.616	25	0.516	K.GQTWSEDM*IAAGSTVK.I
R1/RRR1-21/2	1680.857	1681.849	-1188.749	0.480	2607.788	0.526	24	0.485	K.GQTWSEDMIAAGSTVK.I
R1/RRR1-22/2	1681.392	1681.849	-272.604	0.551	2402.144	0.574	24	0.457	K.GQTWSEDMIAAGSTVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/2	1698.312	1697.848	273.887	0.589	2294.276	0.604	24	0.445	K.GQTWSEDM*IAAGSTVK.I
R1/RRR1-21/2	1697.342	1697.848	-890.348	0.544	1949.650	0.603	22	0.376	K.GQTWSEDM*IAAGSTVK.I
R1/RRR1-22/2	1680.472	1681.849	-1418.671	0.380	1960.643	0.453	22	0.329	K.GQTWSEDMIAAGSTVK.I
R1/RRR1-20/2	1549.083	1549.706	-1050.306	0.421	1432.334	0.505	20	0.272	R.TLSDPLFFGYSSSK.N
R1/RRR1-19/2	1550.461	1549.706	-158.379	0.493	1297.066	0.560	20	0.272	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/2	1550.308	1549.706	-257.193	0.523	1387.324	0.507	21	0.269	R.TLSDPLFFGYSSSK.N
R1/RRR1-20/2	1549.559	1549.706	-95.102	0.476	1368.653	0.504	20	0.266	R.TLSDPLFFGYSSSK.N
R1/RRR1-17/2	1550.214	1549.706	-317.944	0.452	1417.398	0.480	20	0.265	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/2	1549.250	1549.706	-295.224	0.464	1323.010	0.515	20	0.264	R.TLSDPLFFGYSSSK.N
R1/RRR1-23/2	1550.358	1549.706	-224.727	0.484	1370.563	0.480	20	0.260	R.TLSDPLFFGYSSSK.N
R1/RRR1-19/2	1550.290	1549.706	-269.042	0.527	1253.089	0.530	19	0.259	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1549.173	1549.706	-992.234	0.450	1186.234	0.542	19	0.256	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/2	1549.207	1549.706	-322.498	0.458	1144.108	0.549	19	0.254	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1548.650	1549.706	-1331.580	0.361	1283.870	0.459	19	0.246	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1548.787	1549.706	-1242.290	0.365	1203.590	0.478	19	0.243	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1548.455	1549.706	-1457.547	0.350	1312.996	0.429	19	0.242	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/2	1549.268	1549.706	-283.287	0.445	1134.223	0.481	18	0.238	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1825.579	1826.021	-243.014	0.560	708.597	0.609	24	0.236	K.KGQTWSEDM*IAAGSTVK.I
R1/RRR1-21/2	1549.511	1549.706	-126.158	0.487	1008.701	0.496	18	0.233	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1810.082	1810.022	33.238	0.492	754.353	0.584	23	0.232	K.KGQTWSEDMIAAGSTVK.I
R1/RRR1-16/2	1550.107	1549.706	259.578	0.448	1143.736	0.436	19	0.232	R.TLSDPLFFGYSSSK.N
R1/RRR1-18/2	1549.249	1549.706	-295.303	0.345	1041.571	0.462	17	0.226	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1810.200	1810.022	98.574	0.509	609.569	0.593	21	0.225	K.KGQTWSEDMIAAGSTVK.I
R1/RRR1-21/2	1810.476	1810.022	251.530	0.515	646.644	0.574	21	0.223	K.KGQTWSEDMIAAGSTVK.I
R1/RRR1-20/2	1549.026	1549.706	-1087.494	0.379	951.849	0.470	17	0.223	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1825.459	1826.021	-858.412	0.532	588.413	0.549	23	0.220	K.KGQTWSEDM*IAAGSTVK.I
R1/RRR1-21/2	1548.709	1549.706	-1293.028	0.315	1033.020	0.420	18	0.219	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/2	1549.124	1549.706	-1023.722	0.349	825.341	0.467	16	0.214	R.TLSDPLFFGYSSSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/2	1550.406	1549.706	-193.605	0.383	874.513	0.420	17	0.212	R.TLSDPLFFGYSSSK.N
R1/RRR1-14/2	1549.690	1549.706	-10.003	0.400	857.568	0.420	17	0.212	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1548.754	1549.706	-1263.898	0.288	919.687	0.395	16	0.208	R.TLSDPLFFGYSSSK.N
R1/RRR1-18/2	1549.044	1549.706	-1076.100	0.250	1052.304	0.344	17	0.207	R.TLSDPLFFGYSSSK.N
R1/RRR1-18/2	1548.512	1549.706	-1420.728	0.215	1016.106	0.339	17	0.204	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/2	1736.582	1736.931	-201.756	0.305	1447.793	0.407	20	0.204	K.VFGCPEPVDVTATLCA.-
R1/RRR1-19/2	1548.432	1549.706	-1472.989	0.210	891.469	0.357	16	0.200	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/2	1548.385	1549.706	-1503.477	0.214	567.578	0.293	15	0.191	R.TLSDPLFFGYSSSK.N
R1/RRR1-21/2	1737.146	1736.931	124.286	0.396	1347.362	0.455	20	0.184	K.VFGCPEPVDVTATLCA.-
R1/RRR1-22/2	1736.372	1736.931	-900.704	0.275	1330.491	0.346	19	0.166	K.VFGCPEPVDVTATLCA.-
R1/RRR1-22/3	1825.241	1826.021	-978.192	0.519	1085.119	0.416	29	0.113	K.KGQTWSEDM*IAAGSTVK.I
R1/RRR1-21/2	1736.315	1736.931	-933.381	0.266	940.798	0.316	19	0.103	K.VFGCPEPVDVTATLCA.-
R1/RRR1-21/3	1549.527	1549.706	-115.775	0.315	1397.250	0.265	27	0.098	R.TLSDPLFFGYSSSK.N
R1/RRR1-22/3	1825.484	1826.021	-844.558	0.408	734.769	0.272	26	0.076	K.KGQTWSEDM*IAAGSTVK.I
R1/RRR1-22/3	1825.430	1826.021	-874.464	0.425	752.546	0.250	25	0.073	-.KGQTWSEDM*IAAGSTVK.-
R1/RRR1-6/2	1784.172	1783.010	91.571	0.444	1104.678	0.455	19	0.226	K.STTTVGLCQALGAFLDK.K
R1/RRR1-6/2	1114.037	1114.322	-256.692	0.268	784.144	0.466	17	0.207	K.GAPSGFVLPIR.D
R1/RRR1-6/2	1486.010	1486.587	-1064.127	0.356	656.300	0.433	18	0.204	K.FASDTEAEM*DVVR.N
R1/RRR1-6/2	1345.257	1345.483	-168.339	0.415	675.524	0.417	15	0.204	R.LDIDPESITWR.R
R1/RRR1-6/2	1485.973	1486.587	-1089.201	0.374	735.624	0.397	17	0.202	K.FASDTEAEM*DVVR.N
R1/RRR1-6/2	1114.019	1114.322	-273.072	0.377	599.834	0.396	15	0.200	K.GAPSGFVLPIR.D
R1/RRR1-6/2	1485.964	1486.587	-1094.975	0.289	630.440	0.441	17	0.199	K.FASDTEAEM*DVVR.N
R1/RRR1-6/2	1113.798	1114.322	-1372.727	0.319	530.477	0.288	13	0.188	K.GAPSGFVLPIR.D
R1/RRR1-6/2	1099.490	1099.266	204.941	0.314	752.628	0.277	15	0.188	-.GAVDLGLAVQR.-
R1/RRR1-6/2	1345.302	1345.483	-134.751	0.311	540.279	0.276	13	0.186	-.LDIDPESITWR.-
R1/RRR1-4/2	1618.454	1617.821	-227.754	0.503	779.763	0.570	21	0.230	R.SAPGAALWCDVQLTK.D
R1/RRR1-4/2	1668.445	1668.955	-907.727	0.402	833.623	0.477	23	0.219	R.FDPLPIVPVEDVLSK.Y
R1/RRR1-4/2	1201.118	1201.395	-231.048	0.382	700.354	0.434	17	0.204	K.TLSGDSPLVIAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1085.861	1086.219	-330.554	0.355	640.792	0.422	12	0.201	R.LSDFLDFTK.G
R1/RRR1-3/2	1669.947	1668.955	-4.444	0.255	506.114	0.433	18	0.193	R.FDPLPIVPVEDVLSK.Y
R1/RRR1-4/2	1667.685	1668.955	-1364.794	0.190	392.862	0.359	16	0.184	R.FDPLPIVPVEDVLSK.Y
R1/RRR1-4/2	1086.001	1086.219	-201.424	0.206	578.709	0.201	10	0.181	-.LSDFLDFTK.-
R1/RRR1-20/2	1072.027	1072.240	-199.824	0.508	1638.715	0.547	19	0.314	R.VLVVDGGGSLR.C
R1/RRR1-20/2	1071.984	1072.240	-240.035	0.481	1660.602	0.506	19	0.305	R.VLVVDGGGSLR.C
R1/RRR1-21/2	1071.729	1072.240	-1414.157	0.365	1652.718	0.472	19	0.291	R.VLVVDGGGSLR.C
R1/RRR1-20/2	1072.916	1072.240	-303.161	0.521	1498.712	0.483	19	0.279	R.VLVVDGGGSLR.C
R1/RRR1-21/2	1071.968	1072.240	-254.544	0.387	1186.473	0.550	16	0.256	R.VLVVDGGGSLR.C
R1/RRR1-20/2	1106.886	1107.242	-321.953	0.521	1003.228	0.438	15	0.227	K.VYEDNVLVR.E
R1/RRR1-20/2	1106.433	1107.242	-1639.921	0.393	919.835	0.423	15	0.217	K.VYEDNVLVR.E
R1/RRR1-21/2	1278.231	1278.484	-198.814	0.407	564.285	0.546	15	0.216	R.ALQPVFQVYGR.R
R1/RRR1-21/2	1071.378	1072.240	-1743.174	0.290	910.418	0.421	15	0.210	R.VLVVDGGGSLR.C
R1/RRR1-20/2	1278.132	1278.484	-276.422	0.467	588.175	0.440	16	0.209	R.ALQPVFQVYGR.R
R1/RRR1-20/2	1106.331	1107.242	-1731.926	0.355	965.069	0.345	15	0.208	K.VYEDNVLVR.E
R1/RRR1-20/2	1277.724	1278.484	-1381.360	0.374	565.793	0.444	16	0.206	R.ALQPVFQVYGR.R
R1/RRR1-20/2	1329.161	1329.616	-343.279	0.360	1036.235	0.332	16	0.205	R.RQVFAGPIVTLK.V
R1/RRR1-20/2	1277.862	1278.484	-1273.229	0.354	597.481	0.409	16	0.203	R.ALQPVFQVYGR.R
R1/RRR1-20/2	1329.397	1329.616	-165.374	0.336	1006.848	0.303	17	0.200	R.RQVFAGPIVTLK.V
R1/RRR1-17/2	1292.203	1292.509	-237.597	0.453	1368.458	0.498	18	0.266	K.FSGKDVVLVATR.R
R1/RRR1-17/2	1068.138	1068.297	-149.084	0.382	1084.233	0.334	15	0.212	K.AVIIHVPYR.L
R1/RRR1-17/2	1292.162	1292.509	-269.252	0.342	1489.874	0.161	18	0.208	K.FSGKDVVLVATR.R
R1/RRR1-18/2	873.454	873.032	484.220	0.393	1044.390	0.306	13	0.206	K.DVVLVATR.R
R1/RRR1-17/2	1068.260	1068.297	-33.881	0.336	734.887	0.406	13	0.204	K.AVIIHVPYR.L
R1/RRR1-17/2	1291.636	1292.509	-1454.638	0.277	1050.924	0.279	16	0.198	K.FSGKDVVLVATR.R
R1/RRR1-17/2	1197.474	1196.469	3.414	0.420	907.357	0.292	14	0.195	-.KAVIIHVPYR.-
R1/RRR1-17/2	1067.585	1068.297	-1607.616	0.318	434.385	0.375	11	0.194	K.AVIIHVPYR.L
R1/RRR1-19/2	873.153	873.032	139.016	0.276	846.858	0.012	12	0.175	K.DVVLVATR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1098.127	1097.207	-72.652	0.464	1632.788	0.482	16	0.295	R.DIEAHVASVR.A
R1/RRR1-5/2	1752.797	1752.004	-118.162	0.517	1217.622	0.543	20	0.257	K.EFQNGFLPAVLSLSTK.F
R1/RRR1-5/2	1751.365	1752.004	-938.714	0.440	1163.303	0.528	21	0.249	K.EFQNGFLPAVLSLSTK.F
R1/RRR1-5/2	1097.899	1097.207	-281.319	0.420	1190.526	0.501	15	0.249	R.DIEAHVASVR.A
R1/RRR1-5/2	1710.706	1710.825	-69.754	0.469	1185.907	0.507	19	0.247	R.SIQSFDPLASSSWER.V
R1/RRR1-5/2	1097.523	1097.207	288.865	0.375	1155.796	0.494	15	0.242	R.DIEAHVASVR.A
R1/RRR1-5/2	1710.906	1710.825	47.116	0.436	907.967	0.522	17	0.225	R.SIQSFDPLASSSWER.V
R1/RRR1-5/2	1859.900	1860.061	-86.738	0.512	433.405	0.603	18	0.212	R.GVVPASGFSFSSQQFWK.V
R1/RRR1-5/3	1621.076	1620.875	124.491	0.398	1966.262	0.275	29	0.172	K.VIKENKDLDLPAHK.V
R1/RRR1-20/3	1621.893	1620.875	11.269	0.313	912.473	0.228	24	0.069	K.VIKENKDLDLPAHK.V
R1/RRR1-4/2	1521.022	1520.624	262.449	0.554	2186.721	0.580	23	0.418	R.VEQGSLTGETASVNK.T
R1/RRR1-4/2	1519.500	1520.624	-1401.844	0.373	2388.058	0.454	23	0.412	R.VEQGSLTGETASVNK.T
R1/RRR1-1/2	1978.219	1978.232	-6.660	0.535	2278.186	0.505	24	0.404	R.SGYIQLLDGSVVLLDEGAK.A
R1/RRR1-4/2	1519.544	1520.624	-1373.200	0.378	1836.833	0.464	22	0.315	R.VEQGSLTGETASVNK.T
R1/RRR1-2/2	1979.623	1978.232	198.001	0.503	1514.511	0.542	23	0.289	R.SGYIQLLDGSVVLLDEGAK.A
R1/RRR1-3/2	1520.233	1520.624	-258.012	0.494	1255.364	0.446	22	0.243	R.VEQGSLTGETASVNK.T
R1/RRR1-2/2	1979.051	1978.232	-91.971	0.438	1198.399	0.435	23	0.231	R.SGYIQLLDGSVVLLDEGAK.A
R1/RRR1-4/2	895.837	896.028	-213.156	0.337	849.366	0.435	12	0.213	R.HAAPSVWK.L
R1/RRR1-1/2	1130.135	1130.363	-202.225	0.386	971.619	0.376	14	0.209	R.VLQLISSTLR.V
R1/RRR1-4/2	1980.103	1978.232	-65.643	0.439	403.005	0.471	20	0.200	R.SGYIQLLDGSVVLLDEGAK.A
R1/RRR1-4/2	896.263	896.028	263.706	0.301	543.183	0.375	11	0.198	R.HAAPSVWK.L
R1/RRR1-3/2	895.783	896.028	-273.992	0.297	468.626	0.367	11	0.197	R.HAAPSVWK.L
R1/RRR1-1/2	895.432	896.028	-1787.752	0.295	612.031	0.368	10	0.196	R.HAAPSVWK.L
R1/RRR1-4/2	1001.028	1001.119	-90.890	0.432	1031.508	0.226	13	0.193	-.GAVENLLER.-
R1/RRR1-4/2	1000.341	1001.119	-1782.816	0.378	1070.629	0.210	13	0.192	K.GAVENLLER.S
R1/RRR1-2/2	896.632	896.028	-442.784	0.270	230.527	0.372	10	0.191	-.HAAPSVWK.-
R1/RRR1-1/2	1000.848	1001.119	-271.348	0.376	1018.527	0.134	13	0.182	K.GAVENLLER.S
R1/RRR1-16/2	1672.210	1672.857	-987.541	0.576	1955.572	0.593	22	0.377	R.AKDVALVYNECYAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1672.283	1672.857	-944.228	0.581	1866.789	0.602	22	0.365	R.AKDVALVYNECYAR.L
R1/RRR1-16/2	1673.396	1672.857	-276.541	0.604	1876.013	0.579	21	0.357	R.AKDVALVYNECYAR.L
R1/RRR1-16/2	1673.302	1672.857	266.809	0.626	1887.000	0.559	22	0.352	R.AKDVALVYNECYAR.L
R1/RRR1-15/2	1672.355	1672.857	-900.846	0.590	1801.228	0.598	21	0.352	R.AKDVALVYNECYAR.L
R1/RRR1-15/3	1673.519	1672.857	-202.672	0.595	2428.831	0.456	32	0.341	R.AKDVALVYNECYAR.L
R1/RRR1-16/3	1673.227	1672.857	221.993	0.592	2444.495	0.447	33	0.337	R.AKDVALVYNECYAR.L
R1/RRR1-15/2	1672.271	1672.857	-951.337	0.570	1626.805	0.563	21	0.315	R.AKDVALVYNECYAR.L
R1/RRR1-15/2	1446.978	1446.534	307.779	0.515	1720.879	0.507	18	0.311	R.AACYDCGTSVWR.D
R1/RRR1-16/2	1446.028	1446.534	-1044.637	0.447	1806.651	0.457	18	0.309	R.AACYDCGTSVWR.D
R1/RRR1-16/2	1445.890	1446.534	-1140.085	0.473	1757.042	0.454	18	0.301	R.AACYDCGTSVWR.D
R1/RRR1-15/2	1446.022	1446.534	-1048.790	0.446	1690.935	0.469	18	0.296	R.AACYDCGTSVWR.D
R1/RRR1-16/3	1673.676	1672.857	-108.394	0.589	2209.803	0.455	30	0.291	R.AKDVALVYNECYAR.L
R1/RRR1-15/2	1446.116	1446.534	-289.863	0.465	1656.537	0.467	18	0.291	R.AACYDCGTSVWR.D
R1/RRR1-15/2	1474.315	1473.606	-197.867	0.588	1367.472	0.564	19	0.284	K.DVALVYNECYAR.L
R1/RRR1-16/2	1445.963	1446.534	-1089.816	0.459	1518.701	0.473	18	0.276	R.AACYDCGTSVWR.D
R1/RRR1-15/2	1474.081	1473.606	323.134	0.559	1304.496	0.538	19	0.271	K.DVALVYNECYAR.L
R1/RRR1-16/2	1474.046	1473.606	299.220	0.553	1314.642	0.494	19	0.261	K.DVALVYNECYAR.L
R1/RRR1-16/2	1474.057	1473.606	306.859	0.574	1317.732	0.493	19	0.260	K.DVALVYNECYAR.L
R1/RRR1-16/2	1473.198	1473.606	-277.719	0.468	1354.535	0.435	19	0.251	K.DVALVYNECYAR.L
R1/RRR1-16/2	1267.115	1267.367	-199.785	0.540	1332.815	0.420	18	0.246	R.LSDKDDFLADK.V
R1/RRR1-15/2	1473.121	1473.606	-330.261	0.400	1337.630	0.415	19	0.244	K.DVALVYNECYAR.L
R1/RRR1-15/2	1266.620	1267.367	-1383.708	0.502	1372.565	0.361	18	0.237	R.LSDKDDFLADK.V
R1/RRR1-15/2	1267.135	1267.367	-183.453	0.531	1330.243	0.377	18	0.236	R.LSDKDDFLADK.V
R1/RRR1-16/2	1267.031	1267.367	-265.702	0.486	1256.710	0.359	17	0.227	R.LSDKDDFLADK.V
R1/RRR1-15/2	1267.179	1267.367	-148.566	0.499	1253.282	0.342	18	0.224	R.LSDKDDFLADK.V
R1/RRR1-16/2	1267.214	1267.367	-120.929	0.500	1122.509	0.387	17	0.223	R.LSDKDDFLADK.V
R1/RRR1-14/2	1446.006	1446.534	-1060.063	0.437	1045.506	0.392	15	0.215	R.AACYDCGTSVWR.D
R1/RRR1-16/1	1266.635	1267.367	-1371.162	0.323	588.942	0.240	13	0.210	R.LSDKDDFLADK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/3	1673.723	1672.857	-80.191	0.595	1930.631	0.395	30	0.206	R.AKDVALVYNECYAR.L
R1/RRR1-17/2	1268.420	1267.367	42.123	0.411	552.361	0.348	14	0.195	-.LSDKDDFLADK.-
R1/RRR1-15/3	1673.257	1672.857	239.661	0.580	1840.569	0.377	29	0.186	R.AKDVALVYNECYAR.L
R1/RRR1-15/3	1672.392	1672.857	-278.545	0.573	1513.946	0.439	27	0.161	R.AKDVALVYNECYAR.L
R1/RRR1-14/2	1447.304	1446.534	-159.177	0.376	808.866	0.122	13	0.155	-.AACYDCGTSVWR.-
R1/RRR1-13/3	1672.836	1672.857	-12.678	0.452	961.385	0.426	23	0.107	R.AKDVALVYNECYAR.L
R1/RRR1-25/2	1350.061	1350.542	-357.645	0.307	1456.010	0.510	19	0.272	K.ETVASAPVVVYSK.S
R1/RRR1-25/2	1154.194	1154.340	-126.936	0.390	1254.281	0.407	16	0.236	K.LFEQLGATFK.A
R1/RRR1-25/2	1350.099	1350.542	-329.249	0.341	765.166	0.523	16	0.215	K.ETVASAPVVVYSK.S
R1/RRR1-25/2	1541.410	1541.814	-263.364	0.377	738.994	0.481	20	0.210	K.LVPLLTEAGAIASSAK.T
R1/RRR1-25/2	1350.103	1350.542	-326.165	0.304	952.953	0.326	17	0.200	K.ETVASAPVVVYSK.S
R1/RRR1-25/2	1540.759	1541.814	-1337.922	0.292	649.248	0.354	20	0.192	K.LVPLLTEAGAIASSAK.T
R1/RRR1-25/2	1540.782	1541.814	-1323.202	0.272	459.591	0.296	17	0.186	K.LVPLLTEAGAIASSAK.T
R1/RRR1-25/2	1153.424	1154.340	-1666.416	0.190	496.989	0.260	13	0.183	K.LFEQLGATFK.A
R1/RRR1-25/3	1549.322	1549.793	-305.136	0.441	1115.802	0.432	29	0.112	K.AKETVASAPVVVYSK.S
R1/RRR1-25/3	1549.872	1549.793	50.936	0.468	1024.828	0.433	28	0.107	K.AKETVASAPVVVYSK.S
R1/RRR1-16/2	1897.480	1898.104	-858.491	0.593	2673.983	0.536	26	0.509	K.LGWAIDEDFGSFEALVK.K
R1/RRR1-16/2	1898.224	1898.104	63.429	0.612	2520.523	0.510	26	0.460	K.LGWAIDEDFGSFEALVK.K
R1/RRR1-16/2	1897.283	1898.104	-962.542	0.533	2602.221	0.457	26	0.459	K.LGWAIDEDFGSFEALVK.K
R1/RRR1-16/2	1744.597	1744.968	-213.391	0.571	1716.244	0.542	25	0.321	K.KLSVETTANQDPLVTK.G
R1/RRR1-16/2	1616.191	1616.795	-995.180	0.468	1867.263	0.466	21	0.320	K.LSVETTANQDPLVTK.G
R1/RRR1-17/2	1744.575	1744.968	-225.886	0.582	1579.361	0.546	25	0.303	K.KLSVETTANQDPLVTK.G
R1/RRR1-17/2	1616.228	1616.795	-972.203	0.511	1654.049	0.510	20	0.300	K.LSVETTANQDPLVTK.G
R1/RRR1-17/2	1617.315	1616.795	-297.334	0.535	1548.379	0.551	19	0.297	K.LSVETTANQDPLVTK.G
R1/RRR1-16/2	1744.281	1744.968	-969.761	0.542	1483.727	0.545	24	0.291	K.KLSVETTANQDPLVTK.G
R1/RRR1-17/2	1745.413	1744.968	255.785	0.591	1536.859	0.513	24	0.287	K.KLSVETTANQDPLVTK.G
R1/RRR1-17/2	1743.868	1744.968	-1207.861	0.529	1514.067	0.488	24	0.279	K.KLSVETTANQDPLVTK.G
R1/RRR1-17/2	1615.831	1616.795	-1218.932	0.421	1485.878	0.484	19	0.272	K.LSVETTANQDPLVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1745.392	1744.968	243.442	0.549	1365.707	0.509	23	0.267	K.KLSVETTANQDPLVTK.G
R1/RRR1-16/2	1616.394	1616.795	-248.647	0.482	1310.891	0.528	18	0.262	K.LSVETTANQDPLVTK.G
R1/RRR1-16/2	1616.155	1616.795	-1017.475	0.450	1334.588	0.487	18	0.255	K.LSVETTANQDPLVTK.G
R1/RRR1-16/2	1505.278	1505.702	-282.537	0.386	832.567	0.378	15	0.203	K.NVRPDYLSNIWK.V
R1/RRR1-16/2	1504.494	1505.702	-1472.142	0.382	798.112	0.374	15	0.201	K.NVRPDYLSNIWK.V
R1/RRR1-16/2	1505.433	1505.702	-179.788	0.406	793.980	0.357	15	0.199	K.NVRPDYLSNIWK.V
R1/RRR1-17/2	1505.235	1505.702	-311.584	0.293	679.357	0.269	14	0.187	K.NVRPDYLSNIWK.V
R1/RRR1-17/3	1744.284	1744.968	-968.012	0.446	1011.436	0.391	27	0.100	K.KLSVETTANQDPLVTK.G
R1/RRR1-17/3	1744.637	1744.968	-189.954	0.346	734.524	0.376	21	0.084	K.KLSVETTANQDPLVTK.G
R1/RRR1-5/2	1329.107	1329.569	-348.728	0.420	1141.696	0.467	17	0.237	R.ALVEGPFLDVLR.S
R1/RRR1-5/2	1501.208	1501.664	-304.590	0.412	918.917	0.485	18	0.224	K.LPADTPYSQFAYK.F
R1/RRR1-5/2	1502.250	1501.664	-276.423	0.477	829.044	0.514	17	0.223	K.LPADTPYSQFAYK.F
R1/RRR1-5/2	1378.580	1379.504	-1399.577	0.409	1023.780	0.445	18	0.222	R.SSSIGNGVQFLNR.H
R1/RRR1-5/2	1329.246	1329.569	-243.779	0.377	1100.320	0.398	17	0.221	R.ALVEGPFLDVLR.S
R1/RRR1-5/2	1329.378	1329.569	-144.562	0.362	965.507	0.436	16	0.217	R.ALVEGPFLDVLR.S
R1/RRR1-5/2	1501.328	1501.664	-224.318	0.446	905.173	0.412	18	0.212	K.LPADTPYSQFAYK.F
R1/RRR1-5/2	1240.470	1240.433	29.748	0.321	440.141	0.492	16	0.202	R.IVHGIDVFDPK.F
R1/RRR1-5/2	1240.533	1240.433	80.970	0.255	461.962	0.293	16	0.189	R.IVHGIDVFDPK.F
R1/RRR1-5/3	1447.614	1447.573	28.104	0.566	1284.259	0.365	26	0.111	K.SKDREEIAEIEK.M
R1/RRR1-5/3	1447.325	1447.573	-171.873	0.575	1326.958	0.329	28	0.104	K.SKDREEIAEIEK.M
R1/RRR1-19/1	781.220	781.900	-2157.317	-2.522	11.042	0.026	6	1.000	-.DKYMQP.-
R1/RRR1-20/2	1005.015	1005.192	-177.209	0.424	1301.940	0.398	16	0.239	-.FALLADNLK.-
R1/RRR1-21/2	1005.098	1005.192	-93.750	0.402	1339.947	0.351	16	0.234	-.FALLADNLK.-
R1/RRR1-21/2	1004.964	1005.192	-227.656	0.469	1316.523	0.351	16	0.232	R.FALLADNLK.V
R1/RRR1-20/2	1186.178	1186.339	-136.106	0.417	959.562	0.465	18	0.227	K.FLADGLGTYTK.A
R1/RRR1-21/2	1186.166	1186.339	-145.707	0.458	957.838	0.414	18	0.220	K.FLADGLGTYTK.A
R1/RRR1-21/2	1188.389	1188.353	30.227	0.414	968.976	0.436	16	0.220	K.ALGLELDLSEK.G
R1/RRR1-21/2	1185.637	1186.339	-1439.391	0.420	1200.459	0.327	18	0.219	K.FLADGLGTYTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1186.198	1186.339	-119.279	0.368	969.621	0.401	18	0.217	K.FLADGLGTYTK.A
R1/RRR1-21/2	1186.029	1186.339	-261.757	0.466	963.069	0.376	18	0.214	K.FLADGLGTYTK.A
R1/RRR1-20/2	1186.190	1186.339	-125.783	0.401	818.201	0.400	17	0.211	K.FLADGLGTYTK.A
R1/RRR1-21/2	1187.585	1188.353	-1493.321	0.425	710.723	0.433	15	0.208	K.ALGLELDLSEK.G
R1/RRR1-21/2	1187.844	1188.353	-1273.755	0.352	665.862	0.425	13	0.200	K.ALGLELDLSEK.G
R1/RRR1-21/2	1160.316	1161.379	-1783.141	0.338	1360.122	0.149	15	0.198	R.RFALLADNLK.V
R1/RRR1-21/2	1161.259	1161.379	-103.495	0.386	1264.032	0.147	15	0.191	R.RFALLADNLK.V
R1/RRR1-21/2	1004.864	1005.192	-327.713	0.461	902.137	0.276	13	0.190	-.FALLADNLK.-
R1/RRR1-21/2	1162.484	1161.379	91.040	0.392	1138.587	0.080	14	0.175	-.RFALLADNLK.-
R1/RRR1-20/2	1004.621	1005.192	-1569.072	0.294	713.414	0.230	12	0.174	-.FALLADNLK.-
R1/RRR1-11/2	1711.391	1710.809	-244.804	0.587	2320.140	0.519	23	0.425	R.M*SNDNWNDWASVVR.I
R1/RRR1-11/2	1710.278	1710.809	-898.066	0.502	1554.528	0.439	20	0.272	R.M*SNDNWNDWASVVR.I
R1/RRR1-11/2	1274.089	1273.418	-258.560	0.528	1345.952	0.500	18	0.265	K.GLIDINQDSLGK.A
R1/RRR1-11/2	1072.999	1072.283	-265.710	0.583	1390.921	0.422	17	0.252	K.ISQATLALVR.N
R1/RRR1-11/2	1072.103	1072.283	-168.404	0.492	1352.084	0.346	17	0.233	K.ISQATLALVR.N
R1/RRR1-11/2	1273.035	1273.418	-301.958	0.442	1099.249	0.452	17	0.231	K.GLIDINQDSLGK.A
R1/RRR1-11/2	1156.686	1157.342	-1436.253	0.427	845.627	0.402	16	0.210	K.SPIILGNDLSK.I
R1/RRR1-11/2	1157.321	1157.342	-18.578	0.401	745.680	0.345	15	0.198	K.SPIILGNDLSK.I
R1/RRR1-11/2	1157.257	1157.342	-73.912	0.425	618.831	0.372	14	0.197	K.SPIILGNDLSK.I
R1/RRR1-9/2	1274.542	1273.418	97.926	0.228	428.005	0.359	12	0.185	K.GLIDINQDSLGK.A
R1/RRR1-3/2	1072.940	1072.283	-320.842	0.310	783.836	0.226	13	0.185	-.ISQATLALVR.-
R1/RRR1-14/3	1970.272	1970.261	5.486	0.558	3475.122	0.544	38	0.804	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-13/2	1969.711	1970.261	-789.528	0.573	3450.529	0.535	28	0.728	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-13/2	1970.564	1970.261	154.238	0.616	3335.218	0.564	29	0.704	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-13/2	1969.354	1970.261	-971.396	0.507	3227.009	0.532	28	0.658	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-14/2	1970.634	1970.261	189.771	0.634	3097.783	0.581	28	0.639	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-14/2	1970.332	1970.261	35.941	0.619	2957.060	0.574	28	0.596	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-14/2	1968.997	1970.261	-1153.455	0.510	3041.376	0.478	28	0.576	K.SAELIGQAIANNPAFLALR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1662.424	1662.872	-270.117	0.530	1592.924	0.452	22	0.279	K.AVVAQYNASQLITQR.E
R1/RRR1-14/2	1662.386	1662.872	-292.882	0.515	1595.680	0.449	22	0.279	K.AVVAQYNASQLITQR.E
R1/RRR1-14/2	1663.264	1662.872	236.250	0.549	1614.062	0.433	22	0.276	K.AVVAQYNASQLITQR.E
R1/RRR1-14/2	1374.254	1374.485	-169.064	0.523	1209.757	0.506	20	0.253	R.ARPNLVESTSGSR.D
R1/RRR1-14/2	1374.093	1374.485	-286.700	0.506	1269.212	0.468	20	0.250	R.ARPNLVESTSGSR.D
R1/RRR1-14/2	1374.188	1374.485	-217.363	0.523	1122.133	0.496	19	0.243	R.ARPNLVESTSGSR.D
R1/RRR1-13/2	1374.166	1374.485	-233.404	0.480	1120.429	0.491	19	0.241	R.ARPNLVESTSGSR.D
R1/RRR1-13/2	1374.135	1374.485	-255.774	0.486	1095.871	0.479	19	0.237	R.ARPNLVESTSGSR.D
R1/RRR1-13/2	1375.229	1374.485	-187.284	0.536	1028.793	0.468	19	0.230	R.ARPNLVESTSGSR.D
R1/RRR1-14/2	1207.282	1206.459	-147.722	0.343	456.339	0.490	17	0.204	R.VPVPPAGAGTLVK.L
R1/RRR1-14/2	1206.258	1206.459	-167.031	0.284	501.666	0.464	17	0.199	R.VPVPPAGAGTLVK.L
R1/RRR1-13/2	1206.228	1206.459	-192.005	0.254	440.331	0.491	15	0.196	R.VPVPPAGAGTLVK.L
R1/RRR1-14/2	1206.315	1206.459	-120.132	0.279	302.836	0.448	13	0.191	-.VPVPPAGAGTLVK.-
R1/RRR1-13/3	1970.124	1970.261	-70.022	0.448	1473.495	0.433	30	0.161	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-14/3	1969.903	1970.261	-182.559	0.413	1244.840	0.403	29	0.124	K.SAELIGQAIANNPAFLALR.Q
R1/RRR1-8/2	1481.392	1481.590	-133.612	0.420	966.794	0.357	19	0.208	K.SSPFESLTTENLR.F
R1/RRR1-8/2	1332.774	1332.441	250.646	0.400	854.785	0.391	13	0.206	R.YYEFLDYYR.A
R1/RRR1-8/2	1482.119	1481.590	-318.426	0.420	865.224	0.362	18	0.203	K.SSPFESLTTENLR.F
R1/RRR1-16/3	1171.120	1170.303	-156.529	0.460	1860.040	0.416	23	0.200	K.FGAAVVSPEHR.Y
R1/RRR1-8/2	1481.282	1481.590	-208.426	0.410	671.645	0.337	17	0.195	K.SSPFESLTTENLR.F
R1/RRR1-8/3	1169.714	1170.303	-1362.384	0.466	1286.822	0.447	20	0.135	K.FGAAVVSPEHR.Y
R1/RRR1-8/3	1169.472	1170.303	-1570.117	0.458	1147.810	0.414	20	0.113	K.FGAAVVSPEHR.Y
R1/RRR1-9/3	1170.588	1170.303	244.152	0.381	1149.768	0.383	19	0.106	K.FGAAVVSPEHR.Y
R1/RRR1-16/3	1298.869	1298.475	303.509	0.520	1073.931	0.343	21	0.097	K.KFGAAVVSPEHR.Y
R1/RRR1-8/3	1298.434	1298.475	-32.176	0.481	981.199	0.373	23	0.094	K.KFGAAVVSPEHR.Y
R1/RRR1-16/3	1171.209	1170.303	-79.995	0.405	894.795	0.331	18	0.084	-.FGAAVVSPEHR.-
R1/RRR1-8/3	1298.679	1298.475	157.046	0.455	752.651	0.311	19	0.082	K.KFGAAVVSPEHR.Y
R1/RRR1-24/3	1298.263	1298.475	-164.305	0.458	587.485	0.321	19	0.077	-.KFGAAVVSPEHR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1377.154	1376.528	-272.372	0.528	1568.362	0.480	18	0.284	K.CCDSIVQLPQR.I
R1/RRR1-22/2	1376.037	1376.528	-358.367	0.466	1650.663	0.386	18	0.269	K.CCDSIVQLPQR.I
R1/RRR1-21/2	1375.985	1376.528	-1125.219	0.488	1508.075	0.446	18	0.269	K.CCDSIVQLPQR.I
R1/RRR1-21/2	1375.927	1376.528	-1167.000	0.485	1544.779	0.429	18	0.269	K.CCDSIVQLPQR.I
R1/RRR1-15/2	1377.092	1376.528	-317.372	0.486	1487.373	0.457	17	0.268	K.CCDSIVQLPQR.I
R1/RRR1-20/2	1376.234	1376.528	-214.460	0.502	1568.203	0.403	18	0.264	K.CCDSIVQLPQR.I
R1/RRR1-21/2	1377.086	1376.528	-321.908	0.503	1509.326	0.422	17	0.262	K.CCDSIVQLPQR.I
R1/RRR1-1/2	1375.768	1376.528	-1283.630	0.446	1440.396	0.444	17	0.261	K.CCDSIVQLPQR.I
R1/RRR1-22/2	1376.128	1376.528	-291.704	0.466	1437.075	0.432	17	0.258	K.CCDSIVQLPQR.I
R1/RRR1-17/2	1377.091	1376.528	-318.528	0.493	1555.017	0.369	18	0.255	K.CCDSIVQLPQR.I
R1/RRR1-25/2	1376.216	1376.528	-227.185	0.472	1554.900	0.363	18	0.254	K.CCDSIVQLPQR.I
R1/RRR1-19/2	1375.569	1376.528	-1428.364	0.417	1527.697	0.364	17	0.251	K.CCDSIVQLPQR.I
R1/RRR1-17/2	1377.330	1376.528	-144.329	0.481	1428.194	0.397	17	0.249	K.CCDSIVQLPQR.I
R1/RRR1-20/2	1376.143	1376.528	-280.579	0.472	1366.951	0.412	17	0.247	K.CCDSIVQLPQR.I
R1/RRR1-17/2	1376.019	1376.528	-1099.743	0.468	1454.648	0.365	17	0.244	K.CCDSIVQLPQR.I
R1/RRR1-22/2	1377.085	1376.528	-322.975	0.479	1382.426	0.381	17	0.241	K.CCDSIVQLPQR.I
R1/RRR1-16/2	1375.637	1376.528	-1378.808	0.428	1564.999	0.297	17	0.239	K.CCDSIVQLPQR.I
R1/RRR1-17/2	1375.495	1376.528	-1482.828	0.393	1293.621	0.389	17	0.237	K.CCDSIVQLPQR.I
R1/RRR1-14/2	1376.013	1376.528	-1104.375	0.438	1342.434	0.361	17	0.235	K.CCDSIVQLPQR.I
R1/RRR1-14/2	1375.261	1376.528	-1653.747	0.373	1311.982	0.376	16	0.234	K.CCDSIVQLPQR.I
R1/RRR1-17/2	1376.273	1376.528	-185.897	0.464	1195.185	0.411	16	0.233	K.CCDSIVQLPQR.I
R1/RRR1-16/2	1375.462	1376.528	-1506.809	0.439	1459.459	0.285	17	0.228	K.CCDSIVQLPQR.I
R1/RRR1-18/2	1376.058	1376.528	-342.435	0.449	1347.699	0.322	17	0.227	K.CCDSIVQLPQR.I
R1/RRR1-1/2	1376.230	1376.528	-217.129	0.443	1400.125	0.293	17	0.225	K.CCDSIVQLPQR.I
R1/RRR1-19/2	1375.602	1376.528	-1404.298	0.324	1395.884	0.272	17	0.222	K.CCDSIVQLPQR.I
R1/RRR1-3/2	1376.303	1376.528	-163.830	0.382	1328.893	0.288	17	0.221	K.CCDSIVQLPQR.I
R1/RRR1-19/2	1063.002	1063.091	-83.691	0.440	1000.608	0.385	14	0.219	R.CDDELEPGK.C
R1/RRR1-17/2	1377.191	1376.528	-245.871	0.442	1385.813	0.268	17	0.219	K.CCDSIVQLPQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1754.097	1754.855	-1005.586	0.518	783.368	0.488	21	0.219	R.CDDELEPGKCTAACK.S
R1/RRR1-17/2	1754.103	1754.855	-1001.813	0.490	739.680	0.476	21	0.216	R.CDDELEPGKCTAACK.S
R1/RRR1-1/2	1277.965	1277.359	-308.745	0.367	762.228	0.429	16	0.214	K.ECVEAPGDFPR.G
R1/RRR1-3/2	1377.119	1376.528	-298.251	0.415	901.497	0.373	17	0.214	K.CCDSIVQLPQR.I
R1/RRR1-16/2	1062.678	1063.091	-389.728	0.437	996.867	0.348	14	0.214	R.CDDELEPGK.C
R1/RRR1-3/2	1278.268	1277.359	-71.130	0.355	746.734	0.427	16	0.213	K.ECVEAPGDFPR.G
R1/RRR1-1/2	1277.934	1277.359	-333.567	0.358	701.785	0.444	15	0.213	K.ECVEAPGDFPR.G
R1/RRR1-20/2	1375.484	1376.528	-1490.673	0.362	1184.913	0.293	16	0.212	K.CCDSIVQLPQR.I
R1/RRR1-20/2	1062.972	1063.091	-111.913	0.419	906.975	0.351	14	0.211	R.CDDELEPGK.C
R1/RRR1-17/2	1754.462	1754.855	-224.613	0.511	619.718	0.484	19	0.210	R.CDDELEPGKCTAACK.S
R1/RRR1-17/2	1278.398	1277.359	31.355	0.346	699.284	0.416	15	0.209	K.ECVEAPGDFPR.G
R1/RRR1-1/2	1377.456	1376.528	-52.497	0.411	1039.417	0.324	15	0.209	K.CCDSIVQLPQR.I
R1/RRR1-14/2	1277.916	1277.359	-347.560	0.298	690.231	0.436	15	0.209	K.ECVEAPGDFPR.G
R1/RRR1-17/2	1277.018	1277.359	-267.267	0.289	742.322	0.421	15	0.208	K.ECVEAPGDFPR.G
R1/RRR1-18/2	1062.998	1063.091	-87.377	0.455	905.415	0.326	14	0.208	R.CDDELEPGK.C
R1/RRR1-21/2	1062.844	1063.091	-232.999	0.427	920.589	0.290	14	0.204	R.CDDELEPGK.C
R1/RRR1-17/2	1062.219	1063.091	-1767.426	0.329	1005.741	0.270	14	0.203	R.CDDELEPGK.C
R1/RRR1-21/2	1278.017	1277.359	-268.112	0.268	875.674	0.333	15	0.203	K.ECVEAPGDFPR.G
R1/RRR1-18/2	1062.988	1063.091	-96.823	0.406	947.316	0.274	14	0.203	R.CDDELEPGK.C
R1/RRR1-21/2	1062.787	1063.091	-287.157	0.393	956.222	0.270	14	0.202	R.CDDELEPGK.C
R1/RRR1-17/2	1062.957	1063.091	-126.889	0.405	1002.255	0.250	14	0.201	R.CDDELEPGK.C
R1/RRR1-16/2	1063.171	1063.091	75.361	0.457	944.603	0.267	14	0.201	R.CDDELEPGK.C
R1/RRR1-26/2	1277.046	1277.359	-245.594	0.213	736.976	0.373	16	0.201	K.ECVEAPGDFPR.G
R1/RRR1-26/2	1277.140	1277.359	-171.470	0.301	779.315	0.301	16	0.200	K.ECVEAPGDFPR.G
R1/RRR1-21/2	1277.921	1277.359	-343.726	0.281	615.831	0.344	14	0.200	K.ECVEAPGDFPR.G
R1/RRR1-2/2	1276.925	1277.359	-340.734	0.251	774.633	0.308	16	0.199	K.ECVEAPGDFPR.G
R1/RRR1-19/2	1277.966	1277.359	-308.074	0.275	591.708	0.337	14	0.199	K.ECVEAPGDFPR.G
R1/RRR1-16/2	1062.650	1063.091	-416.123	0.384	999.396	0.231	14	0.199	R.CDDELEPGK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1277.263	1277.359	-75.307	0.273	631.087	0.308	15	0.199	K.ECVEAPGDFPR.G
R1/RRR1-25/2	1277.078	1277.359	-220.181	0.238	638.722	0.333	15	0.198	K.ECVEAPGDFPR.G
R1/RRR1-4/2	1276.971	1277.359	-304.671	0.239	803.593	0.291	16	0.198	K.ECVEAPGDFPR.G
R1/RRR1-1/2	1062.997	1063.091	-89.105	0.387	958.303	0.226	14	0.197	R.CDDELEPGK.C
R1/RRR1-20/2	1063.036	1063.091	-52.015	0.331	924.282	0.226	14	0.197	R.CDDELEPGK.C
R1/RRR1-19/2	1278.027	1277.359	-260.542	0.276	428.573	0.342	13	0.197	-.ECVEAPGDFPR.-
R1/RRR1-17/2	1062.763	1063.091	-309.859	0.399	963.983	0.221	14	0.197	R.CDDELEPGK.C
R1/RRR1-3/2	1376.171	1376.528	-260.644	0.321	886.136	0.248	15	0.197	K.CCDSIVQLPQR.I
R1/RRR1-1/2	1277.160	1277.359	-156.033	0.242	701.371	0.297	15	0.197	K.ECVEAPGDFPR.G
R1/RRR1-1/2	1062.956	1063.091	-127.580	0.418	863.224	0.245	14	0.196	-.CDDELEPGK.-
R1/RRR1-7/2	1277.302	1277.359	-44.248	0.305	521.439	0.256	13	0.196	K.ECVEAPGDFPR.G
R1/RRR1-3/2	1277.323	1277.359	-28.144	0.211	693.030	0.292	15	0.195	K.ECVEAPGDFPR.G
R1/RRR1-18/2	1062.766	1063.091	-306.517	0.347	769.160	0.218	13	0.195	R.CDDELEPGK.C
R1/RRR1-12/2	1276.883	1277.359	-373.347	0.235	519.057	0.267	13	0.195	K.ECVEAPGDFPR.G
R1/RRR1-18/2	1376.410	1376.528	-86.072	0.347	953.659	0.219	15	0.195	K.CCDSIVQLPQR.I
R1/RRR1-12/2	1276.930	1277.359	-336.706	0.212	714.537	0.281	15	0.195	K.ECVEAPGDFPR.G
R1/RRR1-19/2	1062.261	1063.091	-1727.822	0.273	843.835	0.221	13	0.194	R.CDDELEPGK.C
R1/RRR1-17/2	1754.140	1754.855	-980.923	0.463	470.919	0.374	17	0.194	R.CDDELEPGKCTAACK.S
R1/RRR1-1/2	1062.402	1063.091	-1595.062	0.312	940.611	0.195	14	0.194	-.CDDELEPGK.-
R1/RRR1-24/2	1062.806	1063.091	-269.411	0.272	697.357	0.170	14	0.194	R.CDDELEPGK.C
R1/RRR1-19/2	1062.343	1063.091	-1650.240	0.298	982.138	0.165	14	0.192	R.CDDELEPGK.C
R1/RRR1-5/2	1276.948	1277.359	-322.222	0.217	692.094	0.196	15	0.192	K.ECVEAPGDFPR.G
R1/RRR1-4/2	1277.229	1277.359	-101.959	0.231	820.128	0.182	16	0.191	K.ECVEAPGDFPR.G
R1/RRR1-18/2	1375.892	1376.528	-1192.747	0.379	1138.331	0.151	16	0.191	K.CCDSIVQLPQR.I
R1/RRR1-25/2	1276.893	1277.359	-365.769	0.223	648.454	0.212	14	0.191	-.ECVEAPGDFPR.-
R1/RRR1-21/2	1062.720	1063.091	-350.310	0.437	967.812	0.189	14	0.191	-.CDDELEPGK.-
R1/RRR1-26/2	1276.966	1277.359	-308.603	0.182	607.493	0.145	14	0.191	K.ECVEAPGDFPR.G
R1/RRR1-11/2	1277.016	1277.359	-268.898	0.199	729.616	0.194	15	0.190	K.ECVEAPGDFPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1062.440	1063.091	-1558.472	0.321	967.596	0.144	14	0.190	R.CDDELEPGK.C
R1/RRR1-17/2	1062.225	1063.091	-1762.461	0.238	983.525	0.147	14	0.190	-.CDDELEPGK.-
R1/RRR1-13/2	1277.361	1277.359	1.763	0.269	780.007	0.126	16	0.189	K.ECVEAPGDFPR.G
R1/RRR1-17/2	1062.284	1063.091	-1706.347	0.276	1012.459	0.111	14	0.188	R.CDDELEPGK.C
R1/RRR1-25/2	1276.871	1277.359	-383.323	0.078	676.224	0.080	15	0.186	K.ECVEAPGDFPR.G
R1/RRR1-24/2	1062.792	1063.091	-282.432	0.222	612.139	0.151	13	0.183	-.CDDELEPGK.-
R1/RRR1-23/2	1062.831	1063.091	-244.982	0.245	372.229	0.303	10	0.181	-.CDDELEPGK.-
R1/RRR1-9/2	1276.763	1277.359	-1253.324	0.296	514.530	0.181	12	0.174	-.ECVEAPGDFPR.-
R1/RRR1-17/3	1755.042	1754.855	106.687	0.442	1014.779	0.527	28	0.129	R.CDDELEPGKCTAACK.S
R1/RRR1-21/3	1756.106	1754.855	143.295	0.423	748.713	0.495	26	0.109	R.CDDELEPGKCTAACK.S
R1/RRR1-20/3	1754.769	1754.855	-49.450	0.412	650.828	0.460	25	0.101	R.CDDELEPGKCTAACK.S
R1/RRR1-21/3	1755.831	1754.855	-13.787	0.407	782.140	0.443	27	0.101	R.CDDELEPGKCTAACK.S
R1/RRR1-21/3	1754.628	1754.855	-130.154	0.406	729.328	0.446	26	0.100	R.CDDELEPGKCTAACK.S
R1/RRR1-17/3	1754.183	1754.855	-956.058	0.406	735.923	0.435	26	0.099	R.CDDELEPGKCTAACK.S
R1/RRR1-17/3	1754.269	1754.855	-906.807	0.430	754.168	0.403	26	0.096	R.CDDELEPGKCTAACK.S
R1/RRR1-16/3	1755.913	1754.855	33.175	0.368	620.915	0.421	24	0.096	R.CDDELEPGKCTAACK.S
R1/RRR1-2/3	1754.569	1754.855	-163.548	0.311	513.232	0.389	23	0.092	R.CDDELEPGKCTAACK.S
R1/RRR1-16/3	1754.688	1754.855	-95.400	0.381	717.663	0.366	25	0.091	R.CDDELEPGKCTAACK.S
R1/RRR1-13/3	1754.695	1754.855	-91.632	0.329	512.679	0.365	22	0.088	-.CDDELEPGKCTAACK.-
R1/RRR1-20/3	1754.308	1754.855	-884.488	0.364	791.102	0.337	26	0.087	R.CDDELEPGKCTAACK.S
R1/RRR1-18/3	1754.540	1754.855	-180.404	0.348	531.040	0.367	22	0.086	-.CDDELEPGKCTAACK.-
R1/RRR1-18/3	1754.483	1754.855	-212.755	0.332	767.723	0.326	26	0.085	R.CDDELEPGKCTAACK.S
R1/RRR1-17/3	1376.573	1376.528	32.622	0.382	1107.278	0.216	21	0.072	-.CCDSIVQLPQR.-
R1/RRR1-9/2	1585.354	1584.672	-200.999	0.572	2332.396	0.562	27	0.442	K.GFAFVGSGVSGGEEGAR.-
R1/RRR1-9/2	1584.312	1584.672	-227.484	0.531	2047.834	0.533	26	0.375	K.GFAFVGSGVSGGEEGAR.-
R1/RRR1-9/2	1585.364	1584.672	-194.433	0.595	1993.913	0.557	25	0.372	K.GFAFVGSGVSGGEEGAR.-
R1/RRR1-9/2	1491.304	1491.628	-217.862	0.478	1227.676	0.565	19	0.265	K.SIVGAHSTEEFVSK.L
R1/RRR1-9/2	1114.783	1115.418	-1471.239	0.391	1465.248	0.321	16	0.237	R.RVMLLVQAGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1490.606	1491.628	-1360.432	0.373	1100.480	0.485	19	0.234	K.SIVGAHSTEEFVSK.L
R1/RRR1-9/2	1120.817	1121.225	-365.361	0.456	1124.193	0.379	15	0.220	K.VDNFLANEAK.G
R1/RRR1-9/2	1490.385	1491.628	-1509.080	0.281	1128.686	0.368	19	0.214	K.SIVGAHSTEEFVSK.L
R1/RRR1-24/2	1486.371	1487.596	-1501.542	0.332	1923.224	0.440	21	0.322	K.ATLDITADYGYGAR.G
R1/RRR1-24/2	1486.585	1487.596	-1356.782	0.369	1810.465	0.449	21	0.309	K.ATLDITADYGYGAR.G
R1/RRR1-24/2	1220.291	1220.400	-89.459	0.555	1722.313	0.477	17	0.304	K.SDFVVQIGVQK.V
R1/RRR1-24/2	1219.520	1220.400	-1546.079	0.432	1671.410	0.430	16	0.284	K.SDFVVQIGVQK.V
R1/RRR1-24/2	1221.074	1220.400	-267.480	0.552	1476.320	0.472	16	0.270	K.SDFVVQIGVQK.V
R1/RRR1-24/2	1544.279	1544.730	-293.240	0.465	1274.193	0.507	21	0.258	K.AGQTVTIEYTGYLK.D
R1/RRR1-24/2	1544.125	1544.730	-1042.895	0.451	1203.344	0.516	21	0.253	K.AGQTVTIEYTGYLK.D
R1/RRR1-24/2	1544.030	1544.730	-1104.334	0.440	1119.542	0.434	20	0.229	K.AGQTVTIEYTGYLK.D
R1/RRR1-24/2	1167.271	1167.274	-2.724	0.484	1063.370	0.422	14	0.223	K.GWDEGVTQM*K.V
R1/RRR1-24/2	1167.991	1167.274	-243.404	0.368	745.835	0.469	13	0.210	K.GWDEGVTQM*K.V
R1/RRR1-23/2	1220.220	1220.400	-147.761	0.423	647.052	0.423	14	0.202	-.SDFVVQIGVQK.-
R1/RRR1-22/2	1891.342	1892.096	-930.544	0.544	2453.240	0.591	25	0.478	R.FAIYDFDFLTAEDVPK.S
R1/RRR1-22/2	1892.374	1892.096	147.088	0.601	2348.602	0.625	24	0.467	R.FAIYDFDFLTAEDVPK.S
R1/RRR1-22/2	1892.368	1892.096	144.112	0.558	2202.600	0.610	25	0.431	R.FAIYDFDFLTAEDVPK.S
R1/RRR1-22/2	1891.458	1892.096	-868.863	0.543	2137.492	0.605	23	0.414	R.FAIYDFDFLTAEDVPK.S
R1/RRR1-23/2	1892.478	1892.096	202.201	0.563	1702.085	0.619	23	0.342	R.FAIYDFDFLTAEDVPK.S
R1/RRR1-22/2	1966.374	1965.999	191.178	0.550	1211.262	0.658	25	0.288	R.TTSYEDFTSSLPEGDCR.F
R1/RRR1-22/2	1468.323	1467.693	-252.208	0.532	1581.382	0.472	19	0.284	R.IFYILWSPDNAK.V
R1/RRR1-22/2	1965.372	1965.999	-830.393	0.499	1250.935	0.618	23	0.280	R.TTSYEDFTSSLPEGDCR.F
R1/RRR1-22/2	1965.342	1965.999	-845.606	0.521	1135.437	0.640	24	0.274	R.TTSYEDFTSSLPEGDCR.F
R1/RRR1-22/2	1466.401	1467.693	-1567.160	0.362	1642.541	0.390	18	0.269	R.IFYILWSPDNAK.V
R1/RRR1-22/2	1468.190	1467.693	339.942	0.506	1356.393	0.471	18	0.258	R.IFYILWSPDNAK.V
R1/RRR1-23/2	1467.702	1467.693	6.539	0.494	1379.515	0.449	18	0.256	R.IFYILWSPDNAK.V
R1/RRR1-22/2	1466.815	1467.693	-1283.584	0.383	1501.327	0.358	19	0.247	R.IFYILWSPDNAK.V
R1/RRR1-22/2	1466.506	1467.693	-1495.415	0.404	1329.005	0.406	18	0.241	R.IFYILWSPDNAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1893.935	1892.096	-85.244	0.537	705.103	0.611	21	0.235	R.FAIYDFDFLTAEDVPK.S
R1/RRR1-23/2	1965.449	1965.999	-790.990	0.421	1147.854	0.402	22	0.223	R.TTSYEDFTSSLPEGDCR.F
R1/RRR1-23/2	1965.452	1965.999	-789.743	0.423	876.150	0.410	21	0.209	R.TTSYEDFTSSLPEGDCR.F
R1/RRR1-22/2	1070.800	1071.190	-364.818	0.374	809.392	0.368	14	0.204	K.MLYASSNER.F
R1/RRR1-24/2	1892.206	1892.096	58.066	0.379	341.564	0.446	17	0.200	R.FAIYDFDFLTAEDVPK.S
R1/RRR1-23/2	1965.278	1965.999	-878.528	0.411	548.776	0.428	18	0.198	R.TTSYEDFTSSLPEGDCR.F
R1/RRR1-22/2	1070.688	1071.190	-1407.071	0.283	779.260	0.316	14	0.195	K.MLYASSNER.F
R1/RRR1-22/2	1070.280	1071.190	-1789.692	0.284	691.467	0.310	13	0.193	K.MLYASSNER.F
R1/RRR1-23/2	1467.172	1467.693	-1039.429	0.267	968.600	0.174	15	0.186	R.IFYILWSPDNAK.V
R1/RRR1-20/2	1301.060	1300.483	-326.320	0.468	1318.739	0.486	20	0.260	R.LPTDDSLLGQIK.T
R1/RRR1-21/2	1299.989	1300.483	-381.403	0.389	1395.039	0.448	20	0.257	R.LPTDDSLLGQIK.T
R1/RRR1-20/2	1300.201	1300.483	-217.490	0.459	1423.168	0.412	20	0.253	R.LPTDDSLLGQIK.T
R1/RRR1-20/2	1299.814	1300.483	-1288.369	0.444	1368.527	0.405	20	0.246	R.LPTDDSLLGQIK.T
R1/RRR1-21/2	1300.091	1300.483	-302.831	0.399	1104.600	0.487	19	0.239	R.LPTDDSLLGQIK.T
R1/RRR1-22/2	1299.854	1300.483	-1257.339	0.441	1175.029	0.366	19	0.223	R.LPTDDSLLGQIK.T
R1/RRR1-20/2	1421.997	1421.619	266.605	0.424	739.228	0.523	15	0.217	K.CHFVAIDIFNGK.K
R1/RRR1-22/2	1135.918	1135.255	-297.664	0.358	277.743	0.517	15	0.214	K.TYPQQAGTIR.K
R1/RRR1-20/2	1799.482	1800.004	-847.886	0.469	497.858	0.473	20	0.205	K.DDLRLPTDDSLLGQIK.T
R1/RRR1-21/2	1134.867	1135.255	-342.820	0.252	205.117	0.512	13	0.203	K.TYPQQAGTIR.K
R1/RRR1-21/2	1134.842	1135.255	-364.729	0.259	284.128	0.401	15	0.203	K.TYPQQAGTIR.K
R1/RRR1-19/2	1134.967	1135.255	-254.763	0.317	209.718	0.273	13	0.201	-.TYPQQAGTIR.-
R1/RRR1-20/2	1134.582	1135.255	-1479.234	0.242	291.344	0.381	15	0.201	K.TYPQQAGTIR.K
R1/RRR1-20/2	1135.854	1135.255	-354.056	0.240	359.430	0.401	16	0.201	K.TYPQQAGTIR.K
R1/RRR1-20/2	1135.099	1135.255	-138.024	0.251	235.256	0.242	14	0.200	-.TYPQQAGTIR.-
R1/RRR1-20/2	1134.950	1135.255	-269.330	0.249	255.517	0.308	14	0.198	-.TYPQQAGTIR.-
R1/RRR1-20/2	1798.682	1800.004	-1294.804	0.405	484.612	0.417	19	0.198	K.DDLRLPTDDSLLGQIK.T
R1/RRR1-19/2	1134.941	1135.255	-277.207	0.244	181.899	0.363	12	0.198	-.TYPQQAGTIR.-
R1/RRR1-20/2	1421.617	1421.619	-1.517	0.301	442.200	0.499	13	0.196	K.CHFVAIDIFNGK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1300.341	1300.483	-109.562	0.327	437.380	0.356	14	0.195	R.LPTDDSLLGQIK.T
R1/RRR1-20/2	1799.451	1800.004	-865.183	0.475	472.167	0.366	20	0.195	K.DDLRLPTDDSLLGQIK.T
R1/RRR1-21/2	1134.489	1135.255	-1561.268	0.216	184.281	0.384	13	0.188	-.TYPQQAGTIR.-
R1/RRR1-20/2	1134.492	1135.255	-1558.674	0.195	142.160	0.471	12	0.171	-.TYPQQAGTIR.-
R1/RRR1-22/3	1800.990	1800.004	-7.323	0.509	1047.520	0.453	27	0.118	K.DDLRLPTDDSLLGQIK.T
R1/RRR1-22/3	1800.051	1800.004	26.172	0.506	1016.402	0.445	28	0.113	K.DDLRLPTDDSLLGQIK.T
R1/RRR1-22/3	1800.342	1800.004	188.365	0.397	1004.229	0.425	27	0.106	K.DDLRLPTDDSLLGQIK.T
R1/RRR1-22/3	1799.275	1800.004	-963.332	0.402	746.290	0.290	24	0.079	K.DDLRLPTDDSLLGQIK.T
R1/RRR1-25/2	1384.060	1384.537	-345.653	0.503	1746.267	0.410	19	0.291	K.M*QGVESFDVDIK.E
R1/RRR1-25/2	1430.079	1429.601	335.303	0.524	953.744	0.537	21	0.240	K.GNVTPDAVLQTVSK.T
R1/RRR1-25/2	1769.248	1769.955	-967.474	0.506	1147.655	0.471	21	0.238	K.M*QGVESFDVDIKEQK.V
R1/RRR1-24/2	1429.158	1429.601	-310.607	0.475	942.808	0.532	21	0.237	K.GNVTPDAVLQTVSK.T
R1/RRR1-25/2	1428.485	1429.601	-1485.677	0.317	970.021	0.540	21	0.233	K.GNVTPDAVLQTVSK.T
R1/RRR1-24/2	1428.980	1429.601	-1137.811	0.419	742.128	0.516	19	0.221	K.GNVTPDAVLQTVSK.T
R1/RRR1-25/2	1428.581	1429.601	-1418.384	0.332	825.678	0.469	20	0.216	K.GNVTPDAVLQTVSK.T
R1/RRR1-26/2	1428.686	1429.601	-1344.236	0.278	910.007	0.431	21	0.212	K.GNVTPDAVLQTVSK.T
R1/RRR1-26/2	1428.422	1429.601	-1530.057	0.220	727.805	0.481	19	0.204	K.GNVTPDAVLQTVSK.T
R1/RRR1-24/2	1428.615	1429.601	-1394.354	0.327	767.302	0.387	19	0.204	K.GNVTPDAVLQTVSK.T
R1/RRR1-26/2	1428.525	1429.601	-1457.265	0.230	665.680	0.445	18	0.200	K.GNVTPDAVLQTVSK.T
R1/RRR1-24/3	1769.825	1769.955	-73.568	0.480	1553.718	0.479	28	0.180	K.M*QGVESFDVDIKEQK.V
R1/RRR1-25/2	1837.199	1837.921	-939.907	0.361	1032.750	0.499	21	0.130	K.TSFWDAEPAPVEATAASS.-
R1/RRR1-25/3	1770.408	1769.955	256.648	0.480	1324.544	0.393	31	0.121	K.M*QGVESFDVDIKEQK.V
R1/RRR1-25/3	1770.104	1769.955	84.565	0.456	1201.746	0.393	26	0.116	K.M*QGVESFDVDIKEQK.V
R1/RRR1-24/3	1769.749	1769.955	-116.326	0.476	1115.969	0.419	27	0.114	K.M*QGVESFDVDIKEQK.V
R1/RRR1-24/3	1769.418	1769.955	-871.275	0.426	1075.220	0.439	28	0.113	K.M*QGVESFDVDIKEQK.V
R1/RRR1-25/2	1837.231	1837.921	-922.564	0.319	966.722	0.393	20	0.106	K.TSFWDAEPAPVEATAASS.-
R1/RRR1-25/3	1770.892	1769.955	-35.705	0.483	1046.424	0.393	28	0.103	K.M*QGVESFDVDIKEQK.V
R1/RRR1-26/3	1770.424	1769.955	265.878	0.452	951.674	0.381	27	0.096	K.M*QGVESFDVDIKEQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1695.327	1695.895	-927.854	0.469	1075.619	0.574	23	0.253	K.LLESHLVPSSTAPESK.V
R1/RRR1-14/2	1695.413	1695.895	-285.443	0.488	777.584	0.573	20	0.229	K.LLESHLVPSSTAPESK.V
R1/RRR1-14/2	1696.358	1695.895	273.359	0.503	680.950	0.607	19	0.228	K.LLESHLVPSSTAPESK.V
R1/RRR1-18/2	1337.303	1337.504	-150.114	0.384	1659.330	0.291	16	0.248	R.DISLTDYIQIR.S
R1/RRR1-18/2	1337.337	1337.504	-124.659	0.349	1358.198	0.327	15	0.227	R.DISLTDYIQIR.S
R1/RRR1-18/1	1030.632	1031.185	-1511.699	0.350	528.327	0.473	13	0.225	K.DVVAEIGSIK.L
R1/RRR1-18/2	1337.117	1337.504	-289.684	0.419	1179.158	0.372	16	0.223	R.DISLTDYIQIR.S
R1/RRR1-18/1	1030.508	1031.185	-1632.594	0.268	541.184	0.394	13	0.213	K.DVVAEIGSIK.L
R1/RRR1-18/2	1183.628	1184.329	-1441.938	0.415	591.524	0.466	16	0.211	R.SPVYIPHSAGR.Y
R1/RRR1-18/2	1197.391	1197.278	93.908	0.412	1079.087	0.289	15	0.206	K.WSYEDVEIR.D
R1/RRR1-17/2	1184.052	1184.329	-234.481	0.414	453.541	0.458	14	0.205	R.SPVYIPHSAGR.Y
R1/RRR1-17/2	1183.970	1184.329	-304.301	0.433	570.863	0.413	15	0.204	R.SPVYIPHSAGR.Y
R1/RRR1-18/2	1030.491	1031.185	-1648.494	0.353	819.404	0.356	14	0.202	K.DVVAEIGSIK.L
R1/RRR1-18/2	1183.344	1184.329	-1682.740	0.337	479.613	0.450	14	0.202	R.SPVYIPHSAGR.Y
R1/RRR1-18/2	1030.993	1031.185	-186.757	0.399	675.855	0.362	13	0.199	K.DVVAEIGSIK.L
R1/RRR1-18/2	1030.734	1031.185	-438.986	0.343	697.058	0.324	14	0.197	K.DVVAEIGSIK.L
R1/RRR1-17/2	1184.135	1184.329	-164.672	0.399	602.406	0.279	16	0.194	R.SPVYIPHSAGR.Y
R1/RRR1-17/2	1031.006	1031.185	-173.691	0.356	507.472	0.337	12	0.192	-.DVVAEIGSIK.-
R1/RRR1-18/2	1196.148	1197.278	-1786.227	0.310	438.235	0.331	11	0.192	K.WSYEDVEIR.D
R1/RRR1-18/2	1196.597	1197.278	-1409.119	0.375	1071.315	0.166	15	0.189	K.WSYEDVEIR.D
R1/RRR1-17/2	1030.970	1031.185	-208.731	0.309	392.887	0.302	11	0.179	-.DVVAEIGSIK.-
R1/RRR1-16/2	1720.294	1720.988	-987.695	0.556	2008.115	0.479	21	0.351	R.DIYTGDKLEIVVINK.A
R1/RRR1-16/2	1688.476	1687.870	-234.189	0.531	1352.654	0.570	24	0.282	R.DAVTPLSETEAVDLVK.D
R1/RRR1-16/2	1688.212	1687.870	203.169	0.520	1281.429	0.547	23	0.268	R.DAVTPLSETEAVDLVK.D
R1/RRR1-16/2	1687.520	1687.870	-208.202	0.494	1208.176	0.543	23	0.259	R.DAVTPLSETEAVDLVK.D
R1/RRR1-16/2	1050.613	1051.264	-1576.483	0.413	1098.075	0.420	16	0.227	K.SPSPLLLPAR.D
R1/RRR1-16/2	1050.890	1051.264	-356.817	0.469	952.468	0.463	15	0.225	K.SPSPLLLPAR.D
R1/RRR1-16/2	995.834	996.056	-223.350	0.398	921.760	0.479	14	0.225	K.DVFASATER.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1051.036	1051.264	-217.677	0.468	927.012	0.437	14	0.218	K.SPSPLLLPAR.D
R1/RRR1-16/2	995.471	996.056	-1597.270	0.319	915.695	0.423	14	0.213	K.DVFASATER.D
R1/RRR1-16/2	995.753	996.056	-305.013	0.365	884.367	0.409	14	0.212	K.DVFASATER.D
R1/RRR1-9/2	1288.093	1287.488	-307.648	0.437	2010.049	0.487	18	0.354	K.DASLVEIVTAIR.E
R1/RRR1-9/2	1405.584	1404.550	24.163	0.548	1420.102	0.460	20	0.263	R.TLAIDFAPDADVR.L
R1/RRR1-9/2	1404.090	1404.550	-328.971	0.466	1185.113	0.498	19	0.248	R.TLAIDFAPDADVR.L
R1/RRR1-9/2	1287.260	1287.488	-177.256	0.487	1363.660	0.368	17	0.235	K.DASLVEIVTAIR.E
R1/RRR1-8/2	822.482	822.932	-548.350	0.282	801.785	0.396	11	0.199	R.LGFAASTR.H
R1/RRR1-9/2	1360.194	1360.582	-286.210	0.294	611.931	0.424	13	0.192	K.SVIEISLDSIKR.V
R1/RRR1-13/2	1594.797	1594.853	-35.174	0.510	1731.790	0.475	18	0.301	K.FASFETIVEM*IYK.H
R1/RRR1-13/2	1898.312	1898.214	51.947	0.559	1455.328	0.587	27	0.297	K.VM*VGLPTTGGVTPVPGAAEK.A
R1/RRR1-13/2	1594.227	1594.853	-1022.988	0.478	1761.027	0.437	19	0.296	K.FASFETIVEM*IYK.H
R1/RRR1-13/2	1897.648	1898.214	-827.832	0.517	1418.617	0.553	27	0.283	K.VM*VGLPTTGGVTPVPGAAEK.A
R1/RRR1-13/2	1579.908	1578.853	34.593	0.499	1544.355	0.461	19	0.275	K.FASFETIVEMIYK.H
R1/RRR1-13/2	1897.512	1898.214	-899.385	0.486	1192.378	0.624	25	0.273	K.VM*VGLPTTGGVTPVPGAAEK.A
R1/RRR1-13/2	1594.613	1594.853	-150.734	0.485	1219.045	0.475	17	0.243	K.FASFETIVEM*IYK.H
R1/RRR1-13/2	1580.146	1578.853	185.993	0.420	1198.458	0.462	18	0.240	K.FASFETIVEMIYK.H
R1/RRR1-14/2	1579.972	1578.853	75.121	0.383	991.732	0.432	17	0.219	K.FASFETIVEMIYK.H
R1/RRR1-14/2	1594.632	1594.853	-138.755	0.423	1058.803	0.411	16	0.219	K.FASFETIVEM*IYK.H
R1/RRR1-14/2	1594.008	1594.853	-1160.695	0.303	454.024	0.304	15	0.193	K.FASFETIVEM*IYK.H
R1/RRR1-16/2	1398.291	1397.561	-193.389	0.541	1576.772	0.488	19	0.288	K.LYGSTLSWNVTR.C
R1/RRR1-15/2	1397.427	1397.561	-95.905	0.509	1529.906	0.465	19	0.276	K.LYGSTLSWNVTR.C
R1/RRR1-15/2	1397.231	1397.561	-236.649	0.515	1530.369	0.447	19	0.271	K.LYGSTLSWNVTR.C
R1/RRR1-16/2	1397.954	1397.561	282.401	0.496	1416.438	0.460	18	0.262	K.LYGSTLSWNVTR.C
R1/RRR1-16/2	1107.095	1107.285	-172.039	0.482	1449.634	0.399	15	0.253	K.KVLEVYEAR.L
R1/RRR1-15/2	1397.061	1397.561	-358.583	0.412	1392.548	0.416	18	0.249	K.LYGSTLSWNVTR.C
R1/RRR1-15/2	1107.061	1107.285	-202.790	0.533	1333.227	0.418	15	0.246	K.KVLEVYEAR.L
R1/RRR1-16/2	1397.286	1397.561	-197.472	0.492	1375.406	0.386	18	0.241	K.LYGSTLSWNVTR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1107.134	1107.285	-136.645	0.513	1349.641	0.383	15	0.240	K.KVLEVYEAR.L
R1/RRR1-16/2	978.891	979.112	-226.027	0.465	945.632	0.429	13	0.224	K.VLEVYEAR.L
R1/RRR1-15/2	978.951	979.112	-164.855	0.510	899.363	0.428	13	0.222	K.VLEVYEAR.L
R1/RRR1-15/2	978.904	979.112	-213.017	0.443	749.428	0.434	13	0.217	K.VLEVYEAR.L
R1/RRR1-15/2	1106.941	1107.285	-311.761	0.509	1001.366	0.384	14	0.216	K.KVLEVYEAR.L
R1/RRR1-16/2	1107.175	1107.285	-98.930	0.512	1129.937	0.334	15	0.215	K.KVLEVYEAR.L
R1/RRR1-18/2	1397.446	1397.561	-82.323	0.398	987.237	0.390	16	0.213	K.LYGSTLSWNVTR.C
R1/RRR1-16/2	978.468	979.112	-1684.775	0.408	781.994	0.395	13	0.212	K.VLEVYEAR.L
R1/RRR1-15/2	978.856	979.112	-261.934	0.501	724.793	0.393	13	0.212	K.VLEVYEAR.L
R1/RRR1-14/2	978.902	979.112	-215.394	0.447	705.238	0.367	13	0.208	K.VLEVYEAR.L
R1/RRR1-1/2	979.085	979.112	-27.025	0.377	815.940	0.321	13	0.204	K.VLEVYEAR.L
R1/RRR1-16/2	978.501	979.112	-1651.310	0.378	781.566	0.297	13	0.201	K.VLEVYEAR.L
R1/RRR1-16/2	1693.372	1693.908	-909.549	0.461	381.434	0.437	16	0.201	K.AWWTDLM*ARPSSQK.V
R1/RRR1-11/2	979.496	979.112	393.235	0.410	942.556	0.258	13	0.199	K.VLEVYEAR.L
R1/RRR1-13/2	979.039	979.112	-74.798	0.317	685.523	0.335	12	0.198	-.VLEVYEAR.-
R1/RRR1-15/2	1694.099	1693.908	113.351	0.470	484.847	0.368	18	0.198	K.AWWTDLM*ARPSSQK.V
R1/RRR1-15/2	1693.144	1693.908	-1044.680	0.411	536.618	0.359	18	0.197	K.AWWTDLM*ARPSSQK.V
R1/RRR1-16/2	1693.352	1693.908	-921.562	0.422	474.147	0.285	18	0.193	K.AWWTDLM*ARPSSQK.V
R1/RRR1-16/2	1677.416	1677.908	-294.345	0.369	870.342	0.252	18	0.190	K.AWWTDLMARPSSQK.V
R1/RRR1-22/2	1654.699	1653.905	-124.798	0.456	1729.665	0.477	23	0.302	R.TLLGATNPLASAPGTIR.G
R1/RRR1-22/2	1390.798	1391.468	-1204.349	0.515	1460.621	0.510	19	0.279	K.AGEVVNWSSENAK.W
R1/RRR1-22/2	1391.121	1391.468	-250.362	0.537	1377.762	0.495	19	0.265	K.AGEVVNWSSENAK.W
R1/RRR1-22/2	1654.535	1653.905	-224.341	0.453	1396.398	0.473	20	0.257	R.TLLGATNPLASAPGTIR.G
R1/RRR1-22/2	1391.203	1391.468	-191.470	0.523	1304.309	0.491	19	0.257	K.AGEVVNWSSENAK.W
R1/RRR1-23/2	1654.713	1653.905	-116.362	0.495	1192.920	0.541	21	0.254	R.TLLGATNPLASAPGTIR.G
R1/RRR1-22/2	949.811	950.031	-231.465	0.481	1336.414	0.429	15	0.250	R.GDFAIDVGR.N
R1/RRR1-21/2	949.898	950.031	-139.542	0.447	1230.018	0.446	15	0.244	R.GDFAIDVGR.N
R1/RRR1-21/2	950.014	950.031	-17.348	0.479	1143.827	0.410	14	0.230	R.GDFAIDVGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/2	911.588	912.112	-1676.151	0.341	972.311	0.445	14	0.221	R.GLVGPIISR.F
R1/RRR1-22/2	1655.412	1653.905	-298.405	0.456	1036.517	0.449	18	0.219	R.TLLGATNPLASAPGTIR.G
R1/RRR1-22/2	911.577	912.112	-1688.394	0.346	872.529	0.455	13	0.217	R.GLVGPIISR.F
R1/RRR1-22/2	949.895	950.031	-142.894	0.461	1068.746	0.345	14	0.214	R.GDFAIDVGR.N
R1/RRR1-21/2	1391.027	1391.468	-318.330	0.415	1082.668	0.369	17	0.214	K.AGEVVNWSSENAK.W
R1/RRR1-21/2	949.947	950.031	-88.625	0.382	1117.869	0.271	14	0.206	R.GDFAIDVGR.N
R1/RRR1-22/2	949.469	950.031	-1649.899	0.374	1083.630	0.279	14	0.205	R.GDFAIDVGR.N
R1/RRR1-22/2	1655.205	1653.905	181.997	0.426	842.570	0.402	17	0.201	R.TLLGATNPLASAPGTIR.G
R1/RRR1-22/2	911.609	912.112	-1653.819	0.296	884.238	0.335	13	0.201	R.GLVGPIISR.F
R1/RRR1-21/2	912.810	912.112	-331.386	0.376	798.415	0.326	13	0.200	R.GLVGPIISR.F
R1/RRR1-24/2	1654.128	1653.905	135.409	0.374	964.728	0.338	18	0.199	R.TLLGATNPLASAPGTIR.G
R1/RRR1-21/2	912.129	912.112	19.382	0.360	703.070	0.350	12	0.199	R.GLVGPIISR.F
R1/RRR1-21/2	912.098	912.112	-14.982	0.238	762.892	0.247	12	0.189	R.GLVGPIISR.F
R1/RRR1-23/2	949.812	950.031	-230.305	0.298	656.586	0.219	13	0.182	-.GDFAIDVGR.-
R1/RRR1-26/2	1654.202	1653.905	180.182	0.272	598.369	0.160	16	0.181	-.TLLGATNPLASAPGTIR.-
R1/RRR1-23/2	949.613	950.031	-441.030	0.343	577.159	0.235	12	0.160	-.GDFAIDVGR.-
R1/RRR1-23/2	949.411	950.031	-1711.256	0.299	594.540	0.169	12	0.154	-.GDFAIDVGR.-
R1/RRR1-3/2	1910.554	1911.144	-835.122	0.564	1735.702	0.604	27	0.345	R.YEAVGVDPSTTLLEFLR.T
R1/RRR1-3/2	1911.383	1911.144	125.384	0.600	1633.222	0.596	26	0.326	R.YEAVGVDPSTTLLEFLR.T
R1/RRR1-1/2	1912.055	1911.144	-46.784	0.577	1126.682	0.615	23	0.267	R.YEAVGVDPSTTLLEFLR.T
R1/RRR1-2/2	1911.233	1911.144	46.470	0.539	1118.570	0.586	22	0.258	R.YEAVGVDPSTTLLEFLR.T
R1/RRR1-3/2	1476.369	1476.684	-214.200	0.437	1374.857	0.431	19	0.249	R.NTATIGGNIIM*AQR.L
R1/RRR1-3/2	1476.364	1476.684	-217.767	0.446	1234.823	0.449	19	0.240	R.NTATIGGNIIM*AQR.L
R1/RRR1-3/2	1267.568	1267.543	19.646	0.398	1035.512	0.525	19	0.240	K.LVSAPVILEAVR.L
R1/RRR1-3/2	1312.190	1312.411	-168.663	0.463	774.710	0.475	16	0.214	K.HSNVDSSDLPIK.S
R1/RRR1-3/2	1312.036	1312.411	-287.010	0.476	635.113	0.459	15	0.206	K.HSNVDSSDLPIK.S
R1/RRR1-3/2	985.140	984.171	-31.955	0.382	339.585	0.490	12	0.206	K.IPTVDTIPK.Q
R1/RRR1-3/2	983.843	984.171	-335.150	0.316	466.806	0.348	13	0.196	K.IPTVDTIPK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	983.769	984.171	-409.849	0.305	329.818	0.352	11	0.194	K.IPTVDTIPK.Q
R1/RRR1-3/2	1267.031	1267.543	-1196.564	0.266	584.993	0.418	14	0.194	K.LVSAPVILEAVR.L
R1/RRR1-1/2	1267.160	1267.543	-303.261	0.279	387.001	0.362	12	0.185	-.LVSAPVILEAVR.-
R1/RRR1-15/2	1491.537	1491.760	-150.434	0.479	1645.702	0.566	22	0.320	R.KTDLLLAANPVHAK.V
R1/RRR1-15/2	1492.101	1491.760	229.052	0.430	1093.488	0.528	19	0.244	R.KTDLLLAANPVHAK.V
R1/RRR1-15/2	1492.143	1491.760	257.272	0.431	1074.671	0.509	20	0.239	R.KTDLLLAANPVHAK.V
R1/RRR1-15/2	1389.197	1389.582	-277.590	0.452	953.260	0.498	20	0.231	K.LLGSTNPSPFVTR.V
R1/RRR1-15/2	1447.781	1446.630	104.729	0.459	939.857	0.503	19	0.230	R.GLPYDLVAVDLDR.K
R1/RRR1-15/2	1389.205	1389.582	-271.948	0.449	756.322	0.464	18	0.213	K.LLGSTNPSPFVTR.V
R1/RRR1-15/2	1446.566	1446.630	-44.064	0.403	685.590	0.510	17	0.213	R.GLPYDLVAVDLDR.K
R1/RRR1-15/2	885.418	885.086	375.833	0.430	791.400	0.383	13	0.207	R.VELALALR.G
R1/RRR1-15/2	885.200	885.086	128.756	0.466	736.834	0.319	13	0.199	R.VELALALR.G
R1/RRR1-16/2	1390.327	1389.582	-183.665	0.191	477.468	0.244	14	0.180	-.LLGSTNPSPFVTR.-
R1/RRR1-15/3	1492.487	1491.760	-183.654	0.574	1466.151	0.456	28	0.159	R.KTDLLLAANPVHAK.V
R1/RRR1-15/3	1493.227	1491.760	313.570	0.550	1564.771	0.414	30	0.155	R.KTDLLLAANPVHAK.V
R1/RRR1-15/3	1491.436	1491.760	-218.221	0.549	1076.234	0.432	24	0.116	R.KTDLLLAANPVHAK.V
R1/RRR1-12/2	1946.599	1946.197	207.335	0.608	2932.231	0.610	30	0.613	R.GINSLVDVGGGYGAVAAAVVR.A
R1/RRR1-12/2	1944.949	1946.197	-1158.967	0.455	2713.070	0.528	28	0.518	R.GINSLVDVGGGYGAVAAAVVR.A
R1/RRR1-12/2	1944.870	1946.197	-1199.997	0.390	2424.645	0.484	28	0.431	R.GINSLVDVGGGYGAVAAAVVR.A
R1/RRR1-12/2	1126.743	1127.187	-394.517	0.460	996.373	0.502	16	0.236	R.DGEATYTLTR.V
R1/RRR1-12/2	1127.143	1127.187	-39.063	0.472	921.710	0.452	16	0.223	R.DGEATYTLTR.V
R1/RRR1-12/2	1500.033	1499.782	167.440	0.362	771.045	0.396	16	0.197	R.VLTLSGIFTVVHGR.D
R1/RRR1-12/2	1633.359	1634.903	-2176.208	0.250	836.992	0.217	18	0.181	R.VFVNPVAVASQFSIR.E
R1/RRR1-18/2	1214.231	1214.437	-169.665	0.412	2328.951	0.373	18	0.374	R.GSDVIIVLVGNK.T
R1/RRR1-18/2	1214.005	1214.437	-356.477	0.433	2117.941	0.414	18	0.349	R.GSDVIIVLVGNK.T
R1/RRR1-18/2	1466.180	1465.633	-310.030	0.516	1768.405	0.535	21	0.329	R.DSSVAVIVFDVASR.Q
R1/RRR1-18/2	1465.108	1465.633	-1044.320	0.344	1793.349	0.441	20	0.302	R.DSSVAVIVFDVASR.Q
R1/RRR1-16/2	1317.103	1317.432	-250.674	0.407	961.847	0.420	16	0.220	R.LQLWDTAGQER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1317.008	1317.432	-323.205	0.454	968.491	0.423	16	0.219	-.LQLWDTAGQER.-
R1/RRR1-18/2	1464.633	1465.633	-1369.677	0.307	1180.800	0.366	17	0.217	R.DSSVAVIVFDVASR.Q
R1/RRR1-17/2	1316.628	1317.432	-1374.299	0.346	1005.780	0.355	16	0.211	R.LQLWDTAGQER.F
R1/RRR1-18/2	1476.278	1476.721	-301.003	0.355	500.539	0.551	19	0.209	K.IAAALPGM*ETLSSAK.Q
R1/RRR1-17/2	1316.975	1317.432	-348.594	0.401	917.846	0.361	16	0.208	-.LQLWDTAGQER.-
R1/RRR1-16/2	1316.570	1317.432	-1418.999	0.302	908.931	0.328	15	0.202	-.LQLWDTAGQER.-
R1/RRR1-18/2	1317.028	1317.432	-308.047	0.389	810.645	0.347	15	0.202	-.LQLWDTAGQER.-
R1/RRR1-18/2	1317.141	1317.432	-221.571	0.329	823.969	0.322	15	0.200	R.LQLWDTAGQER.F
R1/RRR1-17/2	1318.044	1317.432	-295.920	0.377	571.065	0.291	15	0.197	R.LQLWDTAGQER.F
R1/RRR1-21/2	1317.434	1317.432	1.059	0.359	693.388	0.307	14	0.196	R.LQLWDTAGQER.F
R1/RRR1-18/2	1475.871	1476.721	-1257.518	0.280	423.350	0.470	18	0.196	K.IAAALPGM*ETLSSAK.Q
R1/RRR1-19/2	1317.161	1317.432	-206.881	0.306	705.112	0.301	14	0.195	R.LQLWDTAGQER.F
R1/RRR1-17/2	1317.778	1317.432	262.882	0.336	503.475	0.262	15	0.194	-.LQLWDTAGQER.-
R1/RRR1-18/2	1317.052	1317.432	-289.914	0.337	883.091	0.205	15	0.190	R.LQLWDTAGQER.F
R1/RRR1-18/2	1475.974	1476.721	-1187.418	0.228	433.947	0.365	18	0.188	K.IAAALPGM*ETLSSAK.Q
R1/RRR1-18/2	1316.413	1317.432	-1538.217	0.240	879.277	0.115	15	0.184	R.LQLWDTAGQER.F
R1/RRR1-18/2	1316.440	1317.432	-1518.283	0.170	985.592	0.090	15	0.182	R.LQLWDTAGQER.F
R1/RRR1-15/2	1744.375	1743.942	249.059	0.517	898.028	0.592	21	0.243	R.ELNAGLAEKDWLLDR.M
R1/RRR1-15/2	1743.542	1743.942	-230.093	0.495	899.859	0.553	21	0.236	R.ELNAGLAEKDWLLDR.M
R1/RRR1-15/2	1743.327	1743.942	-928.925	0.519	776.167	0.562	20	0.229	R.ELNAGLAEKDWLLDR.M
R1/RRR1-15/2	1042.495	1043.114	-1558.224	0.321	1251.360	0.375	16	0.228	K.YAASPYTNR.G
R1/RRR1-14/2	1043.119	1043.114	4.389	0.355	917.024	0.429	14	0.216	K.YAASPYTNR.G
R1/RRR1-15/2	1720.340	1719.900	256.056	0.403	616.138	0.522	19	0.212	R.ELM*ASPGPGPNTNVYR.N
R1/RRR1-15/2	1719.357	1719.900	-900.330	0.363	694.689	0.484	20	0.210	R.ELM*ASPGPGPNTNVYR.N
R1/RRR1-15/2	1043.009	1043.114	-101.142	0.346	1024.178	0.336	15	0.210	K.YAASPYTNR.G
R1/RRR1-15/2	1719.108	1719.900	-1046.036	0.338	702.975	0.479	20	0.208	R.ELM*ASPGPGPNTNVYR.N
R1/RRR1-14/2	1719.821	1719.900	-46.074	0.331	640.161	0.508	19	0.208	R.ELM*ASPGPGPNTNVYR.N
R1/RRR1-14/2	1719.328	1719.900	-917.578	0.333	588.803	0.444	19	0.201	R.ELM*ASPGPGPNTNVYR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	984.023	984.133	-112.369	0.371	812.691	0.319	11	0.199	R.GFYQSLLR.E
R1/RRR1-15/2	984.094	984.133	-40.449	0.387	777.828	0.315	11	0.197	-.GFYQSLLR.-
R1/RRR1-14/2	984.077	984.133	-57.495	0.353	791.759	0.309	12	0.195	-.GFYQSLLR.-
R1/RRR1-14/2	1042.650	1043.114	-446.769	0.291	790.183	0.266	13	0.192	K.YAASPYTNR.G
R1/RRR1-15/2	983.568	984.133	-1595.873	0.279	744.462	0.231	11	0.189	R.GFYQSLLR.E
R1/RRR1-14/2	984.344	984.133	214.424	0.390	758.366	0.302	11	0.187	-.GFYQSLLR.-
R1/RRR1-15/2	1042.437	1043.114	-1614.218	0.210	639.248	0.244	11	0.185	K.YAASPYTNR.G
R1/RRR1-18/2	1888.333	1888.973	-870.949	0.544	2129.002	0.655	24	0.435	K.GQIQSDGGTYNLYQSTR.Y
R1/RRR1-18/2	1888.499	1888.973	-251.720	0.576	1880.629	0.633	22	0.376	K.GQIQSDGGTYNLYQSTR.Y
R1/RRR1-18/2	1888.439	1888.973	-814.624	0.554	1862.058	0.630	21	0.371	K.GQIQSDGGTYNLYQSTR.Y
R1/RRR1-18/2	1704.250	1703.903	204.490	0.501	1437.141	0.551	19	0.283	R.TGGTITMSNFFNAWR.N
R1/RRR1-18/2	1703.412	1703.903	-288.775	0.470	1479.099	0.524	20	0.282	R.TGGTITMSNFFNAWR.N
R1/RRR1-18/2	1703.367	1703.903	-904.355	0.449	1524.889	0.503	19	0.281	R.TGGTITMSNFFNAWR.N
R1/RRR1-19/2	1720.098	1719.902	113.956	0.503	1378.455	0.510	19	0.266	R.TGGTITM*SNFFNAWR.N
R1/RRR1-18/2	1719.281	1719.902	-945.937	0.461	1422.006	0.489	19	0.265	R.TGGTITM*SNFFNAWR.N
R1/RRR1-19/2	1718.888	1719.902	-1175.086	0.445	1341.739	0.503	19	0.260	R.TGGTITM*SNFFNAWR.N
R1/RRR1-18/2	1719.141	1719.902	-1027.275	0.459	1188.227	0.526	18	0.249	R.TGGTITM*SNFFNAWR.N
R1/RRR1-18/2	1719.351	1719.902	-904.595	0.468	1128.096	0.554	17	0.249	R.TGGTITM*SNFFNAWR.N
R1/RRR1-19/2	1718.642	1719.902	-1319.303	0.392	1102.917	0.456	17	0.227	R.TGGTITM*SNFFNAWR.N
R1/RRR1-18/2	1199.199	1199.342	-120.232	0.502	1234.851	0.344	14	0.223	K.TFNQYWAIR.T
R1/RRR1-19/2	1199.371	1199.342	23.621	0.478	1045.162	0.396	14	0.223	K.TFNQYWAIR.T
R1/RRR1-19/2	1200.093	1199.342	-208.290	0.307	830.341	0.442	13	0.214	K.TFNQYWAIR.T
R1/RRR1-19/2	1200.173	1199.342	-141.966	0.344	751.065	0.429	13	0.212	K.TFNQYWAIR.T
R1/RRR1-19/2	1198.678	1199.342	-1392.986	0.391	819.558	0.365	13	0.208	K.TFNQYWAIR.T
R1/RRR1-19/2	1079.907	1080.173	-247.231	0.336	719.762	0.419	13	0.205	R.YNAPSIEGTK.T
R1/RRR1-18/2	1079.597	1080.173	-1464.072	0.296	784.578	0.381	15	0.204	R.YNAPSIEGTK.T
R1/RRR1-18/2	1199.314	1199.342	-23.747	0.394	685.145	0.336	12	0.201	K.TFNQYWAIR.T
R1/RRR1-26/2	1199.370	1199.342	23.111	0.320	704.643	0.324	13	0.201	K.TFNQYWAIR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1198.586	1199.342	-1470.115	0.385	1166.196	0.214	14	0.200	K.TFNQYWAIR.T
R1/RRR1-18/2	1199.767	1199.342	354.767	0.357	653.865	0.285	13	0.199	K.TFNQYWAIR.T
R1/RRR1-19/2	1198.745	1199.342	-1336.426	0.362	664.510	0.307	12	0.199	K.TFNQYWAIR.T
R1/RRR1-18/2	1199.861	1199.342	-402.823	0.311	611.763	0.304	12	0.198	K.TFNQYWAIR.T
R1/RRR1-19/2	1198.532	1199.342	-1514.925	0.342	782.663	0.272	13	0.198	K.TFNQYWAIR.T
R1/RRR1-17/2	1080.999	1080.173	-161.581	0.347	513.261	0.307	12	0.194	R.YNAPSIEGTK.T
R1/RRR1-19/2	1079.477	1080.173	-1575.615	0.271	659.592	0.319	13	0.194	R.YNAPSIEGTK.T
R1/RRR1-17/2	1199.588	1199.342	205.191	0.340	484.990	0.253	11	0.193	-.TFNQYWAIR.-
R1/RRR1-18/2	1079.612	1080.173	-1450.102	0.253	775.848	0.283	14	0.193	R.YNAPSIEGTK.T
R1/RRR1-18/2	1199.580	1199.342	198.252	0.267	414.958	0.290	11	0.192	-.TFNQYWAIR.-
R1/RRR1-17/2	1079.594	1080.173	-1466.911	0.255	603.759	0.284	13	0.191	R.YNAPSIEGTK.T
R1/RRR1-19/2	1079.936	1080.173	-220.355	0.337	686.774	0.256	13	0.191	R.YNAPSIEGTK.T
R1/RRR1-18/2	1200.366	1199.342	19.624	0.283	757.024	0.211	12	0.191	K.TFNQYWAIR.T
R1/RRR1-26/2	1200.506	1199.342	136.703	0.321	935.647	0.187	13	0.191	-.TFNQYWAIR.-
R1/RRR1-18/2	1079.417	1080.173	-1631.396	0.181	635.170	0.251	13	0.187	R.YNAPSIEGTK.T
R1/RRR1-16/2	1199.702	1199.342	300.696	0.246	448.381	0.262	10	0.186	-.TFNQYWAIR.-
R1/RRR1-17/2	1199.605	1199.342	219.682	0.376	448.464	0.253	11	0.184	-.TFNQYWAIR.-
R1/RRR1-18/3	1889.748	1888.973	-119.033	0.524	903.903	0.531	28	0.124	K.GQIQSDGGTYNLYQSTR.Y
R1/RRR1-18/3	1888.735	1888.973	-125.968	0.352	621.610	0.436	24	0.086	-.GQIQSDGGTYNLYQSTR.-
R1/RRR1-20/2	1299.228	1299.585	-275.609	0.517	1829.681	0.484	19	0.321	R.TLINNLIIGVTK.G
R1/RRR1-17/2	1299.278	1299.585	-236.868	0.545	1741.589	0.499	19	0.312	R.TLINNLIIGVTK.G
R1/RRR1-20/3	1501.422	1501.669	-165.232	0.517	2259.366	0.462	29	0.309	K.SLSHVAVNFSQPSK.N
R1/RRR1-20/2	1501.237	1501.669	-288.436	0.478	1685.862	0.496	21	0.307	K.SLSHVAVNFSQPSK.N
R1/RRR1-20/2	1299.345	1299.585	-185.218	0.530	1698.235	0.463	19	0.296	R.TLINNLIIGVTK.G
R1/RRR1-17/2	1299.327	1299.585	-198.696	0.541	1610.254	0.470	19	0.287	R.TLINNLIIGVTK.G
R1/RRR1-17/2	1299.261	1299.585	-250.064	0.426	1395.384	0.511	18	0.271	R.TLINNLIIGVTK.G
R1/RRR1-17/3	1501.389	1501.669	-187.254	0.540	1964.850	0.431	29	0.229	K.SLSHVAVNFSQPSK.N
R1/RRR1-17/3	1501.789	1501.669	80.245	0.557	1941.571	0.437	30	0.224	K.SLSHVAVNFSQPSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1298.694	1299.585	-1460.403	0.399	1064.445	0.411	17	0.222	R.TLINNLIIGVTK.G
R1/RRR1-17/3	1501.776	1501.669	71.686	0.569	1867.781	0.434	29	0.212	K.SLSHVAVNFSQPSK.N
R1/RRR1-15/2	1299.389	1299.585	-151.196	0.444	637.004	0.473	14	0.209	R.TLINNLIIGVTK.G
R1/RRR1-17/2	870.413	871.016	-1847.085	0.371	517.160	0.447	13	0.207	R.LVTVEGPR.G
R1/RRR1-17/2	870.369	871.016	-1897.961	0.332	521.664	0.494	12	0.207	R.LVTVEGPR.G
R1/RRR1-17/2	871.053	871.016	42.575	0.347	428.877	0.503	11	0.206	R.LVTVEGPR.G
R1/RRR1-17/2	1418.874	1419.521	-1164.554	0.384	815.177	0.281	17	0.191	K.NSETGVWEVEIR.N
R1/RRR1-20/3	1501.827	1501.669	105.312	0.500	1555.860	0.438	27	0.165	K.SLSHVAVNFSQPSK.N
R1/RRR1-20/3	1500.983	1501.669	-1126.430	0.545	1211.538	0.469	25	0.137	K.SLSHVAVNFSQPSK.N
R1/RRR1-24/3	1500.361	1501.669	-1543.082	0.339	747.183	0.228	22	0.074	K.SLSHVAVNFSQPSK.N
R1/RRR1-19/2	1316.068	1316.443	-285.758	0.446	2182.871	0.493	23	0.384	R.ATGGEVGASSALAPK.I
R1/RRR1-20/2	1316.144	1316.443	-227.786	0.429	2236.662	0.456	24	0.381	R.ATGGEVGASSALAPK.I
R1/RRR1-20/2	1681.291	1681.862	-937.494	0.463	1830.249	0.555	22	0.344	K.EILGTAFSVGCQVDGK.S
R1/RRR1-20/2	1316.011	1316.443	-329.125	0.455	1824.684	0.513	22	0.328	R.ATGGEVGASSALAPK.I
R1/RRR1-19/2	1315.785	1316.443	-1263.983	0.414	1695.012	0.505	22	0.306	R.ATGGEVGASSALAPK.I
R1/RRR1-20/2	1316.044	1316.443	-303.998	0.459	1812.772	0.435	22	0.303	R.ATGGEVGASSALAPK.I
R1/RRR1-19/2	1681.596	1681.862	-158.770	0.461	1400.775	0.612	21	0.296	K.EILGTAFSVGCQVDGK.S
R1/RRR1-19/2	1316.083	1316.443	-274.405	0.408	1672.987	0.398	21	0.274	R.ATGGEVGASSALAPK.I
R1/RRR1-19/2	1585.332	1584.882	284.317	0.461	1107.705	0.500	21	0.239	R.QAAVSVVPTASSLIIK.A
R1/RRR1-19/2	1585.271	1584.882	245.788	0.444	1080.642	0.502	22	0.238	R.QAAVSVVPTASSLIIK.A
R1/RRR1-20/2	1584.229	1584.882	-1047.022	0.388	788.260	0.457	18	0.209	R.QAAVSVVPTASSLIIK.A
R1/RRR1-20/2	1583.934	1584.882	-1233.817	0.320	786.398	0.409	20	0.203	R.QAAVSVVPTASSLIIK.A
R1/RRR1-20/2	1584.175	1584.882	-1081.064	0.331	703.214	0.447	18	0.203	R.QAAVSVVPTASSLIIK.A
R1/RRR1-10/2	1791.439	1791.940	-840.553	0.524	1721.513	0.593	25	0.336	K.SYELPDGQVITIGNER.-
R1/RRR1-12/2	1791.408	1791.940	-857.517	0.496	1762.099	0.548	25	0.328	K.SYELPDGQVITIGNER.-
R1/RRR1-9/2	1791.369	1791.940	-879.818	0.506	1637.313	0.545	25	0.310	K.SYELPDGQVITIGNER.-
R1/RRR1-10/2	1791.510	1791.940	-240.744	0.471	1594.993	0.560	25	0.308	K.SYELPDGQVITIGNER.-
R1/RRR1-10/3	1791.858	1791.940	-45.762	0.522	2208.713	0.475	34	0.305	K.SYELPDGQVITIGNER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1791.195	1791.940	-977.240	0.482	1505.518	0.546	24	0.292	K.SYELPDGQVITIGNER.-
R1/RRR1-10/2	1791.524	1791.940	-232.678	0.510	1492.376	0.542	25	0.290	K.SYELPDGQVITIGNER.-
R1/RRR1-12/2	1791.414	1791.940	-854.302	0.500	1429.118	0.565	23	0.287	K.SYELPDGQVITIGNER.-
R1/RRR1-9/2	1792.311	1791.940	207.627	0.568	1387.324	0.570	23	0.284	K.SYELPDGQVITIGNER.-
R1/RRR1-10/2	1791.922	1791.940	-10.291	0.503	1377.954	0.517	24	0.271	K.SYELPDGQVITIGNER.-
R1/RRR1-10/2	1791.306	1791.940	-914.981	0.486	1327.318	0.460	23	0.252	K.SYELPDGQVITIGNER.-
R1/RRR1-2/2	1791.336	1791.940	-898.288	0.473	1141.137	0.541	21	0.251	K.SYELPDGQVITIGNER.-
R1/RRR1-10/2	1955.048	1955.244	-100.427	0.540	1008.954	0.596	22	0.250	R.VAPEEHPVLLTEAPINPK.S
R1/RRR1-9/2	1792.387	1791.940	250.312	0.513	1155.459	0.514	21	0.246	K.SYELPDGQVITIGNER.-
R1/RRR1-1/2	1791.393	1791.940	-866.068	0.433	1380.714	0.392	23	0.242	K.SYELPDGQVITIGNER.-
R1/RRR1-2/2	1791.484	1791.940	-255.510	0.460	1026.147	0.537	20	0.240	K.SYELPDGQVITIGNER.-
R1/RRR1-10/2	1955.001	1955.244	-124.604	0.493	888.941	0.595	21	0.239	R.VAPEEHPVLLTEAPINPK.S
R1/RRR1-11/2	1791.436	1791.940	-842.263	0.418	1212.788	0.439	21	0.236	K.SYELPDGQVITIGNER.-
R1/RRR1-9/2	1954.676	1955.244	-804.432	0.479	703.554	0.577	19	0.222	R.VAPEEHPVLLTEAPINPK.S
R1/RRR1-10/2	1954.706	1955.244	-788.823	0.501	844.403	0.520	20	0.221	R.VAPEEHPVLLTEAPINPK.S
R1/RRR1-1/2	1790.438	1791.940	-1961.966	0.316	981.064	0.450	20	0.220	K.SYELPDGQVITIGNER.-
R1/RRR1-2/2	1790.801	1791.940	-1197.879	0.362	1006.780	0.425	19	0.218	K.SYELPDGQVITIGNER.-
R1/RRR1-4/2	1790.799	1791.940	-1199.385	0.344	1154.883	0.351	20	0.216	K.SYELPDGQVITIGNER.-
R1/RRR1-2/2	1955.282	1955.244	19.624	0.492	687.176	0.533	19	0.215	R.VAPEEHPVLLTEAPINPK.S
R1/RRR1-12/2	1955.575	1955.244	170.196	0.445	700.624	0.513	20	0.214	R.VAPEEHPVLLTEAPINPK.S
R1/RRR1-1/2	1791.704	1791.940	-132.339	0.406	1015.180	0.370	21	0.212	K.SYELPDGQVITIGNER.-
R1/RRR1-9/2	1954.718	1955.244	-782.931	0.460	590.711	0.543	17	0.210	R.VAPEEHPVLLTEAPINPK.S
R1/RRR1-5/2	1791.281	1791.940	-928.732	0.348	914.775	0.344	19	0.203	K.SYELPDGQVITIGNER.-
R1/RRR1-7/2	1791.000	1791.940	-1086.315	0.365	971.930	0.302	20	0.201	K.SYELPDGQVITIGNER.-
R1/RRR1-10/3	1791.517	1791.940	-236.958	0.494	1623.991	0.472	31	0.188	K.SYELPDGQVITIGNER.-
R1/RRR1-10/3	1791.615	1791.940	-182.103	0.468	1325.573	0.521	31	0.159	K.SYELPDGQVITIGNER.-
R1/RRR1-24/2	954.446	955.154	-1794.235	0.369	970.441	0.505	14	0.232	R.YSM*VITPK.N
R1/RRR1-23/2	955.086	955.154	-71.256	0.412	939.672	0.458	13	0.225	R.YSM*VITPK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	954.694	955.154	-483.343	0.420	896.066	0.456	13	0.222	R.YSM*VITPK.N
R1/RRR1-24/2	954.761	955.154	-412.650	0.400	859.089	0.453	13	0.219	R.YSM*VITPK.N
R1/RRR1-24/2	1365.506	1366.552	-1502.642	0.317	933.094	0.292	17	0.196	K.LQAFWNHPAGPK.T
R1/RRR1-23/2	1367.425	1366.552	-92.547	0.287	578.234	0.308	14	0.187	-.LQAFWNHPAGPK.-
R1/RRR1-24/3	1844.066	1844.103	-20.099	0.475	825.622	0.517	25	0.116	K.WGISIANVADFAKPPEK.I
R1/RRR1-24/2	1619.210	1618.637	-264.547	0.417	702.645	0.538	18	0.110	K.DYFSDEKDAAASLEG.-
R1/RRR1-23/3	1844.757	1844.103	-188.074	0.415	777.518	0.470	25	0.101	K.WGISIANVADFAKPPEK.I
R1/RRR1-15/2	1452.174	1452.613	-303.268	0.508	1683.773	0.490	20	0.301	R.EAGTTM*EVVAAQTK.A
R1/RRR1-16/2	1452.125	1452.613	-337.004	0.449	1633.043	0.510	21	0.301	R.EAGTTM*EVVAAQTK.A
R1/RRR1-15/2	1452.038	1452.613	-1088.405	0.480	1642.236	0.465	20	0.289	R.EAGTTM*EVVAAQTK.A
R1/RRR1-15/2	1452.141	1452.613	-325.955	0.456	1569.996	0.495	20	0.288	R.EAGTTM*EVVAAQTK.A
R1/RRR1-16/2	1050.076	1050.233	-150.016	0.454	1629.477	0.420	16	0.278	K.VAYALSQGIK.V
R1/RRR1-16/2	1049.998	1050.233	-224.888	0.443	1617.935	0.403	17	0.273	K.VAYALSQGIK.V
R1/RRR1-15/2	1602.337	1602.773	-273.140	0.509	1176.679	0.565	22	0.262	K.WLATNVSPAVAESTR.I
R1/RRR1-15/2	1389.417	1389.573	-113.289	0.453	1376.688	0.440	19	0.254	K.VIACIGETLEQR.E
R1/RRR1-16/2	1050.046	1050.233	-178.471	0.449	1578.400	0.319	16	0.247	K.VAYALSQGIK.V
R1/RRR1-15/2	1389.089	1389.573	-350.152	0.473	1363.442	0.409	18	0.245	K.VIACIGETLEQR.E
R1/RRR1-15/2	1602.348	1602.773	-266.032	0.502	946.933	0.563	20	0.240	K.WLATNVSPAVAESTR.I
R1/RRR1-15/2	1602.404	1602.773	-230.799	0.527	932.784	0.549	20	0.236	K.WLATNVSPAVAESTR.I
R1/RRR1-16/2	1389.112	1389.573	-333.400	0.416	1015.523	0.386	17	0.215	K.VIACIGETLEQR.E
R1/RRR1-16/2	1389.021	1389.573	-1121.270	0.415	996.113	0.354	17	0.209	K.VIACIGETLEQR.E
R1/RRR1-16/2	1388.698	1389.573	-1354.554	0.298	912.929	0.323	16	0.199	K.VIACIGETLEQR.E
R1/RRR1-22/2	1964.825	1965.195	-189.162	0.534	1991.143	0.625	29	0.394	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-21/2	1964.546	1965.195	-842.272	0.535	1973.444	0.571	29	0.371	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-23/2	1965.214	1965.195	9.681	0.566	1944.069	0.566	29	0.364	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-24/2	1964.550	1965.195	-839.777	0.500	1963.258	0.552	29	0.363	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-21/2	1964.654	1965.195	-786.699	0.494	1788.120	0.581	27	0.343	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-20/2	1964.559	1965.195	-835.660	0.533	1763.559	0.546	27	0.328	R.IWVFSGDTDAVLPVTSTR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/2	1965.263	1965.195	34.726	0.582	1602.402	0.567	26	0.309	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-22/2	1964.456	1965.195	-887.808	0.485	1711.532	0.477	27	0.300	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-21/2	1964.544	1965.195	-842.833	0.512	1531.006	0.557	26	0.298	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-23/2	1965.246	1965.195	25.755	0.579	1492.446	0.576	26	0.298	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-23/2	1964.478	1965.195	-876.580	0.509	1548.611	0.521	26	0.290	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-21/2	905.984	906.064	-88.263	0.400	1189.207	0.404	12	0.231	K.GLNFVTVR.G
R1/RRR1-20/2	905.948	906.064	-128.540	0.446	1120.322	0.405	12	0.227	-.GLNFVTVR.-
R1/RRR1-20/2	905.838	906.064	-250.609	0.413	1126.880	0.373	12	0.222	-.GLNFVTVR.-
R1/RRR1-20/2	906.036	906.064	-30.690	0.449	1121.953	0.374	12	0.221	-.GLNFVTVR.-
R1/RRR1-21/2	905.740	906.064	-358.914	0.404	1133.134	0.368	12	0.221	K.GLNFVTVR.G
R1/RRR1-21/2	905.696	906.064	-407.462	0.390	1104.429	0.376	12	0.221	K.GLNFVTVR.G
R1/RRR1-24/2	906.179	906.064	127.262	0.355	1023.324	0.346	12	0.212	K.GLNFVTVR.G
R1/RRR1-21/2	1091.392	1092.316	-1768.534	0.351	621.459	0.492	13	0.205	K.ALHVSPIINK.S
R1/RRR1-23/2	905.916	906.064	-163.414	0.329	581.452	0.334	12	0.201	K.GLNFVTVR.G
R1/RRR1-23/2	905.759	906.064	-338.224	0.327	579.171	0.345	11	0.200	K.GLNFVTVR.G
R1/RRR1-21/2	1299.465	1298.479	-10.610	0.421	484.294	0.490	13	0.198	-.GAGHEVPLHRPK.-
R1/RRR1-22/2	905.868	906.064	-217.216	0.337	366.126	0.282	11	0.194	-.GLNFVTVR.-
R1/RRR1-22/2	905.676	906.064	-429.372	0.297	282.287	0.279	10	0.191	-.GLNFVTVR.-
R1/RRR1-14/2	1967.016	1965.195	-91.289	0.397	390.661	0.407	14	0.186	-.IWVFSGDTDAVLPVTSTR.-
R1/RRR1-23/3	1298.598	1298.479	91.717	0.508	1417.238	0.471	25	0.152	R.GAGHEVPLHRPK.Q
R1/RRR1-21/3	1297.832	1298.479	-1272.846	0.496	1413.419	0.417	25	0.136	R.GAGHEVPLHRPK.Q
R1/RRR1-21/3	1298.447	1298.479	-24.679	0.489	1319.886	0.435	25	0.130	R.GAGHEVPLHRPK.Q
R1/RRR1-21/3	1965.028	1965.195	-85.220	0.423	1015.374	0.489	27	0.122	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-20/3	1298.136	1298.479	-264.628	0.520	1142.564	0.439	24	0.116	-.GAGHEVPLHRPK.-
R1/RRR1-23/3	1298.858	1298.479	293.048	0.516	1121.472	0.409	24	0.110	R.GAGHEVPLHRPK.Q
R1/RRR1-21/3	1298.422	1298.479	-43.491	0.523	1080.453	0.405	24	0.106	R.GAGHEVPLHRPK.Q
R1/RRR1-23/3	1298.734	1298.479	197.341	0.488	942.816	0.401	23	0.099	R.GAGHEVPLHRPK.Q
R1/RRR1-20/3	1298.542	1298.479	48.867	0.394	526.874	0.429	18	0.093	-.GAGHEVPLHRPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/3	1298.579	1298.479	77.434	0.422	977.575	0.354	22	0.093	R.GAGHEVPLHRPK.Q
R1/RRR1-24/3	1298.627	1298.479	114.626	0.443	778.386	0.367	21	0.091	R.GAGHEVPLHRPK.Q
R1/RRR1-20/3	1298.275	1298.479	-157.231	0.433	936.437	0.355	22	0.090	-.GAGHEVPLHRPK.-
R1/RRR1-24/3	1298.373	1298.479	-81.543	0.459	799.323	0.359	22	0.084	-.GAGHEVPLHRPK.-
R1/RRR1-23/3	1964.927	1965.195	-137.191	0.365	825.185	0.244	25	0.071	R.IWVFSGDTDAVLPVTSTR.Y
R1/RRR1-6/2	1390.995	1391.492	-358.084	0.503	1496.928	0.454	17	0.270	K.NSLENYAYNM*R.N
R1/RRR1-6/2	1392.007	1391.492	-349.292	0.498	1177.176	0.452	16	0.238	K.NSLENYAYNM*R.N
R1/RRR1-6/2	1374.972	1375.492	-1108.684	0.434	1286.450	0.408	16	0.238	K.NSLENYAYNMR.N
R1/RRR1-6/2	1390.991	1391.492	-1081.882	0.482	1246.350	0.384	17	0.231	K.NSLENYAYNM*R.N
R1/RRR1-11/2	1677.198	1677.832	-976.866	0.485	2168.007	0.521	23	0.398	K.ILQSLEESVTDTDVK.Y
R1/RRR1-11/2	1330.369	1329.486	-88.775	0.497	1218.473	0.542	19	0.263	K.IPATWQGIEASR.L
R1/RRR1-11/2	1277.979	1278.439	-360.955	0.424	1587.597	0.301	17	0.244	R.LAYDTQGIIQR.V
R1/RRR1-11/2	1278.138	1278.439	-236.667	0.464	1445.878	0.348	17	0.240	R.LAYDTQGIIQR.V
R1/RRR1-11/2	1329.262	1329.486	-169.352	0.420	1087.260	0.477	18	0.235	K.IPATWQGIEASR.L
R1/RRR1-11/2	978.042	978.127	-86.892	0.447	1282.921	0.269	14	0.214	R.RVEELFGK.I
R1/RRR1-11/2	977.913	978.127	-219.493	0.403	1218.990	0.292	13	0.213	R.RVEELFGK.I
R1/RRR1-11/2	1329.450	1329.486	-27.316	0.458	816.117	0.431	17	0.212	K.IPATWQGIEASR.L
R1/RRR1-11/2	977.862	978.127	-272.217	0.436	960.724	0.275	13	0.199	R.RVEELFGK.I
R1/RRR1-5/2	1611.311	1610.812	310.606	0.504	1567.148	0.615	22	0.321	K.ASNTLSIIDSGVGM*TK.S
R1/RRR1-5/2	1610.454	1610.812	-223.008	0.481	1585.861	0.589	22	0.316	K.ASNTLSIIDSGVGM*TK.S
R1/RRR1-5/2	1610.283	1610.812	-952.579	0.466	1399.540	0.557	21	0.281	K.ASNTLSIIDSGVGM*TK.S
R1/RRR1-5/2	1735.704	1736.004	-173.713	0.497	1205.889	0.537	22	0.258	K.LDAQPELFIHIVPDK.A
R1/RRR1-5/3	1951.496	1951.255	123.803	0.477	1896.196	0.508	32	0.255	K.SKLDAQPELFIHIVPDK.A
R1/RRR1-5/2	1735.816	1736.004	-108.738	0.527	901.995	0.579	19	0.239	K.LDAQPELFIHIVPDK.A
R1/RRR1-5/2	1735.954	1736.004	-28.819	0.546	1034.429	0.503	21	0.236	K.LDAQPELFIHIVPDK.A
R1/RRR1-1/2	1735.757	1736.004	-142.812	0.340	409.162	0.263	13	0.165	-.LDAQPELFIHIVPDK.-
R1/RRR1-5/3	1951.851	1951.255	-207.551	0.478	1040.008	0.519	27	0.133	K.SKLDAQPELFIHIVPDK.A
R1/RRR1-5/3	1735.951	1736.004	-31.013	0.386	898.256	0.448	26	0.103	K.LDAQPELFIHIVPDK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/3	1735.856	1736.004	-85.714	0.372	623.662	0.462	27	0.094	K.LDAQPELFIHIVPDK.A
R1/RRR1-5/3	1736.233	1736.004	132.312	0.405	617.823	0.361	25	0.086	K.LDAQPELFIHIVPDK.A
R1/RRR1-6/3	1735.815	1736.004	-109.416	0.276	589.239	0.318	24	0.079	K.LDAQPELFIHIVPDK.A
R1/RRR1-6/3	1736.218	1736.004	123.745	0.322	676.798	0.310	24	0.079	K.LDAQPELFIHIVPDK.A
R1/RRR1-6/3	1951.764	1951.255	-252.162	0.334	580.749	0.371	21	0.073	-.SKLDAQPELFIHIVPDK.-
R1/RRR1-16/2	1537.201	1537.655	-296.024	0.521	1809.667	0.468	22	0.314	K.IQFDVWDTAGQEK.F
R1/RRR1-17/2	1537.089	1537.655	-1022.100	0.473	1792.919	0.436	21	0.302	K.IQFDVWDTAGQEK.F
R1/RRR1-16/2	1537.122	1537.655	-1000.571	0.495	1720.554	0.422	21	0.288	K.IQFDVWDTAGQEK.F
R1/RRR1-17/2	1537.755	1537.655	65.479	0.515	1624.820	0.432	21	0.279	K.IQFDVWDTAGQEK.F
R1/RRR1-16/2	1516.384	1516.752	-243.488	0.570	1529.997	0.462	21	0.275	R.VCENIPIVLCGNK.V
R1/RRR1-16/2	1517.503	1516.752	-164.723	0.583	1406.884	0.487	21	0.268	R.VCENIPIVLCGNK.V
R1/RRR1-16/2	1537.056	1537.655	-1043.629	0.468	1569.585	0.394	20	0.262	K.IQFDVWDTAGQEK.F
R1/RRR1-17/2	1516.143	1516.752	-1064.000	0.498	1097.443	0.467	21	0.237	R.VCENIPIVLCGNK.V
R1/RRR1-17/2	1516.265	1516.752	-322.318	0.520	1107.578	0.392	21	0.223	R.VCENIPIVLCGNK.V
R1/RRR1-16/2	1516.737	1516.752	-9.898	0.522	974.116	0.407	20	0.217	R.VCENIPIVLCGNK.V
R1/RRR1-17/2	1216.156	1215.337	-148.859	0.490	961.451	0.388	15	0.214	K.NLQYYDISAK.S
R1/RRR1-17/2	1015.841	1016.174	-327.847	0.336	952.039	0.382	17	0.212	K.LVLVGDGGTGK.T
R1/RRR1-17/2	1015.932	1016.174	-238.274	0.379	898.890	0.345	17	0.206	K.LVLVGDGGTGK.T
R1/RRR1-17/2	1215.074	1215.337	-217.109	0.355	1009.799	0.305	15	0.204	K.NLQYYDISAK.S
R1/RRR1-16/2	1214.580	1215.337	-1450.856	0.339	946.566	0.326	15	0.204	K.NLQYYDISAK.S
R1/RRR1-16/2	1016.018	1016.174	-153.659	0.408	856.524	0.328	17	0.203	K.LVLVGDGGTGK.T
R1/RRR1-16/2	1015.862	1016.174	-307.592	0.374	984.300	0.287	17	0.202	K.LVLVGDGGTGK.T
R1/RRR1-17/2	1016.143	1016.174	-30.377	0.375	674.092	0.345	16	0.200	K.LVLVGDGGTGK.T
R1/RRR1-17/2	1215.056	1215.337	-231.622	0.373	985.498	0.282	15	0.200	K.NLQYYDISAK.S
R1/RRR1-16/2	1215.352	1215.337	12.229	0.420	879.358	0.303	15	0.200	K.NLQYYDISAK.S
R1/RRR1-17/2	1017.085	1016.174	-87.529	0.365	894.077	0.269	16	0.196	K.LVLVGDGGTGK.T
R1/RRR1-17/2	1016.055	1016.174	-117.021	0.354	975.543	0.209	17	0.192	K.LVLVGDGGTGK.T
R1/RRR1-17/2	1536.481	1537.655	-1419.023	0.307	668.278	0.173	14	0.182	-.IQFDVWDTAGQEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1751.247	1751.956	-978.418	0.511	2016.318	0.484	25	0.356	R.IIYGGSVNAANCAELAK.K
R1/RRR1-16/2	1450.269	1450.619	-241.924	0.542	1844.461	0.579	22	0.355	K.GPDFATIINSVTSK.K
R1/RRR1-16/2	1450.284	1450.619	-231.538	0.548	1589.672	0.601	21	0.322	K.GPDFATIINSVTSK.K
R1/RRR1-16/2	1230.089	1230.353	-215.553	0.410	1427.498	0.407	21	0.253	K.TNVSPEVASGIR.I
R1/RRR1-16/2	1230.062	1230.353	-237.357	0.461	1259.055	0.480	19	0.252	K.TNVSPEVASGIR.I
R1/RRR1-15/2	1450.184	1450.619	-300.278	0.468	1150.453	0.532	17	0.248	K.GPDFATIINSVTSK.K
R1/RRR1-16/2	1230.008	1230.353	-280.966	0.439	1206.064	0.477	20	0.247	K.TNVSPEVASGIR.I
R1/RRR1-16/2	1606.399	1606.765	-228.319	0.490	1015.959	0.552	21	0.243	K.VATPEQAQEVHAAVR.D
R1/RRR1-15/2	1230.398	1230.353	36.957	0.424	1195.608	0.395	18	0.229	K.TNVSPEVASGIR.I
R1/RRR1-16/2	1449.676	1450.619	-1344.198	0.363	790.541	0.493	16	0.213	K.GPDFATIINSVTSK.K
R1/RRR1-15/2	1230.067	1230.353	-233.175	0.414	925.191	0.384	18	0.211	K.TNVSPEVASGIR.I
R1/RRR1-16/2	1778.322	1779.029	-962.971	0.570	977.063	0.532	23	0.240	K.IWQVPETLHEEVLGK.M
R1/RRR1-16/2	1779.362	1779.029	187.532	0.554	1033.116	0.502	24	0.239	K.IWQVPETLHEEVLGK.M
R1/RRR1-16/2	1778.099	1779.029	-1088.620	0.510	1072.328	0.456	24	0.233	K.IWQVPETLHEEVLGK.M
R1/RRR1-16/2	1046.955	1047.298	-328.248	0.452	795.820	0.469	14	0.218	R.FGM*M*AAQMK.A
R1/RRR1-16/2	1047.920	1048.129	-199.864	0.428	808.384	0.356	15	0.201	-.GASSIEGVEAK.-
R1/RRR1-17/2	1779.785	1779.029	-137.559	0.390	299.112	0.412	14	0.193	K.IWQVPETLHEEVLGK.M
R1/RRR1-16/2	1047.567	1048.129	-1495.630	0.304	818.854	0.216	16	0.189	K.GASSIEGVEAK.I
R1/RRR1-16/2	1047.848	1048.129	-269.634	0.326	635.408	0.266	14	0.187	-.GASSIEGVEAK.-
R1/RRR1-17/2	1048.032	1048.129	-92.714	0.360	842.508	0.154	15	0.183	-.GASSIEGVEAK.-
R1/RRR1-17/2	1047.943	1048.129	-177.894	0.317	656.549	0.155	14	0.181	-.GASSIEGVEAK.-
R1/RRR1-16/2	1014.527	1015.299	-1752.155	0.230	648.299	0.092	12	0.180	R.FGMMAAQMK.A
R1/RRR1-12/2	1204.092	1204.404	-259.559	0.470	1960.597	0.438	18	0.331	R.VVSNFVAQALR.K
R1/RRR1-12/2	1203.768	1204.404	-1363.194	0.397	1616.949	0.420	18	0.276	R.VVSNFVAQALR.K
R1/RRR1-12/2	1227.972	1228.337	-298.582	0.422	795.788	0.452	15	0.212	K.VVQDTIDPNAR.I
R1/RRR1-12/2	1171.330	1171.370	-34.976	0.340	1022.971	0.291	14	0.199	R.AKELLGWEPK.I
R1/RRR1-12/2	1227.188	1228.337	-1756.212	0.335	727.233	0.366	15	0.197	K.VVQDTIDPNAR.I
R1/RRR1-11/2	1424.026	1423.620	286.258	0.477	2249.373	0.580	21	0.428	R.GGDLVSAFAELMGR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1422.950	1423.620	-1176.878	0.415	2218.422	0.523	20	0.399	R.GGDLVSAFAELMGR.Q
R1/RRR1-11/2	1423.434	1423.620	-130.881	0.468	1826.056	0.564	20	0.343	R.GGDLVSAFAELMGR.Q
R1/RRR1-11/2	1439.546	1439.619	-51.229	0.493	1837.688	0.523	20	0.332	R.GGDLVSAFAELM*GR.Q
R1/RRR1-11/2	1439.098	1439.619	-1060.533	0.360	1466.357	0.516	19	0.276	R.GGDLVSAFAELM*GR.Q
R1/RRR1-11/2	1271.436	1270.376	47.223	0.515	1483.953	0.422	18	0.260	K.GFGVESFGADRK.E
R1/RRR1-10/2	1422.788	1423.620	-1291.809	0.425	1138.895	0.486	17	0.237	R.GGDLVSAFAELMGR.Q
R1/RRR1-10/2	1270.122	1270.376	-199.987	0.439	1199.813	0.392	17	0.227	K.GFGVESFGADRK.E
R1/RRR1-11/2	1269.567	1270.376	-1429.294	0.401	1075.017	0.360	16	0.212	K.GFGVESFGADRK.E
R1/RRR1-11/2	1004.865	1005.152	-286.651	0.399	907.047	0.333	14	0.205	K.RGDYVPGLK.V
R1/RRR1-11/2	1004.931	1005.152	-220.597	0.431	941.418	0.313	14	0.203	K.RGDYVPGLK.V
R1/RRR1-10/2	1422.825	1423.620	-1265.271	0.315	631.517	0.367	17	0.197	R.GGDLVSAFAELMGR.Q
R1/RRR1-11/2	1004.560	1005.152	-1590.375	0.342	757.740	0.253	13	0.191	K.RGDYVPGLK.V
R1/RRR1-2/2	1440.098	1439.619	333.589	0.324	523.313	0.350	14	0.191	R.GGDLVSAFAELM*GR.Q
R1/RRR1-10/2	1004.713	1005.152	-439.144	0.354	581.805	0.253	11	0.187	-.RGDYVPGLK.-
R1/RRR1-11/3	1611.852	1611.677	108.389	0.418	917.388	0.416	26	0.096	R.YHGHSM*SDPGSTYR.T
R1/RRR1-11/3	1611.295	1611.677	-238.299	0.350	781.414	0.317	22	0.077	R.YHGHSM*SDPGSTYR.T
R1/RRR1-11/2	1823.648	1824.159	-831.078	0.530	1834.195	0.566	26	0.348	K.TQKPVVAFIAGLTAPPGR.R
R1/RRR1-11/2	1824.541	1824.159	209.798	0.592	1676.108	0.631	26	0.343	K.TQKPVVAFIAGLTAPPGR.R
R1/RRR1-11/2	1822.721	1824.159	-1341.944	0.503	1574.387	0.604	24	0.318	K.TQKPVVAFIAGLTAPPGR.R
R1/RRR1-11/2	1187.056	1187.325	-226.874	0.447	1055.536	0.509	18	0.239	R.EAGVTVVESPAK.I
R1/RRR1-11/2	1187.431	1187.325	89.643	0.450	1002.299	0.519	18	0.238	R.EAGVTVVESPAK.I
R1/RRR1-11/2	1186.528	1187.325	-1518.590	0.355	984.894	0.476	17	0.224	R.EAGVTVVESPAK.I
R1/RRR1-11/3	1955.190	1955.204	-6.933	0.522	1664.518	0.516	34	0.217	K.KGGTEHLGLPVFNSVAEAK.A
R1/RRR1-11/3	1954.513	1955.204	-867.400	0.506	1624.237	0.482	32	0.201	K.KGGTEHLGLPVFNSVAEAK.A
R1/RRR1-11/3	1954.443	1955.204	-903.703	0.443	1592.790	0.468	33	0.186	K.KGGTEHLGLPVFNSVAEAK.A
R1/RRR1-11/3	1826.815	1827.031	-118.375	0.403	1782.608	0.363	29	0.184	K.GGTEHLGLPVFNSVAEAK.A
R1/RRR1-11/3	1826.727	1827.031	-166.539	0.277	701.687	0.239	22	0.066	-.GGTEHLGLPVFNSVAEAK.-
R1/RRR1-16/2	1274.855	1275.352	-391.420	0.493	1437.887	0.480	18	0.271	K.AQIWDTAGQER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1274.928	1275.352	-333.777	0.504	1341.927	0.503	17	0.265	K.AQIWDTAGQER.F
R1/RRR1-17/2	1274.352	1275.352	-1574.192	0.398	1499.294	0.418	17	0.261	K.AQIWDTAGQER.F
R1/RRR1-17/2	1274.257	1275.352	-1648.966	0.340	1377.595	0.417	17	0.247	K.AQIWDTAGQER.F
R1/RRR1-16/2	1081.028	1081.204	-163.502	0.459	1111.881	0.500	16	0.244	K.STIGVEFATR.S
R1/RRR1-16/2	1081.016	1081.204	-174.264	0.466	926.739	0.497	15	0.230	K.STIGVEFATR.S
R1/RRR1-16/2	1081.060	1081.204	-133.598	0.476	977.668	0.468	15	0.228	K.STIGVEFATR.S
R1/RRR1-16/2	1275.027	1275.352	-255.970	0.441	1308.789	0.339	17	0.227	K.AQIWDTAGQER.F
R1/RRR1-16/2	1058.283	1058.254	27.696	0.325	1176.668	0.379	18	0.222	K.IVLIGDSGVGK.S
R1/RRR1-17/2	1274.351	1275.352	-1575.443	0.182	1050.367	0.101	16	0.182	K.AQIWDTAGQER.F
R1/RRR1-16/3	1471.509	1471.598	-60.716	0.484	1511.855	0.411	33	0.152	K.KPVASDEGGAGAAGGVK.E
R1/RRR1-16/3	1471.726	1471.598	87.542	0.512	1286.820	0.399	32	0.124	K.KPVASDEGGAGAAGGVK.E
R1/RRR1-15/2	1668.356	1668.820	-279.211	0.498	2315.511	0.368	22	0.366	R.NDFDTCVDLLSQLK.V
R1/RRR1-15/2	1668.364	1668.820	-274.513	0.522	2053.296	0.455	22	0.349	R.NDFDTCVDLLSQLK.V
R1/RRR1-15/2	1668.345	1668.820	-285.744	0.527	2105.776	0.378	22	0.331	R.NDFDTCVDLLSQLK.V
R1/RRR1-15/2	1191.672	1192.390	-1445.766	0.465	1501.667	0.480	16	0.278	K.LVEVTQLFSR.F
R1/RRR1-15/2	1192.224	1192.390	-139.010	0.511	1469.787	0.471	17	0.273	K.LVEVTQLFSR.F
R1/RRR1-15/2	1832.463	1833.078	-884.274	0.499	1214.426	0.567	24	0.266	K.EIPSLQVINQTLSYAR.E
R1/RRR1-15/2	1832.421	1833.078	-907.213	0.510	1252.162	0.544	24	0.265	K.EIPSLQVINQTLSYAR.E
R1/RRR1-15/2	1191.643	1192.390	-1469.844	0.449	1283.010	0.496	17	0.259	K.LVEVTQLFSR.F
R1/RRR1-15/2	1832.482	1833.078	-873.708	0.507	1115.123	0.525	23	0.247	K.EIPSLQVINQTLSYAR.E
R1/RRR1-15/2	1373.292	1373.579	-209.302	0.436	1161.880	0.386	17	0.223	R.DIYEHAVVLSVK.I
R1/RRR1-15/2	1372.483	1373.579	-1532.025	0.342	879.911	0.372	15	0.202	R.DIYEHAVVLSVK.I
R1/RRR1-15/2	1373.333	1373.579	-179.341	0.387	769.078	0.385	15	0.201	R.DIYEHAVVLSVK.I
R1/RRR1-2/2	1169.806	1170.341	-1315.794	0.373	1987.795	0.330	18	0.300	R.VGLLVESAEPR.E
R1/RRR1-2/2	1170.251	1170.341	-76.649	0.398	1406.838	0.408	16	0.248	R.VGLLVESAEPR.E
R1/RRR1-2/2	1432.173	1432.607	-303.456	0.427	1183.273	0.406	18	0.229	R.VFIETPIQNTNR.A
R1/RRR1-2/2	1087.588	1087.252	310.304	0.402	873.459	0.390	14	0.208	R.AILQTDGQLK.T
R1/RRR1-1/2	1432.616	1432.607	6.358	0.404	943.920	0.348	17	0.205	R.VFIETPIQNTNR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/2	1432.210	1432.607	-277.546	0.444	792.683	0.385	16	0.203	R.VFIETPIQNTNR.A
R1/RRR1-1/2	944.173	944.111	65.861	0.355	842.583	0.348	15	0.202	K.VIGDIAVTR.H
R1/RRR1-1/2	1170.338	1170.341	-2.052	0.319	755.459	0.338	14	0.196	R.VGLLVESAEPR.E
R1/RRR1-2/2	944.121	944.111	10.620	0.374	612.306	0.284	14	0.193	K.VIGDIAVTR.H
R1/RRR1-1/2	1170.058	1170.341	-242.413	0.303	988.466	0.243	14	0.193	R.VGLLVESAEPR.E
R1/RRR1-3/2	1087.967	1087.252	-262.280	0.299	546.651	0.278	13	0.189	R.AILQTDGQLK.T
R1/RRR1-2/2	1087.379	1087.252	117.371	0.254	495.191	0.342	12	0.188	-.AILQTDGQLK.-
R1/RRR1-2/2	1170.318	1170.341	-19.837	0.263	798.752	0.245	14	0.188	R.VGLLVESAEPR.E
R1/RRR1-1/3	1843.169	1844.926	-2044.843	0.475	882.612	0.544	30	0.123	K.GHADHVLISGHDGGTGASR.W
R1/RRR1-8/2	1761.626	1761.957	-188.462	0.540	3161.832	0.528	26	0.630	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-7/2	1761.544	1761.957	-235.387	0.545	2876.979	0.543	25	0.557	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-9/2	1761.415	1761.957	-878.236	0.509	2833.026	0.486	25	0.520	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-9/2	1761.527	1761.957	-244.703	0.556	2745.343	0.506	26	0.506	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-8/2	1762.212	1761.957	145.377	0.563	2673.758	0.513	26	0.491	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-7/2	1762.534	1761.957	-240.951	0.610	2596.821	0.506	25	0.467	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-8/2	1761.865	1761.957	-52.648	0.579	2427.083	0.522	25	0.438	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-10/2	1761.649	1761.957	-175.602	0.499	2556.630	0.446	23	0.437	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-7/2	1761.244	1761.957	-975.506	0.562	2366.572	0.536	25	0.432	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-7/2	1729.473	1728.972	-289.308	0.603	1128.985	0.609	23	0.270	R.WQAVAPSLPDDLFIR.V
R1/RRR1-7/2	1728.315	1728.972	-961.647	0.536	1279.670	0.539	24	0.268	R.WQAVAPSLPDDLFIR.V
R1/RRR1-8/2	1728.465	1728.972	-874.577	0.464	982.756	0.546	22	0.242	R.WQAVAPSLPDDLFIR.V
R1/RRR1-7/2	1728.439	1728.972	-889.537	0.487	942.080	0.538	21	0.237	R.WQAVAPSLPDDLFIR.V
R1/RRR1-6/2	1762.369	1761.957	234.359	0.476	1328.523	0.397	21	0.234	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-10/2	1728.500	1728.972	-273.958	0.434	1062.743	0.471	23	0.234	R.WQAVAPSLPDDLFIR.V
R1/RRR1-4/2	1761.838	1761.957	-67.729	0.474	1202.473	0.435	22	0.233	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-7/2	1828.895	1830.078	-1197.230	0.465	1113.174	0.424	22	0.226	R.SERPEAFAVLDLVNIR.A
R1/RRR1-10/2	1728.059	1728.972	-1110.082	0.435	882.045	0.455	21	0.219	R.WQAVAPSLPDDLFIR.V
R1/RRR1-9/2	1729.675	1728.972	-171.982	0.486	810.775	0.436	20	0.213	R.WQAVAPSLPDDLFIR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1829.399	1830.078	-920.356	0.486	916.870	0.411	21	0.211	R.SERPEAFAVLDLVNIR.A
R1/RRR1-9/2	1727.669	1728.972	-1336.898	0.348	734.046	0.424	18	0.205	R.WQAVAPSLPDDLFIR.V
R1/RRR1-5/2	1762.587	1761.957	-210.380	0.431	695.248	0.383	20	0.200	K.YGLAADNVVDAVLVDAR.G
R1/RRR1-8/2	1730.447	1728.972	275.615	0.410	814.526	0.334	19	0.199	R.WQAVAPSLPDDLFIR.V
R1/RRR1-8/2	1729.479	1728.972	-285.696	0.293	529.710	0.310	16	0.191	R.WQAVAPSLPDDLFIR.V
R1/RRR1-1/2	1829.027	1830.078	-1124.646	0.329	531.030	0.337	15	0.186	R.SERPEAFAVLDLVNIR.A
R1/RRR1-8/3	1831.270	1830.078	105.188	0.475	1205.709	0.424	27	0.125	R.SERPEAFAVLDLVNIR.A
R1/RRR1-7/3	1870.203	1869.134	36.696	0.548	1067.439	0.400	26	0.110	R.LLDKNSM*GSDVFWALR.G
R1/RRR1-7/3	1829.183	1830.078	-1039.082	0.487	762.962	0.402	23	0.091	-.SERPEAFAVLDLVNIR.-
R1/RRR1-1/3	1830.035	1830.078	-23.364	0.365	1235.782	0.247	26	0.088	R.SERPEAFAVLDLVNIR.A
R1/RRR1-9/3	1830.583	1830.078	-270.995	0.451	1132.089	0.249	24	0.087	-.SERPEAFAVLDLVNIR.-
R1/RRR1-7/3	1829.639	1830.078	-240.687	0.463	873.538	0.310	25	0.083	-.SERPEAFAVLDLVNIR.-
R1/RRR1-7/3	1829.841	1830.078	-129.655	0.366	956.953	0.254	26	0.078	R.SERPEAFAVLDLVNIR.A
R1/RRR1-9/3	1830.153	1830.078	41.062	0.350	663.191	0.253	22	0.073	-.SERPEAFAVLDLVNIR.-
R1/RRR1-16/2	1556.875	1557.814	-1249.284	0.507	1562.025	0.555	23	0.306	K.KLPSILVDETSVQK.I
R1/RRR1-16/2	1557.163	1557.814	-1063.570	0.547	1370.402	0.602	22	0.294	K.KLPSILVDETSVQK.I
R1/RRR1-16/2	1558.389	1557.814	-273.222	0.550	1324.778	0.551	22	0.276	K.KLPSILVDETSVQK.I
R1/RRR1-15/2	1073.003	1073.225	-207.972	0.451	899.164	0.573	16	0.241	K.AANGVVIATEK.K
R1/RRR1-16/2	1072.568	1073.225	-1549.464	0.384	1004.556	0.533	17	0.239	K.AANGVVIATEK.K
R1/RRR1-16/2	1072.554	1073.225	-1563.069	0.409	947.530	0.484	17	0.228	K.AANGVVIATEK.K
R1/RRR1-16/2	1561.316	1560.863	291.200	0.538	821.521	0.467	19	0.218	R.LYKETIPVTQLVR.E
R1/RRR1-16/2	1560.421	1560.863	-283.930	0.452	851.359	0.452	19	0.217	R.LYKETIPVTQLVR.E
R1/RRR1-16/2	1072.559	1073.225	-1557.810	0.385	772.352	0.462	15	0.214	K.AANGVVIATEK.K
R1/RRR1-16/2	1560.830	1560.863	-20.914	0.479	733.092	0.452	18	0.211	R.LYKETIPVTQLVR.E
R1/RRR1-15/2	1072.451	1073.225	-1659.575	0.387	812.249	0.400	16	0.209	K.AANGVVIATEK.K
R1/RRR1-16/2	1073.241	1073.225	15.217	0.357	608.506	0.278	15	0.194	K.AANGVVIATEK.K
R1/RRR1-16/2	1073.266	1073.225	38.147	0.232	454.838	0.366	12	0.191	K.AANGVVIATEK.K
R1/RRR1-15/3	1558.193	1557.814	243.883	0.474	1678.805	0.342	26	0.158	K.KLPSILVDETSVQK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1718.154	1718.926	-1034.390	0.437	697.914	0.468	17	0.101	K.VLSPAEIKDFLEEVE.-
R1/RRR1-15/2	1718.116	1718.926	-1056.504	0.350	709.551	0.303	17	0.081	K.VLSPAEIKDFLEEVE.-
R1/RRR1-14/2	1706.577	1706.964	-227.544	0.481	1720.946	0.571	21	0.331	R.IQDNLALVYLSSITR.T
R1/RRR1-14/2	1706.398	1706.964	-920.615	0.473	1736.267	0.517	22	0.318	R.IQDNLALVYLSSITR.T
R1/RRR1-14/2	1651.773	1651.891	-71.649	0.549	1667.239	0.527	22	0.314	R.HLAAQFQEIPLDLR.M
R1/RRR1-14/2	1296.314	1296.411	-75.523	0.409	1735.687	0.440	19	0.298	K.AYISSNLSLGDR.H
R1/RRR1-14/2	1706.532	1706.964	-254.454	0.463	1594.820	0.490	21	0.290	R.IQDNLALVYLSSITR.T
R1/RRR1-14/2	1051.488	1052.120	-1556.657	0.375	881.238	0.481	15	0.222	K.YVDDVVEGR.V
R1/RRR1-14/2	1052.062	1052.120	-54.885	0.494	877.271	0.434	15	0.219	K.YVDDVVEGR.V
R1/RRR1-8/2	1930.447	1931.043	-829.180	0.594	2422.896	0.584	25	0.468	R.YYGGNDVIDEIENLCR.D
R1/RRR1-9/2	1930.646	1931.043	-206.209	0.578	2250.228	0.602	24	0.437	R.YYGGNDVIDEIENLCR.D
R1/RRR1-8/2	1931.104	1931.043	31.599	0.614	2188.063	0.595	24	0.421	R.YYGGNDVIDEIENLCR.D
R1/RRR1-8/2	1931.522	1931.043	248.635	0.607	2139.511	0.597	24	0.412	R.YYGGNDVIDEIENLCR.D
R1/RRR1-8/2	1816.169	1816.986	-1003.779	0.521	2313.058	0.481	23	0.404	K.VSAATGYIDYEKLEEK.A
R1/RRR1-9/2	1930.605	1931.043	-227.712	0.581	2054.307	0.599	23	0.396	R.YYGGNDVIDEIENLCR.D
R1/RRR1-9/2	1929.900	1931.043	-1113.634	0.541	2067.003	0.577	24	0.391	R.YYGGNDVIDEIENLCR.D
R1/RRR1-9/2	1816.591	1816.986	-218.212	0.557	2109.027	0.508	22	0.373	K.VSAATGYIDYEKLEEK.A
R1/RRR1-8/2	1620.303	1619.839	287.324	0.517	1889.443	0.448	21	0.317	K.ISATSIYFESLPYK.V
R1/RRR1-9/2	1619.413	1619.839	-263.985	0.456	2006.063	0.368	21	0.312	K.ISATSIYFESLPYK.V
R1/RRR1-8/2	1207.183	1207.398	-178.364	0.499	1650.279	0.509	19	0.305	K.LIICGGSAYPR.D
R1/RRR1-9/2	1207.066	1207.398	-275.453	0.490	1634.628	0.493	19	0.298	K.LIICGGSAYPR.D
R1/RRR1-9/2	1619.588	1619.839	-155.550	0.418	1764.559	0.430	21	0.295	K.ISATSIYFESLPYK.V
R1/RRR1-9/2	1816.679	1816.986	-169.744	0.538	1644.151	0.500	20	0.295	K.VSAATGYIDYEKLEEK.A
R1/RRR1-9/2	1206.997	1207.398	-333.390	0.515	1431.483	0.503	18	0.276	K.LIICGGSAYPR.D
R1/RRR1-9/2	1619.075	1619.839	-1092.547	0.371	1630.147	0.423	20	0.275	K.ISATSIYFESLPYK.V
R1/RRR1-8/2	1206.630	1207.398	-1469.142	0.364	1406.840	0.433	18	0.254	K.LIICGGSAYPR.D
R1/RRR1-8/2	1816.670	1816.986	-174.530	0.557	1338.898	0.483	19	0.252	K.VSAATGYIDYEKLEEK.A
R1/RRR1-8/2	1206.776	1207.398	-1348.027	0.419	1193.287	0.409	16	0.231	K.LIICGGSAYPR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1207.030	1207.398	-305.182	0.445	1246.483	0.367	18	0.229	K.LIICGGSAYPR.D
R1/RRR1-1/2	1620.881	1619.839	26.241	0.411	808.344	0.406	20	0.209	K.ISATSIYFESLPYK.V
R1/RRR1-8/2	1618.783	1619.839	-1273.587	0.265	1151.536	0.305	18	0.207	K.ISATSIYFESLPYK.V
R1/RRR1-8/2	1618.470	1619.839	-1468.329	0.201	667.942	0.134	18	0.183	K.ISATSIYFESLPYK.V
R1/RRR1-9/3	1931.176	1931.043	69.060	0.443	939.379	0.445	24	0.106	R.YYGGNDVIDEIENLCR.D
R1/RRR1-9/2	1983.706	1984.152	-225.752	0.569	2916.541	0.547	25	0.578	R.ELQDEGFDVQTAGYGLLK.T
R1/RRR1-9/2	1984.357	1984.152	103.743	0.616	2852.110	0.576	25	0.572	R.ELQDEGFDVQTAGYGLLK.T
R1/RRR1-9/2	1983.355	1984.152	-908.795	0.551	2440.010	0.544	25	0.457	R.ELQDEGFDVQTAGYGLLK.T
R1/RRR1-9/2	1488.384	1488.670	-192.871	0.471	1768.126	0.521	22	0.327	R.SNVIVEYPGTVPGR.A
R1/RRR1-9/2	1759.429	1759.984	-886.882	0.485	924.014	0.485	19	0.219	R.DAVGGLDRDPFVSLLGK.L
R1/RRR1-9/2	1759.366	1759.984	-922.475	0.484	843.581	0.433	18	0.205	R.DAVGGLDRDPFVSLLGK.L
R1/RRR1-9/2	1759.352	1759.984	-930.694	0.457	766.103	0.414	18	0.200	R.DAVGGLDRDPFVSLLGK.L
R1/RRR1-9/3	1873.113	1873.056	30.315	0.596	1346.782	0.527	29	0.169	K.KLQEYVHDINENIEK.L
R1/RRR1-15/3	1838.033	1837.934	54.075	0.525	1915.349	0.522	38	0.259	K.HHSNTAVGAELSHSFSR.N
R1/RRR1-14/2	1264.378	1263.420	-33.080	0.419	897.674	0.550	16	0.232	K.SLITISGEVDTK.A
R1/RRR1-15/2	1622.012	1621.816	121.031	0.469	1109.026	0.403	19	0.222	R.KNESVFGELQTQLK.N
R1/RRR1-14/2	1620.800	1621.816	-1247.980	0.481	1099.502	0.399	20	0.222	R.KNESVFGELQTQLK.N
R1/RRR1-15/2	1621.288	1621.816	-945.457	0.444	1167.040	0.377	19	0.221	R.KNESVFGELQTQLK.N
R1/RRR1-15/2	1227.084	1227.435	-287.123	0.436	845.103	0.406	16	0.211	K.SILSLVVPDQR.S
R1/RRR1-15/2	1227.097	1227.435	-276.245	0.423	860.183	0.402	16	0.211	K.SILSLVVPDQR.S
R1/RRR1-15/2	1227.186	1227.435	-204.091	0.414	754.833	0.423	15	0.208	K.SILSLVVPDQR.S
R1/RRR1-14/2	1620.570	1621.816	-1390.194	0.376	879.936	0.338	19	0.201	R.KNESVFGELQTQLK.N
R1/RRR1-14/2	1262.666	1263.420	-1393.374	0.305	748.722	0.374	14	0.196	K.SLITISGEVDTK.A
R1/RRR1-14/2	1226.643	1227.435	-1465.235	0.292	675.365	0.295	14	0.190	K.SILSLVVPDQR.S
R1/RRR1-14/2	1622.378	1621.816	-270.974	0.286	700.394	0.184	17	0.183	R.KNESVFGELQTQLK.N
R1/RRR1-14/2	1263.054	1263.420	-290.191	0.207	595.356	0.190	15	0.182	K.SLITISGEVDTK.A
R1/RRR1-14/3	1622.257	1621.816	272.478	0.433	1152.531	0.273	23	0.086	-.KNESVFGELQTQLK.-
R1/RRR1-10/2	1655.529	1654.974	-269.615	0.556	2369.618	0.490	24	0.419	K.ETLIAGGPFVLPLAQK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1655.414	1654.974	266.511	0.541	2285.473	0.470	23	0.394	K.ETLIAGGPFVLPLAQK.H
R1/RRR1-10/2	1655.245	1654.974	164.018	0.559	2081.998	0.513	23	0.371	K.ETLIAGGPFVLPLAQK.H
R1/RRR1-10/2	1655.638	1654.974	-203.559	0.419	1879.241	0.416	22	0.308	K.ETLIAGGPFVLPLAQK.H
R1/RRR1-10/2	1423.044	1423.575	-1079.158	0.461	1289.511	0.473	20	0.250	R.AGGTM*TGVLSAANEK.A
R1/RRR1-10/2	1424.315	1423.575	-183.076	0.504	1103.724	0.471	20	0.233	R.AGGTM*TGVLSAANEK.A
R1/RRR1-10/2	1423.200	1423.575	-264.345	0.466	1119.240	0.464	20	0.233	R.AGGTM*TGVLSAANEK.A
R1/RRR1-10/2	1209.588	1209.374	177.279	0.426	1016.868	0.466	16	0.228	K.ITVDSATLFNK.G
R1/RRR1-10/2	1208.997	1209.374	-312.382	0.430	860.457	0.452	16	0.217	K.ITVDSATLFNK.G
R1/RRR1-10/2	1337.288	1337.547	-193.696	0.434	918.805	0.328	17	0.200	K.KITVDSATLFNK.G
R1/RRR1-15/2	1951.454	1951.208	126.197	0.548	1900.700	0.545	28	0.352	K.TAFIPFITAGDPDLATTAK.A
R1/RRR1-15/2	1950.401	1951.208	-929.549	0.507	1836.264	0.561	27	0.346	K.TAFIPFITAGDPDLATTAK.A
R1/RRR1-15/2	1950.423	1951.208	-918.427	0.496	1837.740	0.553	27	0.344	K.TAFIPFITAGDPDLATTAK.A
R1/RRR1-15/2	1044.206	1044.227	-20.239	0.400	816.078	0.399	14	0.209	K.VQSLLQDIK.Q
R1/RRR1-15/2	1043.720	1044.227	-1448.354	0.370	793.216	0.367	14	0.204	K.VQSLLQDIK.Q
R1/RRR1-15/2	1329.182	1329.438	-193.312	0.331	869.618	0.330	20	0.200	R.QLGEAASPEEGLK.R
R1/RRR1-15/2	1329.047	1329.438	-295.589	0.341	797.845	0.337	20	0.199	R.QLGEAASPEEGLK.R
R1/RRR1-15/2	1044.995	1044.227	-222.216	0.470	802.476	0.300	15	0.199	K.VQSLLQDIK.Q
R1/RRR1-15/2	1329.193	1329.438	-184.836	0.351	648.872	0.354	18	0.197	R.QLGEAASPEEGLK.R
R1/RRR1-15/2	1912.812	1913.162	-183.552	0.381	803.356	0.315	18	0.188	K.NNLELVLLTTPTTPTER.M
R1/RRR1-8/2	1273.155	1272.388	-183.739	0.480	1303.901	0.509	18	0.262	K.GLTFDSGGYNIK.T
R1/RRR1-8/2	1319.027	1319.360	-253.650	0.502	1407.137	0.459	18	0.262	K.TIEVNNTDAEGR.L
R1/RRR1-8/2	1345.089	1345.506	-311.116	0.444	1287.130	0.501	21	0.258	K.FDM*GGSAAVFGAAK.A
R1/RRR1-8/2	1345.170	1345.506	-250.387	0.450	1129.075	0.514	21	0.246	K.FDM*GGSAAVFGAAK.A
R1/RRR1-8/2	1345.072	1345.506	-323.863	0.378	1171.061	0.489	21	0.242	K.FDM*GGSAAVFGAAK.A
R1/RRR1-8/2	1191.054	1191.271	-182.219	0.413	987.377	0.479	17	0.227	K.EVAAASEISGEK.F
R1/RRR1-8/2	1191.004	1191.271	-224.169	0.421	820.622	0.508	15	0.219	K.EVAAASEISGEK.F
R1/RRR1-8/2	1271.992	1272.388	-312.312	0.347	969.296	0.397	18	0.213	K.GLTFDSGGYNIK.T
R1/RRR1-8/2	1272.017	1272.388	-293.152	0.302	964.670	0.348	18	0.204	K.GLTFDSGGYNIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1255.050	1255.383	-265.851	0.522	1536.629	0.446	17	0.274	K.M*DYVNQALER.L
R1/RRR1-10/2	1354.257	1354.604	-257.323	0.491	1033.911	0.592	21	0.253	R.GGVLGLGGVGHM*GVK.V
R1/RRR1-10/2	1254.959	1255.383	-339.042	0.559	1200.413	0.447	16	0.240	K.M*DYVNQALER.L
R1/RRR1-10/2	1239.049	1239.383	-270.319	0.425	1007.927	0.430	15	0.222	K.MDYVNQALER.L
R1/RRR1-10/2	1131.165	1131.333	-148.952	0.347	1103.284	0.380	16	0.219	K.HFGLM*SPGLR.G
R1/RRR1-10/2	1486.174	1485.651	-321.825	0.385	580.533	0.593	19	0.219	K.SM*GHHVTVISSSAR.K
R1/RRR1-10/2	1354.264	1354.604	-251.535	0.451	760.679	0.505	19	0.216	R.GGVLGLGGVGHM*GVK.V
R1/RRR1-10/2	1130.983	1131.333	-310.170	0.314	995.583	0.416	15	0.215	K.HFGLM*SPGLR.G
R1/RRR1-10/2	1130.297	1131.333	-1806.941	0.294	902.406	0.384	15	0.206	K.HFGLM*SPGLR.G
R1/RRR1-2/2	1486.017	1485.651	246.566	0.323	321.257	0.486	14	0.194	K.SM*GHHVTVISSSAR.K
R1/RRR1-10/3	1486.615	1485.651	-24.669	0.520	1384.715	0.444	27	0.145	K.SM*GHHVTVISSSAR.K
R1/RRR1-9/3	1486.615	1485.651	-24.669	0.507	1204.542	0.419	25	0.123	K.SM*GHHVTVISSSAR.K
R1/RRR1-10/3	1485.724	1485.651	49.278	0.509	1281.557	0.384	28	0.117	K.SM*GHHVTVISSSAR.K
R1/RRR1-10/3	1485.649	1485.651	-1.774	0.562	1259.073	0.375	26	0.116	-.SM*GHHVTVISSSAR.-
R1/RRR1-10/3	1469.333	1469.652	-217.546	0.528	1368.527	0.333	28	0.113	K.SMGHHVTVISSSAR.K
R1/RRR1-1/3	1485.610	1485.651	-28.229	0.502	689.130	0.472	21	0.105	-.SM*GHHVTVISSSAR.-
R1/RRR1-9/3	1485.325	1485.651	-220.257	0.513	930.998	0.377	24	0.099	K.SM*GHHVTVISSSAR.K
R1/RRR1-9/3	1485.133	1485.651	-1025.491	0.435	947.972	0.370	24	0.097	K.SM*GHHVTVISSSAR.K
R1/RRR1-10/3	1469.713	1469.652	41.552	0.551	1000.814	0.344	25	0.094	-.SMGHHVTVISSSAR.-
R1/RRR1-5/3	1485.581	1485.651	-47.515	0.439	903.145	0.333	23	0.091	K.SM*GHHVTVISSSAR.K
R1/RRR1-10/3	1469.279	1469.652	-254.553	0.500	939.633	0.334	24	0.090	-.SMGHHVTVISSSAR.-
R1/RRR1-10/3	1486.050	1485.651	268.756	0.392	600.863	0.312	22	0.088	K.SM*GHHVTVISSSAR.K
R1/RRR1-10/3	1486.149	1485.651	335.594	0.341	834.446	0.211	21	0.074	-.SM*GHHVTVISSSAR.-
R1/RRR1-10/3	1485.262	1485.651	-262.926	0.316	646.530	0.211	21	0.066	-.SM*GHHVTVISSSAR.-
R1/RRR1-12/2	1750.565	1752.092	-2020.502	0.427	1893.718	0.494	26	0.332	K.AVVAGASGGIGQPLSLLLK.L
R1/RRR1-13/2	1752.665	1752.092	-244.124	0.587	1836.950	0.511	26	0.326	K.AVVAGASGGIGQPLSLLLK.L
R1/RRR1-13/2	1752.087	1752.092	-2.768	0.582	1774.714	0.520	27	0.321	K.AVVAGASGGIGQPLSLLLK.L
R1/RRR1-12/2	1750.753	1752.092	-1339.551	0.416	1484.327	0.430	23	0.258	K.AVVAGASGGIGQPLSLLLK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1750.801	1752.092	-1312.101	0.384	1462.382	0.378	23	0.244	K.AVVAGASGGIGQPLSLLLK.L
R1/RRR1-12/2	1211.233	1211.433	-165.132	0.397	1144.913	0.352	17	0.215	K.GLIEIAAEVAPK.A
R1/RRR1-13/2	1234.512	1234.470	34.354	0.448	1080.601	0.335	17	0.211	R.LFGVTTLDIVR.A
R1/RRR1-13/2	1234.143	1234.470	-265.044	0.376	857.856	0.356	17	0.204	R.LFGVTTLDIVR.A
R1/RRR1-13/2	1234.228	1234.470	-196.379	0.412	808.323	0.294	16	0.195	R.LFGVTTLDIVR.A
R1/RRR1-15/2	1879.620	1880.095	-253.626	0.565	1524.908	0.680	33	0.334	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/2	1410.141	1410.578	-310.806	0.493	2169.250	0.350	20	0.334	R.SVQM*EGLTWGASK.L
R1/RRR1-14/2	1879.551	1880.095	-823.752	0.562	1428.198	0.670	32	0.316	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/2	1410.027	1410.578	-1103.267	0.516	1869.017	0.426	20	0.310	R.SVQM*EGLTWGASK.L
R1/RRR1-15/2	1879.502	1880.095	-850.222	0.551	1210.570	0.683	30	0.291	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/2	1511.302	1511.659	-236.691	0.495	1513.546	0.513	22	0.288	K.TYVSGNAISKDDIK.V
R1/RRR1-15/2	1880.330	1880.095	125.110	0.565	1193.246	0.663	30	0.284	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/2	1879.487	1880.095	-858.241	0.531	1141.915	0.669	30	0.280	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/2	1410.969	1410.578	278.143	0.516	1589.268	0.430	20	0.274	R.SVQM*EGLTWGASK.L
R1/RRR1-14/2	1879.567	1880.095	-815.472	0.512	1016.312	0.634	28	0.257	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/2	1511.191	1511.659	-310.761	0.471	1076.574	0.505	20	0.240	K.TYVSGNAISKDDIK.V
R1/RRR1-14/2	1510.721	1511.659	-1286.235	0.480	840.450	0.489	17	0.218	K.TYVSGNAISKDDIK.V
R1/RRR1-21/2	1880.298	1880.095	108.247	0.411	554.942	0.533	22	0.207	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-15/3	1830.982	1830.079	-53.410	0.369	1163.886	0.522	31	0.141	K.VFAAVPSKPGAEFPNAAR.W
R1/RRR1-14/3	1880.702	1880.095	-209.511	0.395	942.867	0.505	32	0.123	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/3	1879.610	1880.095	-258.748	0.344	978.700	0.416	31	0.106	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/3	1830.746	1830.079	-182.826	0.347	689.027	0.494	24	0.104	K.VFAAVPSKPGAEFPNAAR.W
R1/RRR1-14/3	1879.545	1880.095	-826.986	0.344	702.180	0.433	29	0.095	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-15/3	1880.019	1880.095	-40.848	0.335	880.356	0.339	31	0.087	K.AVGVNLPGGGAASSAAAAAPAAK.D
R1/RRR1-14/3	1831.022	1830.079	-31.744	0.278	499.325	0.338	25	0.083	K.VFAAVPSKPGAEFPNAAR.W
R1/RRR1-15/3	1829.691	1830.079	-212.910	0.271	664.510	0.358	26	0.082	K.VFAAVPSKPGAEFPNAAR.W
R1/RRR1-14/3	1829.513	1830.079	-858.737	0.258	979.307	0.308	31	0.081	K.VFAAVPSKPGAEFPNAAR.W
R1/RRR1-15/3	1879.446	1880.095	-879.895	0.278	901.056	0.302	28	0.081	K.AVGVNLPGGGAASSAAAAAPAAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1829.898	1830.079	-99.676	0.247	515.058	0.337	24	0.081	K.VFAAVPSKPGAEFPNAAR.W
R1/RRR1-10/2	1545.734	1545.760	-16.761	0.526	2032.817	0.553	20	0.379	K.TYVVQDGDIIFFK.F
R1/RRR1-10/2	1544.928	1545.760	-1189.521	0.395	1737.010	0.471	19	0.304	K.TYVVQDGDIIFFK.F
R1/RRR1-10/2	1067.093	1067.307	-201.092	0.463	996.642	0.533	17	0.241	K.IGIVGLPNVGK.S
R1/RRR1-10/2	1067.207	1067.307	-93.687	0.450	838.602	0.490	16	0.222	K.IGIVGLPNVGK.S
R1/RRR1-10/2	1067.224	1067.307	-77.509	0.490	831.309	0.473	16	0.220	K.IGIVGLPNVGK.S
R1/RRR1-9/2	1547.144	1545.760	249.154	0.383	389.965	0.369	12	0.185	-.TYVVQDGDIIFFK.-
R1/RRR1-10/3	1514.947	1514.625	213.425	0.438	871.476	0.559	25	0.122	K.APQAAGTIHTDFER.G
R1/RRR1-10/3	1513.526	1514.625	-1390.560	0.396	631.387	0.569	22	0.109	K.APQAAGTIHTDFER.G
R1/RRR1-10/3	1514.510	1514.625	-75.727	0.453	521.039	0.526	21	0.103	K.APQAAGTIHTDFER.G
R1/RRR1-10/3	1538.650	1538.681	-19.951	0.388	1378.383	0.275	27	0.100	K.FDDLKELGSESAVK.A
R1/RRR1-10/2	1201.219	1201.398	-149.283	0.519	1744.787	0.539	20	0.329	K.VIALGDVTGSIR.N
R1/RRR1-10/2	1201.237	1201.398	-134.298	0.544	1733.499	0.521	20	0.322	K.VIALGDVTGSIR.N
R1/RRR1-10/2	1299.197	1299.414	-167.051	0.438	1174.450	0.539	17	0.254	K.DDGTLASFIGFR.V
R1/RRR1-10/2	1298.351	1299.414	-1593.565	0.375	1090.031	0.482	17	0.233	K.DDGTLASFIGFR.V
R1/RRR1-10/2	1733.382	1733.852	-272.268	0.516	729.326	0.537	21	0.219	K.GGIGCAPGELSTSELER.L
R1/RRR1-10/2	1118.487	1119.295	-1622.028	0.327	826.014	0.408	15	0.203	K.TAVAAIPYGGAK.G
R1/RRR1-10/2	1118.919	1119.295	-337.092	0.394	970.797	0.337	16	0.203	K.TAVAAIPYGGAK.G
R1/RRR1-6/3	1720.298	1720.875	-919.020	0.480	2455.804	0.464	39	0.364	R.RVHVAGPAGSAAADRER.I
R1/RRR1-6/2	1352.198	1352.479	-207.859	0.484	1598.630	0.501	17	0.294	R.VAEDGWWSVFR.V
R1/RRR1-6/2	1308.507	1309.407	-1456.281	0.374	1603.793	0.486	18	0.289	R.LEFDAGELTTGR.D
R1/RRR1-6/2	1163.185	1163.348	-140.796	0.580	1468.806	0.454	17	0.268	R.VLETEVAVFR.A
R1/RRR1-6/2	1163.032	1163.348	-272.617	0.495	1444.002	0.460	17	0.268	R.VLETEVAVFR.A
R1/RRR1-6/2	1352.538	1352.479	43.849	0.385	1213.018	0.433	15	0.235	R.VAEDGWWSVFR.V
R1/RRR1-5/2	1353.562	1352.479	62.087	0.368	1030.503	0.452	15	0.225	R.VAEDGWWSVFR.V
R1/RRR1-6/2	1352.386	1352.479	-68.951	0.403	894.711	0.492	15	0.224	R.VAEDGWWSVFR.V
R1/RRR1-6/2	1309.063	1309.407	-263.437	0.381	1093.387	0.409	17	0.222	R.LEFDAGELTTGR.D
R1/RRR1-6/2	1308.418	1309.407	-1524.691	0.328	918.252	0.354	15	0.201	R.LEFDAGELTTGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1353.219	1352.479	-192.049	0.412	401.884	0.420	10	0.194	R.VAEDGWWSVFR.V
R1/RRR1-5/2	1353.202	1352.479	-204.719	0.308	425.413	0.336	11	0.189	-.VAEDGWWSVFR.-
R1/RRR1-5/2	1624.497	1623.811	-193.566	0.379	969.291	0.408	18	0.209	K.ANGTLTIQDSGIGM*TK.A
R1/RRR1-5/2	1561.376	1561.719	-220.788	0.446	891.387	0.335	21	0.202	R.EIISNSSDALDKIR.Y
R1/RRR1-5/2	1291.453	1292.375	-1492.767	0.369	819.452	0.348	16	0.199	R.EIISNSSDALDK.I
R1/RRR1-5/2	1624.371	1623.811	-271.745	0.384	709.950	0.440	16	0.199	K.ANGTLTIQDSGIGM*TK.A
R1/RRR1-5/2	1561.422	1561.719	-190.749	0.452	767.413	0.298	20	0.194	R.EIISNSSDALDKIR.Y
R1/RRR1-5/2	1292.056	1292.375	-247.384	0.404	690.991	0.331	15	0.193	-.EIISNSSDALDK.-
R1/RRR1-5/2	1292.086	1292.375	-224.257	0.399	723.907	0.313	15	0.192	R.EIISNSSDALDK.I
R1/RRR1-5/2	1561.406	1561.719	-201.180	0.456	655.932	0.255	20	0.189	R.EIISNSSDALDKIR.Y
R1/RRR1-6/2	1731.587	1730.986	-231.328	0.587	2540.707	0.645	29	0.527	R.IINEPTAAAIAYGLGAGK.S
R1/RRR1-6/2	1730.486	1730.986	-289.634	0.533	2036.887	0.611	27	0.401	R.IINEPTAAAIAYGLGAGK.S
R1/RRR1-6/2	1730.707	1730.986	-161.905	0.577	2023.773	0.608	27	0.397	R.IINEPTAAAIAYGLGAGK.S
R1/RRR1-6/2	1404.361	1403.563	-144.690	0.325	940.391	0.259	17	0.190	K.SAVDEIVLVGGSTR.I
R1/RRR1-6/2	1623.839	1622.820	11.792	0.343	858.767	0.291	16	0.187	K.LSTTEIEAMVAEAEK.F
R1/RRR1-6/2	1404.497	1403.563	-47.302	0.304	632.487	0.162	14	0.176	K.SAVDEIVLVGGSTR.I
R1/RRR1-6/3	1395.368	1395.588	-158.048	0.351	1183.584	0.126	23	0.064	R.ARFEELNAVAFK.G
R1/RRR1-12/2	1767.831	1767.022	-108.362	0.587	1882.608	0.526	23	0.341	R.VLDTHVEGGNLFIVPR.F
R1/RRR1-12/2	1766.286	1767.022	-985.545	0.503	1652.792	0.528	22	0.307	R.VLDTHVEGGNLFIVPR.F
R1/RRR1-12/2	1205.083	1205.299	-179.996	0.483	1685.255	0.475	18	0.300	R.AWDLAESDAVK.L
R1/RRR1-12/2	1766.504	1767.022	-861.705	0.483	1466.702	0.535	21	0.284	R.VLDTHVEGGNLFIVPR.F
R1/RRR1-12/2	1204.311	1205.299	-1655.884	0.376	1579.663	0.366	17	0.258	R.AWDLAESDAVK.L
R1/RRR1-12/2	1735.202	1734.932	156.248	0.507	1122.127	0.570	24	0.255	K.LSLNAGGLALPSFSDSGK.V
R1/RRR1-12/2	1204.664	1205.299	-1361.062	0.419	1426.831	0.377	17	0.245	R.AWDLAESDAVK.L
R1/RRR1-12/2	1186.062	1186.383	-271.866	0.485	1030.770	0.501	19	0.238	K.LVSSQPASGIVK.I
R1/RRR1-12/2	1734.302	1734.932	-942.231	0.461	895.249	0.573	22	0.235	K.LSLNAGGLALPSFSDSGK.V
R1/RRR1-12/2	1185.991	1186.383	-331.501	0.496	979.446	0.479	19	0.230	K.LVSSQPASGIVK.I
R1/RRR1-13/2	1734.537	1734.932	-227.899	0.449	935.177	0.511	21	0.226	K.LSLNAGGLALPSFSDSGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1734.606	1734.932	-188.292	0.354	476.226	0.358	17	0.188	K.LSLNAGGLALPSFSDSGK.V
R1/RRR1-8/2	1399.495	1399.660	-117.810	0.486	1711.006	0.507	18	0.312	K.VLWLIENVDAVK.N
R1/RRR1-8/2	1463.296	1463.613	-216.677	0.378	1453.888	0.306	19	0.231	R.DSLGIISTASEIEK.L
R1/RRR1-8/2	1399.262	1399.660	-284.956	0.402	755.510	0.468	14	0.209	K.VLWLIENVDAVK.N
R1/RRR1-8/2	1114.059	1114.237	-160.743	0.482	829.080	0.376	16	0.206	R.RLESELPGGR.T
R1/RRR1-8/2	1399.247	1399.660	-295.459	0.284	765.748	0.391	14	0.197	K.VLWLIENVDAVK.N
R1/RRR1-8/2	1463.105	1463.613	-1033.281	0.306	788.865	0.123	17	0.176	R.DSLGIISTASEIEK.L
R1/RRR1-8/3	1578.763	1578.662	63.963	0.458	727.238	0.530	26	0.106	K.VFGQHVTDCSNASR.T
R1/RRR1-8/3	1578.697	1578.662	21.854	0.428	609.714	0.530	25	0.101	K.VFGQHVTDCSNASR.T
R1/RRR1-13/2	1346.217	1346.496	-207.741	0.480	964.416	0.507	19	0.234	R.DM*TALSGAHTIGR.A
R1/RRR1-13/2	1345.995	1346.496	-1118.503	0.477	994.331	0.486	19	0.232	R.DM*TALSGAHTIGR.A
R1/RRR1-13/2	1346.065	1346.496	-320.735	0.486	984.310	0.478	19	0.230	R.DM*TALSGAHTIGR.A
R1/RRR1-14/2	991.527	992.150	-1641.964	0.396	1322.084	0.329	14	0.227	R.GFEVIDAIK.T
R1/RRR1-14/2	1092.987	1093.218	-212.459	0.374	878.195	0.489	16	0.223	R.NINASFASLR.Q
R1/RRR1-14/2	1549.102	1549.732	-1055.386	0.460	870.507	0.455	24	0.220	K.M*GNLLPSSGTATEVR.L
R1/RRR1-14/2	991.415	992.150	-1755.643	0.343	1346.465	0.273	14	0.220	-.GFEVIDAIK.-
R1/RRR1-14/2	1093.408	1093.218	173.720	0.370	831.793	0.483	14	0.218	R.NINASFASLR.Q
R1/RRR1-14/2	1549.504	1549.732	-147.528	0.505	679.995	0.505	21	0.217	K.M*GNLLPSSGTATEVR.L
R1/RRR1-14/2	1093.319	1093.218	92.320	0.285	967.091	0.418	16	0.213	R.NINASFASLR.Q
R1/RRR1-14/2	1346.236	1346.496	-193.641	0.387	872.160	0.405	19	0.211	R.DM*TALSGAHTIGR.A
R1/RRR1-13/2	991.974	992.150	-178.119	0.434	1251.227	0.250	14	0.208	-.GFEVIDAIK.-
R1/RRR1-13/2	992.046	992.150	-105.413	0.448	1304.210	0.230	14	0.206	R.GFEVIDAIK.T
R1/RRR1-14/2	1549.433	1549.732	-193.366	0.452	627.629	0.339	21	0.196	K.M*GNLLPSSGTATEVR.L
R1/RRR1-14/2	1347.031	1346.496	-345.865	0.322	568.717	0.331	17	0.195	R.DM*TALSGAHTIGR.A
R1/RRR1-14/2	991.471	992.150	-1698.738	0.305	989.106	0.237	13	0.192	-.GFEVIDAIK.-
R1/RRR1-14/2	1345.432	1346.496	-1538.397	0.291	712.938	0.240	17	0.189	R.DM*TALSGAHTIGR.A
R1/RRR1-9/2	1969.653	1970.170	-772.954	0.491	1473.635	0.353	19	0.238	R.KNPDLENLLFDDFFNK.A
R1/RRR1-9/2	1352.259	1352.474	-158.866	0.390	837.226	0.453	15	0.214	K.EIGDIFTEWNK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1136.969	1137.276	-270.467	0.440	752.953	0.415	15	0.209	K.AIHTAQPGWR.D
R1/RRR1-9/2	1353.534	1352.474	44.631	0.461	648.242	0.443	14	0.206	K.EIGDIFTEWNK.G
R1/RRR1-9/2	1353.431	1352.474	-31.808	0.404	732.474	0.388	15	0.203	K.EIGDIFTEWNK.G
R1/RRR1-9/2	1137.049	1137.276	-200.349	0.375	627.917	0.370	15	0.200	K.AIHTAQPGWR.D
R1/RRR1-9/2	1137.197	1137.276	-69.079	0.441	491.225	0.298	15	0.196	K.AIHTAQPGWR.D
R1/RRR1-9/3	1672.186	1672.782	-957.177	0.479	1337.493	0.490	29	0.148	K.YPEGQDIHVNWTGR.G
R1/RRR1-9/3	1672.940	1672.782	94.651	0.457	980.501	0.482	27	0.113	K.YPEGQDIHVNWTGR.G
R1/RRR1-9/3	1673.010	1672.782	136.910	0.404	869.698	0.429	25	0.097	K.YPEGQDIHVNWTGR.G
R1/RRR1-7/2	1696.603	1697.953	-1389.306	0.332	2161.904	0.483	23	0.378	R.VIEVGEVDPAAYPLPK.T
R1/RRR1-7/2	1697.470	1697.953	-285.386	0.485	1917.674	0.581	22	0.368	R.VIEVGEVDPAAYPLPK.T
R1/RRR1-7/2	1429.203	1428.487	-199.315	0.428	597.720	0.537	18	0.214	K.ENPAPSASDIEAAR.V
R1/RRR1-7/2	1287.108	1287.445	-262.414	0.441	481.056	0.485	17	0.206	K.QEITAAVAELNK.A
R1/RRR1-7/2	1428.063	1428.487	-297.385	0.361	506.651	0.501	18	0.204	K.ENPAPSASDIEAAR.V
R1/RRR1-7/2	1088.257	1088.283	-24.258	0.318	888.577	0.320	14	0.194	-.TKLTLENLR.-
R1/RRR1-7/2	1567.365	1567.722	-228.928	0.536	2118.510	0.590	25	0.414	K.IAVFAGGVDTSATETK.G
R1/RRR1-7/2	1289.195	1289.457	-203.771	0.469	1650.747	0.349	17	0.263	K.TEEAKVEELIK.A
R1/RRR1-7/2	1181.818	1182.352	-1301.385	0.417	1053.138	0.455	17	0.229	K.HLSGLDEAVLK.N
R1/RRR1-7/2	1425.119	1425.656	-1081.700	0.337	678.026	0.460	21	0.205	R.IIPGAAATEIELAR.R
R1/RRR1-11/2	1420.294	1419.606	-220.738	0.535	1850.409	0.570	19	0.348	R.AFQLYSSGIFTGK.C
R1/RRR1-12/2	1420.369	1419.606	-167.626	0.548	1874.199	0.537	19	0.341	R.AFQLYSSGIFTGK.C
R1/RRR1-13/2	1419.262	1419.606	-243.587	0.477	1925.582	0.465	19	0.327	R.AFQLYSSGIFTGK.C
R1/RRR1-11/2	1420.011	1419.606	286.205	0.484	1609.651	0.538	19	0.303	R.AFQLYSSGIFTGK.C
R1/RRR1-11/2	1539.270	1539.719	-292.365	0.545	1384.148	0.594	24	0.291	K.AVANQPVSVAIEAGGR.A
R1/RRR1-12/2	1540.276	1539.719	-288.200	0.553	1327.598	0.593	24	0.284	K.AVANQPVSVAIEAGGR.A
R1/RRR1-14/2	1540.329	1539.719	-253.931	0.551	1297.981	0.564	23	0.273	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1540.259	1539.719	-299.411	0.561	1140.171	0.620	22	0.270	K.AVANQPVSVAIEAGGR.A
R1/RRR1-14/2	1539.249	1539.719	-305.891	0.520	1131.929	0.612	22	0.267	K.AVANQPVSVAIEAGGR.A
R1/RRR1-15/2	1540.262	1539.719	-297.344	0.530	1202.678	0.563	23	0.264	K.AVANQPVSVAIEAGGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1540.213	1539.719	322.138	0.564	1209.797	0.561	23	0.264	K.AVANQPVSVAIEAGGR.A
R1/RRR1-22/2	1539.224	1539.719	-322.521	0.519	1121.136	0.594	22	0.262	K.AVANQPVSVAIEAGGR.A
R1/RRR1-11/2	1540.261	1539.719	-298.059	0.565	1031.598	0.623	21	0.260	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1540.602	1539.719	-75.627	0.581	1066.100	0.602	22	0.260	K.AVANQPVSVAIEAGGR.A
R1/RRR1-23/2	1539.258	1539.719	-299.844	0.521	1050.300	0.586	23	0.256	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1419.285	1419.606	-227.106	0.407	1434.057	0.438	17	0.256	R.AFQLYSSGIFTGK.C
R1/RRR1-12/2	1539.225	1539.719	-321.805	0.512	1057.564	0.586	21	0.254	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1539.363	1539.719	-231.740	0.513	1047.318	0.582	22	0.254	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1334.291	1334.536	-184.588	0.483	1537.268	0.362	19	0.251	K.CGIAVEPSYPLK.K
R1/RRR1-22/2	1539.176	1539.719	-1004.963	0.489	1052.016	0.543	22	0.246	K.AVANQPVSVAIEAGGR.A
R1/RRR1-23/2	1539.501	1539.719	-142.010	0.533	958.983	0.573	22	0.246	K.AVANQPVSVAIEAGGR.A
R1/RRR1-16/2	1539.169	1539.719	-1009.581	0.477	935.738	0.580	22	0.245	K.AVANQPVSVAIEAGGR.A
R1/RRR1-2/2	1539.266	1539.719	-295.070	0.482	949.160	0.575	21	0.244	K.AVANQPVSVAIEAGGR.A
R1/RRR1-22/2	1539.234	1539.719	-315.758	0.520	839.821	0.600	21	0.242	K.AVANQPVSVAIEAGGR.A
R1/RRR1-3/2	1539.234	1539.719	-315.599	0.473	1049.006	0.521	22	0.242	K.AVANQPVSVAIEAGGR.A
R1/RRR1-22/2	1420.310	1419.606	-209.184	0.451	959.276	0.564	16	0.240	R.AFQLYSSGIFTGK.C
R1/RRR1-12/2	1539.414	1539.719	-198.726	0.523	973.820	0.536	22	0.240	K.AVANQPVSVAIEAGGR.A
R1/RRR1-2/2	1539.263	1539.719	-296.662	0.484	941.274	0.529	22	0.236	K.AVANQPVSVAIEAGGR.A
R1/RRR1-11/2	1335.773	1334.536	178.039	0.464	1413.993	0.349	18	0.236	K.CGIAVEPSYPLK.K
R1/RRR1-16/2	1539.425	1539.719	-191.169	0.497	839.531	0.558	21	0.235	K.AVANQPVSVAIEAGGR.A
R1/RRR1-17/2	1539.079	1539.719	-1068.668	0.498	916.847	0.515	22	0.233	K.AVANQPVSVAIEAGGR.A
R1/RRR1-1/2	1540.236	1539.719	-314.201	0.531	945.484	0.522	20	0.232	K.AVANQPVSVAIEAGGR.A
R1/RRR1-15/2	1539.320	1539.719	-259.585	0.489	963.260	0.490	22	0.231	K.AVANQPVSVAIEAGGR.A
R1/RRR1-14/2	1538.683	1539.719	-1327.235	0.377	852.933	0.506	21	0.225	K.AVANQPVSVAIEAGGR.A
R1/RRR1-23/2	1538.892	1539.719	-1190.288	0.443	799.445	0.499	20	0.222	K.AVANQPVSVAIEAGGR.A
R1/RRR1-9/2	1540.558	1539.719	-104.877	0.439	628.409	0.552	19	0.222	K.AVANQPVSVAIEAGGR.A
R1/RRR1-16/2	1538.562	1539.719	-1406.042	0.395	906.541	0.452	21	0.220	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1334.202	1334.536	-251.499	0.430	1319.478	0.300	18	0.220	K.CGIAVEPSYPLK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1538.548	1539.719	-1415.207	0.404	753.845	0.474	19	0.215	K.AVANQPVSVAIEAGGR.A
R1/RRR1-15/2	1538.808	1539.719	-1245.652	0.353	758.646	0.462	20	0.214	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1334.115	1334.536	-316.491	0.435	1178.594	0.318	17	0.213	K.CGIAVEPSYPLK.K
R1/RRR1-10/2	1419.135	1419.606	-332.817	0.377	756.246	0.454	16	0.211	R.AFQLYSSGIFTGK.C
R1/RRR1-9/2	1540.287	1539.719	-281.044	0.347	408.005	0.460	17	0.205	K.AVANQPVSVAIEAGGR.A
R1/RRR1-13/2	1040.842	1041.099	-246.746	0.378	824.394	0.270	14	0.198	K.SWGESGYVR.M
R1/RRR1-14/2	1040.693	1041.099	-390.902	0.325	662.376	0.253	13	0.194	K.SWGESGYVR.M
R1/RRR1-12/2	1334.409	1334.536	-95.755	0.394	973.416	0.263	15	0.194	K.CGIAVEPSYPLK.K
R1/RRR1-14/2	1419.332	1419.606	-193.887	0.381	665.934	0.297	15	0.193	R.AFQLYSSGIFTGK.C
R1/RRR1-11/2	1040.906	1041.099	-185.684	0.363	700.421	0.234	13	0.193	K.SWGESGYVR.M
R1/RRR1-22/2	1419.344	1419.606	-185.518	0.253	556.531	0.341	14	0.193	R.AFQLYSSGIFTGK.C
R1/RRR1-15/2	1420.287	1419.606	-225.739	0.301	639.526	0.291	16	0.192	-.AFQLYSSGIFTGK.-
R1/RRR1-11/2	1040.973	1041.099	-120.630	0.296	931.423	0.208	14	0.192	K.SWGESGYVR.M
R1/RRR1-14/2	1041.032	1041.099	-63.934	0.304	778.846	0.210	14	0.192	K.SWGESGYVR.M
R1/RRR1-10/2	1419.768	1419.606	114.211	0.263	438.494	0.291	13	0.191	R.AFQLYSSGIFTGK.C
R1/RRR1-14/2	1418.879	1419.606	-1221.071	0.257	551.900	0.264	15	0.191	R.AFQLYSSGIFTGK.C
R1/RRR1-12/2	1334.190	1334.536	-260.403	0.405	749.784	0.287	14	0.190	K.CGIAVEPSYPLK.K
R1/RRR1-13/2	1040.968	1041.099	-125.805	0.263	864.459	0.192	14	0.190	K.SWGESGYVR.M
R1/RRR1-13/2	1041.968	1041.099	-125.332	0.259	767.604	0.210	13	0.190	K.SWGESGYVR.M
R1/RRR1-12/2	1040.875	1041.099	-215.332	0.296	797.972	0.199	14	0.190	-.SWGESGYVR.-
R1/RRR1-15/2	1333.887	1334.536	-1240.037	0.327	736.066	0.263	14	0.189	K.CGIAVEPSYPLK.K
R1/RRR1-12/2	1040.959	1041.099	-134.040	0.374	767.727	0.184	13	0.189	K.SWGESGYVR.M
R1/RRR1-17/2	1418.576	1419.606	-1435.206	0.220	661.513	0.237	15	0.188	R.AFQLYSSGIFTGK.C
R1/RRR1-11/2	1418.578	1419.606	-1433.996	0.188	543.912	0.322	13	0.188	R.AFQLYSSGIFTGK.C
R1/RRR1-13/2	1040.813	1041.099	-275.339	0.258	973.242	0.128	15	0.187	K.SWGESGYVR.M
R1/RRR1-23/2	1420.040	1419.606	306.375	0.200	630.442	0.109	15	0.185	R.AFQLYSSGIFTGK.C
R1/RRR1-13/3	1541.086	1539.719	239.280	0.439	1464.947	0.432	29	0.153	K.AVANQPVSVAIEAGGR.A
R1/RRR1-11/3	1539.465	1539.719	-165.205	0.334	745.567	0.199	24	0.067	K.AVANQPVSVAIEAGGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1769.979	1769.936	24.584	0.501	2096.403	0.566	23	0.400	R.ILNPQYLSQSSDTFR.D
R1/RRR1-17/2	1455.149	1455.595	-307.584	0.509	2169.187	0.536	22	0.399	K.GVISLDTSGSSYLR.A
R1/RRR1-17/2	1456.123	1455.595	-325.120	0.560	2054.957	0.539	21	0.378	K.GVISLDTSGSSYLR.A
R1/RRR1-17/2	1455.334	1455.595	-180.088	0.482	1734.084	0.545	20	0.325	K.GVISLDTSGSSYLR.A
R1/RRR1-16/2	1981.190	1979.268	-39.837	0.489	1287.924	0.509	21	0.254	K.IFVDTGAVVTFGLNALQGR.Q
R1/RRR1-16/2	1002.448	1003.180	-1732.595	0.404	1325.519	0.289	15	0.220	K.AIQAFSPLR.I
R1/RRR1-16/2	1002.921	1003.180	-259.128	0.440	1188.498	0.338	13	0.217	K.AIQAFSPLR.I
R1/RRR1-3/2	1844.542	1843.924	-207.338	0.593	2752.750	0.585	26	0.560	R.LPQDLSDEIEEDPTGGK.I
R1/RRR1-3/2	985.063	985.206	-145.623	0.463	1111.606	0.318	17	0.211	R.LLAGVGSVLR.L
R1/RRR1-3/2	1559.656	1558.867	-135.423	0.409	972.788	0.378	19	0.208	R.SM*LPAEPIAVWTVK.K
R1/RRR1-1/2	1357.531	1356.509	16.450	0.325	732.857	0.357	15	0.193	R.FLAVGSYDNTIR.I
R1/RRR1-7/2	1308.189	1307.434	-188.084	0.471	1809.328	0.511	19	0.329	R.VDAAEVFDTIAR.R
R1/RRR1-7/2	1466.392	1466.835	-303.138	0.459	1268.361	0.538	19	0.264	K.LIFVDPALLPVLR.D
R1/RRR1-7/2	1466.662	1466.835	-118.425	0.453	1180.270	0.556	18	0.258	K.LIFVDPALLPVLR.D
R1/RRR1-7/2	1274.990	1274.492	391.549	0.412	1089.129	0.515	16	0.239	R.LASALVSSLGISR.G
R1/RRR1-7/2	1462.382	1463.621	-1535.466	0.430	1123.905	0.485	18	0.238	R.RVDAAEVFDTIAR.R
R1/RRR1-1/2	1467.236	1466.835	274.073	0.387	1267.725	0.421	17	0.236	K.LIFVDPALLPVLR.D
R1/RRR1-7/2	1308.198	1307.434	-181.064	0.389	903.026	0.504	15	0.222	R.VDAAEVFDTIAR.R
R1/RRR1-2/2	1466.788	1466.835	-32.104	0.387	962.151	0.413	17	0.215	K.LIFVDPALLPVLR.D
R1/RRR1-2/2	1466.658	1466.835	-121.264	0.302	884.533	0.382	15	0.203	K.LIFVDPALLPVLR.D
R1/RRR1-7/2	1273.772	1274.492	-1354.310	0.277	381.845	0.460	15	0.196	R.LASALVSSLGISR.G
R1/RRR1-14/2	1467.566	1466.835	-184.427	0.349	542.483	0.363	14	0.194	K.LIFVDPALLPVLR.D
R1/RRR1-2/2	1275.345	1274.492	-116.126	0.314	745.213	0.302	16	0.191	R.LASALVSSLGISR.G
R1/RRR1-7/2	1274.441	1274.492	-40.216	0.328	369.338	0.421	12	0.187	-.LASALVSSLGISR.-
R1/RRR1-2/2	1466.264	1466.835	-1074.643	0.277	771.000	0.204	15	0.185	K.LIFVDPALLPVLR.D
R1/RRR1-9/2	1466.542	1466.835	-201.003	0.263	432.670	0.295	12	0.184	-.LIFVDPALLPVLR.-
R1/RRR1-5/2	1611.739	1610.835	-59.983	0.534	2693.303	0.527	22	0.510	R.NGILEAYSGILQGFK.S
R1/RRR1-5/2	1338.403	1337.452	-36.739	0.566	1554.930	0.560	19	0.306	R.VVCEATQSTDVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1514.658	1513.764	-70.618	0.541	1450.800	0.606	21	0.303	K.GLLLQTLSSPVASAR.S
R1/RRR1-5/2	1610.410	1610.835	-265.157	0.382	1622.627	0.524	20	0.300	R.NGILEAYSGILQGFK.S
R1/RRR1-5/2	1337.231	1337.452	-165.504	0.532	1690.005	0.474	19	0.299	R.VVCEATQSTDVK.I
R1/RRR1-5/2	1513.518	1513.764	-163.377	0.437	1411.644	0.561	21	0.284	K.GLLLQTLSSPVASAR.S
R1/RRR1-5/2	1367.224	1366.502	-204.052	0.517	1520.749	0.482	17	0.278	R.TAAYETLNEVVR.C
R1/RRR1-5/2	1336.976	1337.452	-356.932	0.475	1611.429	0.432	19	0.278	R.VVCEATQSTDVK.I
R1/RRR1-4/2	1610.917	1610.835	51.104	0.433	1323.697	0.443	19	0.245	R.NGILEAYSGILQGFK.S
R1/RRR1-2/2	1337.452	1337.452	0.036	0.455	1260.493	0.437	18	0.242	R.VVCEATQSTDVK.I
R1/RRR1-2/2	1513.841	1513.764	50.499	0.400	1086.643	0.398	19	0.218	K.GLLLQTLSSPVASAR.S
R1/RRR1-5/2	1365.520	1366.502	-1455.733	0.308	1099.584	0.300	17	0.204	R.TAAYETLNEVVR.C
R1/RRR1-1/2	1610.823	1610.835	-7.495	0.325	647.668	0.376	17	0.194	R.NGILEAYSGILQGFK.S
R1/RRR1-5/2	1365.489	1366.502	-1478.361	0.270	688.962	0.184	16	0.183	R.TAAYETLNEVVR.C
R1/RRR1-4/2	1579.208	1579.672	-294.702	0.542	2377.357	0.477	24	0.420	K.VM*ANADTPEDATTAR.Q
R1/RRR1-4/2	1580.599	1579.672	-46.564	0.453	905.547	0.522	18	0.226	K.VM*ANADTPEDATTAR.Q
R1/RRR1-4/2	970.893	971.048	-160.233	0.414	999.036	0.370	13	0.212	R.SDFEGIFR.A
R1/RRR1-19/3	1699.661	1698.904	-143.547	0.510	2049.180	0.487	29	0.286	R.ILVDHSIVEGFAQGGR.T
R1/RRR1-9/2	1889.840	1889.096	-135.671	0.516	1542.299	0.500	23	0.284	K.SFDGLDVSPGSVVPLDVGK.A
R1/RRR1-19/2	1831.895	1832.090	-107.179	0.513	805.806	0.467	24	0.217	R.VYGSLVPVLDGENLSIR.I
R1/RRR1-19/2	1831.390	1832.090	-931.055	0.454	588.363	0.498	21	0.210	R.VYGSLVPVLDGENLSIR.I
R1/RRR1-18/2	1831.289	1832.090	-986.800	0.445	480.330	0.398	20	0.197	R.VYGSLVPVLDGENLSIR.I
R1/RRR1-19/2	1830.797	1832.090	-1256.442	0.381	579.028	0.342	21	0.194	R.VYGSLVPVLDGENLSIR.I
R1/RRR1-9/2	1114.714	1115.267	-1397.630	0.337	864.104	0.263	15	0.191	K.GWASLQSIPR.T
R1/RRR1-19/3	1697.920	1698.904	-1172.232	0.452	1195.902	0.467	25	0.135	R.ILVDHSIVEGFAQGGR.T
R1/RRR1-10/2	1356.172	1356.467	-217.813	0.477	1671.652	0.518	20	0.310	K.TLEAEAAHGTVTR.H
R1/RRR1-10/2	1357.109	1356.467	-264.666	0.538	900.696	0.637	18	0.253	K.TLEAEAAHGTVTR.H
R1/RRR1-10/2	1774.596	1775.079	-272.706	0.548	1376.899	0.448	20	0.251	R.NILNGTVFREPILCK.N
R1/RRR1-10/2	1356.059	1356.467	-301.709	0.521	1048.607	0.531	19	0.244	K.TLEAEAAHGTVTR.H
R1/RRR1-10/2	1774.633	1775.079	-251.658	0.525	1144.100	0.438	19	0.228	R.NILNGTVFREPILCK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1078.108	1077.302	-180.526	0.409	1075.382	0.442	13	0.225	K.DLALLIHGPK.V
R1/RRR1-10/2	1776.560	1775.079	271.563	0.527	1087.491	0.350	19	0.207	R.NILNGTVFREPILCK.N
R1/RRR1-6/2	1435.938	1434.662	192.478	0.555	2009.240	0.480	20	0.348	R.NVLGGLSLEGFLSK.W
R1/RRR1-6/2	1106.297	1106.300	-2.281	0.490	1703.572	0.525	17	0.319	K.TALLQSFLGR.Q
R1/RRR1-6/2	1889.239	1889.099	74.359	0.542	1553.914	0.528	21	0.293	R.APDQTLELTGQAIDFLR.G
R1/RRR1-6/2	1106.087	1106.300	-192.785	0.459	1398.702	0.527	15	0.277	K.TALLQSFLGR.Q
R1/RRR1-6/2	1433.606	1434.662	-1438.692	0.275	968.801	0.474	15	0.215	R.NVLGGLSLEGFLSK.W
R1/RRR1-6/2	1331.419	1332.533	-1592.978	0.360	759.194	0.370	14	0.198	K.GRLETTWTVLR.K
R1/RRR1-6/2	1332.723	1332.533	142.617	0.322	681.789	0.344	15	0.194	K.GRLETTWTVLR.K
R1/RRR1-6/2	1433.772	1434.662	-1322.389	0.293	504.572	0.398	15	0.191	R.NVLGGLSLEGFLSK.W
R1/RRR1-10/3	1505.010	1504.756	169.074	0.617	3054.787	0.398	31	0.487	K.KVSPQLIAEYTVR.A
R1/RRR1-10/3	1504.543	1504.756	-141.656	0.584	2676.036	0.458	31	0.401	K.KVSPQLIAEYTVR.A
R1/RRR1-1/3	1505.842	1504.756	57.467	0.548	2731.425	0.408	30	0.393	K.KVSPQLIAEYTVR.A
R1/RRR1-11/2	1505.695	1504.756	-40.707	0.577	2000.401	0.484	22	0.347	K.KVSPQLIAEYTVR.A
R1/RRR1-10/3	1504.672	1504.756	-55.716	0.585	2519.596	0.410	29	0.339	K.KVSPQLIAEYTVR.A
R1/RRR1-16/2	1504.311	1504.756	-296.718	0.470	1839.592	0.514	22	0.332	K.KVSPQLIAEYTVR.A
R1/RRR1-10/2	1503.874	1504.756	-1254.885	0.528	1754.270	0.554	21	0.331	K.KVSPQLIAEYTVR.A
R1/RRR1-12/3	1505.474	1504.756	-187.478	0.459	2484.982	0.392	30	0.316	K.KVSPQLIAEYTVR.A
R1/RRR1-11/2	1505.401	1504.756	-236.236	0.564	1789.290	0.471	21	0.310	K.KVSPQLIAEYTVR.A
R1/RRR1-11/2	1504.338	1504.756	-278.318	0.515	1578.312	0.522	21	0.298	K.KVSPQLIAEYTVR.A
R1/RRR1-10/2	1503.767	1504.756	-1326.542	0.471	1640.674	0.462	20	0.288	K.KVSPQLIAEYTVR.A
R1/RRR1-12/3	1503.781	1504.756	-1317.013	0.464	2316.719	0.342	29	0.255	K.KVSPQLIAEYTVR.A
R1/RRR1-10/2	1504.023	1504.756	-1155.527	0.505	1282.436	0.464	19	0.249	K.KVSPQLIAEYTVR.A
R1/RRR1-2/3	1505.070	1504.756	209.091	0.442	2078.277	0.387	27	0.230	K.KVSPQLIAEYTVR.A
R1/RRR1-11/2	1376.075	1376.583	-1098.809	0.422	641.383	0.533	17	0.219	K.VSPQLIAEYTVR.A
R1/RRR1-10/2	1376.094	1376.583	-356.573	0.399	622.587	0.503	17	0.213	K.VSPQLIAEYTVR.A
R1/RRR1-10/2	1376.231	1376.583	-256.274	0.394	599.787	0.474	16	0.208	K.VSPQLIAEYTVR.A
R1/RRR1-10/2	1297.045	1296.501	-352.440	0.352	697.916	0.402	18	0.207	K.KPWALSFSFGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1297.255	1296.501	-190.519	0.396	670.918	0.383	18	0.206	K.KPWALSFSFGR.A
R1/RRR1-11/2	1295.423	1296.501	-1609.455	0.322	674.332	0.424	17	0.206	K.KPWALSFSFGR.A
R1/RRR1-11/2	1296.551	1296.501	38.660	0.365	550.016	0.399	16	0.203	K.KPWALSFSFGR.A
R1/RRR1-10/2	1296.117	1296.501	-297.053	0.287	543.193	0.377	16	0.198	K.KPWALSFSFGR.A
R1/RRR1-11/3	1504.391	1504.756	-243.240	0.456	1909.130	0.400	29	0.197	K.KVSPQLIAEYTVR.A
R1/RRR1-9/2	1504.288	1504.756	-312.105	0.353	370.347	0.338	14	0.195	K.KVSPQLIAEYTVR.A
R1/RRR1-11/2	1376.071	1376.583	-1101.926	0.357	528.012	0.312	15	0.192	K.VSPQLIAEYTVR.A
R1/RRR1-11/2	1295.312	1296.501	-1695.230	0.233	351.388	0.322	12	0.191	K.KPWALSFSFGR.A
R1/RRR1-12/3	1504.995	1504.756	159.557	0.517	1792.486	0.414	27	0.188	K.KVSPQLIAEYTVR.A
R1/RRR1-2/3	1505.268	1504.756	-324.763	0.510	1886.023	0.338	26	0.179	K.KVSPQLIAEYTVR.A
R1/RRR1-11/3	1296.593	1296.501	70.896	0.569	1394.440	0.424	24	0.135	K.KPWALSFSFGR.A
R1/RRR1-11/3	1296.209	1296.501	-226.199	0.518	1327.028	0.400	22	0.125	K.KPWALSFSFGR.A
R1/RRR1-11/3	1296.605	1296.501	79.960	0.536	1219.515	0.419	23	0.117	K.KPWALSFSFGR.A
R1/RRR1-3/3	1504.583	1504.756	-115.531	0.405	1599.947	0.219	27	0.104	K.KVSPQLIAEYTVR.A
R1/RRR1-13/3	1505.587	1504.756	-112.201	0.334	900.449	0.296	23	0.083	K.KVSPQLIAEYTVR.A
R1/RRR1-5/3	1506.142	1504.756	256.823	0.435	670.743	0.318	23	0.081	-.KVSPQLIAEYTVR.-
R1/RRR1-3/3	1504.833	1504.756	51.444	0.385	1306.825	0.184	26	0.078	K.KVSPQLIAEYTVR.A
R1/RRR1-4/3	1505.351	1504.756	-269.722	0.311	1070.609	0.088	23	0.064	-.KVSPQLIAEYTVR.-
R1/RRR1-7/2	974.188	974.137	52.646	0.489	980.535	0.466	15	0.228	K.AGANVVLTTK.G
R1/RRR1-7/2	973.961	974.137	-180.659	0.341	818.136	0.456	14	0.212	K.AGANVVLTTK.G
R1/RRR1-15/2	1284.503	1285.472	-1537.446	0.323	880.802	0.377	15	0.203	K.VLVELAELQDR.E
R1/RRR1-7/2	1100.914	1101.275	-328.926	0.395	727.933	0.345	15	0.199	R.IADDDVILVK.G
R1/RRR1-12/2	974.406	974.137	276.799	0.326	565.086	0.375	13	0.196	K.AGANVVLTTK.G
R1/RRR1-13/2	1561.601	1560.863	-168.226	0.301	1250.449	0.152	17	0.194	-.IIQFATEAAITILR.-
R1/RRR1-16/2	1285.812	1285.472	265.704	0.313	663.937	0.346	13	0.191	K.VLVELAELQDR.E
R1/RRR1-7/2	1562.117	1560.863	163.685	0.353	828.222	0.284	16	0.188	K.IIQFATEAAITILR.I
R1/RRR1-7/2	1100.686	1101.275	-1448.479	0.286	559.337	0.239	13	0.185	-.IADDDVILVK.-
R1/RRR1-4/2	1222.266	1222.329	-51.850	0.446	1965.949	0.375	19	0.314	K.SFNSELAAAPSK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1198.389	1197.406	-14.468	0.500	1508.182	0.403	18	0.261	K.IPADLIINAEK.A
R1/RRR1-4/2	1133.890	1134.265	-332.210	0.421	1501.678	0.338	19	0.245	K.LSSAIEASISR.G
R1/RRR1-4/2	998.400	999.149	-1757.709	0.369	1100.154	0.412	14	0.224	R.GQIGIQQVR.G
R1/RRR1-4/2	998.945	999.149	-205.066	0.436	989.120	0.425	14	0.221	R.GQIGIQQVR.G
R1/RRR1-4/2	1133.474	1134.265	-1585.026	0.328	1169.624	0.304	18	0.210	K.LSSAIEASISR.G
R1/RRR1-12/2	1840.154	1840.028	68.558	0.596	3708.123	0.578	29	0.848	R.AFIAGVADDNGYGWAIAK.A
R1/RRR1-12/2	1840.530	1840.028	-271.519	0.604	3570.384	0.570	29	0.794	R.AFIAGVADDNGYGWAIAK.A
R1/RRR1-13/2	1839.196	1840.028	-998.800	0.515	3083.745	0.467	27	0.588	R.AFIAGVADDNGYGWAIAK.A
R1/RRR1-12/2	1172.985	1172.317	-283.561	0.500	546.888	0.482	17	0.213	R.VNTISAGPLGSR.A
R1/RRR1-12/2	1172.210	1172.317	-91.561	0.477	552.336	0.471	17	0.212	R.VNTISAGPLGSR.A
R1/RRR1-12/2	1172.048	1172.317	-229.884	0.444	583.667	0.450	17	0.210	R.VNTISAGPLGSR.A
R1/RRR1-12/2	1113.141	1113.205	-57.593	0.428	664.021	0.411	16	0.208	R.YAGSSNWTVK.E
R1/RRR1-13/2	1113.070	1113.205	-120.846	0.460	537.565	0.452	14	0.208	R.YAGSSNWTVK.E
R1/RRR1-13/2	1171.990	1172.317	-279.832	0.426	383.219	0.452	14	0.203	R.VNTISAGPLGSR.A
R1/RRR1-12/2	1112.444	1113.205	-1587.806	0.296	659.902	0.421	15	0.202	R.YAGSSNWTVK.E
R1/RRR1-13/2	1171.618	1172.317	-1454.419	0.404	349.742	0.460	13	0.201	R.VNTISAGPLGSR.A
R1/RRR1-13/2	1171.369	1172.317	-1667.644	0.392	421.603	0.376	16	0.201	R.VNTISAGPLGSR.A
R1/RRR1-12/2	1112.379	1113.205	-1646.123	0.217	693.790	0.430	15	0.197	R.YAGSSNWTVK.E
R1/RRR1-6/2	1847.186	1848.002	-985.930	0.482	1891.829	0.404	23	0.306	K.ESSQESIEGDTAILLVR.A
R1/RRR1-6/2	1847.527	1848.002	-257.568	0.530	1597.872	0.454	21	0.277	K.ESSQESIEGDTAILLVR.A
R1/RRR1-5/2	1617.484	1617.778	-182.246	0.456	538.604	0.447	17	0.204	K.DLDLDIPYDEPALK.A
R1/RRR1-5/2	1618.253	1617.778	294.497	0.499	542.672	0.445	17	0.204	K.DLDLDIPYDEPALK.A
R1/RRR1-3/2	1618.487	1617.778	-180.620	0.435	749.334	0.368	19	0.202	K.DLDLDIPYDEPALK.A
R1/RRR1-1/2	1617.573	1617.778	-126.981	0.395	448.460	0.385	15	0.195	K.DLDLDIPYDEPALK.A
R1/RRR1-5/2	1032.137	1033.120	-1926.887	0.334	585.378	0.351	13	0.195	K.FPGDDGVLGR.A
R1/RRR1-6/2	1033.905	1033.120	-207.902	0.283	1169.338	0.188	16	0.194	K.FPGDDGVLGR.A
R1/RRR1-6/2	1617.259	1617.778	-942.437	0.380	450.166	0.346	16	0.194	K.DLDLDIPYDEPALK.A
R1/RRR1-6/2	1617.111	1617.778	-1033.909	0.310	546.251	0.336	17	0.193	K.DLDLDIPYDEPALK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1033.040	1033.120	-77.111	0.343	814.449	0.249	14	0.190	K.FPGDDGVLGR.A
R1/RRR1-6/2	1306.193	1306.634	-338.629	0.312	1027.136	0.205	18	0.189	R.IMSTLACVVALK.S
R1/RRR1-6/2	1678.385	1678.891	-900.381	0.560	2190.776	0.555	23	0.406	K.NQVAM*NPINTVFDAK.R
R1/RRR1-6/2	1663.382	1662.892	295.193	0.565	1998.425	0.565	23	0.374	K.NQVAMNPINTVFDAK.R
R1/RRR1-6/2	1678.363	1678.891	-913.596	0.545	1954.315	0.551	22	0.361	K.NQVAM*NPINTVFDAK.R
R1/RRR1-6/2	1679.226	1678.891	199.955	0.591	1947.704	0.522	22	0.348	K.NQVAM*NPINTVFDAK.R
R1/RRR1-14/2	1679.357	1678.891	277.804	0.541	1982.289	0.480	22	0.341	K.NQVAM*NPINTVFDAK.R
R1/RRR1-6/2	1229.063	1229.325	-214.139	0.480	1843.471	0.398	18	0.300	R.VEIIANDQGNR.I
R1/RRR1-6/2	1661.664	1662.892	-1344.687	0.390	1719.192	0.467	21	0.298	K.NQVAMNPINTVFDAK.R
R1/RRR1-6/2	1229.031	1229.325	-239.847	0.484	1655.488	0.409	19	0.279	R.VEIIANDQGNR.I
R1/RRR1-6/2	1819.506	1819.078	235.612	0.544	1332.601	0.561	22	0.275	K.NQVAMNPINTVFDAKR.L
R1/RRR1-6/2	1229.011	1229.325	-256.289	0.495	1650.809	0.386	19	0.272	R.VEIIANDQGNR.I
R1/RRR1-6/2	1834.227	1835.078	-1012.227	0.499	1204.903	0.526	22	0.254	K.NQVAM*NPINTVFDAKR.L
R1/RRR1-6/2	1834.428	1835.078	-902.189	0.545	1098.226	0.509	22	0.241	K.NQVAM*NPINTVFDAKR.L
R1/RRR1-6/2	1818.187	1819.078	-1043.338	0.436	1056.508	0.482	20	0.231	K.NQVAMNPINTVFDAKR.L
R1/RRR1-6/2	1834.383	1835.078	-926.840	0.555	867.595	0.480	23	0.222	K.NQVAM*NPINTVFDAKR.L
R1/RRR1-8/2	1679.321	1678.891	256.448	0.469	239.924	0.425	16	0.201	K.NQVAM*NPINTVFDAK.R
R1/RRR1-4/2	1688.284	1687.920	216.432	0.504	1841.159	0.545	21	0.344	R.AVSDEIKNVIIASATR.K
R1/RRR1-4/2	1711.776	1710.897	-70.783	0.453	1107.573	0.429	16	0.224	-.IAICVFDDIAEQCR.-
R1/RRR1-4/2	1486.286	1486.653	-247.183	0.384	1102.372	0.381	19	0.216	R.LASSLSSPATPADLR.A
R1/RRR1-4/2	1486.384	1486.653	-180.939	0.412	1047.661	0.392	19	0.215	-.LASSLSSPATPADLR.-
R1/RRR1-4/2	1486.404	1486.653	-167.922	0.297	1110.765	0.270	19	0.202	-.LASSLSSPATPADLR.-
R1/RRR1-4/3	1236.090	1236.402	-253.792	0.489	1132.775	0.429	22	0.113	K.LNNVITHPEAK.H
R1/RRR1-4/3	1236.204	1236.402	-160.916	0.475	1202.964	0.391	21	0.111	K.LNNVITHPEAK.H
R1/RRR1-4/3	1236.746	1236.402	279.007	0.450	1113.354	0.426	21	0.111	K.LNNVITHPEAK.H
R1/RRR1-3/3	1236.142	1236.402	-211.587	0.419	822.970	0.414	19	0.094	K.LNNVITHPEAK.H
R1/RRR1-4/2	1476.474	1476.703	-154.954	0.526	1792.673	0.507	19	0.324	R.VLQQASQIFQSVK.I
R1/RRR1-4/3	1661.528	1661.754	-136.820	0.526	2076.612	0.515	31	0.289	K.YGASHLELENEKDR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1475.949	1476.703	-1191.691	0.384	1590.087	0.392	18	0.264	R.VLQQASQIFQSVK.I
R1/RRR1-4/3	1661.922	1661.754	101.245	0.555	1748.928	0.522	27	0.232	K.YGASHLELENEKDR.N
R1/RRR1-3/2	1566.198	1564.767	276.142	0.469	1092.542	0.459	16	0.228	K.IATELSLWQEAFR.S
R1/RRR1-4/2	1563.959	1564.767	-1159.076	0.309	636.038	0.376	13	0.190	K.IATELSLWQEAFR.S
R1/RRR1-4/3	1971.515	1970.007	-250.257	0.397	1070.716	0.527	31	0.137	R.GGDGGSSAGGQRPAVAPEQDR.W
R1/RRR1-3/3	1970.027	1970.007	10.086	0.439	1145.905	0.479	32	0.134	R.GGDGGSSAGGQRPAVAPEQDR.W
R1/RRR1-4/3	1969.817	1970.007	-96.760	0.499	888.694	0.553	31	0.131	R.GGDGGSSAGGQRPAVAPEQDR.W
R1/RRR1-16/2	1700.092	1699.882	123.394	0.495	2977.424	0.536	25	0.593	K.AITEIFAEAGFSDVTK.N
R1/RRR1-16/2	1699.655	1699.882	-134.463	0.513	2844.694	0.551	25	0.563	K.AITEIFAEAGFSDVTK.N
R1/RRR1-16/2	1699.274	1699.882	-949.404	0.407	2425.268	0.505	23	0.440	K.AITEIFAEAGFSDVTK.N
R1/RRR1-16/2	1191.302	1190.334	-26.990	0.618	2164.050	0.433	19	0.355	K.NFLAVLADNGR.L
R1/RRR1-16/2	1189.880	1190.334	-382.638	0.485	2041.201	0.422	18	0.335	K.NFLAVLADNGR.L
R1/RRR1-16/2	1190.876	1190.334	-385.403	0.623	2085.929	0.407	18	0.331	K.NFLAVLADNGR.L
R1/RRR1-17/2	1190.087	1190.334	-207.778	0.593	1964.131	0.454	18	0.330	K.NFLAVLADNGR.L
R1/RRR1-17/2	1191.014	1190.334	-269.297	0.611	1982.517	0.349	18	0.296	K.NFLAVLADNGR.L
R1/RRR1-17/2	1189.533	1190.334	-1518.254	0.452	1610.699	0.424	17	0.275	K.NFLAVLADNGR.L
R1/RRR1-16/2	1066.926	1067.262	-315.650	0.436	601.764	0.479	12	0.212	K.SPLFSQFIK.D
R1/RRR1-17/2	1067.184	1067.262	-73.726	0.409	596.079	0.402	12	0.204	K.SPLFSQFIK.D
R1/RRR1-17/2	1067.197	1067.262	-61.105	0.360	642.166	0.375	12	0.201	K.SPLFSQFIK.D
R1/RRR1-17/2	1189.517	1190.334	-1532.067	0.399	699.995	0.327	15	0.198	K.NFLAVLADNGR.L
R1/RRR1-16/2	1066.662	1067.262	-1504.783	0.404	509.149	0.386	11	0.197	-.SPLFSQFIK.-
R1/RRR1-17/2	1067.222	1067.262	-38.044	0.365	587.004	0.290	12	0.194	K.SPLFSQFIK.D
R1/RRR1-16/2	1067.069	1067.262	-181.475	0.318	446.816	0.365	10	0.193	-.SPLFSQFIK.-
R1/RRR1-23/3	1718.129	1717.776	205.966	0.620	2461.936	0.491	31	0.378	K.HGYIGEFEELDDHR.S
R1/RRR1-22/3	1718.450	1717.776	-190.712	0.530	1833.062	0.448	29	0.213	K.HGYIGEFEELDDHR.S
R1/RRR1-23/2	898.390	899.073	-1878.899	0.388	716.652	0.412	12	0.204	K.IVVQLNGR.L
R1/RRR1-22/2	961.127	961.095	34.190	0.361	751.817	0.390	13	0.204	R.TSVLNDALK.S
R1/RRR1-22/2	960.941	961.095	-160.236	0.326	663.045	0.386	13	0.200	R.TSVLNDALK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/2	960.801	961.095	-306.806	0.196	425.812	0.281	10	0.175	-.TSVLNDALK.-
R1/RRR1-22/3	1717.628	1717.776	-86.517	0.498	1254.094	0.448	24	0.135	K.HGYIGEFEELDDHR.S
R1/RRR1-15/2	1868.506	1868.124	204.665	0.546	2921.607	0.616	30	0.619	R.LQAQSALAEAAAASGVALPK.G
R1/RRR1-15/2	1867.509	1868.124	-867.352	0.504	2545.981	0.541	29	0.484	R.LQAQSALAEAAAASGVALPK.G
R1/RRR1-15/3	1868.144	1868.124	10.374	0.461	2683.778	0.465	39	0.445	R.LQAQSALAEAAAASGVALPK.G
R1/RRR1-15/3	1867.990	1868.124	-72.113	0.472	2140.310	0.454	35	0.294	R.LQAQSALAEAAAASGVALPK.G
R1/RRR1-15/2	1480.210	1480.565	-240.670	0.491	1006.028	0.502	22	0.236	K.QYLAGGQDTSNLGR.G
R1/RRR1-15/2	1480.132	1480.565	-293.707	0.467	759.253	0.503	20	0.220	K.QYLAGGQDTSNLGR.G
R1/RRR1-15/2	1480.268	1480.565	-201.042	0.463	711.235	0.476	19	0.213	K.QYLAGGQDTSNLGR.G
R1/RRR1-15/2	1102.002	1102.222	-200.388	0.295	710.833	0.417	13	0.198	R.YSGSVDAFKK.I
R1/RRR1-3/2	1664.402	1664.798	-238.606	0.508	1795.857	0.504	24	0.322	K.FTPSAVAIDLNSGESR.E
R1/RRR1-3/2	1664.075	1664.798	-1038.943	0.476	1778.863	0.472	25	0.310	K.FTPSAVAIDLNSGESR.E
R1/RRR1-3/2	1664.504	1664.798	-177.392	0.530	1539.286	0.488	23	0.281	K.FTPSAVAIDLNSGESR.E
R1/RRR1-3/2	1155.032	1155.288	-222.458	0.458	1695.258	0.367	19	0.273	K.FQVTGFSVGGR.V
R1/RRR1-3/2	1155.114	1155.288	-151.320	0.478	1264.637	0.399	18	0.236	K.FQVTGFSVGGR.V
R1/RRR1-3/2	1173.298	1172.272	21.746	0.433	1146.567	0.411	16	0.229	R.AVTDNLGYYR.L
R1/RRR1-3/2	1172.105	1172.272	-143.068	0.450	843.797	0.459	15	0.219	R.AVTDNLGYYR.L
R1/RRR1-3/2	1154.568	1155.288	-1494.243	0.358	1173.140	0.356	16	0.219	K.FQVTGFSVGGR.V
R1/RRR1-3/2	1171.877	1172.272	-338.158	0.399	979.288	0.358	16	0.210	R.AVTDNLGYYR.L
R1/RRR1-3/2	1665.860	1664.798	37.439	0.334	894.314	0.294	20	0.194	K.FTPSAVAIDLNSGESR.E
R1/RRR1-3/2	1666.090	1664.798	175.516	0.394	470.740	0.298	17	0.188	K.FTPSAVAIDLNSGESR.E
R1/RRR1-3/3	1793.691	1795.057	-1322.895	0.386	854.550	0.481	26	0.105	K.AM*VTLTHGPENVKPQR.K
R1/RRR1-3/3	1794.311	1795.057	-975.868	0.444	663.833	0.504	24	0.102	K.AM*VTLTHGPENVKPQR.K
R1/RRR1-14/2	1798.697	1798.032	-186.892	0.573	2454.342	0.606	26	0.486	K.KVLQFAGIEDVFTSSR.G
R1/RRR1-14/2	1669.771	1669.860	-53.132	0.543	2460.334	0.593	24	0.477	K.VLQFAGIEDVFTSSR.G
R1/RRR1-13/2	1798.548	1798.032	-270.232	0.582	2381.171	0.595	25	0.464	K.KVLQFAGIEDVFTSSR.G
R1/RRR1-14/2	1669.498	1669.860	-217.270	0.537	2244.160	0.573	23	0.422	K.VLQFAGIEDVFTSSR.G
R1/RRR1-13/2	1670.385	1669.860	-285.029	0.515	2226.890	0.571	23	0.418	K.VLQFAGIEDVFTSSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1670.471	1669.860	-233.122	0.563	2045.540	0.561	22	0.378	K.VLQFAGIEDVFTSSR.G
R1/RRR1-13/2	1669.632	1669.860	-136.441	0.470	1988.450	0.534	23	0.360	K.VLQFAGIEDVFTSSR.G
R1/RRR1-11/2	1670.343	1669.860	290.297	0.424	1992.599	0.492	21	0.346	K.VLQFAGIEDVFTSSR.G
R1/RRR1-13/2	1798.584	1798.032	-250.009	0.553	1604.100	0.584	22	0.316	K.KVLQFAGIEDVFTSSR.G
R1/RRR1-13/2	1796.523	1798.032	-1959.273	0.459	1638.691	0.494	21	0.294	K.KVLQFAGIEDVFTSSR.G
R1/RRR1-1/2	1670.123	1669.860	158.305	0.376	834.185	0.427	17	0.209	K.VLQFAGIEDVFTSSR.G
R1/RRR1-2/2	1671.081	1669.860	132.717	0.447	609.788	0.503	15	0.209	K.VLQFAGIEDVFTSSR.G
R1/RRR1-12/2	1671.480	1669.860	-227.634	0.418	721.568	0.463	16	0.208	K.VLQFAGIEDVFTSSR.G
R1/RRR1-3/2	1670.315	1669.860	273.663	0.395	762.605	0.400	17	0.203	K.VLQFAGIEDVFTSSR.G
R1/RRR1-2/2	1670.384	1669.860	-285.322	0.347	628.876	0.405	16	0.199	K.VLQFAGIEDVFTSSR.G
R1/RRR1-18/2	1670.040	1669.860	108.459	0.315	417.266	0.404	14	0.195	K.VLQFAGIEDVFTSSR.G
R1/RRR1-2/2	1799.281	1798.032	138.639	0.419	440.324	0.442	13	0.192	K.KVLQFAGIEDVFTSSR.G
R1/RRR1-12/2	1671.268	1669.860	244.936	0.219	481.020	0.268	14	0.187	K.VLQFAGIEDVFTSSR.G
R1/RRR1-2/2	1670.961	1669.860	60.772	0.299	248.900	0.427	11	0.175	-.VLQFAGIEDVFTSSR.-
R1/RRR1-14/3	1797.873	1798.032	-89.057	0.456	1539.573	0.366	32	0.142	K.KVLQFAGIEDVFTSSR.G
R1/RRR1-14/3	1738.498	1738.962	-267.601	0.503	1202.212	0.466	27	0.133	K.SPFQEYTDLLAKPTK.A
R1/RRR1-14/3	1738.761	1738.962	-116.096	0.513	701.719	0.472	23	0.106	K.SPFQEYTDLLAKPTK.A
R1/RRR1-13/3	1738.869	1738.962	-53.352	0.435	735.952	0.475	23	0.104	K.SPFQEYTDLLAKPTK.A
R1/RRR1-13/3	1739.795	1738.962	-96.111	0.466	671.735	0.466	23	0.102	K.SPFQEYTDLLAKPTK.A
R1/RRR1-14/3	1739.090	1738.962	74.224	0.450	862.704	0.395	25	0.096	K.SPFQEYTDLLAKPTK.A
R1/RRR1-13/3	1738.883	1738.962	-45.325	0.361	586.900	0.430	21	0.093	K.SPFQEYTDLLAKPTK.A
R1/RRR1-19/2	1735.154	1735.790	-945.578	0.561	2626.182	0.576	23	0.514	R.WSEYDFDQVFADGR.D
R1/RRR1-19/2	1734.629	1735.790	-1249.657	0.552	2399.075	0.595	22	0.468	R.WSEYDFDQVFADGR.D
R1/RRR1-19/2	1735.493	1735.790	-171.688	0.574	2386.828	0.601	22	0.468	R.WSEYDFDQVFADGR.D
R1/RRR1-18/2	1735.434	1735.790	-205.699	0.577	2299.509	0.603	22	0.449	R.WSEYDFDQVFADGR.D
R1/RRR1-18/2	1736.296	1735.790	-285.774	0.594	2110.853	0.609	21	0.412	R.WSEYDFDQVFADGR.D
R1/RRR1-18/2	1734.687	1735.790	-1216.230	0.476	1727.605	0.542	19	0.321	R.WSEYDFDQVFADGR.D
R1/RRR1-18/2	1518.014	1517.668	228.610	0.529	1700.436	0.432	20	0.287	K.VSDTEVIGYHQLR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1517.338	1517.668	-218.078	0.443	1606.625	0.383	20	0.264	K.VSDTEVIGYHQLR.V
R1/RRR1-19/2	1516.988	1517.668	-1110.703	0.522	1314.099	0.458	20	0.252	K.VSDTEVIGYHQLR.V
R1/RRR1-19/2	1516.853	1517.668	-1200.479	0.470	1389.846	0.388	19	0.242	K.VSDTEVIGYHQLR.V
R1/RRR1-18/2	1517.017	1517.668	-1091.877	0.510	1192.567	0.445	19	0.237	K.VSDTEVIGYHQLR.V
R1/RRR1-19/2	1016.359	1017.123	-1741.226	0.303	623.786	0.365	12	0.197	K.TQHFIGGTR.W
R1/RRR1-18/2	1016.707	1017.123	-410.902	0.267	603.115	0.393	12	0.197	K.TQHFIGGTR.W
R1/RRR1-19/2	1017.204	1017.123	79.187	0.294	727.048	0.339	12	0.197	K.TQHFIGGTR.W
R1/RRR1-18/2	1016.761	1017.123	-357.896	0.347	505.482	0.350	10	0.194	K.TQHFIGGTR.W
R1/RRR1-19/2	1016.345	1017.123	-1755.104	0.287	663.159	0.283	12	0.192	K.TQHFIGGTR.W
R1/RRR1-18/2	1016.871	1017.123	-248.529	0.266	452.867	0.294	11	0.190	-.TQHFIGGTR.-
R1/RRR1-18/3	1517.218	1517.668	-297.632	0.410	734.069	0.448	24	0.096	K.VSDTEVIGYHQLR.V
R1/RRR1-19/3	1517.884	1517.668	142.191	0.372	892.448	0.421	25	0.096	K.VSDTEVIGYHQLR.V
R1/RRR1-19/3	1517.203	1517.668	-307.440	0.405	657.289	0.455	23	0.096	K.VSDTEVIGYHQLR.V
R1/RRR1-19/3	1518.579	1517.668	-58.915	0.442	802.156	0.434	26	0.096	K.VSDTEVIGYHQLR.V
R1/RRR1-18/3	1518.569	1517.668	-65.688	0.383	583.670	0.449	22	0.094	K.VSDTEVIGYHQLR.V
R1/RRR1-18/3	1517.826	1517.668	104.081	0.363	663.715	0.399	25	0.088	K.VSDTEVIGYHQLR.V
R1/RRR1-15/2	1818.501	1818.019	265.838	0.612	2686.842	0.698	27	0.589	K.ALAVGADVSLDTATGNLTK.Y
R1/RRR1-15/2	1818.426	1818.019	224.373	0.568	2579.161	0.641	26	0.533	K.ALAVGADVSLDTATGNLTK.Y
R1/RRR1-14/2	1590.520	1590.845	-205.196	0.588	1896.833	0.496	23	0.334	K.KADLIFGEIQSQIK.N
R1/RRR1-14/2	1591.433	1590.845	-260.163	0.610	1802.184	0.525	23	0.329	K.KADLIFGEIQSQIK.N
R1/RRR1-15/2	1590.555	1590.845	-183.099	0.586	1678.368	0.546	22	0.317	K.KADLIFGEIQSQIK.N
R1/RRR1-15/2	1591.338	1590.845	310.250	0.623	1737.458	0.505	22	0.311	K.KADLIFGEIQSQIK.N
R1/RRR1-15/2	1590.765	1590.845	-50.768	0.603	1667.633	0.490	22	0.298	K.KADLIFGEIQSQIK.N
R1/RRR1-15/2	1462.169	1462.673	-1031.682	0.401	1821.767	0.395	19	0.294	K.ADLIFGEIQSQIK.N
R1/RRR1-14/2	1462.092	1462.673	-1084.241	0.393	1690.210	0.382	19	0.274	K.ADLIFGEIQSQIK.N
R1/RRR1-15/2	1462.203	1462.673	-321.842	0.400	1612.271	0.406	19	0.270	K.ADLIFGEIQSQIK.N
R1/RRR1-14/2	1590.551	1590.845	-185.563	0.562	1352.355	0.502	21	0.265	K.KADLIFGEIQSQIK.N
R1/RRR1-14/2	1462.192	1462.673	-329.715	0.415	1567.939	0.361	19	0.254	K.ADLIFGEIQSQIK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1817.503	1818.019	-836.583	0.369	1206.812	0.375	22	0.220	K.ALAVGADVSLDTATGNLTK.Y
R1/RRR1-14/3	1590.332	1590.845	-954.784	0.444	1566.673	0.229	26	0.111	K.KADLIFGEIQSQIK.N
R1/RRR1-3/2	1217.925	1218.296	-305.669	0.434	1584.680	0.310	18	0.246	R.EGETAAEILER.I
R1/RRR1-3/2	1240.571	1240.473	79.684	0.539	1086.676	0.478	15	0.237	K.SKEDILLFFK.L
R1/RRR1-3/2	1243.162	1243.349	-150.451	0.492	903.137	0.479	17	0.225	K.VELSNPDAELR.L
R1/RRR1-3/2	1217.592	1218.296	-1403.223	0.288	1194.055	0.185	16	0.194	R.EGETAAEILER.I
R1/RRR1-3/3	1736.824	1736.908	-48.128	0.473	1455.206	0.551	28	0.185	R.YPDVPSFLEYVHNR.Q
R1/RRR1-3/3	1737.014	1736.908	61.519	0.461	912.270	0.487	24	0.112	R.YPDVPSFLEYVHNR.Q
R1/RRR1-14/2	1772.407	1772.962	-879.559	0.529	1464.029	0.653	26	0.317	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-13/2	1772.280	1772.962	-951.885	0.506	1530.188	0.593	26	0.308	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-13/2	1772.508	1772.962	-256.450	0.525	1384.398	0.606	25	0.292	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-13/2	1772.227	1772.962	-981.966	0.492	1296.002	0.622	24	0.284	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-13/3	1772.730	1772.962	-131.139	0.451	1292.030	0.519	34	0.158	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-13/3	1772.943	1772.962	-10.547	0.473	914.714	0.629	33	0.148	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-14/3	1772.410	1772.962	-877.976	0.411	764.532	0.594	29	0.129	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-12/3	1773.303	1772.962	192.963	0.450	908.264	0.545	33	0.127	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-13/3	1772.990	1772.962	16.075	0.428	873.651	0.536	33	0.122	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-14/3	1772.368	1772.962	-901.623	0.378	699.490	0.559	30	0.116	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-14/3	1772.796	1772.962	-93.735	0.449	682.116	0.539	30	0.115	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-12/3	1772.801	1772.962	-90.938	0.440	906.924	0.480	33	0.114	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-11/3	1773.497	1772.962	-262.631	0.385	598.496	0.516	25	0.109	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-12/3	1773.812	1772.962	-84.398	0.370	735.415	0.499	29	0.108	R.GM*GDAADLVALSGGHTVGK.-
R1/RRR1-21/2	1495.230	1495.659	-288.202	0.493	1953.762	0.586	22	0.377	K.ITLISDFGEISGSR.G
R1/RRR1-21/2	1496.102	1495.659	296.691	0.550	1762.482	0.588	22	0.345	K.ITLISDFGEISGSR.G
R1/RRR1-20/2	1495.309	1495.659	-235.211	0.455	1820.390	0.553	21	0.342	K.ITLISDFGEISGSR.G
R1/RRR1-21/3	1624.076	1623.832	150.496	0.444	1192.519	0.527	25	0.148	R.KITLISDFGEISGSR.G
R1/RRR1-21/3	1495.918	1495.659	173.498	0.428	1320.748	0.355	27	0.113	K.ITLISDFGEISGSR.G
R1/RRR1-21/3	1624.129	1623.832	183.284	0.386	833.888	0.502	23	0.108	R.KITLISDFGEISGSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/3	1495.580	1495.659	-53.394	0.330	1094.958	0.337	25	0.090	K.ITLISDFGEISGSR.G
R1/RRR1-21/2	1535.418	1535.837	-273.159	0.377	864.102	0.233	19	0.076	K.IM*LTHVLHGQGSII.-
R1/RRR1-21/2	1535.119	1535.837	-1121.986	0.354	712.704	0.215	18	0.072	K.IM*LTHVLHGQGSII.-
R1/RRR1-16/2	1583.317	1582.734	-264.049	0.588	2837.710	0.547	22	0.554	R.SNVGELLEYSLETK.K
R1/RRR1-16/2	1582.019	1582.734	-1087.258	0.397	2583.256	0.430	22	0.444	R.SNVGELLEYSLETK.K
R1/RRR1-16/2	1582.208	1582.734	-967.494	0.403	2381.524	0.409	22	0.393	R.SNVGELLEYSLETK.K
R1/RRR1-16/2	1470.563	1471.679	-1443.666	0.432	1911.513	0.466	20	0.330	R.KYDAFIASDSLIK.Q
R1/RRR1-15/2	1582.055	1582.734	-1064.481	0.417	2053.270	0.294	20	0.298	R.SNVGELLEYSLETK.K
R1/RRR1-16/2	1471.205	1471.679	-323.368	0.500	1599.443	0.468	19	0.285	R.KYDAFIASDSLIK.Q
R1/RRR1-15/2	1581.621	1582.734	-1340.050	0.399	1406.545	0.385	18	0.241	R.SNVGELLEYSLETK.K
R1/RRR1-16/2	1472.107	1471.679	291.463	0.437	1019.163	0.320	16	0.202	-.KYDAFIASDSLIK.-
R1/RRR1-15/3	1490.714	1490.622	62.071	0.569	1575.723	0.491	31	0.178	K.HGGIDSM*SADDLKK.L
R1/RRR1-16/3	1490.661	1490.622	26.590	0.558	1196.616	0.525	28	0.145	K.HGGIDSM*SADDLKK.L
R1/RRR1-16/3	1490.486	1490.622	-91.450	0.556	1156.287	0.498	28	0.134	K.HGGIDSM*SADDLKK.L
R1/RRR1-15/3	1490.543	1490.622	-53.003	0.496	940.184	0.503	27	0.117	K.HGGIDSM*SADDLKK.L
R1/RRR1-16/3	1490.138	1490.622	-325.393	0.538	810.364	0.508	27	0.111	K.HGGIDSM*SADDLKK.L
R1/RRR1-15/3	1489.939	1490.622	-1132.606	0.524	870.726	0.491	28	0.110	K.HGGIDSM*SADDLKK.L
R1/RRR1-16/3	1474.637	1474.622	9.987	0.470	812.652	0.401	22	0.097	K.HGGIDSMSADDLKK.L
R1/RRR1-3/2	1354.237	1354.405	-124.188	0.423	995.094	0.463	20	0.229	R.QAIEEFSSDATR.F
R1/RRR1-4/2	1354.339	1354.405	-48.330	0.402	690.239	0.448	19	0.212	R.QAIEEFSSDATR.F
R1/RRR1-3/2	1354.037	1354.405	-272.048	0.425	643.841	0.446	18	0.210	R.QAIEEFSSDATR.F
R1/RRR1-3/2	1354.101	1354.405	-225.199	0.406	645.832	0.441	18	0.209	R.QAIEEFSSDATR.F
R1/RRR1-3/2	1464.657	1463.571	58.548	0.401	971.584	0.363	19	0.207	R.SFAPDEEINEALK.N
R1/RRR1-3/2	1619.528	1618.813	-175.968	0.472	692.171	0.398	18	0.197	R.ASGEGVQPQEYVLIK.M
R1/RRR1-3/2	1195.541	1196.380	-1542.576	0.296	876.140	0.280	13	0.192	K.LGFYDLQLAR.D
R1/RRR1-3/2	1196.347	1196.380	-27.592	0.415	1007.665	0.180	14	0.186	-.LGFYDLQLAR.-
R1/RRR1-4/2	1196.225	1196.380	-129.538	0.230	596.745	0.174	12	0.177	-.LGFYDLQLAR.-
R1/RRR1-12/2	1205.301	1205.432	-108.348	0.513	2421.058	0.621	21	0.488	R.ILVVGGTGYIGR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/3	1959.264	1959.187	39.137	0.495	2585.130	0.543	36	0.468	R.DADVVISTLGALQIADQTK.L
R1/RRR1-12/2	1205.176	1205.432	-212.796	0.536	1972.858	0.555	20	0.371	R.ILVVGGTGYIGR.H
R1/RRR1-12/2	1205.242	1205.432	-157.318	0.434	1588.445	0.585	20	0.316	R.ILVVGGTGYIGR.H
R1/RRR1-12/2	1959.468	1959.187	143.864	0.473	1487.028	0.542	24	0.287	R.DADVVISTLGALQIADQTK.L
R1/RRR1-12/2	1958.687	1959.187	-768.217	0.450	1517.442	0.493	25	0.278	R.DADVVISTLGALQIADQTK.L
R1/RRR1-12/2	1958.399	1959.187	-915.937	0.368	1366.288	0.521	24	0.265	R.DADVVISTLGALQIADQTK.L
R1/RRR1-13/2	1958.965	1959.187	-113.664	0.428	936.069	0.454	19	0.213	R.DADVVISTLGALQIADQTK.L
R1/RRR1-13/2	1958.654	1959.187	-785.296	0.364	852.627	0.388	19	0.199	R.DADVVISTLGALQIADQTK.L
R1/RRR1-12/3	1065.405	1065.251	145.176	0.518	1280.432	0.351	22	0.104	R.LGHPTTALVR.D
R1/RRR1-12/3	1065.453	1065.251	189.814	0.530	1114.575	0.361	21	0.097	R.LGHPTTALVR.D
R1/RRR1-12/3	1065.671	1065.251	394.857	0.500	1134.651	0.335	21	0.091	-.LGHPTTALVR.-
R1/RRR1-13/3	1065.300	1065.251	46.407	0.503	770.255	0.366	18	0.089	R.LGHPTTALVR.D
R1/RRR1-13/3	1065.467	1065.251	203.774	0.504	733.914	0.344	18	0.083	-.LGHPTTALVR.-
R1/RRR1-13/3	1065.463	1065.251	199.810	0.497	759.608	0.337	18	0.082	-.LGHPTTALVR.-
R1/RRR1-17/2	1551.124	1551.685	-1009.378	0.513	2561.656	0.506	21	0.472	K.LQIWDTAGQESFR.S
R1/RRR1-17/2	1551.428	1551.685	-165.935	0.567	2452.817	0.549	21	0.464	K.LQIWDTAGQESFR.S
R1/RRR1-17/2	1550.770	1551.685	-1238.253	0.460	2372.986	0.548	21	0.446	K.LQIWDTAGQESFR.S
R1/RRR1-17/2	1358.087	1358.435	-257.264	0.408	1098.476	0.476	16	0.234	R.AVSYEEGEQFAK.E
R1/RRR1-17/2	1358.130	1358.435	-225.432	0.410	1117.822	0.456	16	0.231	R.AVSYEEGEQFAK.E
R1/RRR1-17/2	1319.593	1320.519	-1463.995	0.330	1320.285	0.381	16	0.231	R.GAAGALLVYDITR.R
R1/RRR1-17/2	1358.003	1358.435	-318.858	0.374	718.576	0.429	14	0.203	R.AVSYEEGEQFAK.E
R1/RRR1-17/2	1319.587	1320.519	-1469.013	0.299	424.139	0.349	13	0.187	-.GAAGALLVYDITR.-
R1/RRR1-17/2	1320.529	1320.519	7.454	0.221	288.687	0.337	13	0.185	-.GAAGALLVYDITR.-
R1/RRR1-20/2	1325.007	1324.593	312.985	0.536	1598.451	0.513	17	0.298	R.VLQAM*QLM*TEK.R
R1/RRR1-20/2	1323.724	1324.593	-1416.535	0.478	1708.440	0.367	17	0.272	R.VLQAM*QLM*TEK.R
R1/RRR1-20/2	1324.205	1324.593	-293.643	0.502	1597.087	0.401	17	0.268	R.VLQAM*QLM*TEK.R
R1/RRR1-20/2	945.598	946.083	-514.699	0.456	998.690	0.381	15	0.216	K.SIAGIVTER.D
R1/RRR1-20/2	945.426	946.083	-1757.902	0.431	990.460	0.353	15	0.211	K.SIAGIVTER.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1307.297	1308.594	-1761.935	0.268	582.492	0.273	14	0.188	R.VLQAM*QLMTEK.R
R1/RRR1-21/2	946.375	946.083	308.931	0.260	813.386	0.118	13	0.180	-.SIAGIVTER.-
R1/RRR1-20/2	998.878	999.102	-224.630	0.384	1082.851	0.619	15	0.165	R.LNAYIQGGY.-
R1/RRR1-20/2	998.821	999.102	-281.889	0.307	642.190	0.537	12	0.114	R.LNAYIQGGY.-
R1/RRR1-20/2	999.014	999.102	-87.948	0.234	778.292	0.462	13	0.106	R.LNAYIQGGY.-
R1/RRR1-10/2	1870.601	1871.037	-233.838	0.560	2853.664	0.559	24	0.566	K.LAYVALDYEQELDTAR.S
R1/RRR1-10/2	1870.285	1871.037	-939.581	0.523	2924.442	0.491	24	0.553	K.LAYVALDYEQELDTAR.S
R1/RRR1-12/2	1871.633	1871.037	-216.635	0.604	2581.810	0.581	24	0.505	K.LAYVALDYEQELDTAR.S
R1/RRR1-10/2	1871.061	1871.037	13.047	0.573	2592.665	0.558	24	0.498	K.LAYVALDYEQELDTAR.S
R1/RRR1-16/2	1639.002	1638.849	94.004	0.554	2247.803	0.571	22	0.427	K.TNLNVEQVFFSIAR.D
R1/RRR1-16/2	1638.519	1638.849	-201.651	0.543	2122.949	0.564	22	0.400	K.TNLNVEQVFFSIAR.D
R1/RRR1-16/2	1638.475	1638.849	-229.081	0.564	2089.602	0.566	22	0.394	K.TNLNVEQVFFSIAR.D
R1/RRR1-16/2	1164.318	1165.278	-1688.681	0.368	1441.696	0.416	16	0.253	K.GQALADEYGIK.F
R1/RRR1-16/2	1164.169	1165.278	-1816.994	0.306	1625.096	0.178	17	0.222	K.GQALADEYGIK.F
R1/RRR1-17/2	1165.140	1165.278	-118.808	0.342	1118.080	0.351	14	0.212	K.GQALADEYGIK.F
R1/RRR1-16/3	1403.808	1403.520	205.814	0.563	1887.850	0.386	30	0.200	K.IKSEGEAEAAAAQK.S
R1/RRR1-3/2	1639.217	1638.849	225.599	0.352	430.467	0.452	16	0.199	K.TNLNVEQVFFSIAR.D
R1/RRR1-16/3	1403.207	1403.520	-223.653	0.533	1339.057	0.380	27	0.124	K.IKSEGEAEAAAAQK.S
R1/RRR1-10/2	1821.702	1821.066	-200.327	0.588	2740.576	0.585	25	0.541	R.QAVALLQDNYPEFIAK.K
R1/RRR1-10/2	1820.528	1821.066	-847.231	0.512	2013.754	0.587	24	0.383	R.QAVALLQDNYPEFIAK.K
R1/RRR1-4/2	1819.878	1821.066	-1205.650	0.463	1779.207	0.569	22	0.336	R.QAVALLQDNYPEFIAK.K
R1/RRR1-10/2	1820.526	1821.066	-848.442	0.490	1691.797	0.564	22	0.321	R.QAVALLQDNYPEFIAK.K
R1/RRR1-4/2	1820.442	1821.066	-895.023	0.520	1594.542	0.588	22	0.314	R.QAVALLQDNYPEFIAK.K
R1/RRR1-9/2	1821.331	1821.066	146.036	0.548	1412.688	0.589	22	0.291	R.QAVALLQDNYPEFIAK.K
R1/RRR1-4/2	1820.416	1821.066	-909.160	0.533	1379.573	0.560	20	0.277	R.QAVALLQDNYPEFIAK.K
R1/RRR1-9/2	1820.691	1821.066	-206.557	0.471	963.029	0.580	18	0.240	R.QAVALLQDNYPEFIAK.K
R1/RRR1-4/2	1171.044	1170.384	-290.826	0.455	1131.869	0.471	17	0.239	K.IVLTINNPASK.K
R1/RRR1-9/2	1821.309	1821.066	133.870	0.558	842.912	0.590	18	0.235	R.QAVALLQDNYPEFIAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1820.491	1821.066	-867.963	0.403	473.117	0.476	14	0.199	R.QAVALLQDNYPEFIAK.K
R1/RRR1-5/2	1821.199	1821.066	73.036	0.372	451.089	0.429	15	0.197	R.QAVALLQDNYPEFIAK.K
R1/RRR1-5/2	1819.790	1821.066	-1254.622	0.294	511.437	0.429	16	0.196	R.QAVALLQDNYPEFIAK.K
R1/RRR1-9/3	1272.238	1272.496	-203.630	0.407	1176.884	0.343	21	0.100	R.KVPANEEPIM*K.G
R1/RRR1-4/3	1272.022	1272.496	-374.467	0.430	1136.338	0.315	23	0.090	R.KVPANEEPIM*K.G
R1/RRR1-4/3	1256.725	1256.497	182.017	0.398	486.793	0.301	19	0.086	-.KVPANEEPIMK.-
R1/RRR1-4/3	1272.580	1272.496	66.009	0.489	1084.432	0.277	22	0.084	R.KVPANEEPIM*K.G
R1/RRR1-10/3	1272.221	1272.496	-217.491	0.397	1049.161	0.288	22	0.083	R.KVPANEEPIM*K.G
R1/RRR1-9/3	1272.632	1272.496	106.413	0.470	969.628	0.307	20	0.083	-.KVPANEEPIM*K.-
R1/RRR1-4/3	1257.642	1256.497	115.976	0.441	779.164	0.326	21	0.082	-.KVPANEEPIMK.-
R1/RRR1-10/3	1272.626	1272.496	101.940	0.467	895.820	0.275	21	0.078	-.KVPANEEPIM*K.-
R1/RRR1-10/3	1271.670	1272.496	-1440.439	0.346	643.768	0.259	19	0.076	-.KVPANEEPIM*K.-
R1/RRR1-4/3	1272.341	1272.496	-122.637	0.439	886.967	0.244	20	0.070	-.KVPANEEPIM*K.-
R1/RRR1-20/3	1272.835	1272.496	266.844	0.444	726.686	0.228	19	0.064	-.KVPANEEPIM*K.-
R1/RRR1-10/3	1272.090	1272.496	-320.740	0.358	618.933	0.230	17	0.062	-.KVPANEEPIM*K.-
R1/RRR1-24/2	1229.863	1229.385	389.924	0.461	1839.574	0.498	17	0.329	R.ISAM*IYEETR.G
R1/RRR1-23/2	1230.189	1229.385	-160.163	0.520	1500.020	0.501	17	0.284	R.ISAM*IYEETR.G
R1/RRR1-23/2	1229.508	1229.385	99.856	0.541	1457.777	0.476	17	0.273	R.ISAM*IYEETR.G
R1/RRR1-23/2	1327.132	1326.527	-298.414	0.476	1278.934	0.496	18	0.257	R.DNIQGITKPAIR.R
R1/RRR1-24/2	1325.714	1326.527	-1371.715	0.447	1196.761	0.486	18	0.247	R.DNIQGITKPAIR.R
R1/RRR1-23/2	1326.027	1326.527	-1134.833	0.409	1169.619	0.463	18	0.240	R.DNIQGITKPAIR.R
R1/RRR1-24/2	1327.024	1326.527	375.458	0.481	1139.512	0.458	18	0.237	R.DNIQGITKPAIR.R
R1/RRR1-23/2	1465.507	1465.720	-145.337	0.440	1191.925	0.450	18	0.237	K.TVTSLDVVYALKR.Q
R1/RRR1-23/2	1326.321	1326.527	-156.065	0.438	1194.030	0.431	18	0.236	R.DNIQGITKPAIR.R
R1/RRR1-24/2	1327.249	1326.527	-210.198	0.457	1082.184	0.477	17	0.236	R.DNIQGITKPAIR.R
R1/RRR1-20/2	1326.268	1326.527	-195.767	0.421	966.610	0.456	16	0.223	R.DNIQGITKPAIR.R
R1/RRR1-24/2	1228.957	1229.385	-349.813	0.345	1089.161	0.415	15	0.223	R.ISAM*IYEETR.G
R1/RRR1-23/2	1466.025	1465.720	208.656	0.441	1131.445	0.401	16	0.221	K.TVTSLDVVYALKR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-25/2	1325.963	1326.527	-1183.273	0.362	845.129	0.396	15	0.207	R.DNIQGITKPAIR.R
R1/RRR1-21/2	1327.422	1326.527	-79.656	0.316	657.090	0.450	16	0.206	R.DNIQGITKPAIR.R
R1/RRR1-21/2	1327.131	1326.527	-299.152	0.218	533.054	0.240	14	0.188	R.DNIQGITKPAIR.R
R1/RRR1-15/2	1620.409	1618.813	-249.542	0.622	2651.855	0.483	22	0.473	K.VLNFAIDDAILEER.I
R1/RRR1-14/2	1618.128	1618.813	-1044.458	0.515	2332.415	0.402	22	0.377	K.VLNFAIDDAILEER.I
R1/RRR1-14/2	1618.373	1618.813	-272.477	0.509	2324.607	0.368	22	0.364	K.VLNFAIDDAILEER.I
R1/RRR1-14/2	1617.437	1618.813	-1473.051	0.440	2256.076	0.316	22	0.336	K.VLNFAIDDAILEER.I
R1/RRR1-14/2	1611.441	1611.778	-210.282	0.489	1618.527	0.513	23	0.300	K.TPGLDDVTGEPLIQR.K
R1/RRR1-1/2	1620.284	1618.813	291.559	0.460	1860.784	0.380	19	0.293	K.VLNFAIDDAILEER.I
R1/RRR1-15/2	1611.847	1611.778	42.416	0.484	1400.607	0.499	22	0.269	K.TPGLDDVTGEPLIQR.K
R1/RRR1-14/2	1021.890	1022.181	-286.129	0.441	1342.171	0.458	15	0.256	K.GFILDGFPR.T
R1/RRR1-14/2	1611.455	1611.778	-201.238	0.483	1241.836	0.474	20	0.246	K.TPGLDDVTGEPLIQR.K
R1/RRR1-14/2	1611.432	1611.778	-215.905	0.488	1296.607	0.440	21	0.244	K.TPGLDDVTGEPLIQR.K
R1/RRR1-14/2	1022.133	1022.181	-47.568	0.469	1163.232	0.471	14	0.242	K.GFILDGFPR.T
R1/RRR1-14/2	1021.950	1022.181	-227.167	0.465	1188.955	0.457	14	0.241	K.GFILDGFPR.T
R1/RRR1-15/2	1611.026	1611.778	-1090.861	0.448	1177.559	0.471	20	0.239	K.TPGLDDVTGEPLIQR.K
R1/RRR1-13/2	1619.003	1618.813	118.155	0.296	650.544	0.194	15	0.183	K.VLNFAIDDAILEER.I
R1/RRR1-6/2	1620.103	1618.813	179.592	0.277	520.951	0.203	13	0.177	-.VLNFAIDDAILEER.-
R1/RRR1-15/2	1616.566	1616.795	-141.829	0.526	2326.432	0.641	23	0.476	R.IALTDNSIVEENLGK.Y
R1/RRR1-15/2	1616.181	1616.795	-1001.701	0.469	2058.331	0.564	22	0.389	R.IALTDNSIVEENLGK.Y
R1/RRR1-15/2	1635.467	1635.886	-257.426	0.398	1139.456	0.531	17	0.245	K.VVEPWVAYGYPNLK.S
R1/RRR1-15/2	1636.288	1635.886	246.206	0.495	992.928	0.545	16	0.236	K.VVEPWVAYGYPNLK.S
R1/RRR1-15/2	1383.509	1383.488	15.345	0.408	875.414	0.365	18	0.206	K.QSGEFYVPAEQK.L
R1/RRR1-15/2	1384.060	1383.488	-310.024	0.442	745.445	0.301	18	0.195	K.QSGEFYVPAEQK.L
R1/RRR1-15/2	1384.152	1383.488	-243.573	0.434	744.693	0.280	17	0.192	K.QSGEFYVPAEQK.L
R1/RRR1-13/2	1488.358	1488.629	-182.098	0.532	1925.589	0.564	24	0.365	R.TKGEAGTGNVVEAVR.H
R1/RRR1-13/2	1489.281	1488.629	-233.943	0.545	1866.146	0.559	24	0.353	R.TKGEAGTGNVVEAVR.H
R1/RRR1-13/2	1488.253	1488.629	-253.355	0.526	1732.622	0.550	23	0.328	R.TKGEAGTGNVVEAVR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1367.171	1366.608	-320.839	0.424	625.784	0.563	17	0.219	R.IAAPYDLVM*QTK.Q
R1/RRR1-13/2	1450.068	1450.509	-305.686	0.481	867.014	0.402	16	0.207	R.NM*DDDEVFSYAK.R
R1/RRR1-13/3	1488.580	1488.629	-32.795	0.515	1255.704	0.335	28	0.106	-.TKGEAGTGNVVEAVR.-
R1/RRR1-14/3	1489.337	1488.629	-196.456	0.489	1081.208	0.323	27	0.093	R.TKGEAGTGNVVEAVR.H
R1/RRR1-13/3	1488.738	1488.629	73.424	0.518	880.252	0.325	27	0.084	-.TKGEAGTGNVVEAVR.-
R1/RRR1-14/3	1487.902	1488.629	-1164.106	0.444	623.930	0.279	21	0.075	-.TKGEAGTGNVVEAVR.-
R1/RRR1-14/3	1488.554	1488.629	-49.945	0.441	770.100	0.248	24	0.071	-.TKGEAGTGNVVEAVR.-
R1/RRR1-13/3	1487.663	1488.629	-1325.150	0.471	807.892	0.328	25	0.069	-.TKGEAGTGNVVEAVR.-
R1/RRR1-16/2	1479.737	1479.660	52.160	0.421	2199.463	0.441	20	0.370	R.STNEALLVIEAYR.T
R1/RRR1-15/2	1479.436	1479.660	-151.582	0.387	1894.641	0.385	18	0.301	R.STNEALLVIEAYR.T
R1/RRR1-16/2	1479.219	1479.660	-298.771	0.344	1689.467	0.379	18	0.272	R.STNEALLVIEAYR.T
R1/RRR1-15/2	1479.108	1479.660	-1052.481	0.354	1289.037	0.353	16	0.224	R.STNEALLVIEAYR.T
R1/RRR1-15/2	1030.859	1031.188	-320.518	0.482	1091.056	0.340	15	0.215	R.LDNLSSLIR.Q
R1/RRR1-15/2	1031.174	1031.188	-14.083	0.558	1077.203	0.328	15	0.210	R.LDNLSSLIR.Q
R1/RRR1-16/2	1030.978	1031.188	-204.811	0.502	800.982	0.345	13	0.202	R.LDNLSSLIR.Q
R1/RRR1-17/2	1031.239	1031.188	49.318	0.467	825.721	0.312	14	0.201	R.LDNLSSLIR.Q
R1/RRR1-16/2	1031.144	1031.188	-42.581	0.496	800.720	0.308	14	0.199	R.LDNLSSLIR.Q
R1/RRR1-15/2	1031.047	1031.188	-137.228	0.392	776.647	0.276	14	0.197	R.LDNLSSLIR.Q
R1/RRR1-15/2	1547.955	1546.705	162.098	0.409	911.429	0.316	17	0.194	K.DLSGSFAFVVFDNK.S
R1/RRR1-15/2	1528.087	1528.645	-1022.592	0.497	1736.361	0.555	20	0.328	K.SPNSDTYVIFGEAK.I
R1/RRR1-15/2	1520.435	1520.840	-266.917	0.489	1765.827	0.376	19	0.281	K.NILFVISKPDVFK.S
R1/RRR1-15/2	1527.929	1528.645	-1126.229	0.458	1455.180	0.520	20	0.280	K.SPNSDTYVIFGEAK.I
R1/RRR1-15/2	1520.609	1520.840	-152.631	0.502	1438.661	0.429	17	0.257	-.NILFVISKPDVFK.-
R1/RRR1-15/2	1528.023	1528.645	-1064.782	0.499	1184.342	0.520	20	0.252	K.SPNSDTYVIFGEAK.I
R1/RRR1-18/2	1528.081	1528.645	-1026.121	0.448	1102.996	0.457	18	0.230	K.SPNSDTYVIFGEAK.I
R1/RRR1-15/2	1044.112	1044.184	-68.436	0.492	671.694	0.479	14	0.213	K.APDLSNVISK.A
R1/RRR1-15/2	1043.975	1044.184	-200.267	0.378	681.713	0.482	13	0.209	K.APDLSNVISK.A
R1/RRR1-11/2	1577.156	1577.807	-1050.010	0.464	2891.549	0.462	25	0.537	R.IAVLGASGYTGAEIVR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1577.666	1577.807	-89.682	0.529	2631.198	0.558	24	0.513	R.IAVLGASGYTGAEIVR.L
R1/RRR1-11/2	1299.306	1298.597	-224.613	0.572	1900.919	0.556	19	0.359	R.AIIISVIDNLVK.G
R1/RRR1-11/2	1298.353	1298.597	-188.000	0.507	1566.551	0.539	18	0.301	R.AIIISVIDNLVK.G
R1/RRR1-11/2	973.136	973.149	-13.162	0.356	1144.984	0.389	14	0.223	K.VSNIIIDAK.S
R1/RRR1-11/2	973.258	973.149	112.892	0.285	770.411	0.249	13	0.188	K.VSNIIIDAK.S
R1/RRR1-22/2	1225.126	1225.420	-240.012	0.440	1475.020	0.526	18	0.284	R.VLLINEGPNAGK.L
R1/RRR1-22/2	1225.104	1225.420	-258.205	0.391	1382.804	0.454	17	0.255	R.VLLINEGPNAGK.L
R1/RRR1-21/2	1224.534	1225.420	-1544.148	0.436	1284.501	0.470	17	0.250	R.VLLINEGPNAGK.L
R1/RRR1-22/2	1224.340	1225.420	-1703.296	0.364	1172.167	0.472	17	0.239	R.VLLINEGPNAGK.L
R1/RRR1-21/2	1243.146	1243.350	-164.636	0.474	1122.138	0.446	15	0.233	R.SNLTDFDRFK.V
R1/RRR1-21/2	1224.510	1225.420	-1564.176	0.401	1056.984	0.466	16	0.229	R.VLLINEGPNAGK.L
R1/RRR1-21/2	1131.498	1132.206	-1514.321	0.322	1306.012	0.351	17	0.227	R.VLVDGPSSDSR.L
R1/RRR1-21/2	1131.527	1132.206	-1488.313	0.335	1304.379	0.343	17	0.226	R.VLVDGPSSDSR.L
R1/RRR1-21/2	1131.545	1132.206	-1472.709	0.350	1206.190	0.325	18	0.217	R.VLVDGPSSDSR.L
R1/RRR1-22/2	1242.981	1243.350	-298.128	0.386	792.273	0.420	14	0.208	R.SNLTDFDRFK.V
R1/RRR1-3/3	1908.849	1909.022	-91.276	0.519	2725.899	0.505	36	0.470	K.TQEKDADAM*QVDNAVEK.K
R1/RRR1-3/3	1908.928	1909.022	-49.710	0.540	2670.985	0.487	34	0.448	K.TQEKDADAM*QVDNAVEK.K
R1/RRR1-3/3	1908.620	1909.022	-211.567	0.509	2301.115	0.510	32	0.356	K.TQEKDADAM*QVDNAVEK.K
R1/RRR1-4/3	1908.900	1909.022	-64.335	0.505	2150.343	0.520	32	0.321	K.TQEKDADAM*QVDNAVEK.K
R1/RRR1-4/2	1177.620	1178.403	-1518.121	0.389	1038.723	0.453	16	0.227	K.LPTAILSTYAK.A
R1/RRR1-5/2	1178.397	1178.403	-5.155	0.366	629.122	0.466	14	0.206	K.LPTAILSTYAK.A
R1/RRR1-3/2	1911.129	1910.163	-17.977	0.437	644.110	0.482	19	0.204	K.KAPEPEPTFQILTNPAR.V
R1/RRR1-3/2	1178.172	1178.403	-196.630	0.291	943.915	0.251	15	0.192	K.LPTAILSTYAK.A
R1/RRR1-4/2	1177.452	1178.403	-1661.628	0.224	688.630	0.211	15	0.185	K.LPTAILSTYAK.A
R1/RRR1-3/3	1910.006	1910.163	-82.610	0.369	1005.113	0.402	27	0.100	K.KAPEPEPTFQILTNPAR.V
R1/RRR1-4/3	1911.111	1910.163	-27.434	0.448	1164.391	0.281	27	0.090	-.KAPEPEPTFQILTNPAR.-
R1/RRR1-14/2	1634.431	1634.812	-234.067	0.570	2518.840	0.454	22	0.438	K.VLNFAIDDSILEER.I
R1/RRR1-14/2	1633.643	1634.812	-1331.478	0.416	2467.064	0.323	22	0.381	K.VLNFAIDDSILEER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1595.988	1595.779	131.136	0.540	1868.418	0.631	23	0.377	K.VPGVDDVTGEPLIQR.K
R1/RRR1-14/2	1595.396	1595.779	-241.022	0.516	1935.782	0.580	23	0.371	K.VPGVDDVTGEPLIQR.K
R1/RRR1-14/2	1634.548	1634.812	-161.991	0.573	2214.256	0.438	22	0.370	K.VLNFAIDDSILEER.I
R1/RRR1-14/2	1596.451	1595.779	-206.274	0.528	1515.023	0.610	21	0.312	K.VPGVDDVTGEPLIQR.K
R1/RRR1-6/2	1850.693	1850.106	-223.651	0.517	2017.383	0.459	24	0.346	K.LSFKDIDEVILVGGSTR.I
R1/RRR1-6/2	982.358	983.187	-1867.550	0.456	546.156	0.463	15	0.212	R.IPAVQDLVK.K
R1/RRR1-6/2	983.001	983.187	-189.460	0.416	480.325	0.471	14	0.209	R.IPAVQDLVK.K
R1/RRR1-6/2	885.953	885.988	-39.954	0.351	769.749	0.406	12	0.205	R.TPVDNALR.D
R1/RRR1-6/2	885.316	885.988	-1894.269	0.324	706.680	0.423	12	0.204	R.TPVDNALR.D
R1/RRR1-14/2	1987.483	1987.198	144.300	0.573	2428.715	0.590	27	0.470	K.GDVSDEAVAALDKIEAALAK.F
R1/RRR1-14/2	1986.139	1987.198	-1039.442	0.517	2344.701	0.573	27	0.446	K.GDVSDEAVAALDKIEAALAK.F
R1/RRR1-14/2	1988.049	1987.198	-74.926	0.565	1989.715	0.571	25	0.371	K.GDVSDEAVAALDKIEAALAK.F
R1/RRR1-14/2	1888.878	1889.054	-93.315	0.569	1357.111	0.603	22	0.290	K.QQFAEELLAYTDAFNK.A
R1/RRR1-15/2	1986.236	1987.198	-990.386	0.478	1429.886	0.555	22	0.280	K.GDVSDEAVAALDKIEAALAK.F
R1/RRR1-14/2	1889.494	1889.054	233.365	0.364	560.058	0.312	15	0.183	K.QQFAEELLAYTDAFNK.A
R1/RRR1-3/2	1988.673	1987.198	239.766	0.198	443.567	0.285	17	0.181	K.GDVSDEAVAALDKIEAALAK.F
R1/RRR1-14/3	1986.817	1987.198	-191.912	0.383	1380.543	0.463	37	0.148	K.GDVSDEAVAALDKIEAALAK.F
R1/RRR1-14/3	1987.112	1987.198	-43.083	0.370	961.857	0.390	33	0.095	K.GDVSDEAVAALDKIEAALAK.F
R1/RRR1-14/3	1356.360	1356.509	-109.741	0.453	684.175	0.356	20	0.084	K.QDPQFLLEHTK.K
R1/RRR1-14/3	1356.375	1356.509	-98.908	0.404	1118.054	0.286	23	0.083	K.QDPQFLLEHTK.K
R1/RRR1-14/3	1356.580	1356.509	53.140	0.409	697.043	0.348	20	0.082	K.QDPQFLLEHTK.K
R1/RRR1-16/2	1140.993	1141.346	-309.968	0.534	1951.164	0.515	18	0.353	R.LVNILNAANAK.A
R1/RRR1-16/2	1266.391	1266.470	-62.515	0.590	1771.315	0.536	17	0.329	R.LEQAFVNIFGK.K
R1/RRR1-16/2	1141.161	1141.346	-162.182	0.549	1674.387	0.484	18	0.301	R.LVNILNAANAK.A
R1/RRR1-16/2	1142.108	1141.346	-208.788	0.567	1581.407	0.504	17	0.293	R.LVNILNAANAK.A
R1/RRR1-16/2	1266.109	1266.470	-286.300	0.446	1503.556	0.497	17	0.282	R.LEQAFVNIFGK.K
R1/RRR1-16/2	1504.991	1504.583	271.997	0.474	1326.427	0.527	19	0.267	K.VITNDVDAGDWNGK.-
R1/RRR1-16/2	1266.187	1266.470	-224.009	0.337	1231.246	0.436	16	0.236	R.LEQAFVNIFGK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1708.090	1706.877	125.325	0.588	2271.406	0.566	21	0.429	K.LAADVIEFAEDQWAK.-
R1/RRR1-10/2	1706.392	1706.877	-284.754	0.471	1896.088	0.528	20	0.345	K.LAADVIEFAEDQWAK.-
R1/RRR1-10/2	1707.823	1706.877	-31.301	0.507	1474.214	0.499	19	0.275	K.LAADVIEFAEDQWAK.-
R1/RRR1-10/3	1744.159	1744.845	-969.485	0.518	1673.182	0.582	31	0.239	R.THDVGGHFAAYEQPSK.L
R1/RRR1-10/3	1744.409	1744.845	-250.762	0.554	1626.680	0.558	31	0.222	R.THDVGGHFAAYEQPSK.L
R1/RRR1-10/2	1445.440	1445.642	-140.324	0.463	895.798	0.483	17	0.222	R.ENIDPSVIGPIYK.Y
R1/RRR1-10/2	1445.130	1445.642	-1049.183	0.474	970.161	0.439	18	0.220	R.ENIDPSVIGPIYK.Y
R1/RRR1-10/2	1446.257	1445.642	-267.316	0.490	823.730	0.489	17	0.219	R.ENIDPSVIGPIYK.Y
R1/RRR1-10/3	1744.780	1744.845	-37.663	0.535	1461.723	0.579	29	0.204	R.THDVGGHFAAYEQPSK.L
R1/RRR1-10/3	1706.578	1706.877	-175.609	0.448	1322.762	0.371	25	0.123	K.LAADVIEFAEDQWAK.-
R1/RRR1-12/2	1576.846	1576.843	2.515	0.497	2031.693	0.531	23	0.368	R.MFYGPGGPYALFAGK.D
R1/RRR1-12/2	1592.164	1592.842	-1057.158	0.522	1786.592	0.569	23	0.340	R.M*FYGPGGPYALFAGK.D
R1/RRR1-12/2	1592.104	1592.842	-1095.111	0.492	1559.846	0.628	23	0.324	R.M*FYGPGGPYALFAGK.D
R1/RRR1-12/2	1576.491	1576.843	-223.409	0.515	1698.950	0.537	23	0.317	R.MFYGPGGPYALFAGK.D
R1/RRR1-12/2	1593.250	1592.842	256.725	0.545	1547.747	0.549	23	0.300	R.M*FYGPGGPYALFAGK.D
R1/RRR1-12/2	1577.502	1576.843	-216.669	0.507	1413.365	0.577	20	0.288	R.MFYGPGGPYALFAGK.D
R1/RRR1-12/2	1577.102	1576.843	165.157	0.478	1178.358	0.530	19	0.251	R.MFYGPGGPYALFAGK.D
R1/RRR1-12/2	1167.978	1167.254	-236.765	0.483	1240.080	0.477	16	0.251	K.GQIYDVTQSR.M
R1/RRR1-12/2	1167.051	1167.254	-174.111	0.495	1263.045	0.449	16	0.247	K.GQIYDVTQSR.M
R1/RRR1-12/2	1167.122	1167.254	-113.781	0.480	1202.643	0.457	16	0.243	K.GQIYDVTQSR.M
R1/RRR1-12/3	1802.999	1802.875	68.843	0.423	1224.695	0.423	31	0.234	K.EKEEAVAAAAPDEGAKES.-
R1/RRR1-13/2	1167.116	1167.254	-118.397	0.460	1082.074	0.392	15	0.221	K.GQIYDVTQSR.M
R1/RRR1-13/2	1166.801	1167.254	-389.367	0.386	1003.536	0.333	15	0.208	K.GQIYDVTQSR.M
R1/RRR1-1/2	1594.341	1592.842	313.991	0.350	604.634	0.428	15	0.198	R.M*FYGPGGPYALFAGK.D
R1/RRR1-16/2	1166.877	1167.254	-323.658	0.291	1092.651	0.221	15	0.196	K.GQIYDVTQSR.M
R1/RRR1-12/3	1802.520	1802.875	-197.474	0.464	938.478	0.463	28	0.127	K.EKEEAVAAAAPDEGAKES.-
R1/RRR1-7/2	1394.305	1393.607	-217.124	0.517	2404.335	0.495	22	0.426	R.VVSCADILAFAAR.D
R1/RRR1-9/2	1394.151	1393.607	-328.067	0.525	2358.025	0.518	21	0.425	R.VVSCADILAFAAR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1394.193	1393.607	-297.760	0.546	2343.789	0.499	21	0.414	R.VVSCADILAFAAR.D
R1/RRR1-8/2	1394.203	1393.607	-290.556	0.538	2180.544	0.524	21	0.392	R.VVSCADILAFAAR.D
R1/RRR1-8/2	1393.379	1393.607	-163.932	0.514	2266.122	0.473	21	0.389	R.VVSCADILAFAAR.D
R1/RRR1-9/1	949.533	950.070	-1623.855	0.313	866.127	0.165	12	0.379	R.GFEVIDAAK.A
R1/RRR1-9/2	1394.997	1393.607	280.629	0.554	1817.047	0.601	20	0.354	R.VVSCADILAFAAR.D
R1/RRR1-9/1	949.415	950.070	-1748.503	0.287	785.461	0.244	12	0.332	R.GFEVIDAAK.A
R1/RRR1-7/1	949.457	950.070	-1703.936	0.296	760.503	0.239	11	0.324	-.GFEVIDAAK.-
R1/RRR1-8/1	949.499	950.070	-1659.632	0.295	755.370	0.234	11	0.319	-.GFEVIDAAK.-
R1/RRR1-9/1	949.485	950.070	-1674.744	0.240	756.669	0.169	11	0.314	-.GFEVIDAAK.-
R1/RRR1-8/2	1392.683	1393.607	-1385.756	0.385	1888.419	0.425	20	0.310	R.VVSCADILAFAAR.D
R1/RRR1-7/1	949.471	950.070	-1689.082	0.267	728.016	0.206	11	0.293	-.GFEVIDAAK.-
R1/RRR1-4/2	1394.334	1393.607	-196.572	0.478	1562.723	0.460	18	0.276	R.VVSCADILAFAAR.D
R1/RRR1-8/1	949.464	950.070	-1696.573	0.286	700.651	0.214	11	0.275	-.GFEVIDAAK.-
R1/RRR1-11/2	1393.194	1393.607	-297.270	0.473	1517.953	0.458	18	0.270	R.VVSCADILAFAAR.D
R1/RRR1-7/1	949.516	950.070	-1642.454	0.280	694.305	0.224	11	0.270	R.GFEVIDAAK.A
R1/RRR1-8/2	944.987	945.049	-66.092	0.396	1327.815	0.394	14	0.239	K.AAVEAACPR.V
R1/RRR1-7/2	949.445	950.070	-1716.610	0.412	1223.413	0.404	15	0.236	R.GFEVIDAAK.A
R1/RRR1-9/2	949.566	950.070	-1589.516	0.444	1178.808	0.416	14	0.234	R.GFEVIDAAK.A
R1/RRR1-8/2	949.961	950.070	-115.947	0.452	1083.551	0.440	14	0.233	R.GFEVIDAAK.A
R1/RRR1-6/2	949.980	950.070	-95.066	0.447	1103.826	0.424	15	0.232	R.GFEVIDAAK.A
R1/RRR1-8/2	949.490	950.070	-1669.204	0.386	1215.112	0.391	15	0.232	R.GFEVIDAAK.A
R1/RRR1-9/2	949.965	950.070	-111.178	0.456	1079.149	0.426	14	0.230	R.GFEVIDAAK.A
R1/RRR1-11/2	949.958	950.070	-118.267	0.374	1090.548	0.419	14	0.228	R.GFEVIDAAK.A
R1/RRR1-7/2	949.930	950.070	-148.302	0.446	1195.749	0.376	14	0.228	R.GFEVIDAAK.A
R1/RRR1-6/2	949.653	950.070	-441.011	0.362	1110.054	0.405	14	0.227	R.GFEVIDAAK.A
R1/RRR1-12/2	949.397	950.070	-1768.025	0.361	988.634	0.459	14	0.226	-.GFEVIDAAK.-
R1/RRR1-7/2	949.915	950.070	-164.029	0.442	1141.074	0.367	14	0.223	R.GFEVIDAAK.A
R1/RRR1-3/2	950.058	950.070	-13.224	0.371	1092.373	0.386	14	0.223	R.GFEVIDAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	949.812	950.070	-272.973	0.392	1108.554	0.373	14	0.222	R.GFEVIDAAK.A
R1/RRR1-3/2	949.974	950.070	-101.510	0.366	1153.320	0.342	14	0.219	R.GFEVIDAAK.A
R1/RRR1-11/2	950.043	950.070	-28.560	0.371	881.262	0.429	13	0.218	R.GFEVIDAAK.A
R1/RRR1-6/2	949.859	950.070	-223.075	0.415	1086.598	0.352	14	0.218	R.GFEVIDAAK.A
R1/RRR1-2/2	949.893	950.070	-187.750	0.383	874.607	0.423	13	0.217	R.GFEVIDAAK.A
R1/RRR1-1/2	950.286	950.070	227.971	0.474	1036.120	0.351	14	0.215	R.GFEVIDAAK.A
R1/RRR1-4/2	950.068	950.070	-2.656	0.389	946.808	0.389	13	0.214	-.GFEVIDAAK.-
R1/RRR1-3/2	949.928	950.070	-149.978	0.357	1032.141	0.346	14	0.214	R.GFEVIDAAK.A
R1/RRR1-1/2	949.824	950.070	-260.337	0.329	903.841	0.401	13	0.214	R.GFEVIDAAK.A
R1/RRR1-2/2	949.898	950.070	-181.820	0.354	874.755	0.383	13	0.212	R.GFEVIDAAK.A
R1/RRR1-1/2	949.803	950.070	-282.515	0.317	887.795	0.380	13	0.209	-.GFEVIDAAK.-
R1/RRR1-2/2	949.466	950.070	-1695.038	0.292	815.863	0.396	13	0.209	R.GFEVIDAAK.A
R1/RRR1-9/2	1394.596	1393.607	-7.692	0.328	1068.842	0.295	16	0.203	R.VVSCADILAFAAR.D
R1/RRR1-8/2	1394.681	1393.607	53.497	0.301	1016.396	0.311	16	0.202	R.VVSCADILAFAAR.D
R1/RRR1-10/1	949.467	950.070	-1693.473	0.286	562.320	0.225	10	0.201	-.GFEVIDAAK.-
R1/RRR1-12/2	1394.879	1393.607	195.599	0.350	873.783	0.338	15	0.200	R.VVSCADILAFAAR.D
R1/RRR1-3/2	1393.330	1393.607	-199.702	0.441	775.982	0.349	15	0.198	R.VVSCADILAFAAR.D
R1/RRR1-10/1	949.397	950.070	-1768.010	0.225	549.325	0.096	10	0.181	-.GFEVIDAAK.-
R1/RRR1-10/1	949.444	950.070	-1718.598	0.230	524.618	0.135	10	0.170	-.GFEVIDAAK.-
R1/RRR1-8/1	949.445	950.070	-1717.048	0.248	468.546	0.138	10	0.148	-.GFEVIDAAK.-
R1/RRR1-23/2	1806.322	1806.035	159.586	0.533	1760.038	0.475	25	0.307	R.VCCLSIIDPGDSDIIK.T
R1/RRR1-23/2	1805.234	1806.035	-1000.703	0.491	1608.799	0.529	24	0.302	R.VCCLSIIDPGDSDIIK.T
R1/RRR1-23/2	1806.301	1806.035	147.861	0.568	1402.221	0.501	23	0.268	R.VCCLSIIDPGDSDIIK.T
R1/RRR1-22/2	1806.547	1806.035	-270.865	0.492	1406.523	0.455	23	0.258	R.VCCLSIIDPGDSDIIK.T
R1/RRR1-23/2	1334.099	1334.520	-316.597	0.429	1368.334	0.400	15	0.243	K.SEIEYYAM*LAK.T
R1/RRR1-22/2	1805.096	1806.035	-1077.561	0.370	1329.303	0.383	21	0.234	R.VCCLSIIDPGDSDIIK.T
R1/RRR1-22/2	1805.760	1806.035	-152.599	0.374	1097.214	0.362	20	0.213	R.VCCLSIIDPGDSDIIK.T
R1/RRR1-23/2	1396.260	1396.654	-282.763	0.391	1061.114	0.346	16	0.208	K.LVIISNNCPPLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1736.964	1737.720	-1013.813	0.535	2277.983	0.548	24	0.424	K.DATDDFEDVGHSTTAR.A
R1/RRR1-21/2	1737.218	1737.720	-866.787	0.553	2060.237	0.565	23	0.386	K.DATDDFEDVGHSTTAR.A
R1/RRR1-21/2	1887.509	1888.025	-805.425	0.573	1715.372	0.634	28	0.352	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-21/2	1886.681	1888.025	-1245.962	0.527	1602.604	0.638	27	0.335	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-21/2	1887.547	1888.025	-253.793	0.581	1476.938	0.625	26	0.312	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-21/2	1737.085	1737.720	-943.822	0.534	1615.750	0.551	22	0.308	K.DATDDFEDVGHSTTAR.A
R1/RRR1-21/2	1737.283	1737.720	-252.065	0.555	1453.842	0.511	20	0.273	K.DATDDFEDVGHSTTAR.A
R1/RRR1-21/3	1644.038	1643.819	133.625	0.575	1937.895	0.525	30	0.263	K.HNSKDDCWLIIGGK.V
R1/RRR1-21/3	1887.950	1888.025	-39.444	0.496	1428.465	0.432	32	0.151	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-21/3	1643.357	1643.819	-281.827	0.466	1496.616	0.384	24	0.146	K.HNSKDDCWLIIGGK.V
R1/RRR1-20/3	1643.054	1643.819	-1077.654	0.465	1432.218	0.392	24	0.140	K.HNSKDDCWLIIGGK.V
R1/RRR1-21/3	1887.829	1888.025	-103.946	0.510	1248.844	0.445	31	0.135	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-20/3	1887.814	1888.025	-112.021	0.434	1185.999	0.452	30	0.129	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-21/3	1644.146	1643.819	199.298	0.483	989.334	0.515	24	0.125	K.HNSKDDCWLIIGGK.V
R1/RRR1-20/3	1889.011	1888.025	-7.176	0.456	1138.548	0.391	29	0.113	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-21/3	1737.779	1737.720	34.473	0.349	774.182	0.533	27	0.111	K.DATDDFEDVGHSTTAR.A
R1/RRR1-21/3	1887.723	1888.025	-160.379	0.490	1014.524	0.405	28	0.109	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-20/3	1738.416	1737.720	-175.492	0.398	460.636	0.529	22	0.105	K.DATDDFEDVGHSTTAR.A
R1/RRR1-21/3	1738.103	1737.720	221.069	0.339	782.820	0.493	26	0.105	K.DATDDFEDVGHSTTAR.A
R1/RRR1-20/3	1738.678	1737.720	-24.205	0.352	740.686	0.484	26	0.102	K.DATDDFEDVGHSTTAR.A
R1/RRR1-20/3	1737.126	1737.720	-920.126	0.303	745.066	0.437	25	0.094	K.DATDDFEDVGHSTTAR.A
R1/RRR1-22/3	1737.535	1737.720	-106.524	0.332	635.580	0.385	25	0.087	K.DATDDFEDVGHSTTAR.A
R1/RRR1-22/3	1737.624	1737.720	-55.258	0.288	486.872	0.383	21	0.087	K.DATDDFEDVGHSTTAR.A
R1/RRR1-19/3	1889.877	1888.025	-78.437	0.387	952.072	0.257	27	0.080	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-20/3	1887.203	1888.025	-968.177	0.340	841.031	0.178	27	0.070	K.FLEDHPGGDDVLLSSTGK.D
R1/RRR1-22/2	1170.288	1170.256	27.033	0.457	996.684	0.454	17	0.228	K.LQGFAEDYAR.Q
R1/RRR1-22/2	1171.190	1170.256	-56.829	0.454	1000.224	0.435	17	0.225	K.LQGFAEDYAR.Q
R1/RRR1-22/2	1169.383	1170.256	-1606.713	0.357	895.044	0.492	16	0.223	K.LQGFAEDYAR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-22/2	1368.139	1368.556	-305.757	0.372	995.950	0.292	15	0.198	R.GVFIICNYEPR.G
R1/RRR1-22/2	1368.282	1368.556	-200.673	0.226	839.106	0.205	13	0.181	R.GVFIICNYEPR.G
R1/RRR1-12/2	1306.248	1306.490	-185.271	0.511	2427.174	0.405	21	0.401	K.AFGAELVLTDAAK.G
R1/RRR1-12/2	1115.231	1115.310	-70.989	0.557	1699.478	0.476	19	0.304	K.IQGIGAGFVPR.N
R1/RRR1-12/2	1306.294	1306.490	-150.303	0.527	1734.078	0.370	21	0.275	K.AFGAELVLTDAAK.G
R1/RRR1-12/2	1306.090	1306.490	-306.971	0.525	1740.691	0.366	21	0.275	K.AFGAELVLTDAAK.G
R1/RRR1-12/2	1115.218	1115.310	-82.627	0.534	1384.761	0.485	19	0.268	K.IQGIGAGFVPR.N
R1/RRR1-12/2	1308.309	1308.572	-201.404	0.515	1271.028	0.454	17	0.248	K.TPM*VYLNNIVK.G
R1/RRR1-9/2	1636.563	1636.825	-160.221	0.496	1338.327	0.540	19	0.273	K.ELILNYANQLCER.L
R1/RRR1-20/2	1636.497	1636.825	-200.852	0.423	965.089	0.464	17	0.222	K.ELILNYANQLCER.L
R1/RRR1-9/2	1635.492	1636.825	-1430.213	0.297	1148.843	0.372	17	0.217	K.ELILNYANQLCER.L
R1/RRR1-9/3	1867.943	1866.102	-85.028	0.531	1677.299	0.483	28	0.204	K.TKELILNYANQLCER.L
R1/RRR1-11/2	1638.174	1636.825	214.009	0.386	439.560	0.380	13	0.192	K.ELILNYANQLCER.L
R1/RRR1-9/3	1865.456	1866.102	-884.919	0.507	1434.808	0.511	25	0.179	K.TKELILNYANQLCER.L
R1/RRR1-9/3	1865.506	1866.102	-857.822	0.462	1109.627	0.422	24	0.116	K.TKELILNYANQLCER.L
R1/RRR1-9/3	1559.496	1559.710	-137.999	0.446	892.735	0.475	28	0.104	K.HYKGDHTYVPVSR.K
R1/RRR1-14/3	1559.874	1559.710	105.632	0.445	672.491	0.474	24	0.099	K.HYKGDHTYVPVSR.K
R1/RRR1-9/3	1560.771	1559.710	39.402	0.451	554.530	0.466	23	0.097	K.HYKGDHTYVPVSR.K
R1/RRR1-9/3	1559.264	1559.710	-286.897	0.440	657.515	0.466	26	0.096	K.HYKGDHTYVPVSR.K
R1/RRR1-8/3	1559.643	1559.710	-43.312	0.492	618.992	0.423	24	0.094	K.HYKGDHTYVPVSR.K
R1/RRR1-14/3	1560.249	1559.710	-296.408	0.436	558.740	0.421	23	0.092	K.HYKGDHTYVPVSR.K
R1/RRR1-11/2	1495.386	1494.781	-264.919	0.552	2560.240	0.538	23	0.479	K.MVGYALQAAEILSK.E
R1/RRR1-11/2	1510.585	1510.781	-129.802	0.511	2514.007	0.490	23	0.449	K.M*VGYALQAAEILSK.E
R1/RRR1-11/2	1511.303	1510.781	-317.206	0.517	2536.730	0.469	23	0.446	K.M*VGYALQAAEILSK.E
R1/RRR1-12/2	1201.116	1201.355	-199.244	0.395	2084.030	0.369	19	0.327	K.EGISAEVINLR.S
R1/RRR1-11/2	1494.310	1494.781	-316.566	0.466	1935.705	0.446	21	0.325	K.MVGYALQAAEILSK.E
R1/RRR1-12/2	1510.374	1510.781	-270.222	0.361	1713.412	0.383	22	0.276	K.M*VGYALQAAEILSK.E
R1/RRR1-11/2	1202.012	1201.355	-286.186	0.507	1510.243	0.383	18	0.254	K.EGISAEVINLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1201.193	1201.355	-135.526	0.432	1498.253	0.331	17	0.241	K.EGISAEVINLR.S
R1/RRR1-11/2	1201.029	1201.355	-271.842	0.491	1349.925	0.386	18	0.240	K.EGISAEVINLR.S
R1/RRR1-11/2	1510.112	1510.781	-1108.451	0.351	1178.406	0.407	20	0.228	K.M*VGYALQAAEILSK.E
R1/RRR1-11/2	1704.650	1704.929	-164.079	0.448	975.861	0.481	22	0.227	R.IAGADVPM*PYAANLER.M
R1/RRR1-11/2	1704.128	1704.929	-1060.062	0.428	833.792	0.431	21	0.211	R.IAGADVPM*PYAANLER.M
R1/RRR1-11/2	1704.403	1704.929	-898.189	0.434	663.956	0.433	19	0.203	R.IAGADVPM*PYAANLER.M
R1/RRR1-11/2	1688.783	1688.930	-86.899	0.427	474.318	0.467	18	0.202	R.IAGADVPMPYAANLER.M
R1/RRR1-12/2	1511.006	1510.781	149.301	0.271	751.763	0.204	19	0.188	K.M*VGYALQAAEILSK.E
R1/RRR1-12/2	1510.519	1510.781	-173.740	0.305	872.756	0.165	19	0.185	K.M*VGYALQAAEILSK.E
R1/RRR1-12/2	1200.692	1201.355	-1389.222	0.319	641.276	0.213	12	0.180	-.EGISAEVINLR.-
R1/RRR1-14/2	1101.507	1102.263	-1599.570	0.432	2004.018	0.479	18	0.348	R.ALLEVVESGGK.N
R1/RRR1-14/2	1101.995	1102.263	-244.053	0.498	1986.158	0.467	18	0.342	R.ALLEVVESGGK.N
R1/RRR1-14/2	1102.216	1102.263	-42.834	0.556	1915.731	0.499	18	0.340	R.ALLEVVESGGK.N
R1/RRR1-14/2	1101.636	1102.263	-1481.461	0.441	1930.830	0.485	18	0.338	R.ALLEVVESGGK.N
R1/RRR1-14/2	1102.063	1102.263	-182.157	0.501	1847.419	0.508	18	0.333	R.ALLEVVESGGK.N
R1/RRR1-14/2	921.133	921.075	62.790	0.451	758.739	0.371	13	0.206	R.YIAGLQQK.Y
R1/RRR1-14/2	920.955	921.075	-131.165	0.377	756.321	0.370	13	0.204	R.YIAGLQQK.Y
R1/RRR1-14/2	920.171	921.075	-2075.393	0.324	651.216	0.377	12	0.200	R.YIAGLQQK.Y
R1/RRR1-14/2	1104.357	1104.236	109.691	0.444	802.513	0.356	15	0.199	R.GSDTVVLGVEK.K
R1/RRR1-16/2	1501.386	1501.750	-243.229	0.510	2146.562	0.567	24	0.404	K.AVASINSVLTDLVAK.G
R1/RRR1-16/2	1501.437	1501.750	-209.461	0.553	2062.237	0.559	23	0.384	K.AVASINSVLTDLVAK.G
R1/RRR1-16/2	1502.164	1501.750	276.584	0.560	1944.724	0.593	23	0.375	K.AVASINSVLTDLVAK.G
R1/RRR1-16/2	1379.940	1379.540	290.523	0.507	1573.112	0.567	18	0.310	K.ANNVIYGLAQCR.G
R1/RRR1-16/2	1379.388	1379.540	-111.095	0.488	1528.546	0.463	18	0.275	K.ANNVIYGLAQCR.G
R1/RRR1-16/2	1379.266	1379.540	-199.519	0.495	1517.900	0.415	18	0.262	K.ANNVIYGLAQCR.G
R1/RRR1-2/2	1502.603	1501.750	-98.237	0.362	1115.010	0.427	18	0.224	K.AVASINSVLTDLVAK.G
R1/RRR1-1/2	1502.062	1501.750	207.888	0.398	758.356	0.480	18	0.212	K.AVASINSVLTDLVAK.G
R1/RRR1-16/2	1184.883	1185.226	-290.633	0.304	634.152	0.417	18	0.195	K.GSTGGGFATSSAGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1501.824	1501.750	49.273	0.284	733.764	0.363	17	0.195	K.AVASINSVLTDLVAK.G
R1/RRR1-5/2	1129.090	1129.250	-142.554	0.518	1843.278	0.503	18	0.332	K.SPAGANQWVAK.N
R1/RRR1-5/2	1128.539	1129.250	-1521.438	0.450	1822.760	0.391	17	0.295	K.SPAGANQWVAK.N
R1/RRR1-5/2	1129.023	1129.250	-202.207	0.534	1455.849	0.522	17	0.283	K.SPAGANQWVAK.N
R1/RRR1-5/2	1748.319	1746.986	191.072	0.604	1057.482	0.588	23	0.260	R.FLEKPELFYDAFAR.A
R1/RRR1-5/2	1746.061	1746.986	-1105.720	0.385	867.753	0.448	20	0.215	R.FLEKPELFYDAFAR.A
R1/RRR1-5/2	1747.214	1746.986	131.278	0.355	725.734	0.382	19	0.200	R.FLEKPELFYDAFAR.A
R1/RRR1-5/2	1649.714	1650.813	-1276.203	0.441	717.934	0.379	17	0.195	K.NAEAFIPDAFDPSKK.H
R1/RRR1-5/2	1650.659	1650.813	-93.505	0.421	622.908	0.333	16	0.181	-.NAEAFIPDAFDPSKK.-
R1/RRR1-17/2	974.038	974.094	-56.767	0.436	1947.865	0.376	19	0.309	R.LSADAGAGALK.L
R1/RRR1-17/2	974.186	974.094	95.064	0.483	1662.205	0.396	19	0.276	R.LSADAGAGALK.L
R1/RRR1-17/2	1173.098	1173.295	-168.100	0.418	1166.038	0.512	17	0.248	R.AAGPELVEACR.K
R1/RRR1-17/2	974.084	974.094	-9.881	0.435	1369.145	0.389	18	0.243	R.LSADAGAGALK.L
R1/RRR1-17/3	1257.149	1256.417	-213.848	0.392	979.237	0.508	26	0.114	R.M*LGGGGVDGAIHR.A
R1/RRR1-17/3	1256.699	1256.417	224.546	0.449	912.268	0.477	25	0.107	R.M*LGGGGVDGAIHR.A
R1/RRR1-17/3	1255.993	1256.417	-338.724	0.363	957.010	0.386	25	0.091	R.M*LGGGGVDGAIHR.A
R1/RRR1-5/2	1818.462	1817.933	-259.597	0.639	2500.413	0.618	24	0.506	R.NPQDITQEEYAAFYK.S
R1/RRR1-5/2	1817.217	1817.933	-947.009	0.583	2545.269	0.537	24	0.482	R.NPQDITQEEYAAFYK.S
R1/RRR1-5/2	1257.174	1257.422	-197.762	0.484	999.159	0.439	17	0.223	K.ADLVNNLGTIAR.S
R1/RRR1-6/2	1257.162	1257.422	-207.308	0.440	982.103	0.393	16	0.213	K.ADLVNNLGTIAR.S
R1/RRR1-6/2	1257.439	1257.422	13.572	0.407	907.683	0.409	15	0.210	K.ADLVNNLGTIAR.S
R1/RRR1-5/2	1256.808	1257.422	-1287.739	0.396	751.413	0.426	15	0.206	K.ADLVNNLGTIAR.S
R1/RRR1-6/3	1848.013	1847.148	-73.357	0.403	1087.303	0.240	23	0.078	-.HSEFISYPIYLHVLK.-
R1/RRR1-17/2	1312.518	1313.502	-1516.508	0.378	1845.005	0.420	19	0.305	K.FM*EVISGTGDIK.A
R1/RRR1-17/2	1313.030	1313.502	-360.955	0.437	1631.375	0.417	19	0.277	K.FM*EVISGTGDIK.A
R1/RRR1-17/2	1312.922	1313.502	-1206.993	0.398	1269.139	0.461	17	0.246	K.FM*EVISGTGDIK.A
R1/RRR1-17/2	1673.222	1673.805	-948.747	0.480	1133.798	0.455	21	0.233	K.ENHDFLASVGLDDLK.A
R1/RRR1-17/2	1553.429	1552.708	-179.672	0.486	1192.232	0.438	18	0.233	K.GSSSCTNGLLWLTR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1296.474	1297.503	-1569.240	0.362	1146.274	0.394	18	0.224	K.FMEVISGTGDIK.A
R1/RRR1-17/2	1675.333	1673.805	-282.579	0.464	561.123	0.410	18	0.197	K.ENHDFLASVGLDDLK.A
R1/RRR1-18/2	1770.320	1769.934	218.644	0.499	1506.471	0.520	23	0.286	K.DGATDPTFLYFSHGLK.E
R1/RRR1-18/2	1502.440	1502.650	-140.460	0.487	1397.244	0.542	19	0.279	R.EIENGILWEVDGK.W
R1/RRR1-17/2	1770.768	1769.934	-94.284	0.536	1315.674	0.507	23	0.261	K.DGATDPTFLYFSHGLK.E
R1/RRR1-17/2	1769.617	1769.934	-179.724	0.497	1300.891	0.492	23	0.256	K.DGATDPTFLYFSHGLK.E
R1/RRR1-18/2	1502.434	1502.650	-144.454	0.496	1141.396	0.546	18	0.253	R.EIENGILWEVDGK.W
R1/RRR1-17/2	1502.208	1502.650	-295.503	0.475	1103.793	0.518	18	0.244	R.EIENGILWEVDGK.W
R1/RRR1-17/2	1502.209	1502.650	-295.014	0.445	1047.812	0.530	18	0.242	R.EIENGILWEVDGK.W
R1/RRR1-18/2	1769.316	1769.934	-917.218	0.449	1185.664	0.473	22	0.241	K.DGATDPTFLYFSHGLK.E
R1/RRR1-17/2	1501.474	1502.650	-1453.738	0.378	1117.947	0.503	19	0.241	R.EIENGILWEVDGK.W
R1/RRR1-18/2	1769.244	1769.934	-958.223	0.462	1060.927	0.500	21	0.236	K.DGATDPTFLYFSHGLK.E
R1/RRR1-17/2	1770.264	1769.934	186.767	0.493	1127.902	0.459	22	0.234	K.DGATDPTFLYFSHGLK.E
R1/RRR1-18/2	1501.529	1502.650	-1417.237	0.389	1015.782	0.471	18	0.227	R.EIENGILWEVDGK.W
R1/RRR1-18/2	1063.996	1064.217	-207.891	0.391	1121.011	0.332	15	0.215	K.VVDIVDTFR.L
R1/RRR1-17/2	1064.036	1064.217	-170.256	0.485	761.970	0.426	14	0.214	K.VVDIVDTFR.L
R1/RRR1-18/2	1064.025	1064.217	-180.959	0.375	994.551	0.314	15	0.206	K.VVDIVDTFR.L
R1/RRR1-17/2	1063.289	1064.217	-1818.271	0.352	849.339	0.320	14	0.201	K.VVDIVDTFR.L
R1/RRR1-17/2	1063.545	1064.217	-1576.078	0.394	807.354	0.274	14	0.196	K.VVDIVDTFR.L
R1/RRR1-14/2	1347.353	1346.517	-121.915	0.538	1686.906	0.621	21	0.344	R.TLTGIQIWGSGGR.G
R1/RRR1-14/2	1346.434	1346.517	-61.618	0.518	1595.218	0.602	20	0.323	R.TLTGIQIWGSGGR.G
R1/RRR1-14/2	1042.995	1043.202	-199.751	0.528	1787.504	0.467	16	0.312	R.GLVAQAQSLR.S
R1/RRR1-14/2	1043.057	1043.202	-139.874	0.513	1796.591	0.431	16	0.302	R.GLVAQAQSLR.S
R1/RRR1-14/2	1073.017	1073.228	-197.585	0.531	1706.933	0.420	18	0.286	R.SLATAAQAAIR.A
R1/RRR1-14/2	1072.976	1073.228	-235.819	0.501	1607.652	0.437	18	0.279	R.SLATAAQAAIR.A
R1/RRR1-14/2	1042.935	1043.202	-257.052	0.486	1634.244	0.401	16	0.273	R.GLVAQAQSLR.S
R1/RRR1-14/2	1345.539	1346.517	-1474.529	0.367	1339.036	0.514	20	0.264	R.TLTGIQIWGSGGR.G
R1/RRR1-14/2	1072.998	1073.228	-215.047	0.527	1526.748	0.411	18	0.263	R.SLATAAQAAIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1347.683	1346.517	123.500	0.358	832.688	0.541	17	0.224	R.TLTGIQIWGSGGR.G
R1/RRR1-13/2	1073.132	1073.228	-89.975	0.389	1260.786	0.321	18	0.221	R.SLATAAQAAIR.A
R1/RRR1-13/2	1072.951	1073.228	-258.875	0.340	792.043	0.221	15	0.188	R.SLATAAQAAIR.A
R1/RRR1-23/2	1080.871	1080.176	-283.372	0.569	1795.832	0.539	19	0.334	R.LAGSSAAAFER.C
R1/RRR1-23/2	1079.578	1080.176	-1485.079	0.495	1648.450	0.578	19	0.324	R.LAGSSAAAFER.C
R1/RRR1-24/2	1080.941	1080.176	-218.564	0.513	1705.263	0.544	19	0.322	R.LAGSSAAAFER.C
R1/RRR1-23/2	1080.011	1080.176	-153.113	0.561	1611.690	0.528	19	0.305	R.LAGSSAAAFER.C
R1/RRR1-20/2	1080.425	1080.176	231.335	0.443	1489.654	0.547	18	0.292	R.LAGSSAAAFER.C
R1/RRR1-23/2	1734.505	1734.963	-265.104	0.509	1466.085	0.441	21	0.261	R.VGGPCGYGVCYLYLR.R
R1/RRR1-23/2	1472.539	1473.569	-1382.861	0.393	1298.448	0.460	20	0.248	R.TSDAVSLAFGDAYR.N
R1/RRR1-19/2	1080.127	1080.176	-45.637	0.431	935.024	0.496	17	0.231	R.LAGSSAAAFER.C
R1/RRR1-24/2	1734.158	1734.963	-1044.330	0.460	1107.298	0.459	19	0.230	R.VGGPCGYGVCYLYLR.R
R1/RRR1-23/2	1734.173	1734.963	-1035.284	0.474	1106.477	0.428	19	0.224	R.VGGPCGYGVCYLYLR.R
R1/RRR1-23/2	1733.646	1734.963	-1340.835	0.402	1076.533	0.400	19	0.218	R.VGGPCGYGVCYLYLR.R
R1/RRR1-20/2	1080.500	1080.176	300.328	0.403	516.068	0.429	14	0.205	R.LAGSSAAAFER.C
R1/RRR1-19/2	1079.371	1080.176	-1677.633	0.253	552.316	0.233	15	0.191	R.LAGSSAAAFER.C
R1/RRR1-2/2	1081.206	1080.176	27.335	0.304	279.759	0.314	12	0.191	-.LAGSSAAAFER.-
R1/RRR1-19/2	1080.906	1081.324	-387.460	0.540	955.030	0.329	14	0.203	K.TCLLIVFSK.G
R1/RRR1-19/2	1080.981	1081.324	-318.229	0.463	930.048	0.250	14	0.193	K.TCLLIVFSK.G
R1/RRR1-19/3	1772.856	1772.935	-44.733	0.455	960.657	0.494	27	0.118	K.TSQKPVSPEDGEEIKK.K
R1/RRR1-19/3	1772.956	1772.935	11.828	0.497	825.178	0.515	25	0.116	K.TSQKPVSPEDGEEIKK.K
R1/RRR1-19/3	1644.432	1644.762	-201.269	0.481	913.655	0.467	25	0.110	K.TSQKPVSPEDGEEIK.K
R1/RRR1-19/3	1644.882	1644.762	73.004	0.454	853.428	0.472	25	0.106	K.TSQKPVSPEDGEEIK.K
R1/RRR1-19/3	1772.285	1772.935	-933.996	0.428	684.954	0.493	24	0.102	K.TSQKPVSPEDGEEIKK.K
R1/RRR1-19/3	1644.398	1644.762	-222.270	0.412	817.565	0.436	25	0.097	K.TSQKPVSPEDGEEIK.K
R1/RRR1-20/2	1381.008	1381.475	-339.169	0.449	1448.725	0.516	21	0.280	R.WVGAAVDFSEGSR.A
R1/RRR1-20/2	1381.133	1381.475	-248.184	0.494	1308.828	0.501	20	0.261	R.WVGAAVDFSEGSR.A
R1/RRR1-20/2	1381.162	1381.475	-227.258	0.482	999.254	0.523	18	0.237	R.WVGAAVDFSEGSR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	958.989	959.084	-99.471	0.466	726.663	0.348	13	0.205	R.WAADNLLR.A
R1/RRR1-21/2	959.001	959.084	-87.086	0.481	744.949	0.334	13	0.204	R.WAADNLLR.A
R1/RRR1-20/2	958.880	959.084	-212.996	0.475	698.571	0.331	13	0.203	R.WAADNLLR.A
R1/RRR1-21/2	959.153	959.084	72.364	0.473	681.633	0.325	13	0.202	R.WAADNLLR.A
R1/RRR1-21/2	958.432	959.084	-1728.683	0.406	631.943	0.330	12	0.200	R.WAADNLLR.A
R1/RRR1-20/2	959.751	959.084	-348.283	0.442	621.100	0.296	12	0.198	R.WAADNLLR.A
R1/RRR1-20/3	1981.469	1982.204	-878.276	0.465	1527.864	0.412	29	0.162	K.YGAKPDAETLDM*LNTVAR.Q
R1/RRR1-20/3	1981.294	1982.204	-966.969	0.361	1406.316	0.363	27	0.130	K.YGAKPDAETLDM*LNTVAR.Q
R1/RRR1-20/3	1981.437	1982.204	-894.696	0.414	748.980	0.358	24	0.086	K.YGAKPDAETLDM*LNTVAR.Q
R1/RRR1-16/2	1290.115	1289.467	-273.570	0.525	1517.197	0.568	19	0.303	R.VVGGWASPFVNR.V
R1/RRR1-16/2	1113.490	1113.251	215.340	0.445	1257.249	0.592	17	0.277	K.VPNLAAWADR.F
R1/RRR1-16/2	1289.260	1289.467	-161.121	0.439	1328.273	0.563	18	0.276	R.VVGGWASPFVNR.V
R1/RRR1-15/2	1112.971	1113.251	-252.427	0.426	1319.141	0.508	17	0.264	K.VPNLAAWADR.F
R1/RRR1-15/2	1289.086	1289.467	-296.108	0.457	1133.792	0.573	17	0.258	R.VVGGWASPFVNR.V
R1/RRR1-16/2	1289.148	1289.467	-248.132	0.432	1152.730	0.523	17	0.249	R.VVGGWASPFVNR.V
R1/RRR1-15/2	1159.165	1158.327	-139.595	0.534	1102.744	0.522	17	0.248	K.IAGVELLDEAK.V
R1/RRR1-15/2	1289.220	1289.467	-192.561	0.434	1228.469	0.480	18	0.248	R.VVGGWASPFVNR.V
R1/RRR1-16/2	1158.121	1158.327	-178.626	0.505	1141.261	0.506	17	0.248	K.IAGVELLDEAK.V
R1/RRR1-16/2	1158.149	1158.327	-153.883	0.499	1138.920	0.507	17	0.248	K.IAGVELLDEAK.V
R1/RRR1-15/2	1112.775	1113.251	-428.847	0.432	1279.286	0.434	17	0.245	K.VPNLAAWADR.F
R1/RRR1-16/2	1158.127	1158.327	-172.810	0.488	1114.583	0.496	17	0.244	K.IAGVELLDEAK.V
R1/RRR1-15/2	1158.125	1158.327	-174.608	0.410	1220.671	0.434	17	0.238	K.IAGVELLDEAK.V
R1/RRR1-15/2	1158.108	1158.327	-189.834	0.454	1087.776	0.476	17	0.237	K.IAGVELLDEAK.V
R1/RRR1-16/2	1112.544	1113.251	-1538.689	0.287	597.569	0.427	12	0.198	K.VPNLAAWADR.F
R1/RRR1-15/2	1112.355	1113.251	-1709.559	0.302	646.095	0.372	13	0.197	K.VPNLAAWADR.F
R1/RRR1-15/2	1288.335	1289.467	-1660.124	0.251	472.870	0.399	11	0.188	-.VVGGWASPFVNR.-
R1/RRR1-14/2	1687.357	1686.932	252.614	0.500	2236.506	0.443	25	0.379	R.LISEATAAAGTGLIELR.R
R1/RRR1-14/2	1686.546	1686.932	-229.085	0.446	2012.052	0.432	23	0.335	R.LISEATAAAGTGLIELR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1417.089	1417.509	-297.269	0.502	990.674	0.592	20	0.251	R.SPNVAYVPAGDNGR.M
R1/RRR1-14/2	1417.109	1417.509	-282.836	0.531	958.274	0.571	20	0.245	R.SPNVAYVPAGDNGR.M
R1/RRR1-14/2	1219.105	1219.437	-273.072	0.469	1554.251	0.299	16	0.239	K.DLQM*VNLTLR.L
R1/RRR1-14/2	1219.284	1219.437	-125.419	0.506	1571.723	0.296	16	0.239	K.DLQM*VNLTLR.L
R1/RRR1-14/2	1417.935	1417.509	301.304	0.477	984.308	0.524	19	0.236	R.SPNVAYVPAGDNGR.M
R1/RRR1-14/2	1219.082	1219.437	-291.958	0.390	1483.246	0.238	16	0.222	K.DLQM*VNLTLR.L
R1/RRR1-14/2	1417.123	1417.509	-273.243	0.421	725.148	0.506	18	0.216	R.SPNVAYVPAGDNGR.M
R1/RRR1-21/2	1344.112	1343.485	-278.501	0.501	1303.707	0.442	18	0.247	K.EAFELVSGEM*SK.T
R1/RRR1-21/2	1343.422	1343.485	-47.063	0.485	1335.369	0.387	18	0.238	K.EAFELVSGEM*SK.T
R1/RRR1-21/2	1343.117	1343.485	-274.697	0.459	1191.402	0.408	18	0.231	K.EAFELVSGEM*SK.T
R1/RRR1-21/2	1685.485	1685.902	-248.334	0.477	693.734	0.575	25	0.230	R.LDPGVTASHAFVLETK.V
R1/RRR1-21/2	1686.313	1685.902	244.202	0.502	638.570	0.543	24	0.223	R.LDPGVTASHAFVLETK.V
R1/RRR1-21/2	1685.459	1685.902	-263.447	0.430	641.423	0.485	24	0.213	R.LDPGVTASHAFVLETK.V
R1/RRR1-21/2	1240.062	1239.405	-277.405	0.405	800.280	0.430	17	0.212	R.FQGSPAVITYR.V
R1/RRR1-21/2	1238.596	1239.405	-1464.439	0.356	731.492	0.443	16	0.208	R.FQGSPAVITYR.V
R1/RRR1-20/2	1343.197	1343.485	-214.884	0.446	943.660	0.372	16	0.208	K.EAFELVSGEM*SK.T
R1/RRR1-21/2	1239.017	1239.405	-314.003	0.339	640.471	0.394	15	0.199	R.FQGSPAVITYR.V
R1/RRR1-20/2	1343.060	1343.485	-317.372	0.388	761.091	0.277	15	0.191	K.EAFELVSGEM*SK.T
R1/RRR1-9/2	1730.209	1730.813	-930.165	0.532	2473.887	0.566	25	0.479	K.VFFTNSGSEANDSQVK.L
R1/RRR1-9/2	1730.394	1730.813	-242.879	0.543	2325.436	0.565	25	0.444	K.VFFTNSGSEANDSQVK.L
R1/RRR1-9/2	1217.164	1217.399	-193.901	0.480	1198.736	0.527	19	0.257	K.AFAGSPIVGEIR.G
R1/RRR1-9/2	1217.160	1217.399	-197.020	0.471	1169.730	0.512	19	0.251	K.AFAGSPIVGEIR.G
R1/RRR1-9/2	1216.996	1217.399	-332.060	0.473	1200.071	0.495	19	0.250	K.AFAGSPIVGEIR.G
R1/RRR1-9/2	1270.371	1270.500	-102.220	0.563	1471.307	0.347	18	0.240	R.LANNLEELILK.E
R1/RRR1-9/2	1270.300	1270.500	-157.936	0.546	1418.221	0.346	18	0.236	R.LANNLEELILK.E
R1/RRR1-9/2	1269.606	1270.500	-1496.273	0.409	1372.893	0.318	18	0.229	R.LANNLEELILK.E
R1/RRR1-19/2	1215.960	1216.282	-265.383	0.486	712.131	0.536	15	0.224	R.AQGSYTFADQK.T
R1/RRR1-19/2	1215.821	1216.282	-380.214	0.469	697.058	0.490	15	0.216	R.AQGSYTFADQK.T

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1215.575	1216.282	-1408.372	0.474	687.558	0.487	15	0.216	R.AQGSYTFADQK.T
R1/RRR1-18/2	1216.097	1216.282	-152.692	0.490	679.120	0.442	15	0.210	R.AQGSYTFADQK.T
R1/RRR1-19/2	1216.025	1216.282	-211.703	0.509	682.561	0.442	15	0.210	R.AQGSYTFADQK.T
R1/RRR1-18/2	887.867	888.004	-155.014	0.420	1138.237	0.261	13	0.205	R.NEVLSAVR.E
R1/RRR1-18/2	887.997	888.004	-7.323	0.339	1132.367	0.197	13	0.196	R.NEVLSAVR.E
R1/RRR1-18/2	887.859	888.004	-164.117	0.416	1177.709	0.177	13	0.194	R.NEVLSAVR.E
R1/RRR1-19/2	887.587	888.004	-471.367	0.342	1108.484	0.130	13	0.187	R.NEVLSAVR.E
R1/RRR1-19/2	887.988	888.004	-18.353	0.386	1113.598	0.116	13	0.185	R.NEVLSAVR.E
R1/RRR1-18/3	1760.428	1761.017	-905.304	0.415	1013.514	0.563	29	0.135	K.VYFHDVVGGTKPTAIR.V
R1/RRR1-19/3	1760.673	1761.017	-196.152	0.439	943.344	0.453	26	0.109	K.VYFHDVVGGTKPTAIR.V
R1/RRR1-19/3	1760.098	1761.017	-1093.396	0.395	774.641	0.463	26	0.100	K.VYFHDVVGGTKPTAIR.V
R1/RRR1-19/3	1761.527	1761.017	-278.977	0.426	611.024	0.456	25	0.096	K.VYFHDVVGGTKPTAIR.V
R1/RRR1-16/2	1482.151	1480.688	313.197	0.433	1192.905	0.445	16	0.234	K.TATEVTILIEAYR.T
R1/RRR1-16/2	1023.590	1024.199	-1576.477	0.418	682.409	0.587	16	0.230	R.GPLPASQVVR.D
R1/RRR1-16/2	1024.015	1024.199	-179.899	0.449	513.064	0.582	15	0.224	R.GPLPASQVVR.D
R1/RRR1-15/2	1024.057	1024.199	-138.763	0.419	468.046	0.553	14	0.217	R.GPLPASQVVR.D
R1/RRR1-16/2	1023.940	1024.199	-253.809	0.421	319.750	0.589	12	0.214	R.GPLPASQVVR.D
R1/RRR1-15/2	1023.274	1024.199	-1886.982	0.374	426.039	0.512	13	0.208	R.GPLPASQVVR.D
R1/RRR1-18/2	1481.711	1480.688	15.898	0.247	573.836	0.305	13	0.184	K.TATEVTILIEAYR.T
R1/RRR1-16/3	1295.000	1295.473	-366.716	0.461	1730.591	0.422	25	0.182	R.DRGPLPASQVVR.D
R1/RRR1-15/2	1481.954	1480.688	180.058	0.348	686.686	0.127	13	0.175	-.TATEVTILIEAYR.-
R1/RRR1-16/3	1295.570	1295.473	74.874	0.449	1053.539	0.349	22	0.093	R.DRGPLPASQVVR.D
R1/RRR1-16/3	1294.533	1295.473	-1502.844	0.337	1098.662	0.272	22	0.080	R.DRGPLPASQVVR.D
R1/RRR1-13/2	1261.025	1261.407	-304.154	0.428	1316.478	0.471	18	0.254	R.TIITAGEDATIR.I
R1/RRR1-12/2	1260.841	1261.407	-1246.234	0.381	1237.189	0.500	18	0.251	R.TIITAGEDATIR.I
R1/RRR1-13/2	1260.931	1261.279	-277.280	0.444	1128.392	0.500	18	0.244	R.SFSSGGEDGYVR.L
R1/RRR1-13/2	1260.687	1261.407	-1368.562	0.287	1273.930	0.407	18	0.233	R.TIITAGEDATIR.I
R1/RRR1-12/2	1086.023	1086.264	-221.938	0.357	1344.934	0.351	15	0.231	K.ILQEEIGGVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1086.085	1086.264	-164.996	0.374	1282.616	0.329	16	0.223	K.ILQEEIGGVK.G
R1/RRR1-13/2	1260.946	1261.279	-265.334	0.410	917.459	0.467	18	0.223	R.SFSSGGEDGYVR.L
R1/RRR1-12/2	1260.983	1261.279	-235.809	0.403	956.714	0.460	16	0.221	R.SFSSGGEDGYVR.L
R1/RRR1-12/2	1261.021	1261.407	-307.165	0.437	819.658	0.452	16	0.214	R.TIITAGEDATIR.I
R1/RRR1-12/2	1261.101	1261.279	-141.806	0.368	509.171	0.452	13	0.199	R.SFSSGGEDGYVR.L
R1/RRR1-9/3	1977.688	1978.192	-762.824	0.521	3970.733	0.501	42	1.000	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/2	1977.515	1978.192	-850.617	0.597	3957.218	0.544	29	0.899	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/2	1977.514	1978.192	-851.422	0.586	3780.517	0.573	30	0.853	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/2	1977.144	1978.192	-1039.155	0.572	3738.635	0.548	29	0.823	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/3	1977.712	1978.192	-243.498	0.457	3449.564	0.523	40	0.773	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-2/2	1980.121	1978.192	-36.148	0.635	3266.718	0.617	28	0.701	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-3/2	1978.543	1978.192	177.935	0.556	3140.027	0.533	28	0.621	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-4/2	1978.859	1978.192	-169.011	0.574	2653.851	0.536	26	0.491	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-10/2	1978.895	1978.192	-150.756	0.527	2048.241	0.534	24	0.364	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/2	1979.656	1978.192	234.797	0.500	1869.387	0.550	23	0.339	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-8/2	1978.141	1978.192	-26.219	0.501	2020.121	0.450	24	0.331	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-2/2	1977.207	1978.192	-1006.921	0.436	1926.427	0.389	24	0.300	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-15/2	1979.071	1978.192	-61.594	0.424	1622.862	0.503	23	0.290	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-8/2	1978.698	1978.192	-250.393	0.450	1557.525	0.505	22	0.281	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/2	1977.881	1978.192	-158.138	0.408	1695.593	0.391	23	0.270	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/3	1977.152	1978.192	-1034.823	0.455	2018.857	0.436	32	0.262	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-16/2	1978.108	1978.192	-42.870	0.447	1214.601	0.475	21	0.238	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/2	1978.776	1978.192	-210.907	0.426	1080.791	0.494	22	0.232	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-7/2	1977.468	1978.192	-874.413	0.373	1050.958	0.449	23	0.223	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-9/2	1689.410	1688.954	270.860	0.489	570.645	0.513	21	0.210	R.RPVPGSYGVPFVSAVR.D
R1/RRR1-9/2	1979.170	1978.192	-11.297	0.326	845.050	0.373	20	0.200	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-8/2	1979.192	1978.192	-0.409	0.308	904.893	0.316	18	0.193	R.SNFGALLDTVELQLASGGGK.S
R1/RRR1-13/2	1545.146	1545.639	-319.859	0.523	1233.588	0.463	21	0.247	K.FNDLSTNHNNQLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1847.803	1847.104	-163.500	0.498	824.190	0.506	17	0.217	R.IM*YADFYSGVYDMVR.N
R1/RRR1-13/3	1673.328	1673.812	-289.950	0.515	919.885	0.502	26	0.116	K.KFNDLSTNHNNQLK.T
R1/RRR1-13/3	1672.923	1673.812	-1131.965	0.423	945.346	0.442	25	0.104	K.KFNDLSTNHNNQLK.T
R1/RRR1-13/3	1673.719	1673.812	-55.612	0.462	810.672	0.464	25	0.102	K.KFNDLSTNHNNQLK.T
R1/RRR1-16/2	1406.199	1405.487	-205.188	0.518	1485.968	0.526	18	0.289	R.FYCWDTAGQEK.F
R1/RRR1-16/2	1405.015	1405.487	-336.859	0.460	1480.369	0.510	18	0.283	R.FYCWDTAGQEK.F
R1/RRR1-16/2	1763.537	1762.988	-256.921	0.528	1157.745	0.533	18	0.250	K.SNYNFEKPFLYLAR.K
R1/RRR1-16/2	1405.136	1405.487	-250.479	0.450	1252.649	0.442	17	0.243	R.FYCWDTAGQEK.F
R1/RRR1-16/2	1763.568	1762.988	-239.283	0.560	1030.278	0.530	18	0.239	K.SNYNFEKPFLYLAR.K
R1/RRR1-15/2	1762.555	1762.988	-246.714	0.452	1190.890	0.449	19	0.237	K.SNYNFEKPFLYLAR.K
R1/RRR1-16/2	1762.527	1762.988	-262.487	0.564	1027.499	0.498	18	0.232	K.SNYNFEKPFLYLAR.K
R1/RRR1-17/2	1764.080	1762.988	51.873	0.459	787.107	0.466	16	0.212	K.SNYNFEKPFLYLAR.K
R1/RRR1-15/2	1762.438	1762.988	-882.450	0.447	787.015	0.448	16	0.209	K.SNYNFEKPFLYLAR.K
R1/RRR1-16/3	1762.579	1762.988	-232.652	0.523	1606.403	0.529	30	0.197	K.SNYNFEKPFLYLAR.K
R1/RRR1-15/2	1763.837	1762.988	-86.256	0.384	251.298	0.470	13	0.196	-.SNYNFEKPFLYLAR.-
R1/RRR1-16/2	1763.894	1762.988	-53.351	0.310	183.496	0.341	12	0.192	-.SNYNFEKPFLYLAR.-
R1/RRR1-16/3	1763.686	1762.988	-171.624	0.531	1222.915	0.578	27	0.164	K.SNYNFEKPFLYLAR.K
R1/RRR1-16/3	1761.979	1762.988	-1143.546	0.498	1193.543	0.548	26	0.153	K.SNYNFEKPFLYLAR.K
R1/RRR1-15/3	1762.635	1762.988	-200.865	0.448	773.554	0.528	22	0.116	K.SNYNFEKPFLYLAR.K
R1/RRR1-15/3	1762.259	1762.988	-984.331	0.424	929.448	0.419	25	0.101	K.SNYNFEKPFLYLAR.K
R1/RRR1-17/3	1761.978	1762.988	-1144.589	0.411	742.744	0.383	22	0.091	K.SNYNFEKPFLYLAR.K
R1/RRR1-17/3	1761.741	1762.988	-1279.638	0.371	524.298	0.357	19	0.088	K.SNYNFEKPFLYLAR.K
R1/RRR1-3/2	1490.586	1490.749	-110.044	0.482	1073.403	0.549	19	0.249	R.TYIGPM*TPPLVER.I
R1/RRR1-3/2	1011.281	1011.243	36.974	0.455	679.961	0.413	15	0.206	R.LIGASLPAIR.A
R1/RRR1-3/2	1159.002	1159.280	-240.289	0.409	971.043	0.326	16	0.202	R.RFPAAPTEGGR.L
R1/RRR1-3/2	1011.026	1011.243	-215.392	0.438	585.855	0.369	14	0.198	R.LIGASLPAIR.A
R1/RRR1-10/2	1184.965	1185.304	-287.307	0.489	1700.960	0.426	16	0.288	K.FGCTDFVNPK.D
R1/RRR1-10/2	1185.033	1185.304	-229.638	0.431	1647.324	0.397	16	0.274	K.FGCTDFVNPK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1185.215	1185.304	-75.164	0.456	1501.429	0.390	16	0.256	K.FGCTDFVNPK.D
R1/RRR1-3/2	1039.984	1040.238	-245.066	0.407	537.577	0.474	15	0.212	R.IIGVDLNPAK.F
R1/RRR1-10/2	1040.159	1040.238	-76.583	0.454	476.703	0.425	14	0.207	R.IIGVDLNPAK.F
R1/RRR1-3/2	1040.089	1040.238	-144.276	0.391	527.463	0.384	14	0.202	R.IIGVDLNPAK.F
R1/RRR1-3/2	1040.071	1040.238	-160.994	0.347	568.805	0.353	15	0.200	R.IIGVDLNPAK.F
R1/RRR1-10/2	1041.165	1040.238	-70.747	0.474	530.236	0.349	14	0.200	R.IIGVDLNPAK.F
R1/RRR1-10/2	1643.562	1643.908	-211.610	0.486	708.385	0.436	16	0.199	-.IIGVDLNPAKFEQAK.-
R1/RRR1-7/2	1041.236	1040.238	-1.718	0.343	436.712	0.268	14	0.196	R.IIGVDLNPAK.F
R1/RRR1-1/2	1185.070	1185.304	-198.533	0.366	632.003	0.293	14	0.194	K.FGCTDFVNPK.D
R1/RRR1-6/2	1002.507	1003.135	-1629.172	0.351	976.130	0.377	14	0.211	R.VAVTNTLER.R
R1/RRR1-6/2	1002.662	1003.135	-473.257	0.354	534.429	0.325	13	0.192	-.VAVTNTLER.-
R1/RRR1-5/2	1624.260	1623.833	264.085	0.534	1758.025	0.510	19	0.318	R.VINTALFSEYYFR.V
R1/RRR1-5/2	1623.674	1623.833	-97.849	0.507	1737.911	0.516	19	0.317	R.VINTALFSEYYFR.V
R1/RRR1-5/2	1326.050	1326.541	-371.064	0.537	1717.174	0.376	18	0.276	R.M*VEESFILDVK.H
R1/RRR1-4/2	1624.491	1623.833	-210.627	0.502	1394.986	0.505	18	0.269	R.VINTALFSEYYFR.V
R1/RRR1-5/2	1623.106	1623.833	-1066.826	0.337	1223.324	0.411	17	0.230	R.VINTALFSEYYFR.V
R1/RRR1-5/2	974.441	975.083	-1690.482	0.409	914.687	0.473	13	0.225	K.HGESYLLR.V
R1/RRR1-5/2	975.191	975.083	110.722	0.482	746.039	0.463	13	0.219	K.HGESYLLR.V
R1/RRR1-5/2	974.987	975.083	-98.969	0.362	848.649	0.412	13	0.212	K.HGESYLLR.V
R1/RRR1-4/2	1327.498	1326.541	-32.448	0.286	701.190	0.339	14	0.192	R.M*VEESFILDVK.H
R1/RRR1-4/2	975.148	975.083	66.531	0.292	510.138	0.259	11	0.191	K.HGESYLLR.V
R1/RRR1-14/2	1859.775	1859.285	263.954	0.514	1172.718	0.608	22	0.266	R.LPLVGPLLTPPVSVASVAK.V
R1/RRR1-14/2	1586.243	1586.772	-967.040	0.458	1154.179	0.591	21	0.262	K.INGTANINAISVAAEK.G
R1/RRR1-14/2	1586.419	1586.772	-223.323	0.479	1099.090	0.608	21	0.261	K.INGTANINAISVAAEK.G
R1/RRR1-14/2	1859.058	1859.285	-122.736	0.516	967.353	0.609	21	0.246	R.LPLVGPLLTPPVSVASVAK.V
R1/RRR1-14/2	1859.231	1859.285	-29.147	0.501	932.860	0.602	21	0.241	R.LPLVGPLLTPPVSVASVAK.V
R1/RRR1-14/2	962.095	962.080	16.021	0.463	911.919	0.420	15	0.217	R.ATEAELLSK.F
R1/RRR1-14/2	1198.092	1198.305	-178.185	0.520	1595.441	0.415	16	0.271	R.TCYAQASQIR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1198.001	1198.305	-253.827	0.537	1379.752	0.437	17	0.255	R.TCYAQASQIR.Q
R1/RRR1-20/2	1579.327	1579.824	-315.649	0.430	941.559	0.510	20	0.232	K.ATSSIFPLQNVFVR.K
R1/RRR1-18/2	1580.462	1579.824	-230.130	0.483	825.871	0.542	19	0.231	K.ATSSIFPLQNVFVR.K
R1/RRR1-17/2	1198.186	1198.305	-98.875	0.471	1349.281	0.337	16	0.230	R.TCYAQASQIR.Q
R1/RRR1-14/2	1579.382	1579.824	-281.219	0.432	967.652	0.480	20	0.229	K.ATSSIFPLQNVFVR.K
R1/RRR1-14/2	1197.467	1198.305	-1539.278	0.418	1228.355	0.379	15	0.229	R.TCYAQASQIR.Q
R1/RRR1-18/2	1198.158	1198.305	-122.483	0.460	1188.345	0.385	16	0.228	R.TCYAQASQIR.Q
R1/RRR1-14/2	1579.305	1579.824	-964.620	0.432	900.785	0.493	19	0.226	K.ATSSIFPLQNVFVR.K
R1/RRR1-14/2	1580.365	1579.824	-291.735	0.446	862.229	0.503	19	0.226	K.ATSSIFPLQNVFVR.K
R1/RRR1-19/2	1579.516	1579.824	-196.006	0.427	867.331	0.485	20	0.224	K.ATSSIFPLQNVFVR.K
R1/RRR1-14/2	890.008	890.021	-15.492	0.446	814.853	0.455	13	0.221	K.APSVFNVR.N
R1/RRR1-20/2	1580.315	1579.824	311.174	0.489	829.489	0.475	19	0.220	K.ATSSIFPLQNVFVR.K
R1/RRR1-19/2	1579.564	1579.824	-165.382	0.409	914.601	0.396	20	0.213	K.ATSSIFPLQNVFVR.K
R1/RRR1-18/2	1579.369	1579.824	-289.361	0.350	782.316	0.457	17	0.211	K.ATSSIFPLQNVFVR.K
R1/RRR1-15/2	1580.168	1579.824	218.378	0.434	586.562	0.497	16	0.211	K.ATSSIFPLQNVFVR.K
R1/RRR1-18/2	1579.443	1579.824	-242.371	0.403	749.666	0.427	18	0.209	K.ATSSIFPLQNVFVR.K
R1/RRR1-14/2	889.446	890.021	-1776.381	0.360	653.574	0.428	12	0.208	K.APSVFNVR.N
R1/RRR1-16/2	1580.267	1579.824	280.657	0.396	640.050	0.440	17	0.207	K.ATSSIFPLQNVFVR.K
R1/RRR1-14/2	889.629	890.021	-442.553	0.324	660.580	0.395	12	0.203	K.APSVFNVR.N
R1/RRR1-2/2	1581.223	1579.824	252.612	0.391	577.202	0.445	15	0.203	K.ATSSIFPLQNVFVR.K
R1/RRR1-17/2	1197.998	1198.305	-256.893	0.438	1100.848	0.244	16	0.200	R.TCYAQASQIR.Q
R1/RRR1-18/2	1197.758	1198.305	-1294.901	0.428	895.492	0.275	16	0.199	R.TCYAQASQIR.Q
R1/RRR1-25/2	890.176	890.021	173.907	0.273	444.683	0.374	10	0.196	K.APSVFNVR.N
R1/RRR1-1/2	1579.449	1579.824	-238.572	0.308	438.569	0.302	13	0.189	-.ATSSIFPLQNVFVR.-
R1/RRR1-25/2	889.465	890.021	-1754.732	0.171	246.292	0.369	9	0.166	-.APSVFNVR.-
R1/RRR1-25/2	889.591	890.021	-485.100	0.188	134.981	0.429	6	0.138	-.APSVFNVR.-
R1/RRR1-11/2	1720.463	1720.910	-260.364	0.502	1853.467	0.448	19	0.312	K.NLSLGTEAFWLGQQR.K
R1/RRR1-11/2	1517.171	1516.679	325.255	0.537	1374.848	0.493	20	0.265	K.IDTNGVVSALLEER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1515.975	1516.679	-1127.195	0.364	1096.686	0.394	19	0.218	K.IDTNGVVSALLEER.L
R1/RRR1-11/2	1719.970	1720.910	-1131.462	0.414	1199.064	0.355	16	0.214	K.NLSLGTEAFWLGQQR.K
R1/RRR1-11/2	793.186	792.906	353.854	0.320	931.743	0.201	13	0.187	K.SGVGFVAR.Y
R1/RRR1-19/2	1423.741	1423.726	10.697	0.451	796.015	0.477	21	0.218	K.QSLAGIPLLVLGNK.I
R1/RRR1-19/2	1423.343	1423.726	-269.468	0.464	852.430	0.406	22	0.211	K.QSLAGIPLLVLGNK.I
R1/RRR1-19/2	1056.113	1056.195	-77.049	0.293	831.336	0.369	13	0.198	K.SELHDLLTK.Q
R1/RRR1-19/2	1449.291	1449.634	-237.357	0.344	673.325	0.417	13	0.192	R.GVSAILYVVDAADR.D
R1/RRR1-17/2	1574.767	1575.748	-1261.602	0.345	1256.323	0.336	19	0.219	K.EAVNVEQAFEVIAR.N
R1/RRR1-9/2	1423.093	1423.550	-322.256	0.474	2397.083	0.484	23	0.427	K.FIASEGDTVTPGTK.V
R1/RRR1-9/2	1422.773	1423.550	-1252.753	0.381	2220.537	0.473	22	0.386	K.FIASEGDTVTPGTK.V
R1/RRR1-9/2	1423.150	1423.550	-281.635	0.477	2104.440	0.485	22	0.369	K.FIASEGDTVTPGTK.V
R1/RRR1-9/2	1796.279	1795.885	219.642	0.526	1486.294	0.660	22	0.320	K.SAAPAETHVAPSEDSTPK.E
R1/RRR1-9/2	1795.393	1795.885	-274.867	0.505	1252.998	0.650	21	0.285	K.SAAPAETHVAPSEDSTPK.E
R1/RRR1-9/2	1795.313	1795.885	-878.294	0.485	1267.741	0.634	21	0.282	K.SAAPAETHVAPSEDSTPK.E
R1/RRR1-9/2	1398.884	1399.466	-1134.383	0.486	1490.425	0.431	17	0.262	R.DADNM*NFADIEK.G
R1/RRR1-9/2	1399.059	1399.466	-291.573	0.488	1219.385	0.431	17	0.236	R.DADNM*NFADIEK.G
R1/RRR1-9/2	1398.605	1399.466	-1334.379	0.364	1259.237	0.318	17	0.218	R.DADNM*NFADIEK.G
R1/RRR1-11/2	1570.102	1569.657	284.423	0.560	2122.264	0.420	24	0.352	K.NFGDEALIGEGSFGR.V
R1/RRR1-6/2	1181.941	1181.372	-365.216	0.424	1097.977	0.314	16	0.209	R.VYFGVLRNGR.S
R1/RRR1-11/2	996.164	996.189	-24.902	0.384	642.260	0.400	15	0.204	K.ALQPLLNAR.A
R1/RRR1-6/2	1182.051	1181.372	-272.478	0.367	1147.595	0.199	16	0.195	R.VYFGVLRNGR.S
R1/RRR1-12/2	995.593	996.189	-1607.527	0.278	534.036	0.312	13	0.190	K.ALQPLLNAR.A
R1/RRR1-6/2	1949.565	1950.144	-812.570	0.563	1695.412	0.631	27	0.345	K.GAADFQPLALGLGNASYAGR.-
R1/RRR1-6/2	1949.643	1950.144	-772.032	0.550	1668.158	0.626	27	0.339	K.GAADFQPLALGLGNASYAGR.-
R1/RRR1-6/2	1950.617	1950.144	243.376	0.570	1452.145	0.635	26	0.309	K.GAADFQPLALGLGNASYAGR.-
R1/RRR1-6/3	1949.592	1950.144	-798.593	0.476	1805.202	0.517	33	0.250	K.GAADFQPLALGLGNASYAGR.-
R1/RRR1-6/3	1668.829	1668.745	50.534	0.565	1787.281	0.551	29	0.245	K.YGETYKAEHDDLAR.R
R1/RRR1-6/2	1589.359	1589.731	-235.235	0.362	591.118	0.445	21	0.203	K.NLPTYTPSDPAVASR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1589.140	1589.731	-1004.493	0.346	381.984	0.466	17	0.197	K.NLPTYTPSDPAVASR.K
R1/RRR1-6/3	1668.186	1668.745	-937.454	0.531	1380.330	0.533	27	0.172	K.YGETYKAEHDDLAR.R
R1/RRR1-6/3	1667.968	1668.745	-1068.934	0.465	1357.802	0.529	25	0.168	K.YGETYKAEHDDLAR.R
R1/RRR1-6/3	1950.854	1950.144	-148.882	0.315	750.126	0.275	28	0.072	K.GAADFQPLALGLGNASYAGR.-
R1/RRR1-15/2	1908.441	1909.040	-840.666	0.511	2055.079	0.565	24	0.389	R.ASGSCDFAGAASIVNQQPK.I
R1/RRR1-15/3	1962.964	1963.098	-68.656	0.534	1772.078	0.570	31	0.259	K.VAHATYAFNDFYQTTGR.A
R1/RRR1-15/3	1964.042	1963.098	-28.814	0.539	1786.025	0.500	28	0.240	K.VAHATYAFNDFYQTTGR.A
R1/RRR1-15/3	1962.617	1963.098	-245.808	0.495	1595.338	0.516	30	0.204	K.VAHATYAFNDFYQTTGR.A
R1/RRR1-15/2	1285.297	1285.432	-105.320	0.424	762.500	0.323	13	0.193	-.NFGLFYPNGQK.-
R1/RRR1-14/2	1285.961	1285.432	-367.379	0.334	765.643	0.249	14	0.188	R.NFGLFYPNGQK.V
R1/RRR1-12/2	1285.977	1285.432	-354.616	0.363	532.856	0.332	13	0.188	-.NFGLFYPNGQK.-
R1/RRR1-14/2	1286.193	1285.432	-186.732	0.306	589.675	0.237	12	0.185	R.NFGLFYPNGQK.V
R1/RRR1-10/2	1424.168	1424.542	-262.950	0.456	1694.874	0.511	16	0.310	K.YAFEYAYLNNR.K
R1/RRR1-10/2	1280.905	1281.433	-1197.081	0.506	1507.539	0.559	18	0.300	K.LADGLFLESCR.E
R1/RRR1-10/2	1281.176	1281.433	-201.511	0.518	1263.741	0.591	18	0.280	K.LADGLFLESCR.E
R1/RRR1-10/2	1280.712	1281.433	-1347.927	0.408	1422.942	0.506	18	0.274	K.LADGLFLESCR.E
R1/RRR1-10/2	1423.847	1424.542	-1193.765	0.469	1432.113	0.426	16	0.256	K.YAFEYAYLNNR.K
R1/RRR1-10/2	1424.124	1424.542	-293.909	0.406	1005.530	0.460	15	0.225	K.YAFEYAYLNNR.K
R1/RRR1-10/2	1194.209	1194.366	-131.705	0.443	882.898	0.460	16	0.222	R.HQDVDIVVIR.E
R1/RRR1-10/2	1194.218	1194.366	-124.220	0.468	978.772	0.420	16	0.221	R.HQDVDIVVIR.E
R1/RRR1-10/2	1194.237	1194.366	-107.814	0.480	829.317	0.400	15	0.210	R.HQDVDIVVIR.E
R1/RRR1-14/2	1354.292	1354.536	-180.777	0.546	2056.876	0.490	22	0.362	R.IPSGEVWVGNPAK.F
R1/RRR1-14/2	1353.661	1354.536	-1389.072	0.472	1831.038	0.538	21	0.340	R.IPSGEVWVGNPAK.F
R1/RRR1-14/2	1355.193	1354.536	-254.018	0.566	1683.175	0.554	21	0.323	R.IPSGEVWVGNPAK.F
R1/RRR1-14/3	1928.760	1929.100	-177.101	0.514	1906.070	0.463	29	0.246	K.YAHKDEEYDSM*LGVVR.E
R1/RRR1-14/3	1102.689	1102.290	363.447	0.425	1528.016	0.285	25	0.111	K.HSM*VGAGSLVK.Q
R1/RRR1-14/3	1101.993	1102.290	-269.953	0.334	741.227	0.255	20	0.072	K.HSM*VGAGSLVK.Q
R1/RRR1-7/2	1767.942	1766.886	31.676	0.558	2256.366	0.574	24	0.437	R.YPGIFESEIDEDVPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	966.208	966.116	95.722	0.379	757.276	0.330	14	0.197	R.SYGLTGLVR.I
R1/RRR1-14/2	1482.066	1482.586	-1028.653	0.247	927.003	0.125	16	0.176	K.WADAHDGRLPSTR.Q
R1/RRR1-11/2	1557.121	1557.767	-1060.768	0.463	1623.359	0.579	21	0.320	R.VPTPNVSVVDLTCR.I
R1/RRR1-11/2	1508.769	1508.854	-56.611	0.410	1391.005	0.481	19	0.263	R.VLDLIAHMALVNAK.-
R1/RRR1-12/2	1557.373	1557.767	-254.218	0.435	1157.011	0.555	18	0.254	R.VPTPNVSVVDLTCR.I
R1/RRR1-12/2	1372.412	1373.539	-1554.406	0.321	1565.698	0.483	19	0.281	R.AIQQDGLVWGASK.L
R1/RRR1-12/2	1373.073	1373.539	-340.861	0.467	1396.064	0.495	18	0.267	R.AIQQDGLVWGASK.L
R1/RRR1-12/2	1784.263	1784.003	146.325	0.550	1028.053	0.596	24	0.255	R.SYIVGTAPSQADVVTFK.A
R1/RRR1-12/2	1661.196	1661.797	-966.818	0.484	1159.998	0.494	20	0.241	K.ALSSAPDAEKYPNAAR.W
R1/RRR1-12/2	1783.365	1784.003	-921.114	0.456	884.299	0.550	23	0.232	R.SYIVGTAPSQADVVTFK.A
R1/RRR1-12/2	1782.762	1784.003	-1260.627	0.315	835.452	0.528	21	0.218	R.SYIVGTAPSQADVVTFK.A
R1/RRR1-18/2	1877.788	1878.113	-173.348	0.626	3607.002	0.590	27	0.818	R.IVNAGGECLTFDQLALR.A
R1/RRR1-18/2	1878.960	1878.113	-81.362	0.617	3314.229	0.579	26	0.713	R.IVNAGGECLTFDQLALR.A
R1/RRR1-18/2	1877.455	1878.113	-885.451	0.594	3116.214	0.593	26	0.660	R.IVNAGGECLTFDQLALR.A
R1/RRR1-18/2	1182.239	1182.398	-135.213	0.448	1787.350	0.461	19	0.308	R.APLGQNTVLLR.G
R1/RRR1-18/2	1183.119	1182.398	-236.633	0.474	1564.932	0.518	19	0.295	R.APLGQNTVLLR.G
R1/RRR1-18/2	1181.858	1182.398	-1306.624	0.467	1436.845	0.488	18	0.272	R.APLGQNTVLLR.G
R1/RRR1-17/2	1182.796	1182.398	337.187	0.434	1250.187	0.507	17	0.257	R.APLGQNTVLLR.G
R1/RRR1-17/2	1182.463	1182.398	55.229	0.455	1250.946	0.485	18	0.253	R.APLGQNTVLLR.G
R1/RRR1-18/2	1182.684	1182.398	242.908	0.438	1243.730	0.435	18	0.242	R.APLGQNTVLLR.G
R1/RRR1-17/2	1181.996	1182.398	-341.374	0.392	1088.034	0.508	17	0.242	R.APLGQNTVLLR.G
R1/RRR1-19/2	1183.311	1182.398	-73.837	0.393	1197.233	0.453	17	0.240	R.APLGQNTVLLR.G
R1/RRR1-19/2	1183.459	1182.398	51.665	0.408	1272.808	0.405	18	0.238	R.APLGQNTVLLR.G
R1/RRR1-20/2	1182.973	1182.398	-360.343	0.467	944.421	0.527	16	0.237	R.APLGQNTVLLR.G
R1/RRR1-17/2	1183.243	1182.398	-131.063	0.435	1137.111	0.448	17	0.236	R.APLGQNTVLLR.G
R1/RRR1-19/2	1183.268	1182.398	-109.745	0.385	1143.797	0.450	17	0.236	R.APLGQNTVLLR.G
R1/RRR1-20/2	1181.996	1182.398	-341.374	0.391	636.394	0.531	15	0.220	R.APLGQNTVLLR.G
R1/RRR1-17/2	1182.849	1182.398	382.613	0.333	854.919	0.378	14	0.206	R.APLGQNTVLLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1182.910	1182.398	-413.771	0.339	554.958	0.434	13	0.204	R.APLGQNTVLLR.G
R1/RRR1-14/2	1454.106	1454.561	-313.698	0.552	1681.431	0.593	21	0.335	R.DLVGVAYTEEETK.A
R1/RRR1-14/2	1453.966	1454.561	-1100.237	0.498	1691.375	0.580	21	0.332	R.DLVGVAYTEEETK.A
R1/RRR1-14/2	1665.052	1664.883	101.652	0.475	766.194	0.550	21	0.227	R.FANGGAYPPDLSLITK.A
R1/RRR1-14/2	1665.894	1664.883	6.570	0.453	799.361	0.502	23	0.223	R.FANGGAYPPDLSLITK.A
R1/RRR1-14/2	1666.408	1664.883	-285.636	0.508	813.462	0.485	22	0.220	R.FANGGAYPPDLSLITK.A
R1/RRR1-14/2	1666.016	1664.883	79.839	0.459	670.820	0.497	20	0.214	R.FANGGAYPPDLSLITK.A
R1/RRR1-14/2	1665.365	1664.883	290.430	0.454	568.982	0.499	20	0.212	R.FANGGAYPPDLSLITK.A
R1/RRR1-14/2	1665.688	1664.883	-117.359	0.447	464.983	0.444	19	0.204	R.FANGGAYPPDLSLITK.A
R1/RRR1-13/2	1453.998	1454.561	-1077.983	0.374	840.040	0.397	15	0.203	R.DLVGVAYTEEETK.A
R1/RRR1-14/2	1889.369	1890.049	-891.727	0.476	590.601	0.436	18	0.199	K.LSDRFPQPYPNEQAAR.F
R1/RRR1-13/2	1665.484	1664.883	-240.068	0.366	265.827	0.398	15	0.196	R.FANGGAYPPDLSLITK.A
R1/RRR1-13/2	1666.334	1664.883	271.451	0.258	308.710	0.315	17	0.193	R.FANGGAYPPDLSLITK.A
R1/RRR1-14/2	1890.692	1890.049	-189.261	0.480	468.545	0.368	17	0.189	K.LSDRFPQPYPNEQAAR.F
R1/RRR1-8/2	1240.370	1240.388	-14.373	0.513	1889.137	0.530	19	0.346	K.YGVTESTLLTR.N
R1/RRR1-7/2	1241.154	1240.388	-189.266	0.528	1539.535	0.606	19	0.318	K.YGVTESTLLTR.N
R1/RRR1-7/2	1239.670	1240.388	-1389.986	0.543	1556.518	0.548	18	0.303	K.YGVTESTLLTR.N
R1/RRR1-7/2	1239.830	1240.388	-1260.639	0.554	1514.240	0.509	19	0.288	K.YGVTESTLLTR.N
R1/RRR1-9/2	1240.268	1240.388	-97.297	0.410	1525.569	0.466	18	0.276	K.YGVTESTLLTR.N
R1/RRR1-8/2	1239.667	1240.388	-1392.657	0.546	1266.212	0.565	18	0.274	K.YGVTESTLLTR.N
R1/RRR1-7/2	1868.481	1869.154	-897.698	0.534	1384.892	0.512	25	0.270	R.LPIYVVQPQDGLDAIAR.N
R1/RRR1-7/2	1868.583	1869.154	-843.396	0.561	1352.367	0.519	25	0.268	R.LPIYVVQPQDGLDAIAR.N
R1/RRR1-7/2	1868.842	1869.154	-167.495	0.576	1305.610	0.510	24	0.260	R.LPIYVVQPQDGLDAIAR.N
R1/RRR1-8/2	1239.595	1240.388	-1450.815	0.480	1247.312	0.486	18	0.253	K.YGVTESTLLTR.N
R1/RRR1-8/2	1868.761	1869.154	-211.006	0.520	1246.283	0.494	24	0.251	R.LPIYVVQPQDGLDAIAR.N
R1/RRR1-8/2	1868.761	1869.154	-210.941	0.561	1083.298	0.521	23	0.242	R.LPIYVVQPQDGLDAIAR.N
R1/RRR1-8/2	1755.746	1756.097	-200.777	0.393	861.019	0.352	18	0.198	K.LQM*GQILDVPLPVCR.S
R1/RRR1-8/2	1755.040	1756.097	-1175.514	0.348	526.635	0.274	15	0.182	K.LQM*GQILDVPLPVCR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1080.706	1081.244	-1427.222	0.356	848.491	0.408	14	0.210	R.LENTISYIK.G
R1/RRR1-15/2	937.758	938.109	-376.101	0.385	588.668	0.421	13	0.206	R.HVVLQSVR.S
R1/RRR1-14/2	1081.108	1081.244	-126.570	0.419	891.591	0.304	14	0.200	R.LENTISYIK.G
R1/RRR1-15/2	1081.145	1081.244	-91.573	0.399	505.773	0.293	14	0.196	R.LENTISYIK.G
R1/RRR1-15/2	937.477	938.109	-1746.754	0.301	414.862	0.381	11	0.194	-.HVVLQSVR.-
R1/RRR1-23/2	937.997	938.109	-119.645	0.211	349.648	0.345	9	0.188	R.HVVLQSVR.S
R1/RRR1-15/3	1395.459	1395.636	-127.373	0.540	1234.253	0.351	25	0.105	R.RVNALENVVKPR.L
R1/RRR1-15/3	1395.699	1395.636	45.027	0.517	964.199	0.305	22	0.084	R.RVNALENVVKPR.L
R1/RRR1-10/2	1690.459	1689.883	-251.514	0.556	2002.833	0.542	22	0.370	R.SQDEALQIAELICAK.L
R1/RRR1-10/2	1689.364	1689.883	-901.777	0.449	1984.352	0.406	22	0.323	R.SQDEALQIAELICAK.L
R1/RRR1-10/2	1415.166	1415.578	-291.443	0.474	1755.530	0.496	21	0.316	R.GNIASAINTIQANK.V
R1/RRR1-10/2	1524.794	1523.668	82.657	0.556	1253.070	0.414	17	0.234	K.INDDEVEYWIVK.A
R1/RRR1-10/2	1414.944	1415.578	-1157.924	0.388	1032.007	0.365	19	0.210	R.GNIASAINTIQANK.V
R1/RRR1-12/2	855.941	856.005	-75.042	0.432	1158.394	0.418	13	0.232	K.TPAQVALR.W
R1/RRR1-12/2	1109.087	1109.257	-154.067	0.468	1003.746	0.411	15	0.221	K.REDLFITSK.L
R1/RRR1-12/2	856.013	856.005	9.353	0.377	931.738	0.412	13	0.215	K.TPAQVALR.W
R1/RRR1-12/2	1108.878	1109.257	-343.126	0.402	982.864	0.306	14	0.202	K.REDLFITSK.L
R1/RRR1-12/2	1076.858	1077.259	-372.657	0.357	965.979	0.284	13	0.196	K.LFEEGVVKR.E
R1/RRR1-8/2	1682.572	1682.893	-191.714	0.485	1675.845	0.522	21	0.310	K.TTITEDDIVGLTYLK.M
R1/RRR1-8/2	1682.742	1682.893	-90.267	0.500	1630.252	0.492	21	0.295	K.TTITEDDIVGLTYLK.M
R1/RRR1-8/2	1442.054	1442.560	-1047.431	0.475	966.336	0.487	19	0.228	K.GNNFEFLPFGSGR.R
R1/RRR1-8/2	1556.340	1556.701	-232.674	0.473	1223.357	0.348	19	0.220	R.YRDEFLDALNTAK.N
R1/RRR1-8/2	962.895	963.112	-225.968	0.502	1308.924	0.342	13	0.228	R.IGDLELFR.A
R1/RRR1-8/2	963.022	963.112	-94.096	0.508	1256.744	0.356	13	0.227	R.IGDLELFR.A
R1/RRR1-8/2	1001.879	1002.062	-183.690	0.297	706.554	0.396	15	0.200	K.FASTFSADR.T
R1/RRR1-8/2	1040.352	1040.238	109.378	0.410	879.773	0.296	15	0.199	R.LLLGEIPER.T
R1/RRR1-8/2	1040.309	1040.238	68.072	0.379	857.150	0.279	14	0.195	R.LLLGEIPER.T
R1/RRR1-8/2	1001.480	1002.062	-1584.568	0.290	550.074	0.220	14	0.188	K.FASTFSADR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-18/2	1412.219	1412.610	-278.093	0.476	1361.952	0.505	21	0.268	K.VVEVVESSPPEIK.A
R1/RRR1-18/2	1413.170	1412.610	-312.475	0.502	1173.513	0.558	20	0.262	K.VVEVVESSPPEIK.A
R1/RRR1-15/2	1412.273	1412.610	-239.937	0.481	1150.207	0.514	20	0.250	K.VVEVVESSPPEIK.A
R1/RRR1-14/2	1412.106	1412.610	-1068.518	0.443	1203.266	0.492	20	0.249	K.VVEVVESSPPEIK.A
R1/RRR1-18/2	1412.281	1412.610	-233.780	0.433	1072.028	0.550	19	0.249	K.VVEVVESSPPEIK.A
R1/RRR1-19/2	1412.243	1412.610	-260.836	0.468	1113.195	0.528	19	0.249	K.VVEVVESSPPEIK.A
R1/RRR1-15/2	1412.234	1412.610	-267.600	0.461	1210.490	0.480	20	0.248	K.VVEVVESSPPEIK.A
R1/RRR1-20/2	1659.658	1659.948	-175.328	0.419	1169.434	0.504	23	0.247	K.SGTTPLSPAIVFILDK.V
R1/RRR1-14/2	1413.599	1412.610	-8.195	0.532	1076.049	0.529	19	0.247	K.VVEVVESSPPEIK.A
R1/RRR1-18/2	1660.645	1659.948	-182.817	0.471	1085.332	0.517	23	0.244	K.SGTTPLSPAIVFILDK.V
R1/RRR1-19/2	1659.304	1659.948	-993.599	0.392	1095.428	0.497	22	0.238	K.SGTTPLSPAIVFILDK.V
R1/RRR1-19/2	1412.065	1412.610	-1097.595	0.400	1024.146	0.518	18	0.238	K.VVEVVESSPPEIK.A
R1/RRR1-14/2	1412.155	1412.610	-323.538	0.446	978.981	0.524	18	0.237	K.VVEVVESSPPEIK.A
R1/RRR1-19/2	1660.530	1659.948	-252.361	0.418	951.137	0.538	22	0.236	K.SGTTPLSPAIVFILDK.V
R1/RRR1-1/2	1413.246	1412.610	-258.832	0.482	1194.771	0.429	19	0.235	K.VVEVVESSPPEIK.A
R1/RRR1-14/2	1659.507	1659.948	-266.387	0.438	947.071	0.526	21	0.234	K.SGTTPLSPAIVFILDK.V
R1/RRR1-20/2	1659.489	1659.948	-277.309	0.444	876.500	0.548	21	0.233	K.SGTTPLSPAIVFILDK.V
R1/RRR1-18/2	1659.437	1659.948	-913.097	0.440	1021.881	0.487	22	0.233	K.SGTTPLSPAIVFILDK.V
R1/RRR1-20/2	1659.121	1659.948	-1104.255	0.405	1012.746	0.493	22	0.232	K.SGTTPLSPAIVFILDK.V
R1/RRR1-2/2	1660.737	1659.948	-127.293	0.484	911.041	0.512	21	0.230	K.SGTTPLSPAIVFILDK.V
R1/RRR1-20/2	1782.317	1782.844	-859.143	0.329	844.887	0.539	27	0.228	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-15/2	1782.269	1782.844	-886.302	0.313	783.874	0.578	26	0.227	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-18/2	1659.391	1659.948	-941.086	0.376	966.856	0.477	22	0.226	K.SGTTPLSPAIVFILDK.V
R1/RRR1-21/2	1659.183	1659.948	-1066.948	0.353	996.425	0.465	22	0.225	K.SGTTPLSPAIVFILDK.V
R1/RRR1-15/2	1412.046	1412.610	-1110.876	0.405	942.563	0.454	18	0.223	K.VVEVVESSPPEIK.A
R1/RRR1-18/2	1782.287	1782.844	-875.988	0.361	663.678	0.557	25	0.223	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-19/2	1659.337	1659.948	-973.583	0.359	951.956	0.467	21	0.223	K.SGTTPLSPAIVFILDK.V
R1/RRR1-20/2	1782.091	1782.844	-986.561	0.325	708.558	0.563	25	0.222	K.AEPEPEPEAPAAETTSR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1782.145	1782.844	-955.752	0.301	840.634	0.516	26	0.222	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-17/2	1412.187	1412.610	-300.642	0.404	906.290	0.453	18	0.221	K.VVEVVESSPPEIK.A
R1/RRR1-19/2	1782.388	1782.844	-256.539	0.267	816.816	0.533	27	0.220	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-18/2	1782.257	1782.844	-893.040	0.397	570.872	0.552	23	0.219	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-15/2	1782.405	1782.844	-246.851	0.315	723.276	0.536	25	0.219	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-14/2	1782.029	1782.844	-1021.360	0.351	580.547	0.566	23	0.219	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-20/2	1412.142	1412.610	-332.471	0.403	649.268	0.494	17	0.216	K.VVEVVESSPPEIK.A
R1/RRR1-15/2	1782.183	1782.844	-934.572	0.304	591.275	0.562	24	0.216	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-22/2	1660.912	1659.948	-21.570	0.448	745.566	0.477	20	0.216	K.SGTTPLSPAIVFILDK.V
R1/RRR1-21/2	1412.159	1412.610	-320.762	0.400	671.332	0.460	17	0.213	K.VVEVVESSPPEIK.A
R1/RRR1-2/2	1660.070	1659.948	73.930	0.390	741.015	0.455	19	0.211	K.SGTTPLSPAIVFILDK.V
R1/RRR1-10/2	1659.992	1659.948	26.655	0.361	847.548	0.420	20	0.211	K.SGTTPLSPAIVFILDK.V
R1/RRR1-19/2	1782.352	1782.844	-276.603	0.269	714.737	0.471	26	0.210	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-20/2	1412.230	1412.610	-270.462	0.356	570.695	0.455	17	0.209	K.VVEVVESSPPEIK.A
R1/RRR1-11/2	1660.276	1659.948	198.328	0.388	813.750	0.408	20	0.208	K.SGTTPLSPAIVFILDK.V
R1/RRR1-14/2	1782.195	1782.844	-927.696	0.252	646.128	0.489	25	0.207	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-20/2	1412.183	1412.610	-303.243	0.334	645.524	0.410	18	0.206	K.VVEVVESSPPEIK.A
R1/RRR1-14/2	1658.766	1659.948	-1319.210	0.297	827.302	0.398	20	0.206	K.SGTTPLSPAIVFILDK.V
R1/RRR1-20/2	1781.854	1782.844	-1119.720	0.231	716.779	0.425	26	0.203	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-18/2	1782.386	1782.844	-257.433	0.252	588.557	0.448	24	0.203	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-15/3	1782.487	1782.844	-200.551	0.459	1553.801	0.539	31	0.202	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-21/2	1411.624	1412.610	-1411.571	0.309	593.509	0.368	17	0.201	K.VVEVVESSPPEIK.A
R1/RRR1-17/2	1411.640	1412.610	-1400.193	0.262	814.004	0.332	16	0.198	K.VVEVVESSPPEIK.A
R1/RRR1-17/2	1411.573	1412.610	-1447.444	0.273	924.307	0.276	16	0.196	K.VVEVVESSPPEIK.A
R1/RRR1-15/2	1658.656	1659.948	-1385.584	0.236	683.859	0.328	19	0.194	K.SGTTPLSPAIVFILDK.V
R1/RRR1-14/2	1782.340	1782.844	-846.424	0.168	549.988	0.397	23	0.192	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-15/3	1782.846	1782.844	1.290	0.493	1225.356	0.609	31	0.176	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-19/3	1783.488	1782.844	-199.752	0.425	1224.579	0.502	29	0.145	K.AEPEPEPEAPAAETTSR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/3	1783.004	1782.844	90.284	0.429	970.255	0.487	27	0.120	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-15/3	1782.317	1782.844	-858.842	0.457	900.571	0.517	29	0.120	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-19/3	1782.786	1782.844	-32.499	0.382	853.553	0.374	25	0.092	K.AEPEPEPEAPAAETTSR.E
R1/RRR1-10/2	1807.502	1807.127	207.914	0.376	607.220	0.436	21	0.196	R.AVTLIPGDGIGPLVTGAVR.Q
R1/RRR1-8/2	1706.340	1706.840	-293.732	0.525	1550.996	0.602	20	0.314	R.TGFDLQHVQDGLYGR.H
R1/RRR1-8/2	1706.204	1706.840	-961.982	0.496	1552.810	0.550	20	0.300	R.TGFDLQHVQDGLYGR.H
R1/RRR1-8/2	1713.782	1712.969	-109.493	0.510	1013.058	0.575	21	0.247	K.QTLDLGSTGLLPLEVR.F
R1/RRR1-8/2	1705.581	1706.840	-1328.656	0.448	1240.623	0.470	19	0.244	R.TGFDLQHVQDGLYGR.H
R1/RRR1-3/2	1714.172	1712.969	118.667	0.409	551.773	0.432	18	0.198	K.QTLDLGSTGLLPLEVR.F
R1/RRR1-8/2	1483.311	1482.689	-255.933	0.346	686.324	0.341	15	0.189	-.TMISSSWGAPAAFR.-
R1/RRR1-8/2	1714.391	1712.969	246.916	0.335	592.701	0.328	16	0.187	K.QTLDLGSTGLLPLEVR.F
R1/RRR1-8/3	1707.055	1706.840	126.182	0.510	777.077	0.541	25	0.115	R.TGFDLQHVQDGLYGR.H
R1/RRR1-8/2	1535.599	1536.756	-1409.314	0.378	1108.069	0.481	20	0.235	K.AALAPYFELTNAVR.V
R1/RRR1-8/2	1537.201	1536.756	290.431	0.475	901.044	0.532	20	0.232	K.AALAPYFELTNAVR.V
R1/RRR1-14/2	1057.014	1057.139	-119.262	0.416	822.430	0.508	15	0.222	R.APIGEEVEGR.R
R1/RRR1-14/2	1260.117	1260.384	-212.457	0.348	889.717	0.384	15	0.207	K.ATVSHNSQLFR.F
R1/RRR1-14/2	1318.370	1318.538	-128.217	0.336	895.319	0.396	16	0.206	K.LGLDVASCLITR.A
R1/RRR1-14/2	1260.133	1260.384	-199.921	0.314	705.328	0.362	14	0.196	K.ATVSHNSQLFR.F
R1/RRR1-14/2	1259.587	1260.384	-1430.800	0.344	619.720	0.326	15	0.195	K.ATVSHNSQLFR.F
R1/RRR1-14/2	1259.440	1260.384	-1548.404	0.244	401.279	0.351	13	0.190	K.ATVSHNSQLFR.F
R1/RRR1-14/2	1318.074	1318.538	-353.412	0.300	468.738	0.352	12	0.186	-.LGLDVASCLITR.-
R1/RRR1-13/2	1244.869	1245.368	-401.635	0.452	1968.313	0.421	20	0.327	K.SINDIAASQGIR.I
R1/RRR1-12/2	1245.226	1245.368	-114.608	0.544	1860.869	0.453	21	0.320	K.SINDIAASQGIR.I
R1/RRR1-12/2	1612.149	1610.883	165.288	0.533	1500.723	0.462	22	0.270	R.VLNISGVQLIGINNR.S
R1/RRR1-11/2	1611.325	1610.883	275.095	0.507	1420.123	0.437	22	0.256	R.VLNISGVQLIGINNR.S
R1/RRR1-13/2	1611.564	1610.883	-198.718	0.478	1360.347	0.431	21	0.248	R.VLNISGVQLIGINNR.S
R1/RRR1-12/2	1611.867	1610.883	-10.149	0.536	1320.693	0.434	21	0.244	R.VLNISGVQLIGINNR.S
R1/RRR1-11/2	1610.463	1610.883	-261.955	0.455	1334.704	0.411	21	0.241	R.VLNISGVQLIGINNR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1345.559	1346.515	-1458.310	0.308	1067.237	0.457	16	0.225	R.DFYGALASAFKR.N
R1/RRR1-12/2	1346.335	1346.515	-134.557	0.321	971.708	0.489	16	0.224	R.DFYGALASAFKR.N
R1/RRR1-12/2	1610.565	1610.883	-197.929	0.449	1163.770	0.377	20	0.220	R.VLNISGVQLIGINNR.S
R1/RRR1-12/2	1346.140	1346.515	-280.011	0.335	793.045	0.539	15	0.220	R.DFYGALASAFKR.N
R1/RRR1-11/2	1346.434	1346.515	-60.436	0.358	917.837	0.446	16	0.216	R.DFYGALASAFKR.N
R1/RRR1-11/2	1346.176	1346.515	-252.809	0.285	841.419	0.477	15	0.212	R.DFYGALASAFKR.N
R1/RRR1-11/2	1345.526	1346.515	-1483.279	0.285	714.971	0.449	14	0.203	R.DFYGALASAFKR.N
R1/RRR1-13/2	1610.287	1610.883	-994.495	0.335	763.559	0.166	17	0.181	-.VLNISGVQLIGINNR.-
R1/RRR1-17/2	1762.467	1764.013	-2017.625	0.428	1310.979	0.529	22	0.264	K.SGGLGDLKYPLISDVTK.S
R1/RRR1-17/2	1213.067	1213.323	-211.614	0.515	1178.070	0.498	18	0.246	R.AGGVDDAPLVGNK.A
R1/RRR1-17/2	1214.123	1213.323	-165.042	0.541	1182.139	0.485	18	0.243	R.AGGVDDAPLVGNK.A
R1/RRR1-17/2	1213.121	1213.323	-166.995	0.522	1069.522	0.483	17	0.233	R.AGGVDDAPLVGNK.A
R1/RRR1-17/2	1763.200	1764.013	-1031.087	0.474	1053.563	0.465	19	0.224	K.SGGLGDLKYPLISDVTK.S
R1/RRR1-17/2	1486.289	1486.740	-304.846	0.333	961.859	0.342	22	0.206	K.SFGVLIPDQGIALR.G
R1/RRR1-18/2	1488.032	1486.740	196.272	0.492	505.444	0.415	17	0.200	K.SFGVLIPDQGIALR.G
R1/RRR1-17/2	1488.082	1486.740	230.328	0.451	590.041	0.371	18	0.198	K.SFGVLIPDQGIALR.G
R1/RRR1-18/2	1487.156	1486.740	280.528	0.397	620.533	0.332	17	0.192	-.SFGVLIPDQGIALR.-
R1/RRR1-17/2	1486.160	1486.740	-1066.930	0.285	550.127	0.260	18	0.189	K.SFGVLIPDQGIALR.G
R1/RRR1-17/3	1763.410	1764.013	-911.445	0.321	1110.568	0.224	31	0.073	K.SGGLGDLKYPLISDVTK.S
R1/RRR1-17/3	1763.931	1764.013	-46.451	0.342	459.146	0.358	21	0.071	-.SGGLGDLKYPLISDVTK.-
R1/RRR1-12/2	1655.478	1655.833	-214.820	0.513	1773.065	0.516	25	0.327	R.DVAALHYAAAVDPDVK.S
R1/RRR1-12/2	1364.302	1364.534	-170.207	0.460	1413.790	0.314	18	0.231	K.FNWNTVINSLR.R
R1/RRR1-12/2	1365.149	1364.534	-282.749	0.481	1205.488	0.362	18	0.225	K.FNWNTVINSLR.R
R1/RRR1-12/2	1365.127	1364.534	-298.718	0.525	1075.733	0.377	17	0.217	K.FNWNTVINSLR.R
R1/RRR1-12/2	1872.592	1873.056	-248.824	0.451	847.540	0.525	20	0.119	R.GWIPLDQSIRDTVGSDI.-
R1/RRR1-12/2	1873.316	1873.056	139.042	0.455	788.270	0.478	19	0.108	R.GWIPLDQSIRDTVGSDI.-
R1/RRR1-12/2	1872.088	1873.056	-1054.501	0.367	733.927	0.491	18	0.107	R.GWIPLDQSIRDTVGSDI.-
R1/RRR1-3/2	1497.298	1497.725	-286.169	0.464	2530.342	0.399	21	0.421	R.SALLQGQALQALQR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1497.555	1497.725	-114.102	0.470	2171.262	0.395	20	0.349	R.SALLQGQALQALQR.F
R1/RRR1-3/2	1498.319	1497.725	-272.082	0.442	1562.411	0.418	20	0.267	R.SALLQGQALQALQR.F
R1/RRR1-3/2	948.897	949.129	-244.978	0.458	969.790	0.379	13	0.214	K.IEALVFTR.L
R1/RRR1-3/2	949.121	949.129	-7.819	0.431	851.231	0.348	13	0.205	K.IEALVFTR.L
R1/RRR1-3/2	1149.072	1148.377	-266.340	0.428	885.113	0.307	15	0.197	K.ATFEVVQLLK.N
R1/RRR1-11/2	1559.198	1558.868	212.201	0.565	1924.905	0.513	22	0.345	K.GAALNAVQIAEM*LLK.-
R1/RRR1-11/2	1558.406	1558.868	-297.658	0.508	1598.903	0.523	21	0.299	K.GAALNAVQIAEM*LLK.-
R1/RRR1-11/2	1558.415	1558.868	-292.000	0.489	1373.389	0.505	20	0.266	K.GAALNAVQIAEM*LLK.-
R1/RRR1-11/2	1160.966	1160.260	-253.909	0.546	1161.203	0.486	17	0.245	R.AAEGVTIIDDR.A
R1/RRR1-11/2	1159.430	1160.260	-1582.701	0.425	1218.519	0.460	17	0.243	R.AAEGVTIIDDR.A
R1/RRR1-11/3	1997.925	1998.189	-132.106	0.419	1756.704	0.510	31	0.239	R.AHAPAAVASGAVVVDNSSAFR.M
R1/RRR1-11/2	1159.490	1160.260	-1531.195	0.422	1169.131	0.442	17	0.236	R.AAEGVTIIDDR.A
R1/RRR1-11/3	1997.972	1998.189	-108.939	0.400	1718.137	0.515	31	0.233	R.AHAPAAVASGAVVVDNSSAFR.M
R1/RRR1-11/3	1997.478	1998.189	-858.703	0.428	1143.009	0.531	27	0.152	R.AHAPAAVASGAVVVDNSSAFR.M
R1/RRR1-8/2	1260.978	1260.404	-339.163	0.560	2062.854	0.544	19	0.382	R.AFATGGYAAM*QR.V
R1/RRR1-8/2	1259.550	1260.404	-1476.962	0.448	1593.329	0.486	19	0.290	R.AFATGGYAAM*QR.V
R1/RRR1-8/2	1260.007	1260.404	-316.103	0.511	1489.086	0.501	19	0.282	R.AFATGGYAAM*QR.V
R1/RRR1-8/2	1420.267	1420.639	-262.638	0.512	1507.905	0.482	20	0.278	R.AYAQSVATLNLLR.A
R1/RRR1-8/2	1420.246	1420.639	-277.211	0.494	1296.774	0.463	19	0.250	R.AYAQSVATLNLLR.A
R1/RRR1-8/2	1450.620	1451.696	-1435.660	0.461	679.760	0.411	15	0.200	K.LIEILNPSNKPGR.I
R1/RRR1-8/2	1420.122	1420.639	-1071.107	0.427	723.702	0.394	14	0.197	R.AYAQSVATLNLLR.A
R1/RRR1-8/2	1450.649	1451.696	-1415.206	0.409	686.569	0.361	16	0.196	K.LIEILNPSNKPGR.I
R1/RRR1-8/2	1451.018	1451.696	-1159.851	0.439	554.281	0.406	14	0.195	K.LIEILNPSNKPGR.I
R1/RRR1-10/2	1411.478	1410.661	-129.995	0.484	1562.834	0.463	18	0.280	R.ILIGSIMEEYNK.A
R1/RRR1-10/2	1249.888	1250.384	-397.965	0.450	1647.939	0.342	19	0.260	R.AFDEGWGGVIAK.T
R1/RRR1-10/2	1411.751	1410.661	63.605	0.479	1385.929	0.427	17	0.251	R.ILIGSIMEEYNK.A
R1/RRR1-10/2	1250.379	1250.384	-4.074	0.451	1280.050	0.304	17	0.216	R.AFDEGWGGVIAK.T
R1/RRR1-10/2	1249.533	1250.384	-1486.211	0.348	1032.675	0.303	16	0.201	R.AFDEGWGGVIAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	920.283	920.134	162.681	0.497	1223.936	0.339	21	0.096	R.AVHPIALAK.V
R1/RRR1-10/3	920.046	920.134	-96.177	0.453	835.141	0.347	19	0.080	-.AVHPIALAK.-
R1/RRR1-10/3	919.948	920.134	-202.494	0.401	733.908	0.256	18	0.064	-.AVHPIALAK.-
R1/RRR1-14/2	1072.205	1071.249	-41.635	0.510	1095.056	0.452	16	0.234	K.IVAISLDDPK.A
R1/RRR1-14/2	1072.064	1071.249	-173.321	0.533	988.709	0.430	16	0.223	K.IVAISLDDPK.A
R1/RRR1-14/2	1364.074	1364.439	-268.790	0.391	438.709	0.535	15	0.207	K.VIEETNESWEK.L
R1/RRR1-14/2	1071.098	1071.249	-141.585	0.424	929.552	0.286	15	0.198	K.IVAISLDDPK.A
R1/RRR1-14/3	1515.554	1515.737	-120.955	0.408	1015.411	0.376	26	0.094	R.AGDGVFHFVVEIPK.E
R1/RRR1-14/3	1515.915	1515.737	117.741	0.442	1001.199	0.354	25	0.092	R.AGDGVFHFVVEIPK.E
R1/RRR1-16/2	1676.173	1675.904	160.655	0.493	705.512	0.582	18	0.222	K.ALADEIGIPFLETSAK.D
R1/RRR1-17/2	1072.201	1072.280	-74.409	0.408	1045.087	0.372	17	0.215	K.LLLIGDSGVGK.S
R1/RRR1-17/2	1072.328	1072.280	44.802	0.333	1231.013	0.281	17	0.210	K.LLLIGDSGVGK.S
R1/RRR1-17/3	1921.934	1922.177	-126.702	0.396	1288.020	0.425	32	0.131	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-17/3	1922.943	1922.177	-121.988	0.424	780.448	0.503	30	0.112	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-17/3	1922.245	1922.177	35.548	0.386	923.707	0.461	33	0.108	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-17/3	1922.313	1922.177	70.896	0.400	865.485	0.467	31	0.108	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-16/3	1922.406	1922.177	119.328	0.415	823.519	0.467	31	0.106	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-17/3	1922.398	1922.177	115.221	0.418	667.609	0.467	27	0.104	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-16/3	1921.963	1922.177	-111.985	0.377	788.115	0.453	31	0.102	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-16/3	1922.892	1922.177	-148.734	0.400	790.917	0.446	31	0.101	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-16/3	1922.370	1922.177	100.797	0.421	801.658	0.406	29	0.098	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-17/3	1921.583	1922.177	-831.907	0.365	624.192	0.428	28	0.096	R.M*ASQPATNASKPATVQM*R.G
R1/RRR1-17/3	1906.066	1906.178	-58.956	0.280	449.046	0.376	23	0.088	-.MASQPATNASKPATVQM*R.-
R1/RRR1-9/2	1306.060	1306.406	-266.105	0.404	1223.428	0.461	18	0.243	K.LGVSYNQPDGQK.L
R1/RRR1-9/2	1235.019	1235.371	-285.873	0.401	627.595	0.433	15	0.202	R.SYSELPLAAQR.Y
R1/RRR1-9/2	1305.634	1306.406	-1361.209	0.289	683.832	0.373	17	0.195	K.LGVSYNQPDGQK.L
R1/RRR1-9/3	1892.022	1892.191	-89.608	0.333	1190.638	0.333	29	0.099	R.IEELVGVPVHYIGVGPGR.D
R1/RRR1-9/3	1891.912	1892.191	-147.663	0.286	887.181	0.330	28	0.080	R.IEELVGVPVHYIGVGPGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/3	1891.947	1892.191	-129.120	0.278	695.020	0.294	26	0.074	R.IEELVGVPVHYIGVGPGR.D
R1/RRR1-14/3	1878.888	1879.019	-69.968	0.590	3521.184	0.516	33	0.802	R.AWDVLNEIFNEDGSLR.Q
R1/RRR1-14/3	1878.656	1879.019	-193.935	0.527	3037.679	0.528	31	0.613	R.AWDVLNEIFNEDGSLR.Q
R1/RRR1-14/2	1878.379	1879.019	-876.086	0.568	2691.057	0.492	24	0.489	R.AWDVLNEIFNEDGSLR.Q
R1/RRR1-14/2	1879.314	1879.019	157.296	0.629	2143.249	0.532	24	0.385	R.AWDVLNEIFNEDGSLR.Q
R1/RRR1-14/2	1294.174	1294.485	-240.735	0.509	1803.929	0.559	19	0.342	K.VIQDHVATVVGR.W
R1/RRR1-14/2	1879.211	1879.019	102.576	0.614	1997.537	0.468	23	0.336	R.AWDVLNEIFNEDGSLR.Q
R1/RRR1-13/2	1294.174	1294.485	-241.303	0.554	1570.005	0.556	20	0.308	K.VIQDHVATVVGR.W
R1/RRR1-14/2	1294.179	1294.485	-237.139	0.549	1378.112	0.592	19	0.293	K.VIQDHVATVVGR.W
R1/RRR1-14/2	1294.233	1294.485	-195.694	0.527	1336.817	0.567	19	0.281	K.VIQDHVATVVGR.W
R1/RRR1-12/2	1878.341	1879.019	-895.919	0.439	679.432	0.405	19	0.201	R.AWDVLNEIFNEDGSLR.Q
R1/RRR1-13/2	1878.804	1879.019	-114.864	0.464	417.859	0.386	16	0.191	-.AWDVLNEIFNEDGSLR.-
R1/RRR1-12/2	1879.510	1879.019	261.704	0.408	392.208	0.361	15	0.186	-.AWDVLNEIFNEDGSLR.-
R1/RRR1-13/2	1878.500	1879.019	-811.373	0.342	216.803	0.368	13	0.181	-.AWDVLNEIFNEDGSLR.-
R1/RRR1-16/2	1786.972	1788.082	-1184.756	0.468	1111.105	0.481	22	0.237	R.NKFDPLWNSLVIGGVK.K
R1/RRR1-16/2	1787.479	1788.082	-899.884	0.495	952.075	0.507	21	0.229	R.NKFDPLWNSLVIGGVK.K
R1/RRR1-16/2	1643.211	1641.889	196.588	0.450	812.531	0.530	20	0.224	R.TQYPYVTGSSIIALK.Y
R1/RRR1-16/2	1789.542	1788.082	257.346	0.393	820.715	0.431	19	0.207	R.NKFDPLWNSLVIGGVK.K
R1/RRR1-16/2	1643.019	1641.889	79.168	0.385	668.937	0.459	17	0.203	R.TQYPYVTGSSIIALK.Y
R1/RRR1-16/2	1655.212	1654.885	198.343	0.510	670.739	0.405	17	0.197	K.ITTEGATIYPPYSLK.T
R1/RRR1-16/2	1654.402	1654.885	-292.445	0.418	758.169	0.344	19	0.196	K.ITTEGATIYPPYSLK.T
R1/RRR1-16/2	1654.405	1654.885	-290.890	0.385	622.505	0.313	16	0.187	K.ITTEGATIYPPYSLK.T
R1/RRR1-16/3	1787.924	1788.082	-88.868	0.393	1241.809	0.340	26	0.106	R.NKFDPLWNSLVIGGVK.K
R1/RRR1-16/3	1787.988	1788.082	-53.016	0.313	690.462	0.243	21	0.067	-.NKFDPLWNSLVIGGVK.-
R1/RRR1-7/2	1965.331	1966.330	-1019.906	0.398	1136.874	0.504	21	0.239	R.YFELSGLPM*LVLIGPDGK.T
R1/RRR1-7/2	927.972	928.108	-146.402	0.466	642.468	0.594	14	0.231	K.VPVSELVGK.T
R1/RRR1-7/2	1965.489	1966.330	-939.092	0.442	928.500	0.495	21	0.222	R.YFELSGLPM*LVLIGPDGK.T
R1/RRR1-7/2	927.555	928.108	-1679.375	0.427	673.725	0.467	14	0.214	K.VPVSELVGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	928.160	928.108	56.774	0.380	549.025	0.471	13	0.208	K.VPVSELVGK.T
R1/RRR1-7/2	1586.814	1587.719	-1203.646	0.399	561.902	0.459	15	0.197	K.DNQTIHSLFGTPTR.D
R1/RRR1-3/2	1967.937	1966.330	-200.295	0.366	418.796	0.351	14	0.183	R.YFELSGLPM*LVLIGPDGK.T
R1/RRR1-6/2	1687.254	1687.870	-960.667	0.447	2449.757	0.405	24	0.407	R.VVDSLDDLSLDIPSAK.S
R1/RRR1-6/2	1883.705	1883.132	-227.857	0.484	874.303	0.594	24	0.239	R.AVIDDVLAPLNLDEISGK.L
R1/RRR1-6/2	1686.471	1687.870	-1426.765	0.356	1442.281	0.241	19	0.215	R.VVDSLDDLSLDIPSAK.S
R1/RRR1-6/2	1754.952	1755.946	-1139.466	0.323	824.339	0.469	18	0.207	K.SVAPIIEEYFSTGDVK.L
R1/RRR1-6/2	1686.643	1687.870	-1324.119	0.270	1459.496	0.166	20	0.205	R.VVDSLDDLSLDIPSAK.S
R1/RRR1-7/2	1259.641	1258.451	150.892	0.522	1627.633	0.465	17	0.289	R.TDLALWQAALR.R
R1/RRR1-7/2	1503.632	1502.719	-57.507	0.510	916.487	0.567	21	0.239	K.M*GEGLPETLGGVLGR.L
R1/RRR1-7/2	1257.397	1258.451	-1638.847	0.398	1143.769	0.387	15	0.221	R.TDLALWQAALR.R
R1/RRR1-7/3	1786.888	1786.965	-43.148	0.577	1418.521	0.581	32	0.197	R.APGQVKDDGSSIKENIK.A
R1/RRR1-7/3	1786.385	1786.965	-886.940	0.511	1044.390	0.587	28	0.151	R.APGQVKDDGSSIKENIK.A
R1/RRR1-7/2	1479.875	1478.629	166.907	0.510	1242.148	0.472	18	0.248	K.EIQDVLDDIYVR.Y
R1/RRR1-7/2	1060.084	1060.226	-134.509	0.382	852.268	0.457	15	0.216	K.ALSLVDSQVK.N
R1/RRR1-7/2	1480.019	1478.629	264.426	0.489	721.157	0.463	15	0.209	K.EIQDVLDDIYVR.Y
R1/RRR1-7/2	1060.120	1060.226	-100.434	0.390	657.579	0.395	14	0.201	K.ALSLVDSQVK.N
R1/RRR1-7/3	1502.114	1502.632	-1013.617	0.498	1137.006	0.371	25	0.103	K.M*KDAEENPEGPIR.I
R1/RRR1-7/3	1502.747	1502.632	76.255	0.399	555.884	0.325	19	0.079	-.M*KDAEENPEGPIR.-
R1/RRR1-8/3	1502.631	1502.632	-0.617	0.413	664.279	0.256	20	0.061	-.M*KDAEENPEGPIR.-
R1/RRR1-5/2	1742.205	1742.911	-981.668	0.485	2324.689	0.535	23	0.435	K.GLKDETYSGDGIALFR.I
R1/RRR1-5/2	1650.387	1650.815	-259.772	0.324	1027.695	0.320	18	0.198	R.ASALAALSSAFNPSSQK.N
R1/RRR1-5/3	1282.287	1282.556	-210.609	0.482	1504.422	0.358	23	0.130	R.IQDFKPVPLPK.A
R1/RRR1-4/3	1282.918	1282.556	282.804	0.381	1104.082	0.369	21	0.098	R.IQDFKPVPLPK.A
R1/RRR1-5/3	1282.178	1282.556	-295.852	0.412	1360.492	0.216	23	0.085	R.IQDFKPVPLPK.A
R1/RRR1-5/3	1282.314	1282.556	-188.978	0.388	1309.950	0.229	22	0.084	R.IQDFKPVPLPK.A
R1/RRR1-13/2	1851.190	1851.124	36.020	0.422	948.278	0.448	22	0.215	R.VM*QGHAGANLVPLVASNR.I
R1/RRR1-13/2	1075.087	1075.238	-140.262	0.437	695.354	0.555	13	0.116	K.VLLTLDGEKS.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/3	1457.944	1456.585	246.838	0.498	803.505	0.481	22	0.105	-.KSHIPDGPGYQEK.-
R1/RRR1-16/3	1456.434	1456.585	-104.176	0.356	483.951	0.455	20	0.093	R.KSHIPDGPGYQEK.F
R1/RRR1-13/3	1456.238	1456.585	-239.260	0.340	534.118	0.387	21	0.083	-.KSHIPDGPGYQEK.-
R1/RRR1-16/3	1456.925	1456.585	234.194	0.452	382.558	0.444	19	0.079	-.KSHIPDGPGYQEK.-
R1/RRR1-12/3	1457.313	1456.585	-187.205	0.370	549.960	0.343	21	0.078	-.KSHIPDGPGYQEK.-
R1/RRR1-8/2	1688.701	1688.943	-143.311	0.514	1351.837	0.406	21	0.241	R.ALFVDLEPTVIDEVK.T
R1/RRR1-9/2	1539.978	1538.597	248.724	0.441	998.223	0.538	19	0.238	R.DAFNTFFSETSSGK.H
R1/RRR1-9/2	1518.251	1518.781	-1010.831	0.307	1042.611	0.482	17	0.224	R.LISQVISSLTTSLR.F
R1/RRR1-9/2	1517.865	1518.781	-1265.661	0.376	867.345	0.518	17	0.221	R.LISQVISSLTTSLR.F
R1/RRR1-9/2	1688.141	1688.943	-1070.331	0.392	1005.396	0.387	20	0.213	R.ALFVDLEPTVIDEVK.T
R1/RRR1-8/2	1539.907	1538.597	201.984	0.398	765.915	0.460	18	0.210	R.DAFNTFFSETSSGK.H
R1/RRR1-8/2	1688.842	1688.943	-59.710	0.425	920.046	0.363	18	0.203	R.ALFVDLEPTVIDEVK.T
R1/RRR1-9/2	1688.327	1688.943	-959.694	0.455	965.400	0.331	20	0.202	R.ALFVDLEPTVIDEVK.T
R1/RRR1-9/2	1687.918	1688.943	-1203.216	0.374	898.170	0.347	19	0.201	R.ALFVDLEPTVIDEVK.T
R1/RRR1-8/2	1345.188	1344.624	-324.990	0.427	1455.926	0.606	19	0.302	K.VVVESGAVPIFVK.L
R1/RRR1-8/2	1601.054	1601.903	-1158.298	0.385	1682.789	0.410	22	0.280	R.IVTVCLEGLENILK.V
R1/RRR1-7/2	1607.569	1607.833	-164.634	0.458	1348.516	0.431	20	0.246	R.SPPIEEVINTGVVPR.F
R1/RRR1-7/2	1601.530	1601.903	-233.601	0.524	1220.552	0.465	20	0.243	R.IVTVCLEGLENILK.V
R1/RRR1-8/2	1600.607	1601.903	-1438.819	0.369	1510.206	0.335	21	0.243	R.IVTVCLEGLENILK.V
R1/RRR1-8/2	1601.036	1601.903	-1169.936	0.384	1162.120	0.367	19	0.219	R.IVTVCLEGLENILK.V
R1/RRR1-9/2	1344.245	1344.624	-283.047	0.404	1042.476	0.388	16	0.213	K.VVVESGAVPIFVK.L
R1/RRR1-8/2	1344.167	1344.624	-341.178	0.337	739.020	0.416	15	0.200	K.VVVESGAVPIFVK.L
R1/RRR1-7/2	1602.148	1601.903	153.482	0.454	800.752	0.364	17	0.199	R.IVTVCLEGLENILK.V
R1/RRR1-5/2	1608.262	1607.833	267.397	0.371	623.589	0.284	16	0.184	R.SPPIEEVINTGVVPR.F
R1/RRR1-7/2	1612.716	1612.810	-58.125	0.528	1229.931	0.556	20	0.267	K.VLEPLFSYWNSTR.Q
R1/RRR1-7/2	1611.999	1612.810	-1126.356	0.367	1109.848	0.507	19	0.240	K.VLEPLFSYWNSTR.Q
R1/RRR1-7/2	1611.649	1612.810	-1344.406	0.288	1225.143	0.396	19	0.227	K.VLEPLFSYWNSTR.Q
R1/RRR1-6/2	1612.316	1612.810	-307.217	0.365	854.383	0.470	16	0.214	K.VLEPLFSYWNSTR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/3	1337.692	1338.538	-1383.834	0.637	1305.090	0.505	26	0.148	K.VGIKDHESVVVR.I
R1/RRR1-7/3	1338.867	1338.538	246.340	0.597	996.514	0.465	23	0.115	K.VGIKDHESVVVR.I
R1/RRR1-7/3	1243.686	1244.385	-1369.905	0.496	820.423	0.512	20	0.109	R.THRVETTFPR.L
R1/RRR1-6/3	1243.945	1244.385	-354.109	0.464	887.359	0.463	20	0.103	R.THRVETTFPR.L
R1/RRR1-7/3	1244.677	1244.385	235.422	0.498	655.485	0.491	18	0.102	R.THRVETTFPR.L
R1/RRR1-7/3	1337.978	1338.538	-1169.409	0.519	763.248	0.437	21	0.099	K.VGIKDHESVVVR.I
R1/RRR1-6/3	1338.069	1338.538	-351.527	0.488	902.891	0.423	24	0.098	K.VGIKDHESVVVR.I
R1/RRR1-6/3	1244.885	1244.385	-402.723	0.481	852.103	0.407	19	0.094	R.THRVETTFPR.L
R1/RRR1-6/3	1244.531	1244.385	117.690	0.445	619.323	0.455	19	0.094	R.THRVETTFPR.L
R1/RRR1-3/3	1338.005	1338.538	-1149.208	0.360	761.484	0.241	21	0.074	K.VGIKDHESVVVR.I
R1/RRR1-7/2	1369.529	1369.629	-73.005	0.298	756.638	0.385	15	0.194	K.VGPALACGNAVVLK.T
R1/RRR1-7/2	1369.644	1369.629	11.477	0.262	577.581	0.392	14	0.188	K.VGPALACGNAVVLK.T
R1/RRR1-8/2	1362.012	1362.428	-306.233	0.339	1044.567	0.148	18	0.179	K.SGVDSGATLVAGGDR.A
R1/RRR1-9/2	1255.060	1254.504	-354.962	0.597	1536.743	0.580	19	0.310	K.INNAVAQVLLAK.R
R1/RRR1-13/2	1253.996	1254.504	-1205.975	0.494	1173.953	0.553	17	0.259	K.INNAVAQVLLAK.R
R1/RRR1-9/2	1933.638	1933.235	208.788	0.391	631.596	0.423	18	0.196	R.FGLQCIIYMGAQDMER.Q
R1/RRR1-9/2	1253.320	1254.504	-1747.827	0.338	400.062	0.389	14	0.195	K.INNAVAQVLLAK.R
R1/RRR1-13/3	1984.287	1984.197	45.431	0.473	953.509	0.527	29	0.132	R.IIAETGAGQHGVATATVCAR.F
R1/RRR1-13/3	1984.229	1984.197	16.369	0.478	955.569	0.516	30	0.129	R.IIAETGAGQHGVATATVCAR.F
R1/RRR1-14/3	1984.134	1984.197	-31.577	0.455	1200.224	0.416	30	0.126	R.IIAETGAGQHGVATATVCAR.F
R1/RRR1-9/3	1984.243	1984.197	23.588	0.478	1069.747	0.466	31	0.126	R.IIAETGAGQHGVATATVCAR.F
R1/RRR1-9/3	1983.143	1984.197	-1038.921	0.393	989.358	0.301	29	0.087	R.IIAETGAGQHGVATATVCAR.F
R1/RRR1-13/3	1983.135	1984.197	-1042.629	0.406	542.165	0.400	25	0.087	-.IIAETGAGQHGVATATVCAR.-
R1/RRR1-12/2	959.986	960.067	-84.318	0.456	1669.689	0.369	15	0.270	R.TAEELLGAR.K
R1/RRR1-12/2	959.831	960.067	-246.078	0.470	1698.074	0.332	15	0.263	R.TAEELLGAR.K
R1/RRR1-12/2	959.613	960.067	-474.136	0.414	1655.354	0.347	15	0.262	R.TAEELLGAR.K
R1/RRR1-11/2	960.056	960.067	-11.619	0.338	1428.560	0.295	15	0.228	R.TAEELLGAR.K
R1/RRR1-12/2	1058.557	1059.155	-1514.686	0.451	686.675	0.375	15	0.206	K.LVENDDVVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1058.858	1059.155	-281.978	0.468	709.504	0.352	15	0.204	K.LVENDDVVR.I
R1/RRR1-12/2	1058.434	1059.155	-1630.769	0.375	726.737	0.362	15	0.203	K.LVENDDVVR.I
R1/RRR1-11/3	1578.824	1578.665	100.487	0.500	1341.584	0.498	27	0.151	R.HIEEDLGHEETLR.E
R1/RRR1-12/3	1578.858	1578.665	122.353	0.525	1203.262	0.435	25	0.123	R.HIEEDLGHEETLR.E
R1/RRR1-12/3	1578.470	1578.665	-123.988	0.540	950.044	0.521	24	0.123	R.HIEEDLGHEETLR.E
R1/RRR1-6/2	1617.025	1615.990	21.987	0.341	769.744	0.308	18	0.189	K.GVMINKDVVAPGKMR.R
R1/RRR1-9/2	1785.348	1786.063	-963.913	0.348	715.668	0.451	18	0.201	R.DIQAWETIPLGPFLGK.S
R1/RRR1-11/2	1114.201	1113.289	-79.625	0.303	929.049	0.284	15	0.195	K.ILSADEPVLR.D
R1/RRR1-10/2	1113.985	1113.289	-274.069	0.298	661.366	0.223	13	0.184	-.ILSADEPVLR.-
R1/RRR1-9/3	1968.142	1966.271	-65.738	0.492	1156.928	0.435	27	0.122	K.NHVNYDIPLEVWIKPK.E
R1/RRR1-7/2	1502.317	1502.732	-277.145	0.441	1614.958	0.459	20	0.284	R.GCVLVASSPEILTR.V
R1/RRR1-7/2	1501.765	1502.732	-1313.799	0.359	1798.432	0.358	21	0.282	R.GCVLVASSPEILTR.V
R1/RRR1-7/2	1502.430	1502.732	-201.254	0.491	1589.788	0.458	20	0.280	R.GCVLVASSPEILTR.V
R1/RRR1-7/2	1168.034	1168.368	-286.544	0.421	1191.103	0.634	20	0.277	R.AALPVGTVSGAPK.V
R1/RRR1-7/2	1167.909	1168.368	-393.820	0.414	1300.114	0.572	20	0.275	R.AALPVGTVSGAPK.V
R1/RRR1-7/2	1168.039	1168.368	-282.455	0.405	1195.173	0.589	20	0.266	R.AALPVGTVSGAPK.V
R1/RRR1-7/2	1321.368	1320.347	15.973	0.542	1006.364	0.629	19	0.263	R.HATTEDAFQDGK.S
R1/RRR1-7/2	1320.028	1320.347	-242.049	0.516	769.950	0.563	18	0.232	R.HATTEDAFQDGK.S
R1/RRR1-7/2	1503.258	1503.597	-226.229	0.406	1375.841	0.529	21	0.271	R.ASQPTDTTTSPLAGR.L
R1/RRR1-7/2	1503.157	1503.597	-293.199	0.401	1331.588	0.401	21	0.239	R.ASQPTDTTTSPLAGR.L
R1/RRR1-7/2	1502.645	1503.597	-1302.926	0.283	1203.571	0.442	20	0.231	R.ASQPTDTTTSPLAGR.L
R1/RRR1-7/2	1333.528	1332.525	1.688	0.469	668.864	0.566	17	0.222	K.IATTATEIVDVAK.M
R1/RRR1-7/2	1332.430	1332.525	-71.638	0.398	1007.534	0.430	20	0.221	K.IATTATEIVDVAK.M
R1/RRR1-7/2	1072.518	1072.240	259.183	0.394	1025.351	0.363	15	0.212	K.DIGAVNTIIR.K
R1/RRR1-7/2	1073.055	1072.240	-173.275	0.365	866.205	0.287	14	0.195	K.DIGAVNTIIR.K
R1/RRR1-7/2	1072.330	1072.240	83.623	0.267	862.573	0.115	14	0.180	K.DIGAVNTIIR.K
R1/RRR1-10/2	959.278	959.082	204.839	0.422	1470.709	0.406	16	0.256	R.AVVSAIGADR.V
R1/RRR1-10/2	958.972	959.082	-114.794	0.441	1250.179	0.381	15	0.230	R.AVVSAIGADR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1979.491	1981.107	-1831.862	0.245	1103.779	0.329	21	0.202	R.ELGLEAVESGDADLVSYGR.L
R1/RRR1-10/3	1869.956	1869.885	38.322	0.477	1345.389	0.342	28	0.119	K.DGINDRTDEYGGSLSNR.C
R1/RRR1-6/2	1642.372	1642.792	-256.791	0.500	1628.990	0.546	23	0.311	K.LAGLSAGGGEEPQQLSK.N
R1/RRR1-6/2	1324.313	1325.403	-1583.034	0.350	1244.109	0.364	16	0.225	R.TSELEDNEFIK.F
R1/RRR1-6/2	1375.189	1375.550	-263.234	0.444	1028.854	0.401	18	0.219	K.LLFYDLYGGGEK.V
R1/RRR1-6/2	1374.901	1375.550	-1202.957	0.351	984.317	0.417	17	0.216	K.LLFYDLYGGGEK.V
R1/RRR1-6/2	1325.067	1325.403	-254.434	0.467	1057.480	0.372	16	0.214	R.TSELEDNEFIK.F
R1/RRR1-6/2	1375.196	1375.550	-258.158	0.332	872.513	0.237	16	0.189	K.LLFYDLYGGGEK.V
R1/RRR1-3/2	1374.727	1375.550	-1330.112	0.340	359.964	0.323	11	0.171	-.LLFYDLYGGGEK.-
R1/RRR1-5/2	1459.610	1458.599	7.079	0.504	1730.037	0.567	17	0.333	K.YNVESWLDYLR.S
R1/RRR1-5/2	1459.813	1458.599	146.556	0.518	1493.134	0.549	16	0.293	K.YNVESWLDYLR.S
R1/RRR1-6/2	1459.735	1458.599	93.051	0.430	1069.354	0.483	15	0.234	K.YNVESWLDYLR.S
R1/RRR1-5/2	1337.401	1337.550	-111.470	0.388	667.504	0.394	16	0.202	R.EISIDQILHLR.D
R1/RRR1-5/2	1358.112	1358.520	-301.163	0.399	838.854	0.327	17	0.197	K.VSLSENEPILEK.M
R1/RRR1-5/2	1337.210	1337.550	-254.687	0.333	533.027	0.292	15	0.190	R.EISIDQILHLR.D
R1/RRR1-6/2	1458.909	1458.599	213.030	0.352	519.353	0.223	14	0.187	-.YNVESWLDYLR.-
R1/RRR1-1/2	1323.244	1322.449	-155.133	0.540	1995.417	0.516	18	0.358	K.GVADFLQEVTSR.K
R1/RRR1-1/2	1322.319	1322.449	-98.945	0.496	1883.699	0.468	18	0.324	K.GVADFLQEVTSR.K
R1/RRR1-2/2	1321.712	1322.449	-1318.157	0.427	1719.057	0.421	18	0.288	K.GVADFLQEVTSR.K
R1/RRR1-1/2	1321.595	1322.449	-1407.026	0.410	1274.977	0.438	16	0.241	K.GVADFLQEVTSR.K
R1/RRR1-2/2	1922.540	1922.169	193.563	0.502	990.481	0.566	17	0.235	K.AISVGGQETNIITDYVLK.I
R1/RRR1-1/2	1697.513	1696.797	-168.028	0.504	737.491	0.595	22	0.230	K.STSHPASLTTSTYGASK.L
R1/RRR1-1/2	1922.401	1922.169	121.353	0.484	932.445	0.532	17	0.224	K.AISVGGQETNIITDYVLK.I
R1/RRR1-2/2	1922.128	1922.169	-21.442	0.489	828.066	0.543	16	0.218	K.AISVGGQETNIITDYVLK.I
R1/RRR1-2/2	1322.288	1322.449	-121.911	0.380	1183.476	0.297	17	0.210	K.GVADFLQEVTSR.K
R1/RRR1-8/2	1659.495	1659.861	-221.383	0.468	1337.070	0.489	20	0.258	K.ELQGVVFDDVPEALK.H
R1/RRR1-8/2	1659.532	1659.861	-199.097	0.451	1108.078	0.501	19	0.238	K.ELQGVVFDDVPEALK.H
R1/RRR1-8/2	1659.364	1659.861	-300.720	0.484	1193.530	0.414	19	0.228	K.ELQGVVFDDVPEALK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1032.009	1032.132	-119.542	0.301	815.758	0.233	13	0.188	-.VYIYSSGSR.-
R1/RRR1-8/2	1031.440	1032.132	-1644.722	0.253	928.955	0.171	13	0.184	K.VYIYSSGSR.E
R1/RRR1-8/3	1855.190	1854.950	129.702	0.482	914.564	0.535	33	0.120	K.HLTSTYSSDETKEDIK.L
R1/RRR1-8/3	1855.248	1854.950	161.178	0.516	1092.210	0.460	34	0.117	K.HLTSTYSSDETKEDIK.L
R1/RRR1-8/3	1854.783	1854.950	-90.285	0.501	834.919	0.510	31	0.113	K.HLTSTYSSDETKEDIK.L
R1/RRR1-15/3	1854.304	1854.950	-890.109	0.517	702.627	0.500	30	0.108	K.HLTSTYSSDETKEDIK.L
R1/RRR1-15/3	1854.415	1854.950	-829.940	0.516	543.293	0.492	26	0.106	K.HLTSTYSSDETKEDIK.L
R1/RRR1-15/3	1854.469	1854.950	-259.945	0.515	747.132	0.478	30	0.106	K.HLTSTYSSDETKEDIK.L
R1/RRR1-7/3	1854.492	1854.950	-247.761	0.517	786.271	0.457	30	0.104	K.HLTSTYSSDETKEDIK.L
R1/RRR1-1/3	1853.930	1854.950	-1092.871	0.450	355.173	0.341	21	0.098	K.HLTSTYSSDETKEDIK.L
R1/RRR1-7/3	1854.040	1854.950	-1033.075	0.487	701.263	0.414	29	0.096	K.HLTSTYSSDETKEDIK.L
R1/RRR1-7/3	1854.341	1854.950	-870.283	0.509	653.515	0.408	29	0.095	K.HLTSTYSSDETKEDIK.L
R1/RRR1-9/3	1854.682	1854.950	-144.554	0.467	634.661	0.392	28	0.093	K.HLTSTYSSDETKEDIK.L
R1/RRR1-5/2	1241.295	1241.459	-132.529	0.499	1642.730	0.531	20	0.311	K.SPGLDDILVALK.T
R1/RRR1-5/2	1240.750	1241.459	-1381.573	0.523	1207.848	0.527	18	0.257	K.SPGLDDILVALK.T
R1/RRR1-5/2	1589.535	1589.774	-150.865	0.420	346.347	0.549	17	0.209	K.VIPIFNENDAISTR.K
R1/RRR1-5/2	1589.227	1589.774	-976.317	0.389	243.684	0.471	15	0.199	K.VIPIFNENDAISTR.K
R1/RRR1-5/3	1530.909	1531.658	-1146.399	0.541	1516.954	0.510	28	0.182	R.RVDSAAVFHNASTR.F
R1/RRR1-5/2	1589.160	1589.774	-1018.733	0.265	169.873	0.320	14	0.179	-.VIPIFNENDAISTR.-
R1/RRR1-5/3	1531.638	1531.658	-13.527	0.513	1361.901	0.476	27	0.151	R.RVDSAAVFHNASTR.F
R1/RRR1-6/3	1532.735	1531.658	50.427	0.511	1040.638	0.496	25	0.126	R.RVDSAAVFHNASTR.F
R1/RRR1-2/3	1530.659	1531.658	-1310.004	0.339	672.960	0.240	23	0.075	R.RVDSAAVFHNASTR.F
R1/RRR1-4/3	1531.003	1531.658	-1084.190	0.309	685.515	0.242	20	0.074	R.RVDSAAVFHNASTR.F
R1/RRR1-8/2	1576.965	1576.841	79.285	0.450	1334.125	0.445	20	0.246	K.AVQSGLGTAAVIVM*DK.S
R1/RRR1-8/2	1310.360	1310.445	-65.183	0.527	861.043	0.497	17	0.227	R.RGPEWFASFGR.K
R1/RRR1-8/3	1349.821	1349.518	225.384	0.432	2140.988	0.270	28	0.201	K.AREEAYAAGLLGK.N
R1/RRR1-8/2	1577.794	1576.841	-29.552	0.288	206.960	0.496	19	0.197	K.AVQSGLGTAAVIVM*DK.S
R1/RRR1-9/2	1310.547	1310.445	78.139	0.350	405.191	0.423	13	0.196	R.RGPEWFASFGR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1577.843	1576.841	1.798	0.086	122.127	0.413	18	0.177	-.AVQSGLGTAAVIVM*DK.-
R1/RRR1-8/3	1349.439	1349.518	-58.179	0.305	1074.726	0.248	22	0.075	K.AREEAYAAGLLGK.N
R1/RRR1-6/2	1598.158	1596.809	219.061	0.535	1202.255	0.594	20	0.270	K.LGIGGLSAEFTDIFR.R
R1/RRR1-6/2	1173.222	1173.386	-140.636	0.379	1459.463	0.408	19	0.255	K.GILLYGPPGTGK.T
R1/RRR1-6/2	980.389	981.088	-1737.610	0.358	943.673	0.371	14	0.207	K.SAVSYALNR.Q
R1/RRR1-6/2	1878.846	1878.036	-101.633	0.573	1775.532	0.503	22	0.318	R.NLGAIEGSWFGSWAPER.M
R1/RRR1-6/2	1767.767	1767.919	-85.925	0.529	1276.746	0.569	21	0.273	K.HWTTFSFGEVEELGK.T
R1/RRR1-6/2	1209.191	1209.374	-151.742	0.451	1297.361	0.415	18	0.241	R.GEVVVGGYSITK.G
R1/RRR1-6/2	1208.963	1209.374	-340.849	0.430	1043.648	0.379	17	0.214	R.GEVVVGGYSITK.G
R1/RRR1-7/2	1595.185	1593.808	237.276	0.481	785.947	0.478	16	0.210	R.IYGVFDNQLPSALR.K
R1/RRR1-6/2	1086.053	1086.307	-234.333	0.479	805.039	0.417	15	0.208	-.IPSITSLINK.-
R1/RRR1-6/3	1319.573	1319.540	25.681	0.441	1234.408	0.182	21	0.075	R.LQHPWVGIVNR.S
R1/RRR1-9/2	1933.807	1934.223	-215.812	0.593	2362.263	0.654	26	0.487	K.KALSFYDVVFDAVYAPK.V
R1/RRR1-9/2	1933.501	1934.223	-893.220	0.550	1330.487	0.627	21	0.290	K.KALSFYDVVFDAVYAPK.V
R1/RRR1-8/2	1807.743	1806.050	-170.312	0.573	1119.857	0.608	19	0.262	K.ALSFYDVVFDAVYAPK.V
R1/RRR1-9/2	1935.442	1934.223	113.830	0.513	1141.455	0.576	22	0.258	K.KALSFYDVVFDAVYAPK.V
R1/RRR1-9/2	1588.783	1589.821	-1286.461	0.585	2778.592	0.660	24	0.597	K.THINIVVIGHVDSGK.S
R1/RRR1-9/2	1589.382	1589.821	-277.216	0.582	2727.886	0.664	24	0.585	K.THINIVVIGHVDSGK.S
R1/RRR1-9/2	1589.463	1589.821	-225.976	0.574	2676.214	0.621	24	0.551	K.THINIVVIGHVDSGK.S
R1/RRR1-8/3	1589.581	1589.821	-151.293	0.420	2477.932	0.506	32	0.381	K.THINIVVIGHVDSGK.S
R1/RRR1-9/3	1589.102	1589.821	-1084.732	0.471	1821.725	0.586	29	0.267	K.THINIVVIGHVDSGK.S
R1/RRR1-9/3	1588.910	1589.821	-1205.880	0.483	1869.210	0.538	29	0.256	K.THINIVVIGHVDSGK.S
R1/RRR1-2/2	1120.964	1121.268	-272.254	0.416	1063.554	0.515	15	0.243	K.STTTGHLIYK.L
R1/RRR1-3/3	1590.826	1589.821	3.369	0.524	1902.570	0.494	30	0.243	K.THINIVVIGHVDSGK.S
R1/RRR1-8/3	1589.140	1589.821	-1060.667	0.507	1706.108	0.578	29	0.241	K.THINIVVIGHVDSGK.S
R1/RRR1-1/3	1589.966	1589.821	91.312	0.577	1706.737	0.571	29	0.240	K.THINIVVIGHVDSGK.S
R1/RRR1-2/2	1121.061	1121.268	-185.623	0.416	922.074	0.527	14	0.235	K.STTTGHLIYK.L
R1/RRR1-16/2	1121.146	1121.268	-109.164	0.473	765.862	0.560	14	0.234	K.STTTGHLIYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/3	1589.169	1589.821	-1042.273	0.489	1867.282	0.484	30	0.231	K.THINIVVIGHVDSGK.S
R1/RRR1-9/3	1589.739	1589.821	-51.464	0.530	1758.827	0.526	29	0.231	K.THINIVVIGHVDSGK.S
R1/RRR1-8/2	1121.957	1121.268	-278.015	0.428	762.191	0.525	14	0.228	K.STTTGHLIYK.L
R1/RRR1-9/2	1120.986	1121.268	-252.261	0.365	1000.902	0.452	15	0.228	K.STTTGHLIYK.L
R1/RRR1-7/2	1121.087	1121.268	-162.029	0.405	879.898	0.484	14	0.226	K.STTTGHLIYK.L
R1/RRR1-3/2	1121.022	1121.268	-220.142	0.417	881.911	0.476	14	0.226	K.STTTGHLIYK.L
R1/RRR1-4/2	1121.012	1121.268	-228.991	0.428	817.350	0.479	14	0.224	K.STTTGHLIYK.L
R1/RRR1-6/2	1120.349	1121.268	-1718.125	0.316	1012.629	0.424	16	0.223	K.STTTGHLIYK.L
R1/RRR1-4/2	1121.205	1121.268	-56.960	0.414	774.474	0.498	13	0.223	K.STTTGHLIYK.L
R1/RRR1-4/2	1121.039	1121.268	-205.285	0.387	747.825	0.489	13	0.220	K.STTTGHLIYK.L
R1/RRR1-3/2	1122.010	1121.268	-231.079	0.423	762.991	0.461	14	0.220	K.STTTGHLIYK.L
R1/RRR1-3/2	1121.023	1121.268	-219.159	0.386	728.936	0.491	13	0.219	K.STTTGHLIYK.L
R1/RRR1-16/2	1121.098	1121.268	-152.526	0.413	647.706	0.502	13	0.219	K.STTTGHLIYK.L
R1/RRR1-5/2	1120.955	1121.268	-279.792	0.413	730.453	0.479	13	0.219	K.STTTGHLIYK.L
R1/RRR1-1/2	1121.241	1121.268	-24.090	0.397	579.143	0.531	12	0.218	K.STTTGHLIYK.L
R1/RRR1-6/2	1120.929	1121.268	-303.611	0.415	752.908	0.468	13	0.218	K.STTTGHLIYK.L
R1/RRR1-15/2	1120.896	1121.268	-332.675	0.405	775.214	0.448	14	0.218	K.STTTGHLIYK.L
R1/RRR1-8/2	1121.660	1121.268	350.108	0.407	681.747	0.478	13	0.217	K.STTTGHLIYK.L
R1/RRR1-15/2	1121.026	1121.268	-216.428	0.417	775.143	0.453	13	0.217	K.STTTGHLIYK.L
R1/RRR1-6/2	1121.117	1121.268	-134.940	0.387	704.186	0.467	13	0.216	K.STTTGHLIYK.L
R1/RRR1-5/2	1120.471	1121.268	-1608.884	0.367	668.343	0.479	13	0.216	K.STTTGHLIYK.L
R1/RRR1-16/2	1121.040	1121.268	-203.975	0.425	750.547	0.447	13	0.216	K.STTTGHLIYK.L
R1/RRR1-1/2	1120.626	1121.268	-1470.233	0.377	845.019	0.417	14	0.216	K.STTTGHLIYK.L
R1/RRR1-1/2	1121.982	1121.268	-255.747	0.438	678.140	0.454	13	0.215	K.STTTGHLIYK.L
R1/RRR1-11/2	1121.153	1121.268	-103.048	0.403	757.920	0.424	14	0.215	K.STTTGHLIYK.L
R1/RRR1-5/2	1121.122	1121.268	-131.008	0.404	588.244	0.488	12	0.214	K.STTTGHLIYK.L
R1/RRR1-8/2	1120.990	1121.268	-248.765	0.377	754.872	0.439	13	0.214	K.STTTGHLIYK.L
R1/RRR1-9/2	1120.971	1121.268	-265.808	0.360	671.834	0.457	13	0.213	K.STTTGHLIYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1121.090	1121.268	-159.407	0.376	628.490	0.456	13	0.213	K.STTTGHLIYK.L
R1/RRR1-2/2	1121.060	1121.268	-186.606	0.364	711.964	0.441	13	0.213	K.STTTGHLIYK.L
R1/RRR1-13/3	1589.283	1589.821	-970.205	0.417	1760.202	0.481	29	0.211	K.THINIVVIGHVDSGK.S
R1/RRR1-7/3	1589.185	1589.821	-1032.440	0.459	1628.174	0.541	29	0.211	K.THINIVVIGHVDSGK.S
R1/RRR1-14/2	1120.563	1121.268	-1525.930	0.358	724.771	0.402	14	0.211	K.STTTGHLIYK.L
R1/RRR1-21/2	1120.882	1121.268	-346.006	0.315	531.331	0.481	12	0.210	K.STTTGHLIYK.L
R1/RRR1-9/3	1589.825	1589.821	2.717	0.563	1560.880	0.565	30	0.209	K.THINIVVIGHVDSGK.S
R1/RRR1-13/2	1121.177	1121.268	-81.642	0.352	621.999	0.367	13	0.205	K.STTTGHLIYK.L
R1/RRR1-14/2	1120.522	1121.268	-1563.465	0.306	513.306	0.376	13	0.204	K.STTTGHLIYK.L
R1/RRR1-11/2	1121.168	1121.268	-89.505	0.446	601.686	0.395	13	0.204	-.STTTGHLIYK.-
R1/RRR1-11/2	1121.058	1121.268	-188.354	0.359	373.778	0.323	11	0.202	K.STTTGHLIYK.L
R1/RRR1-2/3	1589.214	1589.821	-1014.046	0.483	1548.076	0.551	29	0.202	K.THINIVVIGHVDSGK.S
R1/RRR1-3/3	1589.743	1589.821	-48.807	0.459	1629.385	0.515	29	0.202	K.THINIVVIGHVDSGK.S
R1/RRR1-2/3	1588.609	1589.821	-1396.399	0.463	1494.867	0.557	27	0.200	K.THINIVVIGHVDSGK.S
R1/RRR1-9/2	1121.167	1121.268	-90.597	0.276	623.212	0.312	13	0.199	K.STTTGHLIYK.L
R1/RRR1-15/2	1120.362	1121.268	-1706.302	0.250	562.013	0.263	13	0.197	K.STTTGHLIYK.L
R1/RRR1-2/3	1589.767	1589.821	-33.673	0.511	1514.946	0.516	28	0.187	K.THINIVVIGHVDSGK.S
R1/RRR1-6/3	1590.496	1589.821	-204.592	0.473	1517.704	0.426	25	0.164	K.THINIVVIGHVDSGK.S
R1/RRR1-1/3	1589.181	1589.821	-1035.216	0.390	1861.194	0.273	29	0.154	K.THINIVVIGHVDSGK.S
R1/RRR1-5/3	1589.249	1589.821	-991.952	0.326	851.842	0.335	23	0.090	K.THINIVVIGHVDSGK.S
R1/RRR1-13/3	1589.609	1589.821	-133.498	0.272	566.059	0.349	24	0.090	K.THINIVVIGHVDSGK.S
R1/RRR1-3/3	1589.110	1589.821	-1079.988	0.291	667.846	0.310	20	0.082	-.THINIVVIGHVDSGK.-
R1/RRR1-5/3	1589.263	1589.821	-983.045	0.320	911.502	0.207	22	0.077	K.THINIVVIGHVDSGK.S
R1/RRR1-6/2	1360.266	1360.535	-198.975	0.499	1672.872	0.421	19	0.281	R.NLSQQCLNALAK.A
R1/RRR1-6/2	1360.241	1360.535	-216.981	0.518	1611.617	0.438	19	0.278	R.NLSQQCLNALAK.A
R1/RRR1-6/2	1359.628	1360.535	-1407.109	0.487	1602.891	0.437	19	0.278	R.NLSQQCLNALAK.A
R1/RRR1-6/2	1361.834	1360.535	220.214	0.525	1325.445	0.448	19	0.251	R.NLSQQCLNALAK.A
R1/RRR1-2/2	1359.950	1360.535	-1169.367	0.449	1445.335	0.396	19	0.251	R.NLSQQCLNALAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1800.350	1800.990	-913.648	0.418	702.360	0.408	20	0.198	K.SIISGELPSGWDNSLPK.Y
R1/RRR1-1/2	1359.974	1360.535	-1151.340	0.320	796.619	0.270	16	0.193	R.NLSQQCLNALAK.A
R1/RRR1-2/2	1359.962	1360.535	-1160.173	0.366	456.969	0.302	14	0.191	-.NLSQQCLNALAK.-
R1/RRR1-6/2	1000.970	1001.162	-192.114	0.508	1468.725	0.462	17	0.271	R.IGAATALEVR.A
R1/RRR1-6/2	1001.181	1001.162	19.003	0.501	1358.495	0.461	17	0.259	R.IGAATALEVR.A
R1/RRR1-6/2	1397.254	1396.486	-166.982	0.433	1350.598	0.413	18	0.245	K.GFTISDWEGIDR.I
R1/RRR1-6/2	1000.631	1001.162	-1534.338	0.512	1088.720	0.451	17	0.235	R.IGAATALEVR.A
R1/RRR1-6/2	1231.524	1231.464	49.052	0.420	937.353	0.473	18	0.225	R.ITVGTTILDAVK.A
R1/RRR1-6/2	1230.816	1231.464	-1342.985	0.372	865.074	0.472	18	0.219	R.ITVGTTILDAVK.A
R1/RRR1-6/2	1231.241	1231.464	-181.939	0.371	659.613	0.417	16	0.202	R.ITVGTTILDAVK.A
R1/RRR1-6/2	1396.166	1396.486	-230.252	0.345	1195.488	0.219	17	0.198	K.GFTISDWEGIDR.I
R1/RRR1-6/2	1396.144	1396.486	-246.041	0.323	1171.567	0.186	17	0.193	K.GFTISDWEGIDR.I
R1/RRR1-9/3	1678.769	1678.914	-86.915	0.503	770.210	0.568	29	0.118	R.IVLEVAQHLGENTVR.T
R1/RRR1-9/3	1679.549	1678.914	-218.019	0.491	998.359	0.451	29	0.110	R.IVLEVAQHLGENTVR.T
R1/RRR1-9/3	1679.400	1678.914	289.963	0.423	619.530	0.536	27	0.104	R.IVLEVAQHLGENTVR.T
R1/RRR1-9/3	1677.686	1678.914	-1332.547	0.376	737.112	0.338	28	0.082	R.IVLEVAQHLGENTVR.T
R1/RRR1-26/2	1496.147	1495.605	-306.602	0.588	2957.076	0.589	23	0.608	R.VCACVDSAGAVTER.G
R1/RRR1-27/2	1496.256	1495.605	-233.916	0.603	2840.311	0.576	23	0.569	R.VCACVDSAGAVTER.G
R1/RRR1-27/2	1495.213	1495.605	-262.493	0.539	2783.736	0.531	23	0.534	R.VCACVDSAGAVTER.G
R1/RRR1-26/2	1495.101	1495.605	-1008.465	0.487	2767.671	0.522	23	0.527	R.VCACVDSAGAVTER.G
R1/RRR1-26/2	1494.603	1495.605	-1343.523	0.419	2880.846	0.434	23	0.517	R.VCACVDSAGAVTER.G
R1/RRR1-27/2	1658.008	1658.852	-1115.759	0.455	1387.664	0.540	21	0.276	R.GVTLCYIGAGAM*TGDR.Y
R1/RRR1-10/3	1513.695	1513.812	-77.668	0.561	3686.377	0.511	37	0.840	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-11/3	1514.038	1513.812	149.425	0.563	3262.930	0.518	37	0.660	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-11/3	1513.890	1513.812	51.176	0.583	2653.735	0.565	35	0.476	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-11/2	1513.207	1513.812	-1064.365	0.510	2427.414	0.552	26	0.461	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-11/3	1514.530	1513.812	-187.287	0.594	2641.429	0.552	37	0.457	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-11/2	1512.927	1513.812	-1249.642	0.488	2316.521	0.552	25	0.436	K.HLGVVGLGGLGHLGVK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1513.517	1513.812	-195.816	0.538	2228.608	0.582	25	0.429	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-10/3	1513.285	1513.812	-1012.457	0.557	2617.913	0.480	34	0.417	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-13/3	1513.833	1513.812	13.934	0.495	2373.244	0.506	32	0.364	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-11/3	1513.071	1513.812	-1154.128	0.527	1704.666	0.542	28	0.235	K.HLGVVGLGGLGHLGVK.F
R1/RRR1-6/2	1310.944	1311.469	-1167.223	0.423	627.910	0.464	16	0.210	R.QVLVDLQENPR.A
R1/RRR1-6/2	1311.463	1311.469	-5.192	0.457	746.013	0.422	16	0.209	R.QVLVDLQENPR.A
R1/RRR1-6/2	1312.455	1311.469	-10.598	0.426	620.420	0.412	16	0.202	-.QVLVDLQENPR.-
R1/RRR1-6/3	1659.625	1659.740	-69.216	0.473	1258.700	0.338	25	0.107	K.ANRGDLTQEEIQER.Q
R1/RRR1-6/3	1886.874	1886.098	-118.955	0.267	911.230	0.418	26	0.096	R.LGAAHLGLGDAASAVAAYEK.G
R1/RRR1-6/3	1659.415	1659.740	-196.390	0.399	819.030	0.329	21	0.082	-.ANRGDLTQEEIQER.-
R1/RRR1-6/3	1660.751	1659.740	6.877	0.504	816.225	0.263	21	0.072	-.ANRGDLTQEEIQER.-
R1/RRR1-6/3	1887.792	1886.098	-162.805	0.187	666.372	0.219	23	0.064	R.LGAAHLGLGDAASAVAAYEK.G
R1/RRR1-6/3	1887.734	1886.098	-193.262	0.136	650.409	0.199	23	0.061	R.LGAAHLGLGDAASAVAAYEK.G
R1/RRR1-12/2	1708.549	1708.940	-229.789	0.586	3540.613	0.596	28	0.811	R.HVVIVDDLVQSGGTLR.E
R1/RRR1-12/3	1826.362	1826.237	68.749	0.499	2615.228	0.529	36	0.459	K.VAILGAAGGIGQPLSLLM*K.L
R1/RRR1-12/3	1809.483	1810.238	-972.513	0.452	2220.416	0.451	36	0.303	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-12/3	1809.911	1810.238	-180.871	0.472	1917.200	0.555	33	0.285	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-3/2	1826.355	1826.237	64.802	0.365	1550.941	0.397	22	0.256	K.VAILGAAGGIGQPLSLLM*K.L
R1/RRR1-12/2	1810.587	1810.238	193.495	0.481	1304.822	0.414	21	0.233	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-12/2	1810.872	1810.238	-202.471	0.451	1346.181	0.368	21	0.228	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-12/2	1809.805	1810.238	-239.596	0.415	1236.671	0.362	20	0.218	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-12/2	1825.855	1826.237	-210.048	0.433	409.207	0.566	23	0.214	K.VAILGAAGGIGQPLSLLM*K.L
R1/RRR1-12/3	1809.901	1810.238	-186.555	0.427	1577.650	0.496	33	0.192	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-11/2	1809.471	1810.238	-979.414	0.326	601.874	0.280	18	0.185	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-11/2	1809.396	1810.238	-1020.934	0.262	691.293	0.190	16	0.178	K.VAILGAAGGIGQPLSLLMK.L
R1/RRR1-12/3	1953.865	1954.410	-793.198	0.399	1467.355	0.442	32	0.161	R.KVAILGAAGGIGQPLSLLM*K.L
R1/RRR1-12/2	1825.545	1826.237	-929.460	0.282	169.681	0.416	12	0.146	-.VAILGAAGGIGQPLSLLM*K.-
R1/RRR1-12/3	1825.544	1826.237	-930.340	0.278	1358.677	0.279	29	0.102	K.VAILGAAGGIGQPLSLLM*K.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/3	1938.956	1938.411	-235.326	0.402	816.987	0.396	27	0.095	R.KVAILGAAGGIGQPLSLLMK.L
R1/RRR1-12/3	1954.353	1954.410	-28.974	0.324	1001.841	0.301	27	0.085	R.KVAILGAAGGIGQPLSLLM*K.L
R1/RRR1-12/3	1937.998	1938.411	-213.520	0.356	600.889	0.330	25	0.081	R.KVAILGAAGGIGQPLSLLMK.L
R1/RRR1-4/2	1844.775	1844.098	-175.787	0.520	1408.386	0.375	20	0.235	K.NSPAIIFIDEIDSIAPK.R
R1/RRR1-4/2	1233.010	1232.414	-328.740	0.491	1130.547	0.419	19	0.229	R.FALGVSNPSALR.E
R1/RRR1-4/2	1231.952	1232.414	-376.329	0.407	912.608	0.385	16	0.207	R.FALGVSNPSALR.E
R1/RRR1-3/2	1486.598	1485.753	-104.318	0.500	1690.376	0.474	21	0.300	R.LAVGEALTNLVWAK.V
R1/RRR1-3/2	1254.421	1254.418	2.771	0.459	1126.350	0.408	18	0.225	R.SPNSVIVEVGPR.M
R1/RRR1-3/2	1485.342	1485.753	-277.097	0.391	1022.132	0.408	17	0.214	R.LAVGEALTNLVWAK.V
R1/RRR1-3/2	1676.595	1676.932	-201.745	0.482	1316.514	0.261	18	0.207	R.IPYLQESETIELLK.Q
R1/RRR1-23/3	1364.691	1365.565	-1377.721	0.510	3038.881	0.371	30	0.465	R.HHVIGQYVVGQK.G
R1/RRR1-23/3	1365.597	1365.565	23.381	0.530	2923.712	0.399	30	0.444	R.HHVIGQYVVGQK.G
R1/RRR1-24/3	1365.723	1365.565	115.763	0.521	2854.400	0.424	30	0.436	R.HHVIGQYVVGQK.G
R1/RRR1-24/3	1365.661	1365.565	70.179	0.543	2707.738	0.377	28	0.373	R.HHVIGQYVVGQK.G
R1/RRR1-23/3	1365.593	1365.565	20.288	0.537	2156.694	0.447	27	0.269	R.HHVIGQYVVGQK.G
R1/RRR1-24/2	1270.326	1270.374	-37.937	0.427	780.755	0.589	19	0.236	K.VPPNSASLEEAR.H
R1/RRR1-23/2	1269.985	1270.374	-307.118	0.381	748.605	0.593	19	0.232	K.VPPNSASLEEAR.H
R1/RRR1-23/2	1269.965	1270.374	-323.127	0.429	598.628	0.589	18	0.227	K.VPPNSASLEEAR.H
R1/RRR1-24/2	1270.194	1270.374	-141.851	0.438	608.292	0.534	18	0.221	K.VPPNSASLEEAR.H
R1/RRR1-23/2	1269.486	1270.374	-1491.302	0.282	566.190	0.474	17	0.203	K.VPPNSASLEEAR.H
R1/RRR1-24/2	1269.565	1270.374	-1429.393	0.350	401.794	0.423	16	0.202	K.VPPNSASLEEAR.H
R1/RRR1-24/3	1364.360	1365.565	-1620.888	0.399	798.640	0.324	22	0.082	R.HHVIGQYVVGQK.G
R1/RRR1-25/2	1115.981	1116.290	-277.090	0.549	2707.381	0.661	21	0.567	R.VVGAGGAVVACR.G
R1/RRR1-17/2	1115.945	1116.290	-310.233	0.558	2494.290	0.645	21	0.506	R.VVGAGGAVVACR.G
R1/RRR1-17/2	1115.941	1116.290	-313.635	0.544	2432.662	0.677	20	0.505	R.VVGAGGAVVACR.G
R1/RRR1-17/2	1116.112	1116.290	-159.789	0.502	2459.408	0.650	21	0.500	R.VVGAGGAVVACR.G
R1/RRR1-18/2	1115.976	1116.290	-281.699	0.559	2365.467	0.647	20	0.477	R.VVGAGGAVVACR.G
R1/RRR1-25/2	1115.428	1116.290	-1674.224	0.489	2303.717	0.662	21	0.469	R.VVGAGGAVVACR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-25/2	1116.069	1116.290	-198.411	0.570	2310.158	0.640	21	0.462	R.VVGAGGAVVACR.G
R1/RRR1-26/2	1115.457	1116.290	-1648.277	0.465	2335.492	0.624	21	0.460	R.VVGAGGAVVACR.G
R1/RRR1-16/2	1115.883	1116.290	-365.769	0.504	2272.347	0.655	21	0.460	R.VVGAGGAVVACR.G
R1/RRR1-18/2	1115.961	1116.290	-295.636	0.567	2220.905	0.663	21	0.453	R.VVGAGGAVVACR.G
R1/RRR1-18/2	1116.054	1116.290	-211.797	0.571	2220.644	0.645	21	0.446	R.VVGAGGAVVACR.G
R1/RRR1-19/2	1116.041	1116.290	-223.429	0.526	2226.272	0.628	21	0.440	R.VVGAGGAVVACR.G
R1/RRR1-19/2	1116.006	1116.290	-255.032	0.569	2160.542	0.661	21	0.440	R.VVGAGGAVVACR.G
R1/RRR1-16/2	1115.921	1116.290	-331.854	0.540	2137.498	0.652	21	0.431	R.VVGAGGAVVACR.G
R1/RRR1-26/2	1115.316	1116.290	-1774.948	0.484	2151.143	0.626	20	0.423	R.VVGAGGAVVACR.G
R1/RRR1-19/2	1115.484	1116.290	-1623.430	0.496	2185.361	0.602	21	0.421	R.VVGAGGAVVACR.G
R1/RRR1-16/2	1115.952	1116.290	-303.977	0.544	2110.058	0.635	21	0.419	R.VVGAGGAVVACR.G
R1/RRR1-26/2	1115.310	1116.290	-1780.337	0.474	2159.690	0.597	20	0.413	R.VVGAGGAVVACR.G
R1/RRR1-14/2	1115.826	1116.290	-416.591	0.413	2246.004	0.493	21	0.392	R.VVGAGGAVVACR.G
R1/RRR1-12/2	1116.152	1116.290	-123.584	0.456	1719.598	0.506	19	0.310	R.VVGAGGAVVACR.G
R1/RRR1-18/2	1674.134	1673.852	169.115	0.560	1542.431	0.575	22	0.304	R.GLVSYDFPASFWAGR.V
R1/RRR1-15/2	1116.049	1116.290	-215.967	0.431	1452.382	0.613	20	0.303	R.VVGAGGAVVACR.G
R1/RRR1-17/2	1673.122	1673.852	-1036.837	0.485	1548.971	0.560	20	0.299	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1674.294	1673.852	265.261	0.563	1424.544	0.605	21	0.297	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1673.282	1673.852	-940.884	0.511	1505.606	0.524	20	0.283	R.GLVSYDFPASFWAGR.V
R1/RRR1-19/2	1673.211	1673.852	-983.658	0.455	1424.877	0.552	20	0.282	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1673.297	1673.852	-931.802	0.545	1406.536	0.543	21	0.278	R.GLVSYDFPASFWAGR.V
R1/RRR1-17/2	1674.594	1673.852	-154.462	0.609	1216.965	0.575	21	0.266	R.GLVSYDFPASFWAGR.V
R1/RRR1-24/2	1674.422	1673.852	-257.433	0.575	1240.080	0.569	20	0.266	R.GLVSYDFPASFWAGR.V
R1/RRR1-17/2	1673.301	1673.852	-929.458	0.505	1224.573	0.568	20	0.265	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1674.478	1673.852	-223.716	0.539	1258.705	0.521	20	0.257	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1672.818	1673.852	-1219.493	0.438	1211.374	0.539	20	0.257	R.GLVSYDFPASFWAGR.V
R1/RRR1-19/2	1673.158	1673.852	-1015.155	0.475	1162.028	0.502	20	0.245	R.GLVSYDFPASFWAGR.V
R1/RRR1-19/2	1673.187	1673.852	-997.941	0.478	1074.478	0.529	19	0.243	R.GLVSYDFPASFWAGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1673.507	1673.852	-206.726	0.477	1118.334	0.504	19	0.241	R.GLVSYDFPASFWAGR.V
R1/RRR1-17/2	1675.226	1673.852	224.039	0.550	903.085	0.566	20	0.240	R.GLVSYDFPASFWAGR.V
R1/RRR1-25/2	1673.434	1673.852	-250.415	0.489	1003.221	0.527	18	0.236	R.GLVSYDFPASFWAGR.V
R1/RRR1-25/2	1673.546	1673.852	-183.091	0.462	1006.839	0.481	18	0.228	R.GLVSYDFPASFWAGR.V
R1/RRR1-24/2	1674.898	1673.852	27.734	0.488	746.842	0.563	16	0.225	R.GLVSYDFPASFWAGR.V
R1/RRR1-22/2	1675.138	1673.852	171.426	0.485	791.746	0.470	19	0.218	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1672.867	1673.852	-1190.182	0.308	811.774	0.451	16	0.209	R.GLVSYDFPASFWAGR.V
R1/RRR1-3/2	1673.817	1673.852	-20.672	0.337	891.009	0.415	16	0.209	R.GLVSYDFPASFWAGR.V
R1/RRR1-3/2	1674.793	1673.852	-34.989	0.351	593.978	0.447	17	0.206	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1672.892	1673.852	-1175.087	0.330	860.032	0.401	16	0.206	R.GLVSYDFPASFWAGR.V
R1/RRR1-18/2	1115.309	1116.290	-1781.217	0.316	800.137	0.332	16	0.201	R.VVGAGGAVVACR.G
R1/RRR1-18/2	1116.030	1116.290	-233.304	0.273	755.694	0.352	15	0.200	R.VVGAGGAVVACR.G
R1/RRR1-13/2	1673.721	1673.852	-78.025	0.329	488.047	0.386	16	0.199	R.GLVSYDFPASFWAGR.V
R1/RRR1-16/2	1672.721	1673.852	-1277.242	0.309	767.733	0.358	16	0.199	R.GLVSYDFPASFWAGR.V
R1/RRR1-11/2	1674.348	1673.852	297.281	0.320	779.299	0.347	16	0.198	R.GLVSYDFPASFWAGR.V
R1/RRR1-16/2	1672.895	1673.852	-1173.035	0.307	523.598	0.396	14	0.196	R.GLVSYDFPASFWAGR.V
R1/RRR1-13/2	1673.419	1673.852	-259.197	0.341	594.718	0.180	15	0.186	R.GLVSYDFPASFWAGR.V
R1/RRR1-6/2	1302.163	1302.459	-227.787	0.409	277.406	0.492	13	0.200	R.QLNLTEDSLLR.Y
R1/RRR1-6/3	1515.552	1515.692	-92.640	0.450	907.703	0.530	27	0.117	R.VYEAHVGISSPDLK.V
R1/RRR1-6/3	1614.721	1613.753	-19.921	0.497	547.314	0.588	27	0.111	K.VVLDTDDKAYGGFGR.V
R1/RRR1-6/3	1515.908	1515.692	142.658	0.458	577.095	0.490	23	0.099	R.VYEAHVGISSPDLK.V
R1/RRR1-6/3	1516.184	1515.692	325.175	0.453	647.444	0.439	24	0.093	R.VYEAHVGISSPDLK.V
R1/RRR1-6/3	1613.446	1613.753	-190.754	0.403	570.700	0.444	27	0.090	K.VVLDTDDKAYGGFGR.V
R1/RRR1-6/3	1613.983	1613.753	143.055	0.357	497.951	0.439	26	0.088	K.VVLDTDDKAYGGFGR.V
R1/RRR1-20/2	1792.387	1793.055	-933.101	0.580	2769.953	0.557	23	0.530	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-20/2	1792.448	1793.055	-898.847	0.564	2775.592	0.549	23	0.528	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-15/2	1792.882	1793.055	-96.765	0.565	2725.696	0.550	23	0.516	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-19/2	1792.274	1793.055	-996.760	0.559	2773.212	0.518	23	0.513	K.AM*SIM*NSFINDIFEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1793.537	1793.055	269.514	0.594	2614.260	0.584	22	0.502	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-19/2	1791.996	1793.055	-1152.215	0.561	2553.716	0.591	23	0.493	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-19/2	1792.202	1793.055	-1036.765	0.580	2670.712	0.530	23	0.493	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-16/2	1794.267	1793.055	118.463	0.608	2276.623	0.593	22	0.430	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-18/2	1794.330	1793.055	153.941	0.608	2173.198	0.581	22	0.405	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-16/2	1794.360	1793.055	170.588	0.608	2001.167	0.585	22	0.375	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-18/2	1792.987	1793.055	-37.760	0.584	2040.933	0.545	21	0.367	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-15/2	1793.910	1793.055	-80.739	0.597	1913.023	0.577	21	0.356	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-16/2	1792.997	1793.055	-32.502	0.570	1868.727	0.541	21	0.338	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-23/2	1794.460	1793.055	226.527	0.616	1506.185	0.570	20	0.294	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-18/2	1792.204	1793.055	-1035.671	0.549	1455.914	0.559	19	0.285	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-18/2	1792.445	1793.055	-900.557	0.552	1299.854	0.579	20	0.275	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-1/2	1793.659	1793.055	-221.435	0.504	1363.241	0.552	19	0.274	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-2/2	1794.128	1793.055	40.880	0.529	1168.351	0.557	18	0.255	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-23/2	1794.736	1793.055	-177.846	0.575	1169.299	0.561	18	0.255	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-12/2	1794.805	1793.055	-139.433	0.531	1152.456	0.526	18	0.246	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-11/2	1794.148	1793.055	52.344	0.524	1073.857	0.550	18	0.245	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-12/2	1794.229	1793.055	97.243	0.497	933.070	0.485	18	0.224	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-6/2	1793.225	1793.055	94.976	0.464	576.857	0.575	16	0.220	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-14/2	1794.364	1793.055	172.976	0.479	744.867	0.504	17	0.218	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-3/2	1794.031	1793.055	-13.374	0.446	729.324	0.485	16	0.213	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-15/2	1793.183	1793.055	71.900	0.409	904.746	0.425	17	0.213	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-25/2	1794.702	1793.055	-197.361	0.421	417.438	0.519	14	0.208	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-25/2	1794.194	1793.055	77.865	0.387	543.090	0.427	16	0.203	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-24/2	1793.498	1793.055	247.675	0.435	343.445	0.469	13	0.202	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-21/2	939.966	940.162	-208.424	0.305	538.430	0.390	12	0.201	R.LVLPGELAK.H
R1/RRR1-20/2	939.588	940.162	-1679.824	0.285	358.453	0.428	11	0.201	R.LVLPGELAK.H
R1/RRR1-17/2	940.158	940.162	-3.921	0.340	299.076	0.366	10	0.200	R.LVLPGELAK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	939.996	940.162	-177.157	0.311	322.137	0.387	10	0.199	R.LVLPGELAK.H
R1/RRR1-23/2	939.782	940.162	-405.582	0.310	378.377	0.341	11	0.199	R.LVLPGELAK.H
R1/RRR1-17/2	939.668	940.162	-527.068	0.215	772.394	0.374	14	0.199	R.LVLPGELAK.H
R1/RRR1-18/2	939.579	940.162	-1689.614	0.255	359.037	0.395	11	0.198	R.LVLPGELAK.H
R1/RRR1-7/2	1794.241	1793.055	104.339	0.414	376.560	0.415	13	0.198	K.AM*SIM*NSFINDIFEK.L
R1/RRR1-20/2	939.936	940.162	-240.866	0.282	320.518	0.375	10	0.198	R.LVLPGELAK.H
R1/RRR1-17/2	940.082	940.162	-85.322	0.281	251.479	0.391	9	0.198	R.LVLPGELAK.H
R1/RRR1-21/2	940.105	940.162	-60.314	0.281	306.709	0.291	10	0.197	R.LVLPGELAK.H
R1/RRR1-15/2	939.555	940.162	-1715.198	0.196	492.338	0.272	12	0.191	R.LVLPGELAK.H
R1/RRR1-21/2	1832.252	1832.006	135.075	0.541	2914.328	0.545	29	0.567	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-21/2	1831.385	1832.006	-887.335	0.505	2869.895	0.533	29	0.551	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-22/2	1832.466	1832.006	251.986	0.602	2763.883	0.597	30	0.551	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-22/2	1831.554	1832.006	-247.447	0.457	2787.411	0.555	29	0.540	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-21/2	1831.449	1832.006	-852.273	0.524	2510.524	0.547	29	0.468	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-22/2	1832.136	1832.006	71.197	0.525	2464.444	0.517	29	0.445	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-22/2	978.919	979.072	-156.105	0.479	1110.299	0.534	14	0.253	R.GNLDIFSGR.G
R1/RRR1-20/2	1832.279	1832.006	149.640	0.500	1081.709	0.569	27	0.252	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-22/2	978.296	979.072	-1820.236	0.453	1072.078	0.536	14	0.250	R.GNLDIFSGR.G
R1/RRR1-26/2	978.935	979.072	-140.594	0.454	1056.890	0.541	14	0.249	R.GNLDIFSGR.G
R1/RRR1-18/2	978.764	979.072	-315.123	0.421	1180.268	0.493	14	0.248	R.GNLDIFSGR.G
R1/RRR1-17/2	979.072	979.072	-0.139	0.412	1194.297	0.480	15	0.248	R.GNLDIFSGR.G
R1/RRR1-26/2	978.543	979.072	-1567.283	0.420	1040.642	0.537	14	0.246	R.GNLDIFSGR.G
R1/RRR1-21/2	978.855	979.072	-221.783	0.480	1039.556	0.495	14	0.240	R.GNLDIFSGR.G
R1/RRR1-19/2	978.328	979.072	-1788.265	0.429	1079.422	0.486	14	0.240	R.GNLDIFSGR.G
R1/RRR1-19/2	978.947	979.072	-128.210	0.456	1007.910	0.497	14	0.238	R.GNLDIFSGR.G
R1/RRR1-18/2	979.016	979.072	-56.916	0.452	1019.016	0.489	14	0.237	R.GNLDIFSGR.G
R1/RRR1-25/2	978.847	979.072	-230.290	0.457	1019.648	0.487	14	0.237	R.GNLDIFSGR.G
R1/RRR1-25/2	978.434	979.072	-1678.953	0.387	1012.122	0.500	14	0.237	R.GNLDIFSGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1831.614	1832.006	-214.283	0.426	1128.509	0.470	28	0.236	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-20/2	978.946	979.072	-128.460	0.428	1041.356	0.473	14	0.235	R.GNLDIFSGR.G
R1/RRR1-21/2	978.443	979.072	-1669.677	0.451	849.206	0.537	13	0.234	R.GNLDIFSGR.G
R1/RRR1-19/2	1832.551	1832.006	-248.648	0.477	931.187	0.531	27	0.234	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-26/2	978.517	979.072	-1593.851	0.408	988.786	0.482	14	0.233	R.GNLDIFSGR.G
R1/RRR1-21/2	978.331	979.072	-1784.880	0.431	824.716	0.531	13	0.232	R.GNLDIFSGR.G
R1/RRR1-20/2	1831.713	1832.006	-160.062	0.451	983.750	0.497	25	0.229	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-22/2	978.361	979.072	-1753.664	0.436	824.633	0.506	13	0.228	R.GNLDIFSGR.G
R1/RRR1-19/2	978.343	979.072	-1772.468	0.353	1023.225	0.430	14	0.225	R.GNLDIFSGR.G
R1/RRR1-20/2	979.100	979.072	28.998	0.431	863.070	0.471	13	0.224	R.GNLDIFSGR.G
R1/RRR1-25/2	978.705	979.072	-375.941	0.440	883.753	0.463	13	0.224	R.GNLDIFSGR.G
R1/RRR1-20/2	978.351	979.072	-1763.693	0.384	797.017	0.490	13	0.223	R.GNLDIFSGR.G
R1/RRR1-1/2	978.907	979.072	-169.115	0.434	953.531	0.406	14	0.221	R.GNLDIFSGR.G
R1/RRR1-19/2	1832.392	1832.006	211.505	0.459	668.811	0.512	23	0.215	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-23/2	978.737	979.072	-343.404	0.386	535.384	0.375	12	0.206	R.GNLDIFSGR.G
R1/RRR1-19/2	1831.565	1832.006	-241.228	0.390	586.446	0.442	23	0.204	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-17/2	1831.995	1832.006	-5.788	0.402	465.785	0.410	25	0.203	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-17/2	1831.824	1832.006	-99.630	0.283	263.657	0.362	19	0.196	K.GGTDSVIGVTLLGADGSGVR.I
R1/RRR1-17/2	978.099	979.072	-2023.518	0.240	699.299	0.198	13	0.191	-.GNLDIFSGR.-
R1/RRR1-4/2	1201.938	1202.388	-375.540	0.414	1305.060	0.530	19	0.267	R.HALSAISAIYR.L
R1/RRR1-4/2	1220.620	1221.388	-1452.504	0.381	1713.376	0.257	17	0.247	R.AVAYLLTNAER.V
R1/RRR1-4/2	1202.225	1202.388	-136.123	0.430	1177.104	0.490	18	0.246	R.HALSAISAIYR.L
R1/RRR1-4/2	1221.023	1221.388	-299.579	0.473	1523.158	0.333	17	0.244	R.AVAYLLTNAER.V
R1/RRR1-4/2	1170.201	1169.354	-131.163	0.457	749.107	0.425	14	0.209	R.LIDTFYQIR.A
R1/RRR1-4/2	1427.320	1427.549	-160.548	0.450	736.630	0.494	15	0.213	R.NPVYQNAGNFFR.L
R1/RRR1-4/2	1042.059	1042.209	-144.708	0.349	1005.171	0.379	14	0.212	R.LSDFLTFAK.D
R1/RRR1-4/2	1042.048	1042.209	-155.754	0.366	855.318	0.339	13	0.200	R.LSDFLTFAK.D
R1/RRR1-3/2	1938.946	1938.172	-116.732	0.462	605.035	0.438	19	0.199	K.EYIWPVTTNNYIQPAK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1471.340	1471.596	-174.634	0.364	1646.591	0.434	17	0.282	K.TALSNFEAALDYR.N
R1/RRR1-3/2	1384.501	1384.562	-44.094	0.433	1354.856	0.505	17	0.267	K.YIDNLTNIYVR.F
R1/RRR1-3/2	1264.219	1264.370	-119.666	0.421	1439.707	0.326	19	0.235	R.ADQSLFEAGVAR.E
R1/RRR1-3/2	1263.662	1264.370	-1355.069	0.317	1451.694	0.278	18	0.226	R.ADQSLFEAGVAR.E
R1/RRR1-4/2	1228.304	1228.336	-25.479	0.463	1224.875	0.338	15	0.220	K.LNIDETGFYR.V
R1/RRR1-4/2	1298.971	1299.414	-341.549	0.452	857.435	0.476	14	0.217	K.EAEISQFFATR.T
R1/RRR1-4/2	1729.483	1729.912	-248.742	0.367	882.705	0.364	17	0.198	R.ISEAFSGSSLISDFIR.S
R1/RRR1-4/2	1299.895	1299.414	371.238	0.353	548.138	0.357	12	0.190	K.EAEISQFFATR.T
R1/RRR1-4/2	1729.038	1729.912	-1086.652	0.276	819.780	0.221	17	0.182	R.ISEAFSGSSLISDFIR.S
R1/RRR1-4/2	1728.758	1729.912	-1249.439	0.286	669.477	0.184	16	0.178	R.ISEAFSGSSLISDFIR.S
R1/RRR1-5/2	1674.691	1675.862	-1300.743	0.324	1447.320	0.352	21	0.237	K.AAVAVLGDLADTLGSSSK.D
R1/RRR1-5/2	1498.187	1496.732	304.777	0.361	822.357	0.431	18	0.206	R.GIFEAYSGILQGIK.G
R1/RRR1-5/2	1262.887	1262.442	354.001	0.382	935.398	0.323	14	0.200	K.SNLFHVEFLR.E
R1/RRR1-6/2	1290.967	1291.478	-1174.189	0.428	1025.545	0.393	16	0.216	K.VQDIVSQIFNK.T
R1/RRR1-22/2	1811.282	1811.885	-887.720	0.541	2586.938	0.627	29	0.531	K.SQNADPLTGISSEGYSGK.G
R1/RRR1-22/2	1812.495	1811.885	-216.003	0.601	2368.174	0.688	28	0.504	K.SQNADPLTGISSEGYSGK.G
R1/RRR1-22/2	1812.316	1811.885	238.641	0.571	2061.731	0.645	27	0.418	K.SQNADPLTGISSEGYSGK.G
R1/RRR1-22/2	1212.229	1211.370	-116.324	0.412	988.175	0.452	18	0.224	R.SFAGPAPSTM*TK.E
R1/RRR1-22/2	1211.000	1211.370	-306.113	0.307	1059.826	0.427	18	0.220	R.SFAGPAPSTM*TK.E
R1/RRR1-22/2	1210.494	1211.370	-1554.280	0.401	809.517	0.477	16	0.216	R.SFAGPAPSTM*TK.E
R1/RRR1-14/2	1617.488	1617.743	-157.871	0.532	2897.447	0.489	25	0.544	R.ELTAEVQQSGVTGAAR.V
R1/RRR1-14/2	1617.198	1617.743	-958.447	0.528	2864.973	0.506	25	0.543	R.ELTAEVQQSGVTGAAR.V
R1/RRR1-14/2	1617.372	1617.743	-230.101	0.543	2420.952	0.468	24	0.420	R.ELTAEVQQSGVTGAAR.V
R1/RRR1-13/2	1617.446	1617.743	-184.369	0.560	2309.489	0.498	23	0.408	R.ELTAEVQQSGVTGAAR.V
R1/RRR1-13/2	1617.086	1617.743	-1027.716	0.482	2259.915	0.408	23	0.367	R.ELTAEVQQSGVTGAAR.V
R1/RRR1-14/2	1362.650	1363.455	-1328.693	0.467	1500.471	0.473	19	0.274	K.VFGESSPEAQPSK.S
R1/RRR1-14/2	1363.144	1363.455	-228.735	0.497	1393.813	0.484	19	0.265	K.VFGESSPEAQPSK.S
R1/RRR1-14/2	1363.098	1363.455	-262.515	0.485	1267.554	0.439	18	0.241	K.VFGESSPEAQPSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1616.359	1616.868	-936.599	0.541	2475.378	0.526	23	0.457	K.MGQIQVLTGSQGQIR.A
R1/RRR1-11/2	1632.424	1632.867	-272.563	0.533	2487.188	0.494	23	0.446	K.M*GQIQVLTGSQGQIR.A
R1/RRR1-11/2	1632.372	1632.867	-304.223	0.561	2486.829	0.483	23	0.440	K.M*GQIQVLTGSQGQIR.A
R1/RRR1-11/2	1615.703	1616.868	-1343.989	0.454	2417.337	0.460	23	0.419	K.MGQIQVLTGSQGQIR.A
R1/RRR1-11/2	1616.363	1616.868	-933.794	0.548	2333.547	0.510	23	0.419	K.MGQIQVLTGSQGQIR.A
R1/RRR1-11/2	935.057	935.016	44.047	0.247	975.192	0.141	13	0.182	-.TPNVFDNK.-
R1/RRR1-13/3	1845.649	1845.008	-195.048	0.558	2812.894	0.484	37	0.475	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/3	1844.880	1845.008	-69.267	0.544	2467.359	0.502	37	0.379	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-13/3	1844.271	1845.008	-944.742	0.620	2265.777	0.518	36	0.336	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/3	1844.000	1845.008	-1092.083	0.592	2152.179	0.513	36	0.305	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/2	1152.056	1152.279	-194.232	0.533	1588.316	0.453	17	0.279	R.AALYLASDEAK.Y
R1/RRR1-13/2	1153.028	1152.279	-218.385	0.544	1541.804	0.454	17	0.274	R.AALYLASDEAK.Y
R1/RRR1-14/2	1845.437	1845.008	233.363	0.554	1245.059	0.584	22	0.271	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/2	1151.601	1152.279	-1461.093	0.422	1551.940	0.381	17	0.258	R.AALYLASDEAK.Y
R1/RRR1-13/2	1151.562	1152.279	-1495.699	0.415	1524.066	0.390	17	0.257	R.AALYLASDEAK.Y
R1/RRR1-13/2	1151.950	1152.279	-286.400	0.494	1337.817	0.455	16	0.252	R.AALYLASDEAK.Y
R1/RRR1-14/2	1151.952	1152.279	-284.912	0.487	1470.656	0.394	17	0.252	R.AALYLASDEAK.Y
R1/RRR1-14/2	1845.576	1845.008	-234.621	0.527	798.232	0.548	20	0.224	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-13/3	1845.054	1845.008	25.003	0.550	1813.842	0.472	33	0.221	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/3	1844.967	1845.008	-22.279	0.536	1740.710	0.472	34	0.205	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-13/3	1845.950	1845.008	-31.454	0.438	1331.500	0.417	31	0.133	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-13/3	1845.462	1845.008	246.821	0.528	843.760	0.558	33	0.124	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-13/3	1844.991	1845.008	-8.940	0.489	779.027	0.533	33	0.115	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/3	1846.171	1845.008	88.422	0.506	762.118	0.528	34	0.113	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/3	1845.168	1845.008	86.811	0.517	857.887	0.491	34	0.111	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-14/3	1846.136	1845.008	69.821	0.510	700.010	0.507	33	0.108	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-13/3	1845.938	1845.008	-37.921	0.451	706.530	0.493	32	0.106	K.YVNGHNLVVDGGFTSHK.G
R1/RRR1-4/2	956.157	957.109	-2047.928	0.341	919.102	0.391	13	0.209	R.AVAIENALR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1292.127	1292.335	-161.332	0.378	421.771	0.498	15	0.205	R.QNITESETDVR.S
R1/RRR1-4/2	956.667	957.109	-463.310	0.339	861.169	0.349	13	0.202	R.AVAIENALR.L
R1/RRR1-4/2	1292.195	1292.335	-108.832	0.391	393.491	0.420	14	0.199	R.QNITESETDVR.S
R1/RRR1-4/2	956.160	957.109	-2044.977	0.316	620.768	0.305	12	0.192	R.AVAIENALR.L
R1/RRR1-4/3	1301.275	1300.486	-162.796	0.406	1131.520	0.193	22	0.068	-.AKDTVTVIEAPR.-
R1/RRR1-23/3	1900.651	1901.012	-190.195	0.474	2479.602	0.417	41	0.355	R.RASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-23/2	1744.050	1744.825	-1021.114	0.482	1625.430	0.557	26	0.309	R.ASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-23/2	1744.262	1744.825	-898.711	0.473	1190.516	0.556	24	0.256	R.ASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-22/2	1744.302	1744.825	-875.668	0.484	1172.060	0.563	22	0.254	R.ASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-23/2	1744.232	1744.825	-916.346	0.460	1017.665	0.550	23	0.238	R.ASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-22/2	1744.512	1744.825	-180.111	0.491	967.079	0.549	21	0.232	R.ASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-22/2	1744.253	1744.825	-904.332	0.475	974.021	0.545	21	0.232	R.ASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-22/3	1900.814	1901.012	-104.187	0.468	1692.766	0.334	34	0.161	R.RASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-23/3	1900.203	1901.012	-954.871	0.471	1429.739	0.380	33	0.140	R.RASTAGGSGGFSGGGGSNM*LR.F
R1/RRR1-19/2	1688.245	1687.985	154.413	0.570	2355.262	0.704	25	0.509	R.HVVFGQVIEGM*DIVK.M
R1/RRR1-19/2	1687.173	1687.985	-1077.276	0.513	2175.243	0.676	25	0.455	R.HVVFGQVIEGM*DIVK.M
R1/RRR1-19/2	1687.334	1687.985	-981.391	0.515	2173.398	0.643	25	0.442	R.HVVFGQVIEGM*DIVK.M
R1/RRR1-19/2	1993.603	1994.193	-799.964	0.571	1384.487	0.626	27	0.301	R.VVIGLYGDDVPQTAENFR.A
R1/RRR1-19/2	1994.395	1994.193	101.563	0.595	1344.526	0.644	26	0.301	R.VVIGLYGDDVPQTAENFR.A
R1/RRR1-19/2	1993.584	1994.193	-809.798	0.572	1388.894	0.592	27	0.293	R.VVIGLYGDDVPQTAENFR.A
R1/RRR1-19/3	1994.598	1994.193	203.628	0.408	1350.303	0.457	30	0.147	R.VVIGLYGDDVPQTAENFR.A
R1/RRR1-19/3	1995.754	1994.193	-220.776	0.391	759.455	0.443	26	0.095	-.VVIGLYGDDVPQTAENFR.-
R1/RRR1-19/3	1994.240	1994.193	23.347	0.320	808.359	0.416	27	0.091	R.VVIGLYGDDVPQTAENFR.A
R1/RRR1-11/2	1562.390	1562.774	-246.409	0.502	2407.030	0.482	23	0.424	K.M*GQIGVLSGTQGEIR.L
R1/RRR1-11/2	1562.297	1562.774	-306.063	0.483	2238.638	0.449	23	0.378	K.M*GQIGVLSGTQGEIR.L
R1/RRR1-11/2	1562.244	1562.774	-982.426	0.506	2196.770	0.468	23	0.377	K.M*GQIGVLSGTQGEIR.L
R1/RRR1-10/2	1564.138	1562.774	233.236	0.537	2077.169	0.496	22	0.364	K.M*GQIGVLSGTQGEIR.L
R1/RRR1-10/2	1562.195	1562.774	-1014.120	0.512	2075.398	0.465	24	0.354	K.M*GQIGVLSGTQGEIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1562.833	1562.774	37.653	0.510	2096.694	0.434	23	0.347	K.M*GQIGVLSGTQGEIR.L
R1/RRR1-11/2	893.914	894.010	-108.287	0.334	848.358	0.366	13	0.206	K.ATVNSFVR.S
R1/RRR1-11/2	893.441	894.010	-1761.312	0.287	618.132	0.404	12	0.200	K.ATVNSFVR.S
R1/RRR1-10/2	893.514	894.010	-556.417	0.316	545.266	0.368	12	0.199	K.ATVNSFVR.S
R1/RRR1-10/2	893.531	894.010	-537.909	0.357	580.723	0.339	12	0.199	K.ATVNSFVR.S
R1/RRR1-10/2	893.729	894.010	-315.035	0.307	850.089	0.286	13	0.197	K.ATVNSFVR.S
R1/RRR1-15/2	1606.157	1606.798	-1024.876	0.454	2975.804	0.369	23	0.512	R.FQAQADAVNLICGAK.T
R1/RRR1-15/2	1606.018	1606.798	-1111.797	0.380	2113.359	0.348	22	0.325	R.FQAQADAVNLICGAK.T
R1/RRR1-15/2	1605.983	1606.798	-1133.778	0.393	1542.400	0.332	22	0.245	R.FQAQADAVNLICGAK.T
R1/RRR1-16/2	1130.177	1130.317	-123.783	0.400	866.869	0.482	15	0.221	R.VLVTPTSDLGK.I
R1/RRR1-12/2	1607.591	1606.798	-129.369	0.311	1557.940	0.184	22	0.217	R.FQAQADAVNLICGAK.T
R1/RRR1-16/2	1130.054	1130.317	-233.009	0.362	660.764	0.420	15	0.204	R.VLVTPTSDLGK.I
R1/RRR1-16/2	1129.527	1130.317	-1589.481	0.294	674.134	0.404	15	0.200	R.VLVTPTSDLGK.I
R1/RRR1-15/2	1129.826	1130.317	-435.270	0.294	605.373	0.339	14	0.194	R.VLVTPTSDLGK.I
R1/RRR1-15/2	1130.203	1130.317	-100.814	0.305	446.100	0.314	13	0.180	-.VLVTPTSDLGK.-
R1/RRR1-22/2	1116.044	1116.296	-227.048	0.418	1138.333	0.475	16	0.240	R.KVTIQNLSGR.D
R1/RRR1-22/2	988.150	988.123	27.183	0.420	1130.851	0.428	14	0.230	K.VTIQNLSGR.D
R1/RRR1-22/2	987.949	988.123	-177.420	0.407	1031.618	0.451	14	0.227	K.VTIQNLSGR.D
R1/RRR1-22/2	1116.006	1116.296	-260.737	0.407	954.854	0.467	15	0.224	R.KVTIQNLSGR.D
R1/RRR1-27/3	1484.819	1484.624	131.834	0.474	2614.947	0.356	30	0.339	R.SPCSLYACEAGLR.A
R1/RRR1-27/2	1485.597	1484.624	-18.099	0.493	1747.544	0.500	20	0.313	R.SPCSLYACEAGLR.A
R1/RRR1-27/2	1484.183	1484.624	-297.524	0.478	1831.422	0.421	20	0.301	R.SPCSLYACEAGLR.A
R1/RRR1-27/2	1484.277	1484.624	-234.072	0.417	1812.628	0.368	20	0.285	R.SPCSLYACEAGLR.A
R1/RRR1-23/2	1484.167	1484.624	-308.582	0.430	1749.902	0.375	20	0.279	R.SPCSLYACEAGLR.A
R1/RRR1-26/2	1484.267	1484.624	-240.672	0.459	1732.118	0.383	20	0.278	R.SPCSLYACEAGLR.A
R1/RRR1-27/2	1483.596	1484.624	-1370.987	0.364	1857.755	0.318	20	0.278	R.SPCSLYACEAGLR.A
R1/RRR1-25/2	1484.022	1484.624	-1082.657	0.434	1630.238	0.386	19	0.266	R.SPCSLYACEAGLR.A
R1/RRR1-26/2	1484.136	1484.624	-329.295	0.423	1636.084	0.365	19	0.262	R.SPCSLYACEAGLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-26/2	1483.640	1484.624	-1340.659	0.323	1435.448	0.327	19	0.234	R.SPCSLYACEAGLR.A
R1/RRR1-26/3	1484.429	1484.624	-131.533	0.382	2223.074	0.308	30	0.222	R.SPCSLYACEAGLR.A
R1/RRR1-27/2	993.897	994.080	-184.611	0.361	915.763	0.316	15	0.206	R.AWCGSGVTR.C
R1/RRR1-27/2	993.406	994.080	-1689.698	0.326	876.915	0.332	15	0.205	R.AWCGSGVTR.C
R1/RRR1-27/2	993.952	994.080	-129.539	0.371	749.156	0.342	14	0.204	R.AWCGSGVTR.C
R1/RRR1-27/2	993.922	994.080	-159.477	0.347	1012.760	0.278	15	0.204	R.AWCGSGVTR.C
R1/RRR1-26/2	993.854	994.080	-227.860	0.370	842.717	0.311	15	0.204	R.AWCGSGVTR.C
R1/RRR1-27/3	1484.769	1484.624	98.441	0.490	1946.886	0.379	28	0.202	R.SPCSLYACEAGLR.A
R1/RRR1-26/2	993.878	994.080	-203.340	0.333	701.997	0.264	14	0.197	R.AWCGSGVTR.C
R1/RRR1-26/2	993.392	994.080	-1704.019	0.267	701.300	0.287	14	0.196	R.AWCGSGVTR.C
R1/RRR1-25/2	993.747	994.080	-336.060	0.267	662.612	0.263	14	0.195	R.AWCGSGVTR.C
R1/RRR1-27/2	993.573	994.080	-1521.455	0.249	562.589	0.218	12	0.192	R.AWCGSGVTR.C
R1/RRR1-26/2	993.875	994.080	-207.283	0.299	897.891	0.189	14	0.191	R.AWCGSGVTR.C
R1/RRR1-27/2	993.803	994.080	-279.370	0.241	768.951	0.211	13	0.190	R.AWCGSGVTR.C
R1/RRR1-21/2	1483.160	1484.624	-1666.097	0.240	1053.053	0.176	17	0.189	R.SPCSLYACEAGLR.A
R1/RRR1-25/2	993.256	994.080	-1841.943	0.183	891.856	0.205	14	0.188	R.AWCGSGVTR.C
R1/RRR1-26/3	1484.476	1484.624	-99.981	0.447	1596.119	0.256	26	0.115	R.SPCSLYACEAGLR.A
R1/RRR1-26/3	1484.326	1484.624	-201.202	0.273	803.473	0.260	23	0.073	R.SPCSLYACEAGLR.A
R1/RRR1-3/2	1344.273	1343.510	-176.569	0.377	574.418	0.478	17	0.205	R.YQYLSSAAIQAK.S
R1/RRR1-3/2	1129.934	1129.292	-317.228	0.398	673.233	0.363	13	0.194	-.LVQTLGNDLR.-
R1/RRR1-3/2	1834.387	1834.062	178.102	0.322	735.139	0.391	19	0.193	R.GLYGYVAGLGDSGSILYK.A
R1/RRR1-3/2	1616.462	1616.883	-261.058	0.489	2678.881	0.565	23	0.522	K.SQPDLAILAVNTFVK.D
R1/RRR1-3/2	1617.170	1616.883	178.176	0.522	2224.128	0.502	22	0.393	K.SQPDLAILAVNTFVK.D
R1/RRR1-5/2	1617.694	1616.883	-117.435	0.539	1685.198	0.535	20	0.312	K.SQPDLAILAVNTFVK.D
R1/RRR1-5/2	1616.868	1616.883	-9.209	0.333	1659.550	0.444	20	0.282	K.SQPDLAILAVNTFVK.D
R1/RRR1-4/2	1615.919	1616.883	-1219.321	0.310	1491.855	0.446	19	0.261	K.SQPDLAILAVNTFVK.D
R1/RRR1-6/2	1616.228	1616.883	-1027.202	0.276	1059.403	0.308	17	0.200	K.SQPDLAILAVNTFVK.D
R1/RRR1-15/2	982.660	982.114	-463.078	0.333	739.178	0.378	13	0.200	R.TSFLEAWK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/3	1660.837	1660.893	-33.632	0.552	2489.628	0.456	33	0.382	R.IINEPTAAAIAYGIDK.K
R1/RRR1-6/2	1787.830	1789.066	-1254.177	0.538	1494.758	0.586	25	0.303	R.IINEPTAAAIAYGIDKK.A
R1/RRR1-6/2	1788.673	1789.066	-220.249	0.551	1501.286	0.562	26	0.298	R.IINEPTAAAIAYGIDKK.A
R1/RRR1-6/2	1789.387	1789.066	180.118	0.577	1224.125	0.589	24	0.271	R.IINEPTAAAIAYGIDKK.A
R1/RRR1-6/2	1660.260	1660.893	-986.390	0.413	1405.534	0.467	24	0.262	R.IINEPTAAAIAYGIDK.K
R1/RRR1-10/2	1788.606	1789.066	-257.633	0.519	1034.439	0.551	22	0.243	R.IINEPTAAAIAYGIDKK.A
R1/RRR1-6/2	1660.660	1660.893	-140.422	0.409	952.355	0.499	23	0.229	R.IINEPTAAAIAYGIDK.K
R1/RRR1-6/2	1660.933	1660.893	24.134	0.393	1130.441	0.395	19	0.219	R.IINEPTAAAIAYGIDK.K
R1/RRR1-6/2	1660.940	1660.893	28.557	0.405	737.794	0.515	20	0.217	R.IINEPTAAAIAYGIDK.K
R1/RRR1-6/2	1660.685	1660.893	-125.454	0.451	539.115	0.471	20	0.207	R.IINEPTAAAIAYGIDK.K
R1/RRR1-13/2	1130.043	1130.320	-246.122	0.474	2248.510	0.508	22	0.401	K.VAVITGGASGIGK.A
R1/RRR1-13/2	1129.992	1130.320	-290.882	0.536	2277.865	0.490	22	0.399	K.VAVITGGASGIGK.A
R1/RRR1-15/2	1129.585	1130.320	-1540.515	0.436	2165.020	0.542	22	0.397	K.VAVITGGASGIGK.A
R1/RRR1-16/2	1130.201	1130.320	-105.581	0.522	2169.988	0.515	22	0.388	K.VAVITGGASGIGK.A
R1/RRR1-16/2	1130.183	1130.320	-121.291	0.517	2034.046	0.539	22	0.372	K.VAVITGGASGIGK.A
R1/RRR1-15/2	1129.960	1130.320	-319.062	0.459	2040.694	0.503	21	0.360	K.VAVITGGASGIGK.A
R1/RRR1-15/2	1129.470	1130.320	-1642.569	0.434	1910.255	0.562	21	0.357	K.VAVITGGASGIGK.A
R1/RRR1-14/2	1129.579	1130.320	-1545.509	0.442	1981.402	0.508	21	0.352	K.VAVITGGASGIGK.A
R1/RRR1-15/2	1328.134	1328.497	-274.220	0.470	1943.328	0.508	19	0.348	K.VIIADVQDELGR.S
R1/RRR1-16/2	1129.730	1130.320	-1411.783	0.441	1949.242	0.486	21	0.340	K.VAVITGGASGIGK.A
R1/RRR1-13/2	1129.279	1130.320	-1812.959	0.379	1854.913	0.525	20	0.334	K.VAVITGGASGIGK.A
R1/RRR1-14/1	1129.642	1130.320	-1489.864	0.241	645.624	0.518	15	0.322	K.VAVITGGASGIGK.A
R1/RRR1-14/1	1129.691	1130.320	-1446.230	0.199	610.938	0.361	15	0.257	K.VAVITGGASGIGK.A
R1/RRR1-15/2	1328.115	1328.497	-288.329	0.413	743.423	0.329	14	0.193	K.VIIADVQDELGR.S
R1/RRR1-15/2	1328.394	1328.497	-77.570	0.402	742.117	0.322	14	0.192	-.VIIADVQDELGR.-
R1/RRR1-15/2	1328.127	1328.497	-279.107	0.387	778.745	0.288	14	0.190	K.VIIADVQDELGR.S
R1/RRR1-21/2	1648.471	1647.917	-271.322	0.533	1240.992	0.501	21	0.254	R.SGKM*ELPEWVDIVK.T
R1/RRR1-21/2	1647.478	1647.917	-267.695	0.500	1234.035	0.500	21	0.253	R.SGKM*ELPEWVDIVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1648.470	1647.917	-272.362	0.539	1086.932	0.531	20	0.246	R.SGKM*ELPEWVDIVK.T
R1/RRR1-21/2	1375.315	1375.615	-219.185	0.467	816.359	0.414	18	0.215	K.M*ELPEWVDIVK.T
R1/RRR1-21/2	1376.212	1375.615	-293.685	0.469	719.277	0.443	17	0.215	K.M*ELPEWVDIVK.T
R1/RRR1-22/2	1375.377	1375.615	-173.953	0.398	604.608	0.370	16	0.203	K.M*ELPEWVDIVK.T
R1/RRR1-21/2	1359.276	1359.616	-250.373	0.474	712.565	0.334	17	0.201	K.MELPEWVDIVK.T
R1/RRR1-21/2	1359.099	1359.616	-1119.470	0.412	754.155	0.273	17	0.196	K.MELPEWVDIVK.T
R1/RRR1-21/2	1375.967	1375.615	256.618	0.367	551.564	0.251	15	0.193	K.M*ELPEWVDIVK.T
R1/RRR1-21/2	1358.519	1359.616	-1547.861	0.306	751.799	0.221	17	0.191	K.MELPEWVDIVK.T
R1/RRR1-10/2	1756.206	1756.854	-941.285	0.544	2699.022	0.526	26	0.513	R.LGFTEAAGNFQTSNNGK.G
R1/RRR1-10/2	1756.405	1756.854	-256.431	0.541	2421.535	0.522	25	0.445	R.LGFTEAAGNFQTSNNGK.G
R1/RRR1-10/2	1758.399	1756.854	-259.621	0.523	2166.013	0.535	25	0.397	R.LGFTEAAGNFQTSNNGK.G
R1/RRR1-10/2	1586.765	1586.689	47.716	0.513	1272.099	0.558	21	0.267	K.GGLGNDAVILNSQDGR.S
R1/RRR1-11/2	1586.337	1586.689	-222.717	0.493	972.923	0.625	20	0.253	K.GGLGNDAVILNSQDGR.S
R1/RRR1-11/2	1586.315	1586.689	-236.381	0.494	1072.662	0.544	21	0.246	K.GGLGNDAVILNSQDGR.S
R1/RRR1-11/2	1586.203	1586.689	-307.489	0.485	927.150	0.600	20	0.244	K.GGLGNDAVILNSQDGR.S
R1/RRR1-10/2	1586.363	1586.689	-205.888	0.455	793.830	0.590	19	0.231	K.GGLGNDAVILNSQDGR.S
R1/RRR1-10/2	1587.330	1586.689	-226.588	0.301	284.018	0.460	14	0.193	K.GGLGNDAVILNSQDGR.S
R1/RRR1-16/2	1659.345	1659.866	-919.788	0.442	1207.455	0.489	20	0.245	R.FDPATTPLLAAWAER.F
R1/RRR1-16/2	1659.358	1659.866	-911.665	0.411	1243.378	0.403	20	0.231	R.FDPATTPLLAAWAER.F
R1/RRR1-16/2	1658.834	1659.866	-1228.592	0.322	1121.986	0.313	19	0.206	R.FDPATTPLLAAWAER.F
R1/RRR1-16/2	1815.380	1816.053	-924.159	0.491	605.377	0.438	21	0.204	K.RFDPATTPLLAAWAER.F
R1/RRR1-16/2	1815.896	1816.053	-86.817	0.462	607.949	0.417	22	0.203	K.RFDPATTPLLAAWAER.F
R1/RRR1-16/2	1815.296	1816.053	-970.470	0.437	405.396	0.353	18	0.192	K.RFDPATTPLLAAWAER.F
R1/RRR1-16/3	1816.132	1816.053	43.839	0.416	1305.494	0.388	26	0.124	K.RFDPATTPLLAAWAER.F
R1/RRR1-16/3	1815.044	1816.053	-1109.978	0.354	874.895	0.397	23	0.092	K.RFDPATTPLLAAWAER.F
R1/RRR1-9/2	1386.316	1386.490	-125.907	0.461	2122.078	0.565	22	0.398	K.TYGASTSGNSLSLK.F
R1/RRR1-9/2	1387.294	1386.490	-141.528	0.517	2050.766	0.594	22	0.396	K.TYGASTSGNSLSLK.F
R1/RRR1-9/2	1386.996	1386.490	-356.948	0.534	1776.222	0.583	20	0.342	K.TYGASTSGNSLSLK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1386.338	1386.490	-109.831	0.505	1577.510	0.501	20	0.290	K.TYGASTSGNSLSLK.F
R1/RRR1-10/2	1386.255	1386.490	-169.985	0.476	1375.345	0.503	20	0.267	K.TYGASTSGNSLSLK.F
R1/RRR1-10/2	1386.157	1386.490	-240.571	0.443	1205.845	0.523	18	0.252	K.TYGASTSGNSLSLK.F
R1/RRR1-9/3	1623.031	1623.794	-1089.326	0.477	977.359	0.507	26	0.120	K.FLTKHEYGTNIGSR.F
R1/RRR1-9/3	1623.294	1623.794	-308.919	0.481	916.306	0.492	25	0.113	K.FLTKHEYGTNIGSR.F
R1/RRR1-9/3	1623.139	1623.794	-1023.063	0.442	663.659	0.483	22	0.100	K.FLTKHEYGTNIGSR.F
R1/RRR1-9/2	1469.376	1469.712	-229.113	0.469	2533.038	0.452	21	0.445	K.SGLVALNLDLAQVR.Q
R1/RRR1-9/2	1469.186	1469.712	-1041.338	0.429	1647.041	0.499	19	0.299	K.SGLVALNLDLAQVR.Q
R1/RRR1-9/2	1432.430	1432.653	-156.471	0.455	1353.038	0.479	19	0.261	K.WGNIQFPLPFGR.V
R1/RRR1-9/2	1432.349	1432.653	-212.896	0.484	1174.271	0.413	18	0.231	K.WGNIQFPLPFGR.V
R1/RRR1-9/2	1432.403	1432.653	-174.937	0.374	947.720	0.301	16	0.198	K.WGNIQFPLPFGR.V
R1/RRR1-9/2	1432.592	1432.653	-42.956	0.324	717.786	0.317	14	0.191	-.WGNIQFPLPFGR.-
R1/RRR1-19/2	1625.128	1625.757	-1005.679	0.501	1968.912	0.610	22	0.384	R.YVCQDQFTGQPGPK.C
R1/RRR1-20/2	1625.134	1625.757	-1001.758	0.528	1922.711	0.611	22	0.376	R.YVCQDQFTGQPGPK.C
R1/RRR1-21/2	1625.318	1625.757	-271.086	0.511	1938.761	0.600	22	0.375	R.YVCQDQFTGQPGPK.C
R1/RRR1-18/2	1625.474	1625.757	-174.646	0.501	1849.988	0.633	22	0.371	R.YVCQDQFTGQPGPK.C
R1/RRR1-18/2	1625.220	1625.757	-948.669	0.526	1860.738	0.620	22	0.369	R.YVCQDQFTGQPGPK.C
R1/RRR1-20/2	1625.139	1625.757	-998.515	0.540	1820.651	0.631	22	0.365	R.YVCQDQFTGQPGPK.C
R1/RRR1-19/2	1625.151	1625.757	-991.125	0.506	1800.440	0.620	21	0.357	R.YVCQDQFTGQPGPK.C
R1/RRR1-21/2	1625.300	1625.757	-282.314	0.517	1846.808	0.591	22	0.357	R.YVCQDQFTGQPGPK.C
R1/RRR1-20/2	1625.297	1625.757	-283.745	0.507	1781.984	0.621	22	0.356	R.YVCQDQFTGQPGPK.C
R1/RRR1-21/2	1625.443	1625.757	-193.933	0.543	1767.508	0.626	22	0.355	R.YVCQDQFTGQPGPK.C
R1/RRR1-19/2	1625.302	1625.757	-281.108	0.530	1752.775	0.627	21	0.352	R.YVCQDQFTGQPGPK.C
R1/RRR1-18/2	1625.214	1625.757	-952.138	0.532	1744.782	0.627	21	0.351	R.YVCQDQFTGQPGPK.C
R1/RRR1-21/3	1406.650	1406.554	68.134	0.444	1276.312	0.323	25	0.098	K.CCDNIERLPTK.T
R1/RRR1-21/3	1406.389	1406.554	-117.808	0.469	1090.803	0.386	23	0.098	-.CCDNIERLPTK.-
R1/RRR1-11/2	1257.287	1257.422	-107.276	0.505	1754.674	0.519	19	0.323	K.NVQQGNVGLVTK.F
R1/RRR1-11/2	1257.165	1257.422	-204.775	0.501	1556.136	0.608	18	0.320	K.NVQQGNVGLVTK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	926.987	926.135	-160.558	0.376	972.201	0.314	13	0.205	K.IQIVEVPK.Q
R1/RRR1-11/2	926.323	926.135	203.336	0.281	818.279	0.288	12	0.194	-.IQIVEVPK.-
R1/RRR1-10/2	926.470	926.135	362.549	0.292	541.747	0.312	11	0.193	K.IQIVEVPK.Q
R1/RRR1-10/2	926.536	926.135	433.882	0.298	430.948	0.274	11	0.185	-.IQIVEVPK.-
R1/RRR1-15/3	1948.961	1949.071	-56.647	0.479	2529.520	0.501	33	0.411	K.VAHATYAFNDYYQTAGR.A
R1/RRR1-15/2	1909.539	1910.068	-803.442	0.514	1994.748	0.595	25	0.384	R.ASGSCDFAGAATIVTQQPK.I
R1/RRR1-15/2	1909.597	1910.068	-247.464	0.543	2031.506	0.577	24	0.384	R.ASGSCDFAGAATIVTQQPK.I
R1/RRR1-15/3	1948.420	1949.071	-849.878	0.523	2187.045	0.513	31	0.328	K.VAHATYAFNDYYQTAGR.A
R1/RRR1-15/2	1909.410	1910.068	-871.082	0.522	1756.472	0.533	23	0.321	R.ASGSCDFAGAATIVTQQPK.I
R1/RRR1-14/3	1948.672	1949.071	-205.565	0.488	2184.958	0.488	31	0.314	K.VAHATYAFNDYYQTAGR.A
R1/RRR1-15/3	1948.860	1949.071	-108.858	0.554	2010.241	0.500	30	0.282	K.VAHATYAFNDYYQTAGR.A
R1/RRR1-14/3	1948.887	1949.071	-94.721	0.498	1889.684	0.474	29	0.245	K.VAHATYAFNDYYQTAGR.A
R1/RRR1-14/3	1948.123	1949.071	-1003.012	0.434	1538.386	0.443	30	0.168	K.VAHATYAFNDYYQTAGR.A
R1/RRR1-12/2	1900.632	1901.191	-822.475	0.567	2922.510	0.608	27	0.620	R.FGLITDFVDADLVSFLK.L
R1/RRR1-13/2	1438.144	1438.522	-263.630	0.455	2141.349	0.485	21	0.376	R.ELAEEGYSGVEVR.V
R1/RRR1-13/2	1438.104	1438.522	-291.392	0.537	2005.885	0.531	21	0.368	R.ELAEEGYSGVEVR.V
R1/RRR1-13/2	1439.114	1438.522	-284.126	0.525	2019.282	0.519	21	0.366	R.ELAEEGYSGVEVR.V
R1/RRR1-13/3	1582.781	1582.704	49.181	0.462	895.957	0.520	28	0.115	R.ATHTQEVLGEQGRR.I
R1/RRR1-14/3	1582.346	1582.704	-226.576	0.478	689.587	0.530	24	0.110	R.ATHTQEVLGEQGRR.I
R1/RRR1-13/3	1582.379	1582.704	-205.912	0.416	603.032	0.550	24	0.108	R.ATHTQEVLGEQGRR.I
R1/RRR1-15/3	1582.839	1582.704	85.960	0.349	431.372	0.459	20	0.094	R.ATHTQEVLGEQGRR.I
R1/RRR1-13/3	1581.658	1582.704	-1297.297	0.370	368.151	0.493	21	0.090	-.ATHTQEVLGEQGRR.-
R1/RRR1-14/3	1583.239	1582.704	-294.462	0.342	440.302	0.432	20	0.088	-.ATHTQEVLGEQGRR.-
R1/RRR1-22/3	1901.605	1902.051	-235.506	0.449	1297.223	0.382	28	0.125	K.FLEDHPGGDDVLLSSTAK.D
R1/RRR1-7/2	1555.817	1554.729	57.243	0.526	2304.629	0.582	21	0.445	R.LAIGDLATQYFADR.D
R1/RRR1-7/2	1555.105	1554.729	242.919	0.460	2153.942	0.515	21	0.388	R.LAIGDLATQYFADR.D
R1/RRR1-7/2	1403.023	1403.521	-356.012	0.448	1934.170	0.445	19	0.328	K.TFSYAGFEQQPK.T
R1/RRR1-7/2	1553.893	1554.729	-1184.628	0.309	1942.597	0.366	20	0.303	R.LAIGDLATQYFADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1402.878	1403.521	-1174.429	0.476	1504.416	0.468	18	0.274	K.TFSYAGFEQQPK.T
R1/RRR1-22/2	937.443	937.977	-1641.221	0.411	831.209	0.387	13	0.209	R.ASLNDFDR.F
R1/RRR1-22/2	937.881	937.977	-102.232	0.364	858.843	0.366	13	0.206	R.ASLNDFDR.F
R1/RRR1-22/2	1213.294	1213.324	-25.391	0.405	789.575	0.364	15	0.204	R.ASLNDFDRFK.-
R1/RRR1-23/2	1213.276	1213.324	-40.024	0.373	580.474	0.377	13	0.198	R.ASLNDFDRFK.-
R1/RRR1-22/2	1213.198	1213.324	-104.212	0.398	545.552	0.376	12	0.197	R.ASLNDFDRFK.-
R1/RRR1-22/2	937.357	937.977	-1733.327	0.324	669.206	0.295	13	0.195	R.ASLNDFDR.F
R1/RRR1-22/2	1212.642	1213.324	-1391.282	0.352	747.873	0.306	13	0.194	R.ASLNDFDRFK.-
R1/RRR1-12/2	1658.834	1657.850	-9.788	0.615	1931.722	0.719	31	0.422	K.GLPLGSGLGSSAASAAAAAK.A
R1/RRR1-12/2	1657.361	1657.850	-295.912	0.540	1753.729	0.674	29	0.370	K.GLPLGSGLGSSAASAAAAAK.A
R1/RRR1-12/2	1658.342	1657.850	297.197	0.568	1565.257	0.687	30	0.345	K.GLPLGSGLGSSAASAAAAAK.A
R1/RRR1-12/2	1161.696	1162.364	-1439.755	0.417	994.577	0.299	15	0.199	K.AVDALFGSLLR.Q
R1/RRR1-12/2	1161.816	1162.364	-1336.225	0.329	472.057	0.354	13	0.191	K.AVDALFGSLLR.Q
R1/RRR1-14/2	1420.557	1421.622	-1458.286	0.510	1780.678	0.629	21	0.358	K.LPGLFIWSADSSK.V
R1/RRR1-15/2	1421.129	1421.622	-348.375	0.506	1674.588	0.563	22	0.322	K.LPGLFIWSADSSK.V
R1/RRR1-14/2	1421.269	1421.622	-248.928	0.510	1580.503	0.598	21	0.319	K.LPGLFIWSADSSK.V
R1/RRR1-15/2	1422.377	1421.622	-173.071	0.489	1577.701	0.583	20	0.313	K.LPGLFIWSADSSK.V
R1/RRR1-14/2	1421.214	1421.622	-287.791	0.510	1557.987	0.581	20	0.310	K.LPGLFIWSADSSK.V
R1/RRR1-14/2	1420.600	1421.622	-1428.077	0.479	1453.285	0.603	21	0.303	K.LPGLFIWSADSSK.V
R1/RRR1-15/2	1421.253	1421.622	-260.302	0.507	1417.310	0.577	19	0.290	K.LPGLFIWSADSSK.V
R1/RRR1-14/2	1338.119	1338.404	-213.431	0.443	1451.573	0.530	17	0.283	K.VSSYGFEYETR.G
R1/RRR1-14/2	1421.390	1421.622	-163.888	0.499	1155.022	0.608	17	0.267	K.LPGLFIWSADSSK.V
R1/RRR1-14/2	1337.640	1338.404	-1322.232	0.364	1079.696	0.519	17	0.240	K.VSSYGFEYETR.G
R1/RRR1-14/2	1338.002	1338.404	-300.748	0.447	977.442	0.512	16	0.234	K.VSSYGFEYETR.G
R1/RRR1-15/2	1338.079	1338.404	-243.359	0.271	950.357	0.439	16	0.213	K.VSSYGFEYETR.G
R1/RRR1-3/2	1421.153	1421.622	-330.794	0.383	583.546	0.502	14	0.208	K.LPGLFIWSADSSK.V
R1/RRR1-2/2	1420.422	1421.622	-1553.414	0.376	705.937	0.455	15	0.208	K.LPGLFIWSADSSK.V
R1/RRR1-4/2	1421.412	1421.622	-148.122	0.352	217.556	0.333	12	0.177	-.LPGLFIWSADSSK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1609.448	1608.814	-228.419	0.531	2314.941	0.469	23	0.403	K.FKDLVEEISESLAK.T
R1/RRR1-13/2	1608.146	1608.814	-1040.510	0.460	2143.000	0.426	22	0.356	K.FKDLVEEISESLAK.T
R1/RRR1-13/2	1607.883	1608.814	-1205.007	0.472	2017.367	0.399	22	0.326	K.FKDLVEEISESLAK.T
R1/RRR1-13/3	1894.195	1894.969	-939.201	0.431	1476.517	0.287	30	0.117	K.TEGKETEEDSSAAGLLEK.L
R1/RRR1-13/3	1894.695	1894.969	-144.862	0.425	1093.063	0.359	29	0.100	K.TEGKETEEDSSAAGLLEK.L
R1/RRR1-16/3	1894.274	1894.969	-897.569	0.301	829.070	0.181	27	0.066	K.TEGKETEEDSSAAGLLEK.L
R1/RRR1-11/2	1652.618	1651.932	-190.521	0.576	2166.351	0.569	23	0.414	R.VPQVGSIAINDGVILR.N
R1/RRR1-11/2	1107.134	1107.281	-133.548	0.441	887.596	0.549	14	0.234	K.YGAVEDILVK.M
R1/RRR1-11/2	1107.193	1107.281	-80.351	0.422	732.763	0.474	14	0.214	K.YGAVEDILVK.M
R1/RRR1-11/2	1106.950	1107.281	-299.923	0.302	720.104	0.389	13	0.198	K.YGAVEDILVK.M
R1/RRR1-21/2	1206.235	1206.380	-120.242	0.481	975.163	0.545	18	0.241	R.KGHAVGDIPGVR.F
R1/RRR1-21/2	1206.424	1206.380	37.285	0.517	878.968	0.539	17	0.233	R.KGHAVGDIPGVR.F
R1/RRR1-21/2	1077.963	1078.207	-226.664	0.423	550.638	0.617	15	0.227	K.GHAVGDIPGVR.F
R1/RRR1-21/2	1206.044	1206.380	-278.833	0.454	891.563	0.499	17	0.226	R.KGHAVGDIPGVR.F
R1/RRR1-21/2	1077.886	1078.207	-298.355	0.425	519.311	0.590	15	0.222	K.GHAVGDIPGVR.F
R1/RRR1-26/2	1077.757	1078.207	-418.697	0.346	238.533	0.580	12	0.207	K.GHAVGDIPGVR.F
R1/RRR1-26/2	1077.721	1078.207	-451.543	0.344	321.109	0.546	12	0.205	K.GHAVGDIPGVR.F
R1/RRR1-27/2	1077.743	1078.207	-431.426	0.319	268.093	0.554	11	0.202	K.GHAVGDIPGVR.F
R1/RRR1-24/2	1077.739	1078.207	-434.949	0.311	204.414	0.439	12	0.200	K.GHAVGDIPGVR.F
R1/RRR1-24/2	1077.450	1078.207	-1635.625	0.324	224.572	0.470	12	0.194	-.GHAVGDIPGVR.-
R1/RRR1-26/3	1205.899	1206.380	-399.700	0.450	1215.833	0.378	25	0.108	R.KGHAVGDIPGVR.F
R1/RRR1-26/3	1206.457	1206.380	64.319	0.491	995.461	0.406	23	0.104	R.KGHAVGDIPGVR.F
R1/RRR1-20/3	1206.028	1206.380	-292.147	0.457	956.878	0.410	23	0.102	R.KGHAVGDIPGVR.F
R1/RRR1-25/3	1206.501	1206.380	101.002	0.491	1111.795	0.355	25	0.098	R.KGHAVGDIPGVR.F
R1/RRR1-21/3	1206.452	1206.380	59.752	0.450	887.209	0.394	23	0.097	R.KGHAVGDIPGVR.F
R1/RRR1-21/3	1206.664	1206.380	236.446	0.466	843.879	0.397	23	0.096	R.KGHAVGDIPGVR.F
R1/RRR1-21/3	1206.366	1206.380	-11.643	0.538	928.032	0.380	24	0.096	R.KGHAVGDIPGVR.F
R1/RRR1-19/3	1206.881	1206.380	-414.643	0.423	744.854	0.400	21	0.096	R.KGHAVGDIPGVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-26/3	1205.989	1206.380	-325.051	0.469	796.189	0.383	22	0.095	R.KGHAVGDIPGVR.F
R1/RRR1-18/3	1206.822	1206.380	368.051	0.421	872.001	0.370	22	0.094	R.KGHAVGDIPGVR.F
R1/RRR1-20/3	1206.544	1206.380	136.312	0.453	835.223	0.341	23	0.089	R.KGHAVGDIPGVR.F
R1/RRR1-20/3	1206.760	1206.380	316.022	0.490	751.711	0.330	22	0.088	R.KGHAVGDIPGVR.F
R1/RRR1-22/3	1206.724	1206.380	285.897	0.430	899.892	0.313	23	0.086	R.KGHAVGDIPGVR.F
R1/RRR1-22/3	1206.898	1206.380	-400.181	0.474	946.169	0.310	24	0.086	R.KGHAVGDIPGVR.F
R1/RRR1-25/3	1205.248	1206.380	-1774.276	0.332	953.485	0.290	23	0.083	R.KGHAVGDIPGVR.F
R1/RRR1-18/3	1206.784	1206.380	336.409	0.402	777.889	0.296	21	0.082	-.KGHAVGDIPGVR.-
R1/RRR1-18/3	1205.588	1206.380	-1490.277	0.363	673.513	0.240	21	0.082	R.KGHAVGDIPGVR.F
R1/RRR1-24/3	1206.157	1206.380	-185.379	0.357	455.200	0.368	17	0.082	-.KGHAVGDIPGVR.-
R1/RRR1-22/3	1206.789	1206.380	340.364	0.288	1077.854	0.063	22	0.063	-.KGHAVGDIPGVR.-
R1/RRR1-26/2	1122.912	1123.284	-332.078	0.465	1065.343	0.397	16	0.222	R.VCGNPHGLIR.K
R1/RRR1-26/2	1122.507	1123.284	-1588.296	0.431	879.778	0.417	15	0.215	R.VCGNPHGLIR.K
R1/RRR1-26/2	975.825	976.120	-303.135	0.356	1140.943	0.312	11	0.212	K.YGLM*CCR.Q
R1/RRR1-26/2	975.935	976.120	-189.940	0.365	1105.277	0.317	11	0.211	K.YGLM*CCR.Q
R1/RRR1-26/2	959.824	960.120	-309.606	0.372	1004.864	0.325	11	0.208	K.YGLMCCR.Q
R1/RRR1-25/2	975.826	976.120	-301.503	0.347	996.321	0.332	11	0.208	K.YGLM*CCR.Q
R1/RRR1-25/2	1123.104	1123.284	-160.429	0.389	877.004	0.336	15	0.204	R.VCGNPHGLIR.K
R1/RRR1-25/2	1122.949	1123.284	-299.575	0.374	941.719	0.318	15	0.203	R.VCGNPHGLIR.K
R1/RRR1-26/2	975.919	976.120	-206.001	0.378	860.054	0.290	11	0.199	K.YGLM*CCR.Q
R1/RRR1-26/2	1122.374	1123.284	-1706.952	0.348	888.037	0.258	15	0.195	R.VCGNPHGLIR.K
R1/RRR1-21/2	1473.403	1472.624	-150.790	0.533	2037.612	0.527	20	0.373	R.AFVVHELEDDLGK.G
R1/RRR1-22/2	1472.442	1472.624	-124.030	0.440	1987.682	0.483	20	0.349	R.AFVVHELEDDLGK.G
R1/RRR1-22/2	1324.034	1324.511	-361.438	0.332	411.864	0.492	15	0.202	K.QIPLSGPNSVVGR.A
R1/RRR1-22/2	1323.952	1324.511	-1181.001	0.292	439.064	0.520	15	0.201	K.QIPLSGPNSVVGR.A
R1/RRR1-22/2	1324.401	1324.511	-83.258	0.311	347.348	0.476	13	0.196	K.QIPLSGPNSVVGR.A
R1/RRR1-21/2	1323.943	1324.511	-1188.362	0.235	469.322	0.423	15	0.192	K.QIPLSGPNSVVGR.A
R1/RRR1-21/2	1323.687	1324.511	-1382.140	0.186	238.503	0.393	11	0.161	-.QIPLSGPNSVVGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1344.290	1344.539	-185.948	0.535	1798.040	0.567	21	0.343	R.LVDIGTVTAQQAK.D
R1/RRR1-10/2	1344.201	1344.539	-252.270	0.509	1410.681	0.522	21	0.278	R.LVDIGTVTAQQAK.D
R1/RRR1-10/2	1343.717	1344.539	-1360.262	0.417	1366.322	0.493	21	0.264	R.LVDIGTVTAQQAK.D
R1/RRR1-11/2	1344.074	1344.539	-347.213	0.430	1170.535	0.496	20	0.246	R.LVDIGTVTAQQAK.D
R1/RRR1-10/2	1343.430	1344.539	-1574.360	0.431	931.463	0.505	19	0.230	R.LVDIGTVTAQQAK.D
R1/RRR1-10/2	1415.847	1415.490	253.235	0.428	1135.493	0.368	17	0.218	R.DIDSFTQQFASR.I
R1/RRR1-16/2	1506.469	1505.698	-152.032	0.525	2527.900	0.413	22	0.431	K.ALELFLNAGNDLSK.S
R1/RRR1-15/2	995.893	995.111	-219.402	0.483	1410.140	0.210	13	0.209	R.YDLVDLTR.Q
R1/RRR1-15/2	995.973	995.111	-138.988	0.421	1369.139	0.188	13	0.204	R.YDLVDLTR.Q
R1/RRR1-15/2	995.047	995.111	-64.920	0.415	1012.506	0.217	12	0.192	-.YDLVDLTR.-
R1/RRR1-24/2	1615.387	1614.781	-244.785	0.563	2023.339	0.493	23	0.358	R.YVIANVDDTTIYAR.Q
R1/RRR1-24/2	1614.245	1614.781	-954.512	0.526	1989.257	0.462	23	0.342	R.YVIANVDDTTIYAR.Q
R1/RRR1-24/2	1315.504	1314.473	23.211	0.341	989.942	0.387	18	0.210	K.AIADILSNVNGAR.D
R1/RRR1-25/2	1315.486	1314.473	10.088	0.285	626.124	0.203	15	0.181	K.AIADILSNVNGAR.D
R1/RRR1-24/2	1101.198	1101.322	-112.365	0.465	1099.395	0.552	17	0.254	R.LVTIATLVDR.L
R1/RRR1-24/2	995.507	995.158	351.674	0.435	948.042	0.466	14	0.224	K.AQHAVLLDK.S
R1/RRR1-24/2	1101.019	1101.322	-275.517	0.329	310.601	0.452	12	0.191	-.LVTIATLVDR.-
R1/RRR1-17/2	1759.651	1759.979	-187.213	0.550	2932.075	0.537	25	0.587	K.IAELKEALESVTAEQK.Y
R1/RRR1-12/3	1582.634	1581.752	-74.827	0.471	684.412	0.595	27	0.113	K.TKFGFDDAFNYKK.E
R1/RRR1-12/3	1581.885	1581.752	84.000	0.478	753.371	0.506	26	0.104	K.TKFGFDDAFNYKK.E
R1/RRR1-12/3	1352.443	1352.475	-24.191	0.523	950.875	0.451	24	0.099	-.FGFDDAFNYKK.-
R1/RRR1-12/3	1581.426	1581.752	-207.352	0.354	329.052	0.455	18	0.091	K.TKFGFDDAFNYKK.E
R1/RRR1-12/3	1352.282	1352.475	-143.029	0.465	992.106	0.377	25	0.091	K.FGFDDAFNYKK.E
R1/RRR1-12/3	1352.754	1352.475	206.612	0.470	1089.388	0.348	26	0.090	K.FGFDDAFNYKK.E
R1/RRR1-10/2	1602.981	1602.815	103.831	0.503	2180.835	0.533	23	0.398	R.AVNITINSIGTELTR.D
R1/RRR1-11/2	1602.691	1602.815	-77.510	0.512	2156.289	0.515	23	0.387	R.AVNITINSIGTELTR.D
R1/RRR1-11/2	1602.353	1602.815	-289.107	0.503	1965.683	0.533	22	0.358	R.AVNITINSIGTELTR.D
R1/RRR1-2/2	1604.205	1602.815	244.185	0.480	1599.541	0.429	20	0.272	R.AVNITINSIGTELTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1601.691	1602.815	-1330.138	0.385	940.365	0.426	20	0.215	R.AVNITINSIGTELTR.D
R1/RRR1-11/2	1287.118	1287.422	-236.739	0.458	762.463	0.428	15	0.208	K.ISYGESQM*LDK.A
R1/RRR1-11/2	1287.031	1287.422	-304.108	0.437	730.393	0.420	15	0.206	K.ISYGESQM*LDK.A
R1/RRR1-9/3	1755.734	1755.873	-79.095	0.517	2225.898	0.548	32	0.347	R.TAVHQGIGHQTYAESR.G
R1/RRR1-10/3	1756.019	1755.873	83.444	0.514	2121.755	0.534	32	0.313	R.TAVHQGIGHQTYAESR.G
R1/RRR1-10/3	1755.195	1755.873	-958.506	0.517	2033.730	0.544	31	0.299	R.TAVHQGIGHQTYAESR.G
R1/RRR1-10/3	1755.551	1755.873	-183.612	0.528	1970.324	0.537	30	0.284	R.TAVHQGIGHQTYAESR.G
R1/RRR1-9/3	1755.691	1755.873	-103.575	0.500	1682.893	0.514	29	0.217	R.TAVHQGIGHQTYAESR.G
R1/RRR1-9/3	1755.483	1755.873	-222.433	0.492	1599.954	0.517	28	0.205	R.TAVHQGIGHQTYAESR.G
R1/RRR1-10/3	1773.958	1774.094	-77.109	0.398	865.122	0.575	27	0.124	R.APEYLALNDKVISLVK.G
R1/RRR1-10/3	1773.196	1774.094	-1073.547	0.384	852.512	0.573	28	0.121	R.APEYLALNDKVISLVK.G
R1/RRR1-10/3	1773.847	1774.094	-139.649	0.360	1026.381	0.486	26	0.118	R.APEYLALNDKVISLVK.G
R1/RRR1-5/2	1356.435	1356.550	-84.722	0.482	1988.707	0.511	18	0.358	R.LLVLEAADQLDR.H
R1/RRR1-5/2	1356.070	1356.550	-354.705	0.418	2030.364	0.447	19	0.345	R.LLVLEAADQLDR.H
R1/RRR1-5/2	1240.252	1240.434	-147.152	0.478	1334.590	0.600	20	0.289	R.VPATNILLGEGR.G
R1/RRR1-5/2	1240.143	1240.434	-235.822	0.436	1317.215	0.561	19	0.275	R.VPATNILLGEGR.G
R1/RRR1-1/2	1239.921	1240.434	-1224.306	0.206	590.311	0.265	14	0.183	R.VPATNILLGEGR.G
R1/RRR1-11/2	1324.542	1325.538	-1510.937	0.492	1656.006	0.589	19	0.328	R.YSGNFLVNLLGK.W
R1/RRR1-11/2	1325.288	1325.538	-188.891	0.544	1588.537	0.555	18	0.307	R.YSGNFLVNLLGK.W
R1/RRR1-11/2	1325.190	1325.538	-263.280	0.453	1057.510	0.584	17	0.254	R.YSGNFLVNLLGK.W
R1/RRR1-11/2	1325.073	1325.538	-351.545	0.507	1143.401	0.523	18	0.251	R.YSGNFLVNLLGK.W
R1/RRR1-11/2	1324.642	1325.538	-1435.308	0.441	1022.164	0.500	18	0.236	R.YSGNFLVNLLGK.W
R1/RRR1-11/2	1164.963	1165.278	-271.010	0.402	1038.261	0.340	18	0.209	K.TWIEVSGSSAK.D
R1/RRR1-1/2	1324.876	1325.538	-1258.175	0.350	873.439	0.374	17	0.206	R.YSGNFLVNLLGK.W
R1/RRR1-5/2	1571.473	1571.718	-155.793	0.473	2196.979	0.521	21	0.400	R.GLEGLTVQQAIDGNR.L
R1/RRR1-5/2	1571.367	1571.718	-223.904	0.448	1864.979	0.506	20	0.334	R.GLEGLTVQQAIDGNR.L
R1/RRR1-5/3	1651.349	1649.744	-239.759	0.523	1316.029	0.618	28	0.191	R.YGDQTSTITAAHVER.G
R1/RRR1-5/3	1650.802	1649.744	35.325	0.515	1162.441	0.580	28	0.158	R.YGDQTSTITAAHVER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1147.071	1147.304	-203.829	0.472	1042.837	0.540	18	0.247	K.IGSLVDVQTSK.D
R1/RRR1-20/2	1147.146	1147.304	-138.389	0.461	1164.943	0.460	18	0.241	K.IGSLVDVQTSK.D
R1/RRR1-20/2	1146.397	1147.304	-1668.727	0.400	987.607	0.445	18	0.224	K.IGSLVDVQTSK.D
R1/RRR1-20/3	1815.198	1815.018	99.205	0.390	1368.599	0.473	31	0.150	K.IGSLVDVQTSKDPEGLR.I
R1/RRR1-20/3	1814.392	1815.018	-898.825	0.410	687.753	0.370	26	0.084	K.IGSLVDVQTSKDPEGLR.I
R1/RRR1-9/3	1469.560	1468.637	-52.965	0.599	1830.132	0.505	29	0.230	R.VTSHSLQELQPTK.S
R1/RRR1-9/3	1468.852	1468.637	146.854	0.535	1783.716	0.507	27	0.226	R.VTSHSLQELQPTK.S
R1/RRR1-9/2	1319.202	1318.547	-261.784	0.503	907.518	0.372	19	0.209	K.FTVLLLPSGSQR.V
R1/RRR1-9/2	1318.069	1318.547	-363.446	0.416	785.771	0.315	17	0.196	K.FTVLLLPSGSQR.V
R1/RRR1-9/2	1318.352	1318.547	-147.721	0.366	586.318	0.280	15	0.189	K.FTVLLLPSGSQR.V
R1/RRR1-9/3	1468.301	1468.637	-229.581	0.520	1315.141	0.485	25	0.148	R.VTSHSLQELQPTK.S
R1/RRR1-10/2	1691.320	1691.903	-938.812	0.501	2148.617	0.527	26	0.392	K.FVAPDVSILESDSAIK.S
R1/RRR1-10/2	1691.665	1691.903	-141.106	0.505	2006.268	0.532	25	0.367	K.FVAPDVSILESDSAIK.S
R1/RRR1-10/2	1690.745	1691.903	-1280.209	0.309	1041.247	0.389	20	0.211	K.FVAPDVSILESDSAIK.S
R1/RRR1-10/2	1768.495	1768.088	230.708	0.458	599.388	0.513	19	0.210	R.QSLLPLTVPINTETLK.M
R1/RRR1-10/2	1767.957	1768.088	-74.212	0.441	387.859	0.470	15	0.196	R.QSLLPLTVPINTETLK.M
R1/RRR1-9/2	1767.626	1768.088	-262.007	0.379	462.554	0.416	16	0.193	R.QSLLPLTVPINTETLK.M
R1/RRR1-4/2	1442.408	1441.652	-169.224	0.575	1772.787	0.488	21	0.314	K.LLVSEDLQPLGEK.L
R1/RRR1-4/2	1440.840	1441.652	-1261.007	0.488	1830.515	0.433	21	0.307	K.LLVSEDLQPLGEK.L
R1/RRR1-4/2	1440.840	1441.652	-1261.263	0.361	1052.631	0.465	17	0.227	K.LLVSEDLQPLGEK.L
R1/RRR1-4/2	1163.235	1163.302	-58.060	0.335	748.091	0.309	13	0.192	R.DLLEGDPYLK.Q
R1/RRR1-3/2	1441.979	1441.652	227.843	0.341	590.889	0.361	12	0.189	K.LLVSEDLQPLGEK.L
R1/RRR1-4/2	1163.163	1163.302	-119.431	0.228	498.552	0.152	10	0.156	-.DLLEGDPYLK.-
R1/RRR1-7/2	1315.589	1316.486	-1445.836	0.450	2293.938	0.496	19	0.408	K.SIQVIVVTDGER.I
R1/RRR1-7/2	1316.237	1316.486	-189.957	0.494	2177.693	0.526	19	0.396	K.SIQVIVVTDGER.I
R1/RRR1-6/2	1316.159	1316.486	-248.900	0.385	1908.522	0.444	18	0.321	K.SIQVIVVTDGER.I
R1/RRR1-6/2	1316.174	1316.486	-237.642	0.424	1679.643	0.462	18	0.293	K.SIQVIVVTDGER.I
R1/RRR1-7/2	1802.477	1802.123	197.305	0.516	756.625	0.588	21	0.229	R.ILGLGDLGCQGM*GIPVGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1316.065	1316.486	-321.111	0.349	1124.918	0.385	16	0.219	K.SIQVIVVTDGER.I
R1/RRR1-7/2	1801.074	1802.123	-1140.994	0.429	596.089	0.559	19	0.213	R.ILGLGDLGCQGM*GIPVGK.L
R1/RRR1-7/2	1802.461	1802.123	188.069	0.434	586.346	0.526	19	0.209	R.ILGLGDLGCQGM*GIPVGK.L
R1/RRR1-6/2	1787.331	1786.123	116.344	0.349	495.849	0.399	16	0.190	R.ILGLGDLGCQGMGIPVGK.L
R1/RRR1-6/2	1801.563	1802.123	-868.092	0.343	438.466	0.336	16	0.187	R.ILGLGDLGCQGM*GIPVGK.L
R1/RRR1-21/2	1582.581	1581.685	-65.730	0.550	1679.559	0.551	21	0.317	K.VSDSGELNSLMDDAK.Y
R1/RRR1-21/2	1581.427	1581.685	-163.407	0.489	1573.137	0.536	21	0.298	K.VSDSGELNSLMDDAK.Y
R1/RRR1-21/2	1598.077	1597.684	246.762	0.560	1439.316	0.529	20	0.278	K.VSDSGELNSLM*DDAK.Y
R1/RRR1-21/2	1596.633	1597.684	-1288.309	0.398	1347.458	0.432	20	0.246	K.VSDSGELNSLM*DDAK.Y
R1/RRR1-21/2	1597.286	1597.684	-250.057	0.500	1170.291	0.461	19	0.235	K.VSDSGELNSLM*DDAK.Y
R1/RRR1-21/2	1149.005	1149.237	-202.740	0.418	1136.329	0.431	14	0.231	K.YADTHEWVK.V
R1/RRR1-13/2	1700.392	1700.782	-230.172	0.513	2062.462	0.509	25	0.373	R.ASGYDVESSASSDAILK.A
R1/RRR1-13/2	1425.649	1426.647	-1405.499	0.359	675.898	0.438	14	0.199	K.VWVLDGGLPQWR.A
R1/RRR1-15/2	1439.299	1439.556	-179.032	0.529	1468.041	0.562	22	0.297	R.RGADVVVNYGSSSK.A
R1/RRR1-15/2	844.813	843.994	-215.378	0.439	1255.320	0.438	15	0.243	K.VALVTGAGR.G
R1/RRR1-12/2	1543.123	1543.651	-993.030	0.521	1786.296	0.533	24	0.334	K.ITGCYVVGSAGSDEK.V
R1/RRR1-10/2	1630.280	1630.910	-1002.877	0.519	2075.949	0.554	24	0.388	R.ELLGGNGILADFLVAK.A
R1/RRR1-10/2	1631.137	1630.910	139.870	0.543	1467.874	0.595	21	0.300	R.ELLGGNGILADFLVAK.A
R1/RRR1-10/2	1629.702	1630.910	-1358.664	0.371	1438.669	0.424	22	0.254	R.ELLGGNGILADFLVAK.A
R1/RRR1-10/2	1547.241	1547.821	-1024.177	0.508	823.763	0.490	20	0.218	R.EITGIASFKPAALTK.S
R1/RRR1-15/2	1534.300	1534.721	-274.938	0.494	1855.874	0.534	21	0.338	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-15/2	1534.323	1534.721	-259.852	0.517	1776.004	0.553	21	0.331	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-15/2	1534.233	1534.721	-318.842	0.470	1590.163	0.508	20	0.290	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-16/2	1536.092	1534.721	242.518	0.471	948.540	0.493	21	0.227	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-16/2	1536.090	1534.721	241.323	0.446	830.864	0.529	20	0.225	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-15/3	1534.423	1534.721	-194.533	0.447	1633.986	0.547	27	0.224	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-16/2	1536.152	1534.721	281.324	0.436	774.321	0.495	21	0.218	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-15/2	1007.557	1008.110	-1546.151	0.291	776.647	0.378	14	0.201	R.TTIFSPEGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1007.935	1008.110	-174.266	0.338	628.264	0.344	12	0.195	R.TTIFSPEGR.L
R1/RRR1-15/2	1007.591	1008.110	-1512.196	0.274	625.285	0.258	12	0.187	-.TTIFSPEGR.-
R1/RRR1-15/3	1534.977	1534.721	167.468	0.421	1266.715	0.474	25	0.144	K.AAAVGANSQAAQSM*LK.Q
R1/RRR1-12/2	943.946	944.071	-132.510	0.478	1479.011	0.398	15	0.256	R.SAVQAALQR.E
R1/RRR1-13/2	943.971	944.071	-105.788	0.507	1466.225	0.402	15	0.255	R.SAVQAALQR.E
R1/RRR1-14/2	943.191	944.071	-1998.388	0.440	1316.898	0.459	15	0.254	R.SAVQAALQR.E
R1/RRR1-13/2	944.028	944.071	-45.862	0.536	1468.449	0.395	15	0.253	R.SAVQAALQR.E
R1/RRR1-12/2	943.927	944.071	-152.748	0.450	1465.903	0.385	15	0.252	R.SAVQAALQR.E
R1/RRR1-12/2	943.894	944.071	-187.646	0.460	1344.851	0.405	14	0.244	R.SAVQAALQR.E
R1/RRR1-14/2	943.223	944.071	-1964.311	0.410	1378.768	0.364	15	0.239	R.SAVQAALQR.E
R1/RRR1-12/2	1026.228	1027.243	-1969.121	0.446	1306.549	0.351	16	0.229	R.EIALAAGLIR.I
R1/RRR1-1/2	1026.925	1027.243	-310.180	0.332	888.781	0.335	14	0.199	R.EIALAAGLIR.I
R1/RRR1-9/2	1588.065	1588.785	-1086.633	0.540	2123.253	0.493	22	0.373	K.M*FVLDEADEM*LSR.G
R1/RRR1-9/2	1572.147	1572.786	-1045.605	0.485	2127.068	0.450	21	0.358	K.M*FVLDEADEMLSR.G
R1/RRR1-9/2	1555.997	1556.786	-1153.676	0.496	2231.356	0.390	20	0.355	K.MFVLDEADEMLSR.G
R1/RRR1-9/2	1571.587	1572.786	-1403.646	0.358	1646.938	0.426	20	0.278	K.M*FVLDEADEMLSR.G
R1/RRR1-9/2	1085.077	1085.322	-226.758	0.436	1351.479	0.485	17	0.263	R.VLIATDLLAR.G
R1/RRR1-9/2	1588.038	1588.785	-1103.458	0.457	1350.695	0.436	19	0.249	K.M*FVLDEADEM*LSR.G
R1/RRR1-9/2	1572.286	1572.786	-957.051	0.440	1246.706	0.326	18	0.218	K.MFVLDEADEM*LSR.G
R1/RRR1-9/2	1084.341	1085.322	-1832.878	0.321	545.746	0.444	13	0.199	R.VLIATDLLAR.G
R1/RRR1-9/2	1572.350	1572.786	-278.388	0.398	968.209	0.194	17	0.186	K.MFVLDEADEM*LSR.G
R1/RRR1-15/2	1342.743	1343.513	-1321.948	0.413	1498.675	0.481	19	0.276	R.LDEALATGLFHR.I
R1/RRR1-15/2	1343.319	1343.513	-144.885	0.471	1254.443	0.501	18	0.256	R.LDEALATGLFHR.I
R1/RRR1-24/2	1342.944	1343.513	-1172.232	0.485	1192.080	0.493	18	0.248	R.LDEALATGLFHR.I
R1/RRR1-23/2	1343.292	1343.513	-164.849	0.433	1199.940	0.467	18	0.243	R.LDEALATGLFHR.I
R1/RRR1-15/2	1209.518	1209.399	99.052	0.435	1062.541	0.498	19	0.240	R.GTVGVM*VTATTR.C
R1/RRR1-24/2	1208.986	1209.399	-342.248	0.499	979.523	0.527	18	0.240	R.GTVGVM*VTATTR.C
R1/RRR1-15/2	1208.526	1209.399	-1554.053	0.387	1114.414	0.436	19	0.231	R.GTVGVM*VTATTR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1209.014	1209.399	-319.050	0.455	792.682	0.533	18	0.229	R.GTVGVM*VTATTR.C
R1/RRR1-15/2	1343.436	1343.513	-57.472	0.436	1383.539	0.309	18	0.226	R.LDEALATGLFHR.I
R1/RRR1-24/2	1209.017	1209.399	-317.125	0.466	885.634	0.445	18	0.220	R.GTVGVM*VTATTR.C
R1/RRR1-15/2	1208.902	1209.399	-411.952	0.391	881.618	0.454	18	0.220	R.GTVGVM*VTATTR.C
R1/RRR1-24/2	1342.778	1343.513	-1295.836	0.432	744.707	0.497	15	0.217	R.LDEALATGLFHR.I
R1/RRR1-23/2	1342.537	1343.513	-1476.458	0.428	796.294	0.434	16	0.212	R.LDEALATGLFHR.I
R1/RRR1-23/2	1208.721	1209.399	-1392.340	0.305	634.171	0.504	16	0.209	R.GTVGVM*VTATTR.C
R1/RRR1-23/2	1208.955	1209.399	-368.589	0.351	761.304	0.410	18	0.208	R.GTVGVM*VTATTR.C
R1/RRR1-23/2	1343.036	1343.513	-356.416	0.415	781.537	0.418	15	0.208	R.LDEALATGLFHR.I
R1/RRR1-24/3	1343.382	1343.513	-97.586	0.442	1236.937	0.471	27	0.126	R.LDEALATGLFHR.I
R1/RRR1-15/3	1343.261	1343.513	-188.242	0.471	907.298	0.514	25	0.113	R.LDEALATGLFHR.I
R1/RRR1-23/3	1343.449	1343.513	-47.821	0.469	763.424	0.490	22	0.106	R.LDEALATGLFHR.I
R1/RRR1-15/3	1343.459	1343.513	-40.302	0.510	923.281	0.460	25	0.106	R.LDEALATGLFHR.I
R1/RRR1-23/3	1343.280	1343.513	-174.294	0.481	778.706	0.476	23	0.103	R.LDEALATGLFHR.I
R1/RRR1-24/3	1343.518	1343.513	3.990	0.470	757.065	0.448	24	0.098	R.LDEALATGLFHR.I
R1/RRR1-15/3	1343.610	1343.513	72.470	0.497	695.442	0.413	22	0.094	R.LDEALATGLFHR.I
R1/RRR1-24/3	1343.541	1343.513	21.076	0.479	747.353	0.403	23	0.093	R.LDEALATGLFHR.I
R1/RRR1-10/2	1856.545	1856.027	-260.603	0.543	1896.440	0.611	25	0.377	R.TLGATHTVNAAKEDAVEK.I
R1/RRR1-10/2	1050.034	1050.190	-148.506	0.431	886.724	0.480	14	0.222	K.LAESGAFNLK.N
R1/RRR1-10/2	1049.915	1050.190	-262.690	0.463	850.429	0.443	15	0.217	K.LAESGAFNLK.N
R1/RRR1-10/2	1049.445	1050.190	-1667.488	0.338	746.958	0.409	14	0.204	K.LAESGAFNLK.N
R1/RRR1-10/3	1855.941	1856.027	-46.556	0.522	1052.397	0.573	35	0.142	R.TLGATHTVNAAKEDAVEK.I
R1/RRR1-11/3	1855.918	1856.027	-58.828	0.509	709.700	0.580	31	0.120	R.TLGATHTVNAAKEDAVEK.I
R1/RRR1-10/3	1855.824	1856.027	-109.697	0.505	665.988	0.570	30	0.117	R.TLGATHTVNAAKEDAVEK.I
R1/RRR1-10/3	1855.769	1856.027	-139.389	0.493	790.967	0.525	33	0.112	R.TLGATHTVNAAKEDAVEK.I
R1/RRR1-12/2	1147.424	1146.321	89.888	0.445	1261.556	0.284	17	0.215	R.FPDIASVQLR.M
R1/RRR1-12/2	1146.069	1146.321	-220.245	0.467	1050.854	0.331	16	0.210	R.FPDIASVQLR.M
R1/RRR1-12/2	1146.123	1146.321	-173.018	0.463	981.007	0.327	16	0.204	-.FPDIASVQLR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1146.542	1146.321	193.327	0.386	655.766	0.223	12	0.167	-.FPDIASVQLR.-
R1/RRR1-12/3	1757.319	1758.015	-967.659	0.423	1186.050	0.403	28	0.112	K.EVLNRFPDIASVQLR.M
R1/RRR1-12/3	1757.254	1758.015	-1005.006	0.434	739.109	0.430	25	0.093	K.EVLNRFPDIASVQLR.M
R1/RRR1-9/2	1978.562	1979.049	-247.317	0.547	2126.705	0.642	27	0.429	K.TVGGGDDAFNTFFSETGAGK.H
R1/RRR1-9/2	1978.680	1979.049	-187.342	0.558	1578.308	0.663	24	0.334	K.TVGGGDDAFNTFFSETGAGK.H
R1/RRR1-9/2	1978.313	1979.049	-880.538	0.530	1464.891	0.662	23	0.316	K.TVGGGDDAFNTFFSETGAGK.H
R1/RRR1-9/2	1702.283	1702.929	-969.879	0.496	1446.334	0.543	23	0.286	R.AVFVDLEPTVIDEVR.T
R1/RRR1-9/2	1702.281	1702.929	-971.463	0.506	1116.446	0.526	21	0.247	R.AVFVDLEPTVIDEVR.T
R1/RRR1-14/2	1702.577	1702.929	-207.439	0.485	1112.594	0.490	21	0.240	R.AVFVDLEPTVIDEVR.T
R1/RRR1-9/2	1702.451	1702.929	-282.106	0.501	952.987	0.529	21	0.236	R.AVFVDLEPTVIDEVR.T
R1/RRR1-2/2	1703.645	1702.929	-167.639	0.512	1274.567	0.420	20	0.236	R.AVFVDLEPTVIDEVR.T
R1/RRR1-18/2	1701.968	1702.929	-1155.947	0.339	563.747	0.365	15	0.192	R.AVFVDLEPTVIDEVR.T
R1/RRR1-13/2	1702.737	1702.929	-113.080	0.420	815.952	0.265	18	0.189	R.AVFVDLEPTVIDEVR.T
R1/RRR1-10/2	1702.283	1702.929	-969.951	0.327	642.527	0.188	16	0.183	R.AVFVDLEPTVIDEVR.T
R1/RRR1-8/2	1836.353	1836.018	182.979	0.578	2477.701	0.499	23	0.443	R.MTNFYTNFQVDEIGR.V
R1/RRR1-8/2	1851.410	1852.017	-870.670	0.551	2327.218	0.567	22	0.440	R.M*TNFYTNFQVDEIGR.V
R1/RRR1-8/2	1852.291	1852.017	147.949	0.598	2311.606	0.564	22	0.434	R.M*TNFYTNFQVDEIGR.V
R1/RRR1-8/2	1852.304	1852.017	155.418	0.613	2233.797	0.572	22	0.420	R.M*TNFYTNFQVDEIGR.V
R1/RRR1-8/2	1835.292	1836.018	-943.019	0.567	2214.892	0.523	22	0.398	R.MTNFYTNFQVDEIGR.V
R1/RRR1-8/2	1836.314	1836.018	161.513	0.592	2113.701	0.545	22	0.386	R.MTNFYTNFQVDEIGR.V
R1/RRR1-8/2	1204.141	1204.356	-178.611	0.538	2048.591	0.411	18	0.332	R.AAELTTLLESR.M
R1/RRR1-1/2	1204.104	1204.356	-209.833	0.525	1683.625	0.455	17	0.292	R.AAELTTLLESR.M
R1/RRR1-8/2	1203.785	1204.356	-1308.251	0.501	1806.414	0.394	17	0.291	R.AAELTTLLESR.M
R1/RRR1-3/2	1203.839	1204.356	-1263.340	0.352	927.201	0.386	14	0.208	-.AAELTTLLESR.-
R1/RRR1-2/2	1204.330	1204.356	-21.615	0.355	568.795	0.313	13	0.185	-.AAELTTLLESR.-
R1/RRR1-14/2	1858.737	1858.206	-253.116	0.594	2793.642	0.532	24	0.544	R.GCIVSQDLSVLNLVIVK.Q
R1/RRR1-15/2	1750.061	1750.953	-1084.163	0.413	1776.968	0.498	20	0.319	K.DLVVDMTNFYNQYK.S
R1/RRR1-15/3	1448.666	1448.606	41.310	0.487	1096.730	0.452	23	0.116	K.IKNEQDPSLTFR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/3	1448.603	1448.606	-2.301	0.470	1087.846	0.400	23	0.104	K.IKNEQDPSLTFR.R
R1/RRR1-16/2	1518.354	1518.782	-282.765	0.375	1952.038	0.378	19	0.309	K.ASILLLQDAAAYLR.K
R1/RRR1-15/2	1518.309	1518.782	-312.771	0.373	1773.701	0.381	18	0.284	K.ASILLLQDAAAYLR.K
R1/RRR1-15/2	1101.920	1102.180	-237.181	0.459	1070.624	0.404	16	0.222	K.NVDEAVEGLR.A
R1/RRR1-20/3	1867.067	1867.012	29.856	0.521	1658.149	0.590	28	0.246	R.HDVESAIPYHAELTQR.G
R1/RRR1-20/2	1464.166	1464.604	-300.003	0.449	943.484	0.511	16	0.231	R.LSYLWADDPEVR.A
R1/RRR1-21/2	1464.227	1464.604	-258.349	0.429	817.560	0.473	15	0.216	R.LSYLWADDPEVR.A
R1/RRR1-20/2	1464.135	1464.604	-321.501	0.389	924.420	0.414	16	0.214	R.LSYLWADDPEVR.A
R1/RRR1-21/2	1464.454	1464.604	-102.970	0.443	747.220	0.458	15	0.212	R.LSYLWADDPEVR.A
R1/RRR1-21/2	1464.302	1464.604	-207.080	0.413	800.960	0.434	15	0.210	R.LSYLWADDPEVR.A
R1/RRR1-20/2	1464.181	1464.604	-289.380	0.357	778.247	0.413	15	0.206	R.LSYLWADDPEVR.A
R1/RRR1-20/3	1866.611	1867.012	-215.520	0.495	1471.684	0.558	28	0.198	R.HDVESAIPYHAELTQR.G
R1/RRR1-20/2	1466.052	1464.604	306.865	0.254	654.625	0.160	14	0.183	R.LSYLWADDPEVR.A
R1/RRR1-19/3	1867.904	1867.012	-58.090	0.434	1127.730	0.519	25	0.141	R.HDVESAIPYHAELTQR.G
R1/RRR1-8/2	1419.253	1419.694	-311.395	0.455	1421.849	0.491	19	0.272	R.KLSIQELLTAFR.V
R1/RRR1-8/2	1092.771	1093.132	-331.489	0.424	765.923	0.403	14	0.206	K.NQDLNFADR.H
R1/RRR1-24/2	1260.099	1260.466	-291.552	0.500	1540.134	0.531	18	0.296	R.FTTFALSGFIR.A
R1/RRR1-24/2	1259.982	1260.466	-385.254	0.489	1362.677	0.574	17	0.285	R.FTTFALSGFIR.A
R1/RRR1-25/2	1260.335	1260.466	-103.520	0.514	1030.243	0.576	17	0.254	R.FTTFALSGFIR.A
R1/RRR1-25/2	1260.159	1260.466	-244.027	0.424	994.434	0.515	17	0.237	R.FTTFALSGFIR.A
R1/RRR1-24/2	1260.071	1260.466	-314.004	0.422	841.069	0.537	15	0.228	R.FTTFALSGFIR.A
R1/RRR1-24/2	1674.532	1674.796	-158.123	0.484	1044.300	0.456	17	0.222	R.AQGDADSALDRLWQK.R
R1/RRR1-24/2	1674.310	1674.796	-291.235	0.492	993.339	0.467	17	0.221	R.AQGDADSALDRLWQK.R
R1/RRR1-24/2	1675.052	1674.796	153.234	0.508	1047.387	0.431	18	0.219	R.AQGDADSALDRLWQK.R
R1/RRR1-25/2	1673.934	1674.796	-1115.621	0.337	694.894	0.252	17	0.185	R.AQGDADSALDRLWQK.R
R1/RRR1-8/2	1544.358	1544.735	-244.944	0.459	2143.093	0.514	24	0.390	K.VTALVNDTVGTLAGGR.Y
R1/RRR1-8/2	1850.288	1851.007	-932.067	0.427	1133.707	0.461	20	0.230	K.GFSINGTVGEDVVAELSR.A
R1/RRR1-10/2	1595.447	1594.836	-244.314	0.560	1815.771	0.563	24	0.345	R.LPGYLGEYLALTGAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1594.500	1594.836	-211.134	0.531	1688.726	0.499	23	0.305	R.LPGYLGEYLALTGAR.L
R1/RRR1-10/2	1594.177	1594.836	-1043.637	0.511	1624.759	0.507	23	0.299	R.LPGYLGEYLALTGAR.L
R1/RRR1-10/2	1295.483	1295.424	46.347	0.456	1431.016	0.363	19	0.243	R.SVVTGDVYEGIR.A
R1/RRR1-1/2	1595.560	1594.836	-173.546	0.346	594.063	0.318	14	0.184	-.LPGYLGEYLALTGAR.-
R1/RRR1-16/2	1650.182	1649.825	216.977	0.471	1813.671	0.566	26	0.344	R.CSYTVWPGALPGGGAR.L
R1/RRR1-17/2	1650.283	1649.825	278.469	0.449	1634.907	0.498	25	0.298	R.CSYTVWPGALPGGGAR.L
R1/RRR1-16/2	1649.226	1649.825	-972.202	0.468	1433.615	0.570	24	0.290	R.CSYTVWPGALPGGGAR.L
R1/RRR1-17/2	1885.460	1885.070	207.175	0.553	1406.817	0.553	27	0.282	R.LDPGQSWSISVAAGTPAAR.I
R1/RRR1-16/2	1884.653	1885.070	-221.895	0.542	1372.943	0.556	26	0.278	R.LDPGQSWSISVAAGTPAAR.I
R1/RRR1-16/2	1885.498	1885.070	227.691	0.572	1280.515	0.582	26	0.274	R.LDPGQSWSISVAAGTPAAR.I
R1/RRR1-17/2	1650.231	1649.825	246.723	0.500	1308.083	0.549	22	0.270	R.CSYTVWPGALPGGGAR.L
R1/RRR1-16/2	1649.074	1649.825	-1064.876	0.439	1349.913	0.518	23	0.267	R.CSYTVWPGALPGGGAR.L
R1/RRR1-17/2	1650.232	1649.825	247.093	0.488	1299.213	0.543	21	0.266	R.CSYTVWPGALPGGGAR.L
R1/RRR1-16/2	1884.506	1885.070	-832.631	0.514	1223.956	0.552	24	0.260	R.LDPGQSWSISVAAGTPAAR.I
R1/RRR1-17/2	1884.489	1885.070	-841.410	0.488	1235.190	0.532	25	0.257	R.LDPGQSWSISVAAGTPAAR.I
R1/RRR1-3/2	1884.648	1885.070	-224.689	0.507	984.344	0.528	22	0.232	R.LDPGQSWSISVAAGTPAAR.I
R1/RRR1-5/2	1885.401	1885.070	176.141	0.473	528.473	0.513	20	0.207	R.LDPGQSWSISVAAGTPAAR.I
R1/RRR1-12/2	1089.292	1089.181	101.766	0.568	1609.348	0.394	17	0.268	K.LGGELTVDER.N
R1/RRR1-12/2	1090.047	1089.181	-124.072	0.551	1602.420	0.383	17	0.264	K.LGGELTVDER.N
R1/RRR1-12/2	1390.997	1391.550	-1119.237	0.502	1333.150	0.443	19	0.251	R.IISSIEQKEESK.G
R1/RRR1-12/2	1089.924	1089.181	-236.758	0.528	1439.351	0.307	17	0.230	K.LGGELTVDER.N
R1/RRR1-12/2	1391.199	1391.550	-252.900	0.455	800.135	0.417	16	0.207	R.IISSIEQKEESK.G
R1/RRR1-15/3	1889.017	1888.964	28.083	0.562	1720.260	0.572	33	0.246	R.TIGHTVTSPDDTAEQCR.S
R1/RRR1-15/2	1401.938	1402.405	-334.018	0.471	1090.722	0.383	16	0.217	K.GGNDYEIFESDR.T
R1/RRR1-15/2	1402.273	1402.405	-93.827	0.485	1060.113	0.315	17	0.204	K.GGNDYEIFESDR.T
R1/RRR1-15/2	1402.238	1402.405	-118.889	0.469	749.267	0.353	17	0.200	K.GGNDYEIFESDR.T
R1/RRR1-15/3	1888.671	1888.964	-155.890	0.504	1304.807	0.541	29	0.169	R.TIGHTVTSPDDTAEQCR.S
R1/RRR1-15/3	1888.622	1888.964	-181.566	0.547	1196.752	0.550	28	0.161	R.TIGHTVTSPDDTAEQCR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1936.180	1936.174	3.139	0.532	1923.697	0.571	27	0.363	K.GVYAYDFGDTAGLTPLM*K.M
R1/RRR1-9/2	1920.468	1920.175	153.288	0.528	2099.190	0.470	27	0.359	K.GVYAYDFGDTAGLTPLMK.M
R1/RRR1-9/2	1919.620	1920.175	-812.553	0.411	2109.766	0.394	26	0.337	K.GVYAYDFGDTAGLTPLMK.M
R1/RRR1-9/2	1936.426	1936.174	130.543	0.519	1548.198	0.560	25	0.301	K.GVYAYDFGDTAGLTPLM*K.M
R1/RRR1-9/2	1935.347	1936.174	-947.138	0.516	1387.593	0.530	24	0.273	K.GVYAYDFGDTAGLTPLM*K.M
R1/RRR1-9/2	1552.439	1552.749	-200.450	0.531	1058.113	0.479	22	0.238	R.FIDIPEEVAEVYK.L
R1/RRR1-9/2	1552.388	1552.749	-233.266	0.535	921.240	0.507	21	0.234	R.FIDIPEEVAEVYK.L
R1/RRR1-9/2	1552.297	1552.749	-292.278	0.485	879.248	0.466	21	0.225	R.FIDIPEEVAEVYK.L
R1/RRR1-9/2	1919.428	1920.175	-912.909	0.403	1049.145	0.406	19	0.213	K.GVYAYDFGDTAGLTPLMK.M
R1/RRR1-8/2	1553.706	1552.749	-27.866	0.487	814.409	0.364	20	0.206	R.FIDIPEEVAEVYK.L
R1/RRR1-5/2	1553.536	1552.749	-137.653	0.360	553.730	0.371	17	0.199	R.FIDIPEEVAEVYK.L
R1/RRR1-8/2	1554.078	1552.749	211.881	0.448	549.254	0.322	17	0.196	R.FIDIPEEVAEVYK.L
R1/RRR1-6/2	1553.803	1552.749	34.387	0.395	642.926	0.282	18	0.194	R.FIDIPEEVAEVYK.L
R1/RRR1-2/2	1552.313	1552.749	-282.258	0.303	645.748	0.196	18	0.189	R.FIDIPEEVAEVYK.L
R1/RRR1-24/2	1500.399	1499.673	-183.514	0.513	1077.822	0.590	20	0.260	R.LM*GFFPNDSEVAR.Y
R1/RRR1-25/2	1499.088	1499.673	-1060.690	0.449	969.460	0.473	20	0.229	R.LM*GFFPNDSEVAR.Y
R1/RRR1-25/2	1499.337	1499.673	-224.882	0.442	833.310	0.478	19	0.221	R.LM*GFFPNDSEVAR.Y
R1/RRR1-24/2	1499.177	1499.673	-332.056	0.414	846.187	0.468	19	0.220	R.LM*GFFPNDSEVAR.Y
R1/RRR1-24/2	1499.427	1499.673	-164.607	0.450	723.501	0.490	18	0.217	R.LM*GFFPNDSEVAR.Y
R1/RRR1-25/2	1498.908	1499.673	-1181.464	0.454	870.675	0.423	18	0.214	R.LM*GFFPNDSEVAR.Y
R1/RRR1-25/2	1353.542	1354.536	-1477.208	0.317	644.849	0.498	14	0.205	K.VVGNFSALDYLR.L
R1/RRR1-25/2	1353.468	1354.536	-1532.199	0.250	203.759	0.377	12	0.185	-.VVGNFSALDYLR.-
R1/RRR1-25/2	1353.642	1354.536	-1403.020	0.223	230.807	0.350	10	0.182	-.VVGNFSALDYLR.-
R1/RRR1-9/2	1230.328	1230.436	-88.032	0.493	1136.856	0.465	16	0.237	K.TLNDQIVVLSK.R
R1/RRR1-9/2	1229.997	1230.436	-357.715	0.526	923.535	0.502	16	0.230	K.TLNDQIVVLSK.R
R1/RRR1-9/2	1229.985	1230.436	-367.872	0.503	869.936	0.491	16	0.225	K.TLNDQIVVLSK.R
R1/RRR1-9/2	1295.317	1295.500	-141.747	0.339	1046.444	0.387	15	0.213	K.AAIDIVELCYK.A
R1/RRR1-19/2	1369.639	1369.546	68.153	0.538	1461.302	0.507	20	0.281	K.HLLDETISDVVK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1369.314	1369.546	-169.763	0.482	1507.861	0.478	20	0.279	K.HLLDETISDVVK.S
R1/RRR1-19/2	1369.227	1369.546	-233.173	0.480	1220.522	0.505	19	0.254	K.HLLDETISDVVK.S
R1/RRR1-19/2	1138.928	1139.197	-237.537	0.472	660.341	0.410	15	0.210	R.LIDDYNTER.K
R1/RRR1-19/2	1138.698	1139.197	-439.621	0.406	596.638	0.428	15	0.209	R.LIDDYNTER.K
R1/RRR1-19/2	1138.638	1139.197	-1373.640	0.431	589.465	0.344	14	0.201	R.LIDDYNTER.K
R1/RRR1-18/2	1139.254	1139.197	49.801	0.406	653.300	0.317	14	0.198	R.LIDDYNTER.K
R1/RRR1-15/2	1669.299	1669.904	-964.399	0.549	1378.410	0.519	22	0.273	R.RVEPYVAYGYPNLK.S
R1/RRR1-15/2	1669.451	1669.904	-272.501	0.557	1218.206	0.534	21	0.260	R.RVEPYVAYGYPNLK.S
R1/RRR1-15/2	1514.201	1513.718	319.667	0.494	1142.456	0.498	21	0.246	R.VEPYVAYGYPNLK.S
R1/RRR1-15/2	1514.291	1513.718	-283.119	0.513	1123.057	0.502	21	0.246	R.VEPYVAYGYPNLK.S
R1/RRR1-15/2	1669.432	1669.904	-284.092	0.557	1165.168	0.492	21	0.245	R.RVEPYVAYGYPNLK.S
R1/RRR1-15/2	1513.054	1513.718	-1102.748	0.301	872.142	0.375	20	0.204	R.VEPYVAYGYPNLK.S
R1/RRR1-10/2	1729.226	1729.822	-925.879	0.523	1875.120	0.583	22	0.363	K.EAFVSSSEEPFTVDGK.E
R1/RRR1-9/2	1696.477	1696.923	-263.540	0.498	895.383	0.453	22	0.220	R.NLEVGIPELLENDIK.V
R1/RRR1-9/2	1696.308	1696.923	-955.251	0.456	701.216	0.445	20	0.210	R.NLEVGIPELLENDIK.V
R1/RRR1-9/2	1696.313	1696.923	-951.928	0.477	760.473	0.409	21	0.208	R.NLEVGIPELLENDIK.V
R1/RRR1-10/2	1696.518	1696.923	-239.430	0.464	622.610	0.453	19	0.207	R.NLEVGIPELLENDIK.V
R1/RRR1-10/2	1696.384	1696.923	-909.954	0.435	651.385	0.446	19	0.207	R.NLEVGIPELLENDIK.V
R1/RRR1-10/2	1696.070	1696.923	-1096.008	0.380	654.657	0.447	19	0.206	R.NLEVGIPELLENDIK.V
R1/RRR1-16/2	1728.538	1728.967	-248.736	0.518	1101.172	0.583	24	0.261	K.IWQVPETLSEEVLGK.M
R1/RRR1-16/2	1729.644	1728.967	-186.992	0.553	1043.563	0.506	24	0.240	K.IWQVPETLSEEVLGK.M
R1/RRR1-16/2	1728.579	1728.967	-225.072	0.511	918.783	0.511	23	0.232	K.IWQVPETLSEEVLGK.M
R1/RRR1-4/2	1607.958	1607.833	78.001	0.453	2506.921	0.386	21	0.414	R.SVEQLGYITVLTQR.N
R1/RRR1-5/2	1607.503	1607.833	-206.075	0.220	370.197	0.370	13	0.183	R.SVEQLGYITVLTQR.N
R1/RRR1-4/3	1989.608	1990.205	-804.962	0.528	1004.947	0.431	23	0.113	R.DLNKEELIEFFNNHVK.V
R1/RRR1-19/2	1355.276	1354.446	-125.990	0.537	1519.187	0.511	19	0.288	K.AFNVEEAPSDFK.V
R1/RRR1-19/2	1353.965	1354.446	-356.794	0.470	1374.800	0.447	18	0.255	K.AFNVEEAPSDFK.V
R1/RRR1-19/2	1354.179	1354.446	-198.242	0.466	1026.832	0.393	17	0.216	K.AFNVEEAPSDFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1143.179	1143.315	-119.912	0.371	1081.665	0.333	15	0.111	K.VSGAEVILNQI.-
R1/RRR1-19/2	1142.956	1143.315	-315.006	0.260	682.102	0.258	13	0.078	K.VSGAEVILNQI.-
R1/RRR1-21/2	1268.803	1269.472	-1319.375	0.319	1326.536	0.392	19	0.236	K.VVIIQPVDSGNK.L
R1/RRR1-21/2	1066.196	1066.229	-31.535	0.391	711.551	0.399	13	0.204	R.YTLELEGLK.G
R1/RRR1-21/2	1269.167	1269.472	-241.523	0.395	864.583	0.313	16	0.196	K.VVIIQPVDSGNK.L
R1/RRR1-21/2	1066.209	1066.229	-18.903	0.342	585.016	0.344	12	0.195	R.YTLELEGLK.G
R1/RRR1-21/2	1065.858	1066.229	-349.509	0.237	386.344	0.378	11	0.190	R.YTLELEGLK.G
R1/RRR1-17/2	1431.520	1431.702	-127.576	0.435	1418.400	0.564	19	0.224	K.LGSQIDILAPIKY.-
R1/RRR1-17/2	1432.480	1431.702	-155.269	0.450	1338.249	0.616	19	0.216	K.LGSQIDILAPIKY.-
R1/RRR1-17/2	1432.092	1431.702	273.702	0.431	1100.553	0.567	18	0.157	K.LGSQIDILAPIKY.-
R1/RRR1-17/3	1538.161	1538.759	-1042.198	0.490	1361.533	0.469	26	0.147	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1538.264	1538.759	-322.639	0.448	1396.717	0.399	27	0.129	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1539.051	1538.759	190.525	0.449	1231.524	0.437	24	0.127	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1538.168	1538.759	-1037.537	0.480	1047.766	0.502	24	0.127	R.M*NTKPSHGPIHFR.A
R1/RRR1-16/3	1538.409	1538.759	-228.179	0.457	997.775	0.484	25	0.118	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1537.773	1538.759	-1295.531	0.487	1021.124	0.455	25	0.114	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1538.374	1538.759	-250.747	0.438	992.403	0.423	23	0.108	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1539.103	1538.759	224.407	0.385	1136.856	0.392	25	0.107	R.M*NTKPSHGPIHFR.A
R1/RRR1-16/3	1538.379	1538.759	-247.523	0.413	992.054	0.424	24	0.106	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1538.597	1538.759	-105.444	0.386	1044.222	0.405	24	0.105	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1538.163	1538.759	-1040.884	0.429	926.393	0.400	23	0.100	R.M*NTKPSHGPIHFR.A
R1/RRR1-16/3	1538.969	1538.759	136.954	0.418	631.486	0.437	21	0.099	R.M*NTKPSHGPIHFR.A
R1/RRR1-17/3	1537.442	1538.759	-1511.426	0.417	871.644	0.381	23	0.095	R.M*NTKPSHGPIHFR.A
R1/RRR1-15/3	1537.983	1538.759	-1158.388	0.359	823.929	0.320	23	0.085	R.M*NTKPSHGPIHFR.A
R1/RRR1-9/2	869.977	870.075	-112.956	0.267	1191.312	0.265	12	0.204	K.NLVVLVGR.L
R1/RRR1-9/2	1230.671	1231.336	-1357.570	0.337	723.671	0.342	14	0.192	R.YDTFTAEAGKK.V
R1/RRR1-9/2	870.072	870.075	-3.745	0.239	842.530	0.283	12	0.190	K.NLVVLVGR.L
R1/RRR1-7/2	1346.492	1346.600	-80.710	0.534	2256.492	0.387	20	0.363	R.KFDLGALVDLVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1346.202	1346.600	-296.551	0.475	1751.185	0.513	19	0.321	R.KFDLGALVDLVR.K
R1/RRR1-7/2	1201.129	1201.312	-152.964	0.383	1008.882	0.464	19	0.227	K.IVDPDTGASLGR.N
R1/RRR1-7/2	1200.553	1201.312	-1469.133	0.341	825.631	0.487	18	0.217	K.IVDPDTGASLGR.N
R1/RRR1-7/2	1200.420	1201.312	-1580.981	0.287	562.911	0.397	15	0.194	K.IVDPDTGASLGR.N
R1/RRR1-7/3	1346.740	1346.600	104.257	0.353	1491.859	0.165	26	0.083	R.KFDLGALVDLVR.K
R1/RRR1-7/3	1346.623	1346.600	17.255	0.468	1157.914	0.227	24	0.070	-.KFDLGALVDLVR.-
R1/RRR1-18/2	1369.803	1370.621	-1331.408	0.512	1454.728	0.573	18	0.296	K.VHLVAIDIFTNK.K
R1/RRR1-19/2	1370.362	1370.621	-190.094	0.440	1292.967	0.498	17	0.257	K.VHLVAIDIFTNK.K
R1/RRR1-18/2	1370.508	1370.621	-83.227	0.463	934.873	0.540	17	0.236	K.VHLVAIDIFTNK.K
R1/RRR1-18/2	1707.341	1707.842	-881.350	0.431	863.207	0.501	21	0.122	K.AM*GEEVPTQVKPSSGSS.-
R1/RRR1-19/2	1707.206	1707.842	-960.883	0.429	766.214	0.515	20	0.119	K.AM*GEEVPTQVKPSSGSS.-
R1/RRR1-18/2	1707.421	1707.842	-246.905	0.476	666.114	0.482	19	0.112	K.AM*GEEVPTQVKPSSGSS.-
R1/RRR1-19/2	1707.322	1707.842	-892.835	0.416	676.486	0.470	19	0.111	K.AM*GEEVPTQVKPSSGSS.-
R1/RRR1-19/2	1707.332	1707.842	-886.877	0.411	664.510	0.457	19	0.110	K.AM*GEEVPTQVKPSSGSS.-
R1/RRR1-22/2	1866.124	1867.118	-1071.652	0.509	1797.447	0.498	25	0.321	K.DM*PVLQDGPPPGGFAPVR.Y
R1/RRR1-22/2	1867.616	1867.118	267.366	0.535	1377.544	0.521	23	0.269	K.DM*PVLQDGPPPGGFAPVR.Y
R1/RRR1-22/2	1571.051	1570.726	207.254	0.480	801.594	0.556	22	0.233	R.TALVPVLQAEEDER.F
R1/RRR1-22/2	1569.872	1570.726	-1184.893	0.422	778.966	0.496	21	0.220	R.TALVPVLQAEEDER.F
R1/RRR1-22/2	1569.331	1570.726	-1531.001	0.310	686.634	0.373	20	0.198	R.TALVPVLQAEEDER.F
R1/RRR1-22/2	1779.482	1780.062	-890.718	0.505	1146.599	0.577	19	0.256	R.KLIGATNPLQAEPGTIR.G
R1/RRR1-22/2	943.893	944.111	-230.646	0.511	1130.569	0.421	14	0.230	R.GLVGEIISR.F
R1/RRR1-21/2	943.948	944.111	-172.654	0.472	1144.963	0.409	14	0.229	R.GLVGEIISR.F
R1/RRR1-21/2	944.153	944.111	45.244	0.437	1228.499	0.331	14	0.220	R.GLVGEIISR.F
R1/RRR1-22/2	944.035	944.111	-79.906	0.443	1144.687	0.337	14	0.216	R.GLVGEIISR.F
R1/RRR1-22/3	1780.922	1780.062	-78.561	0.416	991.681	0.405	31	0.099	R.KLIGATNPLQAEPGTIR.G
R1/RRR1-22/3	1779.145	1780.062	-1080.452	0.373	545.473	0.444	27	0.090	R.KLIGATNPLQAEPGTIR.G
R1/RRR1-22/3	1780.534	1780.062	265.861	0.341	914.234	0.269	29	0.075	R.KLIGATNPLQAEPGTIR.G
R1/RRR1-23/2	1243.200	1242.366	-133.409	0.544	960.907	0.578	16	0.247	K.HQYLPADAQAK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1242.124	1242.366	-194.736	0.518	1040.221	0.516	16	0.240	K.HQYLPADAQAK.Q
R1/RRR1-23/2	1242.302	1242.366	-51.408	0.508	920.599	0.540	15	0.235	K.HQYLPADAQAK.Q
R1/RRR1-23/2	1231.125	1231.426	-245.008	0.428	657.561	0.405	16	0.205	R.EALGALPLYQR.T
R1/RRR1-23/2	1231.344	1231.426	-66.383	0.483	516.074	0.371	14	0.197	R.EALGALPLYQR.T
R1/RRR1-23/2	1231.429	1231.426	2.326	0.266	375.744	0.315	12	0.189	R.EALGALPLYQR.T
R1/RRR1-1/2	1861.397	1861.044	190.318	0.535	2276.374	0.523	22	0.419	R.LDIDFAEVYANSALYR.S
R1/RRR1-8/2	1562.775	1562.706	44.609	0.515	1760.705	0.521	22	0.326	K.HFVALSTNESEVTK.F
R1/RRR1-8/2	1572.162	1572.656	-315.297	0.474	1497.620	0.549	22	0.294	K.TFTTAETTTNANTAK.T
R1/RRR1-8/2	1572.190	1572.656	-296.990	0.482	1456.675	0.560	22	0.291	K.TFTTAETTTNANTAK.T
R1/RRR1-8/2	1573.182	1572.656	-302.017	0.514	1204.981	0.593	20	0.269	K.TFTTAETTTNANTAK.T
R1/RRR1-8/2	1957.836	1957.261	-217.853	0.530	1250.534	0.626	23	0.281	K.VLFIGGGIANFTNVASTFK.G
R1/RRR1-8/2	1117.239	1116.250	-9.930	0.328	828.247	0.329	15	0.196	K.AATQELGLNAK.I
R1/RRR1-8/2	1116.005	1116.250	-220.145	0.379	742.661	0.219	16	0.186	K.AATQELGLNAK.I
R1/RRR1-14/2	1610.235	1609.850	239.468	0.458	940.368	0.490	20	0.227	K.STSSIFPLQNVFIR.K
R1/RRR1-14/2	1609.154	1609.850	-1057.130	0.398	634.702	0.368	17	0.194	K.STSSIFPLQNVFIR.K
R1/RRR1-13/2	1390.329	1390.610	-202.158	0.485	1663.718	0.462	18	0.294	K.KLSAILSWENTK.K
R1/RRR1-13/3	1577.666	1577.785	-75.952	0.441	1195.922	0.460	30	0.122	K.RGEEVLKAEEM*AAK.Y
R1/RRR1-14/3	1577.843	1577.785	36.611	0.424	1451.572	0.354	32	0.119	K.RGEEVLKAEEM*AAK.Y
R1/RRR1-13/3	1577.428	1577.785	-227.318	0.441	1021.159	0.451	29	0.108	K.RGEEVLKAEEM*AAK.Y
R1/RRR1-14/3	1577.714	1577.785	-45.568	0.350	935.514	0.359	27	0.088	K.RGEEVLKAEEM*AAK.Y
R1/RRR1-14/3	1577.788	1577.785	1.693	0.421	858.306	0.353	26	0.087	K.RGEEVLKAEEM*AAK.Y
R1/RRR1-13/3	1577.834	1577.785	30.908	0.413	838.197	0.334	26	0.084	K.RGEEVLKAEEM*AAK.Y
R1/RRR1-5/2	1394.466	1395.586	-1524.994	0.452	1273.153	0.552	19	0.267	R.AASIVEDALAHGLK.S
R1/RRR1-5/2	1450.560	1449.634	-51.202	0.456	777.984	0.401	18	0.205	K.TIFTVTPGSEQIR.A
R1/RRR1-5/2	1449.154	1449.634	-332.006	0.415	725.339	0.388	18	0.202	K.TIFTVTPGSEQIR.A
R1/RRR1-9/2	1311.014	1311.380	-280.229	0.566	1352.330	0.515	18	0.270	K.AGNEQFVTETSK.W
R1/RRR1-9/2	1039.020	1039.207	-180.600	0.420	1554.823	0.401	17	0.264	R.LGYTGLSLSK.Q
R1/RRR1-9/2	1038.925	1039.207	-272.186	0.369	1228.893	0.422	16	0.236	R.LGYTGLSLSK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1039.971	1039.207	-227.881	0.374	916.774	0.404	15	0.213	R.LGYTGLSLSK.Q
R1/RRR1-1/2	1040.148	1039.207	-57.515	0.275	663.425	0.315	14	0.193	R.LGYTGLSLSK.Q
R1/RRR1-13/2	1382.801	1383.615	-1315.705	0.411	1546.759	0.515	20	0.292	K.VIVIDVNDPLASK.L
R1/RRR1-13/2	1088.959	1089.138	-164.785	0.521	1127.567	0.395	15	0.226	K.LNDVEDVER.H
R1/RRR1-13/2	1088.902	1089.138	-217.978	0.485	1127.997	0.385	15	0.224	K.LNDVEDVER.H
R1/RRR1-13/2	1088.962	1089.138	-162.311	0.501	1042.871	0.401	15	0.222	K.LNDVEDVER.H
R1/RRR1-7/2	1980.686	1981.204	-769.019	0.534	1822.978	0.614	24	0.361	K.QIGVIGWGSQGPAQAQNLR.D
R1/RRR1-7/2	1980.754	1981.204	-227.819	0.550	1683.580	0.620	24	0.339	K.QIGVIGWGSQGPAQAQNLR.D
R1/RRR1-2/2	1790.173	1789.021	85.382	0.404	837.247	0.338	18	0.194	R.FDYILTQQAFVTVDK.N
R1/RRR1-25/2	1671.294	1671.814	-912.403	0.443	1203.210	0.499	21	0.248	R.VTSGEQQVVSGM*NYR.L
R1/RRR1-25/2	1671.160	1671.814	-992.921	0.499	1127.360	0.483	21	0.239	R.VTSGEQQVVSGM*NYR.L
R1/RRR1-25/2	1042.624	1043.116	-473.084	0.425	687.060	0.612	16	0.235	R.HASLSSDGLR.F
R1/RRR1-25/2	1042.877	1043.116	-229.476	0.404	833.248	0.530	16	0.230	R.HASLSSDGLR.F
R1/RRR1-26/2	1042.876	1043.116	-230.651	0.457	539.039	0.557	15	0.223	R.HASLSSDGLR.F
R1/RRR1-25/3	1671.515	1671.814	-179.289	0.446	2068.226	0.371	33	0.223	R.VTSGEQQVVSGM*NYR.L
R1/RRR1-25/2	1042.991	1043.116	-120.396	0.433	608.232	0.545	15	0.223	R.HASLSSDGLR.F
R1/RRR1-26/2	1043.030	1043.116	-82.594	0.395	581.932	0.550	15	0.220	R.HASLSSDGLR.F
R1/RRR1-26/2	1042.957	1043.116	-152.918	0.416	544.663	0.556	14	0.220	R.HASLSSDGLR.F
R1/RRR1-26/2	1671.978	1671.814	98.378	0.328	356.171	0.433	13	0.190	R.VTSGEQQVVSGM*NYR.L
R1/RRR1-24/2	1042.163	1043.116	-1879.566	0.238	273.643	0.482	11	0.189	-.HASLSSDGLR.-
R1/RRR1-26/3	1672.119	1671.814	183.116	0.450	1510.652	0.320	29	0.125	R.VTSGEQQVVSGM*NYR.L
R1/RRR1-25/3	1671.221	1671.814	-956.188	0.407	1238.555	0.237	28	0.084	R.VTSGEQQVVSGM*NYR.L
R1/RRR1-21/2	1123.992	1124.229	-211.609	0.489	832.975	0.556	17	0.236	K.GISSSAVPYSR.N
R1/RRR1-21/2	1123.384	1124.229	-1647.327	0.345	968.933	0.503	17	0.229	K.GISSSAVPYSR.N
R1/RRR1-21/2	1123.921	1124.229	-275.241	0.513	779.008	0.536	16	0.228	K.GISSSAVPYSR.N
R1/RRR1-21/2	1199.238	1198.397	-133.501	0.432	651.409	0.442	18	0.209	K.GATPSQIGVVLR.D
R1/RRR1-21/2	1199.128	1198.397	-225.407	0.366	678.587	0.381	19	0.202	K.GATPSQIGVVLR.D
R1/RRR1-21/2	1199.174	1198.397	-187.213	0.447	700.549	0.362	18	0.201	K.GATPSQIGVVLR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1123.905	1124.229	-288.862	0.388	645.386	0.366	15	0.199	K.GISSSAVPYSR.N
R1/RRR1-9/2	1184.116	1183.318	-171.189	0.425	844.221	0.513	16	0.227	-.MGNPDFYGPGK.T
R1/RRR1-9/2	1183.881	1183.318	-370.202	0.401	848.845	0.499	16	0.224	-.MGNPDFYGPGK.T
R1/RRR1-9/2	1198.391	1199.318	-1612.803	0.426	866.048	0.410	17	0.214	-.M*GNPDFYGPGK.T
R1/RRR1-9/2	1183.837	1183.318	-408.069	0.356	839.108	0.404	16	0.209	-.MGNPDFYGPGK.T
R1/RRR1-9/2	1378.712	1377.528	134.041	0.358	1057.195	0.351	17	0.209	K.EVGGFTQLDAAIR.I
R1/RRR1-9/2	1198.904	1199.318	-345.778	0.319	816.541	0.392	15	0.205	-.M*GNPDFYGPGK.T
R1/RRR1-9/2	1198.493	1199.318	-1527.465	0.334	928.416	0.327	16	0.203	-.M*GNPDFYGPGK.T
R1/RRR1-9/2	1376.443	1377.528	-1519.166	0.283	467.447	0.348	12	0.184	K.EVGGFTQLDAAIR.I
R1/RRR1-22/2	1308.187	1307.502	-242.103	0.475	1154.046	0.481	19	0.243	R.LM*GSLTNTQGLR.F
R1/RRR1-22/2	1307.094	1307.502	-313.589	0.459	871.473	0.501	17	0.225	R.LM*GSLTNTQGLR.F
R1/RRR1-22/2	1306.948	1307.502	-1192.916	0.405	952.125	0.474	18	0.225	R.LM*GSLTNTQGLR.F
R1/RRR1-22/2	747.338	747.908	-2107.530	0.356	920.338	0.349	12	0.207	R.FGVVVAR.F
R1/RRR1-22/2	747.412	747.908	-666.086	0.359	793.075	0.367	11	0.204	R.FGVVVAR.F
R1/RRR1-22/2	747.687	747.908	-296.740	0.407	764.144	0.342	11	0.202	R.FGVVVAR.F
R1/RRR1-12/2	1343.624	1342.525	73.664	0.456	1823.522	0.319	18	0.282	-.WGLEQGQSVLPK.-
R1/RRR1-12/2	1788.716	1788.978	-146.523	0.506	1569.080	0.491	21	0.288	K.TPSLIFEYVNNTDFK.V
R1/RRR1-12/2	1427.430	1426.680	-175.546	0.449	1080.042	0.428	17	0.223	K.ILQNLCGGPNIVK.L
R1/RRR1-12/2	1279.179	1279.421	-189.765	0.507	1053.765	0.576	20	0.257	R.LVGDVDFAEVSK.V
R1/RRR1-12/2	1466.169	1466.834	-1138.930	0.367	1216.151	0.493	21	0.247	R.SNIVGLPVSLLLLK.A
R1/RRR1-12/2	1279.154	1279.421	-209.487	0.486	985.987	0.553	20	0.246	R.LVGDVDFAEVSK.V
R1/RRR1-12/2	1278.719	1279.421	-1335.188	0.444	1046.181	0.518	20	0.243	R.LVGDVDFAEVSK.V
R1/RRR1-12/2	1279.764	1279.421	269.160	0.486	932.980	0.551	19	0.241	R.LVGDVDFAEVSK.V
R1/RRR1-12/2	1466.361	1466.834	-323.184	0.411	1075.552	0.511	20	0.239	R.SNIVGLPVSLLLLK.A
R1/RRR1-12/2	1466.472	1466.834	-247.350	0.453	958.948	0.547	19	0.237	R.SNIVGLPVSLLLLK.A
R1/RRR1-10/2	1224.030	1224.262	-190.513	0.489	1925.139	0.335	18	0.292	R.GDSVDQFSNVR.H
R1/RRR1-10/2	1223.626	1224.262	-1340.970	0.494	1501.420	0.337	17	0.242	R.GDSVDQFSNVR.H
R1/RRR1-10/2	971.632	972.209	-1627.133	0.393	375.170	0.462	14	0.208	K.GLPILGVFR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1223.226	1224.262	-1669.815	0.376	1217.287	0.264	16	0.207	R.GDSVDQFSNVR.H
R1/RRR1-10/2	971.567	972.209	-1695.294	0.401	449.284	0.420	14	0.205	K.GLPILGVFR.S
R1/RRR1-10/2	971.771	972.209	-451.510	0.385	404.698	0.399	14	0.204	K.GLPILGVFR.S
R1/RRR1-12/2	1449.361	1449.588	-156.755	0.533	1466.047	0.514	19	0.281	K.DGTTLLWDLTEGK.M
R1/RRR1-12/2	1450.261	1449.588	-226.054	0.570	1397.573	0.514	19	0.272	K.DGTTLLWDLTEGK.M
R1/RRR1-12/2	1449.161	1449.588	-295.168	0.446	1080.715	0.473	17	0.232	K.DGTTLLWDLTEGK.M
R1/RRR1-12/3	1771.980	1771.992	-6.890	0.503	1058.020	0.644	28	0.165	K.LDAGAIIHSLCFSPNR.Y
R1/RRR1-12/3	1772.078	1771.992	48.867	0.520	1015.030	0.618	29	0.152	K.LDAGAIIHSLCFSPNR.Y
R1/RRR1-12/3	1771.782	1771.992	-118.528	0.418	676.383	0.472	25	0.098	K.LDAGAIIHSLCFSPNR.Y
R1/RRR1-18/2	1591.115	1590.716	251.580	0.509	1416.050	0.516	24	0.276	R.EYVAEGSAPALPETR.R
R1/RRR1-17/2	1591.159	1590.716	279.351	0.488	1428.150	0.470	24	0.266	R.EYVAEGSAPALPETR.R
R1/RRR1-19/2	1590.159	1590.716	-982.213	0.467	1399.493	0.462	24	0.261	R.EYVAEGSAPALPETR.R
R1/RRR1-17/2	1590.216	1590.716	-315.259	0.474	1290.498	0.507	23	0.260	R.EYVAEGSAPALPETR.R
R1/RRR1-18/2	1590.272	1590.716	-280.294	0.489	1280.557	0.502	23	0.258	R.EYVAEGSAPALPETR.R
R1/RRR1-17/2	1591.146	1590.716	270.812	0.538	1171.962	0.540	22	0.256	R.EYVAEGSAPALPETR.R
R1/RRR1-19/2	1591.167	1590.716	284.505	0.509	1143.038	0.499	22	0.245	R.EYVAEGSAPALPETR.R
R1/RRR1-21/2	1590.347	1590.716	-233.011	0.411	1251.974	0.452	23	0.244	R.EYVAEGSAPALPETR.R
R1/RRR1-21/2	1590.241	1590.716	-299.779	0.418	1282.778	0.428	23	0.242	R.EYVAEGSAPALPETR.R
R1/RRR1-18/2	1590.044	1590.716	-1054.743	0.371	1272.103	0.420	22	0.238	R.EYVAEGSAPALPETR.R
R1/RRR1-19/2	1590.209	1590.716	-950.692	0.480	1101.753	0.469	22	0.236	R.EYVAEGSAPALPETR.R
R1/RRR1-17/2	1542.883	1542.890	-5.048	0.460	992.095	0.482	19	0.229	R.LLELGVKPVFLTGR.T
R1/RRR1-18/2	1542.120	1542.890	-1151.752	0.476	828.885	0.485	18	0.220	R.LLELGVKPVFLTGR.T
R1/RRR1-18/2	1542.345	1542.890	-1004.883	0.409	994.664	0.429	18	0.219	R.LLELGVKPVFLTGR.T
R1/RRR1-18/2	1542.731	1542.890	-103.538	0.452	847.121	0.472	17	0.217	R.LLELGVKPVFLTGR.T
R1/RRR1-17/2	1542.258	1542.890	-1061.623	0.387	869.855	0.429	18	0.213	R.LLELGVKPVFLTGR.T
R1/RRR1-21/2	1541.849	1542.890	-1327.924	0.374	809.636	0.423	16	0.207	R.LLELGVKPVFLTGR.T
R1/RRR1-21/2	1542.523	1542.890	-239.124	0.411	782.784	0.408	17	0.206	R.LLELGVKPVFLTGR.T
R1/RRR1-21/2	1544.206	1542.890	205.148	0.344	597.651	0.456	16	0.204	R.LLELGVKPVFLTGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1541.996	1542.890	-1232.119	0.404	958.869	0.332	18	0.203	R.LLELGVKPVFLTGR.T
R1/RRR1-17/2	1541.360	1542.890	-2297.521	0.312	877.059	0.307	18	0.198	R.LLELGVKPVFLTGR.T
R1/RRR1-18/2	1542.914	1542.890	15.664	0.327	538.609	0.304	13	0.188	R.LLELGVKPVFLTGR.T
R1/RRR1-18/3	1541.455	1542.890	-1584.749	0.436	1611.771	0.477	28	0.183	R.LLELGVKPVFLTGR.T
R1/RRR1-17/3	1542.905	1542.890	9.664	0.479	1295.056	0.445	25	0.137	R.LLELGVKPVFLTGR.T
R1/RRR1-17/3	1542.063	1542.890	-1188.604	0.342	1452.706	0.397	27	0.136	R.LLELGVKPVFLTGR.T
R1/RRR1-18/3	1541.555	1542.890	-1519.479	0.416	1348.292	0.430	27	0.134	R.LLELGVKPVFLTGR.T
R1/RRR1-18/3	1541.559	1542.890	-1516.734	0.367	1230.343	0.422	26	0.120	R.LLELGVKPVFLTGR.T
R1/RRR1-19/3	1542.218	1542.890	-1087.858	0.341	1077.854	0.419	26	0.107	R.LLELGVKPVFLTGR.T
R1/RRR1-18/3	1541.815	1542.890	-1349.959	0.300	715.034	0.263	21	0.076	-.LLELGVKPVFLTGR.-
R1/RRR1-21/3	1541.523	1542.890	-1540.479	0.316	747.998	0.240	20	0.073	-.LLELGVKPVFLTGR.-
R1/RRR1-6/2	1488.376	1488.622	-166.055	0.480	1939.075	0.561	23	0.365	K.IDSPSGVDVTVSPSK.L
R1/RRR1-5/2	1337.143	1337.421	-208.093	0.494	1589.214	0.533	21	0.303	R.NVGSNANAVYEAK.I
R1/RRR1-6/2	1337.039	1337.421	-286.038	0.500	1496.789	0.538	21	0.292	R.NVGSNANAVYEAK.I
R1/RRR1-6/2	1337.139	1337.421	-211.116	0.541	1387.630	0.565	20	0.286	R.NVGSNANAVYEAK.I
R1/RRR1-6/2	1337.161	1337.421	-194.356	0.481	1500.099	0.503	21	0.283	R.NVGSNANAVYEAK.I
R1/RRR1-6/2	1488.129	1488.622	-332.279	0.411	1298.806	0.549	21	0.268	K.IDSPSGVDVTVSPSK.L
R1/RRR1-6/2	1488.191	1488.622	-290.717	0.434	1333.229	0.525	21	0.267	K.IDSPSGVDVTVSPSK.L
R1/RRR1-5/2	1336.956	1337.421	-348.512	0.445	1174.783	0.501	19	0.247	R.NVGSNANAVYEAK.I
R1/RRR1-19/2	844.944	844.976	-38.271	0.350	1120.764	0.317	13	0.209	R.VGDVVDIK.A
R1/RRR1-19/2	937.264	937.075	202.726	0.366	720.068	0.387	14	0.203	K.TGVVYNVGK.A
R1/RRR1-19/2	937.021	937.075	-57.638	0.293	436.699	0.362	12	0.182	-.TGVVYNVGK.-
R1/RRR1-8/2	1197.989	1198.351	-303.397	0.451	1022.576	0.599	17	0.253	R.VVDALGNPIDGK.G
R1/RRR1-9/2	1198.392	1198.351	34.266	0.492	993.266	0.593	17	0.251	R.VVDALGNPIDGK.G
R1/RRR1-8/2	1197.618	1198.351	-1451.470	0.424	990.972	0.558	17	0.242	R.VVDALGNPIDGK.G
R1/RRR1-8/2	723.888	723.887	1.419	0.406	535.560	0.438	10	0.209	K.APGIIPR.L
R1/RRR1-8/2	723.698	723.887	-261.489	0.370	640.268	0.405	11	0.207	K.APGIIPR.L
R1/RRR1-9/2	723.801	723.887	-118.175	0.436	656.501	0.346	11	0.204	K.APGIIPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	723.826	723.887	-84.003	0.371	533.996	0.335	10	0.200	K.APGIIPR.L
R1/RRR1-8/2	723.873	723.887	-19.470	0.342	582.577	0.299	11	0.198	K.APGIIPR.L
R1/RRR1-9/2	723.325	723.887	-2165.902	0.314	472.278	0.313	10	0.197	K.APGIIPR.L
R1/RRR1-23/2	1189.992	1190.289	-250.391	0.490	1202.947	0.470	18	0.244	K.AGNLGDSVTVTR.D
R1/RRR1-23/2	1189.573	1190.289	-1447.082	0.447	1154.971	0.478	19	0.242	K.AGNLGDSVTVTR.D
R1/RRR1-23/2	1189.503	1190.289	-1505.838	0.373	1021.550	0.502	18	0.233	K.AGNLGDSVTVTR.D
R1/RRR1-22/2	1559.010	1559.526	-975.529	0.313	1169.915	0.359	16	0.132	R.YFNIAENEGEEED.-
R1/RRR1-22/2	1558.944	1559.526	-1018.216	0.352	1046.529	0.325	16	0.108	R.YFNIAENEGEEED.-
R1/RRR1-22/2	1558.812	1559.526	-1102.895	0.255	1038.531	0.273	16	0.104	R.YFNIAENEGEEED.-
R1/RRR1-14/2	1382.026	1382.549	-1105.594	0.440	1546.244	0.418	20	0.268	R.IPTGELWAGNPAR.F
R1/RRR1-14/3	1462.831	1461.706	85.347	0.533	1676.797	0.362	24	0.159	R.KLTNEEIM*EIPK.L
R1/RRR1-14/3	1461.573	1461.706	-91.209	0.459	1821.161	0.237	24	0.140	R.KLTNEEIM*EIPK.L
R1/RRR1-20/2	1412.998	1412.617	270.296	0.503	1609.491	0.418	19	0.275	K.IFFIAWSPSTSR.I
R1/RRR1-20/2	1412.182	1412.617	-309.053	0.435	1629.964	0.383	19	0.268	K.IFFIAWSPSTSR.I
R1/RRR1-20/3	1602.240	1602.712	-295.663	0.418	1396.059	0.396	30	0.132	R.SHSNASSGM*GVAPDIR.D
R1/RRR1-20/3	1602.109	1602.712	-1003.470	0.360	701.224	0.266	23	0.072	-.SHSNASSGM*GVAPDIR.-
R1/RRR1-16/2	1465.617	1464.730	-76.991	0.495	1094.699	0.469	18	0.236	K.QSIGCLFWLLAR.M
R1/RRR1-16/2	1203.564	1204.357	-1494.145	0.321	1381.729	0.356	17	0.235	R.YVDIGIPANNK.G
R1/RRR1-15/2	1204.010	1204.357	-289.474	0.346	1031.237	0.419	16	0.219	R.YVDIGIPANNK.G
R1/RRR1-11/2	1204.291	1204.357	-55.165	0.402	976.621	0.376	16	0.212	R.YVDIGIPANNK.G
R1/RRR1-16/2	1203.993	1204.357	-303.715	0.349	887.079	0.393	15	0.208	R.YVDIGIPANNK.G
R1/RRR1-13/2	1466.138	1464.730	279.455	0.447	680.060	0.436	16	0.207	K.QSIGCLFWLLAR.M
R1/RRR1-13/2	1466.027	1464.730	203.394	0.465	417.040	0.438	13	0.199	K.QSIGCLFWLLAR.M
R1/RRR1-15/2	1465.381	1464.730	-238.761	0.384	424.561	0.293	14	0.191	K.QSIGCLFWLLAR.M
R1/RRR1-16/2	1772.943	1772.978	-19.655	0.531	1528.952	0.536	24	0.293	R.NQDVSLTELPATVSAVK.N
R1/RRR1-16/2	1772.836	1772.978	-80.431	0.561	1430.798	0.556	24	0.286	R.NQDVSLTELPATVSAVK.N
R1/RRR1-17/2	1772.425	1772.978	-878.928	0.532	1297.414	0.575	23	0.275	R.NQDVSLTELPATVSAVK.N
R1/RRR1-16/2	1773.558	1772.978	-237.520	0.549	1361.590	0.547	23	0.274	R.NQDVSLTELPATVSAVK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1772.478	1772.978	-849.061	0.519	1331.521	0.518	23	0.264	R.NQDVSLTELPATVSAVK.N
R1/RRR1-15/2	1144.225	1144.346	-106.641	0.502	2362.303	0.630	22	0.476	K.VAVITGAASGIGK.A
R1/RRR1-15/2	1144.109	1144.346	-207.781	0.505	2126.591	0.656	22	0.435	K.VAVITGAASGIGK.A
R1/RRR1-15/2	1143.632	1144.346	-1503.178	0.460	2143.152	0.651	22	0.435	K.VAVITGAASGIGK.A
R1/RRR1-16/2	1144.018	1144.346	-287.637	0.304	1431.976	0.540	20	0.276	K.VAVITGAASGIGK.A
R1/RRR1-3/2	1145.127	1144.346	-192.414	0.273	736.741	0.286	17	0.191	-.VAVITGAASGIGK.-
R1/RRR1-13/2	1115.083	1115.267	-165.866	0.413	1147.809	0.607	19	0.266	R.AHAYAAAVAAAK.G
R1/RRR1-13/2	1114.952	1115.267	-283.275	0.415	941.110	0.643	18	0.254	R.AHAYAAAVAAAK.G
R1/RRR1-13/2	1114.551	1115.267	-1544.378	0.356	806.742	0.551	17	0.224	R.AHAYAAAVAAAK.G
R1/RRR1-13/2	1132.658	1133.196	-1361.543	0.337	804.713	0.419	16	0.209	R.DVHLGDYSAR.L
R1/RRR1-13/2	1132.809	1133.196	-342.795	0.355	647.042	0.366	14	0.198	R.DVHLGDYSAR.L
R1/RRR1-13/2	1132.752	1133.196	-393.505	0.338	356.367	0.295	13	0.192	-.DVHLGDYSAR.-
R1/RRR1-13/3	1114.989	1115.267	-250.006	0.390	1238.522	0.310	22	0.097	R.AHAYAAAVAAAK.G
R1/RRR1-14/2	1808.481	1808.027	251.334	0.555	1324.478	0.586	23	0.281	R.EIPLNYATFQPGTTVR.D
R1/RRR1-13/2	1588.384	1588.791	-257.502	0.483	1556.814	0.423	21	0.268	R.DNVQAYWPNVIIR.Y
R1/RRR1-14/2	1589.277	1588.791	306.569	0.544	1488.461	0.459	20	0.268	R.DNVQAYWPNVIIR.Y
R1/RRR1-14/2	1588.289	1588.791	-948.835	0.480	1600.005	0.407	20	0.268	R.DNVQAYWPNVIIR.Y
R1/RRR1-14/2	1589.400	1588.791	-247.169	0.551	1308.653	0.436	19	0.244	R.DNVQAYWPNVIIR.Y
R1/RRR1-14/2	1589.837	1588.791	29.064	0.604	1146.944	0.461	18	0.233	R.DNVQAYWPNVIIR.Y
R1/RRR1-13/2	1588.270	1588.791	-960.486	0.491	1175.419	0.428	18	0.232	R.DNVQAYWPNVIIR.Y
R1/RRR1-13/2	1587.778	1588.791	-1271.776	0.389	1166.155	0.406	18	0.228	R.DNVQAYWPNVIIR.Y
R1/RRR1-14/2	1807.476	1808.027	-860.732	0.439	907.959	0.481	22	0.224	R.EIPLNYATFQPGTTVR.D
R1/RRR1-13/2	1808.266	1808.027	132.195	0.512	634.663	0.575	19	0.223	R.EIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1588.273	1588.791	-958.943	0.445	1084.420	0.383	18	0.219	R.DNVQAYWPNVIIR.Y
R1/RRR1-3/2	1589.711	1588.791	-50.725	0.476	1141.169	0.368	17	0.217	R.DNVQAYWPNVIIR.Y
R1/RRR1-14/2	1808.419	1808.027	216.949	0.540	647.737	0.515	20	0.217	R.EIPLNYATFQPGTTVR.D
R1/RRR1-13/2	1808.417	1808.027	216.204	0.459	595.676	0.531	19	0.216	R.EIPLNYATFQPGTTVR.D
R1/RRR1-13/2	1807.352	1808.027	-929.687	0.414	671.181	0.501	20	0.215	R.EIPLNYATFQPGTTVR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1809.061	1808.027	18.435	0.504	579.697	0.534	18	0.214	R.EIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1807.390	1808.027	-908.871	0.436	772.431	0.459	21	0.214	R.EIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1807.652	1808.027	-208.522	0.427	513.967	0.554	18	0.214	R.EIPLNYATFQPGTTVR.D
R1/RRR1-1/2	1589.449	1588.791	-215.810	0.449	1009.621	0.394	16	0.214	R.DNVQAYWPNVIIR.Y
R1/RRR1-14/2	1807.921	1808.027	-58.757	0.486	423.296	0.548	17	0.211	R.EIPLNYATFQPGTTVR.D
R1/RRR1-13/2	1808.860	1808.027	-92.637	0.535	424.865	0.554	16	0.210	R.EIPLNYATFQPGTTVR.D
R1/RRR1-12/2	1588.648	1588.791	-90.527	0.458	911.815	0.391	16	0.209	R.DNVQAYWPNVIIR.Y
R1/RRR1-5/2	1589.885	1588.791	59.019	0.386	634.861	0.338	13	0.193	R.DNVQAYWPNVIIR.Y
R1/RRR1-19/2	1589.807	1588.791	9.657	0.369	246.489	0.420	12	0.193	-.DNVQAYWPNVIIR.-
R1/RRR1-14/2	1587.787	1588.791	-1266.140	0.297	723.430	0.223	15	0.188	R.DNVQAYWPNVIIR.Y
R1/RRR1-13/2	1588.607	1588.791	-116.579	0.317	679.827	0.213	14	0.186	R.DNVQAYWPNVIIR.Y
R1/RRR1-9/2	1422.005	1422.469	-327.238	0.513	1301.748	0.534	20	0.270	K.YGTGYCDAQCAR.D
R1/RRR1-9/2	1421.998	1422.469	-332.147	0.522	1090.767	0.582	20	0.261	K.YGTGYCDAQCAR.D
R1/RRR1-9/2	1421.316	1422.469	-1519.185	0.453	1027.536	0.545	18	0.244	K.YGTGYCDAQCAR.D
R1/RRR1-9/3	1637.402	1636.793	-239.558	0.548	1248.959	0.518	27	0.150	K.FVQKHEYGTNIGSR.M
R1/RRR1-9/3	1636.268	1636.793	-934.939	0.479	1414.676	0.403	27	0.136	K.FVQKHEYGTNIGSR.M
R1/RRR1-9/3	1636.645	1636.793	-90.723	0.539	1064.117	0.517	26	0.132	K.FVQKHEYGTNIGSR.M
R1/RRR1-8/3	1636.490	1636.793	-185.898	0.350	388.707	0.389	21	0.091	K.FVQKHEYGTNIGSR.M
R1/RRR1-8/3	1636.385	1636.793	-249.995	0.362	367.957	0.338	21	0.090	K.FVQKHEYGTNIGSR.M
R1/RRR1-8/3	1635.768	1636.793	-1241.846	0.409	547.786	0.363	23	0.088	K.FVQKHEYGTNIGSR.M
R1/RRR1-15/2	1730.328	1730.852	-883.259	0.556	2305.956	0.599	24	0.444	R.SGTALCSYIASTAQSGR.I
R1/RRR1-15/2	1730.378	1730.852	-274.581	0.538	2335.535	0.579	24	0.443	R.SGTALCSYIASTAQSGR.I
R1/RRR1-14/2	1730.396	1730.852	-264.318	0.532	2078.274	0.614	23	0.403	R.SGTALCSYIASTAQSGR.I
R1/RRR1-15/2	1731.372	1730.852	-277.888	0.574	2012.308	0.608	22	0.387	R.SGTALCSYIASTAQSGR.I
R1/RRR1-16/2	1730.277	1730.852	-912.792	0.518	2009.507	0.605	22	0.386	R.SGTALCSYIASTAQSGR.I
R1/RRR1-15/2	1730.252	1730.852	-927.453	0.542	2031.083	0.585	23	0.383	R.SGTALCSYIASTAQSGR.I
R1/RRR1-15/2	1729.658	1730.852	-1272.361	0.489	2003.841	0.574	24	0.376	R.SGTALCSYIASTAQSGR.I
R1/RRR1-14/2	1931.296	1930.151	75.403	0.480	1854.485	0.569	26	0.374	R.ISGIPSGTVNLLAFNGNPSA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1730.282	1730.852	-909.959	0.522	1832.908	0.589	22	0.350	R.SGTALCSYIASTAQSGR.I
R1/RRR1-14/2	1930.266	1930.151	59.966	0.434	1791.006	0.553	26	0.346	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/2	1730.347	1730.852	-872.352	0.510	1841.301	0.566	22	0.344	R.SGTALCSYIASTAQSGR.I
R1/RRR1-14/3	1930.078	1930.151	-37.727	0.442	1418.837	0.475	33	0.343	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/2	1731.669	1730.852	-105.746	0.570	1621.850	0.649	21	0.334	R.SGTALCSYIASTAQSGR.I
R1/RRR1-15/2	1930.753	1930.151	-206.895	0.453	1713.232	0.568	25	0.321	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-15/2	1930.461	1930.151	161.311	0.491	1701.200	0.587	26	0.319	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-15/2	1731.420	1730.852	-250.302	0.518	1550.347	0.583	20	0.303	R.SGTALCSYIASTAQSGR.I
R1/RRR1-15/2	1929.555	1930.151	-829.690	0.371	1672.581	0.528	26	0.299	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/2	1930.349	1930.151	103.030	0.476	1501.168	0.594	25	0.256	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-15/3	1929.816	1930.151	-174.201	0.428	1259.001	0.362	31	0.233	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/2	1930.373	1930.151	115.207	0.425	1458.943	0.530	24	0.231	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/3	1930.831	1930.151	-166.247	0.479	1211.048	0.462	31	0.229	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-15/2	1930.532	1930.151	198.089	0.467	1373.116	0.607	24	0.225	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-15/3	1930.581	1930.151	223.318	0.408	1097.005	0.403	31	0.176	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/2	1929.654	1930.151	-258.280	0.396	1213.563	0.515	23	0.173	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-15/2	1929.516	1930.151	-849.758	0.382	1177.507	0.522	23	0.169	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/3	1930.736	1930.151	-215.338	0.313	1159.367	0.169	28	0.164	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-15/2	1930.428	1930.151	143.808	0.407	1037.662	0.581	21	0.157	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/3	1930.295	1930.151	75.022	0.387	1045.334	0.360	30	0.150	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/2	1931.177	1930.151	13.656	0.435	986.707	0.518	21	0.140	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-14/2	1928.943	1930.151	-1147.828	0.279	557.225	0.412	17	0.119	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-13/2	1931.650	1930.151	258.950	0.387	643.705	0.177	18	0.091	-.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-13/2	1931.874	1930.151	-143.714	0.359	683.500	0.086	18	0.085	R.ISGIPSGTVNLLAFNGNPSA.-
R1/RRR1-16/3	1980.920	1981.147	-114.884	0.530	1364.077	0.555	30	0.185	K.DLSVIATEVGEEGQEYLK.L
R1/RRR1-16/3	1244.953	1245.408	-366.558	0.458	1813.880	0.308	24	0.155	R.AREVLLEASEK.L
R1/RRR1-16/3	1245.392	1245.408	-12.655	0.459	1237.230	0.304	21	0.096	R.AREVLLEASEK.L
R1/RRR1-16/3	1245.545	1245.408	110.762	0.529	1039.591	0.341	20	0.093	R.AREVLLEASEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1094.215	1093.215	0.156	0.511	1790.475	0.509	18	0.325	K.IGYDNAAAVAK.K
R1/RRR1-9/2	1092.947	1093.215	-245.513	0.470	1498.170	0.488	17	0.279	K.IGYDNAAAVAK.K
R1/RRR1-9/2	1092.437	1093.215	-1632.351	0.435	1526.017	0.451	17	0.272	K.IGYDNAAAVAK.K
R1/RRR1-9/2	1166.192	1166.306	-98.228	0.434	507.774	0.473	15	0.207	R.LLGDASVSFEK.N
R1/RRR1-2/2	1093.871	1093.215	-315.710	0.323	640.731	0.338	14	0.194	K.IGYDNAAAVAK.K
R1/RRR1-9/2	1165.970	1166.306	-289.047	0.278	754.968	0.252	14	0.186	R.LLGDASVSFEK.N
R1/RRR1-17/2	1586.301	1586.726	-268.569	0.465	1082.930	0.595	24	0.259	K.DLALPVSGVSAEENGK.A
R1/RRR1-16/2	1587.209	1586.726	305.117	0.510	767.140	0.530	21	0.223	K.DLALPVSGVSAEENGK.A
R1/RRR1-16/2	1586.451	1586.726	-173.617	0.467	763.909	0.502	21	0.218	K.DLALPVSGVSAEENGK.A
R1/RRR1-16/2	1586.093	1586.726	-1032.359	0.396	869.996	0.434	21	0.212	K.DLALPVSGVSAEENGK.A
R1/RRR1-16/2	1417.659	1417.675	-11.280	0.356	913.326	0.359	16	0.199	K.EVVVYATVALPAGK.G
R1/RRR1-12/1	963.558	964.183	-1692.153	0.230	753.979	0.374	12	0.343	R.TALAFVTLK.S
R1/RRR1-12/1	963.539	964.183	-1712.137	0.222	722.576	0.342	12	0.312	R.TALAFVTLK.S
R1/RRR1-12/1	963.598	964.183	-1650.279	0.296	647.471	0.399	11	0.280	-.TALAFVTLK.-
R1/RRR1-12/2	963.968	964.183	-223.938	0.497	969.416	0.453	15	0.227	R.TALAFVTLK.S
R1/RRR1-12/2	964.177	964.183	-6.617	0.523	972.198	0.449	15	0.227	R.TALAFVTLK.S
R1/RRR1-12/2	963.986	964.183	-205.517	0.472	994.560	0.437	15	0.226	R.TALAFVTLK.S
R1/RRR1-12/3	1794.087	1794.037	27.795	0.468	1597.151	0.316	29	0.135	K.IFHYGSISLITEPCR.-
R1/RRR1-12/3	1793.342	1794.037	-947.881	0.433	848.120	0.162	23	0.062	-.IFHYGSISLITEPCR.-
R1/RRR1-10/2	1275.161	1275.434	-214.463	0.465	1427.185	0.532	19	0.282	K.EIVGSIQSQVSK.I
R1/RRR1-10/2	1274.946	1275.434	-383.613	0.451	1346.130	0.483	18	0.260	K.EIVGSIQSQVSK.I
R1/RRR1-10/2	1777.622	1776.068	-251.924	0.470	861.974	0.554	25	0.235	R.YGLPPSFLSAVLAPSQK.G
R1/RRR1-10/2	1775.480	1776.068	-897.276	0.438	734.735	0.548	23	0.224	R.YGLPPSFLSAVLAPSQK.G
R1/RRR1-10/2	1775.767	1776.068	-170.414	0.472	662.734	0.489	23	0.214	R.YGLPPSFLSAVLAPSQK.G
R1/RRR1-10/2	1775.848	1776.068	-124.626	0.332	267.401	0.471	15	0.193	-.YGLPPSFLSAVLAPSQK.-
R1/RRR1-10/2	1775.776	1776.068	-165.311	0.262	296.692	0.412	16	0.191	R.YGLPPSFLSAVLAPSQK.G
R1/RRR1-10/2	1775.903	1776.068	-93.184	0.313	424.221	0.362	17	0.191	R.YGLPPSFLSAVLAPSQK.G
R1/RRR1-11/2	1319.231	1319.491	-197.833	0.435	1615.728	0.428	18	0.277	R.AAIFNQVEASLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1318.661	1319.491	-1392.422	0.348	1661.071	0.405	17	0.275	R.AAIFNQVEASLR.R
R1/RRR1-11/2	1319.201	1319.491	-220.483	0.360	1410.711	0.334	17	0.233	R.AAIFNQVEASLR.R
R1/RRR1-11/3	1773.419	1771.998	238.207	0.408	1040.545	0.300	22	0.086	R.RLDTDYIDLLQIHR.F
R1/RRR1-11/3	1773.490	1771.998	278.170	0.325	744.154	0.201	19	0.065	-.RLDTDYIDLLQIHR.-
R1/RRR1-13/2	1218.170	1217.442	-223.994	0.581	1802.763	0.443	18	0.305	R.EALFVLAQLGR.K
R1/RRR1-13/2	1217.303	1217.442	-115.025	0.516	1728.032	0.470	18	0.305	R.EALFVLAQLGR.K
R1/RRR1-13/2	1289.875	1290.493	-1258.619	0.482	1302.662	0.422	16	0.242	R.YQILAGVIEQR.M
R1/RRR1-13/2	1290.150	1290.493	-267.204	0.463	1280.545	0.400	16	0.236	R.YQILAGVIEQR.M
R1/RRR1-13/2	1216.803	1217.442	-1351.207	0.376	1212.222	0.364	16	0.223	R.EALFVLAQLGR.K
R1/RRR1-18/2	1611.828	1611.847	-11.740	0.456	388.543	0.573	20	0.222	R.VIPNFM*LQGGDFTR.G
R1/RRR1-18/2	1596.101	1595.847	159.279	0.465	523.823	0.506	21	0.219	R.VIPNFMLQGGDFTR.G
R1/RRR1-19/2	1596.028	1595.847	113.796	0.409	599.724	0.502	21	0.218	R.VIPNFMLQGGDFTR.G
R1/RRR1-17/2	1595.146	1595.847	-1069.868	0.380	605.536	0.479	21	0.214	R.VIPNFMLQGGDFTR.G
R1/RRR1-18/2	1612.206	1611.847	223.574	0.386	319.902	0.510	20	0.214	R.VIPNFM*LQGGDFTR.G
R1/RRR1-21/2	1269.536	1269.300	186.363	0.349	783.464	0.432	17	0.210	R.GNGTGGESIYGEK.-
R1/RRR1-20/2	1270.091	1269.300	-164.710	0.385	724.688	0.428	16	0.208	R.GNGTGGESIYGEK.-
R1/RRR1-18/2	1611.311	1611.847	-955.751	0.299	333.003	0.476	20	0.207	R.VIPNFM*LQGGDFTR.G
R1/RRR1-17/2	1594.892	1595.847	-1229.715	0.349	431.448	0.432	19	0.206	R.VIPNFMLQGGDFTR.G
R1/RRR1-20/2	1270.056	1269.300	-192.671	0.396	716.670	0.412	15	0.204	R.GNGTGGESIYGEK.-
R1/RRR1-20/2	1269.065	1269.300	-185.972	0.421	439.652	0.410	16	0.204	R.GNGTGGESIYGEK.-
R1/RRR1-17/2	1612.010	1611.847	101.545	0.284	254.519	0.430	18	0.203	R.VIPNFM*LQGGDFTR.G
R1/RRR1-19/2	1611.290	1611.847	-968.833	0.303	277.957	0.391	18	0.203	R.VIPNFM*LQGGDFTR.G
R1/RRR1-20/2	1269.977	1269.300	-255.156	0.367	717.815	0.389	16	0.203	R.GNGTGGESIYGEK.-
R1/RRR1-20/2	1269.030	1269.300	-213.281	0.320	460.566	0.439	16	0.203	R.GNGTGGESIYGEK.-
R1/RRR1-18/2	1594.798	1595.847	-1289.056	0.318	407.120	0.396	19	0.203	R.VIPNFMLQGGDFTR.G
R1/RRR1-21/2	1268.872	1269.300	-338.072	0.356	440.071	0.391	16	0.202	R.GNGTGGESIYGEK.-
R1/RRR1-20/2	1269.031	1269.300	-212.605	0.449	512.044	0.363	17	0.202	R.GNGTGGESIYGEK.-
R1/RRR1-18/2	1594.788	1595.847	-1294.822	0.289	491.045	0.357	21	0.201	R.VIPNFMLQGGDFTR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-20/2	1268.930	1269.300	-292.418	0.380	467.850	0.368	16	0.201	R.GNGTGGESIYGEK.-
R1/RRR1-18/2	1611.275	1611.847	-978.265	0.252	166.658	0.343	14	0.199	R.VIPNFM*LQGGDFTR.G
R1/RRR1-21/2	1270.193	1269.300	-84.498	0.401	652.068	0.351	16	0.199	R.GNGTGGESIYGEK.-
R1/RRR1-21/2	1269.390	1269.300	71.220	0.267	613.644	0.400	16	0.199	R.GNGTGGESIYGEK.-
R1/RRR1-21/2	1268.938	1269.300	-285.951	0.305	473.949	0.364	16	0.198	R.GNGTGGESIYGEK.-
R1/RRR1-20/2	1268.962	1269.300	-267.131	0.286	554.940	0.362	17	0.198	R.GNGTGGESIYGEK.-
R1/RRR1-21/2	1268.638	1269.300	-1313.756	0.310	477.537	0.320	17	0.198	R.GNGTGGESIYGEK.-
R1/RRR1-17/2	1610.845	1611.847	-1246.529	0.186	303.193	0.366	18	0.195	R.VIPNFM*LQGGDFTR.G
R1/RRR1-7/2	820.901	820.959	-71.086	0.422	754.378	0.507	12	0.221	R.VGVVFSGR.Q
R1/RRR1-7/2	820.923	820.959	-44.387	0.400	746.770	0.479	12	0.216	R.VGVVFSGR.Q
R1/RRR1-7/2	1297.117	1297.526	-315.702	0.368	590.416	0.529	19	0.212	K.VVGVPVSLNGDLK.N
R1/RRR1-7/2	820.983	820.959	28.990	0.405	743.308	0.418	12	0.209	R.VGVVFSGR.Q
R1/RRR1-7/2	1297.267	1297.526	-200.238	0.378	425.262	0.504	16	0.203	K.VVGVPVSLNGDLK.N
R1/RRR1-20/1	1186.660	1187.411	-1480.597	0.319	942.951	0.466	15	0.551	K.AVVVLGSSEVVK.G
R1/RRR1-20/2	1188.047	1187.411	-307.276	0.501	1539.780	0.464	20	0.279	K.AVVVLGSSEVVK.G
R1/RRR1-20/2	1187.939	1187.411	-398.620	0.482	1421.435	0.464	19	0.265	K.AVVVLGSSEVVK.G
R1/RRR1-20/2	1336.179	1336.476	-222.996	0.492	1205.513	0.540	18	0.258	R.AVVVHADPDDLGK.G
R1/RRR1-20/2	1336.117	1336.476	-269.099	0.506	1155.031	0.524	18	0.250	R.AVVVHADPDDLGK.G
R1/RRR1-20/2	1336.176	1336.476	-224.829	0.493	1152.317	0.505	18	0.246	R.AVVVHADPDDLGK.G
R1/RRR1-19/2	1187.001	1187.411	-346.536	0.257	891.140	0.276	16	0.191	K.AVVVLGSSEVVK.G
R1/RRR1-15/2	1427.064	1427.542	-335.858	0.547	1392.003	0.588	19	0.236	K.NLKDEPVAAEQNV.-
R1/RRR1-15/2	1885.644	1886.138	-262.555	0.509	871.929	0.582	21	0.234	K.SGATVLPDLVAAQEWLSK.N
R1/RRR1-14/2	1437.489	1437.690	-139.993	0.431	1344.487	0.486	17	0.258	R.YLMIVEAIGSQGR.Y
R1/RRR1-14/2	1453.228	1453.689	-318.320	0.448	1407.525	0.416	18	0.249	R.YLM*IVEAIGSQGR.Y
R1/RRR1-14/2	1820.269	1819.141	70.181	0.518	676.424	0.571	18	0.220	K.LPNNAVAPSLFFFRPK.N
R1/RRR1-14/2	1818.644	1819.141	-274.450	0.458	611.078	0.489	17	0.204	K.LPNNAVAPSLFFFRPK.N
R1/RRR1-14/2	1438.121	1437.690	300.735	0.399	614.921	0.294	14	0.184	-.YLMIVEAIGSQGR.-
R1/RRR1-14/2	1437.286	1437.690	-281.762	0.276	440.260	0.341	12	0.184	-.YLMIVEAIGSQGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/3	1820.363	1819.141	122.397	0.550	934.670	0.566	28	0.135	K.LPNNAVAPSLFFFRPK.N
R1/RRR1-14/3	1818.779	1819.141	-199.579	0.511	974.005	0.535	28	0.130	K.LPNNAVAPSLFFFRPK.N
R1/RRR1-14/3	1819.898	1819.141	-134.299	0.528	862.060	0.545	27	0.126	K.LPNNAVAPSLFFFRPK.N
R1/RRR1-14/3	1819.779	1819.141	-199.806	0.474	1080.053	0.437	26	0.118	K.LPNNAVAPSLFFFRPK.N
R1/RRR1-15/3	1818.772	1819.141	-203.922	0.365	394.473	0.359	21	0.090	K.LPNNAVAPSLFFFRPK.N
R1/RRR1-15/3	1818.834	1819.141	-169.382	0.349	456.044	0.403	21	0.080	-.LPNNAVAPSLFFFRPK.-
R1/RRR1-22/2	950.095	950.031	68.479	0.420	1449.237	0.253	15	0.222	R.AFVVDGDAR.L
R1/RRR1-22/2	949.946	950.031	-89.527	0.438	1258.405	0.240	14	0.206	R.AFVVDGDAR.L
R1/RRR1-21/2	1359.685	1359.616	51.170	0.395	857.673	0.379	15	0.204	R.LM*FSLIDNVYK.Q
R1/RRR1-22/2	949.429	950.031	-1691.879	0.315	1425.189	0.141	15	0.201	R.AFVVDGDAR.L
R1/RRR1-22/2	1359.720	1359.616	76.922	0.241	927.571	0.113	16	0.179	R.LM*FSLIDNVYK.Q
R1/RRR1-23/2	1376.366	1377.546	-1588.681	0.433	2010.277	0.493	22	0.355	K.GTDPVAIDLGSM*GK.G
R1/RRR1-23/2	1377.081	1377.546	-339.113	0.516	1548.124	0.511	21	0.290	K.GTDPVAIDLGSM*GK.G
R1/RRR1-26/2	1724.413	1723.866	-263.460	0.523	1184.973	0.577	21	0.262	R.IGAQTSVFTVESGSPSR.S
R1/RRR1-24/2	1376.848	1377.546	-1236.959	0.317	859.543	0.475	18	0.213	K.GTDPVAIDLGSM*GK.G
R1/RRR1-11/2	1565.672	1564.871	-127.569	0.392	1343.422	0.413	18	0.240	K.VGGVM*ALLSFPSEIK.V
R1/RRR1-11/2	1566.203	1564.871	212.063	0.468	1327.057	0.405	18	0.236	K.VGGVM*ALLSFPSEIK.V
R1/RRR1-11/2	1235.790	1235.371	340.165	0.431	949.472	0.320	15	0.202	-.IDYINEALQR.-
R1/RRR1-11/2	1565.872	1564.871	0.055	0.266	449.913	0.290	13	0.182	K.VGGVM*ALLSFPSEIK.V
R1/RRR1-2/2	1060.532	1061.133	-1514.290	0.400	1228.299	0.352	15	0.225	R.EAQWATAQR.T
R1/RRR1-2/2	1118.030	1118.219	-170.028	0.498	1067.484	0.379	16	0.219	R.ELSEIAEQAK.R
R1/RRR1-3/2	1117.940	1118.219	-251.196	0.440	964.464	0.391	16	0.216	R.ELSEIAEQAK.R
R1/RRR1-1/2	1117.865	1118.219	-317.914	0.399	994.958	0.355	16	0.212	R.ELSEIAEQAK.R
R1/RRR1-3/2	1117.892	1118.219	-293.483	0.394	983.783	0.319	16	0.206	R.ELSEIAEQAK.R
R1/RRR1-1/2	1117.600	1118.219	-1453.179	0.383	946.362	0.311	15	0.203	R.ELSEIAEQAK.R
R1/RRR1-1/2	1117.999	1118.219	-197.740	0.412	867.637	0.329	15	0.203	R.ELSEIAEQAK.R
R1/RRR1-2/2	1060.858	1061.133	-260.326	0.334	1062.689	0.227	15	0.198	R.EAQWATAQR.T
R1/RRR1-2/2	1060.831	1061.133	-285.609	0.267	711.710	0.293	13	0.193	R.EAQWATAQR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1060.783	1061.133	-331.098	0.367	951.976	0.200	14	0.191	R.EAQWATAQR.T
R1/RRR1-1/2	1060.978	1061.133	-146.051	0.323	869.159	0.188	13	0.188	R.EAQWATAQR.T
R1/RRR1-3/2	1060.492	1061.133	-1552.215	0.291	618.947	0.142	12	0.185	-.EAQWATAQR.-
R1/RRR1-10/2	1485.728	1484.720	5.718	0.492	1041.674	0.503	21	0.239	K.FLPYIISSFGPDK.S
R1/RRR1-10/2	1485.046	1484.720	220.411	0.325	998.704	0.212	18	0.191	-.FLPYIISSFGPDK.-
R1/RRR1-10/3	1489.418	1489.612	-130.600	0.452	1216.828	0.316	27	0.095	K.FKNEPESGPQLDK.F
R1/RRR1-10/3	1489.260	1489.612	-236.545	0.393	680.854	0.316	20	0.071	-.FKNEPESGPQLDK.-
R1/RRR1-10/3	1489.299	1489.612	-210.766	0.316	695.153	0.205	21	0.069	-.FKNEPESGPQLDK.-
R1/RRR1-4/2	1396.389	1395.690	-215.713	0.514	1677.309	0.513	18	0.307	R.VTIDLLEM*VFAK.G
R1/RRR1-4/2	1396.306	1395.690	-275.352	0.551	1684.765	0.489	18	0.300	R.VTIDLLEM*VFAK.G
R1/RRR1-1/2	1396.324	1395.690	-262.459	0.541	1669.985	0.439	17	0.282	R.VTIDLLEM*VFAK.G
R1/RRR1-4/2	1395.179	1395.690	-1086.185	0.438	1668.130	0.418	17	0.279	R.VTIDLLEM*VFAK.G
R1/RRR1-4/2	1395.679	1395.690	-7.825	0.485	1581.739	0.423	17	0.269	R.VTIDLLEM*VFAK.G
R1/RRR1-4/2	1380.934	1379.690	177.270	0.516	546.323	0.519	16	0.217	R.VTIDLLEMVFAK.G
R1/RRR1-4/2	1395.305	1395.690	-276.164	0.401	1195.122	0.288	17	0.209	R.VTIDLLEM*VFAK.G
R1/RRR1-4/2	1394.431	1395.690	-1624.478	0.309	1149.604	0.249	16	0.201	R.VTIDLLEM*VFAK.G
R1/RRR1-22/2	1345.187	1345.486	-222.959	0.447	855.797	0.478	16	0.220	R.HLVDQYLEATR.G
R1/RRR1-22/2	1637.495	1637.682	-114.295	0.308	599.021	0.255	15	0.182	K.VEFDESPPDDFDPK.N
R1/RRR1-22/2	1636.845	1637.682	-1125.566	0.254	887.999	0.166	17	0.180	K.VEFDESPPDDFDPK.N
R1/RRR1-15/2	1085.036	1085.279	-224.735	0.458	865.798	0.518	17	0.229	K.TPIKDALAAGK.E
R1/RRR1-15/2	1058.205	1058.254	-46.004	0.447	608.986	0.401	13	0.196	-.LSGIVGVPTSK.-
R1/RRR1-15/2	1058.076	1058.254	-168.206	0.381	697.665	0.361	14	0.195	-.LSGIVGVPTSK.-
R1/RRR1-15/2	1086.091	1085.279	-173.901	0.371	553.113	0.329	15	0.193	K.TPIKDALAAGK.E
R1/RRR1-20/2	1226.352	1225.461	-89.116	0.413	524.520	0.475	17	0.209	K.LPIPGWVDTVK.T
R1/RRR1-20/2	1713.728	1712.906	-104.361	0.414	518.618	0.504	17	0.208	K.EM*PPQDIDWFYVR.A
R1/RRR1-20/2	1712.201	1712.906	-998.808	0.365	421.004	0.369	15	0.192	K.EM*PPQDIDWFYVR.A
R1/RRR1-20/2	1225.205	1225.461	-209.717	0.265	562.126	0.325	16	0.190	K.LPIPGWVDTVK.T
R1/RRR1-14/2	1098.130	1098.304	-159.221	0.374	1376.565	0.436	18	0.252	K.HGM*VAAGALVR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-14/2	1293.901	1293.491	318.074	0.499	1226.984	0.457	18	0.245	R.KLTDDEIAFIK.E
R1/RRR1-13/2	1097.717	1098.304	-1450.549	0.329	1089.087	0.460	18	0.230	K.HGM*VAAGALVR.Q
R1/RRR1-14/2	1098.138	1098.304	-151.638	0.321	758.238	0.471	15	0.210	K.HGM*VAAGALVR.Q
R1/RRR1-14/2	1293.193	1293.491	-230.882	0.492	840.298	0.404	16	0.209	R.KLTDDEIAFIK.E
R1/RRR1-14/2	1097.390	1098.304	-1749.991	0.312	442.815	0.468	13	0.199	K.HGM*VAAGALVR.Q
R1/RRR1-16/2	1211.173	1211.393	-182.123	0.395	695.882	0.539	17	0.220	R.VPIVPSDGAISR.T
R1/RRR1-16/2	1211.097	1211.393	-244.814	0.279	618.822	0.444	16	0.199	R.VPIVPSDGAISR.T
R1/RRR1-16/2	1210.476	1211.393	-1588.785	0.274	396.464	0.490	15	0.197	R.VPIVPSDGAISR.T
R1/RRR1-16/3	1229.504	1229.324	147.260	0.443	1177.698	0.233	22	0.079	K.FHGVAENPTEK.I
R1/RRR1-16/3	1229.190	1229.324	-109.242	0.405	887.514	0.168	22	0.067	K.FHGVAENPTEK.I
R1/RRR1-9/2	1418.022	1418.534	-1068.895	0.515	1447.147	0.575	19	0.295	R.GPLLDEDGPSYVR.V
R1/RRR1-9/2	1419.290	1418.534	-172.326	0.529	1356.957	0.587	19	0.287	R.GPLLDEDGPSYVR.V
R1/RRR1-9/2	1418.293	1418.534	-170.375	0.487	1419.547	0.534	19	0.280	R.GPLLDEDGPSYVR.V
R1/RRR1-9/2	1048.236	1048.217	17.566	0.362	921.725	0.300	14	0.198	R.ALFVQADGVK.L
R1/RRR1-9/2	1048.108	1048.217	-104.389	0.326	895.325	0.309	14	0.198	R.ALFVQADGVK.L
R1/RRR1-9/2	1048.182	1048.217	-33.712	0.305	841.252	0.320	14	0.197	-.ALFVQADGVK.-
R1/RRR1-13/2	1498.813	1497.677	90.952	0.405	948.968	0.387	16	0.210	R.EQIQSYVFDVIR.A
R1/RRR1-14/2	1497.363	1497.677	-210.521	0.355	1044.358	0.323	16	0.205	R.EQIQSYVFDVIR.A
R1/RRR1-14/2	934.008	934.117	-116.944	0.447	882.778	0.323	15	0.201	K.YLAGLGIAR.Q
R1/RRR1-14/2	1497.174	1497.677	-1007.233	0.231	684.800	0.167	14	0.181	R.EQIQSYVFDVIR.A
R1/RRR1-14/2	1496.701	1497.677	-1323.970	0.190	734.163	0.127	14	0.179	R.EQIQSYVFDVIR.A
R1/RRR1-7/2	1281.269	1280.538	-210.957	0.390	1113.966	0.555	18	0.250	R.GLPTLVLIGPDGK.T
R1/RRR1-7/2	1516.331	1516.639	-203.608	0.417	1302.015	0.448	20	0.247	K.DNQTVQSVLGTPTR.D
R1/RRR1-7/2	1516.177	1516.639	-305.782	0.352	1278.718	0.339	20	0.223	K.DNQTVQSVLGTPTR.D
R1/RRR1-7/2	1516.119	1516.639	-1005.226	0.363	1161.786	0.388	18	0.221	K.DNQTVQSVLGTPTR.D
R1/RRR1-7/2	1280.259	1280.538	-218.678	0.320	948.790	0.409	17	0.210	R.GLPTLVLIGPDGK.T
R1/RRR1-7/2	1280.312	1280.538	-176.974	0.214	495.027	0.346	12	0.183	R.GLPTLVLIGPDGK.T
R1/RRR1-15/2	1617.499	1617.659	-99.207	0.529	1785.320	0.423	21	0.296	K.NSWGADWGDNGYFK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1617.217	1617.659	-273.883	0.526	1363.733	0.432	19	0.247	K.NSWGADWGDNGYFK.M
R1/RRR1-15/2	1617.283	1617.659	-232.764	0.499	1323.274	0.431	18	0.242	K.NSWGADWGDNGYFK.M
R1/RRR1-15/3	1401.863	1401.549	224.790	0.549	1496.289	0.347	29	0.121	K.DWREDGIVSPVK.D
R1/RRR1-15/3	1401.946	1401.549	283.988	0.493	1215.827	0.345	27	0.098	K.DWREDGIVSPVK.D
R1/RRR1-16/3	1401.720	1401.549	122.223	0.475	857.395	0.335	24	0.084	K.DWREDGIVSPVK.D
R1/RRR1-15/3	1401.035	1401.549	-1083.874	0.438	988.852	0.267	24	0.078	K.DWREDGIVSPVK.D
R1/RRR1-20/1	1219.542	1220.357	-1492.278	0.142	813.673	0.205	15	0.366	K.LNPAADAGSIYK.T
R1/RRR1-20/2	1221.064	1220.357	-240.710	0.469	857.117	0.578	20	0.243	K.LNPAADAGSIYK.T
R1/RRR1-21/2	1219.986	1220.357	-304.751	0.456	773.972	0.559	19	0.234	K.LNPAADAGSIYK.T
R1/RRR1-20/2	1220.046	1220.357	-255.563	0.497	661.707	0.583	18	0.233	K.LNPAADAGSIYK.T
R1/RRR1-19/2	1220.771	1220.357	340.438	0.469	775.990	0.530	19	0.230	K.LNPAADAGSIYK.T
R1/RRR1-20/2	1219.938	1220.357	-344.306	0.440	887.134	0.488	20	0.229	K.LNPAADAGSIYK.T
R1/RRR1-21/2	1220.147	1220.357	-172.254	0.474	860.064	0.481	20	0.228	K.LNPAADAGSIYK.T
R1/RRR1-21/2	1219.880	1220.357	-392.097	0.432	549.714	0.542	18	0.222	K.LNPAADAGSIYK.T
R1/RRR1-18/2	1220.170	1220.357	-153.186	0.487	631.904	0.470	18	0.217	K.LNPAADAGSIYK.T
R1/RRR1-19/2	1219.493	1220.357	-1532.559	0.318	793.604	0.475	19	0.216	K.LNPAADAGSIYK.T
R1/RRR1-19/2	1219.565	1220.357	-1473.438	0.362	476.338	0.500	17	0.212	K.LNPAADAGSIYK.T
R1/RRR1-18/2	1219.894	1220.357	-380.049	0.372	581.546	0.444	17	0.209	K.LNPAADAGSIYK.T
R1/RRR1-18/2	1219.607	1220.357	-1439.054	0.262	412.901	0.369	15	0.197	K.LNPAADAGSIYK.T
R1/RRR1-20/1	1219.604	1220.357	-1441.204	0.118	541.754	0.212	13	0.194	K.LNPAADAGSIYK.T
R1/RRR1-5/2	1600.845	1601.871	-1269.885	0.382	1925.956	0.487	21	0.338	R.IPALFVVNISSGEVR.A
R1/RRR1-5/2	1600.754	1601.871	-1326.863	0.394	1205.912	0.560	18	0.257	R.IPALFVVNISSGEVR.A
R1/RRR1-5/2	1632.652	1631.898	-151.156	0.467	891.429	0.371	17	0.200	K.VSTPTLFLLGAQDLR.V
R1/RRR1-5/2	1631.634	1631.898	-162.281	0.364	1094.993	0.254	19	0.196	K.VSTPTLFLLGAQDLR.V
R1/RRR1-5/2	1631.106	1631.898	-1101.603	0.254	781.448	0.237	17	0.184	K.VSTPTLFLLGAQDLR.V
R1/RRR1-10/2	1113.499	1114.314	-1634.791	0.404	1373.100	0.430	15	0.251	K.APLLIGCDVR.S
R1/RRR1-10/2	1114.369	1114.314	49.924	0.421	1264.488	0.438	16	0.244	K.APLLIGCDVR.S
R1/RRR1-10/2	1114.186	1114.314	-115.340	0.470	1163.405	0.459	15	0.239	K.APLLIGCDVR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/2	1113.994	1114.314	-287.805	0.425	1193.235	0.446	15	0.239	K.APLLIGCDVR.S
R1/RRR1-7/2	1114.916	1114.314	-358.290	0.318	549.497	0.378	11	0.193	-.APLLIGCDVR.-
R1/RRR1-6/2	1114.663	1114.314	314.190	0.254	531.826	0.241	12	0.188	K.APLLIGCDVR.S
R1/RRR1-10/3	1501.380	1501.601	-147.731	0.425	962.935	0.388	25	0.093	-.M*PGSLDHEEQDVK.T
R1/RRR1-10/3	1501.221	1501.601	-254.302	0.418	921.707	0.349	23	0.087	-.M*PGSLDHEEQDVK.T
R1/RRR1-13/2	1499.535	1499.693	-105.296	0.503	1409.208	0.452	20	0.260	R.SIGISNYDIFLTR.D
R1/RRR1-13/2	1500.466	1499.693	-151.824	0.521	1168.243	0.509	19	0.249	R.SIGISNYDIFLTR.D
R1/RRR1-13/2	1500.274	1499.693	-280.133	0.523	1157.056	0.466	19	0.239	R.SIGISNYDIFLTR.D
R1/RRR1-12/2	1500.212	1499.693	-321.604	0.535	1124.802	0.470	19	0.237	R.SIGISNYDIFLTR.D
R1/RRR1-12/2	1499.064	1499.693	-1090.007	0.447	1051.435	0.467	18	0.230	R.SIGISNYDIFLTR.D
R1/RRR1-12/2	1499.462	1499.693	-154.620	0.514	1062.618	0.452	18	0.228	R.SIGISNYDIFLTR.D
R1/RRR1-13/2	897.512	898.085	-1758.440	0.413	1207.728	0.357	13	0.225	K.TPAQLVLR.W
R1/RRR1-13/2	897.467	898.085	-1808.596	0.409	1037.594	0.325	13	0.210	K.TPAQLVLR.W
R1/RRR1-12/2	897.573	898.085	-1689.160	0.559	1072.057	0.301	13	0.205	K.TPAQLVLR.W
R1/RRR1-13/2	898.091	898.085	6.801	0.582	1042.703	0.293	13	0.201	K.TPAQLVLR.W
R1/RRR1-12/2	898.335	898.085	279.658	0.506	1026.482	0.204	13	0.190	K.TPAQLVLR.W
R1/RRR1-13/2	898.288	898.085	227.060	0.303	661.010	0.172	11	0.182	-.TPAQLVLR.-
R1/RRR1-15/2	1560.240	1558.804	280.728	0.415	1061.759	0.483	17	0.228	R.LFYGPGGPYALFAGK.D
R1/RRR1-13/2	1152.702	1153.227	-1327.459	0.298	832.440	0.153	14	0.178	-.GQIYDVSQSR.-
R1/RRR1-20/2	1216.114	1216.366	-207.962	0.482	1641.866	0.326	16	0.254	R.LLEELERGEK.G
R1/RRR1-20/2	1215.766	1216.366	-1320.637	0.509	1530.170	0.343	16	0.246	R.LLEELERGEK.G
R1/RRR1-20/2	1216.189	1216.366	-145.936	0.536	1563.036	0.301	16	0.238	R.LLEELERGEK.G
R1/RRR1-21/2	1215.867	1216.366	-412.222	0.458	1298.900	0.247	16	0.209	R.LLEELERGEK.G
R1/RRR1-21/2	1216.064	1216.366	-249.352	0.459	1046.775	0.310	15	0.206	R.LLEELERGEK.G
R1/RRR1-21/2	1215.692	1216.366	-1381.346	0.414	1114.732	0.236	15	0.198	R.LLEELERGEK.G
R1/RRR1-21/3	1806.260	1806.930	-927.327	0.483	1263.122	0.481	27	0.146	R.INM*SCVNHETGAVDSR.K
R1/RRR1-21/3	1805.840	1806.930	-1160.539	0.475	1121.204	0.433	27	0.118	R.INM*SCVNHETGAVDSR.K
R1/RRR1-21/3	1807.056	1806.930	70.125	0.458	843.330	0.458	25	0.105	R.INM*SCVNHETGAVDSR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1951.976	1952.120	-73.865	0.570	1507.369	0.584	23	0.305	K.GLHSSLNHLANEFDQIR.S
R1/RRR1-8/3	1951.957	1952.120	-83.595	0.502	2086.506	0.485	35	0.282	K.GLHSSLNHLANEFDQIR.S
R1/RRR1-8/3	1952.203	1952.120	42.665	0.468	1994.424	0.475	31	0.265	K.GLHSSLNHLANEFDQIR.S
R1/RRR1-8/2	1426.379	1426.561	-127.349	0.523	1334.540	0.448	20	0.251	R.SSGGFWTWLTGAR.S
R1/RRR1-8/2	1426.238	1426.561	-226.943	0.431	989.360	0.466	18	0.225	R.SSGGFWTWLTGAR.S
R1/RRR1-8/2	1425.717	1426.561	-1297.227	0.430	1070.842	0.428	18	0.224	R.SSGGFWTWLTGAR.S
R1/RRR1-8/3	1952.119	1952.120	-0.327	0.471	1389.616	0.478	31	0.157	K.GLHSSLNHLANEFDQIR.S
R1/RRR1-22/2	1464.370	1464.688	-217.940	0.384	878.238	0.461	22	0.219	R.QSGSTYSLVVVVPK.D
R1/RRR1-22/2	1464.474	1464.688	-146.860	0.441	812.416	0.461	21	0.217	R.QSGSTYSLVVVVPK.D
R1/RRR1-22/2	1464.386	1464.688	-207.403	0.390	711.209	0.484	20	0.213	R.QSGSTYSLVVVVPK.D
R1/RRR1-22/3	1488.428	1488.710	-190.407	0.456	1553.641	0.357	26	0.138	K.TLKPDTEIWTVGK.L
R1/RRR1-22/3	1488.528	1488.710	-122.781	0.489	1347.993	0.340	25	0.113	K.TLKPDTEIWTVGK.L
R1/RRR1-22/3	1488.753	1488.710	28.725	0.480	1291.982	0.325	25	0.105	K.TLKPDTEIWTVGK.L
R1/RRR1-23/3	1488.400	1488.710	-209.289	0.419	762.546	0.237	20	0.071	-.TLKPDTEIWTVGK.-
R1/RRR1-15/2	1441.061	1441.620	-1084.686	0.544	1518.395	0.465	18	0.274	R.IYNQNLINHVGR.G
R1/RRR1-15/2	1441.341	1441.620	-193.729	0.561	1355.664	0.486	19	0.263	R.IYNQNLINHVGR.G
R1/RRR1-15/2	1396.310	1396.533	-160.080	0.457	1252.517	0.457	18	0.246	R.NNIQAYPSVSFR.Y
R1/RRR1-15/2	1396.151	1396.533	-274.629	0.445	1248.184	0.444	18	0.242	R.NNIQAYPSVSFR.Y
R1/RRR1-14/2	1441.130	1441.620	-340.991	0.483	1119.810	0.459	18	0.236	R.IYNQNLINHVGR.G
R1/RRR1-15/2	1441.320	1441.620	-209.023	0.556	1039.020	0.468	17	0.230	R.IYNQNLINHVGR.G
R1/RRR1-14/2	1440.531	1441.620	-1454.640	0.489	1004.900	0.465	17	0.228	R.IYNQNLINHVGR.G
R1/RRR1-15/2	1396.295	1396.533	-171.043	0.435	1122.179	0.422	17	0.227	R.NNIQAYPSVSFR.Y
R1/RRR1-15/2	1396.752	1396.533	157.205	0.338	556.895	0.376	14	0.195	R.NNIQAYPSVSFR.Y
R1/RRR1-14/2	1603.382	1603.839	-286.249	0.525	1068.654	0.471	17	0.228	K.LNSSLSQVLVNCLR.Y
R1/RRR1-14/2	1602.599	1603.839	-1402.040	0.372	1291.743	0.359	19	0.227	K.LNSSLSQVLVNCLR.Y
R1/RRR1-14/2	1294.835	1295.379	-1195.834	0.352	900.663	0.353	17	0.202	-.GSVSTESAVTQTK.-
R1/RRR1-14/2	1294.635	1295.379	-1351.117	0.282	1010.024	0.259	17	0.194	K.GSVSTESAVTQTK.F
R1/RRR1-14/2	1294.619	1295.379	-1363.333	0.315	708.154	0.346	16	0.193	-.GSVSTESAVTQTK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1858.619	1858.166	244.488	0.521	1805.809	0.512	22	0.326	K.GVLISNASIICLVAGVDR.L
R1/RRR1-6/2	1250.612	1251.454	-1477.390	0.333	818.676	0.354	15	0.197	K.AKEYILGELSK.V
R1/RRR1-13/2	1305.093	1305.420	-251.668	0.474	965.827	0.432	15	0.217	R.TSNVFDGVYFR.E
R1/RRR1-12/3	1633.635	1634.794	-1325.301	0.462	1097.631	0.495	27	0.127	K.M*GQLDLKEGDAGEVR.T
R1/RRR1-11/2	1167.379	1166.349	26.261	0.520	899.062	0.570	17	0.243	R.LPTSVYSALSK.A
R1/RRR1-11/2	1166.345	1166.349	-3.528	0.467	1036.440	0.508	18	0.241	R.LPTSVYSALSK.A
R1/RRR1-11/2	1166.300	1166.349	-41.846	0.403	875.192	0.486	17	0.224	R.LPTSVYSALSK.A
R1/RRR1-11/2	858.059	858.021	44.432	0.409	1059.391	0.349	15	0.214	R.SAGLIGLAR.N
R1/RRR1-12/2	1166.757	1166.349	350.532	0.319	288.465	0.494	13	0.201	R.LPTSVYSALSK.A
R1/RRR1-12/2	857.941	858.021	-93.705	0.305	573.261	0.347	12	0.194	R.SAGLIGLAR.N
R1/RRR1-12/2	857.748	858.021	-319.258	0.290	419.769	0.324	11	0.187	-.SAGLIGLAR.-
R1/RRR1-24/2	1795.996	1794.946	28.318	0.530	1142.624	0.487	20	0.238	K.LFVGGLSWNTNDDSLR.E
R1/RRR1-24/3	1542.635	1542.675	-26.068	0.420	457.081	0.623	24	0.112	K.SAM*DAM*DGKELEGR.S
R1/RRR1-24/3	1542.302	1542.675	-242.797	0.368	393.747	0.542	23	0.100	K.SAM*DAM*DGKELEGR.S
R1/RRR1-24/3	1542.191	1542.675	-314.742	0.387	374.458	0.559	21	0.099	-.SAM*DAM*DGKELEGR.-
R1/RRR1-23/3	1542.371	1542.675	-197.538	0.324	589.702	0.512	25	0.097	K.SAM*DAM*DGKELEGR.S
R1/RRR1-23/3	1542.462	1542.675	-138.350	0.364	432.874	0.431	23	0.091	K.SAM*DAM*DGKELEGR.S
R1/RRR1-7/2	1648.409	1647.806	-241.590	0.531	2376.682	0.555	24	0.455	R.TEEELIEAIATATGAK.K
R1/RRR1-13/2	1613.583	1613.794	-131.240	0.483	938.250	0.449	19	0.218	K.ILNENDLITPDLSR.V
R1/RRR1-23/2	1247.319	1246.439	-96.355	0.354	945.784	0.084	15	0.172	-.KVDKTSLEVAR.-
R1/RRR1-22/2	1260.206	1259.439	-185.336	0.400	2493.037	0.469	22	0.439	R.FPGVNGLGISAAR.V
R1/RRR1-22/2	1259.225	1259.439	-170.993	0.470	2241.852	0.472	22	0.389	R.FPGVNGLGISAAR.V
R1/RRR1-22/2	1259.167	1259.439	-216.896	0.487	2030.506	0.472	22	0.351	R.FPGVNGLGISAAR.V
R1/RRR1-22/2	1259.225	1259.439	-170.604	0.474	2085.853	0.432	22	0.347	R.FPGVNGLGISAAR.V
R1/RRR1-22/2	1259.718	1259.439	222.028	0.381	1523.115	0.324	18	0.241	R.FPGVNGLGISAAR.V
R1/RRR1-12/2	1442.294	1441.572	-193.177	0.446	1056.651	0.563	22	0.251	R.QGNPDLIGTGALER.A
R1/RRR1-12/2	1441.248	1441.572	-225.089	0.427	1009.971	0.549	22	0.243	R.QGNPDLIGTGALER.A
R1/RRR1-12/2	1220.970	1221.345	-307.714	0.385	1361.358	0.343	20	0.233	K.VFGSPTSAEVAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-12/2	1222.057	1221.345	-236.006	0.414	1076.317	0.437	19	0.229	K.VFGSPTSAEVAR.V
R1/RRR1-12/2	1221.138	1221.345	-169.909	0.415	915.914	0.410	18	0.215	K.VFGSPTSAEVAR.V
R1/RRR1-11/2	1441.392	1441.572	-125.513	0.363	434.556	0.498	16	0.203	R.QGNPDLIGTGALER.A
R1/RRR1-11/2	1221.236	1221.345	-89.389	0.400	826.969	0.328	18	0.201	K.VFGSPTSAEVAR.V
R1/RRR1-12/2	1440.542	1441.572	-1413.492	0.321	452.371	0.475	16	0.199	R.QGNPDLIGTGALER.A
R1/RRR1-11/2	1221.109	1221.345	-193.576	0.355	744.112	0.279	19	0.196	K.VFGSPTSAEVAR.V
R1/RRR1-11/2	1222.029	1221.345	-258.654	0.317	555.819	0.347	15	0.195	K.VFGSPTSAEVAR.V
R1/RRR1-16/2	1419.306	1419.648	-241.681	0.407	957.101	0.554	16	0.235	K.GANEVLLVIEAYK.T
R1/RRR1-16/2	1419.199	1419.648	-317.014	0.310	625.546	0.459	14	0.198	K.GANEVLLVIEAYK.T
R1/RRR1-15/3	1850.690	1851.084	-213.570	0.380	957.630	0.420	30	0.097	K.VTAVPAKEEEICGATFK.V
R1/RRR1-15/2	1595.153	1594.746	255.472	0.505	1175.194	0.553	23	0.262	K.LAEAPYLDSVDWSK.W
R1/RRR1-15/2	1595.278	1594.746	-294.150	0.587	824.131	0.628	20	0.247	K.LAEAPYLDSVDWSK.W
R1/RRR1-15/2	1349.592	1349.601	-6.224	0.408	1332.936	0.356	19	0.230	R.GAFTVVLSGGSLIK.N
R1/RRR1-15/2	1594.236	1594.746	-950.364	0.474	804.074	0.538	20	0.228	K.LAEAPYLDSVDWSK.W
R1/RRR1-15/2	1350.112	1349.601	-362.619	0.446	1141.851	0.372	18	0.217	R.GAFTVVLSGGSLIK.N
R1/RRR1-11/2	1192.031	1192.303	-228.803	0.497	843.562	0.539	17	0.233	K.VLAPYSAEDAR.G
R1/RRR1-11/2	1191.994	1192.303	-260.344	0.387	1142.758	0.430	18	0.231	K.VLAPYSAEDAR.G
R1/RRR1-11/2	1192.184	1192.303	-100.605	0.436	999.563	0.464	18	0.229	K.VLAPYSAEDAR.G
R1/RRR1-11/2	1785.403	1786.045	-922.678	0.468	794.490	0.542	20	0.224	K.SNYM*SAGQISVPIVFR.G
R1/RRR1-11/2	1786.602	1786.045	-248.747	0.516	719.735	0.467	19	0.208	K.SNYM*SAGQISVPIVFR.G
R1/RRR1-11/2	1770.096	1770.046	28.317	0.357	583.065	0.315	16	0.186	K.SNYMSAGQISVPIVFR.G
R1/RRR1-8/2	1465.436	1465.678	-165.813	0.503	1638.713	0.458	21	0.289	K.FLGNSLEVYPLGR.T
R1/RRR1-8/2	1465.432	1465.678	-168.571	0.489	1413.863	0.469	20	0.264	K.FLGNSLEVYPLGR.T
R1/RRR1-8/2	932.593	933.089	-533.495	0.484	1008.493	0.434	13	0.225	K.VNNLIFGR.T
R1/RRR1-8/2	932.917	933.089	-185.129	0.537	866.742	0.372	12	0.206	K.VNNLIFGR.T
R1/RRR1-8/2	1464.876	1465.678	-1233.965	0.209	653.707	0.174	14	0.179	K.FLGNSLEVYPLGR.T
R1/RRR1-11/2	1557.669	1558.671	-1289.206	0.371	1253.307	0.441	21	0.240	R.GCSANVFLDNAAYR.Q
R1/RRR1-11/2	1558.297	1558.671	-240.553	0.501	613.246	0.537	18	0.216	R.GCSANVFLDNAAYR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1314.462	1314.477	-10.862	0.305	410.641	0.454	14	0.198	R.QHAFWVPVSSR.Y
R1/RRR1-11/2	1314.238	1314.477	-182.281	0.259	266.201	0.533	13	0.196	R.QHAFWVPVSSR.Y
R1/RRR1-11/2	1314.111	1314.477	-278.823	0.269	452.056	0.439	14	0.195	R.QHAFWVPVSSR.Y
R1/RRR1-9/2	1536.520	1536.927	-265.875	0.473	1426.557	0.555	21	0.288	R.TLELVAGKPLLLLR.W
R1/RRR1-9/3	1502.605	1502.697	-61.130	0.458	1172.484	0.415	25	0.116	K.LGKPEIFPASTDAR.Y
R1/RRR1-9/3	1501.401	1502.697	-1533.981	0.353	995.508	0.226	23	0.072	K.LGKPEIFPASTDAR.Y
R1/RRR1-8/2	1442.258	1442.688	-298.703	0.406	1637.614	0.468	21	0.291	R.NLGVGLGHSLLAYK.A
R1/RRR1-8/2	1459.349	1459.629	-192.262	0.460	1008.914	0.440	21	0.226	R.QFIEGLDLPEAAR.S
R1/RRR1-8/2	1459.125	1459.629	-1033.834	0.395	987.604	0.360	21	0.211	R.QFIEGLDLPEAAR.S
R1/RRR1-8/2	1460.412	1459.629	-148.862	0.483	941.993	0.366	20	0.209	R.QFIEGLDLPEAAR.S
R1/RRR1-5/2	1123.068	1123.284	-193.359	0.487	1783.746	0.449	17	0.307	K.LSEGYLTLAR.D
R1/RRR1-5/2	1122.395	1123.284	-1687.830	0.442	1640.379	0.453	17	0.288	K.LSEGYLTLAR.D
R1/RRR1-5/2	1122.718	1123.284	-1399.116	0.501	1549.706	0.463	17	0.280	K.LSEGYLTLAR.D
R1/RRR1-5/2	1348.855	1348.486	273.800	0.496	1258.599	0.462	16	0.245	R.NLAGEIAQEFQK.R
R1/RRR1-5/2	1347.466	1348.486	-1504.314	0.366	708.094	0.291	15	0.189	R.NLAGEIAQEFQK.R
R1/RRR1-13/2	1365.298	1365.514	-158.335	0.372	1398.210	0.446	17	0.255	K.EPYTATIVSVER.L
R1/RRR1-13/2	1365.207	1365.514	-225.519	0.344	1176.108	0.440	16	0.231	K.EPYTATIVSVER.L
R1/RRR1-13/2	1365.358	1365.514	-114.299	0.297	840.678	0.377	14	0.199	K.EPYTATIVSVER.L
R1/RRR1-13/2	910.279	911.037	-1937.685	0.280	869.032	0.256	13	0.191	R.LYSIASTR.Y
R1/RRR1-13/2	910.952	911.037	-94.233	0.318	871.787	0.238	13	0.191	R.LYSIASTR.Y
R1/RRR1-9/2	1298.397	1298.471	-57.108	0.496	1324.200	0.566	19	0.278	R.LLAGESGIGPIDR.F
R1/RRR1-9/2	1297.670	1298.471	-1391.547	0.426	907.854	0.563	16	0.233	R.LLAGESGIGPIDR.F
R1/RRR1-9/2	1116.774	1117.278	-1350.979	0.305	1176.731	0.404	19	0.225	K.ALESAGLALGSK.S
R1/RRR1-10/2	1118.294	1117.278	14.604	0.214	334.284	0.503	16	0.191	K.ALESAGLALGSK.S
R1/RRR1-13/2	1391.241	1391.550	-222.619	0.498	971.907	0.460	17	0.223	R.IVTSIEQKEESK.G
R1/RRR1-4/2	1722.396	1720.822	-247.775	0.494	1328.152	0.497	24	0.260	R.TLSFAIADGSQPGNEGR.E
R1/RRR1-4/2	1720.522	1720.822	-174.890	0.409	1132.753	0.445	21	0.229	R.TLSFAIADGSQPGNEGR.E
R1/RRR1-4/2	1268.038	1268.444	-321.493	0.431	585.196	0.430	17	0.204	R.EADGTLRPLPAK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1267.976	1268.444	-370.369	0.361	770.254	0.381	18	0.202	R.EADGTLRPLPAK.H
R1/RRR1-4/2	1719.462	1720.822	-1376.746	0.276	994.551	0.334	20	0.200	R.TLSFAIADGSQPGNEGR.E
R1/RRR1-19/2	1566.408	1566.784	-240.871	0.462	1199.025	0.461	18	0.238	K.IFFVSWSPAAADVR.S
R1/RRR1-19/2	1795.632	1795.879	-138.186	0.441	1296.849	0.387	21	0.231	R.DAGFDELTASLPADGCR.Y
R1/RRR1-19/2	1565.614	1566.784	-1390.037	0.337	1138.558	0.411	19	0.223	K.IFFVSWSPAAADVR.S
R1/RRR1-19/2	1795.488	1795.879	-218.254	0.451	1001.703	0.419	21	0.215	R.DAGFDELTASLPADGCR.Y
R1/RRR1-8/2	1905.810	1904.153	-180.693	0.575	1201.868	0.571	22	0.263	R.SALDYLELQPDLSALVR.G
R1/RRR1-8/2	1905.063	1904.153	-47.598	0.545	1281.519	0.492	23	0.253	R.SALDYLELQPDLSALVR.G
R1/RRR1-8/2	1904.657	1904.153	-261.284	0.466	1134.056	0.410	22	0.223	R.SALDYLELQPDLSALVR.G
R1/RRR1-17/2	1746.629	1746.901	-156.013	0.416	695.432	0.496	18	0.205	R.VTGSLADGAATIQSALDR.M
R1/RRR1-15/2	1712.456	1711.896	-257.936	0.512	1362.928	0.469	25	0.258	K.TEGVFSFLPASQATGAK.F
R1/RRR1-15/2	1711.318	1711.896	-925.266	0.456	1100.146	0.518	25	0.244	K.TEGVFSFLPASQATGAK.F
R1/RRR1-15/2	1132.088	1132.249	-143.366	0.449	687.746	0.531	17	0.221	K.AGNSVGLEVASK.Y
R1/RRR1-15/2	1710.735	1711.896	-1267.254	0.441	791.909	0.507	21	0.218	K.TEGVFSFLPASQATGAK.F
R1/RRR1-15/2	1132.174	1132.249	-67.115	0.462	767.841	0.440	18	0.213	K.AGNSVGLEVASK.Y
R1/RRR1-15/2	1132.028	1132.249	-196.262	0.448	607.112	0.499	16	0.212	K.AGNSVGLEVASK.Y
R1/RRR1-21/2	1077.016	1077.215	-185.597	0.395	919.875	0.445	16	0.220	R.EGELVFGVAR.I
R1/RRR1-22/2	1077.074	1077.215	-131.478	0.383	880.063	0.409	15	0.212	R.EGELVFGVAR.I
R1/RRR1-21/2	1076.789	1077.215	-396.900	0.426	819.732	0.389	15	0.208	R.EGELVFGVAR.I
R1/RRR1-21/2	1076.996	1077.215	-204.699	0.319	600.224	0.296	13	0.192	R.EGELVFGVAR.I
R1/RRR1-21/3	1795.633	1794.993	-201.470	0.398	1064.383	0.436	25	0.113	K.TQRPAQENISLGPQVR.E
R1/RRR1-21/3	1795.011	1794.993	9.773	0.338	1019.636	0.418	27	0.102	K.TQRPAQENISLGPQVR.E
R1/RRR1-21/3	1795.429	1794.993	243.504	0.225	757.564	0.191	22	0.064	K.TQRPAQENISLGPQVR.E
R1/RRR1-20/2	1924.562	1924.960	-207.433	0.536	2104.098	0.647	26	0.426	R.SLNDGDVVEFSVGSGNDGR.T
R1/RRR1-20/2	1924.665	1924.960	-153.986	0.536	2081.652	0.634	25	0.416	R.SLNDGDVVEFSVGSGNDGR.T
R1/RRR1-20/2	1924.544	1924.960	-216.787	0.549	1904.346	0.635	24	0.381	R.SLNDGDVVEFSVGSGNDGR.T
R1/RRR1-9/2	1066.801	1066.269	-440.097	0.386	530.839	0.471	13	0.208	R.LVFQVCTAK.M
R1/RRR1-9/2	1066.546	1066.269	260.634	0.267	521.947	0.363	12	0.193	R.LVFQVCTAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1066.254	1066.269	-14.194	0.232	440.500	0.383	12	0.191	R.LVFQVCTAK.M
R1/RRR1-17/2	1559.271	1558.677	-261.604	0.572	748.972	0.525	21	0.224	K.FVSNGQPGPAQNVDK.S
R1/RRR1-17/2	1558.320	1558.677	-229.707	0.525	817.731	0.492	22	0.223	K.FVSNGQPGPAQNVDK.S
R1/RRR1-16/2	1558.101	1558.677	-1015.074	0.511	875.778	0.460	23	0.221	K.FVSNGQPGPAQNVDK.S
R1/RRR1-16/2	1558.199	1558.677	-307.986	0.521	771.678	0.488	22	0.220	K.FVSNGQPGPAQNVDK.S
R1/RRR1-17/2	1558.320	1558.677	-230.021	0.517	793.292	0.443	22	0.214	K.FVSNGQPGPAQNVDK.S
R1/RRR1-17/2	1521.330	1522.773	-1610.613	0.268	886.328	0.219	16	0.182	K.FVNDLHALISPPAK.G
R1/RRR1-16/3	1523.890	1522.773	77.435	0.346	1039.016	0.442	27	0.105	K.FVNDLHALISPPAK.G
R1/RRR1-17/3	1523.784	1522.773	7.174	0.353	674.973	0.353	22	0.080	K.FVNDLHALISPPAK.G
R1/RRR1-14/2	1282.202	1282.536	-261.412	0.476	1173.451	0.403	15	0.229	R.IQMFLYVPDR.V
R1/RRR1-14/2	1282.226	1282.536	-243.074	0.386	1065.572	0.361	14	0.213	R.IQMFLYVPDR.V
R1/RRR1-14/2	1298.167	1298.536	-284.689	0.312	592.551	0.187	11	0.183	-.IQM*FLYVPDR.-
R1/RRR1-13/2	1298.015	1298.536	-1175.160	0.225	611.183	0.122	11	0.181	-.IQM*FLYVPDR.-
R1/RRR1-14/3	1917.901	1918.183	-147.386	0.371	703.755	0.552	27	0.114	R.VATNPAIIVGLHPCGGNAR.Q
R1/RRR1-13/3	1918.913	1918.183	-141.502	0.382	518.131	0.457	24	0.096	R.VATNPAIIVGLHPCGGNAR.Q
R1/RRR1-13/3	1918.979	1918.183	-106.852	0.328	513.355	0.461	23	0.091	-.VATNPAIIVGLHPCGGNAR.-
R1/RRR1-14/3	1917.367	1918.183	-950.136	0.277	349.480	0.403	19	0.069	-.VATNPAIIVGLHPCGGNAR.-
R1/RRR1-13/3	1917.599	1918.183	-828.677	0.292	244.134	0.473	16	0.067	-.VATNPAIIVGLHPCGGNAR.-
R1/RRR1-11/2	1307.465	1307.650	-141.647	0.463	1043.960	0.499	17	0.236	R.VVLLIDVPIIGR.I
R1/RRR1-10/2	1290.552	1290.530	16.829	0.310	787.435	0.314	15	0.192	K.IPISLIYDDIK.S
R1/RRR1-11/2	1307.189	1307.650	-354.013	0.362	576.903	0.296	15	0.188	-.VVLLIDVPIIGR.-
R1/RRR1-12/2	1389.436	1389.578	-103.154	0.420	1302.141	0.443	16	0.245	K.ALESLKEWEGVK.V
R1/RRR1-12/2	1060.110	1059.243	-126.075	0.495	610.089	0.528	16	0.221	K.LGPQNAIFAK.A
R1/RRR1-12/2	1058.951	1059.243	-276.751	0.204	274.702	0.339	12	0.185	-.LGPQNAIFAK.-
R1/RRR1-8/1	994.510	995.113	-1616.774	0.319	827.708	0.324	12	0.385	R.DSAAVFAWK.G
R1/RRR1-8/1	994.521	995.113	-1605.738	0.344	818.091	0.332	12	0.377	R.DSAAVFAWK.G
R1/RRR1-8/1	994.553	995.113	-1572.692	0.283	762.578	0.298	12	0.327	R.DSAAVFAWK.G
R1/RRR1-1/2	995.003	995.113	-111.067	0.453	1322.495	0.456	14	0.253	R.DSAAVFAWK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	995.010	995.113	-103.438	0.519	1257.810	0.477	14	0.252	R.DSAAVFAWK.G
R1/RRR1-2/2	995.076	995.113	-37.111	0.424	1327.993	0.447	14	0.251	R.DSAAVFAWK.G
R1/RRR1-8/2	994.982	995.113	-131.620	0.435	1291.703	0.446	15	0.249	R.DSAAVFAWK.G
R1/RRR1-3/2	994.821	995.113	-294.591	0.409	1293.743	0.433	15	0.246	R.DSAAVFAWK.G
R1/RRR1-2/2	995.033	995.113	-80.179	0.471	1260.143	0.433	14	0.243	R.DSAAVFAWK.G
R1/RRR1-8/2	994.965	995.113	-149.465	0.501	1233.188	0.438	14	0.242	R.DSAAVFAWK.G
R1/RRR1-2/2	994.908	995.113	-206.083	0.408	1168.943	0.451	14	0.238	R.DSAAVFAWK.G
R1/RRR1-1/2	994.854	995.113	-260.737	0.439	1167.227	0.438	14	0.236	R.DSAAVFAWK.G
R1/RRR1-8/2	1993.317	1994.314	-1004.842	0.463	1054.756	0.443	19	0.220	R.LELELAEVEM*PGLMSCR.T
R1/RRR1-19/2	1663.013	1662.860	91.837	0.528	2412.325	0.501	25	0.435	K.AITSGVLAGCSDAIAQK.I
R1/RRR1-19/2	1663.387	1662.860	-285.492	0.554	2244.240	0.526	24	0.408	K.AITSGVLAGCSDAIAQK.I
R1/RRR1-19/2	1662.595	1662.860	-160.290	0.529	2141.634	0.521	24	0.387	K.AITSGVLAGCSDAIAQK.I
R1/RRR1-17/2	1063.084	1063.181	-90.825	0.391	1254.765	0.323	17	0.220	K.CVVTGDGAVGK.T
R1/RRR1-17/2	1063.088	1063.181	-87.600	0.344	1054.530	0.343	17	0.210	K.CVVTGDGAVGK.T
R1/RRR1-17/2	1062.502	1063.181	-1584.425	0.297	677.446	0.282	14	0.189	K.CVVTGDGAVGK.T
R1/RRR1-17/3	1659.872	1659.823	29.378	0.532	1285.568	0.450	27	0.136	K.LDLREDQATLESLR.S
R1/RRR1-17/3	1659.541	1659.823	-170.257	0.492	857.132	0.386	22	0.093	-.LDLREDQATLESLR.-
R1/RRR1-17/3	1659.991	1659.823	101.511	0.426	685.911	0.332	20	0.074	-.LDLREDQATLESLR.-
R1/RRR1-13/2	1232.083	1231.383	-244.222	0.497	1125.381	0.406	17	0.227	R.ISGTVTVPDWR.N
R1/RRR1-13/2	1194.144	1194.279	-113.257	0.461	1029.236	0.427	16	0.225	K.NLNTGQEVYR.T
R1/RRR1-13/2	1193.897	1194.279	-321.153	0.430	630.699	0.461	15	0.211	K.NLNTGQEVYR.T
R1/RRR1-13/2	1230.539	1231.383	-1502.484	0.372	874.795	0.361	15	0.204	R.ISGTVTVPDWR.N
R1/RRR1-13/2	1231.209	1231.383	-141.172	0.461	984.617	0.310	16	0.202	-.ISGTVTVPDWR.-
R1/RRR1-13/2	1193.100	1194.279	-1832.147	0.319	575.879	0.244	15	0.190	K.NLNTGQEVYR.T
R1/RRR1-14/2	1230.931	1231.383	-368.286	0.308	595.516	0.259	12	0.174	-.ISGTVTVPDWR.-
R1/RRR1-8/2	1472.352	1472.671	-216.758	0.398	451.631	0.567	19	0.212	R.VAPAPPAGEPALPER.A
R1/RRR1-8/2	1314.139	1314.427	-219.469	0.460	502.423	0.496	18	0.210	R.LGPGDDVDAVLSR.M
R1/RRR1-8/2	1472.409	1472.671	-178.416	0.392	394.144	0.546	18	0.207	R.VAPAPPAGEPALPER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1472.079	1472.671	-1084.787	0.372	451.766	0.502	19	0.205	R.VAPAPPAGEPALPER.A
R1/RRR1-8/2	1313.600	1314.427	-1395.084	0.341	584.527	0.412	18	0.199	R.LGPGDDVDAVLSR.M
R1/RRR1-20/2	1553.265	1552.713	-289.337	0.613	2314.939	0.537	23	0.428	K.DFNLAEHPDIPGVK.N
R1/RRR1-20/2	1553.279	1552.713	-279.875	0.587	2233.630	0.557	23	0.420	K.DFNLAEHPDIPGVK.N
R1/RRR1-20/2	1552.101	1552.713	-1041.480	0.523	2127.650	0.526	22	0.388	K.DFNLAEHPDIPGVK.N
R1/RRR1-22/2	1656.182	1656.950	-1071.099	0.476	922.340	0.370	18	0.202	-.DINPQAPTHIVIIPK.-
R1/RRR1-22/2	1656.308	1656.950	-994.583	0.428	716.047	0.283	17	0.185	R.DINPQAPTHIVIIPK.V
R1/RRR1-22/3	1464.593	1464.605	-8.754	0.485	1057.385	0.524	28	0.125	K.VVAKQEGLEDGYR.I
R1/RRR1-22/3	1464.060	1464.605	-1058.624	0.443	982.428	0.504	28	0.114	K.VVAKQEGLEDGYR.I
R1/RRR1-23/3	1464.905	1464.605	205.379	0.507	813.768	0.479	27	0.103	K.VVAKQEGLEDGYR.I
R1/RRR1-22/3	1464.624	1464.605	12.814	0.517	916.957	0.451	28	0.102	K.VVAKQEGLEDGYR.I
R1/RRR1-23/3	1465.053	1464.605	306.145	0.489	622.001	0.465	25	0.097	K.VVAKQEGLEDGYR.I
R1/RRR1-2/2	1421.166	1421.581	-292.712	0.427	855.510	0.458	17	0.215	R.IVTNVGQDNAVYK.A
R1/RRR1-5/2	1421.162	1421.581	-295.555	0.406	937.323	0.408	18	0.213	R.IVTNVGQDNAVYK.A
R1/RRR1-5/2	1421.115	1421.581	-328.476	0.434	756.294	0.457	16	0.209	R.IVTNVGQDNAVYK.A
R1/RRR1-1/2	1822.266	1823.127	-1024.340	0.366	726.231	0.481	18	0.208	K.GSLVDLNLPSITIPNLR.M
R1/RRR1-6/2	1822.655	1823.127	-259.336	0.465	636.143	0.500	17	0.207	K.GSLVDLNLPSITIPNLR.M
R1/RRR1-5/2	1823.622	1823.127	272.746	0.474	570.905	0.510	17	0.207	K.GSLVDLNLPSITIPNLR.M
R1/RRR1-5/2	1822.353	1823.127	-976.186	0.362	665.589	0.466	17	0.203	K.GSLVDLNLPSITIPNLR.M
R1/RRR1-1/2	1822.626	1823.127	-825.565	0.426	476.258	0.483	15	0.199	K.GSLVDLNLPSITIPNLR.M
R1/RRR1-6/2	1822.757	1823.127	-203.502	0.442	537.547	0.456	16	0.198	K.GSLVDLNLPSITIPNLR.M
R1/RRR1-3/2	1824.437	1823.127	170.416	0.438	597.265	0.443	16	0.198	K.GSLVDLNLPSITIPNLR.M
R1/RRR1-7/2	1197.308	1197.453	-120.729	0.504	1778.342	0.355	17	0.278	K.ELVQNLLVLR.F
R1/RRR1-7/2	1347.685	1347.502	136.401	0.459	1269.483	0.429	16	0.241	R.DNIDNIQIVFR.E
R1/RRR1-7/2	1197.286	1197.453	-139.445	0.427	1558.872	0.293	16	0.239	K.ELVQNLLVLR.F
R1/RRR1-7/2	1197.306	1197.453	-122.877	0.491	1449.411	0.336	16	0.238	K.ELVQNLLVLR.F
R1/RRR1-7/2	1348.597	1347.502	70.941	0.459	1033.245	0.414	16	0.221	R.DNIDNIQIVFR.E
R1/RRR1-8/2	1197.270	1197.453	-152.843	0.377	1266.798	0.293	15	0.216	K.ELVQNLLVLR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1348.454	1347.502	-35.467	0.361	1063.975	0.384	15	0.215	R.DNIDNIQIVFR.E
R1/RRR1-8/2	1197.249	1197.453	-170.129	0.352	690.016	0.335	13	0.196	K.ELVQNLLVLR.F
R1/RRR1-15/2	1903.748	1903.081	-175.486	0.472	648.652	0.525	23	0.215	K.DYTDPPPAPLFDVGELR.L
R1/RRR1-16/2	1164.169	1164.336	-143.727	0.307	1224.138	0.166	16	0.195	-.SIGAAVIYNQK.-
R1/RRR1-18/3	1770.782	1770.883	-56.850	0.415	1200.762	0.333	26	0.203	R.HLYLPDENYQVNHQ.-
R1/RRR1-18/2	1067.900	1068.165	-249.323	0.456	737.940	0.357	16	0.201	R.TTTGAYIANR.V
R1/RRR1-11/2	1615.318	1615.641	-200.530	0.489	2405.879	0.475	26	0.423	R.LDFSSGQSTGTASNSR.L
R1/RRR1-11/2	1615.340	1615.641	-186.656	0.483	2306.439	0.461	25	0.398	R.LDFSSGQSTGTASNSR.L
R1/RRR1-11/2	1615.115	1615.641	-947.630	0.483	2150.083	0.455	24	0.365	R.LDFSSGQSTGTASNSR.L
R1/RRR1-1/2	1616.923	1615.641	174.871	0.206	853.282	0.142	19	0.179	R.LDFSSGQSTGTASNSR.L
R1/RRR1-11/2	1554.196	1554.770	-1015.497	0.459	1014.958	0.487	20	0.231	R.VLTDVGDVPIQEIR.D
R1/RRR1-11/2	1554.201	1554.770	-1012.342	0.438	1043.899	0.450	20	0.226	R.VLTDVGDVPIQEIR.D
R1/RRR1-11/2	1101.077	1101.322	-222.907	0.394	985.511	0.430	17	0.220	R.VIDASLTLIR.E
R1/RRR1-10/2	1688.526	1688.969	-263.506	0.438	1160.522	0.460	21	0.235	R.EFDLIVM*PGGLPGAQK.F
R1/RRR1-10/2	1145.132	1145.331	-174.878	0.370	698.220	0.551	15	0.218	R.VVVDGNLITSK.A
R1/RRR1-10/2	1145.199	1145.331	-116.066	0.382	540.971	0.545	15	0.212	R.VVVDGNLITSK.A
R1/RRR1-17/2	1245.005	1245.365	-289.776	0.449	1070.945	0.423	16	0.225	K.EAVNQSLENLK.T
R1/RRR1-17/2	1245.157	1245.365	-167.516	0.428	878.983	0.413	16	0.213	K.EAVNQSLENLK.T
R1/RRR1-16/2	1778.103	1777.874	129.273	0.488	928.694	0.433	18	0.212	K.DGAPDSFHFVEDWVR.T
R1/RRR1-16/2	1245.042	1245.365	-259.971	0.331	974.393	0.378	16	0.210	K.EAVNQSLENLK.T
R1/RRR1-16/2	1245.065	1245.365	-241.479	0.375	806.765	0.358	15	0.202	K.EAVNQSLENLK.T
R1/RRR1-17/2	1244.463	1245.365	-1532.407	0.246	920.052	0.293	16	0.195	K.EAVNQSLENLK.T
R1/RRR1-14/2	1254.221	1254.504	-226.635	0.395	1063.787	0.404	18	0.221	R.ATLSIGNVLPIR.S
R1/RRR1-14/2	1254.267	1254.504	-189.825	0.367	1157.892	0.353	18	0.218	R.ATLSIGNVLPIR.S
R1/RRR1-14/2	1253.562	1254.504	-1554.102	0.292	648.544	0.369	14	0.195	R.ATLSIGNVLPIR.S
R1/RRR1-15/2	1253.990	1254.504	-1210.667	0.274	739.217	0.297	14	0.190	R.ATLSIGNVLPIR.S
R1/RRR1-11/2	1254.413	1254.504	-72.482	0.243	611.919	0.206	13	0.184	R.ATLSIGNVLPIR.S
R1/RRR1-18/2	1255.158	1254.504	-276.214	0.313	330.680	0.340	12	0.179	-.ATLSIGNVLPIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	1975.575	1975.066	-248.937	0.379	1056.140	0.538	30	0.136	R.ASGDYAIVISHNPDNGTSR.I
R1/RRR1-1/3	1974.735	1975.066	-167.914	0.383	935.727	0.451	29	0.108	R.ASGDYAIVISHNPDNGTSR.I
R1/RRR1-2/3	1976.832	1975.066	-118.744	0.373	770.621	0.480	25	0.105	R.ASGDYAIVISHNPDNGTSR.I
R1/RRR1-14/3	1976.085	1975.066	10.055	0.331	592.061	0.350	23	0.082	R.ASGDYAIVISHNPDNGTSR.I
R1/RRR1-9/2	1185.632	1186.340	-1445.180	0.364	1459.703	0.437	18	0.260	R.EISGAVQLPGSK.S
R1/RRR1-9/2	1257.849	1258.490	-1308.429	0.301	873.902	0.388	15	0.202	K.FAEVLEM*M*GAK.V
R1/RRR1-13/2	1872.410	1873.058	-882.933	0.446	796.882	0.520	23	0.223	R.FSPNPQNPVIVSSGWDK.L
R1/RRR1-12/2	1872.635	1873.058	-226.392	0.432	876.056	0.495	23	0.223	R.FSPNPQNPVIVSSGWDK.L
R1/RRR1-12/2	1249.431	1249.398	26.203	0.330	1031.168	0.440	16	0.222	R.LWELATGTTTR.R
R1/RRR1-12/2	1873.502	1873.058	237.514	0.389	668.564	0.504	22	0.212	R.FSPNPQNPVIVSSGWDK.L
R1/RRR1-12/2	1872.368	1873.058	-905.448	0.413	847.290	0.435	23	0.212	R.FSPNPQNPVIVSSGWDK.L
R1/RRR1-13/2	1249.089	1249.398	-248.444	0.314	740.732	0.405	15	0.202	R.LWELATGTTTR.R
R1/RRR1-13/2	1249.259	1249.398	-111.788	0.230	890.305	0.299	15	0.193	R.LWELATGTTTR.R
R1/RRR1-13/2	1249.102	1249.398	-237.463	0.249	512.665	0.328	12	0.188	R.LWELATGTTTR.R
R1/RRR1-18/1	1436.978	1437.661	-1174.795	0.227	648.695	0.106	12	0.237	R.VVFELYDDIVPK.T
R1/RRR1-18/2	1438.272	1437.661	-271.949	0.514	1100.074	0.470	18	0.237	R.VVFELYDDIVPK.T
R1/RRR1-18/2	1437.576	1437.661	-59.329	0.490	1159.100	0.425	18	0.232	R.VVFELYDDIVPK.T
R1/RRR1-17/2	1437.300	1437.661	-252.455	0.463	1078.658	0.423	18	0.227	R.VVFELYDDIVPK.T
R1/RRR1-17/2	1437.283	1437.661	-263.873	0.429	934.718	0.389	17	0.213	R.VVFELYDDIVPK.T
R1/RRR1-18/2	1437.322	1437.661	-236.692	0.398	1060.113	0.342	17	0.211	R.VVFELYDDIVPK.T
R1/RRR1-18/2	1372.322	1373.491	-1585.467	0.276	1016.466	0.240	15	0.192	K.VYFDIEWADSK.I
R1/RRR1-17/2	1437.154	1437.661	-1051.768	0.292	703.094	0.300	14	0.192	R.VVFELYDDIVPK.T
R1/RRR1-19/2	1437.044	1437.661	-1129.041	0.302	611.247	0.261	14	0.190	R.VVFELYDDIVPK.T
R1/RRR1-19/2	1437.147	1437.661	-1057.227	0.284	737.657	0.217	15	0.188	R.VVFELYDDIVPK.T
R1/RRR1-18/2	1374.840	1373.491	254.732	0.289	310.759	0.318	12	0.187	-.VYFDIEWADSK.-
R1/RRR1-19/2	1437.493	1437.661	-117.592	0.331	567.372	0.302	13	0.187	-.VVFELYDDIVPK.-
R1/RRR1-12/2	1200.228	1200.327	-82.793	0.382	1393.326	0.266	17	0.220	K.SGLSLNDQLPR.N
R1/RRR1-12/2	1200.004	1200.327	-270.238	0.294	542.356	0.182	12	0.179	-.SGLSLNDQLPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1359.644	1359.509	99.361	0.298	977.353	0.369	17	0.108	R.IGEVISGEGVHYV.-
R1/RRR1-19/2	1359.776	1359.509	196.776	0.310	526.641	0.458	15	0.106	R.IGEVISGEGVHYV.-
R1/RRR1-19/2	1359.607	1359.509	72.077	0.348	605.293	0.437	13	0.099	R.IGEVISGEGVHYV.-
R1/RRR1-12/2	784.930	784.970	-50.712	0.448	869.162	0.258	13	0.193	R.VGILGLGR.I
R1/RRR1-11/2	1650.524	1650.944	-255.523	0.308	644.228	0.429	15	0.191	K.VIDALGPEGVLINIAR.G
R1/RRR1-9/2	1763.443	1762.985	260.460	0.465	641.883	0.604	22	0.224	K.LLEATGISTVPGSGFGQK.E
R1/RRR1-9/2	1762.722	1762.985	-149.379	0.413	455.990	0.592	19	0.210	K.LLEATGISTVPGSGFGQK.E
R1/RRR1-9/2	1941.857	1942.069	-109.306	0.459	473.397	0.580	19	0.209	R.DGYPSDPELIYLTDGASK.G
R1/RRR1-25/2	1538.431	1539.711	-1485.986	0.367	2286.979	0.480	21	0.401	R.FLFCQSSPASAPAR.E
R1/RRR1-25/2	1539.927	1539.711	140.919	0.530	1675.513	0.571	20	0.325	R.FLFCQSSPASAPAR.E
R1/RRR1-25/2	1540.286	1539.711	-276.274	0.410	812.767	0.547	16	0.223	R.FLFCQSSPASAPAR.E
R1/RRR1-19/2	1504.419	1503.685	-176.980	0.502	2130.587	0.574	21	0.403	R.ALEWITANGGITTR.D
R1/RRR1-19/2	1503.411	1503.685	-182.962	0.427	1204.226	0.471	19	0.242	R.ALEWITANGGITTR.D
R1/RRR1-19/2	1503.121	1503.685	-1043.650	0.365	1132.520	0.364	19	0.217	R.ALEWITANGGITTR.D
R1/RRR1-13/2	1504.466	1503.685	-145.886	0.375	1065.453	0.351	17	0.209	R.ALEWITANGGITTR.D
R1/RRR1-15/2	1502.931	1503.685	-1170.541	0.264	1154.202	0.246	18	0.199	R.ALEWITANGGITTR.D
R1/RRR1-15/2	1503.100	1503.685	-1057.512	0.285	812.834	0.197	18	0.185	R.ALEWITANGGITTR.D
R1/RRR1-12/2	1480.301	1480.603	-205.007	0.195	673.569	0.414	18	0.191	R.FVFPETSGLDDPR.V
R1/RRR1-13/2	1388.772	1389.495	-1244.368	0.272	742.746	0.286	15	0.186	-.EAVGAEAAFGPDVR.-
R1/RRR1-13/2	1479.603	1480.603	-1355.985	0.128	523.693	0.375	17	0.179	R.FVFPETSGLDDPR.V
R1/RRR1-12/2	1388.875	1389.495	-1169.873	0.226	715.883	0.196	16	0.179	K.EAVGAEAAFGPDVR.E
R1/RRR1-11/2	1678.934	1678.013	-47.081	0.473	2161.574	0.555	22	0.405	R.VPQVGLIAVNDGIILR.N
R1/RRR1-11/2	1677.777	1678.013	-140.887	0.483	2004.531	0.590	22	0.387	R.VPQVGLIAVNDGIILR.N
R1/RRR1-8/2	1973.342	1972.074	136.288	0.485	1090.314	0.533	19	0.239	R.SGGDDDILDDLDEM*IFGK.K
R1/RRR1-8/2	1792.112	1791.019	52.086	0.390	891.633	0.436	19	0.210	K.ALMLIEAWGESGDELR.Y
R1/RRR1-19/2	1806.090	1807.018	-1070.776	0.352	526.781	0.275	14	0.179	K.ALM*LIEAWGESGDELR.Y
R1/RRR1-22/2	1773.167	1773.003	92.637	0.596	2181.415	0.544	23	0.403	R.AM*SILNSFVNDIFER.V
R1/RRR1-22/2	1773.061	1773.003	32.911	0.603	2075.820	0.557	22	0.387	R.AM*SILNSFVNDIFER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1772.450	1773.003	-878.763	0.554	1998.251	0.581	21	0.381	R.AM*SILNSFVNDIFER.V
R1/RRR1-1/2	1187.491	1188.316	-1541.692	0.420	1267.352	0.465	19	0.249	K.GKVEDAAAALSR.I
R1/RRR1-3/2	1188.309	1188.316	-6.142	0.410	1452.747	0.266	19	0.224	K.GKVEDAAAALSR.I
R1/RRR1-1/2	1017.061	1017.118	-56.413	0.439	913.819	0.302	14	0.200	K.GLSLEQVDR.M
R1/RRR1-2/2	1017.693	1017.118	-418.865	0.353	706.917	0.221	13	0.187	K.GLSLEQVDR.M
R1/RRR1-22/3	1926.871	1925.291	-218.184	0.431	1442.814	0.225	27	0.097	R.RYLQMIQKNSIFNLR.S
R1/RRR1-23/3	1926.418	1925.291	66.371	0.437	1336.807	0.193	25	0.084	R.RYLQMIQKNSIFNLR.S
R1/RRR1-3/3	1583.211	1581.865	218.723	0.252	1154.549	0.068	23	0.054	K.KKTGVLNTMTGFGAR.M
R1/RRR1-6/2	1208.635	1209.420	-1481.393	0.469	1296.243	0.534	21	0.269	K.VPGATDLGLIPR.K
R1/RRR1-6/2	1208.694	1209.420	-1432.496	0.466	1067.983	0.598	20	0.261	K.VPGATDLGLIPR.K
R1/RRR1-6/2	1208.934	1209.420	-403.750	0.410	831.841	0.551	18	0.230	K.VPGATDLGLIPR.K
R1/RRR1-6/2	1499.955	1500.699	-1166.330	0.296	833.235	0.448	18	0.206	K.TM*SLVTGVLDYER.F
R1/RRR1-9/2	1604.444	1602.840	-247.370	0.484	895.538	0.446	19	0.213	K.VALVYGQMNEPPGAR.M
R1/RRR1-10/2	1506.196	1506.601	-269.196	0.435	2050.575	0.569	22	0.390	K.LASLSQGAAGESSTAR.E
R1/RRR1-4/2	1417.159	1416.607	-317.039	0.356	1133.536	0.528	19	0.245	R.GADPAIVLNNLYR.H
R1/RRR1-16/2	1146.396	1147.307	-1671.825	0.258	957.474	0.158	13	0.185	R.CSVIERRAR.F
R1/RRR1-16/2	1146.509	1147.307	-1572.772	0.268	937.659	0.153	13	0.184	R.CSVIERRAR.F
R1/RRR1-17/2	1146.505	1147.307	-1576.729	0.250	916.266	0.124	13	0.182	R.CSVIERRAR.F
R1/RRR1-17/2	1147.024	1147.307	-247.602	0.279	954.698	0.118	13	0.182	R.CSVIERRAR.F
R1/RRR1-15/2	1621.462	1621.853	-241.829	0.411	940.442	0.394	18	0.208	R.LTVEDPVTIEYITK.Y
R1/RRR1-15/2	1821.899	1822.113	-117.489	0.530	623.827	0.438	18	0.200	K.LIEM*LPVEDIENYVK.N
R1/RRR1-8/2	1374.303	1374.569	-194.270	0.482	1066.150	0.482	17	0.235	R.YATNAVTAFIFR.E
R1/RRR1-8/2	1374.208	1374.569	-263.244	0.422	495.264	0.453	14	0.202	R.YATNAVTAFIFR.E
R1/RRR1-9/2	1375.281	1374.569	-210.157	0.261	426.737	0.421	12	0.190	R.YATNAVTAFIFR.E
R1/RRR1-8/2	1373.957	1374.569	-1176.605	0.282	631.336	0.284	15	0.189	R.YATNAVTAFIFR.E
R1/RRR1-8/3	1284.690	1283.590	77.557	0.509	1931.077	0.233	25	0.156	-.HHPLLLQLIAK.-
R1/RRR1-10/2	1684.290	1684.831	-917.433	0.416	1033.987	0.478	20	0.227	K.ALNLGSFFTSGADEVR.Q
R1/RRR1-10/2	1605.186	1603.844	213.373	0.412	385.330	0.536	13	0.196	R.VPANLTVYDIAGLTR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1724.341	1724.038	175.765	0.510	942.184	0.533	20	0.234	R.IAWEEPFGPVLPVIR.I
R1/RRR1-8/2	1723.398	1724.038	-954.586	0.428	788.698	0.451	19	0.210	R.IAWEEPFGPVLPVIR.I
R1/RRR1-8/2	1334.219	1334.460	-181.111	0.296	765.964	0.300	15	0.191	K.LLVSDSFPGNER.N
R1/RRR1-8/2	1334.000	1334.460	-345.522	0.358	632.029	0.343	13	0.191	K.LLVSDSFPGNER.N
R1/RRR1-8/2	1333.587	1334.460	-1408.328	0.345	481.323	0.281	12	0.185	K.LLVSDSFPGNER.N
R1/RRR1-2/2	1724.107	1724.038	40.009	0.332	502.003	0.258	14	0.182	-.IAWEEPFGPVLPVIR.-
R1/RRR1-11/2	1924.791	1924.228	-227.573	0.458	960.676	0.556	19	0.230	R.TAVTTTLAGSVAALTTLFGK.R
R1/RRR1-1/2	1543.091	1541.620	306.150	0.459	484.636	0.493	19	0.206	R.ISAEDETSGM*DLTR.H
R1/RRR1-15/2	1205.978	1206.330	-292.758	0.417	1055.819	0.379	17	0.215	-.GGAFVEAPVSGSK.-
R1/RRR1-14/2	1206.113	1206.330	-180.451	0.420	866.928	0.392	17	0.207	K.GGAFVEAPVSGSK.K
R1/RRR1-15/2	1206.015	1206.330	-261.581	0.346	1061.683	0.333	17	0.207	K.GGAFVEAPVSGSK.K
R1/RRR1-14/2	1205.531	1206.330	-1496.989	0.297	860.796	0.310	16	0.194	K.GGAFVEAPVSGSK.K
R1/RRR1-15/2	1698.887	1698.961	-43.938	0.411	732.551	0.368	17	0.193	K.VLYDDM*VPAFDVLGK.K
R1/RRR1-8/2	1010.470	1011.240	-1757.433	0.440	1096.461	0.431	14	0.229	R.LLEIAQVPK.E
R1/RRR1-8/2	1010.650	1011.240	-1577.701	0.387	1137.922	0.407	15	0.227	R.LLEIAQVPK.E
R1/RRR1-8/2	861.343	861.020	376.600	0.411	765.777	0.404	12	0.207	R.FGDAPLIK.L
R1/RRR1-8/2	1012.078	1011.240	-160.306	0.550	960.294	0.329	14	0.204	R.LLEIAQVPK.E
R1/RRR1-8/2	861.008	861.020	-14.307	0.346	762.759	0.368	12	0.201	R.FGDAPLIK.L
R1/RRR1-10/2	950.099	950.074	26.532	0.445	639.494	0.414	12	0.206	K.VELFSQAR.D
R1/RRR1-10/2	1664.519	1664.896	-227.327	0.412	760.783	0.321	20	0.192	R.DCLLPM*GLTSENVAK.R
R1/RRR1-10/2	949.989	950.074	-89.329	0.445	608.889	0.244	12	0.190	K.VELFSQAR.D
R1/RRR1-2/2	1437.790	1437.671	82.720	0.404	934.439	0.435	15	0.212	K.VAESLGHVILGWR.W
R1/RRR1-2/2	1900.587	1900.130	241.215	0.520	566.567	0.531	18	0.205	K.NTGDGAGILVALPHNFFR.E
R1/RRR1-2/2	1436.980	1437.671	-1180.298	0.231	617.484	0.317	15	0.185	K.VAESLGHVILGWR.W
R1/RRR1-2/3	1821.950	1823.169	-1221.142	0.402	1166.033	0.155	27	0.070	-.AGLEM*AKKELMESIQK.-
R1/RRR1-7/2	1369.255	1369.635	-278.414	0.407	399.917	0.528	16	0.206	K.QQQILLATQVVK.M
R1/RRR1-6/2	1108.759	1109.214	-412.290	0.277	750.080	0.342	15	0.193	R.IAEGYELASR.I
R1/RRR1-6/2	1012.806	1013.213	-402.693	0.454	473.519	0.446	14	0.208	R.IPSVQELVK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1012.971	1013.213	-239.212	0.340	380.221	0.391	13	0.198	R.IPSVQELVK.K
R1/RRR1-6/2	1788.059	1787.993	37.140	0.467	836.576	0.383	18	0.196	K.LSVDNLDEVILVGGSTR.I
R1/RRR1-14/3	1756.876	1756.896	-11.270	0.560	2212.999	0.504	32	0.324	K.KGDNDLPGLTDTEKPR.M
R1/RRR1-20/3	1756.593	1756.896	-172.804	0.537	2058.713	0.500	31	0.286	K.KGDNDLPGLTDTEKPR.M
R1/RRR1-20/3	1756.575	1756.896	-182.948	0.498	1787.065	0.512	30	0.234	K.KGDNDLPGLTDTEKPR.M
R1/RRR1-14/3	1756.259	1756.896	-934.467	0.535	1685.900	0.511	28	0.220	K.KGDNDLPGLTDTEKPR.M
R1/RRR1-14/3	1757.356	1756.896	262.539	0.548	1513.795	0.542	28	0.202	K.KGDNDLPGLTDTEKPR.M
R1/RRR1-5/2	1607.061	1607.700	-1023.385	0.491	1401.197	0.516	19	0.272	K.VSSSYDASSQTFSLK.F
R1/RRR1-5/2	964.866	965.088	-231.216	0.397	873.227	0.242	12	0.191	K.SLNIFQSR.L
R1/RRR1-5/2	964.905	965.088	-190.349	0.409	915.420	0.174	13	0.186	K.SLNIFQSR.L
R1/RRR1-14/3	1770.299	1770.922	-919.656	0.556	2125.728	0.540	32	0.322	K.KGENDLPGLTDTEKPR.M
R1/RRR1-14/3	1771.005	1770.922	47.030	0.569	1829.949	0.550	31	0.260	K.KGENDLPGLTDTEKPR.M
R1/RRR1-19/3	1771.693	1770.922	-129.867	0.363	263.122	0.382	23	0.072	-.KGENDLPGLTDTEKPR.-
R1/RRR1-5/2	1494.585	1494.678	-61.982	0.476	911.518	0.593	21	0.243	R.LPATGEPIGQLQGGR.E
R1/RRR1-5/2	1494.233	1494.678	-298.555	0.448	680.178	0.574	19	0.222	R.LPATGEPIGQLQGGR.E
R1/RRR1-5/2	1364.801	1365.471	-1226.661	0.405	1047.441	0.379	15	0.213	K.NLEDEIYAEIR.A
R1/RRR1-6/2	1312.111	1311.430	-243.323	0.370	850.545	0.344	16	0.199	R.HDFFNYAGLAR.S
R1/RRR1-21/2	1254.541	1253.344	157.556	0.247	620.250	0.219	13	0.184	-.FDIQTSVSNGGK.-
R1/RRR1-19/2	1254.544	1253.344	160.093	0.241	829.999	0.143	15	0.182	R.FDIQTSVSNGGK.V
R1/RRR1-26/2	1254.486	1253.344	113.838	0.201	715.341	0.136	14	0.181	R.FDIQTSVSNGGK.V
R1/RRR1-27/2	1254.460	1253.344	93.247	0.262	860.606	0.122	15	0.181	R.FDIQTSVSNGGK.V
R1/RRR1-30/2	1254.555	1253.344	169.265	0.238	901.793	0.090	15	0.179	R.FDIQTSVSNGGK.V
R1/RRR1-29/2	1254.468	1253.344	99.395	0.222	534.100	0.112	12	0.174	-.FDIQTSVSNGGK.-
R1/RRR1-5/2	1731.372	1731.934	-905.073	0.522	1304.406	0.511	20	0.260	K.LNSELLNNLGNFINR.V
R1/RRR1-5/2	1730.992	1731.934	-1125.389	0.448	1233.750	0.422	19	0.233	K.LNSELLNNLGNFINR.V
R1/RRR1-7/2	1732.677	1731.934	-149.072	0.399	701.215	0.421	15	0.198	K.LNSELLNNLGNFINR.V
R1/RRR1-5/2	1254.464	1253.470	-4.842	0.299	740.952	0.346	14	0.192	K.LLNPTELIDPK.C
R1/RRR1-26/2	1303.497	1304.437	-1493.064	0.451	2067.844	0.530	23	0.376	K.NVAAGAAGGPYISR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-26/2	1304.033	1304.437	-310.460	0.520	2016.322	0.543	23	0.372	K.NVAAGAAGGPYISR.A
R1/RRR1-25/2	1304.078	1304.437	-276.368	0.527	2035.042	0.531	23	0.371	K.NVAAGAAGGPYISR.A
R1/RRR1-25/2	1303.527	1304.437	-1469.547	0.460	2033.624	0.528	23	0.369	K.NVAAGAAGGPYISR.A
R1/RRR1-25/2	1304.029	1304.437	-313.465	0.509	1935.639	0.550	23	0.360	K.NVAAGAAGGPYISR.A
R1/RRR1-26/2	1304.162	1304.437	-211.760	0.539	1834.758	0.558	22	0.345	K.NVAAGAAGGPYISR.A
R1/RRR1-14/2	1235.798	1236.399	-1299.626	0.515	2339.737	0.413	19	0.388	R.VYVLSVEGDVR.E
R1/RRR1-13/2	1236.135	1236.399	-214.598	0.364	1396.769	0.307	16	0.227	R.VYVLSVEGDVR.E
R1/RRR1-13/2	1236.381	1236.399	-14.816	0.387	597.211	0.286	13	0.187	-.VYVLSVEGDVR.-
R1/RRR1-10/2	1485.564	1484.640	-50.984	0.378	876.391	0.425	20	0.209	K.NGAAPATTDGLLGLGR.G
R1/RRR1-3/2	1485.563	1484.640	-51.644	0.326	584.226	0.340	17	0.188	K.NGAAPATTDGLLGLGR.G
R1/RRR1-10/2	1031.576	1032.216	-1594.419	0.245	1037.637	0.166	13	0.183	R.GSVSLLSQLK.Q
R1/RRR1-10/2	1208.228	1208.300	-59.546	0.367	1371.652	0.341	18	0.232	K.VDFGDIDGLEK.I
R1/RRR1-10/2	1208.248	1208.300	-42.419	0.390	1066.761	0.407	16	0.220	K.VDFGDIDGLEK.I
R1/RRR1-9/2	1741.030	1740.938	52.982	0.425	841.384	0.322	18	0.193	K.AFSDVLEHDLPQLQK.Q
R1/RRR1-10/2	1741.210	1740.938	157.115	0.421	515.634	0.394	13	0.187	K.AFSDVLEHDLPQLQK.Q
R1/RRR1-3/2	1512.371	1512.776	-269.069	0.468	1462.204	0.554	21	0.291	R.LPLITISDSGNLLR.D
R1/RRR1-3/2	1512.214	1512.776	-1036.241	0.485	1268.006	0.574	20	0.273	R.LPLITISDSGNLLR.D
R1/RRR1-4/2	1512.514	1512.776	-174.171	0.471	1070.050	0.500	18	0.236	R.LPLITISDSGNLLR.D
R1/RRR1-3/2	1577.707	1577.892	-117.385	0.420	1268.400	0.422	17	0.236	R.LPVLYVAYAEGLIR.A
R1/RRR1-24/2	1269.054	1268.491	-345.549	0.515	1974.445	0.558	20	0.368	R.IVVAGNQIAVQR.T
R1/RRR1-13/2	1268.192	1268.491	-236.302	0.506	1899.005	0.498	19	0.335	R.IVVAGNQIAVQR.T
R1/RRR1-18/2	1268.238	1268.491	-199.801	0.482	1897.849	0.486	19	0.331	R.IVVAGNQIAVQR.T
R1/RRR1-13/2	1268.194	1268.491	-235.144	0.513	1864.527	0.502	19	0.330	R.IVVAGNQIAVQR.T
R1/RRR1-24/2	1268.111	1268.491	-300.427	0.469	1869.711	0.429	19	0.309	R.IVVAGNQIAVQR.T
R1/RRR1-12/2	1268.279	1268.491	-167.745	0.488	1835.264	0.440	19	0.307	R.IVVAGNQIAVQR.T
R1/RRR1-12/2	1268.003	1268.491	-386.100	0.479	1721.518	0.470	18	0.300	R.IVVAGNQIAVQR.T
R1/RRR1-13/2	1267.627	1268.491	-1475.139	0.409	1557.691	0.483	18	0.282	R.IVVAGNQIAVQR.T
R1/RRR1-12/2	1267.640	1268.491	-1464.209	0.413	1675.486	0.420	19	0.281	R.IVVAGNQIAVQR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1268.057	1268.491	-343.117	0.391	1629.639	0.414	17	0.273	R.IVVAGNQIAVQR.T
R1/RRR1-25/2	1268.146	1268.491	-272.806	0.482	1579.015	0.430	18	0.271	R.IVVAGNQIAVQR.T
R1/RRR1-19/2	1268.067	1268.491	-335.197	0.453	1403.873	0.493	17	0.267	R.IVVAGNQIAVQR.T
R1/RRR1-24/2	1267.745	1268.491	-1381.030	0.400	1503.303	0.357	19	0.248	R.IVVAGNQIAVQR.T
R1/RRR1-12/2	1677.463	1677.873	-245.215	0.572	1880.587	0.600	24	0.368	K.VPNDVCADVVYNAIK.V
R1/RRR1-12/2	1676.808	1677.873	-1235.576	0.575	1703.733	0.573	23	0.330	K.VPNDVCADVVYNAIK.V
R1/RRR1-12/2	1676.224	1677.873	-2183.667	0.363	1277.907	0.498	19	0.251	K.VPNDVCADVVYNAIK.V
R1/RRR1-13/2	1678.862	1677.873	-7.046	0.397	762.111	0.405	18	0.202	K.VPNDVCADVVYNAIK.V
R1/RRR1-6/2	1454.642	1453.621	14.173	0.389	1111.615	0.477	17	0.233	R.IWLDYADASAISK.G
R1/RRR1-6/2	1486.487	1486.740	-171.043	0.356	755.463	0.418	15	0.198	R.SSKPVVLFAIPDGR.Q
R1/RRR1-14/2	1525.947	1526.674	-1135.154	0.379	1918.897	0.547	23	0.354	R.LIAATYSGSTPTTSR.C
R1/RRR1-14/2	1526.301	1526.674	-244.874	0.491	1640.516	0.603	22	0.329	R.LIAATYSGSTPTTSR.C
R1/RRR1-14/2	1526.075	1526.674	-1050.657	0.412	1717.672	0.565	22	0.327	R.LIAATYSGSTPTTSR.C
R1/RRR1-6/2	1413.303	1413.514	-149.925	0.549	2036.540	0.521	23	0.369	R.FGGALDGAAEEFTK.A
R1/RRR1-6/2	1412.604	1413.514	-1355.986	0.475	2050.810	0.499	23	0.365	R.FGGALDGAAEEFTK.A
R1/RRR1-6/2	1413.094	1413.514	-297.849	0.538	1953.922	0.519	23	0.354	R.FGGALDGAAEEFTK.A
R1/RRR1-11/2	1701.086	1700.920	98.059	0.601	1929.097	0.561	27	0.359	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-15/2	1700.457	1700.920	-273.148	0.582	1753.199	0.570	26	0.333	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-11/2	1700.558	1700.920	-213.374	0.581	1675.317	0.560	25	0.318	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-11/2	1700.484	1700.920	-257.087	0.571	1423.913	0.560	24	0.285	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-14/2	1701.418	1700.920	293.343	0.602	1439.810	0.561	23	0.285	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-19/2	1700.322	1700.920	-942.771	0.503	1548.277	0.501	24	0.284	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-15/2	1702.184	1700.920	155.251	0.548	1560.164	0.488	23	0.280	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-15/2	1700.244	1700.920	-988.541	0.532	1330.400	0.572	23	0.277	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-15/2	1700.210	1700.920	-1009.085	0.542	1189.739	0.593	22	0.267	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-19/2	1702.133	1700.920	125.692	0.589	1226.047	0.517	22	0.251	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-15/2	1701.268	1700.920	204.848	0.542	1200.753	0.515	22	0.249	R.NLAGNSAIFVAPNGLNK.G
R1/RRR1-13/2	1700.604	1700.920	-186.441	0.506	1235.166	0.479	22	0.245	R.NLAGNSAIFVAPNGLNK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1702.106	1700.920	109.365	0.373	456.714	0.346	15	0.189	-.NLAGNSAIFVAPNGLNK.-
R1/RRR1-6/2	1667.828	1666.881	-31.735	0.525	2106.542	0.481	22	0.367	R.FASEVAGVQDLGM*LGR.G
R1/RRR1-3/2	1665.589	1666.881	-1380.161	0.229	672.603	0.124	16	0.175	R.FASEVAGVQDLGM*LGR.G
R1/RRR1-5/2	1899.299	1899.178	64.038	0.444	949.262	0.480	19	0.217	K.LALGTLALEDALSTGSPIR.T
R1/RRR1-13/3	1098.147	1098.148	-1.641	0.410	1305.450	0.207	21	0.082	K.DPSSAGAVEHK.S
R1/RRR1-14/2	1313.538	1312.540	-2.014	0.503	1858.589	0.580	22	0.360	K.LEAPVVIVTGASR.G
R1/RRR1-14/2	1312.223	1312.540	-242.369	0.403	1015.035	0.546	17	0.239	K.LEAPVVIVTGASR.G
R1/RRR1-11/2	1139.038	1139.288	-220.530	0.350	906.671	0.286	14	0.195	R.FNVFKDNVR.L
R1/RRR1-10/2	1627.227	1625.862	224.854	0.330	726.374	0.305	15	0.184	K.EGLCGIAMEASYPVK.T
R1/RRR1-9/2	1389.113	1389.487	-270.115	0.462	2210.004	0.427	21	0.373	R.VVLDCATADPDGR.K
R1/RRR1-3/2	1358.438	1357.580	-104.246	0.533	1411.556	0.512	19	0.276	K.IPSVNDIPLNFK.V
R1/RRR1-3/2	1357.245	1357.580	-247.229	0.517	1425.576	0.497	19	0.273	K.IPSVNDIPLNFK.V
R1/RRR1-3/2	1359.459	1359.551	-67.692	0.401	1130.452	0.538	18	0.248	K.LIIGNSEVGVETK.F
R1/RRR1-3/2	1357.297	1357.580	-209.153	0.354	592.336	0.444	13	0.199	K.IPSVNDIPLNFK.V
R1/RRR1-2/2	1358.607	1357.580	20.312	0.362	794.022	0.278	15	0.191	K.IPSVNDIPLNFK.V
R1/RRR1-11/2	1498.356	1497.674	-212.915	0.345	1034.350	0.378	16	0.209	R.VPTFTSVDDFLQK.V
R1/RRR1-13/2	1078.106	1077.174	-63.099	0.171	867.792	0.102	16	0.175	K.SSNSGVSVALR.N
R1/RRR1-11/2	1088.099	1088.283	-169.304	0.500	1999.691	0.523	19	0.364	R.VVGVLLGTSSR.G
R1/RRR1-11/2	1088.158	1088.283	-115.061	0.467	1725.813	0.615	18	0.347	R.VVGVLLGTSSR.G
R1/RRR1-11/2	1087.969	1088.283	-289.626	0.417	1904.278	0.509	18	0.342	R.VVGVLLGTSSR.G
R1/RRR1-12/2	1619.288	1618.813	294.158	0.572	1813.743	0.599	22	0.357	K.VPVENTAQAVYDAIK.L
R1/RRR1-12/2	1617.874	1618.813	-1201.728	0.499	1120.293	0.527	20	0.246	K.VPVENTAQAVYDAIK.L
R1/RRR1-13/2	1767.353	1765.947	230.164	0.563	2019.345	0.512	21	0.364	K.AFLQQWSSSLAEELR.A
R1/RRR1-2/2	1788.922	1789.087	-92.919	0.537	1705.562	0.445	22	0.289	R.M*LAISALNTLLQGSPDK.A
R1/RRR1-2/2	1109.301	1109.218	75.869	0.313	803.648	0.404	15	0.201	K.NAVTSVAFSGR.A
R1/RRR1-3/2	1789.220	1789.087	74.545	0.457	812.243	0.322	17	0.188	-.M*LAISALNTLLQGSPDK.-
R1/RRR1-21/2	1355.056	1355.542	-359.935	0.516	2057.126	0.489	20	0.360	R.FSQVVSNALDM*K.L
R1/RRR1-20/2	1355.018	1355.542	-1128.529	0.471	1849.662	0.455	19	0.316	R.FSQVVSNALDM*K.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1355.144	1355.542	-295.041	0.518	1751.438	0.462	19	0.303	R.FSQVVSNALDM*K.L
R1/RRR1-21/2	1355.166	1355.542	-278.593	0.543	1665.244	0.495	19	0.301	R.FSQVVSNALDM*K.L
R1/RRR1-21/2	1339.185	1339.543	-268.026	0.427	1490.621	0.492	19	0.278	R.FSQVVSNALDMK.L
R1/RRR1-21/2	1338.954	1339.543	-1190.081	0.417	1150.830	0.489	16	0.241	R.FSQVVSNALDMK.L
R1/RRR1-7/2	1752.379	1752.904	-872.913	0.524	1972.231	0.523	22	0.354	R.SFGTDLDTATNELVIR.V
R1/RRR1-7/2	1752.092	1752.904	-1037.204	0.472	1243.208	0.422	21	0.234	R.SFGTDLDTATNELVIR.V
R1/RRR1-1/2	1754.390	1752.904	277.856	0.387	684.479	0.340	18	0.193	R.SFGTDLDTATNELVIR.V
R1/RRR1-1/2	1754.310	1752.904	232.364	0.365	218.479	0.282	13	0.189	R.SFGTDLDTATNELVIR.V
R1/RRR1-4/2	1754.178	1752.904	156.652	0.336	368.285	0.311	15	0.188	R.SFGTDLDTATNELVIR.V
R1/RRR1-19/2	1587.342	1587.755	-260.988	0.471	1988.521	0.506	25	0.351	K.LAFGSLGDSFSATSVK.A
R1/RRR1-19/2	1587.210	1587.755	-976.633	0.481	1854.272	0.545	25	0.342	K.LAFGSLGDSFSATSVK.A
R1/RRR1-18/2	1588.179	1587.755	267.695	0.522	1716.876	0.585	24	0.333	K.LAFGSLGDSFSATSVK.A
R1/RRR1-18/2	1587.410	1587.755	-218.170	0.498	1759.084	0.551	24	0.329	K.LAFGSLGDSFSATSVK.A
R1/RRR1-18/2	1588.278	1587.755	-301.460	0.508	1774.509	0.541	24	0.328	K.LAFGSLGDSFSATSVK.A
R1/RRR1-17/2	1587.291	1587.755	-293.625	0.412	1697.210	0.498	24	0.304	K.LAFGSLGDSFSATSVK.A
R1/RRR1-2/2	1587.687	1587.755	-43.078	0.421	1830.210	0.410	24	0.298	K.LAFGSLGDSFSATSVK.A
R1/RRR1-1/2	1587.871	1587.755	72.819	0.444	1608.759	0.474	23	0.285	K.LAFGSLGDSFSATSVK.A
R1/RRR1-17/2	1587.284	1587.755	-297.637	0.457	1331.998	0.537	22	0.269	K.LAFGSLGDSFSATSVK.A
R1/RRR1-17/2	1586.397	1587.755	-1491.223	0.354	1482.379	0.462	22	0.266	K.LAFGSLGDSFSATSVK.A
R1/RRR1-4/2	1587.325	1587.755	-272.021	0.408	1094.981	0.458	20	0.229	K.LAFGSLGDSFSATSVK.A
R1/RRR1-2/2	1587.453	1587.755	-191.169	0.327	1208.390	0.248	20	0.203	K.LAFGSLGDSFSATSVK.A
R1/RRR1-6/2	1586.743	1587.755	-1271.988	0.273	1175.831	0.230	20	0.199	K.LAFGSLGDSFSATSVK.A
R1/RRR1-13/3	1724.691	1723.826	-78.602	0.597	2061.101	0.485	33	0.276	K.KPTGTNDVVNSGYQSR.N
R1/RRR1-13/3	1723.184	1723.826	-955.707	0.542	1779.155	0.430	30	0.201	K.KPTGTNDVVNSGYQSR.N
R1/RRR1-13/3	1723.761	1723.826	-37.483	0.513	1745.375	0.385	29	0.181	K.KPTGTNDVVNSGYQSR.N
R1/RRR1-14/3	1723.394	1723.826	-251.049	0.516	1369.183	0.403	27	0.138	K.KPTGTNDVVNSGYQSR.N
R1/RRR1-14/3	1723.067	1723.826	-1023.454	0.439	1305.519	0.333	28	0.110	K.KPTGTNDVVNSGYQSR.N
R1/RRR1-14/3	1723.024	1723.826	-1048.955	0.451	829.626	0.359	24	0.091	K.KPTGTNDVVNSGYQSR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1504.054	1503.767	191.331	0.515	2207.786	0.413	21	0.366	-.TNM*VM*VFGEITTK.-
R1/RRR1-10/2	1503.154	1503.767	-1076.291	0.501	2076.471	0.399	20	0.333	K.TNM*VM*VFGEITTK.A
R1/RRR1-9/2	1503.301	1503.767	-310.438	0.505	1911.220	0.433	20	0.318	K.TNM*VM*VFGEITTK.A
R1/RRR1-10/2	1503.020	1503.767	-1165.504	0.490	1885.900	0.422	20	0.315	-.TNM*VM*VFGEITTK.-
R1/RRR1-10/2	1503.360	1503.767	-271.415	0.517	1698.640	0.393	19	0.275	K.TNM*VM*VFGEITTK.A
R1/RRR1-4/2	1032.977	1033.246	-261.071	0.473	947.395	0.446	16	0.224	K.TFASGIIVPK.K
R1/RRR1-4/2	1033.100	1033.246	-141.104	0.395	748.237	0.377	13	0.201	K.TFASGIIVPK.K
R1/RRR1-4/2	1032.414	1033.246	-1779.315	0.350	664.544	0.281	13	0.189	-.TFASGIIVPK.-
R1/RRR1-14/2	1536.481	1536.841	-235.123	0.487	1922.861	0.522	21	0.349	R.ALALQENPGLVILGK.Q
R1/RRR1-14/2	1536.868	1536.841	17.637	0.461	1573.116	0.497	20	0.288	R.ALALQENPGLVILGK.Q
R1/RRR1-4/2	1178.299	1177.332	-28.327	0.393	1205.030	0.405	15	0.232	-.SFEVTELPVR.-
R1/RRR1-4/2	1196.046	1196.338	-244.926	0.471	909.965	0.495	16	0.228	K.HNEIQTVNIK.T
R1/RRR1-4/2	1796.326	1794.924	224.473	0.488	844.914	0.505	18	0.216	K.LAGFSFSSSSSQASM*QR.N
R1/RRR1-6/2	828.903	828.976	-89.159	0.344	1076.284	0.180	11	0.192	-.KDDILPK.-
R1/RRR1-6/2	828.382	828.976	-1930.532	0.257	1143.391	0.107	11	0.186	-.KDDILPK.-
R1/RRR1-6/2	828.894	828.976	-99.056	0.247	1232.801	0.067	12	0.183	R.KDDILPK.L
R1/RRR1-7/2	1919.825	1921.058	-1166.736	0.335	730.163	0.438	16	0.196	R.DGGFNYASTDLAALWYR.L
R1/RRR1-7/3	1658.908	1657.855	31.609	0.369	960.727	0.450	25	0.104	K.TNHVGFGLVLGSDGKR.F
R1/RRR1-3/2	1315.319	1315.458	-105.988	0.456	970.576	0.456	14	0.223	R.FTWTIENFTR.I
R1/RRR1-3/2	1315.044	1315.458	-315.774	0.423	1050.851	0.343	15	0.210	R.FTWTIENFTR.I
R1/RRR1-4/2	1193.382	1193.334	39.745	0.384	1000.274	0.277	17	0.198	R.AVAYLLSNADR.V
R1/RRR1-4/2	1219.410	1220.466	-1691.286	0.353	968.626	0.233	16	0.192	R.M*LGPNYVPGKK.T
R1/RRR1-4/2	1268.428	1267.420	6.119	0.318	872.376	0.229	14	0.182	K.AGIISAKHAGDAR.F
R1/RRR1-4/2	1220.034	1220.466	-355.700	0.361	624.023	0.147	14	0.177	-.M*LGPNYVPGKK.-
R1/RRR1-4/2	1220.203	1220.466	-216.377	0.405	605.897	0.149	14	0.169	-.M*LGPNYVPGKK.-
R1/RRR1-26/2	1376.099	1375.507	-297.315	0.510	1897.058	0.507	18	0.338	R.EGDILTLLESER.E
R1/RRR1-25/2	1375.252	1375.507	-185.857	0.466	1856.257	0.526	18	0.338	R.EGDILTLLESER.E
R1/RRR1-25/2	1376.225	1375.507	-205.387	0.519	1931.828	0.474	18	0.333	R.EGDILTLLESER.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-25/2	1376.352	1375.507	-112.941	0.514	1717.631	0.535	18	0.320	R.EGDILTLLESER.E
R1/RRR1-26/2	1375.151	1375.507	-259.680	0.448	1586.756	0.441	18	0.276	R.EGDILTLLESER.E
R1/RRR1-26/2	1374.555	1375.507	-1424.608	0.350	1457.407	0.467	18	0.265	R.EGDILTLLESER.E
R1/RRR1-16/2	1135.000	1135.204	-180.215	0.536	2141.891	0.409	20	0.351	R.CLAEASADAAR.S
R1/RRR1-16/2	1134.321	1135.204	-1664.472	0.436	1101.274	0.416	17	0.226	R.CLAEASADAAR.S
R1/RRR1-13/2	1794.310	1794.001	172.868	0.522	1781.037	0.551	25	0.334	R.DIPLNYATFQPGTTVR.D
R1/RRR1-13/2	1794.320	1794.001	178.326	0.503	1621.105	0.558	25	0.312	R.DIPLNYATFQPGTTVR.D
R1/RRR1-13/2	1793.386	1794.001	-903.132	0.476	1493.543	0.513	24	0.283	R.DIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1793.845	1794.001	-86.929	0.492	1134.088	0.488	22	0.240	R.DIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1795.400	1794.001	223.091	0.530	1112.085	0.500	20	0.238	R.DIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1794.425	1794.001	236.995	0.556	835.478	0.538	20	0.227	R.DIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1793.331	1794.001	-934.088	0.425	723.501	0.496	18	0.213	R.DIPLNYATFQPGTTVR.D
R1/RRR1-14/2	1792.699	1794.001	-1287.582	0.318	1004.010	0.381	21	0.211	R.DIPLNYATFQPGTTVR.D
R1/RRR1-6/2	961.910	962.084	-181.777	0.379	1022.864	0.275	13	0.200	R.SPINFIDR.F
R1/RRR1-6/2	1494.321	1494.675	-237.578	0.297	988.973	0.224	17	0.185	K.AGSSLYGIADLASLR.A
R1/RRR1-6/2	961.824	962.084	-271.537	0.379	630.632	0.192	11	0.184	-.SPINFIDR.-
R1/RRR1-2/2	1631.810	1630.910	-61.346	0.502	2037.795	0.424	22	0.337	R.LDQPIILTGFSALNK.L
R1/RRR1-2/2	1631.147	1630.910	145.724	0.325	757.855	0.295	17	0.188	R.LDQPIILTGFSALNK.L
R1/RRR1-1/2	1124.217	1124.355	-123.568	0.328	815.670	0.354	13	0.195	R.ILLLDASPPGK.E
R1/RRR1-1/3	1913.556	1914.066	-791.503	0.446	1181.743	0.457	30	0.132	R.LGM*EKGEGM*SAVADSGEGR.G
R1/RRR1-1/3	1913.667	1914.066	-208.791	0.455	954.865	0.435	29	0.110	R.LGM*EKGEGM*SAVADSGEGR.G
R1/RRR1-1/3	1913.314	1914.066	-918.499	0.428	944.847	0.440	29	0.109	R.LGM*EKGEGM*SAVADSGEGR.G
R1/RRR1-9/3	1913.868	1914.066	-103.789	0.417	781.880	0.463	25	0.105	-.LGM*EKGEGM*SAVADSGEGR.-
R1/RRR1-9/3	1914.217	1914.066	79.481	0.471	823.609	0.398	26	0.099	R.LGM*EKGEGM*SAVADSGEGR.G
R1/RRR1-5/3	1912.294	1914.066	-1978.427	0.315	738.038	0.283	25	0.078	R.LGM*EKGEGM*SAVADSGEGR.G
R1/RRR1-20/2	1868.598	1869.018	-225.505	0.560	1568.205	0.613	22	0.321	K.LPDATLSYFDSPDGELK.T
R1/RRR1-10/3	1926.475	1926.157	165.451	0.526	1875.894	0.506	33	0.254	K.SIALDVEELADNLQLGPK.F
R1/RRR1-10/3	1926.604	1926.157	232.358	0.514	1829.779	0.491	36	0.232	K.SIALDVEELADNLQLGPK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1925.187	1926.157	-1026.537	0.351	672.604	0.393	27	0.086	K.SIALDVEELADNLQLGPK.F
R1/RRR1-16/2	1524.289	1524.703	-272.105	0.419	1696.852	0.555	21	0.322	K.GVNPWIEVDGGVGPK.N
R1/RRR1-16/2	1524.165	1524.703	-1011.969	0.316	1166.103	0.516	18	0.241	K.GVNPWIEVDGGVGPK.N
R1/RRR1-1/2	1747.461	1746.982	274.894	0.585	2001.774	0.453	25	0.341	K.NEILAESEFAAPTIIK.L
R1/RRR1-22/2	1524.251	1523.713	-303.841	0.525	1940.507	0.476	22	0.334	R.LSYGAISDLSGIQAK.K
R1/RRR1-23/2	1523.293	1523.713	-276.503	0.481	1980.215	0.448	22	0.332	R.LSYGAISDLSGIQAK.K
R1/RRR1-22/2	1523.148	1523.713	-1030.329	0.428	1868.349	0.451	21	0.316	R.LSYGAISDLSGIQAK.K
R1/RRR1-22/2	1523.246	1523.713	-307.176	0.465	1747.264	0.457	21	0.300	R.LSYGAISDLSGIQAK.K
R1/RRR1-23/2	1523.306	1523.713	-267.539	0.502	1777.923	0.435	21	0.297	R.LSYGAISDLSGIQAK.K
R1/RRR1-1/2	1523.496	1523.713	-142.617	0.319	1138.581	0.221	18	0.194	R.LSYGAISDLSGIQAK.K
R1/RRR1-7/2	1701.201	1699.974	133.893	0.567	1422.800	0.642	20	0.309	K.LALQGLNALLQQSTTK.T
R1/RRR1-11/2	1932.676	1933.152	-246.980	0.517	1700.862	0.559	24	0.323	R.SFLQAVSTVTEEAPSPLR.V
R1/RRR1-11/2	1932.898	1933.152	-131.413	0.502	1519.674	0.577	23	0.302	R.SFLQAVSTVTEEAPSPLR.V
R1/RRR1-11/2	1932.607	1933.152	-801.835	0.432	1325.829	0.475	22	0.252	R.SFLQAVSTVTEEAPSPLR.V
R1/RRR1-6/2	1589.128	1587.888	151.426	0.489	931.973	0.470	19	0.221	K.LLVFQSTLPSLGVGR.L
R1/RRR1-4/2	1560.534	1560.692	-101.259	0.432	434.596	0.505	17	0.208	R.TYINPYATFADAGR.K
R1/RRR1-5/2	1560.621	1560.692	-45.237	0.385	587.254	0.454	17	0.204	R.TYINPYATFADAGR.K
R1/RRR1-5/2	1560.629	1560.692	-39.981	0.358	667.637	0.432	15	0.200	R.TYINPYATFADAGR.K
R1/RRR1-4/2	1560.655	1560.692	-23.505	0.394	353.806	0.447	15	0.199	R.TYINPYATFADAGR.K
R1/RRR1-6/2	1587.981	1587.888	58.782	0.410	695.254	0.373	16	0.194	K.LLVFQSTLPSLGVGR.L
R1/RRR1-4/2	1587.464	1587.888	-268.141	0.345	478.675	0.393	16	0.192	K.LLVFQSTLPSLGVGR.L
R1/RRR1-4/2	1560.935	1560.692	156.279	0.126	242.807	0.376	18	0.186	R.TYINPYATFADAGR.K
R1/RRR1-24/2	1557.074	1557.734	-1069.134	0.422	1880.847	0.477	19	0.328	R.TNYAQWVSAITFR.V
R1/RRR1-19/2	1559.170	1557.734	280.685	0.390	435.013	0.402	15	0.195	R.TNYAQWVSAITFR.V
R1/RRR1-12/2	1476.194	1475.580	-262.558	0.556	1733.760	0.547	21	0.329	K.IEDLQVVDEGETK.S
R1/RRR1-12/2	1475.421	1475.580	-108.179	0.461	1230.775	0.491	20	0.251	K.IEDLQVVDEGETK.S
R1/RRR1-19/2	1239.290	1238.372	-66.550	0.433	1654.378	0.558	20	0.319	K.YSGNDLLGVTAK.V
R1/RRR1-19/2	1238.601	1238.372	185.482	0.264	663.784	0.321	14	0.187	K.YSGNDLLGVTAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1643.437	1643.908	-287.617	0.483	1628.326	0.572	25	0.318	K.NLVAPVIGEANLAAYK.A
R1/RRR1-15/2	1644.066	1643.908	95.949	0.458	1485.714	0.597	24	0.304	K.NLVAPVIGEANLAAYK.A
R1/RRR1-16/2	1643.687	1643.908	-134.870	0.456	1386.528	0.570	23	0.284	K.NLVAPVIGEANLAAYK.A
R1/RRR1-18/2	1643.479	1643.908	-261.982	0.222	181.133	0.357	12	0.182	-.NLVAPVIGEANLAAYK.-
R1/RRR1-17/2	1188.084	1188.268	-155.468	0.501	1750.574	0.536	18	0.324	R.FDDSFSAASLK.A
R1/RRR1-6/2	1187.898	1188.268	-312.571	0.438	1700.495	0.530	18	0.314	R.FDDSFSAASLK.A
R1/RRR1-18/2	1188.025	1188.268	-205.150	0.480	1789.094	0.478	18	0.312	R.FDDSFSAASLK.A
R1/RRR1-16/2	1188.063	1188.268	-173.402	0.435	1669.769	0.534	18	0.311	R.FDDSFSAASLK.A
R1/RRR1-19/2	1189.070	1188.268	-167.077	0.531	1599.572	0.556	18	0.309	R.FDDSFSAASLK.A
R1/RRR1-17/2	1188.104	1188.268	-138.359	0.470	1663.507	0.507	18	0.303	R.FDDSFSAASLK.A
R1/RRR1-10/2	1188.991	1188.268	-234.125	0.477	1426.673	0.577	17	0.292	R.FDDSFSAASLK.A
R1/RRR1-4/2	1188.027	1188.268	-203.707	0.487	1489.080	0.534	17	0.288	R.FDDSFSAASLK.A
R1/RRR1-4/2	1188.079	1188.268	-159.797	0.461	1446.467	0.534	17	0.283	R.FDDSFSAASLK.A
R1/RRR1-5/2	1187.946	1188.268	-272.363	0.401	1555.974	0.487	17	0.283	R.FDDSFSAASLK.A
R1/RRR1-8/2	1187.934	1188.268	-282.466	0.356	1697.730	0.383	17	0.273	R.FDDSFSAASLK.A
R1/RRR1-6/2	1188.207	1188.268	-51.481	0.400	1364.579	0.496	17	0.264	R.FDDSFSAASLK.A
R1/RRR1-16/2	1188.149	1188.268	-100.947	0.414	1472.462	0.438	17	0.262	R.FDDSFSAASLK.A
R1/RRR1-14/2	1188.089	1188.268	-151.242	0.411	1469.601	0.407	17	0.255	R.FDDSFSAASLK.A
R1/RRR1-19/2	1187.952	1188.268	-267.002	0.409	1153.630	0.488	16	0.243	R.FDDSFSAASLK.A
R1/RRR1-17/2	1187.967	1188.268	-254.631	0.417	1235.784	0.453	16	0.243	R.FDDSFSAASLK.A
R1/RRR1-18/2	1187.439	1188.268	-1545.266	0.411	1443.394	0.357	18	0.243	R.FDDSFSAASLK.A
R1/RRR1-13/2	1188.226	1188.268	-36.127	0.429	1223.376	0.446	16	0.241	R.FDDSFSAASLK.A
R1/RRR1-4/2	1188.179	1188.268	-75.698	0.378	1084.288	0.482	15	0.235	R.FDDSFSAASLK.A
R1/RRR1-18/2	1187.576	1188.268	-1429.205	0.396	1212.936	0.338	17	0.222	R.FDDSFSAASLK.A
R1/RRR1-12/2	1187.312	1188.268	-1652.676	0.283	990.403	0.454	15	0.221	R.FDDSFSAASLK.A
R1/RRR1-11/2	1188.027	1188.268	-203.913	0.330	912.860	0.440	16	0.219	R.FDDSFSAASLK.A
R1/RRR1-13/2	1188.241	1188.268	-23.350	0.291	1226.651	0.235	16	0.206	R.FDDSFSAASLK.A
R1/RRR1-16/2	1187.931	1188.268	-285.146	0.315	687.404	0.364	15	0.203	R.FDDSFSAASLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-19/2	1188.055	1188.268	-180.411	0.272	487.157	0.362	12	0.197	R.FDDSFSAASLK.A
R1/RRR1-7/2	1754.046	1754.961	-1095.102	0.466	1649.442	0.563	23	0.318	K.EGVAFYNSLIDDVIAK.G
R1/RRR1-7/2	1754.117	1754.961	-1054.783	0.486	1666.144	0.550	23	0.317	K.EGVAFYNSLIDDVIAK.G
R1/RRR1-7/2	1754.537	1754.961	-242.677	0.480	1186.688	0.564	20	0.259	K.EGVAFYNSLIDDVIAK.G
R1/RRR1-10/2	1908.703	1909.045	-180.098	0.531	1500.305	0.604	24	0.308	R.DSGAFSWEIAPVEISSGR.G
R1/RRR1-10/2	1908.321	1909.045	-906.353	0.464	1224.574	0.563	22	0.262	R.DSGAFSWEIAPVEISSGR.G
R1/RRR1-12/2	1764.309	1764.875	-889.980	0.549	1767.526	0.521	19	0.321	K.LISWYDNEFGYSNR.V
R1/RRR1-12/2	1764.331	1764.875	-877.687	0.530	1508.435	0.598	18	0.307	K.LISWYDNEFGYSNR.V
R1/RRR1-12/2	1764.207	1764.875	-948.120	0.484	1709.187	0.496	19	0.306	K.LISWYDNEFGYSNR.V
R1/RRR1-11/2	1214.810	1215.298	-403.510	0.518	1761.607	0.517	22	0.323	R.AVAGGGAAGEEAVR.A
R1/RRR1-11/2	1215.131	1215.298	-138.405	0.493	1520.606	0.502	21	0.285	R.AVAGGGAAGEEAVR.A
R1/RRR1-11/2	1214.578	1215.298	-1420.415	0.459	1528.739	0.493	21	0.283	R.AVAGGGAAGEEAVR.A
R1/RRR1-10/2	1755.601	1753.845	-139.803	0.411	1875.099	0.457	21	0.322	R.YDATADDLIDVIEGSR.I
R1/RRR1-9/2	1483.745	1483.607	93.361	0.506	1882.465	0.462	22	0.325	R.NPYYGGEAASVNLK.T
R1/RRR1-9/2	1485.010	1483.607	271.782	0.529	1556.820	0.462	20	0.278	R.NPYYGGEAASVNLK.T
R1/RRR1-7/2	1886.295	1886.097	105.566	0.498	1777.497	0.493	23	0.315	R.LVAFVADLFGADSFDAAR.D
R1/RRR1-15/2	1887.759	1886.097	-179.178	0.313	410.922	0.340	16	0.184	R.LVAFVADLFGADSFDAAR.D
R1/RRR1-4/3	1388.689	1388.554	97.273	0.418	1141.784	0.344	22	0.095	K.IHELSDKDFKR.N
R1/RRR1-4/3	1391.680	1390.520	115.099	0.452	1236.385	0.252	23	0.084	K.CYHQIEGLNQK.N
R1/RRR1-4/3	1390.568	1390.520	34.539	0.380	1010.434	0.174	21	0.067	K.CYHQIEGLNQK.N
R1/RRR1-15/2	1264.138	1264.453	-249.167	0.554	1627.800	0.543	19	0.311	K.DIGNAVYALISK.E
R1/RRR1-15/2	1263.893	1264.453	-1237.412	0.557	1679.769	0.518	19	0.311	K.DIGNAVYALISK.E
R1/RRR1-15/2	1264.078	1264.453	-297.511	0.490	1390.058	0.536	18	0.278	K.DIGNAVYALISK.E
R1/RRR1-11/2	1603.022	1603.708	-1055.293	0.504	1364.152	0.617	22	0.295	K.AGDTVGVGYFVDSCR.A
R1/RRR1-11/2	1604.317	1603.708	-244.719	0.553	1342.501	0.624	22	0.295	K.AGDTVGVGYFVDSCR.A
R1/RRR1-11/2	1602.541	1603.708	-1356.249	0.383	1239.441	0.587	21	0.268	K.AGDTVGVGYFVDSCR.A
R1/RRR1-3/2	972.829	972.164	-345.552	0.392	1428.177	0.347	15	0.239	R.VAILETVAR.Y
R1/RRR1-3/2	1157.088	1157.259	-148.416	0.409	1109.284	0.326	16	0.212	R.ISQDDVPQVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1156.829	1157.259	-372.403	0.417	967.934	0.348	16	0.208	R.ISQDDVPQVR.K
R1/RRR1-8/2	1818.441	1818.148	161.148	0.488	1416.236	0.595	24	0.293	R.TSIPGIFAIGDVAAFPLK.M
R1/RRR1-8/2	1818.350	1818.148	111.060	0.493	799.726	0.573	22	0.230	R.TSIPGIFAIGDVAAFPLK.M
R1/RRR1-9/2	1817.094	1818.148	-1134.121	0.312	600.671	0.424	20	0.196	R.TSIPGIFAIGDVAAFPLK.M
R1/RRR1-9/2	1816.974	1818.148	-1200.570	0.291	317.094	0.400	16	0.189	R.TSIPGIFAIGDVAAFPLK.M
R1/RRR1-2/2	1556.282	1555.758	-306.635	0.550	1190.760	0.499	21	0.249	K.LLDVLNTPSEAVQR.A
R1/RRR1-2/2	1555.329	1555.758	-276.515	0.435	1310.861	0.419	21	0.242	K.LLDVLNTPSEAVQR.A
R1/RRR1-1/2	1555.913	1555.758	99.575	0.452	965.169	0.414	20	0.217	K.LLDVLNTPSEAVQR.A
R1/RRR1-1/2	1555.137	1555.758	-1045.272	0.380	966.797	0.418	19	0.216	K.LLDVLNTPSEAVQR.A
R1/RRR1-2/2	1071.163	1070.181	-16.987	0.429	764.138	0.392	14	0.203	R.ALADPNVDVR.G
R1/RRR1-2/2	1557.037	1555.758	179.867	0.467	603.317	0.387	17	0.199	K.LLDVLNTPSEAVQR.A
R1/RRR1-1/2	1556.077	1555.758	205.472	0.409	631.395	0.373	17	0.198	K.LLDVLNTPSEAVQR.A
R1/RRR1-4/2	1761.512	1762.040	-870.264	0.380	1311.670	0.326	20	0.221	K.LVENYAELLASQGLLK.T
R1/RRR1-3/2	1761.305	1762.040	-988.263	0.366	1324.857	0.315	19	0.219	K.LVENYAELLASQGLLK.T
R1/RRR1-12/2	1762.680	1762.040	-204.603	0.411	919.422	0.346	16	0.196	K.LVENYAELLASQGLLK.T
R1/RRR1-7/3	1418.905	1418.663	171.050	0.290	1043.052	0.255	23	0.073	R.KIPGVVAASSFDVK.I
R1/RRR1-12/2	1158.031	1158.244	-184.349	0.486	1816.683	0.457	19	0.313	K.VASDDLDPAVR.E
R1/RRR1-11/2	1158.052	1158.244	-166.372	0.431	1321.271	0.434	19	0.249	K.VASDDLDPAVR.E
R1/RRR1-12/2	1158.072	1158.244	-149.136	0.487	1213.079	0.442	18	0.241	K.VASDDLDPAVR.E
R1/RRR1-12/2	1157.455	1158.244	-1549.753	0.383	1243.714	0.434	19	0.241	K.VASDDLDPAVR.E
R1/RRR1-11/2	1157.979	1158.244	-229.082	0.480	1239.807	0.422	18	0.239	K.VASDDLDPAVR.E
R1/RRR1-11/2	1158.028	1158.244	-187.310	0.476	839.721	0.465	16	0.220	K.VASDDLDPAVR.E
R1/RRR1-11/2	1415.075	1415.531	-323.216	0.504	1687.571	0.508	22	0.311	R.SPNELLNSEGGLGK.Q
R1/RRR1-6/2	1333.608	1334.543	-1455.129	0.327	736.975	0.350	14	0.194	R.AYELQALLGLDK.Q
R1/RRR1-6/2	1334.376	1334.543	-125.486	0.269	356.505	0.362	11	0.187	R.AYELQALLGLDK.Q
R1/RRR1-6/2	1334.106	1334.543	-328.332	0.185	533.768	0.218	13	0.181	R.AYELQALLGLDK.Q
R1/RRR1-6/3	1417.812	1417.552	184.049	0.387	1174.878	0.333	26	0.095	R.SPSSVSHLVSNFR.K
R1/RRR1-15/2	1348.134	1348.482	-258.254	0.478	1536.807	0.546	21	0.300	R.TILGESDEVVASK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1348.183	1348.482	-222.282	0.481	1504.338	0.551	21	0.297	R.TILGESDEVVASK.T
R1/RRR1-15/2	1347.622	1348.482	-1384.031	0.353	1174.127	0.510	19	0.245	R.TILGESDEVVASK.T
R1/RRR1-13/2	1496.533	1495.703	-113.443	0.529	1495.713	0.557	18	0.298	R.SGYLYNLQYFVK.W
R1/RRR1-19/3	1582.238	1582.651	-261.684	0.499	1483.620	0.557	27	0.196	R.SGAEVHTGHELCER.K
R1/RRR1-10/2	1225.983	1226.404	-344.805	0.497	1421.881	0.572	19	0.294	R.IPAEALDVIER.S
R1/RRR1-10/2	1226.183	1226.404	-181.392	0.490	1061.093	0.571	18	0.255	R.IPAEALDVIER.S
R1/RRR1-17/2	1636.291	1634.686	-241.732	0.543	1500.597	0.546	24	0.294	R.ASDFDSLGSDGGPGPVR.S
R1/RRR1-12/2	1817.361	1818.021	-915.741	0.516	1549.532	0.531	25	0.293	K.AAANNIGLDGFDVIDAIK.S
R1/RRR1-12/2	1817.835	1818.021	-102.620	0.523	1339.531	0.559	23	0.274	K.AAANNIGLDGFDVIDAIK.S
R1/RRR1-12/2	1817.244	1818.021	-980.682	0.524	1264.165	0.553	23	0.264	K.AAANNIGLDGFDVIDAIK.S
R1/RRR1-11/2	1817.079	1818.021	-1071.735	0.515	1218.337	0.552	22	0.258	K.AAANNIGLDGFDVIDAIK.S
R1/RRR1-11/2	1819.204	1818.021	100.845	0.549	1118.720	0.589	22	0.257	K.AAANNIGLDGFDVIDAIK.S
R1/RRR1-11/2	1818.726	1818.021	-162.215	0.540	1083.620	0.563	21	0.247	K.AAANNIGLDGFDVIDAIK.S
R1/RRR1-22/2	1343.163	1343.551	-289.656	0.519	1537.856	0.533	19	0.296	R.TPEGTIIELTIR.G
R1/RRR1-23/2	1343.513	1343.551	-28.671	0.490	1457.887	0.517	19	0.282	R.TPEGTIIELTIR.G
R1/RRR1-22/2	1343.265	1343.551	-213.708	0.478	1190.281	0.556	18	0.262	R.TPEGTIIELTIR.G
R1/RRR1-22/2	1343.288	1343.551	-196.204	0.500	1236.212	0.529	18	0.260	R.TPEGTIIELTIR.G
R1/RRR1-23/2	1342.537	1343.551	-1504.638	0.404	718.001	0.512	17	0.219	R.TPEGTIIELTIR.G
R1/RRR1-1/2	1883.063	1884.165	-1119.942	0.438	1159.369	0.617	23	0.266	K.GPDVVGSFGLLQPLADGLK.L
R1/RRR1-3/2	1884.419	1884.165	135.104	0.529	854.221	0.640	24	0.246	K.GPDVVGSFGLLQPLADGLK.L
R1/RRR1-24/2	1586.293	1586.752	-290.337	0.504	1582.849	0.516	20	0.293	K.AGGAYTM*NTASAVTVR.S
R1/RRR1-24/2	1585.487	1586.752	-1433.312	0.371	1591.938	0.436	20	0.273	K.AGGAYTM*NTASAVTVR.S
R1/RRR1-4/2	1512.215	1511.661	-295.329	0.513	1780.762	0.451	19	0.306	R.DNFNQLDQLLYK.L
R1/RRR1-4/2	1511.040	1511.661	-1075.453	0.335	1485.441	0.383	18	0.250	R.DNFNQLDQLLYK.L
R1/RRR1-15/3	1468.396	1468.556	-108.997	0.634	1955.044	0.368	27	0.200	R.HYNDISELSPHR.L
R1/RRR1-15/3	1468.725	1468.556	115.605	0.547	1981.499	0.296	27	0.177	R.HYNDISELSPHR.L
R1/RRR1-15/3	1468.114	1468.556	-302.166	0.588	1459.520	0.324	25	0.119	R.HYNDISELSPHR.L
R1/RRR1-7/2	1457.255	1456.542	-197.747	0.513	1386.754	0.569	18	0.288	-.SFGFNTAVEEAQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1550.276	1550.783	-975.022	0.401	1927.516	0.368	20	0.306	K.TLFVINFDPINTR.T
R1/RRR1-10/2	1458.260	1458.596	-230.943	0.421	1538.441	0.513	20	0.288	R.EADPLDSQVVTVGK.F
R1/RRR1-10/2	1458.184	1458.596	-283.685	0.434	1453.858	0.543	20	0.285	R.EADPLDSQVVTVGK.F
R1/RRR1-10/2	1458.246	1458.596	-240.937	0.376	1403.768	0.520	19	0.271	R.EADPLDSQVVTVGK.F
R1/RRR1-15/3	1581.871	1581.717	97.584	0.560	1506.806	0.530	30	0.184	K.NHAVHISQIGEGYR.A
R1/RRR1-15/3	1581.485	1581.717	-147.538	0.522	1505.772	0.531	30	0.183	K.NHAVHISQIGEGYR.A
R1/RRR1-15/3	1581.218	1581.717	-316.442	0.537	1466.620	0.527	27	0.183	K.NHAVHISQIGEGYR.A
R1/RRR1-9/2	1447.110	1447.533	-293.217	0.551	1368.031	0.564	23	0.284	R.EVEAIGGNVSASASR.E
R1/RRR1-4/2	1589.548	1588.790	-152.636	0.520	1315.632	0.565	18	0.273	K.IGGSNIQLFGESLPR.I
R1/RRR1-14/3	1692.381	1692.896	-898.080	0.479	1556.365	0.510	29	0.186	K.KVNEILSHYPSNYK.Q
R1/RRR1-14/3	1692.967	1692.896	42.039	0.484	1364.917	0.397	26	0.131	K.KVNEILSHYPSNYK.Q
R1/RRR1-1/2	1687.181	1686.844	200.245	0.464	1368.114	0.374	19	0.236	R.YYDLSSQEIGELIR.F
R1/RRR1-2/2	1257.385	1257.377	6.757	0.277	852.019	0.444	14	0.205	K.TGYFQVTDLGR.I
R1/RRR1-1/2	1687.767	1687.870	-61.489	0.316	952.092	0.095	18	0.172	R.LAESIDDLSLDIPSAK.I
R1/RRR1-7/3	1648.855	1648.827	16.927	0.536	1228.183	0.438	30	0.126	R.LRPNSSGSQTVQM*AR.A
R1/RRR1-7/3	1648.547	1648.827	-170.563	0.485	922.180	0.383	28	0.093	R.LRPNSSGSQTVQM*AR.A
R1/RRR1-1/2	1782.570	1782.119	253.545	0.456	824.186	0.605	18	0.230	R.GVLGIWSPVLSAVGNALK.I
R1/RRR1-1/2	1616.423	1616.760	-209.406	0.481	1433.741	0.541	22	0.283	K.GQQPLQGDITAANFR.T
R1/RRR1-1/2	1616.544	1616.760	-133.727	0.481	1450.109	0.524	22	0.281	K.GQQPLQGDITAANFR.T
R1/RRR1-1/2	1615.927	1616.760	-1137.788	0.486	1355.994	0.522	22	0.270	K.GQQPLQGDITAANFR.T
R1/RRR1-18/2	1616.151	1616.760	-998.690	0.483	1257.004	0.528	21	0.260	K.GQQPLQGDITAANFR.T
R1/RRR1-18/2	1615.152	1616.760	-2240.386	0.243	821.245	0.320	16	0.190	K.GQQPLQGDITAANFR.T
R1/RRR1-21/2	1266.486	1267.415	-1527.705	0.376	1029.076	0.301	16	0.203	R.FTWTIENLSR.V
R1/RRR1-3/3	1965.375	1966.147	-903.940	0.385	958.602	0.412	26	0.098	K.VTYHHGTKDEVSVHSIR.L
R1/RRR1-13/2	1263.180	1262.483	-240.245	0.454	1428.735	0.538	18	0.283	R.IVNVSSGFGLLR.-
R1/RRR1-7/2	1423.226	1422.565	-239.037	0.503	1551.474	0.502	23	0.291	R.YGTAGLLSPNTEAK.I
R1/RRR1-7/2	1421.806	1422.565	-1241.291	0.467	1236.439	0.474	21	0.248	R.YGTAGLLSPNTEAK.I
R1/RRR1-16/2	1295.191	1295.467	-213.416	0.439	1188.817	0.594	17	0.267	R.VNQSFVIATSTK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	1295.422	1295.467	-34.556	0.413	1376.327	0.459	18	0.257	R.VNQSFVIATSTK.L
R1/RRR1-15/2	1295.170	1295.467	-229.962	0.435	1161.622	0.553	16	0.255	R.VNQSFVIATSTK.L
R1/RRR1-15/2	1295.041	1295.467	-329.349	0.393	969.671	0.579	16	0.242	R.VNQSFVIATSTK.L
R1/RRR1-15/2	1295.122	1295.467	-267.218	0.407	819.490	0.523	17	0.225	R.VNQSFVIATSTK.L
R1/RRR1-8/2	1238.196	1237.429	-188.432	0.425	1781.977	0.417	17	0.298	K.YVAVGNEPFLK.A
R1/RRR1-21/3	1429.578	1429.511	46.872	0.555	1623.989	0.481	28	0.176	K.DCRPVESSEPPR.Y
R1/RRR1-21/3	1430.563	1429.511	36.526	0.551	1473.048	0.463	28	0.149	K.DCRPVESSEPPR.Y
R1/RRR1-21/3	1429.638	1429.511	88.749	0.542	1206.309	0.501	26	0.135	K.DCRPVESSEPPR.Y
R1/RRR1-20/3	1429.426	1429.511	-60.020	0.514	991.964	0.496	23	0.121	K.DCRPVESSEPPR.Y
R1/RRR1-21/3	1428.879	1429.511	-1146.041	0.438	1321.612	0.394	25	0.120	K.DCRPVESSEPPR.Y
R1/RRR1-20/3	1428.682	1429.511	-1284.132	0.459	1398.433	0.376	27	0.119	K.DCRPVESSEPPR.Y
R1/RRR1-20/3	1429.077	1429.511	-304.851	0.535	952.021	0.468	26	0.108	K.DCRPVESSEPPR.Y
R1/RRR1-21/3	1428.901	1429.511	-1130.472	0.485	859.723	0.481	24	0.108	K.DCRPVESSEPPR.Y
R1/RRR1-19/3	1429.385	1429.511	-88.931	0.472	1113.879	0.375	24	0.102	K.DCRPVESSEPPR.Y
R1/RRR1-19/3	1428.963	1429.511	-1086.853	0.508	765.952	0.424	23	0.098	K.DCRPVESSEPPR.Y
R1/RRR1-17/3	1430.494	1429.511	-11.873	0.481	741.631	0.416	22	0.097	K.DCRPVESSEPPR.Y
R1/RRR1-21/3	1428.842	1429.511	-1172.035	0.453	824.875	0.403	24	0.095	K.DCRPVESSEPPR.Y
R1/RRR1-17/3	1429.554	1429.511	29.786	0.435	315.651	0.362	18	0.093	-.DCRPVESSEPPR.-
R1/RRR1-19/3	1428.973	1429.511	-1079.520	0.455	889.727	0.368	25	0.091	K.DCRPVESSEPPR.Y
R1/RRR1-15/3	1429.597	1429.511	60.360	0.406	640.776	0.256	22	0.084	K.DCRPVESSEPPR.Y
R1/RRR1-19/2	1944.441	1945.166	-889.769	0.498	1410.321	0.531	21	0.274	K.VQASIAANTWVVSGSPQTK.K
R1/RRR1-14/3	1458.833	1458.690	97.841	0.443	1700.135	0.441	28	0.182	K.YSVRPNTGVVLPR.S
R1/RRR1-14/3	1459.079	1458.690	266.995	0.440	1573.116	0.371	28	0.141	K.YSVRPNTGVVLPR.S
R1/RRR1-14/3	1458.382	1458.690	-211.792	0.410	1230.564	0.336	25	0.101	K.YSVRPNTGVVLPR.S
R1/RRR1-1/2	1838.446	1839.148	-928.681	0.377	1049.623	0.226	18	0.191	R.FQMCPRNQLLAGQFK.T
R1/RRR1-17/2	1210.302	1210.494	-159.291	0.318	708.618	0.223	13	0.183	-.LLNIQNLIIR.-
R1/RRR1-1/2	1211.219	1210.494	-227.908	0.333	894.572	0.182	13	0.183	R.LLNIQNLIIR.E
R1/RRR1-30/2	1838.551	1839.148	-871.090	0.381	693.499	0.200	16	0.181	R.FQMCPRNQLLAGQFK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-21/2	1838.693	1839.148	-248.417	0.346	741.189	0.168	16	0.180	R.FQMCPRNQLLAGQFK.T
R1/RRR1-22/2	1838.671	1839.148	-259.940	0.350	770.130	0.123	17	0.178	R.FQMCPRNQLLAGQFK.T
R1/RRR1-1/2	1839.343	1839.148	106.531	0.338	734.590	0.105	16	0.177	-.FQMCPRNQLLAGQFK.-
R1/RRR1-28/2	1839.727	1839.148	-229.377	0.382	576.336	0.160	15	0.177	-.FQMCPRNQLLAGQFK.-
R1/RRR1-1/2	1838.493	1839.148	-903.018	0.339	647.073	0.125	15	0.176	-.FQMCPRNQLLAGQFK.-
R1/RRR1-24/2	1838.436	1839.148	-933.747	0.315	786.554	0.060	17	0.175	R.FQMCPRNQLLAGQFK.T
R1/RRR1-18/2	965.058	965.215	-162.915	0.315	392.345	0.630	14	0.212	K.AAPVIIVPGK.E
R1/RRR1-18/2	965.183	965.215	-33.123	0.207	412.285	0.477	16	0.193	K.AAPVIIVPGK.E
R1/RRR1-18/2	964.916	965.215	-310.256	0.148	327.101	0.352	13	0.184	K.AAPVIIVPGK.E
R1/RRR1-18/2	1829.395	1828.960	238.421	0.559	1212.058	0.571	22	0.264	R.VVGNSVSEFQSGFSDIR.T
R1/RRR1-18/2	1828.264	1828.960	-930.705	0.522	1160.997	0.554	21	0.254	R.VVGNSVSEFQSGFSDIR.T
R1/RRR1-18/2	1828.536	1828.960	-232.656	0.500	1130.438	0.521	21	0.244	R.VVGNSVSEFQSGFSDIR.T
R1/RRR1-22/2	1631.598	1631.963	-223.818	0.475	1447.802	0.516	22	0.279	R.CCVIPVLGQALLCK.T
R1/RRR1-14/2	1633.147	1631.963	113.084	0.517	1544.009	0.464	23	0.277	R.CCVIPVLGQALLCK.T
R1/RRR1-24/2	1631.671	1631.963	-179.461	0.433	1503.494	0.465	22	0.272	R.CCVIPVLGQALLCK.T
R1/RRR1-22/2	1632.127	1631.963	101.152	0.438	1532.369	0.422	23	0.266	R.CCVIPVLGQALLCK.T
R1/RRR1-22/2	1632.566	1631.963	-243.784	0.474	1587.871	0.396	23	0.265	R.CCVIPVLGQALLCK.T
R1/RRR1-1/2	1631.390	1631.963	-967.071	0.411	1253.164	0.443	21	0.243	R.CCVIPVLGQALLCK.T
R1/RRR1-15/2	1631.282	1631.963	-1033.183	0.415	1142.950	0.443	20	0.234	R.CCVIPVLGQALLCK.T
R1/RRR1-1/2	1632.398	1631.963	267.794	0.473	1236.419	0.381	21	0.229	R.CCVIPVLGQALLCK.T
R1/RRR1-19/2	1631.195	1631.963	-1086.831	0.454	979.399	0.472	19	0.228	R.CCVIPVLGQALLCK.T
R1/RRR1-17/2	1630.624	1631.963	-1438.613	0.297	1327.084	0.339	22	0.227	R.CCVIPVLGQALLCK.T
R1/RRR1-19/2	1632.169	1631.963	126.954	0.450	1089.570	0.417	20	0.226	R.CCVIPVLGQALLCK.T
R1/RRR1-18/2	1631.452	1631.963	-928.534	0.389	1126.897	0.383	18	0.220	R.CCVIPVLGQALLCK.T
R1/RRR1-7/2	1633.240	1631.963	170.501	0.405	1162.852	0.344	21	0.219	R.CCVIPVLGQALLCK.T
R1/RRR1-16/2	1631.369	1631.963	-979.466	0.372	1119.245	0.362	20	0.218	R.CCVIPVLGQALLCK.T
R1/RRR1-1/2	1631.210	1631.963	-1077.438	0.387	1129.254	0.351	20	0.217	R.CCVIPVLGQALLCK.T
R1/RRR1-2/2	1632.590	1631.963	-229.006	0.423	818.391	0.332	18	0.201	R.CCVIPVLGQALLCK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1633.545	1631.963	-256.155	0.390	712.552	0.294	17	0.194	R.CCVIPVLGQALLCK.T
R1/RRR1-6/2	1631.663	1631.963	-183.964	0.286	625.198	0.277	15	0.191	R.CCVIPVLGQALLCK.T
R1/RRR1-16/2	1630.452	1631.963	-2159.814	0.179	988.293	0.198	18	0.189	R.CCVIPVLGQALLCK.T
R1/RRR1-15/2	1214.429	1215.342	-1579.479	0.462	1921.370	0.347	18	0.295	R.SLEGLQANVQR.L
R1/RRR1-19/2	1214.932	1215.342	-338.166	0.519	1736.731	0.379	18	0.278	R.SLEGLQANVQR.L
R1/RRR1-19/2	1214.399	1215.342	-1604.421	0.456	1700.911	0.345	18	0.266	R.SLEGLQANVQR.L
R1/RRR1-19/2	1215.217	1215.342	-102.729	0.559	1692.953	0.353	18	0.264	R.SLEGLQANVQR.L
R1/RRR1-15/2	1214.693	1215.342	-1361.719	0.465	1504.682	0.346	17	0.245	R.SLEGLQANVQR.L
R1/RRR1-23/2	1214.676	1215.342	-1375.648	0.415	1594.760	0.291	18	0.242	R.SLEGLQANVQR.L
R1/RRR1-7/2	1376.293	1376.536	-177.710	0.484	1535.939	0.490	21	0.285	R.YGALEGLDVVDPK.T
R1/RRR1-7/2	1376.280	1376.536	-187.141	0.449	1448.140	0.489	19	0.272	R.YGALEGLDVVDPK.T
R1/RRR1-6/2	1596.306	1596.807	-942.919	0.428	1644.617	0.446	22	0.285	R.DGEAILQLIGGDVAPK.D
R1/RRR1-2/2	1615.319	1613.834	301.247	0.396	795.990	0.351	16	0.192	K.LELQLSPGDSVIDVK.Q
R1/RRR1-3/2	1305.796	1305.545	193.190	0.222	759.386	0.187	14	0.179	-.VGSYLLDTVIPK.-
R1/RRR1-7/2	1485.361	1485.663	-203.732	0.523	1655.030	0.445	19	0.286	K.YYNDLINELLSK.G
R1/RRR1-7/2	1484.791	1485.663	-1264.416	0.449	1683.544	0.387	19	0.275	K.YYNDLINELLSK.G
R1/RRR1-7/2	1485.274	1485.663	-262.684	0.364	1145.315	0.352	16	0.215	K.YYNDLINELLSK.G
R1/RRR1-5/2	1486.978	1485.663	212.632	0.380	681.621	0.419	14	0.201	K.YYNDLINELLSK.G
R1/RRR1-13/2	1774.681	1774.996	-178.107	0.531	1148.980	0.571	23	0.259	K.VDALPVASPTGLDLYSR.F
R1/RRR1-13/2	1774.418	1774.996	-892.018	0.486	1083.414	0.523	23	0.242	K.VDALPVASPTGLDLYSR.F
R1/RRR1-13/2	1775.642	1774.996	-200.076	0.470	788.200	0.567	20	0.226	K.VDALPVASPTGLDLYSR.F
R1/RRR1-13/2	1595.856	1594.877	-13.396	0.519	1548.720	0.474	20	0.280	R.NIEGVSLPVLTPNLK.G
R1/RRR1-15/2	1308.086	1308.509	-324.006	0.479	1263.684	0.549	17	0.267	K.SELLLASNPVHK.K
R1/RRR1-10/2	1935.727	1934.179	-234.447	0.533	1324.152	0.530	22	0.265	K.LITELIGSPDDSSLGFLR.S
R1/RRR1-9/2	1488.845	1489.696	-1247.240	0.369	1561.953	0.448	20	0.274	K.IASLQSEITSLQAK.G
R1/RRR1-9/2	1489.185	1489.696	-1017.734	0.437	1321.490	0.435	18	0.244	K.IASLQSEITSLQAK.G
R1/RRR1-9/2	1488.588	1489.696	-1420.345	0.291	686.073	0.368	15	0.192	K.IASLQSEITSLQAK.G
R1/RRR1-24/2	1189.195	1189.384	-159.853	0.515	1524.652	0.473	20	0.279	K.LSAGIASILESK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/2	1189.105	1189.384	-235.441	0.479	1211.473	0.491	18	0.249	K.LSAGIASILESK.L
R1/RRR1-25/2	1189.179	1189.384	-173.034	0.533	1201.166	0.482	18	0.247	K.LSAGIASILESK.L
R1/RRR1-25/2	1189.894	1189.384	-413.400	0.527	1005.218	0.513	17	0.237	K.LSAGIASILESK.L
R1/RRR1-24/2	1189.014	1189.384	-311.762	0.451	1115.505	0.452	18	0.234	K.LSAGIASILESK.L
R1/RRR1-25/2	1188.604	1189.384	-1502.032	0.453	1097.181	0.440	18	0.230	K.LSAGIASILESK.L
R1/RRR1-16/2	1050.099	1050.233	-128.093	0.520	1438.197	0.501	16	0.276	R.SLGAAIIYNK.D
R1/RRR1-16/2	1050.041	1050.233	-183.952	0.528	1193.738	0.595	15	0.272	R.SLGAAIIYNK.D
R1/RRR1-16/2	1049.799	1050.233	-415.152	0.504	1231.921	0.570	16	0.271	R.SLGAAIIYNK.D
R1/RRR1-17/2	1049.835	1050.233	-380.850	0.300	554.675	0.332	13	0.186	-.SLGAAIIYNK.-
R1/RRR1-14/2	1726.460	1726.997	-893.251	0.455	1272.484	0.536	22	0.261	K.QGPGTAILLGPNFLAEK.G
R1/RRR1-14/2	1726.235	1726.997	-1024.157	0.419	1205.803	0.443	21	0.234	K.QGPGTAILLGPNFLAEK.G
R1/RRR1-14/2	1725.652	1726.997	-1363.365	0.328	506.596	0.385	14	0.186	K.QGPGTAILLGPNFLAEK.G
R1/RRR1-12/2	1835.578	1835.005	-233.164	0.512	1262.594	0.538	20	0.259	K.NGVEEVLGLGQLSDFEK.E
R1/RRR1-12/2	1834.354	1835.005	-902.652	0.425	672.211	0.483	19	0.207	K.NGVEEVLGLGQLSDFEK.E
R1/RRR1-12/2	1836.111	1835.005	58.173	0.376	667.175	0.494	19	0.207	K.NGVEEVLGLGQLSDFEK.E
R1/RRR1-25/2	1836.302	1835.005	162.581	0.325	278.027	0.341	11	0.165	-.NGVEEVLGLGQLSDFEK.-
R1/RRR1-14/2	1659.078	1659.735	-1001.852	0.457	1266.377	0.538	19	0.261	K.SGGLESEKDYPYTGR.D
R1/RRR1-14/2	1659.476	1659.735	-156.607	0.509	1001.175	0.566	19	0.243	K.SGGLESEKDYPYTGR.D
R1/RRR1-14/3	1659.842	1659.735	64.453	0.459	1039.906	0.483	25	0.124	K.SGGLESEKDYPYTGR.D
R1/RRR1-14/3	1660.267	1659.735	-282.939	0.429	1128.602	0.461	27	0.123	K.SGGLESEKDYPYTGR.D
R1/RRR1-14/3	1658.815	1659.735	-1161.042	0.412	969.222	0.483	24	0.118	K.SGGLESEKDYPYTGR.D
R1/RRR1-13/3	1660.658	1659.735	-46.428	0.483	866.817	0.477	24	0.112	K.SGGLESEKDYPYTGR.D
R1/RRR1-15/3	1659.779	1659.735	26.614	0.420	1066.049	0.421	25	0.111	K.SGGLESEKDYPYTGR.D
R1/RRR1-20/3	1659.181	1659.735	-939.295	0.390	642.933	0.424	22	0.094	K.SGGLESEKDYPYTGR.D
R1/RRR1-13/2	1523.407	1523.630	-146.403	0.544	1558.093	0.462	20	0.278	K.VLSDNFEQLNTSR.A
R1/RRR1-13/2	1523.334	1523.630	-194.956	0.521	1602.769	0.423	20	0.273	K.VLSDNFEQLNTSR.A
R1/RRR1-13/2	1522.720	1523.630	-1257.847	0.413	1437.564	0.406	19	0.251	K.VLSDNFEQLNTSR.A
R1/RRR1-4/2	1661.497	1659.908	-248.308	0.505	1351.720	0.517	22	0.269	R.ETLAGINPYAIELVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1824.273	1825.076	-991.775	0.509	1257.755	0.537	20	0.258	R.LTQM*NTDLFGGVDAVVK.Y
R1/RRR1-5/2	1810.751	1809.077	-180.374	0.339	495.545	0.292	16	0.182	R.LTQMNTDLFGGVDAVVK.Y
R1/RRR1-6/2	1496.887	1495.703	123.377	0.469	1273.121	0.538	19	0.265	R.LPVTWYPASFADK.V
R1/RRR1-16/2	1312.206	1312.456	-190.961	0.476	1504.769	0.465	16	0.274	K.DNVLAHLESWK.G
R1/RRR1-5/2	1480.819	1480.645	117.854	0.439	1712.627	0.393	20	0.279	R.DGSDFSAAIIGSLVK.A
R1/RRR1-5/2	1480.620	1480.645	-17.085	0.352	1731.585	0.297	18	0.256	R.DGSDFSAAIIGSLVK.A
R1/RRR1-19/2	1846.685	1847.127	-240.264	0.561	1249.199	0.531	25	0.263	K.IFEVAPSASQM*FSFLR.N
R1/RRR1-19/2	1848.361	1847.127	126.861	0.596	1147.139	0.533	24	0.252	K.IFEVAPSASQM*FSFLR.N
R1/RRR1-3/2	1174.295	1173.345	-42.082	0.303	934.808	0.319	16	0.198	K.ITLGDALSLNR.A
R1/RRR1-2/2	1600.865	1600.799	41.253	0.435	1043.377	0.211	20	0.186	K.VSGGIDLDTVNIIQR.D
R1/RRR1-3/3	1281.412	1281.443	-24.195	0.496	1397.709	0.501	23	0.158	K.HVVDDGLELRK.A
R1/RRR1-3/3	1281.889	1281.443	348.457	0.514	1242.318	0.510	22	0.144	K.HVVDDGLELRK.A
R1/RRR1-3/3	1281.659	1281.443	168.828	0.526	863.630	0.530	20	0.118	K.HVVDDGLELRK.A
R1/RRR1-25/2	1780.679	1780.914	-132.127	0.476	1277.202	0.526	20	0.259	K.VDVDELSAVSQEYGIR.A
R1/RRR1-25/2	1779.667	1780.914	-1266.396	0.287	1488.200	0.434	21	0.258	K.VDVDELSAVSQEYGIR.A
R1/RRR1-18/2	1422.102	1422.567	-327.990	0.469	1154.913	0.551	17	0.254	R.GPTESIYQGGVWK.V
R1/RRR1-10/2	1683.210	1683.843	-973.232	0.540	1084.238	0.557	21	0.249	R.VFFANTGTEANEAAIK.F
R1/RRR1-23/2	1273.935	1274.446	-1189.695	0.446	1697.272	0.392	18	0.281	K.LNNETVTIELK.N
R1/RRR1-5/2	1393.004	1393.529	-1097.848	0.457	1582.351	0.438	19	0.275	R.GFVISDWQGLDR.I
R1/RRR1-5/2	1394.284	1393.529	-176.119	0.544	1527.811	0.448	19	0.271	R.GFVISDWQGLDR.I
R1/RRR1-5/2	1394.353	1393.529	-126.235	0.569	1523.336	0.428	19	0.264	R.GFVISDWQGLDR.I
R1/RRR1-6/2	1393.196	1393.529	-239.356	0.508	1501.531	0.430	19	0.264	R.GFVISDWQGLDR.I
R1/RRR1-6/2	1392.556	1393.529	-1420.964	0.357	1543.811	0.336	19	0.247	R.GFVISDWQGLDR.I
R1/RRR1-3/2	1394.196	1393.529	-239.535	0.448	1176.795	0.420	17	0.231	R.GFVISDWQGLDR.I
R1/RRR1-6/2	1393.345	1393.529	-132.477	0.449	1247.897	0.359	18	0.226	R.GFVISDWQGLDR.I
R1/RRR1-3/2	1393.219	1393.529	-223.182	0.484	1164.481	0.356	17	0.218	R.GFVISDWQGLDR.I
R1/RRR1-9/3	1814.491	1814.935	-245.733	0.438	536.899	0.604	23	0.111	R.DPAAWERPDEFVPER.F
R1/RRR1-9/3	1814.670	1814.935	-146.426	0.421	552.826	0.417	23	0.088	R.DPAAWERPDEFVPER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/3	1662.414	1661.924	295.688	0.523	1818.039	0.353	27	0.184	R.VTDHIEHIIELITK.I
R1/RRR1-12/2	1353.959	1353.465	366.452	0.472	1053.854	0.568	18	0.252	R.DNVQAYPGVSFR.Y
R1/RRR1-12/2	1353.243	1353.465	-163.998	0.468	1100.392	0.507	18	0.243	R.DNVQAYPGVSFR.Y
R1/RRR1-12/2	1353.113	1353.465	-260.743	0.409	875.195	0.423	17	0.213	R.DNVQAYPGVSFR.Y
R1/RRR1-21/2	1585.728	1585.739	-7.073	0.501	1181.659	0.540	21	0.256	K.STGFGLIYDNLDAAK.K
R1/RRR1-20/2	1585.246	1585.739	-312.463	0.467	1226.479	0.501	22	0.252	K.STGFGLIYDNLDAAK.K
R1/RRR1-20/2	1584.762	1585.739	-1251.560	0.371	1188.488	0.516	21	0.248	K.STGFGLIYDNLDAAK.K
R1/RRR1-19/2	1585.253	1585.739	-307.596	0.449	927.373	0.500	19	0.226	K.STGFGLIYDNLDAAK.K
R1/RRR1-20/2	1584.813	1585.739	-1218.994	0.390	929.542	0.437	19	0.215	K.STGFGLIYDNLDAAK.K
R1/RRR1-17/2	1586.301	1585.739	-277.445	0.406	611.734	0.485	16	0.206	K.STGFGLIYDNLDAAK.K
R1/RRR1-3/2	1272.441	1272.436	3.598	0.449	1204.550	0.518	18	0.252	K.AAVVGGNVLTSQR.V
R1/RRR1-1/2	1273.094	1272.436	-269.630	0.319	898.354	0.335	16	0.198	K.AAVVGGNVLTSQR.V
R1/RRR1-1/2	1273.171	1272.436	-208.644	0.195	432.054	0.294	11	0.164	-.AAVVGGNVLTSQR.-
R1/RRR1-4/2	1191.637	1192.346	-1438.616	0.444	1543.874	0.438	19	0.273	K.TLFVDAADLAR.N
R1/RRR1-4/2	1191.567	1192.346	-1497.989	0.376	1293.677	0.366	17	0.230	K.TLFVDAADLAR.N
R1/RRR1-22/2	1432.105	1432.567	-323.391	0.455	1221.261	0.529	21	0.258	R.VTGGGHTSQVYAVR.Q
R1/RRR1-22/2	1432.212	1432.567	-248.137	0.521	1099.943	0.523	20	0.246	R.VTGGGHTSQVYAVR.Q
R1/RRR1-22/2	1433.198	1432.567	-258.047	0.516	1071.384	0.500	20	0.239	R.VTGGGHTSQVYAVR.Q
R1/RRR1-12/2	1206.927	1206.288	-300.034	0.493	842.905	0.587	19	0.243	R.VIGSGTNLDSSR.F
R1/RRR1-11/2	1206.976	1206.288	-259.141	0.483	1000.896	0.485	20	0.235	R.VIGSGTNLDSSR.F
R1/RRR1-12/2	1207.086	1206.288	-168.438	0.447	905.336	0.512	19	0.232	R.VIGSGTNLDSSR.F
R1/RRR1-12/2	1206.794	1206.288	-410.959	0.431	825.610	0.541	19	0.231	R.VIGSGTNLDSSR.F
R1/RRR1-11/2	1205.964	1206.288	-270.019	0.355	870.092	0.412	18	0.212	R.VIGSGTNLDSSR.F
R1/RRR1-11/2	1206.179	1206.288	-91.114	0.342	855.688	0.387	19	0.208	R.VIGSGTNLDSSR.F
R1/RRR1-14/3	1571.324	1570.729	-258.748	0.496	1293.103	0.513	29	0.153	R.SPSGVIHLTDTSVTR.F
R1/RRR1-14/3	1570.841	1570.729	71.496	0.483	1005.411	0.516	27	0.126	R.SPSGVIHLTDTSVTR.F
R1/RRR1-13/3	1570.822	1570.729	59.104	0.369	1170.779	0.444	28	0.119	R.SPSGVIHLTDTSVTR.F
R1/RRR1-14/3	1570.558	1570.729	-109.508	0.309	640.733	0.320	20	0.078	R.SPSGVIHLTDTSVTR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-11/2	1275.284	1275.391	-83.489	0.439	1416.449	0.479	19	0.268	R.VSTVVDVDLGDR.S
R1/RRR1-11/2	1628.380	1628.852	-291.103	0.360	1175.038	0.524	18	0.245	R.LPGFYGEYVGLTGVR.L
R1/RRR1-13/2	1702.834	1701.905	-41.675	0.511	1191.513	0.532	23	0.255	R.GWAPTFLGYSAQGAFK.Y
R1/RRR1-13/2	1702.238	1701.905	196.388	0.438	656.067	0.336	18	0.187	-.GWAPTFLGYSAQGAFK.-
R1/RRR1-20/2	1660.258	1658.854	244.156	0.502	393.136	0.569	19	0.214	R.VIPNFM*CQGGDFTR.G
R1/RRR1-9/2	1892.286	1891.070	114.291	0.333	275.020	0.559	18	0.199	R.TDFFLISTTDAFVDAAR.H
R1/RRR1-9/2	1891.851	1891.070	-116.337	0.419	292.839	0.452	16	0.193	R.TDFFLISTTDAFVDAAR.H
R1/RRR1-5/2	1795.633	1795.070	-244.283	0.375	1219.375	0.505	18	0.244	R.LGGISSTLSAYETLLLR.G
R1/RRR1-16/2	1197.133	1197.323	-159.611	0.512	1147.543	0.533	18	0.255	R.HLVAVQTDEGK.A
R1/RRR1-16/2	1197.018	1197.323	-255.365	0.496	1145.518	0.453	18	0.238	R.HLVAVQTDEGK.A
R1/RRR1-17/2	1196.860	1197.323	-388.079	0.492	1013.489	0.458	17	0.229	R.HLVAVQTDEGK.A
R1/RRR1-16/2	1196.328	1197.323	-1672.664	0.441	1082.489	0.415	18	0.226	R.HLVAVQTDEGK.A
R1/RRR1-16/2	967.312	967.190	126.433	0.520	1338.212	0.488	15	0.264	K.AILLQGVPR.N
R1/RRR1-18/2	967.233	967.190	43.911	0.334	417.873	0.299	11	0.192	K.AILLQGVPR.N
R1/RRR1-18/2	967.721	967.190	-486.991	0.309	486.571	0.317	11	0.191	K.AILLQGVPR.N
R1/RRR1-2/2	1172.300	1171.372	-61.580	0.411	1493.217	0.446	17	0.268	R.VSQLELALAAR.A
R1/RRR1-7/2	1476.365	1476.653	-195.436	0.414	1536.100	0.429	19	0.268	K.SPLIVFDDVDIDK.-
R1/RRR1-9/3	1599.249	1598.869	238.272	0.431	1299.698	0.496	25	0.146	R.TPFYLYSKPQVVR.N
R1/RRR1-9/3	1598.631	1598.869	-149.364	0.369	663.555	0.456	22	0.091	R.TPFYLYSKPQVVR.N
R1/RRR1-10/3	1559.639	1560.805	-1392.977	0.386	1461.723	0.105	27	0.075	K.MAARETGALQAAKNK.L
R1/RRR1-14/3	994.156	994.145	11.487	0.514	1567.118	0.123	20	0.071	K.ETQEM*LVK.E
R1/RRR1-8/3	994.545	994.145	403.520	0.528	1321.651	0.115	18	0.063	-.ETQEM*LVK.-
R1/RRR1-5/3	994.189	994.145	44.275	0.269	1153.433	0.089	17	0.063	K.ETQEM*LVK.E
R1/RRR1-11/3	994.039	994.145	-106.848	0.381	1168.823	0.124	18	0.061	-.ETQEM*LVK.-
R1/RRR1-9/3	994.515	994.145	373.523	0.476	1163.073	0.145	18	0.060	-.ETQEM*LVK.-
R1/RRR1-7/3	994.507	994.145	365.401	0.476	1234.579	0.108	18	0.060	-.ETQEM*LVK.-
R1/RRR1-1/3	994.180	994.145	35.224	0.483	1185.676	0.123	18	0.058	-.ETQEM*LVK.-
R1/RRR1-8/3	994.607	994.145	465.630	0.491	1214.386	0.099	18	0.058	-.ETQEM*LVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-2/3	994.123	994.145	-22.043	0.427	1317.293	0.056	18	0.056	-.ETQEM*LVK.-
R1/RRR1-7/3	994.346	994.145	202.740	0.454	1168.833	0.060	17	0.055	-.ETQEM*LVK.-
R1/RRR1-1/3	994.020	994.145	-126.435	0.444	1255.262	0.055	18	0.054	-.ETQEM*LVK.-
R1/RRR1-10/3	994.408	994.145	265.429	0.452	1068.236	0.113	18	0.054	-.ETQEM*LVK.-
R1/RRR1-1/3	993.886	994.145	-261.252	0.469	1012.749	0.096	17	0.054	-.ETQEM*LVK.-
R1/RRR1-9/3	994.343	994.145	199.786	0.500	1253.515	0.083	19	0.054	-.ETQEM*LVK.-
R1/RRR1-4/3	994.316	994.145	172.178	0.435	1173.475	0.077	18	0.053	-.ETQEM*LVK.-
R1/RRR1-10/3	1299.657	1299.420	182.646	0.514	999.726	0.553	22	0.130	R.HLSTLTGYHNR.T
R1/RRR1-10/3	1299.265	1299.420	-119.652	0.525	877.106	0.532	20	0.120	R.HLSTLTGYHNR.T
R1/RRR1-11/3	1298.699	1299.420	-1328.986	0.427	620.570	0.504	19	0.101	R.HLSTLTGYHNR.T
R1/RRR1-10/3	1299.902	1299.420	371.932	0.457	719.756	0.447	20	0.096	R.HLSTLTGYHNR.T
R1/RRR1-11/3	1298.916	1299.420	-1161.641	0.304	357.565	0.382	16	0.070	-.HLSTLTGYHNR.-
R1/RRR1-18/2	899.825	899.047	-247.657	0.069	480.354	0.436	10	0.104	K.MSVFVASTG.-
R1/RRR1-29/2	899.636	899.047	-457.977	0.011	481.798	0.338	10	0.101	K.MSVFVASTG.-
R1/RRR1-5/2	899.924	899.047	-137.019	-0.004	934.697	0.157	12	0.100	K.MSVFVASTG.-
R1/RRR1-25/2	899.588	899.047	-511.898	-0.085	531.924	0.134	10	0.100	-.MSVFVASTG.-
R1/RRR1-7/2	1768.355	1769.034	-952.543	0.440	580.276	0.577	17	0.219	K.QLLQWPIEEIETLR.R
R1/RRR1-7/2	1769.553	1769.034	-272.930	0.455	550.176	0.510	17	0.211	K.QLLQWPIEEIETLR.R
R1/RRR1-6/2	1768.496	1769.034	-872.573	0.383	517.285	0.460	17	0.203	K.QLLQWPIEEIETLR.R
R1/RRR1-6/2	1768.134	1769.034	-1078.067	0.291	311.660	0.411	14	0.193	K.QLLQWPIEEIETLR.R
R1/RRR1-3/2	1769.898	1769.034	-77.175	0.375	293.742	0.446	12	0.191	-.QLLQWPIEEIETLR.-
R1/RRR1-10/2	1791.529	1791.894	-203.906	0.466	1066.122	0.536	22	0.244	K.VVSIDGFEDVPQNDEK.S
R1/RRR1-11/2	1791.243	1791.894	-924.446	0.452	948.143	0.518	21	0.231	K.VVSIDGFEDVPQNDEK.S
R1/RRR1-10/2	1791.137	1791.894	-983.697	0.478	715.197	0.520	21	0.219	K.VVSIDGFEDVPQNDEK.S
R1/RRR1-10/2	1791.442	1791.894	-252.577	0.460	720.082	0.456	21	0.210	K.VVSIDGFEDVPQNDEK.S
R1/RRR1-13/2	1386.257	1385.593	-243.115	0.441	1023.861	0.546	19	0.241	R.DVGVSPAIVGAFPR.K
R1/RRR1-12/2	1386.887	1385.593	212.352	0.343	898.568	0.447	17	0.211	R.DVGVSPAIVGAFPR.K
R1/RRR1-9/2	1904.386	1903.124	137.931	0.508	800.063	0.558	21	0.224	K.ASILLSLDGTTAVAEDIGR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1903.416	1903.124	153.825	0.395	1012.193	0.450	21	0.218	K.ASILLSLDGTTAVAEDIGR.Q
R1/RRR1-6/2	1520.587	1519.766	-118.171	0.410	1165.834	0.514	16	0.245	R.TVVYWEDVLLGPK.V
R1/RRR1-2/2	1802.428	1802.086	190.364	0.426	854.695	0.524	17	0.220	R.QAIQPLVEILSTGM*ER.E
R1/RRR1-2/2	1787.238	1786.087	85.180	0.350	364.654	0.459	13	0.189	-.QAIQPLVEILSTGMER.-
R1/RRR1-2/2	1801.095	1802.086	-1108.981	0.291	602.561	0.330	16	0.186	R.QAIQPLVEILSTGM*ER.E
R1/RRR1-13/2	1460.141	1459.669	324.542	0.413	1534.268	0.419	18	0.265	R.SPWSTLDIIAEVK.Q
R1/RRR1-10/2	1623.523	1623.832	-191.221	0.404	855.968	0.555	21	0.225	K.AGSGVATLGLPDSPGVPK.G
R1/RRR1-1/2	1830.692	1829.000	-168.712	0.495	689.753	0.543	20	0.216	R.WAIPNTDATIDEPTVGK.A
R1/RRR1-18/2	1285.067	1285.409	-266.677	0.435	990.138	0.544	17	0.239	R.AQGLYM*GSDQAK.L
R1/RRR1-16/2	1678.457	1678.863	-242.881	0.469	913.063	0.550	18	0.232	R.VGYTFTTDALDALYK.K
R1/RRR1-9/2	1678.850	1678.863	-7.775	0.401	685.529	0.486	16	0.205	R.VGYTFTTDALDALYK.K
R1/RRR1-3/2	1585.299	1585.658	-227.033	0.459	617.182	0.540	21	0.216	K.TSPIPQDDAQGQATR.Y
R1/RRR1-8/2	1159.250	1159.230	17.046	0.514	1242.457	0.492	15	0.253	R.SAVDYFEATR.A
R1/RRR1-8/2	1158.917	1159.230	-270.944	0.418	1208.787	0.483	15	0.247	R.SAVDYFEATR.A
R1/RRR1-8/2	1158.896	1159.230	-289.332	0.296	871.489	0.380	16	0.205	R.SAVDYFEATR.A
R1/RRR1-16/2	1323.581	1324.508	-1460.232	0.445	1479.428	0.431	18	0.263	K.SELLLSSNPVHK.K
R1/RRR1-12/2	1614.429	1614.744	-195.483	0.524	1570.012	0.409	20	0.264	K.TWQGRPENVEAAQK.A
R1/RRR1-12/2	1614.338	1614.744	-252.149	0.490	1495.527	0.350	20	0.243	K.TWQGRPENVEAAQK.A
R1/RRR1-12/2	1614.368	1614.744	-233.639	0.486	1156.063	0.400	18	0.223	K.TWQGRPENVEAAQK.A
R1/RRR1-1/2	1300.711	1300.400	239.693	0.332	442.633	0.556	15	0.207	R.QPIGTAAQGAEEK.D
R1/RRR1-16/2	1300.049	1300.400	-271.197	0.293	377.550	0.530	15	0.202	R.QPIGTAAQGAEEK.D
R1/RRR1-16/2	1300.001	1300.400	-308.221	0.234	625.156	0.448	19	0.199	R.QPIGTAAQGAEEK.D
R1/RRR1-16/2	1300.170	1300.400	-177.379	0.265	472.792	0.472	16	0.198	R.QPIGTAAQGAEEK.D
R1/RRR1-1/2	1299.928	1300.400	-364.468	0.239	336.814	0.430	14	0.192	R.QPIGTAAQGAEEK.D
R1/RRR1-1/2	1299.948	1300.400	-348.544	0.163	391.734	0.426	16	0.188	R.QPIGTAAQGAEEK.D
R1/RRR1-14/3	1926.002	1926.061	-30.684	0.476	685.106	0.559	29	0.113	K.GGRPIQM*STDHDPNVER.G
R1/RRR1-14/3	1925.133	1926.061	-1004.749	0.438	455.953	0.526	26	0.101	K.GGRPIQM*STDHDPNVER.G
R1/RRR1-14/3	1925.344	1926.061	-894.370	0.411	459.680	0.488	26	0.096	K.GGRPIQM*STDHDPNVER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1832.590	1833.121	-838.448	0.439	1130.676	0.510	21	0.240	K.DAPSAVNVVVVPNVNLPK.E
R1/RRR1-23/2	1832.581	1833.121	-842.861	0.454	996.771	0.569	20	0.239	K.DAPSAVNVVVVPNVNLPK.E
R1/RRR1-23/2	1832.338	1833.121	-976.479	0.397	1037.967	0.504	20	0.229	K.DAPSAVNVVVVPNVNLPK.E
R1/RRR1-15/2	1593.149	1592.754	248.587	0.480	996.447	0.535	25	0.242	-.M*DGAASVPSSNEVALK.Q
R1/RRR1-16/2	1593.232	1592.754	301.214	0.508	941.849	0.528	25	0.237	-.M*DGAASVPSSNEVALK.Q
R1/RRR1-16/2	1592.226	1592.754	-962.542	0.470	900.814	0.488	25	0.227	-.M*DGAASVPSSNEVALK.Q
R1/RRR1-16/2	1592.312	1592.754	-277.995	0.429	923.836	0.491	23	0.226	-.M*DGAASVPSSNEVALK.Q
R1/RRR1-15/2	1592.183	1592.754	-989.560	0.445	995.695	0.417	25	0.220	-.M*DGAASVPSSNEVALK.Q
R1/RRR1-12/2	1268.296	1268.488	-151.814	0.368	628.720	0.559	15	0.215	R.VPQVSNLGLNVK.G
R1/RRR1-11/2	1268.503	1268.488	12.296	0.413	642.202	0.516	15	0.213	R.VPQVSNLGLNVK.G
R1/RRR1-11/2	1269.349	1268.488	-109.440	0.390	648.315	0.514	15	0.212	R.VPQVSNLGLNVK.G
R1/RRR1-13/2	1262.190	1261.452	-208.034	0.410	844.714	0.553	18	0.227	R.AFTVGIGGPVGTGK.T
R1/RRR1-5/2	1687.401	1685.948	268.860	0.450	513.503	0.551	16	0.207	R.TLNSWKPIDAALSLR.N
R1/RRR1-7/2	1064.707	1065.334	-1532.845	0.340	608.988	0.559	17	0.217	K.AVKPVLVGGPK.M
R1/RRR1-7/2	1065.254	1065.334	-75.009	0.364	604.744	0.513	17	0.214	K.AVKPVLVGGPK.M
R1/RRR1-7/2	1066.119	1065.334	-202.768	0.330	642.498	0.488	18	0.211	K.AVKPVLVGGPK.M
R1/RRR1-6/2	1064.991	1065.334	-322.776	0.275	280.726	0.509	12	0.197	K.AVKPVLVGGPK.M
R1/RRR1-19/2	1263.960	1264.371	-326.018	0.418	516.841	0.561	16	0.219	K.GGAPAEFQPSFR.G
R1/RRR1-19/2	1263.973	1264.371	-316.328	0.385	493.519	0.525	16	0.214	K.GGAPAEFQPSFR.G
R1/RRR1-20/2	1264.004	1264.371	-291.329	0.417	467.707	0.528	15	0.213	K.GGAPAEFQPSFR.G
R1/RRR1-19/2	1265.512	1264.371	111.879	0.445	394.914	0.490	15	0.210	K.GGAPAEFQPSFR.G
R1/RRR1-19/2	1264.062	1264.371	-245.017	0.392	371.167	0.487	14	0.207	K.GGAPAEFQPSFR.G
R1/RRR1-20/2	1263.933	1264.371	-347.724	0.390	496.655	0.454	15	0.206	K.GGAPAEFQPSFR.G
R1/RRR1-19/2	1263.977	1264.371	-312.452	0.332	409.020	0.354	14	0.197	K.GGAPAEFQPSFR.G
R1/RRR1-19/2	1265.020	1264.371	-278.126	0.356	358.211	0.299	14	0.197	K.GGAPAEFQPSFR.G
R1/RRR1-19/2	1265.203	1264.371	-133.411	0.360	361.370	0.310	14	0.194	-.GGAPAEFQPSFR.-
R1/RRR1-21/2	1263.935	1264.371	-346.076	0.270	412.150	0.320	14	0.192	-.GGAPAEFQPSFR.-
R1/RRR1-12/3	1909.451	1908.275	92.866	0.496	946.620	0.530	29	0.126	K.LVIQALLPLLLQSSGEGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	1146.283	1146.366	-72.270	0.437	906.259	0.537	15	0.236	K.IPANLIYWR.V
R1/RRR1-6/2	1146.114	1146.366	-220.237	0.436	682.678	0.540	13	0.222	K.IPANLIYWR.V
R1/RRR1-6/2	1145.924	1146.366	-386.845	0.426	717.959	0.483	13	0.216	K.IPANLIYWR.V
R1/RRR1-10/2	1079.942	1080.259	-294.499	0.407	1192.719	0.484	16	0.246	K.AILQSYLSGK.H
R1/RRR1-10/2	1080.183	1080.259	-70.912	0.393	1201.818	0.452	16	0.240	K.AILQSYLSGK.H
R1/RRR1-10/2	1080.038	1080.259	-205.483	0.389	951.831	0.472	15	0.225	K.AILQSYLSGK.H
R1/RRR1-9/2	1628.701	1628.764	-39.212	0.485	1263.661	0.481	21	0.250	R.GDELLTSYPGLGSYR.V
R1/RRR1-9/2	1629.160	1628.764	243.751	0.543	1109.231	0.514	21	0.244	R.GDELLTSYPGLGSYR.V
R1/RRR1-9/2	1628.080	1628.764	-1037.622	0.329	623.057	0.439	16	0.197	R.GDELLTSYPGLGSYR.V
R1/RRR1-6/2	1061.832	1062.246	-390.961	0.479	824.805	0.541	13	0.229	K.GPVQISWFK.G
R1/RRR1-12/2	1245.872	1245.408	373.380	0.395	1061.489	0.515	17	0.237	K.NSLSGTIPASLGK.I
R1/RRR1-12/2	1245.043	1245.408	-293.799	0.444	926.764	0.503	17	0.226	K.NSLSGTIPASLGK.I
R1/RRR1-7/2	1720.351	1721.077	-1006.238	0.406	1319.498	0.455	24	0.248	R.ILGLGDLGVQGIGIPIGK.L
R1/RRR1-7/2	1720.515	1721.077	-911.069	0.360	1010.767	0.454	21	0.219	R.ILGLGDLGVQGIGIPIGK.L
R1/RRR1-7/2	1225.617	1226.408	-1465.663	0.414	1190.684	0.492	19	0.246	R.GIPSLVAIGADGR.T
R1/RRR1-7/3	1585.566	1584.675	-68.665	0.487	1408.737	0.441	26	0.145	K.HQLDDKWDGVNTR.L
R1/RRR1-7/3	1585.790	1584.675	73.099	0.353	1138.085	0.394	23	0.105	K.HQLDDKWDGVNTR.L
R1/RRR1-12/2	1368.242	1368.584	-250.547	0.421	1462.792	0.426	18	0.259	R.VLSGYNDIIM*AR.V
R1/RRR1-12/2	1367.587	1368.584	-1464.569	0.214	545.591	0.228	14	0.181	R.VLSGYNDIIM*AR.V
R1/RRR1-19/3	1351.546	1351.449	72.316	0.442	819.068	0.543	21	0.117	K.YGVGDAHFEVTR.F
R1/RRR1-20/3	1351.270	1351.449	-132.761	0.453	896.177	0.516	22	0.116	K.YGVGDAHFEVTR.F
R1/RRR1-20/3	1352.397	1351.449	-38.723	0.432	792.127	0.537	21	0.114	K.YGVGDAHFEVTR.F
R1/RRR1-20/3	1351.352	1351.449	-71.868	0.500	791.739	0.508	22	0.110	K.YGVGDAHFEVTR.F
R1/RRR1-19/3	1351.383	1351.449	-48.763	0.390	741.360	0.502	20	0.105	K.YGVGDAHFEVTR.F
R1/RRR1-19/3	1351.501	1351.449	38.618	0.412	560.260	0.532	20	0.104	K.YGVGDAHFEVTR.F
R1/RRR1-15/2	1259.975	1260.253	-221.713	0.437	1127.482	0.502	19	0.244	R.SDNPLNDGGNTR.S
R1/RRR1-6/2	1512.164	1510.803	239.129	0.345	609.588	0.544	18	0.208	R.AALGTQISGLAPILGK.Q
R1/RRR1-6/2	1510.323	1510.803	-318.965	0.273	379.514	0.378	13	0.183	R.AALGTQISGLAPILGK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1554.246	1554.724	-308.139	0.450	1426.223	0.434	20	0.256	K.LSTSAQSEVEYVLK.F
R1/RRR1-5/2	1554.314	1554.724	-264.328	0.471	1299.991	0.437	20	0.244	K.LSTSAQSEVEYVLK.F
R1/RRR1-5/2	1555.438	1554.724	-183.927	0.545	1160.838	0.497	19	0.243	K.LSTSAQSEVEYVLK.F
R1/RRR1-6/2	1554.108	1554.724	-1042.735	0.393	1024.768	0.442	19	0.223	K.LSTSAQSEVEYVLK.F
R1/RRR1-24/2	1031.974	1032.173	-193.698	0.426	1410.996	0.433	17	0.257	K.AVQASELVSK.H
R1/RRR1-24/2	1031.927	1032.173	-239.268	0.424	1272.049	0.451	16	0.247	K.AVQASELVSK.H
R1/RRR1-23/2	1032.002	1032.173	-166.643	0.393	1036.564	0.497	15	0.235	K.AVQASELVSK.H
R1/RRR1-23/2	1032.953	1032.173	-214.020	0.436	958.367	0.474	15	0.228	K.AVQASELVSK.H
R1/RRR1-24/2	1031.452	1032.173	-1673.430	0.341	1172.274	0.387	17	0.226	K.AVQASELVSK.H
R1/RRR1-23/2	1031.532	1032.173	-1595.793	0.274	733.099	0.303	13	0.193	K.AVQASELVSK.H
R1/RRR1-23/2	1344.421	1344.539	-87.938	0.470	1447.128	0.429	18	0.257	K.TTLLDQAVNAAVK.A
R1/RRR1-23/2	1344.367	1344.539	-128.743	0.370	997.837	0.379	17	0.210	K.TTLLDQAVNAAVK.A
R1/RRR1-12/2	1810.404	1811.069	-922.438	0.390	1192.525	0.484	20	0.241	R.IEALAEEIQPLLSEVR.D
R1/RRR1-9/2	1891.435	1891.158	147.161	0.480	1015.494	0.517	22	0.236	R.FIQYNIFGNVFEVTAK.Y
R1/RRR1-9/2	1892.528	1891.158	196.374	0.489	550.611	0.521	20	0.212	R.FIQYNIFGNVFEVTAK.Y
R1/RRR1-9/2	1892.448	1891.158	153.552	0.493	403.467	0.537	19	0.210	R.FIQYNIFGNVFEVTAK.Y
R1/RRR1-11/2	1085.234	1085.234	-0.069	0.393	606.926	0.543	13	0.214	K.YGVSGYPTLK.F
R1/RRR1-11/2	1084.954	1085.234	-259.397	0.257	637.058	0.487	14	0.201	K.YGVSGYPTLK.F
R1/RRR1-17/2	1513.081	1513.633	-1029.254	0.396	1611.012	0.365	19	0.261	K.FSFEDISAQNQVK.A
R1/RRR1-17/2	1513.148	1513.633	-321.849	0.408	1271.749	0.317	18	0.218	K.FSFEDISAQNQVK.A
R1/RRR1-18/3	1464.323	1464.645	-220.966	0.490	644.563	0.541	23	0.109	K.KGEEVPLSEYKGK.V
R1/RRR1-19/3	1464.437	1464.645	-142.693	0.478	860.682	0.476	23	0.107	K.KGEEVPLSEYKGK.V
R1/RRR1-18/3	1464.183	1464.645	-316.817	0.450	561.624	0.436	22	0.093	K.KGEEVPLSEYKGK.V
R1/RRR1-25/3	1465.180	1464.645	-318.398	0.371	464.198	0.330	19	0.078	-.KGEEVPLSEYKGK.-
R1/RRR1-12/3	1730.804	1730.946	-82.463	0.430	702.234	0.543	30	0.107	R.VLSIQSHTVQGYVGNK.S
R1/RRR1-12/3	1730.987	1730.946	23.538	0.410	705.229	0.453	27	0.095	R.VLSIQSHTVQGYVGNK.S
R1/RRR1-12/3	1730.327	1730.946	-938.742	0.406	556.721	0.426	26	0.090	R.VLSIQSHTVQGYVGNK.S
R1/RRR1-16/2	1212.442	1212.467	-20.763	0.508	1231.082	0.482	17	0.250	R.VNIGQIILSVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1198.607	1199.382	-1485.309	0.500	1051.047	0.511	17	0.239	K.TPLELGATAGLR.L
R1/RRR1-9/2	1199.011	1199.382	-310.695	0.437	1164.209	0.354	18	0.218	K.TPLELGATAGLR.L
R1/RRR1-16/2	1441.252	1440.715	-322.188	0.446	425.751	0.528	16	0.208	K.LPAQIPAGQYLIR.I
R1/RRR1-16/2	1439.610	1440.715	-1466.286	0.388	426.345	0.469	15	0.199	K.LPAQIPAGQYLIR.I
R1/RRR1-5/3	1867.710	1867.098	-208.576	0.426	742.241	0.525	25	0.107	R.VSLTHQFHQALDASIAK.N
R1/RRR1-6/2	1506.623	1506.729	-70.019	0.515	1488.883	0.405	21	0.255	K.AGASLYGIGDLSLLR.A
R1/RRR1-10/3	1427.765	1427.504	183.280	0.450	1043.800	0.512	28	0.121	R.FGAQVHNDNPAEK.M
R1/RRR1-9/3	1427.108	1427.504	-277.861	0.392	761.400	0.507	24	0.105	R.FGAQVHNDNPAEK.M
R1/RRR1-10/3	1426.976	1427.504	-1073.566	0.431	785.907	0.486	24	0.104	R.FGAQVHNDNPAEK.M
R1/RRR1-9/3	1426.791	1427.504	-1204.097	0.424	639.666	0.449	22	0.096	R.FGAQVHNDNPAEK.M
R1/RRR1-10/3	1427.938	1427.504	305.057	0.433	599.788	0.429	21	0.094	R.FGAQVHNDNPAEK.M
R1/RRR1-9/3	1427.040	1427.504	-326.007	0.400	601.500	0.433	22	0.093	R.FGAQVHNDNPAEK.M
R1/RRR1-16/2	1827.338	1828.100	-967.292	0.368	470.088	0.521	19	0.202	K.GLLTDQTLPLLTDSALR.D
R1/RRR1-16/2	1827.955	1828.100	-79.747	0.303	282.792	0.471	16	0.191	K.GLLTDQTLPLLTDSALR.D
R1/RRR1-7/2	1730.624	1729.955	-191.909	0.519	847.235	0.522	22	0.225	R.GDLGIEIPAAEVFAAQK.K
R1/RRR1-7/2	1730.308	1729.955	204.878	0.488	733.934	0.511	20	0.215	R.GDLGIEIPAAEVFAAQK.K
R1/RRR1-7/2	1729.542	1729.955	-239.601	0.453	776.988	0.488	21	0.214	R.GDLGIEIPAAEVFAAQK.K
R1/RRR1-18/2	1712.411	1712.793	-223.766	0.486	794.909	0.530	20	0.221	K.GTSPEQTSTLEESAFK.I
R1/RRR1-8/2	1395.379	1394.558	-128.774	0.472	1149.954	0.490	18	0.246	R.WEFSNPTPFIR.S
R1/RRR1-8/2	1395.213	1394.558	-248.487	0.492	1057.047	0.406	17	0.222	R.WEFSNPTPFIR.S
R1/RRR1-8/2	1394.030	1394.558	-1099.411	0.378	773.671	0.296	16	0.195	R.WEFSNPTPFIR.S
R1/RRR1-9/2	1292.016	1291.438	-327.941	0.440	688.859	0.540	19	0.221	R.GIAAAPVTNSYAR.R
R1/RRR1-9/2	1290.491	1291.438	-1513.234	0.297	604.789	0.480	18	0.202	R.GIAAAPVTNSYAR.R
R1/RRR1-25/2	1663.606	1663.857	-151.213	0.381	519.444	0.523	16	0.198	K.TISGGAYVVATPAASAAR.S
R1/RRR1-15/2	1403.262	1403.605	-245.491	0.447	1110.419	0.495	17	0.237	R.SALGIDDLPIFGGK.S
R1/RRR1-15/2	1404.284	1403.605	-229.444	0.452	817.486	0.504	17	0.219	R.SALGIDDLPIFGGK.S
R1/RRR1-15/2	1403.298	1403.605	-219.834	0.401	592.468	0.415	15	0.196	R.SALGIDDLPIFGGK.S
R1/RRR1-3/2	1636.946	1637.902	-1198.722	0.419	719.803	0.513	19	0.215	R.IPGTELLPGDIVSIGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1637.330	1637.902	-963.338	0.415	707.329	0.505	19	0.213	R.IPGTELLPGDIVSIGR.S
R1/RRR1-2/2	1638.609	1637.902	-179.298	0.451	549.992	0.442	18	0.200	R.IPGTELLPGDIVSIGR.S
R1/RRR1-3/2	1636.990	1637.902	-1171.839	0.306	370.672	0.309	15	0.187	R.IPGTELLPGDIVSIGR.S
R1/RRR1-21/2	1674.155	1672.880	164.351	0.454	380.552	0.507	19	0.215	R.IIPNFM*CQGGDFTR.X
R1/RRR1-20/2	1673.168	1672.880	172.351	0.354	403.802	0.545	19	0.213	R.IIPNFM*CQGGDFTR.X
R1/RRR1-21/2	1673.135	1672.880	152.669	0.382	379.165	0.521	18	0.212	R.IIPNFM*CQGGDFTR.X
R1/RRR1-20/2	1657.286	1656.881	244.860	0.448	279.810	0.477	18	0.212	R.IIPNFMCQGGDFTR.X
R1/RRR1-20/2	1658.050	1656.881	102.376	0.458	353.146	0.473	18	0.211	R.IIPNFMCQGGDFTR.X
R1/RRR1-20/2	1657.254	1656.881	225.656	0.452	306.977	0.435	18	0.209	R.IIPNFMCQGGDFTR.X
R1/RRR1-20/2	1674.075	1672.880	116.600	0.329	378.473	0.446	19	0.206	R.IIPNFM*CQGGDFTR.X
R1/RRR1-21/2	1657.611	1656.881	-163.504	0.432	286.816	0.451	17	0.203	-.IIPNFMCQGGDFTR.-
R1/RRR1-21/2	1674.234	1672.880	211.658	0.341	308.359	0.410	17	0.203	R.IIPNFM*CQGGDFTR.X
R1/RRR1-20/2	1672.628	1672.880	-151.577	0.273	328.958	0.482	18	0.203	R.IIPNFM*CQGGDFTR.X
R1/RRR1-20/2	1673.390	1672.880	-294.110	0.233	405.365	0.489	19	0.201	R.IIPNFM*CQGGDFTR.X
R1/RRR1-20/2	1674.241	1672.880	215.972	0.287	287.061	0.318	17	0.200	R.IIPNFM*CQGGDFTR.X
R1/RRR1-20/2	1674.336	1672.880	273.070	0.238	294.093	0.420	16	0.197	R.IIPNFM*CQGGDFTR.X
R1/RRR1-5/2	1786.575	1787.050	-266.286	0.535	973.084	0.509	21	0.233	R.LDQLIYIPLPDDKSR.M
R1/RRR1-4/2	1787.473	1787.050	237.780	0.502	829.427	0.411	20	0.208	R.LDQLIYIPLPDDKSR.M
R1/RRR1-5/2	1786.512	1787.050	-863.294	0.480	750.060	0.435	19	0.208	R.LDQLIYIPLPDDKSR.M
R1/RRR1-3/2	1787.559	1787.050	-275.181	0.456	751.839	0.382	19	0.201	R.LDQLIYIPLPDDKSR.M
R1/RRR1-1/2	1788.838	1787.050	-118.588	0.390	440.644	0.313	15	0.188	R.LDQLIYIPLPDDKSR.M
R1/RRR1-17/2	1823.820	1825.078	-1241.876	0.507	782.021	0.524	19	0.221	K.AFM*IDKDQVDWIQAK.F
R1/RRR1-16/2	1824.335	1825.078	-958.645	0.490	715.962	0.520	18	0.216	K.AFM*IDKDQVDWIQAK.F
R1/RRR1-17/3	1824.561	1825.078	-833.920	0.530	1663.476	0.489	30	0.199	K.AFM*IDKDQVDWIQAK.F
R1/RRR1-16/3	1824.103	1825.078	-1086.238	0.522	1266.172	0.491	25	0.151	K.AFM*IDKDQVDWIQAK.F
R1/RRR1-16/3	1825.836	1825.078	-132.852	0.557	1202.337	0.492	26	0.143	K.AFM*IDKDQVDWIQAK.F
R1/RRR1-17/3	1824.838	1825.078	-131.985	0.518	1010.693	0.504	24	0.129	K.AFM*IDKDQVDWIQAK.F
R1/RRR1-4/2	1934.496	1935.166	-865.925	0.430	1007.886	0.497	20	0.227	K.GVPSLFSDLSPLYEQPGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1935.101	1935.166	-33.509	0.378	603.133	0.428	17	0.194	-.GVPSLFSDLSPLYEQPGK.-
R1/RRR1-4/2	1935.068	1935.166	-50.593	0.388	494.745	0.444	15	0.191	-.GVPSLFSDLSPLYEQPGK.-
R1/RRR1-4/3	1933.408	1932.984	219.762	0.432	1076.168	0.496	25	0.130	R.HDFSFEDAHDLDLGTGR.S
R1/RRR1-7/2	1892.577	1891.160	221.405	0.493	715.872	0.515	21	0.215	R.EGINIFLAGFVPTENLR.F
R1/RRR1-7/2	1892.215	1891.160	29.531	0.380	386.835	0.522	18	0.200	R.EGINIFLAGFVPTENLR.F
R1/RRR1-6/2	1148.998	1149.235	-207.216	0.322	337.128	0.499	14	0.202	R.HSTVVDSFEK.K
R1/RRR1-6/2	1148.981	1149.235	-222.138	0.352	371.701	0.439	14	0.201	R.HSTVVDSFEK.K
R1/RRR1-6/2	1259.455	1258.526	-56.832	0.389	581.789	0.531	16	0.210	R.IPSSLCGIIGLK.T
R1/RRR1-3/2	1876.613	1875.067	-242.745	0.511	716.615	0.498	19	0.209	K.ILLLDEATSALDVESER.I
R1/RRR1-6/2	1954.863	1955.302	-225.262	0.412	1491.306	0.390	19	0.249	K.LMSTTYLVALCQAVDLR.H
R1/RRR1-6/2	1970.550	1971.301	-891.485	0.454	1093.559	0.455	21	0.227	K.LM*STTYLVALCQAVDLR.H
R1/RRR1-13/2	1240.076	1240.476	-323.016	0.334	1189.980	0.461	17	0.236	R.DVAWAPVLGLAK.A
R1/RRR1-13/2	1240.138	1240.476	-273.537	0.366	1015.537	0.446	16	0.221	R.DVAWAPVLGLAK.A
R1/RRR1-13/2	1239.345	1240.476	-1724.166	0.269	447.674	0.289	11	0.177	-.DVAWAPVLGLAK.-
R1/RRR1-5/2	1561.810	1560.768	26.998	0.421	741.150	0.519	18	0.218	K.LPLEIGSVSEISCR.R
R1/RRR1-5/2	1560.903	1560.768	86.785	0.314	1138.531	0.368	16	0.213	K.LPLEIGSVSEISCR.R
R1/RRR1-5/2	1562.024	1560.768	164.322	0.312	271.594	0.456	15	0.195	K.LPLEIGSVSEISCR.R
R1/RRR1-7/3	1551.238	1550.615	-244.024	0.381	1173.584	0.470	23	0.129	R.SRDGSVHDSFTVSR.D
R1/RRR1-7/3	1550.723	1550.615	69.660	0.442	1064.111	0.426	23	0.111	R.SRDGSVHDSFTVSR.D
R1/RRR1-8/2	1540.385	1539.800	-270.295	0.344	1521.472	0.368	19	0.250	R.AFQTLLTYIGNVAK.N
R1/RRR1-8/2	1540.461	1539.800	-220.607	0.300	1160.137	0.500	18	0.237	R.AFQTLLTYIGNVAK.N
R1/RRR1-14/2	1536.256	1534.734	-311.747	0.515	831.427	0.513	19	0.221	R.VSTTVTVDEALTGLK.T
R1/RRR1-9/2	1020.979	1021.152	-169.701	0.432	1257.253	0.460	14	0.247	R.AVQIAYEAR.K
R1/RRR1-11/2	1444.112	1444.608	-344.272	0.406	1097.623	0.481	15	0.233	R.APTYSILDTCFR.G
R1/RRR1-17/2	1174.172	1174.374	-172.951	0.370	768.020	0.511	14	0.217	K.LSELGILSWR.L
R1/RRR1-16/2	1174.149	1174.374	-192.454	0.363	699.156	0.462	14	0.208	K.LSELGILSWR.L
R1/RRR1-9/2	1147.265	1146.321	-48.623	0.422	1288.298	0.446	16	0.247	R.ITEGVNLPFR.V
R1/RRR1-12/2	1146.746	1146.321	372.024	0.261	918.303	0.228	14	0.190	-.ITEGVNLPFR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/2	1146.559	1146.321	207.954	0.292	482.257	0.315	12	0.189	-.ITEGVNLPFR.-
R1/RRR1-17/2	1088.864	1088.237	-343.249	0.478	1353.468	0.432	16	0.249	K.GAELADGLTIK.D
R1/RRR1-4/2	1542.558	1542.718	-103.788	0.485	1405.316	0.407	21	0.248	R.FGPIIEQNVDPANK.G
R1/RRR1-4/2	1543.611	1542.718	-69.055	0.444	885.128	0.339	17	0.197	R.FGPIIEQNVDPANK.G
R1/RRR1-3/2	1944.603	1943.188	214.159	0.451	1128.505	0.456	21	0.227	R.AASAAAAAALEDQTLIDIVK.H
R1/RRR1-2/2	1542.334	1541.731	-258.126	0.299	1860.945	0.205	19	0.248	R.ESDLAAAVAVAPVATR.K
R1/RRR1-7/2	1541.740	1541.731	5.590	0.328	1427.927	0.344	18	0.232	R.ESDLAAAVAVAPVATR.K
R1/RRR1-6/2	1542.419	1541.731	-202.943	0.341	1334.152	0.333	18	0.226	-.ESDLAAAVAVAPVATR.-
R1/RRR1-7/2	1543.143	1541.731	267.653	0.376	1301.710	0.330	18	0.222	-.ESDLAAAVAVAPVATR.-
R1/RRR1-7/2	1542.453	1541.731	-181.109	0.310	1283.095	0.246	17	0.204	R.ESDLAAAVAVAPVATR.K
R1/RRR1-1/2	1542.542	1541.731	-123.156	0.331	1332.674	0.199	17	0.199	R.ESDLAAAVAVAPVATR.K
R1/RRR1-1/2	1542.751	1541.731	12.491	0.340	1231.425	0.208	18	0.199	-.ESDLAAAVAVAPVATR.-
R1/RRR1-4/2	1542.515	1541.731	-140.938	0.319	1114.351	0.230	17	0.193	R.ESDLAAAVAVAPVATR.K
R1/RRR1-1/2	1542.505	1541.731	-146.972	0.256	880.381	0.216	15	0.183	R.ESDLAAAVAVAPVATR.K
R1/RRR1-2/2	1542.622	1541.731	-71.322	0.238	918.363	0.121	15	0.179	-.ESDLAAAVAVAPVATR.-
R1/RRR1-14/2	1279.102	1279.427	-254.771	0.472	1002.182	0.494	18	0.234	K.GVVTDIIHDPGR.G
R1/RRR1-14/2	1279.210	1279.427	-170.810	0.413	717.328	0.495	16	0.214	K.GVVTDIIHDPGR.G
R1/RRR1-14/2	1278.673	1279.427	-1376.218	0.372	574.434	0.434	14	0.199	K.GVVTDIIHDPGR.G
R1/RRR1-18/2	1114.993	1114.146	-137.658	0.478	1424.978	0.403	15	0.252	R.FGFDEDDIR.V
R1/RRR1-18/2	1113.814	1114.146	-299.284	0.463	1305.574	0.377	15	0.236	R.FGFDEDDIR.V
R1/RRR1-18/2	1114.120	1114.146	-23.255	0.409	1231.129	0.378	14	0.229	R.FGFDEDDIR.V
R1/RRR1-13/2	1854.435	1855.084	-892.086	0.454	1220.910	0.452	20	0.238	R.HVAETLGIDLEPLYQR.I
R1/RRR1-8/2	1443.264	1442.600	-233.767	0.533	817.287	0.497	18	0.221	K.GLDFEFLPFGSGR.R
R1/RRR1-8/2	1442.216	1442.600	-266.876	0.417	832.261	0.406	17	0.206	K.GLDFEFLPFGSGR.R
R1/RRR1-7/2	1977.637	1978.234	-810.013	0.367	548.269	0.495	17	0.197	R.ELTAPFVDDGLIEVVGFR.D
R1/RRR1-26/2	1337.501	1336.469	23.745	0.483	1445.019	0.392	18	0.247	K.AGGFGPVCTVDQK.N
R1/RRR1-26/2	1336.163	1336.469	-229.505	0.395	1219.939	0.280	17	0.207	K.AGGFGPVCTVDQK.N
R1/RRR1-26/2	1336.079	1336.469	-292.842	0.414	1133.396	0.312	17	0.207	K.AGGFGPVCTVDQK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-4/2	1498.508	1497.719	-140.583	0.313	734.392	0.495	15	0.205	-.VPTPDVSVVDLTVR.-
R1/RRR1-13/3	1297.129	1296.548	-324.205	0.452	1325.152	0.428	25	0.132	K.HITGGMMGGHAVK.L
R1/RRR1-14/3	1295.411	1296.548	-1655.036	0.385	1151.229	0.383	24	0.104	K.HITGGMMGGHAVK.L
R1/RRR1-5/2	1360.281	1360.580	-220.755	0.486	932.674	0.496	18	0.229	K.FTEQALPVDLVK.R
R1/RRR1-5/2	1360.349	1360.580	-170.252	0.444	816.735	0.457	18	0.216	K.FTEQALPVDLVK.R
R1/RRR1-11/3	1504.436	1504.676	-160.222	0.341	833.308	0.491	27	0.107	R.LAAALSSPAHPAGGAGR.N
R1/RRR1-11/3	1504.766	1504.676	59.989	0.388	708.322	0.479	24	0.103	R.LAAALSSPAHPAGGAGR.N
R1/RRR1-12/3	1505.607	1504.676	-46.086	0.378	688.677	0.487	25	0.102	R.LAAALSSPAHPAGGAGR.N
R1/RRR1-12/3	1504.437	1504.676	-159.489	0.343	673.546	0.432	24	0.093	R.LAAALSSPAHPAGGAGR.N
R1/RRR1-12/3	1504.660	1504.676	-10.433	0.345	517.302	0.439	22	0.092	R.LAAALSSPAHPAGGAGR.N
R1/RRR1-13/2	1173.233	1174.290	-1758.396	0.391	1297.851	0.430	19	0.243	K.AVENAGTSVGIR.C
R1/RRR1-13/2	1174.077	1174.290	-181.308	0.437	1312.420	0.422	18	0.243	K.AVENAGTSVGIR.C
R1/RRR1-9/2	1693.070	1692.893	104.742	0.408	1000.852	0.480	21	0.227	R.YFTIHTDAPDAVLTK.L
R1/RRR1-7/2	1941.918	1941.196	-143.391	0.468	535.663	0.479	19	0.203	K.GVIM*LDFPSFQPSWGDK.K
R1/RRR1-7/2	1941.611	1941.196	214.700	0.382	367.582	0.419	17	0.193	K.GVIM*LDFPSFQPSWGDK.K
R1/RRR1-7/2	1942.865	1941.196	-170.860	0.419	601.819	0.350	18	0.190	K.GVIM*LDFPSFQPSWGDK.K
R1/RRR1-10/2	1368.007	1368.474	-343.108	0.478	1239.957	0.441	18	0.241	K.SANVTYTENLQK.Y
R1/RRR1-17/2	1238.300	1237.518	-177.046	0.440	841.287	0.501	18	0.226	K.LPFAPVPLVQR.M
R1/RRR1-17/2	1237.154	1237.518	-294.980	0.230	277.207	0.361	11	0.184	-.LPFAPVPLVQR.-
R1/RRR1-17/2	1237.035	1237.518	-391.906	0.225	376.527	0.362	12	0.176	-.LPFAPVPLVQR.-
R1/RRR1-12/2	1344.022	1344.408	-288.560	0.448	1017.945	0.481	16	0.231	K.TFLSDSPEYER.L
R1/RRR1-12/2	1344.129	1344.408	-208.287	0.441	876.637	0.436	15	0.214	K.TFLSDSPEYER.L
R1/RRR1-22/3	1716.505	1716.868	-212.112	0.422	929.376	0.487	28	0.112	R.VPDEVIDKVQEETSK.S
R1/RRR1-22/3	1717.283	1716.868	242.072	0.447	689.168	0.527	26	0.109	R.VPDEVIDKVQEETSK.S
R1/RRR1-21/3	1716.593	1716.868	-160.533	0.415	716.694	0.506	25	0.106	R.VPDEVIDKVQEETSK.S
R1/RRR1-21/3	1716.606	1716.868	-152.936	0.393	791.111	0.481	27	0.103	R.VPDEVIDKVQEETSK.S
R1/RRR1-22/3	1716.676	1716.868	-112.383	0.409	485.568	0.500	21	0.101	R.VPDEVIDKVQEETSK.S
R1/RRR1-21/3	1716.223	1716.868	-961.581	0.396	589.885	0.464	25	0.096	R.VPDEVIDKVQEETSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-3/2	1440.465	1439.677	-147.778	0.295	596.073	0.464	14	0.196	K.LPACFFILTNSR.S
R1/RRR1-9/3	1836.869	1836.186	-172.751	0.393	1739.099	0.268	30	0.142	K.GMTPISTFILEKGALEK.K
R1/RRR1-9/3	1836.941	1836.186	-133.553	0.341	1409.710	0.143	28	0.078	K.GMTPISTFILEKGALEK.K
R1/RRR1-19/2	1184.041	1184.371	-279.465	0.463	557.253	0.491	15	0.209	K.NNPTLAAINKK.F
R1/RRR1-26/2	1108.999	1109.257	-234.121	0.423	1105.283	0.462	17	0.236	R.YIEATGIVSR.A
R1/RRR1-26/2	1109.383	1109.257	113.387	0.467	1082.892	0.467	16	0.236	R.YIEATGIVSR.A
R1/RRR1-25/2	1109.335	1109.257	70.459	0.370	1113.363	0.345	16	0.215	R.YIEATGIVSR.A
R1/RRR1-26/2	1108.372	1109.257	-1706.202	0.352	1016.004	0.283	16	0.202	R.YIEATGIVSR.A
R1/RRR1-7/2	1550.166	1550.781	-1045.149	0.500	588.558	0.480	16	0.203	R.LLSSTNQPSFLSKK.D
R1/RRR1-22/2	1338.464	1338.535	-53.295	0.458	1067.952	0.468	20	0.235	K.VSGVEIVPDPVAR.G
R1/RRR1-24/2	1338.217	1338.535	-237.753	0.557	1151.735	0.441	20	0.235	K.VSGVEIVPDPVAR.G
R1/RRR1-24/2	1338.176	1338.535	-268.594	0.491	980.024	0.497	19	0.234	K.VSGVEIVPDPVAR.G
R1/RRR1-23/2	1338.908	1338.535	279.857	0.513	971.249	0.491	19	0.233	K.VSGVEIVPDPVAR.G
R1/RRR1-23/2	1337.797	1338.535	-1302.766	0.424	998.949	0.470	19	0.230	K.VSGVEIVPDPVAR.G
R1/RRR1-20/2	1339.215	1338.535	-239.404	0.443	817.850	0.526	18	0.228	K.VSGVEIVPDPVAR.G
R1/RRR1-24/2	1338.520	1338.535	-11.032	0.506	1110.378	0.416	20	0.228	K.VSGVEIVPDPVAR.G
R1/RRR1-23/2	1337.652	1338.535	-1411.921	0.404	1005.352	0.413	19	0.221	K.VSGVEIVPDPVAR.G
R1/RRR1-19/2	1339.702	1338.535	125.333	0.387	690.631	0.499	16	0.215	K.VSGVEIVPDPVAR.G
R1/RRR1-22/2	1338.121	1338.535	-309.779	0.418	839.688	0.420	18	0.214	K.VSGVEIVPDPVAR.G
R1/RRR1-18/2	1338.229	1338.535	-229.242	0.370	694.526	0.360	16	0.199	-.VSGVEIVPDPVAR.-
R1/RRR1-19/2	1337.515	1338.535	-1514.223	0.305	500.309	0.409	14	0.199	K.VSGVEIVPDPVAR.G
R1/RRR1-25/2	1338.540	1338.535	3.969	0.252	345.530	0.318	14	0.196	K.VSGVEIVPDPVAR.G
R1/RRR1-18/2	1338.126	1338.535	-306.027	0.342	591.275	0.327	15	0.196	K.VSGVEIVPDPVAR.G
R1/RRR1-21/2	1338.253	1338.535	-210.848	0.283	396.894	0.377	13	0.193	-.VSGVEIVPDPVAR.-
R1/RRR1-22/2	1337.652	1338.535	-1411.462	0.339	640.563	0.283	15	0.193	K.VSGVEIVPDPVAR.G
R1/RRR1-19/2	1338.481	1338.535	-39.939	0.254	548.332	0.306	14	0.192	K.VSGVEIVPDPVAR.G
R1/RRR1-13/2	1532.879	1532.720	104.426	0.433	1342.651	0.409	19	0.241	K.APDSDLVLADFGIAK.M
R1/RRR1-8/3	1626.785	1626.883	-60.189	0.327	1046.197	0.448	30	0.108	K.VAQGVVGAVADKGSVLR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/3	1625.852	1626.883	-1252.545	0.293	812.998	0.307	27	0.075	K.VAQGVVGAVADKGSVLR.F
R1/RRR1-12/3	1076.436	1076.234	188.674	0.501	1581.064	0.337	25	0.131	K.HVGHLGGALSK.N
R1/RRR1-12/3	1076.328	1076.234	87.850	0.525	1504.117	0.309	25	0.115	K.HVGHLGGALSK.N
R1/RRR1-12/3	1076.271	1076.234	34.274	0.503	1449.740	0.330	25	0.114	K.HVGHLGGALSK.N
R1/RRR1-11/2	1520.800	1521.699	-1252.351	0.343	1001.150	0.462	20	0.222	K.NWGFLPLVDSGSTK.I
R1/RRR1-11/2	1520.541	1521.699	-1423.109	0.312	674.905	0.411	16	0.196	K.NWGFLPLVDSGSTK.I
R1/RRR1-10/2	1785.237	1784.091	82.258	0.550	811.131	0.468	23	0.217	K.AQFIPYGATLTNLFVK.D
R1/RRR1-10/2	1785.665	1784.091	-239.270	0.527	825.789	0.453	23	0.216	K.AQFIPYGATLTNLFVK.D
R1/RRR1-10/2	1784.887	1784.091	-114.598	0.527	638.558	0.504	21	0.214	K.AQFIPYGATLTNLFVK.D
R1/RRR1-9/2	1784.686	1784.091	-227.121	0.467	507.563	0.376	19	0.195	K.AQFIPYGATLTNLFVK.D
R1/RRR1-7/2	1599.050	1598.742	193.261	0.362	507.260	0.486	14	0.196	R.SM*NVDQM*ETVAQGR.V
R1/RRR1-14/2	1439.757	1439.641	80.651	0.431	1067.666	0.468	16	0.230	R.SQIQAYVFDVIR.A
R1/RRR1-13/2	1439.169	1439.641	-328.695	0.398	889.081	0.537	13	0.224	R.SQIQAYVFDVIR.A
R1/RRR1-17/2	1082.402	1082.232	157.501	0.342	892.823	0.478	16	0.221	R.YGSLTGLSGVK.V
R1/RRR1-20/2	1082.246	1082.232	12.602	0.373	810.113	0.490	16	0.220	R.YGSLTGLSGVK.V
R1/RRR1-22/2	1082.379	1082.232	136.012	0.360	762.065	0.509	15	0.218	R.YGSLTGLSGVK.V
R1/RRR1-19/2	1081.792	1082.232	-408.194	0.327	774.731	0.495	16	0.216	R.YGSLTGLSGVK.V
R1/RRR1-20/2	1082.110	1082.232	-112.989	0.364	871.117	0.409	16	0.212	R.YGSLTGLSGVK.V
R1/RRR1-19/2	1081.555	1082.232	-1555.268	0.363	611.501	0.497	14	0.210	R.YGSLTGLSGVK.V
R1/RRR1-18/2	1082.143	1082.232	-82.550	0.344	690.481	0.416	15	0.205	R.YGSLTGLSGVK.V
R1/RRR1-3/2	1819.587	1818.019	-238.241	0.442	812.469	0.484	17	0.208	R.GIAFVGGFSYADVLDSAK.G
R1/RRR1-9/2	1579.356	1579.736	-241.454	0.393	895.892	0.482	17	0.217	R.LQENGLSFDLVSTR.T
R1/RRR1-15/2	1803.886	1804.982	-1165.298	0.444	1275.842	0.422	17	0.236	R.FLEYQLSDYNGWLR.D
R1/RRR1-3/3	1861.014	1860.878	73.473	0.498	1068.383	0.444	29	0.120	K.ASHSGSAAGSAEAESGTVQR.L
R1/RRR1-11/2	1254.281	1254.458	-141.406	0.415	473.931	0.482	15	0.205	K.INEGIPAGILEK.I
R1/RRR1-11/2	1254.301	1254.458	-125.102	0.440	453.086	0.426	15	0.201	K.INEGIPAGILEK.I
R1/RRR1-11/2	1254.208	1254.458	-199.694	0.433	464.661	0.391	15	0.195	-.INEGIPAGILEK.-
R1/RRR1-11/2	1311.122	1311.490	-281.101	0.473	1441.535	0.380	17	0.247	K.LLQEM*GVDAYR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1595.632	1595.738	-66.420	0.469	777.447	0.480	19	0.216	R.DGLLPSFFSDVNQR.T
R1/RRR1-2/2	1596.006	1595.738	168.801	0.426	693.055	0.414	18	0.203	R.DGLLPSFFSDVNQR.T
R1/RRR1-2/2	1596.262	1595.738	-299.031	0.313	460.587	0.326	16	0.190	R.DGLLPSFFSDVNQR.T
R1/RRR1-14/2	1633.262	1633.912	-1013.490	0.439	1120.371	0.453	20	0.230	K.VGPALLSGPVFATFEK.V
R1/RRR1-14/2	1633.326	1633.912	-973.720	0.482	1007.352	0.446	19	0.219	K.VGPALLSGPVFATFEK.V
R1/RRR1-13/2	1632.965	1633.912	-1196.171	0.330	969.924	0.194	18	0.183	K.VGPALLSGPVFATFEK.V
R1/RRR1-9/2	1502.594	1502.779	-123.222	0.411	1333.656	0.403	18	0.243	-.SEM*IMVFGEITTK.-
R1/RRR1-7/2	1178.309	1178.320	-8.792	0.334	724.917	0.468	15	0.208	K.YTSDPGLVLGR.Q
R1/RRR1-7/2	1178.662	1178.320	291.521	0.275	654.375	0.446	14	0.198	K.YTSDPGLVLGR.Q
R1/RRR1-11/2	1470.602	1469.793	-130.430	0.322	681.758	0.487	16	0.204	K.VLDPVPLIGFLTGK.L
R1/RRR1-11/2	1469.808	1469.793	10.112	0.240	581.503	0.275	15	0.182	K.VLDPVPLIGFLTGK.L
R1/RRR1-5/2	1200.410	1199.425	-12.506	0.532	1477.267	0.360	16	0.246	R.LLNLQTLDIR.N
R1/RRR1-11/3	1818.783	1819.015	-127.683	0.418	1384.685	0.389	30	0.131	R.VHNAALSAQPALVQNER.K
R1/RRR1-11/3	1818.826	1819.015	-104.355	0.471	1364.420	0.372	28	0.129	R.VHNAALSAQPALVQNER.K
R1/RRR1-10/3	1818.337	1819.015	-925.862	0.431	1255.899	0.360	29	0.112	R.VHNAALSAQPALVQNER.K
R1/RRR1-16/3	1858.320	1859.081	-950.381	0.353	962.212	0.462	28	0.107	R.AAHGGPAFEPHATVVGAIR.L
R1/RRR1-4/2	1474.067	1474.602	-1044.202	0.449	1464.902	0.359	19	0.243	K.IQSNETSNVVQVR.T
R1/RRR1-4/2	1474.152	1474.602	-306.194	0.471	1371.215	0.403	18	0.243	K.IQSNETSNVVQVR.T
R1/RRR1-4/2	1474.107	1474.602	-336.768	0.463	1316.111	0.384	18	0.234	K.IQSNETSNVVQVR.T
R1/RRR1-18/2	1292.011	1292.420	-316.950	0.349	992.009	0.464	18	0.222	K.AVDVTGPDGSFVK.G
R1/RRR1-18/2	1291.997	1292.420	-328.515	0.403	633.215	0.463	14	0.202	-.AVDVTGPDGSFVK.-
R1/RRR1-18/2	1292.164	1292.420	-198.281	0.328	643.329	0.378	15	0.194	-.AVDVTGPDGSFVK.-
R1/RRR1-15/2	1272.549	1272.440	86.149	0.459	490.660	0.471	13	0.204	K.LVYGLHWNGGR.M
R1/RRR1-15/2	1272.918	1272.440	377.182	0.358	383.921	0.380	12	0.193	K.LVYGLHWNGGR.M
R1/RRR1-15/2	1272.356	1272.440	-65.590	0.260	291.467	0.444	10	0.189	K.LVYGLHWNGGR.M
R1/RRR1-18/2	1678.839	1679.861	-1207.899	0.434	920.211	0.475	21	0.223	R.EALGIHQGTVPSWQR.C
R1/RRR1-18/2	1679.107	1679.861	-1047.798	0.425	773.571	0.513	20	0.219	R.EALGIHQGTVPSWQR.C
R1/RRR1-18/2	1680.252	1679.861	233.424	0.473	836.973	0.457	21	0.216	R.EALGIHQGTVPSWQR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/2	965.098	965.088	9.881	0.496	977.375	0.453	14	0.226	R.AGVANYTLR.A
R1/RRR1-6/2	964.820	965.088	-278.434	0.503	973.259	0.412	14	0.219	R.AGVANYTLR.A
R1/RRR1-6/2	964.208	965.088	-1956.036	0.430	1112.957	0.366	14	0.219	R.AGVANYTLR.A
R1/RRR1-5/2	1689.570	1688.821	-148.962	0.443	554.129	0.476	19	0.204	R.FAPLNSWPDNGNLDK.A
R1/RRR1-12/2	1309.136	1309.541	-310.465	0.402	1210.963	0.430	17	0.235	R.LPEAHLAFAALR.D
R1/RRR1-8/2	1390.262	1390.528	-192.128	0.446	1294.244	0.410	17	0.238	K.IVFANGSQDPWR.H
R1/RRR1-8/2	1390.420	1390.528	-78.072	0.415	910.262	0.388	16	0.208	K.IVFANGSQDPWR.H
R1/RRR1-8/2	1391.052	1390.528	-343.057	0.360	915.221	0.354	16	0.203	K.IVFANGSQDPWR.H
R1/RRR1-12/2	1693.393	1692.976	246.652	0.412	802.209	0.482	18	0.214	R.DFVPAIYDTTVIIPK.D
R1/RRR1-12/2	1693.374	1692.976	235.448	0.329	1036.738	0.336	19	0.205	R.DFVPAIYDTTVIIPK.D
R1/RRR1-1/2	1694.601	1692.976	-221.927	0.422	697.332	0.391	16	0.196	R.DFVPAIYDTTVIIPK.D
R1/RRR1-4/2	1461.245	1460.741	-340.906	0.383	816.523	0.466	19	0.213	R.IPPVGEVLTPFYK.T
R1/RRR1-10/2	1210.199	1210.363	-136.642	0.508	1202.600	0.432	17	0.237	R.FDGILGLGFDR.L
R1/RRR1-10/2	1211.142	1210.363	-183.139	0.562	1217.146	0.411	17	0.233	R.FDGILGLGFDR.L
R1/RRR1-10/2	1209.839	1210.363	-1263.552	0.464	1027.158	0.435	17	0.225	R.FDGILGLGFDR.L
R1/RRR1-11/2	1248.988	1249.357	-295.812	0.373	887.198	0.477	15	0.219	K.TGFTGGLNYYR.C
R1/RRR1-12/2	1249.331	1249.357	-20.738	0.460	670.783	0.468	15	0.211	K.TGFTGGLNYYR.C
R1/RRR1-11/2	1248.788	1249.357	-1259.634	0.428	612.268	0.323	15	0.195	K.TGFTGGLNYYR.C
R1/RRR1-8/2	1232.263	1232.409	-118.497	0.367	656.829	0.485	15	0.205	K.NTVEGITGIISK.T
R1/RRR1-5/2	1164.255	1164.376	-104.176	0.416	1272.102	0.412	16	0.239	K.LLVNYLSDVK.Y
R1/RRR1-12/2	1395.265	1394.595	-236.895	0.395	1083.620	0.448	16	0.225	R.AVVDSAYEVISLK.G
R1/RRR1-7/2	1098.184	1097.242	-52.468	0.316	600.761	0.463	13	0.206	R.SHCASFLFK.N
R1/RRR1-8/2	1097.087	1097.242	-141.914	0.392	317.816	0.509	10	0.206	R.SHCASFLFK.N
R1/RRR1-8/2	1096.825	1097.242	-381.055	0.345	366.409	0.497	11	0.205	R.SHCASFLFK.N
R1/RRR1-7/2	1097.096	1097.242	-133.654	0.332	631.099	0.429	12	0.204	R.SHCASFLFK.N
R1/RRR1-7/2	1096.455	1097.242	-1634.185	0.296	307.681	0.516	9	0.199	R.SHCASFLFK.N
R1/RRR1-8/2	1096.293	1097.242	-1782.964	0.196	382.552	0.332	11	0.190	R.SHCASFLFK.N
R1/RRR1-13/2	1217.079	1217.266	-154.883	0.374	1185.578	0.427	17	0.234	R.DLGYLDDSYR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-13/2	1217.192	1217.266	-61.723	0.343	1235.317	0.328	16	0.219	R.DLGYLDDSYR.A
R1/RRR1-13/2	1217.020	1217.266	-202.979	0.344	844.033	0.426	14	0.210	R.DLGYLDDSYR.A
R1/RRR1-7/2	1587.449	1587.754	-192.712	0.498	1372.620	0.389	22	0.242	R.NCPEFAFSFLGAAR.L
R1/RRR1-6/2	1469.610	1468.636	-17.630	0.483	654.224	0.472	19	0.212	K.GIPTVIDSYAEFR.R
R1/RRR1-6/2	1468.567	1468.636	-46.822	0.449	482.448	0.526	17	0.211	K.GIPTVIDSYAEFR.R
R1/RRR1-6/2	1651.626	1650.856	-139.782	0.567	1236.638	0.404	20	0.229	R.QFLTLNALNEFDPK.I
R1/RRR1-6/2	1650.583	1650.856	-165.758	0.545	1150.211	0.416	20	0.227	R.QFLTLNALNEFDPK.I
R1/RRR1-6/2	1651.413	1650.856	-269.101	0.563	1249.523	0.378	19	0.223	R.QFLTLNALNEFDPK.I
R1/RRR1-14/2	1858.232	1857.057	94.576	0.342	912.255	0.459	22	0.214	K.GITPADAPETSALASWLR.A
R1/RRR1-14/2	1858.419	1857.057	195.498	0.311	998.102	0.404	22	0.210	K.GITPADAPETSALASWLR.A
R1/RRR1-10/2	1142.060	1142.292	-203.973	0.387	911.343	0.466	15	0.222	K.TIFHLNPSGR.F
R1/RRR1-10/2	1141.325	1142.292	-1728.922	0.361	917.898	0.469	15	0.222	K.TIFHLNPSGR.F
R1/RRR1-9/2	1142.080	1142.292	-186.816	0.397	899.167	0.442	15	0.219	K.TIFHLNPSGR.F
R1/RRR1-10/2	1141.578	1142.292	-1506.205	0.346	916.993	0.361	15	0.207	K.TIFHLNPSGR.F
R1/RRR1-9/2	1142.159	1142.292	-116.803	0.344	854.374	0.356	15	0.205	K.TIFHLNPSGR.F
R1/RRR1-13/2	1141.492	1142.292	-1581.615	0.213	717.534	0.165	13	0.184	K.TIFHLNPSGR.F
R1/RRR1-5/2	1120.634	1120.280	316.449	0.489	1284.066	0.413	15	0.239	R.TSGLEVVWTK.T
R1/RRR1-5/2	1120.290	1120.280	9.114	0.333	417.199	0.342	11	0.186	-.TSGLEVVWTK.-
R1/RRR1-12/2	1351.914	1351.490	314.025	0.478	1474.346	0.361	17	0.249	-.FGFNDAFNYKK.-
R1/RRR1-20/2	1129.013	1129.377	-323.017	0.478	1177.450	0.429	16	0.235	R.LAVDKWGIVK.A
R1/RRR1-20/2	1128.390	1129.377	-1765.885	0.345	1358.507	0.351	16	0.233	R.LAVDKWGIVK.A
R1/RRR1-23/1	1531.762	1531.645	76.575	0.491	737.225	0.471	17	0.358	R.AGDCALIHSGSWEK.A
R1/RRR1-23/2	1531.323	1531.645	-211.049	0.538	1825.895	0.455	21	0.308	R.AGDCALIHSGSWEK.A
R1/RRR1-23/2	1531.224	1531.645	-275.750	0.531	1703.799	0.477	22	0.300	R.AGDCALIHSGSWEK.A
R1/RRR1-22/2	1531.254	1531.645	-256.555	0.516	1547.486	0.461	21	0.275	R.AGDCALIHSGSWEK.A
R1/RRR1-22/2	1531.100	1531.645	-1012.583	0.505	1589.710	0.437	22	0.275	R.AGDCALIHSGSWEK.A
R1/RRR1-24/2	1531.137	1531.645	-987.689	0.485	1537.338	0.449	21	0.271	R.AGDCALIHSGSWEK.A
R1/RRR1-24/2	1531.370	1531.645	-180.261	0.540	1434.742	0.459	20	0.261	R.AGDCALIHSGSWEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	1531.177	1531.645	-306.464	0.477	1459.986	0.414	20	0.254	R.AGDCALIHSGSWEK.A
R1/RRR1-24/2	1531.184	1531.645	-301.825	0.491	1401.791	0.429	21	0.252	R.AGDCALIHSGSWEK.A
R1/RRR1-22/2	1530.675	1531.645	-1291.225	0.478	1292.816	0.453	19	0.246	R.AGDCALIHSGSWEK.A
R1/RRR1-21/2	1531.122	1531.645	-998.175	0.489	1299.013	0.433	20	0.243	R.AGDCALIHSGSWEK.A
R1/RRR1-23/1	1530.840	1531.645	-1183.064	0.197	625.831	0.232	16	0.239	R.AGDCALIHSGSWEK.A
R1/RRR1-23/2	1531.221	1531.645	-277.830	0.510	1163.516	0.447	19	0.234	R.AGDCALIHSGSWEK.A
R1/RRR1-2/2	1532.393	1531.645	-165.120	0.508	1162.216	0.413	20	0.228	R.AGDCALIHSGSWEK.A
R1/RRR1-23/2	1531.926	1531.645	183.775	0.382	1332.105	0.257	20	0.213	R.AGDCALIHSGSWEK.A
R1/RRR1-23/1	1530.941	1531.645	-1116.527	0.259	557.968	0.242	16	0.200	R.AGDCALIHSGSWEK.A
R1/RRR1-24/3	1532.679	1531.645	21.831	0.476	1357.169	0.421	29	0.132	R.AGDCALIHSGSWEK.A
R1/RRR1-22/3	1531.819	1531.645	114.081	0.476	1265.355	0.430	27	0.129	R.AGDCALIHSGSWEK.A
R1/RRR1-23/3	1532.576	1531.645	-45.035	0.509	1354.525	0.404	29	0.128	R.AGDCALIHSGSWEK.A
R1/RRR1-23/3	1531.884	1531.645	156.636	0.454	1375.947	0.381	28	0.125	R.AGDCALIHSGSWEK.A
R1/RRR1-25/3	1531.371	1531.645	-179.470	0.404	1348.441	0.349	26	0.117	R.AGDCALIHSGSWEK.A
R1/RRR1-24/3	1531.762	1531.645	76.557	0.488	1139.907	0.422	27	0.117	R.AGDCALIHSGSWEK.A
R1/RRR1-19/3	1530.824	1531.645	-1193.331	0.360	1130.044	0.395	25	0.111	R.AGDCALIHSGSWEK.A
R1/RRR1-22/3	1531.629	1531.645	-10.490	0.443	970.849	0.431	25	0.110	R.AGDCALIHSGSWEK.A
R1/RRR1-22/3	1532.764	1531.645	78.025	0.487	1080.885	0.401	26	0.110	R.AGDCALIHSGSWEK.A
R1/RRR1-21/3	1530.961	1531.645	-1103.134	0.364	1354.707	0.329	28	0.110	R.AGDCALIHSGSWEK.A
R1/RRR1-20/3	1531.189	1531.645	-299.195	0.396	1302.226	0.330	26	0.109	R.AGDCALIHSGSWEK.A
R1/RRR1-1/3	1531.414	1531.645	-151.283	0.449	1139.103	0.366	26	0.106	R.AGDCALIHSGSWEK.A
R1/RRR1-18/3	1531.901	1531.645	167.544	0.443	1117.560	0.357	25	0.104	R.AGDCALIHSGSWEK.A
R1/RRR1-18/3	1531.163	1531.645	-316.112	0.415	1341.854	0.282	27	0.100	R.AGDCALIHSGSWEK.A
R1/RRR1-20/3	1531.102	1531.645	-1010.791	0.388	1098.933	0.341	25	0.099	R.AGDCALIHSGSWEK.A
R1/RRR1-25/3	1531.432	1531.645	-139.888	0.385	1129.853	0.327	26	0.097	R.AGDCALIHSGSWEK.A
R1/RRR1-24/3	1532.466	1531.645	-117.423	0.445	825.377	0.361	23	0.096	R.AGDCALIHSGSWEK.A
R1/RRR1-24/3	1531.838	1531.645	125.949	0.402	859.965	0.365	24	0.095	R.AGDCALIHSGSWEK.A
R1/RRR1-24/3	1531.021	1531.645	-1064.225	0.399	1034.410	0.327	25	0.094	R.AGDCALIHSGSWEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-24/3	1530.918	1531.645	-1131.837	0.421	1097.642	0.299	24	0.093	R.AGDCALIHSGSWEK.A
R1/RRR1-19/3	1531.928	1531.645	185.284	0.456	926.991	0.329	24	0.093	R.AGDCALIHSGSWEK.A
R1/RRR1-3/3	1531.399	1531.645	-161.238	0.367	553.942	0.314	20	0.092	R.AGDCALIHSGSWEK.A
R1/RRR1-21/3	1532.497	1531.645	-97.168	0.488	1273.543	0.265	29	0.090	R.AGDCALIHSGSWEK.A
R1/RRR1-1/3	1530.769	1531.645	-1229.607	0.392	834.453	0.317	23	0.089	R.AGDCALIHSGSWEK.A
R1/RRR1-18/3	1531.710	1531.645	42.627	0.414	856.154	0.300	23	0.088	R.AGDCALIHSGSWEK.A
R1/RRR1-2/3	1530.763	1531.645	-1233.090	0.400	783.862	0.298	22	0.088	R.AGDCALIHSGSWEK.A
R1/RRR1-23/3	1531.462	1531.645	-119.859	0.350	989.403	0.293	25	0.087	R.AGDCALIHSGSWEK.A
R1/RRR1-23/3	1532.966	1531.645	209.679	0.419	1206.833	0.243	26	0.086	R.AGDCALIHSGSWEK.A
R1/RRR1-19/3	1531.586	1531.645	-38.549	0.362	711.177	0.279	21	0.086	R.AGDCALIHSGSWEK.A
R1/RRR1-21/3	1532.577	1531.645	-44.556	0.308	653.657	0.280	21	0.086	R.AGDCALIHSGSWEK.A
R1/RRR1-25/3	1531.882	1531.645	154.718	0.349	866.564	0.264	24	0.082	R.AGDCALIHSGSWEK.A
R1/RRR1-23/3	1531.085	1531.645	-1022.438	0.392	1080.401	0.244	26	0.082	R.AGDCALIHSGSWEK.A
R1/RRR1-20/3	1532.243	1531.645	-263.070	0.383	970.728	0.245	24	0.081	-.AGDCALIHSGSWEK.-
R1/RRR1-2/3	1530.918	1531.645	-1131.356	0.309	911.231	0.245	23	0.080	R.AGDCALIHSGSWEK.A
R1/RRR1-4/3	1531.354	1531.645	-190.506	0.342	913.873	0.244	25	0.080	R.AGDCALIHSGSWEK.A
R1/RRR1-1/3	1531.323	1531.645	-210.898	0.378	941.644	0.226	25	0.078	R.AGDCALIHSGSWEK.A
R1/RRR1-23/3	1531.502	1531.645	-93.834	0.349	1035.191	0.145	24	0.070	R.AGDCALIHSGSWEK.A
R1/RRR1-21/2	1258.236	1258.472	-187.917	0.472	1298.821	0.405	15	0.239	K.FNLFM*QQVSK.S
R1/RRR1-21/2	1257.830	1258.472	-1309.329	0.448	1308.419	0.389	16	0.237	K.FNLFM*QQVSK.S
R1/RRR1-14/2	1441.291	1441.698	-283.357	0.439	973.240	0.463	21	0.225	K.ITPTVLQSAGLNVK.Q
R1/RRR1-14/2	1442.385	1441.698	-217.696	0.463	914.613	0.463	21	0.222	K.ITPTVLQSAGLNVK.Q
R1/RRR1-19/2	1264.165	1264.326	-128.291	0.521	1223.639	0.418	19	0.236	K.FGDAVQEDVGAR.L
R1/RRR1-19/2	1264.195	1264.326	-104.656	0.516	1175.040	0.428	19	0.234	K.FGDAVQEDVGAR.L
R1/RRR1-17/2	1263.998	1264.326	-260.818	0.375	551.756	0.255	17	0.190	-.FGDAVQEDVGAR.-
R1/RRR1-17/2	1264.321	1264.326	-4.320	0.301	757.244	0.206	18	0.188	K.FGDAVQEDVGAR.L
R1/RRR1-15/2	1141.790	1142.332	-1354.836	0.424	721.508	0.483	14	0.215	R.HAGIIDIQFK.R
R1/RRR1-15/2	1141.289	1142.332	-1795.274	0.293	668.461	0.513	15	0.209	R.HAGIIDIQFK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	1141.429	1142.332	-1672.127	0.190	296.210	0.391	13	0.189	R.HAGIIDIQFK.R
R1/RRR1-8/2	1192.039	1192.386	-292.483	0.485	1095.118	0.441	16	0.232	R.ILVQEGIYEK.F
R1/RRR1-8/2	1191.922	1192.386	-390.714	0.516	1111.739	0.424	16	0.230	R.ILVQEGIYEK.F
R1/RRR1-8/2	1192.070	1192.386	-265.874	0.473	1055.751	0.401	16	0.222	R.ILVQEGIYEK.F
R1/RRR1-9/2	1601.867	1601.868	-0.887	0.432	714.144	0.474	16	0.205	R.LPVEFVVVGDLGQTK.W
R1/RRR1-13/3	1597.767	1596.764	1.975	0.470	1141.349	0.432	26	0.119	K.TAGKDLASDKTTYPK.L
R1/RRR1-13/3	1596.617	1596.764	-92.422	0.478	740.867	0.441	26	0.095	K.TAGKDLASDKTTYPK.L
R1/RRR1-24/3	1275.860	1275.396	365.313	0.449	1282.705	0.402	26	0.122	R.HGGSGGPADPVPVK.L
R1/RRR1-24/3	1275.042	1275.396	-277.727	0.409	1274.552	0.385	25	0.117	R.HGGSGGPADPVPVK.L
R1/RRR1-15/2	1194.175	1193.273	-82.378	0.398	1802.563	0.216	18	0.246	R.M*NAAGTNPSSAR.L
R1/RRR1-15/2	1194.044	1193.273	-192.309	0.429	1433.740	0.240	17	0.215	R.M*NAAGTNPSSAR.L
R1/RRR1-15/2	1193.509	1193.273	197.942	0.285	1233.653	0.096	16	0.184	R.M*NAAGTNPSSAR.L
R1/RRR1-11/2	1258.518	1259.396	-1497.004	0.450	537.446	0.460	17	0.207	R.HSDVVYNLVGR.N
R1/RRR1-26/2	1299.206	1299.502	-228.494	0.343	634.718	0.471	15	0.200	R.LLAQAALTVGADR.A
R1/RRR1-13/2	1057.105	1057.139	-32.269	0.502	1067.688	0.449	16	0.231	R.AGGPEVLEER.D
R1/RRR1-13/2	1056.535	1057.139	-1523.379	0.422	933.128	0.379	14	0.209	-.AGGPEVLEER.-
R1/RRR1-11/2	1384.798	1384.516	204.449	0.485	758.399	0.468	14	0.212	K.LTYIFDEETPR.W
R1/RRR1-11/2	1385.222	1384.516	-212.361	0.264	493.579	0.310	14	0.188	K.LTYIFDEETPR.W
R1/RRR1-4/2	1420.594	1420.636	-29.270	0.442	1424.104	0.357	18	0.240	R.VNDQYITNVLLK.I
R1/RRR1-4/2	1420.185	1420.636	-318.087	0.488	1091.043	0.400	15	0.218	R.VNDQYITNVLLK.I
R1/RRR1-6/2	1038.920	1038.136	-208.902	0.321	986.028	0.438	16	0.216	R.SVVESFGAGGK.A
R1/RRR1-9/2	1399.273	1399.618	-247.416	0.402	614.597	0.469	14	0.202	R.VFGTDFLPLSFR.T
R1/RRR1-15/2	1213.002	1213.319	-262.396	0.482	773.830	0.463	15	0.210	-.SAAAVDPVEPEK.-
R1/RRR1-9/2	1407.173	1407.512	-241.938	0.433	959.141	0.449	15	0.220	R.HNEFEISDFLR.R
R1/RRR1-9/2	1406.333	1407.512	-1554.437	0.437	746.578	0.485	15	0.215	R.HNEFEISDFLR.R
R1/RRR1-6/2	1049.915	1050.150	-224.556	0.408	1110.550	0.427	16	0.229	R.GVVQTDAGFR.A
R1/RRR1-6/2	1050.193	1050.150	40.967	0.441	639.759	0.429	14	0.205	R.GVVQTDAGFR.A
R1/RRR1-17/2	1161.009	1161.375	-316.646	0.460	1318.685	0.390	18	0.239	K.LLFLGLDNAGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1161.114	1161.375	-225.933	0.517	1354.229	0.369	18	0.237	K.LLFLGLDNAGK.T
R1/RRR1-17/2	1161.600	1161.375	194.089	0.437	814.102	0.334	15	0.199	K.LLFLGLDNAGK.T
R1/RRR1-18/2	1161.579	1161.375	175.752	0.337	571.063	0.388	13	0.197	K.LLFLGLDNAGK.T
R1/RRR1-18/2	1161.782	1161.375	350.558	0.266	638.762	0.381	14	0.195	K.LLFLGLDNAGK.T
R1/RRR1-12/2	1832.158	1831.018	76.943	0.467	727.585	0.460	19	0.208	K.TPSLIFEYINNTDFR.T
R1/RRR1-11/2	1419.760	1418.620	98.776	0.323	1322.730	0.362	18	0.228	R.LGDAGPAGSSVFLVK.E
R1/RRR1-13/2	1622.063	1621.773	178.771	0.375	637.896	0.462	17	0.206	K.SLAEFFTDFGYAPR.E
R1/RRR1-13/2	1622.344	1621.773	-265.697	0.362	462.283	0.451	17	0.201	K.SLAEFFTDFGYAPR.E
R1/RRR1-13/2	1622.153	1621.773	234.388	0.310	1017.287	0.296	16	0.197	K.SLAEFFTDFGYAPR.E
R1/RRR1-13/2	1622.118	1621.773	213.259	0.320	964.080	0.308	16	0.197	K.SLAEFFTDFGYAPR.E
R1/RRR1-13/2	1622.186	1621.773	255.215	0.276	264.964	0.294	14	0.192	K.SLAEFFTDFGYAPR.E
R1/RRR1-11/2	1176.962	1177.289	-278.233	0.309	874.133	0.449	14	0.210	K.GYDPEVIDIR.S
R1/RRR1-6/2	1143.971	1144.305	-292.786	0.439	789.432	0.458	17	0.214	R.FDLSGIAPAPR.G
R1/RRR1-3/2	1945.630	1944.307	166.723	0.408	608.304	0.440	19	0.196	K.LLVFQSVLPSVGIGSLSAR.E
R1/RRR1-4/2	1945.242	1944.307	-33.460	0.428	496.263	0.444	18	0.193	K.LLVFQSVLPSVGIGSLSAR.E
R1/RRR1-13/2	1031.155	1031.187	-31.182	0.365	723.099	0.460	13	0.211	K.FTDVPINPK.V
R1/RRR1-13/2	1031.136	1031.187	-48.993	0.367	699.875	0.395	13	0.203	K.FTDVPINPK.V
R1/RRR1-13/2	1030.172	1031.187	-1961.701	0.280	642.423	0.333	12	0.192	K.FTDVPINPK.V
R1/RRR1-6/2	1732.540	1732.916	-217.562	0.410	697.216	0.457	20	0.207	K.DGAPGLWPFGPVDFEK.M
R1/RRR1-6/2	1733.029	1732.916	65.731	0.431	570.950	0.488	19	0.206	K.DGAPGLWPFGPVDFEK.M
R1/RRR1-6/2	1732.361	1732.916	-900.174	0.372	705.942	0.417	20	0.202	K.DGAPGLWPFGPVDFEK.M
R1/RRR1-4/3	1929.153	1929.118	18.011	0.387	1119.602	0.408	27	0.111	R.LKEGNLDPNELSIATEGK.K
R1/RRR1-8/2	1965.124	1963.173	-24.835	0.452	957.221	0.436	20	0.211	K.TSTGSAVADLELLEVISEK.V
R1/RRR1-16/2	1359.339	1359.552	-157.408	0.445	924.113	0.452	18	0.220	K.GLDFDLVPVDLR.T
R1/RRR1-2/2	1263.399	1263.425	-20.313	0.334	1152.109	0.407	18	0.226	-.SAEPAFSVLVSR.-
R1/RRR1-15/2	1360.488	1360.580	-68.091	0.458	1037.188	0.437	20	0.227	R.LWSADEITALLK.E
R1/RRR1-15/2	1360.502	1360.580	-57.381	0.290	509.124	0.421	14	0.194	R.LWSADEITALLK.E
R1/RRR1-15/2	1360.098	1360.580	-355.545	0.205	334.185	0.344	12	0.185	R.LWSADEITALLK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-16/2	957.013	957.149	-142.407	0.549	1210.742	0.397	15	0.232	R.AAVLLLDNK.K
R1/RRR1-16/2	956.668	957.149	-504.392	0.501	1058.954	0.447	14	0.230	R.AAVLLLDNK.K
R1/RRR1-10/2	1153.492	1154.301	-1573.228	0.329	1042.360	0.424	16	0.219	R.HLISSGALEAR.L
R1/RRR1-10/2	1154.077	1154.301	-195.271	0.301	725.666	0.359	15	0.195	R.HLISSGALEAR.L
R1/RRR1-16/2	1547.394	1546.841	-289.988	0.415	635.957	0.454	15	0.204	R.AGLRLEMPAADM*VR.E
R1/RRR1-15/2	1547.278	1546.841	282.814	0.370	545.878	0.368	14	0.193	R.AGLRLEMPAADM*VR.E
R1/RRR1-16/2	1546.295	1546.841	-1003.216	0.362	593.005	0.359	14	0.192	R.AGLRLEMPAADM*VR.E
R1/RRR1-24/2	1547.371	1546.841	-304.947	0.373	507.722	0.382	13	0.192	R.AGLRLEMPAADM*VR.E
R1/RRR1-15/2	1547.552	1546.841	-187.345	0.321	497.024	0.364	13	0.191	R.AGLRLEMPAADM*VR.E
R1/RRR1-16/2	1547.328	1546.841	315.326	0.366	363.778	0.342	12	0.188	-.AGLRLEMPAADM*VR.-
R1/RRR1-16/2	1546.621	1546.841	-142.968	0.273	423.940	0.316	13	0.187	-.AGLRLEMPAADM*VR.-
R1/RRR1-25/2	1546.666	1546.841	-113.674	0.289	485.573	0.287	12	0.185	R.AGLRLEMPAADM*VR.E
R1/RRR1-7/2	1221.339	1221.346	-5.976	0.425	1026.133	0.435	15	0.223	R.HFEVDLSAFR.N
R1/RRR1-8/2	1330.515	1330.600	-64.195	0.440	1119.255	0.422	17	0.226	K.VYTLGPLQLVAR.K
R1/RRR1-18/2	1333.321	1334.500	-1638.915	0.290	1408.510	0.326	18	0.230	R.IEVTDPASFQVK.E
R1/RRR1-22/2	1300.324	1299.479	-119.476	0.434	605.567	0.448	16	0.205	K.FATLAM*GTTDVR.V
R1/RRR1-22/2	1299.224	1299.479	-196.570	0.374	552.200	0.385	16	0.197	K.FATLAM*GTTDVR.V
R1/RRR1-5/2	1233.915	1234.387	-383.073	0.442	1239.319	0.418	17	0.239	R.LLQYGEQNIR.R
R1/RRR1-5/2	1234.936	1234.387	-365.803	0.531	1127.601	0.393	16	0.224	R.LLQYGEQNIR.R
R1/RRR1-5/2	1234.335	1234.387	-42.019	0.408	1136.169	0.298	16	0.209	R.LLQYGEQNIR.R
R1/RRR1-23/3	1915.302	1914.959	179.584	0.497	1081.281	0.410	28	0.111	K.KDGEEESSGVVDYDKEK.K
R1/RRR1-11/2	1384.352	1384.476	-89.824	0.443	938.571	0.441	18	0.220	R.QDTAEALDFFAR.G
R1/RRR1-11/2	1384.222	1384.476	-183.679	0.426	779.268	0.480	17	0.217	R.QDTAEALDFFAR.G
R1/RRR1-11/2	1383.305	1384.476	-1574.119	0.149	346.188	0.345	11	0.180	R.QDTAEALDFFAR.G
R1/RRR1-15/2	1203.050	1203.371	-267.315	0.444	874.568	0.446	18	0.218	R.ASPTTALTLATR.A
R1/RRR1-15/2	1203.101	1203.371	-224.561	0.361	906.735	0.270	18	0.195	R.ASPTTALTLATR.A
R1/RRR1-15/2	1202.728	1203.371	-1370.277	0.290	790.136	0.315	18	0.195	R.ASPTTALTLATR.A
R1/RRR1-9/3	1649.984	1649.787	119.713	0.446	958.369	0.434	27	0.103	R.QYELVGDKDGAQVAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-9/3	1650.054	1649.787	162.225	0.281	630.195	0.338	21	0.075	R.QYELVGDKDGAQVAR.L
R1/RRR1-11/2	1456.071	1454.652	288.619	0.322	745.882	0.440	15	0.200	R.GFLVASLAAEYGQK.H
R1/RRR1-11/2	1455.560	1454.652	-63.391	0.220	1021.210	0.251	15	0.189	R.GFLVASLAAEYGQK.H
R1/RRR1-9/2	1655.242	1655.984	-1055.434	0.384	1028.436	0.423	16	0.214	K.TPLQQLMNDALIVAK.Q
R1/RRR1-20/2	1291.198	1291.481	-219.670	0.418	1092.535	0.421	16	0.224	R.GVNVIYALTGQR.R
R1/RRR1-20/2	1291.995	1291.481	-377.698	0.417	1024.208	0.416	16	0.219	R.GVNVIYALTGQR.R
R1/RRR1-13/2	1292.427	1291.481	-41.930	0.356	964.031	0.389	15	0.210	R.GVNVIYALTGQR.R
R1/RRR1-12/2	1292.154	1291.481	-254.188	0.367	1008.237	0.358	16	0.209	R.GVNVIYALTGQR.R
R1/RRR1-12/2	1291.219	1291.481	-203.547	0.302	671.865	0.319	14	0.192	R.GVNVIYALTGQR.R
R1/RRR1-13/2	1291.024	1291.481	-355.032	0.301	700.121	0.281	15	0.191	R.GVNVIYALTGQR.R
R1/RRR1-19/2	1291.155	1291.481	-253.057	0.239	792.766	0.247	15	0.188	R.GVNVIYALTGQR.R
R1/RRR1-8/2	1231.930	1231.381	-367.391	0.443	619.630	0.428	13	0.208	R.LHFHDCFVR.-
R1/RRR1-8/2	1231.040	1231.381	-278.244	0.416	816.524	0.231	15	0.193	R.LHFHDCFVR.-
R1/RRR1-7/2	1230.834	1231.381	-1260.601	0.357	570.394	0.216	12	0.189	R.LHFHDCFVR.-
R1/RRR1-8/2	1231.099	1231.381	-229.598	0.422	622.689	0.200	13	0.188	R.LHFHDCFVR.-
R1/RRR1-8/3	1230.675	1231.381	-1390.108	0.422	1065.412	0.372	21	0.092	R.LHFHDCFVR.-
R1/RRR1-10/3	1230.512	1231.381	-1523.573	0.358	883.089	0.364	19	0.086	R.LHFHDCFVR.-
R1/RRR1-9/3	1231.498	1231.381	95.174	0.415	767.287	0.338	18	0.083	R.LHFHDCFVR.-
R1/RRR1-9/3	1231.460	1231.381	64.604	0.395	699.938	0.327	18	0.082	R.LHFHDCFVR.-
R1/RRR1-9/3	1231.398	1231.381	13.898	0.409	759.328	0.306	19	0.080	R.LHFHDCFVR.-
R1/RRR1-8/3	1231.199	1231.381	-148.245	0.352	731.620	0.308	19	0.080	R.LHFHDCFVR.-
R1/RRR1-15/2	1130.466	1131.331	-1654.949	0.369	844.699	0.444	16	0.212	R.VAGM*VTPAAAAR.S
R1/RRR1-15/2	1130.786	1131.331	-1370.582	0.430	713.964	0.444	17	0.210	R.VAGM*VTPAAAAR.S
R1/RRR1-15/2	1130.721	1131.331	-1428.266	0.391	741.662	0.386	17	0.203	R.VAGM*VTPAAAAR.S
R1/RRR1-6/2	1141.196	1141.346	-132.030	0.377	557.448	0.446	15	0.203	R.AQPTLGLITAR.A
R1/RRR1-6/2	1140.676	1141.346	-1468.541	0.361	467.068	0.459	15	0.202	R.AQPTLGLITAR.A
R1/RRR1-20/2	1344.975	1345.529	-1158.809	0.347	655.046	0.446	18	0.204	R.NSPVPSFSGLLAR.A
R1/RRR1-20/2	1345.338	1345.529	-142.574	0.337	496.537	0.493	17	0.202	R.NSPVPSFSGLLAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-15/2	940.978	941.150	-183.608	0.500	1125.767	0.380	13	0.226	R.ILLITDPR.T
R1/RRR1-15/2	940.579	941.150	-1674.930	0.445	1089.638	0.375	13	0.223	R.ILLITDPR.T
R1/RRR1-14/2	940.984	941.150	-177.101	0.491	1094.505	0.373	13	0.223	R.ILLITDPR.T
R1/RRR1-21/2	940.997	941.150	-163.047	0.501	1174.507	0.341	13	0.221	R.ILLITDPR.T
R1/RRR1-14/2	941.065	941.150	-89.916	0.490	1118.312	0.352	13	0.220	R.ILLITDPR.T
R1/RRR1-10/2	940.989	941.150	-171.115	0.477	1064.157	0.364	13	0.220	R.ILLITDPR.T
R1/RRR1-13/2	940.485	941.150	-1775.861	0.412	1077.630	0.354	13	0.219	R.ILLITDPR.T
R1/RRR1-11/2	940.384	941.150	-1883.726	0.476	1056.192	0.358	13	0.219	R.ILLITDPR.T
R1/RRR1-16/2	941.013	941.150	-146.129	0.459	1074.175	0.352	13	0.219	R.ILLITDPR.T
R1/RRR1-12/2	940.395	941.150	-1872.117	0.465	1188.300	0.319	13	0.218	R.ILLITDPR.T
R1/RRR1-15/2	940.528	941.150	-1729.435	0.468	1070.274	0.351	13	0.218	R.ILLITDPR.T
R1/RRR1-21/2	940.765	941.150	-410.364	0.420	1141.270	0.328	13	0.218	R.ILLITDPR.T
R1/RRR1-10/2	941.242	941.150	98.066	0.538	1084.311	0.350	13	0.217	R.ILLITDPR.T
R1/RRR1-12/2	940.947	941.150	-216.014	0.457	1037.830	0.347	13	0.217	R.ILLITDPR.T
R1/RRR1-22/2	940.413	941.150	-1852.681	0.398	949.895	0.382	12	0.216	R.ILLITDPR.T
R1/RRR1-16/2	941.214	941.150	68.150	0.485	945.090	0.381	12	0.216	R.ILLITDPR.T
R1/RRR1-13/2	941.396	941.150	261.924	0.516	1118.144	0.331	13	0.216	R.ILLITDPR.T
R1/RRR1-14/2	941.041	941.150	-115.940	0.475	948.053	0.374	12	0.215	R.ILLITDPR.T
R1/RRR1-21/2	941.108	941.150	-44.638	0.426	984.430	0.359	12	0.215	R.ILLITDPR.T
R1/RRR1-11/2	940.949	941.150	-214.453	0.441	1091.929	0.314	13	0.214	R.ILLITDPR.T
R1/RRR1-12/2	941.108	941.150	-44.768	0.438	981.011	0.346	12	0.213	R.ILLITDPR.T
R1/RRR1-11/2	941.103	941.150	-49.452	0.505	889.150	0.360	12	0.211	R.ILLITDPR.T
R1/RRR1-13/2	940.742	941.150	-434.581	0.450	880.730	0.340	12	0.209	R.ILLITDPR.T
R1/RRR1-17/2	941.236	941.150	91.562	0.433	880.455	0.352	11	0.208	R.ILLITDPR.T
R1/RRR1-16/2	940.604	941.150	-1648.201	0.422	905.972	0.330	12	0.208	R.ILLITDPR.T
R1/RRR1-17/2	940.965	941.150	-197.013	0.373	433.115	0.305	10	0.202	R.ILLITDPR.T
R1/RRR1-22/2	940.858	941.150	-310.771	0.425	855.010	0.307	11	0.202	R.ILLITDPR.T
R1/RRR1-18/2	940.338	941.150	-1932.775	0.338	702.090	0.291	11	0.200	R.ILLITDPR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-1/2	1643.207	1641.680	-288.998	0.341	651.249	0.429	17	0.197	R.FHEDEHGEVVAESR.R
R1/RRR1-7/2	1435.524	1435.692	-117.326	0.384	867.328	0.444	16	0.213	R.FYNPEVIQLIAK.I
R1/RRR1-7/2	1435.394	1435.692	-207.924	0.393	657.126	0.394	16	0.200	R.FYNPEVIQLIAK.I
R1/RRR1-7/2	1143.233	1143.275	-36.907	0.391	1051.478	0.416	17	0.221	R.APLLAQGETSR.A
R1/RRR1-1/2	1766.677	1765.002	-184.666	0.430	1031.675	0.410	18	0.211	R.TGGLVVLSESFGHSVFK.D
R1/RRR1-4/2	1265.109	1264.645	367.219	0.439	690.888	0.449	14	0.207	R.TVVVTIIFMIK.L
R1/RRR1-4/2	1264.581	1264.645	-51.277	0.325	566.702	0.419	13	0.197	R.TVVVTIIFMIK.L
R1/RRR1-4/2	1265.210	1264.645	-344.857	0.362	595.519	0.378	13	0.195	R.TVVVTIIFMIK.L
R1/RRR1-14/2	1186.167	1186.345	-150.765	0.379	571.526	0.442	16	0.206	R.HSGIIDIQFR.R
R1/RRR1-14/2	1185.732	1186.345	-1364.206	0.324	524.977	0.482	16	0.205	R.HSGIIDIQFR.R
R1/RRR1-10/2	1086.066	1086.224	-145.834	0.374	925.281	0.432	16	0.214	K.EAAIQAINAGK.N
R1/RRR1-2/3	1997.041	1996.057	-8.142	0.459	975.412	0.381	26	0.098	R.QSKPDEVTEDDM*PSTSGR.Q
R1/RRR1-23/2	1132.040	1132.209	-149.753	0.436	904.456	0.427	16	0.217	R.NITVNEAQSR.R
R1/RRR1-22/2	1132.258	1132.209	43.188	0.417	690.537	0.430	15	0.208	R.NITVNEAQSR.R
R1/RRR1-6/2	1530.406	1530.709	-198.295	0.460	850.660	0.436	20	0.216	R.SPQFPEAIDWIAR.N
R1/RRR1-6/2	1530.662	1530.709	-30.445	0.467	860.432	0.417	20	0.214	R.SPQFPEAIDWIAR.N
R1/RRR1-1/2	1531.221	1530.709	-319.409	0.421	697.736	0.451	18	0.210	R.SPQFPEAIDWIAR.N
R1/RRR1-6/2	1529.774	1530.709	-1268.294	0.430	740.588	0.331	19	0.199	R.SPQFPEAIDWIAR.N
R1/RRR1-7/2	1530.429	1530.702	-178.852	0.418	751.649	0.443	17	0.206	R.TPPYSYLFDGIEK.S
R1/RRR1-9/2	1282.381	1282.511	-101.740	0.501	842.701	0.425	17	0.213	R.RLCPGIPLAER.V
R1/RRR1-12/2	1131.833	1132.297	-411.241	0.384	691.118	0.446	16	0.210	R.LQQAPPPPQR.Q
R1/RRR1-12/2	1132.015	1132.297	-250.019	0.408	510.463	0.347	14	0.197	R.LQQAPPPPQR.Q
R1/RRR1-12/2	1132.256	1132.297	-37.156	0.366	513.649	0.299	14	0.194	R.LQQAPPPPQR.Q
R1/RRR1-7/3	1503.412	1503.547	-89.927	0.455	1219.840	0.381	24	0.112	R.VHCAESGEESLER.E
R1/RRR1-7/3	1502.989	1503.547	-1040.044	0.458	969.882	0.375	24	0.095	R.VHCAESGEESLER.E
R1/RRR1-10/3	1504.422	1503.547	-83.437	0.477	611.161	0.409	22	0.088	-.VHCAESGEESLER.-
R1/RRR1-10/3	1503.290	1503.547	-171.298	0.476	772.238	0.353	23	0.084	-.VHCAESGEESLER.-
R1/RRR1-10/3	1503.264	1503.547	-188.772	0.424	903.486	0.114	23	0.062	-.VHCAESGEESLER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-10/3	1752.125	1750.891	133.907	0.501	1050.651	0.407	28	0.103	K.TFEERDTLNEQIVR.S
R1/RRR1-10/3	1751.728	1750.891	-93.360	0.426	859.531	0.447	25	0.100	K.TFEERDTLNEQIVR.S
R1/RRR1-11/3	1752.035	1750.891	82.341	0.315	359.938	0.378	21	0.082	-.TFEERDTLNEQIVR.-
R1/RRR1-8/2	1022.841	1023.125	-277.663	0.486	945.957	0.422	14	0.219	K.SGNFELVTR.E
R1/RRR1-8/2	1023.915	1023.125	-204.908	0.540	1055.781	0.379	14	0.211	-.SGNFELVTR.-
R1/RRR1-8/2	1022.907	1023.125	-213.369	0.430	757.411	0.329	13	0.194	-.SGNFELVTR.-
R1/RRR1-2/2	1715.857	1714.987	-75.538	0.437	1181.249	0.365	18	0.217	K.VQLVQFGILSPDEIR.Q
R1/RRR1-2/2	1715.597	1714.987	-227.632	0.413	1124.407	0.271	18	0.198	K.VQLVQFGILSPDEIR.Q
R1/RRR1-3/2	1716.011	1714.987	14.298	0.316	760.701	0.292	16	0.187	K.VQLVQFGILSPDEIR.Q
R1/RRR1-6/2	1915.694	1916.322	-852.324	0.417	651.068	0.412	15	0.190	-.VELTLVRLSQLGKGVM*R.S
R1/RRR1-12/2	1130.221	1130.273	-46.323	0.532	950.145	0.413	15	0.219	K.IVELEEELR.V
R1/RRR1-12/2	1130.132	1130.273	-125.088	0.501	783.234	0.347	14	0.202	K.IVELEEELR.V
R1/RRR1-12/2	1130.266	1130.273	-6.782	0.369	954.149	0.213	14	0.191	K.IVELEEELR.V
R1/RRR1-10/2	1391.316	1391.594	-200.431	0.376	623.429	0.432	13	0.194	R.LQVYDAVAAELAK.Q
R1/RRR1-24/2	1487.216	1486.719	334.992	0.436	1032.513	0.413	19	0.218	R.GIM*QPVPVSDALSR.F
R1/RRR1-24/2	1485.752	1486.719	-1328.065	0.282	751.593	0.384	17	0.195	R.GIM*QPVPVSDALSR.F
R1/RRR1-20/2	1148.174	1147.261	-75.457	0.404	958.611	0.416	14	0.214	K.KEEVAKEGEK.K
R1/RRR1-6/2	1685.385	1686.028	-977.932	0.511	934.235	0.409	20	0.210	R.KDDFLLPGVVEVIIK.S
R1/RRR1-10/2	1177.570	1178.381	-1543.134	0.330	833.212	0.420	17	0.209	K.EITALAPSTM*K.I
R1/RRR1-10/2	1178.059	1178.381	-274.954	0.395	530.632	0.468	14	0.205	K.EITALAPSTM*K.I
R1/RRR1-10/2	1178.000	1178.381	-325.065	0.379	688.902	0.416	15	0.204	K.EITALAPSTM*K.I
R1/RRR1-8/2	994.230	994.123	107.740	0.467	775.292	0.388	12	0.201	-.YGLAAEEIK.-
R1/RRR1-11/2	1295.057	1295.468	-318.473	0.364	721.563	0.435	14	0.203	R.HWILDPIDGTK.G
R1/RRR1-13/2	1102.155	1102.268	-103.269	0.455	923.446	0.428	13	0.217	R.ILDITHAYR.A
R1/RRR1-13/2	1102.176	1102.268	-83.493	0.406	701.947	0.274	12	0.189	R.ILDITHAYR.A
R1/RRR1-23/2	1213.178	1213.369	-157.500	0.497	929.517	0.418	16	0.215	K.VTLSGNQQPIR.V
R1/RRR1-17/2	1344.502	1345.575	-1547.061	0.442	724.087	0.433	16	0.207	K.SALRPLQFVSAR.-
R1/RRR1-17/2	1345.144	1345.575	-321.542	0.405	746.403	0.327	15	0.194	K.SALRPLQFVSAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/2	1345.361	1345.575	-159.408	0.361	669.276	0.291	15	0.190	K.SALRPLQFVSAR.-
R1/RRR1-17/3	1345.969	1345.575	293.707	0.443	834.003	0.484	24	0.101	K.SALRPLQFVSAR.-
R1/RRR1-1/2	1253.351	1252.400	-39.623	0.386	991.207	0.417	15	0.217	K.NFGVTEFVNPK.D
R1/RRR1-5/2	1253.289	1252.400	-88.959	0.392	725.330	0.345	13	0.195	K.NFGVTEFVNPK.D
R1/RRR1-2/2	1252.704	1252.400	242.721	0.277	523.563	0.307	14	0.191	K.NFGVTEFVNPK.D
R1/RRR1-9/2	1252.945	1252.400	-364.845	0.341	534.898	0.288	14	0.190	-.NFGVTEFVNPK.-
R1/RRR1-19/2	1514.163	1514.663	-330.851	0.351	1138.768	0.381	21	0.217	K.EGGPGTAVSGAEAVLAK.-
R1/RRR1-19/2	1514.809	1514.663	96.538	0.335	856.984	0.428	19	0.205	K.EGGPGTAVSGAEAVLAK.-
R1/RRR1-18/2	1515.985	1514.663	212.925	0.309	629.530	0.361	16	0.188	K.EGGPGTAVSGAEAVLAK.-
R1/RRR1-7/2	897.804	898.042	-265.875	0.309	863.352	0.416	11	0.206	K.AVIVQPDR.V
R1/RRR1-5/2	1731.237	1730.948	167.497	0.361	703.067	0.420	20	0.198	R.TPAFLGLSAGAGAWPASR.Y
R1/RRR1-5/2	1731.630	1730.948	-183.949	0.360	287.187	0.414	15	0.186	-.TPAFLGLSAGAGAWPASR.-
R1/RRR1-8/2	1039.154	1039.210	-54.153	0.402	850.900	0.431	15	0.213	K.SPELAGPVLR.L
R1/RRR1-7/2	1039.328	1039.210	113.962	0.365	797.313	0.320	14	0.196	K.SPELAGPVLR.L
R1/RRR1-1/2	1973.097	1972.224	-64.945	0.421	787.139	0.381	18	0.193	R.IVTSFTSLVDSADFLEVK.N
R1/RRR1-11/2	741.632	740.914	-381.130	0.304	1069.085	0.388	12	0.216	-.QLAIPAK.-
R1/RRR1-11/2	740.920	740.914	8.823	0.319	1058.860	0.301	12	0.206	K.QLAIPAK.V
R1/RRR1-11/2	741.305	740.914	529.248	0.314	1029.185	0.231	12	0.196	K.QLAIPAK.V
R1/RRR1-11/2	741.245	740.914	448.024	0.256	764.183	0.257	11	0.189	-.QLAIPAK.-
R1/RRR1-18/2	1272.142	1272.390	-195.339	0.317	875.081	0.408	16	0.209	K.VLTPISQDDQR.Q
R1/RRR1-17/2	1272.107	1272.390	-222.871	0.308	800.175	0.407	17	0.206	K.VLTPISQDDQR.Q
R1/RRR1-18/2	1271.843	1272.390	-1220.340	0.213	735.424	0.282	16	0.189	K.VLTPISQDDQR.Q
R1/RRR1-17/2	1271.424	1272.390	-1550.950	0.205	568.501	0.303	15	0.188	K.VLTPISQDDQR.Q
R1/RRR1-17/2	1271.589	1272.390	-1420.570	0.178	634.392	0.196	16	0.184	K.VLTPISQDDQR.Q
R1/RRR1-11/2	1198.032	1198.311	-233.380	0.442	957.337	0.418	16	0.216	K.VVVQDGPEAQR.A
R1/RRR1-10/2	1442.715	1441.720	-3.793	0.470	647.016	0.407	13	0.195	R.VLDAM*LPFYLSR.Y
R1/RRR1-17/3	1233.273	1233.359	-69.963	0.467	1297.879	0.360	23	0.110	R.HREPLPDSGPK.K
R1/RRR1-17/3	1233.318	1233.359	-32.882	0.488	912.060	0.415	21	0.098	R.HREPLPDSGPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-17/3	1233.243	1233.359	-93.941	0.508	1003.868	0.325	21	0.088	R.HREPLPDSGPK.K
R1/RRR1-18/3	1233.535	1233.359	143.106	0.455	1075.663	0.315	22	0.088	R.HREPLPDSGPK.K
R1/RRR1-12/2	1428.244	1428.661	-292.804	0.420	1255.812	0.369	16	0.226	R.VAHYSELVQIIR.E
R1/RRR1-22/2	1131.981	1131.225	-215.523	0.438	764.617	0.424	16	0.210	-.NITVNQAQSR.-
R1/RRR1-22/2	1131.222	1131.225	-2.122	0.348	838.923	0.416	15	0.209	R.NITVNQAQSR.G
R1/RRR1-23/2	1131.303	1131.225	69.090	0.396	988.055	0.288	16	0.201	-.NITVNQAQSR.-
R1/RRR1-19/2	1172.021	1172.274	-216.309	0.383	781.704	0.427	16	0.205	K.LAEAGNAGEIAR.L
R1/RRR1-3/2	1788.381	1788.938	-873.278	0.431	852.185	0.375	18	0.196	R.SGGAAASAQIIDLLEDTR.I
R1/RRR1-1/2	1788.713	1788.938	-126.057	0.387	678.450	0.187	16	0.172	R.SGGAAASAQIIDLLEDTR.I
R1/RRR1-13/2	1567.485	1567.769	-181.576	0.464	930.352	0.410	21	0.213	R.SRPSELALPVSDPAK.A
R1/RRR1-13/2	1567.496	1567.769	-174.310	0.468	614.159	0.395	18	0.196	R.SRPSELALPVSDPAK.A
R1/RRR1-14/2	963.602	964.100	-518.233	0.373	766.677	0.428	14	0.207	R.AVATGIFER.I
R1/RRR1-1/2	1707.970	1707.009	-23.126	0.294	954.329	0.391	19	0.204	K.GLWASPTPSPLLPTLR.A
R1/RRR1-20/2	1153.582	1154.297	-1490.425	0.321	661.586	0.420	12	0.202	K.YYNLPEVQK.A
R1/RRR1-20/2	1154.249	1154.297	-41.010	0.365	724.711	0.358	13	0.201	K.YYNLPEVQK.A
R1/RRR1-19/2	1153.331	1154.297	-1709.331	0.229	659.135	0.296	12	0.189	K.YYNLPEVQK.A
R1/RRR1-19/2	1153.443	1154.297	-1611.508	0.215	722.310	0.209	12	0.184	K.YYNLPEVQK.A
R1/RRR1-18/2	1246.094	1246.480	-310.943	0.296	953.015	0.393	15	0.206	R.ALLVGINYPGTK.A
R1/RRR1-14/2	1245.903	1246.480	-1270.217	0.282	301.562	0.339	10	0.164	-.ALLVGINYPGTK.-
R1/RRR1-15/2	973.931	974.220	-297.138	0.402	709.023	0.420	15	0.212	R.VVTSLTLLK.S
R1/RRR1-16/2	973.905	974.220	-324.175	0.395	695.420	0.372	15	0.206	R.VVTSLTLLK.S
R1/RRR1-15/2	973.931	974.220	-296.887	0.354	506.475	0.382	13	0.202	R.VVTSLTLLK.S
R1/RRR1-16/2	973.699	974.220	-1566.718	0.350	458.042	0.249	14	0.197	R.VVTSLTLLK.S
R1/RRR1-16/2	973.665	974.220	-1601.227	0.368	552.219	0.271	14	0.197	R.VVTSLTLLK.S
R1/RRR1-15/2	973.624	974.220	-1643.799	0.357	714.558	0.257	15	0.195	R.VVTSLTLLK.S
R1/RRR1-4/3	1253.354	1254.461	-1685.807	0.272	1535.504	0.241	23	0.104	K.EVKVAVDAPLGR.T
R1/RRR1-6/2	1908.009	1908.149	-73.578	0.463	702.521	0.403	16	0.193	R.ILAAWYLVGQDQNYPR.T
R1/RRR1-8/2	1403.006	1403.594	-1134.877	0.425	1365.115	0.335	17	0.229	R.REDELRAAMVGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-8/2	1403.122	1403.594	-336.702	0.421	1279.491	0.279	16	0.211	R.REDELRAAMVGR.T
R1/RRR1-8/2	1402.944	1403.594	-1179.436	0.424	869.430	0.318	15	0.196	-.REDELRAAMVGR.-
R1/RRR1-20/2	1331.152	1331.497	-260.262	0.368	756.096	0.419	19	0.208	R.QALTLQSVVEDK.T
R1/RRR1-20/2	1331.209	1331.497	-217.023	0.344	476.749	0.524	15	0.206	R.QALTLQSVVEDK.T
R1/RRR1-20/2	1330.561	1331.497	-1459.289	0.307	498.154	0.457	16	0.200	R.QALTLQSVVEDK.T
R1/RRR1-5/2	1217.096	1217.351	-210.410	0.530	940.059	0.392	18	0.215	K.ISQDELLAEAK.R
R1/RRR1-5/2	1217.121	1217.351	-189.381	0.501	971.395	0.355	18	0.210	K.ISQDELLAEAK.R
R1/RRR1-5/2	1216.486	1217.351	-1537.455	0.418	971.111	0.322	18	0.205	K.ISQDELLAEAK.R
R1/RRR1-12/2	1190.419	1189.346	61.957	0.401	673.137	0.417	14	0.200	R.AFGTQVAEPLR.A
R1/RRR1-10/3	1991.874	1991.426	225.635	0.408	1617.013	0.245	28	0.119	R.M*SYM*FM*ITLNGVFFLK.K
R1/RRR1-10/3	1976.227	1975.427	-101.211	0.425	1780.086	0.133	31	0.105	R.M*SYMFM*ITLNGVFFLK.K
R1/RRR1-10/3	1991.360	1991.426	-33.369	0.401	850.227	0.319	28	0.083	R.M*SYM*FM*ITLNGVFFLK.K
R1/RRR1-10/3	1993.161	1991.426	-133.374	0.423	816.103	0.175	24	0.069	-.M*SYM*FM*ITLNGVFFLK.-
R1/RRR1-10/3	1974.418	1975.427	-1020.221	0.271	836.049	0.138	26	0.065	R.M*SYM*FMITLNGVFFLK.K
R1/RRR1-3/2	1040.341	1040.285	54.300	0.415	913.601	0.412	13	0.217	R.IRPVLTVNK.M
R1/RRR1-1/2	1041.016	1040.285	-258.466	0.511	827.673	0.421	13	0.215	R.IRPVLTVNK.M
R1/RRR1-5/2	1039.670	1040.285	-1557.511	0.475	706.695	0.451	12	0.214	R.IRPVLTVNK.M
R1/RRR1-1/2	1040.279	1040.285	-5.368	0.439	741.560	0.437	12	0.213	R.IRPVLTVNK.M
R1/RRR1-3/2	1040.237	1040.285	-45.740	0.420	871.372	0.388	13	0.212	R.IRPVLTVNK.M
R1/RRR1-4/2	1040.973	1040.285	-299.996	0.463	770.039	0.419	12	0.211	R.IRPVLTVNK.M
R1/RRR1-1/2	1040.517	1040.285	224.323	0.461	815.959	0.388	13	0.210	R.IRPVLTVNK.M
R1/RRR1-5/2	1040.119	1040.285	-159.456	0.426	724.099	0.409	12	0.209	R.IRPVLTVNK.M
R1/RRR1-3/2	1040.336	1040.285	49.828	0.441	729.886	0.405	12	0.208	R.IRPVLTVNK.M
R1/RRR1-2/2	1040.067	1040.285	-210.084	0.464	722.154	0.406	12	0.208	R.IRPVLTVNK.M
R1/RRR1-5/2	1040.291	1040.285	5.695	0.508	888.967	0.363	13	0.208	R.IRPVLTVNK.M
R1/RRR1-4/2	1039.557	1040.285	-1666.624	0.437	624.326	0.358	12	0.199	-.IRPVLTVNK.-
R1/RRR1-4/2	1039.574	1040.285	-1650.580	0.416	511.598	0.295	11	0.193	-.IRPVLTVNK.-
R1/RRR1-7/2	1554.443	1553.850	-262.722	0.406	660.903	0.403	18	0.198	K.LFGADLM*AIPGLYR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-6/3	1383.960	1383.556	292.807	0.433	1252.493	0.355	26	0.107	K.FKEETAAAAM*AAR.D
R1/RRR1-10/3	1071.362	1071.299	58.887	0.488	1793.127	0.172	22	0.113	R.KVRAVQLEK.A
R1/RRR1-11/2	1002.199	1001.202	-3.129	0.438	867.228	0.415	15	0.215	K.VTVLQDVVK.G
R1/RRR1-11/2	1000.851	1001.202	-352.025	0.327	673.327	0.361	14	0.198	K.VTVLQDVVK.G
R1/RRR1-8/3	1796.928	1797.006	-43.691	0.398	1015.859	0.395	27	0.098	K.EVLKENDQLLADRPR.N
R1/RRR1-8/3	1796.619	1797.006	-215.943	0.389	805.876	0.376	24	0.086	K.EVLKENDQLLADRPR.N
R1/RRR1-9/2	1020.800	1021.066	-261.246	0.440	757.509	0.413	14	0.211	K.FGDPTEQAR.A
R1/RRR1-9/2	1020.951	1021.066	-112.862	0.432	758.625	0.350	14	0.203	K.FGDPTEQAR.A
R1/RRR1-9/2	1020.914	1021.066	-148.724	0.418	612.193	0.376	13	0.202	K.FGDPTEQAR.A
R1/RRR1-8/2	1020.973	1021.066	-91.154	0.398	717.756	0.303	13	0.196	K.FGDPTEQAR.A
R1/RRR1-6/2	1158.179	1158.287	-93.622	0.460	771.647	0.400	16	0.209	R.IVEVVQGEER.A
R1/RRR1-6/2	1157.359	1158.287	-1670.799	0.382	488.244	0.289	16	0.195	R.IVEVVQGEER.A
R1/RRR1-8/2	1895.404	1894.192	112.359	0.258	705.745	0.379	18	0.187	-.MAEVEVAAAAAAAGVLHRR.I
R1/RRR1-2/2	1253.503	1253.387	93.220	0.255	723.130	0.343	16	0.189	K.ALAAEVTSTFSR.R
R1/RRR1-10/2	1612.905	1612.870	21.992	0.391	1126.301	0.367	18	0.213	R.EVFSAVLM*SSDILGK.S
R1/RRR1-25/2	1495.323	1494.718	-264.849	0.377	806.832	0.408	18	0.097	R.SEPRPSLAQLLSPV.-
R1/RRR1-25/2	1496.072	1494.718	237.691	0.381	552.318	0.338	16	0.087	R.SEPRPSLAQLLSPV.-
R1/RRR1-15/2	1201.963	1202.380	-347.214	0.377	725.779	0.411	13	0.201	R.VLLSNCRPDK.T
R1/RRR1-7/2	996.069	996.099	-30.006	0.350	677.479	0.407	14	0.201	R.AFSVLSESR.A
R1/RRR1-15/2	1854.638	1855.041	-217.828	0.438	665.073	0.393	15	0.191	R.QSFDEITTFQQQILR.V
R1/RRR1-4/2	1231.195	1231.335	-113.329	0.480	835.109	0.391	17	0.207	K.TTAGIEPEDVAK.R
R1/RRR1-4/2	1231.138	1231.335	-160.274	0.433	838.890	0.394	16	0.206	K.TTAGIEPEDVAK.R
R1/RRR1-4/2	1230.580	1231.335	-1429.903	0.380	611.348	0.378	15	0.197	K.TTAGIEPEDVAK.R
R1/RRR1-5/2	1322.183	1321.547	-276.102	0.423	796.526	0.395	18	0.205	K.VYTAGSIIDLLR.F
R1/RRR1-21/2	1254.277	1253.432	-123.543	0.362	640.752	0.400	15	0.200	K.FQGSPAIITYR.V
R1/RRR1-20/2	1253.558	1253.432	101.128	0.320	684.151	0.378	15	0.196	-.FQGSPAIITYR.-
R1/RRR1-19/2	1024.262	1024.242	19.890	0.405	906.201	0.391	16	0.211	R.VAIQLPAGVR.C
R1/RRR1-19/2	1024.340	1024.242	96.266	0.321	642.999	0.365	13	0.194	-.VAIQLPAGVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-5/2	1021.093	1021.149	-54.751	0.452	812.049	0.394	14	0.209	R.YADLLNSPK.K
R1/RRR1-5/2	1020.424	1021.149	-1694.754	0.364	786.564	0.408	14	0.207	R.YADLLNSPK.K
R1/RRR1-18/2	1081.531	1081.207	300.608	0.295	673.412	0.393	12	0.197	R.YGASANIRTK.G
R1/RRR1-17/2	1081.668	1081.207	426.779	0.329	555.191	0.322	12	0.183	-.YGASANIRTK.-
R1/RRR1-18/2	1081.389	1081.207	168.631	0.243	496.863	0.320	10	0.175	-.YGASANIRTK.-
R1/RRR1-18/2	1081.844	1081.207	-336.875	0.269	465.781	0.255	11	0.146	-.YGASANIRTK.-
R1/RRR1-9/2	1438.407	1438.693	-198.976	0.396	852.249	0.397	15	0.205	K.TFVLTPEQYIVK.L
R1/RRR1-9/2	1438.145	1438.693	-1079.309	0.311	356.093	0.451	11	0.179	-.TFVLTPEQYIVK.-
R1/RRR1-23/2	1088.755	1089.316	-1437.925	0.296	758.060	0.396	14	0.201	R.LPVFLTRSR.F
R1/RRR1-23/2	1089.183	1089.316	-122.597	0.275	309.532	0.268	11	0.191	R.LPVFLTRSR.F
R1/RRR1-8/2	1440.269	1440.544	-191.578	0.420	1055.051	0.378	17	0.214	R.GWTWGLSEYQGR.L
R1/RRR1-19/2	1606.959	1606.764	121.784	0.431	1299.123	0.329	19	0.221	K.NVKFNVWDVGGQDK.I
R1/RRR1-19/2	1608.044	1606.764	174.847	0.455	1153.428	0.320	17	0.207	K.NVKFNVWDVGGQDK.I
R1/RRR1-19/2	1606.726	1606.764	-23.136	0.373	1064.397	0.329	17	0.205	K.NVKFNVWDVGGQDK.I
R1/RRR1-17/2	1534.615	1533.831	-140.627	0.406	761.971	0.396	17	0.198	K.ALLYCGLAPTVLGGK.I
R1/RRR1-17/2	1111.059	1111.234	-157.210	0.297	736.953	0.382	13	0.200	R.YGNFPAQWK.A
R1/RRR1-17/2	1110.923	1111.234	-280.225	0.276	611.913	0.433	12	0.198	R.YGNFPAQWK.A
R1/RRR1-17/2	1111.023	1111.234	-190.275	0.266	512.819	0.334	11	0.189	-.YGNFPAQWK.-
R1/RRR1-1/2	1475.164	1475.696	-1041.600	0.331	1778.041	0.144	18	0.228	R.NEQIMSLGVQSLR.S
R1/RRR1-2/2	1475.222	1475.696	-322.653	0.362	1367.578	0.198	16	0.202	R.NEQIMSLGVQSLR.S
R1/RRR1-2/2	1475.226	1475.696	-319.665	0.355	1346.186	0.143	16	0.192	R.NEQIMSLGVQSLR.S
R1/RRR1-2/2	1475.212	1475.696	-329.627	0.341	1285.236	0.145	16	0.190	R.NEQIMSLGVQSLR.S
R1/RRR1-22/2	1059.886	1060.187	-284.015	0.464	1088.443	0.368	13	0.218	K.FTNFVEFR.T
R1/RRR1-13/2	1123.013	1123.286	-243.410	0.339	831.479	0.386	14	0.205	R.VPTDIFFQR.X
R1/RRR1-13/2	1123.042	1123.286	-217.675	0.312	742.456	0.437	13	0.205	R.VPTDIFFQR.X
R1/RRR1-3/2	1153.650	1153.313	292.853	0.259	748.598	0.374	12	0.192	K.NYSKTGKINK.I
R1/RRR1-6/3	1687.791	1688.845	-1220.311	0.405	1039.356	0.376	29	0.095	K.AAQEM*TGSHLDEVKR.M
R1/RRR1-6/3	1688.182	1688.845	-987.874	0.398	764.967	0.279	26	0.075	K.AAQEM*TGSHLDEVKR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-25/2	1402.020	1401.634	276.167	0.340	1462.749	0.259	18	0.222	K.SKLLIVDLAGSER.I
R1/RRR1-26/2	1401.465	1401.634	-121.226	0.313	1624.676	0.160	19	0.218	K.SKLLIVDLAGSER.I
R1/RRR1-26/2	1401.353	1401.634	-200.830	0.275	1283.078	0.234	18	0.205	K.SKLLIVDLAGSER.I
R1/RRR1-25/2	1401.342	1401.634	-209.132	0.231	1044.073	0.131	16	0.182	K.SKLLIVDLAGSER.I
R1/RRR1-4/2	1878.357	1877.130	121.591	0.400	839.602	0.368	17	0.195	R.SVAEALFLPYDLVPDAR.G
R1/RRR1-4/2	1878.343	1877.130	113.901	0.294	713.247	0.152	16	0.174	R.SVAEALFLPYDLVPDAR.G
R1/RRR1-15/2	1530.430	1529.691	-171.059	0.250	773.979	0.371	15	0.195	-.M*LDNEAIYDICR.R
R1/RRR1-15/2	1530.462	1529.691	-150.416	0.293	704.210	0.301	14	0.189	-.M*LDNEAIYDICR.R
R1/RRR1-15/2	1530.138	1529.691	292.845	0.243	609.839	0.300	13	0.185	-.M*LDNEAIYDICR.R
R1/RRR1-5/2	1483.880	1483.647	157.628	0.368	936.873	0.368	16	0.203	K.FGYELEALVGQEK.D
R1/RRR1-9/2	1200.159	1200.410	-209.503	0.352	704.220	0.391	14	0.197	R.LLAAELTEIAR.A
R1/RRR1-25/2	1333.023	1333.497	-356.117	0.386	925.845	0.383	19	0.211	R.NLNM*GNAASIPSK.C
R1/RRR1-25/2	1333.001	1333.497	-373.115	0.388	831.304	0.395	18	0.208	R.NLNM*GNAASIPSK.C
R1/RRR1-25/2	1333.089	1333.497	-307.147	0.435	682.119	0.353	17	0.199	R.NLNM*GNAASIPSK.C
R1/RRR1-26/2	1332.954	1333.497	-1160.956	0.418	624.695	0.367	16	0.198	R.NLNM*GNAASIPSK.C
R1/RRR1-24/2	1333.064	1333.497	-325.338	0.377	825.568	0.309	18	0.198	R.NLNM*GNAASIPSK.C
R1/RRR1-24/2	1333.202	1333.497	-221.621	0.412	634.220	0.337	16	0.195	R.NLNM*GNAASIPSK.C
R1/RRR1-26/2	1333.023	1333.497	-356.668	0.359	427.367	0.332	14	0.193	R.NLNM*GNAASIPSK.C
R1/RRR1-3/2	1918.839	1920.068	-1165.293	0.371	928.946	0.370	18	0.198	K.GPYTFSIGDVSGLGTYER.G
R1/RRR1-12/3	1614.784	1613.898	-70.495	0.471	1088.365	0.363	23	0.098	-.LM*QCKPLPEPEVR.-
R1/RRR1-19/2	1061.535	1062.113	-1490.713	0.399	1142.054	0.354	15	0.220	K.SEEIDAELR.V
R1/RRR1-20/2	1061.961	1062.113	-143.033	0.498	1068.120	0.328	15	0.212	K.SEEIDAELR.V
R1/RRR1-19/2	1061.748	1062.113	-344.865	0.408	1098.085	0.289	14	0.206	K.SEEIDAELR.V
R1/RRR1-19/2	1061.387	1062.113	-1630.847	0.318	755.481	0.195	13	0.187	-.SEEIDAELR.-
R1/RRR1-17/2	1062.131	1062.113	17.221	0.210	543.279	0.203	12	0.184	-.SEEIDAELR.-
R1/RRR1-9/2	944.380	945.052	-1775.536	0.379	874.089	0.379	14	0.100	-.EGIAAAVAVGS.-
R1/RRR1-9/2	944.771	945.052	-298.728	0.306	705.150	0.296	14	0.086	-.EGIAAAVAVGS.-
R1/RRR1-9/2	944.900	945.052	-161.725	0.347	797.007	0.268	13	0.083	K.EGIAAAVAVGS.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-7/2	1765.524	1765.107	236.492	0.410	736.028	0.377	17	0.192	R.LASGALFSM*PITLDLAK.E
R1/RRR1-20/2	969.806	970.191	-398.265	0.422	1139.097	0.360	14	0.220	R.ALLDVGLIR.T
R1/RRR1-13/2	969.797	970.191	-407.737	0.449	1035.725	0.378	15	0.218	R.ALLDVGLIR.T
R1/RRR1-13/2	970.041	970.191	-154.946	0.424	971.224	0.380	14	0.214	R.ALLDVGLIR.T
R1/RRR1-13/2	971.094	970.191	-100.816	0.506	941.228	0.370	14	0.211	R.ALLDVGLIR.T
R1/RRR1-12/2	1278.845	1279.637	-1404.850	0.301	740.183	0.381	14	0.195	K.ELLQLLLPVLK.V
R1/RRR1-3/2	1741.181	1739.912	155.360	0.390	760.897	0.358	17	0.193	R.WGFATEGNDLFNVIR.S
R1/RRR1-13/2	1610.753	1610.883	-80.999	0.373	739.989	0.382	16	0.195	K.IAIVGFGNFGQFLAR.T
R1/RRR1-13/2	1610.792	1610.883	-56.826	0.284	368.642	0.347	13	0.179	-.IAIVGFGNFGQFLAR.-
R1/RRR1-14/2	1543.999	1543.621	245.538	0.301	1343.099	0.280	20	0.214	R.GGEEAGADAAQGGALLR.Q
R1/RRR1-17/2	992.240	992.111	131.278	0.543	1288.564	0.309	13	0.218	K.FAEEVLQR.E
R1/RRR1-17/2	991.392	992.111	-1739.012	0.505	1000.466	0.270	14	0.199	K.FAEEVLQR.E
R1/RRR1-5/2	1617.507	1616.840	-206.692	0.493	908.166	0.361	18	0.201	K.FQQLSPEIVQIEGK.D
R1/RRR1-15/2	1264.015	1263.514	-396.036	0.267	831.297	0.351	15	0.195	K.LVAPWFQVFR.G
R1/RRR1-18/2	1285.361	1284.482	-94.455	0.352	792.453	0.373	16	0.200	R.ALAEAYELIYK.A
R1/RRR1-9/2	1405.088	1404.550	-330.219	0.387	811.887	0.377	15	0.201	R.FFDAFFDLEPR.Y
R1/RRR1-12/2	1594.494	1595.862	-1489.409	0.325	1192.669	0.327	18	0.211	R.LTNLAEIDPLASLPK.L
R1/RRR1-5/2	1317.325	1316.449	-94.580	0.424	740.475	0.369	15	0.202	K.NRDWWPNSLK.L
R1/RRR1-5/2	1317.364	1316.449	-64.650	0.358	711.786	0.234	14	0.187	-.NRDWWPNSLK.-
R1/RRR1-9/2	1059.292	1059.155	129.036	0.502	1209.536	0.332	15	0.219	R.IEEELGNVR.Y
R1/RRR1-9/2	1058.622	1059.155	-1452.832	0.447	886.603	0.327	14	0.202	R.IEEELGNVR.Y
R1/RRR1-21/2	1602.315	1603.798	-1554.119	0.362	1221.877	0.324	19	0.214	R.GDPIEFELGTGQVIK.G
R1/RRR1-7/2	933.277	933.086	205.035	0.429	925.565	0.376	13	0.208	-.GGAQLYVPK.-
R1/RRR1-2/2	1535.830	1534.696	87.883	0.399	787.922	0.375	18	0.197	K.LPSVGLDGSSPYSVR.D
R1/RRR1-4/2	1418.138	1417.575	-309.501	0.424	919.323	0.322	17	0.196	-.M*AAVANGGAAPEWR.-
R1/RRR1-4/2	1418.199	1417.575	-266.235	0.326	942.768	0.289	17	0.195	-.M*AAVANGGAAPEWR.-
R1/RRR1-23/2	981.961	982.244	-288.349	0.488	928.996	0.363	13	0.210	K.LAVLKFYK.V
R1/RRR1-23/2	981.965	982.244	-284.358	0.493	756.716	0.387	13	0.209	K.LAVLKFYK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R1/RRR1-23/2	983.051	982.244	-195.989	0.522	747.625	0.297	13	0.197	K.LAVLKFYK.V
R2/RRR2-2/2	1847.457	1847.062	214.618	0.673	3656.128	0.664	29	0.737	K.YKEAAELAAESPQGLLR.T
R2/RRR2-2/2	1846.734	1847.062	-178.186	0.651	3650.970	0.638	29	0.722	K.YKEAAELAAESPQGLLR.T
R2/RRR2-2/2	1846.465	1847.062	-867.556	0.640	3463.794	0.634	28	0.658	K.YKEAAELAAESPQGLLR.T
R2/RRR2-2/2	1565.403	1565.711	-197.695	0.565	2653.942	0.539	24	0.392	R.SQALEAHAASFASFK.V
R2/RRR2-2/2	1565.233	1565.711	-306.680	0.508	2635.688	0.529	24	0.386	R.SQALEAHAASFASFK.V
R2/RRR2-2/2	1842.595	1843.120	-830.041	0.591	2636.572	0.517	25	0.382	K.FNLNVQAVNVLLDNIR.S
R2/RRR2-2/2	1842.453	1843.120	-907.124	0.567	2574.518	0.505	24	0.365	K.FNLNVQAVNVLLDNIR.S
R2/RRR2-2/2	1565.166	1565.711	-990.466	0.572	2450.191	0.536	24	0.347	R.SQALEAHAASFASFK.V
R2/RRR2-2/2	1842.513	1843.120	-874.467	0.560	2531.134	0.474	24	0.344	K.FNLNVQAVNVLLDNIR.S
R2/RRR2-1/2	1565.128	1565.711	-1014.584	0.493	2257.557	0.503	22	0.299	R.SQALEAHAASFASFK.V
R2/RRR2-2/2	1633.092	1632.740	216.549	0.510	2104.943	0.534	20	0.283	K.EVCFACVDAEEFR.L
R2/RRR2-2/2	1778.804	1779.076	-153.328	0.547	1976.438	0.563	26	0.273	K.LHVIELGAQPGKPGFSK.K
R2/RRR2-2/2	1633.244	1632.740	-304.630	0.526	2090.564	0.499	20	0.270	K.EVCFACVDAEEFR.L
R2/RRR2-2/2	1295.319	1295.424	-80.685	0.550	1932.117	0.521	18	0.254	K.LNAYESLELSR.L
R2/RRR2-1/2	1437.335	1437.534	-138.389	0.535	1958.244	0.523	20	0.253	R.AAEEANVYDDLVK.Y
R2/RRR2-2/2	1778.479	1779.076	-900.307	0.530	1916.248	0.533	23	0.252	K.LHVIELGAQPGKPGFSK.K
R2/RRR2-1/2	1633.254	1632.740	-298.481	0.452	1863.070	0.527	19	0.242	K.EVCFACVDAEEFR.L
R2/RRR2-2/2	1295.040	1295.424	-297.394	0.520	1889.887	0.493	18	0.240	K.LNAYESLELSR.L
R2/RRR2-1/2	1565.120	1565.711	-1019.987	0.380	2164.613	0.339	22	0.237	R.SQALEAHAASFASFK.V
R2/RRR2-2/2	1584.890	1584.801	56.193	0.565	1806.732	0.531	19	0.235	R.ALQHYTELPDIKR.V
R2/RRR2-1/2	1437.030	1437.534	-1049.644	0.449	1860.334	0.494	20	0.231	R.AAEEANVYDDLVK.Y
R2/RRR2-2/2	1226.226	1226.403	-144.541	0.570	1819.841	0.509	18	0.230	K.VDGELIFAYAK.I
R2/RRR2-2/2	1694.402	1694.979	-933.705	0.456	1690.468	0.580	21	0.230	R.AHM*GIFTELGVLYAR.Y
R2/RRR2-2/2	1141.149	1141.346	-172.699	0.502	1647.399	0.576	17	0.226	R.GNLQIVVQAAK.E
R2/RRR2-2/2	1140.650	1141.346	-1491.545	0.488	1650.949	0.574	17	0.225	R.GNLQIVVQAAK.E
R2/RRR2-2/2	1694.433	1694.979	-914.973	0.504	1646.426	0.579	21	0.224	R.AHM*GIFTELGVLYAR.Y
R2/RRR2-2/3	1843.213	1843.120	50.834	0.538	1975.235	0.467	33	0.221	K.FNLNVQAVNVLLDNIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1437.175	1437.534	-249.921	0.514	1879.240	0.446	20	0.220	R.AAEEANVYDDLVK.Y
R2/RRR2-2/2	1225.528	1226.403	-1534.404	0.518	1722.294	0.502	18	0.216	K.VDGELIFAYAK.I
R2/RRR2-2/2	1437.074	1437.534	-321.080	0.485	1701.404	0.521	20	0.216	R.AAEEANVYDDLVK.Y
R2/RRR2-2/2	1480.218	1480.648	-291.125	0.501	1670.661	0.527	20	0.216	R.GKLNAYESLELSR.L
R2/RRR2-2/2	1480.242	1480.648	-274.826	0.513	1657.379	0.521	20	0.212	R.GKLNAYESLELSR.L
R2/RRR2-1/2	1479.503	1480.648	-1454.225	0.414	1754.095	0.472	20	0.212	R.GKLNAYESLELSR.L
R2/RRR2-2/2	1106.140	1105.269	-116.843	0.523	1633.875	0.518	17	0.210	R.DPTLAVVAYR.R
R2/RRR2-2/2	1480.973	1480.648	220.356	0.543	1630.077	0.525	20	0.210	R.GKLNAYESLELSR.L
R2/RRR2-2/2	1632.961	1632.740	135.740	0.509	1810.511	0.433	19	0.209	K.EVCFACVDAEEFR.L
R2/RRR2-2/2	1226.143	1226.403	-212.752	0.572	1638.612	0.507	18	0.206	K.VDGELIFAYAK.I
R2/RRR2-1/3	1846.181	1847.062	-1021.855	0.528	1884.118	0.473	33	0.206	K.YKEAAELAAESPQGLLR.T
R2/RRR2-3/3	1847.472	1847.062	222.396	0.540	1757.071	0.521	30	0.205	K.YKEAAELAAESPQGLLR.T
R2/RRR2-2/3	1517.196	1516.749	295.462	0.491	2311.152	0.266	26	0.199	K.SHQMPEQVVFWK.W
R2/RRR2-1/2	1226.033	1226.403	-302.849	0.421	1724.397	0.419	18	0.196	K.VDGELIFAYAK.I
R2/RRR2-2/2	1437.182	1437.534	-245.490	0.543	1602.780	0.486	20	0.195	R.AAEEANVYDDLVK.Y
R2/RRR2-2/3	1673.924	1673.876	28.692	0.518	2124.766	0.340	31	0.194	R.RPITADSALM*NPNTR.I
R2/RRR2-2/3	1842.763	1843.120	-193.925	0.514	1801.115	0.469	32	0.193	K.FNLNVQAVNVLLDNIR.S
R2/RRR2-2/2	1506.083	1506.591	-1004.445	0.494	1792.808	0.367	19	0.192	R.GQCDDELINVTNK.N
R2/RRR2-1/3	1674.814	1673.876	-37.154	0.517	2049.372	0.361	31	0.189	R.RPITADSALM*NPNTR.I
R2/RRR2-2/2	1304.256	1304.480	-172.599	0.442	1600.081	0.445	18	0.188	K.LKQFQGAVDAAR.K
R2/RRR2-2/2	1584.238	1584.801	-989.439	0.485	1539.907	0.470	18	0.186	R.ALQHYTELPDIKR.V
R2/RRR2-1/3	1673.909	1673.876	19.476	0.547	2081.896	0.338	31	0.184	R.RPITADSALM*NPNTR.I
R2/RRR2-2/2	1140.343	1141.346	-1761.655	0.410	1429.486	0.517	17	0.184	R.GNLQIVVQAAK.E
R2/RRR2-2/2	1450.255	1450.619	-251.298	0.499	1445.087	0.507	19	0.184	R.EGLVSEAIESFIR.A
R2/RRR2-2/2	1554.703	1555.715	-1297.650	0.364	1757.175	0.326	21	0.179	K.EAAELAAESPQGLLR.T
R2/RRR2-1/3	1673.426	1673.876	-270.252	0.476	2180.672	0.269	31	0.179	R.RPITADSALM*NPNTR.I
R2/RRR2-2/2	1372.657	1373.496	-1343.803	0.408	1711.896	0.349	18	0.178	R.ADDATHFLDVIR.A
R2/RRR2-2/2	1450.287	1450.619	-229.427	0.497	1498.925	0.454	19	0.178	R.EGLVSEAIESFIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1629.399	1628.849	-276.794	0.532	1233.659	0.585	21	0.177	R.QLIDQVVSTALPESK.S
R2/RRR2-2/2	1105.118	1105.269	-136.783	0.456	1248.331	0.571	15	0.177	R.DPTLAVVAYR.R
R2/RRR2-2/2	1736.236	1736.941	-984.761	0.495	1302.393	0.545	22	0.176	K.VVGNENPSTLICFASK.T
R2/RRR2-2/2	1505.684	1506.591	-1270.046	0.394	1673.780	0.348	19	0.175	R.GQCDDELINVTNK.N
R2/RRR2-1/2	1225.620	1226.403	-1458.966	0.375	1441.710	0.477	17	0.175	K.VDGELIFAYAK.I
R2/RRR2-1/2	1437.106	1437.534	-298.496	0.443	1435.346	0.474	20	0.175	R.AAEEANVYDDLVK.Y
R2/RRR2-1/2	1226.322	1226.403	-65.956	0.394	1492.145	0.437	17	0.173	K.VDGELIFAYAK.I
R2/RRR2-1/2	1628.412	1628.849	-269.368	0.450	1419.514	0.472	22	0.172	R.QLIDQVVSTALPESK.S
R2/RRR2-2/2	1736.323	1736.941	-934.788	0.518	1173.726	0.588	21	0.172	K.VVGNENPSTLICFASK.T
R2/RRR2-2/2	1555.396	1555.715	-205.343	0.478	1679.953	0.334	22	0.171	K.EAAELAAESPQGLLR.T
R2/RRR2-2/2	1439.190	1439.579	-271.162	0.471	1492.544	0.421	17	0.170	K.GNM*QLFSVDQQR.S
R2/RRR2-2/3	1846.621	1847.062	-239.468	0.554	1623.462	0.481	31	0.169	K.YKEAAELAAESPQGLLR.T
R2/RRR2-2/2	1554.940	1555.715	-1144.618	0.374	1622.857	0.345	21	0.168	K.EAAELAAESPQGLLR.T
R2/RRR2-2/2	1423.340	1423.580	-168.997	0.386	1795.620	0.251	18	0.167	K.GNMQLFSVDQQR.S
R2/RRR2-3/2	1437.401	1437.534	-92.216	0.399	1425.184	0.430	19	0.164	R.AAEEANVYDDLVK.Y
R2/RRR2-2/2	1439.184	1439.579	-275.246	0.474	1404.208	0.432	17	0.163	K.GNM*QLFSVDQQR.S
R2/RRR2-1/3	1846.438	1847.062	-882.164	0.519	1526.881	0.490	30	0.161	K.YKEAAELAAESPQGLLR.T
R2/RRR2-1/2	1345.277	1344.448	-127.472	0.540	1211.575	0.483	18	0.161	R.LYDEELYEAAK.I
R2/RRR2-1/3	1847.000	1847.062	-33.491	0.569	1472.328	0.509	29	0.159	K.YKEAAELAAESPQGLLR.T
R2/RRR2-2/2	1678.619	1678.979	-215.579	0.492	1076.085	0.572	18	0.159	R.AHMGIFTELGVLYAR.Y
R2/RRR2-2/2	1512.335	1512.637	-200.179	0.501	1186.873	0.492	19	0.157	K.EYSEQLGVDACIK.L
R2/RRR2-2/2	1304.189	1304.480	-224.054	0.432	1497.629	0.352	17	0.157	K.LKQFQGAVDAAR.K
R2/RRR2-1/2	1628.549	1628.849	-184.992	0.438	1271.440	0.463	21	0.156	R.QLIDQVVSTALPESK.S
R2/RRR2-1/2	1737.309	1736.941	212.791	0.567	1082.935	0.547	20	0.156	K.VVGNENPSTLICFASK.T
R2/RRR2-2/2	1737.239	1736.941	172.345	0.535	1031.105	0.564	20	0.155	K.VVGNENPSTLICFASK.T
R2/RRR2-2/2	1070.078	1070.306	-213.689	0.503	945.539	0.551	14	0.153	K.YGLIYVITK.L
R2/RRR2-1/2	1304.276	1304.480	-156.638	0.385	1318.161	0.414	17	0.153	K.LKQFQGAVDAAR.K
R2/RRR2-2/2	1450.300	1450.619	-220.054	0.494	1244.720	0.442	18	0.152	R.EGLVSEAIESFIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1344.212	1344.448	-176.212	0.432	1171.653	0.455	18	0.151	R.LYDEELYEAAK.I
R2/RRR2-2/2	1512.197	1512.637	-292.013	0.445	1182.543	0.454	19	0.150	K.EYSEQLGVDACIK.L
R2/RRR2-2/2	1099.010	1099.261	-228.896	0.528	931.395	0.532	14	0.149	K.VANVELYYK.A
R2/RRR2-2/2	1069.978	1070.306	-307.426	0.480	959.017	0.523	14	0.148	K.YGLIYVITK.L
R2/RRR2-2/2	1438.489	1439.579	-1457.793	0.387	1416.244	0.344	17	0.148	K.GNM*QLFSVDQQR.S
R2/RRR2-3/2	1450.181	1450.619	-302.559	0.428	1474.532	0.314	19	0.148	R.EGLVSEAIESFIR.A
R2/RRR2-2/2	1513.269	1512.637	-243.989	0.504	1105.538	0.470	19	0.148	K.EYSEQLGVDACIK.L
R2/RRR2-3/2	1437.219	1437.534	-219.586	0.470	1230.613	0.427	17	0.146	R.AAEEANVYDDLVK.Y
R2/RRR2-1/2	1374.153	1373.496	-250.335	0.461	1207.123	0.423	17	0.146	R.ADDATHFLDVIR.A
R2/RRR2-2/2	1070.189	1070.306	-109.442	0.457	990.953	0.489	14	0.145	K.YGLIYVITK.L
R2/RRR2-2/3	1480.681	1480.648	22.556	0.519	1784.431	0.349	29	0.144	R.GKLNAYESLELSR.L
R2/RRR2-2/2	1105.598	1105.269	298.383	0.331	1162.936	0.444	16	0.144	R.DPTLAVVAYR.R
R2/RRR2-2/3	1673.703	1673.876	-103.967	0.535	1725.769	0.365	30	0.144	R.RPITADSALM*NPNTR.I
R2/RRR2-1/2	1100.087	1099.261	-158.778	0.508	912.059	0.507	14	0.144	K.VANVELYYK.A
R2/RRR2-2/2	1099.085	1099.261	-160.259	0.499	977.812	0.481	14	0.144	K.VANVELYYK.A
R2/RRR2-2/2	1537.149	1537.749	-1044.043	0.523	917.647	0.506	20	0.142	K.RANLPGAENLVVQR.F
R2/RRR2-1/2	1628.591	1628.849	-158.599	0.409	1140.577	0.438	20	0.142	R.QLIDQVVSTALPESK.S
R2/RRR2-2/2	1537.451	1537.749	-194.759	0.534	868.497	0.517	20	0.141	K.RANLPGAENLVVQR.F
R2/RRR2-3/2	1437.327	1437.534	-144.268	0.459	1165.404	0.411	18	0.140	R.AAEEANVYDDLVK.Y
R2/RRR2-2/3	1846.011	1847.062	-1114.323	0.524	1566.680	0.407	31	0.140	K.YKEAAELAAESPQGLLR.T
R2/RRR2-2/3	1584.860	1584.801	37.219	0.573	1394.037	0.479	28	0.138	R.ALQHYTELPDIKR.V
R2/RRR2-2/2	1373.253	1373.496	-177.479	0.402	1185.385	0.353	17	0.133	R.ADDATHFLDVIR.A
R2/RRR2-1/2	1372.454	1373.496	-1492.180	0.386	1100.833	0.373	16	0.130	R.ADDATHFLDVIR.A
R2/RRR2-2/2	969.537	970.190	-1709.766	0.366	820.870	0.469	13	0.130	R.IAAYIYKK.A
R2/RRR2-2/2	1372.935	1373.496	-1140.114	0.376	1081.460	0.375	16	0.129	R.ADDATHFLDVIR.A
R2/RRR2-1/2	1098.664	1099.261	-1457.496	0.359	902.664	0.429	14	0.129	K.VANVELYYK.A
R2/RRR2-2/2	970.113	970.190	-79.525	0.393	839.583	0.440	13	0.129	R.IAAYIYKK.A
R2/RRR2-2/2	1380.689	1381.563	-1361.082	0.343	826.971	0.470	19	0.129	R.ANLPGAENLVVQR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1628.629	1628.849	-135.516	0.434	967.457	0.420	19	0.129	R.QLIDQVVSTALPESK.S
R2/RRR2-2/2	862.893	862.996	-119.204	0.428	617.600	0.474	13	0.129	K.VVAAFAER.R
R2/RRR2-3/2	1099.109	1099.261	-138.311	0.412	927.168	0.397	14	0.128	K.VANVELYYK.A
R2/RRR2-3/2	1326.452	1326.567	-87.006	0.430	1110.559	0.338	15	0.127	K.IIYAFISNWAK.L
R2/RRR2-2/2	1111.610	1112.260	-1488.766	0.411	901.810	0.387	14	0.126	R.FQELFAQTK.Y
R2/RRR2-2/2	1099.126	1099.261	-123.047	0.482	873.961	0.374	14	0.125	K.VANVELYYK.A
R2/RRR2-2/2	1381.209	1381.563	-256.946	0.450	808.145	0.407	19	0.124	R.ANLPGAENLVVQR.F
R2/RRR2-2/2	862.779	862.996	-252.189	0.428	636.079	0.392	13	0.122	K.VVAAFAER.R
R2/RRR2-1/2	1381.144	1381.563	-304.119	0.432	695.400	0.417	18	0.122	R.ANLPGAENLVVQR.F
R2/RRR2-2/2	1261.120	1261.455	-266.559	0.456	733.477	0.389	16	0.120	K.RDPTLAVVAYR.R
R2/RRR2-2/2	1785.739	1785.026	-161.098	0.485	557.307	0.465	18	0.119	R.SLLPVEPLVDECEKR.N
R2/RRR2-1/2	1112.100	1112.260	-144.181	0.417	931.347	0.314	14	0.119	R.FQELFAQTK.Y
R2/RRR2-2/2	1381.035	1381.563	-1109.313	0.411	610.768	0.423	17	0.119	R.ANLPGAENLVVQR.F
R2/RRR2-2/2	1516.206	1516.749	-1020.592	0.371	752.203	0.429	15	0.119	K.SHQMPEQVVFWK.W
R2/RRR2-2/2	1784.503	1785.026	-855.827	0.469	669.428	0.429	19	0.119	R.SLLPVEPLVDECEKR.N
R2/RRR2-1/2	862.427	862.996	-1824.296	0.321	757.604	0.384	13	0.119	K.VVAAFAER.R
R2/RRR2-1/2	1380.993	1381.563	-1140.023	0.389	601.290	0.419	17	0.118	R.ANLPGAENLVVQR.F
R2/RRR2-1/2	862.818	862.996	-207.052	0.321	651.368	0.405	13	0.118	K.VVAAFAER.R
R2/RRR2-2/3	1673.850	1673.876	-16.072	0.469	1760.851	0.249	29	0.118	R.RPITADSALM*NPNTR.I
R2/RRR2-3/2	1381.151	1381.563	-299.064	0.298	945.496	0.325	19	0.117	R.ANLPGAENLVVQR.F
R2/RRR2-1/2	1111.574	1112.260	-1520.756	0.421	773.866	0.318	14	0.116	R.FQELFAQTK.Y
R2/RRR2-2/2	1673.389	1673.876	-292.127	0.360	192.698	0.502	16	0.116	R.RPITADSALM*NPNTR.I
R2/RRR2-2/2	1262.139	1261.455	-251.211	0.349	660.704	0.386	16	0.115	K.RDPTLAVVAYR.R
R2/RRR2-1/2	1372.559	1373.496	-1415.083	0.305	925.409	0.316	16	0.115	R.ADDATHFLDVIR.A
R2/RRR2-3/2	1381.198	1381.563	-264.837	0.305	806.406	0.339	18	0.114	R.ANLPGAENLVVQR.F
R2/RRR2-2/3	1930.759	1930.109	-182.170	0.459	1287.860	0.409	29	0.114	K.VDELVKDRIESQNEVR.A
R2/RRR2-2/2	1111.468	1112.260	-1617.180	0.313	837.851	0.305	14	0.114	R.FQELFAQTK.Y
R2/RRR2-3/2	1564.540	1565.711	-1391.930	0.300	855.347	0.344	18	0.113	R.SQALEAHAASFASFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1381.163	1381.563	-289.931	0.392	629.857	0.344	17	0.113	R.ANLPGAENLVVQR.F
R2/RRR2-1/2	1325.550	1326.567	-1526.507	0.269	1002.995	0.294	13	0.113	K.IIYAFISNWAK.L
R2/RRR2-2/2	1673.319	1673.876	-933.546	0.288	280.997	0.484	18	0.112	R.RPITADSALM*NPNTR.I
R2/RRR2-2/3	1481.465	1480.648	-124.028	0.541	1496.681	0.343	28	0.112	R.GKLNAYESLELSR.L
R2/RRR2-2/2	1673.299	1673.876	-945.557	0.287	270.952	0.482	18	0.112	R.RPITADSALM*NPNTR.I
R2/RRR2-2/2	1627.662	1628.849	-1347.654	0.290	800.259	0.327	17	0.110	R.QLIDQVVSTALPESK.S
R2/RRR2-2/2	1584.313	1584.801	-309.015	0.362	371.992	0.346	15	0.110	R.ALQHYTELPDIKR.V
R2/RRR2-3/2	1628.237	1628.849	-992.931	0.343	814.481	0.320	16	0.109	R.QLIDQVVSTALPESK.S
R2/RRR2-2/3	1450.479	1450.619	-96.627	0.408	1592.468	0.262	26	0.108	R.EGLVSEAIESFIR.A
R2/RRR2-1/2	1679.261	1678.979	168.234	0.343	240.674	0.424	12	0.106	-.AHMGIFTELGVLYAR.-
R2/RRR2-1/3	1480.193	1480.648	-307.972	0.467	1292.698	0.372	24	0.106	R.GKLNAYESLELSR.L
R2/RRR2-1/2	1105.163	1105.269	-95.565	0.299	611.341	0.230	13	0.105	R.DPTLAVVAYR.R
R2/RRR2-3/2	1628.076	1628.849	-1092.410	0.327	792.179	0.258	16	0.104	R.QLIDQVVSTALPESK.S
R2/RRR2-2/3	1584.372	1584.801	-271.571	0.481	1182.916	0.405	26	0.104	R.ALQHYTELPDIKR.V
R2/RRR2-2/3	1480.141	1480.648	-1021.356	0.536	1374.629	0.347	27	0.104	R.GKLNAYESLELSR.L
R2/RRR2-2/2	757.752	757.944	-254.585	0.303	695.262	0.185	10	0.103	-.GLILSVR.-
R2/RRR2-1/2	1438.870	1439.579	-1191.579	0.283	563.069	0.226	13	0.102	K.GNM*QLFSVDQQR.S
R2/RRR2-2/2	757.870	757.944	-98.969	0.278	844.387	0.118	10	0.100	-.GLILSVR.-
R2/RRR2-3/3	1674.029	1673.876	91.224	0.390	1515.294	0.255	31	0.097	R.RPITADSALM*NPNTR.I
R2/RRR2-3/2	1111.848	1112.260	-371.832	0.328	568.094	0.202	12	0.097	-.FQELFAQTK.-
R2/RRR2-2/3	1929.814	1930.109	-153.487	0.474	831.294	0.462	25	0.095	K.VDELVKDRIESQNEVR.A
R2/RRR2-1/3	1778.452	1779.076	-915.474	0.391	846.280	0.448	28	0.094	K.LHVIELGAQPGKPGFSK.K
R2/RRR2-2/3	1532.472	1532.748	-180.515	0.483	1219.550	0.339	23	0.093	K.SHQM*PEQVVFWK.W
R2/RRR2-2/3	1373.610	1373.496	83.500	0.493	724.597	0.450	24	0.093	R.ADDATHFLDVIR.A
R2/RRR2-1/3	1373.086	1373.496	-299.672	0.473	456.517	0.471	19	0.091	R.ADDATHFLDVIR.A
R2/RRR2-1/3	1373.249	1373.496	-180.075	0.463	692.968	0.440	24	0.091	R.ADDATHFLDVIR.A
R2/RRR2-1/3	1374.606	1373.496	80.589	0.422	572.319	0.445	23	0.089	R.ADDATHFLDVIR.A
R2/RRR2-1/3	1480.441	1480.648	-140.323	0.490	1013.669	0.368	24	0.088	R.GKLNAYESLELSR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/3	1428.494	1428.615	-84.915	0.410	1059.822	0.359	21	0.087	R.ALQHYTELPDIK.R
R2/RRR2-2/3	1372.770	1373.496	-1261.158	0.460	553.088	0.419	21	0.087	R.ADDATHFLDVIR.A
R2/RRR2-3/3	1373.495	1373.496	-0.599	0.450	729.734	0.409	24	0.087	R.ADDATHFLDVIR.A
R2/RRR2-2/3	1373.489	1373.496	-5.279	0.450	577.111	0.456	22	0.087	-.ADDATHFLDVIR.-
R2/RRR2-2/3	1779.352	1779.076	155.563	0.450	855.021	0.396	30	0.087	K.LHVIELGAQPGKPGFSK.K
R2/RRR2-1/3	1304.531	1304.480	39.539	0.488	705.389	0.420	23	0.087	K.LKQFQGAVDAAR.K
R2/RRR2-2/3	1696.039	1694.979	35.288	0.442	841.150	0.410	24	0.086	R.AHM*GIFTELGVLYAR.Y
R2/RRR2-2/3	1779.173	1779.076	55.141	0.461	660.110	0.424	27	0.086	K.LHVIELGAQPGKPGFSK.K
R2/RRR2-1/3	1584.825	1584.801	15.086	0.477	1022.895	0.346	24	0.085	R.ALQHYTELPDIKR.V
R2/RRR2-1/3	1584.705	1584.801	-60.706	0.525	963.232	0.357	24	0.085	R.ALQHYTELPDIKR.V
R2/RRR2-1/3	1480.358	1480.648	-196.779	0.461	828.683	0.372	22	0.083	R.GKLNAYESLELSR.L
R2/RRR2-3/3	1373.736	1373.496	175.070	0.394	472.258	0.346	21	0.082	R.ADDATHFLDVIR.A
R2/RRR2-2/3	1304.680	1304.480	154.118	0.502	1033.290	0.327	24	0.082	K.LKQFQGAVDAAR.K
R2/RRR2-1/3	1780.668	1779.076	-229.841	0.384	714.357	0.389	25	0.081	K.LHVIELGAQPGKPGFSK.K
R2/RRR2-2/3	1930.446	1930.109	174.687	0.431	810.971	0.368	23	0.079	K.VDELVKDRIESQNEVR.A
R2/RRR2-2/3	1970.568	1971.293	-877.605	0.340	1290.726	0.218	26	0.078	K.KFNLNVQAVNVLLDNIR.S
R2/RRR2-2/3	1538.679	1537.749	-45.613	0.387	1005.558	0.307	26	0.077	K.RANLPGAENLVVQR.F
R2/RRR2-2/3	1779.173	1779.076	54.832	0.402	562.551	0.372	25	0.077	-.LHVIELGAQPGKPGFSK.-
R2/RRR2-1/3	1778.467	1779.076	-907.308	0.396	772.805	0.345	26	0.077	-.LHVIELGAQPGKPGFSK.-
R2/RRR2-2/3	1537.852	1537.749	67.377	0.315	923.833	0.335	26	0.076	K.RANLPGAENLVVQR.F
R2/RRR2-1/3	1584.776	1584.801	-15.623	0.449	722.417	0.313	22	0.074	-.ALQHYTELPDIKR.-
R2/RRR2-2/3	1303.861	1304.480	-1245.363	0.426	940.703	0.283	23	0.072	-.LKQFQGAVDAAR.-
R2/RRR2-3/3	1584.788	1584.801	-8.206	0.407	786.377	0.265	23	0.070	-.ALQHYTELPDIKR.-
R2/RRR2-2/3	1532.403	1532.748	-225.706	0.442	1054.572	0.220	23	0.069	K.SHQM*PEQVVFWK.W
R2/RRR2-3/3	1584.274	1584.801	-966.472	0.383	711.385	0.298	21	0.069	-.ALQHYTELPDIKR.-
R2/RRR2-2/3	1531.327	1532.748	-1585.811	0.354	1120.792	0.186	22	0.066	K.SHQM*PEQVVFWK.W
R2/RRR2-2/3	1971.845	1971.293	-227.862	0.431	700.929	0.261	24	0.066	K.KFNLNVQAVNVLLDNIR.S
R2/RRR2-2/3	1695.368	1694.979	230.002	0.290	970.592	0.208	24	0.064	R.AHM*GIFTELGVLYAR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1628.810	1628.849	-24.175	0.304	166.479	0.375	11	0.062	-.QLIDQVVSTALPESK.-
R2/RRR2-7/3	1627.549	1627.775	-139.037	0.385	1909.515	0.294	30	0.634	K.EKAESAPAEPLKDEL.-
R2/RRR2-7/1	1037.539	1038.133	-1541.050	0.177	685.582	0.254	11	0.457	K.DFDVTALEK.F
R2/RRR2-7/1	1037.504	1038.133	-1574.380	0.226	569.748	0.338	11	0.377	K.DFDVTALEK.F
R2/RRR2-7/1	1037.482	1038.133	-1596.010	0.194	516.225	0.257	10	0.319	K.DFDVTALEK.F
R2/RRR2-7/2	1489.317	1489.700	-257.614	0.523	1756.431	0.570	20	0.239	K.VVVADNVHDFVFK.S
R2/RRR2-7/2	1446.100	1446.542	-306.799	0.545	1921.212	0.454	19	0.230	K.SPEDATNLIDDKK.I
R2/RRR2-7/2	1523.142	1522.730	271.167	0.499	1528.131	0.558	20	0.203	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/2	1523.281	1522.730	-295.756	0.504	1446.266	0.585	20	0.200	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/2	1445.804	1446.542	-1205.953	0.504	1755.458	0.416	20	0.199	K.SPEDATNLIDDKK.I
R2/RRR2-7/2	1488.708	1489.700	-1341.770	0.501	1447.146	0.567	20	0.199	K.VVVADNVHDFVFK.S
R2/RRR2-7/2	1279.029	1279.464	-341.226	0.493	1522.579	0.487	17	0.189	R.TADEIVDFIKK.N
R2/RRR2-7/2	1523.239	1522.730	-323.173	0.543	1421.153	0.542	20	0.188	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/2	1489.322	1489.700	-254.078	0.517	1438.986	0.526	19	0.188	K.VVVADNVHDFVFK.S
R2/RRR2-7/2	1878.499	1878.071	228.343	0.513	1494.837	0.504	20	0.186	K.SVYYGAAEEFKDKEIK.F
R2/RRR2-7/3	1880.847	1881.000	-81.776	0.508	1423.852	0.595	30	0.180	R.SDYDFGHTLHANHLPR.G
R2/RRR2-7/2	1877.471	1878.071	-855.055	0.498	1484.078	0.475	20	0.178	K.SVYYGAAEEFKDKEIK.F
R2/RRR2-7/3	1880.521	1881.000	-255.627	0.480	1442.949	0.584	32	0.178	R.SDYDFGHTLHANHLPR.G
R2/RRR2-7/2	1279.122	1279.464	-267.976	0.469	1509.665	0.430	17	0.175	R.TADEIVDFIKK.N
R2/RRR2-7/2	1196.342	1196.377	-29.332	0.415	1383.818	0.440	16	0.165	K.YEIQGFPTLK.I
R2/RRR2-7/2	1878.347	1878.071	147.274	0.489	1266.476	0.475	19	0.157	K.SVYYGAAEEFKDKEIK.F
R2/RRR2-7/2	1279.129	1279.464	-262.423	0.485	1280.784	0.436	15	0.153	R.TADEIVDFIKK.N
R2/RRR2-7/3	1522.247	1522.730	-317.883	0.443	2029.475	0.254	29	0.152	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/2	1196.082	1196.377	-246.864	0.381	1245.479	0.423	15	0.149	K.YEIQGFPTLK.I
R2/RRR2-7/2	1151.058	1151.291	-203.016	0.528	1087.327	0.467	16	0.149	R.TADEIVDFIK.K
R2/RRR2-7/2	1150.995	1151.291	-258.342	0.456	1229.511	0.414	16	0.148	R.TADEIVDFIK.K
R2/RRR2-7/2	975.960	976.063	-105.770	0.475	1337.175	0.362	15	0.148	K.SDEDVVIAK.M
R2/RRR2-7/2	1446.075	1446.542	-323.907	0.511	1286.665	0.394	19	0.147	K.SPEDATNLIDDKK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/3	1523.082	1522.730	231.779	0.437	1997.360	0.239	29	0.143	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/2	975.480	976.063	-1627.807	0.422	1399.766	0.295	15	0.141	K.SDEDVVIAK.M
R2/RRR2-7/2	976.302	976.063	245.411	0.513	1236.763	0.346	15	0.138	K.SDEDVVIAK.M
R2/RRR2-7/2	1195.655	1196.377	-1443.919	0.359	1155.098	0.397	15	0.138	K.YEIQGFPTLK.I
R2/RRR2-7/3	1880.815	1881.000	-98.963	0.518	973.104	0.613	29	0.135	R.SDYDFGHTLHANHLPR.G
R2/RRR2-7/2	1280.257	1279.464	-161.967	0.430	376.044	0.518	17	0.128	R.EAEGIVEYLKK.Q
R2/RRR2-7/3	1522.369	1522.730	-237.875	0.397	1877.075	0.229	27	0.128	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/2	1150.558	1151.291	-1510.731	0.393	1108.017	0.312	16	0.125	R.TADEIVDFIK.K
R2/RRR2-7/2	1453.161	1452.591	-297.136	0.441	488.806	0.494	18	0.125	K.SEPIPEVNNEPVK.V
R2/RRR2-7/2	1104.950	1105.229	-252.819	0.422	719.197	0.405	14	0.123	K.NIQEYKGPR.E
R2/RRR2-7/2	1104.852	1105.229	-341.938	0.353	972.493	0.341	15	0.122	K.NIQEYKGPR.E
R2/RRR2-7/2	1453.021	1452.591	296.640	0.428	356.314	0.509	16	0.122	K.SEPIPEVNNEPVK.V
R2/RRR2-7/2	1717.538	1717.990	-263.944	0.459	475.649	0.535	17	0.122	K.AAQELSKHDPPIVLAK.V
R2/RRR2-7/2	1452.210	1452.591	-263.522	0.440	348.457	0.498	16	0.122	K.SEPIPEVNNEPVK.V
R2/RRR2-7/2	965.839	966.070	-240.238	0.358	669.781	0.405	15	0.121	K.FIDASSTPK.V
R2/RRR2-7/2	1718.741	1717.990	-145.864	0.480	415.419	0.549	16	0.121	K.AAQELSKHDPPIVLAK.V
R2/RRR2-7/2	1717.376	1717.990	-942.748	0.484	483.634	0.521	17	0.121	K.AAQELSKHDPPIVLAK.V
R2/RRR2-7/2	1452.265	1452.591	-225.742	0.411	466.451	0.453	18	0.120	K.SEPIPEVNNEPVK.V
R2/RRR2-7/2	989.525	990.181	-1678.261	0.388	371.799	0.478	12	0.120	K.HDPPIVLAK.V
R2/RRR2-7/3	1446.383	1446.542	-110.106	0.504	1249.282	0.458	27	0.120	K.SPEDATNLIDDKK.I
R2/RRR2-2/2	966.983	966.070	-90.165	0.390	631.537	0.379	16	0.119	-.FIDASSTPK.-
R2/RRR2-7/2	1104.846	1105.229	-347.925	0.343	833.785	0.344	15	0.118	K.NIQEYKGPR.E
R2/RRR2-7/2	989.601	990.181	-1601.052	0.371	441.216	0.419	13	0.118	K.HDPPIVLAK.V
R2/RRR2-7/2	966.018	966.070	-54.387	0.340	570.180	0.359	15	0.117	K.FIDASSTPK.V
R2/RRR2-7/2	989.993	990.181	-190.534	0.361	511.089	0.390	14	0.117	K.HDPPIVLAK.V
R2/RRR2-7/2	1280.248	1279.464	-169.237	0.363	296.003	0.306	16	0.117	R.EAEGIVEYLKK.Q
R2/RRR2-7/2	965.866	966.070	-211.709	0.385	624.479	0.342	16	0.116	-.FIDASSTPK.-
R2/RRR2-7/2	1279.287	1279.464	-138.833	0.363	398.794	0.328	17	0.116	R.EAEGIVEYLKK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1523.320	1522.730	-270.028	0.392	760.563	0.396	14	0.116	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/3	1538.521	1537.781	-169.644	0.577	1314.579	0.398	25	0.112	-.LFKPFDELVVDSK.-
R2/RRR2-7/3	1446.764	1446.542	154.089	0.492	1049.749	0.485	25	0.112	K.SPEDATNLIDDKK.I
R2/RRR2-7/2	1523.119	1522.730	256.059	0.295	363.899	0.402	14	0.112	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/3	1446.536	1446.542	-4.335	0.567	1264.858	0.416	27	0.111	K.SPEDATNLIDDKK.I
R2/RRR2-1/2	1523.197	1522.730	307.811	0.270	582.208	0.386	15	0.111	K.AHVEPDQIVSWLK.Q
R2/RRR2-7/2	1038.470	1038.133	325.806	0.366	815.061	0.252	14	0.109	-.DFDVTALEK.-
R2/RRR2-2/2	1523.813	1522.730	54.749	0.365	411.719	0.410	12	0.109	-.AHVEPDQIVSWLK.-
R2/RRR2-7/2	1037.399	1038.133	-1675.874	0.282	734.285	0.278	13	0.107	K.DFDVTALEK.F
R2/RRR2-7/2	1524.191	1522.730	303.433	0.270	472.106	0.290	13	0.106	K.AHVEPDQIVSWLK.Q
R2/RRR2-1/2	965.338	966.070	-1799.391	0.252	667.996	0.137	15	0.106	K.FIDASSTPK.V
R2/RRR2-1/2	966.064	966.070	-6.478	0.339	436.210	0.246	13	0.105	-.FIDASSTPK.-
R2/RRR2-7/2	1524.119	1522.730	256.132	0.237	618.235	0.279	14	0.105	K.AHVEPDQIVSWLK.Q
R2/RRR2-3/2	1523.785	1522.730	36.430	0.300	216.797	0.370	12	0.104	-.AHVEPDQIVSWLK.-
R2/RRR2-5/2	1279.521	1279.464	44.437	0.209	641.157	0.235	14	0.102	R.TADEIVDFIKK.N
R2/RRR2-7/2	1280.347	1279.464	-91.765	0.225	607.345	0.124	12	0.100	-.EAEGIVEYLKK.-
R2/RRR2-7/3	1538.001	1537.781	143.435	0.502	1158.437	0.377	24	0.096	-.LFKPFDELVVDSK.-
R2/RRR2-3/3	1446.554	1446.542	8.234	0.464	971.883	0.421	22	0.096	K.SPEDATNLIDDKK.I
R2/RRR2-7/3	1817.465	1816.988	263.422	0.453	964.322	0.427	25	0.095	K.EIKSPEDATNLIDDKK.I
R2/RRR2-3/3	1446.071	1446.542	-326.415	0.407	803.501	0.458	22	0.094	K.SPEDATNLIDDKK.I
R2/RRR2-3/2	1523.629	1522.730	-66.586	0.275	170.396	0.430	10	0.084	-.AHVEPDQIVSWLK.-
R2/RRR2-7/3	1816.322	1816.988	-919.777	0.392	666.013	0.421	22	0.080	K.EIKSPEDATNLIDDKK.I
R2/RRR2-2/2	965.741	966.070	-342.066	0.343	315.634	0.306	11	0.074	-.FIDASSTPK.-
R2/RRR2-6/3	1446.198	1446.542	-238.509	0.364	718.280	0.286	20	0.072	K.SPEDATNLIDDKK.I
R2/RRR2-5/3	1977.566	1978.201	-829.118	0.608	4324.969	0.514	37	1.000	R.KAEHAFYLDWAVHSFR.I
R2/RRR2-5/3	1978.120	1978.201	-41.081	0.609	3924.909	0.544	38	0.841	R.KAEHAFYLDWAVHSFR.I
R2/RRR2-5/2	1991.322	1992.176	-933.688	0.585	3735.892	0.578	26	0.721	K.IQEELDIDVLVHGEPER.N
R2/RRR2-5/2	1968.666	1969.179	-771.040	0.629	3740.593	0.559	27	0.710	K.KISEDEYVSAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1557.124	1556.618	-318.499	0.572	3680.872	0.568	25	0.698	K.DEAYFAANAAAQASR.R
R2/RRR2-5/2	1968.621	1969.179	-793.696	0.610	3565.184	0.559	26	0.653	K.KISEDEYVSAIKEEISK.V
R2/RRR2-5/2	1850.549	1850.028	-259.727	0.623	3305.788	0.616	24	0.598	K.AEHAFYLDWAVHSFR.I
R2/RRR2-5/2	1556.079	1556.618	-992.395	0.455	3422.712	0.509	25	0.590	K.DEAYFAANAAAQASR.R
R2/RRR2-5/1	1021.569	1022.181	-1582.998	0.197	810.054	0.253	12	0.582	K.SWLAFAAQK.V
R2/RRR2-5/3	1978.115	1978.201	-43.681	0.597	3258.942	0.534	36	0.582	R.KAEHAFYLDWAVHSFR.I
R2/RRR2-5/2	1556.222	1556.618	-255.665	0.452	3338.512	0.486	25	0.554	K.DEAYFAANAAAQASR.R
R2/RRR2-5/2	1991.404	1992.176	-892.579	0.601	3185.163	0.574	26	0.546	K.IQEELDIDVLVHGEPER.N
R2/RRR2-5/2	1849.420	1850.028	-871.664	0.648	3011.877	0.628	23	0.519	K.AEHAFYLDWAVHSFR.I
R2/RRR2-5/2	1850.514	1850.028	263.621	0.636	2986.640	0.618	23	0.508	K.AEHAFYLDWAVHSFR.I
R2/RRR2-5/2	1992.422	1992.176	124.094	0.634	3117.372	0.535	26	0.507	K.IQEELDIDVLVHGEPER.N
R2/RRR2-5/1	1021.558	1022.181	-1594.402	0.140	727.669	0.271	12	0.495	K.SWLAFAAQK.V
R2/RRR2-5/2	1969.523	1969.179	175.145	0.636	2914.154	0.566	26	0.467	K.KISEDEYVSAIKEEISK.V
R2/RRR2-4/2	1808.487	1808.137	194.239	0.608	2825.645	0.590	25	0.443	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/2	1807.489	1808.137	-914.667	0.571	2652.474	0.606	25	0.410	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/2	1808.445	1808.137	170.954	0.605	2523.889	0.655	23	0.399	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/1	1021.501	1022.181	-1649.985	0.211	594.772	0.325	11	0.394	K.SWLAFAAQK.V
R2/RRR2-2/2	1807.733	1808.137	-224.314	0.539	2568.180	0.566	24	0.377	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-1/2	1807.859	1808.137	-154.068	0.573	2426.074	0.619	24	0.365	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-1/2	1807.553	1808.137	-879.074	0.555	2513.425	0.568	24	0.365	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-4/2	1808.930	1808.137	-115.059	0.607	2472.973	0.578	23	0.358	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/2	1792.713	1792.138	-237.578	0.596	2390.441	0.611	23	0.353	K.GMLTGPVTILNWSFVR.N
R2/RRR2-5/2	1808.456	1808.137	176.843	0.599	2341.030	0.635	23	0.352	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-6/2	1807.690	1808.137	-248.026	0.544	2230.312	0.592	23	0.316	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/2	1807.466	1808.137	-927.414	0.545	2269.376	0.562	23	0.314	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/2	1791.534	1792.138	-897.984	0.559	2164.928	0.524	23	0.282	K.GMLTGPVTILNWSFVR.N
R2/RRR2-6/2	1808.020	1808.137	-64.734	0.584	1938.229	0.600	22	0.266	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/3	1807.753	1808.137	-212.907	0.478	2245.601	0.429	31	0.260	K.GM*LTGPVTILNWSFVR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/1	1021.518	1022.181	-1632.937	0.124	432.018	0.233	10	0.258	-.SWLAFAAQK.-
R2/RRR2-5/3	1809.179	1808.137	23.346	0.593	2052.384	0.516	32	0.252	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-4/2	1806.938	1808.137	-1220.472	0.501	1862.093	0.564	22	0.245	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-6/2	1807.601	1808.137	-852.566	0.535	1795.235	0.588	21	0.241	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/3	1850.592	1850.028	-236.142	0.554	2055.489	0.470	31	0.236	K.AEHAFYLDWAVHSFR.I
R2/RRR2-5/2	1791.234	1792.138	-1066.078	0.504	1833.726	0.529	21	0.231	K.GMLTGPVTILNWSFVR.N
R2/RRR2-3/2	1807.565	1808.137	-872.362	0.508	1772.878	0.561	20	0.230	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/3	1850.674	1850.028	-191.674	0.544	1959.231	0.479	30	0.224	K.AEHAFYLDWAVHSFR.I
R2/RRR2-4/2	1792.774	1792.138	-203.696	0.561	1778.919	0.530	22	0.223	K.GMLTGPVTILNWSFVR.N
R2/RRR2-2/2	1851.191	1850.028	88.652	0.487	1678.357	0.524	21	0.214	K.AEHAFYLDWAVHSFR.I
R2/RRR2-5/2	1584.567	1585.862	-1453.075	0.499	1786.974	0.394	21	0.199	R.FETCYQIALAIKK.E
R2/RRR2-5/2	1585.452	1585.862	-259.832	0.547	1578.716	0.494	21	0.198	R.FETCYQIALAIKK.E
R2/RRR2-5/2	1457.318	1457.689	-255.541	0.532	1578.721	0.481	20	0.195	R.FETCYQIALAIK.K
R2/RRR2-1/2	1809.895	1808.137	-134.412	0.539	1569.123	0.511	19	0.190	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/3	1739.777	1740.015	-136.763	0.481	1693.479	0.513	34	0.189	K.YTEVKPALTNM*VSAAK.L
R2/RRR2-5/2	1456.626	1457.689	-1420.999	0.433	1555.721	0.451	20	0.185	R.FETCYQIALAIK.K
R2/RRR2-5/3	1739.291	1740.015	-993.819	0.438	1607.728	0.524	33	0.181	K.YTEVKPALTNM*VSAAK.L
R2/RRR2-5/2	1740.460	1740.015	256.469	0.540	1267.595	0.549	24	0.176	K.YTEVKPALTNM*VSAAK.L
R2/RRR2-5/2	1841.537	1841.006	-255.480	0.537	1548.523	0.413	22	0.172	K.ISEDEYVSAIKEEISK.V
R2/RRR2-5/2	1867.576	1868.188	-865.363	0.532	1078.471	0.605	25	0.170	R.KYTEVKPALTNM*VSAAK.L
R2/RRR2-5/2	1485.724	1486.653	-1302.107	0.461	1555.682	0.367	20	0.166	R.IPSTEEIADRINK.M
R2/RRR2-5/3	1807.851	1808.137	-158.648	0.413	1786.079	0.385	29	0.166	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-5/2	1660.226	1659.826	241.402	0.506	1287.911	0.505	22	0.166	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/2	1659.425	1659.826	-242.863	0.451	1247.008	0.515	21	0.163	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/2	1457.225	1457.689	-319.328	0.507	1379.940	0.416	20	0.161	R.FETCYQIALAIK.K
R2/RRR2-5/2	1659.382	1659.826	-268.768	0.469	1261.760	0.492	21	0.160	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/2	1739.369	1740.015	-948.963	0.501	1086.492	0.550	22	0.159	K.YTEVKPALTNM*VSAAK.L
R2/RRR2-5/2	1739.413	1740.015	-923.458	0.487	1086.506	0.545	22	0.158	K.YTEVKPALTNM*VSAAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/3	1968.779	1969.179	-203.714	0.510	1549.692	0.460	32	0.156	K.KISEDEYVSAIKEEISK.V
R2/RRR2-5/2	1194.194	1194.362	-141.652	0.507	1185.533	0.456	16	0.153	R.SDEKLLSVFR.E
R2/RRR2-5/2	1841.708	1841.006	-162.251	0.527	1207.652	0.439	20	0.145	K.ISEDEYVSAIKEEISK.V
R2/RRR2-5/2	1866.955	1868.188	-1199.655	0.474	853.332	0.559	23	0.144	R.KYTEVKPALTNM*VSAAK.L
R2/RRR2-5/3	1725.274	1724.015	150.398	0.451	1107.785	0.590	29	0.141	K.YTEVKPALTNMVSAAK.L
R2/RRR2-5/2	1867.387	1868.188	-967.340	0.520	729.903	0.567	22	0.139	R.KYTEVKPALTNM*VSAAK.L
R2/RRR2-5/2	1840.503	1841.006	-819.143	0.529	1131.719	0.438	19	0.139	K.ISEDEYVSAIKEEISK.V
R2/RRR2-3/2	1131.067	1131.218	-133.861	0.477	878.912	0.461	17	0.138	R.IPSTEEIADR.I
R2/RRR2-4/2	1130.528	1131.218	-1499.917	0.477	820.544	0.473	17	0.137	R.IPSTEEIADR.I
R2/RRR2-4/2	1130.935	1131.218	-250.799	0.477	855.329	0.460	17	0.137	R.IPSTEEIADR.I
R2/RRR2-5/2	1131.013	1131.218	-182.366	0.487	825.410	0.459	17	0.136	R.IPSTEEIADR.I
R2/RRR2-5/2	1131.022	1131.218	-174.137	0.500	686.640	0.498	16	0.136	R.IPSTEEIADR.I
R2/RRR2-5/2	1194.048	1194.362	-263.793	0.526	1084.633	0.388	16	0.135	R.SDEKLLSVFR.E
R2/RRR2-5/2	1021.571	1022.181	-1581.450	0.417	1175.123	0.346	14	0.134	K.SWLAFAAQK.V
R2/RRR2-2/2	1130.897	1131.218	-284.911	0.480	717.015	0.469	16	0.133	R.IPSTEEIADR.I
R2/RRR2-6/2	1660.084	1659.826	155.501	0.423	922.701	0.484	18	0.133	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-1/2	1130.468	1131.218	-1552.524	0.431	674.106	0.490	16	0.132	R.IPSTEEIADR.I
R2/RRR2-2/2	1130.888	1131.218	-293.033	0.460	873.276	0.420	17	0.132	R.IPSTEEIADR.I
R2/RRR2-10/3	1660.327	1659.826	-301.401	0.431	848.878	0.628	26	0.132	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-4/2	1130.795	1131.218	-375.563	0.461	708.856	0.457	16	0.131	R.IPSTEEIADR.I
R2/RRR2-5/2	1022.041	1022.181	-138.018	0.427	1119.925	0.343	14	0.130	K.SWLAFAAQK.V
R2/RRR2-5/2	1130.524	1131.218	-1502.954	0.458	785.451	0.417	17	0.130	R.IPSTEEIADR.I
R2/RRR2-5/2	1487.341	1486.653	-210.046	0.508	849.968	0.463	16	0.129	R.IPSTEEIADRINK.M
R2/RRR2-3/2	1659.453	1659.826	-225.594	0.438	809.046	0.492	17	0.127	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-7/2	1131.517	1131.218	265.146	0.460	613.625	0.434	15	0.126	R.IPSTEEIADR.I
R2/RRR2-6/3	1659.215	1659.826	-973.810	0.429	866.655	0.595	28	0.125	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-1/2	942.960	943.123	-172.640	0.433	450.049	0.451	13	0.125	K.VVEVNALAK.A
R2/RRR2-6/2	1659.808	1659.826	-11.257	0.337	757.233	0.515	17	0.125	K.YGAGIGPGVYDIHSPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	942.597	943.123	-1623.479	0.404	388.973	0.482	12	0.124	K.VVEVNALAK.A
R2/RRR2-3/2	1130.866	1131.218	-312.202	0.381	633.699	0.440	15	0.124	R.IPSTEEIADR.I
R2/RRR2-3/2	942.343	943.123	-1893.776	0.367	422.857	0.474	13	0.124	K.VVEVNALAK.A
R2/RRR2-2/2	942.570	943.123	-1652.233	0.378	365.763	0.472	12	0.123	K.VVEVNALAK.A
R2/RRR2-5/2	1487.110	1486.653	308.530	0.462	934.928	0.381	17	0.123	R.IPSTEEIADRINK.M
R2/RRR2-1/2	1130.975	1131.218	-216.040	0.457	646.237	0.392	15	0.122	R.IPSTEEIADR.I
R2/RRR2-5/2	943.014	943.123	-115.113	0.359	500.105	0.429	14	0.122	K.VVEVNALAK.A
R2/RRR2-2/2	942.485	943.123	-1743.058	0.379	407.368	0.451	12	0.122	K.VVEVNALAK.A
R2/RRR2-5/2	1021.195	1022.181	-1951.190	0.333	1152.305	0.271	14	0.122	K.SWLAFAAQK.V
R2/RRR2-4/3	1659.749	1659.826	-47.080	0.458	840.935	0.584	28	0.122	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-1/2	1131.181	1131.218	-32.970	0.439	647.525	0.383	15	0.121	R.IPSTEEIADR.I
R2/RRR2-4/2	942.747	943.123	-399.046	0.353	443.594	0.436	13	0.121	K.VVEVNALAK.A
R2/RRR2-5/2	942.917	943.123	-218.874	0.379	648.570	0.371	15	0.121	K.VVEVNALAK.A
R2/RRR2-1/2	942.974	943.123	-157.836	0.357	573.419	0.401	14	0.121	K.VVEVNALAK.A
R2/RRR2-1/2	942.617	943.123	-1601.752	0.345	551.015	0.400	14	0.120	K.VVEVNALAK.A
R2/RRR2-5/3	1659.553	1659.826	-165.055	0.457	839.392	0.574	27	0.120	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-2/2	1130.209	1131.218	-1782.975	0.372	537.692	0.371	14	0.118	R.IPSTEEIADR.I
R2/RRR2-14/2	1132.145	1131.218	-65.062	0.409	563.325	0.360	14	0.118	R.IPSTEEIADR.I
R2/RRR2-5/2	1808.917	1808.137	-121.828	0.437	722.344	0.437	16	0.117	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-4/2	943.151	943.123	30.428	0.325	405.200	0.387	12	0.117	K.VVEVNALAK.A
R2/RRR2-3/2	942.183	943.123	-2064.332	0.315	341.371	0.424	11	0.117	K.VVEVNALAK.A
R2/RRR2-5/3	1660.976	1659.826	90.136	0.473	664.903	0.602	27	0.116	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-2/3	1659.085	1659.826	-1052.702	0.456	633.754	0.609	26	0.116	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-3/2	942.884	943.123	-253.812	0.319	390.402	0.326	12	0.116	K.VVEVNALAK.A
R2/RRR2-4/2	942.946	943.123	-187.445	0.272	355.812	0.296	12	0.115	K.VVEVNALAK.A
R2/RRR2-2/3	1659.202	1659.826	-981.787	0.443	526.474	0.624	23	0.114	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-4/3	1660.027	1659.826	121.201	0.501	551.319	0.602	24	0.112	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/2	1131.251	1131.218	29.048	0.283	532.184	0.255	14	0.111	R.IPSTEEIADR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	942.831	943.123	-310.446	0.283	412.448	0.294	12	0.111	-.VVEVNALAK.-
R2/RRR2-14/2	1132.166	1131.218	-45.919	0.355	446.586	0.249	13	0.111	-.IPSTEEIADR.-
R2/RRR2-5/2	1023.117	1022.181	-63.199	0.409	982.931	0.217	14	0.110	K.SWLAFAAQK.V
R2/RRR2-2/2	1194.426	1194.362	53.446	0.440	610.204	0.313	13	0.110	R.SDEKLLSVFR.E
R2/RRR2-6/3	1659.956	1659.826	78.058	0.431	583.124	0.582	25	0.109	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-4/3	1659.424	1659.826	-243.314	0.390	635.561	0.569	25	0.108	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/2	1808.946	1808.137	-105.785	0.347	549.100	0.345	15	0.107	K.GM*LTGPVTILNWSFVR.N
R2/RRR2-1/3	1659.194	1659.826	-986.884	0.405	495.136	0.590	22	0.107	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-3/3	1659.817	1659.826	-5.807	0.408	607.699	0.563	25	0.107	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-9/3	1660.559	1659.826	-161.453	0.440	502.761	0.584	22	0.107	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/3	1978.468	1978.201	135.390	0.444	1208.604	0.398	25	0.106	R.KAEHAFYLDWAVHSFR.I
R2/RRR2-10/3	1659.848	1659.826	13.114	0.417	522.493	0.574	24	0.106	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-6/3	1659.222	1659.826	-970.154	0.411	562.974	0.566	24	0.106	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-4/2	1022.199	1022.181	17.474	0.198	836.203	0.258	11	0.106	-.SWLAFAAQK.-
R2/RRR2-5/3	1659.734	1659.826	-55.822	0.443	517.337	0.552	24	0.103	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/3	1739.612	1740.015	-232.002	0.433	1120.073	0.416	30	0.102	K.YTEVKPALTNM*VSAAK.L
R2/RRR2-5/3	1991.657	1992.176	-765.097	0.461	616.377	0.555	30	0.101	K.IQEELDIDVLVHGEPER.N
R2/RRR2-1/3	1660.846	1659.826	11.853	0.429	490.662	0.538	25	0.101	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/3	1659.289	1659.826	-929.161	0.401	680.614	0.505	24	0.100	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/3	1708.152	1707.951	118.002	0.429	1263.935	0.354	27	0.100	K.LDSEIKSWLAFAAQK.V
R2/RRR2-5/3	1194.332	1194.362	-25.497	0.478	1321.925	0.337	21	0.098	R.SDEKLLSVFR.E
R2/RRR2-5/3	1992.614	1992.176	220.667	0.494	556.549	0.533	30	0.098	K.IQEELDIDVLVHGEPER.N
R2/RRR2-5/3	1868.163	1868.188	-13.033	0.495	730.878	0.494	29	0.097	R.KYTEVKPALTNM*VSAAK.L
R2/RRR2-5/3	1659.079	1659.826	-1056.470	0.439	523.573	0.484	25	0.096	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/3	1194.556	1194.362	162.535	0.496	1144.298	0.365	20	0.094	R.SDEKLLSVFR.E
R2/RRR2-7/3	1658.761	1659.826	-1248.657	0.365	451.159	0.481	21	0.093	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-7/3	1658.811	1659.826	-1218.616	0.378	427.703	0.470	21	0.092	K.YGAGIGPGVYDIHSPR.I
R2/RRR2-5/3	1852.113	1852.188	-40.703	0.445	597.044	0.487	26	0.091	R.KYTEVKPALTNMVSAAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/3	1659.499	1659.826	-197.597	0.384	332.471	0.487	20	0.090	-.YGAGIGPGVYDIHSPR.-
R2/RRR2-5/3	1992.602	1992.176	214.677	0.467	503.629	0.489	27	0.090	K.IQEELDIDVLVHGEPER.N
R2/RRR2-5/3	1868.307	1868.188	64.133	0.491	683.406	0.451	27	0.089	R.KYTEVKPALTNM*VSAAK.L
R2/RRR2-5/3	1991.727	1992.176	-226.263	0.451	449.790	0.522	26	0.089	-.IQEELDIDVLVHGEPER.-
R2/RRR2-5/3	1194.422	1194.362	50.001	0.519	1116.985	0.346	20	0.089	R.SDEKLLSVFR.E
R2/RRR2-5/3	1867.902	1868.188	-153.438	0.476	411.922	0.489	24	0.089	R.KYTEVKPALTNM*VSAAK.L
R2/RRR2-5/3	1456.806	1457.689	-1296.699	0.411	1154.437	0.325	23	0.086	R.FETCYQIALAIK.K
R2/RRR2-5/3	1791.679	1792.138	-256.515	0.391	454.867	0.375	25	0.079	K.GMLTGPVTILNWSFVR.N
R2/RRR2-3/3	1658.896	1659.826	-1167.074	0.341	394.216	0.370	21	0.079	-.YGAGIGPGVYDIHSPR.-
R2/RRR2-5/3	1708.134	1707.951	107.789	0.331	676.016	0.388	22	0.077	K.LDSEIKSWLAFAAQK.V
R2/RRR2-5/3	1969.674	1969.179	252.328	0.382	690.490	0.376	25	0.076	K.KISEDEYVSAIKEEISK.V
R2/RRR2-1/3	1194.943	1194.362	-351.980	0.377	904.750	0.312	18	0.075	-.SDEKLLSVFR.-
R2/RRR2-5/3	1707.417	1707.951	-901.035	0.373	661.115	0.303	22	0.071	K.LDSEIKSWLAFAAQK.V
R2/RRR2-6/2	1967.710	1968.236	-777.637	0.621	2318.435	0.562	25	0.331	R.VQQLLQDFFNGKELCK.S
R2/RRR2-6/2	1413.182	1413.562	-269.240	0.500	2136.772	0.582	21	0.304	K.SSVHDVVLVGGSTR.I
R2/RRR2-6/2	1437.247	1437.625	-263.369	0.567	2265.899	0.473	19	0.288	R.VQQLLQDFFNGK.E
R2/RRR2-6/2	1967.540	1968.236	-864.450	0.582	2069.007	0.549	23	0.281	R.VQQLLQDFFNGKELCK.S
R2/RRR2-6/2	1215.942	1216.436	-407.968	0.500	2158.738	0.485	21	0.277	K.DAGVIAGLNVMR.I
R2/RRR2-6/2	1437.545	1437.625	-55.839	0.545	2084.727	0.481	18	0.260	R.VQQLLQDFFNGK.E
R2/RRR2-6/2	1413.313	1413.562	-176.693	0.502	1846.428	0.591	21	0.257	K.SSVHDVVLVGGSTR.I
R2/RRR2-6/2	1438.466	1437.625	-110.958	0.579	1975.654	0.528	19	0.257	R.VQQLLQDFFNGK.E
R2/RRR2-6/2	1676.299	1676.683	-229.536	0.500	1881.847	0.556	23	0.252	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/2	1437.991	1437.625	255.381	0.606	1970.743	0.512	18	0.250	R.VQQLLQDFFNGK.E
R2/RRR2-6/2	1309.770	1309.490	214.665	0.487	1897.555	0.505	20	0.243	R.EIAEAYLGTTIK.N
R2/RRR2-5/2	1676.312	1676.683	-221.938	0.486	1714.886	0.541	22	0.223	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/2	1197.045	1197.277	-194.092	0.558	1793.337	0.491	18	0.222	R.FSDASVQSDIK.L
R2/RRR2-6/2	1196.967	1197.277	-259.570	0.516	1816.410	0.473	18	0.221	R.FSDASVQSDIK.L
R2/RRR2-6/2	1967.666	1968.236	-800.180	0.594	1534.797	0.596	22	0.214	R.VQQLLQDFFNGKELCK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1309.228	1309.490	-201.028	0.385	1725.818	0.493	19	0.214	R.EIAEAYLGTTIK.N
R2/RRR2-6/2	1676.225	1676.683	-273.664	0.476	1696.412	0.512	22	0.213	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/2	1216.057	1216.436	-312.481	0.452	1807.214	0.431	20	0.209	K.DAGVIAGLNVMR.I
R2/RRR2-5/2	1413.294	1413.562	-189.864	0.452	1641.881	0.518	21	0.209	K.SSVHDVVLVGGSTR.I
R2/RRR2-6/2	1232.163	1232.436	-221.483	0.525	1796.112	0.422	20	0.205	K.DAGVIAGLNVM*R.I
R2/RRR2-6/2	1215.627	1216.436	-1492.412	0.469	1708.885	0.462	20	0.204	K.DAGVIAGLNVMR.I
R2/RRR2-6/2	1197.170	1197.277	-89.141	0.511	1681.628	0.464	18	0.201	R.FSDASVQSDIK.L
R2/RRR2-6/2	1413.158	1413.562	-286.226	0.473	1450.671	0.571	19	0.197	K.SSVHDVVLVGGSTR.I
R2/RRR2-6/3	1681.552	1681.830	-166.099	0.489	1592.441	0.555	28	0.193	K.NAVVTVPAYFNDSQR.Q
R2/RRR2-10/2	1437.458	1437.625	-116.061	0.551	1512.303	0.509	17	0.189	R.VQQLLQDFFNGK.E
R2/RRR2-6/2	1232.087	1232.436	-283.704	0.486	1734.111	0.380	20	0.188	K.DAGVIAGLNVM*R.I
R2/RRR2-6/2	1676.289	1676.683	-235.599	0.491	1417.638	0.549	21	0.188	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/3	1804.745	1804.019	-152.039	0.499	1770.761	0.444	30	0.186	K.M*DKSSVHDVVLVGGSTR.I
R2/RRR2-6/2	1233.010	1232.436	-346.149	0.526	1618.367	0.399	19	0.178	K.DAGVIAGLNVM*R.I
R2/RRR2-6/2	1437.712	1437.625	61.179	0.528	1204.075	0.477	17	0.154	R.VQQLLQDFFNGK.E
R2/RRR2-4/2	1437.570	1437.625	-38.378	0.505	1027.535	0.504	15	0.144	R.VQQLLQDFFNGK.E
R2/RRR2-6/2	1583.522	1582.844	-203.616	0.561	1054.147	0.469	21	0.144	K.QFAAEEISSM*VLIK.M
R2/RRR2-6/2	1541.544	1541.757	-138.168	0.476	1162.479	0.411	19	0.143	R.ARFEELNMDLFR.K
R2/RRR2-6/2	1541.805	1541.757	31.398	0.526	1004.539	0.456	18	0.140	R.ARFEELNMDLFR.K
R2/RRR2-6/2	1308.505	1309.490	-1521.408	0.283	1160.724	0.438	16	0.140	R.EIAEAYLGTTIK.N
R2/RRR2-6/3	1669.726	1669.929	-122.363	0.548	1685.516	0.361	25	0.139	R.ARFEELNMDLFRK.C
R2/RRR2-6/2	1566.455	1566.844	-249.266	0.529	1098.218	0.404	22	0.137	K.QFAAEEISSMVLIK.M
R2/RRR2-6/2	1582.474	1582.844	-234.235	0.524	978.257	0.451	19	0.135	K.QFAAEEISSM*VLIK.M
R2/RRR2-1/2	1676.516	1676.683	-99.731	0.461	919.666	0.492	19	0.135	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/2	1566.454	1566.844	-250.165	0.531	1140.990	0.365	22	0.133	K.QFAAEEISSMVLIK.M
R2/RRR2-1/2	1437.635	1437.625	7.272	0.460	947.499	0.436	16	0.131	R.VQQLLQDFFNGK.E
R2/RRR2-6/2	1612.385	1612.873	-303.722	0.533	589.990	0.494	22	0.131	K.M*REIAEAYLGTTIK.N
R2/RRR2-6/2	1868.651	1869.109	-246.007	0.469	685.664	0.536	17	0.128	R.FSDASVQSDIKLWPFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1541.117	1541.757	-1067.255	0.426	886.534	0.420	17	0.127	R.ARFEELNMDLFR.K
R2/RRR2-6/2	1868.721	1869.109	-208.390	0.500	751.202	0.489	18	0.126	R.FSDASVQSDIKLWPFK.V
R2/RRR2-6/2	1612.658	1612.873	-133.832	0.498	593.704	0.448	22	0.126	K.M*REIAEAYLGTTIK.N
R2/RRR2-6/3	1677.804	1676.683	72.265	0.487	834.242	0.617	30	0.125	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/2	1612.368	1612.873	-936.270	0.463	542.944	0.454	21	0.124	K.M*REIAEAYLGTTIK.N
R2/RRR2-6/2	1296.048	1295.492	-343.275	0.482	531.140	0.456	14	0.123	R.M*VNHFVQEFK.R
R2/RRR2-6/2	1681.500	1681.830	-197.224	0.399	540.663	0.498	20	0.123	K.NAVVTVPAYFNDSQR.Q
R2/RRR2-2/2	1197.654	1197.277	315.931	0.296	702.031	0.480	15	0.121	R.FSDASVQSDIK.L
R2/RRR2-6/2	1582.195	1582.844	-1044.873	0.438	869.513	0.378	19	0.121	K.QFAAEEISSM*VLIK.M
R2/RRR2-6/2	1295.989	1295.492	384.911	0.483	477.080	0.425	14	0.121	R.M*VNHFVQEFK.R
R2/RRR2-6/2	1329.929	1330.491	-1178.378	0.419	938.219	0.342	14	0.120	R.FEELNM*DLFR.K
R2/RRR2-6/2	1296.068	1295.492	-328.060	0.518	519.985	0.409	14	0.120	R.M*VNHFVQEFK.R
R2/RRR2-6/2	1681.280	1681.830	-925.047	0.362	450.096	0.494	18	0.118	K.NAVVTVPAYFNDSQR.Q
R2/RRR2-6/2	1681.325	1681.830	-898.297	0.318	482.103	0.494	19	0.117	K.NAVVTVPAYFNDSQR.Q
R2/RRR2-1/2	1197.894	1197.277	-320.490	0.358	522.639	0.412	15	0.117	R.FSDASVQSDIK.L
R2/RRR2-2/2	1681.263	1681.830	-934.961	0.381	461.307	0.442	18	0.116	K.NAVVTVPAYFNDSQR.Q
R2/RRR2-6/2	1314.050	1314.492	-337.164	0.371	470.172	0.370	15	0.116	R.FEELNMDLFR.K
R2/RRR2-6/3	1676.975	1676.683	174.734	0.434	726.865	0.608	28	0.115	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-1/2	1681.115	1681.830	-1023.386	0.306	417.321	0.430	17	0.111	K.NAVVTVPAYFNDSQR.Q
R2/RRR2-6/2	1313.824	1314.492	-1273.325	0.251	274.045	0.263	13	0.111	R.FEELNMDLFR.K
R2/RRR2-6/3	1670.977	1669.929	28.597	0.451	1424.149	0.345	24	0.111	R.ARFEELNMDLFRK.C
R2/RRR2-2/2	1197.475	1197.277	166.291	0.303	287.908	0.350	11	0.110	R.FSDASVQSDIK.L
R2/RRR2-6/2	1867.764	1869.109	-1259.434	0.417	378.651	0.427	14	0.108	R.FSDASVQSDIKLWPFK.V
R2/RRR2-6/3	1681.819	1681.830	-6.968	0.461	937.391	0.505	26	0.108	K.NAVVTVPAYFNDSQR.Q
R2/RRR2-6/3	1969.824	1968.236	-209.884	0.484	811.940	0.512	30	0.103	R.VQQLLQDFFNGKELCK.S
R2/RRR2-6/3	1677.747	1676.683	38.224	0.439	622.950	0.546	27	0.101	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/3	1867.776	1869.109	-1252.943	0.398	747.428	0.531	26	0.100	R.FSDASVQSDIKLWPFK.V
R2/RRR2-6/3	1969.028	1968.236	-106.033	0.529	701.979	0.518	28	0.100	R.VQQLLQDFFNGKELCK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1868.618	1869.109	-263.415	0.419	697.432	0.537	26	0.100	R.FSDASVQSDIKLWPFK.V
R2/RRR2-6/3	1670.774	1669.929	-93.193	0.535	1365.847	0.321	23	0.099	-.ARFEELNMDLFRK.-
R2/RRR2-6/3	1452.767	1451.678	61.064	0.488	874.287	0.394	23	0.087	R.M*VNHFVQEFKR.K
R2/RRR2-7/3	1676.063	1676.683	-969.500	0.391	472.725	0.469	22	0.086	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-6/3	1451.077	1451.678	-1106.929	0.447	601.834	0.424	20	0.085	R.M*VNHFVQEFKR.K
R2/RRR2-6/3	1968.814	1968.236	-214.904	0.442	508.391	0.435	23	0.083	R.VQQLLQDFFNGKELCK.S
R2/RRR2-6/3	1451.250	1451.678	-295.952	0.466	556.119	0.386	21	0.083	R.M*VNHFVQEFKR.K
R2/RRR2-6/3	1970.169	1968.236	-33.759	0.378	404.422	0.433	24	0.083	R.VQQLLQDFFNGKELCK.S
R2/RRR2-6/3	1685.104	1685.929	-1086.154	0.406	365.460	0.264	21	0.082	R.ARFEELNM*DLFRK.C
R2/RRR2-6/3	1867.826	1869.109	-1225.969	0.360	579.357	0.430	24	0.081	R.FSDASVQSDIKLWPFK.V
R2/RRR2-6/3	1686.120	1685.929	113.872	0.487	725.359	0.333	26	0.079	R.ARFEELNM*DLFRK.C
R2/RRR2-5/3	1675.840	1676.683	-1103.110	0.307	527.439	0.395	24	0.077	-.ATAGDTHLGGEDFDNR.-
R2/RRR2-5/3	1675.421	1676.683	-1354.080	0.296	532.107	0.345	26	0.076	K.ATAGDTHLGGEDFDNR.M
R2/RRR2-5/1	963.436	964.097	-1728.966	0.336	1034.891	0.147	12	0.809	R.FQELGLEK.G
R2/RRR2-5/1	963.522	964.097	-1639.926	0.291	774.644	0.123	11	0.477	-.FQELGLEK.-
R2/RRR2-5/1	963.451	964.097	-1714.008	0.293	745.137	0.110	11	0.442	-.FQELGLEK.-
R2/RRR2-4/3	1927.205	1927.150	28.384	0.522	2753.333	0.539	37	0.429	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/3	1926.290	1927.150	-968.712	0.532	2546.392	0.597	37	0.404	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-4/3	1928.101	1927.150	-25.573	0.552	2400.818	0.601	36	0.367	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/3	1926.737	1927.150	-214.958	0.512	2273.026	0.626	34	0.354	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-1/3	1927.051	1927.150	-51.859	0.522	1980.416	0.605	35	0.276	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-2/3	1926.889	1927.150	-136.024	0.502	2049.342	0.546	36	0.264	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/2	1863.690	1864.118	-230.369	0.593	1865.324	0.577	23	0.257	K.MFDLIEQYNLNGHIR.W
R2/RRR2-5/3	1926.674	1927.150	-247.756	0.534	1847.403	0.596	34	0.247	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-1/3	1927.046	1927.150	-54.432	0.436	1544.958	0.604	30	0.204	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-2/3	1927.346	1927.150	101.755	0.442	1711.610	0.530	32	0.203	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/2	1864.192	1864.118	39.761	0.570	1483.092	0.565	21	0.201	K.MFDLIEQYNLNGHIR.W
R2/RRR2-5/2	1268.180	1268.491	-245.959	0.474	1464.673	0.541	17	0.194	R.IKQQGLNITPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1268.280	1268.491	-166.586	0.454	1424.206	0.523	17	0.185	R.IKQQGLNITPR.I
R2/RRR2-3/3	1926.649	1927.150	-781.316	0.445	1399.638	0.553	29	0.167	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/2	1268.192	1268.491	-236.109	0.420	1295.571	0.495	16	0.166	R.IKQQGLNITPR.I
R2/RRR2-1/2	1016.064	1016.177	-111.537	0.426	1717.628	0.254	17	0.159	R.SLSALQGALR.K
R2/RRR2-5/2	1927.351	1927.150	104.461	0.539	964.431	0.605	23	0.158	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-4/2	1235.566	1235.414	123.014	0.442	1171.874	0.511	15	0.157	K.NLTGLVELYGR.N
R2/RRR2-5/2	1926.486	1927.150	-866.475	0.512	994.852	0.581	23	0.155	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/2	1747.211	1747.949	-997.867	0.491	906.400	0.611	23	0.155	R.TM*ASTVPLAVEGEPSNK.-
R2/RRR2-5/2	1205.810	1205.349	383.907	0.499	1188.347	0.475	18	0.155	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1748.253	1747.949	174.251	0.518	887.978	0.604	23	0.154	R.TM*ASTVPLAVEGEPSNK.-
R2/RRR2-5/2	1205.435	1205.349	71.850	0.445	1244.700	0.437	17	0.151	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1927.693	1927.150	-237.710	0.494	837.793	0.615	22	0.149	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/2	1206.032	1205.349	-263.304	0.452	1389.454	0.353	18	0.148	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1234.962	1235.414	-367.679	0.457	926.064	0.536	16	0.146	K.NLTGLVELYGR.N
R2/RRR2-5/2	1864.489	1864.118	199.655	0.473	1182.317	0.450	18	0.146	K.MFDLIEQYNLNGHIR.W
R2/RRR2-5/2	1204.766	1205.349	-1317.450	0.476	975.818	0.490	17	0.144	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1268.173	1268.491	-251.657	0.435	981.578	0.499	15	0.142	R.IKQQGLNITPR.I
R2/RRR2-5/2	1205.077	1205.349	-226.327	0.447	1141.029	0.398	17	0.139	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1431.684	1432.712	-1420.443	0.478	1049.840	0.418	18	0.136	R.LM*TLTGVYGFWK.Y
R2/RRR2-5/2	1225.679	1226.406	-1413.645	0.372	794.719	0.539	16	0.136	R.VVHGIDVFDPK.F
R2/RRR2-5/2	1747.408	1747.949	-884.385	0.445	706.357	0.573	21	0.136	R.TM*ASTVPLAVEGEPSNK.-
R2/RRR2-1/2	1204.654	1205.349	-1410.875	0.469	880.956	0.469	16	0.135	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1225.563	1226.406	-1508.085	0.367	769.315	0.546	16	0.135	R.VVHGIDVFDPK.F
R2/RRR2-5/2	1204.611	1205.349	-1446.601	0.467	912.883	0.452	16	0.134	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1416.137	1416.712	-1115.535	0.469	770.843	0.503	17	0.134	R.LMTLTGVYGFWK.Y
R2/RRR2-1/2	1926.602	1927.150	-806.177	0.501	738.553	0.547	21	0.134	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/2	1205.620	1205.349	225.898	0.442	1031.916	0.402	16	0.133	K.SIGNGVQFLNR.H
R2/RRR2-4/2	1926.649	1927.150	-781.373	0.453	759.492	0.544	20	0.132	R.IGDSLSAHPNELVAVFTR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1205.231	1205.349	-98.094	0.436	773.161	0.479	16	0.132	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1192.989	1193.444	-382.750	0.385	661.172	0.529	15	0.131	R.NKPIIFSM*AR.L
R2/RRR2-3/2	1205.094	1205.349	-212.201	0.491	791.434	0.445	17	0.131	K.SIGNGVQFLNR.H
R2/RRR2-1/2	1016.111	1016.177	-64.900	0.398	1435.745	0.211	16	0.129	R.SLSALQGALR.K
R2/RRR2-5/2	1583.553	1584.816	-1433.355	0.500	707.315	0.491	19	0.129	K.M*GVTHCTIAHALEK.T
R2/RRR2-5/2	1015.958	1016.177	-215.672	0.495	1450.827	0.221	16	0.129	R.SLSALQGALR.K
R2/RRR2-5/3	1414.701	1415.574	-1327.978	0.482	1274.421	0.490	24	0.128	K.TKYPNSDLYWK.K
R2/RRR2-2/3	1263.718	1263.425	233.038	0.480	1799.937	0.291	25	0.128	K.LKDGAFEDVLR.S
R2/RRR2-1/2	1206.122	1205.349	-188.469	0.455	853.807	0.401	17	0.127	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1433.269	1432.712	-309.889	0.551	767.958	0.443	17	0.127	R.LM*TLTGVYGFWK.Y
R2/RRR2-5/2	1160.185	1160.408	-192.892	0.456	797.564	0.414	14	0.127	R.YLEM*LYALK.Y
R2/RRR2-4/2	1235.021	1235.414	-319.183	0.412	774.678	0.470	14	0.127	K.NLTGLVELYGR.N
R2/RRR2-1/2	1235.184	1235.414	-186.909	0.384	897.086	0.420	15	0.127	K.NLTGLVELYGR.N
R2/RRR2-5/2	1193.079	1193.444	-307.396	0.311	741.700	0.493	15	0.126	R.NKPIIFSM*AR.L
R2/RRR2-5/2	1015.954	1016.177	-219.770	0.447	1480.044	0.183	16	0.126	R.SLSALQGALR.K
R2/RRR2-3/2	1206.287	1205.349	-51.420	0.388	681.868	0.467	15	0.126	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1415.638	1416.712	-1469.754	0.412	706.296	0.456	17	0.126	R.LMTLTGVYGFWK.Y
R2/RRR2-1/2	1205.081	1205.349	-222.363	0.448	744.722	0.421	16	0.125	K.SIGNGVQFLNR.H
R2/RRR2-4/2	1206.128	1205.349	-183.088	0.394	589.173	0.475	15	0.125	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1159.611	1160.408	-1554.495	0.402	778.212	0.414	14	0.125	R.YLEM*LYALK.Y
R2/RRR2-5/2	1016.024	1016.177	-150.826	0.479	1456.112	0.194	16	0.125	R.SLSALQGALR.K
R2/RRR2-3/2	1016.260	1016.177	81.851	0.350	1476.283	0.160	16	0.125	R.SLSALQGALR.K
R2/RRR2-5/2	1206.157	1205.349	-159.229	0.446	883.949	0.380	16	0.125	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1193.069	1193.444	-315.403	0.317	729.231	0.472	15	0.124	R.NKPIIFSM*AR.L
R2/RRR2-4/2	1205.078	1205.349	-225.412	0.443	637.585	0.437	15	0.124	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1415.121	1415.574	-321.389	0.381	731.255	0.444	16	0.124	K.TKYPNSDLYWK.K
R2/RRR2-5/2	1416.127	1416.712	-1122.806	0.415	640.593	0.460	16	0.124	R.LMTLTGVYGFWK.Y
R2/RRR2-2/2	1206.270	1205.349	-65.631	0.424	594.725	0.469	15	0.123	-.SIGNGVQFLNR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1584.659	1584.816	-99.334	0.576	982.113	0.555	28	0.123	K.M*GVTHCTIAHALEK.T
R2/RRR2-1/2	1015.334	1016.177	-1820.582	0.309	1293.741	0.206	16	0.121	R.SLSALQGALR.K
R2/RRR2-5/2	1415.066	1415.574	-1068.878	0.468	591.261	0.430	15	0.121	K.TKYPNSDLYWK.K
R2/RRR2-5/2	1226.069	1226.406	-275.677	0.361	673.128	0.439	15	0.121	R.VVHGIDVFDPK.F
R2/RRR2-3/2	1205.239	1205.349	-90.779	0.397	600.934	0.404	15	0.120	K.SIGNGVQFLNR.H
R2/RRR2-6/2	1205.070	1205.349	-232.119	0.418	632.605	0.407	14	0.119	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1144.280	1144.350	-60.841	0.356	1217.935	0.232	16	0.119	R.SLSALQGALRK.A
R2/RRR2-5/2	1389.996	1390.518	-1098.374	0.304	468.936	0.504	21	0.118	R.LLPDATGTTCGQR.L
R2/RRR2-5/3	1584.912	1584.816	60.708	0.582	759.555	0.598	26	0.118	K.M*GVTHCTIAHALEK.T
R2/RRR2-5/2	1144.134	1144.350	-189.156	0.343	1151.228	0.242	17	0.118	R.SLSALQGALRK.A
R2/RRR2-5/2	1159.574	1160.408	-1586.009	0.378	753.059	0.341	14	0.118	R.YLEM*LYALK.Y
R2/RRR2-2/2	1205.238	1205.349	-91.693	0.381	719.307	0.342	16	0.118	K.SIGNGVQFLNR.H
R2/RRR2-5/2	1262.534	1263.425	-1502.133	0.388	672.587	0.395	15	0.117	K.LKDGAFEDVLR.S
R2/RRR2-2/2	1205.874	1205.349	-394.519	0.394	629.135	0.363	15	0.117	K.SIGNGVQFLNR.H
R2/RRR2-2/2	1390.044	1390.518	-342.513	0.365	331.098	0.446	18	0.117	R.LLPDATGTTCGQR.L
R2/RRR2-2/2	1206.029	1205.349	-265.741	0.401	547.943	0.416	14	0.117	-.SIGNGVQFLNR.-
R2/RRR2-5/2	1143.483	1144.408	-1688.719	0.342	818.773	0.314	15	0.116	R.YLEMLYALK.Y
R2/RRR2-5/2	1415.141	1415.574	-307.195	0.370	561.465	0.430	14	0.116	K.TKYPNSDLYWK.K
R2/RRR2-5/3	1879.320	1880.117	-959.111	0.495	1017.373	0.513	29	0.116	K.M*FDLIEQYNLNGHIR.W
R2/RRR2-5/2	1143.552	1144.408	-1628.124	0.383	769.023	0.317	14	0.116	R.YLEMLYALK.Y
R2/RRR2-5/2	1177.177	1177.445	-228.050	0.398	589.548	0.357	14	0.116	R.NKPIIFSMAR.L
R2/RRR2-5/2	1177.141	1177.445	-258.845	0.323	584.805	0.376	15	0.116	R.NKPIIFSMAR.L
R2/RRR2-5/2	1177.060	1177.445	-327.723	0.318	589.015	0.368	15	0.115	R.NKPIIFSMAR.L
R2/RRR2-5/2	1145.166	1144.350	-160.974	0.401	832.123	0.322	16	0.115	-.SLSALQGALRK.-
R2/RRR2-1/2	1432.263	1432.712	-314.125	0.321	656.654	0.390	15	0.115	R.LM*TLTGVYGFWK.Y
R2/RRR2-5/2	1138.830	1139.329	-439.304	0.378	983.501	0.253	15	0.114	R.AM*ENEM*LLR.I
R2/RRR2-4/2	1205.144	1205.349	-170.030	0.435	612.477	0.315	15	0.114	K.SIGNGVQFLNR.H
R2/RRR2-4/2	1225.877	1226.406	-1250.916	0.261	644.834	0.428	15	0.114	R.VVHGIDVFDPK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1205.472	1205.349	102.419	0.340	543.306	0.330	14	0.114	K.SIGNGVQFLNR.H
R2/RRR2-1/2	1235.047	1235.414	-298.457	0.410	601.244	0.378	13	0.113	K.NLTGLVELYGR.N
R2/RRR2-4/2	1431.979	1432.712	-1213.493	0.364	655.466	0.331	16	0.113	R.LM*TLTGVYGFWK.Y
R2/RRR2-5/2	1138.241	1139.329	-1839.831	0.303	996.977	0.242	15	0.112	R.AM*ENEM*LLR.I
R2/RRR2-4/2	1194.279	1193.444	-138.648	0.298	580.918	0.329	14	0.112	R.NKPIIFSM*AR.L
R2/RRR2-4/2	1225.978	1226.406	-350.400	0.249	724.721	0.351	16	0.111	R.VVHGIDVFDPK.F
R2/RRR2-2/2	1016.083	1016.177	-92.134	0.327	1223.857	0.132	17	0.110	R.SLSALQGALR.K
R2/RRR2-5/3	1415.376	1415.574	-140.935	0.468	1042.211	0.482	22	0.110	K.TKYPNSDLYWK.K
R2/RRR2-5/2	1138.219	1139.329	-1858.798	0.324	937.801	0.227	14	0.109	R.AM*ENEM*LLR.I
R2/RRR2-5/2	1144.061	1144.408	-304.321	0.419	666.410	0.278	14	0.109	-.YLEMLYALK.-
R2/RRR2-4/2	1143.497	1144.408	-1676.385	0.291	771.619	0.251	13	0.109	R.YLEMLYALK.Y
R2/RRR2-2/2	1193.176	1193.444	-225.690	0.238	499.992	0.317	13	0.108	R.NKPIIFSM*AR.L
R2/RRR2-1/2	1431.727	1432.712	-1390.555	0.285	724.416	0.248	17	0.108	R.LM*TLTGVYGFWK.Y
R2/RRR2-3/2	1416.039	1416.712	-1184.783	0.291	485.135	0.279	14	0.108	R.LMTLTGVYGFWK.Y
R2/RRR2-5/2	1262.921	1263.425	-1193.962	0.301	517.011	0.299	14	0.108	K.LKDGAFEDVLR.S
R2/RRR2-1/2	1263.247	1263.425	-141.178	0.352	499.533	0.328	13	0.108	-.LKDGAFEDVLR.-
R2/RRR2-3/2	1263.107	1263.425	-252.569	0.327	716.281	0.263	15	0.107	K.LKDGAFEDVLR.S
R2/RRR2-6/2	963.910	964.097	-194.610	0.382	925.986	0.155	14	0.107	R.FQELGLEK.G
R2/RRR2-3/2	1416.762	1416.712	35.379	0.331	617.510	0.218	15	0.106	R.LMTLTGVYGFWK.Y
R2/RRR2-5/2	964.931	964.097	-172.960	0.371	934.707	0.133	14	0.105	R.FQELGLEK.G
R2/RRR2-5/3	1415.757	1415.574	129.314	0.504	1011.083	0.469	23	0.105	K.TKYPNSDLYWK.K
R2/RRR2-5/2	963.912	964.097	-192.831	0.312	935.343	0.112	14	0.104	R.FQELGLEK.G
R2/RRR2-5/2	963.940	964.097	-163.612	0.247	751.785	0.129	13	0.103	-.FQELGLEK.-
R2/RRR2-5/3	1584.112	1584.816	-1079.294	0.515	885.722	0.485	27	0.102	K.M*GVTHCTIAHALEK.T
R2/RRR2-5/3	1415.921	1415.574	245.257	0.526	905.271	0.479	22	0.102	K.TKYPNSDLYWK.K
R2/RRR2-5/3	1864.953	1864.118	-88.480	0.460	834.446	0.489	27	0.102	K.MFDLIEQYNLNGHIR.W
R2/RRR2-1/2	963.314	964.097	-1856.553	0.269	787.048	0.048	13	0.101	-.FQELGLEK.-
R2/RRR2-3/2	963.654	964.097	-461.603	0.276	669.349	0.108	12	0.100	-.FQELGLEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	964.049	964.097	-50.307	0.273	784.294	0.054	13	0.100	-.FQELGLEK.-
R2/RRR2-5/3	1263.323	1263.425	-80.898	0.501	1546.556	0.265	24	0.099	-.LKDGAFEDVLR.-
R2/RRR2-5/3	1268.718	1268.491	179.718	0.509	1539.157	0.258	24	0.095	R.IKQQGLNITPR.I
R2/RRR2-5/3	1568.583	1568.817	-149.298	0.452	774.603	0.471	25	0.094	K.MGVTHCTIAHALEK.T
R2/RRR2-5/3	1863.298	1864.118	-979.580	0.425	542.572	0.485	24	0.093	K.MFDLIEQYNLNGHIR.W
R2/RRR2-5/3	1268.508	1268.491	13.685	0.527	1337.796	0.307	23	0.092	R.IKQQGLNITPR.I
R2/RRR2-1/3	1926.265	1927.150	-981.691	0.373	932.251	0.390	24	0.090	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/3	1880.236	1880.117	63.378	0.488	823.854	0.391	27	0.087	K.M*FDLIEQYNLNGHIR.W
R2/RRR2-4/3	1263.377	1263.425	-37.866	0.482	1335.450	0.269	22	0.086	K.LKDGAFEDVLR.S
R2/RRR2-5/3	1263.575	1263.425	119.549	0.536	1493.927	0.235	24	0.086	-.LKDGAFEDVLR.-
R2/RRR2-5/3	1864.760	1864.118	-192.294	0.357	575.259	0.418	23	0.085	K.MFDLIEQYNLNGHIR.W
R2/RRR2-5/3	1864.036	1864.118	-44.055	0.338	454.450	0.406	23	0.084	K.MFDLIEQYNLNGHIR.W
R2/RRR2-5/3	1864.860	1864.118	-138.611	0.386	428.733	0.397	21	0.084	K.MFDLIEQYNLNGHIR.W
R2/RRR2-3/3	1926.195	1927.150	-1018.245	0.320	684.989	0.396	22	0.083	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/3	1864.298	1864.118	97.216	0.402	393.450	0.406	21	0.082	-.MFDLIEQYNLNGHIR.-
R2/RRR2-4/3	1263.558	1263.425	105.452	0.516	1389.131	0.239	23	0.081	-.LKDGAFEDVLR.-
R2/RRR2-1/3	1263.672	1263.425	196.567	0.506	1295.525	0.247	23	0.079	-.LKDGAFEDVLR.-
R2/RRR2-5/3	1263.700	1263.425	218.653	0.532	1426.359	0.211	23	0.078	K.LKDGAFEDVLR.S
R2/RRR2-3/3	1926.876	1927.150	-142.601	0.271	506.925	0.332	22	0.077	R.IGDSLSAHPNELVAVFTR.L
R2/RRR2-5/3	1880.485	1880.117	196.387	0.334	664.218	0.337	21	0.076	-.M*FDLIEQYNLNGHIR.-
R2/RRR2-5/3	1268.183	1268.491	-243.797	0.445	1184.693	0.239	22	0.075	R.IKQQGLNITPR.I
R2/RRR2-1/3	1263.608	1263.425	145.417	0.467	1216.358	0.228	22	0.074	-.LKDGAFEDVLR.-
R2/RRR2-2/3	1268.259	1268.491	-183.542	0.416	911.985	0.260	20	0.073	R.IKQQGLNITPR.I
R2/RRR2-5/3	1880.567	1880.117	240.130	0.296	966.176	0.251	25	0.072	K.M*FDLIEQYNLNGHIR.W
R2/RRR2-1/3	1263.508	1263.425	66.502	0.465	1252.450	0.202	22	0.070	-.LKDGAFEDVLR.-
R2/RRR2-5/3	1177.263	1177.445	-155.036	0.434	917.472	0.245	18	0.070	R.NKPIIFSMAR.L
R2/RRR2-5/3	1177.093	1177.445	-300.005	0.354	945.566	0.235	18	0.068	-.NKPIIFSMAR.-
R2/RRR2-5/3	1192.584	1193.444	-1564.770	0.346	824.300	0.228	17	0.067	R.NKPIIFSM*AR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1926.559	1927.150	-828.636	0.241	566.126	0.267	19	0.066	-.IGDSLSAHPNELVAVFTR.-
R2/RRR2-2/3	1263.494	1263.425	54.729	0.372	743.164	0.149	20	0.065	-.LKDGAFEDVLR.-
R2/RRR2-4/3	1268.452	1268.491	-30.909	0.428	926.476	0.154	21	0.064	R.IKQQGLNITPR.I
R2/RRR2-5/3	1177.628	1177.445	155.982	0.368	849.287	0.186	17	0.063	-.NKPIIFSMAR.-
R2/RRR2-2/3	1268.409	1268.491	-64.502	0.418	789.628	0.238	19	0.060	-.IKQQGLNITPR.-
R2/RRR2-2/3	1268.674	1268.491	144.836	0.401	779.212	0.206	19	0.060	-.IKQQGLNITPR.-
R2/RRR2-1/3	1268.337	1268.491	-121.267	0.483	760.491	0.258	19	0.060	-.IKQQGLNITPR.-
R2/RRR2-4/3	1268.678	1268.491	147.587	0.434	778.577	0.133	20	0.057	-.IKQQGLNITPR.-
R2/RRR2-5/2	1971.577	1971.200	192.040	0.652	3336.711	0.653	26	0.628	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/2	1970.586	1971.200	-821.486	0.629	2785.947	0.644	25	0.469	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/2	1970.853	1971.200	-176.531	0.639	2752.107	0.645	25	0.460	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-1/3	1962.764	1961.210	-227.980	0.601	2413.307	0.536	35	0.334	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/3	1970.838	1971.200	-184.087	0.626	2294.270	0.537	38	0.299	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/2	1970.648	1969.312	171.193	0.615	2362.829	0.459	24	0.297	K.LFQDKESLYPLLNFLK.A
R2/RRR2-4/3	1962.115	1961.210	-48.499	0.556	2169.075	0.543	35	0.285	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/3	1961.477	1961.210	136.719	0.585	2185.223	0.525	33	0.280	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1970.492	1969.312	91.549	0.635	2235.197	0.460	25	0.274	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/3	1971.121	1971.200	-40.295	0.597	2064.974	0.573	35	0.273	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/3	1972.022	1971.200	-90.319	0.584	2022.474	0.582	36	0.268	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/3	1962.269	1961.210	30.217	0.591	2085.651	0.526	33	0.260	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-1/3	1971.113	1971.200	-43.929	0.563	1931.970	0.595	34	0.259	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/3	1970.376	1969.312	32.764	0.475	2237.921	0.427	32	0.254	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/3	1971.595	1971.200	201.160	0.586	1928.720	0.533	35	0.230	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/2	1970.596	1969.312	144.853	0.646	1964.325	0.459	23	0.229	K.LFQDKESLYPLLNFLK.A
R2/RRR2-1/3	1962.470	1961.210	133.156	0.556	1887.081	0.518	32	0.222	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-4/2	1968.488	1969.312	-929.404	0.553	1949.562	0.430	22	0.222	K.LFQDKESLYPLLNFLK.A
R2/RRR2-1/3	1971.941	1971.200	-131.488	0.609	1720.038	0.593	33	0.219	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-4/3	1970.813	1971.200	-196.856	0.580	1760.163	0.564	33	0.216	R.HQLLAEFDALIEADKEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1961.779	1961.210	-220.293	0.578	1786.036	0.518	31	0.205	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-3/3	1961.000	1961.210	-107.310	0.533	1802.989	0.494	31	0.201	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/3	1969.846	1969.312	-237.043	0.405	2120.526	0.315	32	0.191	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/3	1969.618	1969.312	155.983	0.427	1979.653	0.383	33	0.190	K.LFQDKESLYPLLNFLK.A
R2/RRR2-2/3	1972.092	1971.200	-54.741	0.533	1648.911	0.535	33	0.189	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-4/3	1970.732	1971.200	-237.962	0.535	1566.968	0.560	33	0.186	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/3	1973.167	1971.200	-16.488	0.545	1601.868	0.539	31	0.185	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-2/3	1971.299	1971.200	50.450	0.525	1701.290	0.484	33	0.180	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-4/3	1961.318	1961.210	55.264	0.551	1515.915	0.546	29	0.177	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1841.297	1841.009	156.687	0.571	1228.751	0.581	20	0.174	R.DLANLVIVCGDHGNQSK.D
R2/RRR2-4/3	1960.728	1961.210	-246.513	0.536	1593.807	0.506	32	0.173	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/3	1971.197	1971.200	-1.535	0.519	1414.973	0.541	31	0.162	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-2/3	1971.935	1971.200	-134.655	0.542	1415.292	0.539	34	0.159	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/3	1970.056	1969.312	-129.998	0.470	1782.578	0.376	32	0.157	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/2	1840.318	1841.009	-921.882	0.572	993.131	0.589	19	0.154	R.DLANLVIVCGDHGNQSK.D
R2/RRR2-2/2	1968.162	1969.312	-1095.468	0.455	1451.121	0.376	20	0.154	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/2	1541.361	1541.768	-265.040	0.486	1403.586	0.380	18	0.152	K.LGVTQCTIAHALEK.T
R2/RRR2-5/2	1541.193	1541.768	-1024.780	0.482	1430.323	0.367	18	0.151	K.LGVTQCTIAHALEK.T
R2/RRR2-5/2	1841.411	1841.009	218.913	0.566	1027.313	0.547	19	0.149	R.DLANLVIVCGDHGNQSK.D
R2/RRR2-5/2	1540.618	1541.768	-1399.875	0.485	1369.602	0.378	18	0.148	K.LGVTQCTIAHALEK.T
R2/RRR2-5/2	1240.668	1241.462	-1450.151	0.454	1336.148	0.372	17	0.148	R.IKQQGLDITPK.I
R2/RRR2-5/2	1240.692	1241.462	-1431.275	0.483	1260.608	0.390	17	0.146	R.IKQQGLDITPK.I
R2/RRR2-5/2	1253.660	1254.418	-1405.922	0.455	1160.589	0.377	18	0.138	K.VIGTEHTDILR.V
R2/RRR2-5/2	1960.784	1961.210	-218.025	0.510	753.143	0.590	19	0.138	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-1/2	1960.335	1961.210	-959.439	0.487	787.577	0.568	20	0.137	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/3	1961.447	1961.210	121.365	0.385	1492.162	0.405	30	0.136	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1254.235	1254.418	-145.999	0.490	1014.924	0.408	18	0.135	K.VIGTEHTDILR.V
R2/RRR2-1/3	1971.241	1971.200	20.918	0.495	1228.900	0.511	28	0.135	R.HQLLAEFDALIEADKEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1457.686	1457.610	52.394	0.474	1748.149	0.322	27	0.134	K.TKYPNSDIYLDK.F
R2/RRR2-5/2	1228.187	1228.332	-118.591	0.462	1195.602	0.317	16	0.131	K.YPNSDIYLDK.F
R2/RRR2-1/2	1389.549	1388.546	2.854	0.444	615.751	0.496	20	0.130	R.LLPDAVGTTCGQR.V
R2/RRR2-1/2	1387.970	1388.546	-1138.261	0.428	676.399	0.488	20	0.130	R.LLPDAVGTTCGQR.V
R2/RRR2-5/2	1253.565	1254.418	-1482.505	0.444	937.233	0.399	18	0.130	K.VIGTEHTDILR.V
R2/RRR2-5/2	1241.235	1241.462	-183.927	0.472	1116.190	0.346	16	0.129	R.IKQQGLDITPK.I
R2/RRR2-4/2	1960.511	1961.210	-868.986	0.454	704.552	0.532	19	0.128	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-1/2	1960.595	1961.210	-826.296	0.410	828.419	0.491	19	0.128	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-2/2	1961.336	1961.210	64.697	0.475	727.367	0.508	19	0.126	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1388.175	1388.546	-267.563	0.389	672.518	0.447	20	0.125	R.LLPDAVGTTCGQR.V
R2/RRR2-5/2	1388.019	1388.546	-1103.203	0.358	676.915	0.447	21	0.124	R.LLPDAVGTTCGQR.V
R2/RRR2-3/3	1961.564	1961.210	180.904	0.387	1301.135	0.429	27	0.124	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1228.156	1228.332	-143.816	0.468	1142.750	0.286	16	0.123	K.YPNSDIYLDK.F
R2/RRR2-2/2	1241.131	1241.462	-267.399	0.474	1083.540	0.317	16	0.123	R.IKQQGLDITPK.I
R2/RRR2-5/2	1125.114	1124.271	-139.249	0.366	326.781	0.427	15	0.123	K.YAPFEDILR.A
R2/RRR2-5/2	1228.331	1228.332	-0.958	0.463	1178.761	0.268	16	0.123	K.YPNSDIYLDK.F
R2/RRR2-5/2	1276.085	1275.477	-308.286	0.449	764.273	0.403	16	0.122	K.NM*TGLVEM*YGK.N
R2/RRR2-3/2	1242.221	1241.462	-194.918	0.441	831.321	0.393	15	0.122	R.IKQQGLDITPK.I
R2/RRR2-2/2	1388.043	1388.546	-1085.718	0.371	673.712	0.420	20	0.122	R.LLPDAVGTTCGQR.V
R2/RRR2-5/2	1961.564	1961.210	181.036	0.441	622.102	0.480	19	0.120	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-2/2	1387.902	1388.546	-1187.719	0.363	477.695	0.431	17	0.118	R.LLPDAVGTTCGQR.V
R2/RRR2-5/2	1124.007	1124.271	-234.916	0.286	354.992	0.367	15	0.116	K.YAPFEDILR.A
R2/RRR2-3/2	1388.041	1388.546	-1087.396	0.326	400.563	0.395	17	0.115	R.LLPDAVGTTCGQR.V
R2/RRR2-4/2	1960.677	1961.210	-783.986	0.440	563.718	0.454	17	0.114	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1387.653	1388.546	-1367.927	0.265	646.909	0.377	21	0.114	R.LLPDAVGTTCGQR.V
R2/RRR2-5/2	1088.658	1089.291	-1504.858	0.420	855.035	0.278	14	0.114	R.ALENEMLLR.I
R2/RRR2-2/3	1960.647	1961.210	-799.351	0.464	1181.572	0.436	28	0.113	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1275.089	1275.477	-305.646	0.419	698.846	0.316	16	0.113	K.NM*TGLVEM*YGK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1969.067	1969.312	-124.460	0.441	672.114	0.388	17	0.112	K.LFQDKESLYPLLNFLK.A
R2/RRR2-2/2	1971.141	1969.312	-86.874	0.382	753.012	0.407	14	0.112	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/2	1089.282	1089.291	-8.499	0.397	406.830	0.262	13	0.112	-.ALENEMLLR.-
R2/RRR2-5/2	1960.400	1961.210	-925.931	0.336	364.875	0.447	17	0.112	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-3/2	1962.236	1961.210	13.502	0.420	571.773	0.396	18	0.111	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-4/2	1960.613	1961.210	-816.734	0.374	304.563	0.466	14	0.110	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1389.455	1388.546	-65.173	0.241	263.053	0.431	17	0.110	-.LLPDAVGTTCGQR.-
R2/RRR2-5/3	1457.640	1457.610	20.645	0.505	1357.126	0.374	24	0.110	K.TKYPNSDIYLDK.F
R2/RRR2-1/2	1970.316	1969.312	1.951	0.389	587.880	0.438	13	0.110	K.LFQDKESLYPLLNFLK.A
R2/RRR2-4/2	1124.153	1124.271	-104.733	0.208	348.418	0.398	15	0.110	K.YAPFEDILR.A
R2/RRR2-5/2	1259.212	1259.478	-211.579	0.310	382.370	0.356	14	0.109	-.NM*TGLVEMYGK.-
R2/RRR2-5/2	1123.550	1124.271	-1535.712	0.209	252.100	0.354	14	0.108	-.YAPFEDILR.-
R2/RRR2-5/2	1961.150	1961.210	-30.442	0.334	228.063	0.467	12	0.108	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1960.038	1961.210	-1111.628	0.288	330.853	0.394	15	0.107	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-1/2	1960.236	1961.210	-1010.205	0.310	619.266	0.345	17	0.107	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-5/2	1389.451	1388.546	-67.993	0.189	330.848	0.452	19	0.106	-.LLPDAVGTTCGQR.-
R2/RRR2-5/2	1104.887	1105.291	-366.459	0.380	798.575	0.211	13	0.106	-.ALENEM*LLR.-
R2/RRR2-1/2	1105.181	1105.291	-99.594	0.310	673.221	0.150	13	0.105	R.ALENEM*LLR.I
R2/RRR2-5/3	1960.697	1961.210	-773.806	0.442	1032.748	0.437	26	0.104	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-3/3	1960.467	1961.210	-891.839	0.379	998.967	0.437	25	0.103	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-1/2	1125.016	1124.271	-226.979	0.096	300.892	0.295	15	0.101	K.YAPFEDILR.A
R2/RRR2-5/2	1104.927	1105.291	-330.100	0.379	741.540	0.138	12	0.101	-.ALENEM*LLR.-
R2/RRR2-2/2	1967.413	1969.312	-1987.362	0.308	586.411	0.229	14	0.099	K.LFQDKESLYPLLNFLK.A
R2/RRR2-4/3	1241.817	1241.462	286.642	0.509	1440.038	0.305	25	0.098	R.IKQQGLDITPK.I
R2/RRR2-5/3	1456.912	1457.610	-1168.740	0.487	1301.539	0.327	25	0.096	K.TKYPNSDIYLDK.F
R2/RRR2-5/2	1104.982	1105.291	-279.779	0.399	577.713	0.213	11	0.092	-.ALENEM*LLR.-
R2/RRR2-5/3	1840.947	1841.009	-33.967	0.409	675.650	0.488	27	0.090	R.DLANLVIVCGDHGNQSK.D
R2/RRR2-7/3	1960.581	1961.210	-833.053	0.417	772.674	0.428	22	0.089	-.LGATFSSHPNELIALFSR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1970.852	1969.312	-233.971	0.450	1378.275	0.248	28	0.086	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/3	1961.292	1961.210	41.781	0.343	822.793	0.373	24	0.085	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-2/3	1960.786	1961.210	-217.002	0.374	1044.447	0.322	25	0.085	R.LGATFSSHPNELIALFSR.Y
R2/RRR2-3/3	1240.862	1241.462	-1293.445	0.498	729.275	0.332	19	0.080	R.IKQQGLDITPK.I
R2/RRR2-1/3	1241.540	1241.462	63.192	0.501	927.842	0.321	22	0.078	-.IKQQGLDITPK.-
R2/RRR2-1/3	1241.619	1241.462	126.495	0.517	1115.867	0.277	23	0.077	-.IKQQGLDITPK.-
R2/RRR2-5/3	1841.795	1841.009	-116.548	0.395	405.869	0.400	22	0.076	R.DLANLVIVCGDHGNQSK.D
R2/RRR2-6/3	1970.884	1971.200	-160.508	0.374	862.484	0.296	25	0.076	R.HQLLAEFDALIEADKEK.Y
R2/RRR2-5/3	1241.711	1241.462	201.178	0.526	1110.545	0.264	23	0.076	R.IKQQGLDITPK.I
R2/RRR2-5/3	1961.505	1961.210	150.761	0.275	563.906	0.298	20	0.075	-.LGATFSSHPNELIALFSR.-
R2/RRR2-4/3	1968.499	1969.312	-923.777	0.377	1074.155	0.246	28	0.073	K.LFQDKESLYPLLNFLK.A
R2/RRR2-4/3	1241.197	1241.462	-214.523	0.514	841.197	0.289	20	0.073	-.IKQQGLDITPK.-
R2/RRR2-4/3	1241.584	1241.462	98.246	0.514	1025.011	0.254	22	0.073	R.IKQQGLDITPK.I
R2/RRR2-3/3	1241.814	1241.462	284.424	0.436	1009.704	0.242	22	0.071	-.IKQQGLDITPK.-
R2/RRR2-1/3	1241.769	1241.462	247.904	0.511	703.593	0.246	20	0.071	-.IKQQGLDITPK.-
R2/RRR2-4/3	1968.480	1969.312	-933.582	0.265	915.578	0.213	26	0.067	K.LFQDKESLYPLLNFLK.A
R2/RRR2-5/3	1241.697	1241.462	189.496	0.471	929.567	0.227	22	0.067	-.IKQQGLDITPK.-
R2/RRR2-3/3	1241.672	1241.462	169.236	0.506	766.276	0.219	20	0.065	-.IKQQGLDITPK.-
R2/RRR2-5/3	1241.939	1241.462	385.396	0.457	1246.310	0.159	23	0.065	R.IKQQGLDITPK.I
R2/RRR2-2/3	1241.200	1241.462	-211.563	0.507	737.525	0.282	20	0.064	-.IKQQGLDITPK.-
R2/RRR2-1/2	1106.078	1105.291	-193.160	0.390	407.161	0.267	10	0.062	-.ALENEM*LLR.-
R2/RRR2-4/2	1994.345	1994.066	140.611	0.633	2898.156	0.638	28	0.503	K.SEGHDTIVLAGAEYGSGSSR.D
R2/RRR2-2/2	1570.404	1569.783	-242.207	0.602	2562.788	0.468	22	0.341	K.YLLQSGLQEYLNK.Q
R2/RRR2-1/2	1571.289	1569.783	-315.628	0.626	2375.355	0.465	22	0.302	K.YLLQSGLQEYLNK.Q
R2/RRR2-4/2	1569.383	1569.783	-255.939	0.562	2302.192	0.404	22	0.272	K.YLLQSGLQEYLNK.Q
R2/RRR2-6/2	1571.336	1569.783	-285.620	0.630	2099.542	0.481	21	0.259	K.YLLQSGLQEYLNK.Q
R2/RRR2-1/2	1569.413	1569.783	-236.431	0.549	2060.750	0.453	21	0.248	K.YLLQSGLQEYLNK.Q
R2/RRR2-4/2	1570.159	1569.783	240.122	0.554	2144.249	0.399	22	0.245	K.YLLQSGLQEYLNK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1546.018	1545.656	235.236	0.549	1725.132	0.572	20	0.237	K.M*FVDYNEPQTER.V
R2/RRR2-4/2	1545.019	1545.656	-1062.344	0.490	1724.858	0.550	20	0.230	K.M*FVDYNEPQTER.V
R2/RRR2-4/2	1499.352	1498.684	-221.511	0.557	1791.041	0.512	20	0.226	R.SDETVAMIEAYLR.A
R2/RRR2-4/3	1570.939	1569.783	99.510	0.553	1946.064	0.497	28	0.225	K.YLLQSGLQEYLNK.Q
R2/RRR2-4/2	1498.242	1498.684	-295.386	0.403	1899.728	0.434	20	0.222	R.SDETVAMIEAYLR.A
R2/RRR2-4/2	1528.068	1528.563	-325.196	0.416	1669.240	0.561	20	0.222	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/2	1545.229	1545.656	-277.138	0.497	1518.669	0.520	19	0.196	K.M*FVDYNEPQTER.V
R2/RRR2-4/2	1528.250	1528.563	-205.305	0.444	1632.471	0.450	21	0.192	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/2	1528.236	1528.563	-214.680	0.463	1506.376	0.508	21	0.190	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/2	1724.204	1724.761	-905.640	0.619	1610.782	0.449	23	0.189	R.NCDNFQVNQNDVEK.I
R2/RRR2-4/2	1724.353	1724.761	-237.340	0.624	1648.368	0.421	23	0.186	R.NCDNFQVNQNDVEK.I
R2/RRR2-3/2	1568.977	1569.783	-1154.823	0.481	1682.431	0.393	20	0.183	K.YLLQSGLQEYLNK.Q
R2/RRR2-4/2	1725.214	1724.761	263.180	0.643	1641.808	0.415	23	0.183	R.NCDNFQVNQNDVEK.I
R2/RRR2-4/3	1498.411	1498.684	-182.601	0.478	1908.016	0.398	28	0.181	R.SDETVAMIEAYLR.A
R2/RRR2-4/2	1280.170	1280.431	-204.454	0.450	1352.492	0.518	18	0.177	K.FVEFYGEGM*GK.L
R2/RRR2-4/3	1514.806	1514.683	81.731	0.575	1959.602	0.336	28	0.164	R.SDETVAM*IEAYLR.A
R2/RRR2-4/2	1263.776	1264.431	-1313.772	0.296	1398.136	0.429	18	0.160	K.FVEFYGEGMGK.L
R2/RRR2-4/2	1279.914	1280.431	-1188.645	0.373	1413.636	0.400	18	0.159	K.FVEFYGEGM*GK.L
R2/RRR2-4/2	1279.894	1280.431	-1204.639	0.325	1463.573	0.376	17	0.158	K.FVEFYGEGM*GK.L
R2/RRR2-4/2	1514.413	1514.683	-179.134	0.469	1271.724	0.457	19	0.157	R.SDETVAM*IEAYLR.A
R2/RRR2-4/2	1289.123	1289.421	-231.421	0.400	1295.521	0.441	17	0.157	K.FDFHGQPAELK.H
R2/RRR2-4/3	1993.546	1994.066	-764.648	0.477	1472.538	0.483	33	0.155	K.SEGHDTIVLAGAEYGSGSSR.D
R2/RRR2-4/2	1497.910	1498.684	-1187.707	0.362	1401.823	0.368	18	0.151	R.SDETVAMIEAYLR.A
R2/RRR2-4/2	1116.611	1117.278	-1496.900	0.377	928.288	0.555	20	0.147	K.TSLAPGSGVVTK.Y
R2/RRR2-4/3	1528.403	1528.563	-105.199	0.506	1272.577	0.525	30	0.140	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/2	1548.713	1549.897	-1413.902	0.368	921.332	0.509	19	0.137	R.SNLVGMGIIPLCFK.A
R2/RRR2-4/2	1293.174	1293.453	-215.737	0.340	877.729	0.520	17	0.137	K.FYSLPALNDPR.I
R2/RRR2-4/2	1515.093	1514.683	271.469	0.511	1007.579	0.434	17	0.133	R.SDETVAM*IEAYLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1202.634	1203.326	-1411.107	0.501	782.627	0.442	16	0.131	K.IIDWENTSPK.L
R2/RRR2-4/3	1529.687	1528.563	81.063	0.529	1189.624	0.516	30	0.130	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/2	1202.500	1203.326	-1523.264	0.482	756.371	0.428	16	0.128	K.IIDWENTSPK.L
R2/RRR2-4/2	1117.066	1117.278	-189.903	0.378	835.973	0.435	20	0.128	K.TSLAPGSGVVTK.Y
R2/RRR2-4/2	1565.312	1565.896	-1014.861	0.469	473.561	0.589	15	0.128	R.SNLVGM*GIIPLCFK.A
R2/RRR2-4/2	1289.131	1289.421	-225.246	0.330	1263.740	0.264	17	0.126	K.FDFHGQPAELK.H
R2/RRR2-4/2	1565.267	1565.896	-1044.145	0.420	598.250	0.526	17	0.126	R.SNLVGM*GIIPLCFK.A
R2/RRR2-4/2	1203.098	1203.326	-189.961	0.468	708.022	0.413	16	0.126	K.IIDWENTSPK.L
R2/RRR2-4/3	1498.506	1498.684	-118.982	0.505	1700.997	0.297	25	0.124	R.SDETVAMIEAYLR.A
R2/RRR2-4/2	1645.382	1645.881	-303.945	0.452	475.042	0.533	17	0.121	K.NILTTLPKPGGGEYGK.F
R2/RRR2-4/2	1116.560	1117.278	-1542.695	0.303	695.827	0.460	18	0.121	K.TSLAPGSGVVTK.Y
R2/RRR2-1/2	1203.363	1203.326	30.868	0.475	748.776	0.372	15	0.121	K.IIDWENTSPK.L
R2/RRR2-4/2	1289.023	1289.421	-309.706	0.371	988.959	0.334	15	0.120	K.FDFHGQPAELK.H
R2/RRR2-4/2	1549.300	1549.897	-1033.326	0.382	798.689	0.414	17	0.120	R.SNLVGMGIIPLCFK.A
R2/RRR2-1/2	1292.920	1293.453	-1189.082	0.336	690.211	0.440	14	0.120	K.FYSLPALNDPR.I
R2/RRR2-4/2	1645.275	1645.881	-979.076	0.419	448.583	0.525	17	0.119	K.NILTTLPKPGGGEYGK.F
R2/RRR2-2/2	1203.301	1203.326	-20.921	0.432	688.961	0.370	15	0.119	K.IIDWENTSPK.L
R2/RRR2-4/2	1548.712	1549.897	-1414.773	0.311	877.815	0.388	18	0.119	R.SNLVGMGIIPLCFK.A
R2/RRR2-4/2	1766.392	1766.957	-888.708	0.520	392.837	0.487	17	0.119	R.SPNAVQSNM*ELEFKR.N
R2/RRR2-4/2	1645.523	1645.881	-218.054	0.453	418.634	0.522	16	0.118	K.NILTTLPKPGGGEYGK.F
R2/RRR2-4/2	1263.565	1264.431	-1481.916	0.298	969.089	0.327	16	0.118	K.FVEFYGEGMGK.L
R2/RRR2-4/2	1766.268	1766.957	-959.199	0.550	353.750	0.498	16	0.118	R.SPNAVQSNM*ELEFKR.N
R2/RRR2-4/3	1724.551	1724.761	-121.952	0.451	1455.135	0.354	26	0.116	R.NCDNFQVNQNDVEK.I
R2/RRR2-4/3	1528.669	1528.563	69.143	0.507	831.037	0.563	25	0.116	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/2	1292.938	1293.453	-1174.956	0.267	853.525	0.350	16	0.116	K.FYSLPALNDPR.I
R2/RRR2-3/2	1203.271	1203.326	-45.749	0.457	722.106	0.295	16	0.115	K.IIDWENTSPK.L
R2/RRR2-4/2	1513.667	1514.683	-1335.911	0.313	951.733	0.295	17	0.114	R.SDETVAM*IEAYLR.A
R2/RRR2-4/3	1994.140	1994.066	37.501	0.438	1213.574	0.423	30	0.112	K.SEGHDTIVLAGAEYGSGSSR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1292.906	1293.453	-1199.985	0.281	539.839	0.385	13	0.111	K.FYSLPALNDPR.I
R2/RRR2-2/2	1292.181	1293.453	-1763.295	0.256	873.487	0.288	15	0.111	K.FYSLPALNDPR.I
R2/RRR2-4/2	1570.688	1569.783	-60.849	0.427	567.835	0.375	14	0.110	-.YLLQSGLQEYLNK.-
R2/RRR2-4/2	1571.200	1569.783	265.990	0.447	746.867	0.323	15	0.110	K.YLLQSGLQEYLNK.Q
R2/RRR2-4/3	1750.584	1750.958	-214.348	0.557	839.355	0.528	26	0.109	R.SPNAVQSNMELEFKR.N
R2/RRR2-3/2	1202.999	1203.326	-272.720	0.375	550.933	0.205	14	0.108	K.IIDWENTSPK.L
R2/RRR2-4/3	1750.976	1750.958	10.368	0.493	882.827	0.512	26	0.108	R.SPNAVQSNMELEFKR.N
R2/RRR2-3/2	1292.669	1293.453	-1383.670	0.237	457.569	0.365	12	0.108	K.FYSLPALNDPR.I
R2/RRR2-5/2	1117.283	1117.278	4.645	0.300	358.127	0.367	14	0.106	-.TSLAPGSGVVTK.-
R2/RRR2-1/2	1292.273	1293.453	-1691.732	0.156	796.248	0.303	16	0.106	K.FYSLPALNDPR.I
R2/RRR2-4/2	1569.332	1569.783	-288.169	0.494	1119.262	0.186	19	0.106	K.YLLQSGLQEYLNK.Q
R2/RRR2-3/2	1117.109	1117.278	-151.317	0.309	406.023	0.273	14	0.104	-.TSLAPGSGVVTK.-
R2/RRR2-4/3	1767.167	1766.957	119.203	0.509	872.931	0.495	27	0.104	R.SPNAVQSNM*ELEFKR.N
R2/RRR2-4/3	1499.008	1498.684	216.879	0.530	1485.886	0.303	24	0.104	R.SDETVAMIEAYLR.A
R2/RRR2-4/3	1658.715	1657.972	-155.506	0.502	1453.533	0.308	29	0.103	K.KACELGLEVKPWVK.T
R2/RRR2-3/2	1292.302	1293.453	-1669.145	0.212	810.574	0.159	16	0.103	K.FYSLPALNDPR.I
R2/RRR2-1/3	1528.870	1528.563	201.031	0.449	960.468	0.457	28	0.103	K.AGEDADSLGLTGHER.Y
R2/RRR2-5/3	1528.224	1528.563	-222.382	0.495	756.353	0.505	25	0.102	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/3	1724.678	1724.761	-48.360	0.475	1434.468	0.293	28	0.099	R.NCDNFQVNQNDVEK.I
R2/RRR2-2/2	1292.403	1293.453	-1590.953	0.079	745.566	0.173	15	0.098	K.FYSLPALNDPR.I
R2/RRR2-1/3	1528.800	1528.563	155.150	0.480	848.026	0.458	25	0.098	K.AGEDADSLGLTGHER.Y
R2/RRR2-2/3	1528.048	1528.563	-994.543	0.436	870.158	0.452	23	0.098	K.AGEDADSLGLTGHER.Y
R2/RRR2-15/3	1528.454	1528.563	-71.431	0.432	791.270	0.463	24	0.096	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/3	1385.930	1386.580	-1193.898	0.389	723.563	0.507	24	0.096	K.DM*TM*SPPGPHGVK.N
R2/RRR2-9/2	1294.311	1293.453	-109.411	0.197	463.552	0.209	11	0.095	-.FYSLPALNDPR.-
R2/RRR2-4/3	1749.912	1750.958	-1172.351	0.478	635.154	0.492	23	0.094	R.SPNAVQSNMELEFKR.N
R2/RRR2-1/3	1528.389	1528.563	-114.572	0.452	891.037	0.422	25	0.094	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/3	1657.434	1657.972	-930.386	0.537	1115.235	0.373	25	0.093	K.KACELGLEVKPWVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1767.255	1766.957	169.079	0.441	710.336	0.454	25	0.091	R.SPNAVQSNM*ELEFKR.N
R2/RRR2-2/3	1529.588	1528.563	15.991	0.429	856.715	0.410	26	0.091	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/3	1569.734	1569.783	-31.528	0.335	1111.000	0.354	21	0.090	-.YLLQSGLQEYLNK.-
R2/RRR2-4/3	1724.119	1724.761	-954.905	0.428	1120.113	0.345	23	0.089	-.NCDNFQVNQNDVEK.-
R2/RRR2-24/3	1528.567	1528.563	2.586	0.445	689.129	0.418	24	0.088	K.AGEDADSLGLTGHER.Y
R2/RRR2-4/3	1386.614	1386.580	24.333	0.422	531.786	0.468	22	0.088	K.DM*TM*SPPGPHGVK.N
R2/RRR2-5/3	1105.383	1105.312	64.329	0.464	497.785	0.359	18	0.088	R.IDKLPYSIR.I
R2/RRR2-2/3	1528.493	1528.563	-46.077	0.393	530.469	0.434	21	0.087	K.AGEDADSLGLTGHER.Y
R2/RRR2-1/3	1105.190	1105.312	-110.808	0.418	455.593	0.308	17	0.086	R.IDKLPYSIR.I
R2/RRR2-1/3	1105.296	1105.312	-14.425	0.483	564.739	0.336	19	0.085	R.IDKLPYSIR.I
R2/RRR2-4/3	1105.489	1105.312	160.679	0.477	520.462	0.273	19	0.085	R.IDKLPYSIR.I
R2/RRR2-5/3	1105.381	1105.312	63.000	0.431	587.976	0.362	19	0.085	R.IDKLPYSIR.I
R2/RRR2-4/3	1386.592	1386.580	8.969	0.409	599.784	0.434	22	0.085	K.DM*TM*SPPGPHGVK.N
R2/RRR2-3/3	1766.760	1766.957	-111.642	0.468	656.808	0.408	24	0.085	R.SPNAVQSNM*ELEFKR.N
R2/RRR2-4/3	1767.223	1766.957	150.688	0.431	644.021	0.409	24	0.084	R.SPNAVQSNM*ELEFKR.N
R2/RRR2-3/3	1105.457	1105.312	131.776	0.511	456.871	0.332	18	0.084	-.IDKLPYSIR.-
R2/RRR2-2/3	1105.373	1105.312	55.192	0.424	487.462	0.278	17	0.084	R.IDKLPYSIR.I
R2/RRR2-4/3	1105.498	1105.312	168.818	0.575	730.734	0.378	21	0.083	-.IDKLPYSIR.-
R2/RRR2-2/3	1105.247	1105.312	-59.290	0.426	498.813	0.326	19	0.081	-.IDKLPYSIR.-
R2/RRR2-4/3	1993.308	1994.066	-884.424	0.381	948.567	0.345	29	0.081	K.SEGHDTIVLAGAEYGSGSSR.D
R2/RRR2-4/3	1386.680	1386.580	72.673	0.352	325.636	0.426	18	0.078	-.DM*TM*SPPGPHGVK.-
R2/RRR2-1/3	1105.215	1105.312	-87.541	0.380	564.610	0.337	19	0.075	-.IDKLPYSIR.-
R2/RRR2-3/3	1105.295	1105.312	-15.754	0.489	409.482	0.361	16	0.073	-.IDKLPYSIR.-
R2/RRR2-5/3	1528.764	1528.563	131.968	0.364	695.637	0.249	23	0.072	K.AGEDADSLGLTGHER.Y
R2/RRR2-3/3	1104.679	1105.312	-1482.574	0.460	524.102	0.309	18	0.071	-.IDKLPYSIR.-
R2/RRR2-4/3	1814.947	1815.062	-63.259	0.497	2340.894	0.579	32	0.346	K.AYLPVIESFGFSSQLR.A
R2/RRR2-3/2	1815.363	1815.062	166.817	0.602	2105.741	0.582	24	0.291	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1815.624	1815.062	-241.863	0.610	1999.338	0.565	25	0.268	K.AYLPVIESFGFSSQLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1814.640	1815.062	-233.155	0.518	2011.112	0.518	25	0.257	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1819.359	1819.945	-874.290	0.543	1898.173	0.564	22	0.257	K.NATLTNEKESDACPIR.A
R2/RRR2-2/2	1814.690	1815.062	-205.554	0.526	1968.631	0.538	24	0.256	K.AYLPVIESFGFSSQLR.A
R2/RRR2-1/2	1814.608	1815.062	-250.500	0.505	1981.729	0.496	25	0.247	K.AYLPVIESFGFSSQLR.A
R2/RRR2-5/2	1814.627	1815.062	-240.174	0.521	1927.301	0.524	24	0.246	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1814.421	1815.062	-906.630	0.519	1894.697	0.539	24	0.245	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1819.389	1819.945	-858.125	0.539	1867.594	0.536	22	0.245	K.NATLTNEKESDACPIR.A
R2/RRR2-3/2	1814.085	1815.062	-1092.739	0.429	1917.874	0.522	24	0.244	K.AYLPVIESFGFSSQLR.A
R2/RRR2-13/2	1814.610	1815.062	-249.353	0.512	1999.568	0.478	24	0.244	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1815.425	1815.062	201.072	0.613	1830.275	0.572	24	0.243	K.AYLPVIESFGFSSQLR.A
R2/RRR2-1/2	1815.190	1815.062	71.187	0.521	1906.727	0.516	24	0.240	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1819.475	1819.945	-259.183	0.557	1843.622	0.525	22	0.237	K.NATLTNEKESDACPIR.A
R2/RRR2-5/2	1814.688	1815.062	-206.701	0.527	1920.839	0.480	23	0.232	K.AYLPVIESFGFSSQLR.A
R2/RRR2-5/2	1814.497	1815.062	-865.094	0.516	1871.693	0.497	22	0.229	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1388.987	1388.586	290.130	0.541	1589.361	0.493	17	0.197	R.GFVQFCYEPIK.Q
R2/RRR2-3/2	1814.073	1815.062	-1099.361	0.455	1608.000	0.501	23	0.197	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1425.314	1425.569	-179.930	0.519	1523.486	0.516	20	0.194	R.LWGENFFDPATK.K
R2/RRR2-4/3	1814.413	1815.062	-911.231	0.457	1591.928	0.524	30	0.181	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1347.170	1347.588	-311.425	0.448	1279.573	0.571	19	0.180	R.VIYASQLTAKPR.L
R2/RRR2-4/2	1652.398	1651.841	-269.237	0.513	1620.495	0.402	18	0.175	K.ILSEEFGWDKDLAK.K
R2/RRR2-3/2	1652.924	1651.841	50.472	0.543	1628.871	0.394	19	0.174	K.ILSEEFGWDKDLAK.K
R2/RRR2-4/2	1425.311	1425.569	-181.820	0.477	1356.386	0.482	19	0.170	R.LWGENFFDPATK.K
R2/RRR2-4/2	1652.187	1651.841	209.896	0.555	1611.715	0.379	18	0.167	K.ILSEEFGWDKDLAK.K
R2/RRR2-4/2	1424.679	1425.569	-1331.001	0.464	1310.735	0.484	19	0.166	R.LWGENFFDPATK.K
R2/RRR2-4/2	1388.126	1388.586	-332.314	0.474	1344.613	0.463	16	0.165	R.GFVQFCYEPIK.Q
R2/RRR2-4/2	1652.346	1651.841	-300.441	0.523	1531.120	0.390	19	0.164	K.ILSEEFGWDKDLAK.K
R2/RRR2-4/2	1347.204	1347.588	-285.516	0.458	1297.298	0.465	18	0.161	R.VIYASQLTAKPR.L
R2/RRR2-4/2	1347.248	1347.588	-253.153	0.501	1072.381	0.563	17	0.161	R.VIYASQLTAKPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1503.321	1503.774	-302.614	0.595	1081.899	0.532	21	0.160	R.RVIYASQLTAKPR.L
R2/RRR2-4/2	1623.439	1623.846	-251.414	0.542	1038.861	0.558	20	0.158	R.NCDPEGPLMLYVSK.M
R2/RRR2-3/2	1347.086	1347.588	-1118.365	0.423	1190.338	0.493	17	0.156	R.VIYASQLTAKPR.L
R2/RRR2-4/2	1553.294	1553.742	-289.804	0.508	1248.474	0.433	21	0.153	R.LWGENFFDPATKK.W
R2/RRR2-4/2	1388.046	1388.586	-1112.443	0.422	1264.831	0.429	16	0.152	R.GFVQFCYEPIK.Q
R2/RRR2-1/2	1425.283	1425.569	-201.753	0.429	1130.409	0.489	18	0.151	R.LWGENFFDPATK.K
R2/RRR2-4/3	1820.723	1819.945	-122.436	0.489	1398.012	0.515	32	0.151	K.NATLTNEKESDACPIR.A
R2/RRR2-4/2	1553.316	1553.742	-275.376	0.502	1082.039	0.450	20	0.144	R.LWGENFFDPATKK.W
R2/RRR2-13/2	1813.622	1815.062	-1348.879	0.352	1379.885	0.344	21	0.143	K.AYLPVIESFGFSSQLR.A
R2/RRR2-3/3	1503.925	1503.774	100.403	0.502	1545.562	0.423	27	0.140	R.RVIYASQLTAKPR.L
R2/RRR2-5/2	1425.264	1425.569	-215.157	0.416	1090.206	0.430	17	0.139	R.LWGENFFDPATK.K
R2/RRR2-3/3	1819.839	1819.945	-58.379	0.474	1269.566	0.518	31	0.139	K.NATLTNEKESDACPIR.A
R2/RRR2-3/2	1425.992	1425.569	297.197	0.456	964.084	0.466	17	0.137	R.LWGENFFDPATK.K
R2/RRR2-3/2	1348.587	1347.588	-0.782	0.434	922.347	0.482	16	0.136	R.VIYASQLTAKPR.L
R2/RRR2-4/3	1815.116	1815.062	30.238	0.438	1372.681	0.459	28	0.136	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1553.335	1553.742	-263.155	0.438	958.759	0.450	19	0.135	R.LWGENFFDPATKK.W
R2/RRR2-4/2	1119.906	1120.219	-280.601	0.427	1090.329	0.377	17	0.134	K.EGALAEENMR.G
R2/RRR2-4/3	1820.020	1819.945	41.223	0.467	1229.313	0.508	30	0.133	K.NATLTNEKESDACPIR.A
R2/RRR2-4/2	1639.086	1639.845	-1076.452	0.507	1004.411	0.418	20	0.133	R.NCDPEGPLM*LYVSK.M
R2/RRR2-4/3	1503.611	1503.774	-109.050	0.505	1463.772	0.430	28	0.132	R.RVIYASQLTAKPR.L
R2/RRR2-1/2	1651.322	1651.841	-922.403	0.492	1325.303	0.318	17	0.132	K.ILSEEFGWDKDLAK.K
R2/RRR2-4/2	1503.306	1503.774	-312.146	0.576	554.276	0.493	19	0.129	R.RVIYASQLTAKPR.L
R2/RRR2-1/2	1425.396	1425.569	-122.197	0.406	804.742	0.465	16	0.128	R.LWGENFFDPATK.K
R2/RRR2-5/2	1424.613	1425.569	-1377.386	0.381	1062.080	0.365	17	0.128	R.LWGENFFDPATK.K
R2/RRR2-1/3	1820.961	1819.945	8.793	0.433	1275.907	0.466	31	0.126	K.NATLTNEKESDACPIR.A
R2/RRR2-5/2	744.882	744.863	26.363	0.374	356.780	0.441	9	0.125	R.FFAFGR.V
R2/RRR2-4/2	1641.381	1639.845	-283.808	0.546	965.612	0.384	20	0.125	R.NCDPEGPLM*LYVSK.M
R2/RRR2-3/2	1425.349	1425.569	-155.015	0.403	872.392	0.402	16	0.124	R.LWGENFFDPATK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1779.301	1780.014	-965.468	0.473	1243.743	0.284	19	0.123	K.ILSEEFGWDKDLAKK.I
R2/RRR2-4/2	1119.939	1120.219	-250.857	0.391	851.278	0.383	15	0.122	K.EGALAEENMR.G
R2/RRR2-3/2	1388.202	1388.586	-276.995	0.425	1091.344	0.317	14	0.121	R.GFVQFCYEPIK.Q
R2/RRR2-8/3	1820.620	1819.945	-179.135	0.438	1271.605	0.437	29	0.120	K.NATLTNEKESDACPIR.A
R2/RRR2-3/3	1819.273	1819.945	-921.650	0.404	1039.800	0.519	29	0.119	K.NATLTNEKESDACPIR.A
R2/RRR2-4/2	1119.672	1120.219	-1386.192	0.334	908.483	0.338	15	0.118	K.EGALAEENMR.G
R2/RRR2-13/3	1815.426	1815.062	201.199	0.430	1071.995	0.499	27	0.118	K.AYLPVIESFGFSSQLR.A
R2/RRR2-5/3	1820.158	1819.945	117.198	0.420	1204.857	0.448	27	0.118	K.NATLTNEKESDACPIR.A
R2/RRR2-8/2	744.932	744.863	92.598	0.424	409.436	0.369	10	0.118	-.FFAFGR.-
R2/RRR2-4/2	890.932	891.049	-132.493	0.336	453.254	0.420	10	0.117	K.FSVSPVVR.V
R2/RRR2-2/2	744.777	744.863	-115.176	0.306	289.228	0.344	8	0.116	-.FFAFGR.-
R2/RRR2-4/2	890.500	891.049	-1745.062	0.292	650.962	0.381	12	0.116	K.FSVSPVVR.V
R2/RRR2-3/2	744.354	744.863	-2033.324	0.295	299.532	0.374	8	0.115	-.FFAFGR.-
R2/RRR2-2/2	890.599	891.049	-507.166	0.294	527.718	0.402	11	0.115	K.FSVSPVVR.V
R2/RRR2-17/2	1815.555	1815.062	272.474	0.397	624.509	0.434	16	0.115	K.AYLPVIESFGFSSQLR.A
R2/RRR2-1/2	744.698	744.863	-222.549	0.246	288.264	0.257	8	0.115	-.FFAFGR.-
R2/RRR2-2/2	744.885	744.863	29.651	0.251	288.995	0.293	8	0.114	-.FFAFGR.-
R2/RRR2-5/2	744.707	744.863	-209.886	0.329	350.131	0.385	9	0.114	-.FFAFGR.-
R2/RRR2-3/2	890.800	891.049	-280.679	0.303	529.669	0.361	11	0.114	K.FSVSPVVR.V
R2/RRR2-1/2	744.829	744.863	-45.963	0.237	287.289	0.270	8	0.114	-.FFAFGR.-
R2/RRR2-8/2	891.331	891.049	317.020	0.325	539.435	0.381	11	0.114	-.FSVSPVVR.-
R2/RRR2-5/2	890.883	891.049	-186.786	0.264	499.872	0.398	11	0.113	K.FSVSPVVR.V
R2/RRR2-3/2	744.824	744.863	-51.717	0.286	284.976	0.348	8	0.112	-.FFAFGR.-
R2/RRR2-4/2	744.437	744.863	-573.602	0.213	337.781	0.282	9	0.112	-.FFAFGR.-
R2/RRR2-4/3	1819.850	1819.945	-52.727	0.426	1067.034	0.474	30	0.112	K.NATLTNEKESDACPIR.A
R2/RRR2-8/2	890.970	891.049	-89.338	0.299	468.964	0.365	10	0.111	-.FSVSPVVR.-
R2/RRR2-2/2	744.841	744.863	-29.524	0.189	340.323	0.264	9	0.111	-.FFAFGR.-
R2/RRR2-7/2	890.986	891.049	-71.472	0.244	634.519	0.333	11	0.110	K.FSVSPVVR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	744.350	744.863	-2038.269	0.206	341.662	0.349	9	0.110	-.FFAFGR.-
R2/RRR2-5/2	744.595	744.863	-361.361	0.214	286.121	0.280	8	0.110	-.FFAFGR.-
R2/RRR2-4/2	744.425	744.863	-589.401	0.225	278.153	0.366	8	0.109	-.FFAFGR.-
R2/RRR2-7/2	890.545	891.049	-1694.793	0.236	520.106	0.311	10	0.108	K.FSVSPVVR.V
R2/RRR2-1/2	1425.962	1425.569	276.339	0.285	667.235	0.329	13	0.108	R.LWGENFFDPATK.K
R2/RRR2-2/2	1424.471	1425.569	-1477.744	0.253	611.207	0.343	13	0.107	-.LWGENFFDPATK.-
R2/RRR2-4/2	1223.825	1224.344	-1244.510	0.310	789.133	0.255	15	0.106	K.ILSEEFGWDK.D
R2/RRR2-3/2	744.163	744.863	-2290.675	0.119	292.683	0.315	8	0.105	-.FFAFGR.-
R2/RRR2-5/2	1650.594	1651.841	-1365.649	0.416	1047.714	0.171	19	0.104	-.ILSEEFGWDKDLAK.-
R2/RRR2-5/3	1819.871	1819.945	-41.021	0.385	1023.991	0.437	28	0.102	K.NATLTNEKESDACPIR.A
R2/RRR2-1/2	1639.690	1639.845	-95.333	0.416	559.345	0.258	15	0.102	R.NCDPEGPLM*LYVSK.M
R2/RRR2-2/2	890.955	891.049	-105.830	0.285	371.992	0.288	9	0.102	-.FSVSPVVR.-
R2/RRR2-9/2	1814.421	1815.062	-907.103	0.353	785.281	0.204	17	0.101	K.AYLPVIESFGFSSQLR.A
R2/RRR2-3/3	1814.394	1815.062	-921.970	0.393	1104.750	0.389	27	0.098	K.AYLPVIESFGFSSQLR.A
R2/RRR2-5/3	1819.569	1819.945	-207.264	0.371	1091.158	0.366	27	0.094	K.NATLTNEKESDACPIR.A
R2/RRR2-2/3	1814.857	1815.062	-113.252	0.377	893.549	0.422	26	0.092	K.AYLPVIESFGFSSQLR.A
R2/RRR2-1/2	744.304	744.863	-2101.070	0.224	179.988	0.375	6	0.089	-.FFAFGR.-
R2/RRR2-5/3	1503.732	1503.774	-27.946	0.425	982.353	0.340	22	0.083	R.RVIYASQLTAKPR.L
R2/RRR2-4/3	1421.119	1421.624	-1062.094	0.368	888.105	0.376	21	0.083	K.FGVDEFKM*M*ER.L
R2/RRR2-13/3	1504.120	1503.774	230.672	0.443	1155.151	0.292	23	0.082	R.RVIYASQLTAKPR.L
R2/RRR2-1/3	1814.591	1815.062	-260.023	0.378	809.176	0.372	23	0.082	K.AYLPVIESFGFSSQLR.A
R2/RRR2-4/2	1867.226	1868.098	-1005.833	0.533	1122.367	0.593	20	0.081	K.GLKEQM*TPLSDFEDKL.-
R2/RRR2-2/3	1814.570	1815.062	-271.767	0.360	595.882	0.398	21	0.081	K.AYLPVIESFGFSSQLR.A
R2/RRR2-3/3	1503.130	1503.774	-1097.086	0.443	792.279	0.364	21	0.080	-.RVIYASQLTAKPR.-
R2/RRR2-6/3	1502.910	1503.774	-1244.008	0.312	1098.527	0.286	24	0.079	R.RVIYASQLTAKPR.L
R2/RRR2-7/3	1819.943	1819.945	-1.058	0.286	543.110	0.321	23	0.077	K.NATLTNEKESDACPIR.A
R2/RRR2-4/3	1422.604	1421.624	-14.263	0.411	797.770	0.316	20	0.075	K.FGVDEFKM*M*ER.L
R2/RRR2-4/3	1421.363	1421.624	-184.402	0.344	618.197	0.275	19	0.072	K.FGVDEFKM*M*ER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1503.859	1503.774	56.321	0.385	773.020	0.252	20	0.070	R.RVIYASQLTAKPR.L
R2/RRR2-3/3	1422.341	1421.624	-199.813	0.315	723.069	0.197	19	0.066	K.FGVDEFKM*M*ER.L
R2/RRR2-4/2	1868.557	1868.098	246.339	0.546	986.930	0.564	19	0.059	K.GLKEQM*TPLSDFEDKL.-
R2/RRR2-11/2	1917.430	1918.175	-912.711	0.629	3251.689	0.608	25	0.573	K.SLVEEDKLELATSLIEK.A
R2/RRR2-10/2	1917.601	1918.175	-823.369	0.622	3173.958	0.623	25	0.558	K.SLVEEDKLELATSLIEK.A
R2/RRR2-10/2	1917.768	1918.175	-213.084	0.599	3106.046	0.570	26	0.515	K.SLVEEDKLELATSLIEK.A
R2/RRR2-10/2	1918.552	1918.175	197.092	0.615	3001.846	0.557	25	0.480	K.SLVEEDKLELATSLIEK.A
R2/RRR2-11/2	1917.615	1918.175	-815.957	0.623	2754.444	0.576	24	0.426	K.SLVEEDKLELATSLIEK.A
R2/RRR2-11/2	1919.407	1918.175	121.032	0.625	2502.956	0.587	23	0.372	K.SLVEEDKLELATSLIEK.A
R2/RRR2-10/2	1574.462	1574.758	-188.703	0.507	2435.575	0.570	26	0.358	K.GVTTIIGGGDSVAAVEK.A
R2/RRR2-11/2	1920.554	1921.103	-808.588	0.542	2154.325	0.633	25	0.324	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-11/2	1803.374	1804.016	-913.095	0.491	2163.893	0.578	27	0.309	K.M*SHISTGGGASLELLEGK.T
R2/RRR2-11/3	1752.879	1752.048	-96.826	0.555	2390.031	0.423	34	0.284	K.LAATLPDGGVLLLENVR.F
R2/RRR2-11/2	1390.219	1389.578	-259.332	0.491	2012.432	0.487	21	0.257	K.ELDYLVGAVANPK.K
R2/RRR2-11/2	1389.177	1389.578	-289.933	0.506	2018.079	0.483	21	0.257	K.ELDYLVGAVANPK.K
R2/RRR2-10/2	1574.310	1574.758	-285.547	0.457	1877.566	0.565	24	0.253	K.GVTTIIGGGDSVAAVEK.A
R2/RRR2-11/2	1920.351	1921.103	-915.021	0.541	1684.587	0.629	23	0.242	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-11/2	1803.346	1804.016	-928.725	0.463	1739.350	0.562	26	0.233	K.M*SHISTGGGASLELLEGK.T
R2/RRR2-11/2	1920.718	1921.103	-200.836	0.543	1683.661	0.584	23	0.230	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-10/3	1917.717	1918.175	-239.816	0.481	2080.472	0.424	31	0.228	K.SLVEEDKLELATSLIEK.A
R2/RRR2-11/3	1752.105	1752.048	32.514	0.497	1865.882	0.513	30	0.224	K.LAATLPDGGVLLLENVR.F
R2/RRR2-11/3	1751.557	1752.048	-281.194	0.401	1843.744	0.427	28	0.193	K.LAATLPDGGVLLLENVR.F
R2/RRR2-13/2	1916.627	1918.175	-1857.067	0.454	1591.983	0.443	22	0.183	K.SLVEEDKLELATSLIEK.A
R2/RRR2-11/2	1043.087	1043.282	-187.174	0.512	1303.634	0.505	17	0.172	K.IGVIESLLAK.V
R2/RRR2-11/2	1774.409	1774.908	-282.119	0.539	1104.765	0.532	22	0.160	R.FYKEEEKNDPEFAK.K
R2/RRR2-11/2	1042.654	1043.282	-1566.206	0.443	1166.700	0.499	17	0.158	K.IGVIESLLAK.V
R2/RRR2-11/2	1751.464	1752.048	-907.273	0.483	957.794	0.578	25	0.155	K.LAATLPDGGVLLLENVR.F
R2/RRR2-11/2	1150.342	1150.261	69.969	0.440	1042.271	0.521	18	0.152	R.SVGTLTESDLK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1042.969	1043.282	-301.300	0.480	1128.583	0.474	16	0.152	K.IGVIESLLAK.V
R2/RRR2-11/2	1774.341	1774.908	-885.570	0.496	998.937	0.531	21	0.151	R.FYKEEEKNDPEFAK.K
R2/RRR2-11/2	1751.589	1752.048	-262.868	0.503	825.401	0.584	24	0.148	K.LAATLPDGGVLLLENVR.F
R2/RRR2-11/2	1774.153	1774.908	-992.148	0.495	915.631	0.524	20	0.144	R.FYKEEEKNDPEFAK.K
R2/RRR2-11/2	1092.592	1093.258	-1529.247	0.444	1274.629	0.370	17	0.144	K.FAAGTDAIAKK.L
R2/RRR2-11/2	1092.421	1093.258	-1686.845	0.437	1258.102	0.374	17	0.143	K.FAAGTDAIAKK.L
R2/RRR2-10/2	1074.995	1075.286	-271.709	0.455	755.625	0.567	17	0.142	K.KPFAAIVGGSK.V
R2/RRR2-11/2	1752.592	1752.048	-261.390	0.522	751.444	0.573	23	0.142	K.LAATLPDGGVLLLENVR.F
R2/RRR2-11/2	1573.278	1574.758	-1581.402	0.328	1256.080	0.400	18	0.141	K.GVTTIIGGGDSVAAVEK.A
R2/RRR2-11/2	1150.090	1150.261	-149.958	0.431	882.749	0.481	17	0.136	R.SVGTLTESDLK.G
R2/RRR2-11/3	1774.926	1774.908	10.297	0.472	1259.153	0.507	26	0.135	R.FYKEEEKNDPEFAK.K
R2/RRR2-11/2	964.987	965.085	-101.581	0.418	1078.384	0.375	18	0.134	K.FAAGTDAIAK.K
R2/RRR2-11/2	964.878	965.085	-214.781	0.386	1123.542	0.358	18	0.133	K.FAAGTDAIAK.K
R2/RRR2-11/2	1092.960	1093.258	-273.180	0.381	1031.457	0.401	16	0.131	K.FAAGTDAIAKK.L
R2/RRR2-10/2	1528.042	1526.800	159.162	0.479	807.308	0.471	20	0.130	K.GVSLLLPTDVVVADK.F
R2/RRR2-10/2	1075.236	1075.286	-46.414	0.395	751.137	0.453	17	0.127	K.KPFAAIVGGSK.V
R2/RRR2-11/2	1150.062	1150.261	-174.235	0.383	807.427	0.455	15	0.126	R.SVGTLTESDLK.G
R2/RRR2-11/2	1075.089	1075.286	-183.424	0.402	609.326	0.464	18	0.126	K.KPFAAIVGGSK.V
R2/RRR2-11/2	1072.893	1073.313	-392.293	0.398	416.850	0.510	14	0.126	K.YSLKPLVPR.L
R2/RRR2-10/2	965.111	965.085	27.198	0.395	1010.555	0.339	17	0.126	K.FAAGTDAIAK.K
R2/RRR2-10/2	1042.520	1043.282	-1695.359	0.381	997.233	0.346	15	0.124	-.IGVIESLLAK.-
R2/RRR2-11/2	964.966	965.085	-123.533	0.386	934.555	0.343	16	0.122	K.FAAGTDAIAK.K
R2/RRR2-11/2	1072.980	1073.313	-311.359	0.378	330.444	0.469	13	0.121	K.YSLKPLVPR.L
R2/RRR2-11/2	1075.109	1075.286	-164.858	0.363	514.794	0.452	17	0.121	K.KPFAAIVGGSK.V
R2/RRR2-11/3	1075.550	1075.286	245.947	0.442	1447.382	0.395	24	0.121	K.KPFAAIVGGSK.V
R2/RRR2-10/2	1075.169	1075.286	-108.822	0.367	521.637	0.414	17	0.119	K.KPFAAIVGGSK.V
R2/RRR2-11/2	1756.526	1755.030	283.234	0.468	900.727	0.358	18	0.116	K.TVIWNGPMGVFEFEK.F
R2/RRR2-10/3	1921.214	1921.103	57.979	0.334	1049.073	0.508	31	0.116	K.LASVADLYVNDAFGTAHR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1073.840	1073.313	-441.773	0.381	349.838	0.323	13	0.116	K.YSLKPLVPR.L
R2/RRR2-11/2	1526.405	1526.800	-259.055	0.387	589.709	0.394	18	0.112	-.GVSLLLPTDVVVADK.-
R2/RRR2-10/2	964.484	965.085	-1664.708	0.328	820.064	0.252	15	0.110	K.FAAGTDAIAK.K
R2/RRR2-10/2	1526.668	1526.800	-86.663	0.378	497.707	0.366	16	0.109	K.GVSLLLPTDVVVADK.F
R2/RRR2-11/3	1774.988	1774.908	45.476	0.448	884.838	0.509	22	0.107	R.FYKEEEKNDPEFAK.K
R2/RRR2-10/3	1774.914	1774.908	3.468	0.477	885.067	0.507	24	0.107	R.FYKEEEKNDPEFAK.K
R2/RRR2-10/2	964.785	965.085	-311.503	0.323	755.742	0.189	15	0.106	K.FAAGTDAIAK.K
R2/RRR2-11/2	1526.053	1526.800	-1148.153	0.293	467.517	0.348	15	0.105	K.GVSLLLPTDVVVADK.F
R2/RRR2-11/2	1573.430	1574.758	-1484.214	0.272	866.900	0.270	17	0.105	K.GVTTIIGGGDSVAAVEK.A
R2/RRR2-11/3	1922.042	1921.103	-31.514	0.422	922.835	0.488	34	0.104	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-11/3	1389.938	1389.578	259.179	0.453	1380.286	0.331	25	0.104	K.ELDYLVGAVANPK.K
R2/RRR2-11/3	1075.581	1075.286	275.052	0.426	1309.756	0.365	23	0.104	K.KPFAAIVGGSK.V
R2/RRR2-11/2	1803.400	1804.016	-898.825	0.251	542.586	0.350	16	0.102	K.M*SHISTGGGASLELLEGK.T
R2/RRR2-11/3	1921.461	1921.103	187.101	0.415	652.670	0.545	28	0.101	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-11/2	1573.469	1574.758	-1459.433	0.215	611.808	0.293	16	0.101	K.GVTTIIGGGDSVAAVEK.A
R2/RRR2-11/3	1775.031	1774.908	69.479	0.404	865.112	0.428	23	0.092	R.FYKEEEKNDPEFAK.K
R2/RRR2-10/3	1774.157	1774.908	-989.910	0.395	789.495	0.449	22	0.092	R.FYKEEEKNDPEFAK.K
R2/RRR2-10/3	1775.060	1774.908	86.032	0.408	766.977	0.452	22	0.091	R.FYKEEEKNDPEFAK.K
R2/RRR2-11/3	1921.003	1921.103	-51.959	0.327	678.988	0.474	30	0.089	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-11/3	1075.225	1075.286	-56.220	0.344	1440.723	0.241	25	0.086	K.KPFAAIVGGSK.V
R2/RRR2-11/3	1918.200	1918.175	12.816	0.406	874.803	0.404	23	0.086	K.SLVEEDKLELATSLIEK.A
R2/RRR2-11/3	1073.366	1073.313	49.651	0.398	784.855	0.422	18	0.086	K.YSLKPLVPR.L
R2/RRR2-11/3	1389.507	1389.578	-51.743	0.357	1416.148	0.224	25	0.085	K.ELDYLVGAVANPK.K
R2/RRR2-10/3	1920.447	1921.103	-864.393	0.296	488.943	0.465	25	0.083	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-10/3	1920.482	1921.103	-846.112	0.344	471.801	0.451	24	0.083	K.LASVADLYVNDAFGTAHR.A
R2/RRR2-10/3	1075.249	1075.286	-33.844	0.361	974.745	0.337	22	0.081	K.KPFAAIVGGSK.V
R2/RRR2-11/3	1072.917	1073.313	-370.730	0.380	692.080	0.376	17	0.080	K.YSLKPLVPR.L
R2/RRR2-10/3	1075.519	1075.286	217.095	0.360	880.239	0.299	21	0.075	K.KPFAAIVGGSK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1075.597	1075.286	289.903	0.333	847.093	0.282	20	0.072	K.KPFAAIVGGSK.V
R2/RRR2-10/3	1073.165	1073.313	-138.073	0.366	572.742	0.316	16	0.070	-.YSLKPLVPR.-
R2/RRR2-14/3	1917.323	1918.175	-968.932	0.318	746.811	0.298	24	0.069	K.SLVEEDKLELATSLIEK.A
R2/RRR2-10/3	1074.217	1073.313	-90.124	0.294	662.142	0.245	16	0.058	-.YSLKPLVPR.-
R2/RRR2-21/2	1930.543	1931.131	-824.762	0.640	3820.195	0.681	31	0.800	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/2	1930.497	1931.131	-849.010	0.619	3502.094	0.674	29	0.689	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/1	1219.557	1220.313	-1444.573	0.204	849.304	0.320	16	0.670	K.LNPAVDDGGSFK.T
R2/RRR2-22/2	1930.504	1931.131	-845.328	0.620	3368.802	0.692	29	0.655	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-22/2	1930.323	1931.131	-939.344	0.630	3320.791	0.698	29	0.642	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/1	1219.617	1220.313	-1394.809	0.211	768.363	0.342	15	0.588	K.LNPAVDDGGSFK.T
R2/RRR2-21/2	1913.362	1914.037	-878.485	0.594	3278.503	0.594	27	0.583	K.M*NVEYELEDGGSLSPEK.E
R2/RRR2-22/1	1219.527	1220.313	-1468.904	0.116	844.950	0.062	16	0.579	K.LNPAVDDGGSFK.T
R2/RRR2-21/2	1930.599	1931.131	-795.883	0.631	3098.609	0.686	28	0.569	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/2	1914.368	1914.037	173.072	0.641	3155.773	0.637	27	0.566	K.M*NVEYELEDGGSLSPEK.E
R2/RRR2-22/1	1219.589	1220.313	-1417.931	0.188	759.970	0.247	15	0.539	K.LNPAVDDGGSFK.T
R2/RRR2-21/1	1219.556	1220.313	-1445.377	0.136	741.302	0.237	15	0.518	K.LNPAVDDGGSFK.T
R2/RRR2-21/3	1930.605	1931.131	-792.653	0.522	2746.275	0.674	38	0.514	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/3	1951.169	1951.170	-0.453	0.554	2870.283	0.497	37	0.445	R.DNAAHVIKSEVLDVPAGSK.V
R2/RRR2-21/3	1931.921	1931.131	-108.988	0.545	2548.943	0.651	37	0.441	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/3	1931.041	1931.131	-46.331	0.532	2408.124	0.659	37	0.407	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-22/3	1932.145	1931.131	7.463	0.568	2335.878	0.664	37	0.388	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-22/1	1219.569	1220.313	-1434.419	0.121	634.533	0.086	14	0.375	K.LNPAVDDGGSFK.T
R2/RRR2-22/3	1931.138	1931.131	3.695	0.564	2258.218	0.670	36	0.373	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/2	1896.981	1898.038	-1087.328	0.544	2410.017	0.557	25	0.350	K.MNVEYELEDGGSLSPEK.E
R2/RRR2-21/3	1951.522	1951.170	180.894	0.580	2219.723	0.580	35	0.319	R.DNAAHVIKSEVLDVPAGSK.V
R2/RRR2-22/3	1950.888	1951.170	-145.145	0.517	2363.528	0.502	35	0.318	R.DNAAHVIKSEVLDVPAGSK.V
R2/RRR2-22/2	1338.945	1339.455	-1131.290	0.517	2064.928	0.582	22	0.289	K.VEGDGGAGTVTTM*K.L
R2/RRR2-22/2	1668.056	1668.849	-1077.893	0.434	1930.899	0.596	21	0.288	K.M*IEDYLVAHPTEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/3	1931.849	1931.131	-146.068	0.540	1952.607	0.621	35	0.281	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/3	1951.992	1951.170	-91.748	0.570	2000.775	0.565	33	0.267	R.DNAAHVIKSEVLDVPAGSK.V
R2/RRR2-21/2	1339.038	1339.455	-312.491	0.507	1945.213	0.551	23	0.260	K.VEGDGGAGTVTTM*K.L
R2/RRR2-22/2	1668.235	1668.849	-970.331	0.514	1825.341	0.611	21	0.250	K.M*IEDYLVAHPTEYA.-
R2/RRR2-22/3	1950.942	1951.170	-117.465	0.536	2232.653	0.414	36	0.247	R.DNAAHVIKSEVLDVPAGSK.V
R2/RRR2-20/3	1931.072	1931.131	-30.448	0.526	1654.700	0.662	33	0.243	K.SHVTETKIEAAGAGSCLAK.M
R2/RRR2-21/2	1339.007	1339.455	-335.358	0.483	1725.028	0.594	22	0.238	K.VEGDGGAGTVTTM*K.L
R2/RRR2-21/2	1669.193	1668.849	206.772	0.484	1777.383	0.571	20	0.236	K.M*IEDYLVAHPTEYA.-
R2/RRR2-21/2	1339.037	1339.455	-312.949	0.499	1677.222	0.554	21	0.221	K.VEGDGGAGTVTTM*K.L
R2/RRR2-21/2	1651.875	1652.849	-1198.784	0.370	1697.708	0.579	20	0.219	K.MIEDYLVAHPTEYA.-
R2/RRR2-21/2	1652.200	1652.849	-1000.983	0.436	1642.614	0.603	19	0.203	K.MIEDYLVAHPTEYA.-
R2/RRR2-22/3	1950.970	1951.170	-102.684	0.539	1777.588	0.497	32	0.201	R.DNAAHVIKSEVLDVPAGSK.V
R2/RRR2-21/2	1668.242	1668.849	-965.776	0.489	1648.506	0.601	20	0.200	K.M*IEDYLVAHPTEYA.-
R2/RRR2-21/2	1652.093	1652.849	-1066.265	0.408	1620.029	0.565	20	0.193	K.MIEDYLVAHPTEYA.-
R2/RRR2-22/2	1338.926	1339.455	-1145.388	0.498	1396.840	0.550	20	0.186	K.VEGDGGAGTVTTM*K.L
R2/RRR2-21/2	1148.020	1148.285	-231.496	0.462	1386.565	0.476	19	0.171	K.IEAAGAGSCLAK.M
R2/RRR2-21/2	1148.064	1148.285	-193.201	0.471	1183.361	0.496	18	0.157	K.IEAAGAGSCLAK.M
R2/RRR2-22/2	1147.509	1148.285	-1553.050	0.366	1339.275	0.430	19	0.157	K.IEAAGAGSCLAK.M
R2/RRR2-20/2	1147.839	1148.285	-389.826	0.486	1226.901	0.474	18	0.157	K.IEAAGAGSCLAK.M
R2/RRR2-21/2	1270.247	1270.565	-251.535	0.512	958.731	0.558	18	0.155	K.LILDGYFGMLK.M
R2/RRR2-22/2	1287.425	1286.565	-108.617	0.554	1111.829	0.496	18	0.154	K.LILDGYFGM*LK.M
R2/RRR2-22/2	1147.939	1148.285	-302.760	0.459	1228.348	0.448	18	0.152	K.IEAAGAGSCLAK.M
R2/RRR2-21/2	1287.180	1286.565	-299.829	0.541	1081.116	0.495	18	0.152	K.LILDGYFGM*LK.M
R2/RRR2-21/2	1667.293	1668.849	-2138.778	0.347	1472.782	0.458	19	0.152	K.M*IEDYLVAHPTEYA.-
R2/RRR2-22/2	1286.374	1286.565	-148.967	0.478	1119.088	0.474	18	0.150	K.LILDGYFGM*LK.M
R2/RRR2-21/2	1323.183	1323.456	-206.402	0.345	1102.437	0.524	19	0.150	K.VEGDGGAGTVTTMK.L
R2/RRR2-22/2	1148.076	1148.285	-182.641	0.477	1140.651	0.468	18	0.149	K.IEAAGAGSCLAK.M
R2/RRR2-20/2	1338.713	1339.455	-1305.440	0.431	957.295	0.557	20	0.149	K.VEGDGGAGTVTTM*K.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1271.197	1270.565	-290.259	0.492	934.173	0.508	18	0.146	K.LILDGYFGMLK.M
R2/RRR2-21/2	1324.119	1323.456	-254.801	0.342	1013.940	0.540	18	0.145	K.VEGDGGAGTVTTMK.L
R2/RRR2-21/2	1286.109	1286.565	-355.389	0.469	1092.976	0.449	18	0.145	K.LILDGYFGM*LK.M
R2/RRR2-21/2	1286.159	1286.565	-316.631	0.492	1072.681	0.438	18	0.142	K.LILDGYFGM*LK.M
R2/RRR2-21/2	1147.327	1148.285	-1711.767	0.349	1200.066	0.399	18	0.141	K.IEAAGAGSCLAK.M
R2/RRR2-22/2	1101.536	1102.220	-1533.169	0.358	1382.670	0.298	17	0.139	K.SEVLDVPAGSK.V
R2/RRR2-21/2	1270.315	1270.565	-197.451	0.482	890.613	0.467	18	0.138	K.LILDGYFGMLK.M
R2/RRR2-22/2	1270.082	1270.565	-381.901	0.446	901.601	0.458	18	0.136	K.LILDGYFGMLK.M
R2/RRR2-21/2	1285.960	1286.565	-1252.025	0.448	985.738	0.427	17	0.135	K.LILDGYFGM*LK.M
R2/RRR2-22/2	1271.080	1270.565	-382.757	0.524	885.855	0.421	18	0.132	K.LILDGYFGMLK.M
R2/RRR2-21/2	1285.989	1286.565	-1228.956	0.418	1155.268	0.340	18	0.132	K.LILDGYFGM*LK.M
R2/RRR2-21/2	1271.264	1270.565	-238.043	0.468	854.042	0.431	18	0.132	K.LILDGYFGMLK.M
R2/RRR2-21/2	1101.492	1102.220	-1573.135	0.368	1141.044	0.347	16	0.130	K.SEVLDVPAGSK.V
R2/RRR2-20/2	1148.002	1148.285	-247.177	0.409	902.715	0.445	16	0.130	K.IEAAGAGSCLAK.M
R2/RRR2-21/2	1270.019	1270.565	-1221.128	0.481	901.755	0.393	18	0.129	K.LILDGYFGMLK.M
R2/RRR2-22/2	1094.018	1094.279	-239.230	0.323	1158.349	0.332	16	0.129	K.VCAGFIDAIK.V
R2/RRR2-21/2	1285.964	1286.565	-1248.498	0.290	1081.953	0.374	16	0.129	K.LILDGYFGM*LK.M
R2/RRR2-22/2	1269.912	1270.565	-1306.172	0.392	876.164	0.408	18	0.128	K.LILDGYFGMLK.M
R2/RRR2-22/2	1101.399	1102.220	-1658.532	0.360	1076.417	0.365	15	0.128	K.SEVLDVPAGSK.V
R2/RRR2-23/2	1148.374	1148.285	77.659	0.387	932.088	0.420	16	0.128	K.IEAAGAGSCLAK.M
R2/RRR2-21/2	1101.958	1102.220	-238.839	0.408	1041.581	0.354	16	0.127	K.SEVLDVPAGSK.V
R2/RRR2-21/2	1101.904	1102.220	-287.519	0.398	1139.854	0.316	16	0.126	K.SEVLDVPAGSK.V
R2/RRR2-21/2	1093.301	1094.279	-1814.833	0.300	1102.954	0.335	16	0.125	K.VCAGFIDAIK.V
R2/RRR2-21/2	1477.483	1477.604	-82.505	0.387	574.157	0.526	19	0.125	K.LNPAVDDGGSFKTR.V
R2/RRR2-22/2	1078.940	1079.252	-289.207	0.363	606.841	0.459	14	0.122	K.VFSDAPAM*PK.V
R2/RRR2-22/2	1286.001	1286.565	-1219.996	0.378	895.877	0.359	16	0.122	K.LILDGYFGM*LK.M
R2/RRR2-22/2	1102.027	1102.220	-175.385	0.384	1070.755	0.291	16	0.120	K.SEVLDVPAGSK.V
R2/RRR2-21/2	1220.119	1220.313	-160.116	0.308	746.644	0.393	17	0.118	K.LNPAVDDGGSFK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1220.877	1220.313	-358.583	0.401	576.107	0.399	16	0.118	K.LNPAVDDGGSFK.T
R2/RRR2-21/2	1063.021	1063.252	-218.102	0.343	506.168	0.434	13	0.118	K.VFSDAPAMPK.V
R2/RRR2-22/2	1078.820	1079.252	-400.801	0.331	745.267	0.350	15	0.116	K.VFSDAPAM*PK.V
R2/RRR2-21/2	1219.980	1220.313	-274.243	0.331	587.000	0.421	15	0.116	K.LNPAVDDGGSFK.T
R2/RRR2-22/2	1078.959	1079.252	-271.613	0.366	723.540	0.332	15	0.116	K.VFSDAPAM*PK.V
R2/RRR2-21/2	1219.973	1220.313	-279.965	0.269	782.262	0.361	18	0.116	K.LNPAVDDGGSFK.T
R2/RRR2-21/2	1543.393	1543.852	-298.432	0.486	813.890	0.325	19	0.115	K.EKLILDGYFGM*LK.M
R2/RRR2-21/2	1078.822	1079.252	-399.325	0.320	704.608	0.325	15	0.114	K.VFSDAPAM*PK.V
R2/RRR2-21/2	1063.091	1063.252	-152.210	0.319	642.849	0.348	14	0.114	K.VFSDAPAMPK.V
R2/RRR2-22/2	1543.088	1543.852	-1146.531	0.462	786.477	0.328	18	0.113	K.EKLILDGYFGM*LK.M
R2/RRR2-22/2	1219.690	1220.313	-1334.657	0.287	674.603	0.355	15	0.112	K.LNPAVDDGGSFK.T
R2/RRR2-21/2	1078.451	1079.252	-1674.973	0.283	563.866	0.303	14	0.111	K.VFSDAPAM*PK.V
R2/RRR2-22/2	1094.014	1094.279	-243.595	0.291	1104.312	0.188	16	0.110	K.VCAGFIDAIK.V
R2/RRR2-25/2	1219.855	1220.313	-376.648	0.240	385.531	0.442	13	0.110	K.LNPAVDDGGSFK.T
R2/RRR2-20/2	1286.001	1286.565	-1219.614	0.270	707.611	0.295	14	0.110	K.LILDGYFGM*LK.M
R2/RRR2-22/2	1221.270	1220.313	-35.451	0.296	483.827	0.308	14	0.109	K.LNPAVDDGGSFK.T
R2/RRR2-25/2	1101.984	1102.220	-215.279	0.374	787.410	0.292	13	0.109	-.SEVLDVPAGSK.-
R2/RRR2-24/2	1101.246	1102.220	-1798.182	0.292	801.016	0.285	13	0.109	K.SEVLDVPAGSK.V
R2/RRR2-25/2	1101.359	1102.220	-1694.499	0.272	649.895	0.375	12	0.109	-.SEVLDVPAGSK.-
R2/RRR2-21/2	1219.908	1220.313	-333.475	0.258	413.726	0.330	13	0.109	K.LNPAVDDGGSFK.T
R2/RRR2-21/2	1078.389	1079.252	-1732.745	0.223	564.023	0.253	14	0.107	K.VFSDAPAM*PK.V
R2/RRR2-19/2	1080.047	1079.252	-190.059	0.343	303.955	0.306	12	0.106	-.VFSDAPAM*PK.-
R2/RRR2-21/2	1219.146	1220.313	-1783.062	0.205	524.173	0.267	15	0.106	K.LNPAVDDGGSFK.T
R2/RRR2-20/2	1219.239	1220.313	-1706.204	0.182	431.723	0.332	14	0.106	K.LNPAVDDGGSFK.T
R2/RRR2-21/2	1477.389	1477.604	-146.322	0.211	154.597	0.361	14	0.106	K.LNPAVDDGGSFKTR.V
R2/RRR2-19/2	1102.152	1102.220	-62.166	0.343	849.968	0.233	14	0.105	-.SEVLDVPAGSK.-
R2/RRR2-24/2	1219.843	1220.313	-386.689	0.159	473.574	0.301	14	0.104	K.LNPAVDDGGSFK.T
R2/RRR2-22/2	1219.849	1220.313	-381.669	0.160	539.423	0.249	14	0.103	K.LNPAVDDGGSFK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1101.240	1102.220	-1803.640	0.218	672.307	0.118	13	0.102	-.SEVLDVPAGSK.-
R2/RRR2-22/2	1651.796	1652.849	-1246.799	0.321	1214.303	0.484	17	0.101	K.MIEDYLVAHPTEYA.-
R2/RRR2-19/2	1102.127	1102.220	-84.719	0.375	663.838	0.277	12	0.097	-.SEVLDVPAGSK.-
R2/RRR2-25/2	1101.417	1102.220	-1642.053	0.254	501.692	0.292	11	0.086	-.SEVLDVPAGSK.-
R2/RRR2-21/2	1652.404	1652.849	-270.347	0.309	1024.013	0.489	17	0.067	K.MIEDYLVAHPTEYA.-
R2/RRR2-21/2	1667.818	1668.849	-1221.199	0.315	729.322	0.208	18	0.020	K.M*IEDYLVAHPTEYA.-
R2/RRR2-7/2	1983.425	1983.204	111.879	0.593	2628.851	0.584	26	0.401	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-8/2	1746.337	1745.940	227.957	0.581	2590.372	0.581	26	0.393	R.HMDGFGVNTYTFVTR.D
R2/RRR2-7/2	1983.310	1983.204	53.609	0.577	2598.103	0.565	26	0.387	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-8/2	1982.579	1983.204	-822.260	0.602	2602.786	0.562	26	0.386	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-8/2	1746.348	1745.940	234.686	0.569	2459.826	0.599	26	0.372	R.HMDGFGVNTYTFVTR.D
R2/RRR2-2/2	1982.269	1983.204	-979.026	0.546	2527.563	0.531	26	0.360	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-8/2	1745.450	1745.940	-281.609	0.529	2382.432	0.571	26	0.346	R.HMDGFGVNTYTFVTR.D
R2/RRR2-8/2	1982.531	1983.204	-846.303	0.561	2387.375	0.548	25	0.336	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-8/2	1982.168	1983.204	-1030.468	0.536	2391.749	0.520	25	0.328	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-2/2	1982.808	1983.204	-200.413	0.547	2293.530	0.565	25	0.324	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-7/2	1982.705	1983.204	-252.543	0.543	2294.837	0.552	25	0.320	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-1/2	1540.406	1540.785	-246.765	0.558	2001.050	0.549	20	0.265	R.GPILLEDYHLIEK.L
R2/RRR2-5/2	1540.499	1540.785	-186.028	0.550	1941.094	0.518	20	0.247	R.GPILLEDYHLIEK.L
R2/RRR2-2/2	1539.992	1540.785	-1167.972	0.566	1865.604	0.542	20	0.242	R.GPILLEDYHLIEK.L
R2/RRR2-8/2	1540.261	1540.785	-992.570	0.558	1836.328	0.547	20	0.239	R.GPILLEDYHLIEK.L
R2/RRR2-7/2	1539.810	1540.785	-1286.427	0.532	1869.061	0.523	20	0.238	R.GPILLEDYHLIEK.L
R2/RRR2-7/2	1540.406	1540.785	-246.844	0.569	1849.038	0.520	20	0.233	R.GPILLEDYHLIEK.L
R2/RRR2-1/2	1540.316	1540.785	-305.362	0.540	1834.680	0.519	20	0.232	R.GPILLEDYHLIEK.L
R2/RRR2-8/2	1539.695	1540.785	-1361.192	0.547	1854.846	0.507	20	0.231	R.GPILLEDYHLIEK.L
R2/RRR2-2/2	1539.737	1540.785	-1333.880	0.524	1784.655	0.520	20	0.225	R.GPILLEDYHLIEK.L
R2/RRR2-8/2	1527.598	1527.856	-169.566	0.539	1614.122	0.541	20	0.206	R.LGPNYLMLPVNAPK.C
R2/RRR2-1/2	1544.392	1543.855	-301.288	0.560	1428.933	0.561	21	0.191	R.LGPNYLM*LPVNAPK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1540.115	1540.785	-1087.267	0.523	1529.435	0.486	20	0.186	R.GPILLEDYHLIEK.L
R2/RRR2-8/2	1761.375	1761.939	-890.740	0.538	1148.371	0.603	25	0.177	R.HM*DGFGVNTYTFVTR.D
R2/RRR2-8/2	1761.327	1761.939	-917.874	0.553	1148.054	0.585	25	0.174	R.HM*DGFGVNTYTFVTR.D
R2/RRR2-8/2	1527.494	1527.856	-237.869	0.512	1314.579	0.542	19	0.173	R.LGPNYLMLPVNAPK.C
R2/RRR2-1/2	1543.330	1543.855	-991.213	0.521	1378.502	0.507	20	0.173	R.LGPNYLM*LPVNAPK.C
R2/RRR2-7/2	1125.074	1125.303	-204.658	0.499	1345.163	0.486	18	0.169	R.SPGAQTPVIVR.F
R2/RRR2-7/2	1544.505	1543.855	-227.622	0.580	1260.053	0.530	20	0.167	R.LGPNYLM*LPVNAPK.C
R2/RRR2-2/2	1543.346	1543.855	-980.890	0.530	1298.786	0.509	19	0.165	R.LGPNYLM*LPVNAPK.C
R2/RRR2-8/2	1544.446	1543.855	-265.603	0.599	1174.716	0.564	19	0.165	R.LGPNYLM*LPVNAPK.C
R2/RRR2-8/2	1761.412	1761.939	-869.451	0.541	985.390	0.608	24	0.165	R.HM*DGFGVNTYTFVTR.D
R2/RRR2-7/2	1126.050	1125.303	-225.574	0.478	1407.621	0.437	18	0.165	R.SPGAQTPVIVR.F
R2/RRR2-7/2	1543.472	1543.855	-248.954	0.504	1342.099	0.485	19	0.165	R.LGPNYLM*LPVNAPK.C
R2/RRR2-6/2	1543.377	1543.855	-311.164	0.526	1354.533	0.469	19	0.162	R.LGPNYLM*LPVNAPK.C
R2/RRR2-3/2	1544.275	1543.855	272.548	0.519	1136.211	0.548	19	0.160	R.LGPNYLM*LPVNAPK.C
R2/RRR2-8/2	1544.321	1543.855	302.350	0.550	1169.675	0.533	19	0.159	R.LGPNYLM*LPVNAPK.C
R2/RRR2-7/2	1540.568	1540.785	-141.116	0.514	1356.816	0.444	18	0.159	R.GPILLEDYHLIEK.L
R2/RRR2-8/2	969.959	970.107	-153.066	0.497	1270.046	0.460	14	0.158	R.FAGELAHPK.V
R2/RRR2-3/2	1543.344	1543.855	-982.557	0.508	1267.271	0.482	19	0.158	R.LGPNYLM*LPVNAPK.C
R2/RRR2-3/2	1539.394	1540.785	-1558.071	0.348	1394.894	0.402	18	0.155	R.GPILLEDYHLIEK.L
R2/RRR2-8/2	1543.386	1543.855	-304.895	0.496	1130.158	0.525	18	0.154	R.LGPNYLM*LPVNAPK.C
R2/RRR2-8/2	1125.089	1125.303	-191.161	0.489	1245.046	0.446	18	0.154	R.SPGAQTPVIVR.F
R2/RRR2-7/2	1124.592	1125.303	-1526.452	0.478	1228.429	0.451	18	0.153	R.SPGAQTPVIVR.F
R2/RRR2-6/2	1124.531	1125.303	-1580.755	0.496	1132.153	0.487	18	0.153	R.SPGAQTPVIVR.F
R2/RRR2-7/2	970.142	970.107	37.027	0.510	1169.463	0.470	14	0.153	R.FAGELAHPK.V
R2/RRR2-8/2	1527.358	1527.856	-327.191	0.497	1173.103	0.499	18	0.153	R.LGPNYLMLPVNAPK.C
R2/RRR2-6/2	1543.374	1543.855	-312.751	0.463	1163.109	0.501	18	0.153	R.LGPNYLM*LPVNAPK.C
R2/RRR2-6/2	1125.108	1125.303	-174.182	0.495	1165.126	0.464	18	0.152	R.SPGAQTPVIVR.F
R2/RRR2-1/2	1124.433	1125.303	-1667.893	0.457	1185.542	0.457	18	0.151	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1124.867	1125.303	-388.862	0.514	1038.558	0.514	17	0.151	R.SPGAQTPVIVR.F
R2/RRR2-2/2	1543.298	1543.855	-1012.416	0.510	1309.349	0.429	19	0.151	R.LGPNYLM*LPVNAPK.C
R2/RRR2-2/2	1543.417	1543.855	-285.136	0.534	1116.299	0.512	18	0.151	R.LGPNYLM*LPVNAPK.C
R2/RRR2-2/2	1125.204	1125.303	-88.858	0.496	1122.330	0.471	18	0.150	R.SPGAQTPVIVR.F
R2/RRR2-8/3	1951.562	1952.248	-866.390	0.448	1341.368	0.526	31	0.150	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-7/2	969.950	970.107	-162.409	0.499	1143.600	0.444	16	0.149	R.FAGELAHPK.V
R2/RRR2-8/2	1125.398	1125.303	84.793	0.418	1270.297	0.416	17	0.149	R.SPGAQTPVIVR.F
R2/RRR2-3/2	1543.332	1543.855	-990.022	0.486	1125.907	0.496	18	0.149	R.LGPNYLM*LPVNAPK.C
R2/RRR2-7/2	969.998	970.107	-112.542	0.459	1027.887	0.495	15	0.149	R.FAGELAHPK.V
R2/RRR2-8/2	1125.505	1125.303	179.644	0.428	1202.174	0.440	17	0.149	R.SPGAQTPVIVR.F
R2/RRR2-8/2	1273.130	1273.287	-123.541	0.462	1379.713	0.354	15	0.148	R.DEEVDYYPSR.H
R2/RRR2-4/2	1125.086	1125.303	-193.229	0.507	1058.871	0.486	17	0.148	R.SPGAQTPVIVR.F
R2/RRR2-5/2	1125.050	1125.303	-225.340	0.486	1071.471	0.478	17	0.147	R.SPGAQTPVIVR.F
R2/RRR2-8/2	969.939	970.107	-173.266	0.539	1067.862	0.457	15	0.146	R.FAGELAHPK.V
R2/RRR2-3/2	1071.036	1071.168	-123.188	0.491	952.642	0.497	15	0.146	R.VFAYADTQR.Y
R2/RRR2-4/2	1124.627	1125.303	-1494.941	0.487	1066.998	0.463	18	0.146	R.SPGAQTPVIVR.F
R2/RRR2-4/2	1544.572	1543.855	-184.014	0.523	998.976	0.514	18	0.144	R.LGPNYLM*LPVNAPK.C
R2/RRR2-7/2	1070.845	1071.168	-302.032	0.478	1008.093	0.467	15	0.144	R.VFAYADTQR.Y
R2/RRR2-10/2	1125.016	1125.303	-256.254	0.502	978.993	0.486	17	0.143	R.SPGAQTPVIVR.F
R2/RRR2-6/2	1543.412	1543.855	-288.310	0.481	1135.821	0.451	18	0.142	R.LGPNYLM*LPVNAPK.C
R2/RRR2-6/2	1124.711	1125.303	-1420.042	0.487	1015.986	0.466	17	0.142	R.SPGAQTPVIVR.F
R2/RRR2-9/2	1125.375	1125.303	64.123	0.492	1102.982	0.435	17	0.142	R.SPGAQTPVIVR.F
R2/RRR2-8/2	1273.965	1273.287	-253.684	0.454	1311.591	0.350	15	0.142	R.DEEVDYYPSR.H
R2/RRR2-3/2	1124.564	1125.303	-1551.640	0.486	892.537	0.503	17	0.142	R.SPGAQTPVIVR.F
R2/RRR2-7/2	1527.140	1527.856	-1127.212	0.440	1045.481	0.471	19	0.141	R.LGPNYLMLPVNAPK.C
R2/RRR2-1/2	1072.021	1071.168	-137.465	0.486	938.266	0.468	15	0.141	R.VFAYADTQR.Y
R2/RRR2-2/2	1070.815	1071.168	-330.511	0.492	867.994	0.486	15	0.141	R.VFAYADTQR.Y
R2/RRR2-7/2	1124.669	1125.303	-1457.435	0.484	1048.273	0.444	17	0.141	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1125.020	1125.303	-252.662	0.439	1011.848	0.458	17	0.140	R.SPGAQTPVIVR.F
R2/RRR2-7/2	1543.404	1543.855	-293.468	0.502	1089.483	0.458	18	0.140	R.LGPNYLM*LPVNAPK.C
R2/RRR2-8/2	1125.162	1125.303	-125.641	0.502	971.318	0.466	17	0.140	R.SPGAQTPVIVR.F
R2/RRR2-8/3	1951.838	1952.248	-210.783	0.512	1134.308	0.566	28	0.140	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-5/2	1124.601	1125.303	-1518.601	0.465	1009.143	0.449	17	0.139	R.SPGAQTPVIVR.F
R2/RRR2-1/2	1124.447	1125.303	-1655.787	0.470	1081.599	0.414	18	0.139	R.SPGAQTPVIVR.F
R2/RRR2-1/2	969.365	970.107	-1802.337	0.431	948.681	0.470	14	0.139	R.FAGELAHPK.V
R2/RRR2-3/2	1124.720	1125.303	-1411.757	0.489	895.419	0.481	17	0.139	R.SPGAQTPVIVR.F
R2/RRR2-10/2	1125.130	1125.303	-154.808	0.491	988.375	0.450	17	0.139	R.SPGAQTPVIVR.F
R2/RRR2-3/2	1124.255	1125.303	-1827.049	0.407	899.367	0.499	16	0.138	R.SPGAQTPVIVR.F
R2/RRR2-6/2	969.985	970.107	-125.797	0.437	918.964	0.473	14	0.138	R.FAGELAHPK.V
R2/RRR2-1/2	1761.386	1761.939	-884.270	0.500	656.761	0.570	21	0.138	R.HM*DGFGVNTYTFVTR.D
R2/RRR2-1/2	1072.005	1071.168	-152.201	0.478	907.871	0.454	15	0.138	R.VFAYADTQR.Y
R2/RRR2-8/3	1952.317	1952.248	35.451	0.461	1251.018	0.516	30	0.138	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-8/2	969.880	970.107	-234.124	0.525	938.336	0.453	14	0.138	R.FAGELAHPK.V
R2/RRR2-8/2	1125.056	1125.303	-220.441	0.490	936.278	0.459	17	0.138	R.SPGAQTPVIVR.F
R2/RRR2-8/2	1070.969	1071.168	-186.531	0.478	958.244	0.434	15	0.137	R.VFAYADTQR.Y
R2/RRR2-1/2	1124.940	1125.303	-323.969	0.477	1035.246	0.424	17	0.137	R.SPGAQTPVIVR.F
R2/RRR2-3/2	1071.111	1071.168	-52.994	0.456	885.822	0.455	15	0.137	R.VFAYADTQR.Y
R2/RRR2-4/2	1124.990	1125.303	-279.224	0.477	994.894	0.433	17	0.137	R.SPGAQTPVIVR.F
R2/RRR2-5/2	1071.128	1071.168	-37.105	0.505	923.463	0.433	15	0.136	R.VFAYADTQR.Y
R2/RRR2-8/2	1071.002	1071.168	-154.973	0.443	1058.836	0.390	15	0.135	R.VFAYADTQR.Y
R2/RRR2-4/2	1543.106	1543.855	-1136.954	0.463	1126.560	0.405	18	0.135	R.LGPNYLM*LPVNAPK.C
R2/RRR2-7/2	1070.888	1071.168	-261.775	0.495	897.826	0.428	15	0.134	R.VFAYADTQR.Y
R2/RRR2-9/2	1125.213	1125.303	-80.261	0.413	1049.489	0.403	17	0.134	R.SPGAQTPVIVR.F
R2/RRR2-8/3	1982.400	1983.204	-912.945	0.443	1482.933	0.409	30	0.134	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-1/2	1543.442	1543.855	-268.870	0.505	949.052	0.462	18	0.134	R.LGPNYLM*LPVNAPK.C
R2/RRR2-4/2	969.817	970.107	-299.788	0.395	1108.726	0.372	14	0.133	R.FAGELAHPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1071.109	1071.168	-55.395	0.464	918.084	0.416	15	0.133	R.VFAYADTQR.Y
R2/RRR2-5/2	1071.019	1071.168	-138.851	0.413	928.615	0.416	15	0.133	R.VFAYADTQR.Y
R2/RRR2-5/2	1070.900	1071.168	-251.140	0.504	892.230	0.406	15	0.132	R.VFAYADTQR.Y
R2/RRR2-8/2	1104.843	1105.188	-312.574	0.425	784.452	0.481	12	0.131	-.SHVQEYWR.-
R2/RRR2-8/2	1104.962	1105.188	-204.837	0.452	885.643	0.425	13	0.130	-.SHVQEYWR.-
R2/RRR2-12/2	1071.397	1071.168	214.315	0.427	749.047	0.468	13	0.130	R.VFAYADTQR.Y
R2/RRR2-9/2	1124.645	1125.303	-1479.131	0.429	943.896	0.402	17	0.130	R.SPGAQTPVIVR.F
R2/RRR2-2/2	1070.442	1071.168	-1616.822	0.411	925.959	0.393	15	0.130	R.VFAYADTQR.Y
R2/RRR2-2/2	969.325	970.107	-1843.335	0.418	904.700	0.411	14	0.130	R.FAGELAHPK.V
R2/RRR2-8/2	1273.105	1273.287	-143.258	0.388	1307.022	0.267	15	0.129	R.DEEVDYYPSR.H
R2/RRR2-5/2	1125.206	1125.303	-86.681	0.489	700.660	0.473	15	0.129	R.SPGAQTPVIVR.F
R2/RRR2-1/2	969.705	970.107	-415.352	0.457	896.891	0.401	14	0.129	R.FAGELAHPK.V
R2/RRR2-10/2	1071.038	1071.168	-121.016	0.419	926.387	0.393	14	0.129	R.VFAYADTQR.Y
R2/RRR2-4/2	1072.173	1071.168	4.955	0.388	915.247	0.395	14	0.128	R.VFAYADTQR.Y
R2/RRR2-11/2	1125.076	1125.303	-202.699	0.437	930.607	0.382	17	0.128	R.SPGAQTPVIVR.F
R2/RRR2-8/2	1603.177	1603.755	-987.297	0.481	1240.179	0.294	19	0.127	K.LFVQVIDPEEEER.F
R2/RRR2-7/2	989.006	989.110	-105.056	0.479	629.571	0.461	11	0.127	R.FSTVIHER.G
R2/RRR2-10/2	1070.252	1071.168	-1795.688	0.378	925.414	0.370	15	0.127	R.VFAYADTQR.Y
R2/RRR2-1/2	1071.063	1071.168	-98.493	0.465	925.529	0.351	15	0.126	R.VFAYADTQR.Y
R2/RRR2-8/2	1604.328	1603.755	-266.543	0.533	1058.714	0.362	18	0.126	K.LFVQVIDPEEEER.F
R2/RRR2-8/2	988.443	989.110	-1690.998	0.437	615.448	0.455	11	0.125	R.FSTVIHER.G
R2/RRR2-8/2	1104.473	1105.188	-1557.139	0.398	797.809	0.423	12	0.124	-.SHVQEYWR.-
R2/RRR2-7/2	1070.421	1071.168	-1636.299	0.367	923.524	0.351	15	0.124	R.VFAYADTQR.Y
R2/RRR2-8/2	1070.386	1071.168	-1669.754	0.399	832.988	0.379	14	0.124	R.VFAYADTQR.Y
R2/RRR2-6/2	1070.670	1071.168	-465.952	0.397	711.985	0.414	13	0.124	R.VFAYADTQR.Y
R2/RRR2-8/2	1603.113	1603.755	-1027.433	0.486	1093.134	0.331	18	0.124	K.LFVQVIDPEEEER.F
R2/RRR2-8/2	988.868	989.110	-245.724	0.464	602.986	0.429	11	0.123	R.FSTVIHER.G
R2/RRR2-8/2	1125.259	1125.303	-39.237	0.392	784.319	0.388	16	0.123	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1071.124	1071.168	-40.877	0.442	807.634	0.356	14	0.122	R.VFAYADTQR.Y
R2/RRR2-6/2	1071.191	1071.168	22.219	0.414	734.217	0.363	14	0.122	R.VFAYADTQR.Y
R2/RRR2-7/2	1526.941	1527.856	-1258.219	0.363	516.366	0.504	16	0.121	R.LGPNYLMLPVNAPK.C
R2/RRR2-1/2	988.348	989.110	-1788.159	0.393	556.558	0.391	11	0.119	R.FSTVIHER.G
R2/RRR2-7/2	1105.102	1105.188	-77.290	0.410	793.067	0.363	12	0.119	-.SHVQEYWR.-
R2/RRR2-10/3	1541.489	1540.785	-192.470	0.399	915.505	0.552	24	0.119	R.GPILLEDYHLIEK.L
R2/RRR2-1/2	988.892	989.110	-221.080	0.380	600.925	0.390	11	0.119	R.FSTVIHER.G
R2/RRR2-8/2	1544.179	1543.855	209.927	0.447	1100.632	0.299	17	0.117	R.LGPNYLM*LPVNAPK.C
R2/RRR2-7/2	1105.011	1105.188	-160.286	0.334	826.765	0.350	12	0.117	-.SHVQEYWR.-
R2/RRR2-6/2	1071.202	1071.168	31.934	0.359	562.924	0.364	12	0.117	R.VFAYADTQR.Y
R2/RRR2-2/2	989.228	989.110	119.362	0.392	472.315	0.422	10	0.116	-.FSTVIHER.-
R2/RRR2-7/2	1526.824	1527.856	-1334.817	0.326	413.701	0.422	16	0.116	R.LGPNYLMLPVNAPK.C
R2/RRR2-7/2	988.817	989.110	-296.627	0.349	505.561	0.388	10	0.116	R.FSTVIHER.G
R2/RRR2-25/2	969.377	970.107	-1789.937	0.283	874.468	0.320	13	0.116	R.FAGELAHPK.V
R2/RRR2-7/2	988.447	989.110	-1687.524	0.323	601.082	0.358	11	0.115	R.FSTVIHER.G
R2/RRR2-23/2	1541.818	1540.785	21.551	0.384	599.921	0.396	15	0.115	R.GPILLEDYHLIEK.L
R2/RRR2-8/2	988.479	989.110	-1654.521	0.429	531.929	0.346	10	0.115	R.FSTVIHER.G
R2/RRR2-8/3	1951.752	1952.248	-254.547	0.399	1079.116	0.471	28	0.113	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-3/2	988.992	989.110	-120.037	0.335	392.458	0.342	10	0.112	-.FSTVIHER.-
R2/RRR2-6/2	988.450	989.110	-1683.801	0.278	316.645	0.315	10	0.112	-.FSTVIHER.-
R2/RRR2-2/3	1541.849	1540.785	41.394	0.432	858.725	0.526	23	0.111	R.GPILLEDYHLIEK.L
R2/RRR2-4/2	969.854	970.107	-261.146	0.296	732.749	0.278	13	0.111	R.FAGELAHPK.V
R2/RRR2-8/2	1543.294	1543.855	-1015.037	0.414	468.936	0.303	16	0.111	R.LGPNYLM*LPVNAPK.C
R2/RRR2-22/2	969.889	970.107	-224.906	0.259	622.014	0.314	12	0.109	-.FAGELAHPK.-
R2/RRR2-8/2	1541.250	1540.785	302.696	0.444	626.674	0.297	16	0.108	-.GPILLEDYHLIEK.-
R2/RRR2-16/2	1125.275	1125.303	-25.527	0.385	283.540	0.258	13	0.106	-.SPGAQTPVIVR.-
R2/RRR2-8/3	1982.679	1983.204	-771.278	0.444	1061.485	0.449	26	0.106	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-5/3	1540.450	1540.785	-218.312	0.408	873.167	0.486	22	0.105	R.GPILLEDYHLIEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/3	1541.584	1540.785	-130.985	0.426	763.215	0.509	22	0.104	R.GPILLEDYHLIEK.L
R2/RRR2-8/3	1763.116	1761.939	100.428	0.481	955.167	0.468	25	0.102	R.HM*DGFGVNTYTFVTR.D
R2/RRR2-2/2	988.570	989.110	-1561.850	0.314	571.800	0.247	10	0.101	-.FSTVIHER.-
R2/RRR2-7/3	1540.752	1540.785	-21.235	0.451	761.759	0.479	21	0.100	R.GPILLEDYHLIEK.L
R2/RRR2-8/3	1126.252	1126.293	-36.279	0.528	1134.036	0.399	22	0.099	R.RFAGELAHPK.V
R2/RRR2-6/3	1540.725	1540.785	-38.996	0.402	728.287	0.463	21	0.096	R.GPILLEDYHLIEK.L
R2/RRR2-3/3	1540.896	1540.785	72.567	0.415	740.199	0.460	21	0.096	R.GPILLEDYHLIEK.L
R2/RRR2-7/3	1540.005	1540.785	-1159.106	0.417	680.969	0.468	21	0.096	R.GPILLEDYHLIEK.L
R2/RRR2-7/3	1982.325	1983.204	-950.687	0.395	900.769	0.448	25	0.095	R.AIWVNYLSQCDESLGVK.I
R2/RRR2-3/3	1540.387	1540.785	-259.096	0.419	690.986	0.454	21	0.094	R.GPILLEDYHLIEK.L
R2/RRR2-6/3	1540.739	1540.785	-29.937	0.452	806.429	0.434	22	0.094	R.GPILLEDYHLIEK.L
R2/RRR2-1/3	1540.979	1540.785	126.195	0.402	578.458	0.472	19	0.094	R.GPILLEDYHLIEK.L
R2/RRR2-7/3	1540.807	1540.785	14.405	0.438	928.887	0.401	23	0.093	R.GPILLEDYHLIEK.L
R2/RRR2-4/3	1540.240	1540.785	-1006.305	0.315	649.472	0.454	20	0.092	R.GPILLEDYHLIEK.L
R2/RRR2-6/3	1540.218	1540.785	-1020.151	0.368	894.687	0.401	24	0.092	R.GPILLEDYHLIEK.L
R2/RRR2-5/3	1540.307	1540.785	-311.215	0.334	446.338	0.465	18	0.091	R.GPILLEDYHLIEK.L
R2/RRR2-8/3	1126.791	1126.293	443.741	0.514	1128.198	0.359	22	0.091	R.RFAGELAHPK.V
R2/RRR2-8/3	1126.705	1126.293	366.513	0.514	1119.706	0.359	21	0.091	R.RFAGELAHPK.V
R2/RRR2-1/3	1950.480	1952.248	-1937.770	0.406	868.852	0.414	25	0.091	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-4/3	1541.176	1540.785	254.520	0.441	933.616	0.380	23	0.090	R.GPILLEDYHLIEK.L
R2/RRR2-2/3	1952.477	1952.248	117.846	0.327	939.106	0.386	26	0.090	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-5/3	1541.135	1540.785	227.952	0.374	861.989	0.386	23	0.089	R.GPILLEDYHLIEK.L
R2/RRR2-10/3	1540.654	1540.785	-85.011	0.343	569.248	0.424	20	0.089	R.GPILLEDYHLIEK.L
R2/RRR2-3/3	1540.247	1540.785	-1001.292	0.349	606.503	0.413	20	0.088	R.GPILLEDYHLIEK.L
R2/RRR2-2/3	1951.618	1952.248	-837.758	0.348	978.379	0.354	27	0.086	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-8/3	1770.389	1769.943	252.792	0.466	1079.122	0.342	28	0.086	K.ATIHKQNDFKQPGER.Y
R2/RRR2-8/3	1538.635	1538.777	-92.444	0.330	1027.050	0.367	25	0.086	K.FPDVIHAFKPNPR.S
R2/RRR2-2/3	1540.845	1540.785	39.196	0.365	669.382	0.378	20	0.085	R.GPILLEDYHLIEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1540.947	1540.785	105.340	0.289	398.965	0.381	16	0.085	R.GPILLEDYHLIEK.L
R2/RRR2-7/2	1273.032	1273.287	-200.780	0.289	631.174	0.084	12	0.084	-.DEEVDYYPSR.-
R2/RRR2-9/3	1540.876	1540.785	59.458	0.369	559.536	0.367	19	0.084	R.GPILLEDYHLIEK.L
R2/RRR2-7/2	1273.038	1273.287	-196.451	0.292	622.038	0.129	12	0.083	-.DEEVDYYPSR.-
R2/RRR2-1/3	1540.418	1540.785	-239.181	0.356	620.064	0.339	21	0.082	R.GPILLEDYHLIEK.L
R2/RRR2-1/3	1540.165	1540.785	-1055.005	0.347	737.474	0.333	22	0.082	R.GPILLEDYHLIEK.L
R2/RRR2-3/3	1951.267	1952.248	-1018.056	0.317	802.607	0.355	23	0.081	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-8/3	1126.968	1126.293	-289.393	0.440	1070.375	0.286	21	0.079	R.RFAGELAHPK.V
R2/RRR2-9/3	1540.620	1540.785	-107.067	0.359	719.724	0.305	20	0.079	R.GPILLEDYHLIEK.L
R2/RRR2-3/3	1952.616	1952.248	188.944	0.326	838.820	0.327	25	0.078	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-8/3	1538.479	1538.777	-194.399	0.355	738.640	0.368	24	0.078	K.FPDVIHAFKPNPR.S
R2/RRR2-1/3	1950.797	1952.248	-1260.061	0.292	643.661	0.330	23	0.076	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-8/3	1746.144	1745.940	117.398	0.348	802.255	0.354	24	0.076	R.HMDGFGVNTYTFVTR.D
R2/RRR2-8/3	1127.098	1126.293	-173.343	0.401	818.193	0.287	19	0.074	-.RFAGELAHPK.-
R2/RRR2-4/3	1952.293	1952.248	23.034	0.301	592.047	0.307	21	0.074	R.DGIKFPDVIHAFKPNPR.S
R2/RRR2-5/3	1126.648	1126.293	315.998	0.449	874.558	0.308	19	0.072	-.RFAGELAHPK.-
R2/RRR2-5/3	1127.010	1126.293	-252.065	0.430	804.338	0.264	19	0.072	-.RFAGELAHPK.-
R2/RRR2-7/3	1126.604	1126.293	276.886	0.354	780.954	0.201	18	0.070	R.RFAGELAHPK.V
R2/RRR2-8/3	1539.395	1540.785	-1556.964	0.302	353.582	0.398	16	0.070	-.GPILLEDYHLIEK.-
R2/RRR2-7/3	1126.021	1126.293	-242.446	0.400	936.388	0.230	20	0.070	-.RFAGELAHPK.-
R2/RRR2-3/3	1125.912	1126.293	-339.361	0.467	918.339	0.231	20	0.069	-.RFAGELAHPK.-
R2/RRR2-8/3	1126.990	1126.293	-269.832	0.391	843.122	0.231	19	0.068	-.RFAGELAHPK.-
R2/RRR2-7/3	1537.396	1538.777	-1553.653	0.264	555.452	0.286	18	0.067	-.FPDVIHAFKPNPR.-
R2/RRR2-3/3	1126.323	1126.293	26.500	0.376	809.988	0.147	19	0.060	-.RFAGELAHPK.-
R2/RRR2-9/2	1997.682	1997.392	145.831	0.627	3207.959	0.591	29	0.557	R.IGLAGLAVMGQNLALNIAEK.G
R2/RRR2-9/2	1666.294	1666.881	-954.969	0.554	3113.482	0.478	26	0.478	R.GLLYLGMGVSGGEEGAR.N
R2/RRR2-9/2	1682.323	1682.880	-928.332	0.559	2968.000	0.502	26	0.451	R.GLLYLGM*GVSGGEEGAR.N
R2/RRR2-9/2	1996.400	1997.392	-1000.492	0.540	2719.506	0.586	28	0.429	R.IGLAGLAVMGQNLALNIAEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1997.574	1997.392	91.718	0.624	2668.167	0.589	27	0.414	R.IGLAGLAVMGQNLALNIAEK.G
R2/RRR2-9/2	1682.343	1682.880	-916.312	0.543	2791.186	0.475	25	0.397	R.GLLYLGM*GVSGGEEGAR.N
R2/RRR2-9/2	1682.208	1682.880	-996.811	0.562	2664.126	0.486	26	0.372	R.GLLYLGM*GVSGGEEGAR.N
R2/RRR2-9/2	1666.128	1666.881	-1055.078	0.547	2624.468	0.475	25	0.360	R.GLLYLGMGVSGGEEGAR.N
R2/RRR2-9/3	1996.517	1997.392	-941.997	0.493	2546.296	0.498	42	0.360	R.IGLAGLAVMGQNLALNIAEK.G
R2/RRR2-9/2	1666.118	1666.881	-1060.890	0.539	2525.539	0.464	25	0.335	R.GLLYLGMGVSGGEEGAR.N
R2/RRR2-9/3	1997.917	1997.392	-238.493	0.529	2453.457	0.484	41	0.329	R.IGLAGLAVMGQNLALNIAEK.G
R2/RRR2-9/3	1996.562	1997.392	-919.348	0.466	2311.574	0.468	39	0.294	R.IGLAGLAVMGQNLALNIAEK.G
R2/RRR2-9/2	1398.139	1398.647	-1082.082	0.473	1474.417	0.465	20	0.179	K.ICSYAQGMNIIK.A
R2/RRR2-9/2	1109.817	1110.292	-429.328	0.556	1397.809	0.488	17	0.178	R.LPANLVQAQR.D
R2/RRR2-1/2	1683.704	1682.880	-104.978	0.519	1478.727	0.434	24	0.169	R.GLLYLGM*GVSGGEEGAR.N
R2/RRR2-9/2	1110.171	1110.292	-108.809	0.524	1343.614	0.469	16	0.168	R.LPANLVQAQR.D
R2/RRR2-9/2	1823.443	1823.984	-847.690	0.501	1449.817	0.430	19	0.167	K.LTNSELQQVFSEWNK.G
R2/RRR2-9/2	1414.118	1414.646	-1083.724	0.505	1395.466	0.443	19	0.167	K.ICSYAQGM*NIIK.A
R2/RRR2-9/2	1553.138	1553.697	-1006.965	0.456	1342.758	0.432	21	0.159	K.VFQGDFSSNLPVDK.A
R2/RRR2-9/2	1110.466	1110.292	156.939	0.510	1274.038	0.445	17	0.158	R.LPANLVQAQR.D
R2/RRR2-9/2	1414.139	1414.646	-1069.422	0.497	1388.346	0.395	19	0.157	K.ICSYAQGM*NIIK.A
R2/RRR2-9/2	1562.789	1563.780	-1277.617	0.405	1271.838	0.405	20	0.148	R.FLSGLKDERVEAAK.V
R2/RRR2-9/2	1553.327	1553.697	-239.116	0.420	1314.129	0.383	21	0.148	K.VFQGDFSSNLPVDK.A
R2/RRR2-9/2	1562.687	1563.780	-1343.515	0.425	1240.167	0.372	20	0.140	R.FLSGLKDERVEAAK.V
R2/RRR2-9/2	1553.153	1553.697	-997.338	0.480	1011.673	0.456	19	0.138	K.VFQGDFSSNLPVDK.A
R2/RRR2-9/2	1414.158	1414.646	-346.212	0.498	1025.319	0.432	17	0.136	K.ICSYAQGM*NIIK.A
R2/RRR2-9/2	1762.337	1762.978	-934.120	0.494	888.655	0.475	24	0.135	K.VAAQVPDSGPCVTYIGK.G
R2/RRR2-9/2	1763.377	1762.978	226.587	0.467	736.375	0.509	23	0.132	K.VAAQVPDSGPCVTYIGK.G
R2/RRR2-9/2	1762.329	1762.978	-938.709	0.491	731.059	0.510	22	0.131	K.VAAQVPDSGPCVTYIGK.G
R2/RRR2-9/2	1597.228	1597.775	-971.883	0.418	726.216	0.493	17	0.127	R.VDM*PGSFHTEWFK.I
R2/RRR2-2/2	1215.559	1216.371	-1495.114	0.431	1069.355	0.344	16	0.126	K.GWSLNLGELAR.I
R2/RRR2-9/2	1597.112	1597.775	-1044.398	0.424	651.366	0.500	17	0.126	R.VDM*PGSFHTEWFK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1259.036	1259.308	-217.210	0.349	749.501	0.470	14	0.125	R.DYFGAHTYER.V
R2/RRR2-9/2	1053.128	1053.196	-64.246	0.344	430.218	0.533	14	0.123	K.GFPISVYNR.T
R2/RRR2-9/2	1259.092	1259.308	-171.983	0.370	790.018	0.398	15	0.121	R.DYFGAHTYER.V
R2/RRR2-9/2	1053.029	1053.196	-158.432	0.328	399.533	0.460	14	0.118	K.GFPISVYNR.T
R2/RRR2-9/2	1258.791	1259.308	-1209.358	0.298	780.718	0.388	14	0.116	R.DYFGAHTYER.V
R2/RRR2-7/2	1111.019	1110.292	-246.479	0.253	830.514	0.368	14	0.114	R.LPANLVQAQR.D
R2/RRR2-9/2	943.993	944.067	-79.132	0.358	869.374	0.281	13	0.114	K.AQLIEDVR.Q
R2/RRR2-9/2	943.802	944.067	-282.430	0.340	696.645	0.330	12	0.114	K.AQLIEDVR.Q
R2/RRR2-9/2	943.753	944.067	-334.468	0.348	768.378	0.302	12	0.113	K.AQLIEDVR.Q
R2/RRR2-9/3	1538.719	1537.752	-21.541	0.469	1187.761	0.426	24	0.109	R.RDRLPANLVQAQR.D
R2/RRR2-9/2	1553.193	1553.697	-971.694	0.351	756.110	0.321	16	0.109	K.VFQGDFSSNLPVDK.A
R2/RRR2-17/2	944.267	944.067	211.466	0.223	811.779	0.229	13	0.105	K.AQLIEDVR.Q
R2/RRR2-7/2	1997.144	1997.392	-124.550	0.396	633.616	0.367	17	0.105	R.IGLAGLAVMGQNLALNIAEK.G
R2/RRR2-9/3	1381.611	1381.566	32.991	0.514	1148.619	0.348	25	0.089	-.DRLPANLVQAQR.-
R2/RRR2-9/3	1763.452	1762.978	269.234	0.412	714.169	0.453	29	0.086	K.VAAQVPDSGPCVTYIGK.G
R2/RRR2-8/3	1381.200	1381.566	-266.043	0.426	1068.379	0.307	23	0.080	-.DRLPANLVQAQR.-
R2/RRR2-9/3	1380.468	1381.566	-1524.503	0.460	1073.019	0.290	22	0.076	-.DRLPANLVQAQR.-
R2/RRR2-9/3	1380.958	1381.566	-1167.812	0.464	1081.728	0.276	23	0.074	-.DRLPANLVQAQR.-
R2/RRR2-8/3	1381.724	1381.566	114.998	0.391	937.348	0.236	21	0.065	-.DRLPANLVQAQR.-
R2/RRR2-5/2	1847.453	1847.057	214.950	0.613	2300.379	0.599	25	0.342	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/3	1321.393	1321.463	-52.696	0.622	2513.485	0.516	27	0.339	K.HFSVEGQLEFK.A
R2/RRR2-5/2	1847.409	1847.057	190.831	0.633	2166.931	0.568	25	0.305	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/2	1847.539	1847.057	261.726	0.607	2075.585	0.596	24	0.298	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/3	1321.287	1321.463	-133.318	0.615	2177.855	0.505	26	0.262	K.HFSVEGQLEFK.A
R2/RRR2-5/3	1321.389	1321.463	-55.754	0.609	1943.630	0.496	25	0.217	K.HFSVEGQLEFK.A
R2/RRR2-5/2	1965.549	1966.225	-855.422	0.542	1373.217	0.614	22	0.202	K.KHSEFISYPISLWTEK.T
R2/RRR2-6/3	1846.785	1847.057	-148.056	0.525	1590.179	0.557	30	0.188	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/2	1542.270	1542.675	-263.376	0.531	1358.682	0.491	19	0.171	K.SLTNDWEEHLAVK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1529.403	1528.689	-188.018	0.540	1352.286	0.481	21	0.167	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/2	1528.262	1528.689	-280.771	0.486	1442.960	0.432	22	0.166	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/2	1543.101	1542.675	277.102	0.586	1263.857	0.498	19	0.163	K.SLTNDWEEHLAVK.H
R2/RRR2-5/2	1272.629	1273.421	-1412.675	0.431	1397.223	0.431	18	0.163	K.SDLVNNLGTIAR.S
R2/RRR2-5/2	1529.189	1528.689	327.663	0.554	1373.713	0.436	22	0.160	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/2	1273.187	1273.421	-184.312	0.474	1331.008	0.418	17	0.154	K.SDLVNNLGTIAR.S
R2/RRR2-1/3	1846.689	1847.057	-199.679	0.573	1397.291	0.530	30	0.154	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/2	1273.148	1273.421	-214.899	0.514	1267.800	0.429	18	0.152	K.SDLVNNLGTIAR.S
R2/RRR2-4/2	1528.311	1528.689	-248.637	0.471	1407.885	0.364	22	0.151	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/2	1837.403	1838.052	-900.422	0.477	1015.955	0.537	18	0.148	K.HSEFISYPISLWTEK.T
R2/RRR2-5/2	950.075	950.026	52.694	0.430	1329.791	0.358	15	0.147	K.SGDELTSLK.D
R2/RRR2-2/2	1528.161	1528.689	-1003.314	0.428	1370.821	0.363	21	0.147	K.GIVDSEDLPLNISR.Q
R2/RRR2-3/3	1585.377	1584.710	-210.735	0.513	1476.753	0.457	27	0.144	K.SGDELTSLKDYVTR.M
R2/RRR2-6/2	1528.074	1528.689	-1060.420	0.438	1181.877	0.415	20	0.142	K.GIVDSEDLPLNISR.Q
R2/RRR2-6/2	1528.514	1528.689	-114.915	0.495	1217.930	0.384	21	0.140	K.GIVDSEDLPLNISR.Q
R2/RRR2-6/2	1273.398	1273.421	-18.327	0.486	1037.524	0.447	17	0.139	K.SDLVNNLGTIAR.S
R2/RRR2-3/2	1528.981	1528.689	191.015	0.512	1093.713	0.414	21	0.137	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/2	1321.128	1321.463	-254.173	0.471	792.350	0.516	16	0.137	K.HFSVEGQLEFK.A
R2/RRR2-1/2	1529.450	1528.689	-156.952	0.544	1123.271	0.414	20	0.137	K.GIVDSEDLPLNISR.Q
R2/RRR2-2/2	1529.481	1528.689	-136.776	0.523	1040.456	0.438	20	0.137	K.GIVDSEDLPLNISR.Q
R2/RRR2-4/2	1542.313	1542.675	-235.425	0.503	1019.957	0.442	18	0.136	K.SLTNDWEEHLAVK.H
R2/RRR2-6/2	1273.245	1273.421	-138.530	0.442	1206.090	0.357	17	0.135	K.SDLVNNLGTIAR.S
R2/RRR2-4/2	1527.875	1528.689	-1191.018	0.365	1301.003	0.307	21	0.134	K.GIVDSEDLPLNISR.Q
R2/RRR2-4/2	1528.222	1528.689	-307.057	0.436	1198.612	0.354	20	0.134	K.GIVDSEDLPLNISR.Q
R2/RRR2-4/3	1846.424	1847.057	-887.044	0.529	1136.826	0.541	26	0.133	R.KPEEITKEEYAAFYK.S
R2/RRR2-6/2	1528.243	1528.689	-293.033	0.470	1068.751	0.396	19	0.131	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/2	1527.799	1528.689	-1241.405	0.378	1328.055	0.274	22	0.131	K.GIVDSEDLPLNISR.Q
R2/RRR2-6/2	1542.027	1542.675	-1071.707	0.472	942.958	0.415	19	0.130	K.SLTNDWEEHLAVK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1321.086	1321.463	-285.692	0.453	783.586	0.463	16	0.130	K.HFSVEGQLEFK.A
R2/RRR2-5/2	1262.132	1262.437	-241.899	0.549	1039.763	0.385	16	0.130	K.KAVENSPFLEK.L
R2/RRR2-2/2	1528.261	1528.689	-281.413	0.488	1105.322	0.365	20	0.130	K.GIVDSEDLPLNISR.Q
R2/RRR2-6/3	1848.022	1847.057	-19.195	0.549	1137.077	0.527	29	0.128	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/3	1847.029	1847.057	-15.095	0.568	1066.724	0.549	28	0.128	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/2	1320.505	1321.463	-1486.720	0.430	793.857	0.447	16	0.128	K.HFSVEGQLEFK.A
R2/RRR2-7/2	1527.993	1528.689	-1113.361	0.376	1131.517	0.336	19	0.127	K.GIVDSEDLPLNISR.Q
R2/RRR2-7/2	1322.776	1321.463	237.268	0.428	758.215	0.447	16	0.127	K.HFSVEGQLEFK.A
R2/RRR2-5/2	1542.136	1542.675	-1000.732	0.496	932.378	0.409	17	0.126	K.SLTNDWEEHLAVK.H
R2/RRR2-5/2	1584.591	1584.710	-75.151	0.535	1014.780	0.392	17	0.126	-.SGDELTSLKDYVTR.-
R2/RRR2-5/2	1082.036	1082.191	-143.435	0.467	781.628	0.401	14	0.125	R.APFDLFDTR.K
R2/RRR2-2/3	1846.899	1847.057	-85.698	0.490	1237.008	0.467	26	0.124	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/2	1837.518	1838.052	-837.265	0.419	641.361	0.504	16	0.122	K.HSEFISYPISLWTEK.T
R2/RRR2-5/2	1134.047	1134.264	-191.486	0.418	750.049	0.409	14	0.121	K.AVENSPFLEK.L
R2/RRR2-5/2	1837.124	1838.052	-1052.844	0.405	812.945	0.415	18	0.120	K.HSEFISYPISLWTEK.T
R2/RRR2-5/2	1133.930	1134.264	-295.379	0.419	628.340	0.411	14	0.119	K.AVENSPFLEK.L
R2/RRR2-4/2	1272.185	1273.421	-1762.715	0.379	598.551	0.395	17	0.118	K.SDLVNNLGTIAR.S
R2/RRR2-6/3	1846.627	1847.057	-233.500	0.568	940.127	0.539	27	0.117	R.KPEEITKEEYAAFYK.S
R2/RRR2-5/2	1262.035	1262.437	-318.948	0.517	754.087	0.370	15	0.117	K.KAVENSPFLEK.L
R2/RRR2-5/2	1262.228	1262.437	-165.833	0.532	873.016	0.348	15	0.117	K.KAVENSPFLEK.L
R2/RRR2-2/3	1848.097	1847.057	21.848	0.526	1014.090	0.514	28	0.117	R.KPEEITKEEYAAFYK.S
R2/RRR2-1/2	1527.660	1528.689	-1332.564	0.361	981.619	0.286	20	0.116	K.GIVDSEDLPLNISR.Q
R2/RRR2-6/2	1273.280	1273.421	-110.929	0.471	890.406	0.341	15	0.116	K.SDLVNNLGTIAR.S
R2/RRR2-7/2	1321.579	1321.463	88.326	0.394	688.851	0.361	15	0.115	K.HFSVEGQLEFK.A
R2/RRR2-1/3	1847.089	1847.057	17.518	0.528	1064.191	0.490	27	0.115	R.KPEEITKEEYAAFYK.S
R2/RRR2-1/2	1527.851	1528.689	-1206.904	0.316	1021.963	0.265	19	0.115	K.GIVDSEDLPLNISR.Q
R2/RRR2-6/2	1542.208	1542.675	-303.240	0.451	519.715	0.354	17	0.114	K.SLTNDWEEHLAVK.H
R2/RRR2-2/3	1847.249	1847.057	104.013	0.511	1111.117	0.465	27	0.113	R.KPEEITKEEYAAFYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1133.491	1134.264	-1568.367	0.379	641.195	0.332	14	0.112	K.AVENSPFLEK.L
R2/RRR2-5/2	1528.796	1528.689	70.107	0.492	737.573	0.344	17	0.112	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/2	1274.046	1273.421	-295.664	0.494	774.277	0.337	14	0.110	-.SDLVNNLGTIAR.-
R2/RRR2-1/2	1583.462	1584.710	-1424.088	0.414	645.043	0.366	15	0.109	K.SGDELTSLKDYVTR.M
R2/RRR2-5/2	1081.512	1082.191	-1557.028	0.314	655.139	0.307	13	0.109	-.APFDLFDTR.-
R2/RRR2-2/2	1584.121	1584.710	-1006.130	0.411	614.353	0.359	15	0.108	-.SGDELTSLKDYVTR.-
R2/RRR2-6/3	1585.278	1584.710	-273.424	0.480	1020.718	0.478	26	0.107	-.SGDELTSLKDYVTR.-
R2/RRR2-5/3	1837.902	1838.052	-82.121	0.411	1049.959	0.465	27	0.107	K.HSEFISYPISLWTEK.T
R2/RRR2-5/3	1966.573	1966.225	177.393	0.458	1166.073	0.410	28	0.105	K.KHSEFISYPISLWTEK.T
R2/RRR2-1/2	1081.745	1082.191	-413.418	0.288	557.934	0.221	11	0.104	R.APFDLFDTR.K
R2/RRR2-5/2	1528.424	1528.689	-173.960	0.316	867.585	0.179	17	0.103	K.GIVDSEDLPLNISR.Q
R2/RRR2-5/3	1569.844	1569.786	37.107	0.498	754.217	0.527	24	0.103	K.IKEVSHEWSLVNK.Q
R2/RRR2-5/3	1569.768	1569.786	-11.912	0.507	760.994	0.513	24	0.101	K.IKEVSHEWSLVNK.Q
R2/RRR2-6/3	1584.828	1584.710	74.766	0.439	903.781	0.473	23	0.101	K.SGDELTSLKDYVTR.M
R2/RRR2-5/3	1570.432	1569.786	-226.423	0.533	817.880	0.490	25	0.100	K.IKEVSHEWSLVNK.Q
R2/RRR2-5/3	1142.018	1142.204	-163.681	0.439	589.276	0.558	21	0.098	K.LGIHEDSTNR.N
R2/RRR2-5/3	1142.947	1142.204	-226.269	0.461	405.891	0.562	18	0.097	K.LGIHEDSTNR.N
R2/RRR2-5/3	1142.264	1142.204	52.284	0.471	544.994	0.534	20	0.097	K.LGIHEDSTNR.N
R2/RRR2-5/3	1838.006	1838.052	-25.061	0.527	900.303	0.433	26	0.094	K.HSEFISYPISLWTEK.T
R2/RRR2-5/3	1366.699	1366.550	109.767	0.488	1133.317	0.371	23	0.094	K.RAPFDLFDTRK.K
R2/RRR2-6/3	1584.956	1584.710	155.988	0.468	806.228	0.468	24	0.094	-.SGDELTSLKDYVTR.-
R2/RRR2-3/3	1584.068	1584.710	-1039.872	0.393	822.840	0.440	23	0.091	K.SGDELTSLKDYVTR.M
R2/RRR2-5/3	1366.812	1366.550	192.663	0.544	938.466	0.398	23	0.090	K.RAPFDLFDTRK.K
R2/RRR2-5/3	1366.775	1366.550	165.256	0.485	982.034	0.369	22	0.087	K.RAPFDLFDTRK.K
R2/RRR2-5/3	1837.564	1838.052	-266.234	0.371	839.180	0.417	24	0.087	K.HSEFISYPISLWTEK.T
R2/RRR2-1/3	1321.275	1321.463	-142.215	0.466	760.856	0.397	19	0.084	K.HFSVEGQLEFK.A
R2/RRR2-7/3	1846.954	1847.057	-56.163	0.379	344.587	0.395	19	0.081	-.KPEEITKEEYAAFYK.-
R2/RRR2-5/3	1528.129	1528.689	-1024.215	0.354	1124.099	0.255	24	0.074	K.GIVDSEDLPLNISR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/3	1803.382	1803.946	-869.483	0.425	2112.823	0.439	32	0.243	K.NATLTNEKEADACPIR.A
R2/RRR2-4/2	1803.490	1803.946	-253.606	0.543	1830.993	0.508	22	0.232	K.NATLTNEKEADACPIR.A
R2/RRR2-4/2	1803.471	1803.946	-263.927	0.529	1767.617	0.474	22	0.215	K.NATLTNEKEADACPIR.A
R2/RRR2-7/2	1618.911	1619.792	-1165.564	0.497	2263.438	0.551	23	0.318	K.IGDTAGTIDNIIQCK.L
R2/RRR2-7/2	1619.195	1619.792	-989.326	0.493	2216.568	0.527	23	0.301	K.IGDTAGTIDNIIQCK.L
R2/RRR2-7/2	1817.412	1817.977	-864.179	0.498	2016.292	0.566	27	0.279	R.ETPSVAGIINPGSDGFQK.L
R2/RRR2-7/2	1600.461	1599.899	-274.608	0.559	1926.073	0.581	26	0.265	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/2	1599.404	1599.899	-310.003	0.501	1910.908	0.516	25	0.244	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/2	1529.523	1528.729	-135.251	0.569	1572.277	0.662	24	0.239	R.VVAIIAEGVPESDTK.Q
R2/RRR2-7/3	1600.584	1599.899	-197.144	0.512	1932.107	0.511	35	0.231	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/2	1529.334	1528.729	-259.199	0.547	1506.367	0.621	24	0.220	R.VVAIIAEGVPESDTK.Q
R2/RRR2-7/2	1620.193	1619.792	247.896	0.583	1750.400	0.489	22	0.214	K.IGDTAGTIDNIIQCK.L
R2/RRR2-7/2	1817.690	1817.977	-158.535	0.478	1515.952	0.568	24	0.204	R.ETPSVAGIINPGSDGFQK.L
R2/RRR2-1/2	1599.679	1599.899	-137.586	0.435	1762.885	0.434	24	0.202	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/2	1817.449	1817.977	-843.614	0.463	1548.773	0.533	25	0.201	R.ETPSVAGIINPGSDGFQK.L
R2/RRR2-6/2	1599.481	1599.899	-261.840	0.432	1714.215	0.441	24	0.198	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/2	1291.122	1290.464	-265.729	0.517	1505.178	0.464	16	0.182	R.M*LDFDFLCGR.E
R2/RRR2-6/2	1599.481	1599.899	-261.763	0.409	1516.311	0.463	23	0.179	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/2	1527.783	1528.729	-1278.042	0.411	1259.149	0.480	22	0.160	R.VVAIIAEGVPESDTK.Q
R2/RRR2-7/2	1249.162	1249.396	-188.445	0.473	1170.351	0.464	15	0.152	K.TTQALFYNYK.Q
R2/RRR2-7/2	1563.989	1563.696	188.113	0.519	1160.031	0.484	18	0.151	K.SGGM*SNEM*YNTIAR.V
R2/RRR2-7/2	992.708	993.055	-350.596	0.487	1378.132	0.339	17	0.147	R.FGGAIDDAAR.Y
R2/RRR2-7/2	1658.156	1658.920	-1067.166	0.431	932.259	0.512	21	0.141	K.VQKPVVAWVSGTCAR.L
R2/RRR2-7/2	1564.039	1563.696	219.733	0.494	1064.979	0.456	18	0.140	K.SGGM*SNEM*YNTIAR.V
R2/RRR2-7/2	992.344	993.055	-1729.879	0.415	1313.542	0.312	17	0.138	R.FGGAIDDAAR.Y
R2/RRR2-7/2	1562.474	1563.696	-1426.248	0.371	1171.145	0.395	18	0.137	K.SGGM*SNEM*YNTIAR.V
R2/RRR2-7/2	1249.045	1249.396	-282.173	0.442	1061.119	0.414	15	0.136	K.TTQALFYNYK.Q
R2/RRR2-7/2	1290.175	1290.464	-224.168	0.392	1227.256	0.348	14	0.135	R.M*LDFDFLCGR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1628.570	1627.907	-207.995	0.328	1188.514	0.384	19	0.135	K.DLVSSLVSGLLTIGPR.F
R2/RRR2-7/2	1187.013	1187.332	-268.863	0.454	853.083	0.441	16	0.132	K.YAHTHFPSVK.Y
R2/RRR2-7/2	1627.226	1627.907	-1036.285	0.294	1155.455	0.377	19	0.131	K.DLVSSLVSGLLTIGPR.F
R2/RRR2-7/3	1659.392	1658.920	285.417	0.408	1529.587	0.369	29	0.128	K.VQKPVVAWVSGTCAR.L
R2/RRR2-7/2	1310.361	1310.526	-126.010	0.480	1022.191	0.363	17	0.126	K.LYRPGSVGFVSK.S
R2/RRR2-7/2	1187.062	1187.332	-227.905	0.412	781.350	0.411	16	0.125	K.YAHTHFPSVK.Y
R2/RRR2-7/2	1187.258	1187.332	-62.351	0.434	752.390	0.401	16	0.124	K.YAHTHFPSVK.Y
R2/RRR2-7/2	1310.321	1310.526	-156.943	0.443	943.302	0.369	17	0.123	K.LYRPGSVGFVSK.S
R2/RRR2-7/2	992.401	993.055	-1671.793	0.390	1067.265	0.311	15	0.123	-.FGGAIDDAAR.-
R2/RRR2-7/2	1289.828	1290.464	-1272.197	0.439	973.904	0.348	13	0.121	R.M*LDFDFLCGR.E
R2/RRR2-7/2	1310.287	1310.526	-183.204	0.438	831.541	0.337	16	0.115	K.LYRPGSVGFVSK.S
R2/RRR2-7/2	1248.416	1249.396	-1591.204	0.276	910.694	0.301	15	0.113	K.TTQALFYNYK.Q
R2/RRR2-17/2	1600.504	1599.899	-247.597	0.318	356.647	0.475	17	0.112	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/2	1846.410	1847.142	-940.789	0.379	608.558	0.425	17	0.111	-.ISPVTEITPPPIPEDLK.-
R2/RRR2-3/2	1291.257	1290.464	-160.830	0.354	780.523	0.264	15	0.110	R.M*LDFDFLCGR.E
R2/RRR2-7/2	1621.016	1619.792	138.251	0.381	513.232	0.382	16	0.110	K.IGDTAGTIDNIIQCK.L
R2/RRR2-1/2	1598.947	1599.899	-1224.146	0.302	754.809	0.342	18	0.109	K.VILGPATVGGIQAGAFK.I
R2/RRR2-7/3	1658.900	1658.920	-12.084	0.471	1303.298	0.372	27	0.107	K.VQKPVVAWVSGTCAR.L
R2/RRR2-7/2	1315.627	1316.488	-1418.341	0.313	782.231	0.263	15	0.104	R.SIGLIGHTFDQK.R
R2/RRR2-7/2	1629.435	1627.907	-290.614	0.272	247.054	0.358	15	0.103	-.DLVSSLVSGLLTIGPR.-
R2/RRR2-7/3	1078.067	1078.159	-84.976	0.416	652.442	0.491	15	0.090	R.YFKDAYDR.N
R2/RRR2-7/3	1077.984	1078.159	-162.841	0.448	616.566	0.478	15	0.089	R.YFKDAYDR.N
R2/RRR2-7/3	1599.243	1599.899	-1038.272	0.361	1079.441	0.314	27	0.081	K.VILGPATVGGIQAGAFK.I
R2/RRR2-3/2	1492.519	1492.742	-149.843	0.525	2680.370	0.529	21	0.391	K.LSVDKNLVEVFTK.G
R2/RRR2-2/2	1633.783	1633.746	22.811	0.529	2191.632	0.561	22	0.304	R.TALTYIDADGNWHR.A
R2/RRR2-3/2	1492.378	1492.742	-244.369	0.499	2140.680	0.480	19	0.268	K.LSVDKNLVEVFTK.G
R2/RRR2-2/2	1633.289	1633.746	-280.708	0.488	1875.818	0.518	21	0.239	R.TALTYIDADGNWHR.A
R2/RRR2-2/2	1633.413	1633.746	-204.455	0.492	1892.839	0.506	21	0.238	R.TALTYIDADGNWHR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1492.293	1492.742	-301.897	0.476	1971.493	0.461	20	0.237	K.LSVDKNLVEVFTK.G
R2/RRR2-4/2	1559.447	1559.743	-190.677	0.475	1903.508	0.489	22	0.234	K.IDQSALTGESLPVTK.G
R2/RRR2-3/2	1407.110	1407.643	-1092.846	0.552	1802.666	0.534	20	0.233	K.GVDKDHVLLLAAR.A
R2/RRR2-2/2	1398.054	1398.451	-285.027	0.550	1717.634	0.567	22	0.232	K.NPGDEVFSGSTCK.Q
R2/RRR2-4/2	1559.264	1559.743	-308.168	0.413	1890.667	0.450	22	0.223	K.IDQSALTGESLPVTK.G
R2/RRR2-2/2	1406.859	1407.643	-1272.320	0.530	1720.275	0.529	20	0.221	K.GVDKDHVLLLAAR.A
R2/RRR2-3/2	1559.293	1559.743	-290.024	0.444	1840.095	0.471	22	0.221	K.IDQSALTGESLPVTK.G
R2/RRR2-3/2	1559.194	1559.743	-996.851	0.423	1871.048	0.447	22	0.219	K.IDQSALTGESLPVTK.G
R2/RRR2-1/3	1407.935	1407.643	207.385	0.536	2002.231	0.459	29	0.212	K.GVDKDHVLLLAAR.A
R2/RRR2-4/2	1634.253	1633.746	-302.718	0.530	1609.283	0.551	20	0.210	R.TALTYIDADGNWHR.A
R2/RRR2-4/2	1634.079	1633.746	204.355	0.515	1580.241	0.564	20	0.210	R.TALTYIDADGNWHR.A
R2/RRR2-3/2	1407.176	1407.643	-333.470	0.457	1756.189	0.464	20	0.210	K.GVDKDHVLLLAAR.A
R2/RRR2-2/2	1492.431	1492.742	-208.673	0.514	1642.464	0.499	20	0.202	K.LSVDKNLVEVFTK.G
R2/RRR2-4/2	1492.469	1492.742	-183.319	0.512	1570.878	0.525	20	0.200	K.LSVDKNLVEVFTK.G
R2/RRR2-4/2	1406.986	1407.643	-1181.181	0.534	1559.995	0.512	19	0.196	K.GVDKDHVLLLAAR.A
R2/RRR2-3/2	1398.212	1398.451	-171.684	0.534	1347.580	0.591	21	0.193	K.NPGDEVFSGSTCK.Q
R2/RRR2-2/2	1492.354	1492.742	-260.371	0.523	1510.436	0.515	20	0.191	K.LSVDKNLVEVFTK.G
R2/RRR2-4/2	1397.940	1398.451	-1083.724	0.555	1457.939	0.530	21	0.191	K.NPGDEVFSGSTCK.Q
R2/RRR2-2/2	1399.081	1398.451	-265.215	0.531	1396.712	0.552	21	0.189	K.NPGDEVFSGSTCK.Q
R2/RRR2-2/2	1492.419	1492.742	-216.633	0.544	1468.492	0.522	19	0.187	K.LSVDKNLVEVFTK.G
R2/RRR2-3/2	1633.332	1633.746	-254.014	0.464	1560.311	0.473	20	0.187	R.TALTYIDADGNWHR.A
R2/RRR2-1/2	1939.737	1940.229	-254.413	0.574	1564.164	0.479	27	0.187	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-2/2	1397.850	1398.451	-1148.698	0.525	1326.167	0.572	21	0.186	K.NPGDEVFSGSTCK.Q
R2/RRR2-1/2	1492.192	1492.742	-1041.447	0.470	1499.253	0.502	19	0.186	K.LSVDKNLVEVFTK.G
R2/RRR2-1/2	1559.571	1559.743	-110.664	0.447	1595.167	0.451	21	0.185	K.IDQSALTGESLPVTK.G
R2/RRR2-4/2	1407.138	1407.643	-1072.812	0.505	1447.006	0.498	19	0.181	K.GVDKDHVLLLAAR.A
R2/RRR2-2/2	1407.273	1407.643	-264.106	0.542	1430.783	0.488	19	0.177	K.GVDKDHVLLLAAR.A
R2/RRR2-4/3	1429.854	1429.649	144.094	0.596	1977.033	0.393	29	0.176	R.KVHAVIDKYAER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1559.243	1559.743	-965.411	0.403	1502.975	0.449	20	0.174	K.IDQSALTGESLPVTK.G
R2/RRR2-3/2	1940.555	1940.229	168.737	0.562	1386.653	0.501	27	0.174	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-1/2	1633.997	1633.746	153.937	0.516	1436.072	0.479	19	0.174	R.TALTYIDADGNWHR.A
R2/RRR2-2/2	1939.554	1940.229	-866.318	0.493	1504.210	0.448	25	0.174	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-1/2	1398.034	1398.451	-298.781	0.508	1339.258	0.506	20	0.173	K.NPGDEVFSGSTCK.Q
R2/RRR2-3/2	1559.139	1559.743	-1031.909	0.409	1487.873	0.450	20	0.173	K.IDQSALTGESLPVTK.G
R2/RRR2-2/2	1558.859	1559.743	-1212.586	0.297	1672.829	0.348	21	0.172	K.IDQSALTGESLPVTK.G
R2/RRR2-2/2	1406.901	1407.643	-1242.171	0.476	1362.542	0.484	18	0.169	K.GVDKDHVLLLAAR.A
R2/RRR2-2/2	1939.115	1940.229	-1093.441	0.505	1477.746	0.440	24	0.168	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-1/2	1940.731	1940.229	-257.121	0.601	1319.648	0.508	25	0.167	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-4/2	1397.966	1398.451	-348.104	0.521	1128.522	0.544	20	0.163	K.NPGDEVFSGSTCK.Q
R2/RRR2-1/2	1633.332	1633.746	-253.864	0.461	1266.665	0.494	18	0.161	R.TALTYIDADGNWHR.A
R2/RRR2-1/2	1633.197	1633.746	-951.232	0.440	1213.056	0.520	18	0.161	R.TALTYIDADGNWHR.A
R2/RRR2-1/2	1938.929	1940.229	-1189.844	0.503	1281.506	0.481	23	0.158	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-2/2	1915.436	1915.182	133.374	0.574	1212.914	0.500	23	0.157	R.LGM*GTNM*YPSSALLGQNK.D
R2/RRR2-2/2	1914.232	1915.182	-1021.425	0.532	1152.529	0.522	22	0.156	R.LGM*GTNM*YPSSALLGQNK.D
R2/RRR2-4/2	1491.640	1492.742	-1413.417	0.433	1247.445	0.462	19	0.155	K.LSVDKNLVEVFTK.G
R2/RRR2-4/2	1491.787	1492.742	-1314.625	0.496	1141.919	0.494	19	0.153	K.LSVDKNLVEVFTK.G
R2/RRR2-3/2	1493.947	1492.742	138.044	0.477	1211.813	0.472	17	0.152	K.LSVDKNLVEVFTK.G
R2/RRR2-4/2	1939.656	1940.229	-813.123	0.563	1192.586	0.486	24	0.152	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-3/2	1163.021	1163.370	-301.070	0.448	1238.147	0.426	18	0.150	K.M*ITGDQLAIGK.E
R2/RRR2-3/3	1429.843	1429.649	136.260	0.531	1519.395	0.480	27	0.150	R.KVHAVIDKYAER.G
R2/RRR2-4/2	1642.406	1642.829	-258.575	0.480	1208.830	0.441	22	0.149	K.DASLEALPVDELIEK.A
R2/RRR2-3/2	1913.915	1915.182	-1187.729	0.498	1163.957	0.469	22	0.147	R.LGM*GTNM*YPSSALLGQNK.D
R2/RRR2-3/3	1429.186	1429.649	-325.132	0.596	1560.333	0.456	26	0.147	R.KVHAVIDKYAER.G
R2/RRR2-1/3	1429.433	1429.649	-151.755	0.568	1615.795	0.434	27	0.146	R.KVHAVIDKYAER.G
R2/RRR2-3/3	1429.006	1429.649	-1153.008	0.544	1605.046	0.436	27	0.146	R.KVHAVIDKYAER.G
R2/RRR2-2/2	1558.679	1559.743	-1328.668	0.350	1338.952	0.378	19	0.146	K.IDQSALTGESLPVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/3	1408.892	1407.643	176.958	0.540	1659.629	0.399	27	0.144	K.GVDKDHVLLLAAR.A
R2/RRR2-4/2	1940.320	1940.229	47.224	0.571	1182.460	0.435	25	0.143	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-2/3	1429.171	1429.649	-335.287	0.586	1455.732	0.478	26	0.142	R.KVHAVIDKYAER.G
R2/RRR2-3/3	1406.886	1407.643	-1252.854	0.544	1611.087	0.412	27	0.142	K.GVDKDHVLLLAAR.A
R2/RRR2-2/3	1429.248	1429.649	-281.171	0.581	1487.115	0.465	27	0.141	R.KVHAVIDKYAER.G
R2/RRR2-3/2	1642.313	1642.829	-926.196	0.436	1182.521	0.396	23	0.140	K.DASLEALPVDELIEK.A
R2/RRR2-4/2	1990.914	1991.233	-160.669	0.464	1080.849	0.460	22	0.140	R.TENQDAIDAAMVGMLADPK.E
R2/RRR2-3/2	1940.550	1940.229	165.835	0.557	1026.095	0.484	23	0.140	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-4/2	1939.749	1940.229	-248.036	0.532	991.181	0.491	22	0.138	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-2/2	1163.076	1163.370	-253.264	0.450	1224.749	0.356	18	0.138	K.M*ITGDQLAIGK.E
R2/RRR2-4/2	1643.311	1642.829	294.030	0.489	1034.395	0.436	22	0.137	K.DASLEALPVDELIEK.A
R2/RRR2-2/2	1939.794	1940.229	-225.118	0.532	1117.265	0.420	24	0.136	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-2/2	1146.803	1147.371	-1371.013	0.381	1037.425	0.420	17	0.135	K.MITGDQLAIGK.E
R2/RRR2-2/2	1429.737	1429.649	61.691	0.453	825.663	0.505	16	0.135	R.KVHAVIDKYAER.G
R2/RRR2-3/2	1164.235	1163.370	-116.087	0.474	1012.290	0.422	16	0.134	K.M*ITGDQLAIGK.E
R2/RRR2-2/2	1162.581	1163.370	-1543.578	0.347	1178.213	0.357	17	0.134	K.M*ITGDQLAIGK.E
R2/RRR2-1/2	1559.016	1559.743	-1111.468	0.325	1336.033	0.298	19	0.133	K.IDQSALTGESLPVTK.G
R2/RRR2-1/3	1430.135	1429.649	340.674	0.580	1511.719	0.429	27	0.133	R.KVHAVIDKYAER.G
R2/RRR2-1/2	1163.294	1163.370	-65.135	0.448	1059.264	0.384	17	0.133	K.M*ITGDQLAIGK.E
R2/RRR2-2/3	1430.443	1429.649	-144.629	0.607	1668.572	0.376	28	0.132	R.KVHAVIDKYAER.G
R2/RRR2-1/3	1407.446	1407.643	-140.555	0.498	1563.477	0.382	26	0.132	-.GVDKDHVLLLAAR.-
R2/RRR2-2/3	1840.579	1840.094	263.827	0.516	1269.162	0.490	33	0.132	K.KHIVGM*TGDGVNDAPALK.K
R2/RRR2-1/2	1162.928	1163.370	-381.425	0.449	1026.010	0.381	17	0.131	K.M*ITGDQLAIGK.E
R2/RRR2-1/2	1491.361	1492.742	-1601.027	0.328	1115.665	0.361	19	0.130	K.LSVDKNLVEVFTK.G
R2/RRR2-2/2	1643.267	1642.829	266.917	0.500	981.263	0.405	21	0.129	K.DASLEALPVDELIEK.A
R2/RRR2-3/2	1162.501	1163.370	-1612.670	0.416	1029.255	0.371	16	0.128	K.M*ITGDQLAIGK.E
R2/RRR2-3/2	1643.029	1642.829	122.016	0.480	1071.756	0.349	22	0.126	K.DASLEALPVDELIEK.A
R2/RRR2-2/2	1643.497	1642.829	-202.455	0.475	1049.055	0.353	22	0.126	K.DASLEALPVDELIEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1026.353	1027.156	-1762.744	0.375	702.926	0.443	15	0.125	K.LGDIVPADAR.L
R2/RRR2-2/2	1915.705	1915.182	-249.350	0.557	921.714	0.435	21	0.125	R.LGM*GTNM*YPSSALLGQNK.D
R2/RRR2-4/3	1407.834	1407.643	135.781	0.523	1497.094	0.391	27	0.125	K.GVDKDHVLLLAAR.A
R2/RRR2-1/2	1162.566	1163.370	-1556.763	0.368	979.290	0.361	16	0.125	K.M*ITGDQLAIGK.E
R2/RRR2-5/2	1939.683	1940.229	-799.541	0.461	919.784	0.424	20	0.124	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-2/2	1162.482	1163.370	-1628.705	0.399	958.204	0.345	17	0.124	K.M*ITGDQLAIGK.E
R2/RRR2-1/2	1643.208	1642.829	231.459	0.471	852.761	0.405	20	0.123	K.DASLEALPVDELIEK.A
R2/RRR2-4/2	1026.464	1027.156	-1654.128	0.424	794.849	0.372	16	0.123	K.LGDIVPADAR.L
R2/RRR2-2/3	1839.886	1840.094	-113.587	0.542	932.072	0.571	31	0.123	K.HIVGM*TGDGVNDAPALKK.A
R2/RRR2-4/2	1026.821	1027.156	-327.263	0.446	559.781	0.404	14	0.121	K.LGDIVPADAR.L
R2/RRR2-1/2	1026.479	1027.156	-1638.835	0.404	599.390	0.403	14	0.120	K.LGDIVPADAR.L
R2/RRR2-4/3	1407.624	1407.643	-13.849	0.534	1437.630	0.391	26	0.120	K.GVDKDHVLLLAAR.A
R2/RRR2-7/3	1429.846	1429.649	137.930	0.576	1324.404	0.433	26	0.118	R.KVHAVIDKYAER.G
R2/RRR2-3/2	1642.441	1642.829	-237.175	0.419	881.367	0.339	21	0.118	K.DASLEALPVDELIEK.A
R2/RRR2-4/2	1162.518	1163.370	-1598.324	0.356	976.937	0.299	16	0.118	K.M*ITGDQLAIGK.E
R2/RRR2-4/2	1642.283	1642.829	-944.329	0.387	906.455	0.327	21	0.118	K.DASLEALPVDELIEK.A
R2/RRR2-2/3	1839.803	1840.094	-158.713	0.481	1049.687	0.506	32	0.117	K.HIVGM*TGDGVNDAPALKK.A
R2/RRR2-1/3	1839.070	1840.094	-1104.111	0.501	926.410	0.544	27	0.116	K.HIVGM*TGDGVNDAPALKK.A
R2/RRR2-2/2	1026.739	1027.156	-407.424	0.394	706.959	0.369	15	0.116	-.LGDIVPADAR.-
R2/RRR2-3/2	1026.444	1027.156	-1673.245	0.363	570.509	0.374	14	0.115	-.LGDIVPADAR.-
R2/RRR2-1/2	1027.118	1027.156	-37.026	0.441	593.021	0.353	14	0.115	-.LGDIVPADAR.-
R2/RRR2-4/2	1026.890	1027.156	-259.756	0.364	492.975	0.381	13	0.114	-.LGDIVPADAR.-
R2/RRR2-2/2	1147.050	1147.371	-280.259	0.352	646.765	0.337	15	0.114	K.MITGDQLAIGK.E
R2/RRR2-5/2	1026.949	1027.156	-202.753	0.324	423.137	0.362	12	0.114	K.LGDIVPADAR.L
R2/RRR2-4/3	1407.635	1407.643	-6.021	0.559	1370.192	0.393	25	0.114	K.GVDKDHVLLLAAR.A
R2/RRR2-2/2	1642.404	1642.829	-259.917	0.414	822.292	0.318	20	0.114	K.DASLEALPVDELIEK.A
R2/RRR2-5/3	1408.370	1407.643	-194.753	0.501	1437.575	0.361	26	0.113	K.GVDKDHVLLLAAR.A
R2/RRR2-1/2	1026.613	1027.156	-1507.432	0.412	549.816	0.380	13	0.112	-.LGDIVPADAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/3	1839.259	1840.094	-1001.050	0.515	786.270	0.568	27	0.112	K.HIVGM*TGDGVNDAPALKK.A
R2/RRR2-4/2	1162.588	1163.370	-1537.250	0.322	921.813	0.250	16	0.112	K.M*ITGDQLAIGK.E
R2/RRR2-4/2	1643.460	1642.829	-225.182	0.458	778.776	0.319	19	0.112	K.DASLEALPVDELIEK.A
R2/RRR2-7/2	1026.823	1027.156	-325.354	0.377	517.560	0.415	13	0.111	-.LGDIVPADAR.-
R2/RRR2-2/2	1027.001	1027.156	-151.479	0.424	546.556	0.318	14	0.110	-.LGDIVPADAR.-
R2/RRR2-2/3	1407.198	1407.643	-317.161	0.495	1351.215	0.368	25	0.108	K.GVDKDHVLLLAAR.A
R2/RRR2-1/2	1642.541	1642.829	-176.186	0.385	516.361	0.318	16	0.108	K.DASLEALPVDELIEK.A
R2/RRR2-3/2	1147.196	1147.371	-152.364	0.192	515.481	0.301	14	0.107	K.MITGDQLAIGK.E
R2/RRR2-1/3	1408.720	1407.643	54.693	0.550	1369.399	0.363	25	0.107	K.GVDKDHVLLLAAR.A
R2/RRR2-2/3	1406.992	1407.643	-1177.575	0.514	1202.518	0.407	23	0.106	K.GVDKDHVLLLAAR.A
R2/RRR2-4/2	1162.362	1163.370	-1733.050	0.353	759.119	0.226	14	0.106	K.M*ITGDQLAIGK.E
R2/RRR2-1/2	1641.694	1642.829	-1304.289	0.276	633.498	0.252	18	0.106	K.DASLEALPVDELIEK.A
R2/RRR2-5/3	1429.958	1429.649	216.392	0.538	1283.084	0.386	25	0.106	R.KVHAVIDKYAER.G
R2/RRR2-7/2	1026.653	1027.156	-1469.212	0.296	491.447	0.253	12	0.102	-.LGDIVPADAR.-
R2/RRR2-4/2	1941.306	1940.229	40.010	0.337	489.687	0.299	14	0.101	R.WGEQEAAILVPGDIISIK.L
R2/RRR2-3/2	1027.333	1027.156	172.618	0.436	523.314	0.298	13	0.099	-.LGDIVPADAR.-
R2/RRR2-1/3	1429.794	1429.649	101.584	0.546	1298.130	0.345	26	0.097	R.KVHAVIDKYAER.G
R2/RRR2-3/3	1407.119	1407.643	-1086.366	0.475	1131.278	0.378	24	0.097	K.GVDKDHVLLLAAR.A
R2/RRR2-3/3	1407.797	1407.643	109.433	0.538	1250.726	0.346	24	0.095	K.GVDKDHVLLLAAR.A
R2/RRR2-3/3	1492.480	1492.742	-175.943	0.402	1066.171	0.383	25	0.094	K.LSVDKNLVEVFTK.G
R2/RRR2-12/2	1027.027	1027.156	-126.321	0.197	534.433	0.213	12	0.092	-.LGDIVPADAR.-
R2/RRR2-8/3	1429.724	1429.649	52.391	0.488	939.594	0.399	24	0.092	R.KVHAVIDKYAER.G
R2/RRR2-2/3	1492.970	1492.742	153.543	0.456	818.059	0.427	23	0.092	K.LSVDKNLVEVFTK.G
R2/RRR2-3/3	1492.983	1492.742	162.276	0.468	823.447	0.419	23	0.091	K.LSVDKNLVEVFTK.G
R2/RRR2-5/3	1407.200	1407.643	-316.247	0.521	1198.668	0.332	23	0.090	K.GVDKDHVLLLAAR.A
R2/RRR2-4/3	1838.903	1840.094	-1195.095	0.424	945.137	0.387	31	0.088	K.KHIVGM*TGDGVNDAPALK.K
R2/RRR2-2/3	1492.958	1492.742	144.934	0.488	881.284	0.390	25	0.088	K.LSVDKNLVEVFTK.G
R2/RRR2-1/3	1492.622	1492.742	-80.323	0.447	710.277	0.406	23	0.087	K.LSVDKNLVEVFTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/3	1492.939	1492.742	132.142	0.450	734.663	0.405	22	0.087	K.LSVDKNLVEVFTK.G
R2/RRR2-6/3	1407.753	1407.643	77.735	0.487	1119.162	0.320	24	0.085	K.GVDKDHVLLLAAR.A
R2/RRR2-3/3	1839.113	1840.094	-1080.418	0.431	962.809	0.361	29	0.085	K.KHIVGM*TGDGVNDAPALK.K
R2/RRR2-1/3	1492.850	1492.742	72.853	0.429	844.476	0.367	24	0.084	K.LSVDKNLVEVFTK.G
R2/RRR2-1/3	1492.592	1492.742	-100.381	0.393	745.364	0.382	23	0.084	K.LSVDKNLVEVFTK.G
R2/RRR2-3/3	1840.152	1840.094	31.345	0.451	816.734	0.386	28	0.083	K.KHIVGM*TGDGVNDAPALK.K
R2/RRR2-8/3	1429.736	1429.649	60.997	0.506	697.655	0.362	21	0.083	R.KVHAVIDKYAER.G
R2/RRR2-2/3	1492.550	1492.742	-129.177	0.379	779.981	0.363	24	0.082	K.LSVDKNLVEVFTK.G
R2/RRR2-2/2	1027.235	1027.156	76.924	0.392	420.539	0.283	12	0.082	-.LGDIVPADAR.-
R2/RRR2-7/3	1429.160	1429.649	-343.385	0.470	751.097	0.370	20	0.082	-.KVHAVIDKYAER.-
R2/RRR2-4/3	1492.450	1492.742	-196.374	0.395	919.037	0.336	25	0.082	K.LSVDKNLVEVFTK.G
R2/RRR2-4/3	1598.363	1598.829	-292.863	0.390	945.691	0.331	24	0.080	R.EVHFLPFNPVDKR.T
R2/RRR2-4/3	1598.735	1598.829	-59.484	0.397	845.144	0.350	22	0.080	R.EVHFLPFNPVDKR.T
R2/RRR2-2/3	1599.047	1598.829	136.352	0.416	743.812	0.263	22	0.071	R.EVHFLPFNPVDKR.T
R2/RRR2-2/3	1598.766	1598.829	-39.839	0.407	881.763	0.262	22	0.071	R.EVHFLPFNPVDKR.T
R2/RRR2-4/3	1838.376	1840.094	-2028.441	0.388	746.097	0.232	30	0.068	K.KHIVGM*TGDGVNDAPALK.K
R2/RRR2-3/3	1599.049	1598.829	137.844	0.303	859.930	0.214	20	0.065	-.EVHFLPFNPVDKR.-
R2/RRR2-2/2	1592.390	1592.644	-159.975	0.557	2466.436	0.568	22	0.366	R.TQDLENELSTANEK.F
R2/RRR2-2/2	1592.264	1592.644	-239.343	0.548	2536.491	0.526	22	0.365	R.TQDLENELSTANEK.F
R2/RRR2-2/2	1592.229	1592.644	-261.494	0.553	2388.006	0.552	22	0.344	R.TQDLENELSTANEK.F
R2/RRR2-2/2	1203.345	1203.328	14.182	0.521	2424.382	0.395	19	0.298	K.TAALEEQALTR.E
R2/RRR2-2/2	1612.360	1611.732	-231.424	0.580	2066.999	0.553	20	0.282	K.VSQLSDELEAYQTK.A
R2/RRR2-2/2	1610.585	1611.732	-1337.313	0.390	2102.755	0.401	20	0.246	K.VSQLSDELEAYQTK.A
R2/RRR2-2/2	1388.422	1388.509	-62.488	0.477	1927.772	0.421	19	0.224	R.TIANQEEQISVR.E
R2/RRR2-2/2	1611.277	1611.732	-283.327	0.487	1769.275	0.470	18	0.213	K.VSQLSDELEAYQTK.A
R2/RRR2-2/2	1202.894	1203.328	-361.806	0.520	1923.790	0.372	18	0.210	K.TAALEEQALTR.E
R2/RRR2-2/2	1161.062	1161.248	-159.930	0.480	1735.987	0.439	18	0.205	R.GLELQSAAESR.S
R2/RRR2-2/2	1507.247	1507.625	-251.706	0.532	1669.807	0.481	21	0.204	K.INELQASLDSTTSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1388.318	1388.509	-138.160	0.495	1631.431	0.488	18	0.202	R.TIANQEEQISVR.E
R2/RRR2-2/2	1507.282	1507.625	-228.550	0.503	1547.018	0.468	20	0.186	K.INELQASLDSTTSK.N
R2/RRR2-2/2	1160.830	1161.248	-360.572	0.392	1171.175	0.409	17	0.142	R.GLELQSAAESR.S
R2/RRR2-2/2	1202.232	1203.328	-1748.673	0.370	1352.252	0.304	17	0.138	K.TAALEEQALTR.E
R2/RRR2-2/2	1073.486	1074.253	-1651.474	0.324	1082.561	0.401	15	0.133	K.LALVNTEVSK.L
R2/RRR2-2/2	1387.846	1388.509	-1201.882	0.358	1116.915	0.381	17	0.133	R.TIANQEEQISVR.E
R2/RRR2-2/2	1506.649	1507.625	-1315.472	0.335	1236.243	0.308	18	0.128	K.INELQASLDSTTSK.N
R2/RRR2-2/2	1073.307	1074.253	-1818.296	0.273	1127.987	0.349	15	0.127	K.LALVNTEVSK.L
R2/RRR2-2/2	1356.919	1357.535	-1194.266	0.369	645.557	0.514	15	0.124	R.SLELESLLHTSK.S
R2/RRR2-2/2	1297.053	1297.393	-263.139	0.300	1094.099	0.280	15	0.116	R.DFSLDSSTLPSK.Q
R2/RRR2-2/3	1589.625	1588.707	-51.314	0.527	1260.444	0.407	26	0.110	R.QNLHYTSLQEAQR.S
R2/RRR2-2/2	1009.820	1010.123	-300.097	0.421	935.947	0.241	12	0.108	-.YNITLEEK.-
R2/RRR2-2/2	1073.311	1074.253	-1814.982	0.279	886.214	0.217	14	0.106	K.LALVNTEVSK.L
R2/RRR2-2/2	1009.542	1010.123	-1570.580	0.308	813.424	0.143	12	0.101	-.YNITLEEK.-
R2/RRR2-2/3	1833.402	1834.018	-883.995	0.436	901.036	0.471	27	0.098	R.SLADKDKELADATQSLK.E
R2/RRR2-2/3	1527.738	1527.660	51.113	0.484	1422.467	0.277	25	0.094	K.FKEVEADLEQYR.S
R2/RRR2-2/3	1543.909	1543.701	135.273	0.424	918.338	0.434	29	0.093	K.VVEEEKASPIEQGK.T
R2/RRR2-1/3	1317.222	1318.502	-1736.198	0.369	1233.715	0.290	27	0.084	K.RTSLEASLLEAK.Q
R2/RRR2-8/3	1317.784	1318.502	-1307.742	0.340	513.462	0.356	21	0.081	K.RTSLEASLLEAK.Q
R2/RRR2-2/3	1543.658	1543.701	-27.937	0.404	633.032	0.392	24	0.080	K.VVEEEKASPIEQGK.T
R2/RRR2-2/3	1425.652	1425.529	86.592	0.552	801.999	0.356	21	0.080	K.AIDHQQVEESLR.S
R2/RRR2-2/3	1425.323	1425.529	-145.320	0.505	916.097	0.333	22	0.080	K.AIDHQQVEESLR.S
R2/RRR2-2/3	1543.039	1543.701	-1080.018	0.396	799.125	0.352	28	0.078	K.VVEEEKASPIEQGK.T
R2/RRR2-2/3	1317.248	1318.502	-1716.505	0.302	511.742	0.309	21	0.078	K.RTSLEASLLEAK.Q
R2/RRR2-2/3	1317.820	1318.502	-1279.833	0.356	737.951	0.302	23	0.076	K.RTSLEASLLEAK.Q
R2/RRR2-8/3	1317.300	1318.502	-1676.145	0.339	875.152	0.298	25	0.075	K.RTSLEASLLEAK.Q
R2/RRR2-4/3	1317.876	1318.502	-1237.694	0.307	665.783	0.271	22	0.073	K.RTSLEASLLEAK.Q
R2/RRR2-2/3	1416.484	1416.602	-83.993	0.484	1065.752	0.259	21	0.073	R.RIEELELEKEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/3	1588.438	1588.707	-169.824	0.484	713.523	0.311	22	0.073	R.QNLHYTSLQEAQR.S
R2/RRR2-23/3	1317.429	1318.502	-1578.399	0.355	837.442	0.262	23	0.072	K.RTSLEASLLEAK.Q
R2/RRR2-8/3	1317.284	1318.502	-1688.574	0.337	961.822	0.246	25	0.071	K.RTSLEASLLEAK.Q
R2/RRR2-2/3	1415.782	1416.602	-1289.562	0.478	1106.310	0.226	21	0.069	-.RIEELELEKEK.-
R2/RRR2-2/3	1425.680	1425.529	105.913	0.519	765.142	0.304	20	0.068	-.AIDHQQVEESLR.-
R2/RRR2-2/3	1416.736	1416.602	94.785	0.479	1049.888	0.224	20	0.067	-.RIEELELEKEK.-
R2/RRR2-10/3	1317.317	1318.502	-1663.157	0.257	813.823	0.141	24	0.065	K.RTSLEASLLEAK.Q
R2/RRR2-2/3	1526.967	1527.660	-1112.314	0.299	1052.002	0.096	23	0.056	-.FKEVEADLEQYR.-
R2/RRR2-4/2	1431.305	1431.767	-323.229	0.537	2649.185	0.578	22	0.404	R.IVSQLLTLMDGLK.Q
R2/RRR2-4/2	1430.954	1431.767	-1270.832	0.490	2516.031	0.548	21	0.364	R.IVSQLLTLMDGLK.Q
R2/RRR2-4/2	1431.333	1431.767	-304.148	0.528	2435.454	0.570	21	0.355	R.IVSQLLTLMDGLK.Q
R2/RRR2-4/2	1843.513	1844.098	-862.171	0.523	2350.744	0.439	25	0.294	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-4/2	1448.188	1447.766	292.571	0.560	1947.509	0.553	20	0.259	R.IVSQLLTLM*DGLK.Q
R2/RRR2-4/2	1843.430	1844.098	-907.640	0.490	2109.475	0.443	24	0.254	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-4/2	1846.304	1846.969	-904.768	0.516	1714.242	0.525	21	0.219	K.YTQGFSGADITEICQR.A
R2/RRR2-4/2	1430.818	1431.767	-1365.679	0.435	1772.426	0.496	19	0.218	R.IVSQLLTLMDGLK.Q
R2/RRR2-4/2	1447.098	1447.766	-1155.872	0.447	1731.761	0.502	20	0.215	R.IVSQLLTLM*DGLK.Q
R2/RRR2-4/2	1846.644	1846.969	-176.736	0.542	1617.619	0.552	22	0.214	K.YTQGFSGADITEICQR.A
R2/RRR2-4/2	1846.393	1846.969	-856.450	0.510	1598.026	0.546	21	0.209	K.YTQGFSGADITEICQR.A
R2/RRR2-4/2	1843.623	1844.098	-258.511	0.484	1791.798	0.441	23	0.207	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-4/2	1844.539	1844.098	239.849	0.540	1732.914	0.459	23	0.202	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-4/2	1584.100	1584.750	-1044.557	0.452	1512.223	0.542	19	0.200	R.LGDVVSVHQCQDVK.Y
R2/RRR2-4/2	1843.536	1844.098	-849.940	0.502	1887.141	0.366	23	0.199	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-4/2	1843.346	1844.098	-953.312	0.462	1812.087	0.381	23	0.195	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-4/2	1253.022	1252.437	-332.284	0.476	1363.643	0.524	18	0.180	K.GVLFYGPPGCGK.T
R2/RRR2-4/2	1431.478	1431.767	-202.420	0.424	1284.328	0.563	19	0.176	R.IVSQLLTLMDGLK.Q
R2/RRR2-4/2	1565.284	1565.746	-296.423	0.490	1430.400	0.460	18	0.169	K.AIANECQANFISVK.G
R2/RRR2-3/2	1565.257	1565.746	-313.872	0.414	1452.793	0.409	19	0.163	K.AIANECQANFISVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1565.229	1565.746	-972.043	0.489	1317.206	0.469	18	0.161	K.AIANECQANFISVK.G
R2/RRR2-4/2	1565.397	1565.746	-223.897	0.489	1302.914	0.471	18	0.160	K.AIANECQANFISVK.G
R2/RRR2-4/2	1587.676	1587.953	-174.948	0.465	1219.513	0.467	21	0.156	R.RIVSQLLTLMDGLK.Q
R2/RRR2-4/2	1587.331	1587.953	-1025.075	0.453	1344.335	0.404	21	0.154	R.RIVSQLLTLMDGLK.Q
R2/RRR2-4/2	1587.651	1587.953	-190.991	0.507	1178.281	0.476	20	0.153	R.RIVSQLLTLMDGLK.Q
R2/RRR2-3/2	1188.097	1188.316	-185.352	0.471	1355.053	0.387	19	0.152	K.TALGTSNPSALR.E
R2/RRR2-2/2	1187.956	1188.316	-303.692	0.468	1274.582	0.413	18	0.149	K.TALGTSNPSALR.E
R2/RRR2-4/2	1253.015	1252.437	-338.051	0.491	1028.036	0.514	17	0.149	K.GVLFYGPPGCGK.T
R2/RRR2-1/2	1188.037	1188.316	-235.962	0.484	1194.046	0.438	19	0.149	K.TALGTSNPSALR.E
R2/RRR2-4/2	1189.131	1188.316	-156.155	0.486	1222.625	0.418	20	0.148	K.TALGTSNPSALR.E
R2/RRR2-4/2	1952.265	1953.165	-976.022	0.477	1174.720	0.465	21	0.148	K.GPELLTM*WFGESEANVR.E
R2/RRR2-3/2	1188.096	1188.316	-186.176	0.409	1227.537	0.424	18	0.147	K.TALGTSNPSALR.E
R2/RRR2-4/2	1187.538	1188.316	-1501.834	0.363	1310.656	0.382	20	0.147	K.TALGTSNPSALR.E
R2/RRR2-2/2	1187.984	1188.316	-280.393	0.511	1121.974	0.447	20	0.147	K.TALGTSNPSALR.E
R2/RRR2-4/2	1953.292	1953.165	65.328	0.586	1036.598	0.504	20	0.142	K.GPELLTM*WFGESEANVR.E
R2/RRR2-4/2	1187.872	1188.316	-375.452	0.482	1080.192	0.449	18	0.142	K.TALGTSNPSALR.E
R2/RRR2-1/2	1187.611	1188.316	-1440.091	0.417	1223.208	0.375	20	0.141	K.TALGTSNPSALR.E
R2/RRR2-4/2	1801.382	1801.033	193.940	0.507	931.986	0.496	21	0.140	R.LDQLIYIPLPDEQSR.L
R2/RRR2-4/2	1953.306	1953.165	72.285	0.540	1015.091	0.477	20	0.137	K.GPELLTM*WFGESEANVR.E
R2/RRR2-4/2	1300.035	1299.412	-291.260	0.466	725.713	0.534	17	0.136	R.EIDIGVPDEVGR.L
R2/RRR2-4/2	1251.481	1252.437	-1567.447	0.378	878.966	0.468	16	0.130	K.GVLFYGPPGCGK.T
R2/RRR2-4/2	1447.297	1447.766	-325.143	0.413	854.341	0.463	17	0.130	R.IVSQLLTLM*DGLK.Q
R2/RRR2-4/2	1800.485	1801.033	-862.442	0.400	964.815	0.417	21	0.129	R.LDQLIYIPLPDEQSR.L
R2/RRR2-4/2	1800.632	1801.033	-223.750	0.471	862.276	0.453	20	0.129	R.LDQLIYIPLPDEQSR.L
R2/RRR2-3/2	1188.129	1188.316	-158.244	0.474	933.787	0.402	18	0.129	K.TALGTSNPSALR.E
R2/RRR2-2/2	1187.403	1188.316	-1615.944	0.388	973.135	0.388	19	0.129	K.TALGTSNPSALR.E
R2/RRR2-4/2	1299.182	1299.412	-177.702	0.430	557.741	0.532	16	0.128	R.EIDIGVPDEVGR.L
R2/RRR2-4/2	1300.188	1299.412	-172.856	0.439	593.523	0.501	17	0.127	R.EIDIGVPDEVGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	968.609	969.160	-1606.552	0.370	914.170	0.351	13	0.122	R.ELVELPLR.H
R2/RRR2-4/2	1075.763	1076.143	-354.144	0.442	747.005	0.395	15	0.122	K.LAGESESNLR.K
R2/RRR2-1/2	1188.035	1188.316	-237.096	0.475	693.320	0.404	17	0.122	K.TALGTSNPSALR.E
R2/RRR2-4/2	958.428	959.079	-1727.988	0.402	947.983	0.316	15	0.121	K.DVDLNALAK.Y
R2/RRR2-4/2	958.413	959.079	-1743.728	0.355	921.178	0.329	15	0.120	K.DVDLNALAK.Y
R2/RRR2-4/2	958.932	959.079	-153.932	0.388	925.392	0.314	15	0.119	K.DVDLNALAK.Y
R2/RRR2-4/2	969.030	969.160	-134.639	0.343	737.056	0.364	12	0.116	R.ELVELPLR.H
R2/RRR2-4/3	1952.812	1953.165	-181.064	0.447	1091.460	0.488	26	0.116	K.GPELLTM*WFGESEANVR.E
R2/RRR2-4/2	1075.345	1076.143	-1676.513	0.340	688.929	0.369	14	0.115	K.LAGESESNLR.K
R2/RRR2-4/2	968.636	969.160	-1577.940	0.324	697.825	0.348	12	0.114	R.ELVELPLR.H
R2/RRR2-1/2	1566.304	1565.746	-283.567	0.422	902.164	0.308	16	0.111	K.AIANECQANFISVK.G
R2/RRR2-4/2	1075.372	1076.143	-1651.309	0.340	596.161	0.288	13	0.108	K.LAGESESNLR.K
R2/RRR2-5/2	1447.692	1447.766	-51.036	0.352	724.790	0.296	14	0.107	R.IVSQLLTLM*DGLK.Q
R2/RRR2-1/2	958.747	959.079	-347.307	0.264	826.911	0.145	14	0.102	K.DVDLNALAK.Y
R2/RRR2-3/2	1954.239	1953.165	38.294	0.436	471.853	0.332	15	0.102	K.GPELLTM*WFGESEANVR.E
R2/RRR2-4/3	1953.114	1953.165	-25.884	0.450	895.628	0.462	26	0.097	K.GPELLTM*WFGESEANVR.E
R2/RRR2-4/3	1649.106	1649.830	-1048.195	0.469	835.068	0.408	22	0.086	K.YAIRENIEKDIER.E
R2/RRR2-4/3	1843.487	1844.098	-876.270	0.331	980.686	0.105	26	0.055	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-4/3	1843.662	1844.098	-237.329	0.357	1224.430	0.057	30	0.054	K.NAPSIIFIDEIDSIAPK.R
R2/RRR2-6/2	1635.197	1635.906	-1048.305	0.413	2247.016	0.555	24	0.315	R.ASDLDIASILGMGFPK.F
R2/RRR2-6/2	1589.173	1589.814	-1036.214	0.568	1993.975	0.616	24	0.296	K.VPVVVGNCTGFAVNR.T
R2/RRR2-6/2	1717.479	1717.987	-880.742	0.491	1924.697	0.580	26	0.269	K.KVPVVVGNCTGFAVNR.T
R2/RRR2-6/2	1635.183	1635.906	-1057.450	0.392	1966.306	0.505	23	0.250	R.ASDLDIASILGMGFPK.F
R2/RRR2-6/3	1717.953	1717.987	-19.757	0.502	1915.981	0.551	33	0.244	K.KVPVVVGNCTGFAVNR.T
R2/RRR2-6/2	1249.342	1249.443	-80.812	0.506	1909.366	0.493	17	0.242	R.LWALEIANYR.K
R2/RRR2-6/2	1718.372	1717.987	224.897	0.483	1737.599	0.565	25	0.236	K.KVPVVVGNCTGFAVNR.T
R2/RRR2-6/2	1651.093	1651.906	-1101.056	0.464	1712.185	0.571	22	0.230	R.ASDLDIASILGM*GFPK.F
R2/RRR2-6/2	1652.313	1651.906	247.045	0.535	1457.156	0.612	22	0.208	R.ASDLDIASILGM*GFPK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1249.181	1249.443	-210.397	0.547	1549.691	0.501	17	0.197	R.LWALEIANYR.K
R2/RRR2-6/2	1248.739	1249.443	-1368.714	0.509	1552.903	0.472	17	0.191	R.LWALEIANYR.K
R2/RRR2-6/2	1308.674	1309.540	-1429.899	0.472	1319.921	0.589	20	0.190	K.VPGVTDVQLKPR.K
R2/RRR2-6/3	1456.641	1456.709	-47.047	0.526	2024.624	0.365	29	0.189	K.TSPQAILDLITVGK.M
R2/RRR2-6/3	1457.122	1456.709	284.200	0.546	1793.594	0.456	29	0.184	K.TSPQAILDLITVGK.M
R2/RRR2-6/2	1650.804	1651.906	-1277.026	0.376	1328.468	0.462	21	0.160	R.ASDLDIASILGM*GFPK.F
R2/RRR2-6/2	1628.372	1628.769	-244.713	0.472	1001.203	0.590	24	0.160	R.SLPLSAPNATQQASSR.S
R2/RRR2-6/2	1308.727	1309.540	-1389.052	0.424	1089.662	0.548	19	0.159	K.VPGVTDVQLKPR.K
R2/RRR2-6/2	1628.282	1628.769	-300.219	0.463	1099.025	0.530	25	0.157	R.SLPLSAPNATQQASSR.S
R2/RRR2-6/2	1175.446	1175.424	18.587	0.471	1356.067	0.409	18	0.157	K.M*IAANLEGLVK.R
R2/RRR2-6/2	1530.353	1530.739	-252.946	0.459	1330.819	0.434	19	0.157	R.GLVDALCSPDELIK.M
R2/RRR2-6/2	1174.512	1175.424	-1632.423	0.428	1268.572	0.430	18	0.153	K.M*IAANLEGLVK.R
R2/RRR2-6/3	1456.082	1456.709	-1121.099	0.482	1793.920	0.350	28	0.152	K.TSPQAILDLITVGK.M
R2/RRR2-6/2	1160.072	1160.353	-242.811	0.476	1032.155	0.509	16	0.151	K.ALVHAFFAQR.L
R2/RRR2-6/2	1160.065	1160.353	-248.512	0.407	1124.459	0.482	16	0.151	K.ALVHAFFAQR.L
R2/RRR2-5/2	1628.198	1628.769	-968.064	0.499	841.859	0.574	22	0.146	R.SLPLSAPNATQQASSR.S
R2/RRR2-6/2	1530.600	1530.739	-90.840	0.471	1262.894	0.402	19	0.146	R.GLVDALCSPDELIK.M
R2/RRR2-6/2	1530.250	1530.739	-320.572	0.452	1226.353	0.405	19	0.144	R.GLVDALCSPDELIK.M
R2/RRR2-6/2	1628.280	1628.769	-301.272	0.458	755.817	0.579	22	0.141	R.SLPLSAPNATQQASSR.S
R2/RRR2-6/2	1456.313	1456.709	-272.784	0.454	926.673	0.497	21	0.141	K.TSPQAILDLITVGK.M
R2/RRR2-6/2	1457.233	1456.709	-328.233	0.510	898.139	0.491	21	0.139	K.TSPQAILDLITVGK.M
R2/RRR2-6/2	1159.085	1159.425	-293.510	0.454	1081.167	0.400	18	0.137	K.MIAANLEGLVK.R
R2/RRR2-6/2	886.963	887.059	-108.377	0.425	956.795	0.436	16	0.135	K.AIVLTGAGGK.F
R2/RRR2-5/2	1456.509	1456.709	-138.080	0.449	824.549	0.493	20	0.134	K.TSPQAILDLITVGK.M
R2/RRR2-6/2	1456.325	1456.709	-264.795	0.465	946.315	0.438	21	0.134	K.TSPQAILDLITVGK.M
R2/RRR2-6/2	1090.400	1091.264	-1714.771	0.420	960.780	0.418	15	0.133	R.VM*DENVVIR.A
R2/RRR2-6/2	1091.003	1091.264	-239.539	0.497	874.602	0.421	15	0.132	R.VM*DENVVIR.A
R2/RRR2-6/3	1716.308	1717.987	-2150.332	0.413	1414.602	0.425	29	0.131	K.KVPVVVGNCTGFAVNR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1175.096	1175.424	-280.232	0.485	815.363	0.408	16	0.125	K.M*IAANLEGLVK.R
R2/RRR2-6/2	886.357	887.059	-1926.164	0.335	1016.222	0.344	15	0.123	K.AIVLTGAGGK.F
R2/RRR2-6/2	935.787	936.042	-273.924	0.365	446.519	0.482	10	0.121	K.GYYLYEK.G
R2/RRR2-6/2	1090.339	1091.264	-1770.901	0.341	965.579	0.319	15	0.120	R.VM*DENVVIR.A
R2/RRR2-6/2	1158.843	1159.425	-1368.708	0.281	915.936	0.351	15	0.117	K.MIAANLEGLVK.R
R2/RRR2-6/2	886.910	887.059	-168.296	0.311	749.676	0.348	15	0.114	K.AIVLTGAGGK.F
R2/RRR2-6/2	935.920	936.042	-130.768	0.292	405.038	0.416	10	0.113	K.GYYLYEK.G
R2/RRR2-5/2	1456.383	1456.709	-224.936	0.333	437.052	0.363	15	0.109	K.TSPQAILDLITVGK.M
R2/RRR2-1/2	1456.204	1456.709	-1036.664	0.326	413.212	0.314	15	0.108	K.TSPQAILDLITVGK.M
R2/RRR2-5/2	1455.661	1456.709	-1411.174	0.213	302.341	0.402	12	0.103	-.TSPQAILDLITVGK.-
R2/RRR2-6/3	1160.383	1160.353	26.091	0.483	890.667	0.497	22	0.102	K.ALVHAFFAQR.L
R2/RRR2-6/3	1205.393	1205.304	74.685	0.426	1346.272	0.328	24	0.098	R.TDRLGSLSEAR.S
R2/RRR2-6/3	1159.825	1160.353	-1321.403	0.437	854.032	0.442	21	0.091	K.ALVHAFFAQR.L
R2/RRR2-6/3	1770.168	1770.959	-1015.035	0.448	823.073	0.396	26	0.085	K.FCGGFDINVFTEVHK.T
R2/RRR2-6/3	1205.474	1205.304	141.410	0.512	742.554	0.372	22	0.082	R.TDRLGSLSEAR.S
R2/RRR2-6/3	1769.934	1770.959	-1147.676	0.355	524.951	0.397	22	0.077	K.FCGGFDINVFTEVHK.T
R2/RRR2-6/3	1770.316	1770.959	-930.712	0.362	708.604	0.346	25	0.075	K.FCGGFDINVFTEVHK.T
R2/RRR2-6/2	1465.478	1465.683	-140.577	0.495	2524.513	0.552	24	0.379	K.KVLTTGPAGGLHSAR.F
R2/RRR2-6/3	1800.247	1801.027	-991.309	0.472	2478.507	0.442	33	0.312	R.FVREELGCVYLTGEK.L
R2/RRR2-5/2	1707.125	1707.826	-999.402	0.542	1674.752	0.545	23	0.217	R.EVNSVNDNPVIDVHR.G
R2/RRR2-6/3	1800.927	1801.027	-55.457	0.530	1850.671	0.503	31	0.212	R.FVREELGCVYLTGEK.L
R2/RRR2-1/2	1707.428	1707.826	-234.028	0.535	1593.241	0.558	22	0.209	R.EVNSVNDNPVIDVHR.G
R2/RRR2-5/2	1707.390	1707.826	-256.263	0.526	1552.878	0.566	22	0.206	R.EVNSVNDNPVIDVHR.G
R2/RRR2-6/2	1337.450	1337.510	-45.004	0.481	1540.684	0.527	21	0.199	K.VLTTGPAGGLHSAR.F
R2/RRR2-8/2	1707.442	1707.826	-225.492	0.522	1471.883	0.560	22	0.196	R.EVNSVNDNPVIDVHR.G
R2/RRR2-6/2	1707.410	1707.826	-244.715	0.511	1441.078	0.578	21	0.195	R.EVNSVNDNPVIDVHR.G
R2/RRR2-3/2	1707.213	1707.826	-947.571	0.518	1397.719	0.589	21	0.193	R.EVNSVNDNPVIDVHR.G
R2/RRR2-3/2	1707.372	1707.826	-267.166	0.539	1380.797	0.586	21	0.191	R.EVNSVNDNPVIDVHR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1707.313	1707.826	-888.926	0.545	1397.706	0.560	21	0.187	R.EVNSVNDNPVIDVHR.G
R2/RRR2-6/3	1465.332	1465.683	-240.073	0.523	1665.609	0.524	31	0.187	K.KVLTTGPAGGLHSAR.F
R2/RRR2-6/2	1336.633	1337.510	-1408.784	0.433	1497.396	0.494	20	0.186	K.VLTTGPAGGLHSAR.F
R2/RRR2-6/3	1465.713	1465.683	20.489	0.532	1583.757	0.531	30	0.178	K.KVLTTGPAGGLHSAR.F
R2/RRR2-1/2	1707.264	1707.826	-918.068	0.548	1209.377	0.602	20	0.177	R.EVNSVNDNPVIDVHR.G
R2/RRR2-6/2	1376.782	1377.528	-1272.191	0.410	1472.078	0.458	20	0.175	R.VAFETGTAPITNR.I
R2/RRR2-1/2	1707.290	1707.826	-902.779	0.508	1265.559	0.564	20	0.174	R.EVNSVNDNPVIDVHR.G
R2/RRR2-6/2	1709.218	1707.826	230.113	0.590	1236.559	0.551	22	0.171	R.EVNSVNDNPVIDVHR.G
R2/RRR2-5/2	1377.221	1377.528	-223.641	0.402	1421.625	0.450	20	0.168	R.VAFETGTAPITNR.I
R2/RRR2-6/2	1337.202	1337.510	-231.158	0.411	1344.449	0.484	20	0.168	K.VLTTGPAGGLHSAR.F
R2/RRR2-2/2	1708.264	1707.826	257.191	0.536	1202.188	0.554	21	0.167	R.EVNSVNDNPVIDVHR.G
R2/RRR2-5/2	1377.269	1377.528	-188.696	0.478	1310.067	0.480	20	0.165	R.VAFETGTAPITNR.I
R2/RRR2-3/3	1465.101	1465.683	-1083.026	0.456	1534.111	0.497	29	0.163	K.KVLTTGPAGGLHSAR.F
R2/RRR2-8/2	1707.383	1707.826	-260.208	0.519	1226.602	0.517	21	0.162	R.EVNSVNDNPVIDVHR.G
R2/RRR2-4/2	1707.502	1707.826	-190.708	0.524	1142.136	0.560	19	0.162	R.EVNSVNDNPVIDVHR.G
R2/RRR2-2/3	1465.987	1465.683	208.025	0.537	1425.241	0.529	29	0.158	K.KVLTTGPAGGLHSAR.F
R2/RRR2-2/2	1377.077	1377.528	-328.489	0.455	1280.665	0.446	19	0.155	R.VAFETGTAPITNR.I
R2/RRR2-2/2	1707.210	1707.826	-949.437	0.524	1132.995	0.523	19	0.154	R.EVNSVNDNPVIDVHR.G
R2/RRR2-2/2	1377.107	1377.528	-306.344	0.441	1202.158	0.470	19	0.153	R.VAFETGTAPITNR.I
R2/RRR2-6/3	1465.900	1465.683	148.778	0.551	1307.955	0.556	29	0.152	K.KVLTTGPAGGLHSAR.F
R2/RRR2-6/2	1377.225	1377.528	-220.884	0.468	1205.399	0.467	18	0.152	R.VAFETGTAPITNR.I
R2/RRR2-5/3	1465.750	1465.683	46.175	0.552	1407.062	0.520	30	0.152	K.KVLTTGPAGGLHSAR.F
R2/RRR2-6/2	1377.192	1377.528	-244.360	0.418	1265.623	0.427	19	0.150	R.VAFETGTAPITNR.I
R2/RRR2-6/2	1708.160	1707.826	195.994	0.494	983.383	0.550	20	0.150	R.EVNSVNDNPVIDVHR.G
R2/RRR2-1/2	1378.251	1377.528	-201.442	0.402	1046.297	0.521	19	0.149	R.VAFETGTAPITNR.I
R2/RRR2-6/3	1800.996	1801.027	-16.807	0.519	1552.270	0.435	29	0.147	R.FVREELGCVYLTGEK.L
R2/RRR2-1/2	1377.027	1377.528	-1092.892	0.420	1262.328	0.393	19	0.145	R.VAFETGTAPITNR.I
R2/RRR2-6/2	1624.473	1624.865	-242.285	0.425	939.143	0.531	20	0.144	R.TSPQWLGPQIEVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1378.260	1377.528	-194.956	0.458	1056.507	0.466	19	0.143	R.VAFETGTAPITNR.I
R2/RRR2-6/2	1251.674	1252.485	-1451.487	0.554	906.399	0.488	16	0.139	K.VNEVDPLLKPK.Q
R2/RRR2-6/2	1624.406	1624.865	-283.600	0.471	777.614	0.507	19	0.134	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1108.049	1108.226	-160.068	0.482	991.339	0.397	15	0.133	K.ITAFEEELR.E
R2/RRR2-6/2	1251.516	1252.485	-1578.263	0.500	862.442	0.458	16	0.133	K.VNEVDPLLKPK.Q
R2/RRR2-1/2	1625.490	1624.865	-231.513	0.527	999.806	0.427	19	0.132	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1624.563	1624.865	-186.501	0.450	902.752	0.447	19	0.131	R.TSPQWLGPQIEVIR.A
R2/RRR2-5/3	1465.904	1465.683	151.409	0.546	1194.289	0.517	28	0.131	K.KVLTTGPAGGLHSAR.F
R2/RRR2-6/2	1624.342	1624.865	-940.362	0.475	974.313	0.412	20	0.131	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1624.481	1624.865	-237.385	0.485	880.606	0.455	18	0.130	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	959.944	960.107	-170.160	0.443	868.867	0.406	15	0.128	K.TAEAVDILK.L
R2/RRR2-2/2	1625.704	1624.865	-99.308	0.394	846.898	0.449	18	0.128	R.TSPQWLGPQIEVIR.A
R2/RRR2-5/2	1625.345	1624.865	296.150	0.460	782.009	0.449	19	0.127	R.TSPQWLGPQIEVIR.A
R2/RRR2-5/2	1624.444	1624.865	-260.303	0.486	750.487	0.463	18	0.127	R.TSPQWLGPQIEVIR.A
R2/RRR2-3/2	1624.314	1624.865	-957.715	0.488	833.755	0.430	19	0.127	R.TSPQWLGPQIEVIR.A
R2/RRR2-5/2	1625.279	1624.865	255.256	0.471	794.409	0.461	17	0.127	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1252.107	1252.485	-302.605	0.526	869.374	0.397	16	0.125	K.VNEVDPLLKPK.Q
R2/RRR2-6/2	934.931	935.102	-183.224	0.466	887.578	0.360	13	0.124	K.VFLAISER.K
R2/RRR2-1/2	1625.388	1624.865	-294.125	0.502	718.620	0.445	18	0.124	R.TSPQWLGPQIEVIR.A
R2/RRR2-4/2	1625.399	1624.865	-287.871	0.464	790.624	0.416	19	0.124	R.TSPQWLGPQIEVIR.A
R2/RRR2-2/2	1377.017	1377.528	-1100.636	0.318	1328.962	0.222	19	0.124	R.VAFETGTAPITNR.I
R2/RRR2-2/3	1465.945	1465.683	179.467	0.509	1101.739	0.517	27	0.124	K.KVLTTGPAGGLHSAR.F
R2/RRR2-6/2	934.645	935.102	-490.077	0.417	817.669	0.390	12	0.124	K.VFLAISER.K
R2/RRR2-8/2	1624.520	1624.865	-213.111	0.492	677.780	0.455	17	0.123	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1108.067	1108.226	-143.933	0.440	1004.370	0.316	15	0.123	K.ITAFEEELR.E
R2/RRR2-6/2	1624.393	1624.865	-291.667	0.465	607.246	0.461	17	0.123	R.TSPQWLGPQIEVIR.A
R2/RRR2-3/2	1625.245	1624.865	234.545	0.513	632.459	0.459	17	0.123	R.TSPQWLGPQIEVIR.A
R2/RRR2-2/2	1040.849	1041.138	-278.741	0.384	364.554	0.447	12	0.122	R.NPSLDYGFK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1108.222	1108.226	-3.603	0.453	856.202	0.353	14	0.122	K.ITAFEEELR.E
R2/RRR2-2/2	1624.362	1624.865	-928.140	0.424	726.612	0.400	19	0.121	R.TSPQWLGPQIEVIR.A
R2/RRR2-5/2	1041.893	1041.138	-236.627	0.420	349.700	0.397	12	0.121	R.NPSLDYGFK.G
R2/RRR2-2/2	1625.274	1624.865	252.470	0.449	630.965	0.422	18	0.121	R.TSPQWLGPQIEVIR.A
R2/RRR2-3/2	1626.362	1624.865	306.278	0.454	804.033	0.378	19	0.120	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	935.139	935.102	39.919	0.462	877.949	0.318	13	0.120	K.VFLAISER.K
R2/RRR2-1/2	1624.352	1624.865	-934.025	0.433	718.508	0.396	18	0.120	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1040.938	1041.138	-192.971	0.341	468.617	0.420	13	0.120	R.NPSLDYGFK.G
R2/RRR2-6/2	1397.939	1398.534	-1144.070	0.395	727.547	0.445	14	0.119	R.EELGCVYLTGEK.L
R2/RRR2-8/2	1624.352	1624.865	-934.100	0.377	626.072	0.423	17	0.119	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1624.563	1624.865	-186.350	0.407	406.482	0.494	14	0.119	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	1040.563	1041.138	-1518.640	0.324	354.670	0.416	12	0.118	R.NPSLDYGFK.G
R2/RRR2-5/2	1042.146	1041.138	7.330	0.356	302.481	0.390	11	0.118	R.NPSLDYGFK.G
R2/RRR2-2/2	1624.490	1624.865	-231.354	0.433	678.976	0.382	18	0.118	R.TSPQWLGPQIEVIR.A
R2/RRR2-5/2	1041.250	1041.138	107.049	0.314	318.778	0.449	11	0.117	R.NPSLDYGFK.G
R2/RRR2-5/3	1465.079	1465.683	-1098.211	0.439	1042.050	0.505	26	0.117	K.KVLTTGPAGGLHSAR.F
R2/RRR2-3/2	1040.914	1041.138	-216.500	0.391	270.575	0.378	10	0.117	R.NPSLDYGFK.G
R2/RRR2-3/2	1623.937	1624.865	-1190.984	0.329	662.956	0.394	18	0.117	R.TSPQWLGPQIEVIR.A
R2/RRR2-3/2	1040.302	1041.138	-1770.178	0.263	427.178	0.491	12	0.116	R.NPSLDYGFK.G
R2/RRR2-5/2	872.787	873.032	-281.492	0.295	929.597	0.315	12	0.116	K.ALLTAIDR.E
R2/RRR2-8/2	1041.936	1041.138	-194.431	0.315	307.184	0.316	11	0.116	R.NPSLDYGFK.G
R2/RRR2-10/2	1626.003	1624.865	85.042	0.454	496.329	0.390	16	0.115	R.TSPQWLGPQIEVIR.A
R2/RRR2-7/2	1624.232	1624.865	-1008.420	0.364	601.955	0.394	16	0.115	R.TSPQWLGPQIEVIR.A
R2/RRR2-3/2	1040.345	1041.138	-1729.503	0.280	307.096	0.405	11	0.115	R.NPSLDYGFK.G
R2/RRR2-5/2	1626.351	1624.865	299.881	0.428	409.367	0.376	15	0.114	R.TSPQWLGPQIEVIR.A
R2/RRR2-1/2	935.686	935.102	-445.697	0.514	986.690	0.259	13	0.114	-.VFLAISER.-
R2/RRR2-7/2	1041.209	1041.138	68.366	0.273	284.971	0.394	10	0.113	R.NPSLDYGFK.G
R2/RRR2-6/2	1624.907	1624.865	25.799	0.362	493.603	0.379	16	0.112	-.TSPQWLGPQIEVIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1040.420	1041.138	-1656.770	0.246	517.343	0.369	13	0.112	R.NPSLDYGFK.G
R2/RRR2-8/2	1623.993	1624.865	-1156.488	0.363	611.245	0.318	17	0.112	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	872.538	873.032	-568.531	0.317	650.389	0.297	12	0.111	K.ALLTAIDR.E
R2/RRR2-2/2	1625.496	1624.865	-228.047	0.339	436.548	0.365	14	0.110	-.TSPQWLGPQIEVIR.-
R2/RRR2-6/2	1624.805	1624.865	-36.819	0.368	475.362	0.327	15	0.109	-.TSPQWLGPQIEVIR.-
R2/RRR2-3/2	1625.297	1624.865	266.403	0.390	401.507	0.325	13	0.109	R.TSPQWLGPQIEVIR.A
R2/RRR2-6/2	959.753	960.107	-369.587	0.308	789.772	0.263	14	0.108	K.TAEAVDILK.L
R2/RRR2-6/2	872.485	873.032	-1778.779	0.273	722.286	0.267	12	0.108	K.ALLTAIDR.E
R2/RRR2-2/2	1040.860	1041.138	-268.504	0.319	251.840	0.310	10	0.107	-.NPSLDYGFK.-
R2/RRR2-5/2	1625.024	1624.865	98.279	0.319	439.412	0.320	13	0.107	-.TSPQWLGPQIEVIR.-
R2/RRR2-6/2	872.480	873.032	-1784.542	0.268	778.431	0.207	13	0.106	K.ALLTAIDR.E
R2/RRR2-2/2	935.525	935.102	453.335	0.322	1007.582	0.158	13	0.104	-.VFLAISER.-
R2/RRR2-9/2	1626.190	1624.865	200.151	0.327	650.259	0.181	16	0.104	-.TSPQWLGPQIEVIR.-
R2/RRR2-2/3	1466.244	1465.683	-300.339	0.458	889.498	0.479	25	0.103	K.KVLTTGPAGGLHSAR.F
R2/RRR2-2/2	1107.947	1108.226	-252.909	0.206	660.711	0.209	12	0.103	K.ITAFEEELR.E
R2/RRR2-1/3	1465.015	1465.683	-1142.135	0.471	848.617	0.486	26	0.103	K.KVLTTGPAGGLHSAR.F
R2/RRR2-1/3	1465.874	1465.683	130.489	0.471	831.482	0.481	25	0.101	K.KVLTTGPAGGLHSAR.F
R2/RRR2-8/2	1109.041	1108.226	-167.873	0.332	437.849	0.314	10	0.097	-.ITAFEEELR.-
R2/RRR2-3/3	1466.158	1465.683	325.122	0.459	615.608	0.504	22	0.097	K.KVLTTGPAGGLHSAR.F
R2/RRR2-6/3	1252.648	1252.485	130.904	0.415	710.690	0.458	20	0.092	K.VNEVDPLLKPK.Q
R2/RRR2-6/3	1252.249	1252.485	-188.920	0.424	471.879	0.493	16	0.089	-.VNEVDPLLKPK.-
R2/RRR2-1/3	1252.919	1252.485	347.377	0.444	551.799	0.426	18	0.087	K.VNEVDPLLKPK.Q
R2/RRR2-2/3	1252.652	1252.485	133.836	0.373	472.964	0.395	17	0.081	-.VNEVDPLLKPK.-
R2/RRR2-6/3	1251.647	1252.485	-1472.510	0.263	540.481	0.324	19	0.076	K.VNEVDPLLKPK.Q
R2/RRR2-5/3	1252.698	1252.485	170.629	0.376	532.468	0.340	17	0.072	-.VNEVDPLLKPK.-
R2/RRR2-2/3	1252.115	1252.485	-296.453	0.355	410.903	0.366	16	0.069	-.VNEVDPLLKPK.-
R2/RRR2-5/3	1252.453	1252.485	-25.976	0.383	428.266	0.355	16	0.066	-.VNEVDPLLKPK.-
R2/RRR2-13/3	1407.788	1406.647	100.171	0.434	1012.925	0.146	23	0.055	-.SAVKNCVTTVAKK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/3	1252.926	1252.485	352.945	0.322	389.768	0.374	15	0.043	-.VNEVDPLLKPK.-
R2/RRR2-12/3	1407.019	1406.647	265.387	0.334	806.111	0.068	19	0.040	-.SAVKNCVTTVAKK.-
R2/RRR2-13/3	1407.310	1406.647	-240.401	0.401	783.617	0.151	20	0.038	-.SAVKNCVTTVAKK.-
R2/RRR2-11/2	1864.628	1864.133	266.080	0.619	2925.628	0.575	26	0.478	R.M*FVADGGELLM*AQSYAK.N
R2/RRR2-11/2	1831.581	1832.134	-850.742	0.537	2286.365	0.599	24	0.341	R.MFVADGGELLMAQSYAK.N
R2/RRR2-11/2	1575.238	1574.798	279.921	0.568	1894.267	0.586	23	0.264	R.VGALSIVCGSADVAVR.V
R2/RRR2-11/2	1574.467	1574.798	-210.554	0.523	2035.185	0.496	24	0.261	R.VGALSIVCGSADVAVR.V
R2/RRR2-11/2	1531.233	1531.695	-302.695	0.470	2013.430	0.477	22	0.252	K.LIFGADSPAIQENR.V
R2/RRR2-11/2	1449.176	1449.629	-313.498	0.483	1772.795	0.568	22	0.242	R.VATVQCLSGTGSLR.V
R2/RRR2-11/2	1531.383	1531.695	-204.005	0.454	1665.787	0.485	21	0.204	K.LIFGADSPAIQENR.V
R2/RRR2-11/2	1574.295	1574.798	-957.813	0.487	1612.891	0.514	22	0.204	R.VGALSIVCGSADVAVR.V
R2/RRR2-11/2	1448.653	1449.629	-1368.390	0.459	1537.295	0.516	21	0.197	R.VATVQCLSGTGSLR.V
R2/RRR2-11/2	1532.227	1531.695	-306.494	0.496	1506.484	0.504	21	0.190	K.LIFGADSPAIQENR.V
R2/RRR2-11/2	1586.259	1586.748	-309.018	0.472	1699.712	0.389	18	0.186	K.DSAM*FNEWTVELK.G
R2/RRR2-11/2	1708.487	1708.979	-288.633	0.568	1470.261	0.412	24	0.166	R.VKEYLPITGLADFNK.L
R2/RRR2-11/2	1480.886	1481.674	-1211.033	0.392	1024.643	0.518	19	0.147	K.EYLPITGLADFNK.L
R2/RRR2-11/2	1480.702	1481.674	-1335.795	0.356	1078.703	0.465	19	0.142	K.EYLPITGLADFNK.L
R2/RRR2-11/2	1707.866	1708.979	-1240.779	0.515	1092.738	0.415	22	0.138	R.VKEYLPITGLADFNK.L
R2/RRR2-11/2	1586.062	1586.748	-1066.033	0.437	1300.440	0.330	17	0.136	K.DSAM*FNEWTVELK.G
R2/RRR2-11/2	1453.674	1454.697	-1395.416	0.489	596.654	0.563	19	0.136	R.TEEGKPLVLNVVR.R
R2/RRR2-11/2	948.781	949.089	-325.856	0.458	906.212	0.446	15	0.135	K.VNLGVGAYR.D
R2/RRR2-11/2	1709.394	1708.979	243.842	0.565	1123.861	0.390	22	0.134	R.VKEYLPITGLADFNK.L
R2/RRR2-11/2	1481.142	1481.674	-1037.892	0.393	953.939	0.446	19	0.133	K.EYLPITGLADFNK.L
R2/RRR2-11/2	848.848	848.969	-143.750	0.546	1145.879	0.335	13	0.131	R.VGGEFLAR.H
R2/RRR2-11/2	1454.349	1454.697	-239.646	0.529	531.642	0.511	18	0.129	R.TEEGKPLVLNVVR.R
R2/RRR2-11/2	848.515	848.969	-537.587	0.495	1076.800	0.331	13	0.128	R.VGGEFLAR.H
R2/RRR2-11/2	1455.593	1454.697	-71.717	0.501	774.133	0.420	21	0.127	R.TEEGKPLVLNVVR.R
R2/RRR2-11/2	907.962	908.059	-106.303	0.356	893.895	0.394	14	0.124	R.ISM*AGLSGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	848.890	848.969	-93.983	0.518	1056.720	0.315	13	0.124	R.VGGEFLAR.H
R2/RRR2-11/2	1076.611	1077.302	-1575.261	0.454	824.609	0.353	17	0.122	K.VFTLAGLTVR.S
R2/RRR2-11/2	1077.027	1077.302	-255.963	0.416	762.254	0.349	17	0.119	K.VFTLAGLTVR.S
R2/RRR2-11/2	891.609	892.059	-506.042	0.438	769.399	0.365	12	0.117	R.ISMAGLSGR.T
R2/RRR2-11/3	1501.635	1500.618	10.949	0.420	1001.145	0.513	26	0.110	R.QEYHIYMTSDGR.I
R2/RRR2-12/2	1531.617	1531.695	-50.890	0.326	268.606	0.336	14	0.109	K.LIFGADSPAIQENR.V
R2/RRR2-11/3	1531.911	1531.695	141.608	0.482	1355.952	0.350	27	0.106	K.LIFGADSPAIQENR.V
R2/RRR2-11/3	1500.643	1500.618	16.626	0.350	869.080	0.467	24	0.093	R.QEYHIYMTSDGR.I
R2/RRR2-11/3	1530.978	1531.695	-1124.874	0.471	1148.935	0.341	23	0.090	-.LIFGADSPAIQENR.-
R2/RRR2-11/3	1500.221	1500.618	-265.666	0.330	681.034	0.434	23	0.083	R.QEYHIYMTSDGR.I
R2/RRR2-11/3	1515.954	1516.618	-1100.675	0.302	494.453	0.470	22	0.082	R.QEYHIYM*TSDGR.I
R2/RRR2-11/3	1709.709	1708.979	-158.100	0.444	836.083	0.354	23	0.078	R.VKEYLPITGLADFNK.L
R2/RRR2-11/3	1574.683	1574.798	-73.338	0.407	1145.707	0.264	25	0.076	R.VGALSIVCGSADVAVR.V
R2/RRR2-11/3	1429.642	1429.631	7.389	0.444	1063.760	0.270	22	0.075	R.RAEQMLINNPSR.V
R2/RRR2-11/3	1708.165	1708.979	-1064.817	0.389	1007.454	0.285	26	0.074	R.VKEYLPITGLADFNK.L
R2/RRR2-11/3	1429.885	1429.631	178.213	0.451	894.780	0.242	20	0.063	-.RAEQMLINNPSR.-
R2/RRR2-11/3	1429.429	1429.631	-142.033	0.373	885.046	0.143	20	0.060	-.RAEQMLINNPSR.-
R2/RRR2-3/2	1559.068	1558.757	199.894	0.512	1908.689	0.483	20	0.239	K.LVYELFTDTLTSR.L
R2/RRR2-3/2	1674.495	1674.788	-175.602	0.471	1808.037	0.518	25	0.234	K.AIENTAASISDVPEEK.L
R2/RRR2-3/2	1557.753	1558.757	-1290.158	0.353	1967.361	0.403	20	0.226	K.LVYELFTDTLTSR.L
R2/RRR2-25/2	1648.265	1648.774	-918.175	0.512	2006.241	0.350	20	0.214	K.VLNDM*IQDDSEQPK.K
R2/RRR2-3/2	1144.019	1144.343	-283.891	0.424	1652.370	0.470	17	0.201	K.GLALAEIESLK.T
R2/RRR2-3/2	1674.170	1674.788	-969.199	0.442	1594.803	0.486	23	0.196	K.AIENTAASISDVPEEK.L
R2/RRR2-3/2	1144.095	1144.343	-217.736	0.441	1494.882	0.516	17	0.192	K.GLALAEIESLK.T
R2/RRR2-25/2	1648.252	1648.774	-926.205	0.483	1841.941	0.333	20	0.189	K.VLNDM*IQDDSEQPK.K
R2/RRR2-3/2	1096.096	1096.219	-112.776	0.454	1411.285	0.470	14	0.174	R.HDNVQLLEK.L
R2/RRR2-3/2	1835.400	1836.147	-954.701	0.542	1085.494	0.586	24	0.168	R.FINVPIGASWVEVTM*R.T
R2/RRR2-3/2	1836.467	1836.147	174.770	0.607	1012.887	0.610	23	0.166	R.FINVPIGASWVEVTM*R.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-25/2	1648.074	1648.774	-1034.621	0.506	1569.243	0.366	19	0.165	K.VLNDM*IQDDSEQPK.K
R2/RRR2-3/2	1096.083	1096.219	-124.283	0.464	1159.619	0.510	14	0.160	R.HDNVQLLEK.L
R2/RRR2-3/2	1835.721	1836.147	-232.876	0.543	995.163	0.576	23	0.158	R.FINVPIGASWVEVTM*R.T
R2/RRR2-3/2	1095.960	1096.219	-237.242	0.512	1121.145	0.486	14	0.153	R.HDNVQLLEK.L
R2/RRR2-3/2	1226.387	1227.392	-1640.253	0.407	1166.534	0.455	18	0.148	K.IIGLDGSEAPVR.V
R2/RRR2-3/2	1507.527	1508.761	-1486.738	0.296	1242.248	0.423	20	0.145	R.LTEPSFLESLM*PK.K
R2/RRR2-3/2	1237.064	1237.409	-279.613	0.425	945.122	0.420	19	0.132	R.LGSM*ETGTGLVR.A
R2/RRR2-3/2	1237.942	1237.409	-378.714	0.496	894.863	0.419	19	0.131	R.LGSM*ETGTGLVR.A
R2/RRR2-3/2	909.006	909.065	-64.735	0.418	497.769	0.520	13	0.130	K.YGSLTVLR.E
R2/RRR2-2/2	1227.340	1227.392	-42.857	0.388	1072.849	0.366	18	0.130	K.IIGLDGSEAPVR.V
R2/RRR2-3/2	1055.901	1056.153	-239.749	0.428	1132.804	0.341	13	0.129	R.AFEYAQQAK.E
R2/RRR2-2/2	1228.108	1227.392	-232.550	0.453	976.256	0.396	17	0.128	K.IIGLDGSEAPVR.V
R2/RRR2-3/2	1492.397	1492.762	-245.678	0.354	864.430	0.417	19	0.125	R.LTEPSFLESLMPK.K
R2/RRR2-3/2	909.037	909.065	-30.252	0.349	520.188	0.440	13	0.121	K.YGSLTVLR.E
R2/RRR2-3/2	1236.931	1237.409	-387.932	0.444	721.347	0.405	17	0.121	R.LGSM*ETGTGLVR.A
R2/RRR2-25/2	908.826	909.065	-263.189	0.371	472.853	0.439	12	0.121	K.YGSLTVLR.E
R2/RRR2-3/2	1492.138	1492.762	-1091.784	0.416	712.503	0.423	17	0.121	R.LTEPSFLESLMPK.K
R2/RRR2-25/2	909.009	909.065	-61.502	0.349	424.469	0.451	12	0.120	K.YGSLTVLR.E
R2/RRR2-3/2	1507.934	1508.761	-1215.714	0.316	648.789	0.479	16	0.119	R.LTEPSFLESLM*PK.K
R2/RRR2-3/2	1226.369	1227.392	-1654.553	0.356	1196.331	0.236	18	0.119	K.IIGLDGSEAPVR.V
R2/RRR2-1/2	1509.719	1508.761	-28.205	0.395	628.592	0.441	16	0.119	R.LTEPSFLESLM*PK.K
R2/RRR2-2/2	1237.130	1237.409	-226.551	0.422	704.300	0.375	18	0.119	R.LGSM*ETGTGLVR.A
R2/RRR2-3/2	908.812	909.065	-279.225	0.333	562.763	0.406	13	0.118	K.YGSLTVLR.E
R2/RRR2-3/2	1231.052	1231.338	-232.790	0.384	728.270	0.413	16	0.118	R.VAVDTQGLEGNK.N
R2/RRR2-3/2	1433.073	1432.560	-340.943	0.476	683.914	0.375	17	0.117	R.QTSEWTVQLDPK.F
R2/RRR2-3/2	1055.810	1056.153	-325.931	0.359	1018.295	0.257	13	0.114	R.AFEYAQQAK.E
R2/RRR2-3/2	1499.320	1499.647	-218.331	0.443	822.110	0.299	15	0.109	K.DAFEENYKELIK.W
R2/RRR2-3/2	1500.280	1499.647	-245.040	0.506	822.720	0.315	14	0.108	-.DAFEENYKELIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1492.124	1492.762	-1100.984	0.318	563.629	0.310	15	0.107	R.LTEPSFLESLMPK.K
R2/RRR2-3/2	1432.228	1432.560	-232.320	0.320	557.586	0.261	16	0.107	R.QTSEWTVQLDPK.F
R2/RRR2-3/3	1627.060	1626.750	191.119	0.533	650.183	0.570	24	0.105	R.IYDNKFESQYYR.I
R2/RRR2-1/2	1227.375	1227.392	-13.827	0.363	722.668	0.216	16	0.105	-.IIGLDGSEAPVR.-
R2/RRR2-3/2	1055.261	1056.153	-1798.689	0.233	838.361	0.221	12	0.104	R.AFEYAQQAK.E
R2/RRR2-2/2	1226.252	1227.392	-1750.963	0.236	612.909	0.176	15	0.103	-.IIGLDGSEAPVR.-
R2/RRR2-3/2	1431.603	1432.560	-1371.431	0.338	640.443	0.205	15	0.102	-.QTSEWTVQLDPK.-
R2/RRR2-3/2	1498.645	1499.647	-1339.327	0.363	774.430	0.228	14	0.102	K.DAFEENYKELIK.W
R2/RRR2-1/2	1226.318	1227.392	-1696.855	0.274	889.217	0.106	18	0.101	K.IIGLDGSEAPVR.V
R2/RRR2-3/3	1404.629	1403.608	15.061	0.491	741.611	0.447	24	0.091	K.FKLEDGAEIKPR.V
R2/RRR2-3/3	1403.519	1403.608	-64.181	0.508	686.415	0.443	23	0.089	K.FKLEDGAEIKPR.V
R2/RRR2-4/2	1227.469	1227.392	62.381	0.262	588.214	0.051	16	0.083	-.IIGLDGSEAPVR.-
R2/RRR2-3/3	1403.795	1403.608	133.512	0.430	790.677	0.357	22	0.079	K.FKLEDGAEIKPR.V
R2/RRR2-1/2	1953.530	1954.172	-843.198	0.556	3649.591	0.539	28	0.667	R.SPVYAQFSEALNGLSTIR.A
R2/RRR2-1/2	1953.441	1954.172	-889.117	0.562	3442.354	0.536	27	0.600	R.SPVYAQFSEALNGLSTIR.A
R2/RRR2-1/2	1953.477	1954.172	-870.423	0.569	3345.352	0.516	27	0.561	R.SPVYAQFSEALNGLSTIR.A
R2/RRR2-2/2	1953.053	1954.172	-1088.584	0.510	3303.276	0.529	26	0.558	R.SPVYAQFSEALNGLSTIR.A
R2/RRR2-1/2	1486.162	1485.708	306.749	0.529	2998.677	0.553	23	0.488	K.ILVLDEATAAVDVR.T
R2/RRR2-1/2	1485.263	1485.708	-300.111	0.402	3026.893	0.515	23	0.481	K.ILVLDEATAAVDVR.T
R2/RRR2-2/2	1953.722	1954.172	-231.222	0.555	2715.325	0.521	25	0.398	R.SPVYAQFSEALNGLSTIR.A
R2/RRR2-2/2	1952.958	1954.172	-1137.349	0.496	2729.331	0.460	26	0.380	R.SPVYAQFSEALNGLSTIR.A
R2/RRR2-1/2	1485.345	1485.708	-244.784	0.439	2449.525	0.503	21	0.340	K.ILVLDEATAAVDVR.T
R2/RRR2-2/2	1487.283	1487.641	-241.172	0.522	2374.901	0.497	21	0.319	R.LASLAENSLNAVER.V
R2/RRR2-2/2	1487.448	1487.641	-129.529	0.530	2318.063	0.518	21	0.315	R.LASLAENSLNAVER.V
R2/RRR2-1/2	1487.267	1487.641	-251.630	0.486	2223.844	0.496	21	0.291	R.LASLAENSLNAVER.V
R2/RRR2-1/2	1487.259	1487.641	-257.229	0.506	2248.099	0.476	22	0.289	R.LASLAENSLNAVER.V
R2/RRR2-1/2	1487.992	1487.641	237.172	0.528	2136.142	0.527	21	0.284	R.LASLAENSLNAVER.V
R2/RRR2-2/2	1486.704	1487.641	-1306.767	0.417	2261.655	0.438	21	0.280	R.LASLAENSLNAVER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1643.731	1642.705	15.820	0.514	1702.179	0.526	19	0.219	K.LDSWDETETLYNR.F
R2/RRR2-1/2	1201.040	1201.352	-260.116	0.522	1830.833	0.399	17	0.207	R.LEDLLLAEER.L
R2/RRR2-1/2	1201.338	1201.352	-11.171	0.511	1782.056	0.413	17	0.204	R.LEDLLLAEER.L
R2/RRR2-1/2	1642.562	1642.705	-87.108	0.510	1361.310	0.508	18	0.175	K.LDSWDETETLYNR.F
R2/RRR2-1/2	1357.686	1357.538	109.514	0.425	1538.509	0.360	18	0.164	K.RLEDLLLAEER.L
R2/RRR2-1/2	1850.488	1851.007	-823.656	0.526	987.505	0.587	23	0.159	R.HDLDLLPGGDLTEIGER.G
R2/RRR2-1/2	1357.510	1357.538	-20.529	0.482	1211.961	0.460	17	0.154	K.RLEDLLLAEER.L
R2/RRR2-1/2	1123.148	1123.198	-44.979	0.369	1106.765	0.486	17	0.149	K.TLVFGDGEER.L
R2/RRR2-2/2	1357.671	1357.538	98.333	0.491	1300.573	0.380	17	0.146	K.RLEDLLLAEER.L
R2/RRR2-1/2	1357.133	1357.538	-299.576	0.433	1283.891	0.363	17	0.143	K.RLEDLLLAEER.L
R2/RRR2-2/2	1357.834	1357.538	218.608	0.449	1194.419	0.390	17	0.141	K.RLEDLLLAEER.L
R2/RRR2-1/2	844.930	844.941	-12.550	0.393	861.082	0.474	12	0.135	R.HANIFSR.I
R2/RRR2-1/2	1504.062	1503.753	205.790	0.533	619.055	0.515	18	0.131	R.APM*VFFHTNPLGR.I
R2/RRR2-1/2	844.343	844.941	-1898.535	0.312	940.249	0.437	12	0.130	R.HANIFSR.I
R2/RRR2-1/2	844.347	844.941	-1893.014	0.371	688.949	0.477	11	0.127	R.HANIFSR.I
R2/RRR2-1/2	1941.852	1941.343	-253.379	0.423	387.466	0.614	20	0.127	R.LLLPNPPLDPELPAISIK.N
R2/RRR2-2/2	1357.436	1357.538	-75.550	0.433	995.391	0.370	16	0.127	K.RLEDLLLAEER.L
R2/RRR2-1/2	1754.468	1754.109	205.057	0.424	528.838	0.518	21	0.124	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-2/2	1753.667	1754.109	-252.921	0.378	606.914	0.497	22	0.123	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-2/2	1940.356	1941.343	-1026.928	0.398	374.999	0.585	19	0.123	R.LLLPNPPLDPELPAISIK.N
R2/RRR2-2/2	845.114	844.941	205.201	0.346	759.013	0.404	11	0.122	R.HANIFSR.I
R2/RRR2-1/2	1123.306	1123.198	96.613	0.355	784.715	0.396	15	0.121	K.TLVFGDGEER.L
R2/RRR2-2/2	1940.761	1941.343	-817.707	0.403	417.189	0.531	20	0.121	R.LLLPNPPLDPELPAISIK.N
R2/RRR2-1/2	1753.534	1754.109	-901.035	0.389	576.375	0.476	21	0.120	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-2/2	1753.501	1754.109	-920.044	0.376	513.221	0.496	20	0.120	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-1/2	1940.699	1941.343	-849.530	0.346	361.523	0.513	19	0.116	R.LLLPNPPLDPELPAISIK.N
R2/RRR2-2/2	1940.532	1941.343	-935.853	0.360	261.417	0.542	17	0.116	R.LLLPNPPLDPELPAISIK.N
R2/RRR2-1/2	1123.092	1123.198	-94.367	0.286	789.622	0.368	15	0.115	K.TLVFGDGEER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/3	1503.704	1503.753	-32.496	0.500	1027.623	0.510	26	0.115	R.APM*VFFHTNPLGR.I
R2/RRR2-1/2	1753.519	1754.109	-909.352	0.347	463.029	0.420	20	0.113	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-1/3	1503.124	1503.753	-1086.735	0.406	827.440	0.570	23	0.113	R.APM*VFFHTNPLGR.I
R2/RRR2-2/2	1753.595	1754.109	-865.814	0.377	415.566	0.439	18	0.113	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-1/2	1940.746	1941.343	-825.284	0.322	347.139	0.495	18	0.113	R.LLLPNPPLDPELPAISIK.N
R2/RRR2-2/2	1504.292	1503.753	-307.170	0.352	385.009	0.418	15	0.112	R.APM*VFFHTNPLGR.I
R2/RRR2-2/2	844.304	844.941	-1944.446	0.254	507.783	0.348	9	0.109	R.HANIFSR.I
R2/RRR2-1/2	1787.337	1787.094	136.072	0.500	789.069	0.345	16	0.108	R.VLVTNQLHFLPYVDK.I
R2/RRR2-1/2	1488.684	1488.672	7.845	0.275	761.799	0.279	14	0.103	R.DNILFGSPFQPPR.Y
R2/RRR2-1/3	1487.461	1487.641	-120.853	0.480	1284.073	0.363	27	0.103	R.LASLAENSLNAVER.V
R2/RRR2-2/2	1122.309	1123.198	-1688.506	0.176	649.174	0.173	13	0.100	K.TLVFGDGEER.L
R2/RRR2-1/3	1503.820	1503.753	44.934	0.513	862.819	0.474	24	0.100	R.APM*VFFHTNPLGR.I
R2/RRR2-1/2	1487.990	1488.672	-1133.583	0.206	612.478	0.208	14	0.098	R.DNILFGSPFQPPR.Y
R2/RRR2-1/2	1641.527	1642.705	-1330.901	0.175	792.710	0.146	14	0.096	K.LDSWDETETLYNR.F
R2/RRR2-2/2	1787.864	1787.094	-129.473	0.429	693.611	0.222	15	0.096	R.VLVTNQLHFLPYVDK.I
R2/RRR2-2/3	1503.547	1503.753	-137.668	0.483	712.977	0.476	22	0.095	R.APM*VFFHTNPLGR.I
R2/RRR2-2/3	1942.741	1941.343	205.345	0.448	838.476	0.467	24	0.094	R.LLLPNPPLDPELPAISIK.N
R2/RRR2-1/3	1679.999	1679.815	109.813	0.434	979.913	0.412	26	0.091	K.VQDIRDDEISWFR.S
R2/RRR2-2/3	1753.461	1754.109	-942.976	0.342	1092.042	0.349	29	0.087	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-1/3	1502.509	1503.753	-1497.758	0.378	862.322	0.386	25	0.085	R.APM*VFFHTNPLGR.I
R2/RRR2-1/3	951.987	952.136	-156.420	0.432	881.032	0.355	16	0.081	R.AHLKDVIR.R
R2/RRR2-1/3	952.556	952.136	442.517	0.432	652.867	0.368	15	0.080	R.AHLKDVIR.R
R2/RRR2-1/3	952.343	952.136	218.337	0.427	682.721	0.369	15	0.080	R.AHLKDVIR.R
R2/RRR2-1/3	1753.932	1754.109	-101.550	0.347	833.472	0.371	26	0.079	K.VLGIIPQAPVLFSGSVR.F
R2/RRR2-2/3	1503.384	1503.753	-246.162	0.393	589.228	0.350	21	0.078	R.APM*VFFHTNPLGR.I
R2/RRR2-1/3	1487.557	1487.641	-56.399	0.384	710.080	0.336	21	0.073	R.LASLAENSLNAVER.V
R2/RRR2-1/3	1941.050	1941.343	-151.337	0.259	573.653	0.268	22	0.062	-.LLLPNPPLDPELPAISIK.-
R2/RRR2-8/1	1493.830	1492.656	117.369	0.488	831.075	0.469	17	0.737	R.IEEELGAAAVYAGAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1985.427	1985.085	172.755	0.583	2704.862	0.616	26	0.438	R.GNPTVEVDVCCSDGTFAR.A
R2/RRR2-8/2	1984.377	1985.085	-863.532	0.563	2481.939	0.638	26	0.395	R.GNPTVEVDVCCSDGTFAR.A
R2/RRR2-8/2	1985.519	1985.085	218.811	0.589	2383.910	0.660	25	0.381	R.GNPTVEVDVCCSDGTFAR.A
R2/RRR2-8/2	1492.238	1492.656	-280.329	0.495	2473.203	0.598	23	0.372	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/3	1575.660	1574.758	-62.375	0.584	2371.186	0.623	33	0.372	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/1	1491.853	1492.656	-1212.011	0.243	495.235	0.318	18	0.320	R.IEEELGAAAVYAGAK.F
R2/RRR2-7/2	1492.405	1492.656	-168.149	0.498	2181.910	0.526	22	0.290	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1552.578	1552.802	-145.072	0.522	2157.724	0.493	22	0.281	K.IPLYQHIANLAGNK.Q
R2/RRR2-8/3	1574.972	1574.758	136.104	0.556	2123.954	0.529	33	0.270	K.VNQIGSVTESIEAVK.M
R2/RRR2-2/2	1492.252	1492.656	-271.137	0.465	2166.795	0.461	23	0.268	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1902.302	1902.953	-870.346	0.562	1884.194	0.597	23	0.264	K.TYDLNFKEENNDGSQK.I
R2/RRR2-8/2	1492.249	1492.656	-273.517	0.530	1962.954	0.555	23	0.262	R.IEEELGAAAVYAGAK.F
R2/RRR2-7/2	1493.158	1492.656	-334.111	0.556	1897.878	0.551	23	0.250	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/1	1491.749	1492.656	-1281.696	0.277	324.027	0.369	17	0.248	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1902.399	1902.953	-819.072	0.552	1799.387	0.551	23	0.238	K.TYDLNFKEENNDGSQK.I
R2/RRR2-1/2	1492.424	1492.656	-155.760	0.489	1817.417	0.524	22	0.231	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/3	1574.693	1574.758	-41.148	0.562	1825.659	0.556	28	0.230	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/3	1492.645	1492.656	-6.826	0.509	1963.865	0.469	31	0.219	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1491.687	1492.656	-1323.413	0.392	1933.594	0.409	23	0.219	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1872.551	1872.241	165.810	0.569	1481.091	0.639	24	0.215	K.LAM*QEFMILPTGAASFK.E
R2/RRR2-8/3	1493.838	1492.656	122.596	0.526	1945.167	0.468	31	0.215	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1871.429	1872.241	-971.161	0.540	1553.802	0.582	25	0.211	K.LAMQEFM*ILPTGAASFK.E
R2/RRR2-2/2	1574.157	1574.758	-1020.043	0.499	1611.034	0.553	23	0.210	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1903.356	1902.953	212.432	0.537	1536.513	0.580	21	0.209	K.TYDLNFKEENNDGSQK.I
R2/RRR2-2/2	1492.227	1492.656	-288.044	0.472	1780.215	0.444	22	0.206	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1581.425	1581.839	-262.429	0.484	1638.134	0.513	23	0.206	K.AVDNVNSVIAPALIGK.D
R2/RRR2-2/2	1492.047	1492.656	-1081.429	0.411	1766.267	0.437	21	0.203	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1553.369	1552.802	-279.859	0.546	1658.668	0.476	21	0.201	K.IPLYQHIANLAGNK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1581.643	1581.839	-123.905	0.488	1523.743	0.555	22	0.201	K.AVDNVNSVIAPALIGK.D
R2/RRR2-8/2	1581.378	1581.839	-291.935	0.507	1494.343	0.559	22	0.198	K.AVDNVNSVIAPALIGK.D
R2/RRR2-8/2	1871.327	1872.241	-1026.173	0.567	1466.063	0.577	23	0.197	K.LAM*QEFMILPTGAASFK.E
R2/RRR2-8/2	1872.606	1872.241	195.293	0.588	1413.402	0.587	25	0.196	K.LAMQEFM*ILPTGAASFK.E
R2/RRR2-8/2	1574.249	1574.758	-961.341	0.520	1482.043	0.552	22	0.194	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1871.537	1872.241	-913.404	0.549	1536.608	0.523	24	0.194	K.LAMQEFM*ILPTGAASFK.E
R2/RRR2-8/2	1888.435	1888.241	103.271	0.596	1361.096	0.605	24	0.193	K.LAM*QEFM*ILPTGAASFK.E
R2/RRR2-8/2	1575.415	1574.758	-218.432	0.558	1442.255	0.561	22	0.192	K.VNQIGSVTESIEAVK.M
R2/RRR2-7/2	1575.212	1574.758	289.097	0.515	1531.233	0.504	23	0.190	K.VNQIGSVTESIEAVK.M
R2/RRR2-1/2	1492.267	1492.656	-260.961	0.448	1648.572	0.441	21	0.189	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1855.598	1856.242	-888.689	0.569	1445.733	0.542	24	0.188	K.LAMQEFMILPTGAASFK.E
R2/RRR2-8/2	1573.782	1574.758	-1259.124	0.388	1564.118	0.480	23	0.187	K.VNQIGSVTESIEAVK.M
R2/RRR2-4/2	1575.304	1574.758	-289.020	0.543	1484.950	0.511	22	0.185	K.VNQIGSVTESIEAVK.M
R2/RRR2-1/2	1575.314	1574.758	-282.800	0.558	1443.008	0.526	22	0.184	K.VNQIGSVTESIEAVK.M
R2/RRR2-2/2	1573.938	1574.758	-1159.973	0.474	1414.323	0.524	22	0.181	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1580.633	1581.839	-1399.292	0.388	1579.867	0.436	22	0.181	K.AVDNVNSVIAPALIGK.D
R2/RRR2-6/2	1574.310	1574.758	-285.313	0.501	1364.579	0.543	22	0.180	K.VNQIGSVTESIEAVK.M
R2/RRR2-1/2	1574.090	1574.758	-1063.022	0.498	1398.574	0.527	22	0.180	K.VNQIGSVTESIEAVK.M
R2/RRR2-6/2	1574.279	1574.758	-304.918	0.487	1484.841	0.483	22	0.179	K.VNQIGSVTESIEAVK.M
R2/RRR2-2/2	1581.415	1581.839	-268.392	0.445	1327.953	0.561	21	0.179	K.AVDNVNSVIAPALIGK.D
R2/RRR2-8/2	1855.413	1856.242	-988.883	0.542	1374.635	0.522	24	0.177	K.LAMQEFMILPTGAASFK.E
R2/RRR2-1/2	1581.328	1581.839	-958.354	0.418	1476.497	0.465	22	0.176	K.AVDNVNSVIAPALIGK.D
R2/RRR2-8/2	1888.490	1888.241	132.183	0.620	1408.870	0.504	24	0.174	K.LAM*QEFM*ILPTGAASFK.E
R2/RRR2-8/2	1573.924	1574.758	-1168.930	0.431	1418.518	0.468	22	0.170	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1855.414	1856.242	-988.289	0.530	1271.556	0.527	24	0.168	K.LAMQEFMILPTGAASFK.E
R2/RRR2-8/2	1871.542	1872.241	-910.916	0.534	1305.482	0.515	23	0.168	K.LAM*QEFMILPTGAASFK.E
R2/RRR2-10/2	1574.361	1574.758	-252.797	0.493	1259.906	0.524	21	0.166	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1190.003	1190.397	-332.287	0.523	1527.755	0.381	16	0.166	K.MGVEVYHNLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1574.161	1574.758	-1017.551	0.476	1310.197	0.469	21	0.160	K.VNQIGSVTESIEAVK.M
R2/RRR2-7/2	1573.584	1574.758	-1385.798	0.375	1282.498	0.489	20	0.160	K.VNQIGSVTESIEAVK.M
R2/RRR2-5/2	1575.141	1574.758	243.560	0.505	1210.402	0.493	21	0.156	K.VNQIGSVTESIEAVK.M
R2/RRR2-5/2	1574.143	1574.758	-1028.918	0.412	1389.291	0.410	21	0.156	K.VNQIGSVTESIEAVK.M
R2/RRR2-1/2	1492.250	1492.656	-272.779	0.408	1394.004	0.405	20	0.156	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	1554.347	1552.802	-293.625	0.547	1132.819	0.478	20	0.150	K.IPLYQHIANLAGNK.Q
R2/RRR2-8/2	1206.021	1206.397	-312.229	0.522	1189.530	0.439	16	0.150	K.M*GVEVYHNLK.S
R2/RRR2-10/2	1574.307	1574.758	-287.492	0.435	1231.257	0.429	22	0.148	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1887.408	1888.241	-973.907	0.547	888.106	0.555	21	0.143	K.LAM*QEFM*ILPTGAASFK.E
R2/RRR2-8/2	1224.261	1224.388	-104.670	0.500	1036.376	0.449	17	0.142	K.ISGDSLKNVYK.S
R2/RRR2-7/2	1573.437	1574.758	-1479.460	0.378	1160.214	0.429	19	0.140	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1680.404	1680.975	-937.551	0.541	876.937	0.465	22	0.134	K.KIPLYQHIANLAGNK.Q
R2/RRR2-3/2	1574.225	1574.758	-976.755	0.437	1063.707	0.408	20	0.133	K.VNQIGSVTESIEAVK.M
R2/RRR2-8/2	1792.285	1791.983	169.101	0.535	573.003	0.548	23	0.132	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/2	1791.499	1791.983	-271.227	0.475	551.228	0.558	22	0.130	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/2	1680.402	1680.975	-939.229	0.521	734.640	0.484	20	0.129	K.KIPLYQHIANLAGNK.Q
R2/RRR2-8/2	1791.429	1791.983	-870.014	0.506	588.581	0.534	22	0.129	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/2	1680.471	1680.975	-897.588	0.487	720.145	0.460	21	0.127	K.KIPLYQHIANLAGNK.Q
R2/RRR2-9/2	1792.286	1791.983	169.306	0.487	500.388	0.539	21	0.126	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/2	1206.140	1206.397	-213.124	0.500	855.321	0.378	15	0.123	K.M*GVEVYHNLK.S
R2/RRR2-1/2	1792.357	1791.983	209.398	0.519	447.560	0.521	20	0.123	R.AAVPSGASTGVYEALELR.D
R2/RRR2-2/2	1791.237	1791.983	-977.559	0.432	619.269	0.480	22	0.123	R.AAVPSGASTGVYEALELR.D
R2/RRR2-1/2	1793.197	1791.983	119.582	0.497	339.474	0.515	19	0.121	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/2	1206.109	1206.397	-238.913	0.501	756.510	0.370	15	0.120	K.M*GVEVYHNLK.S
R2/RRR2-9/2	1791.208	1791.983	-993.911	0.442	658.772	0.426	23	0.120	R.AAVPSGASTGVYEALELR.D
R2/RRR2-3/2	1791.148	1791.983	-1027.576	0.422	462.688	0.483	20	0.119	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/2	1102.055	1102.252	-179.047	0.488	1033.436	0.291	15	0.118	R.AGWGVMTSHR.S
R2/RRR2-10/2	1574.007	1574.758	-1115.506	0.377	733.055	0.383	19	0.117	K.VNQIGSVTESIEAVK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	918.649	919.094	-485.883	0.435	781.942	0.331	13	0.117	-.SCNALLLK.-
R2/RRR2-11/2	1904.655	1902.953	-157.018	0.410	396.054	0.490	17	0.117	K.TYDLNFKEENNDGSQK.I
R2/RRR2-9/2	1791.411	1791.983	-880.344	0.360	232.856	0.427	18	0.115	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/3	1492.329	1492.656	-219.486	0.461	1478.060	0.328	27	0.112	R.IEEELGAAAVYAGAK.F
R2/RRR2-8/2	918.473	919.094	-1770.631	0.462	752.354	0.269	13	0.111	-.SCNALLLK.-
R2/RRR2-7/2	1581.393	1581.839	-282.952	0.304	1067.772	0.234	20	0.111	K.AVDNVNSVIAPALIGK.D
R2/RRR2-9/2	919.653	919.094	-481.758	0.353	527.311	0.265	13	0.110	-.SCNALLLK.-
R2/RRR2-3/2	1791.046	1791.983	-1085.057	0.322	393.609	0.380	18	0.110	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/2	1117.331	1118.251	-1723.561	0.384	520.192	0.286	13	0.109	R.AGWGVM*TSHR.S
R2/RRR2-8/2	1117.826	1118.251	-381.592	0.346	603.249	0.276	14	0.109	R.AGWGVM*TSHR.S
R2/RRR2-8/2	918.480	919.094	-1763.553	0.445	602.240	0.292	12	0.108	-.SCNALLLK.-
R2/RRR2-2/2	1790.590	1791.983	-1340.656	0.281	259.867	0.348	15	0.108	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/3	1902.945	1902.953	-3.971	0.413	705.495	0.585	29	0.107	K.TYDLNFKEENNDGSQK.I
R2/RRR2-2/2	1205.412	1206.397	-1651.720	0.325	757.452	0.230	14	0.107	K.M*GVEVYHNLK.S
R2/RRR2-8/3	1903.923	1902.953	-15.577	0.421	469.833	0.632	27	0.104	K.TYDLNFKEENNDGSQK.I
R2/RRR2-8/3	1902.328	1902.953	-856.568	0.372	494.617	0.593	26	0.097	K.TYDLNFKEENNDGSQK.I
R2/RRR2-8/3	1791.972	1791.983	-6.506	0.438	766.343	0.444	29	0.089	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/3	1791.804	1791.983	-100.291	0.393	642.555	0.455	27	0.085	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/3	1792.830	1791.983	-85.927	0.432	611.100	0.436	27	0.084	R.AAVPSGASTGVYEALELR.D
R2/RRR2-8/3	1274.355	1274.437	-64.717	0.460	862.449	0.369	21	0.082	K.RAGWGVM*TSHR.S
R2/RRR2-9/3	1553.790	1552.802	-7.740	0.353	924.419	0.360	23	0.082	K.IPLYQHIANLAGNK.Q
R2/RRR2-8/3	1273.863	1274.437	-1240.077	0.452	832.307	0.296	20	0.073	K.RAGWGVM*TSHR.S
R2/RRR2-9/3	1552.997	1552.802	125.573	0.377	732.948	0.279	23	0.070	K.IPLYQHIANLAGNK.Q
R2/RRR2-2/3	1552.425	1552.802	-243.601	0.309	722.344	0.239	23	0.066	K.IPLYQHIANLAGNK.Q
R2/RRR2-2/3	1974.092	1974.290	-100.799	0.513	3109.587	0.512	39	0.534	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/3	1973.748	1974.290	-783.732	0.550	3080.358	0.531	41	0.530	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/3	1973.883	1974.290	-206.599	0.492	3140.693	0.464	37	0.519	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/3	1973.607	1974.290	-855.162	0.488	2983.948	0.509	39	0.494	R.LFASNVLVSGLNGLGAEIAK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1974.161	1974.290	-65.537	0.485	2696.872	0.534	38	0.424	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/2	1647.282	1645.938	209.557	0.592	2843.121	0.476	25	0.414	K.IFM*VGSGALGCEFLK.N
R2/RRR2-3/2	1973.633	1974.290	-841.930	0.567	2501.236	0.551	29	0.360	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/2	1571.322	1570.728	-258.974	0.606	2211.551	0.515	24	0.294	R.YDAQISVFGSNLQK.K
R2/RRR2-2/2	1570.299	1570.728	-274.191	0.516	2247.547	0.475	23	0.289	R.YDAQISVFGSNLQK.K
R2/RRR2-3/2	1631.174	1629.939	144.596	0.557	2237.578	0.478	23	0.289	K.IFMVGSGALGCEFLK.N
R2/RRR2-3/2	1570.176	1570.728	-991.438	0.558	2172.806	0.495	24	0.282	R.YDAQISVFGSNLQK.K
R2/RRR2-3/2	1570.260	1570.728	-299.227	0.557	2162.470	0.490	24	0.279	R.YDAQISVFGSNLQK.K
R2/RRR2-3/2	1973.224	1974.290	-1050.031	0.524	1926.055	0.567	27	0.259	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/2	1973.861	1974.290	-218.008	0.561	1992.840	0.526	27	0.256	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/2	1291.567	1292.380	-1407.887	0.475	1707.872	0.462	20	0.206	R.FPIAGSSDDVQR.L
R2/RRR2-3/2	1292.187	1292.380	-149.670	0.461	1738.034	0.429	20	0.201	R.FPIAGSSDDVQR.L
R2/RRR2-3/2	1974.247	1974.290	-21.558	0.534	1509.546	0.573	24	0.200	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-4/2	1975.655	1974.290	185.446	0.469	1412.107	0.525	22	0.177	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/2	1447.545	1448.566	-1400.564	0.431	1542.936	0.363	19	0.166	R.RFPIAGSSDDVQR.L
R2/RRR2-3/2	1974.677	1974.290	196.513	0.505	1254.069	0.503	22	0.157	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/2	1282.967	1282.342	-293.131	0.493	1147.801	0.482	17	0.154	R.APEIDEDLHSR.Q
R2/RRR2-3/2	1248.123	1248.362	-192.035	0.435	1134.414	0.472	18	0.151	K.LTVTDDDVIEK.S
R2/RRR2-3/2	1292.010	1292.380	-287.384	0.462	1230.111	0.423	18	0.149	R.FPIAGSSDDVQR.L
R2/RRR2-3/2	1080.065	1080.223	-145.850	0.429	1244.708	0.390	15	0.146	K.LHVEALQNR.A
R2/RRR2-3/2	1125.097	1125.265	-150.133	0.423	833.837	0.565	16	0.145	K.LLHHFASGSR.A
R2/RRR2-3/2	1247.547	1248.362	-1458.839	0.400	1144.870	0.379	18	0.137	K.LTVTDDDVIEK.S
R2/RRR2-3/2	1247.475	1248.362	-1517.519	0.388	1152.791	0.373	18	0.136	K.LTVTDDDVIEK.S
R2/RRR2-3/2	1125.018	1125.265	-219.904	0.360	975.895	0.410	17	0.131	K.LLHHFASGSR.A
R2/RRR2-3/2	1281.927	1282.342	-324.600	0.461	1093.840	0.370	15	0.130	R.APEIDEDLHSR.Q
R2/RRR2-3/2	1320.438	1319.447	-6.918	0.524	822.806	0.427	15	0.128	R.LKFEDYFSNR.V
R2/RRR2-3/2	1080.084	1080.223	-128.391	0.411	875.091	0.419	14	0.128	K.LHVEALQNR.A
R2/RRR2-3/2	1319.297	1319.447	-113.928	0.465	827.680	0.414	15	0.127	R.LKFEDYFSNR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1079.712	1080.223	-1403.135	0.410	871.796	0.404	14	0.127	K.LHVEALQNR.A
R2/RRR2-3/2	1319.026	1319.447	-319.648	0.490	801.309	0.406	15	0.125	R.LKFEDYFSNR.V
R2/RRR2-2/2	1571.076	1570.728	221.902	0.429	862.920	0.410	19	0.124	R.YDAQISVFGSNLQK.K
R2/RRR2-3/2	1282.070	1282.342	-212.830	0.435	1070.662	0.320	16	0.123	R.APEIDEDLHSR.Q
R2/RRR2-3/2	1124.119	1124.358	-213.981	0.408	907.753	0.373	15	0.122	R.GGIVTQVKPPK.V
R2/RRR2-3/2	1125.117	1125.265	-132.284	0.312	772.476	0.348	15	0.114	K.LLHHFASGSR.A
R2/RRR2-3/2	958.885	958.053	-174.944	0.425	937.217	0.256	12	0.112	-.DWNIGQPK.-
R2/RRR2-3/2	1123.834	1124.358	-1360.577	0.387	680.100	0.328	14	0.110	R.GGIVTQVKPPK.V
R2/RRR2-3/3	1883.756	1882.198	-235.137	0.430	1236.314	0.400	26	0.109	K.FDRPPLLHLAFQALDK.F
R2/RRR2-3/2	1975.000	1974.290	-147.272	0.337	371.602	0.368	16	0.105	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-3/3	1804.127	1804.100	14.774	0.411	1718.106	0.197	30	0.105	K.M*AEAVDKVIVPDFQPK.Q
R2/RRR2-3/2	1975.363	1974.290	37.213	0.296	400.592	0.360	15	0.103	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-5/2	1974.330	1974.290	20.365	0.342	757.244	0.277	17	0.101	R.LFASNVLVSGLNGLGAEIAK.N
R2/RRR2-1/2	1630.693	1629.939	-151.337	0.356	447.976	0.266	14	0.097	-.IFMVGSGALGCEFLK.-
R2/RRR2-3/3	1319.412	1319.447	-26.421	0.437	1055.693	0.262	20	0.069	-.LKFEDYFSNR.-
R2/RRR2-3/3	1831.322	1831.036	156.242	0.357	1109.139	0.201	25	0.066	K.DAIKEPGEFLM*SDFSK.F
R2/RRR2-3/3	1319.547	1319.447	75.879	0.489	815.654	0.298	19	0.061	-.LKFEDYFSNR.-
R2/RRR2-3/3	1804.597	1804.100	275.913	0.379	807.532	0.228	24	0.059	-.M*AEAVDKVIVPDFQPK.-
R2/RRR2-4/2	1646.493	1646.869	-229.378	0.530	3074.446	0.562	24	0.512	K.LLVAGDLQSFGEQLR.N
R2/RRR2-4/2	1647.063	1646.869	117.778	0.569	3036.752	0.563	24	0.501	K.LLVAGDLQSFGEQLR.N
R2/RRR2-4/2	1645.905	1646.869	-1196.883	0.495	2694.740	0.535	24	0.405	K.LLVAGDLQSFGEQLR.N
R2/RRR2-4/2	1979.612	1980.162	-785.393	0.610	2343.656	0.539	26	0.334	K.VSEDDKLVEYDALLVDR.F
R2/RRR2-4/2	1860.416	1860.958	-831.304	0.619	2020.487	0.492	24	0.253	K.DITADDKQELDEALQR.E
R2/RRR2-3/2	1269.099	1268.444	-272.987	0.523	1607.164	0.531	21	0.211	K.LADLEAAPAAVAR.L
R2/RRR2-4/2	1860.416	1860.958	-831.106	0.593	1722.143	0.489	23	0.210	K.DITADDKQELDEALQR.E
R2/RRR2-4/2	1860.322	1860.958	-881.891	0.604	1603.608	0.495	22	0.195	K.DITADDKQELDEALQR.E
R2/RRR2-3/2	1269.205	1268.444	-189.038	0.536	1487.942	0.519	20	0.193	K.LADLEAAPAAVAR.L
R2/RRR2-4/2	1915.078	1914.112	-17.685	0.588	1346.238	0.588	21	0.189	K.NQTVDLVFTAHPTQSVR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1742.971	1742.932	22.379	0.515	1543.294	0.498	31	0.165	R.INGKQEVM*IGYSDSGK.D
R2/RRR2-4/2	1188.006	1188.293	-242.331	0.414	1117.724	0.563	17	0.163	R.TPPTPQDEM*R.A
R2/RRR2-3/2	1860.301	1860.958	-893.287	0.589	1337.669	0.474	21	0.162	K.DITADDKQELDEALQR.E
R2/RRR2-4/2	1187.436	1188.293	-1568.751	0.432	938.469	0.572	15	0.152	R.TPPTPQDEM*R.A
R2/RRR2-4/2	1113.975	1114.299	-292.065	0.520	1306.842	0.403	14	0.152	R.LSAAWQM*YK.A
R2/RRR2-4/2	1113.903	1114.299	-356.275	0.452	1247.124	0.394	14	0.146	R.LSAAWQM*YK.A
R2/RRR2-4/2	1316.497	1316.491	4.872	0.494	1317.910	0.332	16	0.140	K.RQDWLLSELR.G
R2/RRR2-4/2	1914.642	1914.112	-246.173	0.486	876.540	0.542	18	0.138	K.NQTVDLVFTAHPTQSVR.R
R2/RRR2-4/2	1068.014	1068.169	-145.662	0.466	774.502	0.504	14	0.136	R.HQSIDAQLR.L
R2/RRR2-4/2	1187.432	1188.293	-1572.159	0.375	670.527	0.566	13	0.132	R.TPPTPQDEM*R.A
R2/RRR2-4/2	1097.875	1098.300	-388.162	0.438	1065.427	0.365	14	0.131	R.LSAAWQMYK.A
R2/RRR2-4/2	1068.370	1068.169	188.678	0.481	625.841	0.493	13	0.129	R.HQSIDAQLR.L
R2/RRR2-4/2	1316.257	1316.491	-178.002	0.392	1222.792	0.294	16	0.129	K.RQDWLLSELR.G
R2/RRR2-4/2	1491.461	1490.733	-182.376	0.476	679.045	0.448	18	0.126	R.AIPWIFAWTQTR.F
R2/RRR2-4/2	1119.461	1120.237	-1591.524	0.370	572.360	0.504	17	0.125	K.GDPGIAALYDK.L
R2/RRR2-3/2	1187.404	1188.293	-1596.118	0.324	661.169	0.505	13	0.123	R.TPPTPQDEM*R.A
R2/RRR2-3/2	975.982	976.154	-177.400	0.405	797.896	0.377	12	0.122	R.SIVFKEPR.F
R2/RRR2-4/2	1098.085	1098.300	-195.751	0.335	908.823	0.366	13	0.121	R.LSAAWQMYK.A
R2/RRR2-3/2	975.706	976.154	-461.046	0.399	787.336	0.365	12	0.120	R.SIVFKEPR.F
R2/RRR2-4/2	1022.999	1023.168	-165.177	0.384	817.087	0.327	11	0.118	K.HYIEFWK.K
R2/RRR2-3/2	1316.345	1316.491	-111.114	0.444	968.812	0.308	14	0.117	K.RQDWLLSELR.G
R2/RRR2-3/2	1188.103	1188.293	-160.488	0.370	560.908	0.416	13	0.117	R.TPPTPQDEM*R.A
R2/RRR2-4/2	1022.440	1023.168	-1695.305	0.337	846.125	0.323	11	0.116	K.HYIEFWK.K
R2/RRR2-3/2	975.973	976.154	-186.559	0.454	800.175	0.316	12	0.116	R.SIVFKEPR.F
R2/RRR2-3/2	1067.751	1068.169	-392.692	0.396	740.687	0.334	14	0.116	R.HQSIDAQLR.L
R2/RRR2-3/2	1163.417	1163.391	22.246	0.319	236.569	0.512	13	0.116	R.QVSTFGLALVK.L
R2/RRR2-4/2	976.042	976.154	-115.671	0.422	703.930	0.344	11	0.116	R.SIVFKEPR.F
R2/RRR2-4/2	1490.185	1490.733	-1041.700	0.320	623.487	0.383	18	0.115	R.AIPWIFAWTQTR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1490.071	1490.733	-1118.524	0.307	627.918	0.376	18	0.114	R.AIPWIFAWTQTR.F
R2/RRR2-4/2	1163.142	1163.391	-215.434	0.317	242.496	0.462	13	0.114	R.QVSTFGLALVK.L
R2/RRR2-4/3	1742.025	1742.932	-1098.217	0.499	1192.963	0.437	28	0.112	R.INGKQEVM*IGYSDSGK.D
R2/RRR2-4/2	976.004	976.154	-153.937	0.424	804.352	0.266	12	0.112	R.SIVFKEPR.F
R2/RRR2-3/2	1490.183	1490.733	-1043.262	0.316	641.546	0.301	18	0.111	R.AIPWIFAWTQTR.F
R2/RRR2-3/2	1022.813	1023.168	-348.357	0.345	628.539	0.281	10	0.110	K.HYIEFWK.K
R2/RRR2-4/2	1119.451	1120.237	-1599.959	0.286	443.296	0.372	16	0.110	K.GDPGIAALYDK.L
R2/RRR2-4/2	975.488	976.154	-1713.645	0.402	662.412	0.282	11	0.109	-.SIVFKEPR.-
R2/RRR2-4/2	1163.206	1163.391	-159.424	0.291	399.166	0.341	14	0.109	R.QVSTFGLALVK.L
R2/RRR2-4/2	1113.884	1114.299	-373.868	0.383	675.624	0.314	11	0.109	-.LSAAWQM*YK.-
R2/RRR2-3/2	1023.075	1023.168	-90.727	0.394	818.942	0.198	11	0.107	K.HYIEFWK.K
R2/RRR2-3/2	1490.101	1490.733	-1098.042	0.267	573.053	0.223	17	0.106	R.AIPWIFAWTQTR.F
R2/RRR2-4/3	1860.991	1860.958	18.012	0.529	1065.436	0.400	28	0.096	K.DITADDKQELDEALQR.E
R2/RRR2-3/3	1981.204	1980.162	21.276	0.390	1016.089	0.391	24	0.091	K.VSEDDKLVEYDALLVDR.F
R2/RRR2-4/3	1860.435	1860.958	-820.707	0.495	1064.528	0.358	28	0.088	-.DITADDKQELDEALQR.-
R2/RRR2-3/3	1861.176	1860.958	117.575	0.527	865.090	0.403	25	0.087	K.DITADDKQELDEALQR.E
R2/RRR2-3/3	1861.375	1860.958	224.813	0.443	846.778	0.353	26	0.081	K.DITADDKQELDEALQR.E
R2/RRR2-4/3	1860.828	1860.958	-69.627	0.407	799.597	0.346	27	0.079	K.DITADDKQELDEALQR.E
R2/RRR2-3/3	1860.128	1860.958	-986.713	0.444	673.611	0.366	23	0.078	K.DITADDKQELDEALQR.E
R2/RRR2-3/3	1980.048	1980.162	-57.799	0.310	769.662	0.278	23	0.067	K.VSEDDKLVEYDALLVDR.F
R2/RRR2-3/3	1742.685	1742.932	-142.230	0.362	691.509	0.268	23	0.067	-.INGKQEVM*IGYSDSGK.-
R2/RRR2-3/3	1980.040	1980.162	-61.787	0.273	597.633	0.174	18	0.047	-.VSEDDKLVEYDALLVDR.-
R2/RRR2-18/2	1582.427	1582.827	-253.365	0.524	2615.338	0.595	22	0.401	R.TAISHVQNLITGVTK.G
R2/RRR2-18/3	1915.189	1915.135	28.466	0.583	2744.853	0.463	36	0.381	K.VKDELVLDGNDIELVSR.S
R2/RRR2-18/2	1914.569	1915.135	-820.133	0.621	2462.459	0.561	26	0.360	K.VKDELVLDGNDIELVSR.S
R2/RRR2-18/2	1914.653	1915.135	-252.310	0.632	2470.746	0.544	26	0.355	K.VKDELVLDGNDIELVSR.S
R2/RRR2-18/2	1914.061	1915.135	-1086.324	0.603	2422.383	0.561	26	0.352	K.VKDELVLDGNDIELVSR.S
R2/RRR2-20/2	1582.612	1582.827	-135.820	0.560	2394.472	0.580	23	0.347	R.TAISHVQNLITGVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/3	1915.007	1915.135	-66.763	0.540	2628.224	0.441	36	0.343	K.VKDELVLDGNDIELVSR.S
R2/RRR2-18/2	1582.409	1582.827	-264.587	0.523	2101.223	0.626	22	0.307	R.TAISHVQNLITGVTK.G
R2/RRR2-18/2	1582.089	1582.827	-1101.837	0.524	2097.667	0.599	21	0.297	R.TAISHVQNLITGVTK.G
R2/RRR2-17/2	1582.124	1582.827	-1079.137	0.519	2039.357	0.627	22	0.296	R.TAISHVQNLITGVTK.G
R2/RRR2-23/2	1583.584	1582.827	-153.442	0.566	2023.080	0.611	22	0.288	R.TAISHVQNLITGVTK.G
R2/RRR2-17/2	1582.327	1582.827	-316.444	0.524	2050.743	0.543	21	0.271	R.TAISHVQNLITGVTK.G
R2/RRR2-18/2	1844.590	1844.996	-221.006	0.487	1862.857	0.570	24	0.264	K.FLDGIYVSDKGTITEDA.-
R2/RRR2-19/2	1582.644	1582.827	-115.471	0.479	1889.233	0.578	21	0.256	R.TAISHVQNLITGVTK.G
R2/RRR2-20/3	1914.564	1915.135	-822.988	0.491	2244.147	0.418	36	0.248	K.VKDELVLDGNDIELVSR.S
R2/RRR2-18/2	1373.735	1374.675	-1416.546	0.549	1952.824	0.468	20	0.238	R.KVDMLEGVTILR.S
R2/RRR2-18/2	1375.355	1374.675	-233.380	0.572	1890.258	0.501	20	0.238	R.KVDMLEGVTILR.S
R2/RRR2-17/3	1914.909	1915.135	-118.077	0.556	2079.427	0.461	34	0.233	K.VKDELVLDGNDIELVSR.S
R2/RRR2-18/2	1512.215	1512.695	-318.647	0.542	1677.676	0.582	22	0.232	K.HLNLDFQLLEGGR.K
R2/RRR2-18/2	1583.181	1582.827	224.304	0.552	1647.210	0.615	22	0.231	R.TAISHVQNLITGVTK.G
R2/RRR2-18/2	1512.437	1512.695	-171.265	0.528	1715.393	0.559	22	0.230	K.HLNLDFQLLEGGR.K
R2/RRR2-18/2	1583.261	1582.827	275.254	0.570	1703.003	0.566	20	0.224	R.TAISHVQNLITGVTK.G
R2/RRR2-18/2	1375.141	1374.675	339.884	0.570	1839.035	0.466	20	0.221	R.KVDMLEGVTILR.S
R2/RRR2-17/2	1582.490	1582.827	-213.355	0.517	1568.299	0.613	20	0.219	R.TAISHVQNLITGVTK.G
R2/RRR2-18/2	1512.523	1512.695	-114.106	0.542	1593.715	0.542	21	0.210	K.HLNLDFQLLEGGR.K
R2/RRR2-18/2	1844.457	1844.996	-837.036	0.491	1670.621	0.574	23	0.207	K.FLDGIYVSDKGTITEDA.-
R2/RRR2-19/2	1581.749	1582.827	-1317.494	0.438	1487.491	0.585	20	0.201	R.TAISHVQNLITGVTK.G
R2/RRR2-18/2	1844.619	1844.996	-205.338	0.445	1594.419	0.499	23	0.182	K.FLDGIYVSDKGTITEDA.-
R2/RRR2-23/2	1513.108	1512.695	274.017	0.469	1541.988	0.443	20	0.180	K.HLNLDFQLLEGGR.K
R2/RRR2-18/3	1640.758	1640.868	-67.288	0.470	1665.735	0.494	29	0.180	K.HLNLDFQLLEGGRK.L
R2/RRR2-18/3	1640.497	1640.868	-226.941	0.488	1489.995	0.530	26	0.169	K.HLNLDFQLLEGGRK.L
R2/RRR2-18/2	1321.273	1321.509	-179.550	0.522	1457.652	0.420	17	0.167	R.KLQVDAWFGTR.R
R2/RRR2-18/2	1262.117	1262.502	-305.355	0.386	1702.380	0.272	17	0.164	K.VDM*LEGVTILR.S
R2/RRR2-20/3	1914.784	1915.135	-183.786	0.561	1640.963	0.449	30	0.161	K.VKDELVLDGNDIELVSR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1321.562	1321.509	39.966	0.496	1371.715	0.415	17	0.159	R.KLQVDAWFGTR.R
R2/RRR2-18/2	1391.358	1390.675	-227.933	0.504	1017.312	0.514	19	0.151	R.KVDM*LEGVTILR.S
R2/RRR2-18/2	1391.237	1390.675	-315.607	0.521	1011.004	0.490	19	0.147	R.KVDM*LEGVTILR.S
R2/RRR2-18/2	1321.418	1321.509	-69.270	0.476	1241.094	0.408	16	0.146	R.KLQVDAWFGTR.R
R2/RRR2-18/2	1391.327	1390.675	-250.378	0.512	908.819	0.512	19	0.144	R.KVDM*LEGVTILR.S
R2/RRR2-18/2	1157.111	1157.297	-161.322	0.538	1094.497	0.432	16	0.143	K.FLDGIYVSDK.G
R2/RRR2-18/2	1192.807	1193.336	-1286.111	0.443	1009.432	0.464	17	0.143	K.LQVDAWFGTR.R
R2/RRR2-18/2	1156.801	1157.297	-430.201	0.534	1056.276	0.409	16	0.137	K.FLDGIYVSDK.G
R2/RRR2-18/2	1157.144	1157.297	-132.644	0.534	1081.327	0.390	16	0.135	K.FLDGIYVSDK.G
R2/RRR2-18/2	856.892	856.990	-114.109	0.376	624.917	0.539	13	0.133	K.VVTVEGPR.G
R2/RRR2-24/3	1582.498	1582.827	-208.372	0.492	1493.536	0.415	31	0.132	R.TAISHVQNLITGVTK.G
R2/RRR2-17/2	856.600	856.990	-456.473	0.426	509.485	0.460	12	0.127	K.VVTVEGPR.G
R2/RRR2-18/2	1192.324	1193.336	-1692.760	0.335	884.391	0.424	16	0.126	K.LQVDAWFGTR.R
R2/RRR2-18/2	1284.652	1285.470	-1419.277	0.379	1010.084	0.359	16	0.125	R.KFLDGIYVSDK.G
R2/RRR2-18/2	856.672	856.990	-371.682	0.328	470.977	0.499	12	0.124	K.VVTVEGPR.G
R2/RRR2-17/2	856.386	856.990	-1878.842	0.323	500.131	0.469	12	0.122	K.VVTVEGPR.G
R2/RRR2-20/2	856.635	856.990	-415.148	0.345	465.916	0.439	12	0.122	K.VVTVEGPR.G
R2/RRR2-24/2	856.525	856.990	-543.709	0.327	450.440	0.445	12	0.121	K.VVTVEGPR.G
R2/RRR2-22/2	857.090	856.990	117.051	0.333	570.281	0.426	12	0.121	K.VVTVEGPR.G
R2/RRR2-18/2	856.345	856.990	-1926.399	0.303	419.056	0.436	12	0.120	K.VVTVEGPR.G
R2/RRR2-20/2	857.087	856.990	114.337	0.356	836.025	0.298	13	0.117	K.VVTVEGPR.G
R2/RRR2-22/2	856.417	856.990	-1841.888	0.306	490.479	0.355	12	0.117	K.VVTVEGPR.G
R2/RRR2-18/2	856.955	856.990	-40.520	0.275	306.964	0.402	10	0.116	K.VVTVEGPR.G
R2/RRR2-17/2	856.749	856.990	-282.045	0.291	280.669	0.427	9	0.116	K.VVTVEGPR.G
R2/RRR2-20/2	857.121	856.990	153.330	0.365	555.058	0.293	12	0.116	K.VVTVEGPR.G
R2/RRR2-18/2	856.369	856.990	-1897.893	0.262	292.174	0.245	11	0.115	-.VVTVEGPR.-
R2/RRR2-18/2	1512.419	1512.695	-183.087	0.389	809.384	0.347	16	0.114	K.HLNLDFQLLEGGR.K
R2/RRR2-18/2	1193.252	1193.336	-70.554	0.340	661.175	0.347	14	0.113	K.LQVDAWFGTR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/3	1640.853	1640.868	-9.082	0.472	1028.035	0.494	26	0.112	K.HLNLDFQLLEGGRK.L
R2/RRR2-18/2	857.052	856.990	73.056	0.198	290.180	0.411	9	0.108	-.VVTVEGPR.-
R2/RRR2-18/2	856.695	856.990	-344.661	0.168	412.914	0.334	11	0.106	-.VVTVEGPR.-
R2/RRR2-18/2	1322.198	1321.509	-235.911	0.281	633.300	0.271	14	0.106	R.KLQVDAWFGTR.R
R2/RRR2-18/3	1321.143	1321.509	-277.813	0.410	1316.338	0.344	22	0.100	R.KLQVDAWFGTR.R
R2/RRR2-18/3	1512.875	1512.695	119.394	0.493	1314.127	0.333	24	0.099	-.HLNLDFQLLEGGR.-
R2/RRR2-19/3	1583.665	1582.827	-102.494	0.459	836.100	0.430	26	0.093	R.TAISHVQNLITGVTK.G
R2/RRR2-18/3	1583.004	1582.827	112.480	0.469	981.973	0.377	30	0.090	R.TAISHVQNLITGVTK.G
R2/RRR2-18/3	1582.953	1582.827	80.114	0.452	952.174	0.381	29	0.090	R.TAISHVQNLITGVTK.G
R2/RRR2-20/3	1582.415	1582.827	-260.842	0.454	591.390	0.426	25	0.089	R.TAISHVQNLITGVTK.G
R2/RRR2-23/3	1582.299	1582.827	-968.453	0.434	772.731	0.383	26	0.085	R.TAISHVQNLITGVTK.G
R2/RRR2-24/3	1582.630	1582.827	-124.339	0.438	811.737	0.375	26	0.085	R.TAISHVQNLITGVTK.G
R2/RRR2-20/3	1582.544	1582.827	-179.121	0.441	754.369	0.381	26	0.085	R.TAISHVQNLITGVTK.G
R2/RRR2-18/3	1582.926	1582.827	63.292	0.474	786.624	0.371	28	0.085	R.TAISHVQNLITGVTK.G
R2/RRR2-24/3	1581.917	1582.827	-1210.631	0.267	657.452	0.393	23	0.082	R.TAISHVQNLITGVTK.G
R2/RRR2-19/3	1582.459	1582.827	-232.865	0.359	688.699	0.359	25	0.081	R.TAISHVQNLITGVTK.G
R2/RRR2-21/3	1582.767	1582.827	-37.999	0.347	506.427	0.353	22	0.081	R.TAISHVQNLITGVTK.G
R2/RRR2-18/3	1374.601	1374.675	-54.308	0.529	1119.734	0.297	24	0.076	-.KVDMLEGVTILR.-
R2/RRR2-19/3	1582.633	1582.827	-122.366	0.328	764.373	0.255	25	0.073	R.TAISHVQNLITGVTK.G
R2/RRR2-18/3	1390.165	1390.675	-1089.453	0.399	1338.802	0.178	24	0.072	R.KVDM*LEGVTILR.S
R2/RRR2-17/3	1390.491	1390.675	-132.504	0.428	1028.293	0.220	22	0.068	-.KVDM*LEGVTILR.-
R2/RRR2-18/3	1390.936	1390.675	188.256	0.416	1327.510	0.155	24	0.068	R.KVDM*LEGVTILR.S
R2/RRR2-18/3	1373.758	1374.675	-1399.553	0.492	1289.081	0.177	25	0.067	-.KVDMLEGVTILR.-
R2/RRR2-18/3	1512.071	1512.695	-1077.077	0.373	1130.269	0.181	23	0.065	-.HLNLDFQLLEGGR.-
R2/RRR2-18/3	1321.442	1321.509	-51.073	0.379	787.038	0.211	19	0.065	R.KLQVDAWFGTR.R
R2/RRR2-18/3	1512.139	1512.695	-1032.212	0.375	976.608	0.183	22	0.063	K.HLNLDFQLLEGGR.K
R2/RRR2-18/3	1390.666	1390.675	-6.368	0.413	1175.927	0.144	23	0.063	R.KVDM*LEGVTILR.S
R2/RRR2-18/3	1915.445	1915.135	162.408	0.324	795.612	0.163	23	0.062	-.VKDELVLDGNDIELVSR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/3	1914.579	1915.135	-814.828	0.394	996.077	0.149	25	0.060	K.VKDELVLDGNDIELVSR.S
R2/RRR2-17/3	1390.869	1390.675	140.465	0.514	992.797	0.181	20	0.059	-.KVDM*LEGVTILR.-
R2/RRR2-18/2	1782.599	1783.021	-237.277	0.611	2341.661	0.592	24	0.345	K.HLNLDFQLLEVEGVR.K
R2/RRR2-18/2	1781.971	1783.021	-1153.657	0.573	2168.856	0.588	23	0.310	K.HLNLDFQLLEVEGVR.K
R2/RRR2-18/2	1783.650	1783.021	-208.376	0.643	2063.013	0.602	24	0.295	K.HLNLDFQLLEVEGVR.K
R2/RRR2-18/2	1902.518	1902.048	247.856	0.579	1937.351	0.635	27	0.282	K.FLDGIYVSDKGTITEDQ.-
R2/RRR2-18/2	1901.427	1902.048	-854.971	0.514	1868.590	0.505	26	0.254	K.FLDGIYVSDKGTITEDQ.-
R2/RRR2-18/2	1783.077	1783.021	31.613	0.611	1782.589	0.574	23	0.242	K.HLNLDFQLLEVEGVR.K
R2/RRR2-18/2	1903.239	1902.048	100.574	0.508	1721.411	0.580	25	0.217	K.FLDGIYVSDKGTITEDQ.-
R2/RRR2-18/3	1911.110	1911.194	-43.867	0.542	1829.259	0.432	32	0.183	K.HLNLDFQLLEVEGVRK.L
R2/RRR2-18/3	1911.028	1911.194	-87.307	0.548	1479.105	0.522	30	0.165	K.HLNLDFQLLEVEGVRK.L
R2/RRR2-18/2	1781.949	1783.021	-1166.039	0.377	516.543	0.373	15	0.108	K.HLNLDFQLLEVEGVR.K
R2/RRR2-18/3	1911.162	1911.194	-16.671	0.456	979.357	0.405	25	0.092	K.HLNLDFQLLEVEGVRK.L
R2/RRR2-6/2	1879.553	1880.002	-240.020	0.581	2764.312	0.496	25	0.403	K.SWEDLTSDKDAIETIR.A
R2/RRR2-6/2	1856.298	1855.901	214.321	0.615	2452.961	0.530	25	0.347	R.TAWWDGSAVYGNNEER.A
R2/RRR2-6/2	1856.338	1855.901	236.214	0.601	2347.498	0.526	25	0.325	R.TAWWDGSAVYGNNEER.A
R2/RRR2-6/2	1879.381	1880.002	-865.456	0.538	2410.067	0.476	24	0.321	K.SWEDLTSDKDAIETIR.A
R2/RRR2-6/2	1880.415	1880.002	220.102	0.558	2267.268	0.483	24	0.296	K.SWEDLTSDKDAIETIR.A
R2/RRR2-6/3	1992.652	1993.381	-870.214	0.505	2321.617	0.472	41	0.294	K.IKDTFGHIGGPILGGLVGLK.K
R2/RRR2-6/2	1855.368	1855.901	-828.880	0.555	1884.496	0.500	22	0.236	R.TAWWDGSAVYGNNEER.A
R2/RRR2-6/2	1627.934	1628.720	-1099.838	0.466	1405.228	0.540	20	0.187	R.FFTSNFNEETYTK.K
R2/RRR2-6/2	1751.769	1752.050	-161.076	0.502	1388.431	0.536	24	0.183	K.DTFGHIGGPILGGLVGLK.K
R2/RRR2-6/2	1633.431	1633.915	-297.249	0.451	1492.091	0.454	20	0.176	R.NSWAGVSILQALFVK.E
R2/RRR2-6/2	1751.787	1752.050	-150.521	0.497	1208.982	0.587	23	0.175	K.DTFGHIGGPILGGLVGLK.K
R2/RRR2-6/2	1633.429	1633.915	-298.598	0.407	1367.953	0.483	20	0.169	R.NSWAGVSILQALFVK.E
R2/RRR2-6/2	1633.956	1633.915	25.207	0.505	1349.287	0.478	19	0.166	R.NSWAGVSILQALFVK.E
R2/RRR2-6/2	1629.311	1628.720	-251.560	0.572	956.257	0.601	19	0.161	R.FFTSNFNEETYTK.K
R2/RRR2-6/3	1993.388	1993.381	3.180	0.508	1327.219	0.564	33	0.160	K.IKDTFGHIGGPILGGLVGLK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1455.420	1455.770	-240.732	0.461	921.434	0.628	19	0.159	K.VPVPIGLLYLNTR.R
R2/RRR2-6/2	1455.131	1455.770	-1129.732	0.447	952.322	0.618	19	0.159	K.VPVPIGLLYLNTR.R
R2/RRR2-6/2	1455.430	1455.770	-234.000	0.475	888.012	0.630	19	0.158	K.VPVPIGLLYLNTR.R
R2/RRR2-6/2	1021.483	1022.181	-1667.647	0.449	1157.646	0.490	15	0.156	R.ANWYGLLGK.K
R2/RRR2-6/2	1627.559	1628.720	-1331.490	0.394	1106.501	0.492	19	0.149	R.FFTSNFNEETYTK.K
R2/RRR2-6/3	1455.694	1455.770	-51.703	0.414	1912.091	0.280	26	0.148	K.VPVPIGLLYLNTR.R
R2/RRR2-6/2	1307.930	1308.552	-1243.959	0.503	1160.630	0.424	15	0.143	K.IGFLFIHAFDK.R
R2/RRR2-6/2	1455.380	1455.770	-268.164	0.413	776.007	0.586	18	0.142	K.VPVPIGLLYLNTR.R
R2/RRR2-6/2	1455.351	1454.695	-237.125	0.497	489.260	0.623	18	0.141	K.VHTIDWTVELLK.T
R2/RRR2-6/2	1455.549	1454.695	-100.908	0.533	404.152	0.637	17	0.141	K.VHTIDWTVELLK.T
R2/RRR2-6/2	1293.121	1293.537	-322.927	0.439	996.645	0.465	18	0.140	K.LVIGDDGLLLHK.E
R2/RRR2-6/2	1751.127	1752.050	-1101.542	0.417	963.881	0.484	22	0.136	K.DTFGHIGGPILGGLVGLK.K
R2/RRR2-6/2	1521.400	1521.700	-198.101	0.464	896.227	0.473	18	0.135	R.SDRIDLAALEVYR.D
R2/RRR2-6/3	1521.587	1521.700	-74.530	0.500	1525.293	0.392	26	0.132	-.SDRIDLAALEVYR.-
R2/RRR2-6/2	1131.045	1131.222	-156.597	0.402	1196.246	0.323	18	0.132	K.ENGVALSGDIR.N
R2/RRR2-6/2	1131.070	1131.222	-134.186	0.408	1097.212	0.366	17	0.131	K.ENGVALSGDIR.N
R2/RRR2-6/2	1520.908	1521.700	-1181.903	0.395	966.176	0.432	18	0.131	R.SDRIDLAALEVYR.D
R2/RRR2-6/2	1023.038	1022.181	-140.277	0.446	875.279	0.425	14	0.130	R.ANWYGLLGK.K
R2/RRR2-6/2	1131.144	1131.222	-68.366	0.437	1054.891	0.361	18	0.130	K.ENGVALSGDIR.N
R2/RRR2-6/3	1455.593	1455.770	-121.732	0.447	1713.991	0.307	26	0.130	K.VPVPIGLLYLNTR.R
R2/RRR2-6/2	1454.470	1454.695	-155.110	0.426	352.489	0.504	15	0.122	K.VHTIDWTVELLK.T
R2/RRR2-6/2	1021.579	1022.181	-1573.648	0.371	696.417	0.414	13	0.120	R.ANWYGLLGK.K
R2/RRR2-3/2	1456.702	1455.770	-46.615	0.305	586.903	0.508	16	0.120	K.VPVPIGLLYLNTR.R
R2/RRR2-2/2	1456.472	1455.770	-205.167	0.364	518.507	0.512	14	0.119	K.VPVPIGLLYLNTR.R
R2/RRR2-6/3	1454.583	1454.695	-77.416	0.573	1323.806	0.428	26	0.118	-.VHTIDWTVELLK.-
R2/RRR2-6/2	1521.553	1521.700	-96.852	0.391	807.375	0.358	18	0.117	R.SDRIDLAALEVYR.D
R2/RRR2-6/3	1454.885	1454.695	130.885	0.548	1326.189	0.392	25	0.111	K.VHTIDWTVELLK.T
R2/RRR2-1/2	1455.483	1455.770	-197.735	0.299	454.375	0.432	13	0.111	K.VPVPIGLLYLNTR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1455.594	1455.770	-121.228	0.411	1658.120	0.248	25	0.110	K.VPVPIGLLYLNTR.R
R2/RRR2-2/2	1455.536	1455.770	-161.221	0.355	269.863	0.309	12	0.108	-.VPVPIGLLYLNTR.-
R2/RRR2-6/3	1521.937	1521.700	155.971	0.515	1270.601	0.386	24	0.107	-.SDRIDLAALEVYR.-
R2/RRR2-6/2	1274.274	1274.409	-105.942	0.374	866.017	0.233	14	0.105	K.TTEGLRDVINR.H
R2/RRR2-3/2	1455.995	1455.770	155.434	0.278	507.842	0.297	13	0.105	K.VPVPIGLLYLNTR.R
R2/RRR2-6/3	1454.795	1454.695	68.657	0.564	1197.613	0.402	24	0.104	K.VHTIDWTVELLK.T
R2/RRR2-1/2	1521.677	1521.700	-15.498	0.405	452.833	0.375	13	0.103	-.SDRIDLAALEVYR.-
R2/RRR2-6/2	1273.670	1274.409	-1369.511	0.331	858.117	0.170	14	0.101	K.TTEGLRDVINR.H
R2/RRR2-6/3	1521.860	1521.700	105.414	0.498	1270.459	0.355	23	0.100	-.SDRIDLAALEVYR.-
R2/RRR2-6/3	1880.231	1880.002	121.789	0.474	999.719	0.443	30	0.099	K.SWEDLTSDKDAIETIR.A
R2/RRR2-6/2	1274.155	1274.409	-200.315	0.299	593.102	0.113	13	0.098	-.TTEGLRDVINR.-
R2/RRR2-6/3	1992.842	1993.381	-774.656	0.457	824.679	0.479	30	0.097	K.IKDTFGHIGGPILGGLVGLK.K
R2/RRR2-1/2	1521.771	1521.700	46.696	0.377	475.373	0.259	13	0.095	-.SDRIDLAALEVYR.-
R2/RRR2-3/2	1456.149	1454.695	312.567	0.285	219.768	0.378	12	0.095	-.VHTIDWTVELLK.-
R2/RRR2-7/1	986.525	987.175	-1678.014	0.281	682.968	0.418	12	0.525	K.LVDLALASGK.I
R2/RRR2-7/2	1433.957	1434.578	-1133.520	0.476	2242.021	0.489	21	0.295	R.GWDAQVLGEAPYK.F
R2/RRR2-7/2	1779.544	1779.974	-242.088	0.580	1996.385	0.554	24	0.269	K.SVGPVVDGDAVVTFNFR.A
R2/RRR2-7/2	1434.288	1434.578	-202.621	0.487	2100.781	0.416	21	0.249	R.GWDAQVLGEAPYK.F
R2/RRR2-7/2	1434.223	1434.578	-248.046	0.443	2107.192	0.397	21	0.245	R.GWDAQVLGEAPYK.F
R2/RRR2-7/2	1779.621	1779.974	-199.147	0.525	1787.291	0.553	23	0.236	K.SVGPVVDGDAVVTFNFR.A
R2/RRR2-7/2	1404.226	1404.570	-245.790	0.483	1759.726	0.519	19	0.226	R.YAGM*LQYDGELK.L
R2/RRR2-7/2	1404.049	1404.570	-1087.064	0.487	1851.266	0.461	19	0.223	R.YAGM*LQYDGELK.L
R2/RRR2-7/2	1780.355	1779.974	214.386	0.568	1681.096	0.551	22	0.220	K.SVGPVVDGDAVVTFNFR.A
R2/RRR2-7/2	986.957	987.175	-221.451	0.521	1152.829	0.509	17	0.161	K.LVDLALASGK.I
R2/RRR2-7/2	1070.096	1070.307	-198.468	0.543	1531.394	0.320	14	0.153	R.LDQVQLLLK.G
R2/RRR2-7/2	1482.267	1482.629	-245.292	0.460	1228.180	0.438	18	0.152	K.FGHVTFFWNGNR.S
R2/RRR2-7/2	987.014	987.175	-163.756	0.559	957.046	0.509	17	0.149	K.LVDLALASGK.I
R2/RRR2-7/2	1070.245	1070.307	-58.185	0.477	1531.622	0.283	14	0.148	R.LDQVQLLLK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1070.054	1070.307	-237.951	0.519	1465.747	0.305	14	0.145	R.LDQVQLLLK.G
R2/RRR2-7/2	1348.560	1349.518	-1455.791	0.394	1169.980	0.422	18	0.143	R.DAILSGKFDQVR.V
R2/RRR2-7/2	1349.297	1349.518	-163.752	0.462	1057.344	0.458	17	0.142	R.DAILSGKFDQVR.V
R2/RRR2-6/2	987.059	987.175	-118.598	0.507	997.064	0.441	17	0.140	K.LVDLALASGK.I
R2/RRR2-7/2	1482.178	1482.629	-305.114	0.442	1081.662	0.430	17	0.139	K.FGHVTFFWNGNR.S
R2/RRR2-7/2	986.628	987.175	-1572.557	0.473	845.927	0.492	15	0.137	K.LVDLALASGK.I
R2/RRR2-7/2	911.212	911.041	189.106	0.364	1094.880	0.403	13	0.136	R.VHILTDGR.D
R2/RRR2-7/3	1576.919	1576.782	86.788	0.522	1217.406	0.503	26	0.130	K.ARDAILSGKFDQVR.V
R2/RRR2-9/2	986.644	987.175	-1556.275	0.398	772.291	0.436	15	0.126	K.LVDLALASGK.I
R2/RRR2-7/2	1865.303	1866.060	-945.175	0.385	647.220	0.508	23	0.126	K.ASDQYLPPFVIVDESGK.S
R2/RRR2-7/2	1388.759	1388.571	136.157	0.344	764.329	0.463	16	0.124	R.YAGMLQYDGELK.L
R2/RRR2-7/2	1349.106	1349.518	-306.168	0.394	833.042	0.421	16	0.124	R.DAILSGKFDQVR.V
R2/RRR2-7/2	1866.456	1866.060	212.630	0.420	513.244	0.519	21	0.123	K.ASDQYLPPFVIVDESGK.S
R2/RRR2-7/2	1590.047	1590.764	-1083.463	0.379	872.532	0.411	17	0.121	K.RGWDAQVLGEAPYK.F
R2/RRR2-7/2	911.068	911.041	29.887	0.368	738.980	0.409	12	0.121	R.VHILTDGR.D
R2/RRR2-6/2	1006.041	1006.137	-95.853	0.467	891.697	0.295	16	0.119	K.FQNAVEAVK.T
R2/RRR2-7/3	1483.717	1482.629	59.685	0.483	1373.359	0.400	24	0.118	K.FGHVTFFWNGNR.S
R2/RRR2-7/2	1005.894	1006.137	-242.295	0.442	861.225	0.292	16	0.118	K.FQNAVEAVK.T
R2/RRR2-7/2	1006.019	1006.137	-117.519	0.455	836.073	0.271	16	0.114	-.FQNAVEAVK.-
R2/RRR2-7/3	1866.002	1866.060	-31.411	0.462	986.432	0.512	29	0.112	K.ASDQYLPPFVIVDESGK.S
R2/RRR2-1/2	1779.256	1779.974	-968.727	0.363	468.593	0.475	15	0.110	-.SVGPVVDGDAVVTFNFR.-
R2/RRR2-7/2	1865.695	1866.060	-196.587	0.294	464.188	0.401	20	0.109	K.ASDQYLPPFVIVDESGK.S
R2/RRR2-7/3	1482.858	1482.629	155.003	0.445	1483.205	0.318	24	0.109	K.FGHVTFFWNGNR.S
R2/RRR2-7/2	1042.342	1043.146	-1736.174	0.248	651.177	0.318	13	0.107	R.TFACSETVK.F
R2/RRR2-7/2	1387.950	1388.571	-1171.623	0.265	465.114	0.323	13	0.105	R.YAGMLQYDGELK.L
R2/RRR2-7/2	1042.328	1043.146	-1749.823	0.175	749.240	0.326	14	0.104	R.TFACSETVK.F
R2/RRR2-15/2	1005.800	1006.137	-336.416	0.397	697.628	0.255	14	0.103	-.FQNAVEAVK.-
R2/RRR2-7/3	1576.363	1576.782	-266.892	0.543	846.970	0.483	24	0.100	K.ARDAILSGKFDQVR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1005.968	1006.137	-168.886	0.407	707.609	0.201	15	0.098	-.FQNAVEAVK.-
R2/RRR2-7/3	1734.131	1732.965	96.041	0.378	947.536	0.385	29	0.085	K.GTLHLIGLLSDGGVHSR.L
R2/RRR2-7/3	1575.249	1576.782	-2249.500	0.389	679.096	0.421	22	0.083	K.ARDAILSGKFDQVR.V
R2/RRR2-7/3	1482.263	1482.629	-247.739	0.442	1064.724	0.298	21	0.079	K.FGHVTFFWNGNR.S
R2/RRR2-11/3	1450.897	1450.816	55.803	0.564	2570.214	0.432	29	0.316	K.FLKPAVAGFLMQK.E
R2/RRR2-11/3	1450.403	1450.816	-286.061	0.563	2445.578	0.446	29	0.294	K.FLKPAVAGFLMQK.E
R2/RRR2-11/2	1546.244	1546.705	-298.648	0.482	2196.281	0.516	24	0.292	K.GATTIIGGGDSVAAVEK.A
R2/RRR2-10/2	1546.197	1546.705	-977.911	0.457	2167.726	0.527	24	0.290	K.GATTIIGGGDSVAAVEK.A
R2/RRR2-11/2	1546.351	1546.705	-229.664	0.481	2175.218	0.507	24	0.285	K.GATTIIGGGDSVAAVEK.A
R2/RRR2-11/2	1546.316	1546.705	-251.839	0.493	2093.804	0.530	24	0.278	K.GATTIIGGGDSVAAVEK.A
R2/RRR2-11/3	1467.115	1466.816	204.517	0.574	2294.080	0.464	26	0.275	K.FLKPAVAGFLM*QK.E
R2/RRR2-11/3	1736.970	1736.049	-45.516	0.585	2367.555	0.406	32	0.268	K.LAAALPEGGVLLLENVR.F
R2/RRR2-11/3	1466.564	1466.816	-171.966	0.542	2253.759	0.454	27	0.262	K.FLKPAVAGFLM*QK.E
R2/RRR2-11/3	1466.386	1466.816	-293.974	0.548	2245.825	0.439	27	0.254	K.FLKPAVAGFLM*QK.E
R2/RRR2-10/2	1547.240	1546.705	-301.305	0.536	1973.032	0.508	24	0.250	K.GATTIIGGGDSVAAVEK.A
R2/RRR2-11/3	1450.281	1450.816	-1061.633	0.533	2249.299	0.431	28	0.250	K.FLKPAVAGFLMQK.E
R2/RRR2-11/3	1736.021	1736.049	-16.096	0.559	2379.746	0.355	33	0.248	K.LAAALPEGGVLLLENVR.F
R2/RRR2-10/3	1466.776	1466.816	-27.324	0.538	2166.645	0.448	27	0.242	K.FLKPAVAGFLM*QK.E
R2/RRR2-10/2	1545.778	1546.705	-1250.491	0.380	2100.117	0.384	24	0.238	K.GATTIIGGGDSVAAVEK.A
R2/RRR2-11/3	1736.401	1736.049	203.164	0.548	2085.450	0.405	32	0.214	K.LAAALPEGGVLLLENVR.F
R2/RRR2-10/3	1466.911	1466.816	65.325	0.517	2014.026	0.434	26	0.211	K.FLKPAVAGFLM*QK.E
R2/RRR2-11/2	1736.706	1736.049	-198.076	0.599	1332.216	0.552	27	0.182	K.LAAALPEGGVLLLENVR.F
R2/RRR2-10/2	1735.672	1736.049	-217.804	0.564	1175.616	0.566	26	0.170	K.LAAALPEGGVLLLENVR.F
R2/RRR2-10/2	1735.502	1736.049	-893.959	0.539	1130.268	0.520	25	0.157	K.LAAALPEGGVLLLENVR.F
R2/RRR2-11/2	1735.756	1736.049	-169.193	0.538	1109.721	0.524	25	0.156	K.LAAALPEGGVLLLENVR.F
R2/RRR2-10/3	1735.392	1736.049	-957.380	0.531	1725.552	0.378	30	0.154	-.LAAALPEGGVLLLENVR.-
R2/RRR2-10/2	1735.524	1736.049	-881.461	0.509	1155.678	0.464	26	0.150	K.LAAALPEGGVLLLENVR.F
R2/RRR2-15/2	1737.539	1736.049	283.017	0.485	875.976	0.556	22	0.144	K.LAAALPEGGVLLLENVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1466.189	1466.816	-1112.620	0.492	686.962	0.500	20	0.133	K.FLKPAVAGFLM*QK.E
R2/RRR2-11/2	1467.533	1466.816	-193.535	0.484	688.206	0.474	20	0.130	K.FLKPAVAGFLM*QK.E
R2/RRR2-10/3	1735.988	1736.049	-35.139	0.497	1738.466	0.289	29	0.127	K.LAAALPEGGVLLLENVR.F
R2/RRR2-11/2	1466.217	1466.816	-1093.894	0.457	545.319	0.461	19	0.125	K.FLKPAVAGFLM*QK.E
R2/RRR2-15/2	1735.545	1736.049	-869.105	0.465	534.535	0.527	19	0.124	K.LAAALPEGGVLLLENVR.F
R2/RRR2-1/2	1737.123	1736.049	42.740	0.543	567.387	0.507	19	0.123	K.LAAALPEGGVLLLENVR.F
R2/RRR2-11/2	1451.657	1450.816	-109.866	0.474	659.161	0.400	20	0.122	K.FLKPAVAGFLMQK.E
R2/RRR2-11/2	1450.267	1450.816	-1071.723	0.495	519.576	0.417	18	0.120	K.FLKPAVAGFLMQK.E
R2/RRR2-11/2	1450.516	1450.816	-207.866	0.499	575.806	0.414	18	0.120	K.FLKPAVAGFLMQK.E
R2/RRR2-1/2	1736.723	1736.049	-188.063	0.482	605.234	0.451	20	0.119	K.LAAALPEGGVLLLENVR.F
R2/RRR2-10/3	1466.171	1466.816	-1124.918	0.400	1439.250	0.339	23	0.112	K.FLKPAVAGFLM*QK.E
R2/RRR2-10/3	1737.080	1736.049	18.134	0.496	1028.519	0.311	26	0.074	-.LAAALPEGGVLLLENVR.-
R2/RRR2-10/3	1777.842	1777.908	-37.411	0.588	2996.770	0.496	36	0.479	R.DATDDKVTVEAAEATLK.Y
R2/RRR2-10/2	1760.547	1760.969	-240.528	0.640	2932.220	0.506	24	0.444	R.FKDIFQEVYEAGWK.S
R2/RRR2-10/2	1760.600	1760.969	-210.061	0.634	2835.105	0.525	24	0.428	R.FKDIFQEVYEAGWK.S
R2/RRR2-10/3	1778.341	1777.908	243.813	0.606	2785.863	0.495	35	0.416	R.DATDDKVTVEAAEATLK.Y
R2/RRR2-10/2	1760.396	1760.969	-896.341	0.610	2532.785	0.510	23	0.355	R.FKDIFQEVYEAGWK.S
R2/RRR2-10/3	1778.088	1777.908	101.104	0.559	2366.882	0.492	32	0.314	R.DATDDKVTVEAAEATLK.Y
R2/RRR2-10/2	1436.130	1436.569	-306.970	0.514	2177.391	0.564	20	0.305	R.AFAEASM*TTAYEK.K
R2/RRR2-10/2	1321.062	1321.453	-296.912	0.533	2021.020	0.596	22	0.289	K.LEAACVGTVESGK.M
R2/RRR2-10/2	1321.123	1321.453	-250.467	0.513	2040.484	0.553	22	0.279	K.LEAACVGTVESGK.M
R2/RRR2-10/2	1321.127	1321.453	-247.038	0.534	1970.328	0.587	22	0.277	K.LEAACVGTVESGK.M
R2/RRR2-10/2	1798.570	1798.934	-203.244	0.492	2149.331	0.472	24	0.268	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/2	1485.735	1485.622	76.589	0.503	2172.199	0.416	19	0.264	K.DIFQEVYEAGWK.S
R2/RRR2-10/2	1437.005	1436.569	304.460	0.563	1813.976	0.581	20	0.249	R.AFAEASM*TTAYEK.K
R2/RRR2-10/2	1777.335	1777.908	-888.074	0.582	1861.952	0.513	25	0.237	R.DATDDKVTVEAAEATLK.Y
R2/RRR2-10/2	1594.354	1594.755	-251.854	0.566	1769.085	0.533	19	0.231	K.SKFEAAGIWYEHR.L
R2/RRR2-10/2	1778.346	1777.908	246.780	0.581	1733.305	0.538	24	0.225	R.DATDDKVTVEAAEATLK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1595.541	1594.755	-134.106	0.593	1527.889	0.598	19	0.216	K.SKFEAAGIWYEHR.L
R2/RRR2-10/2	1799.349	1798.934	231.039	0.534	1718.908	0.519	22	0.214	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/2	1420.027	1420.570	-1089.803	0.480	1627.843	0.548	19	0.214	R.AFAEASMTTAYEK.K
R2/RRR2-10/2	1778.353	1777.908	250.635	0.578	1690.730	0.502	24	0.210	R.DATDDKVTVEAAEATLK.Y
R2/RRR2-10/2	1420.143	1420.570	-301.199	0.512	1667.583	0.493	19	0.205	R.AFAEASMTTAYEK.K
R2/RRR2-10/2	1798.530	1798.934	-225.237	0.466	1691.251	0.462	21	0.197	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/2	1495.827	1496.694	-1251.650	0.490	1614.664	0.462	22	0.195	K.DLALLIHGSSNVTR.S
R2/RRR2-10/2	1496.276	1496.694	-279.900	0.522	1624.150	0.431	23	0.189	K.DLALLIHGSSNVTR.S
R2/RRR2-10/2	1797.835	1798.934	-1171.127	0.438	1646.171	0.428	21	0.184	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/2	1799.376	1798.934	246.209	0.535	1545.204	0.481	20	0.182	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/2	1435.218	1436.569	-1643.099	0.337	1534.832	0.468	18	0.182	R.AFAEASM*TTAYEK.K
R2/RRR2-10/2	1056.915	1057.226	-295.008	0.468	1677.839	0.362	18	0.179	R.ATDAVLKGPGK.L
R2/RRR2-10/3	1761.076	1760.969	60.957	0.582	1853.085	0.420	31	0.176	R.FKDIFQEVYEAGWK.S
R2/RRR2-10/2	1057.077	1057.226	-141.146	0.528	1498.407	0.421	17	0.172	R.ATDAVLKGPGK.L
R2/RRR2-10/3	1761.030	1760.969	34.574	0.590	1823.108	0.407	30	0.168	R.FKDIFQEVYEAGWK.S
R2/RRR2-10/2	1137.152	1136.285	-117.102	0.511	1370.517	0.432	15	0.165	K.YYDLGVLHR.D
R2/RRR2-10/2	1057.104	1057.226	-115.893	0.458	1529.964	0.364	17	0.164	R.ATDAVLKGPGK.L
R2/RRR2-10/3	1800.046	1798.934	62.256	0.488	1579.718	0.464	31	0.161	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/3	1800.107	1798.934	96.126	0.539	1509.351	0.490	31	0.159	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/3	1761.476	1760.969	-280.653	0.606	1610.968	0.448	29	0.154	R.FKDIFQEVYEAGWK.S
R2/RRR2-10/2	1252.093	1252.505	-329.890	0.523	1090.000	0.490	18	0.152	R.LIDDMVAYALK.S
R2/RRR2-10/2	1252.231	1252.505	-219.368	0.555	1074.420	0.467	18	0.148	R.LIDDMVAYALK.S
R2/RRR2-10/2	1252.175	1252.505	-264.356	0.566	1034.027	0.462	18	0.144	R.LIDDMVAYALK.S
R2/RRR2-10/2	993.792	994.045	-255.040	0.367	932.474	0.503	13	0.140	R.HAFGDQYR.C
R2/RRR2-10/2	1267.593	1268.505	-1512.338	0.421	979.864	0.437	18	0.136	R.LIDDM*VAYALK.S
R2/RRR2-10/2	993.876	994.045	-170.633	0.394	762.368	0.517	13	0.135	R.HAFGDQYR.C
R2/RRR2-10/2	1268.156	1268.505	-275.673	0.449	1007.008	0.412	18	0.135	R.LIDDM*VAYALK.S
R2/RRR2-10/2	993.102	994.045	-1962.125	0.308	674.462	0.488	12	0.123	R.HAFGDQYR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1577.465	1577.888	-268.987	0.460	1111.625	0.312	18	0.122	K.DKLIFPFLDLDIK.Y
R2/RRR2-10/2	1268.658	1268.505	121.087	0.323	933.983	0.356	17	0.121	R.LIDDM*VAYALK.S
R2/RRR2-10/2	1577.227	1577.888	-1056.172	0.393	1138.817	0.281	18	0.120	K.DKLIFPFLDLDIK.Y
R2/RRR2-10/2	1800.435	1798.934	-277.837	0.412	658.286	0.455	16	0.116	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/3	1595.782	1594.755	17.093	0.581	1040.030	0.503	28	0.115	K.SKFEAAGIWYEHR.L
R2/RRR2-9/2	993.876	994.045	-171.003	0.264	736.421	0.364	12	0.114	R.HAFGDQYR.C
R2/RRR2-11/2	994.075	994.045	30.532	0.328	397.708	0.329	10	0.113	R.HAFGDQYR.C
R2/RRR2-2/2	1800.170	1798.934	131.157	0.376	919.728	0.285	19	0.109	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/2	1799.403	1798.934	261.175	0.376	692.452	0.337	17	0.107	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/3	1595.946	1594.755	120.429	0.590	1037.709	0.463	27	0.107	K.SKFEAAGIWYEHR.L
R2/RRR2-25/2	1321.970	1321.453	-366.078	0.176	218.383	0.426	16	0.105	K.LEAACVGTVESGK.M
R2/RRR2-11/2	994.637	994.045	-411.280	0.174	402.415	0.377	9	0.103	-.HAFGDQYR.-
R2/RRR2-16/2	1760.254	1760.969	-977.516	0.300	692.444	0.238	16	0.103	R.FKDIFQEVYEAGWK.S
R2/RRR2-3/2	1800.586	1798.934	-193.972	0.292	555.186	0.198	17	0.101	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/3	1595.262	1594.755	-309.627	0.605	805.198	0.490	26	0.101	K.SKFEAAGIWYEHR.L
R2/RRR2-10/3	1798.651	1798.934	-157.906	0.388	880.193	0.439	26	0.092	K.GGETSTNSIASIFAWTR.G
R2/RRR2-10/3	1497.070	1496.694	251.959	0.335	794.988	0.471	25	0.091	K.DLALLIHGSSNVTR.S
R2/RRR2-10/3	1760.632	1760.969	-191.775	0.397	1072.273	0.355	25	0.089	R.FKDIFQEVYEAGWK.S
R2/RRR2-10/3	1497.001	1496.694	205.842	0.359	791.540	0.412	27	0.083	K.DLALLIHGSSNVTR.S
R2/RRR2-10/3	1496.485	1496.694	-140.169	0.300	555.488	0.455	22	0.080	K.DLALLIHGSSNVTR.S
R2/RRR2-10/3	1760.151	1760.969	-1036.080	0.397	832.137	0.313	25	0.076	R.FKDIFQEVYEAGWK.S
R2/RRR2-4/2	1569.463	1569.746	-181.269	0.567	2476.333	0.549	22	0.359	R.KYQAFAQTLQQSR.G
R2/RRR2-4/2	1569.259	1569.746	-311.667	0.591	2453.083	0.552	22	0.355	R.KYQAFAQTLQQSR.G
R2/RRR2-4/2	1569.334	1569.746	-263.359	0.614	2389.754	0.541	22	0.338	R.KYQAFAQTLQQSR.G
R2/RRR2-4/2	1441.206	1441.574	-256.019	0.555	2000.710	0.513	19	0.261	K.YQAFAQTLQQSR.G
R2/RRR2-3/2	1569.535	1569.746	-135.236	0.569	1795.881	0.562	20	0.242	R.KYQAFAQTLQQSR.G
R2/RRR2-4/2	1440.751	1441.574	-1268.989	0.559	1914.384	0.477	19	0.236	K.YQAFAQTLQQSR.G
R2/RRR2-4/2	1353.295	1353.503	-153.769	0.469	1919.246	0.450	19	0.231	K.LAEDVDLEHIAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1440.637	1441.574	-1348.638	0.449	1955.874	0.426	19	0.230	K.YQAFAQTLQQSR.G
R2/RRR2-4/2	1353.441	1353.503	-45.558	0.475	1903.119	0.443	19	0.227	K.LAEDVDLEHIAK.D
R2/RRR2-4/2	1352.295	1353.503	-1637.377	0.364	1334.043	0.372	18	0.147	K.LAEDVDLEHIAK.D
R2/RRR2-4/3	1354.229	1353.503	-202.630	0.528	729.753	0.457	27	0.093	K.LAEDVDLEHIAK.D
R2/RRR2-4/3	1353.785	1353.503	208.942	0.460	420.515	0.386	21	0.084	K.LAEDVDLEHIAK.D
R2/RRR2-1/3	1353.438	1353.503	-48.146	0.438	295.767	0.425	19	0.078	-.LAEDVDLEHIAK.-
R2/RRR2-13/2	1689.409	1688.864	-270.368	0.596	1991.872	0.662	26	0.303	K.VDGLVSGIGTGGTITGAGR.Y
R2/RRR2-13/2	1688.609	1688.864	-151.657	0.535	1889.622	0.650	26	0.282	K.VDGLVSGIGTGGTITGAGR.Y
R2/RRR2-13/2	1358.228	1357.512	-209.731	0.541	1903.089	0.517	19	0.244	R.IGYSMITDAEEK.G
R2/RRR2-13/2	1705.421	1706.040	-952.063	0.445	1746.699	0.568	20	0.234	K.AFGAELILTDPLLGM*K.G
R2/RRR2-13/2	1357.288	1357.512	-165.314	0.504	1825.533	0.505	19	0.230	R.IGYSMITDAEEK.G
R2/RRR2-13/2	1688.468	1688.864	-235.495	0.510	1558.126	0.647	25	0.229	K.VDGLVSGIGTGGTITGAGR.Y
R2/RRR2-13/2	1817.462	1818.064	-884.028	0.483	1748.665	0.476	22	0.212	K.DVTELIGNTPLVYLNR.V
R2/RRR2-13/2	1818.497	1818.064	238.706	0.533	1630.288	0.538	22	0.212	K.DVTELIGNTPLVYLNR.V
R2/RRR2-13/2	1356.437	1357.512	-1534.261	0.372	1700.723	0.432	19	0.195	R.IGYSMITDAEEK.G
R2/RRR2-13/2	1706.323	1706.040	166.592	0.532	1443.142	0.572	19	0.194	K.AFGAELILTDPLLGM*K.G
R2/RRR2-13/2	1372.617	1373.511	-1383.949	0.415	1585.089	0.482	18	0.193	R.IGYSM*ITDAEEK.G
R2/RRR2-13/3	1817.932	1818.064	-72.449	0.464	1621.344	0.496	31	0.177	K.DVTELIGNTPLVYLNR.V
R2/RRR2-13/2	1373.026	1373.511	-354.662	0.444	1466.879	0.451	18	0.174	R.IGYSM*ITDAEEK.G
R2/RRR2-13/2	1817.460	1818.064	-885.107	0.453	1507.178	0.431	20	0.172	K.DVTELIGNTPLVYLNR.V
R2/RRR2-13/2	1373.062	1373.511	-328.525	0.429	1448.041	0.452	18	0.172	R.IGYSM*ITDAEEK.G
R2/RRR2-13/2	1613.270	1613.841	-976.718	0.437	1271.359	0.523	28	0.170	K.EGLLVGISSGAAAAAAVR.L
R2/RRR2-13/2	1689.745	1690.041	-175.322	0.444	1427.286	0.424	20	0.162	K.AFGAELILTDPLLGMK.G
R2/RRR2-13/2	1215.144	1215.382	-195.836	0.492	1411.872	0.404	18	0.160	K.GAVQKAEELAAK.T
R2/RRR2-13/2	1413.103	1413.686	-1123.996	0.423	1465.428	0.368	19	0.159	R.YLSSVLFQSIKK.E
R2/RRR2-13/2	1474.179	1474.642	-315.241	0.525	1011.743	0.540	18	0.154	K.IHYETTGPEIWK.S
R2/RRR2-13/2	1285.971	1285.513	356.977	0.468	1121.094	0.471	17	0.150	R.YLSSVLFQSIK.K
R2/RRR2-13/2	1413.277	1413.686	-290.447	0.426	1359.871	0.363	18	0.149	R.YLSSVLFQSIKK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1215.141	1215.382	-198.355	0.481	1176.623	0.429	17	0.145	K.GAVQKAEELAAK.T
R2/RRR2-13/2	1474.273	1474.642	-251.024	0.473	803.037	0.515	17	0.137	K.IHYETTGPEIWK.S
R2/RRR2-13/2	1474.370	1474.642	-185.154	0.503	754.188	0.495	16	0.131	K.IHYETTGPEIWK.S
R2/RRR2-13/3	1985.763	1986.176	-208.631	0.486	1224.141	0.483	30	0.126	K.THNSFILQQFENPANPK.I
R2/RRR2-13/2	1704.537	1706.040	-2061.465	0.311	997.187	0.392	17	0.122	K.AFGAELILTDPLLGM*K.G
R2/RRR2-13/2	1612.690	1613.841	-1337.693	0.303	535.467	0.555	23	0.120	K.EGLLVGISSGAAAAAAVR.L
R2/RRR2-13/2	1514.139	1514.815	-1110.171	0.384	697.406	0.411	19	0.119	R.LVLTM*PASM*SM*ER.R
R2/RRR2-13/3	1817.939	1818.064	-68.812	0.409	1044.278	0.504	26	0.115	K.DVTELIGNTPLVYLNR.V
R2/RRR2-13/2	1514.148	1514.815	-1103.776	0.340	468.121	0.459	16	0.114	R.LVLTM*PASM*SM*ER.R
R2/RRR2-13/3	1985.529	1986.176	-832.021	0.462	1235.306	0.423	30	0.113	K.THNSFILQQFENPANPK.I
R2/RRR2-13/2	1396.872	1397.645	-1273.703	0.279	1024.772	0.215	15	0.108	K.LFVVVFPSFGER.Y
R2/RRR2-13/2	1397.317	1397.645	-235.408	0.349	649.000	0.328	13	0.107	K.LFVVVFPSFGER.Y
R2/RRR2-13/2	1283.350	1283.425	-58.215	0.265	938.588	0.217	15	0.106	K.LESM*EPCSSVK.D
R2/RRR2-13/2	1397.394	1397.645	-180.196	0.330	704.393	0.266	13	0.104	K.LFVVVFPSFGER.Y
R2/RRR2-13/2	1283.082	1283.425	-267.587	0.250	622.830	0.255	13	0.103	K.LESM*EPCSSVK.D
R2/RRR2-13/2	1397.227	1397.645	-300.443	0.260	644.276	0.251	13	0.102	K.LFVVVFPSFGER.Y
R2/RRR2-13/2	1285.609	1285.513	74.417	0.227	746.041	0.241	14	0.102	R.YLSSVLFQSIK.K
R2/RRR2-13/3	1614.555	1613.841	-177.504	0.315	1370.985	0.298	28	0.099	K.EGLLVGISSGAAAAAAVR.L
R2/RRR2-13/2	1283.243	1283.425	-141.896	0.222	680.708	0.109	14	0.099	K.LESM*EPCSSVK.D
R2/RRR2-13/3	1986.935	1986.176	-121.930	0.356	775.965	0.372	25	0.078	K.THNSFILQQFENPANPK.I
R2/RRR2-13/3	1613.386	1613.841	-282.434	0.319	732.137	0.372	24	0.075	K.EGLLVGISSGAAAAAAVR.L
R2/RRR2-8/2	1514.006	1514.829	-1207.508	0.374	2518.354	0.401	23	0.321	K.LGANAILAVSLALCK.A
R2/RRR2-8/2	1581.481	1581.839	-226.575	0.424	2057.537	0.563	24	0.288	K.AVDNVNSIIGPALIGK.D
R2/RRR2-8/2	1998.310	1999.112	-904.567	0.536	1683.055	0.633	24	0.245	R.GNPTVEVDICCSDGTFAR.A
R2/RRR2-8/2	1998.416	1999.112	-851.217	0.520	1665.104	0.614	23	0.237	R.GNPTVEVDICCSDGTFAR.A
R2/RRR2-8/2	1903.550	1904.240	-890.609	0.574	1486.889	0.602	25	0.210	K.LAM*QEFM*ILPTGASSFK.E
R2/RRR2-8/2	1514.042	1514.829	-1183.381	0.432	1654.265	0.504	19	0.206	K.LGANAILAVSLALCK.A
R2/RRR2-8/2	1514.421	1514.829	-270.321	0.431	1563.976	0.492	19	0.192	K.LGANAILAVSLALCK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1903.507	1904.240	-913.334	0.533	1303.634	0.552	24	0.178	K.LAM*QEFM*ILPTGASSFK.E
R2/RRR2-8/2	1905.505	1904.240	139.271	0.529	1065.112	0.603	23	0.166	K.LAM*QEFM*ILPTGASSFK.E
R2/RRR2-8/2	1887.724	1888.241	-805.840	0.489	1162.305	0.448	20	0.143	K.LAM*QEFMILPTGASSFK.E
R2/RRR2-8/2	1871.137	1872.241	-1127.931	0.421	744.857	0.474	18	0.122	K.LAMQEFMILPTGASSFK.E
R2/RRR2-8/2	902.933	903.095	-179.819	0.484	778.103	0.315	13	0.117	K.ACNALLLK.V
R2/RRR2-8/2	903.003	903.095	-102.113	0.455	830.095	0.285	13	0.114	K.ACNALLLK.V
R2/RRR2-6/2	1427.369	1427.588	-154.452	0.515	2249.624	0.609	21	0.336	K.STVHDVVLVGGSTR.I
R2/RRR2-6/2	1427.407	1427.588	-127.515	0.506	2245.182	0.548	21	0.314	K.STVHDVVLVGGSTR.I
R2/RRR2-6/2	1427.335	1427.588	-178.045	0.462	1857.266	0.589	19	0.258	K.STVHDVVLVGGSTR.I
R2/RRR2-6/2	1247.569	1248.435	-1500.588	0.470	1417.182	0.509	20	0.183	K.DAGVISGLNVM*R.I
R2/RRR2-6/2	1544.205	1544.752	-1004.729	0.517	1463.247	0.473	21	0.179	K.M*KETAEAYLGSTVK.N
R2/RRR2-6/2	1247.649	1248.435	-1436.018	0.511	1364.911	0.487	20	0.174	K.DAGVISGLNVM*R.I
R2/RRR2-6/2	1543.547	1544.752	-1432.779	0.477	1362.607	0.470	21	0.168	K.M*KETAEAYLGSTVK.N
R2/RRR2-6/2	1248.028	1248.435	-327.301	0.525	1273.265	0.476	19	0.163	K.DAGVISGLNVM*R.I
R2/RRR2-6/2	1544.243	1544.752	-979.967	0.525	1167.880	0.484	20	0.154	K.M*KETAEAYLGSTVK.N
R2/RRR2-6/2	1584.173	1583.788	243.640	0.555	936.103	0.436	20	0.132	K.QFSAEEISSMVLNK.M
R2/RRR2-6/2	1583.239	1583.788	-981.402	0.476	1057.284	0.380	21	0.131	K.QFSAEEISSMVLNK.M
R2/RRR2-6/2	1599.400	1599.788	-243.054	0.478	785.285	0.358	20	0.118	K.QFSAEEISSM*VLNK.M
R2/RRR2-6/2	1599.141	1599.788	-1032.697	0.453	503.954	0.420	16	0.115	K.QFSAEEISSM*VLNK.M
R2/RRR2-6/2	1599.416	1599.788	-233.253	0.522	632.558	0.373	18	0.114	K.QFSAEEISSM*VLNK.M
R2/RRR2-6/2	1585.226	1583.788	277.076	0.467	612.945	0.334	17	0.110	K.QFSAEEISSMVLNK.M
R2/RRR2-6/3	1544.589	1544.752	-106.064	0.504	1277.792	0.342	28	0.097	K.M*KETAEAYLGSTVK.N
R2/RRR2-6/3	1528.604	1528.753	-97.896	0.447	1184.118	0.345	28	0.093	K.MKETAEAYLGSTVK.N
R2/RRR2-6/3	1528.533	1528.753	-144.519	0.448	1083.840	0.315	29	0.083	K.MKETAEAYLGSTVK.N
R2/RRR2-6/3	1544.674	1544.752	-50.653	0.483	1071.164	0.316	25	0.082	K.M*KETAEAYLGSTVK.N
R2/RRR2-6/3	1528.325	1528.753	-280.809	0.426	955.610	0.206	27	0.067	K.MKETAEAYLGSTVK.N
R2/RRR2-6/3	1544.269	1544.752	-313.732	0.376	1007.395	0.183	24	0.064	-.M*KETAEAYLGSTVK.-
R2/RRR2-14/2	1795.490	1795.025	259.767	0.540	2428.220	0.609	26	0.372	K.LTVSTVSSSGVGLTSTAVK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1794.425	1795.025	-894.558	0.492	2438.390	0.541	26	0.350	K.LTVSTVSSSGVGLTSTAVK.K
R2/RRR2-14/2	1794.492	1795.025	-856.794	0.501	2393.789	0.560	25	0.347	K.LTVSTVSSSGVGLTSTAVK.K
R2/RRR2-14/2	1530.254	1530.747	-323.292	0.514	2376.724	0.497	22	0.323	K.KGGLYTLDVSSVYK.Y
R2/RRR2-14/2	1530.363	1530.747	-251.584	0.512	2277.767	0.550	22	0.321	K.KGGLYTLDVSSVYK.Y
R2/RRR2-14/2	1531.329	1530.747	-273.573	0.571	2073.221	0.576	22	0.292	K.KGGLYTLDVSSVYK.Y
R2/RRR2-14/2	1403.439	1402.574	-96.628	0.567	1914.631	0.617	20	0.277	K.GGLYTLDVSSVYK.Y
R2/RRR2-14/3	1794.767	1795.025	-144.229	0.512	1861.549	0.571	32	0.248	K.LTVSTVSSSGVGLTSTAVK.K
R2/RRR2-14/2	1297.236	1297.436	-155.128	0.468	1594.025	0.627	18	0.229	K.SVLTISGEFDTK.A
R2/RRR2-14/2	1402.159	1402.574	-297.116	0.415	1729.756	0.482	18	0.211	K.GGLYTLDVSSVYK.Y
R2/RRR2-14/2	1298.075	1297.436	-279.344	0.518	1392.441	0.613	18	0.202	K.SVLTISGEFDTK.A
R2/RRR2-14/2	1297.065	1297.436	-287.113	0.446	1545.737	0.513	18	0.196	K.SVLTISGEFDTK.A
R2/RRR2-14/2	1401.713	1402.574	-1331.408	0.384	1508.385	0.529	18	0.193	K.GGLYTLDVSSVYK.Y
R2/RRR2-14/2	1766.350	1766.977	-923.679	0.532	1246.677	0.559	23	0.177	R.RLSTNENTLTVGGLYK.V
R2/RRR2-14/2	1146.415	1147.309	-1657.273	0.442	1320.859	0.502	17	0.171	K.GPGLFSDIGKR.A
R2/RRR2-14/2	1610.304	1610.790	-302.963	0.477	1200.860	0.543	20	0.166	R.LSTNENTLTVGGLYK.V
R2/RRR2-14/3	1794.352	1795.025	-935.065	0.398	1738.553	0.385	32	0.162	K.LTVSTVSSSGVGLTSTAVK.K
R2/RRR2-14/2	1610.177	1610.790	-1005.285	0.498	1136.916	0.530	20	0.159	R.LSTNENTLTVGGLYK.V
R2/RRR2-14/2	1346.585	1347.631	-1524.028	0.432	1328.391	0.432	17	0.158	K.LAALLQHEVKPK.S
R2/RRR2-14/2	961.941	962.083	-147.978	0.460	1561.505	0.307	15	0.155	K.SSVVAELTR.R
R2/RRR2-14/2	1147.215	1147.309	-82.350	0.445	1255.479	0.439	16	0.153	K.GPGLFSDIGKR.A
R2/RRR2-14/2	961.930	962.083	-159.435	0.402	1519.650	0.291	15	0.149	K.SSVVAELTR.R
R2/RRR2-14/2	1610.291	1610.790	-310.796	0.473	970.896	0.537	20	0.147	R.LSTNENTLTVGGLYK.V
R2/RRR2-14/2	961.423	962.083	-1731.646	0.417	1674.587	0.209	15	0.147	K.SSVVAELTR.R
R2/RRR2-14/2	990.203	991.123	-1944.067	0.350	814.056	0.631	15	0.146	K.GPGLFSDIGK.K
R2/RRR2-14/2	1146.582	1147.309	-1510.951	0.475	1020.013	0.487	16	0.145	K.GPGLFSDIGKR.A
R2/RRR2-15/2	961.448	962.083	-1705.750	0.411	1441.796	0.281	15	0.142	K.SSVVAELTR.R
R2/RRR2-15/2	961.284	962.083	-1876.841	0.383	1491.923	0.211	14	0.133	K.SSVVAELTR.R
R2/RRR2-15/2	961.896	962.083	-194.826	0.417	1376.649	0.208	14	0.125	K.SSVVAELTR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1389.100	1389.539	-316.832	0.480	1144.773	0.294	18	0.123	K.VSGVYHLDDKQK.S
R2/RRR2-15/2	1297.215	1297.436	-171.082	0.292	748.281	0.403	16	0.116	K.SVLTISGEFDTK.A
R2/RRR2-14/2	1389.246	1389.539	-210.953	0.445	926.515	0.256	17	0.109	K.VSGVYHLDDKQK.S
R2/RRR2-15/2	1401.402	1402.574	-1554.402	0.325	387.662	0.390	13	0.108	K.GGLYTLDVSSVYK.Y
R2/RRR2-14/2	1118.126	1118.269	-128.403	0.320	987.026	0.177	14	0.104	K.SSVVAELTRR.L
R2/RRR2-14/2	1118.030	1118.269	-214.051	0.299	855.439	0.146	14	0.100	K.SSVVAELTRR.L
R2/RRR2-14/3	1530.730	1530.747	-11.096	0.481	1564.235	0.254	27	0.100	K.KGGLYTLDVSSVYK.Y
R2/RRR2-14/3	1146.986	1147.309	-282.421	0.469	455.653	0.545	18	0.097	K.GPGLFSDIGKR.A
R2/RRR2-15/3	1147.357	1147.309	41.968	0.388	420.945	0.534	18	0.092	K.GPGLFSDIGKR.A
R2/RRR2-15/3	1147.005	1147.309	-265.764	0.285	486.602	0.502	19	0.084	K.GPGLFSDIGKR.A
R2/RRR2-15/3	1530.582	1530.747	-108.169	0.441	1038.061	0.331	23	0.083	K.KGGLYTLDVSSVYK.Y
R2/RRR2-15/3	1530.796	1530.747	32.095	0.401	1238.484	0.250	24	0.080	K.KGGLYTLDVSSVYK.Y
R2/RRR2-15/3	1147.243	1147.309	-57.440	0.289	587.314	0.441	21	0.080	K.GPGLFSDIGKR.A
R2/RRR2-14/3	1795.137	1795.025	62.665	0.309	935.148	0.334	28	0.078	K.LTVSTVSSSGVGLTSTAVK.K
R2/RRR2-14/3	1529.948	1530.747	-1179.129	0.397	1134.165	0.242	23	0.074	K.KGGLYTLDVSSVYK.Y
R2/RRR2-14/3	1530.290	1530.747	-299.370	0.456	1008.979	0.206	24	0.065	-.KGGLYTLDVSSVYK.-
R2/RRR2-8/2	1842.561	1842.085	258.912	0.666	3018.130	0.645	27	0.533	K.HVAEADIIFVSVNTPTK.T
R2/RRR2-8/2	1841.461	1842.085	-884.807	0.618	2846.237	0.600	26	0.469	K.HVAEADIIFVSVNTPTK.T
R2/RRR2-8/2	1621.073	1619.796	171.403	0.607	1919.717	0.547	25	0.255	K.FLNASVGFGGSCFQK.D
R2/RRR2-9/3	1682.592	1682.979	-230.977	0.525	2124.956	0.471	31	0.247	K.CPAIEVVVVDISKPR.I
R2/RRR2-8/2	1476.329	1476.699	-251.836	0.542	1897.943	0.539	22	0.246	R.IITTNLWSAELSK.L
R2/RRR2-8/2	1476.544	1476.699	-105.526	0.587	1965.315	0.498	22	0.244	R.IITTNLWSAELSK.L
R2/RRR2-9/2	1619.542	1619.796	-157.293	0.532	1855.267	0.524	25	0.240	K.FLNASVGFGGSCFQK.D
R2/RRR2-8/2	1621.403	1619.796	-242.895	0.639	1803.455	0.545	25	0.237	K.FLNASVGFGGSCFQK.D
R2/RRR2-9/2	1355.058	1354.450	-289.915	0.578	1707.779	0.590	18	0.233	K.AADLTYWESAAR.M
R2/RRR2-9/3	1682.823	1682.979	-93.326	0.576	1719.002	0.589	29	0.221	K.CPAIEVVVVDISKPR.I
R2/RRR2-5/2	1477.552	1476.699	-99.985	0.560	1719.656	0.534	21	0.220	R.IITTNLWSAELSK.L
R2/RRR2-6/2	1075.219	1075.246	-25.349	0.467	1826.760	0.470	17	0.219	K.LAANAFLAQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1355.339	1354.450	-81.810	0.600	1678.583	0.520	18	0.210	K.AADLTYWESAAR.M
R2/RRR2-9/3	1682.715	1682.979	-157.944	0.518	1729.646	0.544	28	0.209	K.CPAIEVVVVDISKPR.I
R2/RRR2-9/2	1476.408	1476.699	-197.670	0.497	1747.943	0.472	21	0.208	R.IITTNLWSAELSK.L
R2/RRR2-9/2	1618.898	1619.796	-1175.556	0.466	1712.403	0.451	23	0.201	K.FLNASVGFGGSCFQK.D
R2/RRR2-9/2	1354.267	1354.450	-135.034	0.547	1677.667	0.476	18	0.200	K.AADLTYWESAAR.M
R2/RRR2-8/2	1354.172	1354.450	-205.296	0.548	1607.811	0.507	18	0.200	K.AADLTYWESAAR.M
R2/RRR2-9/2	1476.378	1476.699	-218.074	0.503	1717.298	0.447	21	0.198	R.IITTNLWSAELSK.L
R2/RRR2-6/2	1074.693	1075.246	-1449.563	0.439	1725.495	0.425	17	0.196	K.LAANAFLAQR.I
R2/RRR2-8/3	1682.019	1682.979	-1169.119	0.526	1582.934	0.570	27	0.195	K.CPAIEVVVVDISKPR.I
R2/RRR2-3/2	1355.420	1354.450	-22.096	0.431	1484.847	0.529	18	0.190	K.AADLTYWESAAR.M
R2/RRR2-9/2	1354.088	1354.450	-267.969	0.551	1518.026	0.497	18	0.187	K.AADLTYWESAAR.M
R2/RRR2-8/2	1354.086	1354.450	-268.964	0.530	1609.340	0.449	18	0.186	K.AADLTYWESAAR.M
R2/RRR2-9/2	1476.293	1476.699	-275.893	0.497	1607.853	0.448	20	0.185	R.IITTNLWSAELSK.L
R2/RRR2-9/2	1075.004	1075.246	-225.580	0.522	1509.853	0.480	17	0.185	K.LAANAFLAQR.I
R2/RRR2-1/2	1075.139	1075.246	-99.942	0.513	1591.260	0.441	17	0.185	K.LAANAFLAQR.I
R2/RRR2-9/2	1619.044	1619.796	-1085.005	0.501	1579.327	0.442	24	0.184	K.FLNASVGFGGSCFQK.D
R2/RRR2-5/2	1476.411	1476.699	-195.596	0.471	1505.643	0.489	19	0.183	R.IITTNLWSAELSK.L
R2/RRR2-5/2	1075.151	1075.246	-88.211	0.484	1563.318	0.445	17	0.183	K.LAANAFLAQR.I
R2/RRR2-8/2	1075.217	1075.246	-27.171	0.533	1511.473	0.456	17	0.180	K.LAANAFLAQR.I
R2/RRR2-6/2	1477.496	1476.699	-137.942	0.556	1431.732	0.499	20	0.178	R.IITTNLWSAELSK.L
R2/RRR2-8/2	1476.176	1476.699	-1034.665	0.498	1440.558	0.487	20	0.177	R.IITTNLWSAELSK.L
R2/RRR2-1/2	1477.191	1476.699	334.140	0.533	1430.706	0.477	20	0.174	R.IITTNLWSAELSK.L
R2/RRR2-15/2	1478.043	1476.699	233.550	0.538	1404.282	0.463	20	0.168	R.IITTNLWSAELSK.L
R2/RRR2-8/2	1075.120	1075.246	-117.482	0.607	1412.525	0.448	17	0.168	K.LAANAFLAQR.I
R2/RRR2-8/2	1074.993	1075.246	-235.719	0.534	1490.836	0.406	17	0.167	K.LAANAFLAQR.I
R2/RRR2-8/3	1802.187	1802.046	78.092	0.530	1477.078	0.533	29	0.166	R.IFDNM*QKPAFVFDGR.N
R2/RRR2-8/2	1272.018	1272.453	-343.282	0.419	1065.726	0.587	19	0.163	R.VVSSM*FNTVSGK.K
R2/RRR2-7/2	1475.844	1476.699	-1261.048	0.388	1457.559	0.393	20	0.160	R.IITTNLWSAELSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1075.048	1075.246	-184.342	0.435	1443.634	0.388	17	0.160	K.LAANAFLAQR.I
R2/RRR2-8/2	1272.088	1272.453	-288.401	0.388	1215.235	0.480	20	0.156	R.VVSSM*FNTVSGK.K
R2/RRR2-7/2	1476.316	1476.699	-260.463	0.460	1305.427	0.428	19	0.153	R.IITTNLWSAELSK.L
R2/RRR2-2/2	1075.032	1075.246	-199.948	0.442	1228.567	0.440	16	0.152	K.LAANAFLAQR.I
R2/RRR2-5/2	1074.895	1075.246	-327.320	0.390	1327.177	0.395	16	0.151	K.LAANAFLAQR.I
R2/RRR2-8/3	1681.401	1682.979	-2134.607	0.451	1469.375	0.476	28	0.150	K.CPAIEVVVVDISKPR.I
R2/RRR2-3/2	1477.194	1476.699	335.632	0.501	1322.844	0.405	19	0.150	R.IITTNLWSAELSK.L
R2/RRR2-8/2	980.115	980.228	-115.003	0.433	1144.136	0.436	15	0.147	K.IAILGFAFK.K
R2/RRR2-8/3	1801.987	1802.046	-32.888	0.501	1259.650	0.547	28	0.146	R.IFDNM*QKPAFVFDGR.N
R2/RRR2-2/2	1476.185	1476.699	-1028.687	0.428	1210.766	0.385	19	0.140	R.IITTNLWSAELSK.L
R2/RRR2-10/2	1075.207	1075.246	-36.623	0.379	1115.053	0.417	16	0.139	K.LAANAFLAQR.I
R2/RRR2-8/2	1497.201	1496.646	-297.963	0.429	838.903	0.506	20	0.137	K.QVSVVWDAYEATK.G
R2/RRR2-1/2	1074.739	1075.246	-1406.210	0.468	1044.982	0.414	15	0.135	-.LAANAFLAQR.-
R2/RRR2-6/2	1476.129	1476.699	-1066.880	0.388	1155.697	0.351	19	0.132	R.IITTNLWSAELSK.L
R2/RRR2-8/2	1255.541	1256.454	-1528.345	0.332	969.434	0.445	17	0.131	R.VVSSMFNTVSGK.K
R2/RRR2-3/2	1476.251	1476.699	-304.348	0.311	1180.757	0.346	18	0.131	R.IITTNLWSAELSK.L
R2/RRR2-2/2	1619.328	1619.796	-289.630	0.435	883.284	0.468	18	0.130	K.FLNASVGFGGSCFQK.D
R2/RRR2-9/3	1802.211	1802.046	91.440	0.532	1131.305	0.533	30	0.129	R.IFDNM*QKPAFVFDGR.N
R2/RRR2-8/2	1626.356	1625.799	-273.021	0.488	503.959	0.521	21	0.129	R.ETPAIDVCHGLLGDK.A
R2/RRR2-8/2	1624.878	1625.799	-1185.320	0.423	658.029	0.499	22	0.129	R.ETPAIDVCHGLLGDK.A
R2/RRR2-10/2	1476.383	1476.699	-214.591	0.389	985.539	0.395	18	0.128	R.IITTNLWSAELSK.L
R2/RRR2-8/2	1625.323	1625.799	-293.534	0.440	609.273	0.501	22	0.128	R.ETPAIDVCHGLLGDK.A
R2/RRR2-8/2	1496.381	1496.646	-177.685	0.425	811.483	0.432	20	0.128	K.QVSVVWDAYEATK.G
R2/RRR2-8/2	1071.058	1070.224	-155.765	0.384	1000.406	0.347	14	0.124	R.NVVDPEKLR.E
R2/RRR2-9/2	1497.317	1496.646	-220.013	0.453	709.920	0.423	19	0.123	K.QVSVVWDAYEATK.G
R2/RRR2-5/2	1074.950	1075.246	-276.049	0.482	850.645	0.383	14	0.123	K.LAANAFLAQR.I
R2/RRR2-9/2	1625.512	1625.799	-176.676	0.413	411.262	0.514	19	0.122	R.ETPAIDVCHGLLGDK.A
R2/RRR2-7/2	1475.653	1476.699	-1390.812	0.323	1047.295	0.317	18	0.121	R.IITTNLWSAELSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1199.951	1200.322	-310.656	0.356	956.955	0.308	15	0.118	R.NLFFSTDVEK.H
R2/RRR2-16/2	1074.295	1075.246	-1821.297	0.361	690.082	0.330	14	0.115	K.LAANAFLAQR.I
R2/RRR2-8/3	1801.321	1802.046	-960.934	0.452	1144.335	0.465	28	0.115	R.IFDNM*QKPAFVFDGR.N
R2/RRR2-9/2	1496.406	1496.646	-160.745	0.414	614.629	0.368	17	0.114	K.QVSVVWDAYEATK.G
R2/RRR2-10/2	1476.139	1476.699	-1060.072	0.346	759.924	0.339	15	0.113	R.IITTNLWSAELSK.L
R2/RRR2-8/2	1271.382	1272.453	-1633.802	0.263	759.501	0.364	17	0.113	R.VVSSM*FNTVSGK.K
R2/RRR2-2/2	1354.023	1354.450	-315.726	0.298	468.216	0.401	13	0.111	K.AADLTYWESAAR.M
R2/RRR2-2/2	1354.129	1354.450	-237.400	0.333	662.695	0.316	15	0.111	K.AADLTYWESAAR.M
R2/RRR2-1/2	1353.499	1354.450	-1445.685	0.314	985.876	0.247	15	0.111	K.AADLTYWESAAR.M
R2/RRR2-16/2	1074.700	1075.246	-1442.831	0.347	414.623	0.286	14	0.110	-.LAANAFLAQR.-
R2/RRR2-9/3	1802.571	1802.046	-264.496	0.525	806.989	0.538	26	0.108	R.IFDNM*QKPAFVFDGR.N
R2/RRR2-8/2	1199.922	1200.322	-334.540	0.276	894.692	0.231	14	0.108	R.NLFFSTDVEK.H
R2/RRR2-6/2	1475.451	1476.699	-1528.089	0.302	636.035	0.272	14	0.107	R.IITTNLWSAELSK.L
R2/RRR2-1/2	1475.240	1476.699	-1672.220	0.218	419.441	0.326	13	0.106	-.IITTNLWSAELSK.-
R2/RRR2-9/2	1199.389	1200.322	-1616.435	0.259	705.168	0.286	12	0.106	R.NLFFSTDVEK.H
R2/RRR2-10/2	1199.871	1200.322	-377.514	0.296	539.994	0.297	11	0.105	-.NLFFSTDVEK.-
R2/RRR2-9/2	1496.323	1496.646	-216.150	0.305	558.356	0.244	16	0.105	K.QVSVVWDAYEATK.G
R2/RRR2-9/2	1200.080	1200.322	-202.069	0.300	673.717	0.220	13	0.105	R.NLFFSTDVEK.H
R2/RRR2-2/2	1353.744	1354.450	-1263.995	0.296	572.961	0.216	14	0.105	-.AADLTYWESAAR.-
R2/RRR2-10/2	1199.765	1200.322	-1301.817	0.259	673.947	0.060	11	0.098	R.NLFFSTDVEK.H
R2/RRR2-1/2	1355.319	1354.450	-96.897	0.256	323.137	0.331	10	0.092	-.AADLTYWESAAR.-
R2/RRR2-4/2	1832.554	1833.143	-869.999	0.508	2965.347	0.521	25	0.462	R.NGVTATDLVLTVTQMLR.K
R2/RRR2-4/2	1833.454	1833.143	169.779	0.563	2786.835	0.570	24	0.435	R.NGVTATDLVLTVTQMLR.K
R2/RRR2-4/2	1879.850	1879.083	-124.179	0.588	2627.701	0.537	26	0.388	K.FVEFYGGGMSELSLADR.A
R2/RRR2-4/2	1832.356	1833.143	-978.608	0.498	2495.064	0.551	23	0.362	R.NGVTATDLVLTVTQMLR.K
R2/RRR2-4/2	1833.555	1833.143	224.993	0.521	2242.410	0.522	22	0.300	R.NGVTATDLVLTVTQMLR.K
R2/RRR2-4/2	1894.277	1895.082	-955.657	0.538	2069.536	0.562	25	0.286	K.FVEFYGGGM*SELSLADR.A
R2/RRR2-4/2	1894.291	1895.082	-948.541	0.545	1879.167	0.564	24	0.255	K.FVEFYGGGM*SELSLADR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1515.273	1515.630	-236.330	0.549	1677.799	0.560	20	0.228	K.M*FVDYNQPEAER.V
R2/RRR2-4/2	1657.253	1656.768	293.329	0.586	1681.325	0.529	21	0.216	K.SDWLSCLDNDVGFK.G
R2/RRR2-4/2	1514.938	1515.630	-1120.143	0.487	1642.474	0.514	20	0.211	K.M*FVDYNQPEAER.V
R2/RRR2-4/2	1849.429	1849.143	155.126	0.527	1467.226	0.601	20	0.203	R.NGVTATDLVLTVTQM*LR.K
R2/RRR2-4/2	1656.427	1656.768	-206.567	0.500	1582.478	0.511	20	0.200	K.SDWLSCLDNDVGFK.G
R2/RRR2-4/2	1656.091	1656.768	-1015.784	0.504	1460.165	0.501	20	0.184	K.SDWLSCLDNDVGFK.G
R2/RRR2-4/2	1517.337	1516.656	-210.486	0.565	1467.033	0.492	20	0.183	R.SDDTVAM*IESYLR.A
R2/RRR2-4/2	1522.663	1521.843	-118.814	0.561	1106.145	0.623	20	0.175	R.SNLAGMGIIPLCFK.S
R2/RRR2-4/2	1517.245	1516.656	-271.828	0.560	1225.099	0.516	19	0.165	R.SDDTVAM*IESYLR.A
R2/RRR2-4/2	1558.095	1558.589	-318.143	0.520	1098.737	0.563	21	0.163	K.SGEDADTLGLTGHER.F
R2/RRR2-4/2	1558.243	1558.589	-223.197	0.494	1129.981	0.507	22	0.156	K.SGEDADTLGLTGHER.F
R2/RRR2-4/2	1538.547	1537.843	-192.554	0.546	831.408	0.619	20	0.155	R.SNLAGM*GIIPLCFK.S
R2/RRR2-4/2	1537.471	1537.843	-242.302	0.483	915.264	0.582	20	0.152	R.SNLAGM*GIIPLCFK.S
R2/RRR2-4/2	1515.786	1516.656	-1237.262	0.390	1252.518	0.416	19	0.148	R.SDDTVAM*IESYLR.A
R2/RRR2-4/2	1558.144	1558.589	-286.702	0.522	911.771	0.519	20	0.142	K.SGEDADTLGLTGHER.F
R2/RRR2-4/2	1521.578	1521.843	-174.743	0.487	851.932	0.542	18	0.141	R.SNLAGMGIIPLCFK.S
R2/RRR2-4/2	1198.073	1198.258	-154.887	0.406	1212.312	0.375	16	0.140	R.NCDEFQVTGK.D
R2/RRR2-4/2	1617.248	1616.793	282.113	0.418	1017.159	0.419	22	0.135	R.DIWPSTEEIAEVVK.S
R2/RRR2-3/2	1517.309	1516.656	-229.533	0.408	1118.276	0.363	17	0.129	R.SDDTVAM*IESYLR.A
R2/RRR2-4/2	1197.644	1198.258	-1351.967	0.349	1079.585	0.365	15	0.129	R.NCDEFQVTGK.D
R2/RRR2-4/2	1197.733	1198.258	-1276.936	0.335	1091.229	0.357	15	0.128	R.NCDEFQVTGK.D
R2/RRR2-4/2	1290.479	1291.437	-1521.597	0.357	841.089	0.456	17	0.127	K.VAEFSFHGTPAK.L
R2/RRR2-4/2	1172.515	1173.300	-1527.133	0.458	847.132	0.389	16	0.126	K.ILDWENSAPK.Q
R2/RRR2-4/2	1537.390	1537.843	-295.354	0.421	623.448	0.490	17	0.123	R.SNLAGM*GIIPLCFK.S
R2/RRR2-4/2	1282.103	1282.426	-252.742	0.238	1134.694	0.324	17	0.123	K.YYSLPALSDPR.I
R2/RRR2-4/2	1616.241	1616.793	-963.257	0.335	796.319	0.393	21	0.120	R.DIWPSTEEIAEVVK.S
R2/RRR2-1/2	1658.273	1656.768	-299.441	0.451	531.187	0.480	15	0.118	K.SDWLSCLDNDVGFK.G
R2/RRR2-4/2	951.435	952.086	-1740.945	0.250	852.440	0.378	15	0.117	K.LSVFDAATK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1283.301	1282.426	-97.660	0.326	643.300	0.439	13	0.116	K.YYSLPALSDPR.I
R2/RRR2-3/2	1616.867	1616.793	45.540	0.325	548.865	0.425	18	0.114	R.DIWPSTEEIAEVVK.S
R2/RRR2-4/2	1281.548	1282.426	-1470.484	0.272	580.177	0.479	13	0.114	K.YYSLPALSDPR.I
R2/RRR2-4/2	951.273	952.086	-1912.037	0.259	903.368	0.300	15	0.113	K.LSVFDAATK.Y
R2/RRR2-1/2	1173.221	1173.300	-67.271	0.432	718.502	0.295	15	0.113	K.ILDWENSAPK.Q
R2/RRR2-4/2	1015.987	1016.174	-183.670	0.269	508.197	0.430	15	0.112	K.TSLAPGSGVVK.K
R2/RRR2-6/2	1538.892	1537.843	32.171	0.288	526.562	0.421	15	0.110	R.SNLAGM*GIIPLCFK.S
R2/RRR2-3/2	1173.447	1173.300	125.978	0.327	749.295	0.276	15	0.110	K.ILDWENSAPK.Q
R2/RRR2-4/2	1848.189	1849.143	-1060.332	0.410	710.973	0.394	15	0.110	-.NGVTATDLVLTVTQM*LR.-
R2/RRR2-4/2	1015.726	1016.174	-442.278	0.337	396.284	0.511	13	0.110	-.TSLAPGSGVVK.-
R2/RRR2-3/2	1502.101	1500.656	297.055	0.331	931.020	0.274	15	0.109	R.SDDTVAMIESYLR.A
R2/RRR2-1/2	951.939	952.086	-155.192	0.264	558.925	0.320	12	0.108	K.LSVFDAATK.Y
R2/RRR2-4/2	1015.961	1016.174	-210.068	0.294	420.523	0.404	13	0.108	-.TSLAPGSGVVK.-
R2/RRR2-2/2	951.783	952.086	-319.489	0.267	522.364	0.310	11	0.107	K.LSVFDAATK.Y
R2/RRR2-4/2	1616.138	1616.793	-1027.562	0.278	508.849	0.283	18	0.107	R.DIWPSTEEIAEVVK.S
R2/RRR2-1/2	1172.923	1173.300	-322.825	0.358	627.895	0.203	14	0.106	K.ILDWENSAPK.Q
R2/RRR2-4/3	1832.985	1833.143	-86.750	0.366	1128.705	0.393	27	0.098	R.NGVTATDLVLTVTQMLR.K
R2/RRR2-1/3	1558.819	1558.589	148.078	0.469	737.147	0.471	25	0.094	K.SGEDADTLGLTGHER.F
R2/RRR2-4/3	1559.715	1558.589	80.955	0.422	865.272	0.413	26	0.090	K.SGEDADTLGLTGHER.F
R2/RRR2-4/3	1558.607	1558.589	11.059	0.477	640.644	0.453	24	0.089	K.SGEDADTLGLTGHER.F
R2/RRR2-4/3	1558.483	1558.589	-68.484	0.428	736.989	0.420	25	0.087	K.SGEDADTLGLTGHER.F
R2/RRR2-3/3	1558.114	1558.589	-306.008	0.386	969.214	0.353	26	0.084	K.SGEDADTLGLTGHER.F
R2/RRR2-2/2	951.975	952.086	-117.116	0.206	277.347	0.332	9	0.079	-.LSVFDAATK.-
R2/RRR2-3/3	1558.626	1558.589	23.313	0.350	599.271	0.347	22	0.075	-.SGEDADTLGLTGHER.-
R2/RRR2-6/2	1582.933	1582.844	56.726	0.479	717.529	0.358	19	0.114	K.QFSAEEISSMVLIK.M
R2/RRR2-7/1	1030.539	1031.142	-1559.952	0.224	719.076	0.331	12	0.528	R.GVEELADAVK.V
R2/RRR2-7/1	1030.483	1031.142	-1614.454	0.226	589.939	0.353	11	0.416	-.GVEELADAVK.-
R2/RRR2-7/2	1435.435	1434.684	-174.361	0.534	2702.122	0.419	22	0.360	R.GISM*AVDAVVTNLK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1321.066	1321.461	-299.599	0.512	2109.265	0.522	20	0.284	R.NVVIEQSYGSPK.V
R2/RRR2-7/2	1320.793	1321.461	-1266.374	0.463	1820.524	0.505	19	0.232	R.NVVIEQSYGSPK.V
R2/RRR2-7/2	1418.184	1418.685	-1061.694	0.409	1955.429	0.377	19	0.216	R.GISMAVDAVVTNLK.G
R2/RRR2-7/2	1902.607	1902.181	225.000	0.575	1377.127	0.626	27	0.203	K.AAVEEGIVPGGGVALLYASK.E
R2/RRR2-7/2	1146.477	1147.218	-1522.516	0.446	1586.183	0.518	18	0.203	K.IGGASEAEVGEK.K
R2/RRR2-7/3	1902.151	1902.181	-15.527	0.382	1755.733	0.475	31	0.197	K.AAVEEGIVPGGGVALLYASK.E
R2/RRR2-7/2	1146.527	1147.218	-1478.987	0.468	1560.562	0.494	19	0.195	K.IGGASEAEVGEK.K
R2/RRR2-7/2	1386.062	1386.576	-1095.661	0.446	1368.593	0.578	19	0.191	R.GYISPYFVTNPK.T
R2/RRR2-7/2	1901.355	1902.181	-963.121	0.466	1302.699	0.598	27	0.187	K.AAVEEGIVPGGGVALLYASK.E
R2/RRR2-7/3	1901.854	1902.181	-172.159	0.401	1852.757	0.395	34	0.183	K.AAVEEGIVPGGGVALLYASK.E
R2/RRR2-7/2	1386.105	1386.576	-341.278	0.476	1365.814	0.501	19	0.176	R.GYISPYFVTNPK.T
R2/RRR2-7/2	1267.983	1268.447	-366.822	0.443	1465.235	0.400	19	0.165	K.SVAAGM*NAM*DLR.R
R2/RRR2-7/2	1146.449	1147.218	-1547.116	0.389	1350.089	0.463	18	0.165	K.IGGASEAEVGEK.K
R2/RRR2-7/2	1030.445	1031.142	-1652.015	0.435	1322.446	0.429	16	0.158	R.GVEELADAVK.V
R2/RRR2-7/2	1030.659	1031.142	-469.964	0.456	1327.381	0.389	16	0.153	-.GVEELADAVK.-
R2/RRR2-7/2	1267.905	1268.447	-1219.426	0.439	1286.323	0.413	18	0.151	K.SVAAGM*NAM*DLR.R
R2/RRR2-7/2	1586.328	1586.679	-222.410	0.476	1175.468	0.467	19	0.151	R.SAIELSTSDYDKEK.L
R2/RRR2-7/2	1385.602	1386.576	-1429.332	0.327	1193.231	0.467	18	0.149	R.GYISPYFVTNPK.T
R2/RRR2-7/2	1585.632	1586.679	-1294.963	0.478	1173.839	0.435	19	0.145	R.SAIELSTSDYDKEK.L
R2/RRR2-8/2	1196.891	1197.453	-1308.729	0.426	1065.814	0.466	15	0.143	K.IGVQIIQNALK.T
R2/RRR2-7/2	1433.804	1434.684	-1315.407	0.329	1378.491	0.314	17	0.139	R.GISM*AVDAVVTNLK.G
R2/RRR2-7/2	966.764	967.147	-397.745	0.528	788.143	0.487	14	0.136	K.VSNLHAVVK.V
R2/RRR2-7/3	1861.888	1862.072	-98.851	0.487	1366.210	0.454	31	0.133	K.VTVSKDDTVILDGAGDKK.S
R2/RRR2-7/2	1418.392	1418.685	-206.963	0.363	986.226	0.420	18	0.129	R.GISMAVDAVVTNLK.G
R2/RRR2-7/2	1535.177	1535.724	-1010.612	0.416	1109.482	0.316	19	0.124	K.ELDKLLTANFDQK.I
R2/RRR2-7/2	1586.395	1586.679	-179.643	0.522	622.941	0.470	15	0.119	R.SAIELSTSDYDKEK.L
R2/RRR2-7/3	1861.164	1862.072	-1028.167	0.493	1182.783	0.461	28	0.118	K.VTVSKDDTVILDGAGDKK.S
R2/RRR2-7/2	1267.485	1268.447	-1552.030	0.317	975.598	0.303	18	0.116	K.SVAAGM*NAM*DLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/3	1901.278	1902.181	-1003.737	0.337	1349.101	0.355	30	0.110	K.AAVEEGIVPGGGVALLYASK.E
R2/RRR2-7/3	1862.509	1862.072	235.358	0.490	953.283	0.459	26	0.100	K.VTVSKDDTVILDGAGDKK.S
R2/RRR2-7/3	1582.356	1581.786	-272.420	0.458	1158.231	0.382	23	0.098	K.CELDDPLILIHDK.K
R2/RRR2-8/3	1862.819	1862.072	-135.904	0.307	496.817	0.372	24	0.075	K.VTVSKDDTVILDGAGDKK.S
R2/RRR2-8/2	1564.226	1564.722	-318.149	0.466	2489.714	0.469	23	0.337	K.AVVQVFEGTSGIDNK.Y
R2/RRR2-8/2	1563.743	1564.722	-1268.930	0.411	2530.668	0.392	23	0.320	K.AVVQVFEGTSGIDNK.Y
R2/RRR2-8/2	1692.440	1690.967	280.213	0.601	2373.328	0.436	22	0.303	R.NIFQSLDLAWTLLR.I
R2/RRR2-8/2	1703.360	1703.908	-911.619	0.504	1950.710	0.621	21	0.283	R.IALTTAEYLAYECGK.H
R2/RRR2-8/2	1703.264	1703.908	-968.027	0.514	1938.702	0.625	21	0.283	R.IALTTAEYLAYECGK.H
R2/RRR2-8/2	1563.793	1564.722	-1237.416	0.414	2265.722	0.379	22	0.266	K.AVVQVFEGTSGIDNK.Y
R2/RRR2-8/2	1717.558	1716.959	-234.429	0.572	2004.178	0.498	22	0.255	R.VTLFLNLANDPTIER.I
R2/RRR2-8/2	1704.401	1703.908	290.315	0.556	1691.162	0.625	19	0.242	R.IALTTAEYLAYECGK.H
R2/RRR2-8/2	1386.262	1386.575	-226.245	0.463	1646.392	0.544	20	0.217	K.YTTVQFTGEVLK.T
R2/RRR2-8/2	1716.339	1716.959	-947.170	0.493	1670.390	0.473	21	0.201	R.VTLFLNLANDPTIER.I
R2/RRR2-8/2	1385.544	1386.575	-1470.041	0.309	1445.875	0.547	19	0.186	K.YTTVQFTGEVLK.T
R2/RRR2-8/2	1716.525	1716.959	-253.972	0.504	1513.926	0.485	20	0.185	R.VTLFLNLANDPTIER.I
R2/RRR2-8/3	1286.518	1286.418	77.732	0.516	1749.477	0.438	26	0.168	R.KFVTQGAYDTR.N
R2/RRR2-8/2	1913.227	1914.127	-995.990	0.578	1035.504	0.601	24	0.166	R.GYPGYMYTDLATIYER.A
R2/RRR2-8/2	1368.654	1369.632	-1449.268	0.344	1514.159	0.377	21	0.165	R.TVSGVAGPLVILDK.V
R2/RRR2-8/2	1914.309	1914.127	95.323	0.615	872.503	0.650	23	0.163	R.GYPGYMYTDLATIYER.A
R2/RRR2-8/2	1913.573	1914.127	-814.481	0.524	991.657	0.583	23	0.158	R.GYPGYMYTDLATIYER.A
R2/RRR2-8/2	1287.099	1286.418	-249.098	0.509	1090.224	0.492	18	0.153	R.KFVTQGAYDTR.N
R2/RRR2-8/2	1089.216	1089.291	-68.975	0.503	988.576	0.503	16	0.148	K.TPVSLDMLGR.I
R2/RRR2-8/2	1105.125	1105.291	-149.897	0.515	1035.462	0.481	15	0.146	K.TPVSLDM*LGR.I
R2/RRR2-8/2	1089.090	1089.291	-185.338	0.525	831.346	0.559	14	0.145	K.TPVSLDMLGR.I
R2/RRR2-8/2	1088.412	1089.291	-1731.417	0.422	923.648	0.529	15	0.144	K.TPVSLDMLGR.I
R2/RRR2-8/2	1034.944	1035.179	-227.805	0.485	1082.618	0.359	14	0.133	K.YQEIVNIR.L
R2/RRR2-8/2	1929.538	1930.126	-825.708	0.442	621.774	0.528	22	0.130	R.GYPGYM*YTDLATIYER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1034.873	1035.179	-295.967	0.509	1039.015	0.350	14	0.130	K.YQEIVNIR.L
R2/RRR2-8/2	1286.089	1286.418	-257.005	0.476	988.740	0.383	17	0.129	R.KFVTQGAYDTR.N
R2/RRR2-8/2	1229.924	1230.353	-349.474	0.495	755.164	0.456	16	0.129	R.RGQVLEVDGEK.A
R2/RRR2-8/2	1597.573	1597.883	-194.327	0.401	686.556	0.487	19	0.126	R.QIYPPINVLPSLSR.L
R2/RRR2-8/2	1929.333	1930.126	-932.537	0.440	515.829	0.504	22	0.126	R.GYPGYM*YTDLATIYER.A
R2/RRR2-8/2	1229.622	1230.353	-1411.899	0.445	770.421	0.407	16	0.123	R.RGQVLEVDGEK.A
R2/RRR2-8/2	1930.257	1930.126	67.569	0.431	459.353	0.486	21	0.122	R.GYPGYM*YTDLATIYER.A
R2/RRR2-8/2	1597.366	1597.883	-952.334	0.380	660.386	0.470	17	0.121	R.QIYPPINVLPSLSR.L
R2/RRR2-8/2	1229.529	1230.353	-1488.285	0.428	805.810	0.377	16	0.120	R.RGQVLEVDGEK.A
R2/RRR2-8/3	1286.647	1286.418	178.641	0.497	1471.927	0.378	25	0.119	R.KFVTQGAYDTR.N
R2/RRR2-8/2	1597.430	1597.883	-284.403	0.341	794.577	0.416	18	0.119	R.QIYPPINVLPSLSR.L
R2/RRR2-8/2	1105.211	1105.291	-72.450	0.327	469.090	0.448	14	0.117	K.TPVSLDM*LGR.I
R2/RRR2-8/2	1286.116	1286.418	-235.484	0.421	1001.051	0.265	17	0.115	R.KFVTQGAYDTR.N
R2/RRR2-8/2	1386.303	1386.575	-196.210	0.373	450.829	0.428	12	0.107	-.YTTVQFTGEVLK.-
R2/RRR2-8/3	1895.906	1896.007	-53.260	0.458	1001.960	0.441	25	0.099	R.DHSDVSNQLYANYAIGK.D
R2/RRR2-8/3	1230.484	1230.353	106.546	0.320	1270.943	0.245	23	0.077	R.RGQVLEVDGEK.A
R2/RRR2-8/3	1229.788	1230.353	-1276.469	0.318	1321.568	0.139	22	0.066	R.RGQVLEVDGEK.A
R2/RRR2-6/2	1496.170	1496.694	-1021.493	0.570	2961.528	0.569	23	0.484	K.SQIHEIVLVGGSTR.I
R2/RRR2-6/2	1495.818	1496.694	-1257.960	0.547	2845.653	0.573	23	0.456	K.SQIHEIVLVGGSTR.I
R2/RRR2-6/2	1497.563	1496.694	-87.694	0.573	2488.260	0.601	22	0.383	K.SQIHEIVLVGGSTR.I
R2/RRR2-6/3	1537.823	1537.620	132.664	0.536	2489.165	0.393	29	0.291	K.NGHVEIIANDQGNR.I
R2/RRR2-6/2	1156.201	1156.317	-100.665	0.491	1970.320	0.427	20	0.233	K.DAGVIAGLNVAR.I
R2/RRR2-6/2	1156.080	1156.317	-205.523	0.457	1879.308	0.472	19	0.232	K.DAGVIAGLNVAR.I
R2/RRR2-6/3	1652.279	1652.835	-944.663	0.558	2204.690	0.342	29	0.207	R.ARFEELNNDLFRK.T
R2/RRR2-6/2	1537.181	1537.620	-286.231	0.482	1632.135	0.495	20	0.203	K.NGHVEIIANDQGNR.I
R2/RRR2-6/2	1537.196	1537.620	-276.511	0.498	1488.709	0.493	19	0.185	K.NGHVEIIANDQGNR.I
R2/RRR2-6/2	1537.160	1537.620	-299.855	0.465	1477.627	0.483	19	0.181	K.NGHVEIIANDQGNR.I
R2/RRR2-6/2	1508.203	1507.777	283.189	0.449	1471.400	0.467	21	0.178	K.VFSPEEVSAMILGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1524.323	1524.663	-223.746	0.518	1336.312	0.436	19	0.161	R.ARFEELNNDLFR.K
R2/RRR2-6/3	1652.793	1652.835	-25.833	0.553	1869.894	0.343	26	0.158	R.ARFEELNNDLFRK.T
R2/RRR2-6/2	1508.545	1507.777	-154.176	0.466	1169.606	0.487	19	0.153	K.VFSPEEVSAMILGK.M
R2/RRR2-6/2	1524.161	1524.663	-988.194	0.481	1293.029	0.399	19	0.150	R.ARFEELNNDLFR.K
R2/RRR2-6/2	1524.319	1524.663	-226.075	0.493	1212.495	0.425	19	0.149	R.ARFEELNNDLFR.K
R2/RRR2-6/2	1297.306	1297.398	-71.124	0.480	1323.360	0.355	16	0.145	R.FEELNNDLFR.K
R2/RRR2-6/2	1144.107	1144.305	-173.751	0.465	966.818	0.475	19	0.143	K.FDLSGIPAAPR.G
R2/RRR2-6/3	1652.650	1652.835	-112.848	0.547	1626.522	0.388	26	0.140	R.ARFEELNNDLFRK.T
R2/RRR2-6/2	1143.667	1144.305	-1436.437	0.448	887.691	0.484	18	0.137	-.FDLSGIPAAPR.-
R2/RRR2-6/3	1525.843	1524.663	118.419	0.622	1652.754	0.365	24	0.134	R.ARFEELNNDLFR.K
R2/RRR2-6/2	1523.486	1523.776	-191.106	0.392	1383.566	0.269	20	0.133	K.VFSPEEVSAM*ILGK.M
R2/RRR2-6/3	1384.638	1385.612	-1429.734	0.497	1683.834	0.331	25	0.130	K.M*KETAEAYLGKK.I
R2/RRR2-6/2	1144.072	1144.305	-203.935	0.465	839.626	0.414	18	0.127	-.FDLSGIPAAPR.-
R2/RRR2-6/2	1509.882	1509.645	157.671	0.356	551.955	0.552	19	0.127	R.ITPSWVAFTDSER.L
R2/RRR2-6/2	1226.525	1227.305	-1455.194	0.371	899.641	0.347	14	0.119	R.DYFEGKEPNK.G
R2/RRR2-6/2	1509.228	1509.645	-276.687	0.357	526.478	0.461	18	0.119	R.ITPSWVAFTDSER.L
R2/RRR2-6/2	1522.928	1523.776	-1216.941	0.313	969.788	0.326	18	0.117	K.VFSPEEVSAM*ILGK.M
R2/RRR2-6/2	1226.469	1227.305	-1501.382	0.396	742.979	0.372	13	0.116	R.DYFEGKEPNK.G
R2/RRR2-6/2	1227.096	1227.305	-170.281	0.374	728.880	0.351	13	0.114	R.DYFEGKEPNK.G
R2/RRR2-6/3	1524.297	1524.663	-240.827	0.564	1304.593	0.397	25	0.110	R.ARFEELNNDLFR.K
R2/RRR2-6/2	1508.532	1509.645	-1404.976	0.254	431.801	0.434	17	0.110	R.ITPSWVAFTDSER.L
R2/RRR2-6/3	1385.940	1385.612	237.870	0.520	1453.051	0.337	25	0.109	K.M*KETAEAYLGKK.I
R2/RRR2-6/2	1297.928	1297.398	-363.143	0.356	820.351	0.259	13	0.107	-.FEELNNDLFR.-
R2/RRR2-6/3	1501.948	1502.783	-1225.200	0.367	1142.760	0.349	24	0.090	K.IVNKDGKPYIQVK.I
R2/RRR2-6/3	1385.087	1385.612	-1104.281	0.489	1203.929	0.326	24	0.090	K.M*KETAEAYLGKK.I
R2/RRR2-6/3	1368.533	1369.612	-1523.572	0.437	1008.013	0.355	22	0.086	K.MKETAEAYLGKK.I
R2/RRR2-6/3	1524.591	1524.663	-47.078	0.563	1043.688	0.345	23	0.085	R.ARFEELNNDLFR.K
R2/RRR2-6/3	1502.732	1502.783	-33.790	0.360	988.283	0.343	23	0.082	K.IVNKDGKPYIQVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1256.716	1257.439	-1374.617	0.357	923.935	0.357	19	0.079	K.M*KETAEAYLGK.K
R2/RRR2-6/3	1503.016	1502.783	155.246	0.336	877.016	0.349	21	0.078	K.IVNKDGKPYIQVK.I
R2/RRR2-6/3	1537.095	1537.620	-994.862	0.420	931.732	0.300	22	0.074	-.NGHVEIIANDQGNR.-
R2/RRR2-6/3	1538.151	1537.620	-305.601	0.395	1062.909	0.140	23	0.059	-.NGHVEIIANDQGNR.-
R2/RRR2-10/2	1282.812	1283.370	-1217.540	0.521	1748.032	0.613	21	0.249	K.TQGVDIAGYGSSK.V
R2/RRR2-10/2	1557.435	1557.779	-221.583	0.482	1898.235	0.476	23	0.234	R.ISITGAGGFIGSHIAR.R
R2/RRR2-10/2	1283.067	1283.370	-236.903	0.542	1521.891	0.604	20	0.216	K.TQGVDIAGYGSSK.V
R2/RRR2-10/2	1730.385	1730.933	-897.239	0.479	1772.654	0.452	22	0.212	R.FFYASSACIYPEFK.Q
R2/RRR2-10/2	1406.161	1406.524	-259.265	0.480	1578.823	0.453	18	0.190	K.SEGHYIIASDWK.K
R2/RRR2-10/2	1282.674	1283.370	-1325.725	0.457	1272.556	0.580	19	0.180	K.TQGVDIAGYGSSK.V
R2/RRR2-10/2	1557.415	1557.779	-234.557	0.469	1560.919	0.439	21	0.180	R.ISITGAGGFIGSHIAR.R
R2/RRR2-10/2	1729.286	1730.933	-2115.459	0.349	1583.939	0.378	20	0.171	R.FFYASSACIYPEFK.Q
R2/RRR2-10/2	1455.258	1455.685	-294.436	0.529	1200.776	0.538	21	0.167	K.VVSTQAPVQLGSLR.A
R2/RRR2-9/2	1455.299	1455.685	-265.739	0.487	1324.525	0.461	20	0.162	K.VVSTQAPVQLGSLR.A
R2/RRR2-10/2	1557.526	1557.779	-162.613	0.470	1353.068	0.451	20	0.161	R.ISITGAGGFIGSHIAR.R
R2/RRR2-9/2	1456.330	1455.685	-244.701	0.532	1204.251	0.489	19	0.156	K.VVSTQAPVQLGSLR.A
R2/RRR2-10/3	1534.691	1534.697	-4.445	0.539	1373.968	0.530	25	0.153	K.SEGHYIIASDWKK.N
R2/RRR2-9/2	1456.288	1455.685	-273.293	0.531	1242.242	0.430	19	0.148	K.VVSTQAPVQLGSLR.A
R2/RRR2-10/2	1672.292	1672.854	-936.462	0.414	1405.343	0.345	18	0.147	R.SFTFIDECVEGVLR.Y
R2/RRR2-10/2	1455.152	1455.685	-1056.766	0.540	1074.892	0.484	20	0.147	K.VVSTQAPVQLGSLR.A
R2/RRR2-9/2	1454.733	1455.685	-1345.585	0.458	1100.852	0.452	20	0.143	K.VVSTQAPVQLGSLR.A
R2/RRR2-10/2	1673.268	1672.854	248.448	0.485	1212.107	0.397	19	0.141	R.SFTFIDECVEGVLR.Y
R2/RRR2-10/2	1468.202	1467.654	-308.935	0.474	826.911	0.435	16	0.126	R.FHNIYGPFGTWK.G
R2/RRR2-10/2	1907.297	1906.983	165.195	0.474	585.728	0.487	21	0.123	K.ESDAWPAEPQDAYGLEK.L
R2/RRR2-10/2	1906.470	1906.983	-795.937	0.462	611.181	0.480	21	0.123	K.ESDAWPAEPQDAYGLEK.L
R2/RRR2-10/2	1468.990	1467.654	229.488	0.484	608.437	0.436	14	0.118	R.FHNIYGPFGTWK.G
R2/RRR2-10/2	1907.286	1906.983	159.162	0.493	545.012	0.449	20	0.118	K.ESDAWPAEPQDAYGLEK.L
R2/RRR2-10/2	963.989	964.089	-103.845	0.314	306.878	0.387	13	0.117	K.LATEELCK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	963.428	964.089	-1729.059	0.280	284.312	0.424	13	0.116	K.LATEELCK.H
R2/RRR2-10/3	1467.282	1467.654	-254.649	0.473	1214.787	0.441	24	0.114	R.FHNIYGPFGTWK.G
R2/RRR2-9/2	1467.936	1467.654	192.787	0.397	706.541	0.349	15	0.113	R.FHNIYGPFGTWK.G
R2/RRR2-10/2	963.384	964.089	-1774.508	0.223	248.474	0.326	12	0.111	K.LATEELCK.H
R2/RRR2-10/2	1467.264	1467.654	-267.076	0.387	658.361	0.329	15	0.111	R.FHNIYGPFGTWK.G
R2/RRR2-11/2	1468.733	1467.654	53.634	0.350	510.166	0.276	14	0.106	-.FHNIYGPFGTWK.-
R2/RRR2-11/2	1468.429	1467.654	-153.886	0.350	621.735	0.268	14	0.106	R.FHNIYGPFGTWK.G
R2/RRR2-9/2	1283.075	1283.370	-230.412	0.247	841.654	0.232	17	0.105	K.TQGVDIAGYGSSK.V
R2/RRR2-10/3	1533.914	1534.697	-1166.103	0.502	858.455	0.500	24	0.103	K.SEGHYIIASDWKK.N
R2/RRR2-10/3	1775.193	1776.029	-1036.888	0.527	967.198	0.419	29	0.094	R.LKSEGHYIIASDWKK.N
R2/RRR2-10/3	1557.506	1557.779	-175.869	0.380	889.625	0.446	28	0.094	R.ISITGAGGFIGSHIAR.R
R2/RRR2-10/3	1534.698	1534.697	0.102	0.453	743.459	0.460	23	0.091	K.SEGHYIIASDWKK.N
R2/RRR2-10/3	1775.370	1776.029	-936.856	0.482	851.103	0.428	29	0.090	R.LKSEGHYIIASDWKK.N
R2/RRR2-10/3	1405.963	1406.524	-1114.125	0.480	785.291	0.432	19	0.088	K.SEGHYIIASDWK.K
R2/RRR2-10/3	1557.818	1557.779	25.526	0.373	613.950	0.464	25	0.086	R.ISITGAGGFIGSHIAR.R
R2/RRR2-11/3	1557.950	1557.779	110.517	0.328	615.004	0.458	25	0.084	R.ISITGAGGFIGSHIAR.R
R2/RRR2-10/3	1557.288	1557.779	-316.234	0.330	550.748	0.418	23	0.079	R.ISITGAGGFIGSHIAR.R
R2/RRR2-10/3	1406.951	1406.524	304.038	0.470	774.233	0.376	19	0.078	-.SEGHYIIASDWK.-
R2/RRR2-10/3	1540.470	1540.657	-122.099	0.364	865.272	0.352	27	0.076	K.EKTQGVDIAGYGSSK.V
R2/RRR2-10/3	1466.827	1467.654	-1249.402	0.373	986.214	0.287	20	0.075	R.FHNIYGPFGTWK.G
R2/RRR2-10/3	1467.276	1467.654	-258.405	0.380	984.155	0.238	23	0.069	R.FHNIYGPFGTWK.G
R2/RRR2-3/2	1434.326	1434.684	-250.553	0.537	2293.769	0.518	23	0.314	K.TNM*ASVLLEAGLAK.L
R2/RRR2-3/2	1274.177	1274.359	-144.003	0.470	2024.738	0.439	17	0.245	R.DVEIEVEAVDR.T
R2/RRR2-3/2	1274.094	1274.359	-209.069	0.412	2051.131	0.422	17	0.245	R.DVEIEVEAVDR.T
R2/RRR2-3/2	1434.211	1434.684	-330.990	0.518	1881.584	0.523	21	0.245	K.TNM*ASVLLEAGLAK.L
R2/RRR2-3/2	1212.528	1213.324	-1485.523	0.490	1763.231	0.458	17	0.211	K.FYVQTVGDQR.V
R2/RRR2-3/2	1547.261	1547.738	-308.976	0.588	1738.777	0.454	20	0.206	R.KAALQNLEQFQEK.A
R2/RRR2-3/2	1212.853	1213.324	-389.523	0.507	1708.813	0.411	17	0.193	K.FYVQTVGDQR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1213.023	1213.324	-249.371	0.464	1624.671	0.448	17	0.192	K.FYVQTVGDQR.V
R2/RRR2-5/2	1213.208	1213.324	-96.137	0.432	1670.666	0.390	17	0.184	K.FYVQTVGDQR.V
R2/RRR2-3/2	1418.000	1418.685	-1191.780	0.423	1538.743	0.424	21	0.176	K.TNMASVLLEAGLAK.L
R2/RRR2-3/2	1547.555	1547.738	-118.089	0.605	1402.337	0.486	19	0.175	R.KAALQNLEQFQEK.A
R2/RRR2-3/2	1286.309	1286.503	-151.211	0.446	1375.224	0.498	18	0.174	R.VASIQQQLASLK.L
R2/RRR2-3/2	1286.336	1286.503	-130.172	0.414	1385.145	0.482	19	0.171	R.VASIQQQLASLK.L
R2/RRR2-5/2	1286.438	1286.503	-50.501	0.403	1465.358	0.429	18	0.168	R.VASIQQQLASLK.L
R2/RRR2-4/2	1287.444	1286.503	-45.706	0.387	1264.499	0.516	18	0.165	R.VASIQQQLASLK.L
R2/RRR2-4/2	1287.265	1286.503	-185.149	0.439	1206.013	0.465	18	0.153	R.VASIQQQLASLK.L
R2/RRR2-3/2	1647.200	1647.726	-929.246	0.483	1077.813	0.494	24	0.150	R.ISTVDGQPTTNTADAR.V
R2/RRR2-3/2	1057.817	1058.254	-413.626	0.386	1007.651	0.540	16	0.149	K.VVVTEVLGGGK.F
R2/RRR2-3/2	1420.027	1419.565	326.554	0.558	1408.555	0.352	17	0.146	K.AALQNLEQFQEK.A
R2/RRR2-4/2	1287.478	1286.503	-19.458	0.430	939.059	0.541	16	0.145	R.VASIQQQLASLK.L
R2/RRR2-3/2	1647.197	1647.726	-930.957	0.455	1013.688	0.491	24	0.145	R.ISTVDGQPTTNTADAR.V
R2/RRR2-3/2	1418.672	1419.565	-1338.104	0.484	1381.875	0.334	17	0.143	K.AALQNLEQFQEK.A
R2/RRR2-3/3	1502.381	1502.659	-185.256	0.522	1432.267	0.470	27	0.141	R.HSAIVEYVFSGHR.F
R2/RRR2-3/2	1287.078	1286.503	-331.007	0.346	1045.697	0.448	16	0.136	R.VASIQQQLASLK.L
R2/RRR2-3/2	1326.165	1326.479	-237.328	0.485	961.651	0.409	17	0.130	R.TGTFLGSLWESK.T
R2/RRR2-3/2	1212.814	1213.324	-1248.944	0.371	1054.432	0.370	15	0.129	K.FYVQTVGDQR.V
R2/RRR2-3/2	1326.396	1326.479	-63.287	0.461	838.532	0.411	17	0.125	R.TGTFLGSLWESK.T
R2/RRR2-3/2	1287.225	1286.503	-216.734	0.383	741.180	0.445	15	0.122	R.VASIQQQLASLK.L
R2/RRR2-3/3	1502.207	1502.659	-301.177	0.538	1280.768	0.441	26	0.120	R.HSAIVEYVFSGHR.F
R2/RRR2-3/2	1058.010	1058.254	-230.939	0.348	567.278	0.475	14	0.119	K.VVVTEVLGGGK.F
R2/RRR2-3/2	1326.222	1326.479	-194.759	0.436	741.823	0.387	16	0.118	R.TGTFLGSLWESK.T
R2/RRR2-3/2	1263.283	1263.473	-150.381	0.373	870.935	0.341	13	0.116	K.ARDFLPFLQR.N
R2/RRR2-4/2	1057.978	1058.254	-261.382	0.273	658.484	0.415	15	0.114	K.VVVTEVLGGGK.F
R2/RRR2-4/2	1057.973	1058.254	-266.360	0.289	551.256	0.450	13	0.112	-.VVVTEVLGGGK.-
R2/RRR2-3/2	1460.746	1461.595	-1269.556	0.292	868.499	0.263	16	0.105	K.ETCSIAFSFSGVR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1058.159	1058.254	-89.165	0.185	409.850	0.296	14	0.101	-.VVVTEVLGGGK.-
R2/RRR2-3/2	1418.439	1419.565	-1503.018	0.334	833.338	0.115	17	0.099	K.AALQNLEQFQEK.A
R2/RRR2-3/3	1549.169	1547.738	279.169	0.448	1309.859	0.299	25	0.092	R.KAALQNLEQFQEK.A
R2/RRR2-4/3	1502.881	1502.659	148.172	0.515	1071.670	0.371	24	0.091	R.HSAIVEYVFSGHR.F
R2/RRR2-4/2	1263.448	1263.473	-19.537	0.370	552.848	0.182	11	0.091	-.ARDFLPFLQR.-
R2/RRR2-3/3	1248.185	1248.330	-116.456	0.460	896.132	0.381	17	0.084	R.RDEKPDNFAR.E
R2/RRR2-2/2	1459.224	1459.670	-306.809	0.434	2271.510	0.592	25	0.334	K.LVAEAGIGTVASGVSK.G
R2/RRR2-2/2	1459.391	1459.670	-191.837	0.469	2203.418	0.555	24	0.309	K.LVAEAGIGTVASGVSK.G
R2/RRR2-2/2	1459.186	1459.670	-332.996	0.455	1941.494	0.522	24	0.253	K.LVAEAGIGTVASGVSK.G
R2/RRR2-2/2	1906.423	1907.199	-934.358	0.510	1892.220	0.461	26	0.228	R.FGVTPTFLVNAEQIEIK.I
R2/RRR2-2/2	1906.676	1907.199	-800.988	0.547	1622.198	0.503	25	0.202	R.FGVTPTFLVNAEQIEIK.I
R2/RRR2-2/2	1202.235	1202.343	-90.395	0.447	1747.494	0.405	19	0.198	R.NGSQLLVLSDR.S
R2/RRR2-2/2	1676.305	1676.807	-899.088	0.541	1680.866	0.400	23	0.183	K.ASDSANLDSTAELLLR.S
R2/RRR2-2/2	1906.987	1907.199	-111.498	0.534	1440.759	0.500	24	0.180	R.FGVTPTFLVNAEQIEIK.I
R2/RRR2-3/2	1906.899	1907.199	-157.539	0.461	1488.326	0.435	23	0.171	R.FGVTPTFLVNAEQIEIK.I
R2/RRR2-1/2	1907.668	1907.199	246.481	0.506	1420.563	0.460	23	0.169	R.FGVTPTFLVNAEQIEIK.I
R2/RRR2-2/2	1521.189	1521.699	-995.114	0.422	1412.155	0.416	19	0.162	K.VFTDEGLEVLGWR.T
R2/RRR2-2/2	1676.387	1676.807	-251.288	0.515	1440.972	0.414	21	0.161	K.ASDSANLDSTAELLLR.S
R2/RRR2-2/2	1852.444	1852.985	-834.286	0.533	897.910	0.594	20	0.150	K.SVASANPYGSWLQQSTR.S
R2/RRR2-2/2	1852.246	1852.985	-941.923	0.521	877.861	0.596	20	0.149	K.SVASANPYGSWLQQSTR.S
R2/RRR2-2/2	1521.022	1521.699	-1105.665	0.374	1204.061	0.417	18	0.144	K.VFTDEGLEVLGWR.T
R2/RRR2-2/2	1143.802	1144.303	-1316.914	0.416	1054.923	0.413	17	0.136	K.IGGLTLDELGR.E
R2/RRR2-2/2	1143.830	1144.303	-415.277	0.464	850.599	0.465	15	0.131	-.IGGLTLDELGR.-
R2/RRR2-2/2	1614.770	1615.762	-1237.552	0.529	1042.388	0.387	17	0.130	K.YPEVIDFYDYYK.G
R2/RRR2-2/2	1218.453	1219.321	-1537.184	0.439	1219.727	0.294	18	0.129	K.VLCDEADAAVR.N
R2/RRR2-2/2	1275.809	1276.379	-1233.916	0.347	914.261	0.446	18	0.128	K.GLQNGDTATSAIK.Q
R2/RRR2-2/2	1218.375	1219.321	-1601.798	0.392	1085.417	0.312	18	0.124	K.VLCDEADAAVR.N
R2/RRR2-2/2	1048.742	1049.245	-1437.800	0.402	799.294	0.365	15	0.119	K.YLLSSAGLPK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/3	1906.939	1907.199	-136.740	0.458	1188.876	0.450	26	0.116	R.FGVTPTFLVNAEQIEIK.I
R2/RRR2-2/2	1520.388	1521.699	-1524.236	0.273	1075.081	0.267	17	0.114	K.VFTDEGLEVLGWR.T
R2/RRR2-2/2	1155.929	1156.273	-298.549	0.293	1111.138	0.230	14	0.113	K.TFQIYNVDR.A
R2/RRR2-2/2	1049.336	1049.245	86.972	0.403	494.604	0.365	13	0.113	K.YLLSSAGLPK.W
R2/RRR2-2/3	1636.765	1636.877	-68.836	0.428	1062.659	0.482	32	0.111	K.IAQGAKPGEGGQLPGKK.V
R2/RRR2-2/3	1636.869	1636.877	-5.439	0.429	1135.365	0.453	31	0.111	K.IAQGAKPGEGGQLPGKK.V
R2/RRR2-2/3	1636.767	1636.877	-67.602	0.460	962.438	0.505	30	0.110	K.IAQGAKPGEGGQLPGKK.V
R2/RRR2-1/2	1677.304	1676.807	297.049	0.445	911.263	0.303	18	0.109	K.ASDSANLDSTAELLLR.S
R2/RRR2-2/2	1201.827	1202.343	-1264.946	0.322	458.231	0.378	13	0.108	-.NGSQLLVLSDR.-
R2/RRR2-3/2	1675.643	1676.807	-1295.693	0.294	884.368	0.200	19	0.102	K.ASDSANLDSTAELLLR.S
R2/RRR2-2/3	1508.463	1508.705	-160.443	0.381	925.492	0.401	27	0.088	K.IAQGAKPGEGGQLPGK.K
R2/RRR2-2/3	1508.507	1508.705	-131.098	0.359	944.481	0.363	28	0.083	K.IAQGAKPGEGGQLPGK.K
R2/RRR2-2/3	1508.464	1508.705	-160.078	0.310	989.051	0.336	27	0.080	K.IAQGAKPGEGGQLPGK.K
R2/RRR2-2/3	1906.709	1907.199	-257.832	0.381	690.053	0.248	23	0.062	-.FGVTPTFLVNAEQIEIK.-
R2/RRR2-11/2	1909.217	1910.047	-961.271	0.543	1567.780	0.548	25	0.208	K.ESGMTLITAEDLDDAAEK.A
R2/RRR2-11/3	1620.649	1619.824	-108.162	0.496	2103.201	0.350	31	0.193	R.LNIHEYQGAELM*GK.Y
R2/RRR2-11/2	1292.384	1292.616	-179.828	0.553	1441.608	0.526	17	0.190	K.AILVNIFGGIM*K.C
R2/RRR2-11/2	1474.342	1474.642	-203.594	0.508	1571.979	0.447	22	0.184	R.GAAAGSVEEVKNTLK.N
R2/RRR2-11/2	1925.524	1926.046	-793.005	0.475	1329.221	0.517	25	0.174	K.ESGM*TLITAEDLDDAAEK.A
R2/RRR2-11/2	1619.242	1619.824	-979.882	0.467	1024.177	0.560	19	0.155	R.LNIHEYQGAELM*GK.Y
R2/RRR2-11/2	1619.112	1619.824	-1060.723	0.463	1066.588	0.514	20	0.151	R.LNIHEYQGAELM*GK.Y
R2/RRR2-11/2	1019.042	1019.284	-238.350	0.470	1185.499	0.333	16	0.134	K.M*LGQILVTK.Q
R2/RRR2-11/2	1474.307	1474.642	-227.516	0.465	1172.095	0.373	20	0.134	R.GAAAGSVEEVKNTLK.N
R2/RRR2-11/2	1003.134	1003.285	-150.079	0.478	926.547	0.404	15	0.132	K.MLGQILVTK.Q
R2/RRR2-11/2	818.810	818.943	-163.004	0.410	734.947	0.494	11	0.131	K.YGINVPR.G
R2/RRR2-11/2	1184.014	1183.255	-204.087	0.481	875.012	0.421	16	0.130	K.LNFDDNAAFR.Q
R2/RRR2-11/2	1317.233	1318.495	-1722.230	0.331	1053.265	0.394	18	0.129	K.CDVIASGIVNAAK.Q
R2/RRR2-11/2	1003.013	1003.285	-271.433	0.457	929.130	0.378	15	0.128	K.MLGQILVTK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1018.984	1019.284	-294.836	0.455	1073.862	0.321	16	0.127	K.M*LGQILVTK.Q
R2/RRR2-11/2	817.900	817.995	-116.256	0.390	368.163	0.526	11	0.127	K.VPIDVFK.G
R2/RRR2-11/2	1004.153	1003.285	-131.759	0.484	817.707	0.404	14	0.127	K.MLGQILVTK.Q
R2/RRR2-11/2	1094.770	1095.277	-1380.928	0.445	994.974	0.377	15	0.126	K.SGLQGGVHIVK.A
R2/RRR2-11/2	817.906	817.995	-109.369	0.432	360.728	0.530	11	0.126	-.VPIDVFK.-
R2/RRR2-11/2	1388.638	1389.622	-1432.379	0.401	1014.105	0.354	18	0.125	K.NVFPSEKEIVVK.S
R2/RRR2-11/2	1094.984	1095.277	-268.650	0.401	894.484	0.388	15	0.123	K.SGLQGGVHIVK.A
R2/RRR2-11/2	1532.277	1531.607	-216.352	0.468	688.059	0.427	20	0.122	R.DTTQEDPREVAAAK.A
R2/RRR2-11/3	1619.713	1619.824	-68.501	0.502	1381.765	0.402	28	0.119	R.LNIHEYQGAELM*GK.Y
R2/RRR2-11/2	1389.361	1389.622	-188.287	0.395	1025.870	0.288	18	0.118	K.NVFPSEKEIVVK.S
R2/RRR2-11/2	1531.363	1531.607	-159.714	0.421	674.488	0.382	19	0.116	R.DTTQEDPREVAAAK.A
R2/RRR2-11/3	1604.654	1603.825	-106.685	0.502	1189.488	0.451	26	0.115	R.LNIHEYQGAELMGK.Y
R2/RRR2-11/2	1473.714	1474.642	-1311.804	0.409	940.200	0.327	18	0.115	R.GAAAGSVEEVKNTLK.N
R2/RRR2-11/2	817.624	817.995	-455.172	0.336	376.630	0.411	11	0.115	-.VPIDVFK.-
R2/RRR2-11/2	1531.276	1531.607	-216.973	0.415	456.149	0.397	17	0.114	R.DTTQEDPREVAAAK.A
R2/RRR2-11/3	1604.191	1603.825	229.105	0.502	1166.348	0.451	26	0.113	R.LNIHEYQGAELMGK.Y
R2/RRR2-11/2	1095.132	1095.277	-133.335	0.393	793.974	0.333	14	0.113	K.SGLQGGVHIVK.A
R2/RRR2-11/2	1389.205	1389.622	-300.768	0.389	811.333	0.289	16	0.110	K.NVFPSEKEIVVK.S
R2/RRR2-11/2	1183.557	1183.255	256.177	0.326	690.355	0.256	15	0.107	K.LNFDDNAAFR.Q
R2/RRR2-11/3	1619.145	1619.824	-1040.292	0.433	836.721	0.353	24	0.080	R.LNIHEYQGAELM*GK.Y
R2/RRR2-3/2	1602.264	1601.825	274.817	0.556	2137.652	0.460	22	0.266	R.FNAILEELGIEQPK.G
R2/RRR2-3/2	1601.488	1601.825	-211.130	0.541	2198.901	0.426	22	0.266	R.FNAILEELGIEQPK.G
R2/RRR2-3/2	1601.152	1601.825	-1048.190	0.433	2174.511	0.429	22	0.265	R.FNAILEELGIEQPK.G
R2/RRR2-3/2	1657.948	1656.818	78.677	0.557	1705.124	0.491	20	0.213	R.GLDQLSKDDFYQVK.R
R2/RRR2-3/2	1745.804	1746.041	-136.169	0.555	1469.862	0.598	23	0.209	K.LPLNGTVFLSLNDLTK.R
R2/RRR2-3/2	1141.694	1142.331	-1437.525	0.467	1589.333	0.510	18	0.202	K.VPIITTVDGAR.A
R2/RRR2-3/2	1634.355	1633.698	-210.705	0.458	1296.291	0.521	22	0.172	K.IWGTSPDSIDAAEDR.K
R2/RRR2-3/2	1141.591	1142.331	-1528.604	0.393	1351.284	0.475	18	0.168	K.VPIITTVDGAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1633.172	1633.698	-937.002	0.446	1276.256	0.507	22	0.167	K.IWGTSPDSIDAAEDR.K
R2/RRR2-3/2	1535.407	1534.865	-299.321	0.509	1251.333	0.479	21	0.161	K.VLQLEGIPVEPVLK.I
R2/RRR2-3/2	1560.985	1559.831	98.389	0.472	1137.692	0.470	18	0.149	K.LALPIQQYLEDKK.L
R2/RRR2-3/2	1745.667	1746.041	-214.453	0.535	946.528	0.555	19	0.147	K.LPLNGTVFLSLNDLTK.R
R2/RRR2-3/2	1778.369	1777.996	210.356	0.526	967.567	0.523	20	0.144	K.LSVGYTLDQIPNDITK.K
R2/RRR2-3/2	1534.455	1534.865	-267.749	0.368	1036.511	0.455	19	0.137	K.VLQLEGIPVEPVLK.I
R2/RRR2-3/2	1422.425	1422.608	-128.994	0.396	1003.875	0.435	18	0.132	R.ELGFNIIATSGTAK.V
R2/RRR2-3/2	1777.215	1777.996	-1005.457	0.441	750.999	0.468	20	0.125	K.LSVGYTLDQIPNDITK.K
R2/RRR2-3/2	1007.043	1007.147	-103.803	0.382	913.740	0.372	15	0.122	K.SVGEAM*ALGR.T
R2/RRR2-3/2	1105.284	1105.309	-22.555	0.349	937.520	0.372	13	0.121	R.LALEVAPTYK.R
R2/RRR2-3/2	1533.789	1534.865	-1357.493	0.344	857.218	0.380	18	0.118	K.VLQLEGIPVEPVLK.I
R2/RRR2-3/2	1141.372	1142.331	-1721.449	0.355	602.173	0.438	13	0.116	K.VPIITTVDGAR.A
R2/RRR2-3/2	1206.392	1206.419	-23.100	0.475	930.827	0.292	14	0.114	R.LRDYSVAIIR.E
R2/RRR2-3/2	995.349	996.189	-1853.569	0.327	844.057	0.304	14	0.112	K.VLILGGGPNR.I
R2/RRR2-3/2	1104.984	1105.309	-295.138	0.293	734.378	0.303	13	0.108	R.LALEVAPTYK.R
R2/RRR2-3/2	1422.272	1422.608	-237.045	0.305	598.522	0.384	15	0.108	R.ELGFNIIATSGTAK.V
R2/RRR2-3/2	995.315	996.189	-1887.953	0.327	697.417	0.258	13	0.106	K.VLILGGGPNR.I
R2/RRR2-2/2	1207.225	1206.419	-161.725	0.360	1039.770	0.171	13	0.104	R.LRDYSVAIIR.E
R2/RRR2-3/2	1561.094	1559.831	168.969	0.319	393.970	0.335	12	0.103	K.LALPIQQYLEDKK.L
R2/RRR2-3/2	1206.844	1206.419	352.990	0.443	795.234	0.212	13	0.102	R.LRDYSVAIIR.E
R2/RRR2-3/2	995.979	996.189	-211.393	0.403	678.206	0.204	13	0.102	-.VLILGGGPNR.-
R2/RRR2-3/2	1207.268	1206.419	-125.818	0.344	655.796	0.176	12	0.096	-.LRDYSVAIIR.-
R2/RRR2-3/2	1105.170	1105.309	-125.920	0.280	485.364	0.242	10	0.073	-.LALEVAPTYK.-
R2/RRR2-8/2	1911.440	1911.020	220.437	0.617	3025.904	0.511	27	0.472	R.TGELIAHVAEGDAEDINR.A
R2/RRR2-8/3	1911.009	1911.020	-5.876	0.556	2880.707	0.447	36	0.422	R.TGELIAHVAEGDAEDINR.A
R2/RRR2-8/2	1910.486	1911.020	-805.351	0.574	2764.771	0.494	26	0.403	R.TGELIAHVAEGDAEDINR.A
R2/RRR2-8/2	1910.398	1911.020	-851.469	0.553	2665.826	0.472	26	0.372	R.TGELIAHVAEGDAEDINR.A
R2/RRR2-8/3	1912.016	1911.020	-1.967	0.523	2709.735	0.420	34	0.366	R.TGELIAHVAEGDAEDINR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1481.163	1481.550	-261.594	0.504	2325.267	0.584	25	0.341	K.YGVDSGANLVTGGDR.L
R2/RRR2-8/2	1481.012	1481.550	-1041.621	0.477	2151.217	0.544	24	0.295	K.YGVDSGANLVTGGDR.L
R2/RRR2-8/2	1481.110	1481.550	-297.894	0.462	2096.274	0.531	24	0.281	K.YGVDSGANLVTGGDR.L
R2/RRR2-9/2	1481.163	1481.550	-261.677	0.443	1842.719	0.491	22	0.229	K.YGVDSGANLVTGGDR.L
R2/RRR2-8/2	1818.345	1818.879	-846.363	0.559	1664.236	0.567	23	0.224	K.NGVEQGPQIDDEQFNK.I
R2/RRR2-8/2	1819.232	1818.879	194.729	0.611	1495.854	0.588	22	0.206	K.NGVEQGPQIDDEQFNK.I
R2/RRR2-8/2	1400.293	1399.655	-258.777	0.560	1389.392	0.579	21	0.195	K.VGPALACGNTVVLK.T
R2/RRR2-8/2	1399.294	1399.655	-258.175	0.507	1371.964	0.528	21	0.181	K.VGPALACGNTVVLK.T
R2/RRR2-8/2	1465.643	1464.645	-1.805	0.533	1216.866	0.583	20	0.178	K.TAEQTPLSALFASK.L
R2/RRR2-8/2	1818.457	1818.879	-233.070	0.544	1266.819	0.527	21	0.168	K.NGVEQGPQIDDEQFNK.I
R2/RRR2-8/2	1399.240	1399.655	-297.298	0.468	1276.369	0.515	20	0.168	K.VGPALACGNTVVLK.T
R2/RRR2-8/2	1247.661	1248.413	-1408.561	0.486	1382.099	0.408	17	0.160	K.FNDLNEVIKR.A
R2/RRR2-8/3	1820.019	1818.879	77.113	0.551	1573.248	0.461	29	0.159	K.NGVEQGPQIDDEQFNK.I
R2/RRR2-8/3	1672.941	1672.947	-3.273	0.428	1609.611	0.428	28	0.155	K.IAQEEIFGPVQSILK.F
R2/RRR2-8/3	1464.452	1464.645	-132.283	0.497	1384.435	0.525	25	0.155	K.TAEQTPLSALFASK.L
R2/RRR2-8/3	1673.809	1672.947	-82.637	0.427	1388.137	0.501	27	0.148	K.IAQEEIFGPVQSILK.F
R2/RRR2-9/2	1464.186	1464.645	-314.967	0.445	994.699	0.525	19	0.147	K.TAEQTPLSALFASK.L
R2/RRR2-8/2	1379.137	1378.599	-335.545	0.496	1395.330	0.337	17	0.144	K.GIDSLKNYLQVK.A
R2/RRR2-8/2	1398.612	1399.655	-1464.622	0.448	1099.542	0.423	19	0.138	K.VGPALACGNTVVLK.T
R2/RRR2-8/2	1819.425	1818.879	-250.240	0.511	1065.487	0.456	19	0.138	K.NGVEQGPQIDDEQFNK.I
R2/RRR2-8/2	1377.487	1378.599	-1537.302	0.437	1432.459	0.267	18	0.137	K.GIDSLKNYLQVK.A
R2/RRR2-9/2	1673.783	1672.947	-97.992	0.538	1289.816	0.352	19	0.134	K.IAQEEIFGPVQSILK.F
R2/RRR2-8/2	1248.154	1248.413	-207.921	0.472	1199.168	0.334	16	0.133	K.FNDLNEVIKR.A
R2/RRR2-8/2	1247.663	1248.413	-1406.595	0.477	1105.322	0.358	16	0.132	K.FNDLNEVIKR.A
R2/RRR2-8/3	1464.289	1464.645	-244.049	0.509	1281.718	0.484	25	0.132	K.TAEQTPLSALFASK.L
R2/RRR2-8/2	1378.290	1378.599	-224.889	0.435	1381.082	0.248	17	0.129	K.GIDSLKNYLQVK.A
R2/RRR2-9/2	1673.789	1672.947	-94.261	0.507	1223.260	0.338	19	0.129	K.IAQEEIFGPVQSILK.F
R2/RRR2-8/2	1175.159	1175.318	-135.090	0.442	864.404	0.435	14	0.129	R.KAFDEGPWPK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1672.559	1672.947	-232.465	0.529	997.981	0.406	19	0.127	K.IAQEEIFGPVQSILK.F
R2/RRR2-8/3	1175.652	1175.318	285.643	0.587	1165.986	0.511	20	0.126	R.KAFDEGPWPK.M
R2/RRR2-8/2	885.050	885.086	-40.825	0.505	603.949	0.388	13	0.123	K.IVLELAAR.S
R2/RRR2-9/2	1673.525	1672.947	-252.889	0.482	1088.696	0.338	18	0.121	K.IAQEEIFGPVQSILK.F
R2/RRR2-8/2	884.986	885.086	-114.153	0.468	603.104	0.364	13	0.121	K.IVLELAAR.S
R2/RRR2-8/2	884.970	885.086	-131.725	0.467	605.665	0.357	13	0.120	K.IVLELAAR.S
R2/RRR2-8/2	1091.451	1092.227	-1631.693	0.398	1206.518	0.228	14	0.119	K.FNDLNEVIK.R
R2/RRR2-8/2	1097.616	1098.188	-1436.467	0.293	806.069	0.406	16	0.118	K.IAFTGSTDTGK.I
R2/RRR2-8/2	884.893	885.086	-219.182	0.446	622.759	0.336	13	0.118	K.IVLELAAR.S
R2/RRR2-8/2	1175.072	1175.318	-209.704	0.401	648.037	0.386	13	0.116	R.KAFDEGPWPK.M
R2/RRR2-8/2	1093.016	1092.227	-193.746	0.468	1210.354	0.206	14	0.115	K.FNDLNEVIK.R
R2/RRR2-8/3	1175.548	1175.318	196.930	0.569	1022.625	0.501	19	0.114	R.KAFDEGPWPK.M
R2/RRR2-8/2	1174.537	1175.318	-1520.647	0.350	696.597	0.346	13	0.112	R.KAFDEGPWPK.M
R2/RRR2-8/3	1465.102	1464.645	312.278	0.488	958.665	0.505	23	0.110	K.TAEQTPLSALFASK.L
R2/RRR2-8/2	1092.007	1092.227	-201.886	0.412	992.444	0.225	13	0.109	K.FNDLNEVIK.R
R2/RRR2-8/3	1820.011	1818.879	72.774	0.477	1329.448	0.369	27	0.109	K.NGVEQGPQIDDEQFNK.I
R2/RRR2-8/2	1097.278	1098.188	-1746.104	0.257	733.933	0.297	15	0.106	K.IAFTGSTDTGK.I
R2/RRR2-8/2	1672.650	1672.947	-177.919	0.408	513.893	0.304	16	0.106	K.IAQEEIFGPVQSILK.F
R2/RRR2-2/2	1674.114	1672.947	100.443	0.449	550.093	0.322	15	0.105	K.IAQEEIFGPVQSILK.F
R2/RRR2-4/2	1674.113	1672.947	99.712	0.424	452.432	0.283	15	0.103	-.IAQEEIFGPVQSILK.-
R2/RRR2-8/2	1673.175	1672.947	137.014	0.440	710.403	0.291	15	0.101	-.IAQEEIFGPVQSILK.-
R2/RRR2-8/3	1378.301	1378.599	-216.591	0.509	941.840	0.444	28	0.096	K.GIDSLKNYLQVK.A
R2/RRR2-8/3	1175.409	1175.318	78.049	0.515	828.438	0.428	18	0.091	R.KAFDEGPWPK.M
R2/RRR2-8/3	1378.489	1378.599	-79.602	0.501	894.835	0.384	27	0.086	K.GIDSLKNYLQVK.A
R2/RRR2-8/3	1378.686	1378.599	63.477	0.461	828.940	0.394	27	0.085	K.GIDSLKNYLQVK.A
R2/RRR2-1/3	1910.903	1911.020	-61.043	0.280	1267.920	0.262	28	0.085	R.TGELIAHVAEGDAEDINR.A
R2/RRR2-14/2	1367.142	1367.556	-304.342	0.569	2071.336	0.557	22	0.283	K.FDVGNVVM*VTGGR.N
R2/RRR2-14/2	1368.389	1367.556	-122.431	0.539	1806.798	0.579	21	0.248	K.FDVGNVVM*VTGGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1367.250	1367.556	-224.977	0.539	1796.709	0.549	22	0.239	K.FDVGNVVM*VTGGR.N
R2/RRR2-14/2	1351.359	1351.557	-146.922	0.489	1743.890	0.500	22	0.218	K.FDVGNVVMVTGGR.N
R2/RRR2-14/2	1351.184	1351.557	-276.610	0.525	1693.426	0.516	21	0.215	K.FDVGNVVMVTGGR.N
R2/RRR2-14/3	1484.050	1483.818	156.652	0.566	2195.062	0.298	26	0.188	K.SRECLPLILIIR.N
R2/RRR2-13/2	949.395	949.129	281.318	0.466	1048.012	0.553	15	0.159	R.LGNVFTIGK.G
R2/RRR2-14/2	1350.905	1351.557	-1226.773	0.477	1317.763	0.450	18	0.159	K.FDVGNVVMVTGGR.N
R2/RRR2-14/2	948.477	949.129	-1746.762	0.406	1068.638	0.526	15	0.154	R.LGNVFTIGK.G
R2/RRR2-14/2	949.037	949.129	-97.482	0.448	992.847	0.537	15	0.152	R.LGNVFTIGK.G
R2/RRR2-14/2	948.985	949.129	-152.450	0.483	990.346	0.514	15	0.150	R.LGNVFTIGK.G
R2/RRR2-13/2	949.146	949.129	18.626	0.411	986.320	0.529	15	0.149	R.LGNVFTIGK.G
R2/RRR2-15/2	949.405	949.129	291.632	0.427	1082.007	0.480	15	0.149	R.LGNVFTIGK.G
R2/RRR2-14/2	1104.694	1105.334	-1488.528	0.397	1049.877	0.438	14	0.139	R.EVISILM*QR.H
R2/RRR2-14/2	1483.781	1483.818	-25.135	0.512	1164.578	0.367	17	0.133	K.SRECLPLILIIR.N
R2/RRR2-14/2	1104.538	1105.334	-1630.514	0.363	1116.059	0.328	14	0.127	R.EVISILM*QR.H
R2/RRR2-14/2	1483.423	1483.818	-266.808	0.485	1039.940	0.353	17	0.125	K.SRECLPLILIIR.N
R2/RRR2-14/2	1088.941	1089.334	-362.226	0.385	968.644	0.365	13	0.124	R.EVISILMQR.H
R2/RRR2-14/2	1548.243	1548.805	-1011.889	0.452	855.221	0.400	18	0.123	K.IDLETNKIVDFIK.F
R2/RRR2-14/2	1556.255	1555.820	280.641	0.448	317.349	0.477	19	0.123	K.TYPAGFM*DVISIPK.T
R2/RRR2-14/3	1475.473	1475.626	-104.201	0.461	1036.308	0.527	25	0.118	K.ANDTIKIDLETNK.I
R2/RRR2-14/2	1548.336	1548.805	-304.334	0.426	979.977	0.308	19	0.118	K.IDLETNKIVDFIK.F
R2/RRR2-14/2	1089.115	1089.334	-202.084	0.356	850.027	0.330	13	0.116	R.EVISILMQR.H
R2/RRR2-14/2	1555.554	1555.820	-171.732	0.368	266.743	0.484	15	0.116	K.TYPAGFM*DVISIPK.T
R2/RRR2-14/3	1484.512	1483.818	-206.785	0.583	1532.309	0.331	25	0.113	K.SRECLPLILIIR.N
R2/RRR2-14/2	1555.273	1555.820	-997.336	0.292	203.159	0.306	16	0.113	K.TYPAGFM*DVISIPK.T
R2/RRR2-14/2	987.824	988.120	-300.458	0.494	922.036	0.247	13	0.112	K.LSIIEEQR.K
R2/RRR2-14/2	987.811	988.120	-313.848	0.507	957.669	0.242	13	0.112	K.LSIIEEQR.K
R2/RRR2-14/2	987.430	988.120	-1716.726	0.402	895.104	0.230	13	0.110	K.LSIIEEQR.K
R2/RRR2-14/2	1483.543	1483.818	-185.577	0.468	956.096	0.271	16	0.110	K.SRECLPLILIIR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1539.341	1539.820	-312.714	0.278	345.265	0.402	16	0.109	K.TYPAGFMDVISIPK.T
R2/RRR2-14/3	1484.113	1483.818	199.586	0.534	1583.951	0.287	25	0.108	K.SRECLPLILIIR.N
R2/RRR2-14/2	1548.099	1548.805	-1105.624	0.434	987.255	0.216	19	0.107	K.IDLETNKIVDFIK.F
R2/RRR2-14/3	1475.264	1475.626	-246.756	0.481	793.665	0.539	23	0.106	K.ANDTIKIDLETNK.I
R2/RRR2-14/3	1216.327	1216.454	-104.659	0.510	1460.581	0.299	24	0.097	R.TIRYPDPIIK.A
R2/RRR2-14/3	1451.278	1451.655	-260.199	0.335	666.483	0.495	25	0.090	K.LGGAFAPKPSSGPHK.A
R2/RRR2-14/3	1216.598	1216.454	118.480	0.425	1257.462	0.307	23	0.087	R.TIRYPDPIIK.A
R2/RRR2-14/3	1883.908	1884.186	-147.836	0.422	1139.771	0.309	26	0.084	R.TDKTYPAGFMDVISIPK.T
R2/RRR2-14/3	1452.729	1451.655	51.266	0.340	628.276	0.428	24	0.082	K.LGGAFAPKPSSGPHK.A
R2/RRR2-14/3	1216.563	1216.454	89.347	0.507	965.641	0.321	21	0.080	R.TIRYPDPIIK.A
R2/RRR2-14/3	1216.203	1216.454	-207.505	0.434	949.306	0.311	21	0.078	R.TIRYPDPIIK.A
R2/RRR2-14/3	1451.660	1451.655	3.777	0.278	531.428	0.364	22	0.074	K.LGGAFAPKPSSGPHK.A
R2/RRR2-14/3	1216.386	1216.454	-56.490	0.451	966.924	0.269	21	0.073	R.TIRYPDPIIK.A
R2/RRR2-13/3	1451.288	1451.655	-253.617	0.298	561.928	0.314	22	0.072	K.LGGAFAPKPSSGPHK.A
R2/RRR2-14/3	1898.652	1900.185	-1866.124	0.288	720.229	0.248	24	0.064	R.TDKTYPAGFM*DVISIPK.T
R2/RRR2-8/1	1030.591	1031.142	-1509.264	0.210	839.743	0.217	12	0.631	K.AIDDAEGLVK.V
R2/RRR2-8/2	1835.441	1836.033	-869.565	0.549	2289.583	0.602	27	0.341	R.VPYTAGIGLESVGVETDK.A
R2/RRR2-8/2	1836.539	1836.033	-269.642	0.594	2147.098	0.594	27	0.310	R.VPYTAGIGLESVGVETDK.A
R2/RRR2-8/2	1948.389	1948.118	139.466	0.545	1831.405	0.586	27	0.253	K.LASPSEVSVDLSDGGSTVVK.G
R2/RRR2-8/2	1835.422	1836.033	-880.247	0.557	1804.291	0.556	25	0.241	R.VPYTAGIGLESVGVETDK.A
R2/RRR2-8/2	1947.309	1948.118	-931.842	0.524	1657.973	0.609	26	0.233	K.LASPSEVSVDLSDGGSTVVK.G
R2/RRR2-8/2	1947.609	1948.118	-777.302	0.524	1675.377	0.550	26	0.220	K.LASPSEVSVDLSDGGSTVVK.G
R2/RRR2-8/2	1576.224	1575.823	255.433	0.474	1585.178	0.454	22	0.188	K.IVSSTGALCLSEIPK.K
R2/RRR2-8/2	1131.001	1131.305	-269.080	0.440	1555.728	0.441	18	0.183	K.NIIIATGSDVK.S
R2/RRR2-8/2	1362.070	1362.511	-325.097	0.465	1313.904	0.511	19	0.172	K.TKVVGVDTSGDGVK.L
R2/RRR2-8/2	1130.543	1131.305	-1562.493	0.369	1464.904	0.420	18	0.168	K.NIIIATGSDVK.S
R2/RRR2-8/2	1451.289	1451.603	-216.951	0.518	1064.973	0.470	19	0.146	R.TCHAHPTVSEALK.E
R2/RRR2-8/2	1130.400	1131.305	-1690.284	0.384	1021.082	0.446	16	0.137	K.NIIIATGSDVK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1030.876	1031.142	-258.752	0.428	911.773	0.457	17	0.136	K.AIDDAEGLVK.V
R2/RRR2-8/2	1030.913	1031.142	-222.401	0.453	838.553	0.468	17	0.135	K.AIDDAEGLVK.V
R2/RRR2-8/2	1575.207	1575.823	-1028.612	0.351	1227.528	0.341	20	0.133	K.IVSSTGALCLSEIPK.K
R2/RRR2-8/2	1030.535	1031.142	-1564.189	0.475	839.446	0.421	17	0.130	K.AIDDAEGLVK.V
R2/RRR2-8/2	1132.911	1133.234	-286.458	0.449	619.355	0.490	17	0.127	K.VVGVDTSGDGVK.L
R2/RRR2-8/2	1575.366	1575.823	-291.029	0.390	1155.142	0.316	20	0.125	K.IVSSTGALCLSEIPK.K
R2/RRR2-8/2	1186.952	1187.368	-351.399	0.371	356.154	0.418	17	0.118	K.SLPGVTIDEKK.I
R2/RRR2-8/2	1187.034	1187.368	-282.267	0.352	255.246	0.461	15	0.118	K.SLPGVTIDEKK.I
R2/RRR2-8/2	1132.554	1133.234	-1487.720	0.379	548.750	0.411	16	0.116	K.VVGVDTSGDGVK.L
R2/RRR2-8/2	1132.469	1133.234	-1563.621	0.318	548.095	0.373	16	0.111	K.VVGVDTSGDGVK.L
R2/RRR2-8/2	917.845	918.075	-251.265	0.355	789.599	0.284	12	0.109	-.FPLLANSR.-
R2/RRR2-8/2	917.363	918.075	-1871.404	0.358	778.805	0.272	12	0.108	-.FPLLANSR.-
R2/RRR2-8/3	1541.380	1540.729	-226.854	0.509	982.305	0.478	26	0.106	K.ALLHSSHM*YHEAK.S
R2/RRR2-8/3	1949.617	1948.118	256.494	0.431	941.991	0.442	29	0.095	K.LASPSEVSVDLSDGGSTVVK.G
R2/RRR2-8/3	1541.228	1540.729	324.761	0.475	696.010	0.423	22	0.085	K.ALLHSSHM*YHEAK.S
R2/RRR2-8/3	1202.377	1202.431	-44.980	0.458	873.829	0.287	19	0.073	R.VGKFPLLANSR.A
R2/RRR2-8/3	1202.601	1202.431	141.646	0.456	1002.937	0.254	22	0.072	R.VGKFPLLANSR.A
R2/RRR2-8/3	1202.203	1202.431	-190.113	0.407	855.987	0.216	20	0.063	-.VGKFPLLANSR.-
R2/RRR2-8/2	1688.540	1689.011	-279.499	0.505	2335.755	0.560	23	0.331	K.SALGILMNLGLIEESK.I
R2/RRR2-8/2	1704.989	1705.010	-12.414	0.570	2228.074	0.531	23	0.299	K.SALGILM*NLGLIEESK.I
R2/RRR2-8/2	1705.031	1705.010	12.288	0.550	2115.435	0.560	22	0.288	K.SALGILM*NLGLIEESK.I
R2/RRR2-8/2	1688.571	1689.011	-261.294	0.466	1982.890	0.494	22	0.248	K.SALGILMNLGLIEESK.I
R2/RRR2-7/2	1705.387	1705.010	221.637	0.566	1768.106	0.603	21	0.244	K.SALGILM*NLGLIEESK.I
R2/RRR2-7/2	1604.255	1603.761	308.515	0.473	1781.215	0.457	22	0.209	K.GFLTINSQPAVNGER.S
R2/RRR2-8/2	1704.184	1705.010	-1075.003	0.453	1684.186	0.446	20	0.193	K.SALGILM*NLGLIEESK.I
R2/RRR2-8/2	1604.220	1603.761	287.075	0.479	1443.556	0.470	21	0.173	K.GFLTINSQPAVNGER.S
R2/RRR2-8/2	1888.666	1889.052	-205.217	0.486	1443.439	0.466	22	0.172	K.LTSSPWSELDGLQPETK.I
R2/RRR2-8/2	1888.647	1889.052	-215.462	0.492	1370.551	0.473	21	0.165	K.LTSSPWSELDGLQPETK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1199.149	1199.381	-193.547	0.477	1488.917	0.392	16	0.165	K.LQEEWAVPVK.S
R2/RRR2-7/2	1199.027	1199.381	-295.987	0.462	1385.450	0.430	15	0.162	K.LQEEWAVPVK.S
R2/RRR2-8/2	1889.460	1889.052	216.586	0.499	1283.917	0.497	21	0.162	K.LTSSPWSELDGLQPETK.I
R2/RRR2-8/2	1845.268	1845.946	-912.375	0.484	1078.004	0.589	21	0.161	R.SDSTSVGWGGPGGYVYQK.A
R2/RRR2-8/2	1845.403	1845.946	-838.730	0.517	1110.454	0.553	21	0.157	R.SDSTSVGWGGPGGYVYQK.A
R2/RRR2-8/2	1604.398	1603.761	-227.154	0.500	1271.885	0.458	21	0.155	K.GFLTINSQPAVNGER.S
R2/RRR2-8/2	1330.272	1330.433	-121.087	0.450	1180.615	0.465	17	0.153	R.TLGWDQYPHGR.W
R2/RRR2-7/2	1845.305	1845.946	-892.120	0.495	1139.092	0.517	21	0.153	R.SDSTSVGWGGPGGYVYQK.A
R2/RRR2-7/2	1888.404	1889.052	-875.650	0.446	1317.390	0.429	20	0.152	K.LTSSPWSELDGLQPETK.I
R2/RRR2-8/2	1604.220	1603.761	286.617	0.533	1155.738	0.470	21	0.149	K.GFLTINSQPAVNGER.S
R2/RRR2-8/2	1845.263	1845.946	-914.700	0.479	1051.705	0.516	21	0.146	R.SDSTSVGWGGPGGYVYQK.A
R2/RRR2-7/2	1199.480	1199.381	82.822	0.441	1291.538	0.381	15	0.146	K.LQEEWAVPVK.S
R2/RRR2-8/2	1198.589	1199.381	-1499.224	0.339	1280.680	0.381	15	0.144	K.LQEEWAVPVK.S
R2/RRR2-7/2	1604.142	1603.761	237.783	0.462	1174.616	0.422	20	0.141	K.GFLTINSQPAVNGER.S
R2/RRR2-7/2	1199.035	1199.381	-288.939	0.460	1107.173	0.423	15	0.141	K.LQEEWAVPVK.S
R2/RRR2-8/2	1164.858	1165.313	-391.383	0.383	1310.546	0.309	14	0.137	K.AYLEFFCSK.E
R2/RRR2-7/2	1185.160	1185.359	-168.455	0.485	1042.336	0.391	18	0.134	K.SNGIQNVLALR.G
R2/RRR2-7/2	1889.521	1889.052	248.524	0.529	957.218	0.482	19	0.134	K.LTSSPWSELDGLQPETK.I
R2/RRR2-7/2	1705.855	1705.010	-91.360	0.508	711.647	0.568	17	0.133	K.SALGILM*NLGLIEESK.I
R2/RRR2-7/2	1604.154	1603.761	245.871	0.481	1037.291	0.414	20	0.132	K.GFLTINSQPAVNGER.S
R2/RRR2-7/2	1603.195	1603.761	-980.184	0.458	1144.064	0.364	20	0.130	K.GFLTINSQPAVNGER.S
R2/RRR2-7/2	1689.815	1689.011	-116.480	0.408	1013.925	0.438	16	0.129	K.SALGILMNLGLIEESK.I
R2/RRR2-7/2	1185.083	1185.359	-233.038	0.486	870.510	0.417	17	0.129	K.SNGIQNVLALR.G
R2/RRR2-25/2	989.459	990.133	-1696.501	0.412	906.569	0.387	15	0.128	K.IDDALTTIK.S
R2/RRR2-8/2	1603.193	1603.761	-981.025	0.483	1010.764	0.393	20	0.128	K.GFLTINSQPAVNGER.S
R2/RRR2-7/2	1603.051	1603.761	-1070.091	0.431	1077.802	0.363	20	0.127	K.GFLTINSQPAVNGER.S
R2/RRR2-7/2	1888.441	1889.052	-855.663	0.447	950.297	0.443	18	0.127	K.LTSSPWSELDGLQPETK.I
R2/RRR2-7/2	1325.153	1324.550	-299.968	0.471	545.750	0.490	17	0.127	K.AFPSLTYIAVNK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	990.017	990.133	-117.501	0.435	801.294	0.401	14	0.126	K.IDDALTTIK.S
R2/RRR2-7/2	1604.218	1603.761	285.778	0.435	1010.434	0.381	19	0.126	K.GFLTINSQPAVNGER.S
R2/RRR2-8/2	1198.588	1199.381	-1500.349	0.322	996.908	0.381	14	0.125	K.LQEEWAVPVK.S
R2/RRR2-25/2	1186.389	1185.359	25.737	0.469	958.742	0.379	15	0.125	K.SNGIQNVLALR.G
R2/RRR2-25/2	989.552	990.133	-1602.183	0.406	826.632	0.405	14	0.125	-.IDDALTTIK.-
R2/RRR2-25/2	989.522	990.133	-1632.546	0.424	810.219	0.386	14	0.124	K.IDDALTTIK.S
R2/RRR2-7/2	989.538	990.133	-1616.931	0.331	908.904	0.367	14	0.122	K.IDDALTTIK.S
R2/RRR2-7/2	1324.089	1324.550	-348.570	0.415	625.465	0.408	18	0.121	K.AFPSLTYIAVNK.D
R2/RRR2-8/2	989.430	990.133	-1726.002	0.363	887.961	0.342	14	0.120	K.IDDALTTIK.S
R2/RRR2-7/2	1324.105	1324.550	-337.008	0.366	603.915	0.445	17	0.120	K.AFPSLTYIAVNK.D
R2/RRR2-8/2	1603.269	1603.761	-307.805	0.460	892.479	0.374	19	0.120	K.GFLTINSQPAVNGER.S
R2/RRR2-8/2	1886.548	1887.045	-263.922	0.440	598.107	0.457	19	0.119	R.NPSYGALTDYQFTRPR.G
R2/RRR2-8/2	990.110	990.133	-23.385	0.413	986.690	0.299	13	0.118	K.IDDALTTIK.S
R2/RRR2-8/2	1323.895	1324.550	-1253.373	0.388	492.333	0.428	16	0.118	K.AFPSLTYIAVNK.D
R2/RRR2-7/2	1327.078	1327.553	-359.318	0.471	650.864	0.417	14	0.118	K.KLQEEWAVPVK.S
R2/RRR2-8/2	1324.050	1324.550	-378.449	0.346	492.224	0.408	16	0.115	K.AFPSLTYIAVNK.D
R2/RRR2-8/2	989.502	990.133	-1652.996	0.346	727.788	0.333	13	0.115	K.IDDALTTIK.S
R2/RRR2-8/2	1886.575	1887.045	-249.900	0.446	510.265	0.451	17	0.115	R.NPSYGALTDYQFTRPR.G
R2/RRR2-8/2	1886.504	1887.045	-819.224	0.441	586.913	0.407	19	0.115	R.NPSYGALTDYQFTRPR.G
R2/RRR2-7/2	1886.428	1887.045	-859.367	0.363	436.915	0.418	17	0.111	R.NPSYGALTDYQFTRPR.G
R2/RRR2-2/2	989.350	990.133	-1807.324	0.259	569.453	0.209	11	0.106	K.IDDALTTIK.S
R2/RRR2-8/3	1886.325	1887.045	-914.268	0.371	578.757	0.505	23	0.089	R.NPSYGALTDYQFTRPR.G
R2/RRR2-7/3	1885.885	1887.045	-1148.495	0.371	833.422	0.427	25	0.088	R.NPSYGALTDYQFTRPR.G
R2/RRR2-8/3	1885.874	1887.045	-1154.637	0.364	726.467	0.428	24	0.084	R.NPSYGALTDYQFTRPR.G
R2/RRR2-8/3	1327.896	1327.553	259.025	0.531	1487.292	0.213	24	0.084	-.KLQEEWAVPVK.-
R2/RRR2-8/3	1704.475	1705.010	-903.147	0.410	855.444	0.367	22	0.079	K.SALGILM*NLGLIEESK.I
R2/RRR2-8/3	1704.393	1705.010	-951.465	0.326	956.882	0.317	23	0.076	-.SALGILM*NLGLIEESK.-
R2/RRR2-7/3	1327.919	1327.553	276.170	0.521	1170.489	0.249	22	0.073	-.KLQEEWAVPVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1803.554	1804.124	-873.134	0.594	3927.694	0.615	28	0.789	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1819.276	1820.123	-1018.499	0.566	3763.250	0.618	27	0.735	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-14/2	1819.628	1820.123	-273.036	0.602	3734.716	0.620	27	0.724	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1820.072	1820.123	-28.106	0.636	3655.034	0.642	27	0.707	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-14/2	1819.499	1820.123	-895.568	0.574	3643.721	0.604	27	0.687	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1787.219	1788.125	-1069.226	0.536	3500.606	0.591	27	0.636	K.NFMIDFLMGGVSAAVSK.T
R2/RRR2-15/2	1819.433	1820.123	-931.939	0.582	3428.041	0.629	27	0.630	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-14/2	1819.105	1820.123	-1112.621	0.565	3299.955	0.582	26	0.569	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1788.208	1788.125	46.859	0.643	3074.952	0.597	27	0.509	K.NFMIDFLMGGVSAAVSK.T
R2/RRR2-15/3	1821.100	1820.123	-13.071	0.584	2994.388	0.541	35	0.500	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-14/2	1820.960	1820.123	-89.682	0.600	2975.925	0.622	26	0.496	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1787.822	1788.125	-169.539	0.598	2987.820	0.583	27	0.482	K.NFMIDFLMGGVSAAVSK.T
R2/RRR2-14/2	1803.009	1804.124	-1176.330	0.550	2829.685	0.560	26	0.434	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1804.535	1804.124	228.332	0.631	2686.313	0.608	25	0.416	K.NFM*IDFLMGGVSAAVSK.T
R2/RRR2-14/2	1804.017	1804.124	-59.299	0.583	2405.662	0.630	25	0.364	K.NFM*IDFLMGGVSAAVSK.T
R2/RRR2-15/3	1819.502	1820.123	-893.555	0.468	2718.474	0.418	36	0.358	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1803.462	1804.124	-924.096	0.575	2344.688	0.611	25	0.345	K.NFM*IDFLMGGVSAAVSK.T
R2/RRR2-15/2	1803.515	1804.124	-894.606	0.545	2285.989	0.599	25	0.330	K.NFM*IDFLMGGVSAAVSK.T
R2/RRR2-13/2	1821.140	1820.123	9.089	0.553	2258.230	0.598	23	0.323	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1802.813	1804.124	-1285.936	0.419	2200.305	0.527	23	0.291	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-14/3	1804.121	1804.124	-1.855	0.459	2411.008	0.394	33	0.277	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1498.099	1498.745	-1101.824	0.400	2202.037	0.420	20	0.269	R.GFNISCVGIIVYR.G
R2/RRR2-15/2	1498.324	1498.745	-281.724	0.502	2032.691	0.516	20	0.268	R.GFNISCVGIIVYR.G
R2/RRR2-15/3	1498.988	1498.745	162.728	0.518	2056.993	0.350	28	0.187	R.GFNISCVGIIVYR.G
R2/RRR2-15/3	1803.927	1804.124	-109.467	0.485	1680.561	0.505	31	0.187	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1227.113	1227.413	-244.712	0.486	1684.373	0.408	18	0.187	K.SSMDAFSQILK.N
R2/RRR2-15/2	1243.118	1243.412	-236.947	0.468	1522.527	0.408	18	0.171	K.SSM*DAFSQILK.N
R2/RRR2-15/2	1226.998	1227.413	-338.533	0.506	1484.549	0.422	17	0.169	K.SSMDAFSQILK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/3	1803.262	1804.124	-1035.727	0.407	1747.948	0.414	32	0.168	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-14/2	1244.148	1243.412	-213.231	0.475	1474.510	0.423	16	0.167	K.SSM*DAFSQILK.N
R2/RRR2-15/2	1362.347	1361.590	-178.860	0.556	1419.685	0.390	17	0.155	K.LLIQNQDEM*IK.S
R2/RRR2-15/2	1243.098	1243.412	-253.103	0.423	1339.931	0.414	16	0.154	K.SSM*DAFSQILK.N
R2/RRR2-14/2	1345.094	1345.591	-370.161	0.496	1493.691	0.339	18	0.153	K.LLIQNQDEMIK.S
R2/RRR2-14/2	1243.215	1243.412	-158.831	0.404	1327.915	0.416	16	0.153	K.SSM*DAFSQILK.N
R2/RRR2-14/2	1361.111	1361.590	-353.082	0.516	1368.132	0.371	18	0.149	K.LLIQNQDEM*IK.S
R2/RRR2-15/2	1243.000	1243.412	-332.318	0.439	1220.540	0.435	16	0.149	K.SSM*DAFSQILK.N
R2/RRR2-14/2	1244.049	1243.412	-292.277	0.476	1249.717	0.420	16	0.148	K.SSM*DAFSQILK.N
R2/RRR2-15/2	1226.820	1227.413	-1302.051	0.366	1398.566	0.333	17	0.145	K.SSMDAFSQILK.N
R2/RRR2-14/2	1227.134	1227.413	-227.746	0.394	1239.832	0.401	16	0.144	K.SSMDAFSQILK.N
R2/RRR2-14/2	1422.596	1423.598	-1411.269	0.410	1218.693	0.396	19	0.143	R.TIKDEGFASLWR.G
R2/RRR2-13/2	1362.123	1361.590	-343.741	0.551	1217.948	0.393	17	0.141	K.LLIQNQDEM*IK.S
R2/RRR2-14/2	1345.177	1345.591	-308.245	0.505	1326.672	0.346	17	0.141	K.LLIQNQDEMIK.S
R2/RRR2-14/2	1345.122	1345.591	-349.400	0.491	1227.486	0.373	17	0.140	K.LLIQNQDEMIK.S
R2/RRR2-15/2	1422.707	1423.598	-1333.362	0.427	1171.126	0.386	19	0.139	R.TIKDEGFASLWR.G
R2/RRR2-15/2	1424.023	1423.598	299.242	0.471	1078.358	0.419	19	0.139	R.TIKDEGFASLWR.G
R2/RRR2-15/3	1498.016	1498.745	-1157.595	0.397	1777.674	0.312	27	0.139	R.GFNISCVGIIVYR.G
R2/RRR2-14/2	1448.169	1447.661	-341.025	0.492	660.724	0.529	19	0.137	R.YFPTQALNFAFK.D
R2/RRR2-15/2	1345.270	1345.591	-239.055	0.500	1231.169	0.354	17	0.137	K.LLIQNQDEMIK.S
R2/RRR2-14/2	1360.690	1361.590	-1400.662	0.495	1240.326	0.348	17	0.136	K.LLIQNQDEM*IK.S
R2/RRR2-14/2	1447.101	1447.661	-1081.598	0.432	758.858	0.513	19	0.136	R.YFPTQALNFAFK.D
R2/RRR2-15/2	1361.119	1361.590	-347.053	0.541	1279.438	0.338	17	0.135	K.LLIQNQDEM*IK.S
R2/RRR2-15/2	1346.097	1345.591	-367.884	0.548	1130.177	0.386	17	0.135	K.LLIQNQDEMIK.S
R2/RRR2-15/2	1362.332	1361.590	-189.646	0.545	1194.411	0.364	17	0.135	K.LLIQNQDEM*IK.S
R2/RRR2-13/2	1362.196	1361.590	-289.973	0.491	1178.147	0.360	17	0.135	K.LLIQNQDEM*IK.S
R2/RRR2-15/2	1447.288	1447.661	-258.835	0.456	757.308	0.489	19	0.134	R.YFPTQALNFAFK.D
R2/RRR2-15/2	882.798	881.950	-172.686	0.445	617.205	0.537	12	0.134	K.GIGDCFGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1424.208	1423.598	-274.635	0.474	953.173	0.432	18	0.134	R.TIKDEGFASLWR.G
R2/RRR2-14/2	1423.067	1423.598	-1079.302	0.461	984.461	0.412	19	0.133	R.TIKDEGFASLWR.G
R2/RRR2-15/2	1447.307	1447.661	-245.296	0.461	730.775	0.482	19	0.133	R.YFPTQALNFAFK.D
R2/RRR2-13/2	1361.140	1361.590	-331.846	0.485	1273.219	0.311	17	0.132	K.LLIQNQDEM*IK.S
R2/RRR2-14/2	952.006	952.046	-42.712	0.467	732.786	0.472	14	0.132	K.SDGIAGLYR.G
R2/RRR2-15/2	951.920	952.046	-133.136	0.477	841.007	0.427	15	0.132	K.SDGIAGLYR.G
R2/RRR2-14/2	1227.198	1227.413	-175.056	0.355	1289.247	0.303	15	0.132	K.SSMDAFSQILK.N
R2/RRR2-15/2	1361.212	1361.590	-278.310	0.441	1263.309	0.302	17	0.131	K.LLIQNQDEM*IK.S
R2/RRR2-15/2	1345.344	1345.591	-183.891	0.490	1339.879	0.282	17	0.131	K.LLIQNQDEMIK.S
R2/RRR2-15/2	1362.155	1361.590	-320.273	0.523	1261.153	0.312	17	0.131	K.LLIQNQDEM*IK.S
R2/RRR2-14/2	1423.158	1423.598	-310.282	0.433	1048.884	0.377	18	0.130	R.TIKDEGFASLWR.G
R2/RRR2-14/2	951.332	952.046	-1807.478	0.393	864.055	0.423	15	0.130	K.SDGIAGLYR.G
R2/RRR2-15/2	951.956	952.046	-94.804	0.451	689.538	0.428	14	0.127	K.SDGIAGLYR.G
R2/RRR2-14/2	881.834	881.950	-131.500	0.385	612.504	0.485	12	0.126	K.GIGDCFGR.T
R2/RRR2-15/2	1211.180	1211.351	-141.990	0.356	603.541	0.504	17	0.126	R.QFNGLVDVYR.K
R2/RRR2-12/2	1360.894	1361.590	-1249.756	0.367	1296.943	0.237	17	0.125	K.LLIQNQDEM*IK.S
R2/RRR2-14/2	951.369	952.046	-1768.413	0.384	709.765	0.409	14	0.123	K.SDGIAGLYR.G
R2/RRR2-15/2	1211.254	1211.351	-80.827	0.398	470.967	0.446	16	0.122	R.QFNGLVDVYR.K
R2/RRR2-15/2	1211.013	1211.351	-280.217	0.341	523.075	0.496	16	0.122	R.QFNGLVDVYR.K
R2/RRR2-3/2	1362.257	1361.590	-244.841	0.347	1336.836	0.196	17	0.122	K.LLIQNQDEM*IK.S
R2/RRR2-14/2	1226.951	1227.413	-376.965	0.365	987.479	0.305	15	0.118	K.SSMDAFSQILK.N
R2/RRR2-12/2	1360.910	1361.590	-1237.866	0.418	1049.076	0.271	16	0.117	K.LLIQNQDEM*IK.S
R2/RRR2-14/2	1446.789	1447.661	-1297.797	0.328	611.335	0.375	18	0.116	R.YFPTQALNFAFK.D
R2/RRR2-1/2	1243.447	1243.412	27.988	0.289	723.562	0.372	14	0.114	K.SSM*DAFSQILK.N
R2/RRR2-4/2	1819.909	1820.123	-118.191	0.414	660.112	0.388	19	0.114	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	1447.125	1447.661	-1064.997	0.309	386.064	0.410	15	0.114	R.YFPTQALNFAFK.D
R2/RRR2-14/2	881.690	881.950	-295.105	0.259	641.113	0.411	12	0.114	K.GIGDCFGR.T
R2/RRR2-14/2	951.490	952.046	-1640.281	0.333	742.483	0.280	14	0.113	K.SDGIAGLYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-26/2	951.446	952.046	-1686.812	0.196	234.220	0.355	12	0.113	K.SDGIAGLYR.G
R2/RRR2-13/2	1820.749	1820.123	-205.959	0.354	468.564	0.441	16	0.113	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-15/2	952.200	952.046	162.000	0.330	500.908	0.253	12	0.111	K.SDGIAGLYR.G
R2/RRR2-2/2	951.611	952.046	-459.082	0.119	201.429	0.280	13	0.111	K.SDGIAGLYR.G
R2/RRR2-14/2	881.348	881.950	-1822.640	0.218	759.016	0.364	13	0.111	K.GIGDCFGR.T
R2/RRR2-1/2	1447.172	1447.661	-339.314	0.295	374.812	0.288	14	0.110	R.YFPTQALNFAFK.D
R2/RRR2-13/2	881.249	881.950	-1935.800	0.229	783.981	0.307	12	0.109	K.GIGDCFGR.T
R2/RRR2-15/2	1803.316	1804.124	-1005.645	0.310	420.010	0.357	16	0.109	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-14/2	771.817	771.888	-92.184	0.404	935.296	0.200	13	0.109	K.GAGANILR.A
R2/RRR2-12/2	951.728	952.046	-335.138	0.149	174.175	0.344	12	0.108	-.SDGIAGLYR.-
R2/RRR2-14/2	1448.398	1447.661	-182.134	0.281	486.323	0.372	12	0.107	R.YFPTQALNFAFK.D
R2/RRR2-1/2	771.901	771.888	17.113	0.359	735.207	0.177	12	0.105	K.GAGANILR.A
R2/RRR2-14/2	771.604	771.888	-369.261	0.398	816.757	0.181	12	0.105	K.GAGANILR.A
R2/RRR2-14/2	771.806	771.888	-106.938	0.435	749.239	0.184	12	0.105	K.GAGANILR.A
R2/RRR2-15/3	1498.802	1498.745	38.499	0.399	1353.160	0.336	28	0.100	R.GFNISCVGIIVYR.G
R2/RRR2-15/3	1803.222	1804.124	-1057.953	0.456	1006.013	0.418	25	0.097	K.NFM*IDFLMGGVSAAVSK.T
R2/RRR2-14/3	1803.901	1804.124	-123.722	0.289	1379.766	0.231	27	0.088	K.NFMIDFLM*GGVSAAVSK.T
R2/RRR2-15/3	1423.502	1423.598	-67.752	0.460	993.339	0.311	22	0.078	-.TIKDEGFASLWR.-
R2/RRR2-15/3	1294.914	1294.482	334.929	0.348	1179.473	0.259	22	0.077	K.TLKSDGIAGLYR.G
R2/RRR2-15/3	1787.028	1788.125	-1176.778	0.321	607.811	0.283	28	0.075	K.NFMIDFLMGGVSAAVSK.T
R2/RRR2-15/3	1819.713	1820.123	-226.403	0.338	1053.252	0.195	28	0.068	K.NFM*IDFLM*GGVSAAVSK.T
R2/RRR2-12/2	951.760	952.046	-302.195	0.144	124.532	0.376	9	0.063	-.SDGIAGLYR.-
R2/RRR2-14/3	1423.243	1423.598	-250.098	0.396	780.696	0.260	21	0.063	-.TIKDEGFASLWR.-
R2/RRR2-15/3	1294.677	1294.482	151.432	0.337	1098.226	0.150	23	0.061	K.TLKSDGIAGLYR.G
R2/RRR2-14/3	1423.830	1423.598	163.536	0.479	844.934	0.254	20	0.061	-.TIKDEGFASLWR.-
R2/RRR2-15/3	1423.566	1423.598	-22.725	0.393	657.849	0.229	19	0.058	-.TIKDEGFASLWR.-
R2/RRR2-15/3	1424.804	1423.598	144.820	0.436	692.075	0.264	19	0.058	-.TIKDEGFASLWR.-
R2/RRR2-14/3	1423.562	1423.598	-25.176	0.431	864.179	0.246	20	0.056	-.TIKDEGFASLWR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	951.440	952.046	-1693.902	0.226	96.886	0.401	10	0.036	-.SDGIAGLYR.-
R2/RRR2-22/1	1549.779	1548.681	63.281	0.473	917.053	0.613	17	0.971	R.AWSAADAVASWVGEK.K
R2/RRR2-23/1	1548.834	1548.681	99.209	0.363	954.498	0.452	18	0.916	R.AWSAADAVASWVGEK.K
R2/RRR2-23/1	1549.971	1548.681	187.924	0.494	816.539	0.627	16	0.838	R.AWSAADAVASWVGEK.K
R2/RRR2-22/1	1549.886	1548.681	132.952	0.448	771.895	0.605	16	0.763	R.AWSAADAVASWVGEK.K
R2/RRR2-22/1	1549.789	1548.681	69.996	0.461	694.571	0.560	16	0.633	R.AWSAADAVASWVGEK.K
R2/RRR2-22/3	1384.024	1384.522	-361.086	0.533	2990.028	0.636	32	0.537	R.RADGVGPVSWDPK.V
R2/RRR2-23/1	1142.599	1143.274	-1470.612	0.185	725.350	0.273	14	0.504	K.VASFAQSYAAK.R
R2/RRR2-25/2	1548.371	1548.681	-200.739	0.483	2587.642	0.475	24	0.345	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1549.176	1548.681	320.511	0.514	2422.340	0.551	23	0.337	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1548.226	1548.681	-294.786	0.484	2370.454	0.542	23	0.325	R.AWSAADAVASWVGEK.K
R2/RRR2-2/2	1549.341	1548.681	-219.737	0.550	2344.496	0.540	23	0.317	R.AWSAADAVASWVGEK.K
R2/RRR2-23/2	1549.179	1548.681	322.407	0.568	2303.344	0.564	23	0.317	R.AWSAADAVASWVGEK.K
R2/RRR2-19/2	1548.364	1548.681	-205.405	0.498	2326.293	0.527	23	0.311	R.AWSAADAVASWVGEK.K
R2/RRR2-23/2	1549.208	1548.681	-305.980	0.562	2247.497	0.549	23	0.302	R.AWSAADAVASWVGEK.K
R2/RRR2-22/1	1142.603	1143.274	-1466.856	0.192	527.504	0.179	13	0.301	K.VASFAQSYAAK.R
R2/RRR2-1/2	1549.009	1548.681	212.258	0.527	2281.349	0.504	23	0.294	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1548.135	1548.681	-1001.599	0.447	2295.534	0.489	23	0.294	R.AWSAADAVASWVGEK.K
R2/RRR2-1/2	1549.917	1548.681	152.650	0.539	2144.044	0.578	23	0.294	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1549.149	1548.681	303.129	0.535	2230.356	0.526	23	0.292	R.AWSAADAVASWVGEK.K
R2/RRR2-23/3	1384.738	1384.522	156.614	0.556	2125.486	0.592	28	0.291	R.RADGVGPVSWDPK.V
R2/RRR2-22/1	1142.566	1143.274	-1498.943	0.160	496.729	0.188	12	0.291	K.VASFAQSYAAK.R
R2/RRR2-24/2	1548.350	1548.681	-214.501	0.479	2250.531	0.502	23	0.289	R.AWSAADAVASWVGEK.K
R2/RRR2-23/1	1547.824	1548.681	-1203.384	0.140	419.640	0.334	16	0.288	R.AWSAADAVASWVGEK.K
R2/RRR2-24/2	1548.419	1548.681	-169.895	0.506	2172.969	0.530	24	0.285	R.AWSAADAVASWVGEK.K
R2/RRR2-24/2	1549.480	1548.681	-130.191	0.554	2065.181	0.574	23	0.279	R.AWSAADAVASWVGEK.K
R2/RRR2-19/2	1547.810	1548.681	-1212.303	0.366	2420.901	0.357	24	0.278	R.AWSAADAVASWVGEK.K
R2/RRR2-19/2	1548.291	1548.681	-252.309	0.406	2251.362	0.459	23	0.278	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1547.914	1548.681	-1144.751	0.341	2330.216	0.384	24	0.270	R.AWSAADAVASWVGEK.K
R2/RRR2-23/1	1142.504	1143.274	-1553.679	0.139	482.143	0.121	12	0.267	K.VASFAQSYAAK.R
R2/RRR2-14/2	1548.248	1548.681	-280.627	0.460	2114.135	0.504	23	0.267	R.AWSAADAVASWVGEK.K
R2/RRR2-23/3	1384.786	1384.522	191.356	0.562	2093.029	0.550	28	0.265	R.RADGVGPVSWDPK.V
R2/RRR2-25/2	1547.886	1548.681	-1163.123	0.390	2249.047	0.410	23	0.263	R.AWSAADAVASWVGEK.K
R2/RRR2-20/2	1548.288	1548.681	-254.523	0.474	2056.615	0.515	23	0.261	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1548.202	1548.681	-310.212	0.455	2042.196	0.518	23	0.260	R.AWSAADAVASWVGEK.K
R2/RRR2-12/2	1549.131	1548.681	291.356	0.506	2036.015	0.523	23	0.259	R.AWSAADAVASWVGEK.K
R2/RRR2-16/2	1549.229	1548.681	-292.382	0.566	2006.690	0.535	23	0.257	R.AWSAADAVASWVGEK.K
R2/RRR2-22/3	1384.173	1384.522	-252.911	0.524	1949.700	0.575	27	0.251	R.RADGVGPVSWDPK.V
R2/RRR2-16/2	1549.507	1548.681	-112.410	0.528	1924.138	0.551	23	0.250	R.AWSAADAVASWVGEK.K
R2/RRR2-20/2	1548.199	1548.681	-312.506	0.379	2102.089	0.441	23	0.248	R.AWSAADAVASWVGEK.K
R2/RRR2-18/2	1547.556	1548.681	-1377.063	0.330	2122.461	0.427	23	0.247	R.AWSAADAVASWVGEK.K
R2/RRR2-23/3	1384.235	1384.522	-207.790	0.517	1837.532	0.609	27	0.245	R.RADGVGPVSWDPK.V
R2/RRR2-21/2	1548.356	1548.681	-210.230	0.455	2030.107	0.471	23	0.244	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1549.122	1548.681	285.351	0.552	1844.331	0.571	22	0.243	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1549.784	1548.681	67.025	0.532	1780.626	0.597	22	0.241	R.AWSAADAVASWVGEK.K
R2/RRR2-22/3	1384.772	1384.522	180.880	0.496	1917.458	0.563	28	0.240	R.RADGVGPVSWDPK.V
R2/RRR2-13/2	1548.221	1548.681	-297.950	0.482	1933.958	0.503	22	0.238	R.AWSAADAVASWVGEK.K
R2/RRR2-16/2	1548.134	1548.681	-1002.153	0.430	1981.633	0.474	22	0.238	R.AWSAADAVASWVGEK.K
R2/RRR2-14/2	1548.046	1548.681	-1058.998	0.397	2026.291	0.446	23	0.238	R.AWSAADAVASWVGEK.K
R2/RRR2-18/2	1549.190	1548.681	-317.680	0.530	1876.075	0.528	22	0.236	R.AWSAADAVASWVGEK.K
R2/RRR2-23/2	1547.973	1548.681	-1106.821	0.376	2042.626	0.427	22	0.235	R.AWSAADAVASWVGEK.K
R2/RRR2-7/2	1550.029	1548.681	225.231	0.566	1858.664	0.533	22	0.234	R.AWSAADAVASWVGEK.K
R2/RRR2-24/2	1676.602	1676.854	-150.333	0.538	1885.356	0.493	23	0.228	R.AWSAADAVASWVGEKK.N
R2/RRR2-20/2	1549.189	1548.681	-318.550	0.517	1713.287	0.578	22	0.227	R.AWSAADAVASWVGEK.K
R2/RRR2-1/2	1548.282	1548.681	-258.320	0.479	1793.397	0.529	22	0.225	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1548.280	1548.681	-259.744	0.499	1723.000	0.559	22	0.223	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1548.132	1548.681	-1003.499	0.474	1797.227	0.517	22	0.223	R.AWSAADAVASWVGEK.K
R2/RRR2-23/2	1548.057	1548.681	-1052.426	0.474	1707.724	0.564	22	0.223	R.AWSAADAVASWVGEK.K
R2/RRR2-22/3	1384.632	1384.522	79.431	0.566	1735.234	0.594	27	0.220	R.RADGVGPVSWDPK.V
R2/RRR2-18/2	1548.052	1548.681	-1055.356	0.394	1921.646	0.427	23	0.218	R.AWSAADAVASWVGEK.K
R2/RRR2-22/3	1384.786	1384.522	191.223	0.580	1728.740	0.590	27	0.217	R.RADGVGPVSWDPK.V
R2/RRR2-20/2	1548.177	1548.681	-974.367	0.477	1747.075	0.503	22	0.213	R.AWSAADAVASWVGEK.K
R2/RRR2-19/3	1384.781	1384.522	187.510	0.551	1733.068	0.571	26	0.212	R.RADGVGPVSWDPK.V
R2/RRR2-12/2	1548.448	1548.681	-150.598	0.476	1718.522	0.513	22	0.211	R.AWSAADAVASWVGEK.K
R2/RRR2-21/2	1549.148	1548.681	302.102	0.512	1752.169	0.499	21	0.211	R.AWSAADAVASWVGEK.K
R2/RRR2-2/2	1548.122	1548.681	-1010.228	0.415	1809.327	0.451	22	0.208	R.AWSAADAVASWVGEK.K
R2/RRR2-23/2	1548.002	1548.681	-1087.897	0.385	1850.188	0.427	22	0.208	R.AWSAADAVASWVGEK.K
R2/RRR2-17/2	1547.942	1548.681	-1126.934	0.411	1787.349	0.453	22	0.206	R.AWSAADAVASWVGEK.K
R2/RRR2-6/2	1548.539	1548.681	-91.686	0.455	1799.966	0.441	21	0.204	R.AWSAADAVASWVGEK.K
R2/RRR2-21/3	1384.666	1384.522	104.099	0.574	1724.830	0.547	26	0.201	R.RADGVGPVSWDPK.V
R2/RRR2-23/2	1676.488	1676.854	-218.701	0.530	1562.919	0.542	21	0.198	R.AWSAADAVASWVGEKK.N
R2/RRR2-21/2	1676.326	1676.854	-914.342	0.543	1482.391	0.568	22	0.195	R.AWSAADAVASWVGEKK.N
R2/RRR2-12/2	1548.381	1548.681	-194.016	0.456	1681.451	0.464	21	0.195	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1677.205	1676.854	209.758	0.570	1446.660	0.578	22	0.194	R.AWSAADAVASWVGEKK.N
R2/RRR2-23/2	1677.594	1676.854	-155.207	0.570	1496.434	0.556	22	0.194	R.AWSAADAVASWVGEKK.N
R2/RRR2-16/3	1384.242	1384.522	-203.146	0.528	1712.093	0.529	27	0.193	R.RADGVGPVSWDPK.V
R2/RRR2-13/2	1548.035	1548.681	-1066.361	0.382	1832.711	0.369	22	0.193	R.AWSAADAVASWVGEK.K
R2/RRR2-23/2	1548.113	1548.681	-1015.691	0.405	1749.350	0.406	21	0.190	R.AWSAADAVASWVGEK.K
R2/RRR2-4/2	1548.336	1548.681	-223.597	0.413	1626.545	0.467	21	0.189	R.AWSAADAVASWVGEK.K
R2/RRR2-5/2	1549.130	1548.681	290.803	0.467	1593.006	0.473	21	0.187	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1676.343	1676.854	-903.742	0.520	1430.361	0.552	22	0.187	R.AWSAADAVASWVGEKK.N
R2/RRR2-25/2	1548.070	1548.681	-1043.717	0.380	1668.084	0.427	21	0.186	R.AWSAADAVASWVGEK.K
R2/RRR2-20/3	1384.583	1384.522	44.283	0.578	1589.192	0.564	28	0.185	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1548.233	1548.681	-290.198	0.450	1581.854	0.466	21	0.184	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1406.058	1405.579	341.379	0.532	1558.053	0.450	17	0.183	K.VCGHYTQVVWR.K
R2/RRR2-23/3	1384.564	1384.522	30.223	0.502	1506.022	0.575	26	0.182	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1548.151	1548.681	-991.070	0.422	1539.656	0.479	20	0.182	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1404.758	1405.579	-1300.544	0.512	1580.561	0.424	18	0.181	K.VCGHYTQVVWR.K
R2/RRR2-22/2	1676.436	1676.854	-250.112	0.550	1367.335	0.558	21	0.180	R.AWSAADAVASWVGEKK.N
R2/RRR2-23/3	1384.653	1384.522	95.213	0.554	1438.114	0.594	25	0.179	R.RADGVGPVSWDPK.V
R2/RRR2-3/2	1548.160	1548.681	-985.054	0.429	1522.187	0.463	20	0.177	R.AWSAADAVASWVGEK.K
R2/RRR2-19/3	1385.134	1384.522	-280.624	0.528	1416.141	0.593	25	0.177	R.RADGVGPVSWDPK.V
R2/RRR2-23/2	1676.280	1676.854	-941.757	0.510	1349.464	0.542	21	0.175	R.AWSAADAVASWVGEKK.N
R2/RRR2-20/2	1676.323	1676.854	-915.950	0.523	1412.620	0.508	22	0.175	R.AWSAADAVASWVGEKK.N
R2/RRR2-21/2	1675.709	1676.854	-1283.659	0.512	1449.627	0.483	22	0.174	R.AWSAADAVASWVGEKK.N
R2/RRR2-4/2	1548.135	1548.681	-1001.837	0.397	1690.163	0.356	21	0.173	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1676.403	1676.854	-269.837	0.475	1486.920	0.464	21	0.173	R.AWSAADAVASWVGEKK.N
R2/RRR2-23/3	1548.733	1548.681	33.581	0.566	1636.765	0.477	27	0.171	R.AWSAADAVASWVGEK.K
R2/RRR2-16/3	1384.708	1384.522	134.733	0.579	1438.076	0.570	26	0.170	R.RADGVGPVSWDPK.V
R2/RRR2-1/3	1384.453	1384.522	-49.765	0.530	1437.190	0.561	24	0.170	R.RADGVGPVSWDPK.V
R2/RRR2-3/2	1548.601	1548.681	-51.992	0.445	1404.769	0.479	19	0.167	R.AWSAADAVASWVGEK.K
R2/RRR2-19/2	1228.455	1228.336	97.812	0.348	1475.785	0.424	18	0.167	R.ADGVGPVSWDPK.V
R2/RRR2-23/2	1676.284	1676.854	-939.491	0.526	1253.380	0.539	21	0.166	R.AWSAADAVASWVGEKK.N
R2/RRR2-19/2	1142.978	1143.274	-259.726	0.525	1117.748	0.564	18	0.166	K.VASFAQSYAAK.R
R2/RRR2-21/3	1384.152	1384.522	-267.776	0.538	1391.175	0.568	25	0.165	R.RADGVGPVSWDPK.V
R2/RRR2-4/2	1143.177	1143.274	-84.783	0.506	1040.557	0.588	18	0.164	K.VASFAQSYAAK.R
R2/RRR2-17/2	1547.668	1548.681	-1304.815	0.375	1414.315	0.451	20	0.164	R.AWSAADAVASWVGEK.K
R2/RRR2-18/2	1677.446	1676.854	-243.539	0.515	1360.547	0.478	21	0.163	R.AWSAADAVASWVGEKK.N
R2/RRR2-18/2	1143.110	1143.274	-144.019	0.476	1053.899	0.582	18	0.163	K.VASFAQSYAAK.R
R2/RRR2-23/2	1404.561	1405.579	-1441.420	0.491	1444.949	0.401	17	0.162	K.VCGHYTQVVWR.K
R2/RRR2-6/2	1548.183	1548.681	-322.395	0.377	1487.815	0.400	20	0.162	R.AWSAADAVASWVGEK.K
R2/RRR2-1/2	1143.091	1143.274	-160.302	0.516	1035.380	0.567	18	0.160	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1143.047	1143.274	-198.762	0.532	1079.592	0.544	18	0.160	K.VASFAQSYAAK.R
R2/RRR2-22/3	1384.370	1384.522	-109.864	0.485	1484.351	0.515	27	0.159	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1675.608	1676.854	-1344.092	0.498	1360.434	0.455	21	0.159	R.AWSAADAVASWVGEKK.N
R2/RRR2-22/2	1547.393	1548.681	-1483.315	0.383	1468.427	0.388	21	0.158	R.AWSAADAVASWVGEK.K
R2/RRR2-12/2	1143.111	1143.274	-143.269	0.508	1063.443	0.542	18	0.158	K.VASFAQSYAAK.R
R2/RRR2-3/2	1142.998	1143.274	-242.154	0.503	987.417	0.572	18	0.158	K.VASFAQSYAAK.R
R2/RRR2-22/2	1142.575	1143.274	-1491.818	0.466	1029.904	0.558	18	0.157	K.VASFAQSYAAK.R
R2/RRR2-22/2	1143.003	1143.274	-237.868	0.507	1025.623	0.549	18	0.157	K.VASFAQSYAAK.R
R2/RRR2-13/2	1142.972	1143.274	-264.869	0.452	1040.097	0.550	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-20/2	1143.048	1143.274	-198.119	0.490	1048.721	0.539	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-2/2	1143.150	1143.274	-108.562	0.467	1021.987	0.553	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-21/2	1143.006	1143.274	-235.511	0.467	1048.722	0.542	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-1/2	1143.091	1143.274	-160.302	0.458	1046.490	0.544	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-23/2	1142.991	1143.274	-248.475	0.489	952.460	0.574	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-22/2	1675.526	1676.854	-1393.483	0.391	1243.441	0.488	21	0.156	R.AWSAADAVASWVGEKK.N
R2/RRR2-23/2	1142.962	1143.274	-273.441	0.442	1016.594	0.558	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-18/2	1142.980	1143.274	-258.119	0.469	1099.390	0.517	18	0.156	K.VASFAQSYAAK.R
R2/RRR2-7/2	1143.212	1143.274	-54.043	0.502	968.049	0.561	18	0.155	K.VASFAQSYAAK.R
R2/RRR2-20/3	1384.629	1384.522	77.176	0.549	1235.868	0.587	23	0.155	R.RADGVGPVSWDPK.V
R2/RRR2-2/2	1143.136	1143.274	-120.881	0.465	945.747	0.573	18	0.155	K.VASFAQSYAAK.R
R2/RRR2-6/2	1143.093	1143.274	-158.802	0.515	994.695	0.545	18	0.155	K.VASFAQSYAAK.R
R2/RRR2-3/2	1142.980	1143.274	-258.333	0.500	1023.444	0.536	18	0.154	K.VASFAQSYAAK.R
R2/RRR2-13/2	1143.029	1143.274	-215.047	0.519	1001.212	0.541	18	0.154	K.VASFAQSYAAK.R
R2/RRR2-23/2	1142.912	1143.274	-317.268	0.443	1027.011	0.544	18	0.154	K.VASFAQSYAAK.R
R2/RRR2-22/2	1143.908	1143.274	-321.166	0.454	1154.117	0.488	18	0.154	K.VASFAQSYAAK.R
R2/RRR2-17/2	1548.357	1548.681	-209.835	0.432	1357.841	0.427	19	0.154	R.AWSAADAVASWVGEK.K
R2/RRR2-1/2	1143.098	1143.274	-154.303	0.454	1009.553	0.544	18	0.154	K.VASFAQSYAAK.R
R2/RRR2-23/2	1142.991	1143.274	-248.582	0.488	973.121	0.550	18	0.154	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1143.009	1143.274	-232.725	0.512	911.903	0.566	18	0.153	K.VASFAQSYAAK.R
R2/RRR2-12/3	1385.750	1384.522	165.202	0.521	1230.978	0.582	24	0.153	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1586.046	1585.607	278.013	0.486	1127.879	0.501	18	0.153	K.NYHYDTNTCDPGK.V
R2/RRR2-15/2	1675.398	1676.854	-1469.883	0.466	1206.289	0.474	22	0.152	R.AWSAADAVASWVGEKK.N
R2/RRR2-25/2	1143.149	1143.274	-109.312	0.453	994.264	0.538	18	0.152	K.VASFAQSYAAK.R
R2/RRR2-24/2	1142.923	1143.274	-307.945	0.499	961.426	0.541	18	0.152	K.VASFAQSYAAK.R
R2/RRR2-23/2	1548.081	1548.681	-1036.354	0.372	1423.433	0.377	20	0.152	R.AWSAADAVASWVGEK.K
R2/RRR2-2/2	1143.084	1143.274	-166.301	0.495	1050.899	0.508	18	0.152	K.VASFAQSYAAK.R
R2/RRR2-22/2	1228.195	1228.336	-115.201	0.385	1273.529	0.429	19	0.152	R.ADGVGPVSWDPK.V
R2/RRR2-2/3	1384.497	1384.522	-18.060	0.451	1440.606	0.500	26	0.152	R.RADGVGPVSWDPK.V
R2/RRR2-6/2	1143.033	1143.274	-211.511	0.450	1003.531	0.533	18	0.152	K.VASFAQSYAAK.R
R2/RRR2-17/2	1143.026	1143.274	-217.297	0.468	956.536	0.546	18	0.151	K.VASFAQSYAAK.R
R2/RRR2-2/2	1677.455	1676.854	-238.647	0.520	1278.280	0.451	21	0.151	R.AWSAADAVASWVGEKK.N
R2/RRR2-14/2	1142.999	1143.274	-241.297	0.500	931.513	0.543	18	0.151	K.VASFAQSYAAK.R
R2/RRR2-22/2	1405.182	1405.579	-283.668	0.506	1282.415	0.416	16	0.150	K.VCGHYTQVVWR.K
R2/RRR2-9/2	1143.206	1143.274	-59.613	0.477	995.645	0.521	18	0.150	K.VASFAQSYAAK.R
R2/RRR2-16/3	1384.383	1384.522	-100.710	0.546	1236.847	0.573	25	0.150	R.RADGVGPVSWDPK.V
R2/RRR2-5/3	1385.271	1384.522	-181.694	0.502	1355.581	0.524	24	0.150	R.RADGVGPVSWDPK.V
R2/RRR2-15/2	1144.124	1143.274	-131.264	0.532	869.876	0.552	18	0.150	K.VASFAQSYAAK.R
R2/RRR2-20/2	1143.761	1143.274	426.732	0.501	869.564	0.555	18	0.149	K.VASFAQSYAAK.R
R2/RRR2-8/2	1142.900	1143.274	-328.198	0.444	881.482	0.565	18	0.149	K.VASFAQSYAAK.R
R2/RRR2-1/3	1384.135	1384.522	-280.119	0.527	1303.243	0.545	25	0.149	R.RADGVGPVSWDPK.V
R2/RRR2-3/2	1143.117	1143.274	-138.020	0.505	847.005	0.567	17	0.149	K.VASFAQSYAAK.R
R2/RRR2-17/2	1142.892	1143.274	-334.842	0.498	999.965	0.507	18	0.149	K.VASFAQSYAAK.R
R2/RRR2-24/2	1676.357	1676.854	-297.452	0.467	1290.436	0.436	19	0.149	R.AWSAADAVASWVGEKK.N
R2/RRR2-28/2	1142.897	1143.274	-331.199	0.469	929.165	0.535	18	0.149	K.VASFAQSYAAK.R
R2/RRR2-22/2	1143.857	1143.274	-365.280	0.441	1104.631	0.472	18	0.148	K.VASFAQSYAAK.R
R2/RRR2-14/2	1142.667	1143.274	-1410.371	0.468	880.601	0.551	18	0.148	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1228.124	1228.336	-172.531	0.416	1323.215	0.383	19	0.148	R.ADGVGPVSWDPK.V
R2/RRR2-21/2	1675.585	1676.854	-1358.287	0.506	1138.697	0.483	21	0.148	R.AWSAADAVASWVGEKK.N
R2/RRR2-10/2	1549.631	1548.681	-32.126	0.453	1060.329	0.515	19	0.147	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1143.555	1143.274	246.188	0.439	1008.632	0.500	18	0.147	K.VASFAQSYAAK.R
R2/RRR2-23/2	1229.062	1228.336	-223.304	0.447	1152.393	0.456	17	0.147	R.ADGVGPVSWDPK.V
R2/RRR2-21/2	1142.847	1143.274	-374.924	0.452	930.267	0.524	18	0.147	K.VASFAQSYAAK.R
R2/RRR2-22/2	1712.903	1713.780	-1099.176	0.508	856.960	0.566	19	0.146	K.KNYHYDTNTCDPGK.V
R2/RRR2-17/2	1142.520	1143.274	-1539.684	0.418	970.896	0.514	18	0.146	K.VASFAQSYAAK.R
R2/RRR2-19/2	1143.148	1143.274	-110.705	0.502	973.584	0.496	18	0.146	K.VASFAQSYAAK.R
R2/RRR2-23/2	1405.393	1405.579	-132.823	0.498	1190.529	0.427	16	0.146	K.VCGHYTQVVWR.K
R2/RRR2-10/2	1143.075	1143.274	-174.443	0.473	943.919	0.509	18	0.146	K.VASFAQSYAAK.R
R2/RRR2-20/3	1384.597	1384.522	54.496	0.517	1307.056	0.529	24	0.146	R.RADGVGPVSWDPK.V
R2/RRR2-24/2	1143.016	1143.274	-226.404	0.476	941.768	0.505	18	0.145	K.VASFAQSYAAK.R
R2/RRR2-22/2	1143.010	1143.274	-231.439	0.477	776.491	0.556	18	0.145	K.VASFAQSYAAK.R
R2/RRR2-22/2	1142.894	1143.274	-333.664	0.430	1069.575	0.464	18	0.145	K.VASFAQSYAAK.R
R2/RRR2-22/2	1676.444	1676.854	-245.437	0.502	944.484	0.562	18	0.145	R.AWSAADAVASWVGEKK.N
R2/RRR2-6/2	1548.182	1548.681	-323.186	0.378	1376.054	0.357	20	0.145	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1675.432	1676.854	-1449.538	0.423	1261.570	0.410	21	0.145	R.AWSAADAVASWVGEKK.N
R2/RRR2-7/2	1143.012	1143.274	-229.725	0.383	884.590	0.549	18	0.145	K.VASFAQSYAAK.R
R2/RRR2-13/2	1142.520	1143.274	-1539.899	0.439	886.183	0.522	18	0.144	K.VASFAQSYAAK.R
R2/RRR2-1/2	1676.180	1676.854	-1001.784	0.484	1269.711	0.409	20	0.143	R.AWSAADAVASWVGEKK.N
R2/RRR2-12/2	1142.911	1143.274	-318.447	0.462	991.569	0.466	18	0.142	K.VASFAQSYAAK.R
R2/RRR2-23/2	1585.047	1585.607	-986.771	0.411	1090.293	0.455	17	0.141	K.NYHYDTNTCDPGK.V
R2/RRR2-10/2	1143.022	1143.274	-221.154	0.468	853.735	0.510	17	0.141	K.VASFAQSYAAK.R
R2/RRR2-10/2	1143.943	1143.274	-290.546	0.485	797.060	0.513	18	0.141	K.VASFAQSYAAK.R
R2/RRR2-22/2	1228.993	1228.336	-279.405	0.438	1030.991	0.465	17	0.141	R.ADGVGPVSWDPK.V
R2/RRR2-19/2	1142.521	1143.274	-1538.933	0.405	810.692	0.528	18	0.140	K.VASFAQSYAAK.R
R2/RRR2-22/2	1586.004	1585.607	251.233	0.478	1008.400	0.471	17	0.139	K.NYHYDTNTCDPGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1227.756	1228.336	-1290.887	0.359	1358.556	0.312	18	0.139	R.ADGVGPVSWDPK.V
R2/RRR2-23/2	1405.129	1405.579	-321.757	0.490	1193.079	0.384	16	0.139	K.VCGHYTQVVWR.K
R2/RRR2-25/2	1142.792	1143.274	-422.832	0.462	716.493	0.530	17	0.138	K.VASFAQSYAAK.R
R2/RRR2-27/2	1142.268	1143.274	-1761.151	0.360	994.385	0.459	18	0.138	K.VASFAQSYAAK.R
R2/RRR2-9/2	1142.396	1143.274	-1648.849	0.410	811.804	0.514	17	0.138	K.VASFAQSYAAK.R
R2/RRR2-23/2	1142.377	1143.274	-1665.167	0.381	880.184	0.492	18	0.138	K.VASFAQSYAAK.R
R2/RRR2-7/3	1385.394	1384.522	-92.992	0.537	1258.551	0.517	23	0.138	R.RADGVGPVSWDPK.V
R2/RRR2-27/2	1142.950	1143.274	-283.835	0.383	811.907	0.514	18	0.138	K.VASFAQSYAAK.R
R2/RRR2-18/2	1142.340	1143.274	-1697.696	0.381	875.744	0.490	18	0.137	K.VASFAQSYAAK.R
R2/RRR2-5/2	1548.309	1548.681	-240.602	0.354	1212.680	0.388	18	0.137	R.AWSAADAVASWVGEK.K
R2/RRR2-7/2	1142.502	1143.274	-1555.891	0.381	774.256	0.526	17	0.136	K.VASFAQSYAAK.R
R2/RRR2-22/2	1585.214	1585.607	-248.749	0.462	960.953	0.472	17	0.136	K.NYHYDTNTCDPGK.V
R2/RRR2-22/2	1676.390	1676.854	-277.508	0.465	1032.632	0.465	19	0.136	R.AWSAADAVASWVGEKK.N
R2/RRR2-15/2	1548.113	1548.681	-1016.008	0.337	1435.400	0.275	19	0.136	R.AWSAADAVASWVGEK.K
R2/RRR2-22/2	1585.133	1585.607	-299.972	0.393	1029.083	0.446	17	0.136	K.NYHYDTNTCDPGK.V
R2/RRR2-14/2	1142.719	1143.274	-1365.092	0.437	845.146	0.465	18	0.136	K.VASFAQSYAAK.R
R2/RRR2-22/2	1678.138	1676.854	169.660	0.457	789.387	0.552	18	0.135	R.AWSAADAVASWVGEKK.N
R2/RRR2-16/2	1142.547	1143.274	-1515.751	0.376	970.977	0.435	18	0.135	K.VASFAQSYAAK.R
R2/RRR2-22/2	1228.033	1228.336	-246.921	0.382	1176.867	0.364	18	0.135	R.ADGVGPVSWDPK.V
R2/RRR2-23/2	1585.101	1585.607	-952.597	0.454	1090.301	0.409	17	0.134	K.NYHYDTNTCDPGK.V
R2/RRR2-1/3	1384.362	1384.522	-115.968	0.516	1001.372	0.587	22	0.134	R.RADGVGPVSWDPK.V
R2/RRR2-21/2	1142.972	1143.274	-264.655	0.381	766.199	0.493	18	0.134	K.VASFAQSYAAK.R
R2/RRR2-12/2	1142.482	1143.274	-1573.494	0.358	802.953	0.500	17	0.134	K.VASFAQSYAAK.R
R2/RRR2-23/2	1585.101	1585.607	-952.674	0.422	1066.148	0.414	17	0.134	K.NYHYDTNTCDPGK.V
R2/RRR2-15/2	1676.145	1676.854	-1022.476	0.482	928.718	0.482	19	0.134	R.AWSAADAVASWVGEKK.N
R2/RRR2-22/2	1300.138	1299.460	-248.389	0.380	980.853	0.445	16	0.133	K.VASFAQSYAAKR.A
R2/RRR2-28/2	1142.260	1143.274	-1768.453	0.355	803.896	0.480	18	0.133	K.VASFAQSYAAK.R
R2/RRR2-15/3	1384.681	1384.522	115.106	0.521	1173.539	0.525	23	0.133	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1227.600	1228.336	-1417.915	0.316	1117.690	0.380	17	0.132	R.ADGVGPVSWDPK.V
R2/RRR2-25/2	1142.411	1143.274	-1635.645	0.361	708.772	0.497	17	0.131	K.VASFAQSYAAK.R
R2/RRR2-22/2	1142.574	1143.274	-1492.677	0.368	642.719	0.510	17	0.131	K.VASFAQSYAAK.R
R2/RRR2-21/2	1228.154	1228.336	-148.502	0.400	1035.173	0.385	17	0.130	R.ADGVGPVSWDPK.V
R2/RRR2-17/2	1384.448	1384.522	-53.647	0.449	573.596	0.473	20	0.129	R.RADGVGPVSWDPK.V
R2/RRR2-27/2	1142.198	1143.274	-1823.218	0.371	750.576	0.452	18	0.129	K.VASFAQSYAAK.R
R2/RRR2-21/2	1227.994	1228.336	-279.233	0.385	1026.896	0.380	17	0.128	R.ADGVGPVSWDPK.V
R2/RRR2-22/3	1383.711	1384.522	-1312.461	0.439	1404.831	0.424	25	0.128	R.RADGVGPVSWDPK.V
R2/RRR2-4/2	1142.373	1143.274	-1669.139	0.395	742.316	0.434	17	0.128	K.VASFAQSYAAK.R
R2/RRR2-17/3	1385.652	1384.522	94.305	0.489	1073.061	0.539	25	0.128	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1384.160	1384.522	-262.324	0.426	594.700	0.455	20	0.127	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1384.203	1384.522	-231.092	0.435	564.835	0.451	20	0.127	R.RADGVGPVSWDPK.V
R2/RRR2-22/3	1383.473	1384.522	-1485.260	0.459	1501.867	0.388	26	0.127	R.RADGVGPVSWDPK.V
R2/RRR2-20/2	1384.064	1384.522	-332.139	0.457	587.944	0.433	20	0.126	R.RADGVGPVSWDPK.V
R2/RRR2-20/2	1384.182	1384.522	-246.310	0.431	499.014	0.503	19	0.126	-.RADGVGPVSWDPK.-
R2/RRR2-23/2	1675.373	1676.854	-1484.887	0.395	1173.691	0.322	20	0.126	R.AWSAADAVASWVGEKK.N
R2/RRR2-18/2	1385.201	1384.522	-232.429	0.438	511.577	0.444	19	0.126	R.RADGVGPVSWDPK.V
R2/RRR2-20/2	1228.081	1228.336	-208.030	0.345	1018.351	0.362	17	0.125	R.ADGVGPVSWDPK.V
R2/RRR2-23/2	1385.015	1384.522	356.909	0.417	558.074	0.431	20	0.125	R.RADGVGPVSWDPK.V
R2/RRR2-21/2	1228.078	1228.336	-210.124	0.356	857.779	0.426	16	0.125	R.ADGVGPVSWDPK.V
R2/RRR2-20/2	1385.218	1384.522	-220.317	0.413	498.604	0.447	19	0.125	R.RADGVGPVSWDPK.V
R2/RRR2-19/2	1228.984	1228.336	-286.779	0.345	926.364	0.402	16	0.125	R.ADGVGPVSWDPK.V
R2/RRR2-19/2	1228.032	1228.336	-247.919	0.360	1029.609	0.352	17	0.125	R.ADGVGPVSWDPK.V
R2/RRR2-19/2	1384.336	1384.522	-134.489	0.429	486.079	0.435	19	0.125	R.RADGVGPVSWDPK.V
R2/RRR2-21/3	1384.384	1384.522	-99.781	0.534	1089.987	0.521	23	0.125	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1143.038	1143.274	-206.690	0.323	971.229	0.352	18	0.125	K.VASFAQSYAAK.R
R2/RRR2-22/2	1385.115	1384.522	-294.673	0.431	585.644	0.416	20	0.125	R.RADGVGPVSWDPK.V
R2/RRR2-22/3	1384.659	1384.522	99.590	0.485	1075.363	0.521	23	0.124	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1384.151	1384.522	-268.783	0.409	652.176	0.399	21	0.124	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1142.842	1143.274	-379.318	0.362	554.435	0.465	15	0.124	K.VASFAQSYAAK.R
R2/RRR2-1/2	1547.343	1548.681	-1515.646	0.287	1109.898	0.333	18	0.124	R.AWSAADAVASWVGEK.K
R2/RRR2-21/2	1383.660	1384.522	-1349.753	0.429	587.398	0.401	20	0.124	R.RADGVGPVSWDPK.V
R2/RRR2-18/3	1384.390	1384.522	-95.801	0.514	941.650	0.560	24	0.123	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1300.079	1299.460	-293.887	0.399	746.751	0.468	14	0.123	K.VASFAQSYAAKR.A
R2/RRR2-4/3	1384.535	1384.522	9.531	0.524	1039.036	0.531	23	0.123	R.RADGVGPVSWDPK.V
R2/RRR2-21/2	1385.025	1384.522	-359.843	0.462	432.174	0.414	18	0.123	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1384.174	1384.522	-251.973	0.405	655.290	0.378	21	0.123	R.RADGVGPVSWDPK.V
R2/RRR2-19/3	1384.544	1384.522	15.898	0.522	1122.683	0.500	22	0.123	R.RADGVGPVSWDPK.V
R2/RRR2-21/2	1383.675	1384.522	-1338.589	0.404	575.232	0.439	20	0.123	-.RADGVGPVSWDPK.-
R2/RRR2-25/3	1384.460	1384.522	-44.724	0.460	1027.650	0.527	23	0.122	R.RADGVGPVSWDPK.V
R2/RRR2-23/2	1227.647	1228.336	-1379.963	0.283	1102.080	0.310	17	0.122	R.ADGVGPVSWDPK.V
R2/RRR2-22/2	1384.452	1384.522	-50.994	0.460	531.485	0.392	19	0.122	R.RADGVGPVSWDPK.V
R2/RRR2-24/2	1143.173	1143.274	-88.532	0.369	631.169	0.403	16	0.122	K.VASFAQSYAAK.R
R2/RRR2-20/2	1228.183	1228.336	-124.971	0.315	1093.763	0.304	17	0.122	R.ADGVGPVSWDPK.V
R2/RRR2-18/2	1385.173	1384.522	-252.852	0.437	387.282	0.406	17	0.122	R.RADGVGPVSWDPK.V
R2/RRR2-4/2	1142.312	1143.274	-1722.497	0.303	603.236	0.433	17	0.122	K.VASFAQSYAAK.R
R2/RRR2-22/2	1384.067	1384.522	-330.015	0.372	355.693	0.409	17	0.121	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1384.038	1384.522	-350.545	0.377	797.153	0.332	22	0.121	R.RADGVGPVSWDPK.V
R2/RRR2-16/2	1142.539	1143.274	-1522.834	0.366	531.977	0.372	16	0.120	K.VASFAQSYAAK.R
R2/RRR2-20/2	1677.283	1676.854	256.832	0.528	855.372	0.407	19	0.120	R.AWSAADAVASWVGEKK.N
R2/RRR2-23/2	1142.268	1143.274	-1761.580	0.339	502.403	0.376	16	0.120	K.VASFAQSYAAK.R
R2/RRR2-22/3	1384.557	1384.522	25.714	0.512	902.242	0.553	22	0.120	R.RADGVGPVSWDPK.V
R2/RRR2-15/3	1384.009	1384.522	-1096.810	0.514	969.699	0.533	22	0.120	R.RADGVGPVSWDPK.V
R2/RRR2-23/2	1385.188	1384.522	-241.712	0.392	611.555	0.352	20	0.120	R.RADGVGPVSWDPK.V
R2/RRR2-12/3	1384.243	1384.522	-201.951	0.477	852.880	0.564	21	0.120	R.RADGVGPVSWDPK.V
R2/RRR2-21/2	1714.364	1713.780	-243.151	0.411	567.317	0.488	16	0.119	K.KNYHYDTNTCDPGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1547.808	1548.681	-1213.491	0.255	1004.418	0.349	17	0.119	R.AWSAADAVASWVGEK.K
R2/RRR2-1/2	1384.168	1384.522	-256.750	0.397	360.607	0.385	16	0.119	R.RADGVGPVSWDPK.V
R2/RRR2-19/2	1385.085	1384.522	-316.690	0.400	427.896	0.328	18	0.119	R.RADGVGPVSWDPK.V
R2/RRR2-17/2	1384.007	1384.522	-1098.173	0.393	455.050	0.342	18	0.119	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1142.422	1143.274	-1625.769	0.275	617.128	0.416	16	0.119	K.VASFAQSYAAK.R
R2/RRR2-8/3	1384.531	1384.522	6.613	0.484	967.953	0.527	23	0.118	R.RADGVGPVSWDPK.V
R2/RRR2-28/2	1142.388	1143.274	-1655.397	0.365	795.081	0.319	17	0.118	K.VASFAQSYAAK.R
R2/RRR2-23/2	1385.519	1384.522	-1.998	0.395	460.541	0.298	19	0.118	R.RADGVGPVSWDPK.V
R2/RRR2-2/2	1385.181	1384.522	-246.928	0.376	487.505	0.351	18	0.118	R.RADGVGPVSWDPK.V
R2/RRR2-19/2	1383.951	1384.522	-1138.825	0.452	627.255	0.323	20	0.118	R.RADGVGPVSWDPK.V
R2/RRR2-16/2	1676.538	1676.854	-188.752	0.504	894.201	0.373	20	0.118	-.AWSAADAVASWVGEKK.-
R2/RRR2-19/2	1677.244	1676.854	233.186	0.508	678.693	0.398	20	0.118	R.AWSAADAVASWVGEKK.N
R2/RRR2-22/2	1678.102	1676.854	148.651	0.453	584.252	0.440	17	0.117	R.AWSAADAVASWVGEKK.N
R2/RRR2-22/2	1675.396	1676.854	-1471.567	0.351	947.172	0.342	18	0.117	R.AWSAADAVASWVGEKK.N
R2/RRR2-1/2	1385.124	1384.522	-288.130	0.333	307.689	0.326	15	0.117	R.RADGVGPVSWDPK.V
R2/RRR2-17/2	1384.201	1384.522	-232.685	0.410	395.026	0.381	17	0.117	-.RADGVGPVSWDPK.-
R2/RRR2-22/2	1678.215	1676.854	215.979	0.430	581.724	0.434	17	0.117	R.AWSAADAVASWVGEKK.N
R2/RRR2-22/2	1384.254	1384.522	-194.289	0.330	535.639	0.261	20	0.116	R.RADGVGPVSWDPK.V
R2/RRR2-1/2	1384.090	1384.522	-313.202	0.302	370.080	0.271	16	0.115	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1384.135	1384.522	-280.463	0.354	478.151	0.265	18	0.115	R.RADGVGPVSWDPK.V
R2/RRR2-15/2	1384.031	1384.522	-355.855	0.343	410.194	0.300	16	0.115	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1383.537	1384.522	-1438.899	0.357	496.877	0.277	18	0.115	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1383.398	1384.522	-1540.293	0.332	443.457	0.281	17	0.115	R.RADGVGPVSWDPK.V
R2/RRR2-16/2	1383.987	1384.522	-1112.521	0.444	371.700	0.357	16	0.115	-.RADGVGPVSWDPK.-
R2/RRR2-22/2	1384.174	1384.522	-251.884	0.384	361.751	0.335	16	0.115	-.RADGVGPVSWDPK.-
R2/RRR2-23/2	1384.169	1384.522	-256.043	0.334	394.944	0.314	17	0.114	-.RADGVGPVSWDPK.-
R2/RRR2-23/2	1299.132	1299.460	-253.199	0.374	906.979	0.298	17	0.114	K.VASFAQSYAAKR.A
R2/RRR2-13/2	1384.336	1384.522	-134.843	0.379	555.619	0.275	18	0.114	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1385.018	1384.522	359.383	0.400	392.576	0.331	16	0.114	-.RADGVGPVSWDPK.-
R2/RRR2-18/2	1384.184	1384.522	-244.541	0.399	327.929	0.325	15	0.114	-.RADGVGPVSWDPK.-
R2/RRR2-16/2	1384.108	1384.522	-300.195	0.391	408.076	0.291	17	0.114	-.RADGVGPVSWDPK.-
R2/RRR2-2/2	1384.248	1384.522	-198.712	0.338	481.550	0.313	18	0.114	-.RADGVGPVSWDPK.-
R2/RRR2-23/2	1585.784	1585.607	111.906	0.342	797.287	0.356	15	0.114	K.NYHYDTNTCDPGK.V
R2/RRR2-16/2	1383.577	1384.522	-1409.920	0.394	484.689	0.295	18	0.113	-.RADGVGPVSWDPK.-
R2/RRR2-20/2	1299.404	1299.460	-43.024	0.345	750.770	0.360	15	0.113	K.VASFAQSYAAKR.A
R2/RRR2-22/2	1142.243	1143.274	-1783.271	0.231	692.658	0.279	17	0.112	K.VASFAQSYAAK.R
R2/RRR2-18/2	1677.384	1676.854	-280.993	0.410	643.190	0.367	17	0.112	R.AWSAADAVASWVGEKK.N
R2/RRR2-22/2	1677.776	1676.854	-46.457	0.413	482.173	0.404	16	0.111	-.AWSAADAVASWVGEKK.-
R2/RRR2-19/2	1676.283	1676.854	-939.637	0.472	867.756	0.301	20	0.111	R.AWSAADAVASWVGEKK.N
R2/RRR2-22/2	1677.978	1676.854	74.236	0.344	453.682	0.351	16	0.111	R.AWSAADAVASWVGEKK.N
R2/RRR2-17/3	1384.260	1384.522	-190.141	0.461	594.381	0.573	22	0.110	R.RADGVGPVSWDPK.V
R2/RRR2-3/2	1547.391	1548.681	-1484.345	0.297	569.007	0.349	15	0.110	R.AWSAADAVASWVGEK.K
R2/RRR2-15/3	1383.993	1384.522	-1108.102	0.448	992.268	0.476	24	0.110	R.RADGVGPVSWDPK.V
R2/RRR2-22/2	1677.237	1676.854	229.464	0.367	418.609	0.348	14	0.108	R.AWSAADAVASWVGEKK.N
R2/RRR2-11/2	1548.017	1548.681	-1078.396	0.347	618.738	0.234	17	0.107	R.AWSAADAVASWVGEK.K
R2/RRR2-16/2	1676.553	1676.854	-179.695	0.462	649.466	0.303	18	0.106	-.AWSAADAVASWVGEKK.-
R2/RRR2-15/2	1384.105	1384.522	-302.318	0.416	306.684	0.343	15	0.106	-.RADGVGPVSWDPK.-
R2/RRR2-5/3	1384.751	1384.522	165.896	0.430	955.635	0.461	23	0.105	R.RADGVGPVSWDPK.V
R2/RRR2-2/2	1547.284	1548.681	-1554.003	0.279	639.614	0.247	14	0.104	R.AWSAADAVASWVGEK.K
R2/RRR2-21/2	1550.174	1548.681	319.199	0.326	215.002	0.372	13	0.104	-.AWSAADAVASWVGEK.-
R2/RRR2-18/3	1384.203	1384.522	-231.279	0.398	811.471	0.492	23	0.104	R.RADGVGPVSWDPK.V
R2/RRR2-5/2	1547.687	1548.681	-1292.062	0.235	698.330	0.103	17	0.103	R.AWSAADAVASWVGEK.K
R2/RRR2-22/3	1405.459	1405.579	-86.263	0.530	1244.935	0.386	25	0.102	K.VCGHYTQVVWR.K
R2/RRR2-22/3	1384.053	1384.522	-339.582	0.477	730.181	0.495	21	0.102	R.RADGVGPVSWDPK.V
R2/RRR2-22/3	1384.360	1384.522	-117.029	0.489	720.474	0.495	21	0.102	R.RADGVGPVSWDPK.V
R2/RRR2-22/3	1384.145	1384.522	-273.483	0.419	1180.152	0.372	23	0.101	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/3	1384.632	1384.522	79.563	0.482	714.131	0.482	23	0.100	R.RADGVGPVSWDPK.V
R2/RRR2-23/3	1384.816	1384.522	212.836	0.420	905.374	0.428	22	0.098	R.RADGVGPVSWDPK.V
R2/RRR2-22/3	1548.288	1548.681	-254.651	0.423	860.622	0.472	27	0.098	R.AWSAADAVASWVGEK.K
R2/RRR2-26/3	1384.326	1384.522	-142.106	0.390	484.170	0.492	20	0.097	R.RADGVGPVSWDPK.V
R2/RRR2-13/3	1384.693	1384.522	124.124	0.443	517.917	0.481	20	0.097	R.RADGVGPVSWDPK.V
R2/RRR2-17/3	1384.288	1384.522	-169.706	0.400	440.832	0.475	19	0.095	R.RADGVGPVSWDPK.V
R2/RRR2-14/3	1384.196	1384.522	-235.924	0.324	322.288	0.469	20	0.095	R.RADGVGPVSWDPK.V
R2/RRR2-23/3	1405.273	1405.579	-218.794	0.530	1207.663	0.356	24	0.095	K.VCGHYTQVVWR.K
R2/RRR2-22/3	1405.741	1405.579	115.603	0.545	1204.597	0.354	24	0.094	K.VCGHYTQVVWR.K
R2/RRR2-2/3	1384.506	1384.522	-11.427	0.440	952.581	0.392	23	0.093	R.RADGVGPVSWDPK.V
R2/RRR2-22/3	1405.829	1405.579	178.041	0.564	1186.339	0.349	23	0.092	K.VCGHYTQVVWR.K
R2/RRR2-25/3	1384.599	1384.522	55.955	0.475	623.948	0.433	20	0.092	R.RADGVGPVSWDPK.V
R2/RRR2-3/3	1405.313	1405.579	-189.906	0.430	331.306	0.458	16	0.092	-.VCGHYTQVVWR.-
R2/RRR2-14/3	1384.299	1384.522	-161.346	0.288	234.455	0.330	19	0.091	-.RADGVGPVSWDPK.-
R2/RRR2-23/3	1405.779	1405.579	142.381	0.548	1241.091	0.330	24	0.091	K.VCGHYTQVVWR.K
R2/RRR2-20/3	1405.945	1405.579	260.843	0.529	1009.569	0.375	22	0.091	K.VCGHYTQVVWR.K
R2/RRR2-13/3	1384.620	1384.522	71.075	0.450	433.302	0.485	21	0.091	-.RADGVGPVSWDPK.-
R2/RRR2-26/3	1384.824	1384.522	218.803	0.435	535.692	0.449	21	0.091	-.RADGVGPVSWDPK.-
R2/RRR2-7/3	1383.920	1384.522	-1160.712	0.394	731.054	0.409	21	0.090	R.RADGVGPVSWDPK.V
R2/RRR2-20/3	1405.213	1405.579	-261.671	0.514	1021.477	0.369	23	0.090	K.VCGHYTQVVWR.K
R2/RRR2-26/3	1384.213	1384.522	-223.582	0.390	470.442	0.424	20	0.088	-.RADGVGPVSWDPK.-
R2/RRR2-22/3	1585.753	1585.607	92.442	0.326	715.730	0.456	26	0.088	K.NYHYDTNTCDPGK.V
R2/RRR2-24/3	1405.451	1405.579	-91.752	0.523	833.305	0.383	21	0.088	K.VCGHYTQVVWR.K
R2/RRR2-21/3	1405.084	1405.579	-353.583	0.456	754.910	0.368	20	0.086	K.VCGHYTQVVWR.K
R2/RRR2-19/3	1406.502	1405.579	-55.427	0.526	808.333	0.365	21	0.086	K.VCGHYTQVVWR.K
R2/RRR2-23/3	1585.782	1585.607	110.855	0.426	530.707	0.395	24	0.086	K.NYHYDTNTCDPGK.V
R2/RRR2-23/3	1406.399	1405.579	-128.950	0.562	1025.793	0.337	23	0.085	K.VCGHYTQVVWR.K
R2/RRR2-23/3	1405.946	1405.579	261.627	0.496	628.238	0.359	18	0.084	K.VCGHYTQVVWR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1405.511	1405.579	-49.020	0.526	919.888	0.361	22	0.084	-.VCGHYTQVVWR.-
R2/RRR2-22/3	1586.532	1585.607	-47.478	0.376	522.245	0.393	23	0.084	K.NYHYDTNTCDPGK.V
R2/RRR2-2/3	1384.459	1384.522	-45.653	0.371	766.904	0.343	23	0.084	R.RADGVGPVSWDPK.V
R2/RRR2-22/3	1405.864	1405.579	203.118	0.562	963.439	0.338	22	0.083	K.VCGHYTQVVWR.K
R2/RRR2-22/3	1404.863	1405.579	-1225.244	0.535	1086.047	0.313	23	0.083	K.VCGHYTQVVWR.K
R2/RRR2-4/3	1405.421	1405.579	-113.054	0.344	224.109	0.303	17	0.083	-.VCGHYTQVVWR.-
R2/RRR2-1/3	1406.311	1405.579	-191.251	0.480	695.127	0.335	19	0.082	K.VCGHYTQVVWR.K
R2/RRR2-18/3	1404.873	1405.579	-1218.569	0.424	723.119	0.332	19	0.082	K.VCGHYTQVVWR.K
R2/RRR2-2/3	1405.472	1405.579	-76.462	0.405	563.961	0.282	19	0.082	K.VCGHYTQVVWR.K
R2/RRR2-20/3	1405.591	1405.579	7.951	0.517	807.062	0.335	20	0.082	K.VCGHYTQVVWR.K
R2/RRR2-19/3	1405.204	1405.579	-267.816	0.470	634.023	0.314	19	0.082	K.VCGHYTQVVWR.K
R2/RRR2-3/3	1405.087	1405.579	-351.360	0.360	342.090	0.327	17	0.081	-.VCGHYTQVVWR.-
R2/RRR2-4/3	1384.290	1384.522	-168.113	0.346	711.337	0.335	20	0.081	-.RADGVGPVSWDPK.-
R2/RRR2-22/3	1533.618	1533.752	-88.195	0.495	876.770	0.350	24	0.081	K.VCGHYTQVVWRK.S
R2/RRR2-21/3	1406.519	1405.579	-43.152	0.419	644.196	0.297	19	0.081	K.VCGHYTQVVWR.K
R2/RRR2-17/3	1406.026	1405.579	318.693	0.475	627.443	0.341	18	0.080	-.VCGHYTQVVWR.-
R2/RRR2-23/3	1585.692	1585.607	53.762	0.303	431.399	0.335	20	0.080	K.NYHYDTNTCDPGK.V
R2/RRR2-26/3	1405.440	1405.579	-99.854	0.464	536.843	0.291	18	0.079	-.VCGHYTQVVWR.-
R2/RRR2-25/3	1404.681	1405.579	-1355.625	0.409	725.141	0.278	21	0.079	K.VCGHYTQVVWR.K
R2/RRR2-23/3	1404.313	1405.579	-1619.109	0.469	809.335	0.314	21	0.078	-.VCGHYTQVVWR.-
R2/RRR2-23/3	1585.268	1585.607	-214.071	0.381	735.917	0.328	25	0.078	K.NYHYDTNTCDPGK.V
R2/RRR2-24/3	1405.730	1405.579	107.634	0.472	595.395	0.284	19	0.078	-.VCGHYTQVVWR.-
R2/RRR2-21/3	1405.440	1405.579	-99.593	0.489	1028.243	0.278	23	0.078	K.VCGHYTQVVWR.K
R2/RRR2-19/3	1549.594	1548.681	-56.076	0.313	450.569	0.426	23	0.077	-.AWSAADAVASWVGEK.-
R2/RRR2-22/3	1585.807	1585.607	126.604	0.343	668.563	0.308	25	0.076	K.NYHYDTNTCDPGK.V
R2/RRR2-21/3	1405.609	1405.579	21.147	0.517	911.254	0.299	22	0.076	-.VCGHYTQVVWR.-
R2/RRR2-22/3	1585.595	1585.607	-7.623	0.391	786.030	0.298	27	0.076	K.NYHYDTNTCDPGK.V
R2/RRR2-22/3	1584.936	1585.607	-1057.378	0.327	767.238	0.314	25	0.076	K.NYHYDTNTCDPGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/3	1405.237	1405.579	-244.285	0.524	739.311	0.335	19	0.076	-.VCGHYTQVVWR.-
R2/RRR2-24/3	1585.855	1585.607	156.826	0.262	696.047	0.335	25	0.075	K.NYHYDTNTCDPGK.V
R2/RRR2-22/3	1534.320	1533.752	-282.824	0.538	743.458	0.302	23	0.075	K.VCGHYTQVVWRK.S
R2/RRR2-23/3	1404.626	1405.579	-1395.165	0.476	779.528	0.282	20	0.073	-.VCGHYTQVVWR.-
R2/RRR2-15/3	1405.565	1405.579	-10.080	0.333	662.491	0.247	18	0.072	-.VCGHYTQVVWR.-
R2/RRR2-1/3	1549.148	1548.681	302.212	0.378	650.175	0.316	24	0.070	-.AWSAADAVASWVGEK.-
R2/RRR2-1/3	1405.039	1405.579	-1099.346	0.381	591.468	0.333	17	0.066	-.VCGHYTQVVWR.-
R2/RRR2-5/2	1240.697	1241.379	-1359.822	0.496	2021.364	0.521	20	0.265	K.IDNPIGATNIGR.A
R2/RRR2-5/2	1241.266	1241.379	-91.498	0.507	1980.144	0.478	21	0.246	K.IDNPIGATNIGR.A
R2/RRR2-5/2	1240.521	1241.379	-1502.535	0.508	1983.781	0.438	20	0.235	K.IDNPIGATNIGR.A
R2/RRR2-5/2	1950.898	1951.170	-139.991	0.545	1707.095	0.545	21	0.222	R.LEGPIAWDVLYNFEQR.W
R2/RRR2-5/2	1859.543	1860.057	-816.813	0.574	1600.637	0.565	25	0.217	R.AYLPVQELLNGEEIDR.W
R2/RRR2-5/2	1859.735	1860.057	-173.977	0.597	1440.016	0.548	24	0.193	R.AYLPVQELLNGEEIDR.W
R2/RRR2-5/2	1951.070	1951.170	-51.433	0.495	1497.794	0.495	20	0.184	R.LEGPIAWDVLYNFEQR.W
R2/RRR2-5/3	1950.934	1951.170	-121.293	0.518	1725.698	0.446	29	0.178	R.LEGPIAWDVLYNFEQR.W
R2/RRR2-5/2	1509.390	1508.695	-202.679	0.545	1445.811	0.475	21	0.177	R.IVSFVGGLDLCDGR.Y
R2/RRR2-5/2	1880.316	1880.989	-892.178	0.499	1170.698	0.594	25	0.173	R.SIDGGAAFGFPDTPEEAAK.A
R2/RRR2-1/2	1241.487	1241.379	87.515	0.446	1584.600	0.385	19	0.173	K.IDNPIGATNIGR.A
R2/RRR2-5/2	1881.293	1880.989	162.077	0.538	1054.564	0.632	23	0.169	R.SIDGGAAFGFPDTPEEAAK.A
R2/RRR2-5/2	1407.344	1406.561	-154.562	0.516	1340.922	0.469	16	0.166	R.DYLTFFCLGNR.E
R2/RRR2-5/2	1287.026	1287.449	-329.878	0.395	1315.777	0.450	16	0.160	R.SIQDAYIHAIR.R
R2/RRR2-5/2	1372.173	1372.553	-277.643	0.456	1137.322	0.499	18	0.154	K.AGLVSGKDQIIDR.S
R2/RRR2-5/2	1819.393	1820.000	-885.781	0.475	1071.593	0.502	19	0.147	K.IVVVDHELPNQGSQQR.R
R2/RRR2-5/2	1200.983	1201.378	-330.213	0.453	1463.710	0.287	17	0.144	-.M*ITNEPINPR.W
R2/RRR2-5/2	1881.235	1880.989	131.363	0.517	754.744	0.602	20	0.140	R.SIDGGAAFGFPDTPEEAAK.A
R2/RRR2-5/2	1508.673	1508.695	-14.820	0.378	1292.545	0.347	20	0.139	R.IVSFVGGLDLCDGR.Y
R2/RRR2-5/2	1200.969	1201.378	-341.635	0.442	1226.790	0.361	16	0.139	-.M*ITNEPINPR.W
R2/RRR2-5/2	1462.346	1462.633	-196.724	0.361	684.295	0.467	20	0.125	K.YPGVPYTFFSQR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1463.035	1462.633	275.697	0.428	540.567	0.462	18	0.124	K.YPGVPYTFFSQR.Q
R2/RRR2-5/2	1857.523	1858.086	-844.001	0.476	634.940	0.494	17	0.121	K.VTLYQDAHVPDNFIPK.I
R2/RRR2-5/2	1200.495	1201.378	-1573.687	0.362	1002.064	0.292	15	0.118	-.M*ITNEPINPR.-
R2/RRR2-5/3	1819.604	1820.000	-218.363	0.449	1087.005	0.496	28	0.117	K.IVVVDHELPNQGSQQR.R
R2/RRR2-5/2	1462.477	1462.633	-107.043	0.379	518.145	0.333	18	0.114	K.YPGVPYTFFSQR.Q
R2/RRR2-5/2	1858.473	1858.086	208.668	0.474	516.631	0.438	16	0.112	K.VTLYQDAHVPDNFIPK.I
R2/RRR2-5/2	1952.915	1951.170	-131.320	0.357	581.103	0.446	15	0.112	R.LEGPIAWDVLYNFEQR.W
R2/RRR2-5/2	1857.836	1858.086	-135.009	0.475	436.013	0.474	14	0.112	K.VTLYQDAHVPDNFIPK.I
R2/RRR2-3/2	1241.124	1241.379	-205.843	0.314	339.174	0.292	14	0.111	K.IDNPIGATNIGR.A
R2/RRR2-1/2	1859.809	1860.057	-134.142	0.440	789.384	0.347	17	0.110	R.AYLPVQELLNGEEIDR.W
R2/RRR2-5/2	1407.395	1406.561	-118.192	0.310	514.388	0.305	15	0.109	R.DYLTFFCLGNR.E
R2/RRR2-5/3	1820.847	1820.000	-84.302	0.436	889.225	0.530	29	0.109	K.IVVVDHELPNQGSQQR.R
R2/RRR2-2/2	1240.969	1241.379	-331.170	0.394	473.850	0.333	14	0.109	-.IDNPIGATNIGR.-
R2/RRR2-4/2	1407.563	1406.561	1.426	0.277	622.994	0.319	14	0.108	R.DYLTFFCLGNR.E
R2/RRR2-3/2	1952.795	1951.170	-192.772	0.387	639.032	0.352	16	0.107	R.LEGPIAWDVLYNFEQR.W
R2/RRR2-5/2	1406.996	1406.561	310.259	0.316	380.131	0.382	13	0.107	-.DYLTFFCLGNR.-
R2/RRR2-5/2	1508.731	1508.695	23.809	0.389	839.743	0.250	17	0.105	R.IVSFVGGLDLCDGR.Y
R2/RRR2-5/3	1819.522	1820.000	-263.289	0.432	700.177	0.496	26	0.094	K.IVVVDHELPNQGSQQR.R
R2/RRR2-19/2	1637.749	1638.823	-1270.022	0.377	2828.735	0.544	23	0.672	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/2	1977.957	1979.086	-1079.645	0.584	3301.382	0.687	30	0.637	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/2	1924.128	1924.095	16.951	0.647	3244.161	0.624	26	0.585	K.LKVEYELEDGSSLSPEK.E
R2/RRR2-21/2	1638.150	1638.823	-1024.337	0.482	2602.229	0.585	23	0.552	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/2	1923.602	1924.095	-257.247	0.625	3183.160	0.585	26	0.550	K.LKVEYELEDGSSLSPEK.E
R2/RRR2-19/2	1638.365	1638.823	-280.256	0.474	2456.433	0.605	22	0.492	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/2	1923.522	1924.095	-820.198	0.638	2823.638	0.612	25	0.464	K.LKVEYELEDGSSLSPEK.E
R2/RRR2-21/2	1978.452	1979.086	-828.183	0.586	2515.455	0.653	26	0.408	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-22/2	1638.367	1638.823	-278.911	0.493	2225.724	0.543	21	0.389	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/2	1638.207	1638.823	-989.025	0.479	2199.706	0.581	21	0.383	K.M*IEDYLVAHPAEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1979.361	1979.086	139.696	0.584	2321.512	0.664	26	0.369	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-22/2	1638.351	1638.823	-288.853	0.488	2133.375	0.547	21	0.353	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/2	1638.380	1638.823	-270.838	0.445	2120.942	0.535	21	0.350	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/2	1683.299	1682.764	-276.878	0.563	2351.131	0.516	23	0.323	K.VEYELEDGSSLSPEK.E
R2/RRR2-21/2	1682.125	1682.764	-977.280	0.480	2414.805	0.450	23	0.315	K.VEYELEDGSSLSPEK.E
R2/RRR2-21/2	1682.172	1682.764	-949.012	0.494	2422.529	0.423	23	0.307	K.VEYELEDGSSLSPEK.E
R2/RRR2-20/2	1637.535	1638.823	-1400.958	0.348	1948.041	0.421	20	0.287	K.M*IEDYLVAHPAEYA.-
R2/RRR2-19/2	1638.093	1638.823	-1058.904	0.475	1861.129	0.567	20	0.263	K.M*IEDYLVAHPAEYA.-
R2/RRR2-22/2	1638.197	1638.823	-995.534	0.444	1845.139	0.573	20	0.260	K.M*IEDYLVAHPAEYA.-
R2/RRR2-20/2	1638.110	1638.823	-1048.429	0.401	1828.538	0.531	20	0.254	K.M*IEDYLVAHPAEYA.-
R2/RRR2-22/3	1978.991	1979.086	-48.116	0.498	1900.170	0.584	35	0.253	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/2	1637.750	1638.823	-1269.348	0.371	1816.224	0.507	20	0.249	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/3	1978.888	1979.086	-100.276	0.491	1841.989	0.593	35	0.247	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/2	1637.647	1638.823	-1332.229	0.290	1728.603	0.451	19	0.225	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/3	1978.866	1979.086	-111.229	0.496	1739.511	0.584	34	0.225	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/3	1978.328	1979.086	-890.997	0.471	1771.180	0.567	36	0.223	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/3	1978.144	1979.086	-984.665	0.484	1644.103	0.590	35	0.211	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/3	1978.497	1979.086	-805.243	0.477	1587.437	0.606	35	0.208	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/3	1978.873	1979.086	-107.702	0.504	1682.600	0.543	36	0.199	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/2	1207.439	1208.295	-1541.573	0.404	1644.344	0.431	20	0.190	K.LEATGDGSCVAK.L
R2/RRR2-21/2	1207.997	1208.295	-247.267	0.420	1624.419	0.412	20	0.184	K.LEATGDGSCVAK.L
R2/RRR2-21/3	1977.865	1979.086	-1126.222	0.446	1511.508	0.560	32	0.184	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/3	1979.113	1979.086	13.968	0.493	1453.002	0.581	34	0.180	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/2	1207.490	1208.295	-1498.717	0.409	1529.943	0.444	20	0.180	K.LEATGDGSCVAK.L
R2/RRR2-19/3	1978.635	1979.086	-228.750	0.487	1453.202	0.576	32	0.180	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-22/3	1978.502	1979.086	-802.920	0.470	1493.115	0.540	36	0.172	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/2	1269.592	1270.454	-1471.216	0.430	1500.124	0.413	19	0.170	R.VAVCDAASHVLK.S
R2/RRR2-20/3	1978.912	1979.086	-88.303	0.456	1290.160	0.593	32	0.165	K.SHSTETKLEATGDGSCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1270.177	1270.454	-218.872	0.489	1361.991	0.454	18	0.165	R.VAVCDAASHVLK.S
R2/RRR2-21/2	1270.261	1270.454	-152.350	0.425	1452.850	0.403	19	0.164	R.VAVCDAASHVLK.S
R2/RRR2-21/3	1978.720	1979.086	-185.582	0.488	1369.530	0.554	32	0.162	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-18/2	1177.940	1178.320	-323.736	0.415	971.466	0.593	20	0.157	K.LNPAAGVGSTYK.T
R2/RRR2-21/2	1084.244	1083.240	3.547	0.355	1426.026	0.368	16	0.153	K.AFM*DASSLPK.A
R2/RRR2-19/2	1083.726	1083.240	449.584	0.372	1309.113	0.419	16	0.153	K.AFM*DASSLPK.A
R2/RRR2-21/2	1178.058	1178.320	-223.099	0.442	903.933	0.577	20	0.152	K.LNPAAGVGSTYK.T
R2/RRR2-19/3	1978.199	1979.086	-956.414	0.454	1144.512	0.601	30	0.152	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/2	1178.032	1178.320	-244.722	0.467	954.111	0.541	20	0.151	K.LNPAAGVGSTYK.T
R2/RRR2-22/2	1270.378	1270.454	-59.524	0.471	1346.786	0.384	18	0.150	R.VAVCDAASHVLK.S
R2/RRR2-20/2	1083.011	1083.240	-212.265	0.435	1088.710	0.499	15	0.150	K.AFM*DASSLPK.A
R2/RRR2-18/3	1978.343	1979.086	-883.842	0.460	1418.110	0.486	32	0.149	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/2	1177.490	1178.320	-1558.738	0.399	913.243	0.562	20	0.148	K.LNPAAGVGSTYK.T
R2/RRR2-22/2	1177.955	1178.320	-310.740	0.415	909.750	0.551	20	0.148	K.LNPAAGVGSTYK.T
R2/RRR2-18/2	1178.091	1178.320	-194.720	0.375	1025.375	0.514	20	0.147	K.LNPAAGVGSTYK.T
R2/RRR2-21/2	1548.147	1547.755	254.010	0.544	1130.773	0.447	21	0.147	K.EKDIVDGYYGM*LK.M
R2/RRR2-21/3	1923.726	1924.095	-192.542	0.484	1472.056	0.457	32	0.145	K.LKVEYELEDGSSLSPEK.E
R2/RRR2-21/2	1178.014	1178.320	-260.316	0.430	842.453	0.550	19	0.144	K.LNPAAGVGSTYK.T
R2/RRR2-19/2	1178.161	1178.320	-135.577	0.433	794.705	0.559	19	0.143	K.LNPAAGVGSTYK.T
R2/RRR2-21/2	1547.207	1547.755	-1003.432	0.431	1204.192	0.397	21	0.143	K.EKDIVDGYYGM*LK.M
R2/RRR2-22/2	1177.992	1178.320	-279.445	0.421	891.671	0.519	20	0.143	K.LNPAAGVGSTYK.T
R2/RRR2-18/3	1978.377	1979.086	-866.096	0.415	1205.955	0.537	31	0.141	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-21/2	1289.847	1290.467	-1260.046	0.363	1227.728	0.383	16	0.141	K.DIVDGYYGM*LK.M
R2/RRR2-21/2	1547.205	1547.755	-1004.858	0.462	1097.343	0.426	20	0.140	K.EKDIVDGYYGM*LK.M
R2/RRR2-17/2	1179.219	1178.320	-85.930	0.424	650.399	0.592	18	0.140	K.LNPAAGVGSTYK.T
R2/RRR2-22/3	1979.891	1979.086	-98.494	0.519	1078.474	0.584	31	0.140	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/2	1083.042	1083.240	-183.770	0.371	1262.034	0.355	15	0.139	K.AFM*DASSLPK.A
R2/RRR2-21/3	1924.857	1924.095	-124.241	0.468	1578.392	0.388	30	0.139	K.LKVEYELEDGSSLSPEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1177.950	1178.320	-315.003	0.431	787.421	0.521	19	0.138	K.LNPAAGVGSTYK.T
R2/RRR2-19/2	1178.004	1178.320	-268.633	0.366	933.239	0.484	20	0.138	K.LNPAAGVGSTYK.T
R2/RRR2-22/2	1177.936	1178.320	-327.168	0.399	749.565	0.541	19	0.138	K.LNPAAGVGSTYK.T
R2/RRR2-20/2	1084.151	1083.240	-82.169	0.420	857.668	0.494	14	0.136	K.AFM*DASSLPK.A
R2/RRR2-22/2	1082.929	1083.240	-287.918	0.330	1269.501	0.321	16	0.135	K.AFM*DASSLPK.A
R2/RRR2-19/3	1979.906	1979.086	-90.887	0.498	1101.299	0.549	31	0.133	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/2	1177.980	1178.320	-289.010	0.349	680.769	0.545	18	0.132	K.LNPAAGVGSTYK.T
R2/RRR2-21/2	1531.038	1531.755	-1125.062	0.445	968.940	0.408	20	0.131	K.EKDIVDGYYGMLK.M
R2/RRR2-22/2	1082.475	1083.240	-1635.381	0.293	1026.173	0.411	14	0.130	K.AFM*DASSLPK.A
R2/RRR2-19/2	1177.420	1178.320	-1618.311	0.325	592.299	0.548	17	0.127	K.LNPAAGVGSTYK.T
R2/RRR2-18/2	1083.038	1083.240	-187.389	0.366	939.937	0.405	14	0.127	K.AFM*DASSLPK.A
R2/RRR2-21/2	1289.842	1290.467	-1263.753	0.352	1100.933	0.345	16	0.127	K.DIVDGYYGM*LK.M
R2/RRR2-21/2	1068.050	1067.241	-179.589	0.448	575.453	0.490	13	0.126	K.AFMDASSLPK.A
R2/RRR2-18/3	1978.219	1979.086	-946.564	0.456	930.548	0.574	30	0.126	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/2	1178.356	1178.320	30.485	0.379	493.505	0.514	16	0.125	K.LNPAAGVGSTYK.T
R2/RRR2-19/2	1269.995	1270.454	-362.646	0.319	925.486	0.427	15	0.125	R.VAVCDAASHVLK.S
R2/RRR2-17/2	1177.963	1178.320	-304.190	0.342	506.094	0.530	15	0.124	K.LNPAAGVGSTYK.T
R2/RRR2-21/2	1084.257	1083.240	15.065	0.266	978.522	0.370	15	0.123	K.AFM*DASSLPK.A
R2/RRR2-1/2	1178.153	1178.320	-142.021	0.338	619.609	0.416	17	0.120	K.LNPAAGVGSTYK.T
R2/RRR2-21/2	1066.558	1067.241	-1582.647	0.289	695.114	0.424	14	0.119	K.AFMDASSLPK.A
R2/RRR2-19/2	1083.628	1083.240	359.234	0.360	459.058	0.450	12	0.118	K.AFM*DASSLPK.A
R2/RRR2-21/2	1178.319	1178.320	-1.102	0.261	742.531	0.417	17	0.118	K.LNPAAGVGSTYK.T
R2/RRR2-21/2	1179.022	1178.320	-253.447	0.314	667.435	0.370	19	0.118	K.LNPAAGVGSTYK.T
R2/RRR2-17/2	1083.193	1083.240	-44.149	0.318	293.760	0.295	13	0.118	K.AFM*DASSLPK.A
R2/RRR2-18/2	1083.688	1083.240	414.011	0.333	478.055	0.417	12	0.116	K.AFM*DASSLPK.A
R2/RRR2-17/2	1082.791	1083.240	-415.730	0.270	843.807	0.298	15	0.113	K.AFM*DASSLPK.A
R2/RRR2-25/2	1177.971	1178.320	-296.912	0.262	508.509	0.342	16	0.112	K.LNPAAGVGSTYK.T
R2/RRR2-19/2	1547.683	1547.755	-46.688	0.403	842.716	0.283	18	0.111	K.EKDIVDGYYGM*LK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1532.036	1531.755	183.762	0.346	447.594	0.339	15	0.110	K.EKDIVDGYYGMLK.M
R2/RRR2-21/3	1923.873	1924.095	-115.872	0.459	1221.845	0.407	29	0.109	K.LKVEYELEDGSSLSPEK.E
R2/RRR2-21/2	1066.316	1067.241	-1810.468	0.214	597.759	0.247	13	0.107	K.AFMDASSLPK.A
R2/RRR2-21/2	1177.613	1178.320	-1453.981	0.140	627.402	0.129	13	0.102	K.LNPAAGVGSTYK.T
R2/RRR2-19/2	1547.383	1547.755	-240.949	0.333	652.279	0.136	17	0.102	K.EKDIVDGYYGM*LK.M
R2/RRR2-4/3	1978.349	1979.086	-880.590	0.406	588.280	0.537	27	0.102	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-22/3	1270.074	1270.454	-299.925	0.413	380.987	0.567	20	0.101	R.VAVCDAASHVLK.S
R2/RRR2-20/3	1270.375	1270.454	-62.041	0.477	489.753	0.520	23	0.100	R.VAVCDAASHVLK.S
R2/RRR2-19/3	1270.376	1270.454	-61.173	0.441	343.054	0.583	19	0.099	-.VAVCDAASHVLK.-
R2/RRR2-21/3	1270.683	1270.454	181.222	0.431	397.529	0.514	21	0.097	R.VAVCDAASHVLK.S
R2/RRR2-21/2	1623.824	1622.823	0.557	0.443	1223.701	0.469	17	0.097	K.MIEDYLVAHPAEYA.-
R2/RRR2-21/3	1270.811	1270.454	281.644	0.428	536.835	0.477	21	0.094	R.VAVCDAASHVLK.S
R2/RRR2-22/3	1270.229	1270.454	-177.281	0.454	381.442	0.460	20	0.094	R.VAVCDAASHVLK.S
R2/RRR2-20/3	1270.681	1270.454	179.055	0.460	360.343	0.433	20	0.093	R.VAVCDAASHVLK.S
R2/RRR2-11/3	1978.817	1979.086	-136.476	0.399	586.094	0.460	28	0.092	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-20/3	1925.194	1924.095	51.309	0.424	991.336	0.396	25	0.091	K.LKVEYELEDGSSLSPEK.E
R2/RRR2-19/3	1270.451	1270.454	-2.479	0.336	303.278	0.472	18	0.091	R.VAVCDAASHVLK.S
R2/RRR2-22/3	1269.360	1270.454	-1654.809	0.393	280.801	0.407	18	0.091	R.VAVCDAASHVLK.S
R2/RRR2-21/3	1270.121	1270.454	-262.463	0.384	479.991	0.453	22	0.091	R.VAVCDAASHVLK.S
R2/RRR2-18/3	1270.468	1270.454	11.543	0.330	261.496	0.427	17	0.089	R.VAVCDAASHVLK.S
R2/RRR2-11/3	1979.287	1979.086	101.837	0.304	468.743	0.434	28	0.088	K.SHSTETKLEATGDGSCVAK.L
R2/RRR2-18/3	1270.465	1270.454	8.652	0.420	308.286	0.349	19	0.086	-.VAVCDAASHVLK.-
R2/RRR2-20/3	1270.795	1270.454	269.074	0.300	536.089	0.304	21	0.079	R.VAVCDAASHVLK.S
R2/RRR2-2/2	1638.146	1638.823	-1026.283	0.219	1100.473	0.230	19	0.067	K.M*IEDYLVAHPAEYA.-
R2/RRR2-21/2	1623.655	1622.823	-103.958	0.409	1006.132	0.473	17	0.061	K.MIEDYLVAHPAEYA.-
R2/RRR2-2/2	1649.083	1649.735	-1004.954	0.455	2895.685	0.459	23	0.431	R.ALEDDETSATALDGLK.Q
R2/RRR2-2/2	1789.800	1789.919	-66.808	0.502	1704.842	0.621	24	0.248	K.EQAAEGLGELIDVTSEK.T
R2/RRR2-1/2	1555.282	1555.758	-306.910	0.476	1643.744	0.516	22	0.209	K.LLDVLNTPSEAVQR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1451.081	1449.634	308.934	0.438	1747.500	0.448	20	0.209	K.SNDLAQALVGVYAK.E
R2/RRR2-1/2	1697.878	1698.946	-1221.108	0.414	1663.814	0.465	23	0.201	K.VQAAGQTALQQVGSVIK.N
R2/RRR2-2/2	1555.942	1555.758	118.301	0.505	1266.911	0.469	21	0.160	K.LLDVLNTPSEAVQR.A
R2/RRR2-2/2	1555.184	1555.758	-1015.088	0.420	1221.333	0.478	20	0.156	K.LLDVLNTPSEAVQR.A
R2/RRR2-2/2	1260.387	1260.505	-93.898	0.371	1056.738	0.521	19	0.149	R.IIALSTVGTLSGK.S
R2/RRR2-2/2	1696.384	1696.970	-937.381	0.450	1192.039	0.432	22	0.146	K.SAGLQAIDEIVPTLLR.A
R2/RRR2-2/2	877.041	877.066	-28.285	0.324	851.768	0.460	14	0.127	K.YGIAAILR.Q
R2/RRR2-2/2	1070.122	1070.181	-55.103	0.343	959.291	0.363	15	0.123	R.ALADPNVDVR.G
R2/RRR2-2/2	1554.996	1555.758	-1136.309	0.356	900.657	0.388	19	0.122	K.LLDVLNTPSEAVQR.A
R2/RRR2-2/2	1448.661	1449.674	-1393.568	0.449	507.857	0.460	17	0.120	R.QSSVELLGDLLFK.V
R2/RRR2-1/2	1137.288	1137.354	-58.093	0.434	757.278	0.391	13	0.118	K.VLVDPIPEVR.A
R2/RRR2-2/2	1449.522	1449.674	-105.297	0.424	546.433	0.433	17	0.118	R.QSSVELLGDLLFK.V
R2/RRR2-2/2	1696.150	1696.970	-1076.105	0.380	872.653	0.339	20	0.114	K.SAGLQAIDEIVPTLLR.A
R2/RRR2-2/2	1361.871	1361.593	204.384	0.416	980.279	0.255	16	0.110	R.IGM*INALEQLSR.S
R2/RRR2-2/2	1279.602	1280.361	-1378.376	0.258	858.259	0.316	14	0.109	R.TALCDSTQEVR.E
R2/RRR2-1/2	1070.121	1070.181	-56.819	0.309	694.674	0.292	14	0.109	R.ALADPNVDVR.G
R2/RRR2-1/2	1137.258	1137.354	-84.255	0.344	424.787	0.401	10	0.107	-.VLVDPIPEVR.-
R2/RRR2-2/2	1070.290	1070.181	101.857	0.320	818.557	0.241	14	0.107	R.ALADPNVDVR.G
R2/RRR2-2/2	1287.162	1287.443	-219.122	0.302	762.945	0.307	14	0.106	R.ESAGLAFSTLYK.S
R2/RRR2-12/2	1330.045	1330.456	-310.095	0.504	1852.708	0.489	20	0.232	K.FSNACGAICTTK.K
R2/RRR2-12/2	1452.178	1452.588	-283.341	0.481	1822.364	0.471	20	0.222	K.SAGILCSYDPNVR.L
R2/RRR2-12/2	1329.986	1330.456	-354.666	0.470	1812.547	0.442	20	0.214	K.FSNACGAICTTK.K
R2/RRR2-12/2	1329.990	1330.456	-351.627	0.488	1619.918	0.520	19	0.208	K.FSNACGAICTTK.K
R2/RRR2-12/2	1452.210	1452.588	-261.498	0.479	1643.473	0.489	19	0.202	K.SAGILCSYDPNVR.L
R2/RRR2-12/2	1452.171	1452.588	-287.895	0.457	1590.257	0.449	19	0.187	K.SAGILCSYDPNVR.L
R2/RRR2-12/2	1458.116	1458.629	-1041.183	0.466	1374.049	0.487	20	0.175	K.FSNACGAICTTKK.G
R2/RRR2-12/2	1906.685	1907.287	-842.531	0.543	932.493	0.614	23	0.156	K.KGAIPALPTVAVAQELISK.A
R2/RRR2-12/2	1503.401	1503.599	-132.063	0.396	1013.373	0.432	19	0.136	K.DDSIFHNEEKLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1453.313	1452.588	-189.606	0.407	913.266	0.475	15	0.131	K.SAGILCSYDPNVR.L
R2/RRR2-12/2	1906.644	1907.287	-864.319	0.513	677.406	0.564	20	0.131	K.KGAIPALPTVAVAQELISK.A
R2/RRR2-12/2	1778.462	1779.114	-931.571	0.433	585.499	0.584	21	0.131	K.GAIPALPTVAVAQELISK.A
R2/RRR2-12/2	1779.624	1779.114	-275.926	0.421	575.729	0.562	22	0.129	K.GAIPALPTVAVAQELISK.A
R2/RRR2-12/2	1503.162	1503.599	-291.569	0.407	861.744	0.438	17	0.128	K.DDSIFHNEEKLR.E
R2/RRR2-12/2	1778.460	1779.114	-932.880	0.387	644.749	0.519	21	0.125	K.GAIPALPTVAVAQELISK.A
R2/RRR2-12/2	987.894	988.160	-270.568	0.363	689.342	0.433	14	0.122	K.LLIVTDGEK.G
R2/RRR2-12/2	1292.101	1292.508	-315.885	0.442	689.032	0.435	14	0.120	K.NVLSLWFDGLK.L
R2/RRR2-12/2	1255.019	1255.404	-307.853	0.392	681.520	0.390	16	0.119	R.LPLWPSEDAAR.A
R2/RRR2-11/2	1779.651	1779.114	-260.855	0.412	722.183	0.440	20	0.119	K.GAIPALPTVAVAQELISK.A
R2/RRR2-12/2	988.060	988.160	-101.377	0.414	467.824	0.401	13	0.118	K.LLIVTDGEK.G
R2/RRR2-12/2	1254.636	1255.404	-1413.611	0.384	400.354	0.479	13	0.118	R.LPLWPSEDAAR.A
R2/RRR2-12/2	988.034	988.160	-128.394	0.445	443.134	0.380	12	0.116	K.LLIVTDGEK.G
R2/RRR2-12/2	1234.011	1234.254	-197.108	0.394	924.225	0.290	15	0.115	K.DDSIFHNEEK.L
R2/RRR2-11/2	1255.365	1255.404	-30.977	0.307	581.384	0.411	15	0.115	R.LPLWPSEDAAR.A
R2/RRR2-12/2	1234.121	1234.254	-108.397	0.402	942.503	0.270	15	0.113	K.DDSIFHNEEK.L
R2/RRR2-10/2	1778.846	1779.114	-151.191	0.369	438.043	0.470	17	0.113	K.GAIPALPTVAVAQELISK.A
R2/RRR2-16/2	1256.366	1255.404	-30.855	0.293	553.972	0.389	15	0.113	R.LPLWPSEDAAR.A
R2/RRR2-12/2	1233.895	1234.254	-291.988	0.393	870.935	0.286	14	0.112	K.DDSIFHNEEK.L
R2/RRR2-11/2	1254.973	1255.404	-344.743	0.302	327.731	0.412	12	0.111	R.LPLWPSEDAAR.A
R2/RRR2-13/2	1778.749	1779.114	-205.439	0.305	463.191	0.414	17	0.108	K.GAIPALPTVAVAQELISK.A
R2/RRR2-12/2	1906.731	1907.287	-818.303	0.293	370.238	0.375	14	0.101	K.KGAIPALPTVAVAQELISK.A
R2/RRR2-12/3	1907.040	1907.287	-129.831	0.418	907.559	0.452	26	0.095	K.KGAIPALPTVAVAQELISK.A
R2/RRR2-12/3	1906.873	1907.287	-217.776	0.333	1113.451	0.337	27	0.087	K.KGAIPALPTVAVAQELISK.A
R2/RRR2-10/3	1749.029	1748.915	65.402	0.499	2576.165	0.448	34	0.340	K.SYELPDGQVITIGAER.F
R2/RRR2-10/2	1827.329	1827.024	167.333	0.612	1998.075	0.516	22	0.257	K.LAYVALDYEQELEAAK.S
R2/RRR2-10/2	1826.473	1827.024	-851.981	0.527	2038.895	0.445	22	0.245	K.LAYVALDYEQELEAAK.S
R2/RRR2-10/2	1827.398	1827.024	204.847	0.593	1846.753	0.503	21	0.230	K.LAYVALDYEQELEAAK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1748.201	1748.915	-983.457	0.495	1891.475	0.510	32	0.223	K.SYELPDGQVITIGAER.F
R2/RRR2-12/2	1748.537	1748.915	-216.692	0.545	1583.353	0.553	25	0.209	K.SYELPDGQVITIGAER.F
R2/RRR2-10/2	1748.349	1748.915	-898.245	0.545	1582.830	0.541	25	0.206	K.SYELPDGQVITIGAER.F
R2/RRR2-10/2	1749.380	1748.915	266.754	0.540	1522.324	0.548	25	0.201	K.SYELPDGQVITIGAER.F
R2/RRR2-12/2	1748.485	1748.915	-246.598	0.549	1546.827	0.527	25	0.198	K.SYELPDGQVITIGAER.F
R2/RRR2-11/2	1748.174	1748.915	-998.697	0.506	1419.606	0.493	25	0.177	K.SYELPDGQVITIGAER.F
R2/RRR2-10/2	1748.237	1748.915	-962.804	0.516	1399.603	0.494	24	0.175	K.SYELPDGQVITIGAER.F
R2/RRR2-11/2	1748.197	1748.915	-985.728	0.515	1307.268	0.534	24	0.175	K.SYELPDGQVITIGAER.F
R2/RRR2-10/2	976.928	977.013	-87.556	0.463	1171.126	0.478	16	0.154	K.AGFAGDDAPR.A
R2/RRR2-13/2	1750.484	1748.915	-247.226	0.534	1049.478	0.531	21	0.151	K.SYELPDGQVITIGAER.F
R2/RRR2-10/2	1429.676	1430.504	-1282.930	0.439	1129.449	0.485	18	0.151	K.GEYDESGPAIVHR.K
R2/RRR2-12/2	1132.939	1133.193	-224.311	0.418	904.610	0.524	16	0.143	R.GYSFTTTAER.E
R2/RRR2-12/2	1132.938	1133.193	-225.284	0.475	920.735	0.501	16	0.143	R.GYSFTTTAER.E
R2/RRR2-10/2	1132.861	1133.193	-294.144	0.421	835.549	0.539	16	0.142	R.GYSFTTTAER.E
R2/RRR2-10/2	976.298	977.013	-1761.445	0.435	1212.260	0.384	16	0.142	K.AGFAGDDAPR.A
R2/RRR2-10/2	1516.214	1516.687	-312.719	0.390	1096.354	0.422	17	0.139	K.IWHHTFYNELR.V
R2/RRR2-10/2	1516.057	1516.687	-1078.516	0.432	1025.732	0.444	17	0.139	K.IWHHTFYNELR.V
R2/RRR2-10/2	976.968	977.013	-45.694	0.464	1207.044	0.357	16	0.137	K.AGFAGDDAPR.A
R2/RRR2-12/2	1133.010	1133.193	-162.053	0.467	886.478	0.466	16	0.137	R.GYSFTTTAER.E
R2/RRR2-10/3	1748.607	1748.915	-176.780	0.469	1513.107	0.403	29	0.135	K.SYELPDGQVITIGAER.F
R2/RRR2-10/2	976.290	977.013	-1769.862	0.348	1210.785	0.341	16	0.134	K.AGFAGDDAPR.A
R2/RRR2-10/2	976.306	977.013	-1753.530	0.362	1139.982	0.369	15	0.133	K.AGFAGDDAPR.A
R2/RRR2-9/2	976.221	977.013	-1841.477	0.392	1007.699	0.389	15	0.130	K.AGFAGDDAPR.A
R2/RRR2-10/2	1133.168	1133.193	-22.324	0.437	707.911	0.473	15	0.129	R.GYSFTTTAER.E
R2/RRR2-10/2	1164.074	1164.355	-241.706	0.346	922.483	0.403	17	0.127	K.EITALAPSSM*K.I
R2/RRR2-1/2	976.954	977.013	-60.107	0.388	1158.748	0.304	15	0.126	K.AGFAGDDAPR.A
R2/RRR2-9/2	1132.918	1133.193	-243.552	0.370	786.795	0.430	16	0.126	R.GYSFTTTAER.E
R2/RRR2-9/2	976.420	977.013	-1636.334	0.328	1228.532	0.269	16	0.126	K.AGFAGDDAPR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1516.613	1516.687	-49.223	0.488	1506.628	0.394	26	0.125	K.IWHHTFYNELR.V
R2/RRR2-10/3	1516.399	1516.687	-190.568	0.577	1178.203	0.503	23	0.125	K.IWHHTFYNELR.V
R2/RRR2-10/2	1148.056	1148.355	-261.243	0.450	903.724	0.382	16	0.125	K.EITALAPSSMK.I
R2/RRR2-10/2	1132.849	1133.193	-303.982	0.323	696.679	0.478	15	0.124	R.GYSFTTTAER.E
R2/RRR2-12/2	1164.389	1164.355	29.123	0.424	804.745	0.377	16	0.121	K.EITALAPSSM*K.I
R2/RRR2-10/2	1148.161	1148.355	-169.831	0.408	655.963	0.432	14	0.120	K.EITALAPSSMK.I
R2/RRR2-10/2	1163.620	1164.355	-1494.974	0.301	714.323	0.404	16	0.118	K.EITALAPSSM*K.I
R2/RRR2-10/3	1516.169	1516.687	-1004.394	0.499	1315.899	0.416	24	0.115	K.IWHHTFYNELR.V
R2/RRR2-10/2	1144.783	1145.381	-1400.170	0.308	260.365	0.494	16	0.115	R.HTGVMVGMGQK.D
R2/RRR2-12/2	1163.481	1164.355	-1615.119	0.272	718.965	0.365	16	0.114	K.EITALAPSSM*K.I
R2/RRR2-10/2	1163.945	1164.355	-352.814	0.311	515.399	0.382	13	0.112	K.EITALAPSSM*K.I
R2/RRR2-12/2	1163.978	1164.355	-324.614	0.358	467.516	0.334	13	0.112	K.EITALAPSSM*K.I
R2/RRR2-19/2	977.292	977.013	286.317	0.239	807.472	0.290	14	0.110	K.AGFAGDDAPR.A
R2/RRR2-10/2	1148.064	1148.355	-254.309	0.313	604.281	0.311	13	0.109	K.EITALAPSSMK.I
R2/RRR2-12/2	1149.371	1148.355	13.890	0.262	552.262	0.285	12	0.106	K.EITALAPSSMK.I
R2/RRR2-10/2	976.887	977.013	-129.421	0.306	724.212	0.144	13	0.103	K.AGFAGDDAPR.A
R2/RRR2-10/2	1749.496	1748.915	-240.227	0.334	617.176	0.264	15	0.102	K.SYELPDGQVITIGAER.F
R2/RRR2-10/3	1933.457	1934.118	-861.949	0.463	1051.632	0.395	27	0.094	K.YPIEHGIVSNWDDMEK.I
R2/RRR2-11/2	976.434	977.013	-1621.262	0.173	524.209	0.123	13	0.091	-.AGFAGDDAPR.-
R2/RRR2-10/3	1564.377	1564.787	-262.599	0.384	762.449	0.472	24	0.089	R.LDLAGRDLTDSLM*K.I
R2/RRR2-10/3	1137.574	1137.400	153.348	0.457	724.452	0.432	20	0.087	K.IKVVAPPERK.Y
R2/RRR2-10/3	1430.495	1430.504	-6.738	0.349	616.377	0.501	28	0.087	K.GEYDESGPAIVHR.K
R2/RRR2-10/3	1145.432	1145.381	43.909	0.447	1064.406	0.347	22	0.087	R.HTGVMVGMGQK.D
R2/RRR2-10/3	1429.846	1430.504	-1163.034	0.252	777.580	0.479	28	0.083	K.GEYDESGPAIVHR.K
R2/RRR2-10/3	1137.299	1137.400	-89.001	0.458	613.174	0.381	18	0.081	K.IKVVAPPERK.Y
R2/RRR2-10/3	1933.179	1934.118	-1006.333	0.422	729.538	0.410	22	0.081	K.YPIEHGIVSNWDDMEK.I
R2/RRR2-10/3	1137.611	1137.400	186.115	0.452	705.359	0.337	20	0.078	K.IKVVAPPERK.Y
R2/RRR2-10/3	1430.665	1430.504	112.776	0.240	353.621	0.368	23	0.074	K.GEYDESGPAIVHR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1145.459	1145.381	67.477	0.435	1092.599	0.249	21	0.073	R.HTGVMVGMGQK.D
R2/RRR2-10/3	1144.477	1145.381	-1668.970	0.313	566.210	0.349	17	0.069	-.HTGVMVGMGQK.-
R2/RRR2-10/3	1162.427	1161.381	39.419	0.463	925.538	0.263	21	0.068	-.HTGVM*VGMGQK.-
R2/RRR2-10/3	1144.548	1145.381	-1606.286	0.287	613.397	0.179	17	0.048	-.HTGVMVGMGQK.-
R2/RRR2-10/2	1906.261	1907.088	-961.210	0.590	2084.402	0.530	24	0.276	K.LSYIALDYDQEM*ETAK.T
R2/RRR2-10/2	1907.307	1907.088	115.199	0.643	1872.034	0.589	23	0.257	K.LSYIALDYDQEM*ETAK.T
R2/RRR2-10/2	1906.338	1907.088	-920.709	0.564	1962.362	0.504	24	0.249	K.LSYIALDYDQEM*ETAK.T
R2/RRR2-10/2	1461.982	1460.531	309.478	0.478	1847.294	0.537	19	0.246	K.AEYDESGPSIVHR.K
R2/RRR2-10/2	1890.427	1891.089	-881.707	0.529	1522.450	0.504	22	0.189	K.LSYIALDYDQEMETAK.T
R2/RRR2-10/2	1890.698	1891.089	-207.328	0.535	1472.009	0.501	22	0.183	K.LSYIALDYDQEMETAK.T
R2/RRR2-10/3	1640.851	1640.883	-19.811	0.452	822.100	0.430	24	0.091	R.LDLAGRDLTDYLM*K.I
R2/RRR2-10/3	1624.552	1624.884	-204.749	0.329	851.695	0.377	26	0.082	R.LDLAGRDLTDYLMK.I
R2/RRR2-10/3	1641.023	1640.883	85.614	0.359	632.085	0.388	22	0.080	R.LDLAGRDLTDYLM*K.I
R2/RRR2-10/3	1640.888	1640.883	2.798	0.403	644.345	0.360	23	0.079	R.LDLAGRDLTDYLM*K.I
R2/RRR2-10/3	1624.880	1624.884	-2.164	0.292	453.639	0.324	22	0.076	R.LDLAGRDLTDYLMK.I
R2/RRR2-10/3	1641.974	1640.883	55.216	0.516	680.678	0.274	23	0.069	-.LDLAGRDLTDYLM*K.-
R2/RRR2-5/3	1751.699	1751.922	-127.750	0.518	1910.745	0.537	34	0.237	K.IGGVPHGLSTDSEVVQR.E
R2/RRR2-5/3	1752.616	1751.922	-175.502	0.552	1816.310	0.492	32	0.204	K.IGGVPHGLSTDSEVVQR.E
R2/RRR2-4/2	1487.158	1486.653	-333.731	0.530	1421.715	0.461	21	0.172	K.GLVDSDTLPLNVSR.E
R2/RRR2-4/2	1486.495	1486.653	-106.632	0.439	1446.391	0.425	20	0.167	K.GLVDSDTLPLNVSR.E
R2/RRR2-5/3	1751.914	1751.922	-4.873	0.529	1537.661	0.483	30	0.161	K.IGGVPHGLSTDSEVVQR.E
R2/RRR2-4/2	1966.576	1966.054	-243.532	0.529	1050.745	0.577	21	0.159	K.ADGSFAISEDTWNEPLGR.G
R2/RRR2-4/2	1486.303	1486.653	-235.812	0.427	1357.581	0.414	21	0.157	K.GLVDSDTLPLNVSR.E
R2/RRR2-4/2	1164.031	1164.245	-184.450	0.434	1051.151	0.477	17	0.145	K.ALDTESVDSVK.I
R2/RRR2-5/2	1101.753	1102.223	-427.803	0.478	1037.810	0.468	16	0.145	K.LGIIEDATNR.N
R2/RRR2-4/2	1552.290	1552.749	-297.012	0.442	1477.984	0.283	19	0.143	R.VFISDEFDELLPK.Y
R2/RRR2-4/2	1163.271	1164.245	-1702.093	0.384	1013.268	0.482	18	0.142	K.ALDTESVDSVK.I
R2/RRR2-4/2	1102.035	1102.223	-171.162	0.459	1195.016	0.384	17	0.142	K.LGIIEDATNR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1163.887	1164.245	-308.605	0.435	988.461	0.465	17	0.140	K.ALDTESVDSVK.I
R2/RRR2-4/2	1866.494	1864.989	-266.364	0.485	797.550	0.565	18	0.137	R.DKVAQDSESESLKQTAK.L
R2/RRR2-4/2	1167.080	1167.294	-183.864	0.481	1043.998	0.386	17	0.134	K.LASLDEYISR.M
R2/RRR2-4/2	1101.392	1102.223	-1667.658	0.465	1129.426	0.360	16	0.134	K.LGIIEDATNR.N
R2/RRR2-4/2	1167.201	1167.294	-79.891	0.463	1045.865	0.354	17	0.129	K.LASLDEYISR.M
R2/RRR2-5/2	1102.004	1102.223	-199.276	0.392	941.690	0.370	15	0.125	K.LGIIEDATNR.N
R2/RRR2-4/2	1101.335	1102.223	-1719.995	0.406	1024.156	0.332	16	0.124	K.LGIIEDATNR.N
R2/RRR2-4/2	840.940	840.990	-59.637	0.358	518.269	0.437	11	0.117	-.VLEINPR.-
R2/RRR2-4/2	841.058	840.990	80.705	0.378	351.788	0.424	9	0.115	-.VLEINPR.-
R2/RRR2-4/3	1864.720	1864.989	-144.695	0.502	766.657	0.558	30	0.109	R.DKVAQDSESESLKQTAK.L
R2/RRR2-4/3	1701.949	1701.774	103.468	0.490	1139.017	0.439	25	0.109	K.APHDLYESYYNSNK.S
R2/RRR2-5/2	841.037	840.990	55.959	0.336	359.220	0.346	9	0.108	-.VLEINPR.-
R2/RRR2-4/2	1578.195	1578.702	-958.084	0.367	811.683	0.276	15	0.106	K.ETTTEWELLNDVK.A
R2/RRR2-4/2	1578.155	1578.702	-983.012	0.367	634.147	0.317	14	0.105	K.ETTTEWELLNDVK.A
R2/RRR2-4/3	1865.768	1864.989	-118.857	0.526	771.814	0.532	29	0.105	R.DKVAQDSESESLKQTAK.L
R2/RRR2-4/3	1864.787	1864.989	-108.841	0.466	809.088	0.524	30	0.104	R.DKVAQDSESESLKQTAK.L
R2/RRR2-6/2	1553.102	1552.749	227.702	0.313	534.444	0.264	13	0.101	R.VFISDEFDELLPK.Y
R2/RRR2-4/3	1701.443	1701.774	-195.280	0.481	1199.286	0.335	24	0.092	K.APHDLYESYYNSNK.S
R2/RRR2-4/3	1701.289	1701.774	-285.545	0.527	975.145	0.351	22	0.082	K.APHDLYESYYNSNK.S
R2/RRR2-4/3	1615.702	1615.726	-14.453	0.385	1022.100	0.332	25	0.081	R.SSAEKFEFQAEVSR.L
R2/RRR2-10/2	1438.180	1438.656	-331.645	0.557	2791.311	0.591	25	0.450	K.YVILGGGVAAGYAAR.E
R2/RRR2-10/2	1437.581	1438.656	-1447.830	0.420	2902.155	0.516	25	0.449	K.YVILGGGVAAGYAAR.E
R2/RRR2-10/2	1438.131	1438.656	-1063.654	0.561	2670.417	0.576	25	0.415	K.YVILGGGVAAGYAAR.E
R2/RRR2-10/2	1533.034	1533.665	-1066.572	0.527	2591.594	0.336	24	0.310	K.VLGAFLEGGSPDENK.A
R2/RRR2-10/2	1533.352	1533.665	-204.702	0.534	2529.635	0.337	24	0.298	K.VLGAFLEGGSPDENK.A
R2/RRR2-10/2	1916.345	1917.152	-945.620	0.516	1442.905	0.537	24	0.188	K.VLGAFLEGGSPDENKAIAK.V
R2/RRR2-10/2	1316.234	1315.581	-264.700	0.484	1450.634	0.512	17	0.185	K.GIELILSTEIVK.A
R2/RRR2-10/2	1314.808	1315.581	-1352.829	0.433	1625.461	0.418	18	0.185	K.GIELILSTEIVK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1984.497	1985.143	-832.138	0.545	1333.104	0.502	21	0.167	K.LSDFGTQGADSNNILYLR.E
R2/RRR2-10/2	1916.498	1917.152	-865.688	0.520	1113.666	0.557	20	0.157	K.VLGAFLEGGSPDENKAIAK.V
R2/RRR2-10/2	1984.462	1985.143	-849.922	0.540	1152.955	0.497	20	0.149	K.LSDFGTQGADSNNILYLR.E
R2/RRR2-10/2	1984.560	1985.143	-800.154	0.567	1010.606	0.514	19	0.141	K.LSDFGTQGADSNNILYLR.E
R2/RRR2-10/2	1916.695	1917.152	-239.330	0.517	977.689	0.513	20	0.139	K.VLGAFLEGGSPDENKAIAK.V
R2/RRR2-10/2	1586.365	1586.769	-255.283	0.488	949.424	0.416	22	0.130	R.EVDDADKLVAAIQAK.K
R2/RRR2-10/2	1586.196	1586.769	-994.856	0.468	984.452	0.402	22	0.130	R.EVDDADKLVAAIQAK.K
R2/RRR2-10/2	1138.090	1137.273	-160.791	0.475	630.306	0.467	15	0.128	K.GYLFPQNAAR.L
R2/RRR2-10/2	1315.107	1315.581	-361.285	0.360	1054.888	0.363	17	0.127	K.GIELILSTEIVK.A
R2/RRR2-10/2	1201.084	1201.355	-226.365	0.380	1025.364	0.358	15	0.126	K.FGSYWIKDGK.V
R2/RRR2-10/2	1432.104	1431.619	340.300	0.463	598.105	0.480	18	0.125	K.EAVAPYERPALSK.G
R2/RRR2-10/2	1586.356	1586.769	-261.150	0.452	861.492	0.409	21	0.125	R.EVDDADKLVAAIQAK.K
R2/RRR2-9/2	1136.924	1137.273	-307.093	0.389	521.258	0.455	14	0.122	K.GYLFPQNAAR.L
R2/RRR2-10/2	1431.384	1431.619	-164.369	0.464	536.093	0.461	17	0.121	K.EAVAPYERPALSK.G
R2/RRR2-10/2	1431.234	1431.619	-269.694	0.445	548.880	0.439	17	0.119	K.EAVAPYERPALSK.G
R2/RRR2-9/2	1137.077	1137.273	-172.456	0.335	587.824	0.414	15	0.118	K.GYLFPQNAAR.L
R2/RRR2-1/2	1138.108	1137.273	-145.405	0.349	635.149	0.386	13	0.115	K.GYLFPQNAAR.L
R2/RRR2-10/2	1136.506	1137.273	-1559.467	0.316	617.054	0.328	15	0.113	K.GYLFPQNAAR.L
R2/RRR2-10/2	1138.188	1137.273	-74.828	0.339	384.618	0.363	12	0.111	-.GYLFPQNAAR.-
R2/RRR2-9/2	1136.490	1137.273	-1572.955	0.299	439.896	0.334	12	0.109	-.GYLFPQNAAR.-
R2/RRR2-10/3	1471.785	1472.624	-1253.262	0.468	858.698	0.435	27	0.092	R.LPGFHVCVGSGGER.L
R2/RRR2-10/3	1473.592	1472.624	-21.746	0.430	895.840	0.426	26	0.091	R.LPGFHVCVGSGGER.L
R2/RRR2-10/3	1472.453	1472.624	-116.638	0.459	962.228	0.393	28	0.089	R.LPGFHVCVGSGGER.L
R2/RRR2-10/3	1201.392	1201.355	31.163	0.376	840.373	0.391	20	0.081	K.FGSYWIKDGK.V
R2/RRR2-9/3	1201.697	1201.355	285.310	0.353	355.459	0.323	14	0.075	K.FGSYWIKDGK.V
R2/RRR2-10/2	993.079	993.138	-59.994	0.299	1149.594	0.345	14	0.073	K.EGLQFASKI.-
R2/RRR2-10/2	993.107	993.138	-32.006	0.314	793.615	0.415	12	0.031	K.EGLQFASKI.-
R2/RRR2-8/2	1840.962	1841.100	-75.659	0.601	2819.356	0.620	26	0.476	K.HVAEANIIFVSVNTPTK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1841.836	1841.100	-144.166	0.510	1660.339	0.468	28	0.176	K.HVAEANIIFVSVNTPTK.T
R2/RRR2-8/2	965.646	966.201	-1614.968	0.446	998.611	0.400	15	0.134	K.IAVLGFAFK.K
R2/RRR2-8/2	965.931	966.201	-280.523	0.451	996.740	0.389	15	0.132	K.IAVLGFAFK.K
R2/RRR2-8/2	966.079	966.201	-126.369	0.464	995.033	0.380	15	0.131	K.IAVLGFAFK.K
R2/RRR2-8/3	1841.719	1841.100	-207.896	0.486	1521.879	0.376	28	0.130	K.HVAEANIIFVSVNTPTK.T
R2/RRR2-9/2	966.190	966.201	-11.292	0.473	937.895	0.384	15	0.129	K.IAVLGFAFK.K
R2/RRR2-9/2	965.804	966.201	-412.656	0.459	965.604	0.377	15	0.129	K.IAVLGFAFK.K
R2/RRR2-9/2	965.641	966.201	-1620.810	0.454	890.496	0.388	14	0.127	K.IAVLGFAFK.K
R2/RRR2-4/2	1353.210	1352.561	-260.543	0.491	1892.910	0.578	21	0.262	K.YVVTLSSGGSILR.A
R2/RRR2-4/2	1344.148	1343.599	-336.992	0.459	2122.297	0.352	17	0.234	R.IIWSNLLQSLR.S
R2/RRR2-4/2	1770.701	1771.048	-196.900	0.456	1625.937	0.441	21	0.191	R.VVVLTEENVIASLDLR.S
R2/RRR2-4/2	1352.380	1352.561	-134.498	0.456	1554.344	0.474	20	0.189	K.YVVTLSSGGSILR.A
R2/RRR2-4/2	1957.892	1958.163	-138.928	0.526	1509.490	0.514	20	0.189	K.DGVSVANVEHNLFEWLK.G
R2/RRR2-4/2	1959.195	1958.163	16.335	0.550	1200.339	0.574	18	0.168	K.DGVSVANVEHNLFEWLK.G
R2/RRR2-4/2	1280.964	1281.397	-339.086	0.457	1184.595	0.515	17	0.162	K.FTSDVTNEVIR.E
R2/RRR2-4/2	1343.290	1343.599	-230.748	0.405	1643.120	0.291	16	0.160	R.IIWSNLLQSLR.S
R2/RRR2-4/2	1580.525	1579.735	-133.288	0.461	1071.167	0.550	19	0.158	K.ELWSIVFPSDTER.I
R2/RRR2-4/2	1280.669	1281.397	-1353.423	0.438	1023.002	0.503	17	0.148	K.FTSDVTNEVIR.E
R2/RRR2-4/2	1281.050	1281.397	-271.587	0.436	984.856	0.526	16	0.148	K.FTSDVTNEVIR.E
R2/RRR2-1/2	1959.374	1958.163	108.128	0.461	802.656	0.542	17	0.132	K.DGVSVANVEHNLFEWLK.G
R2/RRR2-4/2	1352.521	1352.561	-30.019	0.315	1001.993	0.370	16	0.122	K.YVVTLSSGGSILR.A
R2/RRR2-4/2	1211.900	1212.398	-412.022	0.376	641.285	0.416	15	0.118	K.IIADQDVM*YK.Y
R2/RRR2-4/2	1040.191	1039.212	-20.553	0.489	679.062	0.342	12	0.117	K.VFLNNYIR.T
R2/RRR2-4/2	1078.050	1077.259	-193.937	0.446	926.165	0.280	14	0.115	-.LNLYQLNAK.-
R2/RRR2-4/2	1039.171	1039.212	-40.013	0.437	784.757	0.283	13	0.114	K.VFLNNYIR.T
R2/RRR2-4/2	1039.028	1039.212	-178.007	0.486	651.483	0.297	13	0.112	-.VFLNNYIR.-
R2/RRR2-4/2	1579.232	1579.735	-954.198	0.234	817.151	0.372	17	0.112	K.ELWSIVFPSDTER.I
R2/RRR2-3/2	1343.706	1343.599	80.038	0.360	703.198	0.310	15	0.110	R.IIWSNLLQSLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1077.244	1077.259	-13.481	0.455	718.971	0.270	13	0.109	K.LNLYQLNAK.T
R2/RRR2-4/2	1697.467	1697.998	-904.180	0.367	787.968	0.309	18	0.108	-.QLLIGTIGDQVLALDK.-
R2/RRR2-4/2	1078.288	1077.259	26.955	0.453	853.795	0.183	14	0.104	-.LNLYQLNAK.-
R2/RRR2-4/2	1578.749	1579.735	-1261.367	0.162	574.792	0.280	13	0.098	K.ELWSIVFPSDTER.I
R2/RRR2-4/3	1339.400	1338.493	-69.767	0.464	842.629	0.296	20	0.074	R.ICQWQVPHNR.V
R2/RRR2-4/3	1338.653	1338.493	119.979	0.413	980.200	0.256	21	0.071	R.ICQWQVPHNR.V
R2/RRR2-4/3	1495.505	1495.772	-179.404	0.413	988.847	0.202	20	0.055	-.VM*HENPSILIIGR.-
R2/RRR2-4/3	1496.733	1495.772	-26.531	0.411	731.917	0.126	18	0.046	-.VM*HENPSILIIGR.-
R2/RRR2-4/3	1496.123	1495.772	234.719	0.388	722.183	0.127	19	0.033	-.VM*HENPSILIIGR.-
R2/RRR2-7/1	1143.521	1144.260	-1525.852	0.147	739.506	0.248	14	0.514	R.GGVIDEDALVR.A
R2/RRR2-7/2	1183.160	1183.426	-225.345	0.560	2415.430	0.535	22	0.342	R.LAVQLVAGGGGIK.S
R2/RRR2-7/3	1539.977	1540.767	-1165.468	0.488	2542.525	0.457	32	0.334	K.HAVM*AIGVDEEPKK.S
R2/RRR2-7/2	1183.161	1183.426	-224.310	0.565	2371.996	0.517	22	0.327	R.LAVQLVAGGGGIK.S
R2/RRR2-7/2	1182.971	1183.426	-385.598	0.489	2369.058	0.487	22	0.317	R.LAVQLVAGGGGIK.S
R2/RRR2-7/2	1719.452	1719.960	-879.517	0.477	2165.248	0.565	22	0.304	R.ALDSGIVAQAALDVFTK.E
R2/RRR2-7/2	1719.487	1719.960	-275.893	0.459	2110.515	0.508	22	0.276	R.ALDSGIVAQAALDVFTK.E
R2/RRR2-7/2	1720.318	1719.960	208.416	0.512	1996.040	0.543	22	0.267	R.ALDSGIVAQAALDVFTK.E
R2/RRR2-7/2	1652.533	1651.796	-159.636	0.539	1523.493	0.562	24	0.206	K.FPSAISESGEITVEGK.V
R2/RRR2-7/2	1651.351	1651.796	-270.372	0.505	1455.122	0.542	23	0.193	K.FPSAISESGEITVEGK.V
R2/RRR2-7/3	1721.356	1719.960	230.901	0.478	1560.888	0.527	30	0.182	R.ALDSGIVAQAALDVFTK.E
R2/RRR2-7/2	1651.332	1651.796	-282.015	0.507	1279.044	0.525	22	0.170	K.FPSAISESGEITVEGK.V
R2/RRR2-7/2	1164.201	1164.379	-153.820	0.463	1435.973	0.417	18	0.168	R.NKYVGVSLVGK.T
R2/RRR2-7/3	1539.847	1540.767	-1250.366	0.487	1623.415	0.444	30	0.157	K.HAVM*AIGVDEEPKK.S
R2/RRR2-7/2	919.567	920.131	-1705.947	0.390	685.172	0.415	14	0.122	K.TLAILGFGK.V
R2/RRR2-7/2	1605.998	1605.899	62.163	0.422	652.687	0.378	19	0.116	K.IGEIPAIEEFVFLK.-
R2/RRR2-7/2	1084.938	1085.213	-254.186	0.423	785.666	0.312	14	0.115	K.M*LNDETFAK.M
R2/RRR2-7/2	920.070	920.131	-65.686	0.412	677.217	0.327	14	0.115	K.TLAILGFGK.V
R2/RRR2-7/2	919.514	920.131	-1763.834	0.343	668.358	0.347	14	0.115	K.TLAILGFGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1085.105	1085.213	-99.565	0.429	818.293	0.293	14	0.114	K.M*LNDETFAK.M
R2/RRR2-7/2	1606.677	1605.899	-138.587	0.407	514.011	0.385	18	0.114	K.IGEIPAIEEFVFLK.-
R2/RRR2-7/2	1084.888	1085.213	-300.130	0.429	771.265	0.295	14	0.114	K.M*LNDETFAK.M
R2/RRR2-7/2	1605.707	1605.899	-119.455	0.400	528.322	0.408	16	0.113	K.IGEIPAIEEFVFLK.-
R2/RRR2-7/3	1826.352	1827.014	-913.003	0.492	1138.942	0.438	31	0.108	K.GLGM*HVIAHDPYASADR.A
R2/RRR2-18/2	1145.148	1144.260	-98.323	0.291	392.094	0.306	13	0.108	R.GGVIDEDALVR.A
R2/RRR2-3/2	1145.121	1144.260	-122.275	0.336	872.182	0.245	14	0.107	-.GGVIDEDALVR.-
R2/RRR2-6/2	1143.555	1144.260	-1495.679	0.339	612.097	0.269	13	0.104	-.GGVIDEDALVR.-
R2/RRR2-7/3	1667.932	1668.940	-1207.311	0.469	955.767	0.480	28	0.104	R.KHAVM*AIGVDEEPKK.S
R2/RRR2-6/2	1183.246	1183.426	-152.172	0.175	707.561	0.112	15	0.097	R.LAVQLVAGGGGIK.S
R2/RRR2-7/3	1164.428	1164.379	41.931	0.480	1547.719	0.213	22	0.091	-.NKYVGVSLVGK.-
R2/RRR2-7/3	1668.927	1668.940	-7.849	0.443	860.177	0.407	30	0.087	R.KHAVM*AIGVDEEPKK.S
R2/RRR2-7/3	1826.445	1827.014	-861.573	0.463	818.600	0.417	27	0.087	K.GLGM*HVIAHDPYASADR.A
R2/RRR2-7/3	1165.146	1164.379	-200.573	0.483	1503.851	0.198	22	0.084	-.NKYVGVSLVGK.-
R2/RRR2-7/3	1668.350	1668.940	-955.582	0.436	746.447	0.386	28	0.082	R.KHAVM*AIGVDEEPKK.S
R2/RRR2-7/3	1826.583	1827.014	-236.685	0.422	824.419	0.323	28	0.074	-.GLGM*HVIAHDPYASADR.-
R2/RRR2-7/3	1164.428	1164.379	41.457	0.417	1297.132	0.199	21	0.074	-.NKYVGVSLVGK.-
R2/RRR2-7/2	1726.497	1726.956	-266.688	0.595	2892.692	0.475	25	0.422	R.LDQLQLLLNGASANGAK.K
R2/RRR2-7/2	1726.536	1726.956	-243.777	0.568	2901.926	0.428	26	0.407	R.LDQLQLLLNGASANGAK.K
R2/RRR2-7/2	1134.262	1134.219	38.038	0.545	2389.883	0.494	20	0.324	K.GIDACIASGGGR.M
R2/RRR2-7/2	1133.406	1134.219	-1604.566	0.434	2340.878	0.472	20	0.308	K.GIDACIASGGGR.M
R2/RRR2-7/2	1726.347	1726.956	-934.516	0.493	2436.488	0.398	25	0.300	R.LDQLQLLLNGASANGAK.K
R2/RRR2-7/2	1133.270	1134.219	-1724.464	0.462	2363.668	0.416	20	0.295	K.GIDACIASGGGR.M
R2/RRR2-7/2	1727.339	1726.956	222.738	0.526	1688.875	0.452	23	0.196	R.LDQLQLLLNGASANGAK.K
R2/RRR2-7/2	1549.385	1548.635	-161.729	0.471	1479.563	0.528	17	0.192	K.ALEYEDFDKFDR.V
R2/RRR2-7/2	1548.388	1548.635	-159.460	0.449	1516.463	0.509	17	0.192	K.ALEYEDFDKFDR.V
R2/RRR2-7/2	1547.480	1548.635	-1396.198	0.378	1366.824	0.453	17	0.164	K.ALEYEDFDKFDR.V
R2/RRR2-7/2	975.188	975.121	68.349	0.489	984.794	0.567	17	0.158	K.LVDTALASGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	974.443	975.121	-1727.984	0.412	854.232	0.515	16	0.139	K.LVDTALASGK.I
R2/RRR2-7/2	974.330	975.121	-1844.422	0.377	793.872	0.455	16	0.128	K.LVDTALASGK.I
R2/RRR2-3/2	1648.345	1648.802	-277.847	0.528	2910.696	0.469	25	0.430	K.YLAAEQGGGQTIVANR.V
R2/RRR2-3/2	1649.095	1648.802	178.439	0.565	2859.432	0.503	26	0.430	K.YLAAEQGGGQTIVANR.V
R2/RRR2-3/2	1624.057	1623.746	191.895	0.609	2435.245	0.584	23	0.361	R.LAGESNTELLDFASR.F
R2/RRR2-3/2	1648.147	1648.802	-1007.308	0.500	2480.844	0.465	24	0.333	K.YLAAEQGGGQTIVANR.V
R2/RRR2-3/2	1621.964	1621.817	91.066	0.524	2041.787	0.527	21	0.269	K.SPLTFVGEWAAEWK.V
R2/RRR2-3/2	1622.440	1621.817	-232.627	0.549	1872.022	0.559	22	0.252	K.SPLTFVGEWAAEWK.V
R2/RRR2-3/2	1595.889	1596.767	-1180.306	0.314	2058.674	0.439	19	0.249	R.VVASDWESFTLWR.V
R2/RRR2-3/2	1622.768	1623.746	-1222.322	0.500	1906.101	0.498	21	0.239	R.LAGESNTELLDFASR.F
R2/RRR2-8/2	1268.085	1268.403	-251.867	0.484	1814.215	0.532	17	0.237	R.FAQAQLDVYGR.A
R2/RRR2-2/2	1624.607	1623.746	-85.659	0.587	1624.528	0.583	20	0.220	R.LAGESNTELLDFASR.F
R2/RRR2-3/2	1621.534	1621.817	-174.768	0.503	1723.825	0.503	21	0.216	K.SPLTFVGEWAAEWK.V
R2/RRR2-3/2	1622.744	1623.746	-1237.280	0.514	1694.247	0.519	20	0.214	R.LAGESNTELLDFASR.F
R2/RRR2-3/2	1262.401	1263.340	-1540.310	0.298	1618.523	0.446	16	0.187	K.YYQDAYNAVR.K
R2/RRR2-8/2	1269.071	1268.403	-262.574	0.537	1506.504	0.471	18	0.184	R.FAQAQLDVYGR.A
R2/RRR2-3/2	1262.373	1263.340	-1562.749	0.360	1293.872	0.461	16	0.159	K.YYQDAYNAVR.K
R2/RRR2-8/2	1268.444	1268.403	32.663	0.438	1189.821	0.474	17	0.154	R.FAQAQLDVYGR.A
R2/RRR2-3/2	1277.666	1278.436	-1389.952	0.466	1217.753	0.456	17	0.154	K.DLLDGTQLQFK.S
R2/RRR2-3/2	1279.536	1278.436	78.310	0.462	1132.145	0.444	16	0.145	K.DLLDGTQLQFK.S
R2/RRR2-3/2	1595.699	1596.767	-1299.837	0.253	1358.461	0.304	17	0.136	R.VVASDWESFTLWR.V
R2/RRR2-3/2	1134.102	1134.267	-146.242	0.425	807.229	0.462	14	0.128	-.NGYISLNQPK.-
R2/RRR2-3/2	1133.997	1134.267	-238.353	0.356	779.273	0.482	14	0.128	K.NGYISLNQPK.L
R2/RRR2-3/2	1133.479	1134.267	-1581.778	0.371	833.414	0.442	14	0.124	-.NGYISLNQPK.-
R2/RRR2-3/2	1032.435	1033.163	-1678.834	0.416	630.771	0.458	15	0.124	R.APNGSFLQAK.T
R2/RRR2-3/2	1179.316	1178.323	-5.670	0.480	876.883	0.373	17	0.124	K.FISSNGLNAVR.I
R2/RRR2-3/2	1179.127	1178.323	-166.825	0.471	924.180	0.356	17	0.123	K.FISSNGLNAVR.I
R2/RRR2-3/2	1267.832	1268.403	-1242.452	0.361	1009.348	0.353	15	0.123	R.FAQAQLDVYGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1178.735	1178.323	350.190	0.401	806.658	0.385	17	0.122	K.FISSNGLNAVR.I
R2/RRR2-3/2	1032.971	1033.163	-186.162	0.385	305.232	0.497	12	0.118	R.APNGSFLQAK.T
R2/RRR2-1/2	1622.512	1621.817	-188.246	0.343	595.419	0.493	15	0.118	K.SPLTFVGEWAAEWK.V
R2/RRR2-3/2	1107.887	1108.229	-310.279	0.456	860.435	0.311	14	0.117	R.INETTFNLR.V
R2/RRR2-3/2	1179.326	1178.323	2.636	0.477	815.077	0.311	17	0.116	K.FISSNGLNAVR.I
R2/RRR2-3/2	1108.021	1108.229	-188.470	0.453	842.612	0.303	14	0.116	R.INETTFNLR.V
R2/RRR2-3/2	1447.292	1447.618	-226.010	0.357	667.378	0.421	15	0.115	K.NLNVEQNIEFVK.N
R2/RRR2-3/2	1108.005	1108.229	-202.838	0.466	841.953	0.295	14	0.115	R.INETTFNLR.V
R2/RRR2-3/2	1279.405	1278.436	-24.557	0.395	983.903	0.277	16	0.115	K.DLLDGTQLQFK.S
R2/RRR2-1/2	1622.834	1621.817	10.818	0.271	374.149	0.345	17	0.109	K.SPLTFVGEWAAEWK.V
R2/RRR2-3/2	1179.355	1178.323	26.929	0.457	748.072	0.268	16	0.109	-.FISSNGLNAVR.-
R2/RRR2-3/2	1624.492	1623.746	-156.663	0.238	224.788	0.343	13	0.106	R.LAGESNTELLDFASR.F
R2/RRR2-12/2	1919.453	1919.128	169.763	0.628	3474.951	0.616	29	0.653	K.VQQVDTTGAGDAFVGALLR.R
R2/RRR2-12/2	1918.506	1919.128	-848.317	0.611	3386.687	0.621	29	0.629	K.VQQVDTTGAGDAFVGALLR.R
R2/RRR2-12/2	1917.884	1919.128	-1173.406	0.552	3360.589	0.587	29	0.606	K.VQQVDTTGAGDAFVGALLR.R
R2/RRR2-12/2	1578.386	1578.622	-150.069	0.570	2338.631	0.601	26	0.351	R.DNGVDDAGVVFDAGAR.T
R2/RRR2-12/2	1579.151	1578.622	-299.170	0.583	2332.787	0.599	26	0.349	R.DNGVDDAGVVFDAGAR.T
R2/RRR2-12/2	1579.239	1578.622	-243.643	0.623	2263.032	0.602	26	0.335	R.DNGVDDAGVVFDAGAR.T
R2/RRR2-12/2	1358.106	1358.480	-276.012	0.515	1754.046	0.483	20	0.217	R.IVQDPSSLQDQK.K
R2/RRR2-12/3	1919.062	1919.128	-34.434	0.508	1829.577	0.501	34	0.214	K.VQQVDTTGAGDAFVGALLR.R
R2/RRR2-12/2	1401.235	1401.632	-284.380	0.534	1540.623	0.538	20	0.204	K.ILSIWDQADIVK.V
R2/RRR2-12/2	991.745	992.197	-456.676	0.502	1651.582	0.476	15	0.203	R.TALAFVTLR.A
R2/RRR2-12/3	1918.978	1919.128	-78.651	0.497	1812.103	0.454	33	0.194	K.VQQVDTTGAGDAFVGALLR.R
R2/RRR2-12/2	1225.091	1225.370	-228.726	0.495	1551.484	0.487	19	0.193	K.FANACGAITATK.K
R2/RRR2-12/2	991.990	992.197	-208.849	0.512	1596.570	0.453	15	0.191	R.TALAFVTLR.A
R2/RRR2-12/2	1226.216	1225.370	-126.170	0.562	1724.592	0.395	19	0.190	K.FANACGAITATK.K
R2/RRR2-12/2	991.992	992.197	-207.368	0.470	1638.524	0.417	15	0.187	R.TALAFVTLR.A
R2/RRR2-12/2	1357.554	1358.480	-1423.059	0.474	1470.751	0.477	19	0.181	R.IVQDPSSLQDQK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1318.155	1317.550	-300.910	0.512	1309.075	0.520	18	0.174	K.LLLVTLGDQGCK.Y
R2/RRR2-12/2	1401.413	1401.632	-156.789	0.535	1339.779	0.484	19	0.171	K.ILSIWDQADIVK.V
R2/RRR2-12/2	1317.556	1317.550	4.032	0.529	1095.721	0.513	17	0.154	K.LLLVTLGDQGCK.Y
R2/RRR2-12/2	1358.031	1358.480	-331.474	0.532	1126.287	0.468	18	0.149	R.IVQDPSSLQDQK.K
R2/RRR2-12/2	1420.326	1419.565	-168.666	0.495	939.912	0.459	18	0.135	K.EAGALLSYDPNLR.E
R2/RRR2-12/2	1420.165	1419.565	-282.486	0.472	923.956	0.454	17	0.132	K.EAGALLSYDPNLR.E
R2/RRR2-12/2	1581.418	1581.879	-292.315	0.484	751.128	0.472	20	0.127	K.KGAIPSLPTEVEVLK.L
R2/RRR2-12/2	1316.545	1317.550	-1528.113	0.309	1026.412	0.306	17	0.118	K.LLLVTLGDQGCK.Y
R2/RRR2-12/2	1400.532	1401.632	-1503.964	0.281	1134.520	0.255	17	0.117	K.ILSIWDQADIVK.V
R2/RRR2-12/3	1514.611	1514.666	-36.394	0.547	1081.875	0.477	27	0.112	R.RIVQDPSSLQDQK.K
R2/RRR2-12/3	1514.549	1514.666	-77.261	0.492	1001.522	0.379	25	0.089	R.RIVQDPSSLQDQK.K
R2/RRR2-12/3	1514.160	1514.666	-997.803	0.456	861.965	0.399	23	0.087	R.RIVQDPSSLQDQK.K
R2/RRR2-2/2	1646.705	1646.909	-124.586	0.552	1959.806	0.527	23	0.258	R.LDQPIILTGYSALNK.L
R2/RRR2-2/3	1802.782	1803.135	-196.562	0.595	2163.786	0.478	33	0.255	R.HVEPPLSALLELDKLK.V
R2/RRR2-2/3	1803.255	1803.135	66.559	0.592	2271.543	0.416	33	0.249	R.HVEPPLSALLELDKLK.V
R2/RRR2-2/3	1802.402	1803.135	-964.718	0.511	2024.874	0.469	32	0.229	R.HVEPPLSALLELDKLK.V
R2/RRR2-2/2	1391.305	1390.610	-219.881	0.508	1736.441	0.494	19	0.220	R.EIIVVANDITFR.A
R2/RRR2-2/2	1281.271	1281.483	-165.948	0.443	1762.697	0.490	18	0.220	K.IIEEGPVTVAPR.E
R2/RRR2-2/2	1281.175	1281.483	-241.171	0.471	1626.954	0.477	18	0.199	K.IIEEGPVTVAPR.E
R2/RRR2-1/2	1646.606	1646.909	-184.525	0.512	1546.692	0.486	21	0.190	R.LDQPIILTGYSALNK.L
R2/RRR2-2/2	1646.295	1646.909	-983.229	0.484	1490.112	0.489	21	0.184	R.LDQPIILTGYSALNK.L
R2/RRR2-2/2	1755.055	1754.877	101.671	0.525	1350.929	0.495	20	0.174	R.GFQYIYLSEEDYAR.I
R2/RRR2-2/2	1904.554	1905.095	-811.331	0.492	1006.105	0.543	22	0.148	K.TVTANTATVSDYVGYLTK.G
R2/RRR2-2/2	1904.641	1905.095	-239.237	0.492	806.946	0.625	20	0.147	K.TVTANTATVSDYVGYLTK.G
R2/RRR2-2/2	1204.804	1205.216	-342.737	0.398	1409.106	0.327	17	0.146	R.VGWSDDGSPER.G
R2/RRR2-2/2	1181.742	1181.357	326.506	0.432	895.943	0.525	17	0.143	K.VVEFCTALGGK.T
R2/RRR2-2/2	1204.841	1205.216	-312.444	0.381	1379.896	0.313	17	0.142	R.VGWSDDGSPER.G
R2/RRR2-2/2	1905.900	1905.095	-102.696	0.525	730.567	0.586	19	0.136	K.TVTANTATVSDYVGYLTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/3	1802.740	1803.135	-219.794	0.479	1514.202	0.372	27	0.127	R.HVEPPLSALLELDKLK.V
R2/RRR2-2/2	1021.234	1021.195	38.112	0.415	889.063	0.404	16	0.127	R.TVGIGAYLAR.L
R2/RRR2-1/2	1906.544	1905.095	236.415	0.448	365.006	0.581	18	0.123	K.TVTANTATVSDYVGYLTK.G
R2/RRR2-1/2	1906.365	1905.095	141.898	0.379	225.867	0.607	17	0.120	K.TVTANTATVSDYVGYLTK.G
R2/RRR2-2/2	1727.247	1726.935	181.690	0.433	691.717	0.416	18	0.116	K.FDSGIINDFPANM*LR.V
R2/RRR2-2/2	1428.406	1429.691	-1604.132	0.320	953.092	0.341	14	0.116	R.EGLPLFILANWR.-
R2/RRR2-2/2	993.425	994.123	-1714.254	0.315	596.778	0.429	13	0.116	K.ATELVFADK.H
R2/RRR2-2/2	1359.167	1359.599	-318.855	0.378	763.257	0.356	18	0.114	K.LPLIYLAANSGAR.I
R2/RRR2-1/2	1905.992	1905.095	-54.384	0.305	214.256	0.356	18	0.112	K.TVTANTATVSDYVGYLTK.G
R2/RRR2-3/3	1802.752	1803.135	-213.171	0.407	1463.266	0.309	28	0.107	R.HVEPPLSALLELDKLK.V
R2/RRR2-1/2	1204.834	1205.216	-317.729	0.358	764.173	0.222	16	0.106	R.VGWSDDGSPER.G
R2/RRR2-2/2	1204.083	1205.216	-1776.897	0.239	1161.588	0.133	16	0.106	R.VGWSDDGSPER.G
R2/RRR2-1/2	1180.619	1181.357	-1476.309	0.225	387.516	0.302	13	0.104	K.VVEFCTALGGK.T
R2/RRR2-5/2	1430.918	1429.691	159.612	0.224	221.341	0.356	11	0.100	-.EGLPLFILANWR.-
R2/RRR2-2/2	993.154	994.123	-1988.528	0.156	616.014	0.264	13	0.099	K.ATELVFADK.H
R2/RRR2-3/2	1906.496	1905.095	211.118	0.211	131.286	0.456	15	0.089	-.TVTANTATVSDYVGYLTK.-
R2/RRR2-14/2	1459.945	1460.637	-1162.276	0.543	2059.314	0.462	20	0.254	K.NM*LANEGIGSFYK.G
R2/RRR2-14/2	1460.392	1460.637	-168.355	0.554	2022.352	0.455	20	0.246	K.NM*LANEGIGSFYK.G
R2/RRR2-14/3	1529.452	1529.764	-204.312	0.528	1879.942	0.521	31	0.225	K.VKIQLGEGSAAQVTK.N
R2/RRR2-14/2	1459.678	1460.637	-1345.849	0.415	2055.669	0.323	20	0.218	K.NM*LANEGIGSFYK.G
R2/RRR2-15/2	1302.221	1302.459	-183.775	0.516	1634.215	0.486	22	0.201	K.IQLGEGSAAQVTK.N
R2/RRR2-14/2	1302.055	1302.459	-311.402	0.488	1630.244	0.474	22	0.198	K.IQLGEGSAAQVTK.N
R2/RRR2-14/2	1302.128	1302.459	-255.061	0.536	1512.639	0.513	22	0.193	K.IQLGEGSAAQVTK.N
R2/RRR2-14/2	1302.063	1302.459	-305.288	0.521	1420.258	0.553	21	0.192	K.IQLGEGSAAQVTK.N
R2/RRR2-14/2	1328.281	1328.581	-226.719	0.566	1468.883	0.493	20	0.184	R.IIADEGVLALWK.G
R2/RRR2-14/2	1327.773	1328.581	-1365.807	0.417	1512.714	0.417	20	0.172	R.IIADEGVLALWK.G
R2/RRR2-15/2	1328.265	1328.581	-239.258	0.563	1315.081	0.478	19	0.166	R.IIADEGVLALWK.G
R2/RRR2-14/2	1328.025	1328.581	-1175.812	0.471	1265.333	0.486	18	0.162	R.IIADEGVLALWK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1302.188	1302.459	-208.978	0.487	1152.088	0.480	20	0.153	K.IQLGEGSAAQVTK.N
R2/RRR2-15/2	1328.394	1328.581	-141.720	0.492	1187.430	0.457	18	0.151	R.IIADEGVLALWK.G
R2/RRR2-15/2	1328.407	1328.581	-131.949	0.433	1095.584	0.494	18	0.150	R.IIADEGVLALWK.G
R2/RRR2-14/3	1529.392	1529.764	-244.067	0.531	1283.517	0.548	29	0.148	K.VKIQLGEGSAAQVTK.N
R2/RRR2-15/2	1744.455	1744.890	-249.695	0.530	665.174	0.649	21	0.148	K.QQQQQQTAAAATGVWK.T
R2/RRR2-15/2	1301.654	1302.459	-1390.768	0.419	1073.739	0.410	19	0.135	K.IQLGEGSAAQVTK.N
R2/RRR2-14/2	1347.030	1347.523	-367.276	0.475	1000.922	0.410	18	0.133	R.M*QADSTLPIAQR.R
R2/RRR2-14/2	1348.135	1347.523	-289.325	0.502	936.412	0.426	17	0.131	R.M*QADSTLPIAQR.R
R2/RRR2-14/2	1347.231	1347.523	-217.451	0.464	1018.059	0.381	18	0.129	R.M*QADSTLPIAQR.R
R2/RRR2-14/2	1209.106	1209.420	-260.508	0.459	524.175	0.463	16	0.124	K.NDGKPLPLVQK.A
R2/RRR2-14/2	991.986	992.115	-131.400	0.381	796.021	0.368	13	0.121	K.NAFHALYR.I
R2/RRR2-14/2	1208.616	1209.420	-1497.119	0.382	519.191	0.437	16	0.119	K.NDGKPLPLVQK.A
R2/RRR2-14/2	1410.497	1409.607	-77.569	0.352	763.317	0.403	15	0.119	K.FYTGFPVYCVR.I
R2/RRR2-14/2	1209.063	1209.420	-296.466	0.399	468.076	0.417	15	0.117	K.NDGKPLPLVQK.A
R2/RRR2-14/2	991.940	992.115	-177.570	0.371	841.190	0.304	13	0.116	K.NAFHALYR.I
R2/RRR2-14/2	991.838	992.115	-280.787	0.366	922.438	0.281	13	0.116	K.NAFHALYR.I
R2/RRR2-15/2	992.192	992.115	77.050	0.305	894.339	0.293	13	0.114	K.NAFHALYR.I
R2/RRR2-14/2	1410.142	1409.607	-330.425	0.322	785.128	0.339	15	0.113	K.FYTGFPVYCVR.I
R2/RRR2-14/2	1410.358	1409.607	-176.716	0.354	650.527	0.350	14	0.111	K.FYTGFPVYCVR.I
R2/RRR2-14/2	1329.690	1328.581	81.618	0.332	556.437	0.270	15	0.108	R.IIADEGVLALWK.G
R2/RRR2-15/2	992.120	992.115	4.614	0.296	719.020	0.161	12	0.104	K.NAFHALYR.I
R2/RRR2-14/2	1302.010	1302.459	-346.018	0.099	198.507	0.354	14	0.102	K.IQLGEGSAAQVTK.N
R2/RRR2-14/3	1650.412	1650.944	-931.006	0.422	864.188	0.383	27	0.084	K.AIEKNDGKPLPLVQK.A
R2/RRR2-14/3	1650.916	1650.944	-16.925	0.467	533.998	0.433	23	0.081	-.AIEKNDGKPLPLVQK.-
R2/RRR2-15/3	1649.923	1650.944	-1228.594	0.372	675.947	0.401	23	0.081	K.AIEKNDGKPLPLVQK.A
R2/RRR2-14/3	1209.523	1209.420	84.907	0.376	704.563	0.428	17	0.080	-.NDGKPLPLVQK.-
R2/RRR2-14/3	1651.206	1650.944	159.369	0.433	739.212	0.327	25	0.076	K.AIEKNDGKPLPLVQK.A
R2/RRR2-14/3	1328.838	1328.581	193.746	0.365	1320.680	0.195	22	0.074	R.IIADEGVLALWK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/3	1209.224	1209.420	-162.481	0.307	755.545	0.323	18	0.074	K.NDGKPLPLVQK.A
R2/RRR2-14/3	1209.770	1209.420	290.440	0.390	520.938	0.377	17	0.066	-.NDGKPLPLVQK.-
R2/RRR2-14/3	1208.959	1209.420	-382.333	0.262	627.824	0.310	16	0.065	-.NDGKPLPLVQK.-
R2/RRR2-15/3	1209.866	1209.420	369.656	0.241	618.135	0.280	16	0.060	-.NDGKPLPLVQK.-
R2/RRR2-8/2	1967.488	1968.196	-870.509	0.572	3722.053	0.558	28	0.702	K.EYVFVANSDNLGAIVDIK.I
R2/RRR2-8/2	1968.768	1968.196	-217.887	0.602	3305.119	0.585	27	0.582	K.EYVFVANSDNLGAIVDIK.I
R2/RRR2-8/2	1967.414	1968.196	-908.317	0.571	3189.446	0.534	26	0.526	K.EYVFVANSDNLGAIVDIK.I
R2/RRR2-9/2	1967.669	1968.196	-778.587	0.569	2437.747	0.561	24	0.352	K.EYVFVANSDNLGAIVDIK.I
R2/RRR2-9/2	1314.124	1313.528	-308.542	0.509	2422.455	0.537	22	0.343	K.VLQLETAAGAAIR.F
R2/RRR2-9/2	1967.177	1968.196	-1029.296	0.506	2396.513	0.508	25	0.327	K.EYVFVANSDNLGAIVDIK.I
R2/RRR2-9/2	1313.346	1313.528	-139.335	0.492	2345.848	0.475	21	0.307	K.VLQLETAAGAAIR.F
R2/RRR2-9/2	1313.172	1313.528	-271.937	0.475	2334.724	0.469	21	0.303	K.VLQLETAAGAAIR.F
R2/RRR2-9/2	1476.270	1476.704	-295.221	0.466	2397.402	0.295	19	0.259	K.IFNTNNLWVNLK.A
R2/RRR2-9/2	1476.405	1476.704	-203.309	0.476	2259.246	0.301	19	0.238	K.IFNTNNLWVNLK.A
R2/RRR2-8/2	1452.670	1452.636	23.548	0.577	1795.486	0.529	22	0.233	K.VSGDVWFGSGVTLK.G
R2/RRR2-1/2	1314.247	1313.528	-214.793	0.470	1818.305	0.510	21	0.230	K.VLQLETAAGAAIR.F
R2/RRR2-8/2	1476.395	1476.704	-209.779	0.521	2076.406	0.346	19	0.221	K.IFNTNNLWVNLK.A
R2/RRR2-8/2	1359.189	1359.592	-297.952	0.514	1936.426	0.400	20	0.216	R.IVTEDFLPLPSK.G
R2/RRR2-8/2	1475.557	1476.704	-1459.690	0.421	2073.193	0.276	18	0.205	K.IFNTNNLWVNLK.A
R2/RRR2-8/2	1360.233	1359.592	-264.688	0.504	1837.834	0.396	20	0.203	R.IVTEDFLPLPSK.G
R2/RRR2-8/2	1452.373	1452.636	-181.804	0.535	1661.166	0.481	21	0.202	K.VSGDVWFGSGVTLK.G
R2/RRR2-8/2	1452.137	1452.636	-344.477	0.462	1560.421	0.452	21	0.184	K.VSGDVWFGSGVTLK.G
R2/RRR2-9/2	1476.102	1476.704	-1088.383	0.442	1842.890	0.298	18	0.181	K.IFNTNNLWVNLK.A
R2/RRR2-9/2	1359.323	1359.592	-198.483	0.456	1638.153	0.346	19	0.169	R.IVTEDFLPLPSK.G
R2/RRR2-7/2	1360.494	1359.592	-72.500	0.408	1370.915	0.374	18	0.150	R.IVTEDFLPLPSK.G
R2/RRR2-8/2	1358.773	1359.592	-1343.117	0.345	1320.203	0.337	18	0.140	R.IVTEDFLPLPSK.G
R2/RRR2-8/2	1630.370	1630.780	-252.148	0.451	709.665	0.579	20	0.138	R.TNPSNPSIELGPEFK.K
R2/RRR2-2/2	1313.368	1313.528	-122.459	0.362	1245.984	0.354	17	0.136	K.VLQLETAAGAAIR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1630.347	1630.780	-266.420	0.444	735.716	0.554	19	0.135	R.TNPSNPSIELGPEFK.K
R2/RRR2-8/2	1759.325	1758.953	212.216	0.483	526.656	0.603	19	0.133	R.TNPSNPSIELGPEFKK.V
R2/RRR2-8/2	1630.388	1630.780	-241.106	0.472	546.507	0.585	19	0.133	R.TNPSNPSIELGPEFK.K
R2/RRR2-8/2	1758.295	1758.953	-945.737	0.474	542.672	0.580	19	0.131	R.TNPSNPSIELGPEFKK.V
R2/RRR2-10/2	1476.373	1476.704	-225.041	0.349	1434.175	0.197	17	0.126	K.IFNTNNLWVNLK.A
R2/RRR2-8/3	1313.667	1313.528	105.671	0.453	1773.141	0.272	29	0.125	K.VLQLETAAGAAIR.F
R2/RRR2-8/2	957.777	958.157	-398.291	0.389	1035.462	0.337	12	0.125	K.M*EIIPNPK.E
R2/RRR2-8/3	1313.184	1313.528	-262.807	0.438	1650.981	0.307	28	0.122	K.VLQLETAAGAAIR.F
R2/RRR2-8/2	839.930	840.006	-90.393	0.405	517.185	0.422	12	0.122	K.AIGINVPR.S
R2/RRR2-8/2	1758.354	1758.953	-912.004	0.438	457.705	0.526	18	0.121	R.TNPSNPSIELGPEFKK.V
R2/RRR2-9/2	1452.050	1452.636	-1095.871	0.424	778.172	0.440	16	0.121	K.VSGDVWFGSGVTLK.G
R2/RRR2-8/2	839.893	840.006	-135.005	0.417	521.518	0.394	12	0.120	K.AIGINVPR.S
R2/RRR2-8/2	790.600	790.933	-422.645	0.394	639.514	0.374	11	0.120	K.VANFLAR.F
R2/RRR2-8/2	839.760	840.006	-292.927	0.369	602.565	0.383	13	0.119	K.AIGINVPR.S
R2/RRR2-9/2	790.882	790.933	-64.418	0.402	521.094	0.370	10	0.118	K.VANFLAR.F
R2/RRR2-8/2	790.493	790.933	-557.762	0.384	542.869	0.379	10	0.118	K.VANFLAR.F
R2/RRR2-9/2	839.559	840.006	-533.040	0.372	564.697	0.341	12	0.116	K.AIGINVPR.S
R2/RRR2-8/2	790.559	790.933	-474.239	0.374	546.647	0.347	10	0.115	K.VANFLAR.F
R2/RRR2-9/2	791.032	790.933	125.355	0.375	733.924	0.304	11	0.115	K.VANFLAR.F
R2/RRR2-9/2	839.418	840.006	-1896.472	0.286	620.272	0.351	13	0.114	K.AIGINVPR.S
R2/RRR2-9/2	839.583	840.006	-505.026	0.290	662.146	0.332	13	0.113	K.AIGINVPR.S
R2/RRR2-8/2	958.003	958.157	-161.888	0.364	1044.523	0.224	12	0.112	K.M*EIIPNPK.E
R2/RRR2-9/2	1358.945	1359.592	-1216.181	0.330	1072.592	0.223	16	0.112	R.IVTEDFLPLPSK.G
R2/RRR2-10/2	1477.212	1476.704	-334.237	0.377	904.284	0.226	15	0.106	-.IFNTNNLWVNLK.-
R2/RRR2-9/2	1358.458	1359.592	-1576.142	0.314	682.925	0.260	14	0.106	R.IVTEDFLPLPSK.G
R2/RRR2-7/2	1313.891	1313.528	276.799	0.279	555.542	0.246	16	0.105	K.VLQLETAAGAAIR.F
R2/RRR2-8/2	1359.949	1359.592	262.833	0.305	419.641	0.296	11	0.105	R.IVTEDFLPLPSK.G
R2/RRR2-2/2	1359.471	1359.592	-89.396	0.305	516.903	0.339	13	0.104	-.IVTEDFLPLPSK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1359.663	1359.592	52.534	0.191	526.865	0.235	13	0.101	-.IVTEDFLPLPSK.-
R2/RRR2-8/2	958.184	958.157	27.768	0.362	782.464	0.175	11	0.098	-.M*EIIPNPK.-
R2/RRR2-8/1	975.463	976.154	-1738.526	0.226	730.506	0.302	14	0.519	K.IGLFGGAGVGK.T
R2/RRR2-8/1	975.680	976.154	-487.271	0.255	656.446	0.396	14	0.479	K.IGLFGGAGVGK.T
R2/RRR2-8/1	975.516	976.154	-1684.023	0.270	681.761	0.314	14	0.468	K.IGLFGGAGVGK.T
R2/RRR2-8/2	1866.329	1866.064	142.712	0.560	2607.712	0.495	24	0.370	R.DAEGQDVLLFIDNIFR.F
R2/RRR2-8/2	1493.000	1493.647	-1106.161	0.467	2672.686	0.456	23	0.366	R.FTQANSEVSALLGR.I
R2/RRR2-8/2	1493.390	1493.647	-172.548	0.550	2529.274	0.496	23	0.348	R.FTQANSEVSALLGR.I
R2/RRR2-9/2	1493.209	1493.647	-294.168	0.505	2512.449	0.483	22	0.340	R.FTQANSEVSALLGR.I
R2/RRR2-8/2	1493.269	1493.647	-253.898	0.526	2428.641	0.490	22	0.326	R.FTQANSEVSALLGR.I
R2/RRR2-8/2	1708.586	1709.007	-247.126	0.601	2216.852	0.608	22	0.325	R.LVLEVAQHLGENMVR.T
R2/RRR2-9/2	1474.355	1474.791	-297.124	0.470	2436.742	0.468	20	0.318	K.TVLIM*ELINNVAK.A
R2/RRR2-8/2	1866.361	1866.064	160.028	0.598	2161.032	0.575	23	0.307	R.DAEGQDVLLFIDNIFR.F
R2/RRR2-8/2	1493.412	1493.647	-157.870	0.549	2386.584	0.455	22	0.304	R.FTQANSEVSALLGR.I
R2/RRR2-8/2	1709.513	1709.007	-290.036	0.611	2032.283	0.647	22	0.304	R.LVLEVAQHLGENMVR.T
R2/RRR2-8/2	1474.384	1474.791	-276.856	0.496	2476.303	0.385	20	0.297	K.TVLIM*ELINNVAK.A
R2/RRR2-8/2	1708.542	1709.007	-273.002	0.566	2074.245	0.598	22	0.296	R.LVLEVAQHLGENMVR.T
R2/RRR2-8/2	1475.184	1474.791	266.595	0.553	2330.204	0.451	20	0.290	K.TVLIM*ELINNVAK.A
R2/RRR2-9/2	1458.387	1458.792	-278.525	0.429	2385.974	0.401	20	0.288	K.TVLIMELINNVAK.A
R2/RRR2-8/2	1474.212	1474.791	-1074.355	0.464	2410.846	0.384	20	0.286	K.TVLIM*ELINNVAK.A
R2/RRR2-9/2	1459.272	1458.792	329.602	0.565	2300.922	0.443	20	0.282	K.TVLIMELINNVAK.A
R2/RRR2-8/2	1458.897	1458.792	72.459	0.522	2215.802	0.442	20	0.268	K.TVLIMELINNVAK.A
R2/RRR2-8/2	1459.324	1458.792	-321.890	0.568	2227.697	0.399	20	0.255	K.TVLIMELINNVAK.A
R2/RRR2-8/2	1458.354	1458.792	-301.115	0.531	2139.172	0.437	20	0.254	K.TVLIMELINNVAK.A
R2/RRR2-8/2	1391.990	1391.516	341.575	0.579	1534.400	0.673	23	0.238	K.AHGGFSVFAGVGER.T
R2/RRR2-9/2	1492.813	1493.647	-1232.114	0.420	1965.606	0.445	20	0.233	R.FTQANSEVSALLGR.I
R2/RRR2-8/2	1401.541	1400.608	-47.838	0.507	1688.373	0.534	20	0.220	R.VGLTGLTVAEHFR.D
R2/RRR2-8/2	1409.705	1410.644	-1379.793	0.363	1535.180	0.458	22	0.181	R.VLNTGSPITVPVGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1390.732	1391.516	-1286.986	0.515	1127.146	0.619	23	0.178	K.AHGGFSVFAGVGER.T
R2/RRR2-8/2	1391.124	1391.516	-282.838	0.531	1136.594	0.592	23	0.175	K.AHGGFSVFAGVGER.T
R2/RRR2-8/2	1856.570	1857.040	-254.113	0.541	1117.003	0.587	23	0.170	R.M*LSPHVLGEDHYNTAR.G
R2/RRR2-9/2	1458.131	1458.792	-1142.521	0.416	1584.670	0.381	18	0.169	K.TVLIMELINNVAK.A
R2/RRR2-8/2	1279.157	1279.446	-226.206	0.433	1322.671	0.488	19	0.168	R.TIAM*DGTEGLVR.G
R2/RRR2-9/2	1410.307	1410.644	-239.751	0.452	1321.663	0.487	21	0.166	R.VLNTGSPITVPVGR.A
R2/RRR2-8/2	1280.085	1279.446	-283.048	0.450	1141.182	0.535	19	0.161	R.TIAM*DGTEGLVR.G
R2/RRR2-9/2	1474.256	1474.791	-1044.425	0.301	1789.788	0.222	20	0.161	K.TVLIM*ELINNVAK.A
R2/RRR2-8/2	1410.373	1410.644	-192.948	0.434	1237.450	0.489	21	0.159	R.VLNTGSPITVPVGR.A
R2/RRR2-8/2	1856.420	1857.040	-875.543	0.547	972.637	0.585	23	0.159	R.M*LSPHVLGEDHYNTAR.G
R2/RRR2-8/2	1724.472	1725.007	-892.321	0.531	904.868	0.616	20	0.157	R.LVLEVAQHLGENM*VR.T
R2/RRR2-8/2	1174.109	1174.374	-226.769	0.492	1129.937	0.479	17	0.154	K.VVDLLAPYQR.G
R2/RRR2-8/3	1458.040	1458.792	-1205.414	0.440	2008.380	0.259	28	0.153	K.TVLIMELINNVAK.A
R2/RRR2-8/2	1173.549	1174.374	-1559.590	0.386	1146.271	0.491	17	0.153	K.VVDLLAPYQR.G
R2/RRR2-8/2	1264.161	1263.447	-226.887	0.458	1064.906	0.512	18	0.151	R.TIAMDGTEGLVR.G
R2/RRR2-8/2	1399.594	1400.608	-1443.299	0.427	1175.590	0.469	17	0.150	R.VGLTGLTVAEHFR.D
R2/RRR2-8/2	1410.343	1410.644	-213.961	0.472	1096.503	0.495	20	0.150	R.VLNTGSPITVPVGR.A
R2/RRR2-8/2	1174.099	1174.374	-235.531	0.495	1057.289	0.486	16	0.149	K.VVDLLAPYQR.G
R2/RRR2-9/2	975.584	976.154	-1614.079	0.455	1216.161	0.402	17	0.144	K.IGLFGGAGVGK.T
R2/RRR2-8/2	1278.545	1279.446	-1491.048	0.296	1284.256	0.383	19	0.143	R.TIAM*DGTEGLVR.G
R2/RRR2-8/2	975.970	976.154	-189.069	0.462	1143.352	0.422	17	0.143	K.IGLFGGAGVGK.T
R2/RRR2-8/2	1400.314	1400.608	-210.072	0.440	880.471	0.513	16	0.137	R.VGLTGLTVAEHFR.D
R2/RRR2-8/3	1856.591	1857.040	-242.906	0.529	1246.861	0.503	30	0.132	R.M*LSPHVLGEDHYNTAR.G
R2/RRR2-15/2	1492.580	1493.647	-1388.902	0.366	1192.082	0.334	19	0.130	R.FTQANSEVSALLGR.I
R2/RRR2-8/2	975.507	976.154	-1693.655	0.391	934.554	0.424	16	0.130	K.IGLFGGAGVGK.T
R2/RRR2-9/2	1174.234	1174.374	-120.182	0.439	855.579	0.431	15	0.129	K.VVDLLAPYQR.G
R2/RRR2-9/2	975.640	976.154	-1556.259	0.404	933.454	0.410	16	0.128	K.IGLFGGAGVGK.T
R2/RRR2-8/2	1726.524	1725.007	-280.186	0.501	842.983	0.454	19	0.128	R.LVLEVAQHLGENM*VR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1411.090	1410.644	316.648	0.427	844.996	0.451	17	0.127	R.VLNTGSPITVPVGR.A
R2/RRR2-8/2	975.559	976.154	-1639.848	0.406	942.204	0.385	16	0.126	K.IGLFGGAGVGK.T
R2/RRR2-9/2	975.606	976.154	-1591.327	0.424	991.770	0.358	16	0.125	K.IGLFGGAGVGK.T
R2/RRR2-7/2	1493.202	1493.647	-298.515	0.327	1031.573	0.333	17	0.120	R.FTQANSEVSALLGR.I
R2/RRR2-8/3	1841.020	1841.041	-11.553	0.508	1261.250	0.443	29	0.119	R.MLSPHVLGEDHYNTAR.G
R2/RRR2-8/3	1856.334	1857.040	-921.759	0.515	1177.919	0.470	28	0.119	R.M*LSPHVLGEDHYNTAR.G
R2/RRR2-9/2	1410.215	1410.644	-304.969	0.316	938.433	0.310	19	0.115	R.VLNTGSPITVPVGR.A
R2/RRR2-8/3	1856.810	1857.040	-124.681	0.513	1145.838	0.458	28	0.114	R.M*LSPHVLGEDHYNTAR.G
R2/RRR2-8/2	1458.824	1458.792	22.274	0.312	477.278	0.388	15	0.113	K.TVLIMELINNVAK.A
R2/RRR2-8/3	1840.469	1841.041	-856.586	0.502	1223.543	0.424	29	0.112	R.MLSPHVLGEDHYNTAR.G
R2/RRR2-8/2	1459.866	1458.792	51.109	0.346	552.628	0.365	14	0.111	K.TVLIMELINNVAK.A
R2/RRR2-8/3	1709.201	1709.007	113.631	0.490	851.897	0.551	33	0.110	R.LVLEVAQHLGENMVR.T
R2/RRR2-30/2	1459.188	1458.792	272.228	0.395	277.836	0.313	13	0.110	-.TVLIMELINNVAK.-
R2/RRR2-8/3	1400.526	1400.608	-58.679	0.470	1017.542	0.480	27	0.108	R.VGLTGLTVAEHFR.D
R2/RRR2-8/2	1174.255	1174.374	-101.620	0.261	527.867	0.318	12	0.107	K.VVDLLAPYQR.G
R2/RRR2-9/2	1278.642	1279.446	-1414.713	0.266	602.252	0.289	15	0.106	R.TIAM*DGTEGLVR.G
R2/RRR2-8/3	1494.461	1493.647	-124.506	0.410	1244.808	0.393	27	0.106	R.FTQANSEVSALLGR.I
R2/RRR2-9/2	1410.190	1410.644	-322.860	0.289	770.038	0.234	18	0.106	R.VLNTGSPITVPVGR.A
R2/RRR2-2/2	1410.306	1410.644	-240.532	0.259	702.040	0.282	16	0.105	R.VLNTGSPITVPVGR.A
R2/RRR2-8/3	1400.850	1400.608	173.254	0.445	998.271	0.457	26	0.102	R.VGLTGLTVAEHFR.D
R2/RRR2-8/3	1410.825	1410.644	128.811	0.369	1251.129	0.353	28	0.097	R.VLNTGSPITVPVGR.A
R2/RRR2-8/3	1841.074	1841.041	17.775	0.516	865.208	0.457	26	0.097	R.MLSPHVLGEDHYNTAR.G
R2/RRR2-9/3	1401.298	1400.608	-221.468	0.492	837.554	0.463	24	0.097	R.VGLTGLTVAEHFR.D
R2/RRR2-8/3	1725.984	1725.007	-13.203	0.503	741.314	0.489	29	0.097	R.LVLEVAQHLGENM*VR.T
R2/RRR2-8/3	1867.446	1866.064	205.298	0.493	1004.183	0.421	27	0.096	R.DAEGQDVLLFIDNIFR.F
R2/RRR2-8/3	1708.620	1709.007	-227.495	0.458	560.573	0.494	28	0.092	R.LVLEVAQHLGENMVR.T
R2/RRR2-8/3	1392.462	1391.516	-39.235	0.464	821.854	0.416	23	0.087	K.AHGGFSVFAGVGER.T
R2/RRR2-8/3	1400.294	1400.608	-224.993	0.410	943.732	0.360	25	0.084	R.VGLTGLTVAEHFR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/3	1400.827	1400.608	157.262	0.432	714.957	0.372	24	0.081	R.VGLTGLTVAEHFR.D
R2/RRR2-8/2	1174.278	1174.374	-82.225	0.266	259.922	0.362	9	0.081	-.VVDLLAPYQR.-
R2/RRR2-9/3	1856.520	1857.040	-821.556	0.369	604.460	0.380	22	0.079	R.M*LSPHVLGEDHYNTAR.G
R2/RRR2-8/3	1391.629	1391.516	81.539	0.444	799.069	0.347	23	0.077	K.AHGGFSVFAGVGER.T
R2/RRR2-8/3	1410.502	1410.644	-100.841	0.325	741.458	0.323	24	0.073	R.VLNTGSPITVPVGR.A
R2/RRR2-8/3	1410.667	1410.644	16.211	0.307	662.531	0.315	21	0.070	R.VLNTGSPITVPVGR.A
R2/RRR2-8/3	1458.333	1458.792	-315.653	0.430	781.031	0.222	27	0.068	K.TVLIMELINNVAK.A
R2/RRR2-6/2	1259.090	1259.434	-274.282	0.538	2153.324	0.591	20	0.312	R.VNLVQVLGSDSK.V
R2/RRR2-6/2	1259.124	1259.434	-247.145	0.486	2135.508	0.583	20	0.306	R.VNLVQVLGSDSK.V
R2/RRR2-6/2	1259.079	1259.434	-283.328	0.491	2052.250	0.599	19	0.295	R.VNLVQVLGSDSK.V
R2/RRR2-6/2	1088.067	1088.240	-158.956	0.507	1326.522	0.545	17	0.182	K.GPITTSASVVR.G
R2/RRR2-6/2	1087.853	1088.240	-356.848	0.506	1245.401	0.556	17	0.177	K.GPITTSASVVR.G
R2/RRR2-6/2	1206.973	1207.446	-393.044	0.457	1284.545	0.527	19	0.173	K.FFLGIGLPGSAK.D
R2/RRR2-6/2	1400.058	1400.520	-331.143	0.431	1526.626	0.401	20	0.172	K.DTSVSLSANHLQK.L
R2/RRR2-6/2	1246.219	1246.520	-242.237	0.509	1189.987	0.555	18	0.172	K.IVLDFLGLVEK.F
R2/RRR2-6/3	1453.496	1453.667	-118.538	0.380	1875.301	0.334	29	0.160	K.APKPPAQAVDPFSK.F
R2/RRR2-6/2	1246.180	1246.520	-274.176	0.467	1165.460	0.490	17	0.156	K.IVLDFLGLVEK.F
R2/RRR2-6/3	1453.306	1453.667	-249.474	0.414	1789.937	0.298	28	0.138	K.APKPPAQAVDPFSK.F
R2/RRR2-6/2	1298.725	1299.626	-1468.381	0.383	941.343	0.387	18	0.126	R.VFVPLVLSLPSK.V
R2/RRR2-6/2	1206.977	1207.446	-389.290	0.301	829.195	0.483	15	0.125	K.FFLGIGLPGSAK.D
R2/RRR2-6/3	1453.975	1453.667	211.933	0.453	1428.821	0.396	26	0.124	K.APKPPAQAVDPFSK.F
R2/RRR2-6/2	1299.364	1299.626	-202.459	0.362	802.141	0.395	17	0.120	R.VFVPLVLSLPSK.V
R2/RRR2-6/2	1127.387	1128.258	-1664.284	0.350	650.207	0.427	16	0.118	R.ALSYLSSTSAK.Q
R2/RRR2-6/2	1246.082	1246.520	-352.607	0.263	777.229	0.408	14	0.115	K.IVLDFLGLVEK.F
R2/RRR2-6/2	1486.819	1487.505	-1137.358	0.312	1266.731	0.167	18	0.114	K.SYDDGTFYFDEK.H
R2/RRR2-6/2	1487.143	1487.505	-243.829	0.351	662.718	0.381	16	0.114	K.SYDDGTFYFDEK.H
R2/RRR2-6/2	1298.519	1299.626	-1627.491	0.263	682.519	0.344	16	0.109	R.VFVPLVLSLPSK.V
R2/RRR2-6/2	1035.129	1035.219	-87.127	0.328	769.975	0.277	13	0.108	R.TFQILGVEK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1127.308	1128.258	-1734.345	0.257	694.191	0.302	17	0.107	R.ALSYLSSTSAK.Q
R2/RRR2-6/2	1619.239	1618.813	263.997	0.242	741.910	0.339	15	0.104	R.ALGHVELDLPEAPEK.A
R2/RRR2-6/3	1618.725	1618.813	-54.060	0.401	1001.240	0.242	27	0.068	R.ALGHVELDLPEAPEK.A
R2/RRR2-11/2	1593.121	1593.752	-1026.576	0.457	1613.256	0.489	21	0.200	K.YVFTIDDDCFVAK.D
R2/RRR2-11/2	1593.354	1593.752	-250.629	0.438	1637.950	0.473	21	0.199	K.YVFTIDDDCFVAK.D
R2/RRR2-11/2	1593.158	1593.752	-1003.189	0.418	1663.752	0.454	21	0.198	K.YVFTIDDDCFVAK.D
R2/RRR2-11/2	1502.312	1502.609	-198.499	0.548	1263.223	0.620	19	0.192	R.VPEGFDYELYNR.N
R2/RRR2-11/2	1181.248	1181.324	-64.223	0.516	1571.405	0.420	15	0.178	K.DINALEQHIK.N
R2/RRR2-11/2	1238.984	1239.397	-334.171	0.480	1365.360	0.480	16	0.172	K.CYLSLAEQVR.E
R2/RRR2-11/2	1502.273	1502.609	-224.259	0.498	1169.808	0.546	19	0.167	R.VPEGFDYELYNR.N
R2/RRR2-11/2	1503.162	1502.609	-298.411	0.514	1058.629	0.590	19	0.167	R.VPEGFDYELYNR.N
R2/RRR2-11/2	1181.112	1181.324	-179.917	0.483	1511.981	0.392	15	0.166	K.DINALEQHIK.N
R2/RRR2-11/2	1181.166	1181.324	-133.678	0.497	1480.898	0.395	15	0.164	K.DINALEQHIK.N
R2/RRR2-11/2	1239.126	1239.397	-218.823	0.481	1338.254	0.423	17	0.159	K.CYLSLAEQVR.E
R2/RRR2-11/2	1123.138	1123.348	-187.024	0.547	1031.538	0.531	17	0.157	R.YVDAVMTVPK.G
R2/RRR2-11/2	1123.078	1123.348	-240.671	0.548	908.273	0.581	16	0.156	R.YVDAVMTVPK.G
R2/RRR2-11/2	1123.153	1123.348	-174.158	0.533	922.509	0.564	16	0.154	R.YVDAVMTVPK.G
R2/RRR2-10/2	1503.905	1502.609	197.213	0.502	1005.171	0.521	19	0.151	R.VPEGFDYELYNR.N
R2/RRR2-11/2	1139.237	1139.347	-97.116	0.592	874.344	0.553	16	0.151	R.YVDAVM*TVPK.G
R2/RRR2-11/2	1138.537	1139.347	-1594.865	0.432	832.030	0.566	16	0.146	R.YVDAVM*TVPK.G
R2/RRR2-10/2	1139.029	1139.347	-279.763	0.423	868.198	0.520	16	0.141	R.YVDAVM*TVPK.G
R2/RRR2-1/2	1240.572	1239.397	142.157	0.407	1139.653	0.398	16	0.139	K.CYLSLAEQVR.E
R2/RRR2-11/2	1138.447	1139.347	-1674.253	0.444	808.348	0.478	16	0.135	R.YVDAVM*TVPK.G
R2/RRR2-11/2	993.157	992.167	-10.986	0.421	399.384	0.604	11	0.133	R.CFGYMVSK.K
R2/RRR2-11/2	1242.037	1241.456	-338.279	0.436	757.109	0.441	16	0.126	K.VICDHLSLGVK.T
R2/RRR2-11/2	992.957	992.167	-212.468	0.433	396.144	0.468	11	0.124	R.CFGYMVSK.K
R2/RRR2-11/2	1007.905	1008.167	-260.335	0.426	436.211	0.455	11	0.123	R.CFGYM*VSK.K
R2/RRR2-11/2	1731.874	1731.026	-88.555	0.484	575.617	0.489	18	0.123	K.GTLFPMCGMNLAFDR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1007.962	1008.167	-203.351	0.391	505.581	0.403	12	0.120	R.CFGYM*VSK.K
R2/RRR2-2/2	1139.052	1139.347	-259.334	0.370	492.604	0.452	13	0.120	R.YVDAVM*TVPK.G
R2/RRR2-11/2	1118.041	1118.311	-241.536	0.421	777.381	0.367	15	0.119	K.ASNPFVNLKK.E
R2/RRR2-11/2	1732.035	1731.026	4.976	0.428	523.183	0.483	17	0.119	K.GTLFPMCGMNLAFDR.D
R2/RRR2-11/2	991.440	992.167	-1747.077	0.345	435.701	0.394	11	0.117	R.CFGYMVSK.K
R2/RRR2-11/2	1731.750	1731.026	-160.252	0.375	585.398	0.455	17	0.116	K.GTLFPMCGMNLAFDR.D
R2/RRR2-11/2	1119.143	1118.311	-150.713	0.383	584.356	0.386	14	0.116	K.ASNPFVNLKK.E
R2/RRR2-10/2	1181.384	1181.324	51.445	0.399	896.771	0.299	15	0.116	K.DINALEQHIK.N
R2/RRR2-11/2	1117.501	1118.311	-1624.116	0.327	522.163	0.418	13	0.114	K.ASNPFVNLKK.E
R2/RRR2-11/2	1007.355	1008.167	-1803.703	0.299	404.008	0.249	11	0.112	R.CFGYM*VSK.K
R2/RRR2-11/2	1241.041	1241.456	-334.702	0.354	596.583	0.353	15	0.112	K.VICDHLSLGVK.T
R2/RRR2-1/2	1138.717	1139.347	-1435.265	0.259	714.473	0.310	14	0.110	R.YVDAVM*TVPK.G
R2/RRR2-10/2	1182.041	1181.324	-239.852	0.384	834.960	0.247	15	0.110	K.DINALEQHIK.N
R2/RRR2-1/2	1139.023	1139.347	-285.677	0.287	538.500	0.299	13	0.110	R.YVDAVM*TVPK.G
R2/RRR2-11/3	1666.787	1665.829	-25.542	0.558	839.879	0.515	34	0.106	K.DPSGKDINALEQHIK.N
R2/RRR2-11/3	1665.684	1665.829	-87.487	0.480	614.032	0.466	30	0.090	K.DPSGKDINALEQHIK.N
R2/RRR2-11/3	1665.679	1665.829	-90.244	0.429	689.380	0.424	31	0.085	K.DPSGKDINALEQHIK.N
R2/RRR2-4/2	1735.435	1735.825	-225.242	0.515	2494.388	0.460	26	0.333	R.ELCSETGAAQDDVLAR.V
R2/RRR2-4/2	1445.311	1445.667	-246.820	0.490	2432.333	0.420	21	0.310	K.IAVDMVNEGLVER.R
R2/RRR2-4/2	1735.246	1735.825	-912.648	0.557	1948.822	0.489	23	0.243	R.ELCSETGAAQDDVLAR.V
R2/RRR2-4/2	1578.813	1579.672	-1180.781	0.527	1868.258	0.486	24	0.234	K.VM*ANADTPEDATTAR.Q
R2/RRR2-4/2	1735.247	1735.825	-912.295	0.540	1978.497	0.439	23	0.234	R.ELCSETGAAQDDVLAR.V
R2/RRR2-4/3	1977.345	1976.215	66.240	0.547	1844.399	0.502	34	0.214	K.VGICGEHGGEPLSVAFFAK.A
R2/RRR2-4/2	1579.108	1579.672	-993.469	0.531	1705.435	0.477	23	0.209	K.VM*ANADTPEDATTAR.Q
R2/RRR2-4/2	1461.312	1461.666	-242.999	0.455	1643.329	0.466	18	0.198	K.IAVDM*VNEGLVER.R
R2/RRR2-4/2	1372.029	1372.501	-345.225	0.463	1310.261	0.464	17	0.162	K.AGLDYVSCSPFR.V
R2/RRR2-4/3	1975.679	1976.215	-779.899	0.511	1550.000	0.465	31	0.159	K.VGICGEHGGEPLSVAFFAK.A
R2/RRR2-4/2	970.936	971.048	-115.586	0.407	1136.912	0.392	13	0.138	R.SDFEGIFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	971.006	971.048	-43.201	0.480	982.855	0.438	13	0.138	R.SDFEGIFR.A
R2/RRR2-4/2	1280.207	1279.491	-222.314	0.542	898.876	0.483	16	0.138	K.LSEVNPM*LGFR.G
R2/RRR2-4/2	1372.289	1372.501	-154.941	0.416	968.078	0.466	15	0.135	K.AGLDYVSCSPFR.V
R2/RRR2-4/2	1088.925	1089.291	-337.388	0.436	925.190	0.407	16	0.130	R.AM*DGLPVTIR.L
R2/RRR2-4/2	971.033	971.048	-16.216	0.460	1008.097	0.335	13	0.125	R.SDFEGIFR.A
R2/RRR2-4/2	1623.913	1624.841	-1190.252	0.429	602.809	0.468	18	0.122	R.LGISYPELTEM*QAR.A
R2/RRR2-4/2	1088.470	1089.291	-1677.787	0.436	733.320	0.392	15	0.121	R.AM*DGLPVTIR.L
R2/RRR2-4/2	1514.199	1514.620	-278.689	0.401	801.718	0.400	18	0.119	-.GLHNDTDLTATDLK.-
R2/RRR2-4/2	1624.315	1624.841	-942.117	0.407	645.065	0.402	19	0.118	R.LGISYPELTEM*QAR.A
R2/RRR2-4/2	1608.852	1608.841	6.879	0.435	486.019	0.424	16	0.115	R.LGISYPELTEMQAR.A
R2/RRR2-4/2	1278.622	1279.491	-1465.510	0.347	811.381	0.337	15	0.115	K.LSEVNPM*LGFR.G
R2/RRR2-4/2	1624.298	1624.841	-952.604	0.357	375.123	0.434	15	0.113	R.LGISYPELTEM*QAR.A
R2/RRR2-4/2	1278.531	1279.491	-1537.150	0.321	910.091	0.264	16	0.111	K.LSEVNPM*LGFR.G
R2/RRR2-4/2	1608.485	1608.841	-222.086	0.402	488.877	0.298	16	0.107	R.LGISYPELTEMQAR.A
R2/RRR2-4/3	1157.604	1157.329	238.164	0.398	1375.441	0.351	24	0.107	R.GGMTSHAAVVAR.G
R2/RRR2-4/2	1073.164	1073.292	-119.407	0.268	554.982	0.318	13	0.107	-.AMDGLPVTIR.-
R2/RRR2-4/2	1263.028	1263.491	-367.554	0.298	818.338	0.241	14	0.106	K.LSEVNPMLGFR.G
R2/RRR2-5/2	1279.020	1279.491	-368.887	0.273	517.385	0.292	12	0.105	K.LSEVNPM*LGFR.G
R2/RRR2-4/2	1088.651	1089.291	-1510.833	0.185	564.984	0.213	12	0.098	-.AM*DGLPVTIR.-
R2/RRR2-4/3	1157.243	1157.329	-74.401	0.330	1123.634	0.280	23	0.078	R.GGMTSHAAVVAR.G
R2/RRR2-4/3	1975.645	1976.215	-797.110	0.394	1289.321	0.199	26	0.073	K.VGICGEHGGEPLSVAFFAK.A
R2/RRR2-4/3	1157.311	1157.329	-15.522	0.303	833.898	0.163	20	0.061	-.GGMTSHAAVVAR.-
R2/RRR2-12/2	1740.355	1739.942	238.308	0.606	2116.245	0.496	23	0.272	R.LYEALDKCEEILSR.Q
R2/RRR2-11/2	1498.078	1497.546	-313.399	0.575	1961.707	0.580	22	0.271	R.SALDEVTDTGAFDR.S
R2/RRR2-11/2	1497.259	1497.546	-192.055	0.541	1881.313	0.554	22	0.251	R.SALDEVTDTGAFDR.S
R2/RRR2-12/2	1739.309	1739.942	-941.489	0.606	1941.304	0.522	22	0.251	R.LYEALDKCEEILSR.Q
R2/RRR2-12/2	1497.280	1497.546	-177.987	0.524	1852.673	0.557	22	0.248	R.SALDEVTDTGAFDR.S
R2/RRR2-12/2	1497.218	1497.546	-219.946	0.535	1877.039	0.538	22	0.246	R.SALDEVTDTGAFDR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1539.157	1539.666	-983.418	0.558	1930.566	0.492	21	0.243	R.YICGNQLTEADVR.L
R2/RRR2-12/2	1497.139	1497.546	-272.542	0.576	1786.693	0.559	21	0.238	R.SALDEVTDTGAFDR.S
R2/RRR2-12/2	1739.276	1739.942	-960.443	0.579	1840.028	0.517	22	0.236	R.LYEALDKCEEILSR.Q
R2/RRR2-11/2	1739.456	1739.942	-279.975	0.569	1798.600	0.500	22	0.225	R.LYEALDKCEEILSR.Q
R2/RRR2-12/2	1539.253	1539.666	-268.824	0.546	1831.634	0.470	21	0.223	R.YICGNQLTEADVR.L
R2/RRR2-11/2	1361.140	1361.484	-252.908	0.456	1798.283	0.477	19	0.219	K.TVVNNESSEIIR.M
R2/RRR2-12/3	1887.544	1888.159	-858.283	0.540	1709.930	0.563	32	0.213	K.GLDHAIGFTSVKPIFER.T
R2/RRR2-12/2	1361.036	1361.484	-330.022	0.430	1699.005	0.442	19	0.197	K.TVVNNESSEIIR.M
R2/RRR2-12/2	1539.279	1539.666	-252.195	0.552	1591.951	0.460	20	0.190	R.YICGNQLTEADVR.L
R2/RRR2-11/2	1361.217	1361.484	-196.588	0.484	1498.159	0.503	19	0.189	K.TVVNNESSEIIR.M
R2/RRR2-12/2	1361.104	1361.484	-279.991	0.456	1482.211	0.469	19	0.179	K.TVVNNESSEIIR.M
R2/RRR2-11/2	1361.007	1361.484	-351.530	0.465	1405.236	0.503	19	0.179	K.TVVNNESSEIIR.M
R2/RRR2-12/2	1360.529	1361.484	-1440.554	0.318	1537.648	0.372	19	0.164	K.TVVNNESSEIIR.M
R2/RRR2-12/3	1887.618	1888.159	-818.747	0.442	1468.338	0.463	30	0.148	K.GLDHAIGFTSVKPIFER.T
R2/RRR2-12/3	1887.874	1888.159	-151.449	0.516	1392.735	0.479	30	0.143	K.GLDHAIGFTSVKPIFER.T
R2/RRR2-12/2	1361.797	1361.484	231.189	0.455	986.626	0.484	18	0.142	K.TVVNNESSEIIR.M
R2/RRR2-12/3	1336.590	1336.432	117.965	0.537	1788.010	0.338	26	0.139	K.KQEPYDEAVTR.L
R2/RRR2-12/2	1311.244	1310.502	-196.890	0.492	1083.252	0.406	18	0.138	R.MLNTEFNEIAK.N
R2/RRR2-12/3	1255.282	1255.403	-96.388	0.403	1521.049	0.423	22	0.136	R.FDEVYAVHFK.C
R2/RRR2-12/2	1326.086	1326.501	-313.724	0.460	1130.507	0.376	17	0.135	R.M*LNTEFNEIAK.N
R2/RRR2-12/2	1335.658	1336.432	-1332.444	0.455	1099.693	0.365	17	0.132	K.KQEPYDEAVTR.L
R2/RRR2-12/2	1326.265	1326.501	-178.346	0.557	979.016	0.387	18	0.130	R.M*LNTEFNEIAK.N
R2/RRR2-11/2	1336.085	1336.432	-260.492	0.480	1048.759	0.369	17	0.130	K.KQEPYDEAVTR.L
R2/RRR2-12/2	1336.256	1336.432	-132.365	0.465	1063.491	0.358	17	0.129	K.KQEPYDEAVTR.L
R2/RRR2-12/2	1310.130	1310.502	-284.530	0.464	1020.912	0.358	17	0.127	R.MLNTEFNEIAK.N
R2/RRR2-12/2	1335.778	1336.432	-1242.315	0.433	1005.442	0.321	17	0.122	K.KQEPYDEAVTR.L
R2/RRR2-12/3	1255.168	1255.403	-187.846	0.422	1510.136	0.380	23	0.122	R.FDEVYAVHFK.C
R2/RRR2-12/2	1326.290	1326.501	-159.233	0.502	797.931	0.368	17	0.122	R.M*LNTEFNEIAK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1289.994	1289.417	-328.930	0.366	468.189	0.490	13	0.120	R.EYPNLFNYTK.D
R2/RRR2-11/2	1335.949	1336.432	-363.072	0.485	754.275	0.379	15	0.119	K.KQEPYDEAVTR.L
R2/RRR2-12/3	1255.723	1255.403	255.533	0.426	1282.569	0.446	21	0.119	R.FDEVYAVHFK.C
R2/RRR2-12/2	1310.359	1310.502	-109.379	0.438	986.473	0.278	18	0.117	R.MLNTEFNEIAK.N
R2/RRR2-12/2	1290.077	1289.417	-264.847	0.317	401.504	0.484	13	0.116	R.EYPNLFNYTK.D
R2/RRR2-12/2	743.674	743.876	-273.563	0.368	466.440	0.497	10	0.112	-.FPAVPGR.-
R2/RRR2-7/2	1497.605	1497.546	39.438	0.345	874.494	0.279	19	0.111	R.SALDEVTDTGAFDR.S
R2/RRR2-11/3	1336.772	1336.432	255.061	0.523	1502.054	0.333	24	0.110	K.KQEPYDEAVTR.L
R2/RRR2-12/2	743.827	743.876	-67.094	0.347	399.884	0.424	9	0.109	-.FPAVPGR.-
R2/RRR2-12/2	1289.076	1289.417	-265.432	0.261	350.427	0.315	12	0.108	R.EYPNLFNYTK.D
R2/RRR2-12/3	1336.062	1336.432	-278.285	0.469	1416.046	0.345	24	0.107	K.KQEPYDEAVTR.L
R2/RRR2-12/3	1336.737	1336.432	228.552	0.521	1289.073	0.381	23	0.105	K.KQEPYDEAVTR.L
R2/RRR2-11/2	743.869	743.876	-9.482	0.340	398.405	0.365	9	0.102	-.FPAVPGR.-
R2/RRR2-11/3	1336.072	1336.432	-270.997	0.472	1262.265	0.356	22	0.099	K.KQEPYDEAVTR.L
R2/RRR2-11/2	743.301	743.876	-2125.647	0.203	342.886	0.323	8	0.099	-.FPAVPGR.-
R2/RRR2-12/2	743.416	743.876	-621.328	0.238	313.136	0.324	8	0.087	-.FPAVPGR.-
R2/RRR2-11/3	1335.948	1336.432	-364.091	0.457	1372.967	0.260	24	0.086	K.KQEPYDEAVTR.L
R2/RRR2-11/2	743.438	743.876	-591.501	0.286	271.870	0.365	7	0.086	-.FPAVPGR.-
R2/RRR2-6/2	1741.506	1740.944	-252.367	0.625	2599.450	0.602	24	0.407	R.NIIHFNTLANQAVER.A
R2/RRR2-6/2	1740.346	1740.944	-921.371	0.533	2523.191	0.548	24	0.371	R.NIIHFNTLANQAVER.A
R2/RRR2-6/2	1740.554	1740.944	-225.072	0.547	2423.562	0.528	24	0.343	R.NIIHFNTLANQAVER.A
R2/RRR2-6/2	1562.201	1562.774	-1010.198	0.500	2431.746	0.471	22	0.323	R.TTLVANTSNM*PVAAR.E
R2/RRR2-6/2	1562.346	1562.774	-274.472	0.502	2387.172	0.465	22	0.312	R.TTLVANTSNM*PVAAR.E
R2/RRR2-6/3	1740.218	1740.944	-994.687	0.562	2328.865	0.513	31	0.311	R.NIIHFNTLANQAVER.A
R2/RRR2-6/2	1519.214	1519.635	-277.689	0.515	2218.368	0.548	24	0.310	K.FEDPAEGEDVLVAK.F
R2/RRR2-6/2	1735.494	1734.930	-252.113	0.535	2082.572	0.571	23	0.294	R.EASIYTGITIAEYFR.D
R2/RRR2-6/3	1740.562	1740.944	-220.295	0.598	2332.390	0.475	30	0.293	R.NIIHFNTLANQAVER.A
R2/RRR2-6/2	1519.309	1519.635	-214.975	0.476	2114.054	0.544	24	0.289	K.FEDPAEGEDVLVAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1563.274	1562.774	-320.753	0.516	2196.298	0.488	22	0.284	R.TTLVANTSNM*PVAAR.E
R2/RRR2-6/2	1546.256	1546.775	-985.238	0.502	1970.957	0.458	22	0.239	R.TTLVANTSNMPVAAR.E
R2/RRR2-6/2	1605.170	1605.769	-999.343	0.494	1745.464	0.538	22	0.228	K.DALAESDKITLETAK.L
R2/RRR2-6/2	1812.290	1813.024	-959.970	0.525	1623.718	0.583	24	0.222	R.LAEM*PADSGYPAYLAAR.L
R2/RRR2-6/3	1739.958	1740.944	-1144.824	0.519	2112.904	0.399	30	0.219	R.NIIHFNTLANQAVER.A
R2/RRR2-6/2	1518.843	1519.635	-1182.945	0.415	1597.316	0.571	22	0.215	K.FEDPAEGEDVLVAK.F
R2/RRR2-6/2	1811.823	1813.024	-1218.630	0.534	1567.539	0.578	24	0.213	R.LAEM*PADSGYPAYLAAR.L
R2/RRR2-6/2	1605.241	1605.769	-954.527	0.524	1501.903	0.537	21	0.197	K.DALAESDKITLETAK.L
R2/RRR2-6/2	1812.599	1813.024	-235.427	0.554	1311.059	0.574	22	0.182	R.LAEM*PADSGYPAYLAAR.L
R2/RRR2-6/2	1796.286	1797.025	-970.858	0.456	1277.879	0.525	23	0.169	R.LAEMPADSGYPAYLAAR.L
R2/RRR2-6/2	1201.070	1201.310	-200.781	0.578	1276.443	0.492	17	0.168	K.LYDDLTTGFR.N
R2/RRR2-6/2	1472.068	1472.623	-1059.510	0.382	1489.412	0.385	19	0.163	R.EDDLNEIVQLVGK.D
R2/RRR2-6/2	1605.120	1605.769	-1030.343	0.490	1220.752	0.511	20	0.162	K.DALAESDKITLETAK.L
R2/RRR2-6/2	1471.873	1472.623	-1192.579	0.360	1529.138	0.343	20	0.159	R.EDDLNEIVQLVGK.D
R2/RRR2-6/2	1796.552	1797.025	-264.194	0.498	1104.663	0.522	22	0.153	R.LAEMPADSGYPAYLAAR.L
R2/RRR2-6/2	1200.995	1201.310	-262.879	0.547	1216.580	0.436	17	0.153	K.LYDDLTTGFR.N
R2/RRR2-6/2	1472.149	1472.623	-322.578	0.389	1393.160	0.359	19	0.150	R.EDDLNEIVQLVGK.D
R2/RRR2-6/2	1200.752	1201.310	-1301.155	0.535	1119.149	0.448	17	0.149	K.LYDDLTTGFR.N
R2/RRR2-6/2	1733.624	1734.930	-1334.354	0.339	1294.220	0.399	19	0.146	R.EASIYTGITIAEYFR.D
R2/RRR2-6/2	1577.839	1578.795	-1243.471	0.431	519.198	0.497	18	0.124	K.HFPSVNWLISYSK.Y
R2/RRR2-6/2	918.960	918.052	-100.302	0.464	728.005	0.395	11	0.124	R.M*GDLFYR.L
R2/RRR2-6/2	901.915	902.052	-152.396	0.457	913.320	0.335	11	0.122	R.MGDLFYR.L
R2/RRR2-6/3	1605.396	1605.769	-232.856	0.470	1253.010	0.454	29	0.121	K.DALAESDKITLETAK.L
R2/RRR2-6/2	901.937	902.052	-128.094	0.477	824.459	0.339	11	0.121	R.MGDLFYR.L
R2/RRR2-6/2	1578.206	1578.795	-1009.668	0.432	396.755	0.478	17	0.118	-.HFPSVNWLISYSK.-
R2/RRR2-6/2	1577.613	1578.795	-1387.070	0.352	419.623	0.419	17	0.115	K.HFPSVNWLISYSK.Y
R2/RRR2-6/2	917.839	918.052	-232.487	0.283	373.376	0.243	11	0.114	R.M*GDLFYR.L
R2/RRR2-6/2	917.854	918.052	-215.942	0.317	435.159	0.228	11	0.111	-.M*GDLFYR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1562.918	1562.774	92.596	0.458	1177.704	0.434	29	0.110	R.TTLVANTSNM*PVAAR.E
R2/RRR2-6/3	1605.933	1605.769	102.183	0.508	999.520	0.465	29	0.104	K.DALAESDKITLETAK.L
R2/RRR2-6/3	1734.973	1734.930	24.931	0.418	911.701	0.468	25	0.097	R.EASIYTGITIAEYFR.D
R2/RRR2-6/3	1606.424	1605.769	-215.596	0.516	989.302	0.418	28	0.095	K.DALAESDKITLETAK.L
R2/RRR2-6/3	1562.132	1562.774	-1054.142	0.363	709.052	0.362	23	0.074	-.TTLVANTSNM*PVAAR.-
R2/RRR2-11/1	1436.835	1435.607	159.092	0.402	563.204	0.507	17	0.461	R.AASFNIIPSSTGAAK.A
R2/RRR2-11/1	1436.844	1435.607	165.482	0.369	515.975	0.489	16	0.418	R.AASFNIIPSSTGAAK.A
R2/RRR2-11/1	1434.836	1435.607	-1238.415	0.116	556.797	0.330	16	0.391	R.AASFNIIPSSTGAAK.A
R2/RRR2-11/2	1499.487	1499.734	-165.314	0.535	2467.602	0.633	22	0.381	R.VPTVDVSVVDLTVR.I
R2/RRR2-1/2	1500.367	1499.734	-245.761	0.555	2316.093	0.658	22	0.358	R.VPTVDVSVVDLTVR.I
R2/RRR2-2/2	1500.386	1499.734	-232.619	0.541	2304.133	0.664	22	0.358	R.VPTVDVSVVDLTVR.I
R2/RRR2-1/2	1500.404	1499.734	-221.029	0.544	2230.789	0.663	22	0.342	R.VPTVDVSVVDLTVR.I
R2/RRR2-5/2	1500.281	1499.734	-302.983	0.553	2288.888	0.604	22	0.333	R.VPTVDVSVVDLTVR.I
R2/RRR2-11/1	1434.846	1435.607	-1230.811	0.136	527.780	0.238	16	0.333	R.AASFNIIPSSTGAAK.A
R2/RRR2-11/1	1436.793	1435.607	129.442	0.334	383.009	0.482	14	0.330	-.AASFNIIPSSTGAAK.-
R2/RRR2-1/2	1500.503	1499.734	-154.921	0.539	2174.779	0.658	22	0.330	R.VPTVDVSVVDLTVR.I
R2/RRR2-11/1	1434.818	1435.607	-1250.376	0.185	480.845	0.313	15	0.325	R.AASFNIIPSSTGAAK.A
R2/RRR2-12/2	1499.362	1499.734	-248.947	0.507	2147.670	0.629	21	0.315	R.VPTVDVSVVDLTVR.I
R2/RRR2-2/2	1499.484	1499.734	-167.519	0.488	2118.441	0.628	21	0.309	R.VPTVDVSVVDLTVR.I
R2/RRR2-11/2	1499.407	1499.734	-219.053	0.532	2057.616	0.646	21	0.304	R.VPTVDVSVVDLTVR.I
R2/RRR2-3/2	1499.214	1499.734	-1017.132	0.441	2139.970	0.525	21	0.281	R.VPTVDVSVVDLTVR.I
R2/RRR2-14/2	1499.794	1499.734	40.197	0.496	1794.794	0.612	21	0.250	R.VPTVDVSVVDLTVR.I
R2/RRR2-13/2	1499.365	1499.734	-246.823	0.489	1697.991	0.626	19	0.239	R.VPTVDVSVVDLTVR.I
R2/RRR2-15/2	1499.239	1499.734	-331.613	0.450	1726.474	0.600	20	0.236	R.VPTVDVSVVDLTVR.I
R2/RRR2-13/2	1499.329	1499.734	-270.919	0.513	1576.475	0.641	20	0.227	R.VPTVDVSVVDLTVR.I
R2/RRR2-11/2	1756.360	1757.017	-946.082	0.532	1609.105	0.600	21	0.226	K.TLLFGEKEVTVFGCR.N
R2/RRR2-11/2	1762.507	1762.859	-199.969	0.538	1673.107	0.553	19	0.218	K.LVSWYDNEWGYSSR.V
R2/RRR2-11/2	1756.455	1757.017	-892.008	0.555	1536.265	0.578	21	0.211	K.TLLFGEKEVTVFGCR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/3	1499.568	1499.734	-111.141	0.410	2132.202	0.329	29	0.198	R.VPTVDVSVVDLTVR.I
R2/RRR2-11/2	1756.339	1757.017	-958.153	0.528	1392.003	0.576	20	0.192	K.TLLFGEKEVTVFGCR.N
R2/RRR2-11/2	1763.294	1762.859	247.428	0.554	1456.469	0.545	19	0.190	K.LVSWYDNEWGYSSR.V
R2/RRR2-11/2	1762.217	1762.859	-934.392	0.496	1319.215	0.593	18	0.185	K.LVSWYDNEWGYSSR.V
R2/RRR2-11/2	1763.424	1762.859	-247.078	0.569	1300.471	0.595	18	0.184	K.LVSWYDNEWGYSSR.V
R2/RRR2-11/2	1762.120	1762.859	-989.682	0.484	1452.823	0.516	19	0.183	K.LVSWYDNEWGYSSR.V
R2/RRR2-5/2	1500.349	1499.734	-257.433	0.488	1290.468	0.548	18	0.172	R.VPTVDVSVVDLTVR.I
R2/RRR2-11/2	1162.099	1162.320	-191.395	0.434	1392.671	0.408	17	0.157	K.AGIALNDNFVK.-
R2/RRR2-12/2	1762.406	1762.859	-257.642	0.484	1308.668	0.438	18	0.153	K.LVSWYDNEWGYSSR.V
R2/RRR2-11/2	1162.065	1162.320	-220.691	0.470	1267.055	0.425	16	0.150	K.AGIALNDNFVK.-
R2/RRR2-10/2	1161.972	1162.320	-300.368	0.443	1306.557	0.395	17	0.149	K.AGIALNDNFVK.-
R2/RRR2-11/2	1435.184	1435.607	-295.910	0.484	1026.556	0.513	22	0.148	R.AASFNIIPSSTGAAK.A
R2/RRR2-15/2	1162.240	1162.320	-69.276	0.423	1360.653	0.362	16	0.146	K.AGIALNDNFVK.-
R2/RRR2-11/2	1163.189	1162.320	-113.534	0.456	1240.905	0.397	16	0.143	K.AGIALNDNFVK.-
R2/RRR2-2/2	1162.364	1162.320	37.435	0.471	1147.739	0.432	16	0.143	K.AGIALNDNFVK.-
R2/RRR2-11/2	1133.547	1134.226	-1485.445	0.405	1019.078	0.467	14	0.141	K.YDTVHGQWK.H
R2/RRR2-11/2	1161.538	1162.320	-1538.613	0.372	1257.245	0.347	16	0.137	K.AGIALNDNFVK.-
R2/RRR2-2/2	1161.946	1162.320	-323.029	0.402	1159.855	0.385	16	0.137	K.AGIALNDNFVK.-
R2/RRR2-11/2	1163.090	1162.320	-198.600	0.481	1067.390	0.428	15	0.136	K.AGIALNDNFVK.-
R2/RRR2-15/2	1163.249	1162.320	-61.111	0.455	1266.260	0.339	16	0.136	K.AGIALNDNFVK.-
R2/RRR2-11/2	1133.936	1134.226	-255.966	0.366	995.501	0.442	14	0.135	K.YDTVHGQWK.H
R2/RRR2-11/2	1134.029	1134.226	-173.459	0.376	1052.518	0.408	14	0.135	K.YDTVHGQWK.H
R2/RRR2-16/2	1162.337	1162.320	14.683	0.298	1188.983	0.359	15	0.133	K.AGIALNDNFVK.-
R2/RRR2-2/2	1436.326	1435.607	-196.537	0.548	514.247	0.573	18	0.132	R.AASFNIIPSSTGAAK.A
R2/RRR2-3/2	1161.964	1162.320	-307.851	0.377	1030.931	0.402	16	0.132	K.AGIALNDNFVK.-
R2/RRR2-12/2	1134.040	1134.226	-164.281	0.428	859.261	0.454	13	0.132	K.YDTVHGQWK.H
R2/RRR2-11/3	1499.562	1499.734	-115.060	0.410	1644.807	0.331	25	0.132	R.VPTVDVSVVDLTVR.I
R2/RRR2-10/2	1161.634	1162.320	-1455.852	0.383	1007.696	0.406	15	0.130	K.AGIALNDNFVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1133.430	1134.226	-1589.085	0.397	742.956	0.480	13	0.130	K.YDTVHGQWK.H
R2/RRR2-11/2	928.936	929.139	-219.664	0.455	755.049	0.463	13	0.129	K.KVVISAPSK.D
R2/RRR2-11/2	1435.195	1435.607	-287.888	0.475	764.465	0.462	21	0.129	R.AASFNIIPSSTGAAK.A
R2/RRR2-11/2	1435.239	1435.607	-257.595	0.452	678.109	0.482	20	0.128	R.AASFNIIPSSTGAAK.A
R2/RRR2-13/2	1161.481	1162.320	-1588.234	0.327	1106.577	0.334	15	0.126	K.AGIALNDNFVK.-
R2/RRR2-7/2	1498.370	1499.734	-1582.834	0.329	1121.679	0.339	17	0.125	R.VPTVDVSVVDLTVR.I
R2/RRR2-13/2	833.772	833.958	-223.296	0.420	851.890	0.383	12	0.125	K.IGINGFGR.I
R2/RRR2-11/2	833.523	833.958	-523.460	0.408	741.871	0.405	12	0.125	K.IGINGFGR.I
R2/RRR2-11/2	833.891	833.958	-80.550	0.447	753.259	0.392	12	0.124	K.IGINGFGR.I
R2/RRR2-11/2	1162.201	1162.320	-102.779	0.407	934.189	0.365	16	0.124	K.AGIALNDNFVK.-
R2/RRR2-11/2	1762.821	1762.859	-21.782	0.446	1012.860	0.395	15	0.124	K.LVSWYDNEWGYSSR.V
R2/RRR2-1/2	1162.206	1162.320	-98.986	0.389	969.507	0.367	14	0.123	K.AGIALNDNFVK.-
R2/RRR2-12/2	1293.126	1292.463	-261.192	0.471	665.223	0.390	18	0.123	R.LEKPASYDQIK.A
R2/RRR2-12/2	1133.954	1134.226	-240.306	0.371	818.808	0.396	13	0.123	K.YDTVHGQWK.H
R2/RRR2-11/3	1757.132	1757.017	65.797	0.482	1222.081	0.473	28	0.123	K.TLLFGEKEVTVFGCR.N
R2/RRR2-11/2	833.261	833.958	-2042.508	0.410	761.854	0.371	12	0.122	K.IGINGFGR.I
R2/RRR2-26/2	833.835	833.958	-147.806	0.396	773.459	0.370	12	0.122	K.IGINGFGR.I
R2/RRR2-11/2	1435.240	1435.607	-256.742	0.496	734.033	0.413	20	0.122	R.AASFNIIPSSTGAAK.A
R2/RRR2-26/2	1134.242	1134.226	14.723	0.345	1039.436	0.313	13	0.121	K.YDTVHGQWK.H
R2/RRR2-11/2	1435.345	1435.607	-183.108	0.435	623.544	0.438	19	0.121	R.AASFNIIPSSTGAAK.A
R2/RRR2-10/2	1435.149	1435.607	-319.889	0.417	563.772	0.445	19	0.121	R.AASFNIIPSSTGAAK.A
R2/RRR2-10/2	1435.280	1435.607	-228.499	0.430	588.916	0.419	20	0.121	R.AASFNIIPSSTGAAK.A
R2/RRR2-15/2	1435.277	1435.607	-230.461	0.424	424.592	0.499	16	0.120	R.AASFNIIPSSTGAAK.A
R2/RRR2-2/2	833.851	833.958	-128.128	0.409	761.371	0.338	12	0.119	K.IGINGFGR.I
R2/RRR2-11/2	1435.220	1435.607	-270.395	0.454	613.740	0.413	19	0.119	R.AASFNIIPSSTGAAK.A
R2/RRR2-2/2	1435.274	1435.607	-233.021	0.448	504.167	0.435	18	0.119	R.AASFNIIPSSTGAAK.A
R2/RRR2-11/3	1756.548	1757.017	-268.023	0.434	1159.938	0.477	26	0.119	K.TLLFGEKEVTVFGCR.N
R2/RRR2-12/2	929.310	929.139	184.238	0.382	748.031	0.372	13	0.118	K.KVVISAPSK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	834.193	833.958	282.301	0.317	955.863	0.290	13	0.118	K.IGINGFGR.I
R2/RRR2-11/2	1291.681	1292.463	-1383.876	0.467	625.399	0.349	17	0.118	R.LEKPASYDQIK.A
R2/RRR2-13/2	1435.189	1435.607	-291.984	0.439	484.148	0.452	18	0.118	-.AASFNIIPSSTGAAK.-
R2/RRR2-12/2	834.030	833.958	86.523	0.346	659.808	0.367	11	0.118	K.IGINGFGR.I
R2/RRR2-10/2	834.094	833.958	163.728	0.382	669.624	0.349	11	0.117	K.IGINGFGR.I
R2/RRR2-2/2	1436.448	1435.607	-111.370	0.393	326.125	0.470	15	0.117	R.AASFNIIPSSTGAAK.A
R2/RRR2-16/2	1435.158	1435.607	-313.745	0.349	783.095	0.346	21	0.117	R.AASFNIIPSSTGAAK.A
R2/RRR2-11/2	1761.391	1762.859	-1405.421	0.296	911.355	0.372	15	0.117	K.LVSWYDNEWGYSSR.V
R2/RRR2-26/2	1134.018	1134.226	-183.826	0.305	902.236	0.320	13	0.117	K.YDTVHGQWK.H
R2/RRR2-10/2	833.859	833.958	-118.729	0.403	656.739	0.334	11	0.116	K.IGINGFGR.I
R2/RRR2-25/2	833.540	833.958	-502.591	0.308	762.519	0.349	11	0.116	K.IGINGFGR.I
R2/RRR2-12/2	929.029	929.139	-118.691	0.374	629.350	0.392	12	0.116	K.KVVISAPSK.D
R2/RRR2-13/2	1161.467	1162.320	-1600.692	0.320	786.638	0.369	13	0.116	K.AGIALNDNFVK.-
R2/RRR2-9/2	1436.224	1435.607	-267.307	0.450	470.838	0.451	15	0.116	R.AASFNIIPSSTGAAK.A
R2/RRR2-12/2	1762.351	1762.859	-857.900	0.459	815.270	0.389	15	0.116	K.LVSWYDNEWGYSSR.V
R2/RRR2-26/2	833.477	833.958	-578.135	0.381	700.195	0.324	11	0.116	K.IGINGFGR.I
R2/RRR2-12/2	1292.042	1292.463	-326.703	0.477	627.159	0.314	17	0.115	R.LEKPASYDQIK.A
R2/RRR2-11/2	1161.638	1162.320	-1452.580	0.300	224.199	0.421	12	0.115	-.AGIALNDNFVK.-
R2/RRR2-13/2	1161.743	1162.320	-1361.497	0.271	882.655	0.324	13	0.114	K.AGIALNDNFVK.-
R2/RRR2-9/2	833.919	833.958	-46.925	0.364	573.868	0.311	10	0.113	K.IGINGFGR.I
R2/RRR2-11/2	1435.175	1435.607	-302.224	0.355	459.926	0.383	16	0.113	R.AASFNIIPSSTGAAK.A
R2/RRR2-12/2	1292.116	1292.463	-268.977	0.416	595.920	0.269	17	0.112	R.LEKPASYDQIK.A
R2/RRR2-26/2	833.524	833.958	-522.431	0.321	570.747	0.304	10	0.112	K.IGINGFGR.I
R2/RRR2-12/2	1162.169	1162.320	-130.595	0.375	654.131	0.323	13	0.112	K.AGIALNDNFVK.-
R2/RRR2-12/2	833.429	833.958	-1839.658	0.247	523.040	0.299	11	0.112	K.IGINGFGR.I
R2/RRR2-9/2	1435.316	1435.607	-203.670	0.397	480.806	0.354	16	0.111	R.AASFNIIPSSTGAAK.A
R2/RRR2-2/2	833.539	833.958	-503.473	0.391	986.008	0.213	12	0.111	K.IGINGFGR.I
R2/RRR2-5/2	1162.228	1162.320	-79.706	0.332	933.485	0.250	14	0.111	K.AGIALNDNFVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1161.249	1162.320	-1788.666	0.227	893.639	0.276	14	0.111	K.AGIALNDNFVK.-
R2/RRR2-17/2	1162.124	1162.320	-169.055	0.307	551.240	0.340	12	0.111	K.AGIALNDNFVK.-
R2/RRR2-11/2	834.485	833.958	-568.047	0.289	627.510	0.205	12	0.111	K.IGINGFGR.I
R2/RRR2-12/2	929.156	929.139	17.972	0.382	596.879	0.304	12	0.111	K.KVVISAPSK.D
R2/RRR2-11/2	1292.081	1292.463	-296.559	0.457	704.217	0.239	18	0.111	R.LEKPASYDQIK.A
R2/RRR2-25/2	833.904	833.958	-64.985	0.299	732.431	0.253	11	0.110	K.IGINGFGR.I
R2/RRR2-11/2	1292.162	1292.463	-233.719	0.443	616.618	0.238	17	0.110	R.LEKPASYDQIK.A
R2/RRR2-11/2	1322.053	1322.512	-348.205	0.372	659.230	0.286	17	0.110	K.DAPM*FVVGVNEK.E
R2/RRR2-4/2	1435.164	1435.607	-309.393	0.425	418.171	0.432	15	0.110	-.AASFNIIPSSTGAAK.-
R2/RRR2-2/2	1161.341	1162.320	-1709.667	0.252	798.868	0.272	14	0.110	K.AGIALNDNFVK.-
R2/RRR2-3/2	833.526	833.958	-520.227	0.329	654.590	0.210	11	0.109	K.IGINGFGR.I
R2/RRR2-12/2	1435.289	1435.607	-222.355	0.346	388.913	0.340	15	0.109	-.AASFNIIPSSTGAAK.-
R2/RRR2-8/2	833.155	833.958	-2170.914	0.308	667.205	0.254	10	0.108	-.IGINGFGR.-
R2/RRR2-11/3	1499.462	1499.734	-182.310	0.435	1420.352	0.332	25	0.108	R.VPTVDVSVVDLTVR.I
R2/RRR2-6/2	1499.538	1499.734	-131.016	0.313	784.904	0.303	14	0.108	-.VPTVDVSVVDLTVR.-
R2/RRR2-11/2	1306.156	1306.513	-274.054	0.304	667.328	0.281	16	0.107	K.DAPMFVVGVNEK.E
R2/RRR2-12/2	1161.601	1162.320	-1484.458	0.331	669.136	0.203	14	0.107	K.AGIALNDNFVK.-
R2/RRR2-1/2	1161.537	1162.320	-1540.091	0.276	791.830	0.238	13	0.107	K.AGIALNDNFVK.-
R2/RRR2-11/2	1306.133	1306.513	-291.963	0.270	1074.364	0.175	17	0.107	K.DAPMFVVGVNEK.E
R2/RRR2-11/2	1321.943	1322.512	-1190.878	0.246	654.582	0.291	17	0.107	K.DAPM*FVVGVNEK.E
R2/RRR2-10/2	1133.895	1134.226	-292.688	0.309	617.724	0.206	12	0.106	-.YDTVHGQWK.-
R2/RRR2-12/2	1436.557	1435.607	-35.166	0.336	344.069	0.331	14	0.106	-.AASFNIIPSSTGAAK.-
R2/RRR2-26/2	1134.455	1134.226	202.618	0.205	590.856	0.237	12	0.106	K.YDTVHGQWK.H
R2/RRR2-12/2	1763.381	1762.859	-272.011	0.480	829.948	0.298	15	0.105	K.LVSWYDNEWGYSSR.V
R2/RRR2-1/2	833.571	833.958	-465.559	0.317	641.982	0.158	10	0.105	-.IGINGFGR.-
R2/RRR2-12/2	1161.299	1162.320	-1745.891	0.303	699.693	0.173	13	0.104	K.AGIALNDNFVK.-
R2/RRR2-10/3	1292.381	1292.463	-63.258	0.487	1238.313	0.389	24	0.104	R.LEKPASYDQIK.A
R2/RRR2-11/3	1292.490	1292.463	21.151	0.526	910.772	0.449	24	0.100	R.LEKPASYDQIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1435.557	1435.607	-34.935	0.339	229.179	0.347	12	0.099	-.AASFNIIPSSTGAAK.-
R2/RRR2-12/3	1292.744	1292.463	218.192	0.519	603.702	0.482	21	0.099	R.LEKPASYDQIK.A
R2/RRR2-10/3	1293.640	1292.463	137.072	0.510	818.666	0.457	21	0.099	R.LEKPASYDQIK.A
R2/RRR2-12/3	1292.181	1292.463	-218.329	0.499	836.149	0.439	23	0.096	R.LEKPASYDQIK.A
R2/RRR2-24/2	1162.090	1162.320	-198.455	0.322	552.385	0.305	11	0.096	-.AGIALNDNFVK.-
R2/RRR2-11/2	1134.929	1134.226	-262.323	0.309	637.805	0.129	12	0.095	-.YDTVHGQWK.-
R2/RRR2-11/3	1292.526	1292.463	49.142	0.508	792.596	0.431	23	0.094	R.LEKPASYDQIK.A
R2/RRR2-11/3	1292.256	1292.463	-160.758	0.512	672.510	0.429	21	0.093	R.LEKPASYDQIK.A
R2/RRR2-3/3	1292.585	1292.463	94.607	0.488	833.221	0.416	23	0.093	R.LEKPASYDQIK.A
R2/RRR2-13/2	1435.351	1435.607	-178.928	0.323	225.994	0.374	12	0.092	-.AASFNIIPSSTGAAK.-
R2/RRR2-12/3	1292.464	1292.463	0.832	0.520	823.358	0.406	23	0.092	R.LEKPASYDQIK.A
R2/RRR2-1/3	1293.551	1292.463	68.081	0.471	622.397	0.416	20	0.091	R.LEKPASYDQIK.A
R2/RRR2-13/3	1292.524	1292.463	47.863	0.429	563.168	0.457	19	0.091	-.LEKPASYDQIK.-
R2/RRR2-2/3	1292.556	1292.463	72.727	0.477	687.861	0.411	21	0.091	R.LEKPASYDQIK.A
R2/RRR2-7/3	1293.172	1292.463	-225.168	0.456	536.877	0.404	19	0.090	R.LEKPASYDQIK.A
R2/RRR2-11/3	1757.485	1757.017	266.839	0.414	884.395	0.422	25	0.090	K.TLLFGEKEVTVFGCR.N
R2/RRR2-24/3	1293.744	1292.463	218.402	0.448	643.358	0.401	21	0.090	R.LEKPASYDQIK.A
R2/RRR2-23/3	1292.092	1292.463	-287.992	0.419	864.324	0.379	22	0.088	R.LEKPASYDQIK.A
R2/RRR2-2/3	1292.403	1292.463	-46.204	0.455	569.664	0.379	20	0.088	R.LEKPASYDQIK.A
R2/RRR2-1/3	1292.633	1292.463	131.828	0.455	578.711	0.375	20	0.088	R.LEKPASYDQIK.A
R2/RRR2-6/3	1292.890	1292.463	331.665	0.412	538.269	0.386	18	0.088	R.LEKPASYDQIK.A
R2/RRR2-15/3	1292.594	1292.463	101.568	0.393	484.445	0.370	18	0.088	R.LEKPASYDQIK.A
R2/RRR2-3/3	1292.420	1292.463	-33.273	0.482	604.843	0.435	20	0.086	-.LEKPASYDQIK.-
R2/RRR2-3/3	1292.225	1292.463	-184.781	0.430	658.170	0.360	20	0.085	R.LEKPASYDQIK.A
R2/RRR2-2/3	1292.318	1292.463	-112.432	0.410	394.571	0.379	16	0.083	-.LEKPASYDQIK.-
R2/RRR2-9/3	1292.661	1292.463	153.704	0.381	576.753	0.295	20	0.083	R.LEKPASYDQIK.A
R2/RRR2-8/3	1292.248	1292.463	-166.444	0.346	489.698	0.337	18	0.078	-.LEKPASYDQIK.-
R2/RRR2-4/3	1292.122	1292.463	-264.817	0.389	309.320	0.338	15	0.077	-.LEKPASYDQIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1292.390	1292.463	-56.436	0.366	482.264	0.303	18	0.077	-.LEKPASYDQIK.-
R2/RRR2-11/3	1292.797	1292.463	258.955	0.456	976.285	0.290	24	0.077	-.LEKPASYDQIK.-
R2/RRR2-16/3	1292.837	1292.463	290.625	0.397	498.387	0.360	18	0.076	-.LEKPASYDQIK.-
R2/RRR2-11/3	1292.668	1292.463	159.244	0.448	741.175	0.322	21	0.074	-.LEKPASYDQIK.-
R2/RRR2-24/3	1292.421	1292.463	-32.562	0.374	520.638	0.312	17	0.072	-.LEKPASYDQIK.-
R2/RRR2-11/3	1292.909	1292.463	346.291	0.438	600.000	0.275	19	0.070	-.LEKPASYDQIK.-
R2/RRR2-12/3	1499.275	1499.734	-307.156	0.378	971.939	0.255	21	0.066	-.VPTVDVSVVDLTVR.-
R2/RRR2-24/2	1435.259	1435.607	-243.260	0.297	178.795	0.417	11	0.066	-.AASFNIIPSSTGAAK.-
R2/RRR2-4/2	1532.006	1532.743	-1137.127	0.491	2394.793	0.459	22	0.314	R.M*LQSYLGAETFQK.S
R2/RRR2-4/2	1831.518	1831.958	-240.700	0.552	1960.966	0.551	24	0.264	K.TEDLWAALEEGSGEPVK.T
R2/RRR2-4/2	1832.324	1831.958	200.554	0.592	1957.390	0.554	24	0.263	K.TEDLWAALEEGSGEPVK.T
R2/RRR2-4/2	1831.578	1831.958	-207.803	0.547	1804.399	0.560	23	0.241	K.TEDLWAALEEGSGEPVK.T
R2/RRR2-4/2	1211.652	1212.339	-1397.068	0.454	1707.798	0.485	17	0.211	K.LNVNQTGFYR.V
R2/RRR2-4/2	1517.467	1516.744	-182.881	0.553	1514.129	0.533	19	0.198	R.MLQSYLGAETFQK.S
R2/RRR2-4/2	1212.104	1212.339	-194.711	0.525	1255.050	0.446	17	0.158	K.LNVNQTGFYR.V
R2/RRR2-4/2	1582.923	1582.787	85.964	0.510	1125.801	0.526	20	0.157	R.GVGAAGHEVAWTWLK.E
R2/RRR2-4/2	1030.149	1029.172	-23.130	0.541	1260.331	0.419	17	0.153	R.AEANLGNVLK.E
R2/RRR2-4/2	1169.041	1169.223	-156.115	0.476	1322.234	0.386	16	0.150	R.VSYDEELASR.L
R2/RRR2-4/2	1516.165	1516.744	-1044.684	0.402	1382.802	0.359	18	0.148	R.MLQSYLGAETFQK.S
R2/RRR2-4/2	1029.917	1029.172	-248.888	0.539	1240.744	0.387	17	0.146	R.AEANLGNVLK.E
R2/RRR2-4/2	1169.080	1169.223	-123.435	0.500	1077.925	0.385	15	0.133	R.VSYDEELASR.L
R2/RRR2-4/2	1549.871	1550.583	-1107.788	0.388	1080.068	0.396	17	0.132	R.TDEM*GDDAEEFFK.S
R2/RRR2-4/2	1834.257	1834.148	59.901	0.543	673.883	0.520	22	0.131	R.FNEVLPVGEGTLVIAFK.G
R2/RRR2-4/2	1832.976	1834.148	-1188.619	0.477	706.579	0.497	22	0.128	R.FNEVLPVGEGTLVIAFK.G
R2/RRR2-4/2	1212.161	1212.339	-148.037	0.525	986.727	0.366	15	0.126	K.LNVNQTGFYR.V
R2/RRR2-4/2	1168.063	1168.285	-190.627	0.366	1057.969	0.356	15	0.126	K.SGEGHLDALLR.G
R2/RRR2-4/2	1168.565	1169.223	-1423.014	0.416	991.423	0.322	14	0.120	R.VSYDEELASR.L
R2/RRR2-4/2	1106.040	1106.257	-196.446	0.508	787.273	0.330	14	0.117	R.NQDSIFLLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1168.439	1169.223	-1531.832	0.342	892.216	0.287	14	0.113	R.VSYDEELASR.L
R2/RRR2-4/2	1105.980	1106.257	-250.702	0.438	742.383	0.302	13	0.112	R.NQDSIFLLR.G
R2/RRR2-4/2	1582.841	1582.787	34.607	0.426	551.935	0.422	15	0.111	R.GVGAAGHEVAWTWLK.E
R2/RRR2-4/2	1105.498	1106.257	-1595.566	0.385	749.856	0.244	13	0.107	-.NQDSIFLLR.-
R2/RRR2-4/2	1832.805	1834.148	-1282.254	0.342	292.126	0.448	15	0.107	-.FNEVLPVGEGTLVIAFK.-
R2/RRR2-4/2	1169.056	1168.285	-196.644	0.383	788.409	0.259	13	0.105	K.SGEGHLDALLR.G
R2/RRR2-4/2	1167.423	1168.285	-1599.447	0.311	581.516	0.247	13	0.103	-.SGEGHLDALLR.-
R2/RRR2-4/3	1353.967	1354.488	-1126.753	0.441	1026.621	0.313	23	0.078	-.IYKETDLSQEK.-
R2/RRR2-4/3	1354.177	1354.488	-230.350	0.479	993.430	0.305	23	0.074	-.IYKETDLSQEK.-
R2/RRR2-4/3	1354.769	1354.488	208.293	0.470	709.359	0.352	22	0.068	-.IYKETDLSQEK.-
R2/RRR2-3/3	1298.673	1298.434	184.670	0.511	2691.905	0.405	29	0.331	R.RPGSVSLNQSPR.T
R2/RRR2-3/2	1497.318	1497.637	-213.635	0.533	1228.042	0.549	21	0.174	R.QGNVGIVEYAYQR.T
R2/RRR2-3/2	1252.375	1252.528	-122.264	0.445	1418.008	0.459	18	0.171	R.LILGELQAPAVK.Y
R2/RRR2-3/2	1497.213	1497.637	-283.895	0.514	1027.425	0.549	19	0.156	R.QGNVGIVEYAYQR.T
R2/RRR2-3/2	1322.624	1321.501	93.440	0.451	1133.347	0.478	17	0.151	R.VIGNNIFCLDR.D
R2/RRR2-3/2	992.185	992.114	72.484	0.489	1006.122	0.483	16	0.144	K.GAGGSAVFVAR.N
R2/RRR2-3/2	1120.076	1120.283	-185.895	0.380	1111.276	0.374	14	0.133	R.VTIFDLQQR.L
R2/RRR2-3/2	1321.200	1321.501	-228.675	0.410	870.927	0.438	16	0.129	R.VIGNNIFCLDR.D
R2/RRR2-2/2	1498.251	1497.637	-258.611	0.431	710.064	0.479	18	0.127	R.QGNVGIVEYAYQR.T
R2/RRR2-3/3	1298.512	1298.434	60.089	0.459	1625.065	0.346	26	0.127	R.RPGSVSLNQSPR.T
R2/RRR2-3/2	1192.278	1191.402	-104.192	0.406	773.108	0.428	16	0.126	K.TLDVPIYITR.V
R2/RRR2-3/3	1298.688	1298.434	196.406	0.411	1598.248	0.349	26	0.125	R.RPGSVSLNQSPR.T
R2/RRR2-3/2	1191.133	1191.402	-226.406	0.374	733.219	0.430	16	0.124	K.TLDVPIYITR.V
R2/RRR2-3/2	1191.103	1191.402	-251.493	0.376	679.361	0.447	15	0.124	K.TLDVPIYITR.V
R2/RRR2-3/2	1321.984	1321.501	366.794	0.378	663.121	0.480	14	0.123	R.VIGNNIFCLDR.D
R2/RRR2-3/2	1496.653	1497.637	-1329.985	0.335	804.609	0.388	18	0.118	R.QGNVGIVEYAYQR.T
R2/RRR2-2/3	1298.106	1298.434	-253.693	0.449	1377.620	0.401	25	0.118	R.RPGSVSLNQSPR.T
R2/RRR2-5/2	771.796	771.928	-171.188	0.409	868.733	0.235	11	0.112	R.LGIEALR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	771.280	771.928	-2142.751	0.275	1030.515	0.203	11	0.110	R.LGIEALR.Q
R2/RRR2-3/2	1829.010	1829.107	-52.925	0.433	731.280	0.351	19	0.110	K.YVVWSSDMESIALLSK.H
R2/RRR2-5/3	1298.232	1298.434	-156.199	0.436	1321.997	0.394	26	0.110	R.RPGSVSLNQSPR.T
R2/RRR2-1/2	1253.149	1252.528	-303.330	0.333	618.036	0.380	14	0.110	-.LILGELQAPAVK.-
R2/RRR2-3/2	771.581	771.928	-451.152	0.360	669.529	0.245	10	0.110	R.LGIEALR.Q
R2/RRR2-3/2	1617.511	1616.842	-205.027	0.434	689.130	0.350	16	0.109	K.GFPEVALHFVKDEK.T
R2/RRR2-5/2	1191.386	1191.402	-12.806	0.272	556.700	0.330	13	0.109	K.TLDVPIYITR.V
R2/RRR2-5/2	771.535	771.928	-511.482	0.363	1071.393	0.138	11	0.106	R.LGIEALR.Q
R2/RRR2-2/2	1191.124	1191.402	-234.015	0.268	498.117	0.341	12	0.105	-.TLDVPIYITR.-
R2/RRR2-3/2	772.103	771.928	226.904	0.378	916.228	0.143	11	0.105	R.LGIEALR.Q
R2/RRR2-2/2	772.130	771.928	261.781	0.406	726.676	0.181	10	0.105	-.LGIEALR.-
R2/RRR2-1/2	772.124	771.928	254.489	0.312	702.117	0.070	11	0.104	R.LGIEALR.Q
R2/RRR2-2/2	772.283	771.928	460.695	0.445	708.039	0.125	10	0.102	R.LGIEALR.Q
R2/RRR2-3/2	1251.828	1252.528	-1362.500	0.182	1016.418	0.110	14	0.098	R.LILGELQAPAVK.Y
R2/RRR2-5/3	1298.768	1298.434	258.330	0.407	1214.912	0.337	23	0.093	R.RPGSVSLNQSPR.T
R2/RRR2-5/3	1298.252	1298.434	-140.352	0.384	1165.936	0.267	25	0.078	R.RPGSVSLNQSPR.T
R2/RRR2-5/3	1892.588	1893.091	-796.478	0.476	2090.540	0.481	31	0.256	R.HAQLPDEAKELDKELR.Q
R2/RRR2-4/2	1029.931	1030.160	-223.326	0.499	2011.785	0.393	17	0.232	K.TAIAEGLAQR.I
R2/RRR2-5/2	1159.941	1160.260	-275.666	0.486	1798.309	0.451	18	0.215	K.AIDLIDEAGSR.V
R2/RRR2-5/2	1610.419	1610.834	-258.008	0.460	1518.311	0.534	21	0.199	K.VPEPTVDETIQILR.G
R2/RRR2-5/2	1159.866	1160.260	-340.076	0.520	1584.023	0.488	18	0.197	K.AIDLIDEAGSR.V
R2/RRR2-5/2	1158.558	1159.315	-1521.013	0.437	1576.307	0.461	17	0.190	R.VLELSLEEAR.Q
R2/RRR2-5/2	1610.427	1610.834	-253.370	0.488	1331.868	0.571	21	0.187	K.VPEPTVDETIQILR.G
R2/RRR2-5/2	1160.044	1160.260	-186.140	0.412	1519.487	0.456	18	0.181	K.AIDLIDEAGSR.V
R2/RRR2-5/2	1159.033	1159.315	-244.191	0.426	1442.451	0.366	17	0.157	R.VLELSLEEAR.Q
R2/RRR2-5/2	1477.265	1477.689	-287.729	0.368	968.499	0.399	17	0.125	R.GSGFVAVEIPFTPR.A
R2/RRR2-5/2	1477.142	1477.689	-1050.483	0.323	938.615	0.383	17	0.120	R.GSGFVAVEIPFTPR.A
R2/RRR2-5/3	1960.269	1960.225	22.222	0.419	1428.203	0.292	28	0.101	K.NPNRPIASFIFSGPTGVGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1208.747	1208.349	330.392	0.554	1090.101	0.405	20	0.098	K.HIEKDPALER.R
R2/RRR2-5/3	1383.464	1383.575	-80.953	0.419	1062.044	0.380	26	0.091	K.LAEEGKLDPVVGR.Q
R2/RRR2-5/3	1260.333	1260.419	-68.461	0.467	1294.823	0.274	23	0.085	K.AKDIDLQVTEK.F
R2/RRR2-5/3	1208.581	1208.349	192.307	0.515	832.936	0.364	19	0.082	K.HIEKDPALER.R
R2/RRR2-5/3	1086.490	1086.139	323.733	0.455	1079.001	0.319	17	0.082	K.YRGEFEER.L
R2/RRR2-5/3	1959.811	1960.225	-211.956	0.392	920.056	0.361	25	0.081	K.NPNRPIASFIFSGPTGVGK.S
R2/RRR2-5/3	1383.708	1383.575	96.384	0.418	822.972	0.355	24	0.079	K.LAEEGKLDPVVGR.Q
R2/RRR2-4/3	1208.286	1208.349	-52.512	0.435	1051.571	0.263	20	0.074	K.HIEKDPALER.R
R2/RRR2-5/3	1260.504	1260.419	67.923	0.458	1169.411	0.229	22	0.073	K.AKDIDLQVTEK.F
R2/RRR2-5/3	1085.725	1086.139	-382.933	0.387	838.276	0.235	15	0.067	K.YRGEFEER.L
R2/RRR2-5/3	1261.425	1260.419	4.929	0.443	648.256	0.319	17	0.065	-.AKDIDLQVTEK.-
R2/RRR2-5/3	1959.332	1960.225	-969.311	0.318	661.151	0.255	22	0.064	K.NPNRPIASFIFSGPTGVGK.S
R2/RRR2-5/2	1426.809	1426.728	56.583	0.523	2484.019	0.541	19	0.360	R.LPLLDLNIYVPR.D
R2/RRR2-5/2	1427.366	1426.728	-254.212	0.591	2335.871	0.551	20	0.333	R.LPLLDLNIYVPR.D
R2/RRR2-5/2	1427.315	1426.728	-290.249	0.568	2300.301	0.532	20	0.319	R.LPLLDLNIYVPR.D
R2/RRR2-5/2	1087.160	1087.252	-84.985	0.474	1489.654	0.444	17	0.176	K.VANASALAEIK.K
R2/RRR2-5/2	1086.936	1087.252	-291.027	0.459	1511.394	0.423	18	0.175	K.VANASALAEIK.K
R2/RRR2-5/2	1155.970	1156.273	-262.526	0.464	1320.386	0.469	17	0.168	K.LDGNFIYASR.T
R2/RRR2-5/2	1402.225	1402.576	-250.999	0.490	1204.998	0.453	18	0.152	R.VFFANDTYLPSK.M
R2/RRR2-5/2	1086.623	1087.252	-1503.507	0.443	1212.546	0.442	16	0.150	K.VANASALAEIK.K
R2/RRR2-5/2	1491.951	1491.540	276.672	0.425	1024.677	0.396	16	0.131	-.YDYYNDLGQPDK.-
R2/RRR2-5/2	1401.606	1402.576	-1409.517	0.393	990.552	0.391	16	0.127	R.VFFANDTYLPSK.M
R2/RRR2-5/2	1241.044	1240.474	-347.428	0.464	773.451	0.418	19	0.126	K.SLLPVAGDQVLK.L
R2/RRR2-5/2	1533.996	1534.609	-1054.729	0.447	769.315	0.440	19	0.124	K.STLDPNVYGDHTSK.I
R2/RRR2-5/2	1402.344	1402.576	-166.027	0.471	979.521	0.371	16	0.124	R.VFFANDTYLPSK.M
R2/RRR2-5/3	1782.638	1782.079	-248.544	0.555	1153.470	0.485	33	0.119	K.LVRPVLGGSQELPYPR.R
R2/RRR2-4/2	1402.240	1402.576	-239.820	0.430	607.036	0.423	15	0.117	-.VFFANDTYLPSK.-
R2/RRR2-5/3	1781.672	1782.079	-229.265	0.475	1097.101	0.477	32	0.113	K.LVRPVLGGSQELPYPR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1827.193	1827.117	41.631	0.391	965.669	0.523	25	0.112	R.LPLLDLNIYVPRDER.F
R2/RRR2-4/3	1781.605	1782.079	-267.106	0.455	1108.839	0.465	30	0.112	K.LVRPVLGGSQELPYPR.R
R2/RRR2-4/2	1402.144	1402.576	-308.820	0.347	678.950	0.227	17	0.107	R.VFFANDTYLPSK.M
R2/RRR2-5/2	1000.627	1001.159	-1535.384	0.247	776.960	0.279	16	0.105	K.TLTLDGVPGK.G
R2/RRR2-5/2	1240.017	1240.474	-369.734	0.328	319.484	0.357	10	0.099	-.SLLPVAGDQVLK.-
R2/RRR2-5/3	1781.761	1782.079	-179.056	0.495	890.517	0.429	28	0.093	K.LVRPVLGGSQELPYPR.R
R2/RRR2-4/3	1781.462	1782.079	-910.663	0.398	679.065	0.388	25	0.079	-.LVRPVLGGSQELPYPR.-
R2/RRR2-5/3	1827.312	1827.117	106.856	0.379	574.396	0.340	22	0.074	R.LPLLDLNIYVPRDER.F
R2/RRR2-4/3	1781.537	1782.079	-868.461	0.297	571.274	0.304	24	0.073	K.LVRPVLGGSQELPYPR.R
R2/RRR2-5/3	1826.657	1827.117	-252.642	0.320	435.453	0.369	20	0.068	-.LPLLDLNIYVPRDER.-
R2/RRR2-9/2	1869.584	1870.114	-820.613	0.563	2440.349	0.595	25	0.376	R.AVCMISNNTAVAEVFSR.I
R2/RRR2-9/2	1793.574	1794.107	-857.574	0.582	2283.796	0.612	23	0.341	R.IHFMLSSYAPVISAEK.A
R2/RRR2-9/2	1533.455	1532.807	-230.477	0.535	2284.508	0.597	22	0.339	R.LISQIISSLTTSLR.F
R2/RRR2-9/2	1532.573	1532.807	-153.517	0.476	2134.051	0.530	21	0.288	R.LISQIISSLTTSLR.F
R2/RRR2-9/2	1533.330	1532.807	-312.183	0.534	2000.279	0.581	21	0.281	R.LISQIISSLTTSLR.F
R2/RRR2-9/2	1809.444	1810.107	-921.891	0.574	1946.813	0.603	23	0.276	R.IHFM*LSSYAPVISAEK.A
R2/RRR2-9/2	1809.314	1810.107	-994.026	0.548	1512.352	0.608	22	0.214	R.IHFM*LSSYAPVISAEK.A
R2/RRR2-8/2	1717.372	1716.956	242.709	0.512	1732.937	0.371	23	0.182	R.AIFVDLEPTVIDEVR.T
R2/RRR2-9/2	1809.309	1810.107	-996.803	0.509	1279.249	0.580	22	0.181	R.IHFM*LSSYAPVISAEK.A
R2/RRR2-9/2	1873.340	1873.093	132.243	0.473	1184.788	0.593	26	0.175	K.CGINYQPPSVVPGGDLAK.V
R2/RRR2-9/2	1001.919	1002.147	-227.615	0.457	1338.217	0.506	17	0.174	K.DVNAAVATIK.T
R2/RRR2-9/2	1872.411	1873.093	-901.111	0.474	1213.841	0.555	26	0.170	K.CGINYQPPSVVPGGDLAK.V
R2/RRR2-9/2	1717.035	1716.956	46.235	0.570	1271.430	0.486	23	0.162	R.AIFVDLEPTVIDEVR.T
R2/RRR2-9/2	1717.426	1716.956	274.212	0.560	1314.380	0.468	23	0.162	R.AIFVDLEPTVIDEVR.T
R2/RRR2-9/2	1001.924	1002.147	-223.214	0.460	1126.347	0.512	16	0.157	K.DVNAAVATIK.T
R2/RRR2-9/2	1872.596	1873.093	-266.215	0.491	1028.776	0.546	25	0.153	K.CGINYQPPSVVPGGDLAK.V
R2/RRR2-9/2	1001.450	1002.147	-1699.356	0.430	1058.911	0.510	15	0.150	K.DVNAAVATIK.T
R2/RRR2-9/2	1716.375	1716.956	-923.823	0.526	1199.396	0.445	23	0.149	R.AIFVDLEPTVIDEVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1002.950	1002.147	-196.740	0.393	1203.347	0.438	16	0.149	K.DVNAAVATIK.T
R2/RRR2-1/2	1716.536	1716.956	-245.767	0.452	1238.330	0.434	20	0.148	R.AIFVDLEPTVIDEVR.T
R2/RRR2-20/2	1001.685	1002.147	-462.106	0.379	1024.072	0.485	16	0.143	K.DVNAAVATIK.T
R2/RRR2-1/2	1002.096	1002.147	-50.779	0.332	1129.493	0.374	16	0.133	K.DVNAAVATIK.T
R2/RRR2-13/2	1716.689	1716.956	-156.166	0.535	873.713	0.397	19	0.121	R.AIFVDLEPTVIDEVR.T
R2/RRR2-9/3	1810.443	1810.107	186.153	0.410	1628.318	0.297	31	0.119	R.IHFM*LSSYAPVISAEK.A
R2/RRR2-7/2	1001.956	1002.147	-190.825	0.310	715.036	0.387	14	0.117	K.DVNAAVATIK.T
R2/RRR2-9/2	1132.820	1133.271	-398.669	0.352	868.489	0.330	13	0.116	K.EIVDLCLDR.V
R2/RRR2-2/2	1001.954	1002.147	-193.514	0.374	694.052	0.333	15	0.116	K.DVNAAVATIK.T
R2/RRR2-9/2	1285.714	1284.518	153.189	0.318	649.822	0.413	13	0.115	K.YM*ACCLMYR.G
R2/RRR2-8/2	1716.331	1716.956	-949.957	0.359	1050.624	0.226	21	0.111	R.AIFVDLEPTVIDEVR.T
R2/RRR2-2/2	1718.626	1716.956	-192.750	0.496	637.496	0.379	15	0.108	-.AIFVDLEPTVIDEVR.-
R2/RRR2-9/2	1132.446	1133.271	-1616.197	0.206	766.335	0.277	13	0.105	K.EIVDLCLDR.V
R2/RRR2-20/2	1873.434	1873.093	182.494	0.295	290.055	0.334	15	0.104	K.CGINYQPPSVVPGGDLAK.V
R2/RRR2-9/2	1132.377	1133.271	-1677.710	0.203	757.485	0.239	13	0.103	K.EIVDLCLDR.V
R2/RRR2-4/2	1715.849	1716.956	-1231.652	0.283	687.089	0.201	17	0.102	R.AIFVDLEPTVIDEVR.T
R2/RRR2-8/2	1716.638	1716.956	-185.984	0.333	708.845	0.144	17	0.099	R.AIFVDLEPTVIDEVR.T
R2/RRR2-9/3	1693.107	1692.855	149.675	0.461	667.428	0.477	30	0.095	R.SLDIERPTYTNLNR.L
R2/RRR2-9/3	1693.103	1692.855	147.181	0.447	749.688	0.462	28	0.094	R.SLDIERPTYTNLNR.L
R2/RRR2-9/3	1382.025	1381.625	290.253	0.538	947.909	0.403	23	0.092	R.IDHKFDLMYAK.R
R2/RRR2-2/3	1693.012	1692.855	93.058	0.426	610.125	0.457	26	0.091	R.SLDIERPTYTNLNR.L
R2/RRR2-9/3	1692.768	1692.855	-51.333	0.420	582.129	0.436	27	0.089	R.SLDIERPTYTNLNR.L
R2/RRR2-10/3	1693.163	1692.855	182.320	0.397	489.458	0.441	23	0.088	R.SLDIERPTYTNLNR.L
R2/RRR2-2/3	1693.794	1692.855	-36.159	0.352	393.250	0.420	23	0.086	R.SLDIERPTYTNLNR.L
R2/RRR2-8/3	1693.607	1692.855	-146.663	0.390	494.278	0.380	26	0.084	R.SLDIERPTYTNLNR.L
R2/RRR2-8/3	1692.239	1692.855	-957.700	0.368	659.525	0.371	28	0.081	R.SLDIERPTYTNLNR.L
R2/RRR2-13/3	1692.967	1692.855	66.266	0.395	331.508	0.324	23	0.080	-.SLDIERPTYTNLNR.-
R2/RRR2-9/3	1793.302	1794.107	-1009.724	0.360	1076.688	0.276	29	0.076	R.IHFMLSSYAPVISAEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/3	1397.567	1397.624	-40.743	0.363	967.364	0.276	23	0.071	-.IDHKFDLM*YAK.-
R2/RRR2-9/3	1397.824	1397.624	143.731	0.299	752.750	0.190	21	0.065	R.IDHKFDLM*YAK.R
R2/RRR2-9/3	1793.445	1794.107	-929.667	0.311	923.676	0.209	28	0.064	R.IHFMLSSYAPVISAEK.A
R2/RRR2-9/3	1398.142	1397.624	-346.173	0.214	792.086	0.168	20	0.061	R.IDHKFDLM*YAK.R
R2/RRR2-7/2	1707.620	1705.937	-185.819	0.597	2488.790	0.655	23	0.410	K.WPYEAAALAFEAIPR.T
R2/RRR2-7/2	1158.158	1158.327	-146.271	0.497	1891.900	0.491	18	0.238	K.ALEDALAVLDK.I
R2/RRR2-7/2	1358.981	1359.551	-1158.488	0.475	2031.132	0.361	20	0.227	R.TLAQNCGLNVIR.I
R2/RRR2-7/2	1158.126	1158.327	-173.867	0.442	1638.268	0.413	18	0.186	K.ALEDALAVLDK.I
R2/RRR2-7/2	1158.015	1158.327	-269.781	0.431	1342.025	0.406	17	0.155	K.ALEDALAVLDK.I
R2/RRR2-7/2	1120.231	1121.250	-1808.124	0.334	1278.472	0.382	16	0.144	R.NLQDAM*SVAR.N
R2/RRR2-7/2	1316.840	1317.431	-1211.368	0.444	1169.517	0.377	18	0.137	R.GASKDVLNEVER.N
R2/RRR2-7/2	1317.050	1317.516	-354.709	0.450	966.993	0.454	16	0.135	K.GLSDLAIHYLSK.A
R2/RRR2-7/2	1317.061	1317.516	-346.340	0.409	923.991	0.460	16	0.132	K.GLSDLAIHYLSK.A
R2/RRR2-7/2	1121.076	1121.250	-156.109	0.436	1119.078	0.355	16	0.132	R.NLQDAM*SVAR.N
R2/RRR2-7/2	1120.773	1121.250	-427.292	0.347	1128.891	0.345	15	0.129	R.NLQDAM*SVAR.N
R2/RRR2-7/2	818.936	819.048	-136.691	0.376	1154.427	0.293	13	0.125	R.AAM*LGLVK.S
R2/RRR2-7/2	960.192	960.107	88.735	0.513	911.156	0.357	15	0.125	R.IDDIVSGIK.K
R2/RRR2-7/2	1316.482	1317.431	-1484.660	0.386	996.055	0.346	17	0.122	R.GASKDVLNEVER.N
R2/RRR2-7/2	959.959	960.107	-154.852	0.454	802.368	0.364	14	0.121	R.IDDIVSGIK.K
R2/RRR2-7/2	1316.423	1317.431	-1529.742	0.363	922.488	0.369	16	0.121	R.GASKDVLNEVER.N
R2/RRR2-7/2	959.721	960.107	-403.151	0.414	814.215	0.342	14	0.119	R.IDDIVSGIK.K
R2/RRR2-7/2	1058.015	1058.127	-106.651	0.399	582.699	0.386	15	0.118	K.VPGGQLEDSR.V
R2/RRR2-7/2	1057.798	1058.127	-312.123	0.309	732.211	0.388	16	0.117	K.VPGGQLEDSR.V
R2/RRR2-7/2	763.976	763.904	94.056	0.475	862.793	0.244	11	0.110	R.AGLFEVK.K
R2/RRR2-7/2	763.797	763.904	-141.562	0.394	867.903	0.207	11	0.107	R.AGLFEVK.K
R2/RRR2-7/2	1057.474	1058.127	-1568.107	0.281	735.366	0.230	15	0.106	K.VPGGQLEDSR.V
R2/RRR2-9/2	1505.274	1504.744	-313.690	0.475	1965.931	0.514	22	0.256	K.ECILSGLLSVDGLK.V
R2/RRR2-9/2	1491.124	1491.653	-1028.281	0.483	1668.777	0.588	21	0.235	K.THQGLDLTTM*TTR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1504.906	1504.744	107.994	0.479	1731.519	0.505	21	0.218	K.ECILSGLLSVDGLK.V
R2/RRR2-9/2	1504.402	1504.744	-228.580	0.434	1157.869	0.473	19	0.150	K.ECILSGLLSVDGLK.V
R2/RRR2-9/2	1037.669	1038.243	-1521.503	0.423	1024.675	0.418	14	0.135	K.SPLM*GLFEK.R
R2/RRR2-9/2	1073.025	1073.180	-145.552	0.465	718.971	0.431	16	0.126	K.AVDGSYVFSK.G
R2/RRR2-9/2	1864.064	1864.003	32.670	0.443	859.657	0.428	18	0.124	R.NFFIYVQDYNEADPK.T
R2/RRR2-9/2	1091.141	1091.261	-109.630	0.418	413.799	0.471	14	0.120	K.VPATDM*EALK.S
R2/RRR2-9/3	1626.743	1626.798	-33.773	0.443	1283.075	0.413	29	0.114	R.FRGEDKPPAHLGSSK.D
R2/RRR2-9/2	1038.313	1038.243	68.042	0.313	698.976	0.330	13	0.111	K.SPLM*GLFEK.R
R2/RRR2-9/2	1156.553	1156.404	129.367	0.289	777.044	0.281	13	0.106	K.FMM*ANGTLVR.T
R2/RRR2-9/3	1469.509	1469.732	-152.226	0.476	1331.498	0.351	26	0.103	K.IHKVPATDM*EALK.S
R2/RRR2-9/3	1469.744	1469.732	8.368	0.481	1175.400	0.398	25	0.102	K.IHKVPATDM*EALK.S
R2/RRR2-2/2	1864.652	1864.003	-188.884	0.373	550.303	0.315	13	0.101	R.NFFIYVQDYNEADPK.T
R2/RRR2-9/3	1805.763	1805.970	-115.077	0.434	1455.053	0.269	28	0.097	R.DDRYLNEPAIDTVKR.M
R2/RRR2-9/3	1627.181	1626.798	235.875	0.453	893.459	0.369	25	0.082	R.FRGEDKPPAHLGSSK.D
R2/RRR2-9/3	1806.330	1805.970	199.942	0.472	939.315	0.344	25	0.081	R.DDRYLNEPAIDTVKR.M
R2/RRR2-9/3	1469.125	1469.732	-1097.256	0.459	728.885	0.360	22	0.079	K.IHKVPATDM*EALK.S
R2/RRR2-9/3	1805.495	1805.970	-263.809	0.388	841.654	0.289	22	0.071	R.DDRYLNEPAIDTVKR.M
R2/RRR2-7/2	1471.288	1471.678	-265.930	0.368	2572.228	0.440	21	0.350	K.ESIVDVEGVVSLPK.E
R2/RRR2-7/2	1531.228	1531.652	-277.509	0.557	2240.628	0.529	25	0.307	R.VWTEVGGLDEAAAGR.S
R2/RRR2-7/2	1531.012	1531.652	-1074.459	0.443	2026.606	0.416	24	0.238	R.VWTEVGGLDEAAAGR.S
R2/RRR2-7/2	1467.377	1466.768	-267.280	0.483	1974.755	0.431	18	0.235	R.VVM*LFCALNNIR.K
R2/RRR2-7/2	1530.554	1531.652	-1375.082	0.357	1992.833	0.384	24	0.224	R.VWTEVGGLDEAAAGR.S
R2/RRR2-7/2	1307.337	1307.477	-108.040	0.450	1073.454	0.490	19	0.147	K.LIAGSSEGGAAVFK.L
R2/RRR2-7/2	1307.140	1307.477	-258.954	0.408	993.743	0.453	19	0.135	K.LIAGSSEGGAAVFK.L
R2/RRR2-7/2	1097.980	1098.281	-275.277	0.489	837.676	0.443	13	0.125	R.GAAQAIRPVSK.K
R2/RRR2-7/2	1050.012	1050.235	-213.225	0.443	770.632	0.402	13	0.123	R.VFEVGPVFR.A
R2/RRR2-7/2	1341.949	1341.556	293.971	0.452	767.718	0.397	16	0.122	K.LTYEEGIQM*LK.E
R2/RRR2-7/2	1017.344	1018.151	-1781.843	0.418	613.484	0.395	13	0.118	R.TPANQAIFR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1017.541	1018.151	-1587.051	0.414	611.630	0.395	13	0.118	R.TPANQAIFR.I
R2/RRR2-7/2	1050.121	1050.235	-108.386	0.391	665.222	0.385	12	0.117	R.VFEVGPVFR.A
R2/RRR2-7/2	1341.132	1341.556	-317.150	0.393	1045.955	0.297	14	0.117	K.LTYEEGIQM*LK.E
R2/RRR2-8/2	1049.952	1050.235	-270.027	0.451	714.063	0.363	12	0.113	-.VFEVGPVFR.-
R2/RRR2-7/2	1049.969	1050.235	-253.580	0.286	683.558	0.168	11	0.102	R.VFEVGPVFR.A
R2/RRR2-7/2	1449.972	1450.768	-1242.595	0.294	666.626	0.225	13	0.100	R.VVMLFCALNNIR.K
R2/RRR2-8/2	1049.811	1050.235	-404.884	0.374	501.830	0.264	10	0.099	-.VFEVGPVFR.-
R2/RRR2-6/2	1050.100	1050.235	-128.909	0.346	508.019	0.275	10	0.098	-.VFEVGPVFR.-
R2/RRR2-7/3	1520.518	1519.593	-49.459	0.408	464.439	0.518	25	0.091	R.SEAEIEKAEQAGEK.L
R2/RRR2-7/3	1519.815	1519.593	146.441	0.384	576.759	0.448	26	0.084	R.SEAEIEKAEQAGEK.L
R2/RRR2-7/3	1519.552	1519.593	-26.849	0.341	305.695	0.388	21	0.080	R.SEAEIEKAEQAGEK.L
R2/RRR2-7/3	1064.630	1064.303	308.530	0.345	1027.029	0.138	18	0.053	-.IHLPELLTK.-
R2/RRR2-7/2	1815.475	1815.103	205.652	0.631	2740.689	0.560	25	0.419	R.TLKEWIVSSLGPDAVAK.H
R2/RRR2-7/2	1814.616	1815.103	-269.189	0.565	2217.472	0.563	23	0.311	R.TLKEWIVSSLGPDAVAK.H
R2/RRR2-7/2	1372.103	1372.530	-311.647	0.477	1306.310	0.523	18	0.174	K.TFTTAETM*LNAR.T
R2/RRR2-7/2	1371.953	1372.530	-1152.524	0.446	900.198	0.535	17	0.144	K.TFTTAETM*LNAR.T
R2/RRR2-7/2	1895.450	1896.130	-888.801	0.492	772.058	0.573	22	0.141	R.YLAVEPSTPYNTTTLPK.-
R2/RRR2-7/2	1896.330	1896.130	106.170	0.555	777.786	0.547	22	0.139	R.YLAVEPSTPYNTTTLPK.-
R2/RRR2-7/2	1372.068	1372.530	-337.533	0.445	919.316	0.482	17	0.137	K.TFTTAETM*LNAR.T
R2/RRR2-7/2	950.038	950.031	8.169	0.420	604.668	0.521	16	0.131	R.SGSWVGATGK.A
R2/RRR2-7/2	949.873	950.031	-166.228	0.412	662.384	0.493	16	0.129	R.SGSWVGATGK.A
R2/RRR2-7/2	1233.112	1233.438	-265.167	0.455	526.608	0.498	17	0.128	R.AILPYSQALEK.F
R2/RRR2-7/2	949.756	950.031	-290.263	0.398	583.917	0.468	16	0.125	R.SGSWVGATGK.A
R2/RRR2-7/2	1316.206	1316.488	-214.194	0.428	977.679	0.352	17	0.123	-.FLANVDPVDVAR.-
R2/RRR2-7/2	1426.201	1426.562	-254.248	0.338	889.444	0.406	15	0.121	K.NAFAFWDWVGGR.Y
R2/RRR2-7/3	1844.345	1844.139	111.910	0.477	1328.743	0.422	30	0.121	R.SIKDLDPETTLVVVVSK.T
R2/RRR2-8/2	1316.360	1316.488	-96.975	0.365	1086.272	0.289	17	0.120	R.FLANVDPVDVAR.S
R2/RRR2-7/2	1233.057	1233.438	-310.060	0.429	541.086	0.350	17	0.116	R.AILPYSQALEK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1515.175	1515.731	-1029.771	0.320	849.958	0.376	18	0.116	K.DLDPETTLVVVVSK.T
R2/RRR2-7/2	1233.219	1233.438	-178.570	0.400	464.359	0.327	16	0.114	R.AILPYSQALEK.F
R2/RRR2-7/3	1845.415	1844.139	149.928	0.511	1010.778	0.502	26	0.113	R.SIKDLDPETTLVVVVSK.T
R2/RRR2-8/2	1315.943	1316.488	-1177.583	0.374	741.979	0.350	17	0.113	-.FLANVDPVDVAR.-
R2/RRR2-7/2	1317.182	1316.488	-232.905	0.459	638.731	0.319	15	0.106	-.FLANVDPVDVAR.-
R2/RRR2-7/2	1426.379	1426.562	-128.808	0.244	373.282	0.352	12	0.102	-.NAFAFWDWVGGR.-
R2/RRR2-11/2	1814.503	1815.103	-884.322	0.367	1011.960	0.167	17	0.097	R.TLKEWIVSSLGPDAVAK.H
R2/RRR2-7/3	1703.840	1703.901	-35.640	0.457	1059.990	0.405	28	0.097	K.FAPHIQQLSM*ESNGK.G
R2/RRR2-11/2	1815.032	1815.103	-39.031	0.364	1072.844	0.117	17	0.094	R.TLKEWIVSSLGPDAVAK.H
R2/RRR2-7/3	1844.136	1844.139	-2.106	0.430	1044.172	0.376	27	0.091	R.SIKDLDPETTLVVVVSK.T
R2/RRR2-7/3	1703.331	1703.901	-924.671	0.484	904.366	0.409	27	0.090	K.FAPHIQQLSM*ESNGK.G
R2/RRR2-7/3	1703.444	1703.901	-268.957	0.419	955.174	0.398	27	0.090	K.FAPHIQQLSM*ESNGK.G
R2/RRR2-7/3	1704.042	1703.901	83.133	0.363	507.304	0.309	21	0.065	-.FAPHIQQLSM*ESNGK.-
R2/RRR2-7/2	1501.598	1502.732	-1424.917	0.377	1957.611	0.439	22	0.233	R.GCVLVASSPEILTR.V
R2/RRR2-7/2	1502.075	1502.732	-1105.917	0.395	1691.538	0.427	21	0.194	R.GCVLVASSPEILTR.V
R2/RRR2-7/2	1502.276	1502.732	-304.373	0.448	1637.028	0.444	20	0.191	R.GCVLVASSPEILTR.V
R2/RRR2-7/2	1168.034	1168.368	-287.174	0.449	1151.056	0.647	20	0.182	R.AALPVGTVSGAPK.V
R2/RRR2-7/2	1168.029	1168.368	-290.948	0.321	1318.176	0.531	21	0.171	R.AALPVGTVSGAPK.V
R2/RRR2-7/2	1168.189	1168.368	-153.923	0.333	1190.462	0.565	20	0.165	R.AALPVGTVSGAPK.V
R2/RRR2-7/2	1408.126	1408.535	-291.422	0.400	1555.027	0.391	18	0.164	R.AIDLAESAFVDKE.-
R2/RRR2-7/2	1435.072	1435.626	-1086.088	0.493	1443.247	0.407	18	0.164	K.AM*ELIDELEVTR.R
R2/RRR2-7/2	1319.939	1320.347	-309.594	0.519	736.154	0.552	18	0.141	R.HATTEDAFQDGK.S
R2/RRR2-7/2	1320.189	1320.347	-120.250	0.492	661.793	0.544	18	0.136	R.HATTEDAFQDGK.S
R2/RRR2-7/2	1261.610	1260.379	183.167	0.369	913.405	0.446	13	0.129	R.TYANPFEVYR.A
R2/RRR2-7/2	1625.119	1625.873	-1082.603	0.390	713.208	0.497	18	0.126	R.IVNPSPYM*AYVQAR.G
R2/RRR2-7/2	1610.526	1609.874	-217.015	0.379	727.785	0.423	18	0.119	R.IVNPSPYMAYVQAR.G
R2/RRR2-7/2	1210.009	1210.454	-368.886	0.431	650.538	0.407	14	0.116	K.IINRPLAGTVR.R
R2/RRR2-7/2	1434.575	1435.626	-1433.912	0.342	989.153	0.292	16	0.114	K.AM*ELIDELEVTR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1259.309	1260.379	-1648.998	0.212	435.395	0.315	11	0.101	-.TYANPFEVYR.-
R2/RRR2-7/3	1873.125	1874.154	-1086.463	0.344	1326.244	0.314	25	0.098	K.EHIM*AGDIFQIVLSQR.F
R2/RRR2-7/3	1320.412	1320.347	49.634	0.410	1038.075	0.334	22	0.083	R.HATTEDAFQDGK.S
R2/RRR2-7/3	1458.970	1459.632	-1142.251	0.422	947.830	0.316	24	0.077	K.KKLPFSGAPQDDR.N
R2/RRR2-7/3	1459.463	1459.632	-115.998	0.414	1067.355	0.235	26	0.070	K.KKLPFSGAPQDDR.N
R2/RRR2-7/3	1320.705	1320.347	271.699	0.330	877.407	0.200	20	0.064	R.HATTEDAFQDGK.S
R2/RRR2-7/3	1320.359	1320.347	9.021	0.387	433.633	0.355	16	0.043	-.HATTEDAFQDGK.-
R2/RRR2-13/2	1708.400	1708.932	-899.612	0.527	1892.415	0.595	26	0.265	R.GWVPTLLGYSAQGACK.F
R2/RRR2-14/2	1708.297	1708.932	-960.229	0.514	1864.610	0.584	26	0.258	R.GWVPTLLGYSAQGACK.F
R2/RRR2-13/2	1505.163	1505.610	-297.689	0.504	1795.670	0.567	21	0.243	K.YYSDIAGPEYAQK.Y
R2/RRR2-14/2	1709.232	1708.932	175.957	0.567	1707.894	0.605	26	0.241	R.GWVPTLLGYSAQGACK.F
R2/RRR2-14/2	1505.083	1505.610	-1017.396	0.475	1777.416	0.548	21	0.235	K.YYSDIAGPEYAQK.Y
R2/RRR2-13/2	1708.438	1708.932	-290.147	0.528	1725.235	0.577	25	0.235	R.GWVPTLLGYSAQGACK.F
R2/RRR2-14/2	1708.475	1708.932	-268.570	0.490	1687.379	0.550	26	0.223	R.GWVPTLLGYSAQGACK.F
R2/RRR2-13/2	1504.933	1505.610	-1117.730	0.418	1672.056	0.528	21	0.214	K.YYSDIAGPEYAQK.Y
R2/RRR2-13/2	1506.040	1505.610	286.441	0.549	1291.731	0.601	20	0.189	K.YYSDIAGPEYAQK.Y
R2/RRR2-12/2	1506.015	1505.610	269.780	0.538	1382.739	0.530	20	0.183	K.YYSDIAGPEYAQK.Y
R2/RRR2-13/2	1707.560	1708.932	-1393.369	0.366	1393.211	0.476	24	0.169	R.GWVPTLLGYSAQGACK.F
R2/RRR2-13/2	1094.973	1094.286	-286.655	0.462	1066.836	0.504	17	0.151	K.SITSGFGILAK.E
R2/RRR2-13/2	937.949	938.060	-118.019	0.517	750.823	0.523	15	0.141	K.SEGALGLYK.G
R2/RRR2-13/2	937.996	938.060	-68.543	0.487	745.630	0.515	15	0.139	K.SEGALGLYK.G
R2/RRR2-14/2	1063.463	1063.277	175.733	0.477	838.182	0.482	14	0.137	K.LGLWGLFTR.G
R2/RRR2-13/2	1084.761	1085.234	-437.777	0.312	1032.594	0.452	12	0.136	K.FGFYEFFK.K
R2/RRR2-13/2	937.956	938.060	-110.317	0.485	727.018	0.490	15	0.136	K.SEGALGLYK.G
R2/RRR2-13/2	1064.132	1063.277	-136.183	0.433	917.835	0.453	14	0.135	K.LGLWGLFTR.G
R2/RRR2-13/2	747.777	747.908	-176.032	0.461	766.732	0.481	11	0.134	K.HAVPVPK.S
R2/RRR2-13/2	1063.095	1063.277	-171.904	0.493	699.866	0.498	13	0.133	K.LGLWGLFTR.G
R2/RRR2-13/2	747.334	747.908	-2112.620	0.444	690.225	0.490	11	0.132	K.HAVPVPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	747.378	747.908	-2052.863	0.440	751.762	0.485	11	0.131	-.HAVPVPK.-
R2/RRR2-13/2	1062.952	1063.277	-306.579	0.508	695.048	0.475	13	0.130	K.LGLWGLFTR.G
R2/RRR2-13/2	1212.626	1213.407	-1473.388	0.432	999.502	0.390	13	0.129	K.FGFYEFFKK.C
R2/RRR2-13/2	1062.723	1063.277	-1466.350	0.457	702.588	0.463	13	0.128	K.LGLWGLFTR.G
R2/RRR2-13/2	1093.989	1094.286	-272.476	0.366	799.035	0.457	16	0.127	K.SITSGFGILAK.E
R2/RRR2-13/2	1063.183	1063.277	-88.168	0.499	670.143	0.431	13	0.125	K.LGLWGLFTR.G
R2/RRR2-13/2	1063.321	1063.277	42.073	0.446	673.663	0.436	13	0.125	K.LGLWGLFTR.G
R2/RRR2-13/2	1003.945	1004.125	-179.044	0.433	679.371	0.403	14	0.123	R.VQTQPGFAR.C
R2/RRR2-13/2	1085.063	1085.234	-158.381	0.308	754.641	0.451	12	0.122	K.FGFYEFFK.K
R2/RRR2-13/2	1003.968	1004.125	-155.991	0.399	463.114	0.305	14	0.117	R.VQTQPGFAR.C
R2/RRR2-14/2	937.959	938.060	-107.836	0.406	547.064	0.353	13	0.116	K.SEGALGLYK.G
R2/RRR2-1/2	1003.896	1004.125	-228.691	0.357	262.018	0.251	11	0.116	R.VQTQPGFAR.C
R2/RRR2-14/2	1004.077	1004.125	-47.814	0.305	327.232	0.266	13	0.116	R.VQTQPGFAR.C
R2/RRR2-14/2	937.380	938.060	-1797.417	0.399	666.018	0.315	14	0.115	K.SEGALGLYK.G
R2/RRR2-14/2	937.970	938.060	-95.695	0.429	756.358	0.284	15	0.115	K.SEGALGLYK.G
R2/RRR2-13/2	1085.200	1085.234	-32.224	0.336	863.454	0.321	11	0.114	K.FGFYEFFK.K
R2/RRR2-13/2	1093.838	1094.286	-410.414	0.350	687.726	0.386	14	0.114	K.SITSGFGILAK.E
R2/RRR2-13/2	1004.118	1004.125	-6.964	0.310	334.182	0.241	12	0.114	R.VQTQPGFAR.C
R2/RRR2-13/2	1003.910	1004.125	-214.784	0.295	228.695	0.282	10	0.112	-.VQTQPGFAR.-
R2/RRR2-14/2	1212.862	1213.407	-1278.271	0.355	524.328	0.297	12	0.109	K.FGFYEFFKK.C
R2/RRR2-14/2	1004.729	1004.125	-395.206	0.359	264.035	0.262	11	0.107	-.VQTQPGFAR.-
R2/RRR2-1/2	748.520	747.908	-519.521	0.327	586.438	0.347	10	0.107	-.HAVPVPK.-
R2/RRR2-13/2	1063.252	1063.277	-22.986	0.182	478.159	0.287	12	0.106	K.LGLWGLFTR.G
R2/RRR2-13/3	1213.558	1213.407	124.426	0.482	891.520	0.441	21	0.094	K.FGFYEFFKK.C
R2/RRR2-13/3	1213.902	1213.407	408.670	0.447	692.299	0.475	20	0.092	K.FGFYEFFKK.C
R2/RRR2-13/3	1213.343	1213.407	-52.949	0.412	527.105	0.398	18	0.085	K.FGFYEFFKK.C
R2/RRR2-13/3	1213.713	1213.407	252.273	0.291	350.949	0.404	15	0.082	K.FGFYEFFKK.C
R2/RRR2-14/3	1213.605	1213.407	163.616	0.347	464.928	0.289	17	0.080	K.FGFYEFFKK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/3	1213.420	1213.407	10.169	0.342	545.553	0.338	18	0.078	K.FGFYEFFKK.C
R2/RRR2-13/3	1505.306	1505.610	-202.302	0.342	984.513	0.314	22	0.077	K.YYSDIAGPEYAQK.Y
R2/RRR2-13/3	1505.380	1505.610	-152.883	0.303	941.289	0.218	22	0.064	K.YYSDIAGPEYAQK.Y
R2/RRR2-6/2	1955.321	1956.213	-970.729	0.530	2741.509	0.543	28	0.418	K.GVNPDEAVAM*GAAIQGGILR.G
R2/RRR2-6/2	1778.419	1777.956	260.814	0.565	2210.192	0.615	27	0.330	R.IINEPTAAALSYGTNNK.E
R2/RRR2-6/2	1823.281	1822.957	178.180	0.583	2098.457	0.601	23	0.307	K.SQVFSTAADNQTQVGIR.V
R2/RRR2-6/2	1939.616	1940.214	-826.459	0.549	2111.051	0.556	25	0.289	K.GVNPDEAVAMGAAIQGGILR.G
R2/RRR2-6/2	1777.477	1777.956	-270.749	0.521	2000.997	0.571	26	0.278	R.IINEPTAAALSYGTNNK.E
R2/RRR2-6/2	1522.355	1522.728	-245.669	0.494	1939.088	0.508	21	0.250	R.SKFESLVNSLIER.T
R2/RRR2-6/2	1522.395	1522.728	-219.203	0.540	1902.670	0.514	21	0.246	R.SKFESLVNSLIER.T
R2/RRR2-6/2	1461.216	1461.515	-205.255	0.500	1588.019	0.627	20	0.230	K.APNGDAWVETTDGK.Q
R2/RRR2-6/2	1523.460	1522.728	-176.536	0.593	1702.901	0.538	20	0.223	R.SKFESLVNSLIER.T
R2/RRR2-6/2	1776.870	1777.956	-1177.848	0.515	1574.803	0.576	24	0.215	R.IINEPTAAALSYGTNNK.E
R2/RRR2-6/2	1938.610	1940.214	-1864.619	0.328	1726.827	0.448	24	0.201	K.GVNPDEAVAMGAAIQGGILR.G
R2/RRR2-6/2	1460.993	1461.515	-1045.166	0.439	1266.843	0.603	19	0.184	K.APNGDAWVETTDGK.Q
R2/RRR2-6/2	1355.139	1355.433	-217.346	0.488	1364.871	0.498	18	0.175	R.NNADTTIYSVEK.S
R2/RRR2-6/2	1355.093	1355.433	-251.598	0.476	1268.335	0.468	18	0.160	R.NNADTTIYSVEK.S
R2/RRR2-6/2	1355.169	1355.433	-194.845	0.457	1335.955	0.392	18	0.151	R.NNADTTIYSVEK.S
R2/RRR2-6/2	1553.281	1553.701	-271.283	0.461	487.736	0.579	16	0.128	R.QAVTNPQNTFFGTK.R
R2/RRR2-6/2	1553.259	1553.701	-284.924	0.441	583.348	0.532	18	0.127	R.QAVTNPQNTFFGTK.R
R2/RRR2-6/2	1248.590	1249.438	-1484.588	0.433	943.121	0.394	16	0.127	K.VQEIVSEIFGK.S
R2/RRR2-6/3	1956.387	1956.213	89.135	0.445	1526.777	0.336	32	0.121	K.GVNPDEAVAM*GAAIQGGILR.G
R2/RRR2-6/3	1939.584	1940.214	-842.892	0.370	1177.996	0.423	29	0.110	K.GVNPDEAVAMGAAIQGGILR.G
R2/RRR2-6/3	1565.682	1565.755	-46.468	0.381	1277.939	0.363	24	0.103	K.AVITVPAYFNDAQR.Q
R2/RRR2-1/2	993.921	994.276	-357.902	0.352	1263.284	0.026	13	0.099	K.M*VPYKIVK.A
R2/RRR2-1/2	994.048	994.276	-230.006	0.463	1139.206	0.073	13	0.097	K.M*VPYKIVK.A
R2/RRR2-9/2	993.459	994.276	-1834.392	0.408	908.644	0.053	12	0.095	-.M*VPYKIVK.-
R2/RRR2-1/2	994.101	994.276	-176.664	0.409	949.965	0.050	12	0.095	-.M*VPYKIVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	994.117	994.276	-160.158	0.375	1007.834	0.032	12	0.093	-.M*VPYKIVK.-
R2/RRR2-6/3	1939.418	1940.214	-928.569	0.369	911.079	0.405	27	0.088	K.GVNPDEAVAMGAAIQGGILR.G
R2/RRR2-6/3	1522.794	1522.728	43.359	0.506	1117.925	0.317	24	0.084	R.SKFESLVNSLIER.T
R2/RRR2-6/3	1523.848	1522.728	78.843	0.521	1075.613	0.322	23	0.083	R.SKFESLVNSLIER.T
R2/RRR2-6/3	1522.676	1522.728	-33.950	0.489	1131.999	0.296	25	0.081	R.SKFESLVNSLIER.T
R2/RRR2-8/2	1296.091	1296.501	-317.558	0.532	1909.458	0.606	21	0.271	K.VVAAGANPVQITR.G
R2/RRR2-8/2	1296.207	1296.501	-227.322	0.509	1757.322	0.547	21	0.232	K.VVAAGANPVQITR.G
R2/RRR2-8/2	1296.016	1296.501	-375.676	0.464	1749.294	0.552	20	0.231	K.VVAAGANPVQITR.G
R2/RRR2-7/2	1296.280	1296.501	-171.016	0.533	1682.221	0.575	20	0.228	K.VVAAGANPVQITR.G
R2/RRR2-7/2	1296.172	1296.501	-254.344	0.540	1616.468	0.583	20	0.222	K.VVAAGANPVQITR.G
R2/RRR2-7/2	1296.010	1296.501	-380.118	0.508	1585.371	0.571	20	0.215	K.VVAAGANPVQITR.G
R2/RRR2-7/2	1285.008	1285.472	-362.220	0.408	1658.106	0.409	17	0.187	R.DLINVLEEAIR.G
R2/RRR2-7/2	1284.457	1285.472	-1573.246	0.426	1521.585	0.391	17	0.168	R.DLINVLEEAIR.G
R2/RRR2-7/2	1087.908	1088.240	-305.511	0.446	1057.223	0.541	15	0.156	R.KGVVTLEEGR.S
R2/RRR2-7/2	1044.014	1044.187	-166.367	0.496	1099.564	0.499	17	0.155	K.IVNDGVTVAR.E
R2/RRR2-7/2	1285.040	1285.472	-337.153	0.445	1353.587	0.393	17	0.154	R.DLINVLEEAIR.G
R2/RRR2-7/2	1543.315	1542.670	-230.274	0.541	1399.892	0.356	21	0.148	R.EVELEDPVENIGAK.L
R2/RRR2-7/2	1175.098	1175.274	-150.830	0.481	1144.463	0.439	19	0.147	K.NAGVNGSVVTEK.V
R2/RRR2-7/2	1174.863	1175.274	-351.471	0.421	1183.106	0.432	17	0.146	K.NAGVNGSVVTEK.V
R2/RRR2-7/2	1506.125	1506.638	-1007.344	0.369	1167.407	0.432	20	0.144	R.GYISPYFVTDSEK.M
R2/RRR2-7/2	1043.953	1044.187	-224.666	0.479	1219.905	0.365	17	0.141	K.IVNDGVTVAR.E
R2/RRR2-7/2	1937.503	1938.040	-795.638	0.496	723.634	0.565	19	0.133	K.ESTTIVGDGSTQEEVTKR.V
R2/RRR2-7/2	1174.403	1175.274	-1598.282	0.359	899.866	0.488	16	0.133	K.NAGVNGSVVTEK.V
R2/RRR2-7/2	1507.344	1506.638	-195.318	0.414	921.207	0.442	18	0.131	R.GYISPYFVTDSEK.M
R2/RRR2-7/2	1246.195	1246.383	-150.969	0.529	515.699	0.492	16	0.128	R.CCLEHAASVAK.T
R2/RRR2-7/2	1043.969	1044.187	-209.885	0.444	837.691	0.406	16	0.127	K.IVNDGVTVAR.E
R2/RRR2-7/2	1247.180	1246.383	-163.121	0.538	504.146	0.475	16	0.127	R.CCLEHAASVAK.T
R2/RRR2-7/2	1542.035	1542.670	-1063.523	0.416	1088.627	0.329	19	0.124	R.EVELEDPVENIGAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1505.615	1506.638	-1347.358	0.200	1111.023	0.334	19	0.121	R.GYISPYFVTDSEK.M
R2/RRR2-7/2	1937.324	1938.040	-888.424	0.449	691.964	0.488	18	0.121	K.ESTTIVGDGSTQEEVTKR.V
R2/RRR2-7/2	1542.093	1542.670	-1025.690	0.448	1030.899	0.325	19	0.120	R.EVELEDPVENIGAK.L
R2/RRR2-7/2	1229.508	1230.396	-1540.391	0.427	630.683	0.431	14	0.118	K.LRVEDALNATK.A
R2/RRR2-8/2	1245.964	1246.383	-337.114	0.331	282.834	0.326	13	0.112	R.CCLEHAASVAK.T
R2/RRR2-7/3	1230.680	1230.396	231.583	0.487	1357.558	0.349	24	0.104	K.LRVEDALNATK.A
R2/RRR2-7/3	1230.606	1230.396	171.156	0.448	1278.320	0.332	24	0.094	-.LRVEDALNATK.-
R2/RRR2-7/3	1246.156	1246.383	-182.425	0.432	1008.269	0.375	23	0.087	R.CCLEHAASVAK.T
R2/RRR2-7/3	1246.668	1246.383	229.988	0.425	913.210	0.352	23	0.081	R.CCLEHAASVAK.T
R2/RRR2-7/3	1937.447	1938.040	-824.927	0.204	747.066	0.416	29	0.075	K.ESTTIVGDGSTQEEVTKR.V
R2/RRR2-11/3	1247.620	1246.383	190.755	0.277	705.932	0.274	19	0.068	R.CCLEHAASVAK.T
R2/RRR2-7/3	1937.830	1938.040	-108.624	0.178	821.882	0.268	30	0.063	K.ESTTIVGDGSTQEEVTKR.V
R2/RRR2-4/2	1290.935	1291.478	-1199.067	0.440	2051.147	0.532	19	0.271	R.AIADGSLLDFLR.Q
R2/RRR2-3/2	1291.236	1291.478	-187.993	0.529	2038.479	0.522	19	0.266	R.AIADGSLLDFLR.Q
R2/RRR2-4/2	1291.113	1291.478	-283.695	0.493	1865.262	0.540	19	0.244	R.AIADGSLLDFLR.Q
R2/RRR2-4/2	1290.599	1291.478	-1460.266	0.417	1879.480	0.533	19	0.243	R.AIADGSLLDFLR.Q
R2/RRR2-4/2	1886.499	1886.995	-263.799	0.552	1699.782	0.518	24	0.217	K.DITPDDKQELDEALQR.E
R2/RRR2-1/2	1078.171	1077.212	-37.885	0.447	1523.499	0.519	16	0.194	K.SPAEVFDALK.S
R2/RRR2-4/3	1886.417	1886.995	-838.870	0.496	1916.547	0.414	33	0.189	K.DITPDDKQELDEALQR.E
R2/RRR2-3/2	1291.090	1291.478	-301.623	0.550	1442.726	0.542	17	0.189	R.AIADGSLLDFLR.Q
R2/RRR2-4/2	1852.586	1853.070	-261.821	0.529	1344.110	0.581	22	0.188	K.SQTVDLVLTAHPTQSVR.R
R2/RRR2-3/2	1329.131	1328.497	-276.133	0.512	1521.120	0.478	20	0.185	K.LADLESAPAALTR.L
R2/RRR2-4/2	1077.940	1077.212	-253.475	0.515	1412.967	0.525	16	0.185	K.SPAEVFDALK.S
R2/RRR2-4/2	1076.997	1077.212	-200.379	0.491	1358.085	0.548	16	0.184	K.SPAEVFDALK.S
R2/RRR2-3/2	1077.292	1077.212	74.600	0.412	1433.416	0.507	16	0.181	K.SPAEVFDALK.S
R2/RRR2-4/2	1076.953	1077.212	-241.429	0.518	1345.834	0.512	16	0.175	K.SPAEVFDALK.S
R2/RRR2-4/2	1886.610	1886.995	-204.857	0.556	1205.341	0.521	22	0.163	K.DITPDDKQELDEALQR.E
R2/RRR2-4/2	1328.158	1328.497	-256.147	0.506	1302.780	0.469	19	0.162	K.LADLESAPAALTR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1887.376	1886.995	202.294	0.574	1309.146	0.467	22	0.160	K.DITPDDKQELDEALQR.E
R2/RRR2-4/2	1328.172	1328.497	-245.543	0.489	1201.348	0.476	18	0.154	K.LADLESAPAALTR.L
R2/RRR2-4/2	1328.146	1328.497	-264.538	0.480	1145.789	0.488	18	0.152	K.LADLESAPAALTR.L
R2/RRR2-3/2	1077.392	1077.212	167.666	0.348	1131.896	0.483	14	0.147	K.SPAEVFDALK.S
R2/RRR2-3/2	1078.184	1077.212	-26.642	0.433	1167.164	0.440	15	0.146	K.SPAEVFDALK.S
R2/RRR2-4/2	1852.123	1853.070	-1054.101	0.461	1017.601	0.530	19	0.146	K.SQTVDLVLTAHPTQSVR.R
R2/RRR2-2/2	1078.104	1077.212	-100.349	0.359	948.986	0.468	13	0.134	K.SPAEVFDALK.S
R2/RRR2-3/3	1886.853	1886.995	-75.448	0.539	1486.697	0.407	30	0.131	K.DITPDDKQELDEALQR.E
R2/RRR2-2/2	1291.718	1291.478	186.007	0.325	686.925	0.474	14	0.120	R.AIADGSLLDFLR.Q
R2/RRR2-3/2	1328.089	1328.497	-308.248	0.350	694.617	0.419	15	0.116	K.LADLESAPAALTR.L
R2/RRR2-5/2	1076.999	1077.212	-198.787	0.324	658.627	0.370	13	0.114	K.SPAEVFDALK.S
R2/RRR2-2/2	1291.535	1291.478	44.024	0.250	445.405	0.286	13	0.106	R.AIADGSLLDFLR.Q
R2/RRR2-2/2	1327.919	1328.497	-1191.303	0.242	763.156	0.250	15	0.104	K.LADLESAPAALTR.L
R2/RRR2-3/2	1290.935	1291.478	-1199.067	0.228	806.856	0.220	14	0.103	R.AIADGSLLDFLR.Q
R2/RRR2-2/2	1291.472	1291.478	-4.893	0.205	608.401	0.230	13	0.102	R.AIADGSLLDFLR.Q
R2/RRR2-4/3	1886.289	1886.995	-907.276	0.441	1141.838	0.388	27	0.099	K.DITPDDKQELDEALQR.E
R2/RRR2-2/2	1077.162	1077.212	-46.672	0.192	281.017	0.364	10	0.096	-.SPAEVFDALK.-
R2/RRR2-3/3	1886.819	1886.995	-93.457	0.453	1055.256	0.399	27	0.096	K.DITPDDKQELDEALQR.E
R2/RRR2-4/3	1886.639	1886.995	-188.961	0.503	1074.755	0.385	28	0.094	K.DITPDDKQELDEALQR.E
R2/RRR2-4/3	1167.906	1168.373	-401.014	0.390	1080.612	0.398	21	0.094	K.RPLFGPDLPR.T
R2/RRR2-4/3	1168.233	1168.373	-120.287	0.458	1129.927	0.365	22	0.091	K.RPLFGPDLPR.T
R2/RRR2-4/3	1168.342	1168.373	-26.746	0.418	1051.854	0.348	21	0.085	K.RPLFGPDLPR.T
R2/RRR2-4/3	1394.002	1394.638	-1177.394	0.402	1079.540	0.224	21	0.069	R.IRNCLVQLYSK.D
R2/RRR2-3/3	1168.562	1168.373	162.326	0.399	978.496	0.227	19	0.068	K.RPLFGPDLPR.T
R2/RRR2-4/3	1394.618	1394.638	-14.417	0.392	1159.277	0.172	21	0.065	R.IRNCLVQLYSK.D
R2/RRR2-10/2	1572.398	1571.806	-259.887	0.516	1423.334	0.557	20	0.191	R.ISITGAGGFIASHIAR.R
R2/RRR2-10/2	1572.408	1571.806	-253.422	0.501	1330.341	0.530	19	0.174	R.ISITGAGGFIASHIAR.R
R2/RRR2-6/2	1788.325	1787.948	211.376	0.606	2230.050	0.528	24	0.304	K.CGVNTAEDWLNPAAIR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1475.379	1475.631	-171.335	0.521	2023.354	0.595	24	0.292	K.HLGDFLSTGSITAR.Q
R2/RRR2-6/2	1787.401	1787.948	-868.208	0.531	2073.442	0.512	23	0.273	K.CGVNTAEDWLNPAAIR.E
R2/RRR2-6/2	1604.225	1604.726	-938.953	0.511	1343.889	0.553	20	0.184	K.FGSGAYNSM*DNGVLR.F
R2/RRR2-6/2	1662.430	1662.822	-236.459	0.481	1050.644	0.538	21	0.154	K.TDEFVIHSPTLTSSK.W
R2/RRR2-6/2	1662.396	1662.822	-257.159	0.460	1091.136	0.490	20	0.148	K.TDEFVIHSPTLTSSK.W
R2/RRR2-6/2	1369.236	1369.635	-292.457	0.487	1032.800	0.481	18	0.145	R.LFPLLASAYAFR.F
R2/RRR2-6/2	1663.292	1662.822	283.431	0.541	912.793	0.527	20	0.143	K.TDEFVIHSPTLTSSK.W
R2/RRR2-6/2	1369.216	1369.635	-306.947	0.320	1021.155	0.449	18	0.135	R.LFPLLASAYAFR.F
R2/RRR2-6/3	1992.614	1993.209	-802.949	0.519	1333.045	0.466	31	0.134	R.KQFGPQTGGPETQVLNYK.T
R2/RRR2-6/2	1128.551	1129.249	-1509.163	0.435	556.250	0.523	17	0.130	R.QGALANEQLGK.L
R2/RRR2-6/2	1189.005	1188.313	-259.454	0.522	978.293	0.376	16	0.129	R.LTEEEANLLR.L
R2/RRR2-6/2	1188.262	1188.313	-43.030	0.487	1034.023	0.342	16	0.126	R.LTEEEANLLR.L
R2/RRR2-6/2	1128.488	1129.249	-1565.122	0.307	575.376	0.538	17	0.123	R.QGALANEQLGK.L
R2/RRR2-6/2	1128.371	1129.249	-1668.909	0.338	575.475	0.472	17	0.121	R.QGALANEQLGK.L
R2/RRR2-6/2	1865.556	1865.036	-258.163	0.525	521.525	0.507	18	0.120	K.QFGPQTGGPETQVLNYK.T
R2/RRR2-1/2	1476.165	1475.631	-317.139	0.370	734.613	0.423	17	0.118	K.HLGDFLSTGSITAR.Q
R2/RRR2-6/2	1187.488	1188.313	-1541.696	0.414	873.376	0.301	16	0.116	R.LTEEEANLLR.L
R2/RRR2-6/3	1075.477	1075.203	256.095	0.454	710.802	0.448	18	0.087	K.ASTHAVVYAR.L
R2/RRR2-13/2	1699.335	1699.843	-889.641	0.564	2269.888	0.507	24	0.304	K.GNAYAQVAIGTEDVYK.S
R2/RRR2-13/2	1699.367	1699.843	-280.456	0.528	2027.346	0.581	23	0.285	K.GNAYAQVAIGTEDVYK.S
R2/RRR2-13/2	1700.310	1699.843	275.892	0.600	1968.133	0.602	24	0.281	K.GNAYAQVAIGTEDVYK.S
R2/RRR2-13/2	1046.868	1047.184	-303.102	0.457	1814.643	0.479	16	0.224	K.SAEAVELVTK.E
R2/RRR2-13/2	1046.970	1047.184	-205.191	0.482	1580.826	0.521	15	0.203	K.SAEAVELVTK.E
R2/RRR2-13/2	1046.595	1047.184	-1523.692	0.416	1499.462	0.453	15	0.178	K.SAEAVELVTK.E
R2/RRR2-13/2	1504.004	1504.802	-1199.175	0.447	1300.097	0.429	20	0.155	K.ILRQPGPLPGLNTK.I
R2/RRR2-13/2	1232.676	1233.438	-1433.928	0.430	1132.825	0.483	18	0.153	K.VVLVDNADFLK.E
R2/RRR2-13/2	1184.271	1184.366	-80.394	0.431	1082.066	0.473	15	0.146	K.SPEVVLEWPK.K
R2/RRR2-13/2	1233.223	1233.438	-175.591	0.374	1090.596	0.450	17	0.142	K.VVLVDNADFLK.E

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1184.195	1184.366	-144.399	0.396	1159.666	0.399	16	0.140	K.SPEVVLEWPK.K
R2/RRR2-13/2	1249.185	1249.396	-170.015	0.465	1050.988	0.418	17	0.137	K.IASFLDPDGWK.V
R2/RRR2-13/2	1250.037	1249.396	-288.316	0.440	982.278	0.400	17	0.131	K.IASFLDPDGWK.V
R2/RRR2-13/2	1514.190	1514.766	-1043.918	0.404	419.027	0.564	16	0.125	R.GPTPEPLCQVM*LR.V
R2/RRR2-13/2	1498.261	1498.767	-1007.646	0.397	515.186	0.499	17	0.123	R.GPTPEPLCQVMLR.V
R2/RRR2-13/2	1498.298	1498.767	-313.843	0.377	519.902	0.492	17	0.121	R.GPTPEPLCQVMLR.V
R2/RRR2-13/2	1497.993	1498.767	-1187.232	0.378	428.563	0.494	16	0.120	R.GPTPEPLCQVMLR.V
R2/RRR2-13/2	1248.603	1249.396	-1440.347	0.394	902.801	0.314	17	0.117	K.IASFLDPDGWK.V
R2/RRR2-13/2	1504.148	1504.802	-1102.846	0.466	497.122	0.441	16	0.115	K.ILRQPGPLPGLNTK.I
R2/RRR2-13/2	1514.449	1514.766	-210.222	0.295	551.857	0.402	18	0.113	R.GPTPEPLCQVM*LR.V
R2/RRR2-13/2	1183.271	1184.366	-1775.658	0.295	759.526	0.177	13	0.101	K.SPEVVLEWPK.K
R2/RRR2-13/3	1028.059	1028.236	-172.297	0.497	717.681	0.453	16	0.091	K.RLLHAVYR.V
R2/RRR2-13/3	1028.420	1028.236	180.101	0.486	831.392	0.418	17	0.089	K.RLLHAVYR.V
R2/RRR2-13/3	1028.695	1028.236	447.851	0.526	746.439	0.408	16	0.087	K.RLLHAVYR.V
R2/RRR2-13/2	1602.985	1603.841	-1161.333	0.343	1097.476	0.354	20	0.067	K.VVLVDNADFLKELQ.-
R2/RRR2-13/2	1603.330	1603.841	-945.279	0.458	984.449	0.445	20	0.052	K.VVLVDNADFLKELQ.-
R2/RRR2-13/2	1604.069	1603.841	142.383	0.477	980.179	0.407	20	0.049	K.VVLVDNADFLKELQ.-
R2/RRR2-13/2	1604.395	1603.841	-279.124	0.403	664.451	0.298	16	0.017	K.VVLVDNADFLKELQ.-
R2/RRR2-15/1	1531.854	1531.733	78.968	0.458	837.827	0.348	16	0.645	K.DLYYDVLQFINK.L
R2/RRR2-15/1	1531.819	1531.733	56.350	0.470	794.244	0.324	15	0.589	K.DLYYDVLQFINK.L
R2/RRR2-15/1	1530.902	1531.733	-1199.811	0.260	622.659	0.125	14	0.362	K.DLYYDVLQFINK.L
R2/RRR2-15/2	1609.395	1609.806	-256.195	0.479	2225.587	0.552	24	0.303	K.LDISGHTVSAVGPDIK.H
R2/RRR2-15/2	1264.080	1264.456	-297.995	0.499	1935.147	0.534	19	0.248	R.LQAALSTGLFSR.I
R2/RRR2-23/2	1264.160	1264.456	-235.022	0.516	1685.316	0.578	19	0.225	R.LQAALSTGLFSR.I
R2/RRR2-23/2	1263.654	1264.456	-1430.362	0.493	1705.421	0.565	20	0.225	R.LQAALSTGLFSR.I
R2/RRR2-15/2	1264.331	1264.456	-99.222	0.436	1749.008	0.518	19	0.218	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1263.762	1264.456	-1344.208	0.503	1587.094	0.599	19	0.218	R.LQAALSTGLFSR.I
R2/RRR2-25/2	1312.314	1312.497	-139.724	0.507	1696.335	0.534	21	0.215	R.VLVGVVASPEADR.D

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1263.841	1264.456	-1281.251	0.449	1668.963	0.546	19	0.214	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1609.306	1609.806	-311.367	0.500	1759.118	0.498	23	0.214	K.LDISGHTVSAVGPDIK.H
R2/RRR2-24/2	1609.254	1609.806	-966.982	0.432	1776.057	0.488	22	0.214	K.LDISGHTVSAVGPDIK.H
R2/RRR2-15/2	1609.457	1609.806	-217.464	0.464	1710.197	0.519	21	0.212	K.LDISGHTVSAVGPDIK.H
R2/RRR2-22/2	1312.158	1312.497	-258.990	0.460	1555.951	0.590	20	0.210	R.VLVGVVASPEADR.D
R2/RRR2-23/2	1608.701	1609.806	-1312.241	0.407	1733.061	0.497	21	0.210	K.LDISGHTVSAVGPDIK.H
R2/RRR2-15/2	1609.357	1609.806	-279.557	0.428	1682.018	0.514	21	0.207	K.LDISGHTVSAVGPDIK.H
R2/RRR2-14/2	1312.078	1312.497	-320.781	0.451	1679.266	0.497	20	0.204	R.VLVGVVASPEADR.D
R2/RRR2-21/2	1264.262	1264.456	-153.848	0.504	1598.674	0.537	18	0.203	R.LQAALSTGLFSR.I
R2/RRR2-15/2	1263.733	1264.456	-1367.103	0.513	1470.335	0.594	18	0.202	R.LQAALSTGLFSR.I
R2/RRR2-15/2	1264.034	1264.456	-335.007	0.496	1541.696	0.549	19	0.200	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1312.164	1312.497	-254.883	0.445	1596.663	0.526	20	0.200	R.VLVGVVASPEADR.D
R2/RRR2-22/2	1263.597	1264.456	-1475.483	0.451	1559.944	0.544	18	0.200	R.LQAALSTGLFSR.I
R2/RRR2-1/2	1264.275	1264.456	-143.387	0.486	1599.286	0.523	18	0.200	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1264.335	1264.456	-96.123	0.480	1493.922	0.565	19	0.198	R.LQAALSTGLFSR.I
R2/RRR2-22/2	1609.012	1609.806	-1117.870	0.437	1695.758	0.451	23	0.195	K.LDISGHTVSAVGPDIK.H
R2/RRR2-1/2	1265.036	1264.456	-332.612	0.504	1511.319	0.538	19	0.195	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1609.374	1609.806	-268.979	0.444	1558.955	0.518	22	0.194	K.LDISGHTVSAVGPDIK.H
R2/RRR2-19/2	1313.015	1312.497	-368.108	0.498	1426.619	0.570	20	0.192	R.VLVGVVASPEADR.D
R2/RRR2-24/2	1609.297	1609.806	-940.481	0.503	1661.255	0.453	21	0.189	K.LDISGHTVSAVGPDIK.H
R2/RRR2-25/2	1264.177	1264.456	-221.460	0.410	1407.446	0.559	18	0.186	R.LQAALSTGLFSR.I
R2/RRR2-26/2	1313.141	1312.497	-272.036	0.510	1294.302	0.588	19	0.182	R.VLVGVVASPEADR.D
R2/RRR2-13/2	1311.506	1312.497	-1522.781	0.430	1358.542	0.559	19	0.181	R.VLVGVVASPEADR.D
R2/RRR2-17/2	1312.265	1312.497	-177.797	0.406	1407.474	0.533	19	0.180	R.VLVGVVASPEADR.D
R2/RRR2-25/2	1311.800	1312.497	-1297.690	0.401	1482.104	0.486	20	0.179	R.VLVGVVASPEADR.D
R2/RRR2-21/2	1264.168	1264.456	-228.144	0.418	1319.632	0.570	17	0.179	R.LQAALSTGLFSR.I
R2/RRR2-21/2	1312.158	1312.497	-258.990	0.439	1472.001	0.489	19	0.179	R.VLVGVVASPEADR.D
R2/RRR2-25/2	1048.894	1049.270	-359.258	0.449	1530.516	0.445	16	0.178	R.LGVM*LTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1312.132	1312.497	-279.151	0.438	1435.956	0.501	19	0.177	R.VLVGVVASPEADR.D
R2/RRR2-15/2	1263.622	1264.456	-1455.493	0.471	1334.708	0.545	18	0.177	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1312.165	1312.497	-254.137	0.516	1303.405	0.560	19	0.177	R.VLVGVVASPEADR.D
R2/RRR2-14/2	1264.086	1264.456	-293.151	0.510	1379.313	0.520	18	0.177	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1263.466	1264.456	-1579.906	0.491	1319.627	0.550	17	0.176	R.LQAALSTGLFSR.I
R2/RRR2-23/2	1312.199	1312.497	-227.631	0.423	1352.844	0.537	19	0.176	R.VLVGVVASPEADR.D
R2/RRR2-22/2	1313.023	1312.497	-362.231	0.500	1288.122	0.560	19	0.176	R.VLVGVVASPEADR.D
R2/RRR2-15/2	1312.318	1312.497	-137.112	0.522	1306.827	0.546	19	0.175	R.VLVGVVASPEADR.D
R2/RRR2-24/2	1263.741	1264.456	-1361.088	0.475	1355.600	0.521	18	0.175	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1610.202	1609.806	246.697	0.480	1404.133	0.506	21	0.174	K.LDISGHTVSAVGPDIK.H
R2/RRR2-14/2	1049.060	1049.270	-201.058	0.512	1599.115	0.394	17	0.174	R.LGVM*LTATAR.C
R2/RRR2-15/2	1311.680	1312.497	-1389.472	0.385	1361.420	0.513	20	0.172	R.VLVGVVASPEADR.D
R2/RRR2-26/2	1312.447	1312.497	-38.305	0.467	1315.467	0.528	18	0.171	R.VLVGVVASPEADR.D
R2/RRR2-24/2	1311.589	1312.497	-1459.394	0.386	1563.293	0.400	20	0.170	R.VLVGVVASPEADR.D
R2/RRR2-12/2	1311.589	1312.497	-1459.488	0.379	1335.281	0.520	19	0.170	R.VLVGVVASPEADR.D
R2/RRR2-22/2	1312.114	1312.497	-293.151	0.433	1292.050	0.530	19	0.169	R.VLVGVVASPEADR.D
R2/RRR2-20/2	1312.316	1312.497	-138.418	0.428	1250.494	0.553	18	0.169	R.VLVGVVASPEADR.D
R2/RRR2-14/2	1609.565	1609.806	-150.205	0.467	1445.134	0.456	22	0.169	K.LDISGHTVSAVGPDIK.H
R2/RRR2-25/2	1311.544	1312.497	-1493.611	0.384	1318.713	0.520	19	0.169	R.VLVGVVASPEADR.D
R2/RRR2-23/2	1312.130	1312.497	-280.644	0.444	1296.318	0.521	19	0.168	R.VLVGVVASPEADR.D
R2/RRR2-17/2	1265.132	1264.456	-256.326	0.485	1119.406	0.599	17	0.168	R.LQAALSTGLFSR.I
R2/RRR2-2/2	1263.398	1264.456	-1633.679	0.384	1408.896	0.467	18	0.168	R.LQAALSTGLFSR.I
R2/RRR2-13/2	1313.104	1312.497	-300.017	0.485	1147.719	0.584	18	0.167	R.VLVGVVASPEADR.D
R2/RRR2-24/2	1264.340	1264.456	-91.862	0.408	1264.879	0.523	18	0.166	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1049.026	1049.270	-233.045	0.499	1482.349	0.409	16	0.166	R.LGVM*LTATAR.C
R2/RRR2-20/2	1312.168	1312.497	-251.897	0.403	1214.953	0.548	19	0.165	R.VLVGVVASPEADR.D
R2/RRR2-21/2	1311.485	1312.497	-1539.237	0.368	1383.471	0.465	19	0.165	R.VLVGVVASPEADR.D
R2/RRR2-13/2	1263.623	1264.456	-1454.717	0.429	1460.137	0.419	18	0.164	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-26/2	1311.996	1312.497	-1147.343	0.409	1298.276	0.498	19	0.164	R.VLVGVVASPEADR.D
R2/RRR2-23/2	1312.302	1312.497	-149.242	0.467	1260.875	0.509	19	0.163	R.VLVGVVASPEADR.D
R2/RRR2-21/2	1263.878	1264.456	-1252.249	0.456	1208.987	0.533	17	0.163	R.LQAALSTGLFSR.I
R2/RRR2-1/2	1312.107	1312.497	-298.192	0.439	1313.082	0.484	19	0.163	R.VLVGVVASPEADR.D
R2/RRR2-15/2	1312.154	1312.497	-262.350	0.440	1231.220	0.522	19	0.163	R.VLVGVVASPEADR.D
R2/RRR2-23/2	1263.708	1264.456	-1387.477	0.439	1273.335	0.496	18	0.163	R.LQAALSTGLFSR.I
R2/RRR2-21/2	1312.263	1312.497	-178.917	0.381	1438.178	0.415	19	0.161	R.VLVGVVASPEADR.D
R2/RRR2-19/2	1264.486	1264.456	24.341	0.397	1268.028	0.495	17	0.160	R.LQAALSTGLFSR.I
R2/RRR2-20/2	1264.464	1264.456	6.525	0.456	1128.927	0.548	17	0.160	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1263.401	1264.456	-1631.641	0.400	1374.674	0.432	18	0.159	R.LQAALSTGLFSR.I
R2/RRR2-3/2	1312.174	1312.497	-246.950	0.443	1162.775	0.531	18	0.158	R.VLVGVVASPEADR.D
R2/RRR2-16/2	1312.071	1312.497	-326.008	0.367	1278.599	0.481	18	0.158	R.VLVGVVASPEADR.D
R2/RRR2-15/2	1754.324	1754.945	-926.583	0.384	1201.991	0.495	22	0.157	R.EELEKWM*AAYPQSR.V
R2/RRR2-3/2	1264.270	1264.456	-147.261	0.432	1186.756	0.514	16	0.157	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1048.933	1049.270	-322.593	0.486	1380.506	0.396	16	0.155	R.LGVM*LTATAR.C
R2/RRR2-24/2	1048.942	1049.270	-314.186	0.487	1377.267	0.398	16	0.155	R.LGVM*LTATAR.C
R2/RRR2-19/2	1311.989	1312.497	-1152.948	0.358	1195.030	0.496	19	0.154	R.VLVGVVASPEADR.D
R2/RRR2-24/2	1048.998	1049.270	-260.129	0.484	1350.861	0.399	16	0.153	R.LGVM*LTATAR.C
R2/RRR2-24/2	1264.397	1264.456	-46.443	0.373	1201.439	0.486	17	0.153	R.LQAALSTGLFSR.I
R2/RRR2-1/2	1263.897	1264.456	-1236.730	0.414	1170.485	0.495	17	0.153	R.LQAALSTGLFSR.I
R2/RRR2-2/2	1264.237	1264.456	-173.607	0.422	1115.779	0.523	16	0.153	R.LQAALSTGLFSR.I
R2/RRR2-15/2	1049.050	1049.270	-210.397	0.519	1335.120	0.405	16	0.153	R.LGVM*LTATAR.C
R2/RRR2-17/2	1264.264	1264.456	-152.104	0.461	1067.412	0.528	17	0.152	R.LQAALSTGLFSR.I
R2/RRR2-3/2	1263.626	1264.456	-1452.194	0.479	1077.286	0.531	16	0.152	R.LQAALSTGLFSR.I
R2/RRR2-15/2	1048.789	1049.270	-459.866	0.503	1300.149	0.415	16	0.152	R.LGVM*LTATAR.C
R2/RRR2-2/2	1313.102	1312.497	-301.509	0.459	1140.116	0.500	18	0.152	R.VLVGVVASPEADR.D
R2/RRR2-14/2	1049.115	1049.270	-147.947	0.511	1350.209	0.394	16	0.152	R.LGVM*LTATAR.C
R2/RRR2-14/2	1032.926	1033.271	-334.574	0.516	1260.889	0.428	16	0.152	R.LGVMLTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1311.989	1312.497	-1152.668	0.457	1103.161	0.504	19	0.151	R.VLVGVVASPEADR.D
R2/RRR2-13/2	1312.214	1312.497	-216.805	0.466	1033.117	0.544	17	0.151	R.VLVGVVASPEADR.D
R2/RRR2-2/2	1312.182	1312.497	-240.697	0.385	1170.071	0.479	18	0.150	R.VLVGVVASPEADR.D
R2/RRR2-2/2	1263.442	1264.456	-1598.445	0.383	1264.051	0.418	18	0.148	R.LQAALSTGLFSR.I
R2/RRR2-18/2	1311.428	1312.497	-1582.623	0.358	1127.277	0.498	17	0.148	R.VLVGVVASPEADR.D
R2/RRR2-3/2	1263.645	1264.456	-1437.057	0.418	935.217	0.577	15	0.148	R.LQAALSTGLFSR.I
R2/RRR2-15/2	1111.146	1110.271	-112.791	0.425	1129.621	0.466	13	0.147	K.WMAAYPQSR.V
R2/RRR2-24/2	1109.994	1110.271	-249.685	0.459	1067.552	0.471	15	0.147	K.WMAAYPQSR.V
R2/RRR2-23/2	1048.561	1049.270	-1634.459	0.412	1405.270	0.338	16	0.147	R.LGVM*LTATAR.C
R2/RRR2-24/2	1125.839	1126.270	-383.751	0.415	1116.809	0.457	15	0.147	K.WM*AAYPQSR.V
R2/RRR2-24/3	1895.108	1895.132	-12.806	0.458	1348.021	0.507	26	0.146	R.REELEKWMAAYPQSR.V
R2/RRR2-15/2	1532.200	1531.733	305.523	0.509	1464.742	0.314	18	0.146	K.DLYYDVLQFINK.L
R2/RRR2-2/2	1312.012	1312.497	-370.909	0.342	1138.970	0.471	18	0.145	R.VLVGVVASPEADR.D
R2/RRR2-25/2	1263.652	1264.456	-1431.818	0.421	981.156	0.527	16	0.145	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1531.890	1531.733	102.575	0.470	1379.245	0.325	18	0.142	K.DLYYDVLQFINK.L
R2/RRR2-25/2	1049.303	1049.270	31.072	0.389	1310.555	0.352	15	0.142	R.LGVM*LTATAR.C
R2/RRR2-15/2	1126.083	1126.270	-166.973	0.428	941.914	0.480	15	0.141	K.WM*AAYPQSR.V
R2/RRR2-14/3	1611.008	1609.806	125.991	0.498	1210.078	0.547	30	0.141	K.LDISGHTVSAVGPDIK.H
R2/RRR2-23/2	1608.691	1609.806	-1318.337	0.385	1164.223	0.432	20	0.141	K.LDISGHTVSAVGPDIK.H
R2/RRR2-24/2	1263.735	1264.456	-1365.745	0.418	924.966	0.517	16	0.140	R.LQAALSTGLFSR.I
R2/RRR2-25/2	1048.640	1049.270	-1559.262	0.468	1221.275	0.381	15	0.140	R.LGVM*LTATAR.C
R2/RRR2-13/2	1048.468	1049.270	-1724.289	0.365	1272.336	0.344	16	0.139	R.LGVM*LTATAR.C
R2/RRR2-15/2	1609.406	1609.806	-248.814	0.437	1211.809	0.388	22	0.139	K.LDISGHTVSAVGPDIK.H
R2/RRR2-24/2	1109.864	1110.271	-367.863	0.397	1055.455	0.424	15	0.139	K.WMAAYPQSR.V
R2/RRR2-17/2	1311.656	1312.497	-1408.167	0.318	1170.411	0.405	18	0.138	R.VLVGVVASPEADR.D
R2/RRR2-12/2	1311.553	1312.497	-1486.506	0.390	1077.008	0.441	17	0.138	R.VLVGVVASPEADR.D
R2/RRR2-15/2	1033.001	1033.271	-261.657	0.508	981.768	0.440	15	0.136	R.LGVMLTATAR.C
R2/RRR2-24/2	1032.907	1033.271	-353.428	0.522	1047.960	0.419	15	0.136	R.LGVMLTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1264.250	1264.456	-163.146	0.393	1005.466	0.447	17	0.136	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1754.355	1754.945	-909.119	0.483	814.435	0.505	20	0.136	R.EELEKWM*AAYPQSR.V
R2/RRR2-14/2	1531.385	1531.733	-228.390	0.388	1428.132	0.260	18	0.136	K.DLYYDVLQFINK.L
R2/RRR2-23/2	1126.027	1126.270	-216.455	0.467	938.187	0.441	14	0.136	K.WM*AAYPQSR.V
R2/RRR2-15/2	1109.460	1110.271	-1637.212	0.363	1092.962	0.395	15	0.136	K.WMAAYPQSR.V
R2/RRR2-16/2	1264.212	1264.456	-193.174	0.367	946.874	0.477	16	0.135	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1125.900	1126.270	-329.575	0.442	891.942	0.455	14	0.135	K.WM*AAYPQSR.V
R2/RRR2-5/2	1264.073	1264.456	-303.421	0.352	900.419	0.506	15	0.135	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1033.055	1033.271	-209.021	0.491	1016.610	0.417	15	0.135	R.LGVMLTATAR.C
R2/RRR2-1/2	1312.074	1312.497	-323.581	0.382	897.617	0.496	16	0.134	R.VLVGVVASPEADR.D
R2/RRR2-23/2	1125.873	1126.270	-353.942	0.409	829.766	0.468	14	0.133	K.WM*AAYPQSR.V
R2/RRR2-18/2	1311.947	1312.497	-1184.808	0.351	889.704	0.499	16	0.133	R.VLVGVVASPEADR.D
R2/RRR2-15/2	1109.778	1110.271	-445.340	0.315	1160.087	0.357	15	0.133	K.WMAAYPQSR.V
R2/RRR2-24/3	1910.600	1911.131	-804.060	0.445	1230.787	0.507	28	0.133	R.REELEKWM*AAYPQSR.V
R2/RRR2-16/2	1311.844	1312.497	-1263.860	0.368	910.431	0.447	17	0.130	R.VLVGVVASPEADR.D
R2/RRR2-14/2	1033.199	1033.271	-69.870	0.548	960.419	0.436	14	0.129	-.LGVMLTATAR.-
R2/RRR2-14/2	1125.935	1126.270	-298.029	0.437	746.037	0.457	13	0.129	K.WM*AAYPQSR.V
R2/RRR2-24/2	1125.345	1126.270	-1715.947	0.363	889.605	0.415	15	0.129	K.WM*AAYPQSR.V
R2/RRR2-24/2	1126.992	1126.270	-247.558	0.414	785.190	0.436	14	0.129	K.WM*AAYPQSR.V
R2/RRR2-24/2	1126.052	1126.270	-194.269	0.459	755.635	0.429	14	0.129	K.WM*AAYPQSR.V
R2/RRR2-24/2	1755.215	1754.945	154.615	0.520	683.430	0.485	19	0.128	R.EELEKWM*AAYPQSR.V
R2/RRR2-15/2	1125.968	1126.270	-268.661	0.333	871.076	0.422	15	0.128	K.WM*AAYPQSR.V
R2/RRR2-14/2	1033.374	1033.271	99.808	0.387	989.007	0.377	15	0.128	R.LGVMLTATAR.C
R2/RRR2-15/3	1609.849	1609.806	26.754	0.473	1151.690	0.517	30	0.128	K.LDISGHTVSAVGPDIK.H
R2/RRR2-24/2	1032.790	1033.271	-466.445	0.446	887.544	0.404	15	0.127	-.LGVMLTATAR.-
R2/RRR2-24/2	1127.101	1126.270	-150.854	0.477	806.827	0.398	14	0.127	K.WM*AAYPQSR.V
R2/RRR2-23/3	1609.841	1609.806	22.077	0.465	1132.730	0.515	29	0.126	K.LDISGHTVSAVGPDIK.H
R2/RRR2-20/2	1311.740	1312.497	-1343.859	0.343	740.004	0.466	18	0.126	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1133.077	1133.194	-103.476	0.437	849.983	0.375	16	0.126	R.NTDQLEGSLR.E
R2/RRR2-24/2	1033.014	1033.271	-249.209	0.418	873.331	0.391	15	0.125	-.LGVMLTATAR.-
R2/RRR2-2/2	1050.083	1049.270	-179.175	0.428	1057.299	0.325	15	0.125	R.LGVM*LTATAR.C
R2/RRR2-24/2	1109.271	1110.271	-1807.689	0.267	916.175	0.416	13	0.125	K.WMAAYPQSR.V
R2/RRR2-23/2	1264.491	1264.456	27.730	0.380	742.049	0.439	16	0.124	R.LQAALSTGLFSR.I
R2/RRR2-15/2	1125.450	1126.270	-1621.902	0.335	751.637	0.438	13	0.124	K.WM*AAYPQSR.V
R2/RRR2-17/2	1132.938	1133.194	-226.472	0.409	761.953	0.373	16	0.124	R.NTDQLEGSLR.E
R2/RRR2-14/2	1110.100	1110.271	-154.037	0.338	993.894	0.328	15	0.123	K.WMAAYPQSR.V
R2/RRR2-21/2	1133.016	1133.194	-157.621	0.509	838.560	0.354	16	0.123	R.NTDQLEGSLR.E
R2/RRR2-10/2	1311.583	1312.497	-1463.694	0.281	938.289	0.387	17	0.123	R.VLVGVVASPEADR.D
R2/RRR2-26/2	1132.740	1133.194	-402.156	0.430	725.678	0.362	16	0.123	R.NTDQLEGSLR.E
R2/RRR2-12/2	1311.591	1312.497	-1457.805	0.400	663.899	0.465	15	0.122	R.VLVGVVASPEADR.D
R2/RRR2-20/2	1132.516	1133.194	-1486.690	0.371	742.809	0.372	16	0.122	R.NTDQLEGSLR.E
R2/RRR2-23/2	1132.574	1133.194	-1434.831	0.432	788.749	0.351	16	0.122	R.NTDQLEGSLR.E
R2/RRR2-20/2	1132.926	1133.194	-237.174	0.407	740.031	0.360	16	0.122	R.NTDQLEGSLR.E
R2/RRR2-2/2	1133.085	1133.194	-96.560	0.496	681.456	0.377	15	0.122	R.NTDQLEGSLR.E
R2/RRR2-4/2	1312.023	1312.497	-362.507	0.350	694.862	0.431	17	0.122	R.VLVGVVASPEADR.D
R2/RRR2-26/2	1132.929	1133.194	-235.120	0.413	665.795	0.370	15	0.121	R.NTDQLEGSLR.E
R2/RRR2-18/2	1132.905	1133.194	-255.875	0.406	761.224	0.339	16	0.121	R.NTDQLEGSLR.E
R2/RRR2-1/2	1132.853	1133.194	-301.820	0.390	593.145	0.369	15	0.121	R.NTDQLEGSLR.E
R2/RRR2-24/2	1263.492	1264.456	-1558.845	0.339	723.958	0.454	13	0.121	R.LQAALSTGLFSR.I
R2/RRR2-24/2	1755.271	1754.945	186.348	0.397	709.508	0.444	17	0.120	R.EELEKWM*AAYPQSR.V
R2/RRR2-17/2	1133.023	1133.194	-151.352	0.463	747.114	0.331	16	0.120	R.NTDQLEGSLR.E
R2/RRR2-25/2	1133.097	1133.194	-86.078	0.463	647.058	0.353	15	0.120	R.NTDQLEGSLR.E
R2/RRR2-17/2	1132.397	1133.194	-1592.156	0.395	682.123	0.359	15	0.120	R.NTDQLEGSLR.E
R2/RRR2-19/2	1132.961	1133.194	-206.583	0.512	765.260	0.334	16	0.120	R.NTDQLEGSLR.E
R2/RRR2-26/2	1132.493	1133.194	-1507.045	0.381	763.323	0.349	15	0.120	R.NTDQLEGSLR.E
R2/RRR2-14/2	1530.971	1531.733	-1154.541	0.359	1343.783	0.191	17	0.120	K.DLYYDVLQFINK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1132.903	1133.194	-257.821	0.470	781.351	0.324	16	0.120	R.NTDQLEGSLR.E
R2/RRR2-21/2	1132.870	1133.194	-287.009	0.408	811.578	0.317	16	0.119	R.NTDQLEGSLR.E
R2/RRR2-3/2	1132.968	1133.194	-200.314	0.350	744.300	0.338	16	0.119	R.NTDQLEGSLR.E
R2/RRR2-25/2	1133.027	1133.194	-148.218	0.464	718.588	0.338	15	0.119	R.NTDQLEGSLR.E
R2/RRR2-18/2	1312.111	1312.497	-295.485	0.310	972.574	0.337	16	0.119	R.VLVGVVASPEADR.D
R2/RRR2-3/2	1312.040	1312.497	-349.625	0.312	996.048	0.327	16	0.119	R.VLVGVVASPEADR.D
R2/RRR2-6/2	1264.355	1264.456	-79.659	0.296	783.195	0.387	16	0.119	R.LQAALSTGLFSR.I
R2/RRR2-14/2	1132.975	1133.194	-194.477	0.395	685.527	0.338	15	0.119	R.NTDQLEGSLR.E
R2/RRR2-12/2	1127.116	1126.270	-137.165	0.364	873.724	0.302	15	0.119	K.WM*AAYPQSR.V
R2/RRR2-22/2	1132.842	1133.194	-311.874	0.486	766.825	0.313	16	0.119	R.NTDQLEGSLR.E
R2/RRR2-18/2	1132.408	1133.194	-1581.869	0.334	676.472	0.355	15	0.119	R.NTDQLEGSLR.E
R2/RRR2-25/2	1132.902	1133.194	-258.577	0.457	721.256	0.309	16	0.118	R.NTDQLEGSLR.E
R2/RRR2-24/2	1133.917	1133.194	-245.497	0.458	772.468	0.308	16	0.118	R.NTDQLEGSLR.E
R2/RRR2-23/2	1048.838	1049.270	-413.559	0.359	947.326	0.312	14	0.118	R.LGVM*LTATAR.C
R2/RRR2-18/2	1132.975	1133.194	-194.261	0.385	700.282	0.328	15	0.118	R.NTDQLEGSLR.E
R2/RRR2-25/2	1125.887	1126.270	-341.106	0.323	526.539	0.410	12	0.118	K.WM*AAYPQSR.V
R2/RRR2-16/2	1133.028	1133.194	-146.705	0.398	585.969	0.342	14	0.118	R.NTDQLEGSLR.E
R2/RRR2-6/2	1313.099	1312.497	-304.493	0.373	535.415	0.373	17	0.118	R.VLVGVVASPEADR.D
R2/RRR2-1/2	1132.759	1133.194	-385.504	0.458	679.870	0.317	15	0.117	R.NTDQLEGSLR.E
R2/RRR2-24/2	1132.948	1133.194	-217.825	0.485	761.064	0.293	16	0.117	R.NTDQLEGSLR.E
R2/RRR2-15/3	1609.814	1609.806	5.079	0.459	1101.125	0.482	29	0.117	K.LDISGHTVSAVGPDIK.H
R2/RRR2-2/2	1033.056	1033.271	-208.428	0.409	678.569	0.313	15	0.117	R.LGVMLTATAR.C
R2/RRR2-2/2	1610.595	1609.806	-131.408	0.426	504.723	0.462	16	0.116	K.LDISGHTVSAVGPDIK.H
R2/RRR2-2/2	1132.283	1133.194	-1692.663	0.356	652.735	0.304	15	0.116	R.NTDQLEGSLR.E
R2/RRR2-19/2	1132.187	1133.194	-1777.805	0.370	592.333	0.252	16	0.116	R.NTDQLEGSLR.E
R2/RRR2-1/2	1610.127	1609.806	200.095	0.442	626.999	0.425	17	0.116	K.LDISGHTVSAVGPDIK.H
R2/RRR2-3/2	1132.974	1133.194	-195.342	0.348	784.652	0.279	16	0.116	R.NTDQLEGSLR.E
R2/RRR2-23/2	1132.892	1133.194	-267.226	0.461	753.708	0.276	16	0.116	R.NTDQLEGSLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1133.293	1133.194	87.119	0.375	587.415	0.273	15	0.116	R.NTDQLEGSLR.E
R2/RRR2-15/2	1740.434	1738.945	281.280	0.392	282.809	0.516	13	0.115	R.EELEKWMAAYPQSR.V
R2/RRR2-22/2	1133.036	1133.194	-140.437	0.458	679.088	0.286	15	0.115	R.NTDQLEGSLR.E
R2/RRR2-19/2	1311.318	1312.497	-1666.975	0.313	547.606	0.421	14	0.115	R.VLVGVVASPEADR.D
R2/RRR2-19/2	1132.513	1133.194	-1488.964	0.392	804.260	0.255	16	0.115	R.NTDQLEGSLR.E
R2/RRR2-23/2	1132.502	1133.194	-1498.925	0.392	775.486	0.253	16	0.114	R.NTDQLEGSLR.E
R2/RRR2-2/2	1609.802	1609.806	-2.556	0.375	710.647	0.406	16	0.114	K.LDISGHTVSAVGPDIK.H
R2/RRR2-14/3	1610.724	1609.806	-51.060	0.488	877.626	0.540	27	0.114	K.LDISGHTVSAVGPDIK.H
R2/RRR2-15/2	1312.009	1312.497	-373.243	0.329	937.338	0.297	15	0.114	-.VLVGVVASPEADR.-
R2/RRR2-14/3	1610.848	1609.806	26.586	0.470	881.371	0.537	27	0.114	K.LDISGHTVSAVGPDIK.H
R2/RRR2-20/2	1132.221	1133.194	-1748.123	0.368	593.952	0.229	15	0.114	R.NTDQLEGSLR.E
R2/RRR2-1/2	1132.954	1133.194	-212.636	0.358	810.429	0.243	16	0.114	R.NTDQLEGSLR.E
R2/RRR2-15/2	1263.275	1264.456	-1731.631	0.354	303.708	0.402	12	0.113	-.LQAALSTGLFSR.-
R2/RRR2-24/2	1109.955	1110.271	-284.882	0.331	621.193	0.305	12	0.113	K.WMAAYPQSR.V
R2/RRR2-1/2	1610.565	1609.806	-150.188	0.335	670.982	0.359	18	0.112	K.LDISGHTVSAVGPDIK.H
R2/RRR2-25/2	1126.045	1126.270	-200.142	0.244	577.482	0.309	13	0.112	K.WM*AAYPQSR.V
R2/RRR2-22/2	1132.824	1133.194	-327.767	0.432	768.851	0.242	15	0.112	R.NTDQLEGSLR.E
R2/RRR2-15/2	1133.321	1133.194	112.181	0.386	624.633	0.221	14	0.111	R.NTDQLEGSLR.E
R2/RRR2-24/3	1911.180	1911.131	25.805	0.408	834.858	0.537	23	0.111	R.REELEKWM*AAYPQSR.V
R2/RRR2-23/2	1608.988	1609.806	-1133.335	0.375	940.685	0.256	21	0.111	K.LDISGHTVSAVGPDIK.H
R2/RRR2-1/2	1610.106	1609.806	186.866	0.373	660.826	0.369	16	0.111	K.LDISGHTVSAVGPDIK.H
R2/RRR2-23/3	1609.986	1609.806	112.535	0.481	929.869	0.506	29	0.110	K.LDISGHTVSAVGPDIK.H
R2/RRR2-14/2	1132.287	1133.194	-1689.088	0.386	714.116	0.184	15	0.109	R.NTDQLEGSLR.E
R2/RRR2-15/3	1911.473	1911.131	179.241	0.489	779.216	0.539	25	0.109	R.REELEKWM*AAYPQSR.V
R2/RRR2-1/2	1311.674	1312.497	-1393.771	0.200	643.735	0.342	14	0.108	R.VLVGVVASPEADR.D
R2/RRR2-21/2	1133.111	1133.194	-73.218	0.296	652.832	0.131	14	0.108	R.NTDQLEGSLR.E
R2/RRR2-2/2	1610.082	1609.806	172.192	0.352	413.213	0.356	14	0.108	K.LDISGHTVSAVGPDIK.H
R2/RRR2-13/2	1264.257	1264.456	-158.110	0.360	650.015	0.267	13	0.107	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1313.610	1312.497	85.879	0.219	805.076	0.209	17	0.107	R.VLVGVVASPEADR.D
R2/RRR2-3/2	1610.145	1609.806	211.347	0.347	486.177	0.310	15	0.107	K.LDISGHTVSAVGPDIK.H
R2/RRR2-3/2	1311.748	1312.497	-1337.410	0.279	820.957	0.220	15	0.106	R.VLVGVVASPEADR.D
R2/RRR2-15/3	1911.313	1911.131	95.563	0.461	839.238	0.502	24	0.105	R.REELEKWM*AAYPQSR.V
R2/RRR2-3/2	1610.337	1609.806	-292.008	0.374	525.846	0.287	15	0.105	K.LDISGHTVSAVGPDIK.H
R2/RRR2-24/3	1910.958	1911.131	-90.673	0.457	808.607	0.502	24	0.104	R.REELEKWM*AAYPQSR.V
R2/RRR2-24/3	1909.891	1911.131	-1176.496	0.415	660.773	0.528	23	0.102	R.REELEKWM*AAYPQSR.V
R2/RRR2-24/3	1911.812	1911.131	-167.515	0.458	788.759	0.489	23	0.100	R.REELEKWM*AAYPQSR.V
R2/RRR2-14/3	1911.047	1911.131	-44.252	0.400	837.873	0.474	24	0.100	R.REELEKWM*AAYPQSR.V
R2/RRR2-23/3	1609.509	1609.806	-184.793	0.479	792.357	0.472	26	0.098	K.LDISGHTVSAVGPDIK.H
R2/RRR2-15/3	1312.714	1312.497	165.673	0.462	968.006	0.422	25	0.096	R.VLVGVVASPEADR.D
R2/RRR2-17/3	1610.228	1609.806	262.956	0.376	769.766	0.461	26	0.095	K.LDISGHTVSAVGPDIK.H
R2/RRR2-14/3	1910.901	1911.131	-121.046	0.411	585.116	0.485	22	0.094	R.REELEKWM*AAYPQSR.V
R2/RRR2-24/3	1312.714	1312.497	165.953	0.441	717.487	0.470	22	0.094	R.VLVGVVASPEADR.D
R2/RRR2-15/3	1312.350	1312.497	-112.768	0.446	790.217	0.452	24	0.093	R.VLVGVVASPEADR.D
R2/RRR2-23/3	1910.581	1911.131	-813.680	0.383	636.673	0.463	21	0.091	R.REELEKWM*AAYPQSR.V
R2/RRR2-24/3	1895.015	1895.132	-61.846	0.312	966.333	0.378	22	0.090	R.REELEKWMAAYPQSR.V
R2/RRR2-24/3	1894.505	1895.132	-860.977	0.368	702.046	0.440	21	0.090	R.REELEKWMAAYPQSR.V
R2/RRR2-3/3	1610.262	1609.806	283.937	0.391	632.362	0.446	23	0.089	K.LDISGHTVSAVGPDIK.H
R2/RRR2-22/3	1609.419	1609.806	-241.060	0.366	661.122	0.410	25	0.086	K.LDISGHTVSAVGPDIK.H
R2/RRR2-15/3	1312.519	1312.497	16.677	0.426	641.781	0.418	22	0.086	R.VLVGVVASPEADR.D
R2/RRR2-24/3	1312.227	1312.497	-206.270	0.428	528.739	0.434	19	0.085	R.VLVGVVASPEADR.D
R2/RRR2-15/3	1910.427	1911.131	-894.882	0.350	676.630	0.403	21	0.085	R.REELEKWM*AAYPQSR.V
R2/RRR2-15/3	1312.063	1312.497	-331.852	0.348	543.230	0.439	20	0.085	R.VLVGVVASPEADR.D
R2/RRR2-22/3	1609.835	1609.806	18.084	0.408	677.629	0.397	23	0.085	K.LDISGHTVSAVGPDIK.H
R2/RRR2-14/3	1531.976	1531.733	158.865	0.491	950.545	0.346	24	0.083	K.DLYYDVLQFINK.L
R2/RRR2-25/3	1609.424	1609.806	-237.864	0.373	877.659	0.341	26	0.082	K.LDISGHTVSAVGPDIK.H
R2/RRR2-24/3	1312.404	1312.497	-71.062	0.454	541.249	0.400	20	0.080	-.VLVGVVASPEADR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/3	1531.427	1531.733	-200.490	0.448	395.594	0.339	22	0.080	-.DLYYDVLQFINK.-
R2/RRR2-15/2	1312.865	1312.497	280.839	0.299	208.189	0.440	10	0.080	-.VLVGVVASPEADR.-
R2/RRR2-25/3	1609.967	1609.806	100.216	0.325	611.854	0.318	23	0.077	K.LDISGHTVSAVGPDIK.H
R2/RRR2-15/3	1531.535	1531.733	-129.846	0.438	546.151	0.333	23	0.076	-.DLYYDVLQFINK.-
R2/RRR2-15/3	1531.102	1531.733	-1068.767	0.422	425.651	0.387	22	0.071	-.DLYYDVLQFINK.-
R2/RRR2-12/3	1789.560	1789.922	-202.906	0.541	2698.245	0.492	40	0.386	R.KQSSALSAASSACDHIR.D
R2/RRR2-12/2	1347.191	1347.648	-340.503	0.493	2815.957	0.354	20	0.356	K.MELVDAAFPLLK.G
R2/RRR2-11/2	1348.064	1347.648	309.745	0.550	2576.322	0.408	20	0.323	K.MELVDAAFPLLK.G
R2/RRR2-12/2	1347.036	1347.648	-1200.119	0.468	2624.923	0.364	20	0.321	K.MELVDAAFPLLK.G
R2/RRR2-12/2	1347.331	1347.648	-235.872	0.511	2522.514	0.370	20	0.301	K.MELVDAAFPLLK.G
R2/RRR2-11/2	1347.434	1347.648	-158.981	0.487	2392.732	0.353	20	0.273	K.MELVDAAFPLLK.G
R2/RRR2-12/2	1352.745	1352.451	218.345	0.554	2137.695	0.474	20	0.269	K.MDATAQELSEEK.T
R2/RRR2-12/2	1556.226	1555.668	-285.010	0.613	1801.181	0.655	24	0.269	K.SQASALEAHAAPNCK.V
R2/RRR2-11/2	1352.016	1352.451	-322.443	0.517	2180.004	0.443	20	0.268	K.MDATAQELSEEK.T
R2/RRR2-12/2	1555.218	1555.668	-290.391	0.557	1798.978	0.603	24	0.253	K.SQASALEAHAAPNCK.V
R2/RRR2-12/2	1651.527	1650.987	-279.610	0.570	1860.475	0.563	25	0.248	K.VLVVANPANTNALILK.E
R2/RRR2-11/2	1555.230	1555.668	-282.673	0.535	1764.549	0.559	24	0.236	K.SQASALEAHAAPNCK.V
R2/RRR2-11/2	1351.979	1352.451	-349.711	0.523	1966.601	0.447	20	0.235	K.MDATAQELSEEK.T
R2/RRR2-11/2	1348.227	1347.648	-313.360	0.567	2026.090	0.419	20	0.232	K.MELVDAAFPLLK.G
R2/RRR2-11/2	1555.049	1555.668	-1044.623	0.508	1722.894	0.564	24	0.231	K.SQASALEAHAAPNCK.V
R2/RRR2-12/2	1352.009	1352.451	-327.426	0.522	1802.306	0.469	20	0.218	K.MDATAQELSEEK.T
R2/RRR2-11/3	1843.842	1843.115	-148.259	0.518	1829.928	0.515	32	0.217	R.ALGQISEKLNVQVTDVK.N
R2/RRR2-12/3	1789.439	1789.922	-270.657	0.582	1927.204	0.468	35	0.210	R.KQSSALSAASSACDHIR.D
R2/RRR2-12/2	1555.317	1555.668	-226.765	0.514	1455.201	0.603	22	0.206	K.SQASALEAHAAPNCK.V
R2/RRR2-11/2	1651.341	1650.987	215.194	0.554	1654.323	0.508	24	0.205	K.VLVVANPANTNALILK.E
R2/RRR2-11/2	1555.243	1555.668	-274.090	0.514	1479.573	0.575	22	0.202	K.SQASALEAHAAPNCK.V
R2/RRR2-11/2	1650.499	1650.987	-296.400	0.502	1587.545	0.513	24	0.199	K.VLVVANPANTNALILK.E
R2/RRR2-11/2	1368.150	1368.450	-219.825	0.483	1606.920	0.462	20	0.193	K.M*DATAQELSEEK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1650.158	1650.987	-1111.737	0.442	1437.983	0.516	22	0.181	K.VLVVANPANTNALILK.E
R2/RRR2-11/2	1651.443	1650.987	276.864	0.543	1503.943	0.472	24	0.180	K.VLVVANPANTNALILK.E
R2/RRR2-12/2	1650.570	1650.987	-253.290	0.476	1245.354	0.513	22	0.163	K.VLVVANPANTNALILK.E
R2/RRR2-12/2	1016.148	1016.174	-25.196	0.508	1507.477	0.324	15	0.153	K.LNVQVTDVK.N
R2/RRR2-12/2	1362.596	1363.648	-1510.393	0.400	1324.407	0.403	17	0.150	K.M*ELVDAAFPLLK.G
R2/RRR2-12/2	1363.148	1363.648	-1103.710	0.468	1372.978	0.346	18	0.145	K.M*ELVDAAFPLLK.G
R2/RRR2-11/2	1363.288	1363.648	-264.324	0.459	1326.963	0.340	18	0.141	K.M*ELVDAAFPLLK.G
R2/RRR2-11/2	1363.274	1363.648	-275.104	0.488	1153.182	0.407	17	0.139	K.M*ELVDAAFPLLK.G
R2/RRR2-2/2	1346.918	1347.648	-1288.581	0.372	1623.203	0.189	18	0.138	K.MELVDAAFPLLK.G
R2/RRR2-11/3	1789.304	1789.922	-906.877	0.471	1346.668	0.480	31	0.137	R.KQSSALSAASSACDHIR.D
R2/RRR2-11/2	1015.570	1016.174	-1583.440	0.537	1232.268	0.347	15	0.137	K.LNVQVTDVK.N
R2/RRR2-12/3	1662.714	1661.749	-21.408	0.429	1197.150	0.537	31	0.135	K.QSSALSAASSACDHIR.D
R2/RRR2-12/2	1651.181	1650.987	117.632	0.488	980.979	0.467	19	0.134	K.VLVVANPANTNALILK.E
R2/RRR2-11/3	1843.403	1843.115	156.999	0.462	1109.876	0.551	28	0.132	R.ALGQISEKLNVQVTDVK.N
R2/RRR2-7/2	1651.389	1650.987	243.806	0.464	1002.447	0.402	20	0.127	K.VLVVANPANTNALILK.E
R2/RRR2-11/3	1661.439	1661.749	-187.086	0.468	1274.729	0.468	32	0.125	K.QSSALSAASSACDHIR.D
R2/RRR2-7/2	1651.490	1650.987	-302.228	0.415	1186.347	0.306	21	0.125	K.VLVVANPANTNALILK.E
R2/RRR2-11/3	1608.116	1608.796	-1048.380	0.423	1332.002	0.428	25	0.123	R.KKMDATAQELSEEK.T
R2/RRR2-10/2	1015.316	1016.174	-1835.025	0.392	1178.321	0.257	15	0.123	K.LNVQVTDVK.N
R2/RRR2-3/2	1651.040	1650.987	32.361	0.444	771.145	0.427	19	0.121	K.VLVVANPANTNALILK.E
R2/RRR2-11/3	1624.386	1624.796	-253.184	0.517	1430.599	0.387	27	0.120	R.KKM*DATAQELSEEK.T
R2/RRR2-12/2	1650.372	1650.987	-981.394	0.343	913.437	0.375	19	0.119	K.VLVVANPANTNALILK.E
R2/RRR2-5/2	1016.345	1016.174	169.003	0.433	867.044	0.321	14	0.119	K.LNVQVTDVK.N
R2/RRR2-2/2	1016.450	1016.174	272.817	0.413	431.821	0.314	14	0.119	K.LNVQVTDVK.N
R2/RRR2-10/2	1015.562	1016.174	-1591.651	0.367	829.556	0.277	14	0.114	K.LNVQVTDVK.N
R2/RRR2-15/2	1016.389	1016.174	212.362	0.376	489.408	0.276	12	0.112	K.LNVQVTDVK.N
R2/RRR2-3/2	1016.853	1016.174	-316.203	0.297	557.390	0.230	14	0.111	K.LNVQVTDVK.N
R2/RRR2-15/2	1015.569	1016.174	-1584.648	0.338	425.928	0.293	11	0.110	-.LNVQVTDVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/3	1662.117	1661.749	222.041	0.457	888.241	0.505	26	0.106	K.QSSALSAASSACDHIR.D
R2/RRR2-11/2	1362.340	1363.648	-1698.778	0.247	509.141	0.271	13	0.098	-.M*ELVDAAFPLLK.-
R2/RRR2-12/3	1661.502	1661.749	-149.165	0.379	925.020	0.447	27	0.097	K.QSSALSAASSACDHIR.D
R2/RRR2-11/3	1624.489	1624.796	-189.519	0.483	1148.905	0.362	25	0.094	R.KKM*DATAQELSEEK.T
R2/RRR2-11/3	1662.944	1661.749	117.087	0.438	615.172	0.495	23	0.092	K.QSSALSAASSACDHIR.D
R2/RRR2-12/3	1626.014	1624.796	134.443	0.323	522.138	0.383	20	0.077	R.KKM*DATAQELSEEK.T
R2/RRR2-11/3	1608.576	1608.796	-137.632	0.339	580.466	0.296	23	0.072	-.KKMDATAQELSEEK.-
R2/RRR2-13/2	1549.245	1549.732	-315.456	0.497	1801.746	0.559	23	0.242	R.LAIAGMGTDENSLTR.I
R2/RRR2-13/2	1566.230	1565.732	319.384	0.532	1789.387	0.562	22	0.240	R.LAIAGM*GTDENSLTR.I
R2/RRR2-13/2	1565.063	1565.732	-1069.213	0.521	1609.650	0.490	21	0.197	R.LAIAGM*GTDENSLTR.I
R2/RRR2-13/2	1565.122	1565.732	-1031.467	0.472	1408.221	0.553	20	0.188	R.LAIAGM*GTDENSLTR.I
R2/RRR2-13/2	1369.132	1369.416	-207.792	0.413	1702.294	0.374	19	0.184	R.SITDEISGDFER.A
R2/RRR2-13/2	1030.910	1031.225	-306.369	0.460	1378.785	0.513	15	0.180	R.VLVEIACAR.G
R2/RRR2-13/2	1031.154	1031.225	-68.940	0.501	1540.653	0.425	15	0.179	R.VLVEIACAR.G
R2/RRR2-13/2	1369.091	1369.416	-238.383	0.473	1525.969	0.398	18	0.170	R.SITDEISGDFER.A
R2/RRR2-13/2	958.546	959.127	-1653.817	0.503	1149.832	0.540	14	0.166	R.GPAQLFAVR.Q
R2/RRR2-13/2	958.956	959.127	-179.081	0.510	1143.401	0.529	14	0.163	R.GPAQLFAVR.Q
R2/RRR2-13/2	1369.082	1369.416	-244.913	0.440	1260.127	0.419	17	0.149	R.SITDEISGDFER.A
R2/RRR2-13/2	1058.181	1058.171	9.533	0.439	1292.805	0.376	16	0.147	R.DAVLANEVAR.K
R2/RRR2-13/2	1383.948	1384.605	-1201.021	0.332	1227.343	0.429	15	0.146	R.AVILWTLDPAER.D
R2/RRR2-13/2	1349.785	1350.418	-1213.368	0.516	1238.459	0.379	17	0.143	R.YNDEYGHPINK.D
R2/RRR2-13/2	1145.976	1145.419	-388.003	0.436	726.309	0.447	17	0.128	K.LLVPLISAYR.Y
R2/RRR2-13/2	1146.189	1145.419	-201.529	0.450	632.677	0.459	16	0.127	K.LLVPLISAYR.Y
R2/RRR2-13/2	1122.008	1122.299	-260.106	0.463	784.207	0.368	14	0.121	K.LITEAYQKR.N
R2/RRR2-13/2	1057.799	1058.171	-352.056	0.381	758.844	0.256	14	0.107	R.DAVLANEVAR.K
R2/RRR2-13/2	1121.412	1122.299	-1688.000	0.336	831.629	0.210	14	0.106	K.LITEAYQKR.N
R2/RRR2-13/2	1030.421	1031.225	-1756.141	0.298	725.974	0.192	12	0.103	R.VLVEIACAR.G
R2/RRR2-14/2	1819.461	1820.040	-870.203	0.527	1863.570	0.561	23	0.249	K.SAQDIALADLPTTHPIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1819.470	1820.040	-865.422	0.521	1896.207	0.542	23	0.249	K.SAQDIALADLPTTHPIR.L
R2/RRR2-14/2	1820.459	1820.040	231.252	0.581	1857.623	0.565	23	0.249	K.SAQDIALADLPTTHPIR.L
R2/RRR2-14/2	1337.200	1337.504	-227.312	0.544	1867.860	0.532	20	0.246	R.KEAAENTLVAYK.S
R2/RRR2-14/2	1819.530	1820.040	-831.950	0.507	1862.260	0.521	24	0.238	K.SAQDIALADLPTTHPIR.L
R2/RRR2-14/2	1337.220	1337.504	-212.751	0.521	1751.851	0.550	20	0.234	R.KEAAENTLVAYK.S
R2/RRR2-15/2	1819.842	1820.040	-108.696	0.533	1760.332	0.540	23	0.228	K.SAQDIALADLPTTHPIR.L
R2/RRR2-14/2	1337.108	1337.504	-297.012	0.527	1655.778	0.522	20	0.214	R.KEAAENTLVAYK.S
R2/RRR2-15/3	1820.973	1820.040	-36.793	0.476	1829.298	0.475	34	0.201	K.SAQDIALADLPTTHPIR.L
R2/RRR2-14/2	1319.180	1319.400	-167.305	0.501	1623.674	0.465	19	0.194	K.TADVGELTVEER.N
R2/RRR2-14/2	1639.453	1639.832	-231.632	0.491	1387.275	0.526	24	0.181	K.LLDSHLVPSATAAESK.V
R2/RRR2-14/2	1206.231	1206.438	-172.560	0.531	1847.884	0.300	16	0.180	K.DSTLIM*QLLR.D
R2/RRR2-14/2	1319.077	1319.400	-245.751	0.514	1518.514	0.451	18	0.179	K.TADVGELTVEER.N
R2/RRR2-15/2	1418.587	1419.563	-1397.133	0.450	1554.025	0.433	19	0.179	R.IISSIEQKEESR.G
R2/RRR2-15/2	1319.000	1319.400	-304.709	0.458	1579.448	0.408	19	0.177	K.TADVGELTVEER.N
R2/RRR2-14/2	1419.152	1419.563	-290.366	0.470	1389.251	0.462	19	0.169	R.IISSIEQKEESR.G
R2/RRR2-15/2	1420.091	1419.563	-333.369	0.499	1339.382	0.474	19	0.167	R.IISSIEQKEESR.G
R2/RRR2-14/2	1319.296	1319.400	-79.497	0.502	1391.968	0.440	18	0.164	K.TADVGELTVEER.N
R2/RRR2-14/2	1419.225	1419.563	-239.193	0.469	1350.644	0.448	19	0.163	R.IISSIEQKEESR.G
R2/RRR2-14/2	1638.961	1639.832	-1144.955	0.479	1178.950	0.515	23	0.159	K.LLDSHLVPSATAAESK.V
R2/RRR2-15/2	1639.445	1639.832	-236.861	0.501	1166.050	0.511	23	0.158	K.LLDSHLVPSATAAESK.V
R2/RRR2-15/2	1419.216	1419.563	-245.579	0.503	1245.265	0.461	19	0.157	R.IISSIEQKEESR.G
R2/RRR2-15/2	1318.399	1319.400	-1522.714	0.323	1556.264	0.319	18	0.156	K.TADVGELTVEER.N
R2/RRR2-15/2	1318.276	1319.400	-1616.196	0.314	1592.024	0.299	18	0.156	K.TADVGELTVEER.N
R2/RRR2-14/3	1819.995	1820.040	-24.569	0.408	1576.796	0.432	32	0.152	K.SAQDIALADLPTTHPIR.L
R2/RRR2-14/2	1051.960	1052.163	-193.160	0.411	1029.308	0.536	14	0.151	R.GNEAYVASIK.E
R2/RRR2-14/2	1640.362	1639.832	-287.335	0.474	1138.801	0.483	22	0.150	K.LLDSHLVPSATAAESK.V
R2/RRR2-13/2	1419.446	1419.563	-82.600	0.522	1021.736	0.504	18	0.148	R.IISSIEQKEESR.G
R2/RRR2-14/2	1419.033	1419.563	-1081.593	0.471	1132.647	0.460	18	0.148	R.IISSIEQKEESR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1639.432	1639.832	-244.854	0.478	1095.644	0.479	22	0.146	K.LLDSHLVPSATAAESK.V
R2/RRR2-14/2	1051.493	1052.163	-1593.096	0.414	872.901	0.546	15	0.143	R.GNEAYVASIK.E
R2/RRR2-15/2	1052.095	1052.163	-64.775	0.437	765.240	0.538	14	0.137	R.GNEAYVASIK.E
R2/RRR2-14/2	1051.977	1052.163	-176.979	0.461	945.341	0.455	15	0.137	R.GNEAYVASIK.E
R2/RRR2-14/2	1190.202	1190.439	-199.323	0.510	1560.541	0.193	16	0.131	K.DSTLIMQLLR.D
R2/RRR2-14/2	1209.022	1209.331	-256.070	0.365	905.009	0.445	17	0.131	K.EAAENTLVAYK.S
R2/RRR2-15/2	1209.232	1209.331	-81.873	0.413	857.166	0.447	16	0.130	K.EAAENTLVAYK.S
R2/RRR2-15/2	1051.363	1052.163	-1716.851	0.395	651.844	0.491	14	0.126	R.GNEAYVASIK.E
R2/RRR2-14/2	1208.592	1209.331	-1442.849	0.324	879.428	0.432	17	0.126	K.EAAENTLVAYK.S
R2/RRR2-15/2	1638.779	1639.832	-1256.328	0.454	848.029	0.444	19	0.125	K.LLDSHLVPSATAAESK.V
R2/RRR2-15/2	1210.086	1209.331	-202.523	0.366	784.907	0.438	15	0.124	K.EAAENTLVAYK.S
R2/RRR2-14/2	1206.181	1206.438	-213.373	0.402	1493.563	0.127	16	0.120	K.DSTLIM*QLLR.D
R2/RRR2-14/3	1639.980	1639.832	90.692	0.393	1381.172	0.394	31	0.118	K.LLDSHLVPSATAAESK.V
R2/RRR2-14/2	1419.433	1419.563	-92.089	0.456	721.397	0.357	16	0.116	R.IISSIEQKEESR.G
R2/RRR2-14/2	1419.470	1419.563	-65.952	0.434	478.211	0.368	14	0.113	R.IISSIEQKEESR.G
R2/RRR2-14/2	1419.317	1419.563	-173.789	0.328	355.481	0.403	13	0.113	R.IISSIEQKEESR.G
R2/RRR2-14/2	1208.483	1209.331	-1533.656	0.254	634.496	0.406	14	0.111	K.EAAENTLVAYK.S
R2/RRR2-14/2	1368.050	1367.527	-349.561	0.300	1002.044	0.195	14	0.105	R.YEEM*VEFM*EK.V
R2/RRR2-14/2	1189.957	1190.439	-405.970	0.361	937.346	0.122	14	0.101	-.DSTLIMQLLR.-
R2/RRR2-14/2	1189.740	1190.439	-1432.060	0.379	843.663	0.125	14	0.098	-.DSTLIMQLLR.-
R2/RRR2-14/3	1639.968	1639.832	83.414	0.372	1128.495	0.358	29	0.091	K.LLDSHLVPSATAAESK.V
R2/RRR2-11/2	1684.473	1684.961	-290.132	0.553	2825.007	0.588	26	0.460	R.ILVTGGAGFIGSHLVDK.L
R2/RRR2-11/2	1684.874	1684.961	-51.421	0.550	2564.961	0.577	24	0.393	R.ILVTGGAGFIGSHLVDK.L
R2/RRR2-11/2	1617.308	1617.885	-977.914	0.500	2449.308	0.427	22	0.314	R.SFCYVADMVNGLIK.L
R2/RRR2-11/2	1617.472	1617.885	-255.672	0.502	2413.091	0.405	22	0.299	R.SFCYVADMVNGLIK.L
R2/RRR2-11/2	1462.240	1461.753	334.005	0.568	2084.812	0.579	23	0.291	K.TNVIGTLNM*LGLAK.R
R2/RRR2-11/2	1445.248	1445.753	-1044.523	0.568	2108.709	0.538	23	0.282	K.TNVIGTLNMLGLAK.R
R2/RRR2-11/2	1462.385	1461.753	-252.430	0.580	1938.651	0.571	23	0.264	K.TNVIGTLNM*LGLAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1204.169	1204.404	-195.587	0.556	2139.185	0.444	19	0.262	R.VVSNFIAQAVR.G
R2/RRR2-11/2	1445.340	1445.753	-286.630	0.538	2050.700	0.478	23	0.254	K.TNVIGTLNMLGLAK.R
R2/RRR2-11/2	1203.618	1204.404	-1488.179	0.487	2030.542	0.445	19	0.246	R.VVSNFIAQAVR.G
R2/RRR2-11/2	1461.471	1461.753	-193.107	0.514	1970.074	0.476	23	0.242	K.TNVIGTLNM*LGLAK.R
R2/RRR2-11/2	1444.752	1445.753	-1389.033	0.420	2071.652	0.415	22	0.241	K.TNVIGTLNMLGLAK.R
R2/RRR2-11/2	1618.432	1617.885	-280.788	0.584	2027.394	0.439	21	0.240	R.SFCYVADMVNGLIK.L
R2/RRR2-11/2	1203.496	1204.404	-1589.758	0.460	1710.666	0.438	17	0.199	R.VVSNFIAQAVR.G
R2/RRR2-12/2	1204.155	1204.404	-206.672	0.474	1700.538	0.388	17	0.186	R.VVSNFIAQAVR.G
R2/RRR2-11/2	1157.069	1157.344	-238.151	0.482	1387.547	0.401	15	0.158	K.AKEVLGWEPK.I
R2/RRR2-11/3	1445.560	1445.753	-134.011	0.451	1798.624	0.359	27	0.157	K.TNVIGTLNMLGLAK.R
R2/RRR2-11/2	1157.020	1157.344	-280.701	0.484	1273.813	0.415	16	0.152	K.AKEVLGWEPK.I
R2/RRR2-11/2	1156.420	1157.344	-1668.238	0.468	1126.073	0.462	15	0.148	K.AKEVLGWEPK.I
R2/RRR2-11/2	1513.309	1512.693	-254.500	0.497	837.560	0.576	19	0.146	R.GEPLTVQKPGTQTR.S
R2/RRR2-11/2	1511.640	1512.693	-1362.075	0.440	973.205	0.478	21	0.140	R.GEPLTVQKPGTQTR.S
R2/RRR2-11/2	1512.200	1512.693	-326.989	0.445	848.603	0.528	20	0.140	R.GEPLTVQKPGTQTR.S
R2/RRR2-13/2	1462.767	1461.753	9.790	0.409	1055.743	0.425	19	0.135	K.TNVIGTLNM*LGLAK.R
R2/RRR2-11/2	967.923	968.091	-174.260	0.464	875.728	0.366	13	0.126	R.IFNTYGPR.M
R2/RRR2-12/2	1462.998	1461.753	168.128	0.369	1081.990	0.343	19	0.125	K.TNVIGTLNM*LGLAK.R
R2/RRR2-11/2	967.895	968.091	-202.473	0.427	773.853	0.360	13	0.122	R.IFNTYGPR.M
R2/RRR2-11/3	1382.901	1382.570	240.046	0.521	894.770	0.586	24	0.121	R.VAETLMFDYHR.Q
R2/RRR2-1/2	1513.151	1512.693	303.301	0.420	696.145	0.452	17	0.121	R.GEPLTVQKPGTQTR.S
R2/RRR2-13/2	967.808	968.091	-293.072	0.389	648.922	0.373	12	0.120	R.IFNTYGPR.M
R2/RRR2-12/2	968.168	968.091	79.973	0.444	583.894	0.366	11	0.118	R.IFNTYGPR.M
R2/RRR2-11/2	967.471	968.091	-1678.804	0.405	636.780	0.353	11	0.117	R.IFNTYGPR.M
R2/RRR2-10/2	968.751	968.091	-352.189	0.400	650.104	0.374	11	0.117	-.IFNTYGPR.-
R2/RRR2-13/2	967.746	968.091	-356.982	0.366	645.902	0.334	11	0.115	R.IFNTYGPR.M
R2/RRR2-12/2	967.883	968.091	-215.632	0.390	585.654	0.321	11	0.115	R.IFNTYGPR.M
R2/RRR2-10/2	968.268	968.091	183.148	0.360	779.118	0.293	12	0.115	R.IFNTYGPR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	967.628	968.091	-479.509	0.313	597.454	0.344	11	0.114	R.IFNTYGPR.M
R2/RRR2-10/2	968.992	968.091	-102.424	0.307	581.516	0.346	11	0.114	R.IFNTYGPR.M
R2/RRR2-11/2	968.089	968.091	-2.101	0.363	643.434	0.313	12	0.113	-.IFNTYGPR.-
R2/RRR2-12/2	967.805	968.091	-295.983	0.425	663.462	0.303	12	0.113	-.IFNTYGPR.-
R2/RRR2-11/3	1382.720	1382.570	108.850	0.494	804.305	0.547	23	0.109	R.VAETLMFDYHR.Q
R2/RRR2-11/2	1595.519	1595.759	-150.990	0.399	799.821	0.280	17	0.108	R.DGLVLMEDDFRER.L
R2/RRR2-11/2	1595.072	1595.759	-1061.013	0.429	488.513	0.333	16	0.108	-.DGLVLMEDDFRER.-
R2/RRR2-11/3	1382.193	1382.570	-272.983	0.471	754.747	0.540	22	0.106	R.VAETLMFDYHR.Q
R2/RRR2-13/2	1462.846	1461.753	64.026	0.259	687.890	0.221	17	0.104	K.TNVIGTLNM*LGLAK.R
R2/RRR2-11/3	1445.022	1445.753	-1201.827	0.373	1367.177	0.290	25	0.095	K.TNVIGTLNMLGLAK.R
R2/RRR2-11/3	1399.428	1398.569	-100.992	0.377	432.581	0.534	20	0.094	R.VAETLM*FDYHR.Q
R2/RRR2-11/3	1398.510	1398.569	-42.576	0.406	543.296	0.509	22	0.094	R.VAETLM*FDYHR.Q
R2/RRR2-11/3	1398.184	1398.569	-275.868	0.401	322.718	0.485	17	0.091	R.VAETLM*FDYHR.Q
R2/RRR2-11/3	1398.007	1398.569	-1120.386	0.378	369.688	0.410	18	0.086	R.VAETLM*FDYHR.Q
R2/RRR2-11/3	1445.125	1445.753	-1130.319	0.400	1142.584	0.198	27	0.068	K.TNVIGTLNMLGLAK.R
R2/RRR2-3/2	1469.102	1469.645	-1053.444	0.511	2586.257	0.537	24	0.378	R.FIGTAGAASSTM*NPK.N
R2/RRR2-4/2	1885.387	1885.881	-262.851	0.602	2414.179	0.638	28	0.373	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-3/2	1885.506	1885.881	-199.132	0.599	2002.885	0.606	28	0.283	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-3/2	1885.293	1885.881	-844.623	0.569	1810.963	0.655	27	0.266	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-3/2	1469.070	1469.645	-1075.804	0.501	2127.340	0.455	23	0.262	R.FIGTAGAASSTM*NPK.N
R2/RRR2-4/2	1469.126	1469.645	-1037.260	0.473	1910.564	0.515	22	0.245	R.FIGTAGAASSTM*NPK.N
R2/RRR2-4/2	1885.508	1885.881	-198.158	0.593	1632.213	0.609	26	0.226	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-4/2	1469.162	1469.645	-330.364	0.485	1843.409	0.482	22	0.226	R.FIGTAGAASSTM*NPK.N
R2/RRR2-4/2	1470.145	1469.645	340.943	0.579	1729.805	0.538	22	0.224	R.FIGTAGAASSTM*NPK.N
R2/RRR2-4/2	1885.410	1885.881	-250.574	0.580	1607.224	0.609	26	0.223	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-3/2	1885.338	1885.881	-820.769	0.581	1487.683	0.648	25	0.217	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-4/3	1422.784	1422.655	91.242	0.535	2070.172	0.327	28	0.177	K.HANPVLLSSDLKK.K
R2/RRR2-4/3	1422.838	1422.655	128.928	0.530	2086.135	0.314	28	0.175	K.HANPVLLSSDLKK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1359.031	1359.511	-354.383	0.411	1306.290	0.470	18	0.163	R.GIDVVLNEESKR.E
R2/RRR2-4/3	1791.360	1789.969	219.076	0.540	1552.627	0.478	33	0.155	K.FKDEYKIDVYQNAR.A
R2/RRR2-3/2	1541.296	1541.811	-985.707	0.269	1443.035	0.382	19	0.154	R.AVLDAATIAGLCPLR.L
R2/RRR2-3/3	1422.802	1422.655	103.890	0.498	1918.478	0.316	27	0.154	K.HANPVLLSSDLKK.K
R2/RRR2-4/2	1542.178	1541.811	238.366	0.403	1376.693	0.405	19	0.154	R.AVLDAATIAGLCPLR.L
R2/RRR2-3/3	1422.943	1422.655	202.874	0.490	1799.567	0.358	26	0.153	K.HANPVLLSSDLKK.K
R2/RRR2-4/2	1359.224	1359.511	-211.288	0.461	1105.501	0.498	17	0.151	R.GIDVVLNEESKR.E
R2/RRR2-9/2	1885.972	1885.881	48.715	0.472	889.013	0.613	21	0.148	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-10/3	1423.253	1422.655	-282.915	0.504	1984.898	0.265	28	0.145	K.HANPVLLSSDLKK.K
R2/RRR2-4/2	1359.208	1359.511	-223.632	0.455	1028.240	0.478	16	0.142	R.GIDVVLNEESKR.E
R2/RRR2-4/2	1041.029	1041.183	-148.379	0.433	1047.971	0.361	14	0.129	K.IQQQDALPK.H
R2/RRR2-9/2	1884.110	1885.881	-2007.583	0.335	708.810	0.586	20	0.129	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-3/3	1422.757	1422.655	72.139	0.509	1751.556	0.299	26	0.128	K.HANPVLLSSDLKK.K
R2/RRR2-4/2	936.426	937.077	-1767.606	0.347	651.231	0.521	11	0.127	R.DIAAFPFR.V
R2/RRR2-3/2	1040.877	1041.183	-294.730	0.401	1006.559	0.339	14	0.124	K.IQQQDALPK.H
R2/RRR2-4/2	936.996	937.077	-85.864	0.368	623.457	0.445	11	0.122	R.DIAAFPFR.V
R2/RRR2-1/3	1421.388	1422.655	-1599.270	0.489	1753.891	0.272	26	0.121	K.HANPVLLSSDLKK.K
R2/RRR2-3/3	1885.699	1885.881	-96.856	0.488	1172.554	0.480	34	0.121	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-4/2	1541.389	1541.811	-274.567	0.228	1193.327	0.281	19	0.121	R.AVLDAATIAGLCPLR.L
R2/RRR2-3/2	1041.075	1041.183	-103.682	0.440	1009.971	0.292	15	0.120	K.IQQQDALPK.H
R2/RRR2-4/3	1481.098	1481.638	-1042.809	0.438	969.036	0.540	25	0.119	R.VSEGPDGFPLVHAR.Y
R2/RRR2-3/2	1041.024	1041.183	-153.437	0.400	890.730	0.309	14	0.117	K.IQQQDALPK.H
R2/RRR2-3/2	936.351	937.077	-1848.951	0.398	555.198	0.397	10	0.117	R.DIAAFPFR.V
R2/RRR2-4/2	937.089	937.077	13.182	0.335	423.210	0.470	9	0.116	R.DIAAFPFR.V
R2/RRR2-3/2	936.831	937.077	-263.098	0.301	459.082	0.477	9	0.115	R.DIAAFPFR.V
R2/RRR2-4/2	1040.338	1041.183	-1778.826	0.372	844.880	0.300	14	0.115	K.IQQQDALPK.H
R2/RRR2-4/3	1422.655	1422.655	0.239	0.511	1570.757	0.320	26	0.115	K.HANPVLLSSDLKK.K
R2/RRR2-3/3	1885.262	1885.881	-860.945	0.498	991.537	0.510	31	0.114	K.APADAAADGAENGAPNSEEK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	936.493	937.077	-1695.704	0.284	668.384	0.384	10	0.113	R.DIAAFPFR.V
R2/RRR2-4/3	1885.870	1885.881	-5.598	0.451	936.625	0.522	29	0.113	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-4/3	1789.798	1789.969	-95.718	0.488	1249.864	0.421	30	0.111	K.FKDEYKIDVYQNAR.A
R2/RRR2-4/2	1540.889	1541.811	-1251.121	0.258	992.015	0.282	16	0.111	R.AVLDAATIAGLCPLR.L
R2/RRR2-8/2	936.629	937.077	-479.628	0.250	721.368	0.292	11	0.109	R.DIAAFPFR.V
R2/RRR2-4/3	1885.747	1885.881	-70.947	0.502	992.043	0.479	32	0.108	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-7/2	1543.128	1541.811	206.085	0.310	490.651	0.353	14	0.106	R.AVLDAATIAGLCPLR.L
R2/RRR2-8/2	936.819	937.077	-276.171	0.193	477.497	0.280	10	0.106	R.DIAAFPFR.V
R2/RRR2-7/2	1543.254	1541.811	287.785	0.258	572.281	0.346	15	0.106	R.AVLDAATIAGLCPLR.L
R2/RRR2-4/2	974.703	975.083	-391.553	0.304	914.224	0.189	13	0.104	K.ILSHAYDR.S
R2/RRR2-3/2	1540.468	1541.811	-1525.271	0.273	591.006	0.227	14	0.101	-.AVLDAATIAGLCPLR.-
R2/RRR2-3/2	1541.131	1541.811	-1093.701	0.223	587.936	0.235	13	0.099	R.AVLDAATIAGLCPLR.L
R2/RRR2-3/3	1885.839	1885.881	-22.446	0.518	757.265	0.500	30	0.099	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-4/3	1885.865	1885.881	-8.227	0.482	840.153	0.472	32	0.098	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-4/3	1885.112	1885.881	-941.291	0.462	968.603	0.433	32	0.098	K.APADAAADGAENGAPNSEEK.S
R2/RRR2-7/3	1481.323	1481.638	-213.058	0.405	829.753	0.428	24	0.093	R.VSEGPDGFPLVHAR.Y
R2/RRR2-1/3	1481.611	1481.638	-17.909	0.435	662.623	0.458	22	0.092	R.VSEGPDGFPLVHAR.Y
R2/RRR2-3/3	1481.889	1481.638	170.100	0.399	739.135	0.444	24	0.092	R.VSEGPDGFPLVHAR.Y
R2/RRR2-7/3	1481.815	1481.638	120.161	0.386	776.524	0.425	24	0.091	R.VSEGPDGFPLVHAR.Y
R2/RRR2-4/3	1481.699	1481.638	41.463	0.364	591.439	0.454	22	0.090	R.VSEGPDGFPLVHAR.Y
R2/RRR2-2/3	1481.850	1481.638	143.830	0.391	731.444	0.418	23	0.089	R.VSEGPDGFPLVHAR.Y
R2/RRR2-1/3	1481.662	1481.638	16.550	0.403	693.228	0.413	23	0.088	R.VSEGPDGFPLVHAR.Y
R2/RRR2-8/3	1481.332	1481.638	-206.981	0.356	819.448	0.381	23	0.086	R.VSEGPDGFPLVHAR.Y
R2/RRR2-8/3	1481.790	1481.638	103.307	0.386	615.438	0.375	22	0.083	R.VSEGPDGFPLVHAR.Y
R2/RRR2-3/3	1481.643	1481.638	3.535	0.354	679.836	0.372	24	0.083	R.VSEGPDGFPLVHAR.Y
R2/RRR2-2/3	1481.307	1481.638	-224.094	0.346	703.800	0.365	22	0.082	R.VSEGPDGFPLVHAR.Y
R2/RRR2-4/3	1481.279	1481.638	-242.696	0.301	708.471	0.273	23	0.074	R.VSEGPDGFPLVHAR.Y
R2/RRR2-3/3	1480.196	1481.638	-1654.512	0.276	702.748	0.227	22	0.071	R.VSEGPDGFPLVHAR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1870.239	1871.077	-985.495	0.502	2784.872	0.487	24	0.414	K.LAYIALDYEQELETAK.S
R2/RRR2-10/2	1968.631	1969.270	-834.989	0.473	797.932	0.584	20	0.140	R.VAPEEHPILLTEAPLNPK.A
R2/RRR2-10/2	1968.823	1969.270	-227.707	0.478	870.298	0.521	20	0.135	R.VAPEEHPILLTEAPLNPK.A
R2/RRR2-10/2	1968.670	1969.270	-815.195	0.491	634.373	0.511	18	0.122	R.VAPEEHPILLTEAPLNPK.A
R2/RRR2-5/2	1344.985	1344.495	365.893	0.547	1618.455	0.613	20	0.233	K.VFANAETTISYK.I
R2/RRR2-5/2	1344.177	1344.495	-236.972	0.525	1543.282	0.553	20	0.208	K.VFANAETTISYK.I
R2/RRR2-5/2	1650.146	1650.813	-1013.582	0.481	1742.332	0.415	20	0.197	K.GILQNDPFEVFDQK.G
R2/RRR2-5/2	1823.612	1824.025	-227.241	0.531	1455.495	0.547	24	0.195	R.LLSSGNVYTQEEILTR.I
R2/RRR2-5/2	1344.242	1344.495	-188.505	0.542	1442.748	0.545	19	0.194	K.VFANAETTISYK.I
R2/RRR2-5/2	1824.379	1824.025	194.716	0.599	1126.451	0.596	21	0.171	R.LLSSGNVYTQEEILTR.I
R2/RRR2-5/2	1650.524	1650.813	-175.853	0.496	1448.757	0.407	18	0.161	K.GILQNDPFEVFDQK.G
R2/RRR2-5/2	1650.050	1650.813	-1071.443	0.465	1376.100	0.423	18	0.158	K.GILQNDPFEVFDQK.G
R2/RRR2-5/2	1287.677	1287.361	245.827	0.449	805.949	0.539	18	0.139	K.ANADTPADALTAR.N
R2/RRR2-5/2	996.862	997.129	-268.195	0.463	974.739	0.442	13	0.138	R.LDFEGIFR.A
R2/RRR2-5/2	1287.169	1287.361	-149.873	0.354	617.086	0.441	17	0.117	K.ANADTPADALTAR.N
R2/RRR2-5/2	996.677	997.129	-454.232	0.432	683.170	0.327	12	0.115	R.LDFEGIFR.A
R2/RRR2-5/2	1019.226	1018.213	12.393	0.361	814.151	0.314	15	0.115	K.IGSM*IEVPR.A
R2/RRR2-5/2	996.705	997.129	-426.088	0.414	647.575	0.326	12	0.115	R.LDFEGIFR.A
R2/RRR2-5/2	1017.804	1018.213	-403.449	0.382	516.049	0.281	13	0.110	K.IGSM*IEVPR.A
R2/RRR2-5/2	1595.325	1595.842	-954.090	0.277	841.150	0.270	17	0.104	R.AIFEAAISMTEQGVK.V
R2/RRR2-12/2	1748.561	1748.146	238.100	0.593	2292.688	0.574	27	0.328	K.VAVLGAAGGIGQPLGLLIK.M
R2/RRR2-12/2	1748.594	1748.146	257.211	0.596	2070.325	0.565	26	0.283	K.VAVLGAAGGIGQPLGLLIK.M
R2/RRR2-12/3	1748.178	1748.146	18.369	0.507	2209.726	0.452	38	0.267	K.VAVLGAAGGIGQPLGLLIK.M
R2/RRR2-12/2	1347.924	1348.616	-1259.097	0.543	1742.234	0.454	20	0.208	K.KLFGVTTLDVVR.A
R2/RRR2-12/2	1348.347	1348.616	-200.280	0.520	1819.255	0.409	20	0.206	K.KLFGVTTLDVVR.A
R2/RRR2-12/2	1348.284	1348.616	-247.147	0.509	1726.006	0.443	20	0.203	K.KLFGVTTLDVVR.A
R2/RRR2-12/2	1746.769	1748.146	-1364.616	0.401	1645.052	0.450	24	0.191	K.VAVLGAAGGIGQPLGLLIK.M
R2/RRR2-12/2	1468.942	1469.649	-1165.453	0.375	1499.385	0.474	21	0.180	K.AGAGSATLSMAYAAAR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1279.262	1278.526	-206.789	0.450	1552.893	0.425	20	0.178	K.GVDVVVIPAGVPR.K
R2/RRR2-12/3	1485.762	1485.648	76.921	0.447	1484.436	0.546	26	0.177	K.AGAGSATLSM*AYAAAR.F
R2/RRR2-12/2	1486.149	1485.648	-337.034	0.504	1417.887	0.495	21	0.176	K.AGAGSATLSM*AYAAAR.F
R2/RRR2-12/3	1983.285	1983.123	82.278	0.491	1692.724	0.439	32	0.171	K.TRPSVTFTDEETEQLTK.R
R2/RRR2-12/2	1349.290	1349.514	-166.747	0.546	1517.766	0.360	18	0.161	R.DDLFNINASIVK.S
R2/RRR2-12/2	1485.247	1485.648	-271.208	0.477	1225.628	0.494	20	0.157	K.AGAGSATLSM*AYAAAR.F
R2/RRR2-12/2	1259.990	1259.391	-319.757	0.537	1038.570	0.510	19	0.152	R.IQNAGTEVVEAK.A
R2/RRR2-12/2	1220.106	1220.443	-277.326	0.498	1226.423	0.406	19	0.148	K.LFGVTTLDVVR.A
R2/RRR2-12/2	1485.330	1485.648	-214.645	0.457	1250.569	0.432	19	0.147	K.AGAGSATLSM*AYAAAR.F
R2/RRR2-12/2	1219.650	1220.443	-1474.138	0.502	1104.560	0.444	18	0.145	K.LFGVTTLDVVR.A
R2/RRR2-12/2	1415.484	1415.578	-66.570	0.488	1217.219	0.400	20	0.144	K.RIQNAGTEVVEAK.A
R2/RRR2-13/2	1220.355	1220.443	-72.398	0.409	1326.961	0.331	17	0.140	K.LFGVTTLDVVR.A
R2/RRR2-12/2	1260.089	1259.391	-240.737	0.544	870.764	0.497	18	0.140	R.IQNAGTEVVEAK.A
R2/RRR2-12/2	1279.159	1278.526	-287.782	0.391	1092.055	0.402	17	0.133	K.GVDVVVIPAGVPR.K
R2/RRR2-12/2	1219.979	1220.443	-381.729	0.420	1340.640	0.252	19	0.130	K.LFGVTTLDVVR.A
R2/RRR2-12/2	1258.724	1259.391	-1328.675	0.492	822.253	0.434	17	0.127	R.IQNAGTEVVEAK.A
R2/RRR2-12/2	1415.041	1415.578	-1088.797	0.480	954.862	0.377	18	0.124	K.RIQNAGTEVVEAK.A
R2/RRR2-11/2	1221.042	1220.443	-329.656	0.356	1127.149	0.239	16	0.116	K.LFGVTTLDVVR.A
R2/RRR2-12/2	1415.277	1415.578	-212.955	0.456	704.188	0.348	16	0.111	-.RIQNAGTEVVEAK.-
R2/RRR2-13/2	1278.237	1278.526	-226.304	0.319	780.957	0.315	16	0.109	K.GVDVVVIPAGVPR.K
R2/RRR2-12/2	1748.348	1748.146	116.067	0.327	418.106	0.397	18	0.108	K.VAVLGAAGGIGQPLGLLIK.M
R2/RRR2-11/2	1221.146	1220.443	-244.003	0.313	902.884	0.216	15	0.107	K.LFGVTTLDVVR.A
R2/RRR2-13/2	1220.019	1220.443	-348.598	0.301	491.424	0.323	12	0.107	-.LFGVTTLDVVR.-
R2/RRR2-13/2	1747.561	1748.146	-909.439	0.310	863.560	0.269	21	0.106	K.VAVLGAAGGIGQPLGLLIK.M
R2/RRR2-12/3	1348.819	1348.616	151.163	0.482	1179.097	0.318	28	0.085	K.KLFGVTTLDVVR.A
R2/RRR2-12/3	1485.207	1485.648	-298.099	0.415	682.772	0.394	24	0.079	K.AGAGSATLSM*AYAAAR.F
R2/RRR2-12/3	1348.003	1348.616	-1200.041	0.495	885.598	0.337	26	0.066	-.KLFGVTTLDVVR.-
R2/RRR2-12/3	1348.637	1348.616	15.414	0.535	762.303	0.327	24	0.057	-.KLFGVTTLDVVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1972.488	1974.161	-1867.353	0.498	3166.948	0.532	29	0.520	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-8/2	1972.769	1974.161	-1216.106	0.519	2899.472	0.519	28	0.444	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-8/2	1975.858	1974.161	-153.776	0.632	2735.377	0.602	26	0.433	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-1/2	1974.504	1974.161	174.393	0.568	2476.173	0.595	27	0.373	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-8/2	1972.905	1974.161	-1146.764	0.546	2338.678	0.510	26	0.315	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-9/2	1624.793	1623.946	-93.938	0.523	2144.847	0.588	22	0.305	R.LHFFMVGFAPLTSR.G
R2/RRR2-8/2	1624.889	1623.946	-35.009	0.533	1802.759	0.547	20	0.236	R.LHFFMVGFAPLTSR.G
R2/RRR2-8/2	1343.195	1343.427	-172.882	0.550	1833.981	0.504	20	0.230	R.INVYYNEASGGR.Y
R2/RRR2-9/2	1343.314	1343.427	-84.456	0.563	1759.006	0.519	20	0.224	R.INVYYNEASGGR.Y
R2/RRR2-9/2	1343.113	1343.427	-234.516	0.569	1693.664	0.530	20	0.218	R.INVYYNEASGGR.Y
R2/RRR2-8/2	1343.323	1343.427	-77.437	0.538	1701.581	0.492	19	0.209	R.INVYYNEASGGR.Y
R2/RRR2-9/2	1342.579	1343.427	-1380.749	0.468	1645.882	0.514	19	0.207	R.INVYYNEASGGR.Y
R2/RRR2-8/2	1624.467	1623.946	-295.347	0.458	1524.462	0.577	19	0.206	R.LHFFMVGFAPLTSR.G
R2/RRR2-8/2	1232.008	1232.391	-311.749	0.515	1646.728	0.442	17	0.192	R.VSEQFTAM*FR.R
R2/RRR2-9/2	1232.290	1232.391	-82.163	0.571	1657.586	0.435	17	0.190	R.VSEQFTAM*FR.R
R2/RRR2-8/2	1231.859	1232.391	-1247.559	0.446	1626.806	0.420	17	0.185	R.VSEQFTAM*FR.R
R2/RRR2-8/2	1231.831	1232.391	-1269.752	0.521	1502.890	0.438	17	0.176	R.VSEQFTAM*FR.R
R2/RRR2-9/2	1231.877	1232.391	-1232.732	0.472	1323.575	0.439	16	0.159	R.VSEQFTAM*FR.R
R2/RRR2-9/2	1231.936	1232.391	-370.305	0.519	1316.211	0.415	16	0.154	R.VSEQFTAM*FR.R
R2/RRR2-8/2	1140.212	1140.403	-167.794	0.539	1100.492	0.491	17	0.154	K.LAVNLIPFPR.L
R2/RRR2-8/2	1624.740	1623.946	-127.099	0.354	1232.275	0.460	18	0.151	R.LHFFMVGFAPLTSR.G
R2/RRR2-9/2	1140.168	1140.403	-206.244	0.553	1094.624	0.439	17	0.145	K.LAVNLIPFPR.L
R2/RRR2-8/2	1140.167	1140.403	-206.888	0.567	1076.389	0.445	17	0.145	K.LAVNLIPFPR.L
R2/RRR2-9/2	1418.954	1417.719	166.541	0.392	1134.517	0.449	16	0.143	R.M*M*LTFSVFPSPK.V
R2/RRR2-9/2	1139.861	1140.403	-1356.054	0.507	938.422	0.476	17	0.143	K.LAVNLIPFPR.L
R2/RRR2-10/2	1140.198	1140.403	-180.360	0.460	856.146	0.508	16	0.141	K.LAVNLIPFPR.L
R2/RRR2-9/2	1697.106	1697.871	-1043.612	0.434	981.708	0.480	19	0.139	K.NSSYFVEWIPNNVK.S
R2/RRR2-9/2	1139.732	1140.403	-1470.509	0.475	956.308	0.450	16	0.138	K.LAVNLIPFPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1697.533	1697.871	-200.050	0.522	867.827	0.516	18	0.138	K.NSSYFVEWIPNNVK.S
R2/RRR2-9/2	1385.030	1385.720	-1223.597	0.356	1026.720	0.471	15	0.137	R.MMLTFSVFPSPK.V
R2/RRR2-8/2	1140.210	1140.403	-169.083	0.547	1080.948	0.396	17	0.137	K.LAVNLIPFPR.L
R2/RRR2-9/3	1823.720	1824.025	-167.652	0.429	1547.458	0.372	30	0.133	R.EILHIQGGQCGNQIGAK.F
R2/RRR2-9/2	1732.309	1731.994	182.095	0.473	640.215	0.547	20	0.133	R.ALTVPELTQQMWDAK.N
R2/RRR2-8/2	1697.203	1697.871	-985.912	0.421	856.737	0.492	18	0.133	K.NSSYFVEWIPNNVK.S
R2/RRR2-10/2	1140.097	1140.403	-268.544	0.475	916.568	0.414	16	0.132	K.LAVNLIPFPR.L
R2/RRR2-14/2	1139.966	1140.403	-384.356	0.453	780.118	0.458	15	0.131	K.LAVNLIPFPR.L
R2/RRR2-9/2	1418.898	1417.719	126.510	0.427	913.717	0.453	15	0.130	R.M*M*LTFSVFPSPK.V
R2/RRR2-8/2	1697.234	1697.871	-967.859	0.404	838.581	0.449	18	0.127	K.NSSYFVEWIPNNVK.S
R2/RRR2-2/2	1140.301	1140.403	-89.614	0.379	709.688	0.458	14	0.126	K.LAVNLIPFPR.L
R2/RRR2-1/2	1140.304	1140.403	-86.715	0.417	826.417	0.425	14	0.125	-.LAVNLIPFPR.-
R2/RRR2-9/2	1216.088	1216.391	-250.656	0.364	1033.267	0.330	15	0.123	R.VSEQFTAMFR.R
R2/RRR2-9/2	1731.877	1731.994	-67.628	0.396	367.039	0.509	18	0.121	R.ALTVPELTQQMWDAK.N
R2/RRR2-9/2	1385.309	1385.720	-297.194	0.309	765.771	0.464	13	0.120	R.MMLTFSVFPSPK.V
R2/RRR2-8/3	1972.908	1974.161	-1144.907	0.453	1437.573	0.368	30	0.119	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-9/2	1732.542	1731.994	-261.871	0.320	437.606	0.453	21	0.117	R.ALTVPELTQQMWDAK.N
R2/RRR2-8/2	1731.308	1731.994	-977.098	0.352	609.688	0.454	17	0.117	R.ALTVPELTQQMWDAK.N
R2/RRR2-8/2	1343.657	1343.427	171.618	0.429	651.073	0.388	15	0.116	R.INVYYNEASGGR.Y
R2/RRR2-9/2	1733.080	1731.994	49.692	0.312	280.874	0.501	18	0.116	R.ALTVPELTQQMWDAK.N
R2/RRR2-12/2	1140.283	1140.403	-105.292	0.333	605.414	0.386	13	0.116	K.LAVNLIPFPR.L
R2/RRR2-9/2	1216.134	1216.391	-212.389	0.347	821.752	0.346	13	0.116	R.VSEQFTAMFR.R
R2/RRR2-8/2	1216.060	1216.391	-273.516	0.407	644.969	0.323	15	0.116	R.VSEQFTAMFR.R
R2/RRR2-12/2	1140.141	1140.403	-230.089	0.357	644.276	0.347	13	0.115	K.LAVNLIPFPR.L
R2/RRR2-9/3	1975.257	1974.161	48.986	0.475	1217.940	0.432	27	0.114	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-2/2	1343.705	1343.427	207.695	0.297	281.371	0.306	14	0.113	R.INVYYNEASGGR.Y
R2/RRR2-13/2	1141.194	1140.403	-183.635	0.346	691.954	0.317	13	0.113	K.LAVNLIPFPR.L
R2/RRR2-3/2	1140.135	1140.403	-235.459	0.340	571.505	0.340	12	0.112	K.LAVNLIPFPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1343.753	1343.427	243.678	0.253	265.271	0.379	13	0.111	R.INVYYNEASGGR.Y
R2/RRR2-13/2	1141.276	1140.403	-111.637	0.333	601.005	0.336	12	0.111	-.LAVNLIPFPR.-
R2/RRR2-14/2	1698.309	1697.871	258.410	0.395	680.806	0.364	15	0.110	-.NSSYFVEWIPNNVK.-
R2/RRR2-8/2	1696.580	1697.871	-1354.612	0.283	687.668	0.357	16	0.110	K.NSSYFVEWIPNNVK.S
R2/RRR2-10/2	1973.860	1974.161	-152.567	0.305	483.806	0.411	18	0.109	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-1/2	1140.114	1140.403	-253.935	0.249	514.840	0.363	11	0.108	-.LAVNLIPFPR.-
R2/RRR2-4/2	1625.226	1623.946	173.074	0.308	256.995	0.332	11	0.106	R.LHFFMVGFAPLTSR.G
R2/RRR2-2/2	1640.968	1639.945	14.227	0.311	605.078	0.317	14	0.105	R.LHFFM*VGFAPLTSR.G
R2/RRR2-2/2	1732.429	1731.994	251.413	0.311	292.877	0.383	12	0.105	-.ALTVPELTQQMWDAK.-
R2/RRR2-8/2	1417.445	1417.719	-193.997	0.351	471.373	0.277	12	0.104	R.M*M*LTFSVFPSPK.V
R2/RRR2-2/2	1343.907	1343.427	358.624	0.229	150.562	0.358	10	0.100	-.INVYYNEASGGR.-
R2/RRR2-3/2	1697.220	1697.871	-975.730	0.291	668.376	0.128	14	0.097	K.NSSYFVEWIPNNVK.S
R2/RRR2-9/2	1623.637	1623.946	-190.679	0.217	802.703	0.092	15	0.097	R.LHFFMVGFAPLTSR.G
R2/RRR2-8/3	1974.687	1974.161	-240.430	0.434	1084.275	0.391	25	0.096	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-9/3	1973.463	1974.161	-862.607	0.385	775.819	0.356	25	0.078	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-10/3	1973.923	1974.161	-120.935	0.345	959.228	0.275	26	0.074	-.GHYTEGAELIDSVLDVVR.-
R2/RRR2-7/3	1973.975	1974.161	-94.230	0.375	909.786	0.235	24	0.066	K.GHYTEGAELIDSVLDVVR.K
R2/RRR2-8/2	1664.295	1663.805	295.031	0.593	3328.528	0.542	26	0.572	K.ATDSESTEVILDAALK.S
R2/RRR2-8/2	1663.453	1663.805	-212.171	0.584	3317.016	0.527	26	0.562	K.ATDSESTEVILDAALK.S
R2/RRR2-8/2	1662.819	1663.805	-1198.404	0.448	3253.864	0.432	26	0.506	K.ATDSESTEVILDAALK.S
R2/RRR2-8/2	1761.339	1761.914	-896.903	0.565	1611.003	0.505	22	0.203	K.VENQEGVVNFDEILR.E
R2/RRR2-8/2	956.306	956.208	103.115	0.482	1421.662	0.409	15	0.164	K.AALIVVLTR.G
R2/RRR2-8/2	1814.504	1814.097	224.926	0.576	962.116	0.621	26	0.164	R.SAPLPMSPLESLASSAVR.T
R2/RRR2-8/2	1761.271	1761.914	-935.311	0.527	1275.997	0.471	20	0.159	K.VENQEGVVNFDEILR.E
R2/RRR2-8/2	1155.858	1155.369	424.173	0.461	790.511	0.605	19	0.150	R.GLVPLLAEGSAK.A
R2/RRR2-8/2	1813.299	1814.097	-994.564	0.445	868.302	0.576	25	0.146	R.SAPLPMSPLESLASSAVR.T
R2/RRR2-8/2	1155.108	1155.369	-226.471	0.406	772.398	0.612	18	0.145	R.GLVPLLAEGSAK.A
R2/RRR2-8/2	1187.045	1187.285	-203.050	0.480	1151.190	0.388	17	0.138	K.ILAGLENDDAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1813.511	1814.097	-876.907	0.471	739.545	0.543	22	0.134	R.SAPLPMSPLESLASSAVR.T
R2/RRR2-8/2	955.727	956.208	-504.825	0.448	1087.386	0.371	14	0.133	K.AALIVVLTR.G
R2/RRR2-8/2	1830.508	1830.096	225.593	0.498	409.828	0.561	21	0.127	R.SAPLPM*SPLESLASSAVR.T
R2/RRR2-8/2	955.876	956.208	-347.966	0.440	1013.488	0.346	13	0.124	K.AALIVVLTR.G
R2/RRR2-8/2	1829.546	1830.096	-849.655	0.371	437.251	0.543	22	0.122	R.SAPLPM*SPLESLASSAVR.T
R2/RRR2-8/2	1155.014	1155.369	-308.643	0.283	719.370	0.483	18	0.122	R.GLVPLLAEGSAK.A
R2/RRR2-8/2	1205.167	1204.376	-173.824	0.435	872.737	0.365	16	0.121	R.GDLGM*EIPVEK.I
R2/RRR2-8/2	1829.527	1830.096	-860.572	0.381	350.199	0.551	19	0.119	R.SAPLPM*SPLESLASSAVR.T
R2/RRR2-8/2	786.457	786.983	-1945.720	0.338	697.875	0.388	12	0.117	R.IGVASVIK.I
R2/RRR2-8/2	1186.394	1187.285	-1598.329	0.341	952.420	0.302	16	0.115	K.ILAGLENDDAR.V
R2/RRR2-8/2	787.057	786.983	94.254	0.423	666.254	0.325	12	0.115	R.IGVASVIK.I
R2/RRR2-8/2	786.953	786.983	-38.135	0.352	653.099	0.316	12	0.112	R.IGVASVIK.I
R2/RRR2-8/2	1203.478	1204.376	-1581.682	0.324	947.041	0.263	16	0.112	R.GDLGM*EIPVEK.I
R2/RRR2-7/2	1156.423	1155.369	46.838	0.211	732.719	0.342	16	0.107	R.GLVPLLAEGSAK.A
R2/RRR2-8/2	1203.354	1204.376	-1685.015	0.260	760.643	0.251	15	0.105	R.GDLGM*EIPVEK.I
R2/RRR2-8/2	1055.882	1056.175	-277.739	0.219	926.867	0.165	13	0.100	R.ETDAFM*VAR.G
R2/RRR2-9/3	1639.119	1638.812	187.920	0.541	1594.447	0.532	32	0.181	R.FRGEDKPPAHLGASR.D
R2/RRR2-9/3	1638.859	1638.812	28.597	0.549	1415.802	0.558	30	0.166	R.FRGEDKPPAHLGASR.D
R2/RRR2-9/3	1638.652	1638.812	-98.158	0.533	1200.189	0.514	28	0.131	R.FRGEDKPPAHLGASR.D
R2/RRR2-6/2	1690.305	1689.801	-294.128	0.571	2388.658	0.629	24	0.378	K.YSNSQAVVYVGCGER.G
R2/RRR2-6/2	1257.190	1256.434	-194.545	0.507	1067.860	0.506	19	0.153	K.LAADTPLLTGQR.V
R2/RRR2-6/2	1257.343	1256.434	-72.605	0.483	1045.505	0.496	19	0.149	K.LAADTPLLTGQR.V
R2/RRR2-6/2	1256.213	1256.434	-175.886	0.468	849.463	0.462	17	0.132	K.LAADTPLLTGQR.V
R2/RRR2-6/2	1171.144	1171.284	-120.290	0.375	776.866	0.386	14	0.118	K.LYDDLTAGFR.N
R2/RRR2-7/2	1255.771	1256.434	-1327.704	0.320	644.114	0.442	16	0.117	K.LAADTPLLTGQR.V
R2/RRR2-7/3	1789.223	1789.066	88.328	0.511	2730.972	0.488	34	0.408	K.ALLQDIAIVTGAEFQAK.D
R2/RRR2-7/2	1788.650	1789.066	-232.984	0.494	2537.274	0.494	23	0.360	K.ALLQDIAIVTGAEFQAK.D
R2/RRR2-7/2	1637.418	1637.688	-165.147	0.517	2336.377	0.535	26	0.328	K.TNDSAGDGTTTASVLAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1637.366	1637.688	-197.007	0.534	2332.553	0.532	25	0.325	K.TNDSAGDGTTTASVLAR.E
R2/RRR2-7/2	1636.662	1637.688	-1241.421	0.398	2209.303	0.485	25	0.288	K.TNDSAGDGTTTASVLAR.E
R2/RRR2-7/2	1914.649	1915.178	-800.914	0.514	1422.648	0.520	25	0.186	K.DLGLLVESTTVEQLGIAR.K
R2/RRR2-7/3	1788.967	1789.066	-55.178	0.522	1846.631	0.403	31	0.180	K.ALLQDIAIVTGAEFQAK.D
R2/RRR2-7/2	1291.032	1291.347	-244.925	0.523	1422.087	0.432	19	0.167	K.VGAATETELEDR.K
R2/RRR2-7/2	1290.963	1291.347	-298.049	0.510	1265.368	0.482	18	0.163	K.VGAATETELEDR.K
R2/RRR2-7/2	1480.497	1480.646	-101.192	0.483	1216.682	0.504	19	0.162	R.GYISPQFVTNPEK.S
R2/RRR2-7/2	1479.563	1480.646	-1412.127	0.343	1238.761	0.453	19	0.151	R.GYISPQFVTNPEK.S
R2/RRR2-7/2	1473.992	1473.478	-330.897	0.447	1095.861	0.447	20	0.144	R.ELSQTDSAYDSEK.L
R2/RRR2-7/2	1481.261	1480.646	-260.833	0.512	1054.614	0.465	18	0.142	R.GYISPQFVTNPEK.S
R2/RRR2-7/2	1064.523	1065.161	-1543.576	0.383	1348.892	0.307	15	0.139	K.SLVEFENAR.I
R2/RRR2-7/2	898.920	899.113	-214.877	0.485	909.946	0.444	14	0.135	R.GILNVAAIK.A
R2/RRR2-7/2	1474.031	1473.478	-304.474	0.450	856.499	0.485	18	0.134	R.ELSQTDSAYDSEK.L
R2/RRR2-7/2	898.676	899.113	-488.099	0.437	911.178	0.444	14	0.134	R.GILNVAAIK.A
R2/RRR2-7/2	1290.547	1291.347	-1398.658	0.425	1181.926	0.342	18	0.133	K.VGAATETELEDR.K
R2/RRR2-7/2	898.853	899.113	-290.492	0.451	862.123	0.426	14	0.130	R.GILNVAAIK.A
R2/RRR2-7/2	1473.076	1473.478	-274.002	0.368	855.506	0.427	18	0.125	R.ELSQTDSAYDSEK.L
R2/RRR2-7/2	1064.800	1065.161	-340.887	0.302	1097.250	0.272	14	0.118	K.SLVEFENAR.I
R2/RRR2-7/2	857.451	858.018	-1832.098	0.480	1008.393	0.187	13	0.107	R.LGADIIQK.A
R2/RRR2-7/2	1064.241	1065.161	-1810.317	0.317	725.290	0.309	11	0.105	-.SLVEFENAR.-
R2/RRR2-7/2	858.011	858.018	-7.650	0.535	1049.294	0.178	13	0.105	R.LGADIIQK.A
R2/RRR2-7/2	857.812	858.018	-241.017	0.539	1028.780	0.177	13	0.104	R.LGADIIQK.A
R2/RRR2-10/2	1650.286	1650.767	-291.913	0.538	2505.125	0.572	25	0.378	K.SVIGETGSDVTTDQLK.E
R2/RRR2-10/2	1650.254	1650.767	-919.365	0.558	2537.715	0.539	25	0.372	K.SVIGETGSDVTTDQLK.E
R2/RRR2-10/2	1553.537	1553.781	-157.119	0.550	1852.208	0.527	22	0.242	K.YLTEDPLFQLVSK.L
R2/RRR2-10/2	1553.288	1553.781	-318.340	0.512	1809.551	0.485	21	0.225	K.YLTEDPLFQLVSK.L
R2/RRR2-10/2	1553.503	1553.781	-179.348	0.549	1691.480	0.495	21	0.211	K.YLTEDPLFQLVSK.L
R2/RRR2-10/2	1704.278	1704.052	133.149	0.502	1583.022	0.557	21	0.211	K.VQLGNITVDMVLGGMR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1344.827	1345.529	-1269.462	0.340	1332.342	0.452	18	0.159	R.SIGIGSQLIWDR.A
R2/RRR2-10/2	1344.794	1345.529	-1293.893	0.389	1289.051	0.441	18	0.155	R.SIGIGSQLIWDR.A
R2/RRR2-10/2	1928.210	1928.127	43.013	0.496	1084.514	0.462	22	0.145	K.FWEPTYEDCLNLIAR.L
R2/RRR2-10/2	1344.995	1345.529	-1143.680	0.447	1092.245	0.456	17	0.144	R.SIGIGSQLIWDR.A
R2/RRR2-10/2	1928.474	1928.127	180.650	0.511	1133.698	0.371	22	0.133	K.FWEPTYEDCLNLIAR.L
R2/RRR2-10/2	1139.006	1139.328	-283.850	0.382	1006.653	0.415	15	0.132	R.LPAVASYVYR.R
R2/RRR2-10/2	1094.148	1094.332	-169.263	0.441	530.536	0.517	15	0.129	R.ALGLPLERPK.S
R2/RRR2-10/2	1138.564	1139.328	-1554.175	0.377	1012.458	0.353	16	0.126	R.LPAVASYVYR.R
R2/RRR2-10/2	1093.945	1094.332	-355.085	0.388	583.272	0.481	15	0.125	R.ALGLPLERPK.S
R2/RRR2-10/2	1138.872	1139.328	-401.926	0.240	1136.155	0.332	15	0.124	R.LPAVASYVYR.R
R2/RRR2-10/2	1572.869	1571.882	-8.299	0.389	464.941	0.474	17	0.118	K.LYEVVPPILTELGK.V
R2/RRR2-9/2	1095.056	1094.332	-253.426	0.316	538.195	0.441	14	0.116	R.ALGLPLERPK.S
R2/RRR2-10/2	1734.764	1736.051	-1322.431	0.385	902.652	0.356	19	0.116	K.VQLGNITVDM*VLGGM*R.G
R2/RRR2-10/2	1093.860	1094.332	-433.128	0.340	426.389	0.374	13	0.113	R.ALGLPLERPK.S
R2/RRR2-10/2	1571.603	1571.882	-178.373	0.298	469.160	0.408	17	0.111	K.LYEVVPPILTELGK.V
R2/RRR2-10/2	1571.502	1571.882	-242.583	0.322	445.631	0.435	16	0.111	-.LYEVVPPILTELGK.-
R2/RRR2-10/2	1572.427	1571.882	-290.171	0.217	293.375	0.342	12	0.096	-.LYEVVPPILTELGK.-
R2/RRR2-10/2	1138.148	1138.347	-175.091	0.200	115.283	0.616	13	0.078	-.VVPGFGHGVLR.-
R2/RRR2-21/2	1440.273	1441.695	-1686.550	0.427	1784.493	0.406	20	0.199	K.LLPGVEVKDEITK.A
R2/RRR2-21/3	1841.718	1842.027	-168.573	0.541	1758.617	0.489	27	0.193	K.ERLEFLDVDKCECK.S
R2/RRR2-21/2	1556.074	1556.726	-1064.943	0.440	1615.502	0.424	19	0.185	R.LEFLDVDKCECK.S
R2/RRR2-21/2	1440.379	1441.695	-1612.473	0.410	1688.591	0.357	20	0.177	K.LLPGVEVKDEITK.A
R2/RRR2-20/2	1018.087	1018.146	-58.099	0.452	1496.234	0.409	18	0.169	K.STLVEGGGIGK.A
R2/RRR2-21/3	1842.056	1842.027	15.805	0.533	1544.665	0.500	26	0.167	K.ERLEFLDVDKCECK.S
R2/RRR2-21/2	1017.966	1018.146	-177.781	0.473	1327.983	0.467	17	0.164	K.STLVEGGGIGK.A
R2/RRR2-21/2	1440.413	1441.695	-1589.061	0.399	1620.105	0.329	20	0.164	K.LLPGVEVKDEITK.A
R2/RRR2-21/2	1556.245	1556.726	-310.261	0.492	1321.769	0.463	17	0.163	R.LEFLDVDKCECK.S
R2/RRR2-21/2	1556.214	1556.726	-974.527	0.521	1287.896	0.454	18	0.159	R.LEFLDVDKCECK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1017.815	1018.146	-326.369	0.421	1432.174	0.383	18	0.158	K.STLVEGGGIGK.A
R2/RRR2-21/3	1841.736	1842.027	-158.401	0.539	1266.944	0.525	24	0.141	K.ERLEFLDVDKCECK.S
R2/RRR2-20/2	1018.049	1018.146	-95.504	0.418	1144.214	0.407	16	0.140	-.STLVEGGGIGK.-
R2/RRR2-20/2	1440.814	1441.695	-1309.127	0.437	770.627	0.522	20	0.137	K.LLPGVEVKDEITK.A
R2/RRR2-21/2	1017.439	1018.146	-1683.180	0.353	1093.555	0.389	16	0.133	K.STLVEGGGIGK.A
R2/RRR2-21/2	1341.495	1340.576	-60.476	0.473	904.639	0.458	16	0.132	R.AAVMDWHTLAPK.I
R2/RRR2-21/2	1355.665	1356.575	-1413.556	0.453	973.447	0.429	16	0.132	R.AAVM*DWHTLAPK.I
R2/RRR2-21/2	1356.007	1356.575	-1159.930	0.470	1118.309	0.363	17	0.131	R.AAVM*DWHTLAPK.I
R2/RRR2-21/2	1070.373	1071.209	-1720.217	0.289	1197.372	0.333	15	0.130	K.AIETATSHIK.V
R2/RRR2-20/2	1441.044	1441.695	-1148.762	0.397	721.732	0.495	19	0.130	K.LLPGVEVKDEITK.A
R2/RRR2-21/2	1441.293	1441.695	-279.704	0.403	691.568	0.495	19	0.129	K.LLPGVEVKDEITK.A
R2/RRR2-21/2	1441.218	1441.695	-331.880	0.367	777.825	0.474	20	0.129	K.LLPGVEVKDEITK.A
R2/RRR2-21/2	1070.409	1071.209	-1686.646	0.354	1033.443	0.383	14	0.128	K.AIETATSHIK.V
R2/RRR2-21/2	1441.296	1441.695	-277.495	0.363	779.369	0.457	20	0.127	K.LLPGVEVKDEITK.A
R2/RRR2-21/2	1070.437	1071.209	-1660.294	0.329	1116.390	0.338	15	0.127	K.AIETATSHIK.V
R2/RRR2-21/2	1356.879	1356.575	224.462	0.454	1044.923	0.351	17	0.126	R.AAVM*DWHTLAPK.I
R2/RRR2-20/2	1441.315	1441.695	-264.409	0.382	713.387	0.458	19	0.125	K.LLPGVEVKDEITK.A
R2/RRR2-21/2	1094.239	1094.286	-42.699	0.490	779.462	0.397	15	0.124	K.AKESLTGIFK.T
R2/RRR2-21/2	1094.033	1094.286	-231.392	0.457	759.812	0.401	15	0.123	K.AKESLTGIFK.T
R2/RRR2-20/2	1094.077	1094.286	-191.320	0.395	630.468	0.459	13	0.122	K.AKESLTGIFK.T
R2/RRR2-20/2	1094.139	1094.286	-134.575	0.373	590.576	0.491	13	0.121	-.AKESLTGIFK.-
R2/RRR2-21/2	1094.264	1094.286	-20.208	0.449	703.672	0.384	15	0.121	K.AKESLTGIFK.T
R2/RRR2-21/2	1017.881	1018.146	-261.875	0.350	732.647	0.384	15	0.118	K.STLVEGGGIGK.A
R2/RRR2-22/2	1017.813	1018.146	-328.295	0.325	518.439	0.321	13	0.106	-.STLVEGGGIGK.-
R2/RRR2-20/3	1356.680	1356.575	77.518	0.310	700.919	0.519	20	0.094	R.AAVM*DWHTLAPK.I
R2/RRR2-21/3	1356.891	1356.575	233.429	0.324	629.921	0.525	22	0.092	R.AAVM*DWHTLAPK.I
R2/RRR2-21/3	1356.906	1356.575	244.254	0.355	627.024	0.447	20	0.083	-.AAVM*DWHTLAPK.-
R2/RRR2-21/3	1356.952	1356.575	278.623	0.355	479.909	0.457	19	0.082	-.AAVM*DWHTLAPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/3	1356.462	1356.575	-83.587	0.263	413.109	0.451	18	0.080	R.AAVM*DWHTLAPK.I
R2/RRR2-21/3	1705.364	1705.939	-926.073	0.401	781.468	0.348	24	0.078	R.QFNFTSAM*PFSHM*K.E
R2/RRR2-21/3	1705.628	1705.939	-183.039	0.351	705.248	0.325	22	0.074	R.QFNFTSAM*PFSHM*K.E
R2/RRR2-25/2	1017.416	1018.146	-1706.083	0.142	227.097	0.362	12	0.073	-.STLVEGGGIGK.-
R2/RRR2-21/3	1690.959	1689.939	11.602	0.293	968.084	0.231	23	0.068	R.QFNFTSAM*PFSHMK.E
R2/RRR2-21/3	1705.684	1705.939	-149.654	0.298	727.724	0.220	24	0.065	-.QFNFTSAM*PFSHM*K.-
R2/RRR2-5/2	1863.417	1864.066	-887.785	0.595	2668.981	0.547	24	0.408	R.MKEGQSEIYYITGESK.K
R2/RRR2-5/3	1879.716	1880.066	-186.422	0.516	1404.264	0.558	25	0.169	R.M*KEGQSEIYYITGESK.K
R2/RRR2-5/3	1879.687	1880.066	-202.155	0.553	1326.705	0.567	27	0.160	R.M*KEGQSEIYYITGESK.K
R2/RRR2-5/2	1604.235	1604.696	-288.463	0.444	1005.435	0.489	19	0.142	K.EGQSEIYYITGESK.K
R2/RRR2-5/3	1879.687	1880.066	-202.350	0.537	1346.924	0.491	25	0.141	R.M*KEGQSEIYYITGESK.K
R2/RRR2-11/2	1654.159	1652.751	247.617	0.460	3376.756	0.510	27	1.000	K.AAAVVAGNGATNGATNGVH.-
R2/RRR2-11/2	1653.494	1652.751	-155.618	0.588	2954.041	0.572	27	0.738	K.AAAVVAGNGATNGATNGVH.-
R2/RRR2-11/2	1653.737	1652.751	-8.189	0.422	2827.259	0.524	27	0.681	K.AAAVVAGNGATNGATNGVH.-
R2/RRR2-11/2	1653.532	1652.751	-132.809	0.639	2844.554	0.608	28	0.675	K.AAAVVAGNGATNGATNGVH.-
R2/RRR2-11/2	1654.265	1652.751	-294.541	0.664	2827.587	0.582	27	0.663	K.AAAVVAGNGATNGATNGVH.-
R2/RRR2-11/2	1654.250	1652.751	302.669	0.624	2536.125	0.560	27	0.519	K.AAAVVAGNGATNGATNGVH.-
R2/RRR2-11/2	1169.234	1169.442	-178.394	0.525	1809.239	0.510	19	0.231	R.ALVDVLAALKR.A
R2/RRR2-11/2	1169.546	1169.442	88.816	0.470	1772.187	0.475	18	0.216	R.ALVDVLAALKR.A
R2/RRR2-12/2	1169.257	1169.442	-159.333	0.497	1679.632	0.519	18	0.215	R.ALVDVLAALKR.A
R2/RRR2-11/2	1169.254	1169.442	-161.846	0.521	1699.918	0.495	18	0.212	R.ALVDVLAALKR.A
R2/RRR2-15/2	1150.718	1150.310	356.375	0.481	1711.621	0.486	19	0.209	K.SPLTTVYAAAR.A
R2/RRR2-12/2	1150.161	1150.310	-129.936	0.459	1531.488	0.553	18	0.202	K.SPLTTVYAAAR.A
R2/RRR2-13/2	1149.839	1150.310	-410.338	0.442	1508.656	0.552	18	0.199	K.SPLTTVYAAAR.A
R2/RRR2-12/2	1150.408	1150.310	85.717	0.420	1508.659	0.554	18	0.198	K.SPLTTVYAAAR.A
R2/RRR2-11/2	1150.067	1150.310	-211.708	0.514	1526.425	0.536	18	0.198	K.SPLTTVYAAAR.A
R2/RRR2-13/2	1149.869	1150.310	-384.133	0.454	1559.701	0.501	18	0.193	K.SPLTTVYAAAR.A
R2/RRR2-10/2	1150.259	1150.310	-43.919	0.407	1566.245	0.498	18	0.193	K.SPLTTVYAAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1149.699	1150.310	-1405.152	0.392	1556.447	0.487	19	0.189	K.SPLTTVYAAAR.A
R2/RRR2-1/2	1150.196	1150.310	-98.849	0.434	1407.197	0.545	17	0.185	K.SPLTTVYAAAR.A
R2/RRR2-12/2	1012.536	1013.256	-1703.786	0.474	1314.862	0.521	17	0.175	R.ALVDVLAALK.R
R2/RRR2-11/2	1012.666	1013.256	-1574.440	0.453	1254.709	0.513	17	0.168	R.ALVDVLAALK.R
R2/RRR2-11/2	1012.974	1013.256	-279.461	0.535	1261.521	0.489	17	0.165	R.ALVDVLAALK.R
R2/RRR2-12/2	1012.771	1013.256	-479.836	0.486	1177.921	0.525	17	0.165	R.ALVDVLAALK.R
R2/RRR2-15/2	1150.503	1150.310	168.292	0.511	1108.801	0.558	17	0.163	K.SPLTTVYAAAR.A
R2/RRR2-11/2	1013.157	1013.256	-97.536	0.516	1252.599	0.477	17	0.162	R.ALVDVLAALK.R
R2/RRR2-12/2	1013.084	1013.256	-170.540	0.514	1220.449	0.490	17	0.162	R.ALVDVLAALK.R
R2/RRR2-13/2	1013.160	1013.256	-94.636	0.525	1153.840	0.483	17	0.156	R.ALVDVLAALK.R
R2/RRR2-11/2	1150.991	1150.310	-277.384	0.438	1160.702	0.498	17	0.155	K.SPLTTVYAAAR.A
R2/RRR2-9/2	1151.319	1150.310	8.017	0.353	1106.276	0.499	16	0.148	K.SPLTTVYAAAR.A
R2/RRR2-3/2	1150.027	1150.310	-246.210	0.324	939.666	0.474	17	0.134	K.SPLTTVYAAAR.A
R2/RRR2-3/2	1150.222	1150.310	-75.961	0.419	755.671	0.475	14	0.128	K.SPLTTVYAAAR.A
R2/RRR2-11/2	1297.966	1298.396	-332.319	0.356	1032.866	0.364	14	0.125	R.SDEELM*EICR.R
R2/RRR2-5/2	1149.971	1150.310	-295.411	0.366	690.444	0.387	15	0.118	K.SPLTTVYAAAR.A
R2/RRR2-11/2	1046.502	1047.145	-1573.784	0.312	778.363	0.296	16	0.111	R.SVTGLDDAIR.R
R2/RRR2-11/3	1476.380	1476.789	-278.083	0.450	1380.036	0.365	25	0.110	R.QELMEMGFHLIK.S
R2/RRR2-11/2	1046.498	1047.145	-1578.354	0.255	894.655	0.258	16	0.108	R.SVTGLDDAIR.R
R2/RRR2-20/2	1169.927	1169.442	415.409	0.274	290.466	0.314	12	0.103	-.ALVDVLAALKR.-
R2/RRR2-10/2	1149.561	1150.310	-1525.568	0.110	524.465	0.262	14	0.102	K.SPLTTVYAAAR.A
R2/RRR2-12/3	1523.524	1523.718	-127.676	0.375	1114.035	0.391	23	0.098	R.EVVGDRDFFIVAR.T
R2/RRR2-11/3	1523.682	1523.718	-23.160	0.406	1103.537	0.370	23	0.093	R.EVVGDRDFFIVAR.T
R2/RRR2-12/3	1524.622	1523.718	-62.697	0.389	971.148	0.404	22	0.092	R.EVVGDRDFFIVAR.T
R2/RRR2-11/3	1524.261	1523.718	-300.795	0.392	991.258	0.393	22	0.092	R.EVVGDRDFFIVAR.T
R2/RRR2-12/3	1523.782	1523.718	42.407	0.401	997.248	0.390	23	0.091	R.EVVGDRDFFIVAR.T
R2/RRR2-11/3	1523.814	1523.718	63.377	0.357	945.977	0.338	22	0.081	R.EVVGDRDFFIVAR.T
R2/RRR2-11/3	1476.184	1476.789	-1090.944	0.426	1013.818	0.265	24	0.074	R.QELMEMGFHLIK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/3	1492.596	1492.789	-129.242	0.377	957.135	0.255	22	0.071	R.QELM*EMGFHLIK.S
R2/RRR2-11/3	1493.044	1492.789	171.180	0.417	764.470	0.214	22	0.069	R.QELM*EMGFHLIK.S
R2/RRR2-11/3	1477.035	1476.789	166.805	0.393	1241.039	0.145	23	0.064	R.QELMEMGFHLIK.S
R2/RRR2-16/3	1807.200	1807.001	110.383	0.623	3227.042	0.555	39	0.586	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/2	1806.538	1807.001	-256.905	0.548	2764.732	0.639	28	0.460	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/2	1806.422	1807.001	-876.485	0.565	2572.489	0.669	27	0.425	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/3	1806.567	1807.001	-240.914	0.575	2554.429	0.544	35	0.384	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/2	1807.295	1807.001	163.429	0.595	2075.037	0.674	25	0.320	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/3	1808.040	1807.001	21.418	0.565	2238.444	0.495	33	0.285	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/2	1498.220	1498.663	-296.698	0.545	1774.077	0.550	19	0.237	K.AFFEDYKEAHLK.L
R2/RRR2-16/2	1498.406	1498.663	-172.460	0.518	1814.384	0.505	19	0.231	K.AFFEDYKEAHLK.L
R2/RRR2-16/2	1506.197	1506.644	-297.809	0.504	1686.734	0.493	22	0.210	R.LAWHSAGTFDVSSK.T
R2/RRR2-16/2	1507.105	1506.644	306.711	0.531	1510.395	0.521	22	0.196	R.LAWHSAGTFDVSSK.T
R2/RRR2-16/2	1507.131	1506.644	324.253	0.554	1318.515	0.519	21	0.175	R.LAWHSAGTFDVSSK.T
R2/RRR2-16/2	1498.263	1498.663	-268.170	0.494	1256.378	0.461	18	0.158	K.AFFEDYKEAHLK.L
R2/RRR2-15/2	1807.666	1807.001	-185.897	0.487	881.277	0.568	22	0.145	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/2	1556.500	1556.831	-213.221	0.512	766.370	0.531	19	0.137	K.ALLSDPAFRPLVEK.Y
R2/RRR2-15/2	1807.697	1807.001	-168.420	0.463	784.883	0.540	21	0.134	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-16/2	1556.474	1556.831	-229.822	0.532	717.269	0.514	19	0.133	K.ALLSDPAFRPLVEK.Y
R2/RRR2-16/2	1557.491	1556.831	-218.509	0.476	904.145	0.450	20	0.133	K.ALLSDPAFRPLVEK.Y
R2/RRR2-16/2	1008.833	1009.096	-261.857	0.455	997.850	0.388	14	0.131	R.SGFEGPWTK.N
R2/RRR2-16/2	1009.042	1009.096	-53.949	0.465	983.132	0.369	14	0.128	R.SGFEGPWTK.N
R2/RRR2-15/2	1100.060	1100.247	-171.136	0.479	997.713	0.349	16	0.126	K.EGLLQLPSDK.A
R2/RRR2-16/2	1008.895	1009.096	-200.192	0.448	974.058	0.345	14	0.124	R.SGFEGPWTK.N
R2/RRR2-16/2	911.809	912.046	-260.332	0.355	473.383	0.531	12	0.120	-.TGGPFGTM*K.-
R2/RRR2-15/2	1100.018	1100.247	-208.652	0.480	1011.484	0.299	16	0.120	K.EGLLQLPSDK.A
R2/RRR2-15/2	1099.504	1100.247	-1590.680	0.339	857.460	0.367	14	0.119	K.EGLLQLPSDK.A
R2/RRR2-16/2	1100.039	1100.247	-190.172	0.344	1085.703	0.262	16	0.118	K.EGLLQLPSDK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1008.833	1009.096	-261.979	0.413	993.442	0.281	14	0.117	R.SGFEGPWTK.N
R2/RRR2-16/2	896.061	896.046	16.313	0.190	765.719	0.332	13	0.107	K.TGGPFGTMK.T
R2/RRR2-16/2	911.709	912.046	-370.481	0.337	380.221	0.461	11	0.106	-.TGGPFGTM*K.-
R2/RRR2-16/2	911.378	912.046	-1835.483	0.242	415.920	0.316	11	0.103	-.TGGPFGTM*K.-
R2/RRR2-16/2	1009.346	1009.096	247.505	0.211	630.618	0.197	12	0.103	-.SGFEGPWTK.-
R2/RRR2-16/2	1100.078	1100.247	-154.438	0.331	676.272	0.192	12	0.102	K.EGLLQLPSDK.A
R2/RRR2-15/3	1310.433	1310.441	-6.374	0.449	597.732	0.539	23	0.097	R.LPDATKGSDHLR.Q
R2/RRR2-16/3	1506.415	1506.644	-152.696	0.394	645.914	0.472	23	0.088	R.LAWHSAGTFDVSSK.T
R2/RRR2-16/3	1507.144	1506.644	332.487	0.366	926.941	0.394	24	0.087	R.LAWHSAGTFDVSSK.T
R2/RRR2-15/3	1310.072	1310.441	-283.105	0.417	572.342	0.412	22	0.082	R.LPDATKGSDHLR.Q
R2/RRR2-16/3	1310.603	1310.441	123.387	0.380	826.008	0.320	25	0.075	R.LPDATKGSDHLR.Q
R2/RRR2-1/3	1808.514	1807.001	-270.070	0.466	872.156	0.299	29	0.073	K.TPAELSHAANAGLDIAVR.M
R2/RRR2-15/3	1507.293	1506.644	-233.552	0.221	558.814	0.229	20	0.047	-.LAWHSAGTFDVSSK.-
R2/RRR2-3/2	1269.107	1268.527	-332.124	0.426	1405.489	0.471	17	0.171	R.LILGELQAPSVK.Y
R2/RRR2-5/3	1270.138	1270.420	-223.179	0.584	1526.183	0.497	26	0.156	R.RPGSVSLNQSPK.T
R2/RRR2-3/3	1270.052	1270.420	-291.013	0.528	1692.222	0.396	27	0.145	R.RPGSVSLNQSPK.T
R2/RRR2-5/3	1270.489	1270.420	54.428	0.549	1587.466	0.434	26	0.145	R.RPGSVSLNQSPK.T
R2/RRR2-2/3	1270.533	1270.420	88.973	0.563	1591.995	0.416	25	0.141	R.RPGSVSLNQSPK.T
R2/RRR2-3/2	1269.147	1268.527	-300.471	0.382	1106.549	0.434	16	0.139	R.LILGELQAPSVK.Y
R2/RRR2-2/3	1270.305	1270.420	-91.441	0.541	1477.499	0.447	26	0.137	R.RPGSVSLNQSPK.T
R2/RRR2-3/2	1267.563	1268.527	-1554.418	0.369	929.299	0.482	14	0.133	R.LILGELQAPSVK.Y
R2/RRR2-3/3	1270.215	1270.420	-162.439	0.542	1423.776	0.433	25	0.129	R.RPGSVSLNQSPK.T
R2/RRR2-3/3	1270.607	1270.420	147.073	0.543	1401.294	0.434	26	0.126	R.RPGSVSLNQSPK.T
R2/RRR2-5/3	1270.327	1270.420	-73.657	0.513	1322.245	0.440	25	0.122	R.RPGSVSLNQSPK.T
R2/RRR2-5/2	1269.582	1268.527	43.242	0.399	630.760	0.398	16	0.118	R.LILGELQAPSVK.Y
R2/RRR2-2/3	1270.343	1270.420	-60.934	0.525	1329.402	0.395	24	0.112	R.RPGSVSLNQSPK.T
R2/RRR2-5/2	1268.367	1268.527	-127.190	0.275	520.251	0.288	16	0.109	R.LILGELQAPSVK.Y
R2/RRR2-2/2	1268.367	1268.527	-126.804	0.258	499.631	0.360	13	0.106	-.LILGELQAPSVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1268.381	1268.527	-116.088	0.170	470.833	0.325	13	0.102	R.LILGELQAPSVK.Y
R2/RRR2-3/3	1270.971	1270.420	-354.430	0.424	474.125	0.385	20	0.079	-.RPGSVSLNQSPK.-
R2/RRR2-1/3	1270.169	1270.420	-198.593	0.425	633.484	0.312	19	0.071	-.RPGSVSLNQSPK.-
R2/RRR2-12/3	1939.888	1940.190	-156.382	0.538	3770.915	0.564	39	0.813	K.VLIAVADNVGSNQLQEIR.K
R2/RRR2-12/3	1940.099	1940.190	-47.219	0.585	3262.656	0.599	37	0.640	K.VLIAVADNVGSNQLQEIR.K
R2/RRR2-12/2	1743.517	1743.942	-244.071	0.588	2387.900	0.649	32	0.379	K.FAVAAPVAADSGAAAPSAAK.E
R2/RRR2-12/2	1743.316	1743.942	-935.252	0.552	2245.935	0.627	31	0.341	K.FAVAAPVAADSGAAAPSAAK.E
R2/RRR2-14/2	1940.293	1940.190	53.220	0.539	2388.116	0.538	26	0.337	K.VLIAVADNVGSNQLQEIR.K
R2/RRR2-12/2	1939.631	1940.190	-806.253	0.562	2400.235	0.533	26	0.337	K.VLIAVADNVGSNQLQEIR.K
R2/RRR2-12/2	1743.540	1743.942	-231.076	0.520	2230.287	0.620	31	0.336	K.FAVAAPVAADSGAAAPSAAK.E
R2/RRR2-12/2	1939.705	1940.190	-250.882	0.547	2350.473	0.516	26	0.321	K.VLIAVADNVGSNQLQEIR.K
R2/RRR2-12/2	1939.574	1940.190	-835.820	0.536	2102.182	0.522	26	0.278	K.VLIAVADNVGSNQLQEIR.K
R2/RRR2-12/2	1767.874	1768.131	-145.481	0.482	1436.967	0.482	20	0.176	K.INKGTVEIITPVELIK.K
R2/RRR2-12/2	1411.849	1412.697	-1312.484	0.345	1224.432	0.433	18	0.146	K.GTVEIITPVELIK.K
R2/RRR2-12/2	1412.154	1411.619	-329.954	0.481	1082.971	0.459	16	0.145	K.KLCQLLDEYTK.V
R2/RRR2-12/2	1284.395	1283.446	-39.809	0.513	1252.362	0.368	16	0.142	K.LCQLLDEYTK.V
R2/RRR2-12/2	1284.173	1283.446	-213.531	0.528	1223.920	0.365	16	0.140	K.LCQLLDEYTK.V
R2/RRR2-12/2	1411.239	1411.619	-270.392	0.462	944.480	0.481	15	0.138	K.KLCQLLDEYTK.V
R2/RRR2-14/2	1062.171	1062.199	-26.121	0.424	759.194	0.442	17	0.127	K.VGSSESALLAK.L
R2/RRR2-12/2	1061.992	1062.199	-195.601	0.444	790.703	0.416	17	0.126	K.VGSSESALLAK.L
R2/RRR2-12/2	1061.934	1062.199	-250.262	0.415	784.695	0.408	17	0.124	K.VGSSESALLAK.L
R2/RRR2-12/2	1412.294	1412.697	-285.968	0.408	911.378	0.399	16	0.123	K.GTVEIITPVELIK.K
R2/RRR2-12/2	1062.019	1062.199	-169.772	0.396	722.939	0.357	17	0.118	K.VGSSESALLAK.L
R2/RRR2-15/2	1413.649	1412.697	-34.004	0.369	764.012	0.403	15	0.117	K.GTVEIITPVELIK.K
R2/RRR2-12/2	935.317	936.109	-1920.997	0.338	309.140	0.485	11	0.117	R.GDSIVLM*GK.N
R2/RRR2-12/2	1767.884	1768.131	-140.078	0.463	754.199	0.413	17	0.116	K.INKGTVEIITPVELIK.K
R2/RRR2-12/2	1412.228	1412.697	-332.624	0.374	749.271	0.358	15	0.113	K.GTVEIITPVELIK.K
R2/RRR2-12/3	1940.197	1940.190	3.425	0.413	1120.428	0.460	26	0.113	K.VLIAVADNVGSNQLQEIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1062.065	1062.199	-126.650	0.378	721.928	0.274	17	0.111	K.VGSSESALLAK.L
R2/RRR2-13/2	1411.382	1412.697	-1644.908	0.284	803.994	0.346	14	0.111	K.GTVEIITPVELIK.K
R2/RRR2-14/2	1412.131	1412.697	-1112.024	0.356	656.126	0.335	14	0.109	K.GTVEIITPVELIK.K
R2/RRR2-12/2	935.654	936.109	-487.295	0.239	343.681	0.372	11	0.106	-.GDSIVLM*GK.-
R2/RRR2-14/2	1412.340	1412.697	-253.276	0.353	480.409	0.337	12	0.106	K.GTVEIITPVELIK.K
R2/RRR2-12/2	935.724	936.109	-412.545	0.283	316.077	0.407	11	0.104	-.GDSIVLM*GK.-
R2/RRR2-15/2	1413.016	1412.697	226.534	0.223	578.221	0.165	12	0.099	K.GTVEIITPVELIK.K
R2/RRR2-12/3	1768.833	1768.131	-168.978	0.460	970.628	0.297	25	0.074	-.INKGTVEIITPVELIK.-
R2/RRR2-12/3	1767.553	1768.131	-895.490	0.333	1086.901	0.093	27	0.055	K.INKGTVEIITPVELIK.K
R2/RRR2-14/2	1940.680	1940.234	230.491	0.623	4508.818	0.560	30	1.000	R.SSVQAALQQEIALAAGLLR.I
R2/RRR2-14/2	1939.784	1940.234	-232.315	0.574	4064.217	0.524	29	0.808	R.SSVQAALQQEIALAAGLLR.I
R2/RRR2-14/2	1939.490	1940.234	-901.572	0.571	3966.910	0.529	29	0.776	R.SSVQAALQQEIALAAGLLR.I
R2/RRR2-14/3	1940.340	1940.234	55.010	0.456	2152.662	0.430	35	0.247	R.SSVQAALQQEIALAAGLLR.I
R2/RRR2-14/2	1539.191	1539.676	-315.767	0.482	1772.283	0.531	23	0.230	R.DAADLVALSGGHTVGR.T
R2/RRR2-14/2	1859.218	1859.999	-961.059	0.483	1769.046	0.477	22	0.213	R.GGSNSEQGM*GPNLTLQPR.A
R2/RRR2-14/3	1940.155	1940.234	-40.686	0.449	1779.866	0.445	32	0.188	R.SSVQAALQQEIALAAGLLR.I
R2/RRR2-14/2	1277.274	1277.451	-139.531	0.535	1509.617	0.489	18	0.188	R.VQDLIDLFASR.G
R2/RRR2-14/2	1539.216	1539.676	-299.694	0.493	1371.717	0.553	22	0.185	R.DAADLVALSGGHTVGR.T
R2/RRR2-14/2	1539.210	1539.676	-303.513	0.506	1319.538	0.561	22	0.182	R.DAADLVALSGGHTVGR.T
R2/RRR2-14/2	1277.158	1277.451	-230.138	0.579	1414.754	0.481	17	0.175	R.VQDLIDLFASR.G
R2/RRR2-13/2	1276.564	1277.451	-1482.650	0.462	1300.065	0.528	17	0.174	R.VQDLIDLFASR.G
R2/RRR2-14/2	1276.747	1277.451	-1339.264	0.492	1418.800	0.458	16	0.170	R.VQDLIDLFASR.G
R2/RRR2-13/2	1277.206	1277.451	-192.263	0.536	1275.686	0.481	17	0.163	R.VQDLIDLFASR.G
R2/RRR2-14/2	1860.232	1859.999	125.394	0.519	1262.335	0.508	20	0.161	R.GGSNSEQGM*GPNLTLQPR.A
R2/RRR2-14/2	1860.366	1859.999	197.582	0.526	1346.693	0.471	20	0.161	R.GGSNSEQGM*GPNLTLQPR.A
R2/RRR2-14/3	1859.241	1859.999	-948.608	0.431	1469.032	0.493	31	0.157	R.GGSNSEQGM*GPNLTLQPR.A
R2/RRR2-14/3	1865.661	1866.072	-220.749	0.523	1812.069	0.346	31	0.156	R.GLRDAADLVALSGGHTVGR.T
R2/RRR2-14/3	1867.888	1866.072	-98.632	0.501	1701.065	0.383	32	0.153	R.GLRDAADLVALSGGHTVGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1744.555	1744.970	-238.241	0.465	1043.563	0.548	23	0.153	R.DAVVVSGGPSYAVPLGQK.D
R2/RRR2-14/2	1744.408	1744.970	-897.958	0.472	1025.557	0.538	23	0.150	R.DAVVVSGGPSYAVPLGQK.D
R2/RRR2-13/2	1277.234	1277.451	-170.786	0.454	1231.768	0.414	17	0.148	R.VQDLIDLFASR.G
R2/RRR2-13/2	1745.228	1744.970	148.405	0.495	931.639	0.554	22	0.146	R.DAVVVSGGPSYAVPLGQK.D
R2/RRR2-14/3	1859.450	1859.999	-836.005	0.450	1416.476	0.461	31	0.141	R.GGSNSEQGM*GPNLTLQPR.A
R2/RRR2-14/2	1030.903	1031.188	-277.629	0.368	1002.895	0.471	14	0.139	K.AAFFTQFAK.S
R2/RRR2-14/2	1056.653	1057.226	-1492.966	0.417	956.917	0.442	13	0.134	R.ALQLVEDIR.A
R2/RRR2-14/2	1056.985	1057.226	-228.788	0.475	1229.370	0.324	14	0.133	R.ALQLVEDIR.A
R2/RRR2-13/2	1744.405	1744.970	-899.363	0.485	763.216	0.531	20	0.131	R.DAVVVSGGPSYAVPLGQK.D
R2/RRR2-14/3	1859.317	1859.999	-907.677	0.443	1235.718	0.484	30	0.128	R.GGSNSEQGM*GPNLTLQPR.A
R2/RRR2-14/2	1743.978	1744.970	-1145.232	0.366	911.901	0.446	22	0.127	R.DAVVVSGGPSYAVPLGQK.D
R2/RRR2-13/2	1056.952	1057.226	-259.666	0.485	1138.127	0.329	13	0.127	R.ALQLVEDIR.A
R2/RRR2-14/3	1540.732	1539.676	36.974	0.439	1294.989	0.439	31	0.121	R.DAADLVALSGGHTVGR.T
R2/RRR2-13/2	1058.121	1057.226	-98.888	0.512	1056.809	0.292	13	0.118	-.ALQLVEDIR.-
R2/RRR2-14/2	1031.015	1031.188	-168.465	0.311	830.055	0.360	14	0.117	K.AAFFTQFAK.S
R2/RRR2-14/2	1030.407	1031.188	-1733.587	0.277	981.272	0.295	14	0.115	K.AAFFTQFAK.S
R2/RRR2-14/3	1540.680	1539.676	2.883	0.447	850.336	0.480	26	0.099	R.DAADLVALSGGHTVGR.T
R2/RRR2-14/3	1540.889	1539.676	138.637	0.463	962.732	0.436	28	0.097	R.DAADLVALSGGHTVGR.T
R2/RRR2-13/3	1539.604	1539.676	-46.818	0.377	908.506	0.441	28	0.094	R.DAADLVALSGGHTVGR.T
R2/RRR2-13/3	1539.546	1539.676	-84.277	0.301	635.610	0.363	24	0.076	R.DAADLVALSGGHTVGR.T
R2/RRR2-14/3	1867.776	1866.072	-158.716	0.324	1238.623	0.210	29	0.074	R.GLRDAADLVALSGGHTVGR.T
R2/RRR2-7/2	1272.028	1272.473	-351.190	0.464	1865.293	0.427	17	0.216	R.DLITILEDAIR.G
R2/RRR2-7/2	1271.845	1272.473	-1283.874	0.326	1567.986	0.300	17	0.154	R.DLITILEDAIR.G
R2/RRR2-8/2	1272.542	1272.473	54.591	0.350	1180.825	0.397	15	0.138	R.DLITILEDAIR.G
R2/RRR2-9/2	1702.147	1701.940	122.094	0.390	1213.019	0.343	20	0.131	K.AAVEEGIVVGGGCTLLR.L
R2/RRR2-11/2	1272.681	1272.473	163.680	0.438	670.114	0.383	14	0.116	R.DLITILEDAIR.G
R2/RRR2-8/2	1618.221	1617.737	300.556	0.386	575.831	0.417	15	0.112	K.VDAIIETLENDEQK.V
R2/RRR2-8/2	1618.808	1617.737	44.200	0.365	837.386	0.311	17	0.110	K.VDAIIETLENDEQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1272.199	1272.473	-215.829	0.163	427.449	0.303	13	0.102	-.DLITILEDAIR.-
R2/RRR2-15/2	1687.353	1687.833	-285.355	0.448	2935.722	0.532	26	0.460	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-15/3	1773.589	1773.021	-244.565	0.527	3179.570	0.369	37	0.454	R.ARVEAELSNICAGILR.L
R2/RRR2-14/2	1688.351	1687.833	-286.492	0.524	2788.102	0.603	25	0.450	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-14/2	1687.345	1687.833	-290.436	0.460	2961.185	0.481	26	0.445	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-15/2	1687.372	1687.833	-274.178	0.498	2887.464	0.494	26	0.431	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-15/2	1954.247	1955.136	-969.202	0.521	2524.886	0.622	26	0.399	K.DAADATLAAYQAAQDIAM*K.E
R2/RRR2-15/2	1687.275	1687.833	-926.259	0.455	2732.672	0.473	25	0.387	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-15/3	1772.890	1773.021	-74.013	0.495	2906.685	0.361	34	0.380	R.ARVEAELSNICAGILR.L
R2/RRR2-15/2	1771.673	1773.021	-1329.124	0.499	2538.563	0.505	23	0.356	R.ARVEAELSNICAGILR.L
R2/RRR2-15/2	1772.469	1773.021	-878.354	0.587	2471.311	0.548	23	0.355	R.ARVEAELSNICAGILR.L
R2/RRR2-15/2	1954.467	1955.136	-856.584	0.481	2365.312	0.587	25	0.351	K.DAADATLAAYQAAQDIAM*K.E
R2/RRR2-15/2	1772.025	1773.021	-1129.662	0.548	2452.265	0.532	23	0.346	R.ARVEAELSNICAGILR.L
R2/RRR2-14/2	1773.248	1773.021	128.384	0.502	2222.389	0.515	23	0.297	R.ARVEAELSNICAGILR.L
R2/RRR2-14/2	1545.462	1545.757	-191.373	0.537	2320.145	0.450	23	0.295	R.VEAELSNICAGILR.L
R2/RRR2-14/3	1688.546	1687.833	-170.596	0.443	2191.584	0.523	34	0.293	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-15/2	1545.384	1545.757	-241.691	0.520	2142.781	0.455	22	0.265	R.VEAELSNICAGILR.L
R2/RRR2-14/2	1545.394	1545.757	-235.273	0.506	1961.829	0.436	22	0.232	R.VEAELSNICAGILR.L
R2/RRR2-14/3	1774.386	1773.021	206.198	0.524	2234.555	0.362	32	0.225	R.ARVEAELSNICAGILR.L
R2/RRR2-15/2	1688.981	1687.833	87.815	0.434	1497.966	0.587	22	0.203	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-15/2	1545.308	1545.757	-291.064	0.489	1813.559	0.403	21	0.203	R.VEAELSNICAGILR.L
R2/RRR2-15/3	1774.019	1773.021	-1.223	0.502	1953.570	0.381	30	0.187	R.ARVEAELSNICAGILR.L
R2/RRR2-15/2	1375.153	1375.510	-260.214	0.472	1113.172	0.493	18	0.152	R.IVSSIEQKEEGR.G
R2/RRR2-15/2	1375.244	1375.510	-194.405	0.494	959.610	0.508	18	0.145	R.IVSSIEQKEEGR.G
R2/RRR2-14/2	1771.737	1773.021	-1293.142	0.441	1162.243	0.458	19	0.145	R.ARVEAELSNICAGILR.L
R2/RRR2-15/2	1375.248	1375.510	-191.199	0.481	1071.500	0.459	18	0.144	R.IVSSIEQKEEGR.G
R2/RRR2-15/3	1688.490	1687.833	-203.776	0.497	1180.641	0.515	32	0.130	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-15/2	1025.519	1026.212	-1655.054	0.337	271.134	0.579	13	0.120	R.LVPAAAAVDAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1025.924	1026.212	-280.767	0.296	356.006	0.563	16	0.120	R.LVPAAAAVDAK.V
R2/RRR2-14/2	1025.306	1026.212	-1863.657	0.334	326.743	0.452	16	0.119	R.LVPAAAAVDAK.V
R2/RRR2-15/2	1939.217	1939.136	41.632	0.396	436.765	0.448	17	0.110	K.DAADATLAAYQAAQDIAMK.E
R2/RRR2-14/2	1025.448	1026.212	-1725.017	0.304	254.893	0.530	14	0.108	-.LVPAAAAVDAK.-
R2/RRR2-15/2	1026.123	1026.212	-86.102	0.168	192.954	0.366	11	0.105	R.LVPAAAAVDAK.V
R2/RRR2-15/3	1687.759	1687.833	-44.141	0.482	979.686	0.470	27	0.104	K.VVTAAAAGGGGELTVEER.N
R2/RRR2-7/2	1629.480	1629.877	-244.095	0.478	2039.849	0.465	24	0.254	R.SLAIGQCDVALVVGAR.L
R2/RRR2-7/2	1629.083	1629.877	-1104.474	0.400	1265.274	0.461	21	0.156	R.SLAIGQCDVALVVGAR.L
R2/RRR2-7/2	1831.852	1832.197	-188.590	0.529	801.781	0.584	19	0.142	R.KLVDTTGIPFLPTPM*GK.G
R2/RRR2-7/2	959.046	958.094	-49.995	0.450	1038.695	0.392	15	0.134	K.ATTIADIPR.L
R2/RRR2-7/2	1491.927	1492.662	-1166.701	0.320	637.579	0.573	21	0.128	K.GVVPDTHPLSATAAR.S
R2/RRR2-7/2	1492.316	1492.662	-232.729	0.346	588.547	0.575	20	0.127	K.GVVPDTHPLSATAAR.S
R2/RRR2-7/2	1492.373	1492.662	-193.914	0.292	696.611	0.548	22	0.126	K.GVVPDTHPLSATAAR.S
R2/RRR2-7/2	1687.000	1687.988	-1181.785	0.368	722.481	0.460	18	0.119	R.HM*FGVVGIPVTSLASR.A
R2/RRR2-7/3	1121.053	1121.315	-233.745	0.486	1093.631	0.492	23	0.115	R.KPHVGIVGDAK.R
R2/RRR2-7/3	1970.919	1971.246	-166.313	0.447	1456.578	0.336	29	0.114	R.KPAVINVIIDPYAGAESGR.M
R2/RRR2-7/2	1025.528	1026.172	-1607.643	0.318	716.558	0.354	12	0.112	R.AVLVQNEPR.T
R2/RRR2-7/2	957.416	958.094	-1758.460	0.303	858.888	0.290	14	0.112	K.ATTIADIPR.L
R2/RRR2-7/2	1025.666	1026.172	-1472.416	0.298	708.286	0.258	12	0.104	-.AVLVQNEPR.-
R2/RRR2-7/3	1908.479	1908.144	176.313	0.369	793.657	0.402	27	0.080	R.GDFQELDQIAATKPFVK.I
R2/RRR2-6/3	1121.479	1121.315	146.761	0.374	644.569	0.291	18	0.070	R.KPHVGIVGDAK.R
R2/RRR2-7/3	1970.869	1971.246	-192.036	0.366	1014.763	0.186	26	0.062	R.KPAVINVIIDPYAGAESGR.M
R2/RRR2-7/3	1970.755	1971.246	-249.918	0.365	1005.834	0.175	28	0.061	R.KPAVINVIIDPYAGAESGR.M
R2/RRR2-11/2	1818.256	1818.927	-921.957	0.604	3357.582	0.674	28	0.647	R.HETADINTFSWGVANR.G
R2/RRR2-11/1	1101.571	1102.220	-1501.265	0.090	733.445	0.308	13	0.549	R.TLSGPVTDPSK.L
R2/RRR2-11/2	1818.509	1818.927	-230.572	0.635	2942.866	0.721	28	0.546	R.HETADINTFSWGVANR.G
R2/RRR2-11/1	1101.574	1102.220	-1498.482	0.089	715.122	0.336	13	0.540	R.TLSGPVTDPSK.L
R2/RRR2-11/2	1818.502	1818.927	-234.276	0.603	2632.576	0.668	26	0.442	R.HETADINTFSWGVANR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/1	1101.561	1102.220	-1510.393	0.085	565.387	0.231	12	0.360	-.TLSGPVTDPSK.-
R2/RRR2-11/3	1627.790	1627.700	55.756	0.542	2402.094	0.533	33	0.328	R.HKEHISAYGEGNER.R
R2/RRR2-11/2	1811.275	1811.095	99.914	0.579	2329.564	0.519	25	0.319	K.IIAEYIWIGGSGM*DLR.S
R2/RRR2-11/2	1810.533	1811.095	-864.913	0.531	2259.603	0.493	25	0.299	K.IIAEYIWIGGSGM*DLR.S
R2/RRR2-11/3	1627.982	1627.700	174.089	0.547	2261.692	0.528	31	0.297	R.HKEHISAYGEGNER.R
R2/RRR2-11/2	1810.402	1811.095	-937.609	0.571	2141.407	0.545	25	0.294	K.IIAEYIWIGGSGM*DLR.S
R2/RRR2-11/3	1628.637	1627.700	-38.695	0.578	2192.834	0.553	31	0.292	R.HKEHISAYGEGNER.R
R2/RRR2-11/2	1627.259	1627.700	-271.440	0.472	1962.754	0.585	22	0.279	R.HKEHISAYGEGNER.R
R2/RRR2-11/3	1627.331	1627.700	-227.046	0.469	1935.312	0.444	29	0.204	R.HKEHISAYGEGNER.R
R2/RRR2-11/3	1818.752	1818.927	-96.449	0.529	1545.862	0.476	28	0.160	R.HETADINTFSWGVANR.G
R2/RRR2-11/3	1400.613	1399.555	41.427	0.544	1439.454	0.407	27	0.123	K.SM*RNDGGYEIIK.S
R2/RRR2-11/3	1818.794	1818.927	-73.727	0.485	1224.305	0.464	27	0.122	R.HETADINTFSWGVANR.G
R2/RRR2-11/3	1818.490	1818.927	-240.984	0.486	1178.619	0.476	27	0.121	R.HETADINTFSWGVANR.G
R2/RRR2-11/3	1399.579	1399.555	16.832	0.552	1228.436	0.427	25	0.111	K.SM*RNDGGYEIIK.S
R2/RRR2-11/2	1440.362	1440.667	-212.392	0.372	740.384	0.337	16	0.110	-.TLSGPVTDPSKLPK.-
R2/RRR2-11/2	1440.381	1440.667	-199.214	0.377	671.170	0.321	16	0.107	-.TLSGPVTDPSKLPK.-
R2/RRR2-11/2	1440.319	1440.667	-242.406	0.400	693.633	0.316	16	0.107	-.TLSGPVTDPSKLPK.-
R2/RRR2-11/3	1784.275	1783.886	218.436	0.486	680.425	0.522	28	0.098	R.HKEHISAYGEGNERR.L
R2/RRR2-11/3	1399.460	1399.555	-68.074	0.502	1125.717	0.361	24	0.092	K.SM*RNDGGYEIIK.S
R2/RRR2-11/3	1400.659	1399.555	74.599	0.392	1264.261	0.256	23	0.081	K.SM*RNDGGYEIIK.S
R2/RRR2-11/3	1810.932	1811.095	-89.923	0.376	991.712	0.347	26	0.081	K.IIAEYIWIGGSGM*DLR.S
R2/RRR2-11/3	1629.091	1627.700	240.897	0.390	1176.349	0.274	24	0.081	R.HKEHISAYGEGNER.R
R2/RRR2-11/3	1783.845	1783.886	-22.837	0.383	583.186	0.402	25	0.078	R.HKEHISAYGEGNERR.L
R2/RRR2-11/3	1362.424	1362.387	27.434	0.444	1201.085	0.246	24	0.076	K.EHISAYGEGNER.R
R2/RRR2-11/3	1362.233	1362.387	-113.582	0.483	885.326	0.310	23	0.072	-.EHISAYGEGNER.-
R2/RRR2-6/2	1725.440	1725.815	-218.498	0.565	2242.678	0.598	25	0.333	K.YNM*ENGGPAPESVTDK.I
R2/RRR2-6/2	1316.105	1316.355	-190.209	0.484	2052.317	0.539	20	0.281	R.YDYENVDAGAAK.E
R2/RRR2-6/2	1725.342	1725.815	-275.352	0.567	1784.356	0.568	25	0.244	K.YNM*ENGGPAPESVTDK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1489.224	1489.609	-259.274	0.464	1706.805	0.430	19	0.200	R.VYIEQYEKDSSK.T
R2/RRR2-6/3	1743.729	1743.940	-121.277	0.533	1847.904	0.408	31	0.182	K.DNLGGDKLVTVEDIVR.Q
R2/RRR2-6/3	1986.106	1986.216	-55.680	0.546	1675.448	0.473	30	0.178	K.NKDNLGGDKLVTVEDIVR.Q
R2/RRR2-6/3	1986.107	1986.216	-55.033	0.489	1503.281	0.496	31	0.162	K.NKDNLGGDKLVTVEDIVR.Q
R2/RRR2-6/2	1556.860	1555.755	67.664	0.494	1154.989	0.479	21	0.153	R.DSQDALAPLVDVALK.L
R2/RRR2-6/2	1305.549	1306.511	-1507.603	0.395	773.109	0.582	20	0.141	R.SM*PTSAALDVVAK.N
R2/RRR2-6/2	1305.997	1306.511	-1163.119	0.452	769.060	0.524	20	0.137	R.SM*PTSAALDVVAK.N
R2/RRR2-6/2	1305.767	1306.511	-1339.510	0.375	644.622	0.482	19	0.124	R.SM*PTSAALDVVAK.N
R2/RRR2-6/2	1072.015	1072.192	-166.019	0.463	492.382	0.402	12	0.121	R.VYIEQYEK.D
R2/RRR2-6/2	1073.037	1072.192	-145.437	0.506	590.910	0.416	12	0.121	-.VYIEQYEK.-
R2/RRR2-6/3	1986.080	1986.216	-68.720	0.475	1113.068	0.447	28	0.109	K.NKDNLGGDKLVTVEDIVR.Q
R2/RRR2-6/2	1071.288	1072.192	-1783.437	0.303	444.663	0.324	11	0.101	-.VYIEQYEK.-
R2/RRR2-6/3	1761.968	1761.960	4.362	0.436	967.964	0.380	27	0.087	K.KATTPFDGQKPGTSGLR.K
R2/RRR2-6/3	1761.830	1761.960	-74.235	0.451	952.303	0.346	26	0.081	K.KATTPFDGQKPGTSGLR.K
R2/RRR2-6/3	1761.486	1761.960	-269.948	0.435	990.748	0.318	28	0.079	K.KATTPFDGQKPGTSGLR.K
R2/RRR2-2/2	1548.677	1548.726	-31.197	0.459	1567.794	0.459	19	0.187	K.LGLEFGSNAVITNGR.V
R2/RRR2-2/2	1593.523	1593.932	-257.978	0.534	1302.679	0.584	21	0.185	R.IVLNPISSLADLPLK.N
R2/RRR2-2/2	1740.185	1740.935	-1008.419	0.483	1211.671	0.591	21	0.178	K.VYSIAAETGLPVDNYK.A
R2/RRR2-2/2	1593.317	1593.932	-1016.613	0.460	1260.039	0.550	20	0.172	R.IVLNPISSLADLPLK.N
R2/RRR2-2/2	1593.336	1593.932	-1004.998	0.482	1160.633	0.551	20	0.164	R.IVLNPISSLADLPLK.N
R2/RRR2-2/2	1276.028	1275.479	-354.407	0.507	1254.074	0.465	17	0.159	K.VIFVDADQIVR.A
R2/RRR2-2/2	977.031	977.182	-155.216	0.408	1279.427	0.441	15	0.157	R.GLQFILGTK.R
R2/RRR2-2/3	1886.705	1887.038	-177.079	0.531	1239.372	0.565	30	0.149	K.GVALEDPKTEDLSQEVR.G
R2/RRR2-2/2	1123.047	1123.238	-170.249	0.342	1358.680	0.370	15	0.149	R.SADLYELPSK.F
R2/RRR2-2/2	1544.551	1543.794	-157.399	0.467	991.952	0.469	20	0.140	K.VSPGVWYLQLAPGR.S
R2/RRR2-2/2	1274.312	1274.484	-135.724	0.401	1185.309	0.329	14	0.130	K.VLDFLHELCK.F
R2/RRR2-2/2	1275.227	1275.479	-197.650	0.410	1076.201	0.371	15	0.129	K.VIFVDADQIVR.A
R2/RRR2-3/2	1593.549	1593.932	-241.455	0.425	581.961	0.508	17	0.122	R.IVLNPISSLADLPLK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1275.155	1275.479	-254.408	0.373	851.891	0.392	15	0.121	K.VIFVDADQIVR.A
R2/RRR2-2/2	1359.268	1359.423	-114.180	0.359	850.612	0.387	16	0.118	K.WASSFISGDSSSK.K
R2/RRR2-1/2	1275.286	1275.479	-151.270	0.431	972.778	0.290	15	0.115	K.VIFVDADQIVR.A
R2/RRR2-2/2	1358.966	1359.423	-337.372	0.353	800.981	0.352	16	0.113	K.WASSFISGDSSSK.K
R2/RRR2-2/2	1123.051	1123.238	-167.196	0.280	1060.218	0.244	14	0.112	R.SADLYELPSK.F
R2/RRR2-2/3	1887.002	1887.038	-19.382	0.511	787.548	0.546	26	0.108	K.GVALEDPKTEDLSQEVR.G
R2/RRR2-1/2	1544.862	1543.794	44.651	0.318	537.461	0.370	14	0.106	K.VSPGVWYLQLAPGR.S
R2/RRR2-2/3	1886.529	1887.038	-802.411	0.475	964.131	0.481	27	0.105	K.GVALEDPKTEDLSQEVR.G
R2/RRR2-2/2	1359.682	1359.423	191.027	0.311	376.797	0.358	12	0.104	-.WASSFISGDSSSK.-
R2/RRR2-16/2	1340.163	1340.501	-252.482	0.485	1814.904	0.537	22	0.239	R.IIYGGSVTGANCK.E
R2/RRR2-16/2	1375.154	1375.547	-286.746	0.524	1715.700	0.503	19	0.216	K.VIACVGETLEQR.E
R2/RRR2-16/2	1341.104	1340.501	-297.039	0.526	1520.389	0.588	21	0.213	R.IIYGGSVTGANCK.E
R2/RRR2-18/2	1604.031	1604.746	-1072.643	0.393	1659.740	0.521	23	0.212	K.WLAANVSAEVAESTR.I
R2/RRR2-16/2	1376.130	1375.547	-303.625	0.562	1690.736	0.482	19	0.208	K.VIACVGETLEQR.E
R2/RRR2-16/2	1340.105	1340.501	-296.530	0.497	1540.195	0.534	21	0.202	R.IIYGGSVTGANCK.E
R2/RRR2-16/2	1374.447	1375.547	-1532.419	0.373	1730.288	0.401	19	0.193	K.VIACVGETLEQR.E
R2/RRR2-16/2	1394.988	1395.497	-1084.613	0.440	1336.995	0.529	19	0.177	R.SLLGESNEFVGDK.V
R2/RRR2-16/2	1395.076	1395.497	-302.223	0.452	1213.916	0.563	19	0.172	R.SLLGESNEFVGDK.V
R2/RRR2-16/2	1425.016	1424.560	320.685	0.501	1399.076	0.485	19	0.172	R.ESGSTMDVVAAQTK.A
R2/RRR2-16/2	1394.985	1395.497	-1087.074	0.429	1164.859	0.522	19	0.160	R.SLLGESNEFVGDK.V
R2/RRR2-16/2	1424.097	1424.560	-325.983	0.446	1261.485	0.436	19	0.151	R.ESGSTMDVVAAQTK.A
R2/RRR2-16/2	1636.415	1636.748	-204.379	0.451	987.837	0.489	20	0.141	K.VATPDQAQEVHDGLR.K
R2/RRR2-16/2	1440.172	1440.559	-270.030	0.451	1111.335	0.429	19	0.139	R.ESGSTM*DVVAAQTK.A
R2/RRR2-16/2	1440.146	1440.559	-287.548	0.366	1079.259	0.424	18	0.135	R.ESGSTM*DVVAAQTK.A
R2/RRR2-16/2	1424.034	1424.560	-1074.958	0.455	1161.526	0.376	18	0.133	R.ESGSTMDVVAAQTK.A
R2/RRR2-16/2	1439.986	1440.559	-1095.498	0.376	1022.188	0.431	18	0.133	R.ESGSTM*DVVAAQTK.A
R2/RRR2-16/2	1439.695	1440.559	-1299.144	0.427	1071.829	0.403	18	0.132	R.ESGSTM*DVVAAQTK.A
R2/RRR2-16/2	1764.414	1764.921	-856.828	0.442	957.743	0.460	18	0.131	K.VATPDQAQEVHDGLRK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1764.408	1764.921	-860.161	0.453	896.637	0.468	18	0.129	K.VATPDQAQEVHDGLRK.W
R2/RRR2-16/2	1440.079	1440.559	-334.663	0.378	873.908	0.346	17	0.116	R.ESGSTM*DVVAAQTK.A
R2/RRR2-18/2	1604.448	1604.746	-186.245	0.282	913.253	0.351	19	0.115	K.WLAANVSAEVAESTR.I
R2/RRR2-16/2	1439.606	1440.559	-1361.140	0.347	885.942	0.334	17	0.115	R.ESGSTM*DVVAAQTK.A
R2/RRR2-16/2	1764.374	1764.921	-879.330	0.392	619.429	0.361	17	0.108	K.VATPDQAQEVHDGLRK.W
R2/RRR2-30/2	1341.364	1340.501	-102.560	0.313	294.550	0.366	12	0.107	R.IIYGGSVTGANCK.E
R2/RRR2-16/3	1375.874	1375.547	238.602	0.475	1033.527	0.319	26	0.081	K.VIACVGETLEQR.E
R2/RRR2-16/3	1478.875	1478.624	170.364	0.486	1103.493	0.293	25	0.080	K.CNGTTDQVDKIVK.I
R2/RRR2-16/3	1478.721	1478.624	65.931	0.449	899.614	0.308	24	0.077	K.CNGTTDQVDKIVK.I
R2/RRR2-16/3	1376.351	1375.547	-142.618	0.478	732.421	0.342	24	0.075	-.VIACVGETLEQR.-
R2/RRR2-16/3	1479.702	1478.624	52.814	0.334	716.954	0.258	19	0.069	K.CNGTTDQVDKIVK.I
R2/RRR2-16/3	1479.516	1478.624	-73.421	0.300	686.990	0.214	20	0.067	K.CNGTTDQVDKIVK.I
R2/RRR2-16/3	1478.571	1478.624	-35.915	0.380	889.713	0.152	24	0.063	K.CNGTTDQVDKIVK.I
R2/RRR2-23/3	1776.088	1775.858	130.377	0.563	2820.950	0.483	36	0.406	K.FEANRDVDNPDVIDR.L
R2/RRR2-24/3	1775.343	1775.858	-855.767	0.579	2444.794	0.471	32	0.311	K.FEANRDVDNPDVIDR.L
R2/RRR2-24/3	1775.636	1775.858	-125.166	0.574	2511.703	0.387	33	0.284	K.FEANRDVDNPDVIDR.L
R2/RRR2-23/3	1775.512	1775.858	-195.202	0.551	2074.682	0.445	31	0.225	K.FEANRDVDNPDVIDR.L
R2/RRR2-24/3	1775.431	1775.858	-240.829	0.523	1935.841	0.456	31	0.206	K.FEANRDVDNPDVIDR.L
R2/RRR2-24/2	1414.015	1414.542	-1082.574	0.477	1674.946	0.539	18	0.200	K.GIEIIYNYGKED.-
R2/RRR2-24/3	1622.553	1622.763	-129.618	0.441	1818.474	0.499	30	0.199	R.HLFYQDASDLREK.F
R2/RRR2-23/3	1775.992	1775.858	76.198	0.519	1925.289	0.416	30	0.191	K.FEANRDVDNPDVIDR.L
R2/RRR2-23/3	1621.953	1622.763	-1119.566	0.406	1773.496	0.362	25	0.155	R.HLFYQDASDLREK.F
R2/RRR2-24/2	1194.039	1194.276	-198.990	0.535	1147.256	0.460	17	0.152	R.LIDDAEAQYR.N
R2/RRR2-24/3	1622.204	1622.763	-963.838	0.472	1298.588	0.545	27	0.147	R.HLFYQDASDLREK.F
R2/RRR2-23/2	1193.980	1194.276	-249.144	0.504	1139.455	0.427	17	0.146	R.LIDDAEAQYR.N
R2/RRR2-23/3	1622.800	1622.763	22.618	0.432	1482.176	0.455	26	0.144	R.HLFYQDASDLREK.F
R2/RRR2-24/2	1193.361	1194.276	-1609.929	0.393	1116.993	0.415	17	0.140	R.LIDDAEAQYR.N
R2/RRR2-23/3	1622.595	1622.763	-103.582	0.439	1451.049	0.444	27	0.136	R.HLFYQDASDLREK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1623.479	1622.763	-175.510	0.484	1349.857	0.465	27	0.131	R.HLFYQDASDLREK.F
R2/RRR2-23/3	1423.476	1424.632	-1519.470	0.473	1500.313	0.386	25	0.128	R.ALKDTLNWAVHR.H
R2/RRR2-24/2	1157.831	1158.201	-319.736	0.447	900.180	0.400	15	0.127	R.DVDNPDVIDR.L
R2/RRR2-24/2	1157.950	1158.201	-217.351	0.388	899.104	0.379	15	0.123	R.DVDNPDVIDR.L
R2/RRR2-24/2	1193.434	1194.276	-1547.967	0.410	1050.668	0.305	17	0.123	R.LIDDAEAQYR.N
R2/RRR2-23/2	1193.394	1194.276	-1581.979	0.359	858.906	0.342	15	0.118	R.LIDDAEAQYR.N
R2/RRR2-24/2	1194.846	1194.276	-361.169	0.336	263.485	0.370	13	0.114	-.LIDDAEAQYR.-
R2/RRR2-24/2	1157.775	1158.201	-368.715	0.394	682.936	0.353	13	0.112	-.DVDNPDVIDR.-
R2/RRR2-24/2	1365.515	1365.476	28.907	0.372	784.459	0.329	15	0.112	R.HLFYQDASDLR.E
R2/RRR2-24/2	1414.322	1414.542	-155.791	0.362	729.215	0.419	14	0.026	K.GIEIIYNYGKED.-
R2/RRR2-23/2	1413.946	1414.542	-1131.638	0.298	692.842	0.314	14	0.021	K.GIEIIYNYGKED.-
R2/RRR2-23/2	1414.152	1414.542	-276.328	0.416	648.327	0.385	13	0.018	K.GIEIIYNYGKED.-
R2/RRR2-4/2	1570.202	1570.682	-306.411	0.508	1900.427	0.501	23	0.246	K.VFDAILDDQFGDSK.N
R2/RRR2-4/2	1731.142	1731.758	-936.666	0.563	1801.514	0.555	22	0.242	K.FNSGEYESSVAEQQR.A
R2/RRR2-4/2	1387.140	1387.518	-273.412	0.510	1852.829	0.499	22	0.235	K.VVNADEDVGDLLK.V
R2/RRR2-4/2	1386.722	1387.518	-1299.007	0.473	1780.955	0.517	21	0.229	K.VVNADEDVGDLLK.V
R2/RRR2-4/2	1731.077	1731.758	-974.258	0.534	1691.187	0.505	21	0.213	K.FNSGEYESSVAEQQR.A
R2/RRR2-4/2	1386.682	1387.518	-1327.563	0.451	1728.539	0.459	21	0.207	K.VVNADEDVGDLLK.V
R2/RRR2-4/2	1313.178	1313.480	-231.004	0.427	1319.323	0.497	18	0.170	K.VVFLEDYNVSK.A
R2/RRR2-4/2	1314.166	1313.480	-239.682	0.514	1197.263	0.477	17	0.157	K.VVFLEDYNVSK.A
R2/RRR2-4/2	1312.957	1313.480	-1163.942	0.360	1435.839	0.377	17	0.157	K.VVFLEDYNVSK.A
R2/RRR2-4/2	1792.853	1791.940	-48.392	0.451	753.680	0.518	20	0.131	R.AETISAVLYPNDNLDR.G
R2/RRR2-4/2	1099.834	1100.163	-299.415	0.363	387.746	0.492	13	0.118	K.AASGEFDFQK.F
R2/RRR2-4/2	1777.318	1777.996	-946.981	0.391	880.068	0.377	21	0.118	R.TTGVTVSPDALFDVQVK.R
R2/RRR2-4/2	1100.294	1100.163	119.665	0.297	364.695	0.469	13	0.113	K.AASGEFDFQK.F
R2/RRR2-4/2	1289.387	1289.527	-109.217	0.418	936.228	0.284	15	0.110	R.ALDNAM*LNLGLK.D
R2/RRR2-4/3	1824.053	1823.984	38.078	0.409	433.434	0.551	27	0.094	K.LVDEAYRDQEGWITK.T
R2/RRR2-4/3	1823.933	1823.984	-28.074	0.396	255.168	0.544	21	0.090	K.LVDEAYRDQEGWITK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1823.286	1823.984	-933.656	0.309	308.490	0.417	22	0.079	K.LVDEAYRDQEGWITK.T
R2/RRR2-9/2	1994.557	1995.225	-838.807	0.587	2847.354	0.577	27	0.452	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-10/2	1916.972	1916.121	-77.896	0.598	2634.922	0.602	24	0.409	R.LFTSGLAAFYEGYYANK.G
R2/RRR2-10/2	1995.580	1995.225	178.686	0.619	2488.141	0.586	25	0.370	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-10/2	1915.564	1916.121	-815.552	0.543	2493.737	0.557	24	0.362	R.LFTSGLAAFYEGYYANK.G
R2/RRR2-9/2	1915.671	1916.121	-235.495	0.545	2479.085	0.562	24	0.361	R.LFTSGLAAFYEGYYANK.G
R2/RRR2-9/2	1915.472	1916.121	-863.403	0.537	2499.675	0.535	24	0.356	R.LFTSGLAAFYEGYYANK.G
R2/RRR2-10/2	1915.691	1916.121	-225.458	0.566	2444.925	0.552	24	0.349	R.LFTSGLAAFYEGYYANK.G
R2/RRR2-10/2	1807.406	1807.939	-851.147	0.553	2274.502	0.622	26	0.343	K.GTVAVGFDADANGDVTAVK.L
R2/RRR2-10/2	1995.416	1995.225	96.235	0.610	2386.446	0.569	25	0.343	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-9/2	1994.507	1995.225	-863.873	0.569	2427.943	0.533	25	0.339	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-10/2	1807.519	1807.939	-233.058	0.565	2197.823	0.612	25	0.323	K.GTVAVGFDADANGDVTAVK.L
R2/RRR2-9/2	1914.823	1916.121	-1203.928	0.416	2339.797	0.516	23	0.319	R.LFTSGLAAFYEGYYANK.G
R2/RRR2-9/2	1994.750	1995.225	-238.803	0.590	2134.929	0.571	24	0.295	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-10/2	1994.669	1995.225	-782.227	0.576	2020.564	0.581	23	0.278	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-10/2	1620.174	1620.807	-1010.855	0.499	939.444	0.615	21	0.160	R.DIDDADKLVAAM*QAK.K
R2/RRR2-10/3	1995.325	1995.225	50.456	0.454	1546.022	0.463	33	0.157	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-10/2	1621.298	1620.807	303.701	0.559	774.947	0.579	21	0.146	R.DIDDADKLVAAM*QAK.K
R2/RRR2-10/3	1995.304	1995.225	39.964	0.393	1459.297	0.451	32	0.143	K.LTDFGVQGAEANNILYLR.D
R2/RRR2-10/2	1447.212	1447.618	-281.267	0.434	556.636	0.461	18	0.122	K.ESVAPYERPALSK.G
R2/RRR2-10/2	1446.752	1447.618	-1293.938	0.412	588.617	0.463	18	0.122	K.ESVAPYERPALSK.G
R2/RRR2-10/2	1447.248	1447.618	-256.304	0.394	463.493	0.485	17	0.121	K.ESVAPYERPALSK.G
R2/RRR2-10/2	1474.175	1474.597	-287.169	0.370	561.052	0.434	17	0.114	R.LPGFHTCVGSGGER.L
R2/RRR2-9/2	1447.147	1447.618	-326.798	0.358	485.491	0.388	17	0.114	K.ESVAPYERPALSK.G
R2/RRR2-10/2	1808.321	1807.939	211.882	0.353	578.156	0.463	17	0.112	K.GTVAVGFDADANGDVTAVK.L
R2/RRR2-10/3	1620.730	1620.807	-47.594	0.341	1347.084	0.354	26	0.108	R.DIDDADKLVAAM*QAK.K
R2/RRR2-11/2	1809.210	1807.939	150.060	0.367	315.909	0.420	15	0.106	K.GTVAVGFDADANGDVTAVK.L
R2/RRR2-2/2	1915.939	1916.121	-95.576	0.368	612.623	0.278	16	0.102	R.LFTSGLAAFYEGYYANK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1620.854	1620.807	29.005	0.420	1387.465	0.308	26	0.100	R.DIDDADKLVAAM*QAK.K
R2/RRR2-9/3	1620.842	1620.807	21.867	0.305	1710.509	0.123	27	0.090	R.DIDDADKLVAAM*QAK.K
R2/RRR2-10/3	1916.116	1916.121	-2.474	0.386	886.617	0.360	25	0.078	R.LFTSGLAAFYEGYYANK.G
R2/RRR2-15/2	1237.052	1237.387	-271.943	0.516	1676.452	0.572	19	0.227	K.TLASDGLAGLYR.G
R2/RRR2-14/2	1236.542	1237.387	-1496.676	0.448	1598.234	0.580	19	0.217	K.TLASDGLAGLYR.G
R2/RRR2-14/2	1237.187	1237.387	-162.559	0.535	1526.137	0.569	19	0.208	K.TLASDGLAGLYR.G
R2/RRR2-14/2	1237.191	1237.387	-159.391	0.499	1571.847	0.495	18	0.195	K.TLASDGLAGLYR.G
R2/RRR2-15/2	1237.184	1237.387	-165.132	0.440	1634.402	0.449	19	0.192	K.TLASDGLAGLYR.G
R2/RRR2-14/2	1361.219	1361.590	-273.541	0.512	1537.674	0.399	17	0.171	K.LLVQNQEEM*LK.A
R2/RRR2-14/2	1361.017	1361.590	-1159.504	0.522	1522.828	0.401	18	0.171	K.LLVQNQEEM*LK.A
R2/RRR2-14/2	1365.361	1364.552	-140.394	0.382	1249.797	0.387	15	0.141	R.TTAEEGVMALWR.G
R2/RRR2-14/2	1475.263	1475.675	-279.986	0.476	782.432	0.511	19	0.138	R.YFPTQALNFAFR.D
R2/RRR2-14/2	1476.196	1475.675	-325.344	0.492	712.461	0.519	19	0.136	R.YFPTQALNFAFR.D
R2/RRR2-14/2	1360.417	1361.590	-1601.911	0.386	1301.659	0.309	17	0.135	K.LLVQNQEEM*LK.A
R2/RRR2-14/2	1365.868	1364.552	231.396	0.412	1022.630	0.411	16	0.131	R.TTAEEGVMALWR.G
R2/RRR2-14/2	1046.018	1046.115	-92.892	0.357	802.953	0.431	13	0.123	K.YSSSLDAFR.Q
R2/RRR2-14/2	1365.591	1364.552	28.457	0.409	1031.080	0.332	15	0.120	R.TTAEEGVMALWR.G
R2/RRR2-14/2	1474.396	1475.675	-1550.026	0.344	510.405	0.479	17	0.119	R.YFPTQALNFAFR.D
R2/RRR2-15/2	1237.502	1237.387	93.140	0.379	737.458	0.332	17	0.114	K.TLASDGLAGLYR.G
R2/RRR2-14/2	1323.143	1322.537	-299.036	0.298	758.563	0.367	15	0.110	R.GFGPSVAGIVVYR.G
R2/RRR2-14/2	1379.986	1380.552	-1137.944	0.316	822.532	0.267	14	0.107	-.TTAEEGVM*ALWR.-
R2/RRR2-4/2	1433.027	1433.508	-337.024	0.534	2100.702	0.453	20	0.261	R.WSNEVQEAVQSR.A
R2/RRR2-4/2	1246.082	1245.534	-363.906	0.561	1999.427	0.446	19	0.239	R.SIATLAITTLLK.T
R2/RRR2-4/2	1245.245	1245.534	-232.398	0.460	1754.409	0.525	19	0.226	R.SIATLAITTLLK.T
R2/RRR2-4/2	1402.277	1402.619	-244.354	0.504	1997.661	0.374	19	0.221	R.IIDSTLLTQIER.Y
R2/RRR2-4/2	1433.000	1433.508	-1055.415	0.531	1707.364	0.475	20	0.210	R.WSNEVQEAVQSR.A
R2/RRR2-4/2	1402.341	1402.619	-198.855	0.510	1784.168	0.432	18	0.207	R.IIDSTLLTQIER.Y
R2/RRR2-4/2	1401.665	1402.619	-1397.665	0.378	1793.575	0.389	18	0.198	R.IIDSTLLTQIER.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1171.115	1171.408	-251.081	0.531	1622.015	0.417	17	0.185	R.SPLAQCLLIR.Y
R2/RRR2-4/2	1170.506	1171.408	-1630.171	0.496	1555.618	0.405	17	0.175	R.SPLAQCLLIR.Y
R2/RRR2-4/2	1171.239	1171.408	-144.846	0.561	1373.292	0.458	16	0.168	R.SPLAQCLLIR.Y
R2/RRR2-1/2	1245.268	1245.534	-214.401	0.395	1284.685	0.448	18	0.156	R.SIATLAITTLLK.T
R2/RRR2-5/2	1170.826	1171.408	-1355.327	0.448	1254.886	0.427	15	0.151	R.SPLAQCLLIR.Y
R2/RRR2-4/2	1160.803	1161.291	-421.229	0.426	946.355	0.423	18	0.133	R.AITELNGVTSR.E
R2/RRR2-4/2	1160.523	1161.291	-1527.827	0.371	841.599	0.473	17	0.131	R.AITELNGVTSR.E
R2/RRR2-4/2	1526.228	1526.758	-1005.868	0.423	929.896	0.428	19	0.131	K.LLYLLNQGDTFTK.V
R2/RRR2-4/2	1014.975	1015.189	-211.478	0.430	678.505	0.430	15	0.126	R.VILENATVR.A
R2/RRR2-4/2	1015.121	1015.189	-67.074	0.446	695.541	0.399	15	0.124	R.VILENATVR.A
R2/RRR2-4/2	1367.563	1366.587	-17.244	0.404	535.834	0.488	18	0.123	K.LLSSIPEFAGFGK.L
R2/RRR2-4/2	1525.584	1526.758	-1429.239	0.319	913.850	0.394	18	0.122	K.LLYLLNQGDTFTK.V
R2/RRR2-4/2	1014.727	1015.189	-456.710	0.345	723.443	0.377	15	0.119	R.VILENATVR.A
R2/RRR2-4/2	1366.247	1366.587	-249.095	0.382	537.110	0.396	16	0.114	K.LLSSIPEFAGFGK.L
R2/RRR2-7/2	1015.065	1015.189	-121.839	0.267	560.497	0.252	14	0.108	R.VILENATVR.A
R2/RRR2-4/2	1366.255	1366.587	-243.359	0.268	562.795	0.287	18	0.107	K.LLSSIPEFAGFGK.L
R2/RRR2-4/2	1525.935	1526.758	-1198.148	0.250	700.640	0.228	16	0.102	K.LLYLLNQGDTFTK.V
R2/RRR2-4/2	1244.953	1245.534	-1273.349	0.254	838.560	0.163	16	0.101	R.SIATLAITTLLK.T
R2/RRR2-1/2	1367.223	1366.587	-266.738	0.306	308.078	0.330	12	0.101	-.LLSSIPEFAGFGK.-
R2/RRR2-4/3	1198.687	1198.313	312.941	0.358	722.927	0.335	18	0.075	R.VFHDPQLDAR.R
R2/RRR2-4/3	1198.531	1198.313	182.427	0.395	940.858	0.293	20	0.074	R.VFHDPQLDAR.R
R2/RRR2-4/3	1198.390	1198.313	64.905	0.350	676.800	0.209	18	0.064	-.VFHDPQLDAR.-
R2/RRR2-21/2	1993.309	1993.113	99.100	0.645	3402.197	0.688	28	0.661	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-20/2	1992.444	1993.113	-840.065	0.604	2894.681	0.688	27	0.513	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	1992.337	1993.113	-894.066	0.613	2645.445	0.687	26	0.447	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-20/2	1992.507	1993.113	-808.085	0.593	2638.342	0.670	27	0.439	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-22/2	1992.223	1993.113	-951.396	0.627	2326.466	0.675	28	0.370	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	1992.590	1993.113	-766.514	0.609	2297.841	0.666	27	0.360	K.SHSTETKLEATGDASCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/3	1992.533	1993.113	-795.116	0.496	2195.119	0.565	36	0.306	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-22/3	1993.908	1993.113	-103.113	0.530	1953.405	0.604	36	0.271	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-20/3	1992.497	1993.113	-813.012	0.511	1956.153	0.598	36	0.270	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/3	1992.194	1993.113	-965.982	0.484	2066.539	0.502	35	0.253	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-20/3	1993.422	1993.113	155.595	0.534	1678.432	0.590	35	0.216	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/3	1993.873	1993.113	-120.524	0.543	1651.133	0.590	36	0.210	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-20/3	1992.783	1993.113	-165.625	0.511	1752.805	0.531	35	0.207	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-22/2	1221.911	1222.321	-336.936	0.492	1568.736	0.535	20	0.204	K.LEATGDASCVAK.L
R2/RRR2-21/2	1222.113	1222.321	-170.575	0.470	1638.335	0.476	20	0.198	K.LEATGDASCVAK.L
R2/RRR2-21/2	1222.002	1222.321	-261.766	0.477	1610.937	0.488	20	0.198	K.LEATGDASCVAK.L
R2/RRR2-20/2	1221.996	1222.321	-266.877	0.460	1562.273	0.482	20	0.191	K.LEATGDASCVAK.L
R2/RRR2-22/2	1221.424	1222.321	-1557.502	0.417	1527.118	0.501	20	0.190	K.LEATGDASCVAK.L
R2/RRR2-22/3	1993.010	1993.113	-51.525	0.535	1452.976	0.595	34	0.184	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-19/3	1993.254	1993.113	71.025	0.483	1472.251	0.554	33	0.175	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	1222.101	1222.321	-180.795	0.468	1405.495	0.471	19	0.172	K.LEATGDASCVAK.L
R2/RRR2-20/2	1222.009	1222.321	-256.354	0.462	1322.488	0.440	19	0.159	K.LEATGDASCVAK.L
R2/RRR2-20/2	1221.985	1222.321	-275.897	0.473	1267.975	0.451	19	0.157	K.LEATGDASCVAK.L
R2/RRR2-22/2	1221.971	1222.321	-287.423	0.447	1265.598	0.429	19	0.152	K.LEATGDASCVAK.L
R2/RRR2-21/3	1992.515	1993.113	-804.248	0.471	1210.329	0.542	30	0.142	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	1221.972	1222.329	-293.134	0.393	1001.476	0.450	20	0.138	K.LNPSADAGSVYK.T
R2/RRR2-21/2	1161.099	1161.201	-88.325	0.448	1061.324	0.416	17	0.137	K.DGASLSPEQEK.M
R2/RRR2-21/3	1992.774	1993.113	-170.234	0.504	1146.472	0.549	30	0.137	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	1221.975	1222.329	-290.628	0.380	848.329	0.500	19	0.136	K.LNPSADAGSVYK.T
R2/RRR2-22/2	1221.508	1222.329	-1495.350	0.375	914.487	0.465	19	0.134	K.LNPSADAGSVYK.T
R2/RRR2-22/2	1222.034	1222.329	-242.623	0.374	830.398	0.466	19	0.131	K.LNPSADAGSVYK.T
R2/RRR2-21/2	1222.044	1222.329	-234.506	0.333	977.797	0.389	20	0.127	K.LNPSADAGSVYK.T
R2/RRR2-21/3	1993.385	1993.113	137.171	0.481	1117.597	0.521	31	0.127	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	1342.236	1342.560	-241.693	0.393	947.705	0.392	18	0.127	K.IVVCDSATHVLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	996.093	995.151	-58.952	0.466	610.249	0.418	13	0.126	K.LTVEYELK.D
R2/RRR2-18/3	1992.679	1993.113	-218.444	0.462	1103.204	0.498	31	0.121	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	1341.926	1342.560	-1221.478	0.416	875.566	0.362	17	0.120	K.IVVCDSATHVLK.A
R2/RRR2-19/3	1993.212	1993.113	49.834	0.442	1074.332	0.500	31	0.119	K.SHSTETKLEATGDASCVAK.L
R2/RRR2-21/2	995.087	995.151	-65.041	0.323	729.618	0.388	13	0.119	K.LTVEYELK.D
R2/RRR2-20/2	1221.881	1222.329	-368.208	0.353	519.309	0.453	16	0.119	K.LNPSADAGSVYK.T
R2/RRR2-21/2	1167.983	1168.361	-325.029	0.498	779.358	0.362	14	0.118	K.VCLDVHSLPK.V
R2/RRR2-22/2	1221.537	1222.329	-1471.961	0.238	798.027	0.410	19	0.117	K.LNPSADAGSVYK.T
R2/RRR2-20/2	1168.093	1168.361	-230.558	0.491	685.239	0.351	14	0.116	K.VCLDVHSLPK.V
R2/RRR2-22/2	994.965	995.151	-187.613	0.365	539.247	0.336	12	0.116	K.LTVEYELK.D
R2/RRR2-22/2	1160.915	1161.201	-247.381	0.401	871.319	0.294	16	0.114	-.DGASLSPEQEK.-
R2/RRR2-21/2	994.803	995.151	-350.719	0.298	568.185	0.348	12	0.113	K.LTVEYELK.D
R2/RRR2-21/2	1168.166	1168.361	-168.181	0.471	800.048	0.305	14	0.113	K.VCLDVHSLPK.V
R2/RRR2-22/2	1343.799	1342.560	178.069	0.425	545.117	0.395	14	0.113	K.IVVCDSATHVLK.A
R2/RRR2-21/2	1161.027	1161.201	-150.338	0.415	1000.298	0.247	16	0.113	-.DGASLSPEQEK.-
R2/RRR2-20/2	1167.812	1168.361	-1330.727	0.432	924.078	0.272	14	0.112	K.VCLDVHSLPK.V
R2/RRR2-22/2	1168.187	1168.361	-149.417	0.439	700.863	0.292	14	0.112	K.VCLDVHSLPK.V
R2/RRR2-22/2	1167.510	1168.361	-1590.309	0.475	591.442	0.319	13	0.112	K.VCLDVHSLPK.V
R2/RRR2-22/2	994.438	995.151	-1727.960	0.260	456.325	0.329	11	0.110	K.LTVEYELK.D
R2/RRR2-20/2	1168.358	1168.361	-2.893	0.442	651.121	0.258	14	0.109	K.VCLDVHSLPK.V
R2/RRR2-21/2	1168.116	1168.361	-210.428	0.475	700.199	0.283	14	0.109	-.VCLDVHSLPK.-
R2/RRR2-21/2	996.097	995.151	-54.281	0.303	293.213	0.321	9	0.107	-.LTVEYELK.-
R2/RRR2-21/2	1160.248	1161.201	-1688.483	0.337	590.734	0.295	13	0.107	-.DGASLSPEQEK.-
R2/RRR2-22/2	1160.374	1161.201	-1579.091	0.290	773.280	0.156	15	0.103	-.DGASLSPEQEK.-
R2/RRR2-22/2	1160.470	1161.201	-1496.456	0.323	708.240	0.177	14	0.102	-.DGASLSPEQEK.-
R2/RRR2-20/3	1168.093	1168.361	-230.569	0.385	944.224	0.307	22	0.076	K.VCLDVHSLPK.V
R2/RRR2-22/3	1168.628	1168.361	228.741	0.351	701.695	0.231	19	0.071	K.VCLDVHSLPK.V
R2/RRR2-20/3	1168.532	1168.361	146.404	0.329	935.242	0.271	23	0.071	K.VCLDVHSLPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/3	1168.671	1168.361	265.662	0.301	835.195	0.266	21	0.070	K.VCLDVHSLPK.V
R2/RRR2-20/3	1168.567	1168.361	176.104	0.358	706.621	0.183	19	0.065	-.VCLDVHSLPK.-
R2/RRR2-21/3	1168.499	1168.361	118.275	0.338	654.854	0.226	19	0.065	-.VCLDVHSLPK.-
R2/RRR2-21/3	1168.521	1168.361	137.133	0.303	815.955	0.158	21	0.065	K.VCLDVHSLPK.V
R2/RRR2-20/2	952.075	952.090	-14.803	0.465	933.596	0.439	13	0.136	K.TSQIYAIR.Q
R2/RRR2-21/2	951.968	952.090	-128.242	0.466	1038.820	0.389	13	0.134	K.TSQIYAIR.Q
R2/RRR2-21/2	884.670	885.043	-422.752	0.357	1010.329	0.416	12	0.132	-.TLLVADPR.-
R2/RRR2-21/2	951.914	952.090	-185.358	0.370	1001.549	0.372	13	0.128	K.TSQIYAIR.Q
R2/RRR2-21/2	951.952	952.090	-144.965	0.455	917.268	0.382	13	0.128	K.TSQIYAIR.Q
R2/RRR2-21/2	1086.536	1087.297	-1625.102	0.360	677.287	0.530	14	0.128	K.AFEPILLAGR.S
R2/RRR2-21/2	1309.155	1309.490	-256.872	0.418	762.874	0.478	16	0.128	K.TAVAVSYCKPGR.G
R2/RRR2-21/2	885.129	885.043	97.297	0.383	805.131	0.453	11	0.127	R.TLLVADPR.R
R2/RRR2-21/2	884.972	885.043	-80.743	0.358	894.619	0.416	12	0.127	R.TLLVADPR.R
R2/RRR2-21/2	955.912	956.120	-217.628	0.383	841.617	0.401	13	0.125	K.ALVAYYQK.Y
R2/RRR2-21/2	1309.028	1309.490	-354.264	0.385	824.594	0.431	17	0.125	K.TAVAVSYCKPGR.G
R2/RRR2-19/2	952.053	952.090	-38.981	0.365	1008.102	0.310	13	0.122	K.TSQIYAIR.Q
R2/RRR2-19/2	951.870	952.090	-231.672	0.421	821.720	0.308	13	0.118	K.TSQIYAIR.Q
R2/RRR2-21/2	955.619	956.120	-1575.283	0.300	793.469	0.377	13	0.118	K.ALVAYYQK.Y
R2/RRR2-20/2	951.873	952.090	-228.070	0.346	935.223	0.294	13	0.117	K.TSQIYAIR.Q
R2/RRR2-21/2	955.585	956.120	-1610.445	0.344	622.064	0.372	12	0.116	K.ALVAYYQK.Y
R2/RRR2-21/2	1328.237	1328.628	-295.124	0.296	697.866	0.381	16	0.112	R.LKAFEPILLAGR.S
R2/RRR2-22/2	884.898	885.043	-164.874	0.242	724.005	0.376	11	0.112	R.TLLVADPR.R
R2/RRR2-21/2	1309.070	1309.490	-321.892	0.328	677.764	0.351	15	0.111	K.TAVAVSYCKPGR.G
R2/RRR2-22/2	884.935	885.043	-121.976	0.259	440.630	0.356	10	0.109	R.TLLVADPR.R
R2/RRR2-19/2	955.830	956.120	-303.598	0.263	451.836	0.262	11	0.107	-.ALVAYYQK.-
R2/RRR2-20/2	951.481	952.090	-1695.630	0.199	742.159	0.109	13	0.103	K.TSQIYAIR.Q
R2/RRR2-21/2	1327.427	1328.628	-1662.979	0.219	529.886	0.312	13	0.101	R.LKAFEPILLAGR.S
R2/RRR2-21/2	1086.310	1087.297	-1834.628	0.144	325.651	0.387	11	0.098	-.AFEPILLAGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/3	1041.361	1041.229	126.718	0.326	735.644	0.325	18	0.072	R.TLLVADPRR.C
R2/RRR2-21/3	1041.351	1041.229	117.108	0.288	1177.466	0.181	19	0.065	R.TLLVADPRR.C
R2/RRR2-21/3	1041.326	1041.229	93.037	0.286	941.401	0.204	20	0.062	R.TLLVADPRR.C
R2/RRR2-12/2	1685.654	1684.828	-103.258	0.575	2054.870	0.582	21	0.289	R.TESFLTWESLESVR.R
R2/RRR2-12/2	1879.369	1879.302	35.556	0.577	1840.139	0.524	22	0.239	K.NLANPTALMLSAVM*M*LR.H
R2/RRR2-12/2	1423.647	1424.628	-1395.091	0.524	1841.061	0.476	21	0.227	R.IHNAILQTISEGK.F
R2/RRR2-12/2	1424.277	1424.628	-246.683	0.534	1750.391	0.500	21	0.220	R.IHNAILQTISEGK.F
R2/RRR2-12/2	1684.091	1684.828	-1034.446	0.400	1832.007	0.434	20	0.213	R.TESFLTWESLESVR.R
R2/RRR2-12/2	1802.136	1802.018	65.860	0.481	1524.725	0.566	27	0.205	R.ATLFPGDGIGPEIAESVK.Q
R2/RRR2-12/2	1424.150	1424.628	-336.632	0.522	1697.704	0.448	21	0.201	R.IHNAILQTISEGK.F
R2/RRR2-12/2	1802.348	1802.018	183.850	0.519	1351.761	0.607	25	0.194	R.ATLFPGDGIGPEIAESVK.Q
R2/RRR2-12/2	1684.472	1684.828	-212.068	0.492	1593.163	0.461	20	0.189	R.TESFLTWESLESVR.R
R2/RRR2-12/2	1802.303	1802.018	158.515	0.528	1259.148	0.591	25	0.181	R.ATLFPGDGIGPEIAESVK.Q
R2/RRR2-12/2	1242.977	1243.314	-271.829	0.494	1200.681	0.419	17	0.149	R.HLQFNNQADR.I
R2/RRR2-11/2	1686.037	1684.828	124.205	0.488	1057.987	0.466	18	0.141	R.TESFLTWESLESVR.R
R2/RRR2-11/2	1801.500	1802.018	-845.034	0.402	1051.184	0.475	22	0.140	R.ATLFPGDGIGPEIAESVK.Q
R2/RRR2-12/2	1465.378	1465.637	-177.267	0.512	1221.946	0.368	18	0.139	K.TRYDDVNLVTIR.E
R2/RRR2-11/2	1801.857	1802.018	-89.328	0.428	944.779	0.512	22	0.139	R.ATLFPGDGIGPEIAESVK.Q
R2/RRR2-12/2	1242.550	1243.314	-1423.321	0.440	1177.801	0.360	17	0.137	R.HLQFNNQADR.I
R2/RRR2-12/2	1242.746	1243.314	-1265.562	0.408	1016.764	0.427	16	0.136	R.HLQFNNQADR.I
R2/RRR2-12/2	1847.321	1847.921	-868.214	0.456	606.571	0.528	19	0.126	R.ENTEGEYSGLEHQVVR.G
R2/RRR2-12/2	1847.123	1847.921	-976.021	0.399	643.877	0.525	20	0.126	R.ENTEGEYSGLEHQVVR.G
R2/RRR2-11/2	1801.934	1802.018	-46.993	0.410	592.390	0.502	18	0.119	R.ATLFPGDGIGPEIAESVK.Q
R2/RRR2-12/2	1847.317	1847.921	-870.868	0.449	438.407	0.506	17	0.119	R.ENTEGEYSGLEHQVVR.G
R2/RRR2-12/2	888.277	888.067	236.594	0.356	667.837	0.371	13	0.115	K.GPM*ATPIGK.G
R2/RRR2-12/2	887.672	888.067	-446.825	0.331	435.888	0.416	12	0.098	-.GPM*ATPIGK.-
R2/RRR2-10/2	1669.231	1669.773	-926.517	0.550	2313.531	0.554	25	0.412	K.KLESSAHYSADFGKE.-
R2/RRR2-10/2	1722.538	1722.964	-247.967	0.560	2005.679	0.589	22	0.284	K.IVSSAIIDKYIGESAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1260.041	1260.378	-267.662	0.576	1820.606	0.589	18	0.255	K.HGEIDYEAVVK.L
R2/RRR2-10/2	1162.955	1163.265	-267.477	0.528	2087.313	0.372	19	0.237	K.LAEGFNGADLR.N
R2/RRR2-10/2	1259.612	1260.378	-1405.596	0.564	1671.127	0.586	18	0.233	K.HGEIDYEAVVK.L
R2/RRR2-10/2	1259.882	1260.378	-394.419	0.580	1693.748	0.569	17	0.231	K.HGEIDYEAVVK.L
R2/RRR2-10/2	1277.310	1277.451	-111.154	0.458	1646.281	0.546	19	0.218	R.AIASNIDANFLK.I
R2/RRR2-10/2	1276.743	1277.451	-1341.857	0.434	1769.313	0.477	19	0.217	R.AIASNIDANFLK.I
R2/RRR2-10/2	1722.370	1722.964	-927.930	0.503	1515.351	0.571	20	0.205	K.IVSSAIIDKYIGESAR.L
R2/RRR2-10/2	1276.545	1277.451	-1497.731	0.441	1500.180	0.487	18	0.186	R.AIASNIDANFLK.I
R2/RRR2-10/2	1159.173	1159.360	-161.775	0.399	1132.574	0.547	18	0.160	K.GVLLYGPPGTGK.T
R2/RRR2-10/2	1159.095	1159.360	-228.650	0.493	1063.380	0.516	17	0.151	K.GVLLYGPPGTGK.T
R2/RRR2-9/2	1158.466	1159.360	-1639.504	0.444	1091.332	0.507	17	0.151	K.GVLLYGPPGTGK.T
R2/RRR2-9/2	1159.186	1159.360	-150.577	0.471	931.220	0.540	16	0.145	K.GVLLYGPPGTGK.T
R2/RRR2-10/3	1723.950	1722.964	-7.828	0.454	1196.011	0.514	31	0.130	K.IVSSAIIDKYIGESAR.L
R2/RRR2-10/2	1158.610	1159.360	-1514.604	0.366	867.695	0.459	16	0.129	K.GVLLYGPPGTGK.T
R2/RRR2-9/2	1158.593	1159.360	-1529.632	0.377	810.087	0.434	15	0.123	K.GVLLYGPPGTGK.T
R2/RRR2-10/3	1652.631	1652.751	-72.435	0.462	1200.221	0.441	25	0.114	R.RFSEGTSADREIQR.T
R2/RRR2-4/2	1159.321	1159.360	-33.754	0.304	666.344	0.248	13	0.103	K.GVLLYGPPGTGK.T
R2/RRR2-10/3	1652.591	1652.751	-97.219	0.441	1131.202	0.383	23	0.097	R.RFSEGTSADREIQR.T
R2/RRR2-10/3	1722.516	1722.964	-260.702	0.342	955.630	0.456	29	0.097	K.IVSSAIIDKYIGESAR.L
R2/RRR2-10/3	1408.428	1408.628	-142.282	0.465	1220.841	0.346	27	0.093	R.KIEIPLPNEQAR.M
R2/RRR2-10/3	1652.963	1652.751	129.015	0.446	1164.249	0.336	22	0.090	R.RFSEGTSADREIQR.T
R2/RRR2-10/3	1723.370	1722.964	236.350	0.389	811.251	0.422	27	0.087	K.IVSSAIIDKYIGESAR.L
R2/RRR2-10/3	1408.505	1408.628	-87.772	0.369	831.489	0.307	23	0.072	R.KIEIPLPNEQAR.M
R2/RRR2-7/2	1415.366	1414.577	-149.101	0.527	1919.220	0.548	18	0.256	K.SVTDYITDIVCK.R
R2/RRR2-7/2	1415.193	1414.577	-271.972	0.519	1813.135	0.557	18	0.243	K.SVTDYITDIVCK.R
R2/RRR2-7/2	1414.090	1414.577	-345.347	0.498	1737.906	0.535	18	0.226	K.SVTDYITDIVCK.R
R2/RRR2-7/2	1653.111	1652.828	172.006	0.495	1597.374	0.587	21	0.222	K.YVELTADYVYPYR.N
R2/RRR2-7/2	1652.396	1652.828	-262.198	0.398	1594.229	0.415	21	0.181	K.YVELTADYVYPYR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1652.205	1652.828	-985.196	0.310	1529.645	0.436	20	0.175	K.YVELTADYVYPYR.N
R2/RRR2-6/2	1415.912	1414.577	237.572	0.433	1331.708	0.499	16	0.169	K.SVTDYITDIVCK.R
R2/RRR2-7/2	1285.380	1285.349	24.041	0.457	1166.619	0.553	16	0.166	R.GQSHFFGYEGR.C
R2/RRR2-7/2	1285.111	1285.349	-185.555	0.435	1109.145	0.583	16	0.166	R.GQSHFFGYEGR.C
R2/RRR2-7/2	1571.096	1570.763	212.781	0.439	1387.542	0.441	17	0.164	K.SVTDYITDIVCKR.A
R2/RRR2-7/2	1285.016	1285.349	-259.792	0.437	1201.962	0.523	16	0.163	R.GQSHFFGYEGR.C
R2/RRR2-7/2	1243.323	1243.435	-90.066	0.478	1400.910	0.283	16	0.138	K.TIQEQLLLER.D
R2/RRR2-7/2	1351.931	1352.520	-1178.567	0.442	1362.928	0.293	17	0.137	K.FASLRDEWSLK.N
R2/RRR2-7/2	1243.156	1243.435	-225.106	0.420	1381.281	0.260	16	0.134	K.TIQEQLLLER.D
R2/RRR2-7/2	1244.370	1243.435	-52.110	0.458	1252.659	0.250	15	0.124	-.TIQEQLLLER.-
R2/RRR2-7/2	1235.143	1235.368	-182.455	0.405	918.991	0.370	15	0.123	R.DKIETPEQFK.Q
R2/RRR2-7/2	1569.525	1570.763	-1430.024	0.349	942.784	0.357	16	0.119	K.SVTDYITDIVCKR.A
R2/RRR2-7/2	1235.030	1235.368	-274.173	0.413	833.312	0.318	14	0.114	R.DKIETPEQFK.Q
R2/RRR2-7/2	1352.215	1352.520	-226.056	0.442	921.248	0.263	14	0.108	K.FASLRDEWSLK.N
R2/RRR2-7/2	1352.218	1352.520	-223.701	0.433	967.051	0.215	15	0.106	K.FASLRDEWSLK.N
R2/RRR2-7/3	1176.473	1176.309	140.056	0.431	765.464	0.463	21	0.091	K.AEGKYPAHFR.G
R2/RRR2-7/3	1176.259	1176.309	-42.440	0.421	711.094	0.477	21	0.091	K.AEGKYPAHFR.G
R2/RRR2-7/3	1176.226	1176.309	-70.233	0.386	420.932	0.459	17	0.085	K.AEGKYPAHFR.G
R2/RRR2-5/2	1996.642	1997.232	-799.053	0.642	2475.259	0.610	24	0.380	K.KISEEEYISAIKEEISK.V
R2/RRR2-5/2	1996.770	1997.232	-232.001	0.628	2389.890	0.612	24	0.363	K.KISEEEYISAIKEEISK.V
R2/RRR2-5/2	1996.644	1997.232	-798.010	0.635	2355.511	0.607	24	0.354	K.KISEEEYISAIKEEISK.V
R2/RRR2-5/3	1995.983	1997.232	-1130.353	0.556	2157.194	0.505	38	0.260	K.KISEEEYISAIKEEISK.V
R2/RRR2-5/2	1868.453	1869.059	-862.196	0.585	1796.617	0.529	23	0.232	K.ISEEEYISAIKEEISK.V
R2/RRR2-3/3	1998.102	1997.232	-65.610	0.519	1988.980	0.504	36	0.232	K.KISEEEYISAIKEEISK.V
R2/RRR2-2/3	1998.648	1997.232	208.423	0.567	1743.053	0.587	35	0.221	K.KISEEEYISAIKEEISK.V
R2/RRR2-5/2	1868.511	1869.059	-831.109	0.608	1678.234	0.552	22	0.221	K.ISEEEYISAIKEEISK.V
R2/RRR2-5/2	1869.542	1869.059	258.908	0.578	1720.740	0.515	23	0.218	K.ISEEEYISAIKEEISK.V
R2/RRR2-5/3	1996.333	1997.232	-954.350	0.594	1731.365	0.551	35	0.204	K.KISEEEYISAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1997.242	1997.232	4.737	0.507	1726.454	0.487	33	0.185	K.KISEEEYISAIKEEISK.V
R2/RRR2-6/3	1996.623	1997.232	-808.511	0.547	1705.627	0.487	35	0.179	K.KISEEEYISAIKEEISK.V
R2/RRR2-4/3	1997.160	1997.232	-36.276	0.576	1633.492	0.504	34	0.175	K.KISEEEYISAIKEEISK.V
R2/RRR2-3/3	1996.870	1997.232	-182.147	0.545	1459.450	0.563	33	0.173	K.KISEEEYISAIKEEISK.V
R2/RRR2-1/3	1996.802	1997.232	-216.276	0.569	1480.040	0.547	32	0.170	K.KISEEEYISAIKEEISK.V
R2/RRR2-4/3	1996.647	1997.232	-796.452	0.556	1390.552	0.522	33	0.151	K.KISEEEYISAIKEEISK.V
R2/RRR2-1/3	1997.016	1997.232	-108.562	0.562	1225.543	0.572	31	0.149	K.KISEEEYISAIKEEISK.V
R2/RRR2-2/3	1997.177	1997.232	-27.815	0.547	1516.122	0.466	34	0.149	K.KISEEEYISAIKEEISK.V
R2/RRR2-1/3	1996.360	1997.232	-940.722	0.543	1165.350	0.507	30	0.126	K.KISEEEYISAIKEEISK.V
R2/RRR2-5/3	1869.795	1869.059	-142.043	0.440	640.157	0.502	30	0.094	K.ISEEEYISAIKEEISK.V
R2/RRR2-5/3	1868.538	1869.059	-816.886	0.458	689.868	0.480	30	0.093	K.ISEEEYISAIKEEISK.V
R2/RRR2-5/3	1868.799	1869.059	-139.531	0.399	497.265	0.408	26	0.082	K.ISEEEYISAIKEEISK.V
R2/RRR2-3/3	1868.773	1869.059	-153.881	0.402	369.381	0.424	21	0.081	K.ISEEEYISAIKEEISK.V
R2/RRR2-8/2	1241.157	1240.477	-258.811	0.603	2359.096	0.497	18	0.316	R.ALNILADILQR.S
R2/RRR2-8/2	1240.301	1240.477	-142.506	0.493	2242.603	0.405	18	0.268	R.ALNILADILQR.S
R2/RRR2-8/2	1240.117	1240.477	-291.116	0.539	2145.447	0.412	18	0.253	R.ALNILADILQR.S
R2/RRR2-8/2	1188.977	1189.344	-309.301	0.462	1262.170	0.445	18	0.157	R.IDAVDATTVKR.V
R2/RRR2-8/2	1251.054	1251.372	-255.688	0.410	1317.916	0.403	16	0.153	K.YIETHYTAPR.M
R2/RRR2-8/2	1212.556	1212.469	71.832	0.470	1191.110	0.436	16	0.150	R.RIPIPELFAR.I
R2/RRR2-8/2	1188.913	1189.344	-363.692	0.475	1060.477	0.490	17	0.149	R.IDAVDATTVKR.V
R2/RRR2-8/2	1211.574	1212.469	-1568.750	0.447	1089.717	0.428	16	0.141	R.RIPIPELFAR.I
R2/RRR2-8/2	1189.089	1189.344	-215.469	0.461	1088.898	0.431	17	0.141	R.IDAVDATTVKR.V
R2/RRR2-8/2	1057.190	1057.209	-17.906	0.406	960.431	0.458	15	0.138	K.HMGSELVQR.V
R2/RRR2-8/2	1212.380	1212.469	-73.480	0.472	1067.324	0.417	15	0.138	R.RIPIPELFAR.I
R2/RRR2-8/2	1057.083	1057.209	-119.370	0.472	830.146	0.447	15	0.133	K.HMGSELVQR.V
R2/RRR2-8/2	1056.051	1056.282	-219.541	0.417	594.428	0.517	15	0.131	R.IPIPELFAR.I
R2/RRR2-8/2	1056.199	1056.282	-78.898	0.388	577.867	0.498	15	0.127	R.IPIPELFAR.I
R2/RRR2-7/2	1240.268	1240.477	-169.756	0.439	867.947	0.387	14	0.121	R.ALNILADILQR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1056.129	1056.282	-146.026	0.349	560.011	0.443	15	0.121	R.IPIPELFAR.I
R2/RRR2-8/2	1056.680	1057.209	-1451.679	0.385	811.076	0.332	15	0.118	K.HMGSELVQR.V
R2/RRR2-8/2	960.984	961.205	-229.857	0.344	736.997	0.341	14	0.113	-.MVITAAGAVK.-
R2/RRR2-8/2	961.109	961.205	-99.889	0.327	630.950	0.276	14	0.108	R.MVITAAGAVK.H
R2/RRR2-8/2	961.062	961.205	-149.196	0.303	625.412	0.321	13	0.104	-.MVITAAGAVK.-
R2/RRR2-8/3	1212.431	1212.469	-31.024	0.438	1096.356	0.402	22	0.095	R.RIPIPELFAR.I
R2/RRR2-8/3	1998.185	1998.184	0.844	0.489	783.083	0.432	29	0.087	K.SSIQLHLDGSTAVVEDIGR.Q
R2/RRR2-8/3	1212.678	1212.469	173.282	0.392	1074.735	0.350	21	0.085	R.RIPIPELFAR.I
R2/RRR2-8/3	1998.203	1998.184	9.576	0.461	794.664	0.407	28	0.084	K.SSIQLHLDGSTAVVEDIGR.Q
R2/RRR2-8/3	1212.170	1212.469	-246.931	0.413	964.628	0.357	21	0.083	R.RIPIPELFAR.I
R2/RRR2-5/2	1597.294	1596.852	277.972	0.598	2402.187	0.654	24	0.378	R.TGAATNVIFGLALGYK.S
R2/RRR2-5/2	1596.340	1596.852	-949.802	0.507	2426.709	0.619	23	0.371	R.TGAATNVIFGLALGYK.S
R2/RRR2-5/2	1490.286	1490.598	-210.124	0.485	2188.358	0.575	25	0.306	K.TDALDAAGNTTAAIGK.G
R2/RRR2-5/2	1491.233	1490.598	-245.624	0.535	2103.109	0.618	24	0.304	K.TDALDAAGNTTAAIGK.G
R2/RRR2-6/2	1491.161	1490.598	-293.915	0.535	2124.487	0.595	24	0.301	K.TDALDAAGNTTAAIGK.G
R2/RRR2-5/2	1596.498	1596.852	-222.373	0.541	1953.442	0.626	23	0.283	R.TGAATNVIFGLALGYK.S
R2/RRR2-6/2	1596.552	1596.852	-188.316	0.552	1905.829	0.619	23	0.272	R.TGAATNVIFGLALGYK.S
R2/RRR2-6/2	1490.220	1490.598	-254.500	0.472	2080.335	0.521	24	0.270	K.TDALDAAGNTTAAIGK.G
R2/RRR2-2/2	1490.352	1490.598	-165.588	0.456	2092.160	0.512	24	0.270	K.TDALDAAGNTTAAIGK.G
R2/RRR2-6/2	1490.223	1490.598	-252.117	0.464	2075.678	0.510	24	0.267	K.TDALDAAGNTTAAIGK.G
R2/RRR2-1/2	1490.321	1490.598	-186.459	0.486	2015.522	0.499	24	0.254	K.TDALDAAGNTTAAIGK.G
R2/RRR2-1/2	1490.220	1490.598	-254.171	0.450	1970.646	0.516	24	0.252	K.TDALDAAGNTTAAIGK.G
R2/RRR2-6/2	1596.497	1596.852	-222.527	0.564	1634.475	0.620	22	0.231	R.TGAATNVIFGLALGYK.S
R2/RRR2-2/2	1490.175	1490.598	-284.908	0.382	1922.833	0.461	24	0.229	K.TDALDAAGNTTAAIGK.G
R2/RRR2-1/2	1489.531	1490.598	-1391.910	0.378	1870.300	0.493	22	0.229	K.TDALDAAGNTTAAIGK.G
R2/RRR2-1/2	1596.294	1596.852	-978.899	0.472	1775.808	0.518	21	0.224	R.TGAATNVIFGLALGYK.S
R2/RRR2-6/2	1271.183	1270.457	-216.098	0.419	1812.860	0.455	20	0.215	K.AAVIGDTIGDPLK.D
R2/RRR2-2/2	1490.268	1490.598	-221.957	0.391	1951.125	0.383	23	0.214	K.TDALDAAGNTTAAIGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1400.007	1400.563	-1115.008	0.479	1679.880	0.499	22	0.207	K.AADVGADLVGKVER.N
R2/RRR2-3/2	1490.171	1490.598	-287.127	0.418	1702.875	0.468	23	0.201	K.TDALDAAGNTTAAIGK.G
R2/RRR2-1/2	1401.208	1400.563	-253.803	0.510	1528.915	0.548	22	0.201	K.AADVGADLVGKVER.N
R2/RRR2-5/2	1269.981	1270.457	-376.244	0.334	1668.540	0.445	19	0.193	K.AAVIGDTIGDPLK.D
R2/RRR2-5/2	1400.261	1400.563	-216.463	0.463	1498.797	0.502	21	0.186	K.AADVGADLVGKVER.N
R2/RRR2-5/2	1400.247	1400.563	-226.259	0.464	1393.178	0.550	20	0.185	K.AADVGADLVGKVER.N
R2/RRR2-6/2	1400.141	1400.563	-302.004	0.485	1437.309	0.501	21	0.180	K.AADVGADLVGKVER.N
R2/RRR2-5/2	1400.027	1400.563	-1100.474	0.470	1332.954	0.545	20	0.178	K.AADVGADLVGKVER.N
R2/RRR2-2/2	1400.315	1400.563	-177.371	0.470	1461.951	0.468	21	0.175	K.AADVGADLVGKVER.N
R2/RRR2-5/2	1270.176	1270.457	-222.342	0.389	1528.506	0.430	19	0.175	K.AAVIGDTIGDPLK.D
R2/RRR2-6/2	1400.258	1400.563	-218.212	0.498	1361.080	0.506	21	0.174	K.AADVGADLVGKVER.N
R2/RRR2-6/2	1015.472	1016.130	-1637.971	0.433	1300.006	0.490	18	0.166	K.AADVGADLVGK.V
R2/RRR2-6/2	1015.936	1016.130	-192.236	0.469	1276.500	0.489	18	0.165	K.AADVGADLVGK.V
R2/RRR2-2/2	1401.526	1400.563	-26.611	0.465	1345.310	0.469	20	0.164	K.AADVGADLVGKVER.N
R2/RRR2-6/2	1015.677	1016.130	-448.206	0.425	1356.521	0.450	19	0.164	K.AADVGADLVGK.V
R2/RRR2-1/3	1332.540	1332.447	70.132	0.563	1342.779	0.589	27	0.162	K.KYIEAGASEHAR.T
R2/RRR2-2/2	1015.927	1016.130	-200.915	0.430	1279.051	0.448	18	0.157	K.AADVGADLVGK.V
R2/RRR2-1/2	1016.133	1016.130	2.156	0.425	1328.025	0.419	18	0.156	K.AADVGADLVGK.V
R2/RRR2-5/3	1332.596	1332.447	112.301	0.567	1184.883	0.615	25	0.154	K.KYIEAGASEHAR.T
R2/RRR2-2/2	1400.364	1400.563	-142.305	0.453	1138.877	0.510	19	0.154	K.AADVGADLVGKVER.N
R2/RRR2-1/2	1399.355	1400.563	-1582.400	0.419	1203.736	0.460	19	0.150	K.AADVGADLVGKVER.N
R2/RRR2-3/2	1489.434	1490.598	-1457.352	0.365	1392.580	0.378	20	0.150	K.TDALDAAGNTTAAIGK.G
R2/RRR2-3/2	1400.332	1400.563	-165.216	0.415	1166.269	0.446	20	0.146	K.AADVGADLVGKVER.N
R2/RRR2-1/2	1015.862	1016.130	-265.409	0.437	1115.525	0.437	17	0.143	K.AADVGADLVGK.V
R2/RRR2-6/2	1270.379	1270.457	-61.837	0.273	1353.545	0.324	17	0.138	K.AAVIGDTIGDPLK.D
R2/RRR2-2/2	1015.867	1016.130	-259.743	0.391	1119.410	0.397	17	0.137	K.AADVGADLVGK.V
R2/RRR2-4/3	1332.399	1332.447	-36.134	0.531	1209.884	0.536	24	0.136	K.KYIEAGASEHAR.T
R2/RRR2-5/3	1332.751	1332.447	228.454	0.545	1113.965	0.569	24	0.136	K.KYIEAGASEHAR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1015.362	1016.130	-1746.795	0.379	1114.144	0.373	17	0.133	K.AADVGADLVGK.V
R2/RRR2-1/3	1332.670	1332.447	167.832	0.488	1001.953	0.562	24	0.125	K.KYIEAGASEHAR.T
R2/RRR2-6/2	1230.612	1231.381	-1441.605	0.390	1014.568	0.350	15	0.125	K.FTIFNFGEQK.E
R2/RRR2-3/3	1332.569	1332.447	91.906	0.509	1115.264	0.503	25	0.120	K.KYIEAGASEHAR.T
R2/RRR2-5/3	1331.752	1332.447	-1276.788	0.482	956.906	0.543	23	0.118	K.KYIEAGASEHAR.T
R2/RRR2-3/2	1015.251	1016.130	-1856.367	0.341	958.875	0.289	17	0.117	K.AADVGADLVGK.V
R2/RRR2-6/2	1230.781	1231.381	-1303.629	0.375	697.888	0.356	14	0.114	K.FTIFNFGEQK.E
R2/RRR2-2/2	1015.482	1016.130	-1628.551	0.314	945.254	0.267	16	0.113	K.AADVGADLVGK.V
R2/RRR2-3/2	1015.313	1016.130	-1795.598	0.286	836.846	0.301	16	0.113	K.AADVGADLVGK.V
R2/RRR2-3/2	1596.080	1596.852	-1113.350	0.276	815.217	0.331	17	0.110	-.TGAATNVIFGLALGYK.-
R2/RRR2-5/2	1258.131	1258.446	-251.038	0.307	808.491	0.322	15	0.109	K.DTSGPSLNILIK.L
R2/RRR2-6/2	1270.504	1270.457	36.947	0.316	524.695	0.325	13	0.105	-.AAVIGDTIGDPLK.-
R2/RRR2-2/3	1332.336	1332.447	-83.830	0.468	786.836	0.511	21	0.103	K.KYIEAGASEHAR.T
R2/RRR2-5/2	1270.015	1270.457	-349.529	0.242	519.536	0.239	13	0.099	-.AAVIGDTIGDPLK.-
R2/RRR2-8/3	1869.816	1869.112	-158.772	0.503	2006.469	0.484	30	0.236	K.WGAPNKIDFLSLSYTR.H
R2/RRR2-8/3	1869.133	1869.112	10.892	0.474	1778.616	0.467	30	0.191	K.WGAPNKIDFLSLSYTR.H
R2/RRR2-7/2	1321.348	1321.504	-118.569	0.525	1511.135	0.490	19	0.187	K.LGDLSQTQIFAK.I
R2/RRR2-7/2	1321.215	1321.504	-219.591	0.542	1451.142	0.488	19	0.180	K.LGDLSQTQIFAK.I
R2/RRR2-8/2	1321.139	1321.504	-277.155	0.507	1480.283	0.452	19	0.176	K.LGDLSQTQIFAK.I
R2/RRR2-8/2	1322.212	1321.504	-221.277	0.532	1334.101	0.517	19	0.175	K.LGDLSQTQIFAK.I
R2/RRR2-7/2	1321.363	1321.504	-107.356	0.510	1405.902	0.464	19	0.171	K.LGDLSQTQIFAK.I
R2/RRR2-2/2	1322.582	1321.504	59.191	0.501	1199.338	0.533	18	0.166	K.LGDLSQTQIFAK.I
R2/RRR2-8/2	1172.145	1172.274	-110.577	0.400	1444.734	0.381	17	0.160	R.WSFTGAFEAR.Q
R2/RRR2-8/2	1321.113	1321.504	-296.715	0.492	1327.626	0.425	19	0.157	K.LGDLSQTQIFAK.I
R2/RRR2-8/3	1645.516	1645.006	-298.481	0.523	1701.508	0.406	28	0.154	K.YRPTM*PVLSVVIPR.L
R2/RRR2-1/2	1321.242	1321.504	-198.829	0.501	981.851	0.467	17	0.139	K.LGDLSQTQIFAK.I
R2/RRR2-8/2	1214.267	1215.380	-1745.457	0.367	1200.545	0.309	16	0.129	K.IDFLSLSYTR.H
R2/RRR2-8/2	1376.305	1376.623	-231.885	0.343	874.230	0.450	19	0.128	R.GLYPVETISIVGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1376.138	1376.623	-353.448	0.398	694.303	0.460	19	0.125	R.GLYPVETISIVGK.I
R2/RRR2-7/2	1377.339	1376.623	-206.732	0.336	675.722	0.452	19	0.122	R.GLYPVETISIVGK.I
R2/RRR2-7/2	1172.051	1172.274	-190.605	0.307	1009.679	0.291	15	0.116	R.WSFTGAFEAR.Q
R2/RRR2-7/2	1376.206	1376.623	-303.787	0.304	604.596	0.421	18	0.116	R.GLYPVETISIVGK.I
R2/RRR2-8/2	1375.847	1376.623	-1294.502	0.288	744.090	0.352	18	0.113	R.GLYPVETISIVGK.I
R2/RRR2-8/3	1320.443	1320.538	-72.099	0.374	1514.305	0.320	25	0.111	K.CNM*AGKPAVVTR.V
R2/RRR2-7/2	1376.271	1376.623	-256.444	0.275	505.552	0.390	16	0.110	R.GLYPVETISIVGK.I
R2/RRR2-8/2	1171.650	1172.274	-1390.427	0.266	533.784	0.354	13	0.108	R.WSFTGAFEAR.Q
R2/RRR2-7/3	1320.189	1320.538	-264.784	0.385	1376.014	0.330	24	0.103	K.CNM*AGKPAVVTR.V
R2/RRR2-8/3	1305.639	1304.538	77.531	0.479	1128.117	0.393	22	0.098	-.CNMAGKPAVVTR.-
R2/RRR2-8/3	1304.385	1304.538	-118.338	0.366	1323.049	0.303	23	0.094	K.CNMAGKPAVVTR.V
R2/RRR2-8/3	1598.396	1598.697	-188.490	0.365	1043.443	0.383	29	0.091	R.HPAESTNATNESVLK.V
R2/RRR2-8/3	1304.849	1304.538	238.782	0.403	1136.480	0.339	21	0.090	-.CNMAGKPAVVTR.-
R2/RRR2-8/3	1598.871	1598.697	109.411	0.494	902.534	0.406	27	0.090	R.HPAESTNATNESVLK.V
R2/RRR2-8/3	1598.464	1598.697	-146.201	0.455	719.105	0.420	25	0.086	R.HPAESTNATNESVLK.V
R2/RRR2-7/3	1303.779	1304.538	-1353.530	0.388	1427.535	0.223	25	0.084	K.CNMAGKPAVVTR.V
R2/RRR2-8/3	1868.527	1869.112	-851.226	0.351	1020.114	0.341	24	0.083	K.WGAPNKIDFLSLSYTR.H
R2/RRR2-7/3	1598.601	1598.697	-59.910	0.385	437.221	0.416	22	0.082	R.HPAESTNATNESVLK.V
R2/RRR2-8/3	1644.422	1645.006	-966.323	0.426	930.632	0.340	20	0.081	K.YRPTM*PVLSVVIPR.L
R2/RRR2-8/3	1645.178	1645.006	104.822	0.387	1078.033	0.293	22	0.080	K.YRPTM*PVLSVVIPR.L
R2/RRR2-7/3	1599.271	1598.697	-266.974	0.381	651.592	0.328	23	0.075	R.HPAESTNATNESVLK.V
R2/RRR2-8/3	1629.023	1629.007	9.942	0.383	638.447	0.271	21	0.072	K.YRPTMPVLSVVIPR.L
R2/RRR2-7/3	1645.228	1645.006	135.294	0.345	583.736	0.276	22	0.072	-.YRPTM*PVLSVVIPR.-
R2/RRR2-8/3	1304.756	1304.538	167.434	0.305	885.755	0.267	19	0.072	K.CNMAGKPAVVTR.V
R2/RRR2-7/3	1645.138	1645.006	80.153	0.332	539.817	0.289	18	0.067	-.YRPTM*PVLSVVIPR.-
R2/RRR2-7/3	1644.959	1645.006	-28.917	0.225	587.261	0.255	17	0.060	-.YRPTM*PVLSVVIPR.-
R2/RRR2-24/3	1456.389	1456.668	-191.947	0.465	2313.690	0.367	30	1.000	R.SGTLIDAIGIYVHP.-
R2/RRR2-23/2	1537.426	1536.798	-242.624	0.578	2172.806	0.608	24	0.318	K.KLLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1537.296	1536.798	325.059	0.588	2085.821	0.563	23	0.287	K.KLLGVTIYSSDAIR.S
R2/RRR2-24/2	1536.355	1536.798	-289.015	0.539	2061.984	0.572	23	0.286	K.KLLGVTIYSSDAIR.S
R2/RRR2-24/2	1536.301	1536.798	-324.171	0.541	1830.943	0.555	23	0.245	K.KLLGVTIYSSDAIR.S
R2/RRR2-23/2	1536.451	1536.798	-226.522	0.523	1699.420	0.554	22	0.226	K.KLLGVTIYSSDAIR.S
R2/RRR2-24/2	1837.836	1838.014	-96.640	0.525	1671.486	0.582	26	0.221	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.600	1838.014	-225.911	0.533	1656.217	0.575	26	0.217	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1409.238	1408.625	-275.032	0.565	1597.018	0.573	21	0.215	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1837.700	1838.014	-171.267	0.517	1600.183	0.588	26	0.214	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1536.234	1536.798	-1021.154	0.532	1620.916	0.540	21	0.211	K.KLLGVTIYSSDAIR.S
R2/RRR2-24/2	1837.956	1838.014	-31.616	0.524	1566.416	0.588	25	0.209	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1408.237	1408.625	-276.271	0.545	1614.190	0.536	21	0.208	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1966.651	1966.187	236.847	0.466	1696.774	0.493	25	0.206	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/2	1408.143	1408.625	-343.153	0.507	1645.432	0.509	21	0.205	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1838.253	1838.014	130.705	0.569	1567.157	0.572	26	0.205	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-22/2	1409.029	1408.625	288.001	0.514	1655.664	0.501	21	0.205	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1967.363	1966.187	89.952	0.465	1657.649	0.505	25	0.204	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-22/2	1408.182	1408.625	-315.147	0.497	1732.203	0.455	22	0.203	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1408.236	1408.625	-277.315	0.551	1534.582	0.551	21	0.202	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1837.571	1838.014	-241.639	0.502	1556.973	0.558	26	0.202	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1837.698	1838.014	-172.399	0.537	1479.855	0.597	25	0.201	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.510	1838.014	-820.611	0.516	1475.218	0.598	25	0.201	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1837.785	1838.014	-124.823	0.528	1477.423	0.591	25	0.199	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1836.855	1838.014	-1178.844	0.463	1431.359	0.611	26	0.199	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.514	1838.014	-272.764	0.511	1537.933	0.556	25	0.198	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1839.261	1838.014	134.893	0.496	1568.547	0.534	26	0.197	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1455.845	1456.668	-1255.916	0.356	1665.835	0.439	21	0.196	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1838.119	1838.014	57.643	0.563	1450.335	0.582	25	0.194	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.731	1838.014	-154.008	0.560	1526.014	0.540	26	0.193	K.IGPWGGNGGSAQDISVPPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1456.289	1456.668	-260.934	0.426	1651.088	0.482	21	0.192	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1837.414	1838.014	-872.895	0.529	1452.790	0.570	25	0.191	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1838.549	1838.014	-253.698	0.498	1361.635	0.613	25	0.191	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1837.982	1838.014	-17.161	0.500	1463.383	0.562	24	0.190	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1839.383	1838.014	201.581	0.536	1452.179	0.565	25	0.190	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1839.383	1838.014	201.648	0.531	1509.044	0.536	25	0.190	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-3/2	1993.303	1993.210	46.645	0.507	1342.745	0.612	23	0.190	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/2	1837.464	1838.014	-845.952	0.477	1342.223	0.611	25	0.189	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1837.681	1838.014	-181.729	0.538	1350.284	0.601	24	0.187	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.534	1838.014	-261.967	0.553	1419.707	0.563	25	0.186	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-22/2	1456.420	1456.668	-170.539	0.477	1636.536	0.486	21	0.185	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1837.528	1838.014	-264.766	0.494	1376.021	0.573	25	0.184	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1837.520	1838.014	-269.631	0.499	1354.268	0.577	25	0.183	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1839.370	1838.014	194.527	0.520	1440.895	0.536	25	0.183	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-22/2	1456.206	1456.668	-318.459	0.466	1607.464	0.529	21	0.181	R.SGTLIDAIGIYVHP.-
R2/RRR2-23/2	1408.453	1408.625	-122.189	0.506	1455.674	0.495	21	0.181	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1992.428	1993.210	-897.098	0.510	1198.059	0.639	22	0.180	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/2	1839.376	1838.014	197.722	0.535	1403.559	0.532	25	0.178	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.363	1838.014	-901.107	0.478	1342.933	0.554	25	0.177	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1838.366	1838.014	192.103	0.534	1245.672	0.597	24	0.176	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1993.396	1993.210	93.445	0.542	1140.426	0.642	22	0.176	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-23/2	1407.701	1408.625	-1370.973	0.407	1550.418	0.422	21	0.175	K.LLGVTIYSSDAIR.S
R2/RRR2-23/2	1837.498	1838.014	-827.279	0.482	1314.532	0.562	24	0.175	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1838.358	1838.014	187.841	0.527	1256.399	0.593	23	0.175	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.707	1838.014	-167.268	0.553	1290.966	0.572	24	0.175	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1836.773	1838.014	-1223.224	0.470	1177.594	0.618	24	0.173	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-22/2	1408.268	1408.625	-253.834	0.515	1364.795	0.500	20	0.173	K.LLGVTIYSSDAIR.S
R2/RRR2-23/2	1838.485	1838.014	256.955	0.485	1359.943	0.522	24	0.171	K.IGPWGGNGGSAQDISVPPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1457.397	1456.668	-186.638	0.524	1542.120	0.659	21	0.171	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1837.580	1838.014	-236.908	0.518	1220.749	0.583	24	0.171	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1838.319	1838.014	166.798	0.490	1226.674	0.572	23	0.168	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.652	1838.014	-197.455	0.537	1217.875	0.571	24	0.168	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-19/2	1455.571	1456.668	-1445.245	0.339	1547.534	0.421	20	0.166	R.SGTLIDAIGIYVHP.-
R2/RRR2-23/2	1992.295	1993.210	-964.144	0.483	1047.573	0.631	23	0.166	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/2	1736.359	1735.876	278.485	0.523	1265.556	0.519	25	0.166	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1837.488	1838.014	-832.748	0.477	1241.325	0.548	23	0.165	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1837.545	1838.014	-255.835	0.505	1173.144	0.556	24	0.162	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/3	1838.125	1838.014	61.066	0.362	1579.232	0.455	32	0.162	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-15/2	1992.707	1993.210	-756.761	0.509	998.712	0.614	23	0.160	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/2	1456.956	1456.668	198.525	0.469	1517.436	0.544	21	0.159	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1966.274	1966.187	44.422	0.491	1219.164	0.520	22	0.158	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/2	1736.356	1735.876	276.793	0.508	1139.921	0.532	24	0.158	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1992.486	1993.210	-868.191	0.505	893.388	0.654	21	0.157	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-23/2	1992.418	1993.210	-902.572	0.484	963.455	0.617	22	0.157	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-22/2	1992.630	1993.210	-795.562	0.538	921.312	0.615	23	0.155	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-23/2	1736.304	1735.876	247.255	0.532	958.517	0.599	22	0.155	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/2	1993.448	1993.210	119.608	0.512	951.015	0.609	22	0.155	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/2	1456.226	1456.668	-304.161	0.412	1509.868	0.439	20	0.154	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1838.456	1838.014	241.375	0.497	1122.605	0.541	23	0.154	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-22/2	1993.013	1993.210	-99.497	0.500	870.311	0.635	22	0.154	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-17/2	1408.404	1408.625	-157.141	0.518	1289.703	0.431	20	0.153	K.LLGVTIYSSDAIR.S
R2/RRR2-21/2	1408.228	1408.625	-282.794	0.422	1115.377	0.524	17	0.153	K.LLGVTIYSSDAIR.S
R2/RRR2-24/2	1992.488	1993.210	-867.084	0.483	907.497	0.624	21	0.153	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/2	1736.333	1735.876	263.540	0.485	1042.179	0.549	23	0.153	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/2	1735.373	1735.876	-869.191	0.490	1031.261	0.552	23	0.153	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-22/2	1735.402	1735.876	-274.491	0.445	1017.572	0.560	23	0.152	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/2	1456.244	1456.668	-292.219	0.443	1498.865	0.470	20	0.152	R.SGTLIDAIGIYVHP.-
R2/RRR2-23/2	1837.587	1838.014	-232.909	0.520	1123.758	0.529	23	0.152	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/2	1737.248	1735.876	214.490	0.473	1114.059	0.511	24	0.152	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1736.400	1735.876	-275.462	0.505	1064.099	0.532	23	0.152	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1737.292	1735.876	239.644	0.478	1048.917	0.530	23	0.150	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-20/2	1993.664	1993.210	228.234	0.503	804.337	0.638	21	0.149	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/2	1737.228	1735.876	203.075	0.555	972.933	0.550	22	0.148	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-20/2	1735.424	1735.876	-261.224	0.487	928.321	0.563	22	0.147	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-20/2	1992.432	1993.210	-895.130	0.471	838.833	0.615	21	0.147	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-1/2	1735.372	1735.876	-869.262	0.497	916.733	0.565	22	0.147	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-1/2	1735.515	1735.876	-209.146	0.432	1005.822	0.527	22	0.146	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/2	1457.157	1456.668	336.802	0.471	1455.878	0.541	20	0.145	R.SGTLIDAIGIYVHP.-
R2/RRR2-26/2	1735.297	1735.876	-912.762	0.474	920.872	0.554	22	0.145	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-25/2	1735.486	1735.876	-225.729	0.458	959.905	0.539	22	0.145	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-1/2	1992.295	1993.210	-964.390	0.453	922.018	0.568	21	0.145	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-23/2	1837.279	1838.014	-946.664	0.452	1066.688	0.506	23	0.145	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-24/2	1735.963	1735.876	49.821	0.479	919.441	0.550	22	0.145	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1735.363	1735.876	-874.840	0.503	875.482	0.564	22	0.145	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/2	1735.390	1735.876	-281.266	0.443	1101.935	0.472	23	0.144	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-18/2	1735.477	1735.876	-230.880	0.417	956.516	0.534	22	0.143	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1735.355	1735.876	-879.430	0.447	910.420	0.541	22	0.142	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1736.393	1735.876	-278.988	0.446	1041.748	0.483	23	0.142	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-22/2	1735.208	1735.876	-964.318	0.424	929.996	0.528	22	0.141	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-21/2	1455.597	1456.668	-1427.050	0.384	1415.587	0.511	19	0.140	R.SGTLIDAIGIYVHP.-
R2/RRR2-15/2	1992.408	1993.210	-907.554	0.486	718.561	0.608	20	0.140	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-25/2	1736.526	1735.876	-202.326	0.523	830.613	0.550	21	0.139	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-18/2	1991.969	1993.210	-1128.659	0.459	753.438	0.602	19	0.139	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-20/2	1456.117	1456.668	-1068.258	0.441	1436.973	0.477	20	0.138	R.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1735.517	1735.876	-207.735	0.487	886.814	0.512	22	0.138	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1993.110	1993.210	-50.410	0.520	703.274	0.605	19	0.138	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-21/2	1407.645	1408.625	-1410.777	0.528	848.423	0.523	16	0.137	K.LLGVTIYSSDAIR.S
R2/RRR2-21/2	1456.188	1456.668	-330.991	0.431	1435.677	0.460	20	0.137	R.SGTLIDAIGIYVHP.-
R2/RRR2-21/2	1736.324	1735.876	258.323	0.465	791.886	0.541	21	0.136	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-9/2	1457.329	1456.668	-233.527	0.416	1380.577	0.599	19	0.136	R.SGTLIDAIGIYVHP.-
R2/RRR2-2/2	1735.456	1735.876	-242.947	0.458	821.726	0.528	21	0.136	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-20/2	1735.201	1735.876	-968.697	0.466	723.844	0.567	20	0.136	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/3	1737.044	1735.876	97.008	0.510	1239.747	0.512	29	0.135	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-20/2	1735.289	1735.876	-917.282	0.420	865.789	0.511	21	0.135	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-2/2	1993.453	1993.210	121.880	0.460	706.189	0.588	19	0.135	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-26/2	1735.499	1735.876	-218.249	0.453	857.867	0.509	21	0.135	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/2	1455.874	1456.668	-1235.960	0.390	1431.641	0.412	20	0.135	R.SGTLIDAIGIYVHP.-
R2/RRR2-20/2	1457.589	1456.668	-54.231	0.492	1388.431	0.619	20	0.134	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1965.557	1966.187	-831.436	0.456	994.422	0.469	22	0.134	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-3/2	1993.356	1993.210	73.485	0.483	709.068	0.560	20	0.133	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/3	1965.603	1966.187	-807.878	0.431	1332.399	0.476	43	0.133	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-26/2	1735.383	1735.876	-285.430	0.447	808.013	0.518	20	0.133	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-12/2	1993.313	1993.210	51.804	0.467	662.848	0.572	19	0.131	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-19/2	1735.322	1735.876	-898.709	0.436	818.392	0.488	21	0.130	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/3	1736.496	1735.876	-219.612	0.467	1217.673	0.502	30	0.130	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-15/2	1735.482	1735.876	-227.705	0.454	699.746	0.533	19	0.129	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-26/2	1736.332	1735.876	262.976	0.417	899.130	0.429	22	0.127	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/2	1966.531	1966.187	175.536	0.432	1095.693	0.385	22	0.127	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/2	1838.779	1838.014	-128.085	0.446	916.926	0.453	20	0.127	-.IGPWGGNGGSAQDISVPPK.-
R2/RRR2-14/2	1456.561	1456.668	-73.603	0.397	1365.826	0.489	19	0.126	R.SGTLIDAIGIYVHP.-
R2/RRR2-18/2	1456.355	1456.668	-215.860	0.412	1387.063	0.423	19	0.126	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1408.049	1408.625	-1122.465	0.388	768.505	0.477	15	0.125	K.LLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/3	1736.572	1735.876	-175.819	0.483	978.074	0.564	27	0.125	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/3	1966.530	1966.187	175.280	0.406	1216.979	0.473	39	0.124	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-25/2	1736.244	1735.876	212.146	0.392	662.751	0.493	19	0.124	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-24/2	1967.379	1966.187	98.104	0.440	1064.464	0.372	21	0.123	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-1/2	1993.568	1993.210	179.665	0.471	511.107	0.545	17	0.122	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-1/2	1994.038	1993.210	-86.675	0.457	398.330	0.574	16	0.122	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/3	1737.462	1735.876	-238.975	0.479	1185.509	0.472	30	0.120	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/3	1966.461	1966.187	139.796	0.448	1115.443	0.481	39	0.118	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/2	1408.402	1408.625	-158.880	0.354	629.963	0.433	15	0.117	K.LLGVTIYSSDAIR.S
R2/RRR2-3/2	1457.353	1456.668	-216.889	0.443	1295.720	0.613	19	0.117	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1838.442	1838.014	233.918	0.425	627.234	0.485	17	0.117	-.IGPWGGNGGSAQDISVPPK.-
R2/RRR2-24/3	1966.380	1966.187	98.801	0.456	1145.277	0.458	38	0.115	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/2	1965.569	1966.187	-825.451	0.402	958.147	0.336	22	0.115	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/2	1837.996	1838.014	-9.566	0.364	295.383	0.392	17	0.113	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-13/2	1407.503	1408.625	-1511.999	0.345	460.038	0.358	15	0.113	K.LLGVTIYSSDAIR.S
R2/RRR2-24/3	1967.266	1966.187	40.285	0.445	1047.512	0.474	38	0.112	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-26/2	1408.042	1408.625	-1127.514	0.379	495.481	0.394	14	0.111	-.LLGVTIYSSDAIR.-
R2/RRR2-23/3	1736.965	1735.876	51.018	0.424	1047.534	0.478	27	0.111	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-11/2	1992.815	1993.210	-199.284	0.359	539.421	0.393	16	0.109	K.EFSIPLQDSGHVVGFFGR.S
R2/RRR2-24/3	1965.596	1966.187	-811.618	0.446	1064.687	0.448	38	0.108	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1735.157	1735.876	-993.920	0.415	908.362	0.503	26	0.107	K.IVTSANNTYEAGVPNGK.E
R2/RRR2-23/3	1966.000	1966.187	-95.391	0.427	1089.728	0.430	35	0.107	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1967.301	1966.187	58.208	0.395	972.125	0.464	36	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1967.294	1966.187	55.034	0.463	1073.724	0.430	39	0.105	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1965.707	1966.187	-244.612	0.435	897.613	0.472	36	0.104	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1966.539	1966.187	179.575	0.472	887.269	0.471	36	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1967.740	1966.187	-227.528	0.457	977.424	0.447	36	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1967.858	1966.187	-167.598	0.445	999.893	0.435	37	0.102	K.IGPWGGNGGSAQDISVPPKK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1967.641	1966.187	231.619	0.468	971.561	0.443	36	0.102	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1966.220	1966.187	17.079	0.416	966.585	0.442	38	0.102	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1966.369	1966.187	93.104	0.442	846.064	0.459	35	0.100	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1966.794	1966.187	-200.247	0.431	1040.699	0.407	37	0.099	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1966.934	1966.187	-128.617	0.461	881.044	0.448	35	0.099	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1967.427	1966.187	122.427	0.478	1163.902	0.376	39	0.099	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1965.853	1966.187	-169.949	0.452	652.160	0.484	33	0.098	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1966.181	1966.187	-2.723	0.449	867.291	0.441	35	0.098	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1965.705	1966.187	-245.827	0.413	602.406	0.483	31	0.097	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1967.730	1966.187	-232.663	0.421	894.420	0.425	36	0.096	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1967.845	1966.187	-174.226	0.426	953.122	0.411	34	0.096	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1966.589	1966.187	205.252	0.362	1019.286	0.385	35	0.095	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1967.183	1966.187	-1.725	0.408	827.392	0.430	34	0.095	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1967.800	1966.187	-196.816	0.429	943.458	0.404	38	0.095	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1966.872	1966.187	-160.555	0.442	706.737	0.445	34	0.094	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1967.358	1966.187	87.518	0.494	1009.095	0.391	34	0.094	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1965.969	1966.187	-110.806	0.381	905.188	0.401	35	0.093	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1966.021	1966.187	-84.367	0.384	773.823	0.425	33	0.093	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1965.817	1966.187	-188.357	0.365	624.727	0.434	31	0.091	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1967.337	1966.187	76.690	0.445	503.212	0.424	31	0.091	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1838.683	1838.014	-180.305	0.401	907.276	0.411	27	0.090	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/3	1966.275	1966.187	45.100	0.362	967.648	0.367	37	0.090	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-13/2	1456.288	1456.668	-261.775	0.468	1180.440	0.539	18	0.090	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/3	1839.837	1838.014	-96.276	0.425	992.587	0.382	31	0.090	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/3	1966.202	1966.187	7.926	0.337	489.585	0.462	27	0.090	-.IGPWGGNGGSAQDISVPPKK.-
R2/RRR2-24/3	1965.586	1966.187	-816.668	0.412	691.291	0.391	34	0.088	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-14/2	1456.351	1456.668	-218.551	0.373	1170.600	0.466	18	0.088	R.SGTLIDAIGIYVHP.-
R2/RRR2-23/3	1537.723	1536.798	-48.826	0.442	925.670	0.378	24	0.085	K.KLLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/3	1966.412	1966.187	115.237	0.291	955.283	0.311	33	0.083	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-23/3	1967.182	1966.187	-2.285	0.423	886.326	0.331	33	0.082	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-21/2	1456.462	1456.668	-142.204	0.401	1163.140	0.412	18	0.082	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/3	1537.613	1536.798	-120.375	0.396	789.009	0.379	27	0.081	K.KLLGVTIYSSDAIR.S
R2/RRR2-12/2	1456.385	1456.668	-195.259	0.438	1127.213	0.525	18	0.081	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/2	1456.377	1456.668	-200.472	0.452	1137.314	0.474	18	0.079	R.SGTLIDAIGIYVHP.-
R2/RRR2-24/3	1838.072	1838.014	31.792	0.358	627.982	0.374	24	0.077	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-23/3	1536.746	1536.798	-34.117	0.386	565.796	0.346	21	0.075	K.KLLGVTIYSSDAIR.S
R2/RRR2-24/3	1838.240	1838.014	123.405	0.388	638.041	0.335	25	0.074	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-1/2	1456.515	1456.668	-105.128	0.376	1051.911	0.529	17	0.071	R.SGTLIDAIGIYVHP.-
R2/RRR2-14/3	1967.375	1966.187	96.293	0.247	734.157	0.132	27	0.069	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-24/3	1837.385	1838.014	-889.210	0.264	785.834	0.257	25	0.068	K.IGPWGGNGGSAQDISVPPK.K
R2/RRR2-14/2	1456.060	1456.668	-1107.905	0.401	1030.936	0.513	17	0.066	R.SGTLIDAIGIYVHP.-
R2/RRR2-22/3	1965.470	1966.187	-875.957	0.209	867.981	0.060	26	0.063	K.IGPWGGNGGSAQDISVPPKK.L
R2/RRR2-20/2	1455.494	1456.668	-1498.486	0.275	996.098	0.355	16	0.059	R.SGTLIDAIGIYVHP.-
R2/RRR2-15/2	1456.174	1456.668	-340.075	0.435	1006.907	0.457	18	0.058	R.SGTLIDAIGIYVHP.-
R2/RRR2-23/2	1455.388	1456.668	-1571.364	0.317	964.924	0.415	17	0.054	R.SGTLIDAIGIYVHP.-
R2/RRR2-10/2	1456.409	1456.668	-178.695	0.424	930.971	0.478	17	0.050	R.SGTLIDAIGIYVHP.-
R2/RRR2-19/2	1455.821	1456.668	-1272.421	0.279	837.206	0.315	16	0.036	R.SGTLIDAIGIYVHP.-
R2/RRR2-18/2	1456.018	1456.668	-1136.948	0.308	798.081	0.429	15	0.036	R.SGTLIDAIGIYVHP.-
R2/RRR2-4/2	1456.321	1456.668	-238.733	0.403	785.887	0.444	16	0.032	R.SGTLIDAIGIYVHP.-
R2/RRR2-17/2	1456.200	1456.668	-322.664	0.245	722.584	0.398	16	0.027	R.SGTLIDAIGIYVHP.-
R2/RRR2-12/2	1455.911	1456.668	-1210.447	0.270	730.696	0.338	15	0.026	R.SGTLIDAIGIYVHP.-
R2/RRR2-18/2	1456.278	1456.668	-268.839	0.326	676.182	0.423	14	0.023	R.SGTLIDAIGIYVHP.-
R2/RRR2-15/2	1455.612	1456.668	-1416.690	0.261	691.723	0.279	13	0.023	R.SGTLIDAIGIYVHP.-
R2/RRR2-12/2	1456.143	1456.668	-1050.497	0.333	686.121	0.338	14	0.022	R.SGTLIDAIGIYVHP.-
R2/RRR2-22/2	1456.114	1456.668	-1070.446	0.309	612.467	0.438	15	0.018	R.SGTLIDAIGIYVHP.-
R2/RRR2-2/2	1456.323	1456.668	-237.556	0.244	580.181	0.396	13	0.017	R.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1455.678	1456.668	-1371.459	0.322	608.073	0.282	15	0.016	-.SGTLIDAIGIYVHP.-
R2/RRR2-8/2	1443.690	1444.573	-1307.962	0.381	2506.445	0.308	20	0.289	K.AESLDDAIQIVNR.N
R2/RRR2-8/2	1443.689	1444.573	-1308.641	0.422	2241.277	0.339	19	0.250	K.AESLDDAIQIVNR.N
R2/RRR2-8/2	1932.882	1933.303	-218.479	0.441	2199.917	0.329	25	0.243	K.DPGAAMMLAELAM*EAGLPK.G
R2/RRR2-8/2	1443.703	1444.573	-1298.875	0.427	2168.682	0.311	19	0.230	K.AESLDDAIQIVNR.N
R2/RRR2-8/2	1163.097	1163.305	-179.125	0.455	1621.804	0.501	17	0.203	R.IPLTTADEFR.A
R2/RRR2-8/3	1968.847	1968.071	-114.158	0.485	1753.122	0.500	32	0.200	R.ADEHVDVTNPATQEVVSR.I
R2/RRR2-8/2	1290.148	1290.405	-200.204	0.446	1356.342	0.571	18	0.188	K.ASFAGDLNFYGK.A
R2/RRR2-8/2	1203.494	1204.312	-1515.801	0.525	1246.324	0.529	18	0.172	K.LAENITTEQGK.T
R2/RRR2-8/2	1163.089	1163.305	-186.179	0.448	1473.143	0.430	16	0.171	R.IPLTTADEFR.A
R2/RRR2-8/2	1203.513	1204.312	-1499.397	0.483	1152.492	0.522	18	0.162	K.LAENITTEQGK.T
R2/RRR2-8/2	1289.803	1290.405	-1245.778	0.407	1239.031	0.475	18	0.158	K.ASFAGDLNFYGK.A
R2/RRR2-8/2	1162.612	1163.305	-1460.209	0.410	1359.393	0.400	16	0.155	R.IPLTTADEFR.A
R2/RRR2-8/2	1203.282	1204.312	-1692.506	0.445	1267.375	0.436	18	0.155	K.LAENITTEQGK.T
R2/RRR2-9/2	1163.229	1163.305	-65.954	0.446	1262.386	0.403	16	0.148	R.IPLTTADEFR.A
R2/RRR2-9/2	1203.878	1204.312	-362.019	0.539	1027.133	0.495	17	0.148	K.LAENITTEQGK.T
R2/RRR2-8/3	1967.827	1968.071	-124.359	0.429	1335.610	0.502	28	0.145	R.ADEHVDVTNPATQEVVSR.I
R2/RRR2-8/3	1967.914	1968.071	-80.397	0.437	1210.166	0.469	29	0.122	R.ADEHVDVTNPATQEVVSR.I
R2/RRR2-8/2	1220.525	1220.400	103.062	0.392	740.226	0.383	17	0.120	R.LLIGGEFVESR.A
R2/RRR2-9/2	1221.448	1220.400	39.433	0.320	783.808	0.367	14	0.114	R.LLIGGEFVESR.A
R2/RRR2-8/2	1220.319	1220.400	-66.380	0.265	569.937	0.414	17	0.112	R.LLIGGEFVESR.A
R2/RRR2-9/2	1162.323	1163.305	-1710.750	0.345	600.134	0.347	13	0.112	R.IPLTTADEFR.A
R2/RRR2-3/2	1163.303	1163.305	-1.748	0.304	607.505	0.258	12	0.106	R.IPLTTADEFR.A
R2/RRR2-12/2	1101.608	1102.183	-1434.597	0.276	882.577	0.078	15	0.096	-.LIQSGADNGAR.-
R2/RRR2-8/2	1850.580	1851.159	-855.570	0.488	1937.859	0.506	25	0.249	K.AVGEEMGIGFLGIGFQPK.W
R2/RRR2-8/2	1530.295	1530.662	-240.794	0.407	1971.747	0.466	23	0.243	R.EVDAVISSGVTPAER.L
R2/RRR2-8/2	1529.650	1530.662	-1319.464	0.368	1766.117	0.465	22	0.212	R.EVDAVISSGVTPAER.L
R2/RRR2-8/2	1259.151	1259.431	-223.025	0.436	1801.073	0.407	17	0.204	R.DLAEEILQLSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1530.288	1530.662	-245.596	0.357	1672.531	0.475	22	0.202	R.EVDAVISSGVTPAER.L
R2/RRR2-8/2	1850.507	1851.159	-895.170	0.494	1598.929	0.490	22	0.196	K.AVGEEMGIGFLGIGFQPK.W
R2/RRR2-8/2	1258.698	1259.431	-1380.840	0.449	1801.824	0.373	17	0.196	R.DLAEEILQLSK.N
R2/RRR2-8/2	1260.235	1259.431	-156.185	0.556	1588.946	0.459	17	0.190	R.DLAEEILQLSK.N
R2/RRR2-8/2	1930.743	1931.267	-791.448	0.512	1113.636	0.609	26	0.172	R.AGLALQPIATAIFANSPFK.E
R2/RRR2-8/2	1930.489	1931.267	-923.788	0.557	1025.438	0.642	25	0.171	R.AGLALQPIATAIFANSPFK.E
R2/RRR2-8/2	1930.396	1931.267	-972.036	0.504	1053.572	0.586	25	0.162	R.AGLALQPIATAIFANSPFK.E
R2/RRR2-8/2	1287.070	1287.553	-376.018	0.410	1286.899	0.359	17	0.142	K.WALSDIPIM*PK.G
R2/RRR2-8/2	1931.448	1931.199	129.282	0.401	768.861	0.543	18	0.133	R.YVDYALDVPM*YFVYR.N
R2/RRR2-8/2	994.019	994.166	-148.930	0.508	604.872	0.378	13	0.119	-.LLNLYETK.-
R2/RRR2-8/2	994.222	994.166	56.265	0.483	617.774	0.351	13	0.117	-.LLNLYETK.-
R2/RRR2-8/2	994.199	994.166	32.621	0.450	705.444	0.336	13	0.116	-.LLNLYETK.-
R2/RRR2-8/2	1286.511	1287.553	-1592.066	0.289	636.388	0.419	14	0.113	K.WALSDIPIM*PK.G
R2/RRR2-8/3	1930.974	1931.267	-152.222	0.501	1046.297	0.480	27	0.111	R.AGLALQPIATAIFANSPFK.E
R2/RRR2-8/3	1920.061	1920.155	-48.891	0.491	1105.471	0.455	28	0.110	R.FDWDKIVEENNVIGLK.Q
R2/RRR2-8/2	1286.335	1287.553	-1729.156	0.291	592.486	0.145	12	0.098	-.WALSDIPIM*PK.-
R2/RRR2-5/2	1323.641	1324.468	-1384.871	0.466	2222.832	0.598	22	0.327	K.ILVAGSHADDLGR.Q
R2/RRR2-5/2	1324.244	1324.468	-169.531	0.507	2143.997	0.560	22	0.300	K.ILVAGSHADDLGR.Q
R2/RRR2-5/2	1324.037	1324.468	-326.761	0.483	2098.249	0.580	21	0.298	K.ILVAGSHADDLGR.Q
R2/RRR2-5/2	1717.621	1717.924	-177.345	0.526	1981.305	0.504	23	0.253	R.GVSTVM*VSYSSWNGVK.M
R2/RRR2-5/2	1058.915	1059.198	-268.435	0.554	1866.473	0.431	17	0.215	R.IGEATALEVR.A
R2/RRR2-5/2	1058.886	1059.198	-296.424	0.573	1757.065	0.419	17	0.198	R.IGEATALEVR.A
R2/RRR2-5/2	1059.088	1059.198	-104.925	0.539	1626.946	0.410	17	0.182	R.IGEATALEVR.A
R2/RRR2-1/2	1059.954	1059.198	-231.324	0.483	1560.831	0.436	17	0.182	R.IGEATALEVR.A
R2/RRR2-6/2	1059.107	1059.198	-86.658	0.561	1568.144	0.407	17	0.175	R.IGEATALEVR.A
R2/RRR2-5/2	1701.334	1701.925	-937.748	0.496	1399.353	0.455	19	0.164	R.GVSTVMVSYSSWNGVK.M
R2/RRR2-5/2	1702.191	1701.925	156.761	0.471	1180.543	0.528	18	0.158	R.GVSTVMVSYSSWNGVK.M
R2/RRR2-5/2	1782.285	1782.063	124.711	0.476	1086.260	0.506	21	0.150	R.ATGIPYVFAPCVAVCR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1700.633	1701.925	-1351.816	0.317	1428.869	0.346	19	0.148	R.GVSTVMVSYSSWNGVK.M
R2/RRR2-5/2	1781.532	1782.063	-862.065	0.428	1098.250	0.475	21	0.145	R.ATGIPYVFAPCVAVCR.D
R2/RRR2-2/2	1059.225	1059.198	25.475	0.410	1107.097	0.387	16	0.136	R.IGEATALEVR.A
R2/RRR2-3/2	1058.833	1059.198	-346.161	0.411	1149.392	0.355	16	0.134	R.IGEATALEVR.A
R2/RRR2-5/2	1188.243	1188.398	-130.511	0.493	903.465	0.437	17	0.133	K.SSYSPVLPLPK.K
R2/RRR2-5/2	1454.789	1454.659	90.127	0.422	777.992	0.508	20	0.133	K.ATIFPHNVGLGATR.D
R2/RRR2-5/2	1188.116	1188.398	-237.698	0.460	900.098	0.434	17	0.132	K.SSYSPVLPLPK.K
R2/RRR2-5/2	1454.359	1454.659	-206.559	0.342	900.838	0.475	20	0.131	K.ATIFPHNVGLGATR.D
R2/RRR2-4/2	1059.571	1059.198	352.713	0.359	1050.935	0.297	16	0.121	R.IGEATALEVR.A
R2/RRR2-5/2	1187.914	1188.398	-408.523	0.406	701.214	0.389	15	0.118	K.SSYSPVLPLPK.K
R2/RRR2-5/2	1780.538	1782.063	-1985.871	0.281	852.323	0.317	20	0.110	R.ATGIPYVFAPCVAVCR.D
R2/RRR2-5/2	851.933	851.927	6.954	0.267	823.525	0.303	11	0.110	R.IDDAVYR.I
R2/RRR2-5/2	851.950	851.927	26.930	0.260	800.906	0.228	10	0.104	R.IDDAVYR.I
R2/RRR2-5/3	1454.359	1454.659	-206.653	0.347	1038.748	0.462	28	0.102	K.ATIFPHNVGLGATR.D
R2/RRR2-5/3	1593.716	1593.835	-74.488	0.396	1235.505	0.341	23	0.096	K.M*HANHHLITDFLK.N
R2/RRR2-5/3	1454.736	1454.659	53.341	0.391	1016.748	0.405	27	0.093	K.ATIFPHNVGLGATR.D
R2/RRR2-5/3	1593.683	1593.835	-95.694	0.410	1227.388	0.323	22	0.092	K.M*HANHHLITDFLK.N
R2/RRR2-5/3	1594.035	1593.835	125.768	0.409	1046.747	0.358	21	0.088	K.M*HANHHLITDFLK.N
R2/RRR2-2/3	1454.689	1454.659	21.149	0.389	781.139	0.430	23	0.087	K.ATIFPHNVGLGATR.D
R2/RRR2-2/3	1454.807	1454.659	102.194	0.426	669.620	0.417	23	0.084	K.ATIFPHNVGLGATR.D
R2/RRR2-7/2	1858.174	1859.069	-1023.258	0.464	2262.252	0.470	22	0.294	R.ELQAIEDEWLATAQLK.T
R2/RRR2-7/2	1858.481	1859.069	-857.335	0.513	2236.357	0.478	22	0.291	R.ELQAIEDEWLATAQLK.T
R2/RRR2-7/2	1323.988	1324.487	-377.604	0.520	1924.970	0.575	23	0.266	K.TVQGGISSTAAM*GK.G
R2/RRR2-7/2	1659.063	1659.823	-1063.999	0.381	2265.406	0.321	23	0.251	R.TDAVAATLIQTNVDAR.D
R2/RRR2-7/2	1323.522	1324.487	-1488.944	0.402	1899.556	0.541	23	0.250	K.TVQGGISSTAAM*GK.G
R2/RRR2-7/2	1337.067	1337.525	-343.955	0.420	1744.344	0.537	20	0.230	R.SLAAVLSDAM*SAGK.N
R2/RRR2-7/2	1323.666	1324.487	-1379.542	0.420	1682.420	0.556	22	0.223	K.TVQGGISSTAAM*GK.G
R2/RRR2-7/2	1659.338	1659.823	-293.198	0.402	2022.587	0.304	22	0.209	R.TDAVAATLIQTNVDAR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1324.951	1324.487	351.218	0.443	1664.264	0.504	21	0.208	K.TVQGGISSTAAM*GK.G
R2/RRR2-7/3	1133.078	1133.329	-221.486	0.500	1858.607	0.314	23	0.148	R.FRGSVAAAVVR.G
R2/RRR2-7/3	1501.501	1501.626	-83.028	0.476	1471.401	0.358	26	0.117	R.KLQEWSAATSHDK.C
R2/RRR2-7/3	1501.118	1501.626	-1007.287	0.467	1223.853	0.414	26	0.109	R.KLQEWSAATSHDK.C
R2/RRR2-7/2	1707.038	1708.016	-1162.194	0.332	708.311	0.349	16	0.107	R.LQFDIM*GVETVLVAR.T
R2/RRR2-7/3	1627.204	1627.781	-972.087	0.452	1104.104	0.411	30	0.100	R.GAAGVHLEDQSSVTKK.C
R2/RRR2-7/3	1501.299	1501.626	-218.460	0.490	1435.816	0.303	27	0.100	R.KLQEWSAATSHDK.C
R2/RRR2-7/3	1628.363	1627.781	-257.354	0.481	731.662	0.513	25	0.099	R.GAAGVHLEDQSSVTKK.C
R2/RRR2-7/3	1133.281	1133.329	-42.374	0.416	1496.927	0.230	21	0.092	R.FRGSVAAAVVR.G
R2/RRR2-7/3	1627.623	1627.781	-97.545	0.407	601.679	0.463	24	0.086	R.GAAGVHLEDQSSVTKK.C
R2/RRR2-7/2	1474.303	1474.730	-290.549	0.514	2034.454	0.568	20	0.281	R.LGANSLLDIVVFGR.A
R2/RRR2-7/2	1790.509	1790.992	-270.351	0.537	1783.726	0.629	23	0.262	R.AAIGLSEHGFNTACITK.L
R2/RRR2-7/2	1474.404	1474.730	-221.771	0.521	1565.034	0.585	20	0.216	R.LGANSLLDIVVFGR.A
R2/RRR2-7/2	1473.793	1474.730	-1317.799	0.398	1669.266	0.499	20	0.207	R.LGANSLLDIVVFGR.A
R2/RRR2-7/2	1295.104	1295.427	-249.827	0.425	1582.030	0.476	20	0.193	R.ATNTILATGGYGR.A
R2/RRR2-7/2	1294.623	1295.427	-1397.186	0.362	1426.499	0.491	20	0.176	R.ATNTILATGGYGR.A
R2/RRR2-7/2	1295.056	1295.427	-287.464	0.386	1451.458	0.439	20	0.170	R.ATNTILATGGYGR.A
R2/RRR2-7/2	1116.043	1116.338	-265.336	0.455	1234.257	0.456	15	0.157	K.TIAWLDKLR.N
R2/RRR2-7/2	1165.976	1166.336	-309.630	0.506	1263.415	0.426	17	0.154	R.VM*QNNAAVFR.T
R2/RRR2-7/2	1127.043	1127.231	-167.690	0.498	1041.753	0.498	18	0.151	R.AFGGQSLDFGK.G
R2/RRR2-7/2	1608.239	1608.819	-985.636	0.372	1184.744	0.463	21	0.150	K.AVIELENYGLPFSR.T
R2/RRR2-7/2	1128.059	1127.231	-152.887	0.487	1084.996	0.478	18	0.150	R.AFGGQSLDFGK.G
R2/RRR2-7/2	1608.339	1608.819	-299.603	0.469	1045.143	0.497	20	0.147	K.AVIELENYGLPFSR.T
R2/RRR2-7/2	1166.064	1166.336	-234.006	0.486	1229.040	0.397	17	0.147	R.VM*QNNAAVFR.T
R2/RRR2-7/2	1166.005	1166.336	-284.421	0.514	1117.976	0.435	16	0.145	R.VM*QNNAAVFR.T
R2/RRR2-7/2	1126.976	1127.231	-227.127	0.419	1030.297	0.442	18	0.139	R.AFGGQSLDFGK.G
R2/RRR2-7/3	1790.860	1790.992	-73.681	0.394	1273.740	0.497	32	0.133	R.AAIGLSEHGFNTACITK.L
R2/RRR2-7/3	1790.765	1790.992	-127.219	0.458	970.679	0.565	29	0.123	R.AAIGLSEHGFNTACITK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1134.881	1135.210	-290.708	0.454	898.437	0.324	14	0.119	K.AWESYHDVK.I
R2/RRR2-7/3	1790.795	1790.992	-109.988	0.423	656.028	0.633	26	0.114	R.AAIGLSEHGFNTACITK.L
R2/RRR2-7/2	1135.094	1135.210	-102.537	0.441	658.421	0.309	12	0.110	K.AWESYHDVK.I
R2/RRR2-7/3	1474.556	1474.730	-117.925	0.466	1063.362	0.438	25	0.103	R.LGANSLLDIVVFGR.A
R2/RRR2-7/2	1473.868	1474.730	-1266.726	0.246	105.155	0.488	8	0.067	-.LGANSLLDIVVFGR.-
R2/RRR2-8/2	1726.640	1725.963	-187.601	0.530	1368.944	0.578	20	0.191	K.QIVVIYAAVNGFCDR.M
R2/RRR2-8/2	1705.348	1705.914	-921.038	0.494	1480.644	0.533	19	0.190	R.DNGMHALIIYDDLSK.Q
R2/RRR2-8/2	1313.168	1312.580	-315.107	0.477	1558.029	0.322	18	0.156	K.AILSTINPELLK.S
R2/RRR2-8/2	1721.268	1721.913	-958.422	0.483	1136.052	0.505	19	0.152	R.DNGM*HALIIYDDLSK.Q
R2/RRR2-8/3	1439.644	1439.689	-30.933	0.495	1800.627	0.338	29	0.148	R.GIRPAINVGLSVSR.V
R2/RRR2-8/2	1312.138	1312.580	-338.308	0.421	1318.756	0.365	17	0.144	K.AILSTINPELLK.S
R2/RRR2-8/2	1721.421	1721.913	-286.630	0.472	1028.647	0.496	19	0.143	R.DNGM*HALIIYDDLSK.Q
R2/RRR2-8/2	1704.589	1705.914	-1367.929	0.403	1338.142	0.339	21	0.141	R.DNGMHALIIYDDLSK.Q
R2/RRR2-8/2	1312.276	1312.580	-232.936	0.415	1232.059	0.370	17	0.139	K.AILSTINPELLK.S
R2/RRR2-8/3	1439.832	1439.689	99.685	0.470	1713.935	0.319	27	0.134	R.GIRPAINVGLSVSR.V
R2/RRR2-7/2	1313.544	1312.580	-27.834	0.462	1146.675	0.346	16	0.128	K.AILSTINPELLK.S
R2/RRR2-8/2	1439.306	1439.689	-266.905	0.448	543.947	0.526	17	0.125	R.GIRPAINVGLSVSR.V
R2/RRR2-8/2	1438.740	1439.689	-1358.671	0.412	536.203	0.512	17	0.122	R.GIRPAINVGLSVSR.V
R2/RRR2-8/2	1725.147	1725.963	-1056.031	0.365	687.343	0.471	19	0.121	K.QIVVIYAAVNGFCDR.M
R2/RRR2-8/2	1538.425	1538.688	-171.556	0.417	456.822	0.480	17	0.121	R.EAFPGDVFYLHSR.L
R2/RRR2-7/2	1301.822	1301.514	237.231	0.391	1013.748	0.329	16	0.120	K.TAIAIDTILNQK.Q
R2/RRR2-8/2	1077.164	1077.298	-124.760	0.466	873.421	0.333	14	0.120	R.KIELDAFLK.Q
R2/RRR2-8/2	1076.877	1077.298	-392.206	0.471	673.069	0.333	13	0.115	R.KIELDAFLK.Q
R2/RRR2-8/2	1077.120	1077.298	-166.028	0.404	746.470	0.326	13	0.114	R.KIELDAFLK.Q
R2/RRR2-8/2	1439.335	1439.689	-246.569	0.409	489.351	0.427	16	0.114	R.GIRPAINVGLSVSR.V
R2/RRR2-8/2	1704.449	1705.914	-1450.218	0.379	906.549	0.336	16	0.113	R.DNGMHALIIYDDLSK.Q
R2/RRR2-8/2	1538.680	1538.688	-4.982	0.348	379.202	0.407	14	0.111	R.EAFPGDVFYLHSR.L
R2/RRR2-8/3	1439.227	1439.689	-322.013	0.457	1516.267	0.306	25	0.110	R.GIRPAINVGLSVSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1077.246	1077.298	-49.295	0.533	1615.916	0.304	23	0.109	R.KIELDAFLK.Q
R2/RRR2-8/2	1312.240	1312.580	-260.280	0.350	835.800	0.253	16	0.108	K.AILSTINPELLK.S
R2/RRR2-8/2	1538.085	1538.688	-1044.920	0.263	336.215	0.324	15	0.108	R.EAFPGDVFYLHSR.L
R2/RRR2-8/2	1538.256	1538.688	-281.255	0.298	506.002	0.273	17	0.107	R.EAFPGDVFYLHSR.L
R2/RRR2-13/2	1312.227	1312.580	-269.800	0.249	571.467	0.246	14	0.104	K.AILSTINPELLK.S
R2/RRR2-8/2	1311.455	1312.580	-1625.162	0.288	616.533	0.206	14	0.103	K.AILSTINPELLK.S
R2/RRR2-7/2	1301.271	1301.514	-187.296	0.342	733.645	0.228	13	0.101	K.TAIAIDTILNQK.Q
R2/RRR2-9/2	1302.327	1301.514	-144.462	0.250	845.812	0.146	14	0.098	K.TAIAIDTILNQK.Q
R2/RRR2-8/3	1355.516	1355.589	-53.944	0.417	1333.038	0.322	28	0.094	R.KSVHEPMQTGLK.A
R2/RRR2-8/3	1077.424	1077.298	116.738	0.480	1147.967	0.314	21	0.083	R.KIELDAFLK.Q
R2/RRR2-8/3	1077.069	1077.298	-213.678	0.460	1184.572	0.301	22	0.081	R.KIELDAFLK.Q
R2/RRR2-8/3	1355.553	1355.589	-26.304	0.442	963.535	0.304	24	0.077	R.KSVHEPMQTGLK.A
R2/RRR2-8/3	1355.919	1355.589	244.461	0.429	865.730	0.307	23	0.075	R.KSVHEPMQTGLK.A
R2/RRR2-6/2	1891.707	1891.160	-239.837	0.489	1380.853	0.543	23	0.183	R.EGINIFLAGFVPTENLR.F
R2/RRR2-6/2	1244.989	1245.325	-270.111	0.493	1263.391	0.501	19	0.168	R.NVGDLSGGELQR.F
R2/RRR2-6/2	1892.115	1891.160	-23.529	0.439	1160.179	0.546	23	0.162	R.EGINIFLAGFVPTENLR.F
R2/RRR2-6/2	1890.696	1891.160	-245.664	0.441	1087.072	0.510	22	0.150	R.EGINIFLAGFVPTENLR.F
R2/RRR2-6/2	1530.332	1530.784	-295.913	0.445	884.219	0.505	20	0.140	K.CPFDAIEIINLPK.D
R2/RRR2-6/2	1530.374	1530.784	-268.143	0.431	916.564	0.486	19	0.138	K.CPFDAIEIINLPK.D
R2/RRR2-6/2	1530.392	1530.784	-256.620	0.387	791.493	0.531	19	0.135	K.CPFDAIEIINLPK.D
R2/RRR2-6/2	1215.251	1215.297	-38.346	0.345	1102.820	0.214	15	0.112	R.GSELQNYFTR.I
R2/RRR2-7/2	1892.262	1891.160	54.376	0.260	172.631	0.424	15	0.107	R.EGINIFLAGFVPTENLR.F
R2/RRR2-26/2	1118.077	1118.299	-199.478	0.235	812.672	0.240	14	0.103	K.LCIEVTPASK.L
R2/RRR2-6/3	1522.964	1522.816	97.178	0.434	814.053	0.500	24	0.099	K.AIIKPQYVDHIPK.A
R2/RRR2-6/3	1756.991	1756.899	52.562	0.409	677.785	0.482	26	0.091	K.AVQGNVGQVLDQKDER.G
R2/RRR2-6/3	1522.532	1522.816	-186.865	0.393	603.084	0.478	25	0.087	K.AIIKPQYVDHIPK.A
R2/RRR2-6/3	1756.856	1756.899	-24.372	0.345	600.411	0.431	24	0.081	K.AVQGNVGQVLDQKDER.G
R2/RRR2-6/3	1143.768	1143.274	433.194	0.541	1345.726	0.215	22	0.077	R.FRDESLTFK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1756.728	1756.899	-97.345	0.344	620.793	0.381	23	0.076	K.AVQGNVGQVLDQKDER.G
R2/RRR2-6/2	1281.179	1281.437	-201.415	0.324	974.161	0.421	14	0.126	R.EIAEAYLGSSIK.N
R2/RRR2-6/2	1281.073	1281.437	-285.058	0.263	800.868	0.324	13	0.107	R.EIAEAYLGSSIK.N
R2/RRR2-15/2	1435.361	1435.650	-202.043	0.556	2714.066	0.478	23	0.382	K.YIGLLATGLTADAR.S
R2/RRR2-15/2	1435.292	1435.650	-250.164	0.536	2590.248	0.521	23	0.372	K.YIGLLATGLTADAR.S
R2/RRR2-15/2	1435.390	1435.650	-181.994	0.569	2639.008	0.487	23	0.368	K.YIGLLATGLTADAR.S
R2/RRR2-16/2	1436.288	1435.650	-253.401	0.572	2531.909	0.540	23	0.365	K.YIGLLATGLTADAR.S
R2/RRR2-16/2	1435.088	1435.650	-1091.931	0.472	2417.585	0.440	22	0.309	K.YIGLLATGLTADAR.S
R2/RRR2-16/2	1435.092	1435.650	-1088.856	0.507	2012.743	0.491	22	0.254	K.YIGLLATGLTADAR.S
R2/RRR2-15/3	1849.741	1850.063	-174.528	0.461	1577.911	0.530	32	0.181	K.ATSAGLKEQEAINFLEK.K
R2/RRR2-16/3	1850.249	1850.063	101.065	0.542	1526.566	0.505	32	0.164	K.ATSAGLKEQEAINFLEK.K
R2/RRR2-15/2	946.509	947.071	-1655.965	0.409	1097.658	0.430	17	0.142	K.SAGVTSIGVR.G
R2/RRR2-15/2	947.044	947.071	-29.038	0.454	926.842	0.442	16	0.135	K.SAGVTSIGVR.G
R2/RRR2-15/2	1156.549	1157.304	-1522.173	0.409	704.820	0.530	15	0.134	R.HITIFSPEGR.L
R2/RRR2-15/2	946.391	947.071	-1780.626	0.419	979.199	0.422	16	0.134	K.SAGVTSIGVR.G
R2/RRR2-15/2	1162.430	1161.331	85.673	0.520	883.987	0.441	14	0.134	R.LYQVEYAFK.A
R2/RRR2-16/2	1158.174	1157.304	-112.017	0.381	655.152	0.538	15	0.131	R.HITIFSPEGR.L
R2/RRR2-15/2	1161.105	1161.331	-195.144	0.490	929.486	0.413	14	0.131	R.LYQVEYAFK.A
R2/RRR2-16/2	1157.219	1157.304	-73.386	0.418	674.074	0.491	15	0.129	R.HITIFSPEGR.L
R2/RRR2-16/2	1158.147	1157.304	-135.700	0.376	673.147	0.494	15	0.128	R.HITIFSPEGR.L
R2/RRR2-15/2	1156.913	1157.304	-338.722	0.333	569.017	0.474	14	0.121	R.HITIFSPEGR.L
R2/RRR2-16/3	1850.033	1850.063	-16.063	0.412	1260.399	0.428	30	0.117	K.ATSAGLKEQEAINFLEK.K
R2/RRR2-15/2	1158.053	1157.304	-217.649	0.292	445.132	0.372	13	0.112	R.HITIFSPEGR.L
R2/RRR2-15/3	1849.717	1850.063	-187.437	0.390	1131.246	0.447	30	0.110	K.ATSAGLKEQEAINFLEK.K
R2/RRR2-16/3	1221.947	1221.380	-354.873	0.463	1461.255	0.316	21	0.106	R.GKDSVCVVTQK.K
R2/RRR2-16/2	1073.102	1073.225	-115.421	0.303	853.708	0.187	14	0.102	K.ATEIEVGVVR.K
R2/RRR2-15/2	1160.322	1161.331	-1736.809	0.301	781.062	0.227	12	0.101	-.LYQVEYAFK.-
R2/RRR2-15/3	1849.462	1850.063	-868.110	0.370	1125.677	0.374	29	0.096	K.ATSAGLKEQEAINFLEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/3	1849.708	1850.063	-192.303	0.330	795.658	0.390	27	0.083	K.ATSAGLKEQEAINFLEK.K
R2/RRR2-15/3	1220.791	1221.380	-1305.082	0.390	677.382	0.196	18	0.060	-.GKDSVCVVTQK.-
R2/RRR2-15/3	1221.265	1221.380	-93.659	0.427	797.833	0.244	18	0.055	-.GKDSVCVVTQK.-
R2/RRR2-15/3	1221.335	1221.380	-36.362	0.396	781.174	0.243	18	0.043	-.GKDSVCVVTQK.-
R2/RRR2-10/2	1502.384	1502.729	-229.702	0.408	2654.290	0.211	21	0.289	K.CDVIVINTPLTEK.T
R2/RRR2-10/2	1846.829	1848.090	-1227.900	0.496	1679.996	0.517	23	0.216	R.YFKGEDFPVQNYIVK.E
R2/RRR2-10/2	1847.560	1848.090	-830.328	0.559	1578.114	0.556	22	0.212	R.YFKGEDFPVQNYIVK.E
R2/RRR2-10/2	1084.151	1084.297	-135.927	0.544	1393.303	0.422	17	0.164	K.KGVIIVNNAR.G
R2/RRR2-10/2	1083.575	1084.297	-1594.515	0.461	1377.843	0.401	17	0.159	K.KGVIIVNNAR.G
R2/RRR2-10/2	1084.028	1084.297	-249.341	0.523	1192.730	0.447	16	0.152	K.KGVIIVNNAR.G
R2/RRR2-10/2	1256.047	1255.426	-303.012	0.459	381.261	0.494	16	0.126	R.YAAGVKDM*LDR.Y
R2/RRR2-10/2	1410.184	1409.568	-273.459	0.432	679.483	0.417	17	0.120	K.GEDFPVQNYIVK.E
R2/RRR2-10/2	1255.074	1255.426	-281.395	0.412	384.375	0.349	16	0.116	R.YAAGVKDM*LDR.Y
R2/RRR2-11/2	956.085	956.125	-41.634	0.444	912.200	0.281	14	0.114	-.GVIIVNNAR.-
R2/RRR2-10/2	1255.196	1255.426	-183.434	0.339	232.999	0.277	13	0.111	-.YAAGVKDM*LDR.-
R2/RRR2-11/2	956.080	956.125	-46.372	0.412	796.052	0.281	13	0.111	-.GVIIVNNAR.-
R2/RRR2-11/2	955.398	956.125	-1812.601	0.268	607.366	0.147	11	0.093	-.GVIIVNNAR.-
R2/RRR2-10/3	1847.919	1848.090	-92.873	0.410	458.547	0.485	19	0.080	-.YFKGEDFPVQNYIVK.-
R2/RRR2-10/3	1847.100	1848.090	-1080.573	0.302	968.172	0.285	25	0.072	R.YFKGEDFPVQNYIVK.E
R2/RRR2-10/3	1085.255	1085.276	-19.430	0.490	1530.223	0.142	22	0.071	R.LKIDPELEK.E
R2/RRR2-10/3	1085.246	1085.276	-27.299	0.495	1263.800	0.182	20	0.066	-.LKIDPELEK.-
R2/RRR2-10/3	1085.630	1085.276	327.204	0.468	1332.759	0.127	21	0.062	R.LKIDPELEK.E
R2/RRR2-21/2	1721.212	1721.929	-1000.755	0.517	2215.963	0.475	24	0.285	R.AAEACEQFGGVLVTLR.M
R2/RRR2-21/2	1837.281	1838.095	-990.045	0.495	1892.379	0.640	24	0.283	K.ITLIGTSGISGSYVELRA.-
R2/RRR2-21/2	1721.555	1721.929	-218.025	0.491	2247.778	0.432	24	0.278	R.AAEACEQFGGVLVTLR.M
R2/RRR2-21/2	1721.345	1721.929	-923.361	0.538	2177.213	0.473	24	0.277	R.AAEACEQFGGVLVTLR.M
R2/RRR2-21/2	1767.054	1767.017	21.299	0.486	1925.356	0.521	26	0.251	K.ITLIGTSGISGSYVELR.-
R2/RRR2-21/2	1837.354	1838.095	-950.357	0.486	1748.404	0.612	23	0.237	K.ITLIGTSGISGSYVELRA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1218.434	1218.387	38.626	0.430	1446.963	0.506	17	0.184	K.AGQEALLNVFR.A
R2/RRR2-21/2	1617.156	1617.740	-982.245	0.490	1420.426	0.454	21	0.172	K.YLESFGPEENYLR.K
R2/RRR2-21/2	1616.952	1617.740	-1109.201	0.507	1463.056	0.428	21	0.171	K.YLESFGPEENYLR.K
R2/RRR2-21/2	1747.589	1748.918	-1336.792	0.449	960.006	0.487	23	0.140	K.ATDDKAGQEALLNVFR.A
R2/RRR2-21/2	1217.854	1218.387	-1262.374	0.409	1015.241	0.433	16	0.135	K.AGQEALLNVFR.A
R2/RRR2-21/2	1748.093	1748.918	-1047.211	0.439	826.392	0.505	22	0.134	K.ATDDKAGQEALLNVFR.A
R2/RRR2-21/2	1766.791	1767.017	-128.384	0.411	954.211	0.448	23	0.132	K.ITLIGTSGISGSYVELR.-
R2/RRR2-21/2	1617.377	1617.740	-225.256	0.504	957.396	0.428	18	0.131	K.YLESFGPEENYLR.K
R2/RRR2-21/2	1218.560	1218.387	142.113	0.405	855.019	0.439	13	0.125	K.AGQEALLNVFR.A
R2/RRR2-21/2	1654.982	1654.845	83.035	0.473	453.451	0.527	19	0.124	K.HLPAISDPEIESAFK.D
R2/RRR2-21/2	1766.417	1767.017	-908.396	0.310	653.666	0.414	22	0.114	K.ITLIGTSGISGSYVELR.-
R2/RRR2-21/2	1747.607	1748.918	-1326.339	0.264	231.951	0.330	15	0.106	K.ATDDKAGQEALLNVFR.A
R2/RRR2-13/2	1782.379	1782.884	-846.749	0.494	1604.029	0.462	22	0.192	K.ASEISVSAEEEFNIEK.L
R2/RRR2-13/2	1782.218	1782.884	-937.371	0.475	1481.047	0.454	21	0.175	K.ASEISVSAEEEFNIEK.L
R2/RRR2-13/2	1153.092	1153.307	-186.731	0.467	1119.866	0.531	19	0.161	R.FCSGGVVLASR.D
R2/RRR2-13/2	1190.946	1191.310	-306.939	0.481	1187.998	0.421	17	0.148	K.IVCENTLDAR.L
R2/RRR2-13/2	1191.091	1191.310	-184.988	0.434	1199.042	0.411	17	0.146	-.IVCENTLDAR.-
R2/RRR2-14/2	1190.863	1191.310	-377.079	0.468	1093.090	0.444	17	0.144	-.IVCENTLDAR.-
R2/RRR2-14/2	1191.027	1191.310	-238.557	0.444	1115.060	0.431	17	0.144	K.IVCENTLDAR.L
R2/RRR2-13/2	1152.494	1153.307	-1577.884	0.444	897.248	0.529	17	0.144	R.FCSGGVVLASR.D
R2/RRR2-14/2	1190.641	1191.310	-1406.605	0.468	1172.420	0.402	17	0.143	K.IVCENTLDAR.L
R2/RRR2-13/2	1190.917	1191.310	-330.901	0.437	1140.543	0.379	17	0.138	K.IVCENTLDAR.L
R2/RRR2-13/2	1152.541	1153.307	-1536.602	0.369	925.140	0.476	17	0.135	R.FCSGGVVLASR.D
R2/RRR2-13/2	1026.756	1027.243	-475.268	0.364	1061.787	0.345	14	0.127	K.ELVVQGLLR.L
R2/RRR2-13/2	1027.109	1027.243	-130.960	0.448	1034.993	0.327	14	0.124	K.ELVVQGLLR.L
R2/RRR2-13/3	1584.784	1584.823	-24.668	0.556	1426.366	0.404	26	0.122	R.KKIEYSM*QLNASR.I
R2/RRR2-14/2	1152.427	1153.307	-1635.771	0.305	840.307	0.395	16	0.120	R.FCSGGVVLASR.D
R2/RRR2-14/2	1027.253	1027.243	9.701	0.392	955.277	0.305	13	0.117	K.ELVVQGLLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1026.941	1027.243	-294.796	0.386	1075.973	0.249	14	0.116	K.ELVVQGLLR.L
R2/RRR2-13/3	1568.856	1568.823	21.015	0.514	1298.053	0.400	25	0.111	R.KKIEYSMQLNASR.I
R2/RRR2-13/3	1456.026	1456.650	-1118.583	0.523	1167.282	0.414	25	0.104	K.KIEYSM*QLNASR.I
R2/RRR2-13/3	1456.803	1456.650	105.662	0.544	1100.638	0.421	23	0.102	K.KIEYSM*QLNASR.I
R2/RRR2-13/3	1456.182	1456.650	-322.094	0.515	1357.055	0.342	26	0.102	K.KIEYSM*QLNASR.I
R2/RRR2-13/3	1583.872	1584.823	-1235.503	0.516	1298.533	0.348	26	0.099	R.KKIEYSM*QLNASR.I
R2/RRR2-13/3	1620.094	1619.809	176.675	0.522	819.940	0.410	25	0.088	R.VSHNHHEYKNLLK.E
R2/RRR2-13/3	1584.210	1584.823	-1021.120	0.476	768.020	0.419	22	0.088	R.KKIEYSM*QLNASR.I
R2/RRR2-13/3	1619.603	1619.809	-127.284	0.517	919.209	0.382	25	0.087	R.VSHNHHEYKNLLK.E
R2/RRR2-13/3	1619.395	1619.809	-256.133	0.538	751.559	0.370	24	0.082	R.VSHNHHEYKNLLK.E
R2/RRR2-13/3	1618.406	1619.809	-1489.161	0.430	451.544	0.374	20	0.069	-.VSHNHHEYKNLLK.-
R2/RRR2-13/3	1568.861	1568.823	23.942	0.456	781.711	0.283	21	0.068	-.KKIEYSMQLNASR.-
R2/RRR2-13/3	1568.745	1568.823	-50.046	0.338	963.357	0.058	22	0.056	R.KKIEYSMQLNASR.I
R2/RRR2-15/2	1311.122	1311.466	-263.397	0.469	1932.903	0.569	20	0.267	R.VNQSYVIATSTK.V
R2/RRR2-15/2	1740.478	1740.890	-237.111	0.595	1882.249	0.575	23	0.261	K.KTEGELFETEKEATK.N
R2/RRR2-16/2	1740.583	1740.890	-176.954	0.591	1595.844	0.584	22	0.221	K.KTEGELFETEKEATK.N
R2/RRR2-15/2	1311.217	1311.466	-190.171	0.500	1490.264	0.552	18	0.201	R.VNQSYVIATSTK.V
R2/RRR2-15/2	1133.041	1132.377	-297.555	0.551	1491.290	0.464	16	0.178	K.SGLLLVTGPFK.I
R2/RRR2-15/3	1498.446	1498.793	-232.358	0.372	1974.454	0.305	30	0.170	R.SSITPGTVLILLAGR.F
R2/RRR2-19/3	1211.175	1211.350	-144.933	0.523	1529.845	0.476	26	0.155	K.AEKPDAAAAAAPK.F
R2/RRR2-15/3	1211.431	1211.350	67.188	0.494	1655.042	0.418	26	0.153	K.AEKPDAAAAAAPK.F
R2/RRR2-15/3	1211.357	1211.350	5.638	0.516	1638.041	0.402	25	0.147	K.AEKPDAAAAAAPK.F
R2/RRR2-15/2	1498.416	1498.793	-252.209	0.396	1103.074	0.447	23	0.143	R.SSITPGTVLILLAGR.F
R2/RRR2-15/2	1132.096	1132.377	-249.028	0.423	1115.465	0.431	14	0.139	K.SGLLLVTGPFK.I
R2/RRR2-15/2	1060.069	1060.183	-108.177	0.418	957.362	0.473	15	0.138	K.VDISGVNVEK.F
R2/RRR2-15/2	1059.611	1060.183	-1487.757	0.469	748.272	0.511	14	0.134	K.VDISGVNVEK.F
R2/RRR2-15/2	1211.103	1211.350	-204.577	0.463	689.273	0.516	20	0.133	K.AEKPDAAAAAAPK.F
R2/RRR2-15/2	1498.537	1498.793	-171.383	0.404	1106.809	0.373	23	0.132	R.SSITPGTVLILLAGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1131.844	1132.377	-1358.411	0.451	936.091	0.445	14	0.131	K.SGLLLVTGPFK.I
R2/RRR2-15/3	1211.478	1211.350	106.297	0.526	1479.685	0.387	25	0.124	K.AEKPDAAAAAAPK.F
R2/RRR2-15/2	1211.149	1211.350	-166.458	0.457	550.443	0.459	18	0.122	K.AEKPDAAAAAAPK.F
R2/RRR2-16/2	955.814	956.118	-319.487	0.355	745.935	0.398	14	0.120	K.AIEAVPDLK.T
R2/RRR2-15/2	1498.395	1498.793	-266.103	0.333	679.966	0.425	19	0.116	R.SSITPGTVLILLAGR.F
R2/RRR2-13/2	1132.149	1132.377	-202.406	0.400	838.957	0.276	15	0.110	K.SGLLLVTGPFK.I
R2/RRR2-19/3	1211.762	1211.350	341.190	0.517	1377.802	0.354	23	0.108	K.AEKPDAAAAAAPK.F
R2/RRR2-16/2	955.994	956.118	-129.751	0.309	478.706	0.325	11	0.107	K.AIEAVPDLK.T
R2/RRR2-15/3	1740.839	1740.890	-29.274	0.529	983.511	0.477	26	0.107	K.KTEGELFETEKEATK.N
R2/RRR2-15/2	1131.490	1132.377	-1672.748	0.336	809.559	0.219	13	0.103	K.SGLLLVTGPFK.I
R2/RRR2-16/3	1741.655	1740.890	-135.376	0.496	806.880	0.477	26	0.099	K.KTEGELFETEKEATK.N
R2/RRR2-15/3	1740.805	1740.890	-49.108	0.511	924.775	0.446	27	0.099	K.KTEGELFETEKEATK.N
R2/RRR2-18/3	1740.868	1740.890	-12.288	0.492	725.258	0.470	25	0.095	K.KTEGELFETEKEATK.N
R2/RRR2-18/3	1740.816	1740.890	-42.356	0.518	775.506	0.451	26	0.094	K.KTEGELFETEKEATK.N
R2/RRR2-15/3	1740.933	1740.890	24.845	0.441	867.391	0.417	27	0.092	K.KTEGELFETEKEATK.N
R2/RRR2-18/3	1741.844	1740.890	-26.340	0.554	791.611	0.419	26	0.090	K.KTEGELFETEKEATK.N
R2/RRR2-16/3	1740.638	1740.890	-144.810	0.473	866.697	0.381	26	0.086	K.KTEGELFETEKEATK.N
R2/RRR2-19/3	1740.551	1740.890	-195.465	0.417	703.468	0.392	24	0.084	K.KTEGELFETEKEATK.N
R2/RRR2-16/3	1740.801	1740.890	-51.113	0.461	871.370	0.356	27	0.083	K.KTEGELFETEKEATK.N
R2/RRR2-13/3	1740.554	1740.890	-193.354	0.392	698.060	0.358	24	0.081	K.KTEGELFETEKEATK.N
R2/RRR2-21/2	1218.991	1218.386	-324.686	0.471	1364.799	0.526	16	0.180	K.AEIGLWFEPR.E
R2/RRR2-22/2	1218.022	1218.386	-299.613	0.442	1627.876	0.385	17	0.178	K.AEIGLWFEPR.E
R2/RRR2-22/2	1340.038	1339.436	-298.464	0.476	1269.529	0.494	19	0.164	R.NIIHGSDGPETAK.A
R2/RRR2-21/2	1338.953	1339.436	-362.441	0.442	1257.936	0.408	19	0.147	R.NIIHGSDGPETAK.A
R2/RRR2-22/2	885.971	886.031	-68.491	0.478	1119.609	0.451	14	0.147	R.GDLAVVVGR.N
R2/RRR2-21/2	1218.133	1218.386	-208.120	0.409	1306.200	0.364	16	0.145	K.AEIGLWFEPR.E
R2/RRR2-22/2	987.910	988.163	-256.745	0.457	1254.395	0.371	14	0.142	R.GLISEILSR.F
R2/RRR2-22/2	885.925	886.031	-120.044	0.423	1182.380	0.388	15	0.141	R.GDLAVVVGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1217.404	1218.386	-1632.241	0.374	1106.847	0.441	14	0.141	K.AEIGLWFEPR.E
R2/RRR2-21/2	1299.878	1299.366	-376.067	0.463	1054.122	0.446	16	0.140	R.ELVSYTSNEEK.W
R2/RRR2-21/2	1338.955	1339.436	-360.245	0.431	1145.031	0.409	18	0.139	R.NIIHGSDGPETAK.A
R2/RRR2-22/2	1339.171	1339.436	-198.818	0.414	1136.479	0.412	18	0.138	R.NIIHGSDGPETAK.A
R2/RRR2-22/2	1339.106	1339.436	-247.378	0.448	1123.047	0.406	18	0.137	R.NIIHGSDGPETAK.A
R2/RRR2-21/2	1299.054	1299.366	-240.491	0.445	1132.501	0.376	16	0.134	R.ELVSYTSNEEK.W
R2/RRR2-22/2	1217.795	1218.386	-1309.789	0.365	1094.034	0.386	15	0.133	K.AEIGLWFEPR.E
R2/RRR2-21/2	1217.906	1218.386	-395.347	0.433	1015.642	0.413	13	0.131	K.AEIGLWFEPR.E
R2/RRR2-22/2	988.071	988.163	-93.259	0.454	1196.311	0.322	14	0.131	R.GLISEILSR.F
R2/RRR2-21/2	987.588	988.163	-1599.977	0.416	1124.354	0.343	13	0.129	R.GLISEILSR.F
R2/RRR2-21/2	1339.159	1339.436	-207.414	0.443	966.757	0.401	17	0.127	R.NIIHGSDGPETAK.A
R2/RRR2-21/2	987.385	988.163	-1806.644	0.445	1040.640	0.352	13	0.127	R.GLISEILSR.F
R2/RRR2-22/2	987.480	988.163	-1709.510	0.472	949.557	0.366	13	0.125	R.GLISEILSR.F
R2/RRR2-21/2	1299.017	1299.366	-269.056	0.351	1060.401	0.322	16	0.122	R.ELVSYTSNEEK.W
R2/RRR2-22/2	885.924	886.031	-121.426	0.311	964.455	0.358	13	0.122	-.GDLAVVVGR.-
R2/RRR2-21/2	988.153	988.163	-9.988	0.467	971.894	0.329	13	0.121	R.GLISEILSR.F
R2/RRR2-22/2	1345.375	1345.572	-146.938	0.362	684.737	0.443	16	0.120	R.TFIAIKPDGVQR.G
R2/RRR2-21/2	1345.268	1345.572	-226.859	0.417	643.501	0.441	15	0.120	R.TFIAIKPDGVQR.G
R2/RRR2-21/2	1070.948	1071.252	-284.740	0.361	695.725	0.387	15	0.119	R.KLIGATDPQK.S
R2/RRR2-21/2	1217.870	1218.386	-1248.384	0.382	433.705	0.420	12	0.116	K.AEIGLWFEPR.E
R2/RRR2-21/2	885.346	886.031	-1908.517	0.341	796.299	0.329	13	0.114	-.GDLAVVVGR.-
R2/RRR2-21/2	886.042	886.031	12.490	0.331	783.003	0.324	13	0.114	R.GDLAVVVGR.N
R2/RRR2-21/2	1345.309	1345.572	-195.727	0.413	584.605	0.394	14	0.113	R.TFIAIKPDGVQR.G
R2/RRR2-21/2	1345.237	1345.572	-250.073	0.382	516.427	0.405	14	0.113	R.TFIAIKPDGVQR.G
R2/RRR2-21/2	885.258	886.031	-2009.257	0.309	743.720	0.309	14	0.113	R.GDLAVVVGR.N
R2/RRR2-21/2	1070.918	1071.252	-313.559	0.428	592.684	0.332	14	0.112	-.KLIGATDPQK.-
R2/RRR2-22/2	1071.276	1071.252	22.560	0.380	651.661	0.308	14	0.112	R.KLIGATDPQK.S
R2/RRR2-21/2	1070.506	1071.252	-1636.628	0.277	573.737	0.281	14	0.109	R.KLIGATDPQK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1071.250	1071.252	-2.127	0.258	565.303	0.247	13	0.105	-.KLIGATDPQK.-
R2/RRR2-22/2	1070.929	1071.252	-302.466	0.322	437.414	0.265	12	0.103	-.KLIGATDPQK.-
R2/RRR2-21/2	987.376	988.163	-1816.085	0.158	526.740	0.258	11	0.103	-.GLISEILSR.-
R2/RRR2-21/2	987.419	988.163	-1771.614	0.102	675.201	0.126	12	0.100	-.GLISEILSR.-
R2/RRR2-21/2	987.420	988.163	-1770.744	0.131	453.904	0.265	11	0.090	-.GLISEILSR.-
R2/RRR2-5/2	1211.144	1211.310	-136.940	0.508	1312.728	0.427	18	0.159	R.VDDVINVSGHR.I
R2/RRR2-5/2	1226.000	1226.315	-257.218	0.469	1218.539	0.432	17	0.152	K.TNICYNAVDR.N
R2/RRR2-5/2	1061.573	1062.246	-1580.737	0.407	1088.090	0.486	13	0.148	K.GPVQISWFK.G
R2/RRR2-5/2	1582.191	1582.785	-1010.762	0.482	779.579	0.595	19	0.144	R.VLGSVGEPINPSAWR.W
R2/RRR2-5/2	1110.108	1109.294	-168.263	0.451	1289.209	0.302	14	0.134	R.VCQLANYLK.S
R2/RRR2-5/2	1225.809	1226.315	-1232.208	0.392	1075.891	0.391	16	0.134	K.TNICYNAVDR.N
R2/RRR2-5/2	1582.295	1582.785	-310.802	0.433	762.236	0.533	19	0.133	R.VLGSVGEPINPSAWR.W
R2/RRR2-5/2	1707.944	1708.894	-1145.523	0.336	1042.937	0.380	16	0.125	R.DVWWQDVVTSFPTK.C
R2/RRR2-5/2	1708.094	1708.894	-1056.896	0.366	774.478	0.385	14	0.112	R.DVWWQDVVTSFPTK.C
R2/RRR2-5/2	1110.190	1109.294	-93.699	0.380	1141.599	0.184	14	0.111	R.VCQLANYLK.S
R2/RRR2-5/2	1061.509	1062.246	-1640.810	0.264	496.087	0.387	10	0.106	K.GPVQISWFK.G
R2/RRR2-5/3	1538.481	1538.727	-160.735	0.383	1189.737	0.398	27	0.104	R.IGTAEVESALVSHPK.C
R2/RRR2-5/3	1211.236	1211.310	-60.774	0.466	866.609	0.479	21	0.098	R.VDDVINVSGHR.I
R2/RRR2-5/3	1538.391	1538.727	-219.241	0.391	823.811	0.426	25	0.089	R.IGTAEVESALVSHPK.C
R2/RRR2-6/3	1540.123	1538.727	257.715	0.434	548.054	0.495	21	0.088	-.IGTAEVESALVSHPK.-
R2/RRR2-5/3	1512.840	1512.683	103.939	0.369	1035.458	0.340	25	0.082	K.CAEAAVVAVEHEVK.G
R2/RRR2-1/3	1538.947	1538.727	143.268	0.393	607.675	0.363	22	0.073	-.IGTAEVESALVSHPK.-
R2/RRR2-5/3	1538.515	1538.727	-138.528	0.289	437.415	0.335	22	0.062	-.IGTAEVESALVSHPK.-
R2/RRR2-12/2	1308.097	1308.457	-276.268	0.505	2285.285	0.473	20	0.292	K.VSCADITTLATR.D
R2/RRR2-12/2	1308.171	1308.457	-219.628	0.438	2155.184	0.455	20	0.265	K.VSCADITTLATR.D
R2/RRR2-13/2	1308.198	1308.457	-198.752	0.453	2088.932	0.487	20	0.264	K.VSCADITTLATR.D
R2/RRR2-12/2	1308.201	1308.457	-196.412	0.485	2150.173	0.439	20	0.259	K.VSCADITTLATR.D
R2/RRR2-13/2	1308.186	1308.457	-207.739	0.470	2083.478	0.427	19	0.245	K.VSCADITTLATR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1308.027	1308.457	-330.105	0.429	2012.564	0.438	20	0.238	K.VSCADITTLATR.D
R2/RRR2-13/2	1308.090	1308.457	-281.323	0.462	2019.705	0.419	19	0.233	K.VSCADITTLATR.D
R2/RRR2-17/2	1308.045	1308.457	-316.060	0.439	1881.493	0.423	19	0.215	K.VSCADITTLATR.D
R2/RRR2-12/2	1734.382	1734.933	-897.360	0.508	1564.540	0.572	25	0.208	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-13/2	1736.327	1734.933	227.649	0.600	1359.034	0.602	24	0.191	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-17/2	1308.376	1308.457	-62.568	0.451	1824.058	0.345	19	0.189	K.VSCADITTLATR.D
R2/RRR2-12/2	1734.339	1734.933	-922.020	0.501	1371.489	0.584	24	0.188	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-16/2	1735.675	1734.933	-149.096	0.549	1390.559	0.569	24	0.187	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-14/2	1308.038	1308.457	-321.397	0.350	1835.751	0.314	19	0.185	K.VSCADITTLATR.D
R2/RRR2-13/2	1736.450	1734.933	-279.402	0.557	1218.818	0.613	23	0.179	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-17/2	1735.265	1734.933	191.804	0.571	1254.098	0.596	23	0.179	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-14/2	1736.268	1734.933	193.315	0.580	1328.075	0.543	24	0.175	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-12/2	1735.392	1734.933	265.164	0.554	1267.441	0.568	23	0.174	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-1/2	1735.162	1734.933	132.190	0.566	1290.615	0.554	23	0.173	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-16/2	1734.291	1734.933	-949.932	0.482	1179.208	0.562	22	0.164	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-10/2	1735.190	1734.933	148.276	0.525	1271.752	0.513	23	0.164	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-13/2	984.597	985.163	-1594.702	0.465	1409.810	0.418	17	0.163	R.DIGIAAGLVR.I
R2/RRR2-12/2	985.002	985.163	-163.096	0.560	1256.159	0.475	16	0.160	R.DIGIAAGLVR.I
R2/RRR2-17/2	984.720	985.163	-450.857	0.471	1253.552	0.461	16	0.157	R.DIGIAAGLVR.I
R2/RRR2-3/2	1735.163	1734.933	132.825	0.519	1080.888	0.549	22	0.155	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-12/2	984.507	985.163	-1686.877	0.449	1233.375	0.453	16	0.154	R.DIGIAAGLVR.I
R2/RRR2-17/2	985.038	985.163	-127.169	0.537	1307.392	0.421	16	0.154	R.DIGIAAGLVR.I
R2/RRR2-13/2	984.503	985.163	-1690.739	0.422	1270.650	0.436	16	0.154	R.DIGIAAGLVR.I
R2/RRR2-11/2	984.971	985.163	-195.421	0.500	1218.290	0.451	16	0.153	R.DIGIAAGLVR.I
R2/RRR2-12/2	984.652	985.163	-1538.907	0.449	1236.357	0.441	16	0.152	R.DIGIAAGLVR.I
R2/RRR2-13/2	984.995	985.163	-171.053	0.482	1256.970	0.428	16	0.152	R.DIGIAAGLVR.I
R2/RRR2-14/2	984.471	985.163	-1724.001	0.453	1313.794	0.401	16	0.151	R.DIGIAAGLVR.I
R2/RRR2-17/2	985.197	985.163	35.032	0.496	1272.063	0.417	16	0.151	R.DIGIAAGLVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1734.512	1734.933	-243.361	0.488	1174.228	0.488	22	0.151	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-14/2	985.020	985.163	-145.070	0.472	1315.276	0.399	16	0.151	R.DIGIAAGLVR.I
R2/RRR2-1/2	1734.173	1734.933	-1017.916	0.426	1120.633	0.502	22	0.149	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-12/3	1735.104	1734.933	98.457	0.456	1185.219	0.580	28	0.148	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-2/2	1734.424	1734.933	-872.772	0.506	1056.789	0.524	21	0.148	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-14/2	1733.727	1734.933	-1276.083	0.349	1154.127	0.485	22	0.148	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-10/2	1734.381	1734.933	-897.431	0.479	1026.135	0.534	21	0.148	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-12/2	1571.596	1571.714	-75.460	0.515	755.102	0.559	22	0.144	K.DVPVNSVTQELDVR.T
R2/RRR2-14/2	984.982	985.163	-183.610	0.511	1231.240	0.393	16	0.144	R.DIGIAAGLVR.I
R2/RRR2-11/2	985.131	985.163	-32.452	0.464	1214.703	0.396	16	0.144	R.DIGIAAGLVR.I
R2/RRR2-11/2	985.319	985.163	159.413	0.452	1230.876	0.382	16	0.142	R.DIGIAAGLVR.I
R2/RRR2-14/2	1734.247	1734.933	-975.513	0.481	1075.766	0.470	21	0.141	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-11/2	1734.285	1734.933	-953.395	0.461	1061.375	0.470	21	0.140	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-16/2	1733.843	1734.933	-1208.913	0.362	1126.342	0.438	21	0.139	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-11/2	1571.411	1571.714	-193.744	0.451	836.657	0.495	22	0.137	K.DVPVNSVTQELDVR.T
R2/RRR2-12/2	1572.160	1571.714	284.440	0.519	672.565	0.522	21	0.136	K.DVPVNSVTQELDVR.T
R2/RRR2-14/2	1572.302	1571.714	-263.173	0.519	728.273	0.487	22	0.134	K.DVPVNSVTQELDVR.T
R2/RRR2-14/2	1572.299	1571.714	-264.653	0.524	769.928	0.474	22	0.134	K.DVPVNSVTQELDVR.T
R2/RRR2-2/2	1733.880	1734.933	-1187.774	0.325	1192.055	0.372	21	0.133	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-13/2	1571.248	1571.714	-297.558	0.436	781.003	0.471	22	0.132	K.DVPVNSVTQELDVR.T
R2/RRR2-12/2	1571.284	1571.714	-274.408	0.435	764.755	0.475	22	0.132	K.DVPVNSVTQELDVR.T
R2/RRR2-12/2	1571.451	1571.714	-168.028	0.474	799.028	0.448	22	0.131	K.DVPVNSVTQELDVR.T
R2/RRR2-13/2	1571.253	1571.714	-294.674	0.478	666.668	0.484	21	0.131	K.DVPVNSVTQELDVR.T
R2/RRR2-1/2	1571.359	1571.714	-226.554	0.441	738.436	0.468	21	0.130	K.DVPVNSVTQELDVR.T
R2/RRR2-12/2	1571.204	1571.714	-963.905	0.444	753.778	0.445	22	0.129	K.DVPVNSVTQELDVR.T
R2/RRR2-13/2	1572.261	1571.714	-289.345	0.518	766.396	0.435	22	0.129	K.DVPVNSVTQELDVR.T
R2/RRR2-1/2	1571.480	1571.714	-149.560	0.434	806.553	0.433	22	0.129	K.DVPVNSVTQELDVR.T
R2/RRR2-12/2	1141.392	1141.349	37.479	0.510	1024.933	0.362	18	0.129	R.RDIGIAAGLVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1572.054	1571.714	216.468	0.413	273.152	0.535	19	0.128	K.DVPVNSVTQELDVR.T
R2/RRR2-6/2	1571.451	1571.714	-168.340	0.420	646.712	0.472	20	0.127	K.DVPVNSVTQELDVR.T
R2/RRR2-3/2	1734.194	1734.933	-1005.831	0.360	981.810	0.384	20	0.123	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-11/2	1571.191	1571.714	-972.641	0.408	666.364	0.415	21	0.123	K.DVPVNSVTQELDVR.T
R2/RRR2-12/3	1547.652	1546.856	-132.568	0.539	1149.698	0.502	30	0.122	R.FDGSKPIMDPVLVK.K
R2/RRR2-12/2	1734.476	1734.933	-264.685	0.418	992.878	0.348	21	0.120	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-6/2	985.919	985.163	-247.763	0.388	675.583	0.362	15	0.119	R.DIGIAAGLVR.I
R2/RRR2-12/2	1138.159	1138.307	-130.230	0.396	677.079	0.387	13	0.118	R.WHVAEALRR.D
R2/RRR2-12/2	1137.578	1138.307	-1524.740	0.396	765.677	0.376	12	0.118	R.WHVAEALRR.D
R2/RRR2-3/2	985.248	985.163	87.348	0.378	799.780	0.326	15	0.118	R.DIGIAAGLVR.I
R2/RRR2-14/2	1570.984	1571.714	-1104.793	0.333	782.833	0.333	22	0.117	K.DVPVNSVTQELDVR.T
R2/RRR2-2/2	1733.536	1734.933	-1387.040	0.291	868.649	0.384	19	0.117	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-3/2	1734.619	1734.933	-181.515	0.406	823.165	0.387	19	0.117	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-9/2	1571.364	1571.714	-223.826	0.381	504.265	0.383	18	0.117	K.DVPVNSVTQELDVR.T
R2/RRR2-12/2	1141.136	1141.349	-187.293	0.518	905.973	0.309	17	0.116	R.RDIGIAAGLVR.I
R2/RRR2-11/2	1570.636	1571.714	-1327.283	0.306	519.901	0.341	20	0.115	K.DVPVNSVTQELDVR.T
R2/RRR2-4/2	986.064	985.163	-99.968	0.333	580.899	0.320	14	0.114	R.DIGIAAGLVR.I
R2/RRR2-11/2	1733.528	1734.933	-1391.778	0.258	683.617	0.394	21	0.114	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-12/2	1141.369	1141.349	17.849	0.431	742.561	0.319	16	0.114	R.RDIGIAAGLVR.I
R2/RRR2-1/2	1570.907	1571.714	-1153.872	0.312	577.791	0.356	20	0.113	-.DVPVNSVTQELDVR.-
R2/RRR2-2/2	1570.862	1571.714	-1182.821	0.294	422.473	0.276	17	0.112	K.DVPVNSVTQELDVR.T
R2/RRR2-2/2	1571.210	1571.714	-960.239	0.415	362.354	0.336	15	0.110	-.DVPVNSVTQELDVR.-
R2/RRR2-12/2	1138.245	1138.307	-54.494	0.379	388.665	0.346	10	0.108	-.WHVAEALRR.-
R2/RRR2-17/2	1307.741	1308.457	-1316.323	0.276	1131.429	0.149	16	0.107	K.VSCADITTLATR.D
R2/RRR2-9/2	1733.985	1734.933	-1127.048	0.284	400.011	0.355	14	0.107	R.DAIVASGGPYFDVPLGR.R
R2/RRR2-12/3	1564.093	1562.856	152.355	0.387	392.629	0.487	23	0.089	R.FDGSKPIM*DPVLVK.K
R2/RRR2-12/3	1546.378	1546.856	-309.834	0.442	912.853	0.380	28	0.086	R.FDGSKPIMDPVLVK.K
R2/RRR2-12/3	1563.818	1562.856	-24.366	0.372	348.021	0.402	21	0.076	-.FDGSKPIM*DPVLVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/3	1546.950	1546.856	61.163	0.342	699.346	0.278	25	0.072	R.FDGSKPIMDPVLVK.K
R2/RRR2-15/3	1819.993	1820.945	-1075.577	0.585	2489.969	0.526	35	0.359	K.NPGEQSHAANAGLDIAVR.L
R2/RRR2-15/2	1820.353	1820.945	-877.109	0.567	2014.882	0.609	26	0.291	K.NPGEQSHAANAGLDIAVR.L
R2/RRR2-15/2	1820.474	1820.945	-259.512	0.540	2072.731	0.566	26	0.288	K.NPGEQSHAANAGLDIAVR.L
R2/RRR2-15/3	1821.206	1820.945	144.055	0.572	1951.211	0.553	35	0.251	K.NPGEQSHAANAGLDIAVR.L
R2/RRR2-15/2	1820.401	1820.945	-850.451	0.558	1677.190	0.632	25	0.243	K.NPGEQSHAANAGLDIAVR.L
R2/RRR2-15/3	1820.566	1820.945	-208.664	0.565	1826.202	0.578	31	0.241	K.NPGEQSHAANAGLDIAVR.L
R2/RRR2-15/2	1534.978	1534.657	209.732	0.510	1662.530	0.559	22	0.224	R.LAWHSAGTFDVSSR.T
R2/RRR2-15/2	1534.266	1534.657	-256.131	0.513	1388.569	0.496	20	0.175	R.LAWHSAGTFDVSSR.T
R2/RRR2-15/2	1534.262	1534.657	-258.845	0.478	1260.181	0.547	20	0.173	R.LAWHSAGTFDVSSR.T
R2/RRR2-15/2	1310.117	1310.398	-215.096	0.465	1355.426	0.444	19	0.164	R.LPDATQGSDHLR.Q
R2/RRR2-15/2	1310.059	1310.398	-259.966	0.493	1487.414	0.375	20	0.163	R.LPDATQGSDHLR.Q
R2/RRR2-15/2	1310.093	1310.398	-233.698	0.470	1391.088	0.386	19	0.156	R.LPDATQGSDHLR.Q
R2/RRR2-15/3	1534.790	1534.657	86.856	0.552	1385.309	0.505	27	0.147	R.LAWHSAGTFDVSSR.T
R2/RRR2-15/2	1601.111	1600.751	225.768	0.473	537.683	0.589	21	0.135	K.SYPTVSDEYLAAVGK.A
R2/RRR2-15/2	1600.252	1600.751	-312.440	0.398	627.459	0.548	22	0.131	K.SYPTVSDEYLAAVGK.A
R2/RRR2-15/2	1600.277	1600.751	-296.827	0.400	647.883	0.511	22	0.128	K.SYPTVSDEYLAAVGK.A
R2/RRR2-15/3	1534.243	1534.657	-271.267	0.495	1231.304	0.463	27	0.121	R.LAWHSAGTFDVSSR.T
R2/RRR2-15/2	1559.329	1558.870	294.869	0.447	688.083	0.385	18	0.116	K.ALMADPAFRPLVEK.Y
R2/RRR2-15/2	1574.619	1574.870	-159.701	0.388	593.525	0.361	19	0.114	K.ALM*ADPAFRPLVEK.Y
R2/RRR2-15/2	1574.516	1574.870	-225.498	0.393	528.767	0.340	18	0.111	K.ALM*ADPAFRPLVEK.Y
R2/RRR2-15/2	1574.425	1574.870	-283.058	0.391	688.341	0.256	20	0.108	K.ALM*ADPAFRPLVEK.Y
R2/RRR2-15/3	1534.490	1534.657	-109.768	0.516	1176.619	0.420	25	0.107	-.LAWHSAGTFDVSSR.-
R2/RRR2-15/3	1310.196	1310.398	-154.632	0.459	689.510	0.445	24	0.091	R.LPDATQGSDHLR.Q
R2/RRR2-15/3	1310.275	1310.398	-94.772	0.457	680.966	0.433	24	0.090	R.LPDATQGSDHLR.Q
R2/RRR2-15/3	1310.281	1310.398	-90.006	0.397	615.379	0.435	23	0.088	R.LPDATQGSDHLR.Q
R2/RRR2-17/3	1309.648	1310.398	-1340.126	0.343	533.283	0.455	22	0.087	R.LPDATQGSDHLR.Q
R2/RRR2-16/3	1309.916	1310.398	-369.176	0.389	495.735	0.415	21	0.086	R.LPDATQGSDHLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/3	1310.917	1310.398	-368.381	0.485	980.396	0.356	26	0.086	R.LPDATQGSDHLR.Q
R2/RRR2-17/3	1310.826	1310.398	327.127	0.347	528.921	0.401	22	0.084	R.LPDATQGSDHLR.Q
R2/RRR2-16/3	1534.217	1534.657	-287.910	0.370	1000.196	0.335	25	0.082	R.LAWHSAGTFDVSSR.T
R2/RRR2-14/3	1310.471	1310.398	55.617	0.369	479.881	0.327	21	0.081	R.LPDATQGSDHLR.Q
R2/RRR2-16/3	1310.682	1310.398	217.308	0.320	490.130	0.312	19	0.078	R.LPDATQGSDHLR.Q
R2/RRR2-16/2	1608.837	1608.861	-14.810	0.518	3117.305	0.477	22	0.485	K.ALLTELQALEEHLK.A
R2/RRR2-16/2	1608.768	1608.861	-57.887	0.522	2902.524	0.462	22	0.423	K.ALLTELQALEEHLK.A
R2/RRR2-16/2	1608.703	1608.861	-98.531	0.559	2615.168	0.500	20	0.370	K.ALLTELQALEEHLK.A
R2/RRR2-17/2	1607.830	1608.861	-1267.033	0.510	2547.685	0.438	21	0.335	K.ALLTELQALEEHLK.A
R2/RRR2-16/3	1829.852	1828.957	-57.458	0.537	1576.012	0.463	33	0.157	K.AAVGHPDTLGDCPFSQR.V
R2/RRR2-16/3	1122.162	1122.301	-124.243	0.531	1580.509	0.409	22	0.138	K.EHLIAGWAPK.V
R2/RRR2-17/3	1828.769	1828.957	-102.951	0.492	1466.238	0.424	31	0.135	K.AAVGHPDTLGDCPFSQR.V
R2/RRR2-16/3	1828.529	1828.957	-234.539	0.526	1312.491	0.458	31	0.127	K.AAVGHPDTLGDCPFSQR.V
R2/RRR2-17/2	990.429	990.095	338.581	0.330	680.056	0.538	13	0.127	K.VPVFNGGDGK.W
R2/RRR2-17/3	1122.244	1122.301	-50.755	0.482	1543.138	0.383	22	0.127	K.EHLIAGWAPK.V
R2/RRR2-16/2	1616.722	1616.885	-100.617	0.494	1063.860	0.356	17	0.125	K.LIDVQNKPDWFLK.I
R2/RRR2-17/2	1265.329	1264.488	-125.947	0.324	951.151	0.332	16	0.119	K.IFSCFTTFLK.S
R2/RRR2-16/2	990.145	990.095	50.561	0.342	562.071	0.444	13	0.118	K.VPVFNGGDGK.W
R2/RRR2-16/2	1616.475	1616.885	-254.467	0.456	949.042	0.328	16	0.115	K.LIDVQNKPDWFLK.I
R2/RRR2-17/2	989.737	990.095	-362.101	0.324	387.137	0.370	13	0.114	K.VPVFNGGDGK.W
R2/RRR2-17/2	989.472	990.095	-1644.508	0.283	457.677	0.434	13	0.114	K.VPVFNGGDGK.W
R2/RRR2-16/3	1498.071	1498.753	-1126.250	0.457	1381.705	0.384	26	0.114	K.LYHLQVALEHFK.G
R2/RRR2-17/2	990.926	990.095	-171.141	0.315	506.467	0.400	11	0.111	K.VPVFNGGDGK.W
R2/RRR2-16/2	989.281	990.095	-1838.763	0.227	422.758	0.454	12	0.110	K.VPVFNGGDGK.W
R2/RRR2-16/2	989.220	990.095	-1901.009	0.232	319.126	0.481	11	0.107	-.VPVFNGGDGK.-
R2/RRR2-16/2	1264.024	1264.488	-367.749	0.296	745.383	0.213	15	0.105	K.IFSCFTTFLK.S
R2/RRR2-17/3	1828.940	1828.957	-9.153	0.534	979.517	0.473	28	0.105	K.AAVGHPDTLGDCPFSQR.V
R2/RRR2-16/3	1498.423	1498.753	-221.044	0.491	1061.386	0.448	24	0.104	K.LYHLQVALEHFK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1616.735	1616.885	-92.968	0.395	633.101	0.269	15	0.104	-.LIDVQNKPDWFLK.-
R2/RRR2-16/2	1264.025	1264.488	-366.974	0.195	777.829	0.130	15	0.099	K.IFSCFTTFLK.S
R2/RRR2-17/3	1827.906	1828.957	-1125.243	0.449	1074.893	0.404	29	0.098	K.AAVGHPDTLGDCPFSQR.V
R2/RRR2-17/3	1122.568	1122.301	238.835	0.491	1202.912	0.316	20	0.088	K.EHLIAGWAPK.V
R2/RRR2-16/3	1121.933	1122.301	-329.051	0.442	1251.001	0.299	20	0.088	K.EHLIAGWAPK.V
R2/RRR2-16/3	1121.839	1122.301	-412.733	0.353	644.798	0.279	17	0.073	K.EHLIAGWAPK.V
R2/RRR2-17/3	1121.817	1122.301	-432.387	0.372	701.688	0.274	16	0.045	-.EHLIAGWAPK.-
R2/RRR2-14/2	1419.170	1419.517	-245.242	0.524	2204.610	0.557	19	0.306	K.TVDVEELTVEER.N
R2/RRR2-14/2	1418.579	1419.517	-1370.040	0.379	2173.305	0.473	19	0.275	K.TVDVEELTVEER.N
R2/RRR2-14/2	1418.651	1419.517	-1319.223	0.413	2074.367	0.512	19	0.269	K.TVDVEELTVEER.N
R2/RRR2-15/2	1419.075	1419.517	-312.038	0.464	1948.195	0.531	18	0.254	K.TVDVEELTVEER.N
R2/RRR2-15/2	1419.128	1419.517	-274.928	0.515	1857.966	0.561	18	0.249	K.TVDVEELTVEER.N
R2/RRR2-15/2	1418.681	1419.517	-1297.706	0.416	1979.304	0.450	18	0.237	K.TVDVEELTVEER.N
R2/RRR2-16/2	1418.883	1419.517	-1154.537	0.406	1877.260	0.500	18	0.235	K.TVDVEELTVEER.N
R2/RRR2-14/2	1774.542	1774.014	-266.643	0.597	1517.377	0.609	23	0.213	K.AAQDIALADLAPTHPIR.L
R2/RRR2-15/2	1215.910	1216.343	-357.460	0.417	1805.069	0.427	18	0.209	K.EAAESTM*VAYK.A
R2/RRR2-15/2	1773.456	1774.014	-881.248	0.548	1443.467	0.610	22	0.204	K.AAQDIALADLAPTHPIR.L
R2/RRR2-14/2	1774.473	1774.014	259.186	0.568	1483.858	0.587	22	0.203	K.AAQDIALADLAPTHPIR.L
R2/RRR2-14/2	1773.367	1774.014	-931.555	0.516	1522.513	0.557	23	0.201	K.AAQDIALADLAPTHPIR.L
R2/RRR2-15/2	1774.526	1774.014	-275.684	0.568	1455.403	0.573	22	0.196	K.AAQDIALADLAPTHPIR.L
R2/RRR2-15/2	1773.556	1774.014	-259.059	0.589	1451.443	0.569	22	0.194	K.AAQDIALADLAPTHPIR.L
R2/RRR2-14/3	1774.204	1774.014	107.570	0.462	1458.698	0.587	30	0.184	K.AAQDIALADLAPTHPIR.L
R2/RRR2-15/2	1655.284	1655.831	-937.430	0.494	1475.382	0.478	25	0.181	K.LLDSHLVPSSTAAESK.V
R2/RRR2-14/2	1655.207	1655.831	-984.223	0.466	1185.728	0.537	23	0.164	K.LLDSHLVPSSTAAESK.V
R2/RRR2-15/3	1774.887	1774.014	-71.930	0.411	1387.131	0.546	29	0.162	K.AAQDIALADLAPTHPIR.L
R2/RRR2-14/2	1655.494	1655.831	-204.242	0.454	1284.044	0.458	23	0.158	K.LLDSHLVPSSTAAESK.V
R2/RRR2-15/2	1655.362	1655.831	-283.991	0.485	1101.937	0.527	22	0.155	K.LLDSHLVPSSTAAESK.V
R2/RRR2-15/3	1773.390	1774.014	-918.501	0.390	1574.542	0.428	31	0.150	K.AAQDIALADLAPTHPIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/3	1655.858	1655.831	16.288	0.366	1376.024	0.495	30	0.144	K.LLDSHLVPSSTAAESK.V
R2/RRR2-15/3	1774.421	1774.014	229.999	0.451	1350.060	0.493	29	0.142	K.AAQDIALADLAPTHPIR.L
R2/RRR2-14/3	1656.197	1655.831	221.430	0.325	1405.428	0.479	31	0.142	K.LLDSHLVPSSTAAESK.V
R2/RRR2-14/3	1774.519	1774.014	-279.764	0.417	1238.148	0.533	28	0.141	K.AAQDIALADLAPTHPIR.L
R2/RRR2-15/2	1655.338	1655.831	-298.936	0.479	1033.845	0.477	21	0.141	K.LLDSHLVPSSTAAESK.V
R2/RRR2-14/2	1654.788	1655.831	-1238.551	0.415	1085.724	0.451	21	0.140	K.LLDSHLVPSSTAAESK.V
R2/RRR2-15/2	1215.934	1216.343	-337.717	0.434	949.385	0.462	16	0.136	K.EAAESTM*VAYK.A
R2/RRR2-14/3	1774.024	1774.014	5.713	0.386	1216.020	0.511	28	0.133	K.AAQDIALADLAPTHPIR.L
R2/RRR2-15/2	1215.448	1216.343	-1564.082	0.322	1080.170	0.398	16	0.132	K.EAAESTM*VAYK.A
R2/RRR2-15/2	1140.982	1140.271	-254.385	0.488	608.490	0.414	13	0.119	R.GNEEHVTLIK.E
R2/RRR2-14/2	1140.043	1140.271	-200.789	0.491	668.234	0.337	13	0.113	R.GNEEHVTLIK.E
R2/RRR2-14/2	1139.546	1140.271	-1518.776	0.416	561.318	0.317	13	0.112	R.GNEEHVTLIK.E
R2/RRR2-14/3	1655.686	1655.831	-88.201	0.322	1155.867	0.440	28	0.110	K.LLDSHLVPSSTAAESK.V
R2/RRR2-14/2	1139.627	1140.271	-1447.223	0.502	509.572	0.343	12	0.109	-.GNEEHVTLIK.-
R2/RRR2-15/3	1655.238	1655.831	-965.350	0.270	1162.061	0.427	28	0.107	K.LLDSHLVPSSTAAESK.V
R2/RRR2-15/2	1141.010	1140.271	-229.484	0.521	631.208	0.323	12	0.104	-.GNEEHVTLIK.-
R2/RRR2-15/2	1139.291	1140.271	-1743.507	0.397	530.916	0.299	12	0.103	-.GNEEHVTLIK.-
R2/RRR2-15/3	1655.275	1655.831	-942.917	0.341	927.628	0.360	26	0.083	K.LLDSHLVPSSTAAESK.V
R2/RRR2-14/2	1406.956	1407.463	-1073.908	0.466	1928.108	0.366	19	0.209	K.TVDSEELTVEER.N
R2/RRR2-14/2	1407.139	1407.463	-230.632	0.457	1849.492	0.397	19	0.207	K.TVDSEELTVEER.N
R2/RRR2-14/2	1407.140	1407.463	-229.849	0.468	1632.987	0.389	18	0.178	K.TVDSEELTVEER.N
R2/RRR2-14/2	1228.975	1229.342	-299.458	0.487	1304.307	0.409	17	0.153	K.DAAENTM*VAYK.A
R2/RRR2-14/2	1813.618	1814.078	-254.485	0.503	1200.603	0.475	21	0.151	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/2	1813.700	1814.078	-209.109	0.543	967.255	0.539	22	0.147	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/2	1813.627	1814.078	-249.353	0.556	989.884	0.529	22	0.147	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/3	1813.766	1814.078	-172.454	0.423	1361.410	0.496	33	0.142	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/2	1814.452	1814.078	206.376	0.563	933.134	0.510	21	0.139	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/2	1681.338	1681.869	-913.073	0.445	738.339	0.567	20	0.136	K.LLDSHLVPSSTAPESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1229.096	1229.342	-200.611	0.481	1035.608	0.401	17	0.134	K.DAAENTM*VAYK.A
R2/RRR2-14/2	1229.020	1229.342	-263.185	0.483	993.686	0.396	16	0.130	K.DAAENTM*VAYK.A
R2/RRR2-14/2	1814.364	1814.078	158.136	0.458	858.970	0.460	19	0.126	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/2	1681.420	1681.869	-267.648	0.429	449.986	0.524	16	0.118	K.LLDSHLVPSSTAPESK.V
R2/RRR2-14/2	1813.134	1814.078	-1075.350	0.348	596.836	0.402	18	0.111	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/3	1814.346	1814.078	148.177	0.376	1059.653	0.477	30	0.111	K.AAQDIALAELPPTHPIR.L
R2/RRR2-13/2	1407.013	1407.463	-320.630	0.289	738.295	0.331	14	0.109	K.TVDSEELTVEER.N
R2/RRR2-14/3	1814.234	1814.078	86.334	0.407	1079.470	0.447	30	0.107	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/3	1815.208	1814.078	71.584	0.368	1051.280	0.461	31	0.107	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/3	1814.746	1814.078	-183.729	0.386	719.539	0.483	27	0.094	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/3	1990.837	1991.106	-135.929	0.406	703.909	0.475	27	0.090	R.IISSIEQKEESRGNEDR.V
R2/RRR2-14/3	1813.543	1814.078	-849.084	0.312	1145.290	0.342	32	0.090	K.AAQDIALAELPPTHPIR.L
R2/RRR2-14/3	1990.975	1991.106	-65.998	0.381	653.722	0.460	28	0.086	R.IISSIEQKEESRGNEDR.V
R2/RRR2-14/3	1991.175	1991.106	34.451	0.380	547.997	0.475	26	0.085	R.IISSIEQKEESRGNEDR.V
R2/RRR2-14/2	1706.603	1706.964	-212.259	0.504	1976.550	0.550	22	0.266	R.IQDNLALVYLSSITR.T
R2/RRR2-14/2	1706.775	1706.964	-111.593	0.495	1853.150	0.560	23	0.250	R.IQDNLALVYLSSITR.T
R2/RRR2-14/2	1771.200	1771.000	113.048	0.525	1743.078	0.566	20	0.238	R.VEAVVVFNICDSYVR.R
R2/RRR2-14/2	1707.553	1706.964	-241.683	0.474	1680.360	0.498	22	0.209	R.IQDNLALVYLSSITR.T
R2/RRR2-14/2	1707.294	1706.964	193.799	0.532	1493.878	0.593	21	0.208	R.IQDNLALVYLSSITR.T
R2/RRR2-14/2	1295.973	1296.411	-339.127	0.443	1819.621	0.381	19	0.200	K.AYISSNLSLGDR.H
R2/RRR2-14/2	1296.017	1296.411	-305.011	0.403	1754.843	0.406	19	0.198	K.AYISSNLSLGDR.H
R2/RRR2-14/2	1296.151	1296.411	-201.355	0.450	1748.855	0.368	19	0.188	K.AYISSNLSLGDR.H
R2/RRR2-14/2	1181.994	1182.372	-320.536	0.398	1361.182	0.365	18	0.150	R.FISDAVASM*PK.L
R2/RRR2-14/2	1182.204	1182.372	-142.034	0.480	1259.315	0.397	18	0.148	R.FISDAVASM*PK.L
R2/RRR2-14/2	1052.796	1052.120	-307.908	0.485	858.509	0.466	15	0.137	K.YVDDVVEGR.V
R2/RRR2-14/2	1833.853	1834.153	-164.081	0.469	832.119	0.542	20	0.136	R.VIGTLLGSVLPDGTVHVR.N
R2/RRR2-14/2	1052.884	1052.120	-224.505	0.449	873.662	0.435	15	0.132	K.YVDDVVEGR.V
R2/RRR2-14/2	1833.692	1834.153	-251.966	0.446	560.982	0.538	18	0.122	R.VIGTLLGSVLPDGTVHVR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1052.851	1052.120	-255.910	0.353	801.285	0.376	13	0.119	K.YVDDVVEGR.V
R2/RRR2-14/2	1800.321	1800.993	-931.753	0.406	471.823	0.528	17	0.118	R.EVQSPIHLTVDTGFTR.G
R2/RRR2-14/2	1833.551	1834.153	-876.271	0.452	373.998	0.471	15	0.110	R.VIGTLLGSVLPDGTVHVR.N
R2/RRR2-14/2	1182.338	1182.372	-28.419	0.253	615.899	0.363	13	0.107	-.FISDAVASM*PK.-
R2/RRR2-14/3	1834.892	1834.153	-142.643	0.467	747.452	0.516	32	0.100	R.VIGTLLGSVLPDGTVHVR.N
R2/RRR2-14/3	1833.578	1834.153	-861.207	0.399	716.122	0.452	30	0.088	R.VIGTLLGSVLPDGTVHVR.N
R2/RRR2-14/3	1833.397	1834.153	-960.463	0.374	661.340	0.441	29	0.084	R.VIGTLLGSVLPDGTVHVR.N
R2/RRR2-15/2	1951.285	1951.208	39.241	0.601	2003.493	0.592	28	0.283	K.TAFIPFITAGDPDLATTAK.A
R2/RRR2-15/2	1951.407	1951.208	101.856	0.600	1958.184	0.599	28	0.278	K.TAFIPFITAGDPDLATTAK.A
R2/RRR2-15/2	1951.342	1951.208	68.855	0.600	1949.582	0.598	28	0.276	K.TAFIPFITAGDPDLATTAK.A
R2/RRR2-15/2	1096.126	1096.325	-182.663	0.386	1245.451	0.423	15	0.149	R.GIANFM*TVVK.E
R2/RRR2-15/2	1513.691	1512.735	-29.007	0.535	1054.035	0.465	19	0.141	K.AVAVGFGISTPEHVK.Q
R2/RRR2-15/2	1329.230	1329.438	-157.197	0.353	1051.437	0.454	22	0.140	R.QLGEAASPEEGLK.R
R2/RRR2-15/2	1329.159	1329.438	-210.541	0.379	785.371	0.484	19	0.129	R.QLGEAASPEEGLK.R
R2/RRR2-15/2	1096.147	1096.325	-163.112	0.332	968.997	0.411	14	0.127	R.GIANFM*TVVK.E
R2/RRR2-15/2	1329.171	1329.438	-201.419	0.379	830.971	0.390	20	0.122	R.QLGEAASPEEGLK.R
R2/RRR2-15/2	1913.601	1913.162	230.041	0.437	889.300	0.401	20	0.121	K.NNLELVLLTTPTTPTER.M
R2/RRR2-15/2	1044.074	1044.227	-146.539	0.446	738.871	0.350	14	0.118	K.VQSLLQDIK.Q
R2/RRR2-15/3	1922.140	1922.086	28.395	0.483	817.285	0.560	29	0.111	R.AEAAAVGEDERVISGTFAK.L
R2/RRR2-15/2	1913.505	1913.162	179.696	0.427	832.474	0.336	19	0.111	K.NNLELVLLTTPTTPTER.M
R2/RRR2-15/2	1043.453	1044.227	-1705.108	0.253	433.305	0.383	11	0.108	K.VQSLLQDIK.Q
R2/RRR2-15/2	1044.307	1044.227	77.191	0.332	664.410	0.253	13	0.108	K.VQSLLQDIK.Q
R2/RRR2-15/3	1921.365	1922.086	-898.232	0.226	558.951	0.332	21	0.065	-.AEAAAVGEDERVISGTFAK.-
R2/RRR2-4/2	1698.830	1698.943	-66.421	0.529	1395.970	0.469	20	0.171	R.LIWSTQFENFLATK.W
R2/RRR2-4/2	1197.253	1197.416	-136.483	0.499	1332.541	0.489	17	0.171	R.GRLNVLGNVVR.K
R2/RRR2-4/2	1698.256	1698.943	-995.826	0.417	1357.840	0.416	20	0.157	R.LIWSTQFENFLATK.W
R2/RRR2-4/2	1373.803	1374.524	-1256.322	0.452	1293.038	0.425	16	0.154	R.DWLSAYWTGFK.S
R2/RRR2-4/2	1216.954	1216.278	-267.379	0.497	821.739	0.489	15	0.139	K.VYYELDEER.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1197.162	1197.416	-212.891	0.426	991.181	0.425	16	0.133	R.GRLNVLGNVVR.K
R2/RRR2-4/2	1215.910	1216.278	-303.557	0.515	849.829	0.387	15	0.127	K.VYYELDEER.K
R2/RRR2-4/2	1215.925	1216.278	-291.269	0.559	842.642	0.352	15	0.122	K.VYYELDEER.K
R2/RRR2-4/2	1778.446	1779.023	-889.033	0.489	809.834	0.403	19	0.122	R.VEQLCPFPYDLIQR.E
R2/RRR2-4/2	983.680	984.178	-507.843	0.406	822.273	0.352	13	0.119	R.LNVLGNVVR.K
R2/RRR2-3/2	984.125	984.178	-53.884	0.407	723.787	0.358	12	0.116	R.LNVLGNVVR.K
R2/RRR2-1/2	1780.240	1779.023	122.378	0.479	602.807	0.415	16	0.115	R.VEQLCPFPYDLIQR.E
R2/RRR2-4/2	1466.149	1466.583	-296.925	0.370	666.777	0.376	15	0.113	K.YHLGTSYDRPTR.G
R2/RRR2-4/2	984.210	984.178	32.704	0.474	838.155	0.286	13	0.113	R.LNVLGNVVR.K
R2/RRR2-4/2	1777.991	1779.023	-1146.186	0.438	543.321	0.381	16	0.111	R.VEQLCPFPYDLIQR.E
R2/RRR2-4/2	984.221	984.178	43.402	0.455	697.411	0.305	12	0.110	-.LNVLGNVVR.-
R2/RRR2-3/2	983.698	984.178	-489.786	0.372	560.556	0.268	11	0.108	R.LNVLGNVVR.K
R2/RRR2-4/2	1465.541	1466.583	-1397.651	0.347	531.007	0.324	14	0.108	K.YHLGTSYDRPTR.G
R2/RRR2-7/2	984.526	984.178	355.036	0.277	618.187	0.235	12	0.106	R.LNVLGNVVR.K
R2/RRR2-4/2	1466.075	1466.583	-1032.023	0.395	444.444	0.274	13	0.105	K.YHLGTSYDRPTR.G
R2/RRR2-4/2	1373.661	1374.524	-1360.202	0.259	568.062	0.264	13	0.103	R.DWLSAYWTGFK.S
R2/RRR2-3/2	1375.105	1374.524	-305.543	0.339	670.644	0.207	14	0.103	R.DWLSAYWTGFK.S
R2/RRR2-4/3	1013.626	1013.323	300.701	0.397	984.697	0.294	18	0.074	R.KPLIVM*APK.N
R2/RRR2-3/2	1565.513	1565.711	-126.980	0.543	1759.526	0.460	19	0.212	K.IENINDQYWTLR.A
R2/RRR2-3/2	1217.982	1218.296	-258.308	0.411	1745.073	0.261	19	0.165	R.EGETAAEILER.I
R2/RRR2-3/2	1564.714	1565.711	-1280.506	0.396	1428.553	0.364	19	0.155	K.IENINDQYWTLR.A
R2/RRR2-3/2	1219.462	1218.296	136.285	0.507	1372.400	0.339	17	0.145	R.EGETAAEILER.I
R2/RRR2-3/2	1241.436	1240.473	-29.549	0.551	1106.746	0.435	15	0.143	K.SKEDILLFFK.L
R2/RRR2-3/2	1244.154	1243.349	-156.925	0.483	1090.173	0.424	18	0.142	K.VELSNPDAELR.L
R2/RRR2-3/2	1240.405	1240.473	-54.349	0.540	1089.581	0.423	15	0.140	K.SKEDILLFFK.L
R2/RRR2-3/2	1241.513	1240.473	32.879	0.584	1048.986	0.405	15	0.134	K.SKEDILLFFK.L
R2/RRR2-3/2	1160.342	1159.360	-15.048	0.412	1143.049	0.359	16	0.134	K.AEAHLYTIIK.V
R2/RRR2-3/2	1243.165	1243.349	-148.481	0.464	924.713	0.403	17	0.129	K.VELSNPDAELR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1217.757	1218.296	-1267.603	0.360	1166.492	0.273	16	0.122	R.EGETAAEILER.I
R2/RRR2-3/2	1356.454	1357.490	-1505.267	0.328	968.364	0.347	14	0.119	K.ESFYDLQLDVK.G
R2/RRR2-3/2	1160.351	1159.360	-7.028	0.377	836.606	0.265	15	0.111	K.AEAHLYTIIK.V
R2/RRR2-1/2	1357.683	1357.490	142.340	0.415	542.095	0.352	14	0.110	-.ESFYDLQLDVK.-
R2/RRR2-3/2	1158.788	1159.360	-1359.897	0.296	431.858	0.337	11	0.107	K.AEAHLYTIIK.V
R2/RRR2-3/3	1158.854	1159.360	-1302.990	0.478	452.699	0.494	18	0.091	K.AEAHLYTIIK.V
R2/RRR2-3/3	1939.808	1939.146	-174.882	0.464	764.936	0.426	24	0.083	-.SLEKPKEDDFCLELSK.-
R2/RRR2-3/3	1159.148	1159.360	-183.232	0.392	269.268	0.401	15	0.078	-.AEAHLYTIIK.-
R2/RRR2-3/3	1501.799	1501.667	87.868	0.424	953.605	0.283	27	0.073	K.VARDEDLKEQIGK.N
R2/RRR2-3/3	1501.087	1501.667	-1056.207	0.396	744.242	0.264	23	0.069	K.VARDEDLKEQIGK.N
R2/RRR2-11/2	1442.189	1442.643	-315.866	0.492	1754.877	0.595	21	0.243	R.VPTANVSVVDLTAR.I
R2/RRR2-11/2	1441.718	1442.643	-1339.219	0.491	1710.116	0.603	20	0.238	R.VPTANVSVVDLTAR.I
R2/RRR2-11/2	1675.180	1675.781	-958.894	0.477	1749.038	0.549	19	0.232	K.LVSWYDNEWGYSR.R
R2/RRR2-11/2	1277.354	1277.538	-143.932	0.446	1775.345	0.435	18	0.208	R.RVLDLLSYVAK.V
R2/RRR2-11/2	1675.655	1675.781	-75.304	0.449	1418.657	0.547	18	0.189	K.LVSWYDNEWGYSR.R
R2/RRR2-12/2	1443.607	1442.643	-24.732	0.490	1274.379	0.575	19	0.180	-.VPTANVSVVDLTAR.-
R2/RRR2-11/2	1675.428	1675.781	-211.239	0.465	1358.086	0.515	18	0.176	K.LVSWYDNEWGYSR.R
R2/RRR2-12/2	1442.385	1442.643	-179.244	0.493	1139.946	0.600	20	0.172	R.VPTANVSVVDLTAR.I
R2/RRR2-11/2	1441.675	1442.643	-1368.983	0.468	1306.033	0.530	18	0.171	R.VPTANVSVVDLTAR.I
R2/RRR2-11/2	1277.369	1277.538	-132.236	0.437	1350.242	0.446	16	0.162	R.RVLDLLSYVAK.V
R2/RRR2-11/2	1276.672	1277.538	-1465.838	0.440	1332.658	0.452	16	0.162	R.RVLDLLSYVAK.V
R2/RRR2-11/2	1121.283	1121.351	-61.106	0.475	1029.166	0.558	16	0.159	R.VLDLLSYVAK.V
R2/RRR2-11/2	1122.231	1121.351	-107.640	0.547	1045.837	0.499	16	0.151	R.VLDLLSYVAK.V
R2/RRR2-11/2	1121.542	1121.351	170.890	0.404	1066.759	0.500	16	0.149	R.VLDLLSYVAK.V
R2/RRR2-11/2	1178.023	1178.320	-253.039	0.407	1205.412	0.352	16	0.135	K.AGISLNDNFVK.L
R2/RRR2-11/2	1178.203	1178.320	-99.305	0.427	1147.003	0.354	17	0.133	K.AGISLNDNFVK.L
R2/RRR2-11/2	1387.078	1386.536	-331.417	0.467	763.513	0.491	20	0.131	R.GAAQNIIPSSTGAAK.A
R2/RRR2-11/2	1386.184	1386.536	-255.229	0.445	832.131	0.455	21	0.129	R.GAAQNIIPSSTGAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1386.106	1386.536	-311.422	0.416	807.225	0.462	21	0.129	R.GAAQNIIPSSTGAAK.A
R2/RRR2-12/2	1386.108	1386.536	-310.096	0.462	843.938	0.399	21	0.123	R.GAAQNIIPSSTGAAK.A
R2/RRR2-12/2	1386.112	1386.536	-307.269	0.415	997.433	0.357	20	0.123	R.GAAQNIIPSSTGAAK.A
R2/RRR2-12/2	1386.201	1386.536	-242.242	0.411	647.553	0.346	18	0.111	R.GAAQNIIPSSTGAAK.A
R2/RRR2-12/2	1441.692	1442.643	-1357.588	0.396	751.169	0.264	16	0.105	-.VPTANVSVVDLTAR.-
R2/RRR2-11/3	1388.087	1388.488	-289.705	0.418	413.680	0.544	18	0.093	K.YM*LEYDSTHGR.F
R2/RRR2-11/3	1388.298	1388.488	-136.736	0.420	448.627	0.500	18	0.089	K.YM*LEYDSTHGR.F
R2/RRR2-11/3	1388.433	1388.488	-39.368	0.434	509.138	0.479	19	0.088	K.YM*LEYDSTHGR.F
R2/RRR2-15/2	1400.434	1401.636	-1576.809	0.342	824.214	0.417	16	0.121	R.TIKDEGVIALWR.G
R2/RRR2-15/2	1400.561	1401.636	-1485.925	0.313	813.482	0.395	17	0.118	R.TIKDEGVIALWR.G
R2/RRR2-15/2	895.943	895.976	-36.844	0.239	790.095	0.310	12	0.108	K.GIADCFGR.T
R2/RRR2-15/2	895.768	895.976	-233.265	0.186	782.052	0.354	12	0.107	K.GIADCFGR.T
R2/RRR2-15/3	1401.106	1401.636	-1095.136	0.367	1079.081	0.279	21	0.076	R.TIKDEGVIALWR.G
R2/RRR2-15/3	1401.218	1401.636	-298.636	0.322	878.345	0.104	20	0.035	-.TIKDEGVIALWR.-
R2/RRR2-12/2	1726.585	1725.878	-170.588	0.543	1973.167	0.648	25	0.296	K.ATGTVVVSDSGDFATIGK.Y
R2/RRR2-12/2	1725.302	1725.878	-916.205	0.486	1956.741	0.588	25	0.274	K.ATGTVVVSDSGDFATIGK.Y
R2/RRR2-12/2	1725.380	1725.878	-289.427	0.496	1737.302	0.604	24	0.244	K.ATGTVVVSDSGDFATIGK.Y
R2/RRR2-12/3	1558.309	1558.759	-289.430	0.577	1603.673	0.500	32	0.172	K.KLDADGAAALDIEKK.S
R2/RRR2-12/2	1918.790	1919.168	-197.784	0.546	1060.219	0.617	25	0.170	K.YKPQDATTNPSLILAASK.K
R2/RRR2-12/2	1918.506	1919.168	-868.994	0.517	826.264	0.603	22	0.148	K.YKPQDATTNPSLILAASK.K
R2/RRR2-12/2	1522.247	1522.639	-258.315	0.447	946.278	0.439	21	0.134	K.EYAKEEDPGVASVK.S
R2/RRR2-12/2	1522.015	1522.639	-1070.192	0.418	881.824	0.438	20	0.129	K.EYAKEEDPGVASVK.S
R2/RRR2-12/2	1405.184	1405.664	-342.743	0.455	984.709	0.404	17	0.128	K.FAADAVTLKDILK.K
R2/RRR2-12/2	1150.005	1150.306	-262.930	0.429	571.214	0.454	15	0.123	K.LIDQAVEYAK.K
R2/RRR2-12/2	1150.130	1150.306	-153.892	0.365	480.181	0.421	16	0.118	K.LIDQAVEYAK.K
R2/RRR2-12/3	1229.583	1229.450	108.516	0.486	1715.262	0.268	21	0.118	K.ALHIIELYEK.E
R2/RRR2-12/3	1229.010	1229.450	-359.309	0.380	1810.657	0.199	22	0.111	K.ALHIIELYEK.E
R2/RRR2-12/3	1558.560	1558.759	-127.948	0.520	1130.942	0.428	29	0.106	K.KLDADGAAALDIEKK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1406.325	1405.664	-241.997	0.288	368.419	0.328	14	0.105	K.FAADAVTLKDILK.K
R2/RRR2-11/3	1644.492	1643.995	303.564	0.514	1751.781	0.530	33	0.200	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/3	1643.912	1643.995	-50.364	0.485	1617.223	0.555	32	0.190	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/3	1643.967	1643.995	-16.625	0.479	1551.824	0.523	31	0.171	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/3	1644.085	1643.995	54.869	0.502	1506.803	0.532	31	0.168	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/2	1643.570	1643.995	-259.136	0.510	1297.804	0.492	22	0.165	K.TLLLGEKPVTVFGIR.N
R2/RRR2-13/3	1644.623	1643.995	-226.706	0.481	1427.695	0.552	32	0.163	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/3	1644.992	1643.995	-1.803	0.526	1437.013	0.517	32	0.154	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/2	1643.703	1643.995	-177.774	0.514	1073.507	0.488	20	0.146	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/2	1644.758	1643.995	-144.460	0.489	976.040	0.509	20	0.143	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/2	1643.788	1643.995	-125.775	0.498	966.186	0.501	20	0.141	K.TLLLGEKPVTVFGIR.N
R2/RRR2-10/3	1644.036	1643.995	25.491	0.451	1051.972	0.595	30	0.137	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/2	1643.747	1643.995	-151.104	0.507	710.160	0.529	19	0.133	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/2	1643.663	1643.995	-202.211	0.459	758.435	0.500	19	0.130	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/2	1643.430	1643.995	-955.069	0.468	771.506	0.482	20	0.130	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/3	1643.931	1643.995	-39.080	0.459	1158.829	0.510	29	0.126	K.TLLLGEKPVTVFGIR.N
R2/RRR2-13/3	1644.088	1643.995	57.214	0.388	1232.155	0.420	28	0.113	K.TLLLGEKPVTVFGIR.N
R2/RRR2-10/3	1643.848	1643.995	-89.692	0.311	1009.641	0.459	29	0.103	K.TLLLGEKPVTVFGIR.N
R2/RRR2-2/3	1643.930	1643.995	-39.415	0.366	904.267	0.474	26	0.103	K.TLLLGEKPVTVFGIR.N
R2/RRR2-11/3	1644.153	1643.995	96.643	0.452	830.711	0.482	26	0.101	K.TLLLGEKPVTVFGIR.N
R2/RRR2-10/3	1644.053	1643.995	35.656	0.396	972.259	0.396	27	0.093	K.TLLLGEKPVTVFGIR.N
R2/RRR2-2/3	1644.020	1643.995	15.549	0.359	699.080	0.431	23	0.089	K.TLLLGEKPVTVFGIR.N
R2/RRR2-10/2	1710.774	1711.936	-1267.726	0.502	1598.428	0.503	20	0.202	K.KLEEVYGTFEAPSLK.K
R2/RRR2-10/2	1349.248	1349.557	-229.729	0.474	1413.697	0.564	18	0.192	R.KGPLIVYGTEGSK.I
R2/RRR2-10/2	1350.241	1349.557	-234.819	0.525	1457.304	0.531	19	0.190	R.KGPLIVYGTEGSK.I
R2/RRR2-10/2	1349.064	1349.557	-366.712	0.473	1380.561	0.512	19	0.178	R.KGPLIVYGTEGSK.I
R2/RRR2-10/2	1446.242	1446.680	-303.129	0.536	1249.658	0.546	22	0.173	R.LNLLDLAPGGHLGR.F
R2/RRR2-10/2	1447.609	1446.680	-49.023	0.535	1147.000	0.510	22	0.158	R.LNLLDLAPGGHLGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1446.346	1446.680	-231.068	0.518	1112.240	0.510	21	0.155	R.LNLLDLAPGGHLGR.F
R2/RRR2-13/2	1798.429	1797.132	165.256	0.466	1082.803	0.496	21	0.144	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-9/2	1797.150	1797.132	9.769	0.381	1300.767	0.384	23	0.143	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-10/2	1283.126	1283.416	-226.968	0.444	488.713	0.553	19	0.134	R.NLPGVDVANVER.L
R2/RRR2-10/2	1283.118	1283.416	-233.172	0.426	422.404	0.579	18	0.133	R.NLPGVDVANVER.L
R2/RRR2-2/2	1798.223	1797.132	50.479	0.463	951.008	0.482	20	0.132	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-6/3	1446.514	1446.680	-114.582	0.447	1575.262	0.371	27	0.131	R.LNLLDLAPGGHLGR.F
R2/RRR2-13/2	1872.180	1870.971	111.987	0.446	759.005	0.517	18	0.129	K.TMISDSDYAEFDNFSK.W
R2/RRR2-9/2	1284.122	1283.416	-229.939	0.429	405.292	0.502	18	0.127	R.NLPGVDVANVER.L
R2/RRR2-13/3	1446.760	1446.680	55.921	0.446	1474.688	0.394	28	0.126	R.LNLLDLAPGGHLGR.F
R2/RRR2-10/2	1283.082	1283.416	-260.756	0.351	488.544	0.530	19	0.126	R.NLPGVDVANVER.L
R2/RRR2-10/2	1796.474	1797.132	-925.979	0.299	1080.133	0.377	22	0.126	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-9/2	1283.274	1283.416	-110.733	0.460	516.857	0.461	18	0.126	R.NLPGVDVANVER.L
R2/RRR2-9/2	1445.574	1446.680	-1460.830	0.405	774.529	0.448	18	0.124	R.LNLLDLAPGGHLGR.F
R2/RRR2-1/3	1446.352	1446.680	-226.971	0.456	1428.701	0.397	26	0.124	R.LNLLDLAPGGHLGR.F
R2/RRR2-13/2	1283.174	1283.416	-189.270	0.373	369.998	0.502	17	0.124	R.NLPGVDVANVER.L
R2/RRR2-10/3	1446.637	1446.680	-29.514	0.394	1428.777	0.394	28	0.123	R.LNLLDLAPGGHLGR.F
R2/RRR2-7/3	1446.916	1446.680	164.184	0.482	1507.173	0.370	28	0.122	R.LNLLDLAPGGHLGR.F
R2/RRR2-14/2	1446.092	1446.680	-1101.148	0.401	717.911	0.437	18	0.122	R.LNLLDLAPGGHLGR.F
R2/RRR2-13/2	1283.065	1283.416	-274.596	0.332	275.939	0.527	15	0.120	R.NLPGVDVANVER.L
R2/RRR2-3/2	1797.378	1797.132	137.151	0.356	877.949	0.412	20	0.120	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-9/2	1796.048	1797.132	-1164.044	0.231	1216.404	0.260	21	0.119	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-9/2	1886.427	1886.970	-820.576	0.435	646.169	0.448	19	0.119	K.TM*ISDSDYAEFDNFSK.W
R2/RRR2-10/2	1039.002	1039.169	-161.513	0.329	462.603	0.447	14	0.118	K.LNPYFGTAR.K
R2/RRR2-13/2	1445.632	1446.680	-1420.711	0.393	455.266	0.487	15	0.118	R.LNLLDLAPGGHLGR.F
R2/RRR2-9/2	1282.382	1283.416	-1591.260	0.294	395.221	0.401	18	0.116	R.NLPGVDVANVER.L
R2/RRR2-13/3	1446.736	1446.680	39.292	0.377	1321.091	0.391	27	0.114	R.LNLLDLAPGGHLGR.F
R2/RRR2-9/2	1038.313	1039.169	-1792.554	0.315	332.196	0.433	11	0.113	K.LNPYFGTAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1446.425	1446.680	-176.542	0.347	431.950	0.406	16	0.113	R.LNLLDLAPGGHLGR.F
R2/RRR2-13/2	1282.519	1283.416	-1483.881	0.250	327.252	0.348	16	0.112	R.NLPGVDVANVER.L
R2/RRR2-8/3	1446.718	1446.680	26.344	0.470	1293.634	0.399	26	0.112	R.LNLLDLAPGGHLGR.F
R2/RRR2-5/3	1446.722	1446.680	29.517	0.371	1374.254	0.364	27	0.112	R.LNLLDLAPGGHLGR.F
R2/RRR2-2/3	1446.404	1446.680	-191.410	0.451	1343.763	0.379	26	0.112	R.LNLLDLAPGGHLGR.F
R2/RRR2-13/2	1349.231	1349.557	-242.346	0.324	301.250	0.414	14	0.111	R.KGPLIVYGTEGSK.I
R2/RRR2-12/3	1446.523	1446.680	-108.741	0.442	1212.355	0.411	26	0.110	R.LNLLDLAPGGHLGR.F
R2/RRR2-12/3	1446.406	1446.680	-189.505	0.459	1331.716	0.372	26	0.109	R.LNLLDLAPGGHLGR.F
R2/RRR2-13/3	1446.830	1446.680	104.534	0.390	1353.541	0.357	26	0.109	R.LNLLDLAPGGHLGR.F
R2/RRR2-2/2	1446.991	1446.680	216.139	0.343	426.309	0.378	14	0.109	R.LNLLDLAPGGHLGR.F
R2/RRR2-9/3	1797.262	1797.132	72.571	0.363	1390.664	0.343	35	0.109	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-10/2	1796.037	1797.132	-1169.981	0.263	845.933	0.319	19	0.108	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-10/3	1446.826	1446.680	101.488	0.398	1310.617	0.363	25	0.108	R.LNLLDLAPGGHLGR.F
R2/RRR2-9/3	1446.717	1446.680	25.836	0.428	1262.331	0.383	25	0.108	R.LNLLDLAPGGHLGR.F
R2/RRR2-7/3	1446.583	1446.680	-66.841	0.392	1183.298	0.405	26	0.107	R.LNLLDLAPGGHLGR.F
R2/RRR2-14/3	1446.882	1446.680	140.071	0.431	1375.584	0.343	26	0.107	R.LNLLDLAPGGHLGR.F
R2/RRR2-2/3	1445.872	1446.680	-1253.919	0.406	1209.288	0.377	25	0.103	R.LNLLDLAPGGHLGR.F
R2/RRR2-1/3	1446.351	1446.680	-227.860	0.427	1192.332	0.382	25	0.103	R.LNLLDLAPGGHLGR.F
R2/RRR2-15/3	1446.241	1446.680	-303.942	0.412	1353.739	0.320	26	0.101	R.LNLLDLAPGGHLGR.F
R2/RRR2-11/3	1446.389	1446.680	-201.697	0.406	1139.673	0.382	24	0.100	R.LNLLDLAPGGHLGR.F
R2/RRR2-1/2	1796.503	1797.132	-909.676	0.219	694.403	0.271	16	0.100	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-10/2	1796.296	1797.132	-1025.381	0.173	791.146	0.225	17	0.099	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-10/2	1038.415	1039.169	-1694.162	0.128	316.108	0.449	11	0.099	K.LNPYFGTAR.K
R2/RRR2-9/3	1446.827	1446.680	101.869	0.444	1194.605	0.359	24	0.098	R.LNLLDLAPGGHLGR.F
R2/RRR2-9/3	1446.776	1446.680	66.964	0.411	1310.874	0.319	26	0.098	R.LNLLDLAPGGHLGR.F
R2/RRR2-8/3	1446.241	1446.680	-304.451	0.437	1067.574	0.380	24	0.096	R.LNLLDLAPGGHLGR.F
R2/RRR2-4/3	1446.756	1446.680	53.001	0.423	1179.819	0.334	24	0.093	R.LNLLDLAPGGHLGR.F
R2/RRR2-10/3	1797.040	1797.132	-51.489	0.388	1138.875	0.356	35	0.093	R.VAVASALAATSVPSLVLAR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1446.208	1446.680	-326.808	0.444	1106.329	0.348	24	0.092	R.LNLLDLAPGGHLGR.F
R2/RRR2-6/3	1446.709	1446.680	20.124	0.354	944.624	0.334	23	0.085	R.LNLLDLAPGGHLGR.F
R2/RRR2-10/3	1797.538	1797.132	226.530	0.364	709.457	0.409	28	0.083	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-4/3	1446.703	1446.680	16.061	0.366	1036.945	0.298	22	0.083	-.LNLLDLAPGGHLGR.-
R2/RRR2-9/3	1797.507	1797.132	209.267	0.264	626.819	0.271	28	0.070	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-1/3	1796.564	1797.132	-875.577	0.265	782.063	0.262	26	0.068	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-7/3	1797.155	1797.132	12.895	0.340	729.634	0.229	28	0.067	R.VAVASALAATSVPSLVLAR.G
R2/RRR2-7/2	1346.491	1346.600	-80.892	0.568	2821.874	0.433	20	0.392	R.KFDLGALVDLVR.K
R2/RRR2-7/2	1346.321	1346.600	-207.493	0.541	2475.399	0.394	20	0.306	R.KFDLGALVDLVR.K
R2/RRR2-7/2	1346.059	1346.600	-1148.416	0.552	2245.175	0.414	19	0.270	R.KFDLGALVDLVR.K
R2/RRR2-7/2	1075.108	1075.198	-83.432	0.464	1524.897	0.367	16	0.164	R.VTAEDLASIR.M
R2/RRR2-7/2	1006.100	1006.202	-101.922	0.439	1205.750	0.318	14	0.132	K.GDVVM*SLLR.N
R2/RRR2-7/2	1200.380	1201.312	-1614.285	0.307	998.078	0.420	19	0.130	K.IVDPDTGASLGR.N
R2/RRR2-7/2	1075.038	1075.198	-149.380	0.458	1180.376	0.288	16	0.126	R.VTAEDLASIR.M
R2/RRR2-7/2	1201.064	1201.312	-206.695	0.361	720.221	0.466	17	0.124	K.IVDPDTGASLGR.N
R2/RRR2-7/2	1108.022	1108.183	-146.259	0.331	1022.776	0.322	15	0.121	K.GYLNDPEATK.N
R2/RRR2-2/2	1076.083	1075.198	-106.681	0.348	900.714	0.326	15	0.117	R.VTAEDLASIR.M
R2/RRR2-7/2	1200.462	1201.312	-1545.841	0.262	785.286	0.405	18	0.116	K.IVDPDTGASLGR.N
R2/RRR2-7/2	1958.671	1959.363	-866.427	0.396	475.704	0.530	17	0.116	K.HNITIAPFVPPIVVEIAK.S
R2/RRR2-7/2	1107.086	1108.183	-1899.953	0.266	929.037	0.316	15	0.114	K.GYLNDPEATK.N
R2/RRR2-7/2	1475.738	1474.773	-23.862	0.333	962.625	0.284	17	0.112	R.KFDLGALVDLVRK.H
R2/RRR2-7/2	1107.328	1108.183	-1680.833	0.292	1050.605	0.166	14	0.105	K.GYLNDPEATK.N
R2/RRR2-7/3	1346.395	1346.600	-152.430	0.451	1451.308	0.241	26	0.088	R.KFDLGALVDLVR.K
R2/RRR2-7/3	1346.448	1346.600	-113.413	0.393	1204.905	0.204	24	0.065	-.KFDLGALVDLVR.-
R2/RRR2-10/2	1664.170	1663.850	192.714	0.496	2809.025	0.453	25	0.407	K.AFGASEVIAVDVLDEK.L
R2/RRR2-10/2	1855.564	1856.027	-250.645	0.543	2471.490	0.602	27	0.379	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-10/2	1855.283	1856.027	-943.021	0.524	2390.314	0.636	26	0.374	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-10/2	1736.216	1736.813	-922.716	0.550	1858.419	0.543	20	0.250	K.GQEDLCESFFAYNR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1855.568	1856.027	-248.071	0.558	1469.211	0.655	23	0.220	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-10/2	1058.920	1058.210	-275.371	0.544	1585.945	0.553	17	0.213	R.GVDVAVEALGK.A
R2/RRR2-10/2	1059.055	1058.210	-147.010	0.555	1448.076	0.550	17	0.197	R.GVDVAVEALGK.A
R2/RRR2-10/3	1856.264	1856.027	127.978	0.495	1045.888	0.591	36	0.135	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-10/2	1049.972	1050.190	-207.986	0.422	856.185	0.430	14	0.127	K.LAESGAFNLK.N
R2/RRR2-10/2	1049.909	1050.190	-268.522	0.409	868.922	0.425	14	0.127	K.LAESGAFNLK.N
R2/RRR2-10/2	1049.636	1050.190	-1485.217	0.382	784.947	0.461	14	0.127	K.LAESGAFNLK.N
R2/RRR2-11/3	1856.181	1856.027	82.866	0.476	819.783	0.586	32	0.117	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-11/3	1855.981	1856.027	-24.786	0.529	688.044	0.614	30	0.116	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-10/3	1855.852	1856.027	-94.752	0.475	883.014	0.533	33	0.111	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-10/3	1856.454	1856.027	230.652	0.459	873.636	0.523	33	0.108	R.TLGATHTVNAAKEDAVEK.I
R2/RRR2-10/2	1167.516	1168.371	-1593.762	0.361	939.953	0.200	14	0.105	-.ARQDLPQIVK.-
R2/RRR2-10/2	1167.388	1168.371	-1703.852	0.388	790.505	0.232	13	0.104	-.ARQDLPQIVK.-
R2/RRR2-10/3	1990.219	1991.238	-1017.386	0.395	614.543	0.568	24	0.100	R.GAVFWEPGRPLTLEDFR.M
R2/RRR2-2/2	1051.202	1050.190	11.576	0.211	462.574	0.279	12	0.098	-.LAESGAFNLK.-
R2/RRR2-10/3	1991.325	1991.238	44.010	0.444	711.319	0.466	25	0.090	R.GAVFWEPGRPLTLEDFR.M
R2/RRR2-10/3	1990.543	1991.238	-854.098	0.308	578.219	0.413	22	0.077	R.GAVFWEPGRPLTLEDFR.M
R2/RRR2-3/2	1964.442	1965.190	-892.739	0.509	1890.330	0.506	25	0.241	K.TGLYLEGSVSPAISDVDIK.I
R2/RRR2-3/2	1664.213	1664.798	-955.133	0.484	1716.505	0.505	24	0.216	K.FTPSAVAIDLNSGESR.E
R2/RRR2-3/2	1965.321	1965.190	66.559	0.566	1679.916	0.485	26	0.205	K.TGLYLEGSVSPAISDVDIK.I
R2/RRR2-3/2	1664.258	1664.798	-928.034	0.513	1607.603	0.495	24	0.200	K.FTPSAVAIDLNSGESR.E
R2/RRR2-3/2	1664.315	1664.798	-291.439	0.517	1544.121	0.482	23	0.189	K.FTPSAVAIDLNSGESR.E
R2/RRR2-3/2	1155.769	1155.288	417.743	0.504	1516.695	0.388	19	0.170	K.FQVTGFSVGGR.V
R2/RRR2-3/2	1171.945	1172.272	-280.365	0.402	1090.060	0.352	16	0.130	R.AVTDNLGYYR.L
R2/RRR2-3/2	1316.476	1317.389	-1457.324	0.378	694.230	0.479	16	0.125	R.ASHPNYEIETR.G
R2/RRR2-3/2	1171.726	1172.272	-1323.356	0.345	992.427	0.310	15	0.118	R.AVTDNLGYYR.L
R2/RRR2-3/2	1740.365	1740.015	201.820	0.445	385.874	0.561	15	0.118	R.VAYSAM*GSVTLLTGQPK.E
R2/RRR2-3/2	1739.966	1740.015	-28.234	0.364	608.114	0.427	19	0.114	R.VAYSAM*GSVTLLTGQPK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	798.660	798.997	-422.748	0.384	1238.003	0.154	12	0.113	K.LGQILVR.I
R2/RRR2-3/3	1794.635	1795.057	-235.670	0.457	1049.693	0.486	29	0.111	K.AM*VTLTHGPENVKPQR.K
R2/RRR2-3/2	798.847	798.997	-187.385	0.437	1028.790	0.212	11	0.111	K.LGQILVR.I
R2/RRR2-3/2	799.016	798.997	24.884	0.433	1019.157	0.185	11	0.108	K.LGQILVR.I
R2/RRR2-3/2	1740.101	1740.015	49.588	0.331	223.272	0.344	13	0.103	-.VAYSAM*GSVTLLTGQPK.-
R2/RRR2-3/3	1793.630	1795.057	-1357.037	0.423	726.899	0.460	26	0.089	K.AM*VTLTHGPENVKPQR.K
R2/RRR2-3/3	1317.784	1317.389	300.732	0.470	1061.442	0.259	21	0.073	R.ASHPNYEIETR.G
R2/RRR2-3/3	1317.299	1317.389	-68.893	0.419	1007.124	0.188	21	0.065	R.ASHPNYEIETR.G
R2/RRR2-3/3	1318.418	1317.389	22.082	0.432	719.609	0.220	17	0.045	-.ASHPNYEIETR.-
R2/RRR2-16/2	1007.934	1008.107	-171.654	0.507	1905.593	0.358	16	0.204	R.FGELDVAEK.V
R2/RRR2-16/2	1007.983	1008.107	-123.181	0.480	1876.368	0.327	16	0.193	R.FGELDVAEK.V
R2/RRR2-15/2	1009.013	1008.107	-93.447	0.419	1920.202	0.260	16	0.183	R.FGELDVAEK.V
R2/RRR2-15/2	1008.066	1008.107	-40.823	0.434	1715.354	0.308	15	0.171	R.FGELDVAEK.V
R2/RRR2-15/2	1008.069	1008.107	-37.301	0.468	1681.390	0.293	15	0.163	R.FGELDVAEK.V
R2/RRR2-15/2	1097.666	1097.295	339.245	0.490	1186.931	0.444	15	0.151	K.APLLAAWAQR.F
R2/RRR2-16/2	1844.458	1845.091	-887.950	0.520	987.231	0.496	21	0.143	K.VFDEEKAPLLAAWAQR.F
R2/RRR2-16/3	1844.760	1845.091	-179.711	0.423	1607.924	0.374	28	0.140	K.VFDEEKAPLLAAWAQR.F
R2/RRR2-15/2	1456.388	1456.709	-221.656	0.423	976.857	0.446	19	0.134	K.QLLAAVETLEGALK.D
R2/RRR2-16/2	1389.902	1388.590	224.840	0.453	572.956	0.556	19	0.133	K.VLPDVDGVVEFAK.M
R2/RRR2-16/2	1007.416	1008.107	-1683.641	0.394	1263.989	0.289	13	0.129	R.FGELDVAEK.V
R2/RRR2-15/2	1945.988	1947.213	-1147.023	0.426	698.379	0.518	20	0.126	K.QLLAAVETLEGALKDCSK.G
R2/RRR2-15/2	1388.173	1388.590	-301.785	0.205	309.787	0.339	16	0.106	K.VLPDVDGVVEFAK.M
R2/RRR2-15/2	1946.002	1947.213	-1139.653	0.345	350.625	0.409	15	0.105	K.QLLAAVETLEGALKDCSK.G
R2/RRR2-15/2	1388.087	1388.590	-1086.301	0.185	360.757	0.394	16	0.103	K.VLPDVDGVVEFAK.M
R2/RRR2-15/3	1845.379	1845.091	156.533	0.406	1476.185	0.272	27	0.101	K.VFDEEKAPLLAAWAQR.F
R2/RRR2-16/3	1845.147	1845.091	30.741	0.307	1077.033	0.275	25	0.076	K.VFDEEKAPLLAAWAQR.F
R2/RRR2-12/2	1767.421	1767.022	226.692	0.571	1941.948	0.580	23	0.270	R.VLDTHVEGGNLFIVPR.F
R2/RRR2-12/2	1766.684	1767.022	-191.665	0.532	1900.177	0.536	23	0.250	R.VLDTHVEGGNLFIVPR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1767.396	1767.022	212.563	0.557	1654.247	0.570	22	0.223	R.VLDTHVEGGNLFIVPR.F
R2/RRR2-12/2	1206.018	1205.299	-233.663	0.516	1648.361	0.482	18	0.203	R.AWDLAESDAVK.L
R2/RRR2-12/2	1204.370	1205.299	-1606.090	0.375	1672.380	0.392	18	0.185	R.AWDLAESDAVK.L
R2/RRR2-12/2	1204.559	1205.299	-1448.493	0.410	1486.598	0.378	17	0.162	R.AWDLAESDAVK.L
R2/RRR2-12/2	1185.702	1186.383	-1422.377	0.457	1082.235	0.516	19	0.154	K.LVSSQPASGIVK.I
R2/RRR2-12/2	1735.292	1734.932	208.240	0.498	972.993	0.562	22	0.150	K.LSLNAGGLALPSFSDSGK.V
R2/RRR2-13/2	1186.134	1186.383	-210.948	0.423	1058.443	0.492	19	0.148	K.LVSSQPASGIVK.I
R2/RRR2-13/2	1736.306	1734.932	216.440	0.501	860.140	0.586	22	0.147	K.LSLNAGGLALPSFSDSGK.V
R2/RRR2-12/2	1413.762	1414.739	-1402.560	0.372	1117.098	0.452	19	0.143	R.VVVLNTANLPM*VK.E
R2/RRR2-12/2	1399.390	1398.740	-250.545	0.428	857.705	0.519	18	0.138	R.VVVLNTANLPMVK.E
R2/RRR2-12/2	1413.644	1414.739	-1486.603	0.376	1039.910	0.455	18	0.138	R.VVVLNTANLPM*VK.E
R2/RRR2-12/2	1030.072	1029.172	-97.302	0.467	912.939	0.456	17	0.137	K.EVGLGADLVR.I
R2/RRR2-12/2	1185.682	1186.383	-1439.543	0.426	792.651	0.486	17	0.131	K.LVSSQPASGIVK.I
R2/RRR2-12/2	1185.597	1186.383	-1510.798	0.403	768.004	0.491	17	0.130	K.LVSSQPASGIVK.I
R2/RRR2-12/2	1028.933	1029.172	-233.419	0.370	900.525	0.407	17	0.127	K.EVGLGADLVR.I
R2/RRR2-12/2	1232.035	1232.402	-299.087	0.398	913.554	0.401	16	0.124	K.GTCGIVLPEASK.E
R2/RRR2-12/2	1029.034	1029.172	-135.117	0.345	768.036	0.404	16	0.121	K.EVGLGADLVR.I
R2/RRR2-12/2	1736.246	1734.932	181.823	0.489	603.138	0.497	18	0.120	K.LSLNAGGLALPSFSDSGK.V
R2/RRR2-13/2	1734.547	1734.932	-222.180	0.389	601.315	0.477	19	0.117	K.LSLNAGGLALPSFSDSGK.V
R2/RRR2-12/2	1398.322	1398.740	-299.420	0.354	713.495	0.395	16	0.116	R.VVVLNTANLPMVK.E
R2/RRR2-12/2	1398.009	1398.740	-1242.014	0.265	523.568	0.291	14	0.104	R.VVVLNTANLPMVK.E
R2/RRR2-12/2	1231.871	1232.402	-1246.619	0.299	596.305	0.200	14	0.101	-.GTCGIVLPEASK.-
R2/RRR2-12/3	1766.715	1767.022	-174.344	0.497	1175.553	0.379	29	0.099	R.VLDTHVEGGNLFIVPR.F
R2/RRR2-12/3	1765.726	1767.022	-1303.722	0.346	526.504	0.365	20	0.048	-.VLDTHVEGGNLFIVPR.-
R2/RRR2-9/2	1887.440	1887.209	122.693	0.517	1868.726	0.531	26	0.247	R.LGIAPYVAVSEEAAIAALK.R
R2/RRR2-9/2	1575.286	1575.815	-973.533	0.498	1658.172	0.473	19	0.202	R.YFWTMVNQPNFK.K
R2/RRR2-9/2	1121.995	1122.296	-269.166	0.436	1600.970	0.448	16	0.188	K.ALIAAEYSGVK.V
R2/RRR2-9/2	1575.635	1575.815	-114.509	0.484	1509.326	0.468	18	0.183	R.YFWTMVNQPNFK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1121.996	1122.296	-268.293	0.476	1355.248	0.490	16	0.172	K.ALIAAEYSGVK.V
R2/RRR2-9/2	1123.025	1122.296	-242.536	0.546	1297.959	0.470	16	0.162	K.ALIAAEYSGVK.V
R2/RRR2-9/2	1337.267	1336.434	-125.398	0.517	972.464	0.510	16	0.146	K.SFTSEFPHVER.Y
R2/RRR2-9/2	1336.104	1336.434	-248.117	0.443	886.785	0.504	16	0.139	K.SFTSEFPHVER.Y
R2/RRR2-9/2	1335.563	1336.434	-1405.604	0.444	779.362	0.481	15	0.130	K.SFTSEFPHVER.Y
R2/RRR2-9/2	1218.029	1218.490	-380.028	0.420	1105.345	0.349	15	0.128	K.MLVIGSEPPFK.V
R2/RRR2-9/2	1575.394	1575.815	-267.864	0.372	1054.070	0.362	16	0.126	R.YFWTMVNQPNFK.K
R2/RRR2-9/2	1094.057	1094.286	-209.789	0.297	665.511	0.448	14	0.117	K.NPLDLLPPSK.M
R2/RRR2-9/2	1219.187	1218.490	-249.918	0.324	798.862	0.380	13	0.114	-.MLVIGSEPPFK.-
R2/RRR2-9/2	776.546	776.906	-465.532	0.502	859.832	0.253	11	0.112	K.VGGFLQR.M
R2/RRR2-8/2	777.300	776.906	508.363	0.437	604.304	0.160	11	0.108	K.VGGFLQR.M
R2/RRR2-9/2	1094.040	1094.286	-225.124	0.233	571.321	0.352	13	0.106	K.NPLDLLPPSK.M
R2/RRR2-9/2	777.074	776.906	216.708	0.465	856.025	0.190	11	0.105	-.VGGFLQR.-
R2/RRR2-9/2	776.925	776.906	24.015	0.518	886.789	0.194	11	0.105	K.VGGFLQR.M
R2/RRR2-8/2	777.125	776.906	281.605	0.446	717.438	0.195	11	0.103	-.VGGFLQR.-
R2/RRR2-9/2	1218.030	1218.490	-379.424	0.250	819.297	0.175	13	0.101	K.MLVIGSEPPFK.V
R2/RRR2-9/2	1234.452	1234.490	-30.793	0.262	550.886	0.150	12	0.087	-.M*LVIGSEPPFK.-
R2/RRR2-9/2	1234.190	1234.490	-243.592	0.306	615.531	0.154	13	0.087	-.M*LVIGSEPPFK.-
R2/RRR2-9/2	1951.438	1952.155	-882.437	0.514	1008.763	0.599	23	0.159	K.VPVLETPDGPVSESNAIAR.Y
R2/RRR2-9/2	1951.182	1952.155	-1014.265	0.516	861.232	0.595	22	0.147	K.VPVLETPDGPVSESNAIAR.Y
R2/RRR2-9/2	1951.826	1952.155	-169.094	0.490	747.019	0.582	21	0.137	K.VPVLETPDGPVSESNAIAR.Y
R2/RRR2-9/3	1907.947	1908.099	-79.716	0.403	805.291	0.476	25	0.092	K.AAEKPEEEEEAPKPKPK.N
R2/RRR2-7/2	1930.526	1930.106	218.067	0.547	2968.568	0.554	26	0.487	K.DLGLLVENATEEQLGTAR.K
R2/RRR2-7/2	1043.364	1044.187	-1752.897	0.437	1148.804	0.430	17	0.146	K.VVNDGVTIAR.A
R2/RRR2-7/2	1043.825	1044.187	-348.089	0.456	1135.177	0.415	17	0.143	K.VVNDGVTIAR.A
R2/RRR2-7/2	1555.119	1554.856	169.460	0.446	1032.813	0.431	20	0.137	K.EILPILEKTTQLR.A
R2/RRR2-7/2	1684.390	1685.002	-959.829	0.415	1017.446	0.475	19	0.137	K.LGLLSVTSGANPVSLKK.G
R2/RRR2-7/2	1554.363	1554.856	-318.198	0.364	1043.865	0.330	20	0.123	K.EILPILEKTTQLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1555.931	1554.856	48.425	0.317	440.427	0.264	16	0.106	-.EILPILEKTTQLR.-
R2/RRR2-9/2	1968.719	1969.163	-226.164	0.541	2452.303	0.549	24	0.357	R.TMLELLNQLDGFSSDER.I
R2/RRR2-9/2	1968.669	1969.163	-251.669	0.516	2273.940	0.546	24	0.321	R.TMLELLNQLDGFSSDER.I
R2/RRR2-9/2	1662.311	1661.947	219.489	0.499	1485.338	0.489	21	0.181	K.LAGPQLVQM*FIGDGAK.L
R2/RRR2-9/2	1661.349	1661.947	-964.769	0.428	1397.505	0.483	20	0.170	K.LAGPQLVQM*FIGDGAK.L
R2/RRR2-9/2	1646.372	1645.948	258.456	0.419	1347.436	0.445	19	0.158	K.LAGPQLVQMFIGDGAK.L
R2/RRR2-9/2	1669.838	1669.986	-88.545	0.496	1128.797	0.475	22	0.150	R.QTIFLPVIGLVDPEK.L
R2/RRR2-9/2	1669.411	1669.986	-945.852	0.451	1105.611	0.478	22	0.148	R.QTIFLPVIGLVDPEK.L
R2/RRR2-9/2	1645.783	1645.948	-100.477	0.362	1115.184	0.451	19	0.140	K.LAGPQLVQMFIGDGAK.L
R2/RRR2-9/2	1195.989	1196.249	-217.502	0.508	909.988	0.457	16	0.135	R.STDDFNGAQLK.A
R2/RRR2-9/2	1646.126	1645.948	108.547	0.480	1045.867	0.445	18	0.134	K.LAGPQLVQMFIGDGAK.L
R2/RRR2-9/2	1195.445	1196.249	-1513.306	0.447	905.264	0.445	17	0.133	R.STDDFNGAQLK.A
R2/RRR2-9/2	1661.419	1661.947	-922.797	0.403	1135.494	0.399	18	0.133	K.LAGPQLVQM*FIGDGAK.L
R2/RRR2-9/2	1669.363	1669.986	-974.776	0.385	906.462	0.439	20	0.128	R.QTIFLPVIGLVDPEK.L
R2/RRR2-9/2	1887.416	1888.021	-853.274	0.446	597.723	0.463	18	0.118	K.DSYLILDTLPSEYDSR.V
R2/RRR2-9/2	1887.304	1888.021	-912.489	0.425	588.380	0.440	18	0.115	K.DSYLILDTLPSEYDSR.V
R2/RRR2-9/3	1440.505	1440.586	-56.243	0.491	1379.453	0.383	24	0.114	R.KIEFPHPSEEAR.A
R2/RRR2-9/3	1440.352	1440.586	-162.973	0.487	1034.307	0.405	21	0.095	R.KIEFPHPSEEAR.A
R2/RRR2-9/3	1440.552	1440.586	-23.094	0.473	1156.702	0.366	23	0.095	R.KIEFPHPSEEAR.A
R2/RRR2-9/3	1645.731	1645.948	-131.958	0.377	973.269	0.203	24	0.062	-.LAGPQLVQMFIGDGAK.-
R2/RRR2-5/2	1212.502	1213.406	-1574.315	0.382	453.707	0.474	13	0.115	-.AVDEIEPALKK.-
R2/RRR2-5/2	1212.360	1213.406	-1692.456	0.300	470.890	0.408	14	0.111	K.AVDEIEPALKK.Q
R2/RRR2-5/2	1215.280	1215.422	-116.727	0.310	764.252	0.348	15	0.110	R.AAISTVDVLTPK.V
R2/RRR2-5/2	1213.171	1213.406	-194.136	0.368	390.596	0.434	12	0.106	-.AVDEIEPALKK.-
R2/RRR2-10/2	1653.783	1654.910	-1289.669	0.487	1975.012	0.571	25	0.269	R.TPM*GGFLGALSSLSATK.L
R2/RRR2-10/2	1198.178	1198.397	-183.894	0.502	2076.568	0.488	18	0.266	K.AQELGLQVIAR.I
R2/RRR2-10/2	1638.429	1638.910	-294.474	0.475	1758.063	0.569	23	0.234	R.TPMGGFLGALSSLSATK.L
R2/RRR2-10/2	1638.356	1638.910	-951.824	0.467	1692.979	0.602	23	0.233	R.TPMGGFLGALSSLSATK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1942.549	1942.207	176.939	0.409	2028.179	0.451	34	0.231	R.NSGAFAWEIVPIEVPVGR.G
R2/RRR2-10/2	1942.912	1942.207	-152.288	0.554	1568.977	0.620	25	0.225	R.NSGAFAWEIVPIEVPVGR.G
R2/RRR2-10/2	1197.586	1198.397	-1516.632	0.537	1735.965	0.521	18	0.224	K.AQELGLQVIAR.I
R2/RRR2-10/2	1538.863	1539.543	-1094.755	0.447	1892.724	0.432	20	0.222	R.EDQDAYAIQSNER.G
R2/RRR2-10/2	1539.131	1539.543	-268.288	0.505	1759.856	0.486	21	0.218	R.EDQDAYAIQSNER.G
R2/RRR2-10/2	1654.506	1654.910	-244.717	0.472	1586.196	0.582	23	0.214	R.TPM*GGFLGALSSLSATK.L
R2/RRR2-10/2	1540.120	1539.543	-275.668	0.574	1499.677	0.536	19	0.197	R.EDQDAYAIQSNER.G
R2/RRR2-10/2	1638.467	1638.910	-271.152	0.481	1414.658	0.590	24	0.196	R.TPMGGFLGALSSLSATK.L
R2/RRR2-10/2	1088.820	1089.185	-336.291	0.462	1357.579	0.550	18	0.185	K.ALANAGLESSR.V
R2/RRR2-10/2	1655.868	1654.910	-25.577	0.465	1198.475	0.608	22	0.176	R.TPM*GGFLGALSSLSATK.L
R2/RRR2-10/2	1941.678	1942.207	-789.387	0.519	1322.044	0.535	24	0.176	R.NSGAFAWEIVPIEVPVGR.G
R2/RRR2-10/2	1089.154	1089.185	-27.947	0.442	1320.193	0.513	18	0.174	K.ALANAGLESSR.V
R2/RRR2-10/2	1088.992	1089.185	-176.923	0.480	1240.168	0.539	17	0.171	K.ALANAGLESSR.V
R2/RRR2-10/2	1941.651	1942.207	-803.333	0.498	1084.568	0.540	23	0.155	R.NSGAFAWEIVPIEVPVGR.G
R2/RRR2-1/2	1655.765	1654.910	-87.471	0.433	1079.330	0.482	20	0.142	R.TPM*GGFLGALSSLSATK.L
R2/RRR2-10/2	974.826	975.118	-300.571	0.401	1404.975	0.287	14	0.140	R.DVCVVGVAR.T
R2/RRR2-11/2	1655.757	1654.910	-92.795	0.397	892.459	0.428	18	0.123	R.TPM*GGFLGALSSLSATK.L
R2/RRR2-10/2	1198.263	1198.397	-112.356	0.405	938.191	0.346	14	0.119	K.AQELGLQVIAR.I
R2/RRR2-10/3	1960.964	1960.180	-110.402	0.508	939.976	0.515	32	0.111	K.INVHGGAVSLGHPLGCSGAR.I
R2/RRR2-3/2	1638.637	1638.910	-167.415	0.280	274.278	0.371	13	0.104	-.TPMGGFLGALSSLSATK.-
R2/RRR2-10/3	1941.214	1942.207	-1029.320	0.309	1464.061	0.281	28	0.104	R.NSGAFAWEIVPIEVPVGR.G
R2/RRR2-10/3	1959.458	1960.180	-881.676	0.427	963.539	0.446	30	0.098	K.INVHGGAVSLGHPLGCSGAR.I
R2/RRR2-4/2	1746.306	1746.858	-891.093	0.571	1602.264	0.497	20	0.200	R.FGHNEIDEPSFTQPK.M
R2/RRR2-4/2	1495.275	1495.616	-229.075	0.483	973.674	0.422	17	0.130	K.VSTILNDEFQNSK.E
R2/RRR2-4/2	1495.169	1495.616	-300.006	0.441	812.983	0.358	16	0.115	K.VSTILNDEFQNSK.E
R2/RRR2-4/2	1494.593	1495.616	-1358.032	0.331	809.814	0.276	16	0.107	K.VSTILNDEFQNSK.E
R2/RRR2-4/3	1623.842	1623.789	32.669	0.479	1299.317	0.278	25	0.088	K.KVSTILNDEFQNSK.E
R2/RRR2-8/2	1257.054	1257.423	-294.498	0.533	2232.261	0.321	17	0.239	K.GWNLNLAELAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1124.053	1124.318	-236.650	0.570	1608.523	0.506	17	0.203	R.LPANLIQAQR.D
R2/RRR2-8/2	1123.844	1124.318	-423.097	0.547	1475.998	0.563	17	0.202	R.LPANLIQAQR.D
R2/RRR2-8/2	1124.220	1124.318	-87.520	0.519	1568.749	0.493	17	0.196	R.LPANLIQAQR.D
R2/RRR2-8/2	1123.989	1124.318	-293.634	0.544	1561.663	0.486	17	0.193	R.LPANLIQAQR.D
R2/RRR2-9/2	1124.228	1124.318	-80.767	0.521	1465.630	0.496	17	0.185	R.LPANLIQAQR.D
R2/RRR2-9/2	1123.567	1124.318	-1563.696	0.542	1425.794	0.478	17	0.178	R.LPANLIQAQR.D
R2/RRR2-8/2	1257.069	1257.423	-282.515	0.446	1670.028	0.363	16	0.177	K.GWNLNLAELAR.I
R2/RRR2-8/2	1209.462	1209.292	140.651	0.389	912.700	0.387	17	0.127	R.DLFGAHTYER.I
R2/RRR2-8/2	1257.180	1257.423	-194.255	0.424	1393.502	0.221	16	0.126	K.GWNLNLAELAR.I
R2/RRR2-8/2	1964.668	1965.112	-227.005	0.398	605.031	0.574	18	0.126	R.VGGLSNSEIADVFAEWNR.G
R2/RRR2-8/2	1210.361	1209.292	56.991	0.402	860.892	0.398	16	0.126	R.DLFGAHTYER.I
R2/RRR2-8/2	1055.830	1056.284	-431.683	0.425	1067.720	0.326	14	0.123	R.TVVLLVQAGR.A
R2/RRR2-8/2	1055.491	1056.284	-1704.338	0.416	999.426	0.344	14	0.123	R.TVVLLVQAGR.A
R2/RRR2-8/3	1574.480	1574.722	-153.677	0.516	1053.875	0.496	23	0.115	R.IDRPGSFHTEWTK.L
R2/RRR2-8/2	1209.167	1209.292	-104.356	0.377	895.219	0.281	16	0.114	R.DLFGAHTYER.I
R2/RRR2-8/2	1965.803	1965.112	-157.615	0.382	473.076	0.429	17	0.109	R.VGGLSNSEIADVFAEWNR.G
R2/RRR2-8/3	1574.334	1574.722	-246.899	0.398	672.297	0.326	21	0.073	R.IDRPGSFHTEWTK.L
R2/RRR2-18/2	1837.498	1837.967	-256.108	0.577	1717.033	0.610	22	0.244	R.NNTEYKLDTFSSVYR.R
R2/RRR2-18/2	1837.528	1837.967	-239.779	0.564	1589.426	0.606	22	0.225	R.NNTEYKLDTFSSVYR.R
R2/RRR2-18/2	1293.374	1292.509	-104.757	0.529	1665.066	0.542	18	0.217	K.FSGKDVVLVATR.R
R2/RRR2-18/2	1837.221	1837.967	-953.158	0.563	1554.964	0.583	21	0.214	R.NNTEYKLDTFSSVYR.R
R2/RRR2-18/2	1292.012	1292.509	-386.033	0.455	1400.927	0.549	18	0.187	K.FSGKDVVLVATR.R
R2/RRR2-18/2	1292.149	1292.509	-279.488	0.479	1365.664	0.507	18	0.175	K.FSGKDVVLVATR.R
R2/RRR2-18/2	1291.696	1292.509	-1408.125	0.438	1379.941	0.466	19	0.169	K.FSGKDVVLVATR.R
R2/RRR2-18/2	1292.283	1292.509	-175.619	0.455	1385.414	0.443	18	0.164	K.FSGKDVVLVATR.R
R2/RRR2-18/2	1292.197	1292.509	-242.335	0.492	1315.010	0.470	18	0.164	K.FSGKDVVLVATR.R
R2/RRR2-18/2	873.807	873.032	-258.884	0.513	1178.635	0.284	13	0.125	K.DVVLVATR.R
R2/RRR2-18/2	1028.863	1029.219	-346.606	0.382	1054.819	0.314	14	0.123	K.DVVLVATRR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	872.233	873.032	-2069.441	0.353	1220.205	0.229	13	0.121	K.DVVLVATR.R
R2/RRR2-18/2	1068.132	1068.297	-154.472	0.382	891.468	0.328	14	0.119	K.AVIIHVPYR.L
R2/RRR2-18/2	1067.675	1068.297	-1523.309	0.355	608.831	0.400	12	0.116	K.AVIIHVPYR.L
R2/RRR2-18/2	1068.078	1068.297	-205.033	0.397	516.439	0.365	11	0.113	K.AVIIHVPYR.L
R2/RRR2-18/2	872.869	873.032	-187.204	0.306	889.257	0.242	12	0.110	K.DVVLVATR.R
R2/RRR2-17/2	1068.467	1068.297	160.472	0.274	450.536	0.318	10	0.106	K.AVIIHVPYR.L
R2/RRR2-18/2	1028.491	1029.219	-1685.152	0.348	726.464	0.224	13	0.106	K.DVVLVATRR.I
R2/RRR2-17/2	873.194	873.032	185.982	0.329	692.734	0.178	11	0.104	K.DVVLVATR.R
R2/RRR2-18/3	1838.055	1837.967	47.713	0.531	715.038	0.535	30	0.103	R.NNTEYKLDTFSSVYR.R
R2/RRR2-18/3	1420.811	1420.682	91.110	0.403	1525.961	0.262	25	0.101	K.KFSGKDVVLVATR.R
R2/RRR2-18/3	1837.304	1837.967	-908.208	0.489	732.067	0.518	27	0.100	R.NNTEYKLDTFSSVYR.R
R2/RRR2-17/2	872.412	873.032	-1863.133	0.308	1093.640	0.054	12	0.099	K.DVVLVATR.R
R2/RRR2-18/2	1029.108	1029.219	-108.219	0.380	683.693	0.126	13	0.099	-.DVVLVATRR.-
R2/RRR2-18/3	1293.496	1292.509	-10.338	0.425	1150.473	0.221	22	0.071	K.FSGKDVVLVATR.R
R2/RRR2-18/3	1419.769	1420.682	-1351.308	0.342	1062.095	0.201	25	0.065	K.KFSGKDVVLVATR.R
R2/RRR2-18/3	1292.836	1292.509	253.643	0.379	1327.587	0.128	23	0.065	K.FSGKDVVLVATR.R
R2/RRR2-18/3	1292.049	1292.509	-357.130	0.273	913.322	0.087	20	0.053	-.FSGKDVVLVATR.-
R2/RRR2-18/3	1633.242	1632.831	252.354	0.617	2966.245	0.460	35	0.436	K.TIAECLADELINAAK.G
R2/RRR2-18/3	1633.568	1632.831	-161.572	0.608	2854.822	0.438	34	0.395	K.TIAECLADELINAAK.G
R2/RRR2-19/2	1632.477	1632.831	-217.772	0.554	2759.005	0.474	22	0.387	K.TIAECLADELINAAK.G
R2/RRR2-19/3	1633.520	1632.831	-191.258	0.583	2729.337	0.423	33	0.357	K.TIAECLADELINAAK.G
R2/RRR2-18/2	1633.140	1632.831	189.853	0.586	2535.432	0.512	21	0.351	K.TIAECLADELINAAK.G
R2/RRR2-18/2	1632.311	1632.831	-933.746	0.509	2608.965	0.434	22	0.341	K.TIAECLADELINAAK.G
R2/RRR2-18/2	1632.307	1632.831	-936.299	0.495	2600.867	0.428	22	0.338	K.TIAECLADELINAAK.G
R2/RRR2-17/2	1633.655	1632.831	-108.043	0.583	2356.870	0.501	21	0.311	K.TIAECLADELINAAK.G
R2/RRR2-19/2	1633.209	1632.831	231.902	0.572	2317.685	0.486	21	0.299	K.TIAECLADELINAAK.G
R2/RRR2-19/2	1632.248	1632.831	-972.488	0.516	2297.608	0.476	21	0.294	K.TIAECLADELINAAK.G
R2/RRR2-19/2	1420.283	1420.639	-251.429	0.514	2165.895	0.541	21	0.292	R.VNQAIYLLTTGAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1420.310	1420.639	-232.114	0.502	1952.118	0.541	20	0.256	R.VNQAIYLLTTGAR.E
R2/RRR2-18/2	1420.232	1420.639	-287.559	0.503	1924.916	0.552	20	0.255	R.VNQAIYLLTTGAR.E
R2/RRR2-19/2	1420.293	1420.639	-244.617	0.508	1938.117	0.520	20	0.248	R.VNQAIYLLTTGAR.E
R2/RRR2-17/2	1632.188	1632.831	-1009.581	0.421	2363.792	0.249	20	0.239	K.TIAECLADELINAAK.G
R2/RRR2-19/2	1420.374	1420.639	-187.107	0.523	1412.473	0.531	19	0.184	R.VNQAIYLLTTGAR.E
R2/RRR2-19/3	1632.570	1632.831	-160.283	0.550	1870.782	0.387	30	0.172	K.TIAECLADELINAAK.G
R2/RRR2-17/2	1420.180	1420.639	-324.037	0.393	1211.888	0.475	18	0.153	R.VNQAIYLLTTGAR.E
R2/RRR2-18/2	1224.184	1224.354	-138.682	0.390	910.440	0.564	19	0.148	K.HATYLPHTAGR.Y
R2/RRR2-18/2	1420.154	1420.639	-342.320	0.364	1089.921	0.458	19	0.142	R.VNQAIYLLTTGAR.E
R2/RRR2-18/2	1576.372	1576.825	-288.280	0.603	614.256	0.598	19	0.141	R.RVNQAIYLLTTGAR.E
R2/RRR2-18/2	1224.220	1224.354	-109.274	0.414	955.148	0.489	18	0.141	K.HATYLPHTAGR.Y
R2/RRR2-18/2	1224.155	1224.354	-162.889	0.395	596.028	0.617	17	0.138	K.HATYLPHTAGR.Y
R2/RRR2-18/2	1576.155	1576.825	-1062.639	0.554	561.351	0.536	19	0.132	R.RVNQAIYLLTTGAR.E
R2/RRR2-19/2	1576.541	1576.825	-181.076	0.592	567.082	0.521	20	0.132	R.RVNQAIYLLTTGAR.E
R2/RRR2-18/2	1576.405	1576.825	-267.537	0.555	480.061	0.543	18	0.130	R.RVNQAIYLLTTGAR.E
R2/RRR2-19/2	1224.156	1224.354	-161.689	0.367	538.925	0.528	16	0.126	K.HATYLPHTAGR.Y
R2/RRR2-19/2	1223.380	1224.354	-1618.063	0.324	486.506	0.517	15	0.121	K.HATYLPHTAGR.Y
R2/RRR2-19/2	1577.446	1576.825	-241.048	0.497	402.109	0.470	17	0.121	R.RVNQAIYLLTTGAR.E
R2/RRR2-19/2	1225.014	1224.354	-277.814	0.318	399.838	0.496	15	0.119	K.HATYLPHTAGR.Y
R2/RRR2-21/2	1420.848	1420.639	147.301	0.359	621.949	0.479	13	0.118	R.VNQAIYLLTTGAR.E
R2/RRR2-19/2	998.978	999.146	-168.475	0.311	319.144	0.342	13	0.117	R.QAVDISPLR.R
R2/RRR2-18/2	998.687	999.146	-461.655	0.331	335.969	0.430	14	0.117	-.QAVDISPLR.-
R2/RRR2-18/2	998.999	999.146	-148.249	0.260	361.726	0.478	14	0.116	R.QAVDISPLR.R
R2/RRR2-18/2	999.109	999.146	-37.329	0.308	303.274	0.409	13	0.115	-.QAVDISPLR.-
R2/RRR2-17/2	1420.329	1420.639	-219.094	0.329	692.885	0.414	13	0.114	R.VNQAIYLLTTGAR.E
R2/RRR2-19/2	998.455	999.146	-1698.812	0.224	361.512	0.463	14	0.112	R.QAVDISPLR.R
R2/RRR2-17/2	1631.720	1632.831	-1297.856	0.305	1500.091	0.070	19	0.112	K.TIAECLADELINAAK.G
R2/RRR2-18/2	1420.812	1420.639	122.400	0.277	475.980	0.406	14	0.110	R.VNQAIYLLTTGAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	999.846	999.146	-301.437	0.284	367.663	0.366	11	0.110	-.QAVDISPLR.-
R2/RRR2-19/2	1576.279	1576.825	-984.182	0.499	283.793	0.392	16	0.109	-.RVNQAIYLLTTGAR.-
R2/RRR2-18/2	1420.343	1420.639	-208.834	0.259	312.346	0.318	13	0.109	R.VNQAIYLLTTGAR.E
R2/RRR2-18/2	999.104	999.146	-42.108	0.274	267.080	0.368	11	0.108	-.QAVDISPLR.-
R2/RRR2-18/3	1224.466	1224.354	92.120	0.551	718.212	0.521	22	0.106	K.HATYLPHTAGR.Y
R2/RRR2-17/3	1224.138	1224.354	-176.705	0.538	678.264	0.505	22	0.103	K.HATYLPHTAGR.Y
R2/RRR2-18/2	999.707	999.146	-440.485	0.224	318.588	0.325	11	0.103	-.QAVDISPLR.-
R2/RRR2-16/3	1224.462	1224.354	89.271	0.515	655.262	0.506	21	0.103	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.417	1224.354	51.626	0.517	707.453	0.496	22	0.102	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1223.522	1224.354	-1501.506	0.519	681.519	0.500	21	0.102	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.524	1224.354	139.510	0.555	763.266	0.482	23	0.102	K.HATYLPHTAGR.Y
R2/RRR2-16/3	1224.079	1224.354	-225.325	0.532	531.382	0.508	19	0.101	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.551	1224.354	161.404	0.519	493.082	0.495	20	0.100	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.562	1224.354	170.551	0.549	744.594	0.475	23	0.100	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.809	1224.354	372.943	0.518	428.641	0.490	19	0.100	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.526	1224.354	141.159	0.495	472.232	0.495	19	0.100	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.672	1224.354	260.963	0.531	433.119	0.496	18	0.100	K.HATYLPHTAGR.Y
R2/RRR2-17/3	1224.258	1224.354	-78.279	0.510	571.691	0.480	21	0.099	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.549	1224.354	160.204	0.521	688.018	0.472	22	0.099	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.374	1224.354	16.528	0.455	341.460	0.485	17	0.099	K.HATYLPHTAGR.Y
R2/RRR2-17/3	1224.553	1224.354	163.353	0.532	552.262	0.476	21	0.099	K.HATYLPHTAGR.Y
R2/RRR2-16/3	1224.552	1224.354	162.603	0.534	395.091	0.478	18	0.099	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1223.533	1224.354	-1492.637	0.491	637.048	0.476	22	0.099	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.622	1224.354	219.882	0.497	551.544	0.476	21	0.098	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.802	1224.354	367.397	0.497	558.006	0.469	21	0.098	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.632	1224.354	227.978	0.527	633.169	0.461	23	0.098	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1225.202	1224.354	-124.437	0.411	243.370	0.459	15	0.097	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.509	1224.354	127.063	0.523	466.810	0.458	18	0.096	K.HATYLPHTAGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/3	1224.170	1224.354	-150.146	0.515	630.578	0.444	22	0.095	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.075	1224.354	-228.176	0.485	410.745	0.453	17	0.095	K.HATYLPHTAGR.Y
R2/RRR2-4/3	1225.301	1224.354	-43.039	0.442	476.709	0.445	20	0.095	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.307	1224.354	-38.374	0.467	471.570	0.438	19	0.094	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.523	1224.354	139.210	0.499	528.563	0.430	21	0.094	K.HATYLPHTAGR.Y
R2/RRR2-19/2	1421.539	1420.639	-70.507	0.321	222.355	0.386	11	0.094	-.VNQAIYLLTTGAR.-
R2/RRR2-17/2	1632.139	1632.831	-1039.767	0.268	735.804	0.044	14	0.094	-.TIAECLADELINAAK.-
R2/RRR2-15/3	1224.703	1224.354	286.299	0.356	251.155	0.330	15	0.093	K.HATYLPHTAGR.Y
R2/RRR2-20/3	1224.125	1224.354	-187.059	0.409	442.802	0.417	19	0.093	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1223.372	1224.354	-1624.189	0.484	521.787	0.423	19	0.093	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.884	1224.354	-384.159	0.361	340.343	0.387	17	0.092	K.HATYLPHTAGR.Y
R2/RRR2-16/3	1224.580	1224.354	185.246	0.452	468.779	0.389	19	0.091	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.893	1224.354	-377.409	0.352	365.545	0.341	17	0.090	K.HATYLPHTAGR.Y
R2/RRR2-5/3	1224.659	1224.354	250.168	0.386	372.352	0.365	16	0.090	K.HATYLPHTAGR.Y
R2/RRR2-5/3	1224.776	1224.354	345.962	0.421	368.415	0.355	16	0.090	K.HATYLPHTAGR.Y
R2/RRR2-18/3	1224.733	1224.354	310.885	0.406	333.690	0.417	16	0.090	-.HATYLPHTAGR.-
R2/RRR2-20/3	1224.532	1224.354	146.558	0.436	447.030	0.366	18	0.090	K.HATYLPHTAGR.Y
R2/RRR2-24/3	1224.797	1224.354	363.350	0.359	427.151	0.331	18	0.088	K.HATYLPHTAGR.Y
R2/RRR2-19/3	1224.216	1224.354	-112.336	0.497	327.080	0.494	16	0.088	-.HATYLPHTAGR.-
R2/RRR2-5/3	1224.312	1224.354	-33.874	0.412	468.031	0.267	19	0.086	K.HATYLPHTAGR.Y
R2/RRR2-20/3	1224.385	1224.354	25.828	0.407	587.097	0.391	20	0.083	-.HATYLPHTAGR.-
R2/RRR2-18/3	1101.053	1101.275	-202.547	0.455	847.282	0.315	19	0.077	R.KAQCPLVER.L
R2/RRR2-18/3	1100.988	1101.275	-261.859	0.416	826.497	0.278	19	0.073	R.KAQCPLVER.L
R2/RRR2-18/3	1101.468	1101.275	175.855	0.388	660.092	0.304	18	0.073	-.KAQCPLVER.-
R2/RRR2-18/3	1101.483	1101.275	189.608	0.343	1009.836	0.248	19	0.069	-.KAQCPLVER.-
R2/RRR2-18/3	1100.957	1101.275	-289.724	0.407	875.738	0.183	19	0.064	-.KAQCPLVER.-
R2/RRR2-7/2	1514.196	1514.615	-277.153	0.416	1352.292	0.508	19	0.175	K.EIAQGYCDSFAPR.D
R2/RRR2-7/2	1221.042	1221.346	-249.639	0.383	1375.158	0.455	17	0.166	R.HFEVDLSAFR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1221.311	1221.346	-28.933	0.466	1185.973	0.516	16	0.163	R.HFEVDLSAFR.N
R2/RRR2-7/2	1211.616	1211.348	221.445	0.438	1164.274	0.496	16	0.158	K.GEFVEYIPTR.E
R2/RRR2-7/2	1339.155	1339.521	-273.883	0.404	960.103	0.439	17	0.134	K.KGEFVEYIPTR.E
R2/RRR2-7/2	1373.046	1373.604	-1138.179	0.383	718.526	0.443	19	0.124	K.VEPLVNM*GQITR.A
R2/RRR2-7/2	1373.120	1373.604	-353.718	0.401	585.208	0.449	18	0.122	K.VEPLVNM*GQITR.A
R2/RRR2-7/2	1373.112	1373.604	-359.695	0.385	526.280	0.451	17	0.120	K.VEPLVNM*GQITR.A
R2/RRR2-7/2	1116.127	1115.264	-123.148	0.407	878.570	0.351	14	0.119	K.VGDALEFVHK.E
R2/RRR2-7/2	1220.490	1221.346	-1525.791	0.412	595.974	0.394	12	0.114	R.HFEVDLSAFR.N
R2/RRR2-7/2	1115.285	1115.264	19.364	0.307	845.889	0.304	14	0.112	K.VGDALEFVHK.E
R2/RRR2-1/2	1116.144	1115.264	-107.130	0.316	695.820	0.181	14	0.103	K.VGDALEFVHK.E
R2/RRR2-7/3	1448.557	1448.611	-37.336	0.511	1157.376	0.365	23	0.095	R.ARHFEVDLSAFR.N
R2/RRR2-6/3	1449.304	1448.611	-212.611	0.391	963.726	0.291	21	0.074	R.ARHFEVDLSAFR.N
R2/RRR2-9/2	1513.840	1514.706	-1236.190	0.522	1799.696	0.486	22	0.223	R.KLAEDNNVPLSSVK.G
R2/RRR2-9/2	1514.366	1514.706	-225.136	0.522	1632.276	0.542	21	0.215	R.KLAEDNNVPLSSVK.G
R2/RRR2-9/2	1514.208	1514.706	-329.709	0.553	1546.917	0.514	21	0.197	R.KLAEDNNVPLSSVK.G
R2/RRR2-9/2	1233.217	1233.438	-180.357	0.422	1520.992	0.485	19	0.188	R.VIDGAIGAEFLK.A
R2/RRR2-9/2	1233.040	1233.438	-324.065	0.528	1426.142	0.450	19	0.171	R.VIDGAIGAEFLK.A
R2/RRR2-9/2	1987.568	1987.203	184.212	0.508	1137.325	0.588	23	0.167	K.EALAAPGLSYTDVPNAQIR.K
R2/RRR2-9/2	1232.557	1233.438	-1531.017	0.404	1371.470	0.442	18	0.163	R.VIDGAIGAEFLK.A
R2/RRR2-9/2	1986.514	1987.203	-852.681	0.474	1224.228	0.477	23	0.154	K.EALAAPGLSYTDVPNAQIR.K
R2/RRR2-9/2	1985.880	1987.203	-1172.873	0.439	1121.287	0.489	22	0.147	K.EALAAPGLSYTDVPNAQIR.K
R2/RRR2-9/2	1143.081	1143.402	-281.553	0.426	963.613	0.372	15	0.126	K.KISINDLVIK.A
R2/RRR2-9/2	1142.824	1143.402	-1384.894	0.489	682.989	0.377	14	0.118	K.KISINDLVIK.A
R2/RRR2-9/2	1015.092	1015.229	-135.103	0.433	958.381	0.273	15	0.116	K.ISINDLVIK.A
R2/RRR2-9/2	1015.162	1015.229	-65.865	0.469	921.109	0.268	15	0.115	K.ISINDLVIK.A
R2/RRR2-9/2	1014.743	1015.229	-479.869	0.427	887.097	0.265	15	0.114	K.ISINDLVIK.A
R2/RRR2-9/2	1038.019	1038.133	-110.121	0.306	702.378	0.365	13	0.112	K.ADIEDYLAK.G
R2/RRR2-8/2	1015.677	1015.229	442.393	0.308	589.305	0.250	14	0.109	K.ISINDLVIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1142.645	1143.402	-1541.659	0.295	619.756	0.332	13	0.109	K.KISINDLVIK.A
R2/RRR2-9/3	1585.364	1585.744	-240.277	0.361	1070.061	0.382	24	0.093	K.LRGELNPLQESSGGK.K
R2/RRR2-9/3	1585.390	1585.744	-224.403	0.408	946.245	0.361	25	0.083	-.LRGELNPLQESSGGK.-
R2/RRR2-9/3	1143.441	1143.402	34.295	0.446	990.985	0.295	20	0.076	K.KISINDLVIK.A
R2/RRR2-9/3	1585.460	1585.744	-179.680	0.345	837.131	0.284	24	0.070	-.LRGELNPLQESSGGK.-
R2/RRR2-9/3	1143.074	1143.402	-287.351	0.441	701.797	0.251	18	0.067	-.KISINDLVIK.-
R2/RRR2-12/2	1990.678	1991.298	-815.900	0.529	1599.786	0.559	26	0.211	R.AFSGLGGLGVDEPAMVSALAK.W
R2/RRR2-12/2	1578.145	1578.665	-966.183	0.533	1351.290	0.566	20	0.191	R.HIEEDLGHEETLR.E
R2/RRR2-12/2	1989.700	1991.298	-1813.356	0.450	1507.221	0.516	25	0.190	R.AFSGLGGLGVDEPAMVSALAK.W
R2/RRR2-12/2	1990.478	1991.298	-916.861	0.527	1242.029	0.591	24	0.177	R.AFSGLGGLGVDEPAMVSALAK.W
R2/RRR2-12/2	959.623	960.067	-464.180	0.409	1690.206	0.338	15	0.176	R.TAEELLGAR.K
R2/RRR2-12/2	1812.908	1812.096	-103.641	0.514	1213.995	0.564	19	0.171	R.DKPYCGLLVGLVSAYR.Y
R2/RRR2-12/2	1172.934	1173.338	-345.369	0.540	1295.677	0.430	18	0.157	R.EAALCLATPAR.Y
R2/RRR2-12/2	960.296	960.067	239.684	0.481	1630.837	0.278	15	0.156	R.TAEELLGAR.K
R2/RRR2-12/2	959.155	960.067	-1999.659	0.374	1565.401	0.275	15	0.151	R.TAEELLGAR.K
R2/RRR2-12/2	1174.063	1173.338	-234.912	0.525	1283.879	0.363	18	0.143	R.EAALCLATPAR.Y
R2/RRR2-12/2	1172.889	1173.338	-384.215	0.444	1110.742	0.386	17	0.135	R.EAALCLATPAR.Y
R2/RRR2-12/2	1058.986	1059.155	-160.547	0.523	711.458	0.447	15	0.131	K.LVENDDVVR.I
R2/RRR2-12/2	1186.231	1186.385	-129.907	0.446	566.252	0.493	15	0.128	R.SKPHLVETFK.H
R2/RRR2-12/2	1058.653	1059.155	-1423.761	0.485	711.122	0.416	15	0.127	K.LVENDDVVR.I
R2/RRR2-12/3	1578.626	1578.665	-25.146	0.484	1220.465	0.478	26	0.123	R.HIEEDLGHEETLR.E
R2/RRR2-12/3	1578.830	1578.665	104.558	0.510	1060.908	0.525	25	0.121	R.HIEEDLGHEETLR.E
R2/RRR2-12/2	1058.450	1059.155	-1616.171	0.399	718.435	0.383	15	0.121	K.LVENDDVVR.I
R2/RRR2-12/2	1185.883	1186.385	-1270.183	0.394	480.087	0.423	14	0.118	R.SKPHLVETFK.H
R2/RRR2-12/2	1186.150	1186.385	-198.868	0.396	472.511	0.418	14	0.118	R.SKPHLVETFK.H
R2/RRR2-12/3	1578.488	1578.665	-112.875	0.528	964.300	0.480	23	0.106	R.HIEEDLGHEETLR.E
R2/RRR2-13/3	1578.438	1578.665	-144.643	0.431	665.930	0.468	20	0.090	R.HIEEDLGHEETLR.E
R2/RRR2-20/3	1639.603	1639.905	-184.390	0.537	2986.248	0.427	35	0.445	K.IKHTGPGLLSM*ANAGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1565.830	1566.739	-1223.295	0.516	1675.589	0.591	21	0.233	K.VYFDVEIDGKPAGR.V
R2/RRR2-20/2	1566.282	1566.739	-292.717	0.528	1653.965	0.562	20	0.222	K.VYFDVEIDGKPAGR.V
R2/RRR2-20/2	1566.365	1566.739	-239.783	0.504	1633.283	0.553	21	0.217	K.VYFDVEIDGKPAGR.V
R2/RRR2-20/2	1924.418	1925.198	-927.784	0.531	1115.610	0.566	26	0.164	R.IIPSFMIQGGDFTLGDGR.G
R2/RRR2-20/2	1924.415	1925.198	-929.121	0.512	1078.489	0.583	26	0.164	R.IIPSFMIQGGDFTLGDGR.G
R2/RRR2-20/2	1924.045	1925.198	-1122.432	0.510	1109.434	0.517	26	0.155	R.IIPSFMIQGGDFTLGDGR.G
R2/RRR2-20/2	1940.499	1941.197	-877.711	0.460	629.612	0.579	25	0.136	R.IIPSFM*IQGGDFTLGDGR.G
R2/RRR2-20/2	1940.479	1941.197	-888.131	0.505	608.514	0.569	25	0.136	R.IIPSFM*IQGGDFTLGDGR.G
R2/RRR2-20/2	1940.320	1941.197	-970.362	0.448	688.425	0.539	26	0.134	R.IIPSFM*IQGGDFTLGDGR.G
R2/RRR2-20/2	1013.630	1014.115	-479.248	0.416	827.630	0.351	15	0.120	K.ADLTEVTHK.V
R2/RRR2-20/2	866.434	867.091	-1918.793	0.380	640.275	0.369	13	0.119	R.VVM*GLFGK.T
R2/RRR2-20/2	1014.134	1014.115	19.122	0.439	989.699	0.280	15	0.118	K.ADLTEVTHK.V
R2/RRR2-20/2	866.863	867.091	-263.629	0.398	794.253	0.319	13	0.117	R.VVM*GLFGK.T
R2/RRR2-20/2	866.482	867.091	-1862.871	0.364	629.819	0.315	13	0.115	R.VVM*GLFGK.T
R2/RRR2-18/2	1942.689	1941.197	253.933	0.456	242.108	0.461	17	0.115	R.IIPSFM*IQGGDFTLGDGR.G
R2/RRR2-20/2	850.860	851.092	-273.493	0.247	332.517	0.337	11	0.111	R.VVMGLFGK.T
R2/RRR2-20/2	850.692	851.092	-471.445	0.212	389.619	0.348	11	0.108	R.VVMGLFGK.T
R2/RRR2-20/3	1924.756	1925.198	-230.319	0.316	1096.556	0.369	27	0.090	R.IIPSFMIQGGDFTLGDGR.G
R2/RRR2-20/3	1399.718	1398.574	103.578	0.310	995.057	0.235	25	0.066	K.HTGPGLLSM*ANAGR.D
R2/RRR2-4/2	1760.497	1760.968	-268.214	0.569	3035.882	0.607	24	0.513	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-4/2	1760.690	1760.968	-157.965	0.520	2925.243	0.541	24	0.457	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-4/2	1760.449	1760.968	-864.947	0.552	2714.083	0.578	24	0.420	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-3/2	1760.707	1760.968	-148.298	0.489	2536.094	0.541	22	0.366	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-4/2	1726.472	1726.951	-278.039	0.516	2141.294	0.409	21	0.249	R.TYNELVEYNIVLQK.A
R2/RRR2-4/2	1744.369	1744.835	-268.167	0.415	1530.343	0.538	24	0.200	R.QEPVDETVTDPLSGEK.V
R2/RRR2-4/3	1930.833	1931.146	-162.505	0.515	1596.298	0.484	33	0.168	K.VRPAYSFGVDPVWHGSR.S
R2/RRR2-2/2	1760.260	1760.968	-973.060	0.414	1201.327	0.422	19	0.142	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-4/2	1744.488	1744.835	-199.719	0.387	791.078	0.547	19	0.134	R.QEPVDETVTDPLSGEK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1727.186	1726.951	136.274	0.409	1234.132	0.345	17	0.132	R.TYNELVEYNIVLQK.A
R2/RRR2-4/2	971.172	971.176	-3.985	0.415	753.565	0.453	16	0.129	K.LGSLSGLVPK.E
R2/RRR2-4/2	1176.107	1176.262	-132.899	0.432	1138.853	0.330	15	0.129	K.AGEFFYSAQR.S
R2/RRR2-1/2	1762.153	1760.968	105.430	0.435	845.003	0.448	21	0.128	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-4/2	970.637	971.176	-1590.076	0.365	596.340	0.473	15	0.123	K.LGSLSGLVPK.E
R2/RRR2-4/2	970.598	971.176	-1630.254	0.318	755.346	0.444	16	0.123	K.LGSLSGLVPK.E
R2/RRR2-4/2	1175.926	1176.262	-286.600	0.380	959.786	0.313	14	0.117	K.AGEFFYSAQR.S
R2/RRR2-4/3	1930.496	1931.146	-856.754	0.501	1110.153	0.485	29	0.117	K.VRPAYSFGVDPVWHGSR.S
R2/RRR2-1/2	971.313	971.176	141.858	0.387	414.498	0.402	13	0.117	K.LGSLSGLVPK.E
R2/RRR2-1/2	970.859	971.176	-327.589	0.331	396.727	0.366	13	0.113	K.LGSLSGLVPK.E
R2/RRR2-1/2	1760.138	1760.968	-1042.619	0.412	371.957	0.418	16	0.112	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-1/2	1760.771	1760.968	-111.856	0.305	335.218	0.326	15	0.107	K.FTSAFQEIVDAYGIAK.Y
R2/RRR2-19/2	1727.507	1726.951	-257.531	0.395	529.462	0.303	14	0.104	R.TYNELVEYNIVLQK.A
R2/RRR2-20/2	1726.630	1726.951	-186.326	0.391	627.785	0.245	16	0.103	R.TYNELVEYNIVLQK.A
R2/RRR2-4/2	1175.427	1176.262	-1566.161	0.322	756.664	0.224	13	0.103	-.AGEFFYSAQR.-
R2/RRR2-20/2	1728.081	1726.951	75.413	0.399	794.488	0.271	14	0.103	R.TYNELVEYNIVLQK.A
R2/RRR2-4/2	979.241	979.024	222.543	0.194	982.420	0.186	13	0.102	K.FYEGDGYK.F
R2/RRR2-3/2	1726.262	1726.951	-981.515	0.290	639.322	0.205	14	0.100	-.TYNELVEYNIVLQK.-
R2/RRR2-4/3	1930.395	1931.146	-909.696	0.309	756.519	0.373	23	0.077	K.VRPAYSFGVDPVWHGSR.S
R2/RRR2-7/2	1121.201	1121.268	-60.127	0.393	1449.813	0.406	16	0.163	R.GAINFATIDAK.A
R2/RRR2-8/2	1121.272	1121.268	3.318	0.403	1361.168	0.422	16	0.158	R.GAINFATIDAK.A
R2/RRR2-7/2	1199.463	1199.334	107.832	0.354	1363.494	0.288	16	0.137	K.YEELGELFAK.S
R2/RRR2-7/2	1199.864	1199.334	-392.924	0.498	1139.061	0.323	16	0.128	K.YEELGELFAK.S
R2/RRR2-7/2	1314.143	1314.513	-282.357	0.388	1099.831	0.342	16	0.126	K.TLSDALRPIAEK.H
R2/RRR2-7/2	1192.700	1193.414	-1441.234	0.311	869.009	0.405	16	0.122	R.TIEDLITFIK.E
R2/RRR2-7/2	1493.486	1493.640	-103.345	0.405	538.936	0.495	17	0.120	K.ALAPEYEEAATSLK.E
R2/RRR2-8/2	1100.850	1101.237	-352.635	0.358	660.792	0.430	14	0.118	K.HGVEGYPTLK.V
R2/RRR2-8/2	1122.110	1121.268	-141.477	0.367	702.664	0.408	14	0.117	-.GAINFATIDAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1368.990	1369.459	-343.756	0.349	595.830	0.409	19	0.117	K.SEPIPESNDGPVK.V
R2/RRR2-7/2	1368.590	1369.459	-1370.252	0.290	530.147	0.455	19	0.115	K.SEPIPESNDGPVK.V
R2/RRR2-7/2	1120.460	1121.268	-1618.953	0.321	1106.371	0.245	15	0.115	R.GAINFATIDAK.A
R2/RRR2-8/2	1192.459	1193.414	-1644.516	0.330	565.031	0.320	13	0.108	R.TIEDLITFIK.E
R2/RRR2-8/2	1369.116	1369.459	-251.703	0.270	413.985	0.307	17	0.108	K.SEPIPESNDGPVK.V
R2/RRR2-8/2	1315.781	1314.513	204.286	0.271	370.869	0.316	13	0.105	K.TLSDALRPIAEK.H
R2/RRR2-8/2	1104.907	1105.224	-287.735	0.454	756.858	0.568	17	0.141	K.VVGVDTSGSGVK.L
R2/RRR2-8/2	1104.872	1105.224	-319.326	0.408	764.738	0.545	19	0.138	K.VVGVDTSGSGVK.L
R2/RRR2-8/2	1105.144	1105.224	-72.634	0.415	674.105	0.459	18	0.125	K.VVGVDTSGSGVK.L
R2/RRR2-7/2	1203.119	1202.419	-250.101	0.548	1631.304	0.508	19	0.206	R.LLAVEGCAALGK.L
R2/RRR2-7/2	1201.405	1202.419	-1681.800	0.400	1680.557	0.440	18	0.195	R.LLAVEGCAALGK.L
R2/RRR2-7/2	1202.261	1202.419	-132.350	0.459	1649.802	0.452	19	0.195	R.LLAVEGCAALGK.L
R2/RRR2-7/2	1533.388	1533.749	-236.316	0.414	1760.315	0.335	20	0.182	K.ESDIVDWFVPVVK.R
R2/RRR2-7/2	1121.607	1122.258	-1476.260	0.396	1309.601	0.529	17	0.174	R.LAAGEWFTAR.V
R2/RRR2-7/2	1533.220	1533.749	-1000.562	0.378	1640.691	0.349	19	0.172	K.ESDIVDWFVPVVK.R
R2/RRR2-7/2	1122.066	1122.258	-171.271	0.405	1314.118	0.487	17	0.167	R.LAAGEWFTAR.V
R2/RRR2-7/2	1284.190	1284.442	-197.034	0.511	1402.322	0.435	18	0.166	K.FAATVEQNYLK.T
R2/RRR2-6/2	1285.509	1284.442	52.326	0.500	1396.504	0.430	18	0.164	K.FAATVEQNYLK.T
R2/RRR2-7/2	1284.202	1284.442	-187.593	0.495	1403.430	0.398	18	0.159	K.FAATVEQNYLK.T
R2/RRR2-7/2	1765.305	1766.115	-1028.609	0.432	1050.048	0.516	24	0.150	K.VLQALIPILDQSVVEK.N
R2/RRR2-6/2	1767.043	1766.115	-41.061	0.532	905.429	0.560	23	0.149	K.VLQALIPILDQSVVEK.N
R2/RRR2-7/3	1765.668	1766.115	-254.192	0.499	1301.310	0.514	30	0.142	K.VLQALIPILDQSVVEK.N
R2/RRR2-7/2	1765.330	1766.115	-1014.099	0.433	879.638	0.490	23	0.136	K.VLQALIPILDQSVVEK.N
R2/RRR2-6/2	1283.983	1284.442	-359.172	0.420	1174.620	0.354	17	0.134	K.FAATVEQNYLK.T
R2/RRR2-7/2	1190.034	1190.335	-253.777	0.434	1004.402	0.397	14	0.132	K.INNPHYLYR.M
R2/RRR2-7/2	1190.098	1190.335	-199.854	0.489	890.101	0.425	14	0.131	K.INNPHYLYR.M
R2/RRR2-6/2	1765.491	1766.115	-922.464	0.417	845.236	0.457	22	0.129	K.VLQALIPILDQSVVEK.N
R2/RRR2-7/2	1283.457	1284.442	-1551.577	0.347	1075.367	0.324	16	0.124	K.FAATVEQNYLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1765.238	1766.115	-1066.241	0.350	921.782	0.368	23	0.121	K.VLQALIPILDQSVVEK.N
R2/RRR2-7/2	1121.449	1122.258	-1617.524	0.357	750.505	0.367	14	0.116	R.LAAGEWFTAR.V
R2/RRR2-7/2	1190.058	1190.335	-233.710	0.404	906.008	0.292	14	0.116	K.INNPHYLYR.M
R2/RRR2-7/2	1215.216	1215.342	-104.139	0.477	657.578	0.366	14	0.115	-.LLRDNEAEVR.-
R2/RRR2-6/2	1285.666	1284.442	174.788	0.328	383.799	0.427	15	0.114	-.FAATVEQNYLK.-
R2/RRR2-7/2	1532.767	1533.749	-1297.291	0.269	943.619	0.314	16	0.113	K.ESDIVDWFVPVVK.R
R2/RRR2-1/2	1203.435	1202.419	12.859	0.301	533.208	0.396	13	0.109	R.LLAVEGCAALGK.L
R2/RRR2-7/2	1215.188	1215.342	-126.711	0.430	577.340	0.282	13	0.107	-.LLRDNEAEVR.-
R2/RRR2-7/2	1215.033	1215.342	-254.803	0.433	568.390	0.229	13	0.105	R.LLRDNEAEVR.I
R2/RRR2-6/3	1765.559	1766.115	-884.088	0.385	1105.228	0.382	25	0.095	K.VLQALIPILDQSVVEK.N
R2/RRR2-16/2	1629.330	1628.852	294.298	0.581	2502.977	0.614	25	0.387	R.GELLVGIIGTLDTGNR.Y
R2/RRR2-15/2	1629.533	1628.852	-196.677	0.588	2380.920	0.664	25	0.379	R.GELLVGIIGTLDTGNR.Y
R2/RRR2-16/2	1629.718	1628.852	-82.461	0.592	2301.803	0.632	25	0.351	R.GELLVGIIGTLDTGNR.Y
R2/RRR2-16/2	1628.299	1628.852	-956.725	0.479	2223.447	0.539	25	0.305	R.GELLVGIIGTLDTGNR.Y
R2/RRR2-15/2	1629.372	1628.852	-295.284	0.572	2037.524	0.590	24	0.287	R.GELLVGIIGTLDTGNR.Y
R2/RRR2-15/2	1628.580	1628.852	-167.321	0.534	1700.074	0.594	23	0.235	R.GELLVGIIGTLDTGNR.Y
R2/RRR2-16/2	1698.454	1698.866	-243.482	0.514	1340.659	0.619	22	0.195	R.VDFAPGGTNPPHVHPR.A
R2/RRR2-15/2	1698.466	1698.866	-236.199	0.501	1435.765	0.562	21	0.192	R.VDFAPGGTNPPHVHPR.A
R2/RRR2-16/2	1698.485	1698.866	-224.951	0.493	1315.966	0.564	23	0.181	R.VDFAPGGTNPPHVHPR.A
R2/RRR2-16/2	1278.211	1278.508	-232.439	0.470	1478.453	0.406	16	0.164	R.GLMHFQFNVGK.T
R2/RRR2-15/2	1698.423	1698.866	-261.581	0.493	1098.032	0.581	20	0.163	R.VDFAPGGTNPPHVHPR.A
R2/RRR2-15/2	1698.229	1698.866	-966.859	0.447	1097.082	0.552	21	0.157	R.VDFAPGGTNPPHVHPR.A
R2/RRR2-16/2	1278.983	1278.508	373.000	0.495	1324.486	0.394	16	0.149	R.GLMHFQFNVGK.T
R2/RRR2-16/2	1698.532	1698.866	-197.049	0.481	884.740	0.530	19	0.139	R.VDFAPGGTNPPHVHPR.A
R2/RRR2-16/2	957.872	958.137	-277.514	0.442	1198.616	0.363	14	0.138	R.ATEVGIVLR.G
R2/RRR2-16/2	957.984	958.137	-160.283	0.465	1165.871	0.350	14	0.134	R.ATEVGIVLR.G
R2/RRR2-16/2	1278.125	1278.508	-300.085	0.429	1244.714	0.322	16	0.132	R.GLMHFQFNVGK.T
R2/RRR2-16/2	989.902	990.138	-239.036	0.462	893.663	0.413	14	0.131	R.AGETFVIPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	990.026	990.138	-113.605	0.488	846.137	0.371	14	0.125	R.AGETFVIPR.G
R2/RRR2-18/2	989.195	990.138	-1969.689	0.451	745.960	0.387	14	0.125	R.AGETFVIPR.G
R2/RRR2-15/2	1277.980	1278.508	-1199.151	0.379	1352.573	0.219	16	0.124	R.GLMHFQFNVGK.T
R2/RRR2-14/2	989.347	990.138	-1815.808	0.419	848.169	0.357	14	0.123	R.AGETFVIPR.G
R2/RRR2-15/2	989.474	990.138	-1686.390	0.417	868.823	0.352	14	0.123	R.AGETFVIPR.G
R2/RRR2-15/2	989.904	990.138	-236.438	0.449	864.807	0.349	14	0.123	R.AGETFVIPR.G
R2/RRR2-16/2	957.564	958.137	-1648.418	0.421	982.778	0.329	14	0.122	R.ATEVGIVLR.G
R2/RRR2-15/2	1293.997	1294.507	-1170.298	0.446	705.344	0.399	16	0.122	R.GLM*HFQFNVGK.T
R2/RRR2-15/2	1278.016	1278.508	-385.949	0.386	1212.558	0.255	16	0.122	R.GLMHFQFNVGK.T
R2/RRR2-15/2	1278.916	1278.508	320.174	0.471	1323.784	0.230	16	0.122	R.GLMHFQFNVGK.T
R2/RRR2-13/2	990.026	990.138	-113.357	0.443	740.377	0.348	14	0.121	R.AGETFVIPR.G
R2/RRR2-16/2	989.955	990.138	-185.223	0.472	793.342	0.338	14	0.121	R.AGETFVIPR.G
R2/RRR2-14/2	989.303	990.138	-1860.690	0.390	806.803	0.340	14	0.121	R.AGETFVIPR.G
R2/RRR2-15/2	989.988	990.138	-152.072	0.428	765.772	0.332	14	0.120	R.AGETFVIPR.G
R2/RRR2-15/2	1294.237	1294.507	-208.931	0.460	695.356	0.393	15	0.120	R.GLM*HFQFNVGK.T
R2/RRR2-16/2	1294.223	1294.507	-220.475	0.455	677.144	0.376	16	0.120	R.GLM*HFQFNVGK.T
R2/RRR2-15/2	1294.135	1294.507	-288.041	0.430	690.119	0.376	16	0.120	R.GLM*HFQFNVGK.T
R2/RRR2-16/2	1293.754	1294.507	-1359.176	0.432	678.353	0.373	16	0.119	R.GLM*HFQFNVGK.T
R2/RRR2-16/2	989.873	990.138	-268.233	0.376	864.231	0.304	14	0.118	R.AGETFVIPR.G
R2/RRR2-18/2	989.848	990.138	-293.226	0.443	674.329	0.329	13	0.118	R.AGETFVIPR.G
R2/RRR2-11/2	990.023	990.138	-115.955	0.384	752.800	0.305	14	0.117	R.AGETFVIPR.G
R2/RRR2-13/2	989.390	990.138	-1771.549	0.384	807.097	0.299	14	0.117	R.AGETFVIPR.G
R2/RRR2-16/2	989.946	990.138	-194.377	0.446	673.416	0.321	13	0.117	R.AGETFVIPR.G
R2/RRR2-1/2	989.799	990.138	-343.091	0.323	758.950	0.315	14	0.117	R.AGETFVIPR.G
R2/RRR2-19/2	989.764	990.138	-378.730	0.401	842.905	0.286	14	0.117	R.AGETFVIPR.G
R2/RRR2-18/2	989.395	990.138	-1767.210	0.404	724.545	0.287	14	0.116	R.AGETFVIPR.G
R2/RRR2-12/2	989.765	990.138	-377.863	0.380	754.153	0.289	14	0.116	R.AGETFVIPR.G
R2/RRR2-17/2	989.541	990.138	-1618.472	0.382	757.593	0.307	13	0.116	R.AGETFVIPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	989.374	990.138	-1787.665	0.401	792.275	0.276	14	0.115	R.AGETFVIPR.G
R2/RRR2-19/2	989.934	990.138	-206.129	0.387	575.687	0.305	12	0.115	R.AGETFVIPR.G
R2/RRR2-16/2	1413.467	1413.688	-156.924	0.425	1137.071	0.245	17	0.114	K.ALRVDTGVVELLK.S
R2/RRR2-24/2	990.029	990.138	-110.636	0.415	750.779	0.256	14	0.114	R.AGETFVIPR.G
R2/RRR2-19/2	989.373	990.138	-1788.657	0.375	836.311	0.254	14	0.114	R.AGETFVIPR.G
R2/RRR2-25/2	989.600	990.138	-1558.989	0.329	660.892	0.267	13	0.113	R.AGETFVIPR.G
R2/RRR2-19/2	958.191	958.137	55.825	0.338	1042.323	0.230	14	0.113	R.ATEVGIVLR.G
R2/RRR2-16/2	1413.465	1413.688	-158.137	0.448	1038.054	0.257	17	0.112	-.ALRVDTGVVELLK.-
R2/RRR2-12/2	990.011	990.138	-128.076	0.430	698.393	0.280	13	0.112	-.AGETFVIPR.-
R2/RRR2-24/2	989.354	990.138	-1808.121	0.359	772.286	0.241	13	0.112	R.AGETFVIPR.G
R2/RRR2-10/2	989.878	990.138	-263.656	0.415	952.879	0.213	14	0.111	R.AGETFVIPR.G
R2/RRR2-24/2	989.688	990.138	-456.079	0.362	815.604	0.227	13	0.111	R.AGETFVIPR.G
R2/RRR2-14/2	989.905	990.138	-235.448	0.363	838.179	0.189	14	0.110	R.AGETFVIPR.G
R2/RRR2-2/2	990.184	990.138	46.664	0.332	677.550	0.182	13	0.109	R.AGETFVIPR.G
R2/RRR2-16/2	989.357	990.138	-1804.898	0.369	724.080	0.212	13	0.109	-.AGETFVIPR.-
R2/RRR2-7/2	990.087	990.138	-51.395	0.222	643.133	0.158	13	0.108	R.AGETFVIPR.G
R2/RRR2-25/2	989.709	990.138	-434.915	0.316	727.619	0.107	14	0.107	R.AGETFVIPR.G
R2/RRR2-16/3	1414.258	1413.688	-305.059	0.519	934.916	0.394	26	0.087	-.ALRVDTGVVELLK.-
R2/RRR2-16/3	1413.679	1413.688	-6.342	0.509	1037.711	0.313	26	0.080	K.ALRVDTGVVELLK.S
R2/RRR2-16/3	1412.567	1413.688	-1505.852	0.460	1104.173	0.264	25	0.073	-.ALRVDTGVVELLK.-
R2/RRR2-14/2	1606.145	1606.584	-274.093	0.578	2799.078	0.528	25	0.422	K.DAAEGQEGEAATEEAK.K
R2/RRR2-15/2	1720.186	1719.920	155.050	0.584	2732.582	0.531	24	0.406	R.ILDVVYNASNNELVR.T
R2/RRR2-14/2	1720.409	1719.920	284.839	0.586	2594.129	0.553	24	0.383	R.ILDVVYNASNNELVR.T
R2/RRR2-15/2	1606.065	1606.584	-948.853	0.571	2446.091	0.556	24	0.353	K.DAAEGQEGEAATEEAK.K
R2/RRR2-15/2	1606.167	1606.584	-260.369	0.558	2394.626	0.551	23	0.341	K.DAAEGQEGEAATEEAK.K
R2/RRR2-15/2	1720.058	1719.920	80.392	0.567	2452.208	0.504	24	0.336	R.ILDVVYNASNNELVR.T
R2/RRR2-14/2	1605.843	1606.584	-1087.825	0.513	2161.632	0.596	23	0.312	K.DAAEGQEGEAATEEAK.K
R2/RRR2-14/2	1720.385	1719.920	270.751	0.569	2299.642	0.494	24	0.303	R.ILDVVYNASNNELVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1719.375	1719.920	-901.418	0.527	2220.539	0.470	23	0.287	-.ILDVVYNASNNELVR.-
R2/RRR2-14/2	1657.244	1656.735	-297.041	0.595	1973.910	0.564	23	0.268	R.LDTGNYSWGSEAVTR.K
R2/RRR2-15/2	1606.121	1606.584	-289.649	0.526	1996.956	0.512	22	0.256	K.DAAEGQEGEAATEEAK.K
R2/RRR2-15/2	1656.294	1656.735	-266.903	0.548	1813.709	0.541	22	0.237	R.LDTGNYSWGSEAVTR.K
R2/RRR2-14/2	1656.166	1656.735	-949.794	0.496	1829.795	0.513	23	0.232	R.LDTGNYSWGSEAVTR.K
R2/RRR2-1/2	1720.158	1719.920	138.753	0.499	1781.986	0.500	22	0.225	-.ILDVVYNASNNELVR.-
R2/RRR2-15/2	1656.274	1656.735	-278.882	0.520	1761.707	0.488	22	0.215	R.LDTGNYSWGSEAVTR.K
R2/RRR2-15/3	1734.673	1734.757	-48.611	0.567	1843.656	0.493	31	0.211	K.KDAAEGQEGEAATEEAK.K
R2/RRR2-15/2	1657.298	1656.735	-264.304	0.571	1535.129	0.557	21	0.203	R.LDTGNYSWGSEAVTR.K
R2/RRR2-14/3	1862.941	1862.930	5.933	0.631	1563.418	0.594	38	0.198	K.KDAAEGQEGEAATEEAKK.S
R2/RRR2-14/3	1734.831	1734.757	42.859	0.523	1805.350	0.455	30	0.192	K.KDAAEGQEGEAATEEAK.K
R2/RRR2-14/2	1655.590	1656.735	-1299.110	0.461	1529.993	0.499	21	0.189	R.LDTGNYSWGSEAVTR.K
R2/RRR2-15/2	1246.067	1246.437	-298.078	0.390	1560.146	0.471	18	0.188	K.SAIVQVDAAPFK.Q
R2/RRR2-14/2	1247.478	1246.437	32.819	0.395	1299.523	0.448	16	0.156	K.SAIVQVDAAPFK.Q
R2/RRR2-15/3	1720.134	1719.920	124.653	0.478	1489.761	0.422	27	0.139	R.ILDVVYNASNNELVR.T
R2/RRR2-14/2	1245.520	1246.437	-1544.082	0.280	1369.406	0.312	16	0.138	K.SAIVQVDAAPFK.Q
R2/RRR2-15/3	1863.007	1862.930	41.422	0.576	1166.210	0.535	35	0.133	K.KDAAEGQEGEAATEEAKK.S
R2/RRR2-15/2	1616.666	1616.797	-80.779	0.575	2418.616	0.512	23	0.335	K.FPTLVTHQESLESK.V
R2/RRR2-15/2	1616.394	1616.797	-249.556	0.526	2263.994	0.526	23	0.311	K.FPTLVTHQESLESK.V
R2/RRR2-15/2	1616.361	1616.797	-270.240	0.538	2263.145	0.519	23	0.308	K.FPTLVTHQESLESK.V
R2/RRR2-15/2	1491.323	1491.759	-293.309	0.538	2393.125	0.436	21	0.305	K.KYHAFLASEAIIK.Q
R2/RRR2-15/2	1491.447	1491.759	-209.468	0.516	2257.293	0.416	21	0.274	K.KYHAFLASEAIIK.Q
R2/RRR2-15/2	1491.456	1491.759	-203.310	0.505	1818.136	0.460	20	0.219	K.KYHAFLASEAIIK.Q
R2/RRR2-15/2	1506.265	1506.769	-1001.398	0.466	1728.812	0.457	20	0.207	R.KFTETVELQIGLK.N
R2/RRR2-15/3	1491.508	1491.759	-168.834	0.535	2079.171	0.387	30	0.200	K.KYHAFLASEAIIK.Q
R2/RRR2-15/2	1146.889	1147.261	-325.135	0.427	1340.594	0.491	17	0.171	K.EAISQVVGESK.E
R2/RRR2-15/2	1363.020	1363.586	-1152.271	0.412	1512.826	0.340	19	0.159	K.YHAFLASEAIIK.Q
R2/RRR2-15/3	1491.764	1491.759	3.798	0.537	1706.095	0.422	28	0.159	K.KYHAFLASEAIIK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1506.122	1506.769	-1096.361	0.393	1120.953	0.423	17	0.138	R.KFTETVELQIGLK.N
R2/RRR2-15/3	1491.749	1491.759	-6.297	0.521	1633.577	0.381	28	0.138	K.KYHAFLASEAIIK.Q
R2/RRR2-15/2	1146.253	1147.261	-1756.844	0.306	1319.594	0.296	17	0.134	K.EAISQVVGESK.E
R2/RRR2-15/3	1873.099	1873.099	-0.014	0.463	1032.156	0.559	29	0.127	K.AGKFPTLVTHQESLESK.V
R2/RRR2-15/3	1872.743	1873.099	-190.755	0.496	790.111	0.556	28	0.110	K.AGKFPTLVTHQESLESK.V
R2/RRR2-15/3	1491.672	1491.759	-58.254	0.502	1377.912	0.358	26	0.108	K.KYHAFLASEAIIK.Q
R2/RRR2-15/3	1873.341	1873.099	129.295	0.474	788.286	0.502	27	0.100	K.AGKFPTLVTHQESLESK.V
R2/RRR2-13/3	1872.109	1873.099	-1066.399	0.421	811.977	0.463	24	0.094	K.AGKFPTLVTHQESLESK.V
R2/RRR2-15/3	1616.785	1616.797	-7.097	0.430	949.437	0.392	24	0.088	K.FPTLVTHQESLESK.V
R2/RRR2-15/3	1616.130	1616.797	-1034.545	0.396	847.210	0.400	23	0.085	K.FPTLVTHQESLESK.V
R2/RRR2-15/3	1616.795	1616.797	-1.304	0.350	860.664	0.255	23	0.068	K.FPTLVTHQESLESK.V
R2/RRR2-16/3	1458.869	1458.775	64.269	0.516	1938.326	0.424	27	0.196	K.VRPAWLAILFGSK.T
R2/RRR2-16/2	1295.343	1294.482	-107.433	0.532	1326.850	0.471	17	0.165	K.SDLLLASNPVHK.S
R2/RRR2-16/2	1294.007	1294.482	-368.122	0.478	1189.124	0.504	17	0.159	K.SDLLLASNPVHK.S
R2/RRR2-16/2	1294.321	1294.482	-124.356	0.486	1296.804	0.448	18	0.159	K.SDLLLASNPVHK.S
R2/RRR2-16/2	1363.190	1362.601	-302.735	0.497	1171.113	0.463	19	0.152	K.LLGVWSSPYAIR.V
R2/RRR2-16/3	1458.579	1458.775	-135.166	0.492	1671.031	0.373	25	0.144	K.VRPAWLAILFGSK.T
R2/RRR2-16/2	1362.196	1362.601	-297.923	0.430	1047.521	0.399	18	0.133	K.LLGVWSSPYAIR.V
R2/RRR2-16/2	1362.079	1362.601	-1120.616	0.435	1035.083	0.402	18	0.133	K.LLGVWSSPYAIR.V
R2/RRR2-16/2	1363.107	1362.601	-363.653	0.479	908.356	0.430	17	0.130	K.LLGVWSSPYAIR.V
R2/RRR2-16/2	1656.288	1656.771	-292.703	0.507	733.211	0.469	21	0.130	K.SLPYEYVEENLGDK.S
R2/RRR2-16/2	1363.574	1362.601	-20.168	0.439	957.241	0.403	18	0.130	K.LLGVWSSPYAIR.V
R2/RRR2-16/2	1656.266	1656.771	-911.666	0.482	680.899	0.470	21	0.128	K.SLPYEYVEENLGDK.S
R2/RRR2-16/2	1656.245	1656.771	-924.541	0.473	589.715	0.493	20	0.127	K.SLPYEYVEENLGDK.S
R2/RRR2-16/2	1115.960	1115.219	-232.990	0.408	912.365	0.368	14	0.124	R.FWAAYVDDK.V
R2/RRR2-15/2	1362.334	1362.601	-196.876	0.418	664.839	0.427	15	0.119	K.LLGVWSSPYAIR.V
R2/RRR2-16/2	1115.734	1115.219	-435.720	0.222	688.572	0.336	13	0.106	R.FWAAYVDDK.V
R2/RRR2-16/2	941.345	941.196	158.080	0.504	1036.301	0.192	13	0.106	-.VRVVLNLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/3	1458.263	1458.775	-1039.995	0.464	1263.869	0.352	23	0.100	K.VRPAWLAILFGSK.T
R2/RRR2-16/2	940.991	941.196	-218.672	0.445	882.307	0.136	12	0.098	-.VRVVLNLK.-
R2/RRR2-16/2	941.296	941.196	106.580	0.448	875.906	0.128	12	0.096	-.VRVVLNLK.-
R2/RRR2-5/2	1771.550	1771.950	-226.801	0.542	2727.901	0.458	25	0.381	R.LYLDQYGGSGDVWIGK.V
R2/RRR2-5/2	1771.572	1771.950	-213.943	0.548	2693.040	0.475	25	0.380	R.LYLDQYGGSGDVWIGK.V
R2/RRR2-5/2	1847.572	1848.002	-233.506	0.526	2153.495	0.455	23	0.268	K.ESSQESIEGDTAILLVR.A
R2/RRR2-5/2	1771.459	1771.950	-277.958	0.501	1863.259	0.472	23	0.227	R.LYLDQYGGSGDVWIGK.V
R2/RRR2-5/2	1847.464	1848.002	-835.011	0.493	1766.285	0.420	22	0.200	K.ESSQESIEGDTAILLVR.A
R2/RRR2-5/2	1386.260	1386.581	-232.339	0.491	1574.988	0.425	19	0.180	R.VALLADAVSSHFR.R
R2/RRR2-5/2	1618.224	1617.778	276.041	0.507	780.476	0.502	20	0.135	K.DLDLDIPYDEPALK.A
R2/RRR2-5/2	1618.450	1617.778	-203.395	0.488	992.266	0.414	22	0.134	K.DLDLDIPYDEPALK.A
R2/RRR2-5/2	1385.726	1386.581	-1342.350	0.380	1096.421	0.382	17	0.131	R.VALLADAVSSHFR.R
R2/RRR2-2/2	1387.413	1386.581	-121.218	0.398	920.387	0.460	15	0.130	R.VALLADAVSSHFR.R
R2/RRR2-5/2	1119.178	1118.263	-75.661	0.478	819.097	0.374	15	0.122	R.VLQGCSAINR.L
R2/RRR2-5/2	1118.023	1118.263	-214.819	0.432	821.888	0.341	15	0.118	R.VLQGCSAINR.L
R2/RRR2-5/2	1418.109	1418.677	-1108.717	0.300	1040.857	0.302	16	0.117	R.MTLFCNDLYLK.A
R2/RRR2-5/2	1618.340	1617.778	-271.726	0.459	724.287	0.370	19	0.117	K.DLDLDIPYDEPALK.A
R2/RRR2-2/2	1617.543	1617.778	-146.134	0.357	564.578	0.329	17	0.110	K.DLDLDIPYDEPALK.A
R2/RRR2-1/2	1617.324	1617.778	-281.510	0.340	566.019	0.318	17	0.109	K.DLDLDIPYDEPALK.A
R2/RRR2-5/2	1117.456	1118.263	-1621.662	0.287	732.413	0.280	14	0.108	R.VLQGCSAINR.L
R2/RRR2-5/2	1244.140	1244.412	-219.319	0.231	727.418	0.337	13	0.106	K.CFEYLDGIVK.K
R2/RRR2-4/2	1617.570	1617.778	-128.949	0.363	401.732	0.308	14	0.099	-.DLDLDIPYDEPALK.-
R2/RRR2-2/2	1728.273	1728.924	-957.915	0.444	2017.638	0.519	23	0.269	R.YFAAQALASLVCNGSR.G
R2/RRR2-2/2	1887.701	1886.184	-256.756	0.496	1343.394	0.512	22	0.172	R.LLAALALGDLFQNEGLAR.S
R2/RRR2-2/2	1888.068	1886.184	-61.645	0.483	1143.867	0.565	22	0.164	R.LLAALALGDLFQNEGLAR.S
R2/RRR2-2/2	1216.116	1216.414	-245.918	0.527	1205.171	0.445	15	0.150	K.ALNALLSNFPR.L
R2/RRR2-2/2	1568.669	1567.857	-119.856	0.499	996.602	0.505	18	0.143	K.ALANLALAWPNTIAK.E
R2/RRR2-2/2	959.997	960.112	-120.347	0.477	1238.746	0.343	13	0.138	K.APFLVQER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	960.083	960.112	-29.664	0.423	1134.442	0.380	13	0.137	K.APFLVQER.V
R2/RRR2-2/2	960.037	960.112	-78.128	0.458	1186.487	0.311	13	0.130	K.APFLVQER.V
R2/RRR2-2/2	1231.318	1231.509	-155.776	0.313	656.759	0.479	17	0.121	K.VVQPLFSLLSK.A
R2/RRR2-2/2	981.828	982.119	-297.118	0.292	884.564	0.305	13	0.112	-.LTLGNNPPR.-
R2/RRR2-2/2	1705.701	1705.983	-165.714	0.405	580.861	0.425	17	0.112	R.SNAALHSIPVLSNLLR.S
R2/RRR2-2/2	1231.338	1231.509	-139.467	0.297	443.461	0.418	14	0.111	K.VVQPLFSLLSK.A
R2/RRR2-6/2	1397.669	1396.613	40.418	0.497	1894.646	0.364	18	0.208	K.FEELNIDLFKK.T
R2/RRR2-6/2	1212.238	1212.424	-154.087	0.593	1750.173	0.447	20	0.206	K.DAGIIAGLNVLR.I
R2/RRR2-6/3	1442.186	1442.603	-290.365	0.541	1774.549	0.399	26	0.167	K.GKVEILVNDQGNR.I
R2/RRR2-6/2	1265.996	1266.299	-240.581	0.416	1317.659	0.380	19	0.148	K.LYSGGAGGSDEPR.S
R2/RRR2-6/2	1647.330	1646.866	282.387	0.394	978.180	0.432	21	0.131	R.IVNEPTAAAIAYGLDK.T
R2/RRR2-6/2	1211.465	1212.424	-1622.153	0.274	705.926	0.331	15	0.108	-.DAGIIAGLNVLR.-
R2/RRR2-6/2	1212.070	1212.424	-292.801	0.321	867.445	0.250	14	0.105	K.DAGIIAGLNVLR.I
R2/RRR2-6/2	1004.827	1005.069	-241.517	0.306	910.284	0.183	13	0.103	K.NQAASNPFR.T
R2/RRR2-6/3	1556.059	1556.786	-1112.999	0.413	649.638	0.492	23	0.090	K.GGKPIVSVEVKGEEK.Q
R2/RRR2-6/3	1556.502	1556.786	-182.748	0.418	608.103	0.387	23	0.077	K.GGKPIVSVEVKGEEK.Q
R2/RRR2-6/3	1396.160	1396.613	-325.281	0.498	913.671	0.270	23	0.073	K.FEELNIDLFKK.T
R2/RRR2-6/3	1396.325	1396.613	-206.868	0.459	1035.592	0.248	24	0.071	K.FEELNIDLFKK.T
R2/RRR2-6/2	1520.252	1520.712	-303.351	0.433	2069.439	0.414	20	0.244	R.TLFDLQEVSAQIR.E
R2/RRR2-6/2	1316.068	1316.386	-242.870	0.409	1590.641	0.438	18	0.187	K.TEYVSCPSCGR.T
R2/RRR2-6/2	1820.588	1820.101	268.122	0.488	932.389	0.601	19	0.151	K.SAIGIGTLLM*DGLGDTIR.V
R2/RRR2-6/2	1819.728	1820.101	-206.029	0.411	850.489	0.500	21	0.131	K.SAIGIGTLLM*DGLGDTIR.V
R2/RRR2-5/2	1520.531	1520.712	-119.544	0.370	1026.384	0.329	18	0.121	R.TLFDLQEVSAQIR.E
R2/RRR2-6/2	1091.985	1092.230	-225.548	0.400	871.238	0.347	16	0.120	R.IADKGADFVR.I
R2/RRR2-6/2	1092.030	1092.230	-183.830	0.392	697.162	0.389	14	0.117	R.IADKGADFVR.I
R2/RRR2-6/2	861.941	862.008	-78.142	0.417	685.493	0.365	11	0.116	-.APELLYR.-
R2/RRR2-6/2	1224.889	1225.333	-363.905	0.256	208.801	0.488	14	0.112	R.ELPPVEDAQAR.L
R2/RRR2-3/2	1521.074	1520.712	238.534	0.325	936.241	0.236	15	0.106	R.TLFDLQEVSAQIR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1225.029	1225.333	-249.126	0.194	209.600	0.481	14	0.101	-.ELPPVEDAQAR.-
R2/RRR2-6/2	1225.001	1225.333	-271.820	0.108	208.035	0.372	14	0.100	R.ELPPVEDAQAR.L
R2/RRR2-6/3	1803.372	1804.102	-962.230	0.477	1272.442	0.328	30	0.095	K.SAIGIGTLLMDGLGDTIR.V
R2/RRR2-6/3	1530.508	1529.787	-182.870	0.488	1003.592	0.265	21	0.072	R.KLDFHNFVFSM*K.A
R2/RRR2-6/3	1819.938	1820.101	-89.963	0.298	608.399	0.293	23	0.066	K.SAIGIGTLLM*DGLGDTIR.V
R2/RRR2-2/2	1318.141	1318.416	-209.143	0.472	1949.375	0.502	21	0.244	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1318.090	1318.416	-247.700	0.491	1947.135	0.478	20	0.237	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1319.108	1318.416	-233.772	0.574	1693.887	0.590	20	0.231	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1318.299	1318.416	-88.845	0.487	1746.369	0.526	21	0.222	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1460.142	1460.527	-264.773	0.466	1664.479	0.547	20	0.220	K.AISTSNAYDDQFK.Q
R2/RRR2-10/2	1318.151	1318.416	-200.967	0.482	1634.701	0.465	21	0.194	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1286.081	1286.493	-321.553	0.484	1460.718	0.531	20	0.193	K.IPATAECVPSIK.E
R2/RRR2-10/2	1319.022	1318.416	-299.413	0.509	1489.029	0.528	21	0.192	R.LANDTQGTVEAAK.W
R2/RRR2-12/2	1319.221	1318.416	-147.810	0.509	1399.561	0.555	21	0.188	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1318.273	1318.416	-108.536	0.474	1510.325	0.497	20	0.186	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1318.086	1318.416	-250.859	0.439	1521.842	0.483	20	0.184	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1459.538	1460.527	-1367.161	0.349	1582.032	0.440	20	0.183	K.AISTSNAYDDQFK.Q
R2/RRR2-1/2	1318.050	1318.416	-277.897	0.459	1523.666	0.443	20	0.176	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1460.044	1460.527	-332.045	0.484	1264.564	0.549	19	0.175	K.AISTSNAYDDQFK.Q
R2/RRR2-10/2	1425.832	1424.580	177.613	0.513	1675.671	0.340	18	0.174	K.DAESAYWELVIK.D
R2/RRR2-10/2	1286.136	1286.493	-278.415	0.436	1122.178	0.564	19	0.165	K.IPATAECVPSIK.E
R2/RRR2-10/2	1286.329	1286.493	-127.984	0.462	1162.458	0.504	18	0.158	K.IPATAECVPSIK.E
R2/RRR2-7/2	1317.735	1318.416	-1279.395	0.408	1365.678	0.360	20	0.147	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1318.019	1318.416	-301.406	0.433	1070.798	0.480	19	0.145	R.LANDTQGTVEAAK.W
R2/RRR2-12/2	1317.566	1318.416	-1408.169	0.343	1318.563	0.374	19	0.145	R.LANDTQGTVEAAK.W
R2/RRR2-6/2	1318.100	1318.416	-240.453	0.418	1043.118	0.446	18	0.138	R.LANDTQGTVEAAK.W
R2/RRR2-12/2	1317.458	1318.416	-1490.531	0.366	1085.795	0.413	19	0.136	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1317.862	1318.416	-1182.557	0.428	881.488	0.469	19	0.134	R.LANDTQGTVEAAK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1177.971	1178.320	-297.328	0.493	683.743	0.456	15	0.125	R.GVTSNPSIFQK.A
R2/RRR2-10/2	1177.995	1178.320	-276.846	0.445	679.871	0.404	15	0.119	R.GVTSNPSIFQK.A
R2/RRR2-10/2	1178.012	1178.320	-261.667	0.402	666.170	0.383	15	0.116	R.GVTSNPSIFQK.A
R2/RRR2-10/2	1203.151	1203.416	-220.990	0.407	762.536	0.339	14	0.114	K.VVDRPNVYIK.I
R2/RRR2-18/2	1319.254	1318.416	-122.748	0.155	417.944	0.335	15	0.105	R.LANDTQGTVEAAK.W
R2/RRR2-10/2	1203.001	1203.416	-345.693	0.322	490.901	0.271	12	0.085	-.VVDRPNVYIK.-
R2/RRR2-7/2	1371.974	1372.553	-1154.210	0.503	3889.855	0.513	25	0.736	R.NVNSALAASGIGGIK.V
R2/RRR2-7/2	1372.332	1372.553	-161.182	0.571	3339.096	0.606	24	0.602	R.NVNSALAASGIGGIK.V
R2/RRR2-7/2	1372.265	1372.553	-210.530	0.500	3252.867	0.511	24	0.535	R.NVNSALAASGIGGIK.V
R2/RRR2-9/2	1372.285	1372.553	-195.894	0.479	2594.973	0.435	23	0.343	R.NVNSALAASGIGGIK.V
R2/RRR2-7/3	1373.562	1372.553	7.111	0.497	2431.013	0.453	32	0.307	R.NVNSALAASGIGGIK.V
R2/RRR2-9/2	1372.192	1372.553	-263.899	0.454	2384.004	0.446	22	0.305	R.NVNSALAASGIGGIK.V
R2/RRR2-9/2	1372.080	1372.553	-345.123	0.465	2056.985	0.433	22	0.244	R.NVNSALAASGIGGIK.V
R2/RRR2-7/2	1612.109	1611.845	164.033	0.535	2036.297	0.430	22	0.243	R.SEVVQM*YVSLGINR.M
R2/RRR2-7/3	1372.497	1372.553	-40.341	0.445	1809.805	0.405	31	0.172	R.NVNSALAASGIGGIK.V
R2/RRR2-7/2	1756.243	1755.949	167.901	0.560	1187.592	0.568	21	0.169	R.DISLNYATFQPGTTVK.D
R2/RRR2-7/2	1799.156	1797.989	93.054	0.532	1121.903	0.553	22	0.162	R.EISLNYATFQPGTTVR.D
R2/RRR2-14/2	1755.187	1755.949	-1007.264	0.482	1156.441	0.542	21	0.161	R.DISLNYATFQPGTTVK.D
R2/RRR2-7/2	1611.201	1611.845	-1023.383	0.475	1374.483	0.412	20	0.158	R.SEVVQM*YVSLGINR.M
R2/RRR2-7/2	1755.545	1755.949	-230.682	0.475	1094.982	0.508	21	0.150	R.DISLNYATFQPGTTVK.D
R2/RRR2-8/2	1755.477	1755.949	-270.027	0.497	1078.447	0.511	20	0.149	R.DISLNYATFQPGTTVK.D
R2/RRR2-7/2	1799.442	1797.989	252.528	0.531	1003.061	0.522	21	0.147	R.EISLNYATFQPGTTVR.D
R2/RRR2-7/2	1799.331	1797.989	190.214	0.509	871.321	0.518	20	0.138	R.EISLNYATFQPGTTVR.D
R2/RRR2-14/2	1074.966	1075.201	-219.323	0.381	973.891	0.422	14	0.132	R.HFGLFNPDK.T
R2/RRR2-7/2	1755.343	1755.949	-917.684	0.483	714.882	0.546	18	0.132	R.DISLNYATFQPGTTVK.D
R2/RRR2-8/2	1756.148	1755.949	113.460	0.498	771.271	0.498	18	0.128	R.DISLNYATFQPGTTVK.D
R2/RRR2-14/2	1075.205	1075.201	3.005	0.395	841.968	0.372	13	0.121	R.HFGLFNPDK.T
R2/RRR2-8/2	1074.840	1075.201	-336.905	0.368	773.808	0.388	13	0.120	R.HFGLFNPDK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1075.032	1075.201	-157.809	0.363	589.835	0.406	12	0.117	R.HFGLFNPDK.T
R2/RRR2-12/2	1074.978	1075.201	-208.045	0.309	610.730	0.401	11	0.113	-.HFGLFNPDK.-
R2/RRR2-7/2	1074.492	1075.201	-1595.573	0.191	624.847	0.284	13	0.104	-.HFGLFNPDK.-
R2/RRR2-7/3	1231.944	1231.388	-361.286	0.512	1206.479	0.339	20	0.093	R.RHFGLFNPDK.T
R2/RRR2-7/3	1372.250	1372.553	-221.427	0.338	963.582	0.272	25	0.072	R.NVNSALAASGIGGIK.V
R2/RRR2-3/2	1175.024	1175.274	-213.985	0.502	2432.878	0.533	21	0.347	R.LAGEEASGITAR.H
R2/RRR2-3/2	1175.006	1175.274	-229.410	0.502	2399.534	0.519	21	0.335	R.LAGEEASGITAR.H
R2/RRR2-3/2	1174.948	1175.274	-278.814	0.509	2374.014	0.501	21	0.324	R.LAGEEASGITAR.H
R2/RRR2-3/2	1607.293	1606.802	306.484	0.399	2542.865	0.173	22	0.254	K.IDDIYAVELIGGATR.V
R2/RRR2-3/2	1359.349	1359.511	-119.578	0.561	1565.023	0.503	17	0.200	R.LVNYFADQFNK.Q
R2/RRR2-3/2	1606.691	1606.802	-69.240	0.399	1862.238	0.244	21	0.174	K.IDDIYAVELIGGATR.V
R2/RRR2-3/2	1002.223	1002.192	30.894	0.454	844.100	0.395	14	0.126	K.AIGDPILFR.L
R2/RRR2-3/2	1068.144	1068.251	-99.875	0.358	966.918	0.319	14	0.119	K.LGGLEM*EM*R.L
R2/RRR2-3/2	1001.897	1002.192	-295.505	0.372	636.254	0.377	14	0.117	K.AIGDPILFR.L
R2/RRR2-3/2	1632.694	1632.750	-34.354	0.376	647.203	0.400	21	0.116	K.FVEYSVSGLTDASEK.Y
R2/RRR2-3/2	1001.957	1002.192	-234.999	0.344	688.930	0.319	14	0.113	K.AIGDPILFR.L
R2/RRR2-3/2	1632.390	1632.750	-220.859	0.333	435.577	0.359	19	0.110	K.FVEYSVSGLTDASEK.Y
R2/RRR2-3/2	977.284	978.167	-1932.747	0.335	893.925	0.166	13	0.103	R.LYLAELQK.I
R2/RRR2-18/2	1611.311	1610.741	-267.364	0.593	1662.104	0.523	20	0.212	K.DGTNVEEAFQCIVK.N
R2/RRR2-18/2	1611.483	1610.741	-160.207	0.579	1537.828	0.506	20	0.193	K.DGTNVEEAFQCIVK.N
R2/RRR2-18/2	1611.148	1610.741	253.467	0.559	1461.910	0.492	20	0.182	K.DGTNVEEAFQCIVK.N
R2/RRR2-17/2	1059.084	1058.254	-160.647	0.477	1210.330	0.417	18	0.147	K.VIILGDSGVGK.T
R2/RRR2-18/2	1037.222	1037.191	29.439	0.422	1078.888	0.459	17	0.145	K.ATIGADFLTK.E
R2/RRR2-17/2	1058.171	1058.254	-78.288	0.407	1215.537	0.399	18	0.144	K.VIILGDSGVGK.T
R2/RRR2-18/2	1057.473	1058.254	-1689.101	0.343	1269.275	0.354	18	0.140	K.VIILGDSGVGK.T
R2/RRR2-18/2	1189.079	1188.359	-236.785	0.570	1064.858	0.408	17	0.138	R.FQSLGVAFYR.G
R2/RRR2-18/2	1036.865	1037.191	-315.709	0.363	1089.339	0.425	16	0.138	K.ATIGADFLTK.E
R2/RRR2-18/2	1187.913	1188.359	-376.779	0.517	1083.203	0.392	17	0.137	R.FQSLGVAFYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1036.964	1037.191	-219.686	0.350	872.693	0.469	15	0.131	K.ATIGADFLTK.E
R2/RRR2-18/2	1213.948	1214.374	-352.253	0.425	1007.333	0.403	14	0.131	K.TSLM*NQYVNK.K
R2/RRR2-18/2	1226.983	1227.348	-298.024	0.425	514.483	0.529	17	0.130	K.GNIPYFETSAK.D
R2/RRR2-18/2	1036.922	1037.191	-260.904	0.336	758.667	0.498	14	0.128	K.ATIGADFLTK.E
R2/RRR2-18/2	1188.015	1188.359	-290.588	0.448	887.471	0.391	16	0.127	R.FQSLGVAFYR.G
R2/RRR2-18/2	1226.455	1227.348	-1547.719	0.373	501.151	0.480	17	0.123	K.GNIPYFETSAK.D
R2/RRR2-17/2	1058.122	1058.254	-124.576	0.314	994.371	0.353	16	0.123	K.VIILGDSGVGK.T
R2/RRR2-17/2	1188.038	1188.359	-271.002	0.387	977.981	0.334	15	0.122	R.FQSLGVAFYR.G
R2/RRR2-17/2	1036.778	1037.191	-399.463	0.341	731.270	0.426	14	0.121	K.ATIGADFLTK.E
R2/RRR2-17/2	1228.199	1227.348	-121.281	0.381	299.189	0.459	14	0.119	K.GNIPYFETSAK.D
R2/RRR2-17/2	1226.969	1227.348	-309.503	0.415	374.322	0.392	15	0.118	K.GNIPYFETSAK.D
R2/RRR2-18/2	1057.419	1058.254	-1740.134	0.341	777.028	0.379	15	0.118	K.VIILGDSGVGK.T
R2/RRR2-16/2	1058.085	1058.254	-159.873	0.314	853.745	0.353	16	0.117	-.VIILGDSGVGK.-
R2/RRR2-18/2	1226.506	1227.348	-1506.328	0.245	445.704	0.468	16	0.113	K.GNIPYFETSAK.D
R2/RRR2-18/2	1214.044	1214.374	-272.452	0.365	729.950	0.311	15	0.112	K.TSLM*NQYVNK.K
R2/RRR2-16/2	1057.453	1058.254	-1707.658	0.336	670.035	0.341	14	0.111	-.VIILGDSGVGK.-
R2/RRR2-18/2	1058.349	1058.254	90.165	0.215	625.331	0.187	13	0.103	-.VIILGDSGVGK.-
R2/RRR2-19/2	1036.722	1037.191	-454.165	0.311	322.450	0.308	10	0.100	-.ATIGADFLTK.-
R2/RRR2-4/2	1195.502	1196.338	-1540.886	0.494	1438.468	0.473	16	0.178	K.HNEIQTVNIK.T
R2/RRR2-4/2	1195.867	1196.338	-395.671	0.492	995.718	0.528	16	0.152	K.HNEIQTVNIK.T
R2/RRR2-4/2	1298.827	1298.341	375.031	0.369	1120.441	0.465	17	0.145	K.DTNTFASASLDR.T
R2/RRR2-4/2	1178.239	1177.332	-78.727	0.400	1119.365	0.448	15	0.144	K.SFEVTELPVR.S
R2/RRR2-4/2	1321.901	1322.449	-1174.776	0.473	1171.454	0.404	17	0.142	R.LENTLNYGLER.V
R2/RRR2-4/2	1322.334	1322.449	-87.370	0.471	1137.783	0.375	18	0.137	R.LENTLNYGLER.V
R2/RRR2-4/2	1024.289	1024.239	48.816	0.392	856.987	0.497	13	0.133	R.ANALLPSIPK.E
R2/RRR2-4/2	1195.392	1196.338	-1632.799	0.438	949.612	0.421	16	0.133	K.HNEIQTVNIK.T
R2/RRR2-4/2	1557.408	1557.799	-252.168	0.496	1069.342	0.396	18	0.133	R.QMYLLGYLANQSR.V
R2/RRR2-4/2	1557.822	1557.799	14.453	0.403	1082.776	0.305	18	0.121	R.QMYLLGYLANQSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1177.079	1177.332	-215.483	0.275	598.926	0.207	12	0.101	K.SFEVTELPVR.S
R2/RRR2-4/2	1297.380	1298.341	-1516.335	0.131	590.920	0.127	14	0.096	K.DTNTFASASLDR.T
R2/RRR2-23/2	942.826	942.095	-285.839	0.323	951.661	0.046	12	0.094	-.DLQKVNPK.-
R2/RRR2-14/2	1198.020	1198.305	-237.879	0.527	1859.963	0.475	17	0.228	R.TCYAQASQIR.Q
R2/RRR2-14/2	1778.322	1777.978	193.779	0.521	1401.507	0.589	21	0.199	K.NVLTNFWGM*SFTTDK.L
R2/RRR2-16/2	1198.040	1198.305	-221.626	0.501	1693.744	0.394	17	0.187	R.TCYAQASQIR.Q
R2/RRR2-14/2	1198.037	1198.305	-224.284	0.534	1409.428	0.434	17	0.167	R.TCYAQASQIR.Q
R2/RRR2-14/3	1354.495	1354.491	2.827	0.492	1744.892	0.396	23	0.159	K.RTCYAQASQIR.Q
R2/RRR2-14/2	1197.464	1198.305	-1542.043	0.481	1333.228	0.402	16	0.154	R.TCYAQASQIR.Q
R2/RRR2-13/2	1580.453	1579.824	-235.786	0.483	876.164	0.552	19	0.144	K.ATSSIFPLQNVFVR.K
R2/RRR2-16/2	1198.175	1198.305	-108.482	0.461	1212.506	0.349	16	0.136	R.TCYAQASQIR.Q
R2/RRR2-14/2	1579.472	1579.824	-223.762	0.449	879.466	0.460	20	0.133	K.ATSSIFPLQNVFVR.K
R2/RRR2-14/2	889.940	890.021	-92.262	0.404	675.913	0.498	12	0.130	K.APSVFNVR.N
R2/RRR2-16/2	1579.603	1579.824	-140.730	0.395	776.914	0.490	18	0.129	K.ATSSIFPLQNVFVR.K
R2/RRR2-18/2	1579.619	1579.824	-130.342	0.419	875.267	0.443	19	0.129	K.ATSSIFPLQNVFVR.K
R2/RRR2-17/2	1579.455	1579.824	-234.230	0.423	837.345	0.454	19	0.129	K.ATSSIFPLQNVFVR.K
R2/RRR2-2/2	1581.195	1579.824	235.194	0.441	768.378	0.456	18	0.126	K.ATSSIFPLQNVFVR.K
R2/RRR2-18/2	1579.208	1579.824	-1026.859	0.352	805.007	0.445	18	0.124	K.ATSSIFPLQNVFVR.K
R2/RRR2-20/2	1580.704	1579.824	-76.652	0.468	681.496	0.470	17	0.124	K.ATSSIFPLQNVFVR.K
R2/RRR2-17/2	1579.442	1579.824	-243.069	0.380	680.724	0.479	17	0.124	K.ATSSIFPLQNVFVR.K
R2/RRR2-14/2	889.956	890.021	-73.825	0.383	656.975	0.442	12	0.123	K.APSVFNVR.N
R2/RRR2-14/2	985.611	986.182	-1599.336	0.357	609.889	0.453	13	0.123	R.LFCIGFTK.R
R2/RRR2-14/2	889.596	890.021	-479.455	0.337	754.675	0.400	13	0.121	K.APSVFNVR.N
R2/RRR2-20/2	1580.362	1579.824	-293.363	0.409	580.954	0.471	16	0.120	K.ATSSIFPLQNVFVR.K
R2/RRR2-14/2	985.572	986.182	-1639.277	0.368	644.881	0.361	13	0.118	R.LFCIGFTK.R
R2/RRR2-14/2	985.495	986.182	-1717.426	0.322	612.868	0.398	13	0.117	R.LFCIGFTK.R
R2/RRR2-8/2	1580.662	1579.824	-103.300	0.349	630.643	0.425	16	0.116	K.ATSSIFPLQNVFVR.K
R2/RRR2-18/2	1579.394	1579.824	-273.542	0.387	620.891	0.367	17	0.114	K.ATSSIFPLQNVFVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1579.778	1579.824	-29.731	0.389	432.179	0.396	14	0.112	K.ATSSIFPLQNVFVR.K
R2/RRR2-16/2	890.265	890.021	273.872	0.355	636.268	0.288	12	0.111	K.APSVFNVR.N
R2/RRR2-17/2	1579.237	1579.824	-1008.001	0.358	565.878	0.331	16	0.110	K.ATSSIFPLQNVFVR.K
R2/RRR2-16/2	985.988	986.182	-198.013	0.327	591.267	0.239	13	0.110	R.LFCIGFTK.R
R2/RRR2-14/2	1578.923	1579.824	-1207.567	0.248	668.513	0.307	17	0.108	K.ATSSIFPLQNVFVR.K
R2/RRR2-13/2	1579.018	1579.824	-1147.324	0.292	514.161	0.308	15	0.108	K.ATSSIFPLQNVFVR.K
R2/RRR2-13/2	1578.506	1579.824	-1473.314	0.273	632.039	0.137	16	0.103	K.ATSSIFPLQNVFVR.K
R2/RRR2-15/2	1197.788	1198.305	-1270.132	0.318	928.422	0.106	16	0.102	R.TCYAQASQIR.Q
R2/RRR2-14/3	1354.010	1354.491	-356.204	0.364	406.585	0.293	19	0.077	K.RTCYAQASQIR.Q
R2/RRR2-17/2	1613.473	1613.746	-169.798	0.477	1111.192	0.499	19	0.152	K.EGFNVEAAFECIAR.N
R2/RRR2-17/2	1613.095	1613.746	-1026.995	0.444	1110.744	0.499	18	0.150	K.EGFNVEAAFECIAR.N
R2/RRR2-16/2	1406.078	1406.551	-337.362	0.557	3059.552	0.489	25	0.469	K.AM*AQVSQAGSGGLGR.V
R2/RRR2-16/2	1407.006	1406.551	324.120	0.576	2627.879	0.508	25	0.373	K.AM*AQVSQAGSGGLGR.V
R2/RRR2-16/2	1406.146	1406.551	-288.672	0.563	2478.591	0.561	25	0.361	K.AM*AQVSQAGSGGLGR.V
R2/RRR2-16/2	1390.112	1390.552	-317.218	0.498	2621.275	0.458	25	0.355	K.AMAQVSQAGSGGLGR.V
R2/RRR2-16/2	1531.447	1531.776	-215.429	0.588	2358.637	0.604	24	0.352	K.AVASINSVLTDLVTK.G
R2/RRR2-16/2	1532.515	1531.776	-170.939	0.534	2265.055	0.634	23	0.343	K.AVASINSVLTDLVTK.G
R2/RRR2-16/2	1406.107	1406.551	-316.892	0.551	2432.348	0.509	25	0.333	K.AM*AQVSQAGSGGLGR.V
R2/RRR2-16/2	1389.874	1390.552	-1210.700	0.495	2513.260	0.455	25	0.332	K.AMAQVSQAGSGGLGR.V
R2/RRR2-16/2	1531.310	1531.776	-305.638	0.517	2184.091	0.561	23	0.304	K.AVASINSVLTDLVTK.G
R2/RRR2-17/2	1406.233	1406.551	-226.488	0.521	2276.015	0.482	25	0.295	K.AM*AQVSQAGSGGLGR.V
R2/RRR2-16/2	1531.406	1531.776	-242.298	0.553	2032.368	0.607	23	0.291	K.AVASINSVLTDLVTK.G
R2/RRR2-17/2	1531.355	1531.776	-276.207	0.479	1901.970	0.575	22	0.259	K.AVASINSVLTDLVTK.G
R2/RRR2-17/2	1531.237	1531.776	-1008.495	0.409	2009.495	0.505	23	0.257	K.AVASINSVLTDLVTK.G
R2/RRR2-16/2	1879.362	1880.077	-915.433	0.543	1749.984	0.615	26	0.251	R.DLSPLTCAQCLSTAVSR.F
R2/RRR2-16/2	1879.516	1880.077	-833.279	0.538	1593.975	0.619	25	0.229	R.DLSPLTCAQCLSTAVSR.F
R2/RRR2-16/2	1879.230	1880.077	-986.123	0.513	1291.582	0.608	24	0.189	R.DLSPLTCAQCLSTAVSR.F
R2/RRR2-16/2	1393.212	1393.567	-255.347	0.519	1486.727	0.446	18	0.176	K.GNNVIYGLVQCR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1489.946	1490.547	-1077.531	0.496	1580.753	0.399	18	0.175	R.FDQYCGAQQGCR.I
R2/RRR2-17/2	1241.838	1241.333	-399.362	0.467	1122.942	0.562	20	0.164	K.GSTGVGFATSTAGK.G
R2/RRR2-16/2	1393.018	1393.567	-1115.416	0.505	1288.174	0.482	17	0.163	K.GNNVIYGLVQCR.G
R2/RRR2-16/2	1393.362	1393.567	-147.414	0.476	1311.051	0.467	17	0.163	K.GNNVIYGLVQCR.G
R2/RRR2-1/2	1532.104	1531.776	214.440	0.396	1297.470	0.493	19	0.162	K.AVASINSVLTDLVTK.G
R2/RRR2-16/2	1490.145	1490.547	-270.617	0.498	1486.229	0.383	17	0.161	R.FDQYCGAQQGCR.I
R2/RRR2-16/2	1240.774	1241.333	-1259.827	0.422	1101.959	0.551	19	0.158	K.GSTGVGFATSTAGK.G
R2/RRR2-16/2	1489.325	1490.547	-1496.014	0.378	1472.276	0.360	17	0.157	R.FDQYCGAQQGCR.I
R2/RRR2-16/2	1241.122	1241.333	-170.034	0.443	1213.776	0.477	21	0.156	K.GSTGVGFATSTAGK.G
R2/RRR2-16/3	1531.958	1531.776	119.106	0.434	982.661	0.464	27	0.103	K.AVASINSVLTDLVTK.G
R2/RRR2-16/3	1532.663	1531.776	-74.510	0.410	1014.484	0.436	26	0.099	K.AVASINSVLTDLVTK.G
R2/RRR2-16/3	1531.746	1531.776	-19.961	0.425	1043.523	0.428	28	0.099	K.AVASINSVLTDLVTK.G
R2/RRR2-15/2	1282.089	1281.503	-323.955	0.495	1472.880	0.543	17	0.196	K.NM*GLLLAEFEK.I
R2/RRR2-15/2	1251.456	1251.414	33.987	0.489	1458.921	0.506	17	0.188	R.TYLNTLQEIR.I
R2/RRR2-15/2	1251.272	1251.414	-113.859	0.521	1381.232	0.453	17	0.170	R.TYLNTLQEIR.I
R2/RRR2-15/2	1281.323	1281.503	-140.874	0.440	1408.673	0.445	17	0.168	K.NM*GLLLAEFEK.I
R2/RRR2-15/2	1281.314	1281.503	-148.329	0.460	1310.637	0.461	16	0.162	K.NM*GLLLAEFEK.I
R2/RRR2-15/2	1370.168	1370.490	-235.962	0.455	1149.364	0.489	21	0.155	K.ITIDPDDPAAVSR.Y
R2/RRR2-16/2	1370.268	1370.490	-162.586	0.455	1016.426	0.494	20	0.146	K.ITIDPDDPAAVSR.Y
R2/RRR2-15/2	1369.614	1370.490	-1374.323	0.377	1072.842	0.483	20	0.145	K.ITIDPDDPAAVSR.Y
R2/RRR2-16/2	1370.017	1370.490	-346.626	0.446	1055.593	0.455	20	0.142	K.ITIDPDDPAAVSR.Y
R2/RRR2-15/2	1370.198	1370.490	-213.796	0.466	1044.746	0.453	20	0.142	K.ITIDPDDPAAVSR.Y
R2/RRR2-15/2	1071.444	1072.194	-1638.165	0.360	1017.308	0.485	15	0.141	R.TPVNGDDLLK.G
R2/RRR2-16/2	1370.173	1370.490	-232.118	0.428	1036.480	0.441	20	0.139	K.ITIDPDDPAAVSR.Y
R2/RRR2-15/2	1072.059	1072.194	-126.497	0.459	939.909	0.470	15	0.138	R.TPVNGDDLLK.G
R2/RRR2-15/2	1072.131	1072.194	-59.225	0.462	995.863	0.445	15	0.138	R.TPVNGDDLLK.G
R2/RRR2-16/2	1072.074	1072.194	-112.676	0.355	944.752	0.465	15	0.134	R.TPVNGDDLLK.G
R2/RRR2-15/2	1263.131	1262.352	-175.310	0.200	116.921	0.481	14	0.107	R.QKADLLSDSER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1262.934	1262.352	-331.906	0.234	105.602	0.456	13	0.104	-.QKADLLSDSER.-
R2/RRR2-15/3	1230.093	1230.435	-278.818	0.419	999.914	0.363	21	0.086	R.IKYTIDTFTK.G
R2/RRR2-15/3	1230.531	1230.435	78.881	0.417	698.016	0.414	18	0.085	R.IKYTIDTFTK.G
R2/RRR2-15/3	1230.514	1230.435	64.703	0.345	940.202	0.334	20	0.079	R.IKYTIDTFTK.G
R2/RRR2-16/3	1230.685	1230.435	203.776	0.366	997.368	0.307	19	0.078	R.IKYTIDTFTK.G
R2/RRR2-16/3	1230.599	1230.435	133.648	0.335	798.453	0.265	19	0.070	R.IKYTIDTFTK.G
R2/RRR2-13/2	1594.323	1594.754	-271.057	0.575	2796.130	0.576	26	0.444	R.VADHAGVALAGLTADGR.V
R2/RRR2-13/2	1594.221	1594.754	-964.965	0.519	2606.705	0.604	25	0.411	R.VADHAGVALAGLTADGR.V
R2/RRR2-13/2	1595.163	1594.754	256.698	0.583	2580.108	0.578	25	0.393	R.VADHAGVALAGLTADGR.V
R2/RRR2-13/2	1711.337	1711.770	-254.098	0.547	2148.564	0.545	24	0.296	R.NQYDTDVTTWSPAGR.L
R2/RRR2-13/2	1711.400	1711.770	-217.173	0.510	2040.770	0.536	23	0.274	R.NQYDTDVTTWSPAGR.L
R2/RRR2-13/2	1712.514	1711.770	-149.898	0.576	1909.530	0.557	23	0.258	R.NQYDTDVTTWSPAGR.L
R2/RRR2-13/2	1444.035	1444.678	-1141.048	0.514	2053.585	0.448	19	0.248	R.LFQVEYAM*EAVK.Q
R2/RRR2-13/2	1444.138	1444.678	-1069.241	0.536	2085.407	0.432	19	0.247	R.LFQVEYAM*EAVK.Q
R2/RRR2-13/2	1427.706	1428.678	-1385.465	0.572	2132.112	0.409	19	0.246	R.LFQVEYAMEAVK.Q
R2/RRR2-13/2	1379.125	1378.551	-309.269	0.524	1857.043	0.514	20	0.239	K.LTSSNCTVAIVGR.K
R2/RRR2-13/2	1444.324	1444.678	-245.809	0.513	1932.392	0.402	19	0.217	R.LFQVEYAM*EAVK.Q
R2/RRR2-13/2	1429.536	1428.678	-99.832	0.578	1789.710	0.424	19	0.202	R.LFQVEYAMEAVK.Q
R2/RRR2-13/2	1504.187	1503.680	-328.487	0.525	1421.885	0.474	20	0.174	K.DALSAIKETLQGEK.L
R2/RRR2-13/2	1378.008	1378.551	-1122.945	0.468	1585.716	0.379	19	0.171	K.LTSSNCTVAIVGR.K
R2/RRR2-13/2	1503.157	1503.680	-1016.501	0.428	1442.852	0.419	19	0.165	K.DALSAIKETLQGEK.L
R2/RRR2-13/2	1503.786	1503.680	70.622	0.491	1281.674	0.475	19	0.160	K.DALSAIKETLQGEK.L
R2/RRR2-13/2	1377.614	1378.551	-1410.158	0.325	1267.694	0.372	18	0.140	K.LTSSNCTVAIVGR.K
R2/RRR2-13/2	1872.586	1874.043	-1315.821	0.500	990.679	0.457	18	0.135	R.RFEGYNDYTPEQLIK.D
R2/RRR2-13/2	1429.414	1428.678	-185.238	0.302	837.414	0.317	13	0.111	-.LFQVEYAMEAVK.-
R2/RRR2-13/3	1503.447	1503.680	-155.563	0.408	773.362	0.466	27	0.091	K.DALSAIKETLQGEK.L
R2/RRR2-13/3	1503.411	1503.680	-179.266	0.447	644.960	0.473	24	0.090	K.DALSAIKETLQGEK.L
R2/RRR2-13/3	1503.475	1503.680	-136.626	0.348	585.781	0.464	23	0.084	K.DALSAIKETLQGEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/3	1408.614	1408.587	19.364	0.449	1867.555	0.390	27	0.178	K.AANKAPDAFYALR.L
R2/RRR2-9/2	1025.029	1024.154	-122.745	0.508	1173.175	0.487	15	0.159	K.APDAFYALR.L
R2/RRR2-9/2	1024.215	1024.154	59.100	0.472	1249.089	0.449	15	0.157	K.APDAFYALR.L
R2/RRR2-9/2	1501.205	1501.689	-323.795	0.332	1157.707	0.290	17	0.121	R.GGYM*EITGFSAPVR.E
R2/RRR2-9/2	1839.011	1838.160	-81.398	0.409	606.560	0.454	15	0.113	K.TEGAMYLFPQLTLPQK.A
R2/RRR2-9/2	972.750	973.109	-369.494	0.423	970.900	0.215	15	0.109	K.DGILQSLAR.R
R2/RRR2-9/2	1838.137	1838.160	-12.763	0.396	446.605	0.403	14	0.106	K.TEGAMYLFPQLTLPQK.A
R2/RRR2-9/3	1301.231	1301.474	-187.454	0.442	1179.602	0.255	22	0.077	K.AEKDGILQSLAR.R
R2/RRR2-9/3	1301.767	1301.474	225.568	0.330	1172.347	0.173	21	0.066	K.AEKDGILQSLAR.R
R2/RRR2-9/3	1301.308	1301.474	-128.168	0.362	798.323	0.235	19	0.064	-.AEKDGILQSLAR.-
R2/RRR2-17/2	1241.066	1241.401	-270.695	0.500	1933.198	0.538	18	0.255	K.AFM*DATGGLWR.T
R2/RRR2-17/2	1240.625	1241.401	-1435.721	0.435	1887.925	0.525	18	0.244	K.AFM*DATGGLWR.T
R2/RRR2-17/2	1240.450	1241.401	-1577.958	0.461	1691.098	0.573	18	0.228	K.AFM*DATGGLWR.T
R2/RRR2-17/2	1224.998	1225.402	-330.090	0.380	1762.604	0.442	18	0.205	K.AFMDATGGLWR.T
R2/RRR2-17/2	1225.364	1225.402	-30.636	0.377	1661.713	0.400	17	0.183	K.AFMDATGGLWR.T
R2/RRR2-17/2	1699.443	1699.889	-263.369	0.485	1264.801	0.582	19	0.179	R.VATELELQQAFHQGK.Y
R2/RRR2-17/2	1240.461	1241.401	-1568.666	0.346	1630.330	0.390	18	0.177	K.AFM*DATGGLWR.T
R2/RRR2-17/2	1699.361	1699.889	-901.876	0.497	1202.106	0.577	19	0.172	R.VATELELQQAFHQGK.Y
R2/RRR2-17/2	1473.167	1473.486	-217.469	0.421	1115.080	0.616	23	0.171	K.GGSPYGSGTFAGDGSR.V
R2/RRR2-17/2	1744.488	1744.966	-275.027	0.535	1111.814	0.580	24	0.169	K.LWQVPETLSDDVLTK.M
R2/RRR2-17/2	1744.352	1744.966	-928.309	0.472	1046.841	0.562	24	0.159	K.LWQVPETLSDDVLTK.M
R2/RRR2-17/2	1744.061	1744.966	-1095.685	0.475	1043.637	0.558	24	0.159	K.LWQVPETLSDDVLTK.M
R2/RRR2-17/2	1699.425	1699.889	-274.034	0.500	1101.921	0.541	18	0.156	R.VATELELQQAFHQGK.Y
R2/RRR2-17/2	1473.147	1473.486	-231.103	0.443	1054.628	0.528	21	0.151	K.GGSPYGSGTFAGDGSR.V
R2/RRR2-17/2	1062.685	1063.276	-1501.533	0.500	1142.438	0.432	14	0.145	R.FGM*M*AAQFK.A
R2/RRR2-17/2	1472.540	1473.486	-1325.822	0.340	927.536	0.486	22	0.134	K.GGSPYGSGTFAGDGSR.V
R2/RRR2-17/3	1875.786	1875.067	-150.108	0.512	1276.657	0.474	28	0.131	K.LAEEIEKGASSVEGVEVK.L
R2/RRR2-17/2	1063.009	1063.276	-251.265	0.453	977.740	0.391	14	0.130	R.FGM*M*AAQFK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1744.176	1744.966	-1029.276	0.441	544.768	0.518	18	0.124	K.LWQVPETLSDDVLTK.M
R2/RRR2-17/2	1062.829	1063.276	-421.456	0.452	1094.803	0.308	14	0.124	R.FGM*M*AAQFK.A
R2/RRR2-17/2	1224.994	1225.402	-333.690	0.297	1144.329	0.279	15	0.120	K.AFMDATGGLWR.T
R2/RRR2-17/2	1744.230	1744.966	-998.288	0.431	511.551	0.445	17	0.116	K.LWQVPETLSDDVLTK.M
R2/RRR2-17/2	1047.097	1047.276	-171.235	0.314	874.073	0.162	14	0.104	R.FGMM*AAQFK.A
R2/RRR2-15/3	1621.980	1621.816	101.436	0.559	2626.662	0.371	32	0.305	R.KNESVFGELQTQLK.N
R2/RRR2-15/3	1621.836	1621.816	12.326	0.520	2465.555	0.321	31	0.251	R.KNESVFGELQTQLK.N
R2/RRR2-15/3	1837.573	1837.934	-196.871	0.549	1991.064	0.534	36	0.247	K.HHSNTAVGAELSHSFSR.N
R2/RRR2-15/2	1621.373	1621.816	-274.162	0.577	1874.790	0.499	23	0.235	R.KNESVFGELQTQLK.N
R2/RRR2-15/3	1836.873	1837.934	-1125.115	0.494	1913.790	0.497	35	0.221	K.HHSNTAVGAELSHSFSR.N
R2/RRR2-15/2	966.051	966.203	-156.854	0.399	1764.364	0.463	15	0.216	K.VGLSLVLKH.-
R2/RRR2-15/2	1620.579	1621.816	-1384.520	0.539	1816.144	0.427	22	0.208	R.KNESVFGELQTQLK.N
R2/RRR2-14/3	1837.544	1837.934	-212.966	0.518	1661.203	0.529	34	0.191	K.HHSNTAVGAELSHSFSR.N
R2/RRR2-15/2	1620.656	1621.816	-1337.162	0.526	1637.003	0.428	20	0.185	R.KNESVFGELQTQLK.N
R2/RRR2-15/2	1263.105	1263.420	-250.243	0.404	1406.634	0.514	18	0.179	K.SLITISGEVDTK.A
R2/RRR2-14/2	1264.092	1263.420	-260.121	0.380	1379.610	0.495	18	0.172	K.SLITISGEVDTK.A
R2/RRR2-15/3	1837.836	1837.934	-53.444	0.542	1403.448	0.537	34	0.158	K.HHSNTAVGAELSHSFSR.N
R2/RRR2-15/2	1263.143	1263.420	-219.897	0.441	1222.600	0.471	17	0.155	K.SLITISGEVDTK.A
R2/RRR2-14/2	1263.926	1263.420	-391.898	0.393	1153.736	0.499	17	0.153	K.SLITISGEVDTK.A
R2/RRR2-15/2	1263.224	1263.420	-155.331	0.540	1086.526	0.496	17	0.150	K.SLITISGEVDTK.A
R2/RRR2-15/2	1997.035	1998.217	-1095.816	0.455	967.381	0.561	21	0.147	K.FTLTTCTPEGVTITAAGTR.K
R2/RRR2-15/2	1997.239	1998.217	-993.144	0.469	914.837	0.556	23	0.145	K.FTLTTCTPEGVTITAAGTR.K
R2/RRR2-14/2	1621.401	1621.816	-257.016	0.491	1089.514	0.420	19	0.137	R.KNESVFGELQTQLK.N
R2/RRR2-14/2	1263.998	1263.420	-334.629	0.406	841.514	0.472	16	0.130	K.SLITISGEVDTK.A
R2/RRR2-15/2	1227.178	1227.435	-210.178	0.491	833.067	0.379	16	0.122	K.SILSLVVPDQR.S
R2/RRR2-14/2	1620.567	1621.816	-1392.161	0.382	887.697	0.361	19	0.119	R.KNESVFGELQTQLK.N
R2/RRR2-15/2	1227.240	1227.435	-159.487	0.422	774.746	0.348	15	0.116	K.SILSLVVPDQR.S
R2/RRR2-14/2	1227.036	1227.435	-326.649	0.357	673.014	0.351	14	0.113	K.SILSLVVPDQR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	965.982	966.203	-228.858	0.478	1338.927	0.506	14	0.111	K.VGLSLVLKH.-
R2/RRR2-14/2	1227.037	1227.435	-325.650	0.310	371.595	0.312	12	0.108	K.SILSLVVPDQR.S
R2/RRR2-14/2	1227.194	1227.435	-197.505	0.308	528.904	0.311	12	0.106	-.SILSLVVPDQR.-
R2/RRR2-14/3	1621.772	1621.816	-27.195	0.379	886.443	0.236	21	0.066	-.KNESVFGELQTQLK.-
R2/RRR2-14/2	1081.374	1081.244	120.174	0.498	748.722	0.435	14	0.128	R.LENTISYIK.G
R2/RRR2-14/2	937.959	938.109	-161.160	0.397	561.008	0.452	13	0.125	R.HVVLQSVR.S
R2/RRR2-14/2	937.503	938.109	-1718.626	0.370	575.938	0.444	13	0.124	R.HVVLQSVR.S
R2/RRR2-14/2	1081.053	1081.244	-177.656	0.460	783.642	0.355	14	0.120	R.LENTISYIK.G
R2/RRR2-14/2	938.065	938.109	-47.459	0.388	385.594	0.418	11	0.120	R.HVVLQSVR.S
R2/RRR2-15/2	938.124	938.109	15.582	0.395	398.910	0.393	11	0.119	R.HVVLQSVR.S
R2/RRR2-15/3	1394.687	1395.636	-1401.640	0.545	1342.566	0.424	26	0.119	R.RVNALENVVKPR.L
R2/RRR2-15/2	938.010	938.109	-106.068	0.378	489.220	0.367	12	0.118	R.HVVLQSVR.S
R2/RRR2-14/2	1080.424	1081.244	-1689.143	0.363	813.873	0.338	14	0.117	R.LENTISYIK.G
R2/RRR2-14/2	1010.969	1011.111	-140.499	0.325	523.323	0.452	14	0.116	R.ASSFSLAEAK.Y
R2/RRR2-14/2	1010.684	1011.111	-423.527	0.298	497.334	0.371	14	0.110	R.ASSFSLAEAK.Y
R2/RRR2-15/2	937.468	938.109	-1756.174	0.302	355.808	0.279	10	0.110	-.HVVLQSVR.-
R2/RRR2-15/2	1080.880	1081.244	-337.402	0.293	455.106	0.268	13	0.108	-.LENTISYIK.-
R2/RRR2-15/3	1395.517	1395.636	-85.518	0.512	1263.189	0.387	24	0.105	R.RVNALENVVKPR.L
R2/RRR2-14/3	1655.953	1655.747	124.864	0.475	672.268	0.573	24	0.105	K.GELDELEREDFFR.L
R2/RRR2-14/3	1655.776	1655.747	17.952	0.471	597.576	0.579	24	0.103	K.GELDELEREDFFR.L
R2/RRR2-15/3	1394.384	1395.636	-1619.529	0.520	1497.461	0.301	26	0.102	R.RVNALENVVKPR.L
R2/RRR2-22/2	938.127	938.109	18.975	0.217	350.626	0.329	9	0.101	-.HVVLQSVR.-
R2/RRR2-14/3	1395.840	1395.636	146.991	0.536	1160.387	0.379	24	0.097	R.RVNALENVVKPR.L
R2/RRR2-14/3	1394.940	1395.636	-1219.302	0.535	1124.004	0.351	24	0.090	R.RVNALENVVKPR.L
R2/RRR2-14/3	1395.862	1395.636	162.383	0.535	1172.188	0.329	24	0.088	R.RVNALENVVKPR.L
R2/RRR2-14/3	1293.436	1293.497	-47.493	0.468	1182.930	0.274	22	0.080	K.KKSDALTVQFR.A
R2/RRR2-14/3	1293.423	1293.497	-57.149	0.451	1083.679	0.277	23	0.076	K.KKSDALTVQFR.A
R2/RRR2-14/3	1293.456	1293.497	-31.589	0.428	848.097	0.300	21	0.074	K.KKSDALTVQFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1788.465	1787.905	-246.836	0.586	3739.656	0.576	28	0.726	K.GGYVVTEAGFGSDIGTEK.F
R2/RRR2-6/2	1787.633	1787.905	-152.639	0.556	3524.294	0.509	28	0.621	K.GGYVVTEAGFGSDIGTEK.F
R2/RRR2-6/2	1099.062	1099.266	-185.550	0.497	1721.704	0.448	17	0.204	K.GAVDLGLAVQR.A
R2/RRR2-6/2	1346.225	1345.483	-191.683	0.527	1234.967	0.489	18	0.163	R.LDIDPESITWR.R
R2/RRR2-6/2	1263.075	1263.468	-311.997	0.448	1216.769	0.459	17	0.154	K.SYGVNVVVAINK.F
R2/RRR2-6/2	1345.146	1345.483	-250.636	0.499	1108.149	0.463	17	0.148	R.LDIDPESITWR.R
R2/RRR2-6/2	1098.581	1099.266	-1538.185	0.450	1273.431	0.394	16	0.147	K.GAVDLGLAVQR.A
R2/RRR2-6/2	1345.033	1345.483	-335.314	0.506	971.342	0.470	17	0.141	R.LDIDPESITWR.R
R2/RRR2-6/2	1485.890	1486.587	-1145.129	0.358	767.188	0.418	17	0.119	K.FASDTEAEM*DVVR.N
R2/RRR2-6/2	1486.020	1486.587	-1057.363	0.371	549.951	0.411	16	0.113	K.FASDTEAEM*DVVR.N
R2/RRR2-6/3	1186.521	1186.340	152.853	0.412	1038.843	0.304	21	0.075	-.KITIGQGPDEK.-
R2/RRR2-12/2	1678.771	1678.996	-134.167	0.478	1400.468	0.468	18	0.170	R.IAAKLEFLQPSFSVK.D
R2/RRR2-12/2	1215.675	1216.373	-1400.804	0.459	1388.419	0.378	18	0.154	K.IRDSASQLIGR.T
R2/RRR2-12/2	1216.204	1216.373	-139.289	0.482	1325.722	0.410	17	0.154	K.IRDSASQLIGR.T
R2/RRR2-12/2	1296.816	1297.569	-1355.831	0.394	1181.599	0.458	19	0.150	K.LIVTVLPSLGER.Y
R2/RRR2-12/2	1216.131	1216.373	-199.805	0.465	1190.381	0.407	17	0.144	K.IRDSASQLIGR.T
R2/RRR2-12/2	1297.076	1297.569	-381.033	0.420	1008.027	0.441	18	0.137	K.LIVTVLPSLGER.Y
R2/RRR2-12/2	1296.102	1295.508	-314.627	0.493	897.261	0.333	16	0.118	K.LEFLQPSFSVK.D
R2/RRR2-12/2	946.993	947.028	-36.926	0.383	990.888	0.252	14	0.113	R.DSASQLIGR.T
R2/RRR2-12/2	1295.813	1295.508	235.686	0.407	787.011	0.334	14	0.113	K.LEFLQPSFSVK.D
R2/RRR2-12/2	946.431	947.028	-1692.322	0.339	884.049	0.221	14	0.108	R.DSASQLIGR.T
R2/RRR2-12/2	982.051	982.179	-131.071	0.429	620.207	0.316	12	0.107	-.TPM*VYLNK.-
R2/RRR2-12/2	981.394	982.179	-1824.496	0.327	772.890	0.252	13	0.107	-.TPM*VYLNK.-
R2/RRR2-12/2	981.501	982.179	-1714.772	0.374	640.283	0.344	12	0.103	-.TPM*VYLNK.-
R2/RRR2-12/3	1216.323	1216.373	-41.293	0.420	890.160	0.280	19	0.055	-.IRDSASQLIGR.-
R2/RRR2-12/3	1216.281	1216.373	-75.420	0.412	752.668	0.216	18	0.053	-.IRDSASQLIGR.-
R2/RRR2-3/2	1307.983	1307.481	-381.412	0.404	1287.956	0.427	16	0.152	R.AALSLAYQNLSR.V
R2/RRR2-3/2	1619.375	1617.765	-241.830	0.485	1085.482	0.478	18	0.144	K.GFTDGTM*IVGEFNGR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1355.061	1354.405	-254.224	0.505	782.721	0.495	20	0.138	R.QAIEEFSSDATR.F
R2/RRR2-3/2	1355.015	1354.405	-288.297	0.465	743.321	0.497	19	0.134	R.QAIEEFSSDATR.F
R2/RRR2-3/2	1308.526	1307.481	34.937	0.395	1021.039	0.373	15	0.125	R.AALSLAYQNLSR.V
R2/RRR2-3/2	1949.398	1948.122	142.158	0.421	620.917	0.522	16	0.120	K.YGAFEINDTDVFIVTSR.A
R2/RRR2-3/2	1602.330	1601.766	-272.683	0.354	958.356	0.372	17	0.120	K.GFTDGTMIVGEFNGR.K
R2/RRR2-3/2	1453.238	1452.640	-277.152	0.373	684.323	0.457	17	0.120	K.AGWPIAGTPDPTLR.I
R2/RRR2-3/2	1196.265	1196.380	-96.680	0.449	837.365	0.345	13	0.116	K.LGFYDLQLAR.D
R2/RRR2-3/2	1353.391	1354.405	-1492.662	0.282	524.233	0.373	17	0.111	R.QAIEEFSSDATR.F
R2/RRR2-3/2	1196.045	1196.380	-281.062	0.321	962.060	0.230	14	0.109	K.LGFYDLQLAR.D
R2/RRR2-4/2	1835.364	1835.071	159.729	0.287	741.900	0.352	16	0.106	K.EIAWMEEVIAAESSLR.A
R2/RRR2-3/2	1451.563	1452.640	-1435.150	0.245	626.785	0.354	16	0.105	K.AGWPIAGTPDPTLR.I
R2/RRR2-3/2	1195.850	1196.380	-1283.145	0.324	450.963	0.276	12	0.101	-.LGFYDLQLAR.-
R2/RRR2-13/2	1826.514	1826.237	152.006	0.506	2350.018	0.541	25	0.325	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-13/2	1826.385	1826.237	81.225	0.523	1916.479	0.519	25	0.242	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-12/2	1810.474	1810.238	131.087	0.542	1809.744	0.558	25	0.237	K.VAILGASGGIGQPLALLMK.M
R2/RRR2-12/2	1809.581	1810.238	-918.460	0.495	1894.576	0.495	26	0.233	K.VAILGASGGIGQPLALLMK.M
R2/RRR2-13/2	1825.734	1826.237	-825.821	0.499	1790.685	0.524	25	0.225	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-12/2	1826.185	1826.237	-28.720	0.467	1747.869	0.487	23	0.209	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-12/2	1825.776	1826.237	-253.243	0.494	1466.559	0.536	22	0.186	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-13/2	1809.897	1810.238	-188.983	0.496	1530.263	0.495	24	0.185	K.VAILGASGGIGQPLALLMK.M
R2/RRR2-12/2	1457.302	1457.635	-229.267	0.449	1370.354	0.536	22	0.183	K.AGAGSATLSM*AYAAAK.F
R2/RRR2-13/2	1186.308	1186.427	-100.381	0.557	1525.638	0.438	19	0.179	R.LLGVTTLDVVR.A
R2/RRR2-12/2	1348.601	1347.502	73.937	0.483	1770.267	0.321	19	0.179	R.DDLFNINAGIVR.T
R2/RRR2-12/2	1186.128	1186.427	-252.342	0.467	1371.227	0.461	19	0.169	R.LLGVTTLDVVR.A
R2/RRR2-13/2	1810.028	1810.238	-116.050	0.459	1353.657	0.501	22	0.167	K.VAILGASGGIGQPLALLMK.M
R2/RRR2-13/2	1347.352	1347.502	-111.737	0.434	1397.138	0.426	16	0.161	R.DDLFNINAGIVR.T
R2/RRR2-12/2	1809.534	1810.238	-944.263	0.468	1284.584	0.497	22	0.160	K.VAILGASGGIGQPLALLMK.M
R2/RRR2-12/2	1502.337	1502.697	-240.467	0.316	1546.926	0.341	20	0.159	R.ANTFVAEVLGLDPR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1348.274	1347.502	-169.143	0.474	1336.084	0.440	17	0.159	R.DDLFNINAGIVR.T
R2/RRR2-12/2	1187.229	1186.427	-167.027	0.559	1276.060	0.447	19	0.159	R.LLGVTTLDVVR.A
R2/RRR2-13/2	1185.654	1186.427	-1499.574	0.426	1224.226	0.457	18	0.154	R.LLGVTTLDVVR.A
R2/RRR2-13/2	1346.956	1347.502	-1151.015	0.435	1215.104	0.415	16	0.144	R.DDLFNINAGIVR.T
R2/RRR2-12/2	1245.985	1245.365	-305.860	0.494	942.426	0.454	20	0.139	R.IQNGGTEVVEAK.A
R2/RRR2-13/2	1809.537	1810.238	-942.909	0.446	943.531	0.498	21	0.135	K.VAILGASGGIGQPLALLMK.M
R2/RRR2-13/3	1826.371	1826.237	73.576	0.403	1308.876	0.463	30	0.131	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-13/2	1246.010	1245.365	-285.710	0.520	728.983	0.468	18	0.131	R.IQNGGTEVVEAK.A
R2/RRR2-13/2	1502.425	1502.697	-181.615	0.362	1054.926	0.406	16	0.129	R.ANTFVAEVLGLDPR.D
R2/RRR2-12/2	1246.239	1245.365	-101.056	0.504	734.432	0.448	18	0.128	R.IQNGGTEVVEAK.A
R2/RRR2-13/2	1185.377	1186.427	-1734.080	0.336	1026.321	0.377	17	0.128	R.LLGVTTLDVVR.A
R2/RRR2-13/2	1245.142	1245.365	-179.121	0.476	734.292	0.428	18	0.126	R.IQNGGTEVVEAK.A
R2/RRR2-12/2	1245.062	1245.365	-243.544	0.466	682.500	0.402	17	0.121	R.IQNGGTEVVEAK.A
R2/RRR2-13/2	1245.036	1245.365	-264.299	0.474	703.674	0.383	18	0.121	R.IQNGGTEVVEAK.A
R2/RRR2-12/2	1245.298	1245.365	-53.546	0.365	486.235	0.378	17	0.116	R.IQNGGTEVVEAK.A
R2/RRR2-13/2	1246.008	1245.365	-286.890	0.263	257.567	0.333	14	0.112	R.IQNGGTEVVEAK.A
R2/RRR2-12/2	1502.026	1502.697	-1115.980	0.304	900.493	0.309	15	0.110	R.ANTFVAEVLGLDPR.D
R2/RRR2-12/2	1824.918	1826.237	-1274.764	0.280	927.973	0.299	18	0.109	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-12/2	1185.770	1186.427	-1401.438	0.250	413.482	0.293	11	0.104	-.LLGVTTLDVVR.-
R2/RRR2-13/2	1502.227	1502.697	-313.756	0.240	782.948	0.269	14	0.104	-.ANTFVAEVLGLDPR.-
R2/RRR2-12/3	1502.526	1502.697	-114.304	0.461	972.409	0.376	26	0.087	R.ANTFVAEVLGLDPR.D
R2/RRR2-12/3	1502.966	1502.697	179.486	0.420	668.228	0.437	23	0.085	R.ANTFVAEVLGLDPR.D
R2/RRR2-13/3	1502.160	1502.697	-1026.069	0.323	697.238	0.325	23	0.072	R.ANTFVAEVLGLDPR.D
R2/RRR2-12/3	1824.980	1826.237	-1240.378	0.370	595.698	0.359	24	0.072	K.VAILGASGGIGQPLALLM*K.M
R2/RRR2-8/2	1594.463	1594.702	-150.322	0.573	2312.871	0.584	24	0.345	R.IEEELGDAAVYAGEK.F
R2/RRR2-8/2	1791.412	1791.983	-879.660	0.489	738.011	0.560	23	0.137	R.GAVPSGASTGIYEALELR.D
R2/RRR2-8/2	1791.491	1791.983	-275.602	0.485	717.416	0.508	23	0.130	R.GAVPSGASTGIYEALELR.D
R2/RRR2-8/2	1225.253	1225.373	-98.390	0.430	857.410	0.399	16	0.124	K.ISGDSLKDVYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1923.314	1924.165	-965.494	0.532	3090.668	0.534	26	0.507	R.TMLELLNQLDGFEASNK.I
R2/RRR2-10/2	1923.302	1924.165	-971.292	0.541	2715.325	0.526	24	0.407	R.TMLELLNQLDGFEASNK.I
R2/RRR2-10/3	1924.140	1924.165	-13.186	0.509	2610.419	0.495	34	0.376	R.TMLELLNQLDGFEASNK.I
R2/RRR2-10/3	1923.549	1924.165	-842.344	0.488	2355.662	0.495	32	0.317	R.TMLELLNQLDGFEASNK.I
R2/RRR2-10/3	1776.635	1776.995	-203.126	0.495	1571.014	0.536	27	0.185	R.RVHVTQEDFEM*AVAK.V
R2/RRR2-10/2	946.932	947.068	-144.052	0.474	1121.638	0.410	15	0.142	R.VSGSELVQK.Y
R2/RRR2-10/3	1427.598	1428.571	-1386.437	0.426	707.235	0.507	22	0.096	R.AVAHHTDCTFIR.V
R2/RRR2-10/3	1427.989	1428.571	-1111.602	0.397	632.618	0.431	21	0.084	R.AVAHHTDCTFIR.V
R2/RRR2-10/3	1481.125	1480.738	262.070	0.411	727.365	0.407	21	0.081	-.IDILDQALLRPGR.-
R2/RRR2-10/3	1427.473	1428.571	-1474.174	0.341	580.935	0.430	23	0.081	R.AVAHHTDCTFIR.V
R2/RRR2-10/3	1480.717	1480.738	-14.075	0.351	869.890	0.317	24	0.073	-.IDILDQALLRPGR.-
R2/RRR2-10/3	1480.739	1480.738	1.057	0.360	615.771	0.361	20	0.071	-.IDILDQALLRPGR.-
R2/RRR2-10/3	1923.189	1924.165	-1030.627	0.323	903.089	0.253	26	0.068	R.TMLELLNQLDGFEASNK.I
R2/RRR2-9/2	1296.100	1295.420	-247.935	0.552	2205.115	0.560	20	0.311	K.ADIEDYLASVAK.G
R2/RRR2-9/2	1651.455	1649.910	-275.841	0.547	1797.005	0.529	23	0.235	R.ILKADIEDYLASVAK.G
R2/RRR2-9/2	1295.230	1295.420	-147.144	0.472	1840.445	0.449	18	0.219	K.ADIEDYLASVAK.G
R2/RRR2-9/2	1528.403	1528.733	-216.579	0.559	1577.077	0.488	21	0.197	R.KLAEDNNVPLSSIK.G
R2/RRR2-9/2	1649.449	1649.910	-279.888	0.506	1669.497	0.447	22	0.197	R.ILKADIEDYLASVAK.G
R2/RRR2-9/2	1294.690	1295.420	-1340.373	0.376	1634.688	0.355	18	0.172	K.ADIEDYLASVAK.G
R2/RRR2-9/3	1649.582	1649.910	-198.933	0.445	1314.800	0.524	27	0.146	R.ILKADIEDYLASVAK.G
R2/RRR2-9/3	1649.920	1649.910	6.032	0.479	1272.967	0.463	25	0.126	R.ILKADIEDYLASVAK.G
R2/RRR2-9/3	1650.119	1649.910	127.457	0.468	1152.196	0.413	26	0.104	R.ILKADIEDYLASVAK.G
R2/RRR2-9/3	1615.671	1615.770	-61.854	0.319	881.182	0.340	25	0.074	K.LRSELNPLQDTSGGK.K
R2/RRR2-11/2	1290.972	1290.530	343.739	0.536	1581.139	0.533	18	0.208	K.IPISLIYDDIK.S
R2/RRR2-11/2	1290.929	1290.530	309.986	0.460	1614.981	0.477	18	0.198	K.IPISLIYDDIK.S
R2/RRR2-11/2	1290.431	1290.530	-76.626	0.404	1516.443	0.441	17	0.178	K.IPISLIYDDIK.S
R2/RRR2-11/2	1313.218	1313.464	-187.575	0.510	1148.262	0.513	17	0.160	K.DFGSAVWDM*IR.G
R2/RRR2-11/2	1307.449	1307.650	-154.478	0.464	1166.245	0.510	17	0.158	R.VVLLIDVPIIGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1307.561	1307.650	-68.600	0.482	1085.945	0.490	17	0.149	R.VVLLIDVPIIGR.I
R2/RRR2-11/2	1524.403	1524.699	-194.900	0.486	1211.249	0.431	19	0.149	R.FSFEETTATLHLK.L
R2/RRR2-11/2	1307.285	1307.650	-280.186	0.396	1032.238	0.467	17	0.140	R.VVLLIDVPIIGR.I
R2/RRR2-11/2	1524.165	1524.699	-1009.318	0.465	1040.462	0.422	17	0.134	R.FSFEETTATLHLK.L
R2/RRR2-11/2	1786.520	1787.003	-271.503	0.483	977.122	0.400	20	0.126	K.SGEIPIPYKPDVDVEK.I
R2/RRR2-11/2	1786.709	1787.003	-165.122	0.459	609.115	0.427	17	0.114	K.SGEIPIPYKPDVDVEK.I
R2/RRR2-11/2	1312.768	1313.464	-1295.638	0.295	564.912	0.386	15	0.111	K.DFGSAVWDM*IR.G
R2/RRR2-11/3	1976.739	1977.314	-799.183	0.461	858.229	0.379	27	0.081	K.GKIDVDTPFGNM*KLPISK.E
R2/RRR2-11/2	1480.331	1480.711	-257.574	0.465	1640.028	0.436	21	0.190	R.ASIYNAM*PLAGVEK.L
R2/RRR2-11/2	1239.097	1239.405	-249.064	0.507	1099.873	0.578	18	0.168	K.KFSAASVAWSGK.D
R2/RRR2-11/2	1480.501	1480.711	-142.675	0.489	1413.783	0.398	20	0.157	R.ASIYNAM*PLAGVEK.L
R2/RRR2-11/2	1283.472	1283.502	-23.525	0.433	930.782	0.546	18	0.146	K.NVGPSGVTIAIVR.K
R2/RRR2-10/2	1284.261	1283.502	-188.729	0.453	960.200	0.489	18	0.140	K.NVGPSGVTIAIVR.K
R2/RRR2-11/2	1068.099	1068.250	-141.638	0.478	1061.765	0.409	16	0.137	R.FGLIYAGAQK.N
R2/RRR2-11/2	1282.980	1283.502	-1190.374	0.361	825.995	0.556	17	0.137	K.NVGPSGVTIAIVR.K
R2/RRR2-11/2	1948.407	1949.109	-876.269	0.513	764.759	0.536	22	0.136	K.YTSLPPFDAIEQNPEAR.F
R2/RRR2-11/2	1283.151	1283.502	-274.387	0.474	822.720	0.509	17	0.135	K.NVGPSGVTIAIVR.K
R2/RRR2-11/2	1948.917	1949.109	-99.298	0.558	635.018	0.565	21	0.134	K.YTSLPPFDAIEQNPEAR.F
R2/RRR2-11/2	1067.766	1068.250	-455.065	0.463	1049.184	0.386	16	0.133	R.FGLIYAGAQK.N
R2/RRR2-11/2	1067.573	1068.250	-1575.407	0.423	1057.005	0.376	15	0.131	R.FGLIYAGAQK.N
R2/RRR2-10/2	1480.568	1480.711	-97.351	0.482	853.267	0.439	20	0.129	R.ASIYNAM*PLAGVEK.L
R2/RRR2-10/2	1068.015	1068.250	-220.980	0.439	1093.228	0.335	16	0.128	R.FGLIYAGAQK.N
R2/RRR2-10/2	1068.092	1068.250	-148.746	0.435	1140.250	0.314	16	0.128	R.FGLIYAGAQK.N
R2/RRR2-11/2	1479.554	1480.711	-1462.500	0.322	1146.130	0.307	19	0.124	R.ASIYNAM*PLAGVEK.L
R2/RRR2-10/2	1282.535	1283.502	-1538.851	0.339	799.137	0.446	15	0.121	K.NVGPSGVTIAIVR.K
R2/RRR2-11/2	1238.356	1237.494	-111.259	0.509	658.229	0.388	16	0.118	R.SLM*NVPFTLAK.G
R2/RRR2-10/2	1546.338	1545.760	-273.768	0.577	2188.777	0.573	20	0.313	K.TYVVQDGDIIFFK.F
R2/RRR2-10/2	1545.288	1545.760	-306.360	0.526	2020.138	0.556	20	0.278	K.TYVVQDGDIIFFK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1066.745	1067.307	-1468.627	0.407	1100.778	0.515	18	0.154	K.IGIVGLPNVGK.S
R2/RRR2-10/2	1067.021	1067.307	-269.035	0.468	967.560	0.511	17	0.146	K.IGIVGLPNVGK.S
R2/RRR2-10/3	1948.156	1948.206	-25.687	0.520	1036.934	0.551	32	0.125	R.LKDIEFVQNKIDDLEK.S
R2/RRR2-10/3	1514.474	1514.625	-99.375	0.446	908.284	0.590	24	0.123	K.APQAAGTIHTDFER.G
R2/RRR2-10/2	1286.528	1287.465	-1510.140	0.359	864.686	0.391	16	0.120	R.LLADM*PPDEAAK.Y
R2/RRR2-10/3	1514.546	1514.625	-52.200	0.450	894.248	0.575	25	0.119	K.APQAAGTIHTDFER.G
R2/RRR2-10/3	1538.251	1538.681	-280.230	0.491	1137.411	0.486	29	0.117	K.FDDLKELGSESAVK.A
R2/RRR2-10/3	1948.398	1948.206	98.550	0.552	779.327	0.501	29	0.101	R.LKDIEFVQNKIDDLEK.S
R2/RRR2-10/3	1538.826	1538.681	94.506	0.451	963.526	0.398	26	0.090	K.FDDLKELGSESAVK.A
R2/RRR2-10/3	1948.349	1948.206	73.762	0.473	636.924	0.461	26	0.088	R.LKDIEFVQNKIDDLEK.S
R2/RRR2-10/3	1514.827	1514.625	133.789	0.407	697.620	0.400	22	0.081	K.APQAAGTIHTDFER.G
R2/RRR2-6/2	1786.318	1786.919	-898.755	0.545	1496.741	0.513	24	0.188	R.AVFASGSPFDPVEYDGK.I
R2/RRR2-7/2	1786.495	1786.919	-238.131	0.524	1532.850	0.463	24	0.184	-.AVFASGSPFDPVEYDGK.-
R2/RRR2-6/2	1166.009	1166.355	-298.068	0.457	1475.813	0.482	20	0.182	K.ISAHIAANVAAK.A
R2/RRR2-7/2	1786.452	1786.919	-262.124	0.557	1365.191	0.522	23	0.177	-.AVFASGSPFDPVEYDGK.-
R2/RRR2-7/2	980.287	980.100	191.081	0.538	1455.513	0.459	15	0.177	K.AYELGLASR.L
R2/RRR2-7/2	1787.365	1786.919	250.604	0.560	1379.844	0.509	23	0.174	R.AVFASGSPFDPVEYDGK.I
R2/RRR2-6/2	1786.208	1786.919	-960.364	0.551	1339.257	0.520	23	0.173	R.AVFASGSPFDPVEYDGK.I
R2/RRR2-6/2	1166.208	1166.355	-126.993	0.506	1231.468	0.530	19	0.169	K.ISAHIAANVAAK.A
R2/RRR2-6/2	979.939	980.100	-164.314	0.519	1431.711	0.431	15	0.168	K.AYELGLASR.L
R2/RRR2-7/2	980.009	980.100	-93.090	0.516	1480.601	0.403	15	0.167	K.AYELGLASR.L
R2/RRR2-6/2	1786.406	1786.919	-849.432	0.548	1336.170	0.478	23	0.165	-.AVFASGSPFDPVEYDGK.-
R2/RRR2-7/2	1166.054	1166.355	-259.521	0.464	1279.776	0.457	19	0.159	K.ISAHIAANVAAK.A
R2/RRR2-6/2	1165.588	1166.355	-1520.767	0.465	1072.565	0.518	18	0.153	K.ISAHIAANVAAK.A
R2/RRR2-7/2	979.939	980.100	-164.939	0.515	1261.148	0.422	14	0.152	K.AYELGLASR.L
R2/RRR2-6/2	979.894	980.100	-210.927	0.530	1267.736	0.412	14	0.150	K.AYELGLASR.L
R2/RRR2-6/2	1316.237	1315.584	-264.606	0.475	600.238	0.614	19	0.141	K.TIKPTVLIGTSGK.G
R2/RRR2-7/2	1314.654	1315.584	-1472.662	0.422	715.147	0.572	19	0.138	K.TIKPTVLIGTSGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1165.400	1166.355	-1682.805	0.409	963.067	0.470	17	0.137	K.ISAHIAANVAAK.A
R2/RRR2-7/2	1315.089	1315.584	-377.955	0.471	594.549	0.542	19	0.133	K.TIKPTVLIGTSGK.G
R2/RRR2-6/2	1315.170	1315.584	-315.744	0.409	585.482	0.523	19	0.129	K.TIKPTVLIGTSGK.G
R2/RRR2-6/2	1540.971	1540.716	166.328	0.335	738.618	0.384	15	0.114	K.YAESCMYSPLYR.N
R2/RRR2-6/2	1314.687	1315.584	-1447.387	0.295	583.073	0.324	18	0.110	K.TIKPTVLIGTSGK.G
R2/RRR2-6/3	1294.627	1294.528	76.347	0.498	1021.634	0.468	24	0.107	R.KISAHIAANVAAK.A
R2/RRR2-6/2	1540.360	1540.716	-231.670	0.357	717.775	0.250	15	0.104	K.YAESCMYSPLYR.N
R2/RRR2-7/3	1294.707	1294.528	138.756	0.459	929.099	0.402	23	0.090	R.KISAHIAANVAAK.A
R2/RRR2-6/3	1294.738	1294.528	162.300	0.472	1007.604	0.373	24	0.089	R.KISAHIAANVAAK.A
R2/RRR2-7/3	1294.501	1294.528	-21.396	0.439	924.166	0.361	22	0.084	R.KISAHIAANVAAK.A
R2/RRR2-6/3	1294.878	1294.528	270.641	0.447	829.398	0.365	22	0.082	R.KISAHIAANVAAK.A
R2/RRR2-10/3	1769.923	1769.891	17.728	0.581	2330.143	0.561	31	0.333	R.HYAHVDCPGHADYVK.N
R2/RRR2-10/3	1769.208	1769.891	-954.444	0.581	2248.576	0.475	31	0.274	R.HYAHVDCPGHADYVK.N
R2/RRR2-10/3	1769.831	1769.891	-33.948	0.544	2171.438	0.496	30	0.270	R.HYAHVDCPGHADYVK.N
R2/RRR2-10/2	1727.401	1726.949	262.493	0.493	1433.798	0.500	23	0.180	K.TGEDVEILGLTPSGPLK.T
R2/RRR2-10/2	1726.724	1726.949	-130.725	0.483	1308.621	0.494	22	0.166	K.TGEDVEILGLTPSGPLK.T
R2/RRR2-10/2	1757.171	1756.016	88.461	0.550	987.978	0.540	20	0.149	K.SFLM*PIEDVFSIQGR.G
R2/RRR2-10/2	1561.224	1561.676	-290.764	0.448	1257.046	0.423	20	0.149	R.GSALSALQGTNDEIGK.N
R2/RRR2-10/2	1158.097	1157.344	-213.518	0.471	1160.643	0.430	17	0.147	K.FPGDEIPIIR.G
R2/RRR2-10/2	1755.852	1756.016	-93.678	0.475	1010.626	0.488	20	0.142	K.SFLM*PIEDVFSIQGR.G
R2/RRR2-10/2	1756.379	1756.016	207.495	0.510	916.165	0.494	20	0.138	K.SFLM*PIEDVFSIQGR.G
R2/RRR2-10/2	1157.544	1157.344	173.403	0.429	1096.203	0.391	17	0.137	K.FPGDEIPIIR.G
R2/RRR2-10/2	1740.709	1740.016	-177.082	0.425	720.845	0.492	18	0.126	K.SFLMPIEDVFSIQGR.G
R2/RRR2-11/2	1158.325	1157.344	-15.814	0.358	886.901	0.371	15	0.122	K.FPGDEIPIIR.G
R2/RRR2-11/2	1755.616	1756.016	-228.324	0.296	752.793	0.334	17	0.109	K.SFLM*PIEDVFSIQGR.G
R2/RRR2-10/2	1156.984	1157.344	-312.033	0.282	566.013	0.292	13	0.104	-.FPGDEIPIIR.-
R2/RRR2-12/2	1726.182	1726.949	-1027.097	0.325	352.423	0.361	15	0.104	-.TGEDVEILGLTPSGPLK.-
R2/RRR2-10/3	1692.706	1692.898	-113.830	0.450	1103.606	0.384	30	0.095	K.ILDHGEAGDNVGLLLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1693.808	1692.898	-53.181	0.414	755.060	0.329	26	0.074	K.ILDHGEAGDNVGLLLR.G
R2/RRR2-11/2	1525.768	1525.820	-34.234	0.475	1590.832	0.474	18	0.194	K.TVFNILGPLLNPAR.V
R2/RRR2-11/2	1099.078	1099.266	-171.623	0.424	1444.418	0.342	15	0.152	K.VLQDVLAGQR.G
R2/RRR2-11/3	1752.768	1752.910	-81.185	0.501	1823.535	0.308	29	0.148	K.VNTLHDGVALAQETQR.S
R2/RRR2-11/2	1216.065	1216.323	-212.804	0.487	1303.583	0.370	17	0.147	R.LLLEEENEAR.I
R2/RRR2-11/2	1767.981	1767.151	-96.718	0.443	903.128	0.509	17	0.135	K.IKTVFNILGPLLNPAR.V
R2/RRR2-11/2	1216.143	1216.323	-148.961	0.481	1109.275	0.367	16	0.134	R.LLLEEENEAR.I
R2/RRR2-11/2	1215.985	1216.323	-279.273	0.450	1120.942	0.355	16	0.132	R.LLLEEENEAR.I
R2/RRR2-11/2	1098.339	1099.266	-1759.913	0.347	1199.375	0.303	15	0.128	K.VLQDVLAGQR.G
R2/RRR2-11/2	1449.131	1448.603	-326.435	0.451	799.733	0.398	16	0.119	R.SGEAINTLESWIK.I
R2/RRR2-11/2	1447.761	1448.603	-1275.699	0.399	1026.538	0.301	16	0.116	R.SGEAINTLESWIK.I
R2/RRR2-11/2	1448.470	1448.603	-92.103	0.408	636.800	0.355	14	0.109	R.SGEAINTLESWIK.I
R2/RRR2-6/3	1721.006	1720.875	76.605	0.478	2846.284	0.412	38	0.393	R.RVHVAGPAGSAAADRER.I
R2/RRR2-6/2	1162.392	1163.348	-1688.424	0.479	1804.452	0.483	17	0.224	R.VLETEVAVFR.A
R2/RRR2-6/2	1310.202	1309.407	-156.957	0.514	1873.158	0.439	20	0.223	R.LEFDAGELTTGR.D
R2/RRR2-6/2	1352.114	1352.479	-270.443	0.460	1672.571	0.520	17	0.213	R.VAEDGWWSVFR.V
R2/RRR2-6/2	1586.393	1586.683	-182.807	0.430	1770.768	0.448	24	0.210	R.VDVSPETLEPTGGER.R
R2/RRR2-6/2	1163.041	1163.348	-264.615	0.539	1623.325	0.502	17	0.206	R.VLETEVAVFR.A
R2/RRR2-6/2	1352.154	1352.479	-240.373	0.446	1579.248	0.473	17	0.191	R.VAEDGWWSVFR.V
R2/RRR2-5/2	1352.489	1352.479	7.640	0.406	1635.274	0.439	17	0.190	R.VAEDGWWSVFR.V
R2/RRR2-6/2	1351.584	1352.479	-1406.244	0.325	1652.330	0.434	17	0.189	R.VAEDGWWSVFR.V
R2/RRR2-6/2	1586.347	1586.683	-212.296	0.448	1474.233	0.481	22	0.181	R.VDVSPETLEPTGGER.R
R2/RRR2-6/2	1162.677	1163.348	-1441.805	0.427	1516.643	0.452	17	0.181	R.VLETEVAVFR.A
R2/RRR2-6/2	1586.289	1586.683	-249.044	0.444	1433.066	0.456	22	0.172	R.VDVSPETLEPTGGER.R
R2/RRR2-6/2	1309.105	1309.407	-231.723	0.401	1275.536	0.482	18	0.162	R.LEFDAGELTTGR.D
R2/RRR2-5/2	1353.680	1352.479	149.454	0.437	1304.699	0.451	15	0.158	R.VAEDGWWSVFR.V
R2/RRR2-6/2	856.909	857.033	-144.612	0.392	680.254	0.478	12	0.127	K.TPGVTILR.S
R2/RRR2-6/2	856.530	857.033	-1759.952	0.401	852.913	0.369	13	0.123	K.TPGVTILR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	856.545	857.033	-571.213	0.320	669.300	0.355	12	0.114	K.TPGVTILR.S
R2/RRR2-6/3	1720.813	1720.875	-35.982	0.458	1116.277	0.454	30	0.110	R.RVHVAGPAGSAAADRER.I
R2/RRR2-2/2	857.086	857.033	62.125	0.196	404.320	0.272	10	0.094	-.TPGVTILR.-
R2/RRR2-9/2	1137.078	1136.323	-215.634	0.459	1135.843	0.483	15	0.151	K.ALIAAEYTGVK.V
R2/RRR2-9/2	1136.065	1136.323	-227.789	0.372	1207.372	0.431	15	0.146	K.ALIAAEYTGVK.V
R2/RRR2-9/2	1135.971	1136.323	-310.153	0.318	1132.576	0.402	15	0.135	K.ALIAAEYTGVK.V
R2/RRR2-9/2	1190.318	1190.480	-136.867	0.273	677.714	0.351	12	0.106	-.MLVIGSTPPFK.-
R2/RRR2-8/2	945.111	945.055	59.513	0.475	960.728	0.330	15	0.123	R.LDAANTLAR.A
R2/RRR2-8/2	1362.151	1362.428	-204.543	0.421	1095.031	0.260	19	0.113	K.SGVDSGATLVAGGDR.A
R2/RRR2-8/3	1762.035	1761.914	69.019	0.477	832.270	0.548	27	0.110	R.TGVEQGPQIDGEQFKK.I
R2/RRR2-8/3	1762.062	1761.914	84.235	0.430	868.020	0.485	27	0.100	R.TGVEQGPQIDGEQFKK.I
R2/RRR2-8/3	1760.372	1761.914	-2017.948	0.387	736.883	0.499	25	0.095	R.TGVEQGPQIDGEQFKK.I
R2/RRR2-8/3	1356.094	1356.593	-369.110	0.353	984.992	0.321	22	0.077	R.SNLKPVTLELGGK.S
R2/RRR2-8/2	1663.417	1663.898	-289.903	0.452	1329.346	0.599	24	0.189	K.EAGFPAGVLNVISGFGK.I
R2/RRR2-8/2	1820.465	1821.131	-918.148	0.508	1258.405	0.622	23	0.188	K.TAEQTPLSGLVMAQFVK.E
R2/RRR2-8/2	1522.175	1522.642	-307.231	0.502	1476.731	0.453	21	0.178	R.ELGEAALANYTQNK.S
R2/RRR2-8/2	1820.416	1821.131	-944.806	0.508	1206.273	0.571	23	0.172	K.TAEQTPLSGLVMAQFVK.E
R2/RRR2-8/2	1663.268	1663.898	-983.355	0.447	1181.073	0.571	23	0.168	K.EAGFPAGVLNVISGFGK.I
R2/RRR2-8/2	1663.573	1663.898	-195.964	0.406	1093.743	0.562	22	0.157	K.EAGFPAGVLNVISGFGK.I
R2/RRR2-8/2	1108.824	1108.273	-405.751	0.528	877.396	0.506	16	0.141	K.VAFTGSTLVGR.T
R2/RRR2-8/2	1663.684	1663.898	-129.423	0.395	819.148	0.544	19	0.134	K.EAGFPAGVLNVISGFGK.I
R2/RRR2-8/2	1354.321	1354.620	-221.817	0.452	938.343	0.444	17	0.130	K.IGPALATGNTVVLK.T
R2/RRR2-8/2	1353.839	1354.620	-1320.067	0.380	904.756	0.418	17	0.124	K.IGPALATGNTVVLK.T
R2/RRR2-8/2	1354.142	1354.620	-354.306	0.454	714.354	0.458	16	0.121	K.IGPALATGNTVVLK.T
R2/RRR2-8/2	1662.610	1663.898	-1380.227	0.296	619.994	0.467	17	0.114	K.EAGFPAGVLNVISGFGK.I
R2/RRR2-9/2	1354.381	1354.620	-177.240	0.309	501.444	0.378	14	0.107	K.IGPALATGNTVVLK.T
R2/RRR2-9/2	1820.414	1821.131	-945.749	0.308	441.324	0.356	16	0.104	K.TAEQTPLSGLVMAQFVK.E
R2/RRR2-7/2	1663.843	1663.898	-33.159	0.222	447.730	0.294	13	0.099	K.EAGFPAGVLNVISGFGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1878.655	1878.159	264.488	0.385	461.185	0.545	26	0.092	R.VYVQEGIYDKFVAAFK.A
R2/RRR2-8/3	1878.149	1878.159	-5.621	0.323	411.198	0.550	22	0.088	R.VYVQEGIYDKFVAAFK.A
R2/RRR2-8/3	1877.866	1878.159	-156.429	0.319	621.339	0.465	27	0.084	R.VYVQEGIYDKFVAAFK.A
R2/RRR2-11/2	1560.621	1559.788	-107.373	0.542	1990.134	0.502	22	0.251	K.ATAELLFGADNPVLK.Q
R2/RRR2-10/2	1560.424	1559.788	-233.791	0.518	1923.117	0.478	21	0.234	K.ATAELLFGADNPVLK.Q
R2/RRR2-11/2	1560.248	1559.788	295.793	0.480	1794.823	0.460	21	0.212	K.ATAELLFGADNPVLK.Q
R2/RRR2-10/2	1561.066	1559.788	178.227	0.527	1703.431	0.469	20	0.201	K.ATAELLFGADNPVLK.Q
R2/RRR2-11/2	1390.219	1390.568	-252.110	0.525	1533.164	0.526	22	0.198	R.VATLQSLSGTGSLR.L
R2/RRR2-10/2	1389.724	1390.568	-1331.177	0.405	1467.922	0.450	22	0.173	R.VATLQSLSGTGSLR.L
R2/RRR2-10/2	1390.008	1390.568	-1125.406	0.449	1317.050	0.513	22	0.172	R.VATLQSLSGTGSLR.L
R2/RRR2-11/2	1390.120	1390.568	-323.558	0.482	1309.879	0.506	22	0.171	R.VATLQSLSGTGSLR.L
R2/RRR2-11/2	1390.250	1390.568	-229.647	0.492	1231.852	0.527	22	0.168	R.VATLQSLSGTGSLR.L
R2/RRR2-11/2	1700.327	1700.912	-934.631	0.520	1147.564	0.562	20	0.166	R.IGAINVVCSTPEVANR.V
R2/RRR2-10/2	1390.181	1390.568	-278.979	0.498	1244.703	0.493	21	0.162	R.VATLQSLSGTGSLR.L
R2/RRR2-11/2	973.131	973.192	-63.174	0.487	1303.194	0.401	17	0.153	R.ISLAGLSLAK.C
R2/RRR2-10/2	1559.092	1559.788	-1091.310	0.364	1339.458	0.423	18	0.153	K.ATAELLFGADNPVLK.Q
R2/RRR2-11/2	1532.575	1532.763	-122.679	0.508	1133.070	0.447	20	0.146	R.TEELQPYVLNVVK.K
R2/RRR2-10/2	1533.417	1532.763	-226.091	0.553	929.390	0.497	20	0.143	R.TEELQPYVLNVVK.K
R2/RRR2-11/2	1532.332	1532.763	-282.263	0.504	943.126	0.457	20	0.137	R.TEELQPYVLNVVK.K
R2/RRR2-10/2	890.032	890.065	-36.951	0.443	940.789	0.448	13	0.137	R.LAAAFIQR.Y
R2/RRR2-10/2	1532.253	1532.763	-988.249	0.427	1034.366	0.422	20	0.136	R.TEELQPYVLNVVK.K
R2/RRR2-10/2	890.061	890.065	-3.936	0.473	866.598	0.439	13	0.133	R.LAAAFIQR.Y
R2/RRR2-11/2	890.179	890.065	128.930	0.488	898.473	0.423	13	0.133	R.LAAAFIQR.Y
R2/RRR2-11/2	1559.269	1559.788	-977.251	0.334	1276.238	0.322	18	0.132	K.ATAELLFGADNPVLK.Q
R2/RRR2-11/2	889.262	890.065	-2032.564	0.432	902.898	0.419	13	0.131	R.LAAAFIQR.Y
R2/RRR2-11/2	889.593	890.065	-531.481	0.439	861.118	0.411	13	0.129	R.LAAAFIQR.Y
R2/RRR2-11/2	1532.146	1532.763	-1058.720	0.432	1034.950	0.346	20	0.126	R.TEELQPYVLNVVK.K
R2/RRR2-11/2	972.714	973.192	-492.610	0.426	879.515	0.338	15	0.119	R.ISLAGLSLAK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1560.918	1559.788	83.097	0.349	387.672	0.326	13	0.105	K.ATAELLFGADNPVLK.Q
R2/RRR2-9/2	1599.389	1598.730	-213.933	0.518	2349.820	0.482	22	0.314	R.SSICYIDGDEGILR.Y
R2/RRR2-9/2	1117.547	1118.311	-1583.184	0.477	1840.589	0.524	18	0.240	K.APTIAAAAYLR.L
R2/RRR2-9/2	1478.947	1479.662	-1162.618	0.481	1649.920	0.562	20	0.223	K.IYDPGYLNTAPVR.S
R2/RRR2-9/2	1118.108	1118.311	-181.842	0.538	1697.788	0.530	18	0.222	K.APTIAAAAYLR.L
R2/RRR2-9/2	1117.984	1118.311	-293.240	0.486	1724.799	0.516	18	0.221	K.APTIAAAAYLR.L
R2/RRR2-9/2	1480.052	1479.662	264.502	0.515	1598.972	0.532	20	0.210	K.IYDPGYLNTAPVR.S
R2/RRR2-9/2	1597.949	1598.730	-1118.101	0.348	1464.107	0.390	19	0.161	R.SSICYIDGDEGILR.Y
R2/RRR2-9/2	915.030	915.029	0.454	0.496	974.666	0.486	14	0.142	R.GGALAVVDGR.T
R2/RRR2-9/2	915.814	915.029	-235.913	0.547	1046.705	0.437	16	0.141	R.GGALAVVDGR.T
R2/RRR2-9/2	1721.630	1720.948	-185.373	0.501	487.879	0.553	20	0.132	K.LYPNVDFYSGLIYR.A
R2/RRR2-10/2	1721.651	1720.948	-172.997	0.285	353.916	0.371	15	0.106	K.LYPNVDFYSGLIYR.A
R2/RRR2-9/3	1764.034	1764.088	-30.341	0.364	1033.092	0.302	22	0.077	K.IM*RPQQVYTGVWLR.H
R2/RRR2-2/2	1949.089	1949.149	-31.070	0.580	2336.729	0.503	24	0.319	R.FGVSSYYLTNADELQIK.M
R2/RRR2-2/2	1170.073	1170.341	-229.644	0.469	1999.312	0.383	18	0.225	R.VGLLVESAEPR.E
R2/RRR2-2/2	1767.413	1767.020	222.883	0.546	1655.888	0.573	23	0.222	K.VAIIGSGPAGLAAADQLNK.M
R2/RRR2-2/2	1169.524	1170.341	-1558.468	0.381	1850.956	0.377	18	0.203	R.VGLLVESAEPR.E
R2/RRR2-2/2	1846.429	1844.926	-270.054	0.489	1092.576	0.671	21	0.179	K.GHADHVLISGHDGGTGASR.W
R2/RRR2-2/2	1433.279	1432.607	-229.416	0.504	1479.698	0.445	19	0.176	R.VFIETPIQNTNR.A
R2/RRR2-2/3	1844.386	1844.926	-837.507	0.536	1331.468	0.612	37	0.174	K.GHADHVLISGHDGGTGASR.W
R2/RRR2-2/2	1432.885	1432.607	194.597	0.492	1083.243	0.441	18	0.142	R.VFIETPIQNTNR.A
R2/RRR2-2/2	1417.356	1416.607	-177.830	0.393	763.608	0.546	16	0.133	R.GQSLVVWAITEGR.Q
R2/RRR2-2/2	1431.796	1432.607	-1268.631	0.412	894.656	0.423	17	0.128	R.VFIETPIQNTNR.A
R2/RRR2-1/2	1766.559	1767.020	-261.680	0.387	943.717	0.427	20	0.125	K.VAIIGSGPAGLAAADQLNK.M
R2/RRR2-2/2	1169.602	1170.341	-1491.367	0.310	834.840	0.430	14	0.121	R.VGLLVESAEPR.E
R2/RRR2-2/2	1767.362	1767.020	194.278	0.364	342.157	0.370	14	0.098	-.VAIIGSGPAGLAAADQLNK.-
R2/RRR2-2/3	1994.877	1995.303	-213.754	0.369	867.504	0.364	24	0.077	R.HGCTSIVNLELLTKPPSK.R
R2/RRR2-11/3	1491.594	1491.714	-80.502	0.570	3033.043	0.391	30	0.413	K.KVSPEVIAEYTVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/3	1491.327	1491.714	-260.313	0.531	3010.677	0.365	29	0.398	K.KVSPEVIAEYTVR.T
R2/RRR2-10/3	1491.742	1491.714	18.859	0.550	2781.272	0.433	29	0.371	K.KVSPEVIAEYTVR.T
R2/RRR2-11/3	1491.334	1491.714	-255.509	0.559	2782.602	0.409	29	0.358	K.KVSPEVIAEYTVR.T
R2/RRR2-11/2	1570.219	1569.698	-305.940	0.564	1994.501	0.534	24	0.265	K.GDAVLGEGASESLHVK.D
R2/RRR2-11/2	1569.222	1569.698	-304.418	0.493	1862.597	0.493	24	0.233	K.GDAVLGEGASESLHVK.D
R2/RRR2-11/2	1491.326	1491.714	-260.715	0.546	1733.249	0.526	21	0.225	K.KVSPEVIAEYTVR.T
R2/RRR2-16/3	1491.474	1491.714	-161.039	0.493	2236.432	0.361	29	0.219	K.KVSPEVIAEYTVR.T
R2/RRR2-11/3	1491.507	1491.714	-139.118	0.519	2232.462	0.348	26	0.216	K.KVSPEVIAEYTVR.T
R2/RRR2-11/2	1492.233	1491.714	-323.406	0.604	1478.609	0.596	20	0.210	K.KVSPEVIAEYTVR.T
R2/RRR2-11/2	1491.415	1491.714	-201.017	0.503	1414.386	0.513	19	0.182	K.KVSPEVIAEYTVR.T
R2/RRR2-11/2	1569.175	1569.698	-973.422	0.515	1386.055	0.528	22	0.181	K.GDAVLGEGASESLHVK.D
R2/RRR2-10/3	1490.946	1491.714	-1189.198	0.445	1722.339	0.380	25	0.152	K.KVSPEVIAEYTVR.T
R2/RRR2-11/3	1312.489	1312.501	-8.603	0.499	1498.998	0.398	23	0.129	K.KPWSLSFSFGR.A
R2/RRR2-11/2	1363.255	1363.541	-210.215	0.457	740.104	0.453	18	0.128	K.VSPEVIAEYTVR.T
R2/RRR2-11/2	1363.071	1363.541	-345.698	0.444	763.837	0.432	18	0.126	K.VSPEVIAEYTVR.T
R2/RRR2-11/2	1154.933	1155.240	-266.578	0.445	407.669	0.489	15	0.123	K.ANSEATLGTYK.G
R2/RRR2-11/2	1363.157	1363.541	-282.803	0.439	717.793	0.424	17	0.123	K.VSPEVIAEYTVR.T
R2/RRR2-11/2	1155.011	1155.240	-198.823	0.421	517.098	0.457	16	0.122	K.ANSEATLGTYK.G
R2/RRR2-11/3	1312.562	1312.501	46.666	0.541	1370.880	0.409	22	0.120	K.KPWSLSFSFGR.A
R2/RRR2-11/2	1312.038	1312.501	-353.545	0.397	582.502	0.420	16	0.119	K.KPWSLSFSFGR.A
R2/RRR2-11/3	1312.777	1312.501	211.319	0.516	1330.669	0.420	22	0.119	K.KPWSLSFSFGR.A
R2/RRR2-11/2	1154.982	1155.240	-224.270	0.476	493.641	0.413	15	0.119	K.ANSEATLGTYK.G
R2/RRR2-11/2	1311.597	1312.501	-1455.651	0.298	675.972	0.373	17	0.114	K.KPWSLSFSFGR.A
R2/RRR2-11/2	1362.426	1363.541	-1557.173	0.276	668.041	0.355	18	0.112	K.VSPEVIAEYTVR.T
R2/RRR2-11/2	1311.574	1312.501	-1473.039	0.325	476.088	0.385	14	0.112	K.KPWSLSFSFGR.A
R2/RRR2-5/2	1364.276	1363.541	-194.711	0.289	281.915	0.353	14	0.111	K.VSPEVIAEYTVR.T
R2/RRR2-16/3	1491.276	1491.714	-294.435	0.402	1639.654	0.241	27	0.104	K.KVSPEVIAEYTVR.T
R2/RRR2-10/2	1386.455	1386.619	-118.918	0.501	1887.274	0.456	25	0.228	K.IVIIGGGDTATVAAK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1386.280	1386.619	-245.407	0.447	1654.689	0.420	24	0.189	K.IVIIGGGDTATVAAK.Y
R2/RRR2-10/2	1386.046	1386.619	-1138.782	0.432	1537.576	0.430	24	0.178	K.IVIIGGGDTATVAAK.Y
R2/RRR2-10/2	1842.324	1843.006	-915.384	0.530	1130.373	0.596	23	0.171	K.TLDGM*AIGNSLFDEAGSK.T
R2/RRR2-10/2	1399.291	1399.575	-203.489	0.487	1583.531	0.343	18	0.164	K.AADGDIVLLENLR.F
R2/RRR2-10/2	1764.282	1765.042	-1000.822	0.425	712.086	0.530	18	0.128	K.VVLPVDFVTADKFDAK.A
R2/RRR2-10/3	1649.770	1649.788	-11.000	0.449	1072.191	0.531	28	0.123	K.LGDVYINDAFGTAHR.A
R2/RRR2-10/2	989.348	990.133	-1809.308	0.274	1101.311	0.322	15	0.123	K.LSITDVDVK.G
R2/RRR2-10/2	990.004	990.133	-130.736	0.373	837.295	0.324	14	0.116	K.LSITDVDVK.G
R2/RRR2-10/3	1649.883	1649.788	57.236	0.428	822.904	0.498	26	0.100	K.LGDVYINDAFGTAHR.A
R2/RRR2-10/3	1649.463	1649.788	-197.946	0.387	766.349	0.448	24	0.089	K.LGDVYINDAFGTAHR.A
R2/RRR2-25/2	1351.309	1350.542	-173.475	0.487	1740.031	0.644	20	0.257	K.ETVASAPVVVYSK.S
R2/RRR2-25/2	1549.516	1549.793	-179.335	0.529	1566.350	0.624	22	0.230	K.AKETVASAPVVVYSK.S
R2/RRR2-25/2	1351.133	1350.542	-303.534	0.416	1230.131	0.612	18	0.181	K.ETVASAPVVVYSK.S
R2/RRR2-25/2	1351.012	1350.542	348.492	0.441	1189.596	0.589	18	0.173	K.ETVASAPVVVYSK.S
R2/RRR2-25/2	1155.332	1154.340	-6.847	0.533	1103.999	0.418	16	0.141	K.LFEQLGATFK.A
R2/RRR2-25/3	1549.822	1549.793	18.587	0.571	1399.429	0.468	30	0.138	K.AKETVASAPVVVYSK.S
R2/RRR2-25/2	1281.850	1282.513	-1300.788	0.454	967.772	0.450	16	0.136	K.KLFEQLGATFK.A
R2/RRR2-25/2	1541.218	1541.814	-1039.142	0.312	920.391	0.368	22	0.120	K.LVPLLTEAGAIASSAK.T
R2/RRR2-25/2	1541.218	1541.814	-1039.063	0.292	622.437	0.424	20	0.113	K.LVPLLTEAGAIASSAK.T
R2/RRR2-25/2	1282.123	1282.513	-304.879	0.459	560.799	0.381	13	0.112	K.KLFEQLGATFK.A
R2/RRR2-25/2	1153.990	1154.340	-303.824	0.318	465.683	0.370	13	0.111	K.LFEQLGATFK.A
R2/RRR2-25/2	1541.247	1541.814	-1020.296	0.288	513.276	0.308	18	0.105	K.LVPLLTEAGAIASSAK.T
R2/RRR2-24/2	1542.035	1541.814	143.585	0.358	664.418	0.289	18	0.105	K.LVPLLTEAGAIASSAK.T
R2/RRR2-25/2	1154.214	1154.340	-109.219	0.221	300.253	0.328	11	0.104	-.LFEQLGATFK.-
R2/RRR2-25/3	1549.270	1549.793	-986.333	0.404	1183.582	0.404	30	0.103	K.AKETVASAPVVVYSK.S
R2/RRR2-25/3	1549.247	1549.793	-1000.810	0.368	994.789	0.233	26	0.068	K.AKETVASAPVVVYSK.S
R2/RRR2-8/2	1970.301	1970.240	31.095	0.571	1413.157	0.533	22	0.182	R.EGNFDLVGNNMPVFFIR.D
R2/RRR2-8/2	1740.300	1740.961	-957.327	0.580	1379.355	0.503	24	0.180	R.HM*EGFGVNTYTLINK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1969.508	1970.240	-882.236	0.511	1476.722	0.482	23	0.179	R.EGNFDLVGNNMPVFFIR.D
R2/RRR2-8/2	1680.311	1680.796	-289.830	0.529	1314.067	0.440	20	0.156	K.DLTDSIAAGNYPEWK.L
R2/RRR2-8/2	1969.647	1970.240	-811.310	0.538	1180.148	0.496	20	0.152	R.EGNFDLVGNNMPVFFIR.D
R2/RRR2-8/2	1515.039	1515.802	-1167.389	0.351	1202.614	0.461	18	0.149	R.LGPNYLM*LPANAPK.C
R2/RRR2-8/2	1152.248	1151.384	-118.543	0.473	827.778	0.522	16	0.139	R.APGVQTPIIVR.F
R2/RRR2-8/2	1152.388	1151.384	3.866	0.443	863.655	0.494	17	0.137	R.APGVQTPIIVR.F
R2/RRR2-8/2	1680.168	1680.796	-972.006	0.372	1167.298	0.325	19	0.126	K.DLTDSIAAGNYPEWK.L
R2/RRR2-8/2	1515.078	1515.802	-1141.095	0.427	788.086	0.466	16	0.125	R.LGPNYLM*LPANAPK.C
R2/RRR2-8/2	1985.661	1986.240	-797.621	0.496	956.365	0.414	19	0.124	R.EGNFDLVGNNM*PVFFIR.D
R2/RRR2-8/2	1680.257	1680.796	-918.761	0.409	982.801	0.381	18	0.123	K.DLTDSIAAGNYPEWK.L
R2/RRR2-8/2	1514.457	1515.802	-1553.227	0.263	694.488	0.422	15	0.111	R.LGPNYLM*LPANAPK.C
R2/RRR2-1/2	1987.444	1986.240	103.082	0.419	575.909	0.450	14	0.111	R.EGNFDLVGNNM*PVFFIR.D
R2/RRR2-7/2	1567.052	1567.722	-1068.890	0.455	2012.626	0.510	25	0.266	K.IAVFAGGVDTSATETK.G
R2/RRR2-7/3	1774.675	1773.968	-165.249	0.519	1917.111	0.489	29	0.220	K.GTVLIHSAEQLENYAK.T
R2/RRR2-7/3	1773.704	1773.968	-148.945	0.524	1768.093	0.496	27	0.199	K.GTVLIHSAEQLENYAK.T
R2/RRR2-7/2	1259.891	1260.341	-357.974	0.516	1423.202	0.542	18	0.191	K.NPANFNVDNVR.V
R2/RRR2-7/2	1228.711	1229.387	-1367.955	0.398	1641.521	0.405	17	0.186	K.FAESFEM*VPR.T
R2/RRR2-8/2	1260.011	1260.341	-262.907	0.429	1245.228	0.496	18	0.163	K.NPANFNVDNVR.V
R2/RRR2-8/2	1259.866	1260.341	-378.098	0.428	1153.818	0.535	17	0.161	K.NPANFNVDNVR.V
R2/RRR2-7/2	1259.989	1260.341	-280.403	0.455	1058.946	0.481	17	0.147	K.NPANFNVDNVR.V
R2/RRR2-8/3	1775.321	1773.968	199.779	0.503	1342.115	0.494	26	0.141	K.GTVLIHSAEQLENYAK.T
R2/RRR2-8/3	1774.376	1773.968	230.867	0.422	1553.390	0.389	27	0.138	K.GTVLIHSAEQLENYAK.T
R2/RRR2-7/2	1425.260	1425.656	-278.298	0.476	603.532	0.535	21	0.133	R.IIPGAAATEIELAR.R
R2/RRR2-7/2	1182.016	1182.352	-285.020	0.430	815.020	0.435	17	0.128	K.HLSGLDEAVLK.N
R2/RRR2-7/2	1181.668	1182.352	-1429.306	0.402	881.905	0.396	17	0.125	K.HLSGLDEAVLK.N
R2/RRR2-8/2	1260.862	1260.341	-380.810	0.343	654.456	0.423	16	0.119	K.NPANFNVDNVR.V
R2/RRR2-7/3	1774.631	1773.968	-190.193	0.458	1177.093	0.434	24	0.112	K.GTVLIHSAEQLENYAK.T
R2/RRR2-8/2	1425.178	1425.656	-336.303	0.313	367.936	0.402	16	0.109	R.IIPGAAATEIELAR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1773.470	1773.968	-281.517	0.515	932.523	0.462	25	0.099	-.GTVLIHSAEQLENYAK.-
R2/RRR2-23/3	1721.084	1721.810	-1006.102	0.555	2400.332	0.509	30	0.322	K.HGYIGEFEFVDDHR.S
R2/RRR2-23/3	1721.766	1721.810	-25.509	0.566	1980.383	0.523	28	0.242	K.HGYIGEFEFVDDHR.S
R2/RRR2-23/3	1721.078	1721.810	-1009.520	0.491	1942.077	0.448	28	0.208	K.HGYIGEFEFVDDHR.S
R2/RRR2-23/3	1638.780	1637.818	-22.804	0.551	1677.187	0.489	31	0.177	R.FDVGVKEIESWTAR.L
R2/RRR2-23/2	1638.224	1637.818	248.531	0.496	811.823	0.500	21	0.137	R.FDVGVKEIESWTAR.L
R2/RRR2-23/3	1637.522	1637.818	-181.258	0.507	1522.932	0.406	30	0.133	R.FDVGVKEIESWTAR.L
R2/RRR2-23/2	1638.101	1637.818	173.657	0.514	826.188	0.466	21	0.133	R.FDVGVKEIESWTAR.L
R2/RRR2-23/2	958.514	959.122	-1683.061	0.397	844.766	0.404	15	0.127	R.VSVLNDALK.T
R2/RRR2-23/2	1637.398	1637.818	-256.823	0.476	659.877	0.449	19	0.123	R.FDVGVKEIESWTAR.L
R2/RRR2-23/2	788.427	788.909	-612.489	0.343	691.660	0.360	11	0.117	K.CGVISPR.F
R2/RRR2-23/2	958.870	959.122	-263.563	0.392	885.153	0.291	15	0.117	R.VSVLNDALK.T
R2/RRR2-23/2	958.514	959.122	-1682.166	0.363	832.361	0.307	14	0.115	R.VSVLNDALK.T
R2/RRR2-23/2	789.398	788.909	621.008	0.255	611.322	0.313	10	0.108	K.CGVISPR.F
R2/RRR2-23/2	788.540	788.909	-469.087	0.239	479.131	0.287	9	0.105	-.CGVISPR.-
R2/RRR2-22/2	958.253	959.122	-1956.181	0.199	910.749	0.218	14	0.105	R.VSVLNDALK.T
R2/RRR2-22/2	958.463	959.122	-1736.419	0.197	578.907	0.203	12	0.101	-.VSVLNDALK.-
R2/RRR2-23/2	788.355	788.909	-1976.600	0.246	491.246	0.245	9	0.097	-.CGVISPR.-
R2/RRR2-23/3	1812.812	1813.066	-140.549	0.344	900.902	0.362	26	0.079	R.VSVLNDALKTM*YNAEK.R
R2/RRR2-23/3	1722.642	1721.810	-97.495	0.390	486.030	0.345	21	0.077	K.HGYIGEFEFVDDHR.S
R2/RRR2-23/3	1637.957	1637.818	85.534	0.324	553.521	0.315	20	0.064	-.FDVGVKEIESWTAR.-
R2/RRR2-9/2	1437.171	1436.595	-296.012	0.506	2025.153	0.566	21	0.282	R.FTQAGSEVSALLGR.I
R2/RRR2-9/2	1436.234	1436.595	-252.046	0.510	2079.087	0.520	21	0.277	R.FTQAGSEVSALLGR.I
R2/RRR2-9/2	1502.630	1503.768	-1426.790	0.451	2198.272	0.371	20	0.252	K.TVFIQELINNIAK.A
R2/RRR2-9/2	1503.274	1503.768	-329.420	0.491	2140.288	0.340	20	0.232	K.TVFIQELINNIAK.A
R2/RRR2-9/2	1751.525	1751.964	-251.553	0.467	1788.569	0.510	20	0.229	R.SQGQDVLLFVDNIFR.F
R2/RRR2-9/2	1502.696	1503.768	-1382.566	0.419	2112.829	0.321	20	0.225	K.TVFIQELINNIAK.A
R2/RRR2-9/2	1775.553	1774.992	-248.149	0.499	1345.864	0.553	21	0.181	R.GISELGIYPAVDPLDSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1775.393	1774.992	226.433	0.503	1100.131	0.562	20	0.159	R.GISELGIYPAVDPLDSK.S
R2/RRR2-9/2	1775.367	1774.992	211.747	0.497	1060.810	0.564	19	0.155	R.GISELGIYPAVDPLDSK.S
R2/RRR2-9/2	1149.296	1149.322	-22.437	0.495	752.056	0.405	13	0.123	R.VQQILQEYK.S
R2/RRR2-9/2	1149.994	1149.322	-285.610	0.504	774.429	0.372	13	0.120	R.VQQILQEYK.S
R2/RRR2-9/2	1148.260	1149.322	-1801.117	0.334	765.498	0.241	13	0.107	R.VQQILQEYK.S
R2/RRR2-15/2	1247.309	1248.325	-1621.672	0.376	1041.322	0.380	17	0.130	R.EAISQITNESR.E
R2/RRR2-15/2	1247.972	1248.325	-283.986	0.483	971.944	0.361	17	0.125	R.EAISQITNESR.E
R2/RRR2-15/2	1247.568	1248.325	-1412.591	0.402	1042.735	0.316	17	0.122	R.EAISQITNESR.E
R2/RRR2-22/2	1559.086	1559.526	-283.466	0.383	1854.815	0.374	20	0.244	R.YFNIAENEGEEED.-
R2/RRR2-22/2	1559.018	1559.526	-970.576	0.376	1565.561	0.372	19	0.164	R.YFNIAENEGEEED.-
R2/RRR2-23/2	1190.117	1190.289	-144.606	0.489	1232.776	0.445	20	0.156	K.AGNLGDSVTVTR.D
R2/RRR2-22/2	1267.872	1268.401	-1210.063	0.377	1090.062	0.467	17	0.144	K.VTVTSDGAFSKR.Y
R2/RRR2-22/2	1559.984	1559.526	294.038	0.476	1444.102	0.446	18	0.137	R.YFNIAENEGEEED.-
R2/RRR2-22/2	1111.934	1112.215	-253.433	0.480	913.630	0.462	16	0.135	K.VTVTSDGAFSK.R
R2/RRR2-22/2	1112.080	1112.215	-121.724	0.447	826.110	0.487	16	0.134	K.VTVTSDGAFSK.R
R2/RRR2-22/2	1049.996	1050.252	-244.690	0.405	969.754	0.264	14	0.115	K.IM*EIASLEK.F
R2/RRR2-22/2	1035.216	1034.252	-34.962	0.393	845.685	0.269	14	0.112	-.IMEIASLEK.-
R2/RRR2-22/2	1111.366	1112.215	-1668.445	0.282	886.765	0.289	16	0.111	K.VTVTSDGAFSK.R
R2/RRR2-22/2	1049.926	1050.252	-311.294	0.369	784.735	0.248	14	0.110	K.IM*EIASLEK.F
R2/RRR2-22/2	1049.685	1050.252	-1497.140	0.352	773.534	0.233	13	0.107	K.IM*EIASLEK.F
R2/RRR2-16/2	1663.343	1663.767	-255.688	0.551	2968.810	0.630	28	0.506	K.DLASAGADVGSATDWVK.N
R2/RRR2-17/2	1662.998	1663.767	-1067.004	0.482	2537.359	0.621	26	0.396	K.DLASAGADVGSATDWVK.N
R2/RRR2-17/2	1664.317	1663.767	-270.987	0.595	2609.703	0.571	26	0.391	K.DLASAGADVGSATDWVK.N
R2/RRR2-17/2	1663.332	1663.767	-262.535	0.561	2373.780	0.677	25	0.380	K.DLASAGADVGSATDWVK.N
R2/RRR2-16/2	1663.173	1663.767	-961.326	0.489	2299.515	0.575	25	0.329	K.DLASAGADVGSATDWVK.N
R2/RRR2-16/2	1662.377	1663.767	-1442.141	0.389	2593.955	0.353	27	0.316	K.DLASAGADVGSATDWVK.N
R2/RRR2-16/2	1662.481	1663.767	-1379.304	0.379	2421.636	0.326	25	0.275	K.DLASAGADVGSATDWVK.N
R2/RRR2-17/2	1248.073	1248.478	-325.463	0.537	1893.657	0.506	19	0.238	K.LLNANSITM*VR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1662.337	1663.767	-1466.186	0.327	2359.265	0.208	24	0.232	K.DLASAGADVGSATDWVK.N
R2/RRR2-16/2	1248.017	1248.478	-370.606	0.537	1713.868	0.494	19	0.211	K.LLNANSITM*VR.I
R2/RRR2-17/2	1248.068	1248.478	-329.290	0.507	1765.469	0.463	19	0.210	K.LLNANSITM*VR.I
R2/RRR2-17/2	1248.110	1248.478	-295.926	0.511	1657.100	0.515	18	0.208	K.LLNANSITM*VR.I
R2/RRR2-15/2	1247.656	1248.478	-1465.095	0.448	1603.031	0.487	18	0.195	K.LLNANSITM*VR.I
R2/RRR2-17/2	1534.438	1534.736	-194.583	0.528	1492.282	0.521	24	0.194	R.IYDTDPTVLNALAK.T
R2/RRR2-17/2	1534.196	1534.736	-1006.310	0.498	1441.156	0.540	22	0.191	R.IYDTDPTVLNALAK.T
R2/RRR2-16/2	1534.404	1534.736	-216.929	0.496	1443.694	0.483	24	0.181	R.IYDTDPTVLNALAK.T
R2/RRR2-16/2	1247.887	1248.478	-1279.190	0.491	1463.751	0.484	18	0.180	K.LLNANSITM*VR.I
R2/RRR2-16/2	1232.147	1232.479	-269.746	0.483	1384.495	0.487	18	0.173	K.LLNANSITMVR.I
R2/RRR2-16/2	1248.089	1248.478	-312.706	0.515	1353.181	0.491	17	0.170	K.LLNANSITM*VR.I
R2/RRR2-15/2	1248.236	1248.478	-194.964	0.515	1289.350	0.482	17	0.163	K.LLNANSITM*VR.I
R2/RRR2-16/2	1232.167	1232.479	-254.142	0.450	1235.643	0.451	17	0.153	K.LLNANSITMVR.I
R2/RRR2-17/2	1232.147	1232.479	-270.442	0.518	1143.886	0.471	17	0.151	K.LLNANSITMVR.I
R2/RRR2-17/2	1534.129	1534.736	-1050.249	0.460	1109.368	0.478	21	0.149	R.IYDTDPTVLNALAK.T
R2/RRR2-17/2	1233.053	1232.479	-346.006	0.510	1087.717	0.442	17	0.143	K.LLNANSITMVR.I
R2/RRR2-16/2	1231.495	1232.479	-1615.951	0.363	1149.216	0.416	17	0.140	K.LLNANSITMVR.I
R2/RRR2-17/2	1232.148	1232.479	-269.448	0.449	1070.164	0.420	16	0.137	K.LLNANSITMVR.I
R2/RRR2-15/2	1231.930	1232.479	-1261.169	0.382	792.156	0.416	16	0.124	K.LLNANSITMVR.I
R2/RRR2-16/2	1397.165	1397.556	-280.301	0.441	1073.365	0.329	18	0.123	R.DASNLIDPPEVVK.L
R2/RRR2-16/2	964.050	964.229	-186.132	0.431	750.176	0.388	13	0.122	-.VM*VM*LPNK.-
R2/RRR2-16/2	1398.125	1397.556	-309.358	0.491	978.577	0.354	17	0.121	R.DASNLIDPPEVVK.L
R2/RRR2-17/2	1397.201	1397.556	-254.531	0.398	769.676	0.366	16	0.115	R.DASNLIDPPEVVK.L
R2/RRR2-17/2	963.930	964.229	-310.760	0.497	558.778	0.405	12	0.114	-.VM*VM*LPNK.-
R2/RRR2-16/2	963.963	964.229	-276.202	0.416	635.184	0.285	12	0.113	K.VM*VM*LPNK.D
R2/RRR2-15/2	1231.986	1232.479	-401.065	0.334	840.693	0.271	16	0.112	K.LLNANSITMVR.I
R2/RRR2-16/2	1397.239	1397.556	-227.622	0.415	982.010	0.260	18	0.112	R.DASNLIDPPEVVK.L
R2/RRR2-17/2	1397.903	1397.556	248.866	0.407	748.288	0.334	15	0.110	-.DASNLIDPPEVVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	964.838	964.229	-406.022	0.398	711.500	0.294	13	0.108	-.VM*VM*LPNK.-
R2/RRR2-17/2	1397.314	1397.556	-173.634	0.428	702.508	0.284	15	0.105	-.DASNLIDPPEVVK.-
R2/RRR2-17/2	963.325	964.229	-1981.783	0.394	455.303	0.401	10	0.104	-.VM*VM*LPNK.-
R2/RRR2-6/2	1235.352	1235.411	-48.327	0.537	1143.439	0.488	18	0.157	K.VQEVVSEIFGK.A
R2/RRR2-23/2	1805.299	1806.035	-964.722	0.476	1761.792	0.520	25	0.227	R.VCCLSIIDPGDSDIIK.T
R2/RRR2-23/2	1804.800	1806.035	-1241.841	0.435	1821.833	0.441	25	0.215	R.VCCLSIIDPGDSDIIK.T
R2/RRR2-23/2	1805.425	1806.035	-894.262	0.477	1788.536	0.441	25	0.210	R.VCCLSIIDPGDSDIIK.T
R2/RRR2-23/2	1334.213	1334.520	-230.768	0.382	1428.200	0.317	16	0.146	K.SEIEYYAM*LAK.T
R2/RRR2-23/2	1333.594	1334.520	-1448.543	0.340	1497.608	0.256	16	0.145	-.SEIEYYAM*LAK.-
R2/RRR2-23/2	1396.462	1396.654	-138.144	0.404	1098.812	0.414	16	0.136	K.LVIISNNCPPLR.K
R2/RRR2-23/2	1396.175	1396.654	-343.815	0.371	1035.888	0.365	16	0.125	K.LVIISNNCPPLR.K
R2/RRR2-23/3	1462.676	1462.693	-11.705	0.402	1358.904	0.391	24	0.115	R.KSEIEYYAM*LAK.T
R2/RRR2-23/2	1333.314	1334.520	-1659.411	0.265	848.932	0.214	16	0.105	K.SEIEYYAM*LAK.T
R2/RRR2-23/3	1634.248	1634.880	-1001.848	0.422	717.893	0.460	25	0.090	K.STDNINNKLQLVM*K.S
R2/RRR2-23/3	1634.821	1634.880	-36.239	0.487	634.791	0.450	24	0.088	K.STDNINNKLQLVM*K.S
R2/RRR2-23/3	1634.496	1634.880	-235.913	0.424	541.567	0.424	23	0.083	K.STDNINNKLQLVM*K.S
R2/RRR2-17/2	1700.236	1699.882	208.285	0.534	2709.302	0.577	24	0.425	K.AITEIFAEAGFSDVTK.N
R2/RRR2-17/2	1699.638	1699.882	-144.118	0.473	2760.221	0.543	25	0.424	K.AITEIFAEAGFSDVTK.N
R2/RRR2-17/2	1700.459	1699.882	-249.819	0.546	2582.264	0.589	23	0.399	K.AITEIFAEAGFSDVTK.N
R2/RRR2-17/2	1191.040	1190.334	-247.395	0.614	2192.115	0.376	19	0.247	K.NFLAVLADNGR.L
R2/RRR2-17/2	1191.010	1190.334	-272.896	0.636	2158.107	0.374	19	0.240	K.NFLAVLADNGR.L
R2/RRR2-17/2	1190.115	1190.334	-184.626	0.603	1892.891	0.419	18	0.216	K.NFLAVLADNGR.L
R2/RRR2-17/2	1066.612	1067.262	-1551.458	0.445	636.806	0.495	12	0.127	K.SPLFSQFIK.D
R2/RRR2-17/2	1196.092	1195.435	-287.910	0.470	631.162	0.459	14	0.125	K.KSPLFSQFIK.D
R2/RRR2-17/3	1699.850	1699.882	-18.995	0.479	980.152	0.553	26	0.121	K.AITEIFAEAGFSDVTK.N
R2/RRR2-17/2	1067.002	1067.262	-244.713	0.407	593.855	0.421	12	0.119	K.SPLFSQFIK.D
R2/RRR2-17/2	1066.993	1067.262	-253.207	0.378	630.646	0.422	12	0.118	K.SPLFSQFIK.D
R2/RRR2-17/2	1706.556	1707.006	-264.639	0.408	846.329	0.354	18	0.114	K.SPLFSQFIKDLSVPK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1195.102	1195.435	-279.337	0.392	540.652	0.362	13	0.113	K.KSPLFSQFIK.D
R2/RRR2-17/2	1194.419	1195.435	-1693.379	0.363	718.347	0.294	15	0.111	K.KSPLFSQFIK.D
R2/RRR2-22/2	1892.284	1892.096	99.538	0.630	2674.342	0.613	26	0.424	R.FAIYDFDFLTAEDVPK.S
R2/RRR2-22/2	1892.438	1892.096	180.791	0.608	2207.870	0.627	24	0.329	R.FAIYDFDFLTAEDVPK.S
R2/RRR2-23/2	1891.157	1892.096	-1028.524	0.558	2205.707	0.607	23	0.322	R.FAIYDFDFLTAEDVPK.S
R2/RRR2-23/2	1890.923	1892.096	-1152.712	0.508	2231.472	0.579	24	0.319	R.FAIYDFDFLTAEDVPK.S
R2/RRR2-22/2	1891.335	1892.096	-934.302	0.540	2137.634	0.602	23	0.308	R.FAIYDFDFLTAEDVPK.S
R2/RRR2-23/2	1891.678	1892.096	-221.654	0.563	2142.165	0.598	23	0.307	R.FAIYDFDFLTAEDVPK.S
R2/RRR2-23/2	1965.365	1965.999	-834.072	0.475	1386.128	0.626	24	0.201	R.TTSYEDFTSSLPEGDCR.F
R2/RRR2-23/2	1468.279	1467.693	-282.569	0.510	1556.193	0.421	19	0.176	R.IFYILWSPDNAK.V
R2/RRR2-23/2	1965.491	1965.999	-769.732	0.497	1126.655	0.614	24	0.173	R.TTSYEDFTSSLPEGDCR.F
R2/RRR2-22/2	1965.203	1965.999	-916.940	0.530	1038.843	0.643	23	0.171	R.TTSYEDFTSSLPEGDCR.F
R2/RRR2-22/2	1468.135	1467.693	302.009	0.537	1375.363	0.456	18	0.165	R.IFYILWSPDNAK.V
R2/RRR2-22/2	1965.331	1965.999	-851.155	0.504	970.863	0.606	23	0.159	R.TTSYEDFTSSLPEGDCR.F
R2/RRR2-23/2	1467.422	1467.693	-184.946	0.474	1354.469	0.420	18	0.157	R.IFYILWSPDNAK.V
R2/RRR2-23/2	1467.025	1467.693	-1139.767	0.356	1425.432	0.372	18	0.154	R.IFYILWSPDNAK.V
R2/RRR2-22/2	1467.423	1467.693	-184.445	0.464	1274.351	0.433	18	0.153	R.IFYILWSPDNAK.V
R2/RRR2-22/2	1467.016	1467.693	-1146.034	0.376	1490.264	0.325	18	0.151	R.IFYILWSPDNAK.V
R2/RRR2-23/2	1467.405	1467.693	-196.379	0.363	1450.106	0.342	19	0.151	R.IFYILWSPDNAK.V
R2/RRR2-22/2	1965.199	1965.999	-918.748	0.500	886.856	0.591	22	0.150	R.TTSYEDFTSSLPEGDCR.F
R2/RRR2-23/2	1965.156	1965.999	-940.824	0.466	979.840	0.542	23	0.148	R.TTSYEDFTSSLPEGDCR.F
R2/RRR2-22/2	1467.175	1467.693	-1037.341	0.375	1470.146	0.305	18	0.146	R.IFYILWSPDNAK.V
R2/RRR2-23/2	1467.114	1467.693	-1079.027	0.425	1206.399	0.408	17	0.143	R.IFYILWSPDNAK.V
R2/RRR2-23/2	1466.987	1467.693	-1165.921	0.340	1164.586	0.391	17	0.136	R.IFYILWSPDNAK.V
R2/RRR2-23/2	1071.095	1071.190	-88.431	0.370	1048.367	0.377	15	0.131	K.MLYASSNER.F
R2/RRR2-23/2	1158.004	1158.330	-282.154	0.448	806.279	0.383	17	0.124	K.EIIVDKIGDR.T
R2/RRR2-23/2	1070.824	1071.190	-342.285	0.351	798.163	0.413	14	0.123	K.MLYASSNER.F
R2/RRR2-23/2	1157.860	1158.330	-406.861	0.422	714.187	0.380	16	0.121	K.EIIVDKIGDR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1157.934	1158.330	-343.181	0.479	535.030	0.365	14	0.116	K.EIIVDKIGDR.T
R2/RRR2-22/2	1467.132	1467.693	-1067.081	0.316	1104.866	0.181	16	0.109	R.IFYILWSPDNAK.V
R2/RRR2-23/2	1070.711	1071.190	-448.096	0.267	640.687	0.302	13	0.108	K.MLYASSNER.F
R2/RRR2-5/2	1648.293	1648.754	-280.678	0.401	2010.528	0.415	24	0.236	K.GTETIDVTDAVGSNIR.V
R2/RRR2-5/2	1648.286	1648.754	-284.765	0.435	1817.947	0.419	23	0.209	K.GTETIDVTDAVGSNIR.V
R2/RRR2-5/2	1933.608	1934.140	-794.645	0.517	1290.121	0.602	25	0.187	R.ALSEVAGAQLPYDSLSGVR.D
R2/RRR2-5/2	1933.420	1934.140	-891.864	0.503	1310.272	0.553	25	0.179	R.ALSEVAGAQLPYDSLSGVR.D
R2/RRR2-5/2	1862.589	1862.975	-208.024	0.427	1345.414	0.467	19	0.165	R.LNEDINEEWISDKTR.F
R2/RRR2-5/2	1270.243	1269.340	-76.109	0.496	817.002	0.468	15	0.129	R.GSGEEIGTYVEK.L
R2/RRR2-5/2	1270.424	1269.516	-72.243	0.433	704.757	0.475	14	0.123	R.SVVDKNLGPLVK.T
R2/RRR2-5/2	1269.761	1269.516	194.237	0.407	501.564	0.473	14	0.118	R.SVVDKNLGPLVK.T
R2/RRR2-5/2	1269.314	1269.516	-159.505	0.418	779.461	0.396	14	0.117	R.SVVDKNLGPLVK.T
R2/RRR2-5/2	1363.094	1363.541	-329.165	0.336	704.154	0.340	15	0.109	R.ANVILPSSAFSEK.E
R2/RRR2-5/2	1363.123	1363.541	-307.421	0.285	985.851	0.221	17	0.107	R.ANVILPSSAFSEK.E
R2/RRR2-5/2	1362.675	1363.541	-1373.594	0.300	708.466	0.302	15	0.106	R.ANVILPSSAFSEK.E
R2/RRR2-5/2	1268.391	1269.340	-1541.145	0.274	634.035	0.272	15	0.104	R.GSGEEIGTYVEK.L
R2/RRR2-25/2	1768.696	1769.955	-1280.877	0.475	1836.835	0.488	24	0.232	K.M*QGVESFDVDIKEQK.V
R2/RRR2-24/2	1430.043	1429.601	310.139	0.512	1001.424	0.568	21	0.157	K.GNVTPDAVLQTVSK.T
R2/RRR2-26/2	1429.171	1429.601	-301.695	0.497	955.213	0.570	21	0.154	K.GNVTPDAVLQTVSK.T
R2/RRR2-25/2	1371.227	1370.542	-230.416	0.437	1387.505	0.374	19	0.152	R.VGM*SCEGCVGAVK.R
R2/RRR2-25/2	1430.285	1429.601	-221.507	0.507	785.791	0.563	20	0.143	K.GNVTPDAVLQTVSK.T
R2/RRR2-26/2	1429.323	1429.601	-195.016	0.497	858.998	0.535	20	0.142	K.GNVTPDAVLQTVSK.T
R2/RRR2-26/2	1429.048	1429.601	-1090.206	0.474	793.247	0.531	20	0.138	K.GNVTPDAVLQTVSK.T
R2/RRR2-25/2	1428.448	1429.601	-1511.429	0.389	728.630	0.540	19	0.133	K.GNVTPDAVLQTVSK.T
R2/RRR2-25/3	1527.416	1526.729	-205.510	0.485	1149.708	0.532	27	0.130	R.VGM*SCEGCVGAVKR.V
R2/RRR2-25/2	1428.684	1429.601	-1346.124	0.357	791.613	0.487	20	0.129	K.GNVTPDAVLQTVSK.T
R2/RRR2-25/2	1369.471	1370.542	-1516.702	0.359	963.201	0.305	17	0.115	R.VGM*SCEGCVGAVK.R
R2/RRR2-25/3	1769.810	1769.955	-81.870	0.496	1119.529	0.471	28	0.115	K.M*QGVESFDVDIKEQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-25/3	1769.337	1769.955	-916.779	0.470	1235.913	0.429	28	0.114	K.M*QGVESFDVDIKEQK.V
R2/RRR2-25/2	1837.274	1837.921	-898.752	0.318	1274.817	0.472	22	0.113	K.TSFWDAEPAPVEATAASS.-
R2/RRR2-26/3	1769.654	1769.955	-170.401	0.496	1202.684	0.431	29	0.111	K.M*QGVESFDVDIKEQK.V
R2/RRR2-24/2	1428.569	1429.601	-1426.796	0.230	655.308	0.306	17	0.106	K.GNVTPDAVLQTVSK.T
R2/RRR2-25/2	1369.664	1370.542	-1375.697	0.347	720.413	0.272	15	0.105	R.VGM*SCEGCVGAVK.R
R2/RRR2-25/2	1837.255	1837.921	-909.424	0.431	1207.339	0.584	22	0.101	K.TSFWDAEPAPVEATAASS.-
R2/RRR2-26/3	1769.291	1769.955	-942.961	0.466	1079.935	0.408	28	0.099	K.M*QGVESFDVDIKEQK.V
R2/RRR2-26/3	1769.918	1769.955	-20.644	0.439	1181.790	0.360	29	0.096	K.M*QGVESFDVDIKEQK.V
R2/RRR2-25/3	1526.772	1526.729	28.527	0.460	801.082	0.480	25	0.096	R.VGM*SCEGCVGAVKR.V
R2/RRR2-25/3	1769.740	1769.955	-121.515	0.450	1068.463	0.391	28	0.096	K.M*QGVESFDVDIKEQK.V
R2/RRR2-24/3	1769.524	1769.955	-243.792	0.431	1028.100	0.365	26	0.089	K.M*QGVESFDVDIKEQK.V
R2/RRR2-24/3	1769.882	1769.955	-40.982	0.451	797.499	0.383	25	0.085	K.M*QGVESFDVDIKEQK.V
R2/RRR2-24/3	1769.903	1769.955	-29.360	0.352	857.768	0.362	25	0.083	K.M*QGVESFDVDIKEQK.V
R2/RRR2-25/2	1837.157	1837.921	-963.121	0.300	913.850	0.458	19	0.052	K.TSFWDAEPAPVEATAASS.-
R2/RRR2-19/3	1274.473	1274.574	-79.181	0.533	2719.367	0.175	26	0.230	R.VRFPCIQIIK.T
R2/RRR2-19/2	1576.524	1576.776	-160.187	0.556	1694.472	0.506	21	0.213	K.SNGQILAINEIFEK.N
R2/RRR2-19/3	1274.743	1274.574	133.341	0.481	2236.805	0.195	24	0.159	R.VRFPCIQIIK.T
R2/RRR2-19/2	1134.083	1134.272	-167.405	0.389	1024.373	0.406	15	0.134	R.FHQYQVVGR.G
R2/RRR2-19/2	1575.454	1576.776	-1478.110	0.453	988.347	0.422	17	0.129	K.SNGQILAINEIFEK.N
R2/RRR2-19/2	1133.950	1134.272	-285.008	0.398	874.331	0.401	15	0.127	R.FHQYQVVGR.G
R2/RRR2-18/2	1133.947	1134.272	-287.168	0.358	1070.551	0.339	15	0.127	R.FHQYQVVGR.G
R2/RRR2-18/2	1133.988	1134.272	-250.772	0.432	810.105	0.415	14	0.127	R.FHQYQVVGR.G
R2/RRR2-19/2	1575.893	1576.776	-1198.469	0.396	976.780	0.366	17	0.121	K.SNGQILAINEIFEK.N
R2/RRR2-18/2	1133.839	1134.272	-383.409	0.434	939.353	0.323	14	0.121	R.FHQYQVVGR.G
R2/RRR2-19/2	1193.304	1192.303	0.861	0.342	318.717	0.519	14	0.119	R.GLPTPTDEHPK.I
R2/RRR2-19/2	1133.920	1134.272	-311.038	0.404	648.133	0.373	13	0.118	R.FHQYQVVGR.G
R2/RRR2-19/2	1191.839	1192.303	-390.639	0.269	316.307	0.521	14	0.114	R.GLPTPTDEHPK.I
R2/RRR2-19/2	1275.814	1274.574	189.285	0.448	925.886	0.295	14	0.114	R.VRFPCIQIIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1192.191	1192.303	-94.443	0.261	312.137	0.491	14	0.112	R.GLPTPTDEHPK.I
R2/RRR2-19/2	1191.946	1192.303	-300.313	0.237	333.414	0.534	14	0.111	R.GLPTPTDEHPK.I
R2/RRR2-19/2	1264.017	1264.479	-367.193	0.396	920.638	0.188	15	0.105	-.M*KLWATNEVR.-
R2/RRR2-19/2	1264.199	1264.479	-222.157	0.398	736.298	0.185	15	0.104	R.M*KLWATNEVR.A
R2/RRR2-19/2	1264.138	1264.479	-270.497	0.425	928.997	0.143	16	0.102	R.M*KLWATNEVR.A
R2/RRR2-21/2	1877.581	1878.179	-853.556	0.502	1693.157	0.483	23	0.206	K.GVDDILLVSVNDPFVM*K.A
R2/RRR2-21/2	1878.618	1878.179	234.013	0.530	1252.251	0.532	20	0.166	K.GVDDILLVSVNDPFVM*K.A
R2/RRR2-21/2	1004.707	1005.192	-484.723	0.399	1345.889	0.373	16	0.150	R.FALLADNLK.V
R2/RRR2-21/2	1185.910	1186.339	-362.651	0.490	1019.494	0.480	18	0.146	K.FLADGLGTYTK.A
R2/RRR2-21/2	1863.371	1862.180	102.594	0.454	932.611	0.515	18	0.137	K.GVDDILLVSVNDPFVMK.A
R2/RRR2-21/2	1187.138	1186.339	-169.515	0.535	929.785	0.432	18	0.135	K.FLADGLGTYTK.A
R2/RRR2-21/2	1188.161	1188.353	-161.641	0.439	887.560	0.440	16	0.131	K.ALGLELDLSEK.G
R2/RRR2-21/2	1004.715	1005.192	-476.311	0.373	1140.549	0.332	15	0.129	-.FALLADNLK.-
R2/RRR2-21/2	1187.775	1188.353	-1332.070	0.419	900.466	0.399	16	0.126	K.ALGLELDLSEK.G
R2/RRR2-21/2	1186.020	1186.339	-269.708	0.471	980.203	0.341	18	0.124	K.FLADGLGTYTK.A
R2/RRR2-21/2	1188.095	1188.353	-218.123	0.431	809.465	0.402	15	0.122	K.ALGLELDLSEK.G
R2/RRR2-21/2	1161.140	1161.379	-206.526	0.382	1504.508	0.127	16	0.121	R.RFALLADNLK.V
R2/RRR2-21/2	1004.546	1005.192	-1643.903	0.374	898.740	0.339	13	0.117	-.FALLADNLK.-
R2/RRR2-22/2	1162.377	1161.379	-1.328	0.327	1059.508	0.108	14	0.100	R.RFALLADNLK.V
R2/RRR2-14/2	1696.467	1695.895	-253.294	0.521	1000.865	0.638	22	0.168	K.LLESHLVPSSTAPESK.V
R2/RRR2-14/2	1696.266	1695.895	218.878	0.512	887.273	0.581	21	0.149	K.LLESHLVPSSTAPESK.V
R2/RRR2-14/2	1696.327	1695.895	255.175	0.480	719.790	0.597	19	0.140	K.LLESHLVPSSTAPESK.V
R2/RRR2-12/2	1319.150	1319.488	-257.061	0.501	2225.164	0.387	19	0.259	R.DDLFNINAGIVK.G
R2/RRR2-12/2	1319.242	1319.488	-187.436	0.538	2135.329	0.388	19	0.243	R.DDLFNINAGIVK.G
R2/RRR2-12/2	1318.627	1319.488	-1415.950	0.408	1766.408	0.401	18	0.197	R.DDLFNINAGIVK.G
R2/RRR2-12/2	1234.013	1234.295	-229.254	0.478	892.019	0.501	18	0.140	R.TQDGGTEVVEAK.A
R2/RRR2-12/2	1233.559	1234.295	-1412.257	0.452	871.226	0.499	18	0.138	R.TQDGGTEVVEAK.A
R2/RRR2-12/2	1234.160	1234.295	-109.981	0.457	878.036	0.375	17	0.122	R.TQDGGTEVVEAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1234.233	1234.295	-50.355	0.379	947.573	0.326	18	0.119	R.TQDGGTEVVEAK.A
R2/RRR2-12/2	1390.016	1390.482	-336.002	0.379	880.959	0.343	16	0.116	-.RTQDGGTEVVEAK.-
R2/RRR2-13/2	1319.537	1319.488	37.058	0.438	971.288	0.332	15	0.115	-.DDLFNINAGIVK.-
R2/RRR2-12/3	1390.424	1390.482	-41.758	0.377	974.614	0.417	27	0.090	K.RTQDGGTEVVEAK.A
R2/RRR2-12/3	1390.421	1390.482	-43.872	0.345	543.556	0.326	22	0.073	K.RTQDGGTEVVEAK.A
R2/RRR2-7/2	1577.196	1577.721	-969.481	0.559	2196.533	0.464	27	0.280	K.FAGAISDGGDIVLEGR.V
R2/RRR2-6/2	1548.427	1548.722	-191.560	0.483	1854.214	0.485	23	0.228	R.AIGAELVSFDEAIGR.A
R2/RRR2-7/2	1029.149	1029.215	-64.316	0.462	2007.821	0.320	17	0.210	K.LSEAGLAVLR.G
R2/RRR2-7/2	1577.264	1577.721	-290.291	0.529	1639.951	0.484	24	0.202	K.FAGAISDGGDIVLEGR.V
R2/RRR2-7/2	1548.398	1548.722	-209.908	0.448	1584.279	0.429	22	0.181	R.AIGAELVSFDEAIGR.A
R2/RRR2-6/2	1549.356	1548.722	-237.042	0.476	1124.846	0.550	19	0.159	R.AIGAELVSFDEAIGR.A
R2/RRR2-6/2	1548.192	1548.722	-991.440	0.435	1171.979	0.433	20	0.144	R.AIGAELVSFDEAIGR.A
R2/RRR2-6/2	1342.314	1342.567	-188.775	0.336	1103.334	0.438	17	0.137	K.LAVQLVAGESGGIK.G
R2/RRR2-7/2	1549.909	1548.722	120.737	0.396	1030.249	0.371	20	0.126	R.AIGAELVSFDEAIGR.A
R2/RRR2-7/2	1341.581	1342.567	-1484.081	0.328	796.439	0.409	16	0.116	K.LAVQLVAGESGGIK.G
R2/RRR2-7/2	1547.560	1548.722	-1401.348	0.293	929.069	0.322	18	0.114	R.AIGAELVSFDEAIGR.A
R2/RRR2-6/2	1028.429	1029.215	-1742.399	0.295	510.500	0.249	15	0.108	K.LSEAGLAVLR.G
R2/RRR2-7/2	1028.750	1029.215	-453.876	0.309	838.303	0.235	13	0.106	K.LSEAGLAVLR.G
R2/RRR2-7/3	1151.634	1151.381	220.953	0.333	1308.103	0.179	22	0.070	R.TKYVGVSLVGK.T
R2/RRR2-3/2	1698.708	1698.861	-90.283	0.462	1347.062	0.510	21	0.174	K.GAGVDGIITDFPATAHR.Y
R2/RRR2-4/2	1163.038	1163.351	-270.195	0.560	1427.031	0.445	17	0.171	K.VNLVQSLFSR.V
R2/RRR2-4/2	1164.112	1163.351	-206.209	0.497	1312.229	0.494	17	0.171	K.VNLVQSLFSR.V
R2/RRR2-3/2	1118.974	1118.351	-337.733	0.540	1272.870	0.472	18	0.162	K.LGFGVVDAVIK.A
R2/RRR2-3/2	1118.067	1118.351	-254.124	0.515	1244.605	0.472	18	0.160	K.LGFGVVDAVIK.A
R2/RRR2-4/2	1118.234	1118.351	-104.959	0.513	1249.388	0.459	18	0.158	K.LGFGVVDAVIK.A
R2/RRR2-4/2	1119.000	1118.351	-314.528	0.560	1276.316	0.447	18	0.158	K.LGFGVVDAVIK.A
R2/RRR2-3/2	1162.934	1163.351	-360.446	0.462	1419.005	0.377	17	0.157	K.VNLVQSLFSR.V
R2/RRR2-4/2	1118.228	1118.351	-109.558	0.552	1311.439	0.423	18	0.156	K.LGFGVVDAVIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1163.041	1163.351	-267.562	0.501	1211.108	0.428	16	0.150	-.VNLVQSLFSR.-
R2/RRR2-3/2	1163.223	1163.351	-110.899	0.443	1305.348	0.381	17	0.149	K.VNLVQSLFSR.V
R2/RRR2-3/2	1212.538	1212.421	96.875	0.445	744.543	0.512	17	0.133	K.TLSGNPPTIIAK.G
R2/RRR2-3/2	1117.480	1118.351	-1678.600	0.450	999.168	0.387	16	0.129	K.LGFGVVDAVIK.A
R2/RRR2-4/2	1211.318	1212.421	-1740.912	0.330	756.916	0.415	16	0.119	K.TLSGNPPTIIAK.G
R2/RRR2-4/2	864.209	863.984	261.020	0.441	991.776	0.293	12	0.117	K.FANAVSVR.T
R2/RRR2-4/2	1211.479	1212.421	-1607.277	0.332	597.111	0.420	15	0.115	K.TLSGNPPTIIAK.G
R2/RRR2-4/2	1211.426	1212.421	-1651.616	0.278	591.769	0.344	15	0.108	-.TLSGNPPTIIAK.-
R2/RRR2-3/2	1186.238	1187.322	-1761.928	0.280	979.845	0.198	15	0.106	-.DGAGICLPDIR.-
R2/RRR2-3/2	1212.170	1212.421	-207.528	0.313	356.830	0.337	12	0.100	-.TLSGNPPTIIAK.-
R2/RRR2-3/3	1699.264	1698.861	238.082	0.402	816.378	0.484	27	0.096	K.GAGVDGIITDFPATAHR.Y
R2/RRR2-3/3	1699.343	1698.861	284.327	0.262	850.751	0.322	24	0.072	K.GAGVDGIITDFPATAHR.Y
R2/RRR2-6/2	976.934	977.144	-215.138	0.527	1048.271	0.561	13	0.163	K.ANVLAFWR.Q
R2/RRR2-6/2	977.058	977.144	-88.296	0.469	968.791	0.497	13	0.146	K.ANVLAFWR.Q
R2/RRR2-1/2	1389.519	1390.615	-1512.624	0.444	946.537	0.476	16	0.135	K.LPFAAAQIGQAFR.N
R2/RRR2-6/2	1606.159	1606.847	-1054.071	0.379	849.688	0.474	19	0.129	R.VFTPSVIEPSFGIGR.I
R2/RRR2-5/2	1391.410	1390.615	-147.093	0.455	861.285	0.448	17	0.129	K.LPFAAAQIGQAFR.N
R2/RRR2-5/2	1390.435	1390.615	-129.496	0.405	842.565	0.433	16	0.124	K.LPFAAAQIGQAFR.N
R2/RRR2-1/2	1390.991	1390.615	271.755	0.385	779.571	0.445	15	0.122	K.LPFAAAQIGQAFR.N
R2/RRR2-6/2	1116.382	1116.247	121.560	0.369	1054.211	0.293	15	0.118	K.AEVDAAVEALK.A
R2/RRR2-6/2	1115.715	1116.290	-1415.579	0.322	695.132	0.301	16	0.109	R.VGIDEVASVVK.Q
R2/RRR2-6/2	1115.530	1116.290	-1582.095	0.308	761.476	0.292	14	0.107	R.VGIDEVASVVK.Q
R2/RRR2-6/2	1605.729	1606.847	-1322.905	0.273	712.690	0.291	17	0.104	R.VFTPSVIEPSFGIGR.I
R2/RRR2-6/3	1334.791	1334.543	186.232	0.358	1133.229	0.157	23	0.061	-.IKEYGIVAPDTK.-
R2/RRR2-6/3	1334.091	1334.543	-339.680	0.401	1150.034	0.172	21	0.059	-.IKEYGIVAPDTK.-
R2/RRR2-6/3	1334.194	1334.543	-262.018	0.368	1097.661	0.093	21	0.048	-.IKEYGIVAPDTK.-
R2/RRR2-5/2	1293.109	1293.320	-163.293	0.477	2133.616	0.387	21	0.250	K.DSSQDEAGTAAIK.T
R2/RRR2-5/2	1587.429	1587.714	-179.834	0.421	1376.519	0.442	19	0.163	K.EGTESSAFWFALGGK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1744.254	1742.911	197.694	0.469	997.255	0.557	20	0.152	K.GLKDETYSGDGIALFR.I
R2/RRR2-3/2	1649.685	1650.815	-1294.855	0.319	759.711	0.364	19	0.110	R.ASALAALSSAFNPSSQK.N
R2/RRR2-5/3	1932.055	1932.170	-59.963	0.533	662.044	0.540	30	0.101	R.KAASAAVEEFIATQNRPK.T
R2/RRR2-5/3	1282.604	1282.556	37.304	0.412	1274.177	0.278	22	0.085	R.IQDFKPVPLPK.A
R2/RRR2-3/3	1282.585	1282.556	22.555	0.405	1191.541	0.298	22	0.084	R.IQDFKPVPLPK.A
R2/RRR2-5/3	1932.515	1932.170	179.062	0.403	511.915	0.374	26	0.075	R.KAASAAVEEFIATQNRPK.T
R2/RRR2-3/3	1282.817	1282.556	204.228	0.430	1261.763	0.203	23	0.072	R.IQDFKPVPLPK.A
R2/RRR2-5/3	1282.575	1282.556	14.680	0.384	1000.451	0.246	21	0.071	R.IQDFKPVPLPK.A
R2/RRR2-5/3	1282.464	1282.556	-71.814	0.384	941.681	0.177	20	0.064	R.IQDFKPVPLPK.A
R2/RRR2-3/2	1249.446	1249.441	3.664	0.400	1317.636	0.421	17	0.154	R.AALNLAYQGLSK.V
R2/RRR2-3/2	1249.246	1249.441	-157.069	0.363	977.421	0.413	17	0.129	R.AALNLAYQGLSK.V
R2/RRR2-3/2	1425.959	1424.586	262.515	0.338	699.173	0.408	16	0.113	K.AGWPVAGSPDPTLR.I
R2/RRR2-3/2	1845.857	1846.109	-136.880	0.565	2078.896	0.520	24	0.279	R.IVCQQVNVSSLEEVIK.H
R2/RRR2-3/2	1476.214	1476.703	-331.726	0.470	1995.043	0.474	20	0.249	R.VLQQASQIFQSVK.I
R2/RRR2-3/2	1475.929	1476.703	-1204.938	0.475	1697.786	0.507	19	0.214	R.VLQQASQIFQSVK.I
R2/RRR2-4/2	1476.013	1476.703	-1148.173	0.390	1767.575	0.471	19	0.214	R.VLQQASQIFQSVK.I
R2/RRR2-6/2	1565.787	1564.767	12.933	0.468	1178.643	0.432	18	0.145	K.IATELSLWQEAFR.S
R2/RRR2-3/3	1969.666	1970.007	-173.785	0.413	971.218	0.542	31	0.118	R.GGDGGSSAGGQRPAVAPEQDR.W
R2/RRR2-4/2	1563.877	1564.767	-1211.983	0.246	860.218	0.369	16	0.114	K.IATELSLWQEAFR.S
R2/RRR2-3/3	1265.928	1266.433	-1192.636	0.409	1139.670	0.466	23	0.112	K.VNHLSGAVHFGK.M
R2/RRR2-4/2	1565.248	1564.767	308.303	0.287	515.700	0.245	13	0.101	K.IATELSLWQEAFR.S
R2/RRR2-3/2	1321.138	1321.504	-277.711	0.200	825.053	0.208	16	0.101	R.IANLVNFSLDSK.R
R2/RRR2-2/3	1970.908	1970.007	-50.612	0.411	900.954	0.470	28	0.099	R.GGDGGSSAGGQRPAVAPEQDR.W
R2/RRR2-3/2	1320.362	1321.504	-1626.995	0.208	470.809	0.265	12	0.091	-.IANLVNFSLDSK.-
R2/RRR2-3/3	1266.026	1266.433	-322.547	0.356	662.934	0.422	22	0.080	K.VNHLSGAVHFGK.M
R2/RRR2-3/3	1970.637	1970.007	-188.735	0.318	600.168	0.380	27	0.074	R.GGDGGSSAGGQRPAVAPEQDR.W
R2/RRR2-18/2	1502.392	1502.650	-172.818	0.471	1270.280	0.549	19	0.175	R.EIENGILWEVDGK.W
R2/RRR2-18/2	1769.323	1769.934	-913.270	0.469	1304.548	0.496	23	0.167	K.DGATDPTFLYFSHGLK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1502.235	1502.650	-277.404	0.498	1121.061	0.545	18	0.161	R.EIENGILWEVDGK.W
R2/RRR2-18/2	1769.435	1769.934	-282.843	0.497	1144.247	0.517	22	0.157	K.DGATDPTFLYFSHGLK.E
R2/RRR2-18/2	1502.210	1502.650	-294.280	0.462	1127.758	0.501	18	0.153	R.EIENGILWEVDGK.W
R2/RRR2-18/2	1768.764	1769.934	-1230.662	0.452	1169.879	0.466	22	0.150	K.DGATDPTFLYFSHGLK.E
R2/RRR2-17/2	1063.913	1064.217	-286.738	0.342	1053.378	0.307	15	0.122	K.VVDIVDTFR.L
R2/RRR2-18/2	1063.891	1064.217	-306.998	0.383	780.522	0.347	14	0.118	K.VVDIVDTFR.L
R2/RRR2-17/2	1063.702	1064.217	-1428.398	0.380	826.111	0.341	14	0.118	-.VVDIVDTFR.-
R2/RRR2-18/2	1064.044	1064.217	-162.430	0.401	796.408	0.314	14	0.116	K.VVDIVDTFR.L
R2/RRR2-18/2	1063.989	1064.217	-214.566	0.376	802.906	0.265	14	0.112	K.VVDIVDTFR.L
R2/RRR2-17/2	1063.282	1064.217	-1825.423	0.296	640.173	0.263	12	0.107	-.VVDIVDTFR.-
R2/RRR2-18/2	1229.419	1230.395	-1611.509	0.430	640.357	0.155	13	0.097	-.LQEQPPFDKK.-
R2/RRR2-18/2	1230.909	1230.395	-395.348	0.442	892.109	0.107	14	0.096	-.LQEQPPFDKK.-
R2/RRR2-18/2	1230.257	1230.395	-112.121	0.408	796.748	0.087	13	0.094	R.LQEQPPFDKK.Q
R2/RRR2-18/2	1230.117	1230.395	-226.696	0.484	706.785	0.171	13	0.094	-.LQEQPPFDKK.-
R2/RRR2-18/3	1364.806	1365.514	-1255.285	0.426	497.005	0.492	21	0.092	K.LDAEKQEEFKK.N
R2/RRR2-18/3	1365.729	1365.514	158.390	0.479	596.071	0.458	24	0.092	K.LDAEKQEEFKK.N
R2/RRR2-17/3	1365.124	1365.514	-286.038	0.459	320.011	0.441	17	0.090	K.LDAEKQEEFKK.N
R2/RRR2-18/3	1365.721	1365.514	152.474	0.422	387.224	0.420	20	0.088	K.LDAEKQEEFKK.N
R2/RRR2-17/3	1365.787	1365.514	200.607	0.452	528.089	0.368	21	0.084	K.LDAEKQEEFKK.N
R2/RRR2-17/3	1365.861	1365.514	255.052	0.404	292.699	0.350	17	0.079	-.LDAEKQEEFKK.-
R2/RRR2-13/2	1565.266	1564.680	-265.686	0.576	2326.642	0.508	22	0.317	K.SADWSHFLTGSLDK.S
R2/RRR2-13/2	1563.653	1564.680	-1300.481	0.470	2303.846	0.482	22	0.306	K.SADWSHFLTGSLDK.S
R2/RRR2-13/2	1261.113	1261.407	-233.551	0.348	1598.940	0.492	19	0.195	R.TIITAGEDATIR.I
R2/RRR2-13/2	1260.952	1261.407	-362.140	0.495	1557.354	0.495	19	0.194	R.TIITAGEDATIR.I
R2/RRR2-13/2	1261.126	1261.407	-223.258	0.391	1554.848	0.486	19	0.190	R.TIITAGEDATIR.I
R2/RRR2-13/2	1261.953	1261.279	-259.203	0.505	1249.173	0.512	18	0.166	R.SFSSGGEDGYVR.L
R2/RRR2-12/2	1262.381	1261.407	-20.815	0.456	1253.594	0.479	18	0.160	R.TIITAGEDATIR.I
R2/RRR2-13/2	1262.100	1261.279	-142.955	0.501	1128.969	0.516	18	0.157	R.SFSSGGEDGYVR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1260.355	1261.279	-1531.737	0.351	1110.164	0.420	17	0.137	R.SFSSGGEDGYVR.L
R2/RRR2-13/2	1086.306	1086.264	38.929	0.355	1278.724	0.323	16	0.136	K.ILQEEIGGVK.G
R2/RRR2-13/2	1684.675	1683.851	-104.917	0.395	918.505	0.484	19	0.133	K.GHFGPINALAFNPDGR.S
R2/RRR2-12/2	1260.410	1261.279	-1487.957	0.324	679.653	0.452	14	0.118	R.SFSSGGEDGYVR.L
R2/RRR2-12/2	1261.015	1261.279	-210.267	0.397	860.868	0.350	16	0.118	R.SFSSGGEDGYVR.L
R2/RRR2-15/2	1261.223	1261.407	-146.646	0.279	232.888	0.317	15	0.111	-.TIITAGEDATIR.-
R2/RRR2-12/2	1260.263	1261.279	-1605.003	0.279	563.203	0.265	14	0.105	R.SFSSGGEDGYVR.L
R2/RRR2-12/2	1085.290	1086.264	-1823.716	0.236	828.030	0.116	13	0.098	-.ILQEEIGGVK.-
R2/RRR2-14/2	1987.620	1987.198	212.974	0.560	2538.097	0.591	27	0.389	K.GDVSDEAVAALDKIEAALAK.F
R2/RRR2-14/2	1987.494	1987.198	149.720	0.585	2154.250	0.594	26	0.309	K.GDVSDEAVAALDKIEAALAK.F
R2/RRR2-14/2	1986.733	1987.198	-234.282	0.562	2020.747	0.600	25	0.287	K.GDVSDEAVAALDKIEAALAK.F
R2/RRR2-14/2	1889.093	1889.054	20.571	0.520	1301.325	0.593	23	0.190	K.QQFAEELLAYTDAFNK.A
R2/RRR2-14/3	1986.591	1987.198	-810.899	0.416	1454.810	0.431	38	0.136	K.GDVSDEAVAALDKIEAALAK.F
R2/RRR2-14/3	1987.144	1987.198	-26.908	0.419	1037.812	0.498	36	0.113	K.GDVSDEAVAALDKIEAALAK.F
R2/RRR2-14/2	1101.117	1101.322	-186.094	0.359	747.239	0.307	13	0.112	R.FQIFFSAIK.N
R2/RRR2-14/2	1101.239	1101.322	-75.448	0.313	743.020	0.275	14	0.110	R.FQIFFSAIK.N
R2/RRR2-14/2	1100.962	1101.322	-327.355	0.259	548.467	0.251	13	0.106	R.FQIFFSAIK.N
R2/RRR2-14/3	1986.734	1987.198	-233.796	0.361	1071.541	0.390	35	0.094	K.GDVSDEAVAALDKIEAALAK.F
R2/RRR2-14/3	1823.013	1823.039	-13.984	0.447	588.043	0.523	23	0.091	K.FIEEVNKIHAYTETK.Q
R2/RRR2-14/3	1356.652	1356.509	105.797	0.471	960.418	0.401	23	0.090	K.QDPQFLLEHTK.K
R2/RRR2-14/3	1355.867	1356.509	-1214.166	0.379	690.393	0.312	21	0.074	K.QDPQFLLEHTK.K
R2/RRR2-14/3	1356.300	1356.509	-154.431	0.363	676.884	0.267	20	0.068	-.QDPQFLLEHTK.-
R2/RRR2-20/2	1317.256	1316.443	-142.174	0.533	1836.087	0.535	22	0.241	R.ATGGEVGASSALAPK.I
R2/RRR2-20/2	1315.998	1316.443	-339.270	0.372	1929.546	0.405	22	0.220	R.ATGGEVGASSALAPK.I
R2/RRR2-20/2	1316.179	1316.443	-200.710	0.430	1746.926	0.376	22	0.189	R.ATGGEVGASSALAPK.I
R2/RRR2-20/2	1584.747	1584.882	-85.805	0.424	1078.035	0.502	20	0.148	R.QAAVSVVPTASSLIIK.A
R2/RRR2-20/2	1681.280	1681.862	-943.981	0.376	876.345	0.583	19	0.143	K.EILGTAFSVGCQVDGK.S
R2/RRR2-20/2	1359.148	1359.551	-297.240	0.422	1115.899	0.428	16	0.140	K.SITIDEVIEIAR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	882.093	882.082	12.269	0.368	335.882	0.474	12	0.121	K.IGPLGLSPK.K
R2/RRR2-19/2	881.390	882.082	-1925.835	0.366	336.006	0.458	12	0.120	K.IGPLGLSPK.K
R2/RRR2-19/2	881.473	882.082	-1830.924	0.331	326.876	0.445	12	0.118	K.IGPLGLSPK.K
R2/RRR2-19/2	881.984	882.082	-111.834	0.329	346.393	0.396	11	0.114	K.IGPLGLSPK.K
R2/RRR2-18/2	882.020	882.082	-70.880	0.306	372.568	0.385	12	0.114	K.IGPLGLSPK.K
R2/RRR2-20/2	881.318	882.082	-2008.515	0.221	321.224	0.309	11	0.087	-.IGPLGLSPK.-
R2/RRR2-8/2	1761.479	1761.957	-272.026	0.540	3585.518	0.534	27	0.642	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-8/2	1762.272	1761.957	179.277	0.609	2812.895	0.550	26	0.430	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-9/2	1762.161	1761.957	116.130	0.546	2856.281	0.513	26	0.427	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-7/2	1762.168	1761.957	120.298	0.611	2818.643	0.537	27	0.425	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-7/2	1761.527	1761.957	-244.634	0.570	2716.294	0.537	26	0.403	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-7/2	1762.231	1761.957	156.005	0.616	2684.610	0.542	26	0.396	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-8/2	1761.425	1761.957	-872.392	0.520	2129.600	0.485	24	0.268	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-7/2	1829.669	1830.078	-223.879	0.530	1366.664	0.484	24	0.171	R.SERPEAFAVLDLVNIR.A
R2/RRR2-7/2	1728.607	1728.972	-211.470	0.562	928.314	0.573	21	0.153	R.WQAVAPSLPDDLFIR.V
R2/RRR2-7/2	1829.564	1830.078	-829.930	0.511	1116.886	0.478	22	0.148	R.SERPEAFAVLDLVNIR.A
R2/RRR2-8/2	1728.643	1728.972	-190.500	0.454	984.512	0.468	22	0.139	R.WQAVAPSLPDDLFIR.V
R2/RRR2-7/2	1728.426	1728.972	-897.194	0.485	791.547	0.494	20	0.132	R.WQAVAPSLPDDLFIR.V
R2/RRR2-8/2	1730.385	1728.972	239.539	0.545	769.469	0.479	20	0.129	R.WQAVAPSLPDDLFIR.V
R2/RRR2-7/2	1830.509	1830.078	236.470	0.492	954.253	0.395	21	0.125	R.SERPEAFAVLDLVNIR.A
R2/RRR2-7/2	1763.675	1761.957	-160.544	0.371	820.126	0.372	20	0.116	K.YGLAADNVVDAVLVDAR.G
R2/RRR2-7/2	1438.719	1439.659	-1352.980	0.315	944.585	0.325	15	0.114	R.DFYAFM*APFVSK.D
R2/RRR2-7/3	1890.796	1890.130	-176.954	0.404	1400.089	0.353	29	0.113	R.KYGLAADNVVDAVLVDAR.G
R2/RRR2-9/2	1829.531	1830.078	-848.148	0.285	777.601	0.231	16	0.100	R.SERPEAFAVLDLVNIR.A
R2/RRR2-7/3	1830.247	1830.078	92.937	0.468	875.500	0.372	24	0.082	-.SERPEAFAVLDLVNIR.-
R2/RRR2-8/3	1830.983	1830.078	-51.671	0.460	1105.506	0.296	26	0.080	-.SERPEAFAVLDLVNIR.-
R2/RRR2-7/3	1830.376	1830.078	163.368	0.535	988.306	0.314	24	0.074	-.SERPEAFAVLDLVNIR.-
R2/RRR2-7/3	1830.098	1830.078	10.957	0.433	820.131	0.340	23	0.073	-.SERPEAFAVLDLVNIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1829.769	1830.078	-169.106	0.370	737.717	0.245	22	0.062	-.SERPEAFAVLDLVNIR.-
R2/RRR2-4/2	1221.231	1221.388	-128.791	0.531	1529.047	0.412	17	0.174	R.AVAYLLTNAER.V
R2/RRR2-4/2	1162.908	1163.257	-301.284	0.416	1621.045	0.354	17	0.173	R.LLCNTGDDVR.K
R2/RRR2-4/2	1202.076	1202.388	-260.300	0.448	1151.000	0.507	18	0.158	R.HALSAISAIYR.L
R2/RRR2-4/2	1220.533	1221.388	-1524.634	0.446	1241.622	0.337	17	0.136	R.AVAYLLTNAER.V
R2/RRR2-4/3	1819.195	1819.009	103.059	0.486	1144.847	0.475	28	0.117	K.LVDRPQNYTLAPESSK.Q
R2/RRR2-4/3	1818.961	1819.009	-26.367	0.505	968.555	0.521	27	0.114	K.LVDRPQNYTLAPESSK.Q
R2/RRR2-4/2	1057.999	1058.171	-162.548	0.312	735.843	0.345	15	0.112	R.ALSSPNVDVR.R
R2/RRR2-1/2	1201.954	1202.388	-361.783	0.298	445.406	0.347	13	0.109	R.HALSAISAIYR.L
R2/RRR2-3/2	1202.809	1202.388	351.528	0.235	461.609	0.408	12	0.106	R.HALSAISAIYR.L
R2/RRR2-3/2	1202.052	1202.388	-280.371	0.139	429.049	0.270	11	0.096	-.HALSAISAIYR.-
R2/RRR2-4/2	943.989	944.064	-79.716	0.179	840.444	0.120	11	0.096	R.EIIETNPK.L
R2/RRR2-4/3	1819.376	1819.009	202.579	0.472	817.727	0.461	25	0.094	K.LVDRPQNYTLAPESSK.Q
R2/RRR2-3/3	1820.089	1819.009	44.349	0.420	911.872	0.381	25	0.085	K.LVDRPQNYTLAPESSK.Q
R2/RRR2-3/2	1471.831	1471.596	159.751	0.486	2105.387	0.474	19	0.265	K.TALSNFEAALDYR.N
R2/RRR2-3/2	1471.334	1471.596	-179.129	0.423	2013.519	0.455	18	0.245	K.TALSNFEAALDYR.N
R2/RRR2-3/2	1385.086	1384.562	-344.534	0.475	1547.891	0.522	17	0.201	K.YIDNLTNIYVR.F
R2/RRR2-3/2	1264.173	1264.370	-155.796	0.403	1756.741	0.319	19	0.178	R.ADQSLFEAGVAR.E
R2/RRR2-3/2	1471.007	1471.596	-1083.913	0.425	1400.507	0.462	17	0.168	K.TALSNFEAALDYR.N
R2/RRR2-3/2	1264.071	1264.370	-236.685	0.408	1488.811	0.307	19	0.150	R.ADQSLFEAGVAR.E
R2/RRR2-3/2	1322.367	1323.479	-1601.289	0.329	1268.261	0.339	17	0.137	K.YVAEWEAVVTR.T
R2/RRR2-1/2	1472.929	1471.596	226.547	0.425	899.930	0.520	14	0.136	K.TALSNFEAALDYR.N
R2/RRR2-3/2	1174.181	1174.417	-202.042	0.420	1398.958	0.242	16	0.132	R.LYLINSPVVR.A
R2/RRR2-3/2	1264.291	1264.370	-62.135	0.450	1159.781	0.331	17	0.128	R.ADQSLFEAGVAR.E
R2/RRR2-3/2	1175.097	1174.417	-273.778	0.430	1197.620	0.282	15	0.125	R.LYLINSPVVR.A
R2/RRR2-3/2	1384.140	1384.562	-305.584	0.348	824.835	0.404	14	0.119	K.YIDNLTNIYVR.F
R2/RRR2-3/2	1105.814	1105.269	-412.613	0.254	207.002	0.530	11	0.108	R.QQVFDLGIGK.Y
R2/RRR2-2/2	1322.945	1323.479	-1162.928	0.278	626.365	0.175	13	0.100	K.YVAEWEAVVTR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1885.893	1885.107	-113.823	0.591	2757.611	0.531	34	0.435	K.IYQEYGITAENVIATAK.S
R2/RRR2-6/2	1885.425	1885.107	169.060	0.612	2607.784	0.618	26	0.410	K.IYQEYGITAENVIATAK.S
R2/RRR2-6/2	1884.291	1885.107	-966.580	0.561	2618.814	0.591	26	0.403	K.IYQEYGITAENVIATAK.S
R2/RRR2-6/2	1884.449	1885.107	-882.295	0.563	2554.118	0.598	26	0.391	K.IYQEYGITAENVIATAK.S
R2/RRR2-6/2	1403.289	1403.608	-228.560	0.543	2544.288	0.505	24	0.357	K.AIGIDKFGASAPAGK.I
R2/RRR2-2/2	1885.807	1885.107	-159.366	0.602	2415.224	0.578	25	0.352	K.IYQEYGITAENVIATAK.S
R2/RRR2-1/2	1884.099	1885.107	-1068.833	0.470	2336.500	0.500	26	0.313	K.IYQEYGITAENVIATAK.S
R2/RRR2-1/2	1884.395	1885.107	-911.364	0.510	2163.725	0.573	25	0.303	K.IYQEYGITAENVIATAK.S
R2/RRR2-6/2	1402.590	1403.608	-1443.533	0.503	2132.814	0.547	23	0.291	K.AIGIDKFGASAPAGK.I
R2/RRR2-4/2	1884.611	1885.107	-263.738	0.516	2108.909	0.551	25	0.286	K.IYQEYGITAENVIATAK.S
R2/RRR2-6/3	1886.474	1885.107	195.212	0.574	1995.750	0.566	32	0.268	K.IYQEYGITAENVIATAK.S
R2/RRR2-6/2	1402.650	1403.608	-1400.700	0.509	1969.729	0.550	23	0.265	K.AIGIDKFGASAPAGK.I
R2/RRR2-6/2	1376.184	1376.540	-259.663	0.526	1914.375	0.467	20	0.234	R.VSLEAGSTLGWQK.Y
R2/RRR2-6/2	1376.235	1376.540	-221.844	0.508	1696.128	0.450	19	0.200	R.VSLEAGSTLGWQK.Y
R2/RRR2-1/2	1376.213	1376.540	-238.217	0.422	1347.308	0.340	18	0.142	R.VSLEAGSTLGWQK.Y
R2/RRR2-1/2	1443.303	1442.640	-234.185	0.466	639.837	0.575	20	0.138	K.LAQLPGTSIEGVEK.G
R2/RRR2-5/2	1442.069	1442.640	-1092.419	0.448	623.197	0.518	20	0.131	K.LAQLPGTSIEGVEK.G
R2/RRR2-1/2	1442.551	1442.640	-61.332	0.444	504.393	0.497	19	0.126	K.LAQLPGTSIEGVEK.G
R2/RRR2-2/2	1442.375	1442.640	-184.253	0.409	544.243	0.502	19	0.126	K.LAQLPGTSIEGVEK.G
R2/RRR2-5/2	1442.309	1442.640	-229.932	0.444	479.933	0.511	18	0.126	K.LAQLPGTSIEGVEK.G
R2/RRR2-6/2	1442.318	1442.640	-223.649	0.395	642.294	0.450	20	0.124	K.LAQLPGTSIEGVEK.G
R2/RRR2-2/2	1443.114	1442.640	329.983	0.444	417.436	0.505	17	0.124	K.LAQLPGTSIEGVEK.G
R2/RRR2-6/2	1171.605	1172.314	-1463.005	0.400	625.124	0.438	17	0.122	K.ESVLPEAVTAR.V
R2/RRR2-6/2	1441.580	1442.640	-1432.687	0.341	659.462	0.455	20	0.122	K.LAQLPGTSIEGVEK.G
R2/RRR2-5/2	1442.282	1442.640	-248.442	0.413	341.713	0.491	16	0.121	K.LAQLPGTSIEGVEK.G
R2/RRR2-3/2	1442.146	1442.640	-343.553	0.404	368.200	0.468	16	0.119	K.LAQLPGTSIEGVEK.G
R2/RRR2-4/2	1442.157	1442.640	-335.654	0.400	311.028	0.417	15	0.116	K.LAQLPGTSIEGVEK.G
R2/RRR2-6/2	1172.011	1172.314	-259.038	0.335	488.736	0.450	16	0.115	-.ESVLPEAVTAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1442.926	1442.640	199.353	0.320	369.359	0.386	16	0.113	K.LAQLPGTSIEGVEK.G
R2/RRR2-6/2	1171.471	1172.314	-1577.930	0.343	466.092	0.425	15	0.113	-.ESVLPEAVTAR.-
R2/RRR2-5/2	1403.808	1403.608	142.286	0.392	541.354	0.427	15	0.112	K.AIGIDKFGASAPAGK.I
R2/RRR2-6/2	1441.478	1442.640	-1504.392	0.262	325.102	0.371	15	0.111	K.LAQLPGTSIEGVEK.G
R2/RRR2-1/2	1441.483	1442.640	-1500.564	0.245	399.170	0.324	17	0.110	K.LAQLPGTSIEGVEK.G
R2/RRR2-5/2	1403.534	1403.608	-53.266	0.327	360.724	0.332	14	0.088	-.AIGIDKFGASAPAGK.-
R2/RRR2-14/2	1618.421	1617.743	-199.843	0.599	2619.209	0.524	24	0.383	R.ELTAEVQQSGVTGAAR.V
R2/RRR2-14/2	1618.196	1617.743	280.586	0.570	2574.897	0.530	24	0.376	R.ELTAEVQQSGVTGAAR.V
R2/RRR2-14/2	1363.080	1363.455	-275.992	0.481	1744.977	0.536	20	0.230	K.VFGESSPEAQPSK.S
R2/RRR2-14/2	1363.130	1363.455	-239.156	0.519	1430.036	0.490	19	0.180	K.VFGESSPEAQPSK.S
R2/RRR2-14/2	1318.079	1318.416	-256.434	0.434	635.856	0.399	15	0.117	R.KVDDTVQELDR.H
R2/RRR2-14/2	1299.526	1299.495	23.873	0.315	1012.101	0.228	16	0.109	-.ACAVALGVPDVAR.-
R2/RRR2-14/3	1818.990	1819.012	-12.030	0.334	755.134	0.411	25	0.078	K.DHAGPLRPGVDAVESAVK.G
R2/RRR2-14/2	1687.344	1686.932	245.142	0.524	2506.524	0.492	26	0.347	R.LISEATAAAGTGLIELR.R
R2/RRR2-14/2	1686.495	1686.932	-259.728	0.413	2334.281	0.381	25	0.279	R.LISEATAAAGTGLIELR.R
R2/RRR2-14/2	1686.678	1686.932	-150.960	0.498	2030.381	0.453	24	0.247	R.LISEATAAAGTGLIELR.R
R2/RRR2-14/2	1220.131	1220.470	-278.424	0.496	1740.773	0.575	19	0.240	R.MLLGLNAAGFGR.-
R2/RRR2-14/2	1236.220	1236.469	-202.064	0.439	1730.270	0.537	20	0.228	R.M*LLGLNAAGFGR.-
R2/RRR2-14/2	1417.179	1417.509	-233.232	0.486	1420.761	0.595	21	0.201	R.SPNVAYVPAGDNGR.M
R2/RRR2-14/2	1417.215	1417.509	-207.740	0.418	989.004	0.542	20	0.149	R.SPNVAYVPAGDNGR.M
R2/RRR2-14/2	1218.933	1219.437	-1237.187	0.446	1610.323	0.239	16	0.147	K.DLQM*VNLTLR.L
R2/RRR2-14/2	1417.109	1417.509	-282.750	0.452	994.813	0.503	20	0.144	R.SPNVAYVPAGDNGR.M
R2/RRR2-14/2	1418.262	1417.509	-174.350	0.457	960.633	0.520	19	0.144	R.SPNVAYVPAGDNGR.M
R2/RRR2-14/2	1219.059	1219.437	-310.544	0.403	1172.660	0.296	15	0.126	K.DLQM*VNLTLR.L
R2/RRR2-14/2	1220.221	1219.437	-177.198	0.546	1214.380	0.265	16	0.122	K.DLQM*VNLTLR.L
R2/RRR2-14/2	872.881	872.989	-124.713	0.354	904.691	0.244	13	0.110	R.EIAAELAR.S
R2/RRR2-14/3	1686.588	1686.932	-204.623	0.409	1012.814	0.434	31	0.097	R.LISEATAAAGTGLIELR.R
R2/RRR2-16/2	1406.094	1405.487	-280.350	0.516	1524.366	0.527	18	0.200	R.FYCWDTAGQEK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1405.016	1405.487	-335.900	0.481	1503.254	0.508	18	0.192	R.FYCWDTAGQEK.F
R2/RRR2-16/2	1404.291	1405.487	-1568.555	0.332	1527.380	0.421	18	0.173	R.FYCWDTAGQEK.F
R2/RRR2-15/3	1763.068	1762.988	45.332	0.557	1467.312	0.558	30	0.170	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/2	1762.747	1762.988	-137.360	0.568	1264.169	0.519	19	0.167	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/3	1762.477	1762.988	-860.104	0.545	1306.697	0.607	28	0.167	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/2	1516.218	1516.752	-1014.931	0.535	1387.660	0.379	21	0.153	R.VCENIPIVLCGNK.V
R2/RRR2-16/2	1762.465	1762.988	-867.015	0.539	994.859	0.538	17	0.148	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/2	1515.658	1516.752	-1385.769	0.390	1328.013	0.332	21	0.141	R.VCENIPIVLCGNK.V
R2/RRR2-15/3	1762.210	1762.988	-1012.185	0.472	1210.652	0.549	28	0.140	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/2	1763.396	1762.988	231.653	0.532	929.247	0.491	17	0.136	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/3	1763.246	1762.988	146.673	0.464	1205.921	0.526	27	0.134	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/2	1216.089	1215.337	-204.846	0.454	961.811	0.361	16	0.126	K.NLQYYEVSAK.S
R2/RRR2-16/2	1515.442	1516.752	-1528.807	0.410	954.421	0.339	19	0.120	R.VCENIPIVLCGNK.V
R2/RRR2-16/2	1214.697	1215.337	-1354.053	0.394	920.523	0.338	15	0.120	K.NLQYYEVSAK.S
R2/RRR2-16/3	1762.939	1762.988	-27.900	0.487	969.211	0.528	25	0.116	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/2	1215.264	1215.337	-59.906	0.368	796.368	0.354	14	0.116	K.NLQYYEVSAK.S
R2/RRR2-16/3	1762.326	1762.988	-945.944	0.402	903.271	0.472	21	0.101	K.SNYNFEKPFLYLAR.K
R2/RRR2-17/3	1762.771	1762.988	-123.857	0.434	614.731	0.418	20	0.084	K.SNYNFEKPFLYLAR.K
R2/RRR2-16/3	1089.443	1089.226	199.767	0.463	1004.969	0.321	19	0.079	R.HLTGEFEKK.Y
R2/RRR2-11/3	1762.884	1762.988	-59.154	0.349	675.676	0.344	21	0.077	K.SNYNFEKPFLYLAR.K
R2/RRR2-13/2	1075.002	1074.255	-235.375	0.513	1734.798	0.552	17	0.208	R.TFLLSLVGSH.-
R2/RRR2-14/2	1116.278	1115.393	-103.278	0.575	1745.771	0.412	17	0.198	K.LLLAYVGIPR.Y
R2/RRR2-14/2	1190.078	1190.286	-175.269	0.422	1773.760	0.378	18	0.192	R.EALSGDTIDLR.A
R2/RRR2-14/2	1190.090	1190.286	-165.185	0.368	1580.622	0.381	17	0.171	R.EALSGDTIDLR.A
R2/RRR2-13/2	1189.952	1190.286	-281.164	0.373	1675.411	0.312	17	0.167	R.EALSGDTIDLR.A
R2/RRR2-14/2	1189.581	1190.286	-1436.985	0.311	1680.723	0.289	17	0.163	R.EALSGDTIDLR.A
R2/RRR2-14/2	1075.305	1074.255	47.183	0.538	1514.551	0.474	16	0.145	R.TFLLSLVGSH.-
R2/RRR2-13/2	1074.331	1074.255	71.045	0.440	1444.387	0.526	16	0.137	R.TFLLSLVGSH.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1189.898	1190.286	-326.554	0.346	1263.266	0.341	16	0.136	R.EALSGDTIDLR.A
R2/RRR2-13/2	1020.885	1021.152	-261.824	0.367	1030.929	0.373	13	0.129	R.ALIQQEYR.T
R2/RRR2-14/2	1021.029	1021.152	-120.767	0.494	939.659	0.350	13	0.125	R.ALIQQEYR.T
R2/RRR2-13/2	1021.056	1021.152	-94.384	0.421	952.265	0.343	12	0.123	R.ALIQQEYR.T
R2/RRR2-13/2	1189.508	1190.286	-1498.626	0.297	1073.269	0.313	16	0.121	R.EALSGDTIDLR.A
R2/RRR2-14/2	1115.176	1115.393	-195.495	0.400	902.466	0.340	15	0.120	K.LLLAYVGIPR.Y
R2/RRR2-14/2	1021.079	1021.152	-71.719	0.338	829.847	0.345	13	0.118	R.ALIQQEYR.T
R2/RRR2-14/2	1074.137	1074.255	-109.952	0.516	1386.341	0.501	17	0.117	R.TFLLSLVGSH.-
R2/RRR2-14/2	1114.546	1115.393	-1662.147	0.277	636.242	0.212	13	0.103	K.LLLAYVGIPR.Y
R2/RRR2-14/3	1436.604	1436.554	34.775	0.343	768.065	0.435	21	0.085	K.FGTYLEHDIGQR.T
R2/RRR2-13/3	1436.962	1436.554	284.566	0.311	631.271	0.384	19	0.076	K.FGTYLEHDIGQR.T
R2/RRR2-13/3	1436.556	1436.554	1.601	0.262	646.365	0.353	19	0.072	K.FGTYLEHDIGQR.T
R2/RRR2-14/2	1073.503	1074.255	-1636.734	0.373	1080.034	0.511	14	0.071	R.TFLLSLVGSH.-
R2/RRR2-13/2	1074.012	1074.255	-226.586	0.301	816.639	0.373	14	0.032	R.TFLLSLVGSH.-
R2/RRR2-15/2	1160.028	1160.303	-237.438	0.472	1668.532	0.497	19	0.208	K.AVDNSGTVVGIK.C
R2/RRR2-15/2	1160.103	1160.303	-173.043	0.479	1505.034	0.498	19	0.189	K.AVDNSGTVVGIK.C
R2/RRR2-16/2	1084.155	1084.248	-85.559	0.423	867.675	0.573	16	0.148	K.VPADLLEQAK.V
R2/RRR2-15/2	1083.660	1084.248	-1470.108	0.481	641.918	0.620	16	0.147	K.VPADLLEQAK.V
R2/RRR2-16/2	1085.042	1085.234	-178.131	0.442	1049.032	0.466	14	0.144	R.VFQVEYATK.A
R2/RRR2-16/2	1083.924	1084.248	-299.743	0.409	794.342	0.568	16	0.143	K.VPADLLEQAK.V
R2/RRR2-15/2	1084.182	1084.248	-61.164	0.434	828.878	0.523	16	0.140	K.VPADLLEQAK.V
R2/RRR2-15/2	1085.269	1085.234	32.084	0.488	1012.946	0.440	14	0.139	R.VFQVEYATK.A
R2/RRR2-15/2	1159.339	1160.303	-1698.889	0.365	1036.141	0.457	18	0.139	K.AVDNSGTVVGIK.C
R2/RRR2-15/2	1085.324	1085.234	82.509	0.452	1033.960	0.414	14	0.136	R.VFQVEYATK.A
R2/RRR2-15/2	1084.142	1084.248	-98.434	0.392	702.102	0.538	16	0.135	K.VPADLLEQAK.V
R2/RRR2-15/2	1145.124	1145.290	-144.942	0.437	868.018	0.389	15	0.124	K.IIYGVHDEAK.D
R2/RRR2-16/2	1083.623	1084.248	-1504.393	0.304	709.982	0.453	16	0.122	K.VPADLLEQAK.V
R2/RRR2-16/2	1084.511	1085.234	-1594.268	0.365	931.880	0.344	14	0.121	R.VFQVEYATK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1159.981	1160.303	-277.768	0.418	638.636	0.412	15	0.117	K.AVDNSGTVVGIK.C
R2/RRR2-16/2	1084.375	1085.234	-1720.137	0.352	950.890	0.273	14	0.115	R.VFQVEYATK.A
R2/RRR2-15/2	1350.014	1350.435	-312.788	0.373	1201.663	0.454	18	0.090	K.VAAQAALEEM*DAD.-
R2/RRR2-21/2	1965.366	1965.195	86.929	0.587	1879.958	0.623	28	0.270	R.IWVFSGDTDAVLPVTSTR.Y
R2/RRR2-22/2	1964.417	1965.195	-908.207	0.547	1882.481	0.544	28	0.248	R.IWVFSGDTDAVLPVTSTR.Y
R2/RRR2-22/2	1964.457	1965.195	-887.309	0.558	1749.427	0.608	27	0.245	R.IWVFSGDTDAVLPVTSTR.Y
R2/RRR2-21/2	1964.440	1965.195	-896.292	0.501	1716.428	0.626	27	0.245	R.IWVFSGDTDAVLPVTSTR.Y
R2/RRR2-20/2	1964.176	1965.195	-1030.931	0.545	1773.221	0.561	27	0.236	R.IWVFSGDTDAVLPVTSTR.Y
R2/RRR2-21/2	1965.107	1965.195	-44.835	0.570	1576.626	0.634	26	0.228	R.IWVFSGDTDAVLPVTSTR.Y
R2/RRR2-22/2	1964.386	1965.195	-923.928	0.532	1545.654	0.514	26	0.194	R.IWVFSGDTDAVLPVTSTR.Y
R2/RRR2-21/3	1298.252	1298.479	-175.482	0.511	1789.867	0.472	28	0.182	R.GAGHEVPLHRPK.Q
R2/RRR2-21/2	1536.221	1536.713	-321.398	0.570	801.450	0.545	20	0.145	K.HSTVYFNLAEVQK.A
R2/RRR2-21/2	905.848	906.064	-239.252	0.443	1164.936	0.418	12	0.144	K.GLNFVTVR.G
R2/RRR2-24/2	906.010	906.064	-59.881	0.377	1273.357	0.359	13	0.142	K.GLNFVTVR.G
R2/RRR2-24/2	905.847	906.064	-240.334	0.412	1218.977	0.371	12	0.140	-.GLNFVTVR.-
R2/RRR2-24/2	906.025	906.064	-42.718	0.439	1124.013	0.370	12	0.134	-.GLNFVTVR.-
R2/RRR2-21/2	905.398	906.064	-1845.356	0.399	1123.622	0.371	12	0.134	K.GLNFVTVR.G
R2/RRR2-21/2	905.857	906.064	-228.842	0.465	1037.046	0.387	12	0.132	K.GLNFVTVR.G
R2/RRR2-24/3	1298.221	1298.479	-199.111	0.488	1628.313	0.362	27	0.129	R.GAGHEVPLHRPK.Q
R2/RRR2-21/2	1091.972	1092.316	-316.034	0.388	680.883	0.451	14	0.122	K.ALHVSPIINK.S
R2/RRR2-21/3	1298.414	1298.479	-49.857	0.513	1340.386	0.434	26	0.121	R.GAGHEVPLHRPK.Q
R2/RRR2-22/2	905.834	906.064	-254.259	0.412	872.957	0.311	12	0.117	K.GLNFVTVR.G
R2/RRR2-24/3	1299.328	1298.479	-116.584	0.457	1390.436	0.395	25	0.117	R.GAGHEVPLHRPK.Q
R2/RRR2-22/3	1298.064	1298.479	-320.245	0.500	1295.408	0.428	24	0.117	R.GAGHEVPLHRPK.Q
R2/RRR2-22/2	905.501	906.064	-1731.432	0.328	451.105	0.284	12	0.112	-.GLNFVTVR.-
R2/RRR2-21/2	1092.058	1092.316	-237.641	0.275	686.893	0.367	14	0.111	K.ALHVSPIINK.S
R2/RRR2-23/3	1298.447	1298.479	-24.820	0.489	1036.999	0.392	23	0.094	R.GAGHEVPLHRPK.Q
R2/RRR2-20/3	1297.981	1298.479	-384.928	0.449	871.991	0.417	21	0.092	R.GAGHEVPLHRPK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/3	1298.230	1298.479	-191.895	0.506	930.691	0.394	22	0.090	R.GAGHEVPLHRPK.Q
R2/RRR2-22/3	1297.968	1298.479	-1167.300	0.444	1129.278	0.337	24	0.089	R.GAGHEVPLHRPK.Q
R2/RRR2-22/3	1297.878	1298.479	-1236.859	0.481	837.651	0.391	22	0.088	R.GAGHEVPLHRPK.Q
R2/RRR2-23/3	1298.265	1298.479	-165.154	0.416	697.702	0.266	20	0.068	-.GAGHEVPLHRPK.-
R2/RRR2-13/2	1901.580	1902.181	-844.214	0.585	2708.824	0.588	25	0.427	K.NPINYTQIAVLADDILK.N
R2/RRR2-13/2	1901.628	1902.181	-818.953	0.570	2678.014	0.591	25	0.422	K.NPINYTQIAVLADDILK.N
R2/RRR2-13/2	1901.487	1902.181	-893.127	0.560	2525.376	0.599	25	0.390	K.NPINYTQIAVLADDILK.N
R2/RRR2-13/2	1613.247	1612.674	-264.994	0.591	2512.920	0.590	24	0.384	K.VGDLDSYEIEGGETK.S
R2/RRR2-13/2	1613.202	1612.674	-293.538	0.576	2469.100	0.574	24	0.368	K.VGDLDSYEIEGGETK.S
R2/RRR2-13/2	1612.138	1612.674	-955.380	0.543	2429.536	0.563	24	0.356	K.VGDLDSYEIEGGETK.S
R2/RRR2-13/3	1902.877	1902.181	-160.228	0.458	2214.344	0.443	35	0.258	K.NPINYTQIAVLADDILK.N
R2/RRR2-13/3	1902.581	1902.181	210.838	0.480	2102.148	0.410	34	0.223	K.NPINYTQIAVLADDILK.N
R2/RRR2-13/2	1192.995	1193.326	-278.599	0.492	1189.075	0.509	19	0.162	K.GLCGGINSTSVK.V
R2/RRR2-13/2	1193.163	1193.326	-137.054	0.481	1170.163	0.455	19	0.151	K.GLCGGINSTSVK.V
R2/RRR2-13/2	1753.270	1753.910	-938.610	0.539	914.640	0.483	19	0.135	R.DSKDNIEM*TVSELQK.N
R2/RRR2-13/2	1192.168	1193.326	-1815.915	0.379	860.024	0.467	18	0.131	K.GLCGGINSTSVK.V
R2/RRR2-13/2	1060.100	1060.226	-119.839	0.325	1046.681	0.373	15	0.127	K.NVIVAITSDK.G
R2/RRR2-13/2	1059.536	1060.226	-1599.838	0.297	885.892	0.441	15	0.125	K.NVIVAITSDK.G
R2/RRR2-13/2	1059.854	1060.226	-351.951	0.339	798.266	0.414	15	0.122	K.NVIVAITSDK.G
R2/RRR2-13/2	1755.498	1753.910	-235.579	0.431	604.900	0.463	16	0.117	R.DSKDNIEM*TVSELQK.N
R2/RRR2-13/3	1902.194	1902.181	6.873	0.265	868.689	0.259	25	0.068	-.NPINYTQIAVLADDILK.-
R2/RRR2-12/2	1204.313	1204.404	-75.294	0.567	1853.516	0.441	18	0.217	R.VVSNFVAQALR.K
R2/RRR2-12/2	1203.690	1204.404	-1428.178	0.477	1672.375	0.416	18	0.189	R.VVSNFVAQALR.K
R2/RRR2-11/2	1205.235	1204.404	-140.049	0.435	1664.100	0.318	18	0.168	R.VVSNFVAQALR.K
R2/RRR2-12/2	1204.158	1204.404	-204.537	0.405	1622.215	0.316	17	0.163	R.VVSNFVAQALR.K
R2/RRR2-12/2	1171.099	1171.370	-232.057	0.437	1502.734	0.332	16	0.156	R.AKELLGWEPK.I
R2/RRR2-12/2	1228.122	1228.337	-175.921	0.409	1201.984	0.424	18	0.147	K.VVQDTIDPNAR.I
R2/RRR2-12/2	1228.011	1228.337	-266.069	0.482	1101.916	0.456	16	0.145	K.VVQDTIDPNAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1227.984	1228.337	-288.409	0.373	862.940	0.462	16	0.130	-.VVQDTIDPNAR.-
R2/RRR2-12/2	1171.737	1171.370	313.620	0.465	1084.588	0.332	14	0.125	R.AKELLGWEPK.I
R2/RRR2-12/2	1170.804	1171.370	-1341.548	0.505	900.674	0.302	13	0.111	R.AKELLGWEPK.I
R2/RRR2-12/3	1354.096	1354.471	-277.833	0.438	791.053	0.486	23	0.095	R.TAETLTM*DYHR.G
R2/RRR2-11/2	1204.995	1204.404	-339.837	0.401	856.179	0.140	14	0.094	-.VVSNFVAQALR.-
R2/RRR2-12/3	1354.371	1354.471	-74.374	0.428	583.716	0.421	20	0.084	R.TAETLTM*DYHR.G
R2/RRR2-12/3	1354.248	1354.471	-165.649	0.375	590.594	0.354	20	0.077	R.TAETLTM*DYHR.G
R2/RRR2-16/1	1015.574	1016.174	-1579.804	0.305	832.258	0.405	16	0.657	K.LVLVGDGGTGK.T
R2/RRR2-16/1	1015.686	1016.174	-481.339	0.259	662.957	0.413	15	0.481	K.LVLVGDGGTGK.T
R2/RRR2-16/1	1015.667	1016.174	-1487.561	0.276	689.796	0.325	14	0.481	K.LVLVGDGGTGK.T
R2/RRR2-16/2	1015.948	1016.174	-222.483	0.425	1225.851	0.363	18	0.139	K.LVLVGDGGTGK.T
R2/RRR2-16/2	1015.957	1016.174	-214.045	0.397	1028.568	0.325	19	0.125	K.LVLVGDGGTGK.T
R2/RRR2-16/2	1770.966	1771.998	-1150.871	0.391	620.503	0.422	15	0.112	K.SNYNFEKPFLWLGR.K
R2/RRR2-17/2	1016.043	1016.174	-128.952	0.353	630.387	0.318	14	0.111	K.LVLVGDGGTGK.T
R2/RRR2-16/2	1215.120	1215.337	-179.214	0.316	796.741	0.297	14	0.110	K.NLQYYDISAK.S
R2/RRR2-16/2	1015.887	1016.174	-283.240	0.393	776.631	0.227	17	0.109	K.LVLVGDGGTGK.T
R2/RRR2-18/2	1015.915	1016.174	-255.392	0.360	859.835	0.225	16	0.108	-.LVLVGDGGTGK.-
R2/RRR2-17/2	1015.769	1016.174	-398.987	0.296	486.740	0.274	13	0.108	K.LVLVGDGGTGK.T
R2/RRR2-15/2	1015.899	1016.174	-270.581	0.327	579.522	0.282	13	0.107	K.LVLVGDGGTGK.T
R2/RRR2-16/2	1214.450	1215.337	-1558.381	0.276	600.301	0.297	13	0.106	K.NLQYYDISAK.S
R2/RRR2-16/2	1016.942	1016.174	-228.286	0.396	944.600	0.191	16	0.106	K.LVLVGDGGTGK.T
R2/RRR2-16/2	1214.508	1215.337	-1510.118	0.270	862.028	0.183	14	0.103	K.NLQYYDISAK.S
R2/RRR2-8/2	1788.842	1789.021	-100.450	0.571	3351.476	0.580	26	0.602	R.FDYILTQQAFVTVDK.N
R2/RRR2-8/2	1789.659	1789.021	-202.682	0.575	3249.152	0.600	26	0.581	R.FDYILTQQAFVTVDK.N
R2/RRR2-8/2	1980.632	1981.204	-796.239	0.511	1895.235	0.576	25	0.264	K.QIGVIGWGSQGPAQAQNLR.D
R2/RRR2-8/2	1359.512	1359.512	-0.595	0.415	742.971	0.436	16	0.123	K.VSLAGHDEYIVR.G
R2/RRR2-8/2	1359.170	1359.512	-252.915	0.375	655.791	0.440	14	0.117	K.VSLAGHDEYIVR.G
R2/RRR2-8/2	1087.078	1087.288	-194.016	0.313	885.200	0.348	14	0.116	-.NISVVAVCPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1358.580	1359.512	-1426.489	0.293	574.151	0.192	14	0.101	K.VSLAGHDEYIVR.G
R2/RRR2-8/3	1616.668	1616.800	-81.961	0.407	817.727	0.500	22	0.097	K.EKVSLAGHDEYIVR.G
R2/RRR2-12/2	1603.286	1603.887	-1001.816	0.550	2481.621	0.599	24	0.381	K.HIVQDLKPEIPVSK.N
R2/RRR2-12/2	1603.420	1603.887	-292.275	0.548	2028.482	0.617	22	0.297	K.HIVQDLKPEIPVSK.N
R2/RRR2-12/2	1604.180	1603.887	182.977	0.563	2037.099	0.606	23	0.296	K.HIVQDLKPEIPVSK.N
R2/RRR2-12/2	1456.005	1456.618	-1111.731	0.487	2231.668	0.449	20	0.285	R.YWLCAATQDSIK.I
R2/RRR2-12/2	1249.173	1249.398	-180.602	0.536	2077.843	0.457	19	0.257	R.LWDLSTGVTTR.R
R2/RRR2-12/2	1249.313	1249.398	-67.976	0.506	1617.775	0.468	19	0.197	R.LWDLSTGVTTR.R
R2/RRR2-12/2	1249.053	1249.398	-276.682	0.499	1494.119	0.509	18	0.192	R.LWDLSTGVTTR.R
R2/RRR2-12/2	1939.436	1940.104	-862.962	0.489	1170.473	0.554	23	0.165	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-12/2	1939.651	1940.104	-234.288	0.504	1099.581	0.529	24	0.155	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-13/2	1939.554	1940.104	-801.677	0.443	1148.131	0.513	23	0.155	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-12/2	1940.460	1940.104	183.888	0.513	1096.985	0.492	23	0.148	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-12/2	1573.480	1573.775	-188.276	0.513	1011.164	0.521	18	0.147	K.DGVTLLWDLAEGKR.L
R2/RRR2-12/2	1572.996	1573.775	-1134.359	0.494	1109.436	0.457	19	0.144	K.DGVTLLWDLAEGKR.L
R2/RRR2-12/2	1573.332	1573.775	-282.300	0.459	1033.280	0.489	19	0.144	K.DGVTLLWDLAEGKR.L
R2/RRR2-13/2	1939.351	1940.104	-906.940	0.451	818.641	0.544	21	0.137	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-10/2	1574.798	1573.775	14.802	0.406	1128.156	0.412	17	0.136	K.DGVTLLWDLAEGKR.L
R2/RRR2-11/2	1940.098	1940.104	-3.131	0.448	744.572	0.550	19	0.133	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-13/2	1939.618	1940.104	-251.462	0.429	501.193	0.477	17	0.116	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-1/2	1941.488	1940.104	198.295	0.384	482.643	0.386	16	0.108	R.FSPNTFQPTIVSGSWDR.T
R2/RRR2-12/3	1573.946	1573.775	108.849	0.326	992.187	0.373	29	0.083	K.DGVTLLWDLAEGKR.L
R2/RRR2-12/3	1574.166	1573.775	248.952	0.384	911.905	0.338	28	0.078	K.DGVTLLWDLAEGKR.L
R2/RRR2-13/2	1108.772	1108.293	433.615	0.420	1314.542	0.369	16	0.146	K.M*EGLLWGASK.L
R2/RRR2-14/2	1272.312	1272.480	-131.896	0.510	992.780	0.470	17	0.144	R.WFTHIDALLR.L
R2/RRR2-14/2	1108.249	1108.293	-39.687	0.460	1152.288	0.425	15	0.143	K.M*EGLLWGASK.L
R2/RRR2-14/2	1146.076	1146.276	-175.268	0.457	1128.146	0.417	20	0.142	R.LSGVTADGQGIK.V
R2/RRR2-14/2	1145.863	1146.276	-361.863	0.439	1107.965	0.430	19	0.142	R.LSGVTADGQGIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1150.470	1151.338	-1628.018	0.487	1070.948	0.422	15	0.141	K.KLDEYLLTR.S
R2/RRR2-14/2	1107.925	1108.293	-333.434	0.408	1121.121	0.418	14	0.139	K.M*EGLLWGASK.L
R2/RRR2-14/2	1145.931	1146.276	-301.901	0.482	1028.014	0.431	19	0.138	R.LSGVTADGQGIK.V
R2/RRR2-14/2	1746.213	1745.866	199.015	0.490	545.876	0.576	22	0.131	K.VESTAVPSASTPDVADAK.A
R2/RRR2-14/2	1745.320	1745.866	-888.650	0.440	612.986	0.548	23	0.130	K.VESTAVPSASTPDVADAK.A
R2/RRR2-14/2	1272.201	1272.480	-219.967	0.421	761.115	0.443	16	0.128	R.WFTHIDALLR.L
R2/RRR2-13/2	1151.109	1151.338	-198.859	0.441	907.848	0.397	14	0.128	K.KLDEYLLTR.S
R2/RRR2-14/2	1108.209	1108.293	-76.258	0.430	920.078	0.392	14	0.126	K.M*EGLLWGASK.L
R2/RRR2-14/2	1745.248	1745.866	-929.867	0.462	494.181	0.534	21	0.124	K.VESTAVPSASTPDVADAK.A
R2/RRR2-14/2	1150.661	1151.338	-1461.010	0.461	893.806	0.357	14	0.123	K.KLDEYLLTR.S
R2/RRR2-13/2	1745.189	1745.866	-963.924	0.436	436.706	0.517	19	0.119	K.VESTAVPSASTPDVADAK.A
R2/RRR2-13/2	1108.793	1108.293	-452.098	0.337	867.377	0.331	14	0.116	K.M*EGLLWGASK.L
R2/RRR2-13/2	1109.042	1108.293	-227.005	0.322	778.495	0.359	12	0.114	K.M*EGLLWGASK.L
R2/RRR2-14/2	1271.321	1272.480	-1702.661	0.315	434.690	0.413	12	0.112	R.WFTHIDALLR.L
R2/RRR2-14/2	1092.146	1092.294	-135.941	0.217	644.142	0.360	14	0.109	K.MEGLLWGASK.L
R2/RRR2-13/2	1273.696	1272.480	170.567	0.246	391.366	0.441	11	0.108	R.WFTHIDALLR.L
R2/RRR2-14/3	1272.499	1272.480	15.229	0.386	911.158	0.403	19	0.087	R.WFTHIDALLR.L
R2/RRR2-14/3	1272.263	1272.480	-170.839	0.365	1047.668	0.350	20	0.084	R.WFTHIDALLR.L
R2/RRR2-14/3	1272.405	1272.480	-59.103	0.363	1091.750	0.332	20	0.083	R.WFTHIDALLR.L
R2/RRR2-15/2	1372.905	1373.579	-1222.631	0.501	1779.315	0.491	19	0.222	R.DIYEHAVVLSVK.I
R2/RRR2-15/2	1192.177	1192.390	-178.658	0.439	1619.884	0.478	17	0.199	K.LVEVTQLFSR.F
R2/RRR2-15/2	1192.267	1192.390	-103.063	0.566	1513.037	0.481	17	0.188	K.LVEVTQLFSR.F
R2/RRR2-15/2	1191.634	1192.390	-1477.458	0.444	1554.611	0.449	17	0.185	K.LVEVTQLFSR.F
R2/RRR2-15/2	1832.508	1833.078	-859.264	0.508	1258.051	0.528	24	0.171	K.EIPSLQVINQTLSYAR.E
R2/RRR2-15/2	1373.282	1373.579	-217.060	0.410	1492.984	0.418	18	0.170	R.DIYEHAVVLSVK.I
R2/RRR2-15/2	1667.607	1668.820	-1331.232	0.341	1690.949	0.254	22	0.160	R.NDFDTCVDLLSQLK.V
R2/RRR2-15/2	1832.416	1833.078	-909.888	0.465	1184.536	0.494	23	0.157	K.EIPSLQVINQTLSYAR.E
R2/RRR2-15/2	1831.907	1833.078	-1188.912	0.379	1179.736	0.488	23	0.153	K.EIPSLQVINQTLSYAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1373.180	1373.579	-291.617	0.440	1099.456	0.489	17	0.149	R.DIYEHAVVLSVK.I
R2/RRR2-15/2	1123.058	1123.155	-86.084	0.527	791.481	0.342	15	0.120	K.IEDQDAFER.D
R2/RRR2-15/2	1122.828	1123.155	-291.647	0.480	818.107	0.311	15	0.117	K.IEDQDAFER.D
R2/RRR2-15/2	1122.508	1123.155	-1471.367	0.464	859.990	0.249	15	0.112	K.IEDQDAFER.D
R2/RRR2-20/1	1255.770	1254.544	180.276	0.338	705.679	0.350	14	0.532	K.VSVVPSAAALVIK.A
R2/RRR2-20/3	1344.636	1344.496	104.284	0.471	2877.779	0.392	34	0.390	R.VTGGEVGAASSLAPK.I
R2/RRR2-19/3	1639.618	1639.792	-106.427	0.521	2328.072	0.412	32	0.261	K.HSGNISLDDVIEIAR.I
R2/RRR2-20/2	1344.184	1344.496	-232.507	0.495	1880.069	0.478	22	0.230	R.VTGGEVGAASSLAPK.I
R2/RRR2-20/3	1254.644	1254.544	80.097	0.451	2133.494	0.423	29	0.229	K.VSVVPSAAALVIK.A
R2/RRR2-20/2	1344.199	1344.496	-221.392	0.451	1632.297	0.488	21	0.199	R.VTGGEVGAASSLAPK.I
R2/RRR2-20/2	1344.247	1344.496	-185.498	0.470	1742.250	0.427	21	0.198	R.VTGGEVGAASSLAPK.I
R2/RRR2-19/2	1344.099	1344.496	-296.286	0.438	1585.119	0.495	20	0.194	R.VTGGEVGAASSLAPK.I
R2/RRR2-20/3	1639.246	1639.792	-945.751	0.502	1975.792	0.395	30	0.192	K.HSGNISLDDVIEIAR.I
R2/RRR2-19/2	1344.119	1344.496	-281.434	0.458	1617.389	0.457	21	0.190	R.VTGGEVGAASSLAPK.I
R2/RRR2-19/2	1344.154	1344.496	-255.102	0.439	1476.402	0.475	20	0.178	R.VTGGEVGAASSLAPK.I
R2/RRR2-20/2	1639.384	1639.792	-249.417	0.586	1106.189	0.599	22	0.171	K.HSGNISLDDVIEIAR.I
R2/RRR2-20/2	1640.283	1639.792	300.619	0.634	1031.857	0.612	23	0.169	K.HSGNISLDDVIEIAR.I
R2/RRR2-19/3	1639.324	1639.792	-286.143	0.518	1897.065	0.363	29	0.169	K.HSGNISLDDVIEIAR.I
R2/RRR2-19/2	1638.687	1639.792	-1288.602	0.516	1029.839	0.588	21	0.161	K.HSGNISLDDVIEIAR.I
R2/RRR2-20/2	1639.372	1639.792	-256.738	0.562	960.454	0.598	22	0.160	K.HSGNISLDDVIEIAR.I
R2/RRR2-20/3	1254.291	1254.544	-202.034	0.443	1609.122	0.458	27	0.160	K.VSVVPSAAALVIK.A
R2/RRR2-19/2	1255.196	1254.544	-278.352	0.513	962.114	0.549	22	0.154	K.VSVVPSAAALVIK.A
R2/RRR2-20/2	1254.501	1254.544	-34.609	0.490	1044.255	0.525	21	0.154	K.VSVVPSAAALVIK.A
R2/RRR2-20/2	1255.491	1254.544	-42.579	0.505	877.745	0.577	22	0.153	K.VSVVPSAAALVIK.A
R2/RRR2-20/3	1254.286	1254.544	-205.988	0.441	1488.838	0.477	25	0.152	K.VSVVPSAAALVIK.A
R2/RRR2-19/2	1639.337	1639.792	-278.253	0.553	826.012	0.604	21	0.152	K.HSGNISLDDVIEIAR.I
R2/RRR2-19/2	1640.261	1639.792	287.037	0.571	816.399	0.577	21	0.147	K.HSGNISLDDVIEIAR.I
R2/RRR2-19/2	1254.229	1254.544	-251.916	0.498	779.847	0.565	21	0.146	K.VSVVPSAAALVIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1254.225	1254.544	-255.432	0.468	881.762	0.517	22	0.144	K.VSVVPSAAALVIK.A
R2/RRR2-19/3	1640.558	1639.792	-142.898	0.503	1534.476	0.391	26	0.133	K.HSGNISLDDVIEIAR.I
R2/RRR2-19/2	1253.647	1254.544	-1517.763	0.305	584.853	0.462	18	0.118	K.VSVVPSAAALVIK.A
R2/RRR2-20/2	1254.220	1254.544	-258.752	0.257	539.291	0.343	14	0.106	K.VSVVPSAAALVIK.A
R2/RRR2-20/3	1638.609	1639.792	-1336.044	0.428	1243.164	0.298	26	0.088	K.HSGNISLDDVIEIAR.I
R2/RRR2-20/3	1640.021	1639.792	140.187	0.505	963.508	0.388	23	0.088	-.HSGNISLDDVIEIAR.-
R2/RRR2-20/3	1344.506	1344.496	7.447	0.384	1112.524	0.313	27	0.083	R.VTGGEVGAASSLAPK.I
R2/RRR2-20/2	1732.205	1731.793	238.652	0.383	1119.105	0.263	22	0.066	K.DLQEEISDGEVEIPSA.-
R2/RRR2-20/2	1732.085	1731.793	168.758	0.337	1006.838	0.253	21	0.051	K.DLQEEISDGEVEIPSA.-
R2/RRR2-19/2	1732.425	1731.793	-213.194	0.373	998.103	0.265	21	0.050	K.DLQEEISDGEVEIPSA.-
R2/RRR2-19/2	1733.221	1731.793	247.483	0.427	713.435	0.275	18	0.020	K.DLQEEISDGEVEIPSA.-
R2/RRR2-4/2	1761.610	1762.000	-221.964	0.546	3925.421	0.586	27	0.791	R.FLVLNAAELAVDGSSVR.F
R2/RRR2-4/2	1761.469	1762.000	-871.814	0.540	3824.487	0.581	26	0.753	R.FLVLNAAELAVDGSSVR.F
R2/RRR2-4/2	1755.712	1754.916	-116.572	0.622	2224.771	0.560	24	0.314	R.ETALLYDELLSSASNK.Q
R2/RRR2-4/2	1760.890	1762.000	-1201.887	0.392	1883.578	0.472	23	0.229	R.FLVLNAAELAVDGSSVR.F
R2/RRR2-8/2	1763.349	1762.000	198.261	0.495	1517.866	0.561	20	0.200	R.FLVLNAAELAVDGSSVR.F
R2/RRR2-4/2	1753.609	1754.916	-1319.496	0.386	1526.536	0.454	21	0.180	R.ETALLYDELLSSASNK.Q
R2/RRR2-4/2	1156.107	1156.269	-141.129	0.418	1133.209	0.413	15	0.139	K.AAEVSEFFAGK.T
R2/RRR2-4/2	1213.075	1213.324	-205.960	0.446	939.564	0.358	15	0.123	K.LNVDQTGFYR.V
R2/RRR2-4/2	1213.110	1213.324	-177.089	0.453	1026.963	0.302	15	0.120	K.LNVDQTGFYR.V
R2/RRR2-4/2	1213.045	1213.324	-230.795	0.379	961.636	0.286	16	0.116	K.LNVDQTGFYR.V
R2/RRR2-4/3	1451.354	1451.603	-172.493	0.447	1137.321	0.219	24	0.070	-.VKYDDELAAGLEK.-
R2/RRR2-5/3	1451.602	1451.603	-1.031	0.433	1191.799	0.183	24	0.068	-.VKYDDELAAGLEK.-
R2/RRR2-5/3	1452.081	1451.603	330.086	0.408	1050.740	0.178	22	0.064	-.VKYDDELAAGLEK.-
R2/RRR2-4/3	1451.543	1451.603	-41.392	0.465	1050.610	0.123	22	0.055	-.VKYDDELAAGLEK.-
R2/RRR2-4/3	1451.662	1451.603	40.213	0.425	1019.211	0.116	22	0.055	-.VKYDDELAAGLEK.-
R2/RRR2-17/2	1226.275	1226.449	-142.838	0.512	1449.374	0.523	17	0.189	K.LLANILYSYR.G
R2/RRR2-17/2	1227.187	1226.449	-214.167	0.545	1364.309	0.493	17	0.175	K.LLANILYSYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1225.598	1226.449	-1515.136	0.452	1405.660	0.480	17	0.175	K.LLANILYSYR.G
R2/RRR2-17/2	1333.110	1333.429	-239.949	0.507	1414.124	0.449	18	0.169	K.LSGDDVGELHYK.Y
R2/RRR2-17/2	1334.074	1333.429	-266.299	0.533	1307.633	0.475	18	0.165	K.LSGDDVGELHYK.Y
R2/RRR2-17/2	1332.991	1333.429	-329.617	0.482	1217.906	0.478	18	0.158	K.LSGDDVGELHYK.Y
R2/RRR2-16/2	1226.236	1226.449	-174.295	0.417	1169.289	0.503	16	0.157	K.LLANILYSYR.G
R2/RRR2-17/2	1495.286	1494.695	-274.414	0.522	963.863	0.519	21	0.149	R.YVM*PVEEAAELAR.R
R2/RRR2-17/2	1478.317	1478.696	-257.129	0.396	1018.377	0.486	21	0.143	R.YVMPVEEAAELAR.R
R2/RRR2-17/2	1494.215	1494.695	-322.054	0.486	970.165	0.484	21	0.143	R.YVM*PVEEAAELAR.R
R2/RRR2-17/2	1373.107	1373.518	-300.331	0.463	979.164	0.480	20	0.142	R.ASM*GGYISSQTVR.K
R2/RRR2-17/2	1494.323	1494.695	-249.683	0.506	892.354	0.501	20	0.141	R.YVM*PVEEAAELAR.R
R2/RRR2-17/2	1373.033	1373.518	-354.207	0.461	909.010	0.496	19	0.139	R.ASM*GGYISSQTVR.K
R2/RRR2-17/2	1478.311	1478.696	-260.940	0.471	912.583	0.464	20	0.136	R.YVMPVEEAAELAR.R
R2/RRR2-17/2	1373.084	1373.518	-316.743	0.488	853.564	0.497	18	0.136	R.ASM*GGYISSQTVR.K
R2/RRR2-17/2	1478.301	1478.696	-267.567	0.390	932.939	0.451	20	0.134	R.YVMPVEEAAELAR.R
R2/RRR2-16/2	970.151	970.107	46.366	0.388	951.706	0.395	13	0.129	R.AIYQATFR.D
R2/RRR2-17/2	1226.318	1226.449	-107.090	0.466	915.729	0.396	14	0.126	K.LLANILYSYR.G
R2/RRR2-16/2	970.832	970.107	-283.836	0.309	813.181	0.398	12	0.120	R.AIYQATFR.D
R2/RRR2-19/2	1226.347	1226.449	-83.626	0.347	625.277	0.429	14	0.119	K.LLANILYSYR.G
R2/RRR2-16/2	969.963	970.107	-148.774	0.355	638.399	0.356	12	0.115	R.AIYQATFR.D
R2/RRR2-16/2	1226.108	1226.449	-279.064	0.209	323.296	0.373	10	0.106	K.LLANILYSYR.G
R2/RRR2-17/2	1357.626	1357.518	79.488	0.294	128.356	0.457	13	0.094	-.ASMGGYISSQTVR.-
R2/RRR2-11/2	1823.356	1824.159	-992.235	0.508	1818.632	0.604	26	0.257	K.TQKPVVAFIAGLTAPPGR.R
R2/RRR2-11/2	1824.305	1824.159	79.959	0.566	1741.356	0.597	26	0.244	K.TQKPVVAFIAGLTAPPGR.R
R2/RRR2-11/2	1823.694	1824.159	-255.965	0.569	1687.011	0.615	25	0.240	K.TQKPVVAFIAGLTAPPGR.R
R2/RRR2-11/2	1187.040	1187.325	-240.389	0.477	1181.961	0.519	19	0.163	R.EAGVTVVESPAK.I
R2/RRR2-11/2	1186.450	1187.325	-1584.942	0.331	1147.081	0.540	19	0.157	R.EAGVTVVESPAK.I
R2/RRR2-11/2	1084.731	1085.263	-1416.509	0.330	1077.131	0.481	18	0.143	R.MGHAGAIVSGGK.G
R2/RRR2-11/2	1084.826	1085.263	-403.215	0.405	902.753	0.495	17	0.137	R.MGHAGAIVSGGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1172.277	1173.406	-1822.287	0.405	634.007	0.496	16	0.129	K.IGSTMFEIFK.Q
R2/RRR2-12/2	1187.059	1187.325	-224.708	0.384	799.767	0.468	17	0.128	R.EAGVTVVESPAK.I
R2/RRR2-11/2	1186.654	1187.325	-1412.569	0.294	953.347	0.413	17	0.126	R.EAGVTVVESPAK.I
R2/RRR2-12/2	1186.924	1187.325	-338.822	0.297	876.907	0.423	17	0.123	R.EAGVTVVESPAK.I
R2/RRR2-11/3	1955.271	1955.204	34.583	0.458	1129.391	0.470	27	0.115	K.KGGTEHLGLPVFNSVAEAK.A
R2/RRR2-11/2	1173.115	1173.406	-249.609	0.266	389.785	0.418	13	0.112	K.IGSTMFEIFK.Q
R2/RRR2-11/2	1188.786	1189.406	-1366.518	0.261	334.896	0.449	12	0.111	K.IGSTM*FEIFK.Q
R2/RRR2-11/2	1173.064	1173.406	-293.144	0.214	436.491	0.364	13	0.107	K.IGSTMFEIFK.Q
R2/RRR2-11/2	1188.573	1189.406	-1546.827	0.312	195.013	0.321	10	0.105	-.IGSTM*FEIFK.-
R2/RRR2-17/2	1102.072	1101.262	-172.982	0.286	515.284	0.126	12	0.077	-.M*GHAGAIVSGGK.-
R2/RRR2-7/2	1431.428	1431.617	-132.716	0.365	966.993	0.446	16	0.132	R.GYISPYFITNQK.N
R2/RRR2-11/2	1439.285	1439.619	-232.772	0.503	2196.876	0.541	21	0.300	R.GGDLVSAFAELM*GR.Q
R2/RRR2-11/2	1424.192	1423.620	-301.374	0.541	2071.878	0.590	21	0.293	R.GGDLVSAFAELMGR.Q
R2/RRR2-11/2	1423.166	1423.620	-319.916	0.478	2050.491	0.542	21	0.275	R.GGDLVSAFAELMGR.Q
R2/RRR2-11/2	1439.262	1439.619	-249.364	0.498	2006.384	0.505	21	0.257	R.GGDLVSAFAELM*GR.Q
R2/RRR2-11/2	1438.895	1439.619	-1202.188	0.409	1738.729	0.468	20	0.208	R.GGDLVSAFAELM*GR.Q
R2/RRR2-11/3	1595.793	1595.678	72.565	0.462	1669.160	0.475	29	0.173	R.YHGHSMSDPGSTYR.T
R2/RRR2-11/2	1270.172	1270.376	-161.036	0.425	1154.214	0.424	18	0.143	K.GFGVESFGADRK.E
R2/RRR2-11/2	1005.085	1005.152	-67.317	0.427	1079.040	0.378	15	0.134	K.RGDYVPGLK.V
R2/RRR2-11/3	1595.479	1595.678	-125.294	0.444	1455.633	0.419	29	0.130	R.YHGHSMSDPGSTYR.T
R2/RRR2-11/2	1270.151	1270.376	-177.426	0.410	1045.851	0.384	17	0.130	K.GFGVESFGADRK.E
R2/RRR2-11/2	1004.409	1005.152	-1741.403	0.433	1084.709	0.345	15	0.130	K.RGDYVPGLK.V
R2/RRR2-11/2	1958.356	1958.178	90.866	0.482	771.609	0.497	20	0.128	K.ESPMPDTSELFTNVYVK.G
R2/RRR2-11/2	1269.992	1270.376	-302.778	0.381	1000.205	0.382	17	0.127	K.GFGVESFGADRK.E
R2/RRR2-11/3	1595.324	1595.678	-222.699	0.469	1326.980	0.450	27	0.126	R.YHGHSMSDPGSTYR.T
R2/RRR2-11/2	1004.430	1005.152	-1719.912	0.425	931.058	0.305	14	0.118	K.RGDYVPGLK.V
R2/RRR2-11/2	1422.264	1423.620	-1661.506	0.242	928.746	0.373	16	0.116	R.GGDLVSAFAELMGR.Q
R2/RRR2-11/3	1611.649	1611.677	-17.517	0.370	885.098	0.371	25	0.083	R.YHGHSM*SDPGSTYR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/3	1611.869	1611.677	119.326	0.358	635.434	0.298	22	0.073	R.YHGHSM*SDPGSTYR.T
R2/RRR2-4/2	1820.651	1821.066	-228.418	0.561	1823.670	0.594	23	0.253	R.QAVALLQDNYPEFIAK.K
R2/RRR2-10/2	1820.376	1821.066	-931.375	0.505	1832.002	0.590	22	0.252	R.QAVALLQDNYPEFIAK.K
R2/RRR2-3/2	1821.260	1821.066	106.916	0.514	1408.633	0.596	20	0.196	R.QAVALLQDNYPEFIAK.K
R2/RRR2-9/2	1820.462	1821.066	-883.580	0.486	1416.911	0.570	22	0.192	R.QAVALLQDNYPEFIAK.K
R2/RRR2-4/2	1821.332	1821.066	146.439	0.531	1216.197	0.602	19	0.176	R.QAVALLQDNYPEFIAK.K
R2/RRR2-4/2	1171.136	1170.384	-212.081	0.507	1318.125	0.500	18	0.172	K.IVLTINNPASK.K
R2/RRR2-6/2	1170.905	1170.384	-410.275	0.429	1164.199	0.515	17	0.159	K.IVLTINNPASK.K
R2/RRR2-4/3	1820.960	1821.066	-58.679	0.455	1482.813	0.498	30	0.159	R.QAVALLQDNYPEFIAK.K
R2/RRR2-9/2	1822.766	1821.066	-165.012	0.527	740.035	0.556	20	0.137	R.QAVALLQDNYPEFIAK.K
R2/RRR2-4/2	1096.525	1096.303	202.592	0.391	1192.385	0.344	15	0.134	K.SKFIFASPAK.S
R2/RRR2-6/2	1170.056	1170.384	-281.131	0.368	1004.838	0.420	16	0.132	K.IVLTINNPASK.K
R2/RRR2-10/2	1169.776	1170.384	-1378.419	0.402	838.746	0.459	15	0.129	K.IVLTINNPASK.K
R2/RRR2-4/2	1722.268	1722.024	142.137	0.518	480.883	0.451	17	0.118	K.VFINVPWWYLAANK.M
R2/RRR2-4/2	1721.454	1722.024	-914.697	0.451	575.554	0.349	19	0.112	K.VFINVPWWYLAANK.M
R2/RRR2-6/3	1273.651	1272.496	121.564	0.482	1099.968	0.329	22	0.086	R.KVPANEEPIM*K.G
R2/RRR2-4/3	1273.689	1272.496	151.841	0.533	1029.833	0.340	23	0.085	R.KVPANEEPIM*K.G
R2/RRR2-4/3	1820.538	1821.066	-841.752	0.379	820.810	0.397	23	0.082	R.QAVALLQDNYPEFIAK.K
R2/RRR2-4/3	1272.239	1272.496	-203.197	0.448	1058.319	0.311	22	0.082	R.KVPANEEPIM*K.G
R2/RRR2-4/3	1272.419	1272.496	-61.287	0.482	899.405	0.327	21	0.080	R.KVPANEEPIM*K.G
R2/RRR2-5/3	1272.829	1272.496	261.651	0.353	779.857	0.277	20	0.073	R.KVPANEEPIM*K.G
R2/RRR2-7/3	1272.911	1272.496	326.848	0.343	845.134	0.288	20	0.071	-.KVPANEEPIM*K.-
R2/RRR2-7/3	1272.508	1272.496	9.148	0.318	666.375	0.199	18	0.067	-.KVPANEEPIM*K.-
R2/RRR2-9/3	1272.508	1272.496	9.148	0.417	730.819	0.282	20	0.064	-.KVPANEEPIM*K.-
R2/RRR2-8/2	1678.279	1678.953	-1000.458	0.475	1712.328	0.505	22	0.215	R.AATGFGVSTLVEWVLK.N
R2/RRR2-8/2	1346.265	1345.506	-179.883	0.497	1578.356	0.555	22	0.213	K.FDM*GGSAAVFGAAK.A
R2/RRR2-8/2	1678.238	1678.953	-1024.995	0.511	1660.064	0.494	22	0.205	R.AATGFGVSTLVEWVLK.N
R2/RRR2-8/2	1679.519	1678.953	-259.203	0.544	1601.215	0.505	22	0.200	R.AATGFGVSTLVEWVLK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1344.885	1345.506	-1208.895	0.409	1442.142	0.506	22	0.184	K.FDM*GGSAAVFGAAK.A
R2/RRR2-8/2	1273.196	1272.388	-151.807	0.495	939.733	0.481	18	0.140	K.GLTFDSGGYNIK.T
R2/RRR2-8/2	1272.152	1272.388	-186.675	0.397	1060.235	0.434	18	0.138	K.GLTFDSGGYNIK.T
R2/RRR2-8/2	1318.857	1319.360	-1143.324	0.390	1125.721	0.381	18	0.134	K.TIEVNNTDAEGR.L
R2/RRR2-8/2	1272.104	1272.388	-223.930	0.404	1107.992	0.387	18	0.134	K.GLTFDSGGYNIK.T
R2/RRR2-8/2	1164.291	1164.275	14.132	0.260	1031.721	0.196	17	0.106	K.SGVADMVNTGGR.Q
R2/RRR2-11/2	1577.174	1577.807	-1038.353	0.468	2626.033	0.536	25	0.396	R.IAVLGASGYTGAEIVR.L
R2/RRR2-11/2	1992.585	1993.205	-815.673	0.541	2124.415	0.579	23	0.302	K.EANLYTEIAEGIHAYGIK.G
R2/RRR2-11/2	1993.026	1993.205	-90.343	0.539	1517.052	0.529	21	0.194	K.EANLYTEIAEGIHAYGIK.G
R2/RRR2-11/2	973.436	973.149	295.627	0.534	1264.295	0.415	15	0.153	K.VSNIIIDAK.S
R2/RRR2-11/2	1035.970	1036.163	-187.632	0.484	1184.553	0.436	15	0.150	K.IVDLSADFR.L
R2/RRR2-11/2	1298.117	1298.597	-370.635	0.394	1106.102	0.468	16	0.145	R.AIIISVIDNLVK.G
R2/RRR2-11/2	1035.374	1036.163	-1733.431	0.414	1159.560	0.366	15	0.136	K.IVDLSADFR.L
R2/RRR2-11/2	1298.243	1298.597	-273.272	0.355	1048.067	0.411	16	0.132	R.AIIISVIDNLVK.G
R2/RRR2-11/2	1036.042	1036.163	-117.304	0.227	615.604	0.335	11	0.105	K.IVDLSADFR.L
R2/RRR2-10/2	1353.972	1354.604	-1209.038	0.499	1131.147	0.621	22	0.177	R.GGVLGLGGVGHM*GVK.V
R2/RRR2-10/2	1254.856	1255.383	-1220.324	0.563	1560.639	0.403	17	0.175	K.M*DYVNQALER.L
R2/RRR2-10/2	1254.497	1255.383	-1507.611	0.520	1527.524	0.405	17	0.173	K.M*DYVNQALER.L
R2/RRR2-10/2	1254.927	1255.383	-364.320	0.510	1396.533	0.357	16	0.150	K.M*DYVNQALER.L
R2/RRR2-10/2	1353.730	1354.604	-1388.333	0.484	1017.443	0.528	21	0.150	R.GGVLGLGGVGHM*GVK.V
R2/RRR2-10/2	1354.380	1354.604	-166.176	0.502	851.350	0.583	20	0.148	R.GGVLGLGGVGHM*GVK.V
R2/RRR2-10/2	1130.809	1131.333	-1351.482	0.348	1306.636	0.366	17	0.144	K.HFGLM*SPGLR.G
R2/RRR2-10/2	1486.359	1485.651	-197.401	0.380	715.193	0.555	21	0.133	K.SM*GHHVTVISSSAR.K
R2/RRR2-10/3	1486.120	1485.651	316.569	0.484	1457.207	0.413	27	0.129	K.SM*GHHVTVISSSAR.K
R2/RRR2-10/2	1238.827	1239.383	-1259.780	0.445	921.552	0.383	15	0.126	K.MDYVNQALER.L
R2/RRR2-10/2	1073.900	1074.253	-330.018	0.435	505.812	0.486	15	0.125	K.GLTSQIEVVK.M
R2/RRR2-10/2	1130.770	1131.333	-1385.961	0.337	884.314	0.408	15	0.124	K.HFGLM*SPGLR.G
R2/RRR2-10/3	1485.128	1485.651	-1029.081	0.495	1359.254	0.428	28	0.123	K.SM*GHHVTVISSSAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1073.448	1074.253	-1686.205	0.480	453.508	0.453	14	0.122	K.GLTSQIEVVK.M
R2/RRR2-10/2	1130.838	1131.333	-438.943	0.300	1120.150	0.270	16	0.119	K.HFGLM*SPGLR.G
R2/RRR2-10/3	1468.792	1469.652	-1269.987	0.524	1376.264	0.394	28	0.116	K.SMGHHVTVISSSAR.K
R2/RRR2-10/3	1485.546	1485.651	-71.377	0.513	1233.744	0.423	27	0.112	K.SM*GHHVTVISSSAR.K
R2/RRR2-10/2	1115.293	1115.333	-36.733	0.266	1011.503	0.206	15	0.108	K.HFGLMSPGLR.G
R2/RRR2-10/3	1485.257	1485.651	-266.142	0.545	1230.447	0.397	27	0.105	K.SM*GHHVTVISSSAR.K
R2/RRR2-7/3	1485.787	1485.651	91.426	0.486	1171.608	0.392	26	0.101	K.SM*GHHVTVISSSAR.K
R2/RRR2-9/3	1485.632	1485.651	-13.147	0.484	1193.188	0.383	26	0.101	-.SM*GHHVTVISSSAR.-
R2/RRR2-10/3	1485.738	1485.651	58.672	0.446	1310.476	0.336	23	0.101	K.SM*GHHVTVISSSAR.K
R2/RRR2-10/3	1469.138	1469.652	-1033.297	0.520	1029.299	0.296	26	0.078	K.SMGHHVTVISSSAR.K
R2/RRR2-10/3	1485.144	1485.651	-1018.312	0.373	730.966	0.288	22	0.074	K.SM*GHHVTVISSSAR.K
R2/RRR2-10/3	1468.701	1469.652	-1332.088	0.516	870.833	0.276	23	0.066	-.SMGHHVTVISSSAR.-
R2/RRR2-10/2	1794.794	1795.160	-204.558	0.368	1023.983	0.417	21	0.128	R.IAVASALAATAVPSLVLAR.G
R2/RRR2-12/2	856.047	856.005	48.684	0.406	1173.979	0.402	13	0.142	K.TPAQVALR.W
R2/RRR2-12/2	1366.552	1366.547	3.708	0.384	1120.194	0.401	16	0.135	R.GNFIVNPQSVYK.T
R2/RRR2-12/2	1366.347	1366.547	-146.206	0.421	1040.766	0.386	16	0.129	R.GNFIVNPQSVYK.T
R2/RRR2-12/2	1108.917	1109.257	-308.224	0.423	706.781	0.382	13	0.118	K.REDLFITSK.L
R2/RRR2-12/2	1009.834	1010.126	-289.605	0.367	696.519	0.352	16	0.116	R.AIGVSNFSSK.K
R2/RRR2-12/2	1009.416	1010.126	-1699.288	0.345	527.364	0.393	14	0.115	R.AIGVSNFSSK.K
R2/RRR2-12/2	1009.297	1010.126	-1817.157	0.304	665.705	0.377	15	0.114	R.AIGVSNFSSK.K
R2/RRR2-12/2	1076.230	1077.259	-1890.946	0.349	852.950	0.309	12	0.112	-.LFEEGVVKR.-
R2/RRR2-12/2	1076.184	1077.259	-1933.234	0.269	959.379	0.243	13	0.109	K.LFEEGVVKR.E
R2/RRR2-14/2	1511.217	1511.659	-293.093	0.498	1756.579	0.521	23	0.225	K.TYVSGNAISKDDIK.V
R2/RRR2-14/2	1410.039	1410.578	-1094.661	0.466	1971.787	0.403	20	0.225	R.SVQM*EGLTWGASK.L
R2/RRR2-14/2	1880.415	1880.095	170.617	0.563	1417.256	0.688	32	0.221	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-15/2	1880.601	1880.095	-263.520	0.571	1378.445	0.676	31	0.213	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-14/2	1879.485	1880.095	-859.024	0.546	1288.903	0.677	30	0.202	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-15/2	1410.375	1410.578	-144.250	0.449	1758.208	0.386	20	0.193	R.SVQM*EGLTWGASK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1409.882	1410.578	-1206.896	0.492	1699.824	0.420	19	0.192	R.SVQM*EGLTWGASK.L
R2/RRR2-15/2	1511.256	1511.659	-267.323	0.501	1486.764	0.516	21	0.190	K.TYVSGNAISKDDIK.V
R2/RRR2-14/2	1879.504	1880.095	-849.114	0.546	1120.568	0.690	29	0.186	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-14/2	1511.309	1511.659	-232.396	0.504	1354.725	0.551	21	0.183	K.TYVSGNAISKDDIK.V
R2/RRR2-15/2	1511.250	1511.659	-271.618	0.491	1383.000	0.518	21	0.179	K.TYVSGNAISKDDIK.V
R2/RRR2-14/2	1409.863	1410.578	-1219.764	0.450	1704.350	0.348	20	0.178	R.SVQM*EGLTWGASK.L
R2/RRR2-14/2	1324.081	1324.467	-292.074	0.461	1437.365	0.423	18	0.167	R.WYDTVAAALASR.F
R2/RRR2-15/2	1879.382	1880.095	-914.512	0.536	980.278	0.654	28	0.166	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-15/2	1879.490	1880.095	-856.351	0.509	1033.907	0.617	28	0.163	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-15/2	1511.131	1511.659	-1014.216	0.508	1125.975	0.543	20	0.161	K.TYVSGNAISKDDIK.V
R2/RRR2-14/2	1511.208	1511.659	-299.415	0.477	1181.189	0.502	20	0.157	K.TYVSGNAISKDDIK.V
R2/RRR2-14/2	1324.146	1324.467	-242.961	0.450	1297.428	0.439	18	0.157	R.WYDTVAAALASR.F
R2/RRR2-14/3	1880.649	1880.095	-237.837	0.477	1328.119	0.549	37	0.157	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-14/3	1879.717	1880.095	-201.576	0.436	1110.524	0.523	33	0.127	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-14/2	1829.553	1830.079	-837.029	0.455	540.631	0.508	20	0.120	K.VFAAVPSKPGAEFPNAAR.W
R2/RRR2-15/3	1830.211	1830.079	72.335	0.344	775.710	0.478	29	0.092	K.VFAAVPSKPGAEFPNAAR.W
R2/RRR2-15/3	1830.627	1830.079	-248.048	0.303	912.299	0.420	27	0.089	K.VFAAVPSKPGAEFPNAAR.W
R2/RRR2-15/3	1879.903	1880.095	-102.593	0.339	836.030	0.423	31	0.087	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-15/3	1880.020	1880.095	-40.164	0.355	791.426	0.341	28	0.074	K.AVGVNLPGGGAASSAAAAAPAAK.D
R2/RRR2-15/3	1829.666	1830.079	-226.664	0.275	581.796	0.359	24	0.071	K.VFAAVPSKPGAEFPNAAR.W
R2/RRR2-13/2	1900.460	1900.935	-250.587	0.530	1320.161	0.610	25	0.193	K.SADLFDSEGQSSQSNSIK.Q
R2/RRR2-13/2	1900.259	1900.935	-884.877	0.527	1211.852	0.576	25	0.175	K.SADLFDSEGQSSQSNSIK.Q
R2/RRR2-13/3	1491.673	1491.671	1.665	0.547	1597.525	0.470	25	0.164	K.VAEIAAQLEQYQK.A
R2/RRR2-13/2	1400.002	1400.475	-338.677	0.469	1271.694	0.456	18	0.158	R.YQDIDPTFSGTR.E
R2/RRR2-13/2	1134.052	1134.267	-190.514	0.458	1403.936	0.351	16	0.151	K.ANEIFEAIAR.Q
R2/RRR2-13/2	1134.057	1134.267	-186.087	0.501	1101.087	0.425	15	0.141	K.ANEIFEAIAR.Q
R2/RRR2-13/2	1400.239	1400.475	-168.987	0.470	1077.844	0.431	17	0.139	R.YQDIDPTFSGTR.E
R2/RRR2-13/2	1133.583	1134.267	-1489.718	0.436	1067.214	0.398	15	0.134	K.ANEIFEAIAR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1400.049	1400.475	-304.997	0.470	911.399	0.394	16	0.124	R.YQDIDPTFSGTR.E
R2/RRR2-13/2	1308.011	1308.444	-332.351	0.417	860.958	0.378	16	0.120	R.GDVVAITNSM*ER.Y
R2/RRR2-13/3	1491.684	1491.671	9.175	0.462	1112.655	0.437	23	0.106	K.VAEIAAQLEQYQK.A
R2/RRR2-12/2	1645.587	1645.838	-153.018	0.626	2687.280	0.563	24	0.411	K.IKDEEGNPAFALVNK.A
R2/RRR2-12/2	1646.200	1645.838	220.700	0.633	2431.815	0.532	23	0.342	K.IKDEEGNPAFALVNK.A
R2/RRR2-12/2	1646.199	1645.838	220.105	0.612	2370.240	0.524	23	0.328	K.IKDEEGNPAFALVNK.A
R2/RRR2-12/2	1845.439	1845.993	-844.353	0.569	1390.074	0.693	28	0.223	K.ILPWGDEAYAGGSANAPR.G
R2/RRR2-12/2	1722.221	1722.922	-990.856	0.566	1840.437	0.467	22	0.222	K.IRDEEGYPAFALVNK.V
R2/RRR2-12/2	1722.605	1722.922	-184.629	0.589	1761.912	0.502	22	0.220	K.IRDEEGYPAFALVNK.V
R2/RRR2-12/2	1845.601	1845.993	-212.725	0.558	1316.426	0.674	28	0.209	K.ILPWGDEAYAGGSANAPR.G
R2/RRR2-12/2	1845.181	1845.993	-984.944	0.519	1314.930	0.667	27	0.206	K.ILPWGDEAYAGGSANAPR.G
R2/RRR2-12/2	1722.418	1722.922	-876.013	0.556	1670.378	0.457	22	0.197	K.IRDEEGYPAFALVNK.V
R2/RRR2-12/2	1080.427	1081.161	-1610.154	0.417	1754.695	0.380	17	0.193	K.ADEGFSVTVR.G
R2/RRR2-12/2	1080.875	1081.161	-265.473	0.484	1552.452	0.432	17	0.182	K.ADEGFSVTVR.G
R2/RRR2-12/3	1774.710	1774.959	-140.719	0.454	799.392	0.493	28	0.096	R.VTGEAIKHSQGEGHPVK.L
R2/RRR2-12/3	1646.214	1645.838	228.797	0.387	859.273	0.430	26	0.089	K.IKDEEGNPAFALVNK.A
R2/RRR2-12/3	1645.657	1645.838	-110.277	0.359	646.817	0.326	23	0.070	-.IKDEEGNPAFALVNK.-
R2/RRR2-10/2	1104.007	1103.299	-265.345	0.458	852.164	0.468	17	0.134	K.RPFAAIVGGSK.V
R2/RRR2-10/2	1104.359	1103.299	54.146	0.491	792.805	0.479	17	0.134	K.RPFAAIVGGSK.V
R2/RRR2-10/2	1103.202	1103.299	-88.854	0.466	808.660	0.436	17	0.129	K.RPFAAIVGGSK.V
R2/RRR2-10/3	1935.185	1935.129	28.931	0.397	1131.395	0.527	30	0.127	K.LASLADLYVNDAFGTAHR.A
R2/RRR2-10/2	999.885	1000.219	-335.161	0.424	783.923	0.400	15	0.124	K.FSLAPLVPR.L
R2/RRR2-10/3	1103.863	1103.299	-396.107	0.502	1365.596	0.349	23	0.105	K.RPFAAIVGGSK.V
R2/RRR2-10/3	1103.115	1103.299	-167.983	0.421	1257.781	0.341	22	0.096	K.RPFAAIVGGSK.V
R2/RRR2-8/2	1132.865	1133.320	-403.625	0.437	1849.401	0.545	19	0.243	K.ALVSAGLSSSIK.V
R2/RRR2-7/2	1134.175	1133.320	-128.745	0.535	1709.529	0.510	19	0.216	K.ALVSAGLSSSIK.V
R2/RRR2-7/2	1133.126	1133.320	-172.301	0.519	1468.495	0.558	19	0.198	K.ALVSAGLSSSIK.V
R2/RRR2-8/2	1133.042	1133.320	-246.118	0.458	1535.764	0.483	19	0.188	K.ALVSAGLSSSIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1132.546	1133.320	-1571.189	0.397	1656.417	0.420	19	0.188	K.ALVSAGLSSSIK.V
R2/RRR2-7/2	1783.451	1783.963	-849.947	0.540	1340.635	0.543	23	0.183	R.DISLNYATFQPGTTVR.D
R2/RRR2-14/2	1133.221	1133.320	-88.013	0.413	1320.491	0.534	18	0.175	K.ALVSAGLSSSIK.V
R2/RRR2-14/2	1563.270	1562.751	-308.475	0.532	1377.761	0.432	20	0.161	R.DNVEAYWPSVIIR.Y
R2/RRR2-7/2	1562.247	1562.751	-965.121	0.413	1456.815	0.305	20	0.145	R.DNVEAYWPSVIIR.Y
R2/RRR2-7/2	1562.616	1562.751	-86.707	0.492	1237.828	0.401	19	0.144	R.DNVEAYWPSVIIR.Y
R2/RRR2-7/2	1563.186	1562.751	279.259	0.535	1251.773	0.396	19	0.143	R.DNVEAYWPSVIIR.Y
R2/RRR2-7/2	1567.068	1567.767	-1087.709	0.380	801.417	0.504	18	0.132	R.IYYPDKEALDALR.G
R2/RRR2-7/2	1567.550	1567.767	-139.156	0.442	736.801	0.513	17	0.132	R.IYYPDKEALDALR.G
R2/RRR2-9/2	1567.286	1567.767	-307.841	0.436	847.047	0.459	18	0.131	R.IYYPDKEALDALR.G
R2/RRR2-14/2	1562.048	1562.751	-1093.164	0.370	1096.997	0.339	18	0.126	R.DNVEAYWPSVIIR.Y
R2/RRR2-7/2	915.955	916.097	-155.340	0.518	730.408	0.396	13	0.126	R.SEVVQLLK.S
R2/RRR2-8/2	1567.504	1567.767	-168.217	0.415	816.457	0.421	18	0.125	R.IYYPDKEALDALR.G
R2/RRR2-7/2	1567.445	1567.767	-205.951	0.447	693.326	0.459	17	0.125	R.IYYPDKEALDALR.G
R2/RRR2-14/2	915.944	916.097	-167.640	0.399	734.271	0.356	13	0.120	R.SEVVQLLK.S
R2/RRR2-14/2	915.380	916.097	-1881.410	0.369	774.475	0.341	13	0.119	R.SEVVQLLK.S
R2/RRR2-14/2	1566.621	1567.767	-1374.060	0.380	681.316	0.401	17	0.118	R.IYYPDKEALDALR.G
R2/RRR2-8/2	1562.244	1562.751	-967.631	0.318	908.142	0.343	17	0.117	R.DNVEAYWPSVIIR.Y
R2/RRR2-7/2	915.609	916.097	-534.499	0.346	708.002	0.336	13	0.117	R.SEVVQLLK.S
R2/RRR2-7/2	915.904	916.097	-211.360	0.423	622.023	0.363	12	0.114	-.SEVVQLLK.-
R2/RRR2-14/2	916.074	916.097	-25.275	0.391	642.390	0.343	12	0.112	-.SEVVQLLK.-
R2/RRR2-13/2	1566.997	1567.767	-1133.076	0.320	639.880	0.332	17	0.112	R.IYYPDKEALDALR.G
R2/RRR2-13/2	1567.423	1567.767	-220.405	0.350	734.185	0.305	17	0.111	R.IYYPDKEALDALR.G
R2/RRR2-13/2	1567.086	1567.767	-1076.055	0.336	566.258	0.334	15	0.110	R.IYYPDKEALDALR.G
R2/RRR2-13/2	1567.165	1567.767	-1025.531	0.318	536.471	0.290	15	0.108	R.IYYPDKEALDALR.G
R2/RRR2-13/2	1567.109	1567.767	-1061.351	0.369	673.952	0.254	17	0.108	R.IYYPDKEALDALR.G
R2/RRR2-13/2	915.962	916.097	-148.388	0.285	736.155	0.241	11	0.107	-.SEVVQLLK.-
R2/RRR2-13/2	1561.777	1562.751	-1267.470	0.295	725.346	0.188	15	0.101	R.DNVEAYWPSVIIR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/3	1567.732	1567.767	-22.548	0.431	634.547	0.445	27	0.091	R.IYYPDKEALDALR.G
R2/RRR2-13/3	1566.671	1567.767	-1341.866	0.367	366.983	0.405	21	0.087	R.IYYPDKEALDALR.G
R2/RRR2-13/3	1567.769	1567.767	0.998	0.365	852.971	0.399	26	0.087	R.IYYPDKEALDALR.G
R2/RRR2-9/3	1567.870	1567.767	66.009	0.366	429.346	0.398	23	0.086	R.IYYPDKEALDALR.G
R2/RRR2-9/3	1567.755	1567.767	-7.671	0.351	662.898	0.422	25	0.086	R.IYYPDKEALDALR.G
R2/RRR2-8/3	1567.326	1567.767	-282.453	0.340	607.868	0.427	24	0.086	R.IYYPDKEALDALR.G
R2/RRR2-14/3	1567.495	1567.767	-174.163	0.373	427.694	0.371	21	0.085	R.IYYPDKEALDALR.G
R2/RRR2-14/3	1567.143	1567.767	-1039.695	0.305	372.940	0.330	20	0.083	R.IYYPDKEALDALR.G
R2/RRR2-14/3	1567.518	1567.767	-159.398	0.353	549.679	0.368	23	0.082	R.IYYPDKEALDALR.G
R2/RRR2-14/3	1567.412	1567.767	-227.016	0.349	376.049	0.348	21	0.081	-.IYYPDKEALDALR.-
R2/RRR2-13/3	1567.890	1567.767	78.307	0.361	545.953	0.315	24	0.080	R.IYYPDKEALDALR.G
R2/RRR2-26/1	418.965	419.368	-965.547	-2.568	2.146	0.000	1	0.852	-.GGGDGG.-
R2/RRR2-1/1	418.964	419.368	-968.472	-2.384	1.726	0.000	1	0.847	R.GGGDGG.-
R2/RRR2-13/1	419.031	419.368	-806.735	-2.333	21.497	0.000	2	0.807	R.GGGDGG.-
R2/RRR2-11/1	419.034	419.368	-800.887	-2.284	23.527	0.000	2	0.802	R.GGGDGG.-
R2/RRR2-24/1	418.958	419.368	-983.098	-1.905	15.277	0.000	2	0.753	R.GGGDGG.-
R2/RRR2-23/1	418.986	419.368	-915.090	-0.817	39.598	0.000	3	0.738	R.GGGDGG.-
R2/RRR2-14/1	418.990	419.368	-905.731	-2.024	6.815	0.000	2	0.728	-.GGGDGG.-
R2/RRR2-11/1	418.962	419.368	-972.421	-1.288	22.583	0.000	2	0.722	R.GGGDGG.-
R2/RRR2-4/1	418.976	419.368	-938.782	-1.009	1.288	0.000	1	0.704	R.GGGDGG.-
R2/RRR2-11/1	419.152	419.368	-518.487	-0.929	6.144	0.202	1	0.580	-.GGGDGG.-
R2/RRR2-13/1	419.018	419.368	-838.611	-1.042	1.523	0.326	1	0.499	-.GGGDGG.-
R2/RRR2-9/1	418.980	419.368	-929.861	-0.614	8.680	0.825	2	0.446	R.GGGDGG.-
R2/RRR2-13/1	419.031	419.368	-807.613	-0.381	37.585	0.904	3	0.441	-.GGGDGG.-
R2/RRR2-11/2	1245.038	1245.368	-265.380	0.602	1753.638	0.508	20	0.223	K.SINDIAASQGIR.I
R2/RRR2-11/2	1245.055	1245.368	-251.806	0.557	1673.464	0.475	20	0.204	K.SINDIAASQGIR.I
R2/RRR2-11/2	1245.078	1245.368	-233.806	0.581	1597.575	0.472	19	0.194	K.SINDIAASQGIR.I
R2/RRR2-11/2	1190.030	1190.329	-251.926	0.435	1529.889	0.485	17	0.191	R.DFYGALASAFK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1611.373	1610.883	304.720	0.505	1217.677	0.425	20	0.145	R.VLNISGVQLIGINNR.S
R2/RRR2-11/2	1610.323	1610.883	-971.511	0.427	1323.854	0.366	21	0.144	R.VLNISGVQLIGINNR.S
R2/RRR2-12/2	1611.439	1610.883	-276.232	0.503	1197.374	0.392	20	0.138	R.VLNISGVQLIGINNR.S
R2/RRR2-12/2	1652.396	1652.786	-236.709	0.473	1114.282	0.379	19	0.132	R.ENFNPVEIAQAYEK.N
R2/RRR2-12/2	1653.280	1652.786	299.959	0.513	969.576	0.440	18	0.132	R.ENFNPVEIAQAYEK.N
R2/RRR2-12/2	1609.778	1610.883	-1311.743	0.371	1188.589	0.355	19	0.132	R.VLNISGVQLIGINNR.S
R2/RRR2-12/2	1610.512	1610.883	-231.386	0.437	1130.934	0.366	20	0.131	R.VLNISGVQLIGINNR.S
R2/RRR2-12/2	1346.239	1346.515	-205.596	0.292	934.831	0.458	16	0.128	R.DFYGALASAFKR.N
R2/RRR2-11/2	1346.107	1346.515	-304.212	0.282	606.153	0.530	14	0.119	R.DFYGALASAFKR.N
R2/RRR2-11/2	1345.499	1346.515	-1502.781	0.180	664.977	0.330	14	0.102	R.DFYGALASAFKR.N
R2/RRR2-8/2	1532.128	1531.821	200.612	0.545	2274.732	0.610	24	0.341	K.ALGVDILTGFGAIVGK.Q
R2/RRR2-8/2	1531.356	1531.821	-304.670	0.484	2176.575	0.589	24	0.315	K.ALGVDILTGFGAIVGK.Q
R2/RRR2-8/2	1531.452	1531.821	-241.652	0.534	2058.420	0.601	23	0.296	K.ALGVDILTGFGAIVGK.Q
R2/RRR2-8/2	1413.855	1413.605	177.819	0.524	1855.344	0.490	20	0.233	K.GLGLENINVVTQR.G
R2/RRR2-8/2	1413.191	1413.605	-293.584	0.470	1688.777	0.519	19	0.217	K.GLGLENINVVTQR.G
R2/RRR2-8/3	1427.099	1426.640	322.223	0.511	1870.454	0.383	25	0.174	K.DGKPVQIELIDAK.T
R2/RRR2-8/2	1351.956	1352.477	-1128.555	0.427	1330.947	0.491	19	0.170	R.NIDYHTGVFASK.I
R2/RRR2-8/2	1352.148	1352.477	-244.177	0.441	1180.484	0.428	19	0.147	R.NIDYHTGVFASK.I
R2/RRR2-8/3	1426.654	1426.640	9.507	0.468	1596.962	0.330	24	0.124	K.DGKPVQIELIDAK.T
R2/RRR2-8/2	1456.505	1456.754	-171.622	0.264	761.784	0.194	16	0.099	-.NIIIATGSVPFVPK.-
R2/RRR2-8/3	1425.773	1426.640	-1313.802	0.367	1098.015	0.279	22	0.077	K.DGKPVQIELIDAK.T
R2/RRR2-3/2	1512.721	1512.776	-36.310	0.544	1664.355	0.575	22	0.228	R.LPLITISDSGNLLR.D
R2/RRR2-3/2	1577.537	1577.892	-225.667	0.394	1967.069	0.399	20	0.227	R.LPVLYVAYAEGLIR.A
R2/RRR2-3/2	1513.412	1512.776	-241.539	0.560	1618.237	0.552	22	0.216	R.LPLITISDSGNLLR.D
R2/RRR2-1/2	1513.203	1512.776	282.739	0.528	1210.922	0.482	19	0.156	R.LPLITISDSGNLLR.D
R2/RRR2-3/2	1873.764	1873.120	-190.436	0.401	997.263	0.460	19	0.132	K.FNLAAVIFADM*SGTEAAK.N
R2/RRR2-3/2	1365.049	1365.603	-1141.678	0.403	923.660	0.419	16	0.127	R.LLLVNPTDINPR.Q
R2/RRR2-3/2	1963.091	1963.128	-18.998	0.410	606.306	0.446	17	0.113	R.SCDFATEQTLVLHSPEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/3	1902.953	1903.001	-25.396	0.418	910.736	0.508	31	0.105	K.AIAAASGDNARPASSESAQK.N
R2/RRR2-4/2	1873.903	1873.120	-116.002	0.366	281.510	0.371	13	0.102	K.FNLAAVIFADM*SGTEAAK.N
R2/RRR2-18/2	1630.763	1630.999	-145.174	0.596	2941.294	0.608	23	0.493	R.IKQVLLSLQAFTLR.L
R2/RRR2-18/2	1631.634	1630.999	-224.263	0.655	2798.070	0.633	23	0.465	R.IKQVLLSLQAFTLR.L
R2/RRR2-18/2	1630.299	1630.999	-1045.973	0.588	2749.984	0.592	23	0.438	R.IKQVLLSLQAFTLR.L
R2/RRR2-19/2	1464.244	1464.562	-217.875	0.535	1643.452	0.448	22	0.193	K.FDSDGNLIDAQIR.E
R2/RRR2-19/2	1464.299	1464.562	-180.324	0.554	1478.903	0.472	22	0.181	K.FDSDGNLIDAQIR.E
R2/RRR2-19/2	1464.347	1464.562	-147.709	0.534	1343.535	0.451	21	0.163	K.FDSDGNLIDAQIR.E
R2/RRR2-18/2	1463.973	1464.562	-1089.079	0.529	1328.039	0.401	21	0.152	K.FDSDGNLIDAQIR.E
R2/RRR2-18/2	1464.259	1464.562	-207.420	0.568	1252.231	0.409	20	0.146	K.FDSDGNLIDAQIR.E
R2/RRR2-17/2	1464.249	1464.562	-214.362	0.523	1261.188	0.385	20	0.144	K.FDSDGNLIDAQIR.E
R2/RRR2-19/2	1390.461	1389.668	-149.218	0.462	793.856	0.500	18	0.135	K.QVLLSLQAFTLR.L
R2/RRR2-18/2	1389.249	1389.668	-302.697	0.458	954.633	0.425	19	0.133	K.QVLLSLQAFTLR.L
R2/RRR2-18/2	1389.390	1389.668	-200.444	0.461	910.782	0.373	19	0.125	K.QVLLSLQAFTLR.L
R2/RRR2-17/2	1389.588	1389.668	-58.030	0.456	753.308	0.402	18	0.123	K.QVLLSLQAFTLR.L
R2/RRR2-17/2	932.904	933.003	-106.386	0.358	871.488	0.333	13	0.120	K.NALDWASR.G
R2/RRR2-18/2	932.936	933.003	-71.998	0.413	868.197	0.314	13	0.119	K.NALDWASR.G
R2/RRR2-18/2	933.170	933.003	179.408	0.428	889.284	0.306	13	0.119	K.NALDWASR.G
R2/RRR2-17/2	932.885	933.003	-126.732	0.347	820.589	0.301	13	0.116	K.NALDWASR.G
R2/RRR2-19/2	932.384	933.003	-1741.324	0.346	901.832	0.276	13	0.115	K.NALDWASR.G
R2/RRR2-19/2	932.338	933.003	-1791.313	0.334	829.035	0.280	13	0.114	K.NALDWASR.G
R2/RRR2-19/2	932.954	933.003	-52.574	0.403	868.767	0.258	13	0.114	K.NALDWASR.G
R2/RRR2-18/2	932.880	933.003	-132.376	0.338	832.712	0.273	13	0.114	K.NALDWASR.G
R2/RRR2-19/2	1389.340	1389.668	-236.583	0.418	747.789	0.278	16	0.109	K.QVLLSLQAFTLR.L
R2/RRR2-18/2	1631.422	1630.999	259.699	0.335	540.849	0.253	17	0.105	R.IKQVLLSLQAFTLR.L
R2/RRR2-19/3	1630.014	1630.999	-1221.404	0.358	905.638	0.405	26	0.087	R.IKQVLLSLQAFTLR.L
R2/RRR2-18/3	1630.778	1630.999	-135.834	0.326	744.216	0.428	21	0.083	R.IKQVLLSLQAFTLR.L
R2/RRR2-17/3	1630.934	1630.999	-39.992	0.342	697.763	0.420	22	0.082	R.IKQVLLSLQAFTLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1274.274	1274.448	-136.497	0.507	1513.212	0.543	18	0.204	K.HALVVYDDLTK.Q
R2/RRR2-8/2	1740.693	1741.879	-1259.863	0.398	1595.097	0.503	22	0.198	R.EVAAFAQFGSDLDAATK.Q
R2/RRR2-8/2	1586.257	1585.827	271.724	0.431	1231.767	0.336	18	0.134	R.ILEWEADFLAHLK.T
R2/RRR2-8/2	1742.059	1741.879	103.413	0.492	567.374	0.577	19	0.130	R.EVAAFAQFGSDLDAATK.Q
R2/RRR2-8/2	1740.571	1741.879	-1329.942	0.317	936.286	0.394	19	0.120	R.EVAAFAQFGSDLDAATK.Q
R2/RRR2-8/2	1053.226	1053.237	-10.301	0.336	715.051	0.408	14	0.117	-.GLLDSVPVPR.-
R2/RRR2-8/2	1053.219	1053.237	-16.927	0.381	801.504	0.320	13	0.112	-.GLLDSVPVPR.-
R2/RRR2-8/2	1053.099	1053.237	-131.332	0.170	503.694	0.327	11	0.100	R.GLLDSVPVPR.I
R2/RRR2-8/2	1727.435	1726.953	280.349	0.578	2438.442	0.554	26	0.360	R.LNLEAAGVEVDNIGAIK.V
R2/RRR2-8/2	1630.187	1629.799	238.716	0.552	1558.461	0.551	22	0.205	R.TSVPNIWAVGDVTNR.M
R2/RRR2-8/2	1630.326	1629.799	-290.530	0.500	1109.801	0.563	22	0.163	R.TSVPNIWAVGDVTNR.M
R2/RRR2-9/2	1629.494	1629.799	-187.590	0.496	1055.494	0.549	21	0.156	R.TSVPNIWAVGDVTNR.M
R2/RRR2-9/2	1630.113	1629.799	193.210	0.551	996.159	0.558	21	0.154	R.TSVPNIWAVGDVTNR.M
R2/RRR2-8/2	1629.406	1629.799	-241.627	0.474	1043.279	0.519	21	0.150	R.TSVPNIWAVGDVTNR.M
R2/RRR2-8/2	1046.013	1046.160	-140.883	0.353	1368.347	0.341	17	0.145	R.TVVASNLEGR.G
R2/RRR2-8/2	1043.244	1042.213	29.973	0.513	1055.199	0.387	15	0.135	K.ILVYGSSFR.G
R2/RRR2-8/2	1045.938	1046.160	-212.885	0.327	872.700	0.376	15	0.121	R.TVVASNLEGR.G
R2/RRR2-9/2	1628.716	1629.799	-1282.583	0.334	707.938	0.452	18	0.119	R.TSVPNIWAVGDVTNR.M
R2/RRR2-8/2	1045.424	1046.160	-1665.353	0.321	694.927	0.421	14	0.118	R.TVVASNLEGR.G
R2/RRR2-9/2	1814.306	1814.154	84.111	0.379	835.297	0.396	19	0.118	R.MNLTPVALMEATCFSK.T
R2/RRR2-9/2	1046.048	1046.160	-106.818	0.360	772.492	0.292	15	0.112	R.TVVASNLEGR.G
R2/RRR2-9/2	1045.990	1046.160	-162.658	0.284	709.054	0.275	15	0.109	R.TVVASNLEGR.G
R2/RRR2-10/2	1695.317	1694.909	241.244	0.566	2068.696	0.505	21	0.266	R.IVTFNSDWQLLTEK.E
R2/RRR2-10/2	1742.486	1742.950	-267.051	0.453	2143.933	0.438	25	0.262	R.DEDPAAVAATIPSFLPK.L
R2/RRR2-10/2	1694.387	1694.909	-901.200	0.525	1844.553	0.502	21	0.232	R.IVTFNSDWQLLTEK.E
R2/RRR2-10/2	1928.187	1929.246	-1071.255	0.501	1643.021	0.580	25	0.225	K.TAPINIGLAAFELIDEIK.A
R2/RRR2-10/2	1928.622	1929.246	-844.439	0.505	1612.503	0.573	25	0.219	K.TAPINIGLAAFELIDEIK.A
R2/RRR2-10/2	1694.205	1694.909	-1008.831	0.517	1703.911	0.525	20	0.218	R.IVTFNSDWQLLTEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1929.544	1929.246	154.725	0.563	1527.632	0.600	25	0.215	K.TAPINIGLAAFELIDEIK.A
R2/RRR2-10/2	1742.618	1742.950	-191.502	0.435	1674.479	0.475	22	0.202	R.DEDPAAVAATIPSFLPK.L
R2/RRR2-11/2	1694.298	1694.909	-954.000	0.470	1507.643	0.459	18	0.177	R.IVTFNSDWQLLTEK.E
R2/RRR2-10/2	1742.226	1742.950	-992.620	0.385	1437.740	0.343	20	0.148	R.DEDPAAVAATIPSFLPK.L
R2/RRR2-11/2	1608.429	1607.786	-223.083	0.527	1030.759	0.472	21	0.143	R.DLPDSTFTISELIR.N
R2/RRR2-1/2	1694.315	1694.909	-943.873	0.448	795.340	0.460	15	0.123	R.IVTFNSDWQLLTEK.E
R2/RRR2-10/2	1607.280	1607.786	-940.290	0.427	815.683	0.380	19	0.120	R.DLPDSTFTISELIR.N
R2/RRR2-10/2	1607.137	1607.786	-1029.355	0.377	884.385	0.330	20	0.117	R.DLPDSTFTISELIR.N
R2/RRR2-11/2	1606.591	1607.786	-1370.663	0.324	995.478	0.285	21	0.116	R.DLPDSTFTISELIR.N
R2/RRR2-10/2	1116.237	1117.231	-1791.691	0.315	494.050	0.456	15	0.115	-.SCPGVENVVR.-
R2/RRR2-10/2	1116.365	1117.231	-1677.316	0.295	343.295	0.421	13	0.113	K.SCPGVENVVR.Y
R2/RRR2-11/2	1606.503	1607.786	-1425.612	0.281	874.330	0.231	20	0.108	R.DLPDSTFTISELIR.N
R2/RRR2-10/2	1606.955	1607.786	-1142.844	0.291	836.695	0.215	20	0.106	R.DLPDSTFTISELIR.N
R2/RRR2-10/2	1116.485	1117.231	-1569.118	0.334	378.391	0.395	13	0.104	-.SCPGVENVVR.-
R2/RRR2-3/2	1607.219	1607.786	-978.415	0.250	679.454	0.147	17	0.101	R.DLPDSTFTISELIR.N
R2/RRR2-13/2	1738.325	1738.839	-873.279	0.439	1345.348	0.450	23	0.163	R.GDGADPWLLDHADLSR.L
R2/RRR2-13/2	1390.129	1389.495	-264.633	0.456	1217.356	0.463	19	0.153	K.EAVGAEAAFGPDVR.E
R2/RRR2-13/2	1480.047	1480.603	-1054.874	0.287	663.604	0.523	17	0.121	R.FVFPETSGLDDPR.V
R2/RRR2-12/2	1388.952	1389.495	-1114.361	0.266	1135.751	0.275	18	0.118	K.EAVGAEAAFGPDVR.E
R2/RRR2-13/2	1134.152	1134.224	-63.975	0.356	841.218	0.330	15	0.115	R.VNPFVDDATR.A
R2/RRR2-12/2	1390.151	1389.495	-248.599	0.347	692.936	0.374	17	0.112	K.EAVGAEAAFGPDVR.E
R2/RRR2-13/2	1500.465	1500.591	-84.342	0.425	660.236	0.372	17	0.112	K.ANGYGGEVELFESK.G
R2/RRR2-13/2	1480.042	1480.603	-1058.352	0.217	572.734	0.413	16	0.107	R.FVFPETSGLDDPR.V
R2/RRR2-13/2	1479.624	1480.603	-1341.402	0.133	529.456	0.421	16	0.100	R.FVFPETSGLDDPR.V
R2/RRR2-10/2	1300.321	1299.414	-71.524	0.508	1167.294	0.567	18	0.171	K.DDGTLASFIGFR.V
R2/RRR2-10/2	1733.417	1733.852	-251.991	0.518	1145.890	0.536	26	0.164	K.GGIGCAPGELSTSELER.L
R2/RRR2-11/2	1202.010	1201.398	-323.976	0.420	1089.166	0.516	18	0.153	K.VIALGDVTGSIR.N
R2/RRR2-10/2	1118.979	1119.295	-284.007	0.432	945.783	0.419	17	0.130	K.TAVAAIPYGGAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1119.008	1119.295	-257.411	0.424	1028.876	0.379	17	0.128	K.TAVAAIPYGGAK.G
R2/RRR2-10/2	1118.613	1119.295	-1508.231	0.329	906.544	0.392	16	0.122	K.TAVAAIPYGGAK.G
R2/RRR2-10/2	1298.402	1299.414	-1553.803	0.290	654.311	0.463	13	0.114	K.DDGTLASFIGFR.V
R2/RRR2-10/2	1039.916	1040.238	-310.662	0.343	746.960	0.314	15	0.112	K.NGLDIPALVK.H
R2/RRR2-11/2	1041.002	1040.238	-227.537	0.302	666.478	0.321	12	0.106	-.NGLDIPALVK.-
R2/RRR2-4/2	1513.349	1513.760	-272.374	0.385	1125.552	0.469	17	0.145	K.LLVSEELWPLGEK.L
R2/RRR2-4/2	1513.258	1513.760	-995.152	0.349	1050.542	0.357	17	0.124	K.LLVSEELWPLGEK.L
R2/RRR2-4/2	1079.754	1080.261	-1400.133	0.383	960.619	0.363	13	0.123	R.LSAAWQLYK.S
R2/RRR2-4/2	1130.263	1131.261	-1773.358	0.282	847.918	0.348	14	0.114	K.SQEELINVAK.E
R2/RRR2-4/2	1131.034	1131.261	-201.739	0.155	729.795	0.225	13	0.098	K.SQEELINVAK.E
R2/RRR2-8/2	1157.140	1157.302	-140.474	0.530	2119.575	0.567	21	0.298	R.DPAAATSGVVIR.R
R2/RRR2-8/2	1158.022	1157.302	-243.030	0.592	1946.359	0.530	20	0.257	R.DPAAATSGVVIR.R
R2/RRR2-8/2	1156.918	1157.302	-333.111	0.471	1795.426	0.519	20	0.232	R.DPAAATSGVVIR.R
R2/RRR2-8/2	1713.145	1711.882	154.115	0.467	1029.944	0.440	18	0.136	K.GQDMVFTVYGDHWR.K
R2/RRR2-8/2	1163.605	1164.290	-1452.440	0.390	1070.723	0.403	17	0.135	K.LAGYDIPAESK.I
R2/RRR2-8/2	1164.046	1164.290	-209.902	0.465	889.623	0.440	16	0.131	K.LAGYDIPAESK.I
R2/RRR2-8/2	1103.070	1103.342	-247.700	0.438	1130.990	0.327	16	0.130	R.RFGDILLLR.M
R2/RRR2-8/2	1102.851	1103.342	-446.583	0.473	1072.661	0.308	16	0.125	R.RFGDILLLR.M
R2/RRR2-8/2	1164.072	1164.290	-188.020	0.448	840.589	0.400	15	0.123	K.LAGYDIPAESK.I
R2/RRR2-8/2	1102.611	1103.342	-1574.537	0.412	1082.005	0.272	16	0.121	R.RFGDILLLR.M
R2/RRR2-8/2	1459.655	1459.589	45.496	0.376	314.510	0.523	16	0.119	K.EVLHTQGVEFGSR.T
R2/RRR2-8/2	1458.939	1459.589	-1134.084	0.350	488.671	0.436	17	0.115	K.EVLHTQGVEFGSR.T
R2/RRR2-13/2	1419.364	1419.606	-170.937	0.513	1916.615	0.507	19	0.240	R.AFQLYSSGIFTGK.C
R2/RRR2-13/2	1419.367	1419.606	-169.125	0.470	1939.779	0.488	19	0.238	R.AFQLYSSGIFTGK.C
R2/RRR2-23/2	1419.236	1419.606	-261.362	0.473	1828.978	0.468	19	0.218	R.AFQLYSSGIFTGK.C
R2/RRR2-11/2	1419.278	1419.606	-231.938	0.454	1551.023	0.598	19	0.213	R.AFQLYSSGIFTGK.C
R2/RRR2-11/2	1420.012	1419.606	286.981	0.510	1707.065	0.497	19	0.209	R.AFQLYSSGIFTGK.C
R2/RRR2-12/2	1419.152	1419.606	-321.339	0.416	1634.080	0.433	19	0.186	R.AFQLYSSGIFTGK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1420.235	1419.606	-262.041	0.471	1379.929	0.520	18	0.177	R.AFQLYSSGIFTGK.C
R2/RRR2-23/2	1419.152	1419.606	-321.339	0.364	1502.691	0.439	18	0.172	R.AFQLYSSGIFTGK.C
R2/RRR2-12/2	1540.326	1539.719	-255.441	0.574	1152.613	0.600	22	0.171	K.AVANQPVSVAIEAGGR.A
R2/RRR2-13/2	1335.160	1334.536	-282.406	0.505	1469.242	0.428	19	0.170	K.CGIAVEPSYPLK.K
R2/RRR2-15/2	1539.485	1539.719	-152.191	0.532	1168.209	0.582	23	0.170	K.AVANQPVSVAIEAGGR.A
R2/RRR2-12/2	1539.194	1539.719	-993.338	0.505	1231.374	0.549	23	0.168	K.AVANQPVSVAIEAGGR.A
R2/RRR2-14/2	1539.356	1539.719	-236.514	0.516	1149.964	0.578	23	0.168	K.AVANQPVSVAIEAGGR.A
R2/RRR2-11/2	1539.204	1539.719	-986.808	0.537	1137.785	0.576	22	0.165	K.AVANQPVSVAIEAGGR.A
R2/RRR2-11/2	1539.257	1539.719	-300.958	0.498	1057.654	0.604	22	0.164	K.AVANQPVSVAIEAGGR.A
R2/RRR2-13/2	1539.392	1539.719	-212.647	0.521	1096.857	0.574	23	0.163	K.AVANQPVSVAIEAGGR.A
R2/RRR2-13/2	1539.156	1539.719	-1018.181	0.465	1160.320	0.542	22	0.160	K.AVANQPVSVAIEAGGR.A
R2/RRR2-13/2	1540.312	1539.719	-264.505	0.445	1194.651	0.528	21	0.160	K.AVANQPVSVAIEAGGR.A
R2/RRR2-13/2	1540.366	1539.719	-229.364	0.477	1095.570	0.559	22	0.159	K.AVANQPVSVAIEAGGR.A
R2/RRR2-14/2	1539.329	1539.719	-253.618	0.531	1092.677	0.558	22	0.159	K.AVANQPVSVAIEAGGR.A
R2/RRR2-13/2	1540.178	1539.719	299.012	0.552	1007.389	0.594	21	0.158	K.AVANQPVSVAIEAGGR.A
R2/RRR2-11/2	1539.156	1539.719	-1018.500	0.522	1028.062	0.571	22	0.156	K.AVANQPVSVAIEAGGR.A
R2/RRR2-15/2	1539.215	1539.719	-979.642	0.539	955.429	0.592	21	0.154	K.AVANQPVSVAIEAGGR.A
R2/RRR2-23/2	1540.212	1539.719	321.343	0.557	1010.954	0.567	21	0.153	K.AVANQPVSVAIEAGGR.A
R2/RRR2-12/2	1335.368	1334.536	-126.034	0.506	1212.876	0.459	17	0.152	K.CGIAVEPSYPLK.K
R2/RRR2-16/2	1539.146	1539.719	-1024.870	0.475	1036.822	0.542	22	0.152	K.AVANQPVSVAIEAGGR.A
R2/RRR2-14/2	1539.307	1539.719	-268.098	0.506	955.095	0.563	22	0.151	K.AVANQPVSVAIEAGGR.A
R2/RRR2-9/2	1539.370	1539.719	-227.285	0.486	961.612	0.561	21	0.149	K.AVANQPVSVAIEAGGR.A
R2/RRR2-16/2	1539.443	1539.719	-179.395	0.529	943.083	0.553	22	0.148	K.AVANQPVSVAIEAGGR.A
R2/RRR2-1/2	1538.949	1539.719	-1153.409	0.381	1104.699	0.503	22	0.148	K.AVANQPVSVAIEAGGR.A
R2/RRR2-17/2	1539.299	1539.719	-273.429	0.494	954.574	0.556	21	0.148	K.AVANQPVSVAIEAGGR.A
R2/RRR2-23/2	1539.313	1539.719	-264.279	0.506	936.761	0.542	22	0.146	K.AVANQPVSVAIEAGGR.A
R2/RRR2-23/2	1538.675	1539.719	-1332.255	0.362	1048.755	0.478	22	0.141	K.AVANQPVSVAIEAGGR.A
R2/RRR2-12/2	1419.547	1419.606	-41.798	0.451	1107.460	0.451	16	0.140	R.AFQLYSSGIFTGK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1539.259	1539.719	-299.287	0.523	795.123	0.552	20	0.139	K.AVANQPVSVAIEAGGR.A
R2/RRR2-13/2	1335.293	1334.536	-182.983	0.511	1142.271	0.400	17	0.137	K.CGIAVEPSYPLK.K
R2/RRR2-15/2	1538.613	1539.719	-1372.335	0.358	942.081	0.491	21	0.136	K.AVANQPVSVAIEAGGR.A
R2/RRR2-1/2	1539.179	1539.719	-1002.972	0.447	791.718	0.522	20	0.134	K.AVANQPVSVAIEAGGR.A
R2/RRR2-12/2	1539.129	1539.719	-1035.939	0.427	823.986	0.477	20	0.130	K.AVANQPVSVAIEAGGR.A
R2/RRR2-14/2	1419.268	1419.606	-239.100	0.407	910.320	0.450	16	0.129	R.AFQLYSSGIFTGK.C
R2/RRR2-12/2	1334.076	1334.536	-345.777	0.365	1317.025	0.224	17	0.123	K.CGIAVEPSYPLK.K
R2/RRR2-13/2	1462.194	1462.709	-1039.703	0.458	1097.867	0.310	18	0.122	K.CGIAVEPSYPLKK.G
R2/RRR2-13/2	1040.865	1041.099	-224.744	0.381	985.358	0.309	15	0.121	K.SWGESGYVR.M
R2/RRR2-14/2	1334.641	1334.536	78.563	0.396	949.222	0.300	16	0.115	K.CGIAVEPSYPLK.K
R2/RRR2-2/2	1538.646	1539.719	-1351.219	0.300	396.072	0.442	15	0.112	K.AVANQPVSVAIEAGGR.A
R2/RRR2-11/2	1040.863	1041.099	-226.862	0.391	798.546	0.247	14	0.111	K.SWGESGYVR.M
R2/RRR2-13/2	1041.074	1041.099	-23.593	0.382	797.017	0.235	14	0.110	K.SWGESGYVR.M
R2/RRR2-11/2	1040.869	1041.099	-221.097	0.379	660.877	0.245	13	0.110	K.SWGESGYVR.M
R2/RRR2-11/2	1418.679	1419.606	-1362.867	0.280	509.238	0.347	14	0.109	R.AFQLYSSGIFTGK.C
R2/RRR2-23/2	1419.123	1419.606	-341.275	0.292	582.742	0.305	15	0.108	R.AFQLYSSGIFTGK.C
R2/RRR2-11/2	1040.866	1041.099	-224.509	0.308	885.029	0.205	14	0.108	K.SWGESGYVR.M
R2/RRR2-12/2	1040.879	1041.099	-211.685	0.323	658.051	0.205	13	0.108	K.SWGESGYVR.M
R2/RRR2-13/2	1418.653	1419.606	-1380.583	0.297	760.652	0.241	16	0.107	R.AFQLYSSGIFTGK.C
R2/RRR2-12/2	1334.052	1334.536	-363.772	0.373	970.830	0.210	15	0.105	K.CGIAVEPSYPLK.K
R2/RRR2-12/2	1040.903	1041.099	-188.860	0.297	795.756	0.148	14	0.105	K.SWGESGYVR.M
R2/RRR2-15/2	1420.289	1419.606	-223.842	0.264	663.584	0.201	16	0.105	R.AFQLYSSGIFTGK.C
R2/RRR2-23/2	1040.981	1041.099	-113.219	0.363	707.691	0.144	13	0.104	K.SWGESGYVR.M
R2/RRR2-11/2	1462.478	1462.709	-158.447	0.289	541.460	0.219	15	0.101	K.CGIAVEPSYPLKK.G
R2/RRR2-14/2	1419.000	1419.606	-1135.287	0.212	637.601	0.100	14	0.101	R.AFQLYSSGIFTGK.C
R2/RRR2-13/2	1040.302	1041.099	-1732.517	0.185	829.604	0.086	14	0.101	K.SWGESGYVR.M
R2/RRR2-13/3	1462.543	1462.709	-113.745	0.401	790.494	0.318	23	0.076	K.CGIAVEPSYPLKK.G
R2/RRR2-11/3	1462.496	1462.709	-146.147	0.433	962.260	0.296	25	0.075	-.CGIAVEPSYPLKK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/3	1463.011	1462.709	207.026	0.432	793.454	0.295	24	0.070	-.CGIAVEPSYPLKK.-
R2/RRR2-11/3	1462.014	1462.709	-1162.735	0.359	850.367	0.198	23	0.065	-.CGIAVEPSYPLKK.-
R2/RRR2-13/3	1462.697	1462.709	-8.389	0.396	830.601	0.189	24	0.064	-.CGIAVEPSYPLKK.-
R2/RRR2-2/1	401.057	401.396	-847.546	-2.499	10.000	0.000	1	0.873	-.GPGGGG.-
R2/RRR2-23/1	401.095	401.396	-753.753	-2.100	1.085	0.000	1	0.838	R.GPGGGG.-
R2/RRR2-19/1	401.396	401.396	-1.296	-1.742	2.034	0.000	1	0.793	R.GPGGGG.-
R2/RRR2-28/1	401.327	401.396	-172.904	-0.812	10.719	0.000	2	0.776	R.GPGGGG.-
R2/RRR2-24/1	401.465	401.396	171.167	-1.270	1.046	0.000	1	0.758	R.GPGGGG.-
R2/RRR2-23/1	401.236	401.396	-399.515	-1.060	1.517	0.000	1	0.751	R.GPGGGG.-
R2/RRR2-17/1	401.235	401.396	-403.637	-1.667	20.769	0.000	2	0.735	-.GPGGGG.-
R2/RRR2-27/1	401.657	401.396	651.038	-1.083	32.757	0.133	3	0.725	R.GPGGGG.-
R2/RRR2-28/1	401.483	401.396	216.294	-1.216	13.425	0.000	2	0.723	-.GPGGGG.-
R2/RRR2-2/1	401.094	401.396	-755.739	-0.737	10.000	0.000	1	0.703	-.GPGGGG.-
R2/RRR2-21/1	401.206	401.396	-476.144	-1.229	34.732	0.386	3	0.641	R.GPGGGG.-
R2/RRR2-13/1	401.232	401.396	-408.826	-1.238	21.194	0.448	2	0.620	R.GPGGGG.-
R2/RRR2-30/1	401.073	401.396	-806.758	-1.460	33.096	0.472	3	0.592	-.GPGGGG.-
R2/RRR2-24/1	401.194	401.396	-505.760	-1.049	1.288	0.485	1	0.559	-.GPGGGG.-
R2/RRR2-1/1	401.229	401.396	-416.763	-1.100	49.857	0.681	4	0.542	R.GPGGGG.-
R2/RRR2-25/1	401.206	401.396	-473.854	-1.200	19.760	0.686	3	0.541	R.GPGGGG.-
R2/RRR2-29/1	401.403	401.396	16.700	-0.483	45.572	0.826	4	0.535	R.GPGGGG.-
R2/RRR2-2/1	401.175	401.396	-552.479	-1.556	21.671	0.741	2	0.533	-.GPGGGG.-
R2/RRR2-19/1	401.177	401.396	-547.746	-1.144	21.126	0.700	2	0.530	R.GPGGGG.-
R2/RRR2-30/1	401.230	401.396	-415.237	-1.128	20.996	0.707	2	0.526	R.GPGGGG.-
R2/RRR2-20/1	401.343	401.396	-133.543	-1.164	10.000	0.695	1	0.500	-.GPGGGG.-
R2/RRR2-18/1	401.176	401.396	-549.578	-0.341	55.897	0.970	4	0.487	R.GPGGGG.-
R2/RRR2-20/1	401.239	401.396	-392.342	-0.678	21.355	0.787	2	0.473	-.GPGGGG.-
R2/RRR2-7/3	1363.605	1363.547	42.450	0.585	2414.030	0.526	26	0.333	R.IRHQLACATHR.F
R2/RRR2-7/2	1697.539	1697.953	-244.623	0.498	2120.927	0.545	23	0.290	R.VIEVGEVDPAAYPLPK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1698.249	1697.953	174.932	0.506	1872.257	0.590	22	0.261	R.VIEVGEVDPAAYPLPK.T
R2/RRR2-7/2	1697.267	1697.953	-996.262	0.429	1898.799	0.528	22	0.248	R.VIEVGEVDPAAYPLPK.T
R2/RRR2-7/2	1428.018	1428.487	-329.461	0.416	713.562	0.579	20	0.138	K.ENPAPSASDIEAAR.V
R2/RRR2-7/2	1287.336	1287.445	-84.705	0.459	514.962	0.456	17	0.123	K.QEITAAVAELNK.A
R2/RRR2-7/2	1287.369	1287.445	-59.024	0.451	516.626	0.392	17	0.118	K.QEITAAVAELNK.A
R2/RRR2-7/2	1287.125	1287.445	-248.902	0.460	383.913	0.397	16	0.117	K.QEITAAVAELNK.A
R2/RRR2-7/3	1088.235	1088.283	-43.903	0.528	1111.794	0.280	18	0.078	K.TKLTLENLR.D
R2/RRR2-7/3	1088.694	1088.283	378.775	0.527	1187.985	0.204	19	0.069	K.TKLTLENLR.D
R2/RRR2-6/2	1851.364	1852.034	-904.742	0.509	1419.652	0.533	24	0.185	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-6/2	1852.535	1852.034	-269.891	0.568	1344.120	0.534	24	0.177	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-6/2	1851.336	1852.034	-919.834	0.506	1425.961	0.463	24	0.170	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-6/2	1334.195	1334.632	-328.953	0.442	1105.328	0.528	21	0.158	K.KPAAPVKPVAEVK.K
R2/RRR2-6/2	1334.279	1334.632	-265.524	0.420	982.523	0.475	20	0.140	K.KPAAPVKPVAEVK.K
R2/RRR2-6/2	1334.283	1334.632	-262.587	0.457	905.925	0.452	20	0.134	K.KPAAPVKPVAEVK.K
R2/RRR2-6/2	1468.244	1468.641	-271.234	0.453	1011.379	0.397	17	0.130	K.WHAPLIDNPNYK.G
R2/RRR2-6/2	1468.259	1468.641	-260.808	0.440	993.831	0.391	17	0.128	K.WHAPLIDNPNYK.G
R2/RRR2-6/2	1468.948	1468.641	209.657	0.467	877.958	0.429	16	0.127	K.WHAPLIDNPNYK.G
R2/RRR2-6/3	1851.911	1852.034	-66.260	0.381	1451.552	0.368	26	0.123	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-6/2	1306.245	1306.531	-219.858	0.415	616.011	0.423	17	0.122	K.LADIPFLEPYK.T
R2/RRR2-6/2	1143.330	1144.343	-1765.726	0.342	1004.240	0.323	16	0.120	K.IIDVIEKGEK.Q
R2/RRR2-2/2	1851.436	1852.034	-865.491	0.454	748.549	0.440	19	0.120	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-6/2	1306.371	1306.531	-122.928	0.409	437.625	0.415	15	0.118	K.LADIPFLEPYK.T
R2/RRR2-6/2	1306.238	1306.531	-225.296	0.389	406.502	0.414	14	0.116	K.LADIPFLEPYK.T
R2/RRR2-3/2	1851.246	1852.034	-968.754	0.390	845.915	0.317	19	0.110	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-2/2	1306.011	1306.531	-1167.413	0.381	259.366	0.326	11	0.106	-.LADIPFLEPYK.-
R2/RRR2-1/2	1851.179	1852.034	-1004.902	0.347	642.497	0.252	17	0.102	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-6/2	1853.706	1852.034	-177.516	0.321	545.029	0.237	16	0.101	K.ANFLSADDFEPSLIPSK.T
R2/RRR2-6/3	1468.991	1468.641	239.272	0.511	1464.520	0.278	25	0.097	K.WHAPLIDNPNYK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1468.128	1468.641	-1033.216	0.484	1540.480	0.227	26	0.091	K.WHAPLIDNPNYK.G
R2/RRR2-6/3	1469.024	1468.641	261.895	0.449	1437.935	0.171	23	0.075	-.WHAPLIDNPNYK.-
R2/RRR2-11/2	1173.028	1173.385	-304.843	0.450	1355.024	0.542	20	0.183	K.VIAISDVTGAVK.N
R2/RRR2-10/2	1065.672	1066.259	-1493.658	0.441	1406.308	0.478	17	0.175	R.MGAFTLGVNR.V
R2/RRR2-10/2	1081.618	1082.259	-1521.020	0.430	1447.418	0.443	17	0.172	R.M*GAFTLGVNR.V
R2/RRR2-11/2	1172.969	1173.385	-355.275	0.452	1333.958	0.494	20	0.171	K.VIAISDVTGAVK.N
R2/RRR2-10/2	1173.271	1173.385	-96.905	0.433	1356.778	0.474	20	0.169	K.VIAISDVTGAVK.N
R2/RRR2-11/2	1302.541	1301.387	118.850	0.480	1125.993	0.554	18	0.164	K.DDGTLASYVGFR.V
R2/RRR2-11/2	1162.796	1162.320	410.375	0.485	1298.866	0.476	19	0.164	K.TAVANIPYGGAK.G
R2/RRR2-11/2	1162.106	1162.320	-185.072	0.452	1273.346	0.466	19	0.160	K.TAVANIPYGGAK.G
R2/RRR2-10/2	1161.369	1162.320	-1685.483	0.403	1183.777	0.508	18	0.158	K.TAVANIPYGGAK.G
R2/RRR2-11/2	1302.091	1301.387	-227.329	0.414	907.686	0.522	15	0.139	K.DDGTLASYVGFR.V
R2/RRR2-11/2	1173.083	1173.385	-257.757	0.398	1019.517	0.440	18	0.137	K.VIAISDVTGAVK.N
R2/RRR2-10/2	1162.207	1162.320	-97.828	0.473	1179.396	0.353	18	0.134	K.TAVANIPYGGAK.G
R2/RRR2-10/2	1081.319	1082.259	-1799.078	0.402	961.780	0.404	14	0.128	R.M*GAFTLGVNR.V
R2/RRR2-11/2	1162.078	1162.320	-209.098	0.443	974.214	0.315	17	0.118	K.TAVANIPYGGAK.G
R2/RRR2-10/2	1161.912	1162.320	-352.755	0.425	815.537	0.365	15	0.117	K.TAVANIPYGGAK.G
R2/RRR2-11/2	1557.745	1556.788	-27.479	0.355	737.859	0.401	15	0.112	R.GVLFATEALLAEHGK.G
R2/RRR2-1/2	1081.734	1082.259	-1414.011	0.263	673.216	0.142	14	0.102	-.M*GAFTLGVNR.-
R2/RRR2-17/2	1456.115	1455.595	-330.923	0.559	2191.872	0.576	22	0.313	K.GVISLDTSGSSYLR.A
R2/RRR2-17/2	1455.300	1455.595	-203.734	0.535	2292.861	0.509	22	0.310	K.GVISLDTSGSSYLR.A
R2/RRR2-17/2	1456.174	1455.595	-289.962	0.541	2143.766	0.580	22	0.306	K.GVISLDTSGSSYLR.A
R2/RRR2-17/2	1770.413	1769.936	270.293	0.563	1824.078	0.580	23	0.256	R.ILNPQYLSQSSDTFR.D
R2/RRR2-17/3	1771.000	1769.936	35.969	0.526	1883.840	0.441	31	0.198	R.ILNPQYLSQSSDTFR.D
R2/RRR2-17/2	1978.718	1979.268	-785.872	0.448	1508.439	0.414	22	0.169	K.IFVDTGAVVTFGLNALQGR.Q
R2/RRR2-17/3	1519.373	1519.769	-261.310	0.471	1165.732	0.512	29	0.125	R.KPLVVAPGGFYDQK.W
R2/RRR2-17/2	1003.275	1003.180	95.114	0.414	1048.945	0.315	13	0.122	K.AIQAFSPLR.I
R2/RRR2-17/2	1003.002	1003.180	-177.931	0.391	1004.661	0.279	13	0.116	K.AIQAFSPLR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1003.998	1003.180	-181.291	0.423	855.193	0.318	12	0.114	K.AIQAFSPLR.I
R2/RRR2-17/2	1002.321	1003.180	-1859.976	0.338	777.004	0.230	12	0.106	-.AIQAFSPLR.-
R2/RRR2-7/2	1563.516	1563.737	-141.786	0.568	2089.103	0.565	24	0.293	R.GINQVYIIGGDGTQK.G
R2/RRR2-7/2	1563.304	1563.737	-277.532	0.504	1686.909	0.561	22	0.228	R.GINQVYIIGGDGTQK.G
R2/RRR2-7/3	1980.809	1980.168	-182.079	0.536	1782.580	0.521	33	0.213	R.AINAAHVEAESAENGIGVVK.L
R2/RRR2-8/2	1458.984	1457.527	314.561	0.478	1109.449	0.515	18	0.155	K.SFGFDTAVEEAQR.A
R2/RRR2-7/2	1217.253	1217.351	-80.629	0.428	723.761	0.386	16	0.118	K.TIDNDIAVIDK.S
R2/RRR2-7/2	1066.983	1067.224	-226.472	0.257	864.221	0.348	12	0.114	R.HAYIPFYR.I
R2/RRR2-7/3	1981.033	1980.168	-68.586	0.497	1065.779	0.456	29	0.107	R.AINAAHVEAESAENGIGVVK.L
R2/RRR2-8/2	1067.117	1067.224	-100.693	0.135	718.636	0.301	12	0.100	R.HAYIPFYR.I
R2/RRR2-7/2	1066.455	1067.224	-1663.969	0.146	727.535	0.138	11	0.098	R.HAYIPFYR.I
R2/RRR2-7/3	1979.062	1980.168	-1067.727	0.399	832.074	0.446	25	0.090	R.AINAAHVEAESAENGIGVVK.L
R2/RRR2-8/2	1555.337	1554.729	-252.268	0.489	1756.126	0.566	20	0.240	R.LAIGDLATQYFADR.D
R2/RRR2-8/2	1402.882	1403.521	-1171.109	0.426	1276.947	0.467	18	0.161	K.TFSYAGFEQQPK.T
R2/RRR2-8/2	1321.889	1322.363	-359.339	0.417	1307.763	0.259	17	0.127	R.GGADQFIEEAER.S
R2/RRR2-8/2	1322.191	1322.363	-130.161	0.401	1253.821	0.226	16	0.118	R.GGADQFIEEAER.S
R2/RRR2-8/2	1175.089	1175.318	-195.530	0.264	997.654	0.310	15	0.115	K.SQFFVNSFAK.A
R2/RRR2-8/2	1326.181	1325.538	-270.008	0.357	641.065	0.420	13	0.112	R.DSFLVNGVAFKK.T
R2/RRR2-8/2	1356.198	1355.560	-268.275	0.557	1560.552	0.538	18	0.207	R.TFLDQLVEVYK.Q
R2/RRR2-8/2	1359.249	1359.581	-244.367	0.484	1818.695	0.306	18	0.181	K.VGLM*VQQQVNAR.F
R2/RRR2-8/2	1355.283	1355.560	-205.489	0.530	1353.705	0.517	17	0.178	R.TFLDQLVEVYK.Q
R2/RRR2-8/2	1151.379	1150.349	25.350	0.464	856.170	0.474	17	0.135	R.IPLVSFTGSTK.V
R2/RRR2-8/2	1360.874	1359.581	216.296	0.509	1271.748	0.333	17	0.135	K.VGLM*VQQQVNAR.F
R2/RRR2-8/2	1354.830	1355.560	-1281.417	0.327	804.272	0.389	15	0.118	R.TFLDQLVEVYK.Q
R2/RRR2-8/2	1150.923	1150.349	-372.080	0.382	619.947	0.381	15	0.116	R.IPLVSFTGSTK.V
R2/RRR2-8/2	889.095	889.077	20.366	0.440	719.739	0.302	11	0.115	K.RPDIIFK.W
R2/RRR2-8/2	888.370	889.077	-1927.175	0.366	787.493	0.308	11	0.115	K.RPDIIFK.W
R2/RRR2-8/2	1426.224	1425.717	-346.787	0.370	595.560	0.419	13	0.112	R.EELFGPVLYVMK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1425.964	1425.717	173.389	0.292	585.837	0.443	14	0.112	R.EELFGPVLYVMK.V
R2/RRR2-8/2	888.312	889.077	-1992.770	0.344	697.342	0.256	11	0.110	K.RPDIIFK.W
R2/RRR2-2/2	1151.135	1150.349	-187.261	0.254	447.426	0.370	13	0.108	R.IPLVSFTGSTK.V
R2/RRR2-1/2	1151.210	1150.349	-121.947	0.235	487.110	0.329	12	0.102	-.IPLVSFTGSTK.-
R2/RRR2-7/2	1150.478	1150.349	112.423	0.251	327.015	0.318	10	0.091	-.IPLVSFTGSTK.-
R2/RRR2-6/2	1505.252	1505.742	-327.035	0.520	2073.491	0.485	21	0.260	K.IAGIQGGFFELQPK.E
R2/RRR2-6/2	1336.079	1335.534	-341.593	0.576	1462.274	0.505	19	0.184	R.INTLLQGYSGIR.F
R2/RRR2-1/2	1507.150	1505.742	271.201	0.518	1481.550	0.498	19	0.183	K.IAGIQGGFFELQPK.E
R2/RRR2-2/2	1505.683	1505.742	-39.651	0.493	1596.241	0.423	20	0.180	K.IAGIQGGFFELQPK.E
R2/RRR2-6/2	1335.180	1335.534	-265.895	0.517	1468.599	0.429	20	0.170	R.INTLLQGYSGIR.F
R2/RRR2-6/2	1336.174	1335.534	-270.096	0.536	1335.328	0.480	20	0.168	R.INTLLQGYSGIR.F
R2/RRR2-6/2	1335.174	1335.534	-270.298	0.555	1317.636	0.454	19	0.160	R.INTLLQGYSGIR.F
R2/RRR2-2/2	1335.769	1335.534	176.664	0.512	1205.694	0.471	19	0.155	R.INTLLQGYSGIR.F
R2/RRR2-1/2	1336.561	1335.534	20.555	0.504	1094.109	0.474	19	0.148	R.INTLLQGYSGIR.F
R2/RRR2-6/2	1334.410	1335.534	-1596.288	0.428	1080.756	0.458	18	0.143	R.INTLLQGYSGIR.F
R2/RRR2-5/2	1335.260	1335.534	-206.003	0.451	1121.073	0.427	18	0.141	R.INTLLQGYSGIR.F
R2/RRR2-17/2	1336.077	1335.534	-343.060	0.473	992.783	0.447	18	0.138	R.INTLLQGYSGIR.F
R2/RRR2-2/2	1335.251	1335.534	-212.514	0.487	1126.188	0.397	18	0.137	R.INTLLQGYSGIR.F
R2/RRR2-1/2	1505.575	1505.742	-111.542	0.432	1113.542	0.407	18	0.135	K.IAGIQGGFFELQPK.E
R2/RRR2-5/2	1335.154	1335.534	-285.708	0.436	958.728	0.404	18	0.130	R.INTLLQGYSGIR.F
R2/RRR2-7/2	1505.865	1505.742	81.501	0.410	959.285	0.439	16	0.129	K.IAGIQGGFFELQPK.E
R2/RRR2-2/2	1334.642	1335.534	-1422.261	0.350	827.298	0.415	18	0.124	R.INTLLQGYSGIR.F
R2/RRR2-6/2	1481.195	1481.759	-1059.347	0.349	780.683	0.436	16	0.120	K.LLNANVTPCLPLR.G
R2/RRR2-5/2	1334.443	1335.534	-1571.476	0.343	754.618	0.372	16	0.117	R.INTLLQGYSGIR.F
R2/RRR2-5/2	1507.090	1505.742	231.567	0.351	249.984	0.370	16	0.115	K.IAGIQGGFFELQPK.E
R2/RRR2-6/2	1480.862	1481.759	-1284.720	0.235	593.844	0.276	15	0.102	K.LLNANVTPCLPLR.G
R2/RRR2-5/2	1507.087	1505.742	229.130	0.250	214.641	0.325	14	0.101	-.IAGIQGGFFELQPK.-
R2/RRR2-6/2	1442.154	1442.509	-246.512	0.441	1693.030	0.388	17	0.187	K.ELEQQEYYDPK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1442.125	1442.509	-266.553	0.343	1292.400	0.281	15	0.129	K.ELEQQEYYDPK.L
R2/RRR2-6/2	1311.365	1311.469	-79.698	0.452	697.986	0.462	17	0.128	R.QVLVDLQENPR.A
R2/RRR2-6/2	1312.169	1311.469	-229.689	0.476	702.452	0.461	16	0.127	R.QVLVDLQENPR.A
R2/RRR2-6/2	1187.082	1187.370	-243.063	0.340	941.753	0.282	14	0.112	K.TVELKPDWAK.G
R2/RRR2-6/3	1659.645	1659.740	-57.596	0.493	1248.119	0.400	24	0.109	K.ANRGDLTQEEIQER.Q
R2/RRR2-6/2	1318.207	1318.372	-125.632	0.436	953.552	0.197	15	0.104	-.GDLTQEEIQER.-
R2/RRR2-6/2	1317.846	1318.372	-1161.760	0.389	1047.010	0.164	15	0.103	R.GDLTQEEIQER.Q
R2/RRR2-6/3	1660.555	1659.740	-111.905	0.514	1331.717	0.331	27	0.099	K.ANRGDLTQEEIQER.Q
R2/RRR2-6/3	1659.185	1659.740	-940.068	0.460	1060.376	0.339	24	0.085	-.ANRGDLTQEEIQER.-
R2/RRR2-13/2	1970.643	1970.261	194.119	0.650	3958.251	0.551	30	0.772	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-14/2	1969.730	1970.261	-779.948	0.607	3723.089	0.544	30	0.691	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-14/3	1969.812	1970.261	-228.812	0.512	3555.290	0.477	37	0.671	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-14/3	1970.987	1970.261	-139.627	0.563	3085.659	0.569	37	0.561	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-13/2	1969.461	1970.261	-916.636	0.573	3073.000	0.579	28	0.513	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-14/2	1969.629	1970.261	-831.085	0.577	3077.257	0.560	28	0.505	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-13/2	1969.619	1970.261	-836.248	0.583	3094.980	0.539	28	0.500	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-14/2	1969.750	1970.261	-769.497	0.583	2925.556	0.543	28	0.457	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-14/2	1661.848	1662.872	-1221.649	0.389	1862.041	0.357	23	0.199	K.AVVAQYNASQLITQR.E
R2/RRR2-14/2	1662.421	1662.872	-271.738	0.502	1661.370	0.424	22	0.188	K.AVVAQYNASQLITQR.E
R2/RRR2-13/3	1969.651	1970.261	-820.018	0.466	1684.734	0.486	32	0.185	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-14/2	1662.401	1662.872	-284.262	0.515	1710.074	0.384	23	0.185	K.AVVAQYNASQLITQR.E
R2/RRR2-13/2	1661.903	1662.872	-1188.235	0.377	1724.735	0.345	22	0.179	K.AVVAQYNASQLITQR.E
R2/RRR2-14/2	1373.699	1374.485	-1304.280	0.516	1243.842	0.506	20	0.165	R.ARPNLVESTSGSR.D
R2/RRR2-14/2	1374.104	1374.485	-278.412	0.536	1168.810	0.519	19	0.160	R.ARPNLVESTSGSR.D
R2/RRR2-13/2	1374.185	1374.485	-219.145	0.508	1202.442	0.469	20	0.155	R.ARPNLVESTSGSR.D
R2/RRR2-14/2	1374.074	1374.485	-300.248	0.519	1234.547	0.455	20	0.155	R.ARPNLVESTSGSR.D
R2/RRR2-13/2	1662.471	1662.872	-242.124	0.457	1463.094	0.360	21	0.154	K.AVVAQYNASQLITQR.E
R2/RRR2-13/2	1374.179	1374.485	-223.423	0.479	1183.379	0.464	20	0.152	R.ARPNLVESTSGSR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/3	1969.085	1970.261	-1108.361	0.365	1361.839	0.505	30	0.149	K.SAELIGQAIANNPAFLALR.Q
R2/RRR2-13/2	1373.574	1374.485	-1395.764	0.495	1110.626	0.466	19	0.147	R.ARPNLVESTSGSR.D
R2/RRR2-14/2	1205.506	1206.459	-1625.398	0.305	570.240	0.527	16	0.120	R.VPVPPAGAGTLVK.L
R2/RRR2-14/2	1206.264	1206.459	-162.260	0.273	493.260	0.462	17	0.113	R.VPVPPAGAGTLVK.L
R2/RRR2-14/2	1207.178	1206.459	-234.047	0.246	372.129	0.553	16	0.113	R.VPVPPAGAGTLVK.L
R2/RRR2-13/2	1206.348	1206.459	-92.320	0.280	476.734	0.437	16	0.112	R.VPVPPAGAGTLVK.L
R2/RRR2-13/3	1663.059	1662.872	113.029	0.336	1061.569	0.287	24	0.076	-.AVVAQYNASQLITQR.-
R2/RRR2-6/2	1678.335	1678.891	-929.879	0.550	2340.314	0.545	23	0.328	K.NQVAM*NPINTVFDAK.R
R2/RRR2-6/2	1678.277	1678.891	-965.076	0.551	2395.687	0.504	23	0.325	K.NQVAM*NPINTVFDAK.R
R2/RRR2-6/2	1678.222	1678.891	-997.864	0.555	2069.070	0.537	22	0.275	K.NQVAM*NPINTVFDAK.R
R2/RRR2-6/2	1678.045	1678.891	-1103.475	0.540	2141.191	0.482	22	0.270	K.NQVAM*NPINTVFDAK.R
R2/RRR2-6/2	1228.592	1229.325	-1414.976	0.427	2023.038	0.373	19	0.226	R.VEIIANDQGNR.I
R2/RRR2-6/2	1228.703	1229.325	-1324.369	0.492	1802.834	0.457	18	0.217	R.VEIIANDQGNR.I
R2/RRR2-6/2	1662.289	1662.892	-967.361	0.519	1718.880	0.509	22	0.215	K.NQVAMNPINTVFDAK.R
R2/RRR2-6/2	1662.460	1662.892	-260.758	0.535	1684.684	0.525	22	0.215	K.NQVAMNPINTVFDAK.R
R2/RRR2-6/2	1229.130	1229.325	-159.241	0.514	1613.815	0.431	18	0.187	R.VEIIANDQGNR.I
R2/RRR2-6/2	1834.452	1835.078	-889.096	0.492	493.032	0.482	20	0.121	K.NQVAM*NPINTVFDAKR.L
R2/RRR2-6/2	1834.291	1835.078	-977.082	0.513	329.166	0.486	17	0.117	K.NQVAM*NPINTVFDAKR.L
R2/RRR2-6/2	1474.148	1474.554	-275.962	0.261	497.846	0.464	18	0.112	R.TTPSYVGFTDTER.L
R2/RRR2-6/2	1473.946	1474.554	-1093.879	0.262	476.893	0.447	18	0.112	R.TTPSYVGFTDTER.L
R2/RRR2-6/2	1473.567	1474.554	-1352.150	0.245	448.586	0.443	18	0.110	R.TTPSYVGFTDTER.L
R2/RRR2-8/2	999.985	1000.174	-189.793	0.539	1910.967	0.486	17	0.240	K.AAGEVLALQK.R
R2/RRR2-8/2	1217.924	1218.336	-339.145	0.461	2040.511	0.414	20	0.240	R.ALIAEGSCGSPR.S
R2/RRR2-8/2	1000.095	1000.174	-79.345	0.522	1810.346	0.463	17	0.220	K.AAGEVLALQK.R
R2/RRR2-8/2	999.803	1000.174	-372.784	0.498	1780.720	0.465	17	0.216	K.AAGEVLALQK.R
R2/RRR2-8/2	1816.080	1816.951	-1033.290	0.487	1219.724	0.639	22	0.187	K.QGVAVTQENSLLDNTAR.I
R2/RRR2-8/2	1264.389	1264.453	-50.123	0.544	1350.741	0.539	20	0.183	R.ILAFSQDVVSGK.I
R2/RRR2-8/2	1263.538	1264.453	-1520.126	0.414	1263.074	0.597	20	0.182	R.ILAFSQDVVSGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1816.349	1816.951	-884.569	0.494	1063.387	0.596	20	0.163	K.QGVAVTQENSLLDNTAR.I
R2/RRR2-7/2	1264.413	1264.453	-31.142	0.392	1205.526	0.494	19	0.157	R.ILAFSQDVVSGK.I
R2/RRR2-8/2	1217.286	1218.336	-1688.523	0.347	1341.881	0.396	19	0.152	R.ALIAEGSCGSPR.S
R2/RRR2-7/2	1264.238	1264.453	-170.218	0.383	876.976	0.485	16	0.133	R.ILAFSQDVVSGK.I
R2/RRR2-7/2	1264.578	1264.453	99.859	0.419	736.669	0.420	14	0.119	R.ILAFSQDVVSGK.I
R2/RRR2-8/2	1186.429	1187.330	-1607.468	0.361	842.005	0.319	16	0.115	R.DPGLAPNSFLR.T
R2/RRR2-8/2	1187.198	1187.330	-111.753	0.391	613.152	0.370	15	0.115	R.DPGLAPNSFLR.T
R2/RRR2-7/2	1187.293	1187.330	-31.515	0.301	569.262	0.317	13	0.107	R.DPGLAPNSFLR.T
R2/RRR2-1/2	1264.800	1264.453	275.733	0.224	252.270	0.393	11	0.102	-.ILAFSQDVVSGK.-
R2/RRR2-8/2	1217.247	1218.336	-1720.865	0.264	807.675	0.113	17	0.099	R.ALIAEGSCGSPR.S
R2/RRR2-8/2	1423.191	1422.565	-263.905	0.511	1857.684	0.483	24	0.235	R.YGTAGLLSPNTEAK.I
R2/RRR2-8/2	1732.481	1732.873	-226.756	0.531	1119.954	0.492	20	0.150	K.NAEATQSTLTPDGWLK.T
R2/RRR2-8/2	1367.260	1367.536	-202.525	0.435	774.766	0.559	19	0.138	R.HSGVVALIDAATGR.R
R2/RRR2-8/3	1562.806	1562.799	5.036	0.400	849.554	0.557	31	0.109	R.AVAGAASALAAHPVSLR.K
R2/RRR2-8/2	1784.566	1784.989	-237.908	0.258	704.312	0.332	19	0.104	R.IVATIEEISATTPDPAR.R
R2/RRR2-8/3	1563.693	1562.799	-67.590	0.409	878.131	0.500	31	0.101	R.AVAGAASALAAHPVSLR.K
R2/RRR2-13/2	1488.292	1488.629	-227.106	0.531	1893.596	0.560	24	0.258	R.TKGEAGTGNVVEAVR.H
R2/RRR2-13/2	1488.375	1488.629	-170.661	0.539	1743.688	0.568	23	0.237	R.TKGEAGTGNVVEAVR.H
R2/RRR2-13/2	1488.316	1488.629	-210.731	0.534	1583.849	0.570	22	0.215	R.TKGEAGTGNVVEAVR.H
R2/RRR2-13/2	1450.248	1450.509	-181.038	0.475	1393.695	0.524	18	0.184	R.NM*DDDEVFSYAK.R
R2/RRR2-13/2	1258.976	1259.351	-299.398	0.454	1206.600	0.387	21	0.142	K.GEAGTGNVVEAVR.H
R2/RRR2-13/2	1367.071	1366.608	339.472	0.500	595.167	0.574	17	0.137	R.IAAPYDLVM*QTK.Q
R2/RRR2-13/2	1366.286	1366.608	-236.722	0.444	790.313	0.505	18	0.135	R.IAAPYDLVM*QTK.Q
R2/RRR2-13/2	1259.024	1259.351	-260.487	0.487	1052.441	0.409	19	0.135	K.GEAGTGNVVEAVR.H
R2/RRR2-13/2	1366.234	1366.608	-274.907	0.376	569.731	0.366	16	0.113	R.IAAPYDLVM*QTK.Q
R2/RRR2-13/3	1488.573	1488.629	-37.730	0.510	1068.418	0.359	27	0.088	-.TKGEAGTGNVVEAVR.-
R2/RRR2-13/3	1488.031	1488.629	-1076.746	0.516	956.678	0.338	26	0.076	-.TKGEAGTGNVVEAVR.-
R2/RRR2-14/3	1488.689	1488.629	40.857	0.434	802.561	0.312	25	0.073	-.TKGEAGTGNVVEAVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/3	1487.154	1488.629	-1668.670	0.356	940.382	0.199	23	0.064	R.TKGEAGTGNVVEAVR.H
R2/RRR2-13/3	1488.274	1488.629	-239.005	0.447	532.127	0.336	21	0.047	-.TKGEAGTGNVVEAVR.-
R2/RRR2-4/2	1978.525	1978.232	148.171	0.604	2966.736	0.509	25	0.454	R.SGYIQLLDGSVVLLDEGAK.A
R2/RRR2-4/2	1521.137	1520.624	-321.285	0.547	2315.473	0.537	23	0.322	R.VEQGSLTGETASVNK.T
R2/RRR2-4/2	1520.227	1520.624	-261.718	0.517	2215.612	0.545	22	0.306	R.VEQGSLTGETASVNK.T
R2/RRR2-4/2	1976.980	1978.232	-1142.914	0.409	2366.389	0.422	24	0.296	R.SGYIQLLDGSVVLLDEGAK.A
R2/RRR2-4/2	1519.452	1520.624	-1433.798	0.387	2110.967	0.426	22	0.253	R.VEQGSLTGETASVNK.T
R2/RRR2-2/2	1979.783	1978.232	-227.560	0.570	1453.123	0.543	23	0.188	R.SGYIQLLDGSVVLLDEGAK.A
R2/RRR2-3/2	1520.091	1520.624	-1011.298	0.454	1641.351	0.318	21	0.163	R.VEQGSLTGETASVNK.T
R2/RRR2-4/2	1468.986	1469.576	-1085.487	0.301	1049.995	0.473	20	0.138	R.EIGVFGSTEDISSK.S
R2/RRR2-4/2	896.035	896.028	8.115	0.427	735.615	0.431	11	0.124	R.HAAPSVWK.L
R2/RRR2-4/2	896.103	896.028	83.945	0.365	716.134	0.380	11	0.117	R.HAAPSVWK.L
R2/RRR2-4/2	896.282	896.028	284.055	0.342	559.133	0.401	11	0.116	R.HAAPSVWK.L
R2/RRR2-4/2	1000.531	1001.119	-1591.822	0.401	1101.639	0.216	13	0.112	K.GAVENLLER.S
R2/RRR2-1/2	1470.242	1469.576	-227.312	0.435	469.942	0.414	15	0.111	R.EIGVFGSTEDISSK.S
R2/RRR2-1/2	1001.165	1001.119	45.725	0.378	972.955	0.226	13	0.110	K.GAVENLLER.S
R2/RRR2-5/2	896.491	896.028	518.758	0.220	283.964	0.293	9	0.109	R.HAAPSVWK.L
R2/RRR2-1/2	895.981	896.028	-52.284	0.220	401.935	0.372	10	0.108	R.HAAPSVWK.L
R2/RRR2-4/2	1000.478	1001.119	-1645.141	0.382	903.872	0.180	12	0.103	K.GAVENLLER.S
R2/RRR2-2/2	1978.872	1978.232	-182.622	0.281	481.718	0.315	18	0.103	R.SGYIQLLDGSVVLLDEGAK.A
R2/RRR2-1/2	1001.131	1001.119	12.094	0.371	734.733	0.207	12	0.101	-.GAVENLLER.-
R2/RRR2-6/3	1695.873	1694.874	-0.630	0.439	2173.951	0.355	30	0.226	R.AHDAVSAGSIALNAIQR.R
R2/RRR2-6/2	1729.244	1728.924	185.887	0.538	1375.317	0.565	22	0.190	K.SALAATVGIDSDFAYVK.I
R2/RRR2-6/2	980.904	981.088	-188.055	0.408	1125.777	0.416	15	0.141	K.SAVSYALNR.Q
R2/RRR2-6/2	1695.147	1694.874	161.818	0.405	1308.683	0.346	23	0.140	R.AHDAVSAGSIALNAIQR.R
R2/RRR2-5/2	981.784	981.088	-310.600	0.443	809.288	0.385	14	0.123	K.SAVSYALNR.Q
R2/RRR2-6/2	1173.010	1173.386	-321.548	0.278	790.772	0.346	14	0.109	K.GILLYGPPGTGK.T
R2/RRR2-6/2	1518.382	1519.724	-1546.973	0.325	990.672	0.207	16	0.104	K.SQFGIIILDDIER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1841.563	1840.028	-253.482	0.597	3761.487	0.577	29	0.726	R.AFIAGVADDNGYGWAIAK.A
R2/RRR2-13/2	1839.196	1840.028	-998.867	0.515	3323.701	0.527	28	0.565	R.AFIAGVADDNGYGWAIAK.A
R2/RRR2-13/2	1839.211	1840.028	-990.937	0.554	3354.988	0.500	28	0.560	R.AFIAGVADDNGYGWAIAK.A
R2/RRR2-12/2	1841.720	1840.028	-167.901	0.541	1737.634	0.502	26	0.216	R.AFIAGVADDNGYGWAIAK.A
R2/RRR2-12/2	1171.664	1172.317	-1415.071	0.424	732.104	0.471	18	0.129	R.VNTISAGPLGSR.A
R2/RRR2-12/2	1113.010	1113.205	-175.745	0.333	787.152	0.455	16	0.126	R.YAGSSNWTVK.E
R2/RRR2-12/2	1112.932	1113.205	-246.055	0.410	726.782	0.432	16	0.126	R.YAGSSNWTVK.E
R2/RRR2-12/2	1172.145	1172.317	-147.137	0.449	545.427	0.481	17	0.125	R.VNTISAGPLGSR.A
R2/RRR2-13/2	1171.980	1172.317	-288.296	0.512	610.736	0.456	17	0.125	R.VNTISAGPLGSR.A
R2/RRR2-12/2	1173.018	1172.317	-255.266	0.466	383.159	0.458	15	0.120	R.VNTISAGPLGSR.A
R2/RRR2-13/3	1441.371	1441.661	-202.017	0.425	1620.210	0.309	29	0.120	K.IRVNTISAGPLGSR.A
R2/RRR2-13/2	1171.538	1172.317	-1523.077	0.411	428.874	0.486	14	0.119	R.VNTISAGPLGSR.A
R2/RRR2-12/2	1112.800	1113.205	-364.692	0.402	614.180	0.369	15	0.118	R.YAGSSNWTVK.E
R2/RRR2-13/2	1112.920	1113.205	-256.179	0.420	538.415	0.380	14	0.117	R.YAGSSNWTVK.E
R2/RRR2-13/2	1112.906	1113.205	-269.384	0.423	592.429	0.351	15	0.117	R.YAGSSNWTVK.E
R2/RRR2-13/2	1112.400	1113.205	-1626.941	0.330	622.509	0.347	16	0.115	R.YAGSSNWTVK.E
R2/RRR2-13/3	1441.613	1441.661	-33.566	0.426	1000.626	0.282	23	0.074	K.IRVNTISAGPLGSR.A
R2/RRR2-20/2	1910.325	1910.072	132.824	0.635	3234.914	0.553	27	0.557	R.YALYDFDFVTGENVQK.S
R2/RRR2-20/2	1413.336	1412.617	-199.647	0.451	1645.502	0.451	19	0.196	K.IFFIAWSPSTSR.I
R2/RRR2-20/2	1411.999	1412.617	-1149.327	0.286	897.308	0.421	15	0.121	K.IFFIAWSPSTSR.I
R2/RRR2-20/2	1170.078	1169.394	-270.871	0.322	718.809	0.247	12	0.102	-.YVIFKIEEK.-
R2/RRR2-20/2	1169.581	1169.394	159.998	0.414	870.348	0.184	12	0.096	-.YVIFKIEEK.-
R2/RRR2-20/3	1602.129	1602.712	-990.848	0.413	1180.152	0.326	28	0.089	R.SHSNASSGM*GVAPDIR.D
R2/RRR2-20/3	1910.469	1910.072	208.622	0.331	1189.268	0.286	26	0.082	R.YALYDFDFVTGENVQK.S
R2/RRR2-20/3	1602.542	1602.712	-106.285	0.371	1074.791	0.269	27	0.075	R.SHSNASSGM*GVAPDIR.D
R2/RRR2-8/2	1192.057	1192.346	-243.383	0.494	1645.172	0.422	18	0.191	K.VGGIEVDSLFR.T
R2/RRR2-9/2	1376.241	1377.480	-1631.484	0.322	1825.435	0.303	19	0.185	R.DVADADSLVSSLGK.A
R2/RRR2-9/2	1817.463	1818.148	-929.904	0.449	879.236	0.515	23	0.137	R.TSIPGIFAIGDVAAFPLK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1817.787	1818.148	-199.546	0.457	685.915	0.569	21	0.134	R.TSIPGIFAIGDVAAFPLK.M
R2/RRR2-8/2	1818.601	1818.148	249.598	0.489	568.084	0.524	19	0.123	R.TSIPGIFAIGDVAAFPLK.M
R2/RRR2-10/2	1474.131	1473.612	-327.294	0.365	557.310	0.476	18	0.117	-.LPGFHTCVGSGGQR.-
R2/RRR2-8/2	1817.465	1818.148	-929.095	0.370	581.177	0.460	20	0.116	R.TSIPGIFAIGDVAAFPLK.M
R2/RRR2-9/2	1816.959	1818.148	-1208.598	0.322	388.072	0.449	17	0.110	R.TSIPGIFAIGDVAAFPLK.M
R2/RRR2-9/3	1401.850	1402.536	-1205.693	0.352	1301.313	0.362	26	0.104	K.GALIDKLEAGSDGR.V
R2/RRR2-10/2	1474.064	1473.612	307.688	0.362	335.837	0.323	14	0.102	-.LPGFHTCVGSGGQR.-
R2/RRR2-9/3	1401.523	1402.536	-1440.274	0.388	899.326	0.407	23	0.087	K.GALIDKLEAGSDGR.V
R2/RRR2-5/2	1459.015	1458.599	285.687	0.541	1832.816	0.547	18	0.245	K.YNVESWLDYLR.S
R2/RRR2-5/2	1459.090	1458.599	336.943	0.506	1791.820	0.499	18	0.226	K.YNVESWLDYLR.S
R2/RRR2-5/2	1459.027	1458.599	294.160	0.521	1797.831	0.463	17	0.217	K.YNVESWLDYLR.S
R2/RRR2-5/2	1177.092	1177.249	-133.412	0.503	1076.145	0.401	16	0.137	R.SLATDAEWQR.S
R2/RRR2-5/2	1250.174	1250.343	-135.603	0.474	963.899	0.426	16	0.135	R.LQNDIQSFER.E
R2/RRR2-5/2	936.955	937.098	-153.071	0.340	856.973	0.338	12	0.116	K.M*GLEFPAR.E
R2/RRR2-5/2	1358.030	1358.520	-361.226	0.381	753.729	0.346	16	0.113	K.VSLSENEPILEK.M
R2/RRR2-5/2	1064.092	1064.257	-155.404	0.344	852.500	0.376	14	0.121	-.FEILEAITK.-
R2/RRR2-2/2	1064.294	1064.257	34.902	0.390	810.729	0.365	14	0.118	-.FEILEAITK.-
R2/RRR2-2/2	1064.069	1064.257	-176.694	0.381	817.031	0.358	14	0.117	-.FEILEAITK.-
R2/RRR2-6/2	1064.094	1064.257	-152.815	0.492	792.700	0.327	14	0.116	-.FEILEAITK.-
R2/RRR2-1/2	1064.124	1064.257	-125.254	0.374	701.207	0.358	13	0.116	-.FEILEAITK.-
R2/RRR2-6/2	1065.005	1064.257	-236.550	0.495	842.341	0.358	14	0.114	-.FEILEAITK.-
R2/RRR2-2/2	1063.996	1064.257	-245.635	0.358	830.482	0.300	14	0.113	-.FEILEAITK.-
R2/RRR2-5/2	1064.093	1064.257	-154.483	0.234	550.078	0.381	12	0.109	-.FEILEAITK.-
R2/RRR2-1/2	1064.221	1064.257	-33.319	0.332	676.583	0.255	13	0.101	-.FEILEAITK.-
R2/RRR2-15/2	1817.529	1818.019	-270.441	0.559	3161.465	0.667	29	0.579	K.ALAVGADVSLDTATGNLTK.Y
R2/RRR2-15/2	1818.399	1818.019	209.698	0.612	2881.004	0.704	27	0.516	K.ALAVGADVSLDTATGNLTK.Y
R2/RRR2-14/2	1817.172	1818.019	-1019.530	0.481	2834.470	0.620	27	0.470	K.ALAVGADVSLDTATGNLTK.Y
R2/RRR2-15/2	1817.588	1818.019	-237.560	0.571	2673.626	0.653	28	0.441	K.ALAVGADVSLDTATGNLTK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1817.573	1818.019	-246.117	0.576	2484.823	0.682	26	0.408	K.ALAVGADVSLDTATGNLTK.Y
R2/RRR2-14/2	1817.488	1818.019	-844.876	0.517	2547.484	0.584	25	0.385	K.ALAVGADVSLDTATGNLTK.Y
R2/RRR2-15/2	1462.440	1462.673	-159.623	0.499	1869.301	0.460	20	0.225	K.ADLIFGEIQSQIK.N
R2/RRR2-15/2	1590.421	1590.845	-267.950	0.600	1721.519	0.510	22	0.217	K.KADLIFGEIQSQIK.N
R2/RRR2-15/2	1591.307	1590.845	290.943	0.637	1725.349	0.507	22	0.216	K.KADLIFGEIQSQIK.N
R2/RRR2-14/2	1591.635	1590.845	-132.820	0.613	1630.071	0.530	22	0.211	K.KADLIFGEIQSQIK.N
R2/RRR2-15/2	1590.375	1590.845	-296.982	0.616	1627.252	0.521	22	0.208	K.KADLIFGEIQSQIK.N
R2/RRR2-15/2	1463.337	1462.673	-230.309	0.554	1631.528	0.506	19	0.204	K.ADLIFGEIQSQIK.N
R2/RRR2-15/2	1463.176	1462.673	-340.288	0.527	1630.678	0.468	19	0.195	K.ADLIFGEIQSQIK.N
R2/RRR2-14/2	1461.836	1462.673	-1260.401	0.355	1670.654	0.336	18	0.171	K.ADLIFGEIQSQIK.N
R2/RRR2-14/2	1234.091	1233.399	-249.578	0.521	613.366	0.417	16	0.120	-.SILSFAVPDQR.-
R2/RRR2-15/2	1234.020	1233.399	-307.734	0.463	604.982	0.370	16	0.118	K.SILSFAVPDQR.S
R2/RRR2-15/2	1233.015	1233.399	-312.255	0.420	533.051	0.426	15	0.117	-.SILSFAVPDQR.-
R2/RRR2-15/2	1232.674	1233.399	-1403.636	0.416	610.104	0.388	16	0.117	-.SILSFAVPDQR.-
R2/RRR2-14/2	1232.703	1233.399	-1379.865	0.384	444.936	0.378	14	0.113	-.SILSFAVPDQR.-
R2/RRR2-14/2	1232.808	1233.399	-1293.839	0.370	653.555	0.228	15	0.106	-.SILSFAVPDQR.-
R2/RRR2-15/3	1590.967	1590.845	76.363	0.453	1218.617	0.186	23	0.067	K.KADLIFGEIQSQIK.N
R2/RRR2-14/3	1590.353	1590.845	-310.467	0.293	832.534	0.178	23	0.061	-.KADLIFGEIQSQIK.-
R2/RRR2-14/3	1590.367	1590.845	-301.688	0.253	804.375	0.152	21	0.060	-.KADLIFGEIQSQIK.-
R2/RRR2-24/2	1798.258	1798.924	-929.486	0.550	2502.468	0.616	24	0.389	K.CANGGLDLDWDTVFSK.I
R2/RRR2-24/2	1798.548	1798.924	-210.190	0.574	2410.723	0.580	24	0.355	K.CANGGLDLDWDTVFSK.I
R2/RRR2-24/2	1797.585	1798.924	-1305.265	0.489	2176.964	0.526	24	0.293	K.CANGGLDLDWDTVFSK.I
R2/RRR2-24/3	1840.348	1842.041	-2012.551	0.531	2086.371	0.570	32	0.291	R.SKYGWTAFCGPVGPTGR.D
R2/RRR2-24/2	1627.790	1626.790	0.029	0.548	1630.969	0.597	21	0.226	K.YGWTAFCGPVGPTGR.D
R2/RRR2-24/2	1627.186	1626.790	244.197	0.543	1568.106	0.569	21	0.210	K.YGWTAFCGPVGPTGR.D
R2/RRR2-24/2	1627.303	1626.790	-299.873	0.536	1478.972	0.571	21	0.200	K.YGWTAFCGPVGPTGR.D
R2/RRR2-24/3	1842.675	1842.041	-199.117	0.536	1404.873	0.572	28	0.173	R.SKYGWTAFCGPVGPTGR.D
R2/RRR2-24/2	1626.337	1626.790	-279.273	0.443	1437.362	0.472	20	0.173	K.YGWTAFCGPVGPTGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1625.729	1626.790	-1271.535	0.411	1206.954	0.528	19	0.161	K.YGWTAFCGPVGPTGR.D
R2/RRR2-24/2	1136.977	1137.185	-183.347	0.523	880.687	0.416	17	0.132	K.IDTDGQGFQR.G
R2/RRR2-24/2	1136.992	1137.185	-169.454	0.506	862.532	0.401	17	0.130	K.IDTDGQGFQR.G
R2/RRR2-22/2	1137.065	1137.185	-105.805	0.466	732.079	0.412	16	0.127	K.IDTDGQGFQR.G
R2/RRR2-24/2	1137.086	1137.185	-86.852	0.468	704.304	0.398	16	0.125	K.IDTDGQGFQR.G
R2/RRR2-23/2	1136.330	1137.185	-1637.179	0.398	799.876	0.383	17	0.125	K.IDTDGQGFQR.G
R2/RRR2-23/2	1137.076	1137.185	-95.359	0.485	555.078	0.409	15	0.123	K.IDTDGQGFQR.G
R2/RRR2-24/2	1137.272	1137.185	77.018	0.406	653.048	0.396	16	0.123	K.IDTDGQGFQR.G
R2/RRR2-24/2	1136.960	1137.185	-197.780	0.496	622.131	0.391	15	0.122	K.IDTDGQGFQR.G
R2/RRR2-22/2	1798.934	1798.924	5.471	0.462	550.409	0.527	16	0.122	K.CANGGLDLDWDTVFSK.I
R2/RRR2-23/2	1799.161	1798.924	131.911	0.406	872.343	0.416	18	0.121	K.CANGGLDLDWDTVFSK.I
R2/RRR2-24/2	1137.471	1137.185	252.671	0.491	633.460	0.382	15	0.121	K.IDTDGQGFQR.G
R2/RRR2-24/2	1136.432	1137.185	-1546.424	0.443	768.001	0.349	16	0.121	K.IDTDGQGFQR.G
R2/RRR2-23/2	1136.446	1137.185	-1534.339	0.455	653.055	0.355	15	0.119	K.IDTDGQGFQR.G
R2/RRR2-24/2	1137.304	1137.185	105.652	0.277	504.807	0.344	16	0.115	K.IDTDGQGFQR.G
R2/RRR2-23/2	1626.256	1626.790	-945.806	0.315	309.427	0.439	16	0.112	K.YGWTAFCGPVGPTGR.D
R2/RRR2-24/2	1136.706	1137.185	-422.080	0.248	518.905	0.261	15	0.111	K.IDTDGQGFQR.G
R2/RRR2-22/2	1136.905	1137.185	-246.898	0.240	569.632	0.230	15	0.109	K.IDTDGQGFQR.G
R2/RRR2-5/2	1883.695	1884.120	-226.558	0.539	1555.212	0.536	24	0.203	K.ILLDVADALEANEDLIR.S
R2/RRR2-5/2	1241.282	1241.459	-142.985	0.457	1552.414	0.457	19	0.186	K.SPGLDDILVALK.T
R2/RRR2-5/2	1241.230	1241.459	-184.717	0.527	1264.173	0.500	20	0.168	K.SPGLDDILVALK.T
R2/RRR2-5/2	1241.536	1241.459	62.364	0.454	1369.918	0.434	19	0.163	K.SPGLDDILVALK.T
R2/RRR2-6/3	1532.278	1531.658	-248.961	0.468	1387.874	0.457	26	0.136	R.RVDSAAVFHNASTR.F
R2/RRR2-5/2	1589.379	1589.774	-249.638	0.427	431.509	0.569	20	0.129	K.VIPIFNENDAISTR.K
R2/RRR2-5/2	1882.826	1884.120	-1222.177	0.403	967.368	0.411	21	0.127	K.ILLDVADALEANEDLIR.S
R2/RRR2-5/2	1589.300	1589.774	-299.186	0.412	351.133	0.539	18	0.123	K.VIPIFNENDAISTR.K
R2/RRR2-5/2	1588.872	1589.774	-1201.240	0.247	229.837	0.393	15	0.108	K.VIPIFNENDAISTR.K
R2/RRR2-5/3	1922.183	1922.169	7.630	0.416	1085.133	0.325	24	0.083	K.FREQLTETVESLLDLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1884.189	1884.120	36.635	0.401	1069.031	0.183	24	0.061	K.ILLDVADALEANEDLIR.S
R2/RRR2-14/2	1737.826	1738.962	-1232.774	0.548	2666.938	0.576	23	0.411	K.SPFQEYTDLLAKPTK.A
R2/RRR2-14/2	1797.569	1798.032	-258.664	0.619	2647.164	0.592	26	0.409	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1796.927	1798.032	-1174.989	0.574	2493.961	0.595	26	0.377	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-13/2	1669.745	1669.860	-68.898	0.539	2450.416	0.550	24	0.346	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1670.312	1669.860	271.684	0.589	2428.113	0.566	24	0.346	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1669.658	1669.860	-121.040	0.530	2344.989	0.575	24	0.334	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1738.361	1738.962	-923.620	0.559	2321.139	0.539	21	0.322	K.SPFQEYTDLLAKPTK.A
R2/RRR2-14/2	1670.003	1669.860	86.321	0.558	2256.096	0.583	24	0.319	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1738.489	1738.962	-272.666	0.565	2222.000	0.563	21	0.311	K.SPFQEYTDLLAKPTK.A
R2/RRR2-14/2	1798.312	1798.032	155.871	0.586	2122.347	0.600	25	0.305	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-13/2	1669.945	1669.860	51.351	0.536	2250.615	0.541	23	0.304	K.VLQFAGIEDVFTSSR.G
R2/RRR2-13/2	1738.360	1738.962	-924.113	0.509	1944.413	0.558	20	0.261	K.SPFQEYTDLLAKPTK.A
R2/RRR2-14/3	1798.092	1798.032	33.418	0.523	2246.965	0.446	35	0.261	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-13/2	1737.547	1738.962	-1393.914	0.526	1928.828	0.548	21	0.256	K.SPFQEYTDLLAKPTK.A
R2/RRR2-13/2	1670.087	1669.860	136.315	0.537	1850.280	0.554	21	0.241	K.VLQFAGIEDVFTSSR.G
R2/RRR2-16/2	1670.795	1669.860	-38.957	0.516	1268.761	0.605	19	0.181	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1404.117	1403.565	-320.071	0.509	1097.963	0.556	16	0.162	K.TYGFLTPDFWR.E
R2/RRR2-17/2	1669.816	1669.860	-26.295	0.419	1197.477	0.511	18	0.156	K.VLQFAGIEDVFTSSR.G
R2/RRR2-15/2	1670.847	1669.860	-7.592	0.468	1187.302	0.503	17	0.152	K.VLQFAGIEDVFTSSR.G
R2/RRR2-12/2	1670.589	1669.860	-162.234	0.508	974.963	0.529	17	0.142	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1403.094	1403.565	-337.233	0.453	787.674	0.554	14	0.139	K.TYGFLTPDFWR.E
R2/RRR2-13/2	1403.186	1403.565	-270.896	0.503	850.904	0.518	14	0.138	K.TYGFLTPDFWR.E
R2/RRR2-14/3	1797.679	1798.032	-197.154	0.421	1383.409	0.456	30	0.135	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1403.018	1403.565	-1106.069	0.473	856.954	0.468	15	0.132	K.TYGFLTPDFWR.E
R2/RRR2-15/2	1670.964	1669.860	62.384	0.418	906.777	0.487	17	0.132	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1403.222	1403.565	-245.673	0.420	824.698	0.454	14	0.127	K.TYGFLTPDFWR.E
R2/RRR2-1/2	1798.311	1798.032	155.599	0.459	803.357	0.459	18	0.124	K.KVLQFAGIEDVFTSSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1403.663	1403.565	69.466	0.387	761.154	0.429	14	0.122	K.TYGFLTPDFWR.E
R2/RRR2-14/2	1799.443	1798.032	228.714	0.424	925.979	0.392	18	0.121	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-15/2	1403.593	1403.565	19.399	0.417	915.922	0.360	14	0.120	-.TYGFLTPDFWR.-
R2/RRR2-14/3	1739.098	1738.962	78.448	0.472	1137.304	0.486	27	0.119	K.SPFQEYTDLLAKPTK.A
R2/RRR2-9/2	1671.236	1669.860	225.892	0.386	430.999	0.427	16	0.115	K.VLQFAGIEDVFTSSR.G
R2/RRR2-9/2	1798.667	1798.032	-203.573	0.436	649.288	0.414	17	0.114	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1670.783	1669.860	-45.772	0.401	427.773	0.422	14	0.112	K.VLQFAGIEDVFTSSR.G
R2/RRR2-14/2	1671.195	1669.860	200.989	0.343	626.654	0.387	15	0.111	K.VLQFAGIEDVFTSSR.G
R2/RRR2-8/2	1671.256	1669.860	237.904	0.367	461.982	0.376	15	0.111	K.VLQFAGIEDVFTSSR.G
R2/RRR2-17/2	1671.008	1669.860	89.346	0.395	494.728	0.393	14	0.110	K.VLQFAGIEDVFTSSR.G
R2/RRR2-16/2	1669.417	1669.860	-265.685	0.298	792.916	0.296	17	0.109	K.VLQFAGIEDVFTSSR.G
R2/RRR2-17/2	1671.294	1669.860	260.756	0.347	562.159	0.331	15	0.108	K.VLQFAGIEDVFTSSR.G
R2/RRR2-10/2	1671.145	1669.860	171.396	0.285	458.246	0.306	15	0.108	K.VLQFAGIEDVFTSSR.G
R2/RRR2-2/2	1670.740	1669.860	-71.935	0.249	353.784	0.366	13	0.106	-.VLQFAGIEDVFTSSR.-
R2/RRR2-11/2	1797.261	1798.032	-988.520	0.276	451.078	0.322	12	0.101	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-14/3	1738.662	1738.962	-173.037	0.488	797.790	0.464	25	0.095	K.SPFQEYTDLLAKPTK.A
R2/RRR2-14/3	1797.802	1798.032	-128.696	0.429	911.263	0.432	25	0.093	K.KVLQFAGIEDVFTSSR.G
R2/RRR2-13/3	1739.328	1738.962	211.269	0.467	764.606	0.438	24	0.090	K.SPFQEYTDLLAKPTK.A
R2/RRR2-14/3	1738.649	1738.962	-180.538	0.426	931.734	0.394	25	0.089	K.SPFQEYTDLLAKPTK.A
R2/RRR2-13/3	1739.366	1738.962	232.910	0.456	870.184	0.393	24	0.086	K.SPFQEYTDLLAKPTK.A
R2/RRR2-20/2	1072.050	1072.240	-178.348	0.466	1812.409	0.527	19	0.234	R.VLVVDGGGSLR.C
R2/RRR2-20/2	1071.537	1072.240	-1594.260	0.460	1686.354	0.552	19	0.223	R.VLVVDGGGSLR.C
R2/RRR2-21/2	1071.522	1072.240	-1608.452	0.457	1593.191	0.577	19	0.217	R.VLVVDGGGSLR.C
R2/RRR2-21/2	1071.948	1072.240	-273.395	0.419	1466.389	0.526	19	0.190	R.VLVVDGGGSLR.C
R2/RRR2-21/2	1072.229	1072.240	-11.032	0.465	1522.466	0.473	19	0.186	R.VLVVDGGGSLR.C
R2/RRR2-20/2	1107.355	1107.242	102.428	0.392	1363.087	0.363	15	0.149	K.VYEDNVLVR.E
R2/RRR2-21/2	1106.661	1107.242	-1432.250	0.355	1134.659	0.320	15	0.127	K.VYEDNVLVR.E
R2/RRR2-21/2	1278.129	1278.484	-278.818	0.405	539.239	0.458	16	0.122	R.ALQPVFQVYGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1106.974	1107.242	-242.181	0.406	971.928	0.319	15	0.121	K.VYEDNVLVR.E
R2/RRR2-21/2	1278.066	1278.484	-327.784	0.393	573.690	0.425	16	0.119	R.ALQPVFQVYGR.R
R2/RRR2-21/2	1277.566	1278.484	-1505.542	0.343	555.627	0.410	15	0.115	R.ALQPVFQVYGR.R
R2/RRR2-21/2	1330.443	1329.616	-130.458	0.438	891.875	0.271	16	0.109	R.RQVFAGPIVTLK.V
R2/RRR2-22/2	1072.186	1072.240	-50.543	0.235	325.788	0.362	11	0.105	-.VLVVDGGGSLR.-
R2/RRR2-22/2	1369.205	1369.592	-283.253	0.515	2142.668	0.512	19	0.282	R.LVVIVDVVDQNR.A
R2/RRR2-22/2	1370.064	1369.592	345.522	0.583	2004.005	0.522	19	0.261	R.LVVIVDVVDQNR.A
R2/RRR2-23/2	1369.340	1369.592	-184.334	0.558	1975.736	0.482	19	0.246	R.LVVIVDVVDQNR.A
R2/RRR2-23/2	1369.198	1369.592	-288.441	0.441	1843.256	0.386	19	0.203	R.LVVIVDVVDQNR.A
R2/RRR2-23/2	1368.543	1369.592	-1501.543	0.441	1651.383	0.396	18	0.182	R.LVVIVDVVDQNR.A
R2/RRR2-22/2	1356.525	1355.524	0.938	0.503	1331.056	0.519	18	0.175	R.VALVNYGKDYGR.L
R2/RRR2-23/2	1355.191	1355.524	-246.430	0.458	1344.033	0.494	18	0.171	R.VALVNYGKDYGR.L
R2/RRR2-22/2	1356.486	1355.524	-28.306	0.485	1213.510	0.503	17	0.160	R.VALVNYGKDYGR.L
R2/RRR2-23/2	1355.223	1355.524	-222.392	0.450	1126.024	0.501	17	0.153	R.VALVNYGKDYGR.L
R2/RRR2-23/2	1355.164	1355.524	-265.950	0.429	1130.114	0.465	17	0.147	R.VALVNYGKDYGR.L
R2/RRR2-22/2	1355.156	1355.524	-272.185	0.445	1009.849	0.454	16	0.137	R.VALVNYGKDYGR.L
R2/RRR2-23/2	1102.796	1103.275	-434.967	0.403	914.410	0.364	16	0.124	R.ALVDAPDM*VR.C
R2/RRR2-23/2	1102.270	1103.275	-1824.411	0.297	897.881	0.352	15	0.119	R.ALVDAPDM*VR.C
R2/RRR2-23/2	1102.956	1103.275	-289.595	0.402	702.522	0.352	14	0.116	R.ALVDAPDM*VR.C
R2/RRR2-22/2	1102.474	1103.275	-1638.499	0.295	700.816	0.289	14	0.110	R.ALVDAPDM*VR.C
R2/RRR2-22/2	1102.399	1103.275	-1706.136	0.279	601.236	0.276	13	0.108	R.ALVDAPDM*VR.C
R2/RRR2-23/2	1086.976	1087.275	-275.810	0.301	742.081	0.264	13	0.108	R.ALVDAPDMVR.C
R2/RRR2-22/2	1102.460	1103.275	-1651.069	0.276	760.040	0.233	14	0.107	R.ALVDAPDM*VR.C
R2/RRR2-23/2	1086.844	1087.275	-397.847	0.189	472.102	0.162	11	0.078	-.ALVDAPDMVR.-
R2/RRR2-23/3	1415.559	1415.704	-102.254	0.395	935.678	0.291	24	0.072	R.LSLTDIKIDIKR.V
R2/RRR2-12/3	1958.873	1959.187	-161.023	0.471	2526.790	0.566	36	0.396	R.DADVVISTLGALQIADQTK.L
R2/RRR2-12/3	1958.746	1959.187	-225.822	0.447	2323.083	0.513	33	0.322	R.DADVVISTLGALQIADQTK.L
R2/RRR2-12/2	1205.203	1205.432	-189.934	0.523	2077.307	0.542	20	0.281	R.ILVVGGTGYIGR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/3	1958.985	1959.187	-103.545	0.467	1924.701	0.554	34	0.252	R.DADVVISTLGALQIADQTK.L
R2/RRR2-12/2	1206.185	1205.432	-205.208	0.581	1911.247	0.515	21	0.246	R.ILVVGGTGYIGR.H
R2/RRR2-13/3	1959.525	1959.187	172.970	0.438	1802.836	0.579	32	0.241	R.DADVVISTLGALQIADQTK.L
R2/RRR2-12/2	1958.629	1959.187	-797.995	0.450	1858.481	0.498	26	0.232	R.DADVVISTLGALQIADQTK.L
R2/RRR2-12/2	1958.491	1959.187	-868.632	0.424	1634.228	0.570	25	0.218	R.DADVVISTLGALQIADQTK.L
R2/RRR2-12/2	1205.210	1205.432	-184.650	0.526	1584.248	0.530	20	0.206	R.ILVVGGTGYIGR.H
R2/RRR2-13/2	1959.642	1959.187	232.446	0.487	1481.067	0.527	24	0.189	R.DADVVISTLGALQIADQTK.L
R2/RRR2-13/2	1205.246	1205.432	-154.473	0.370	1484.812	0.480	19	0.180	R.ILVVGGTGYIGR.H
R2/RRR2-12/2	1958.005	1959.187	-1117.784	0.315	1285.506	0.434	23	0.149	R.DADVVISTLGALQIADQTK.L
R2/RRR2-12/2	962.556	963.116	-1624.795	0.440	747.323	0.347	12	0.118	K.AQLLQSFR.D
R2/RRR2-12/2	962.778	963.116	-351.385	0.478	722.279	0.347	12	0.118	K.AQLLQSFR.D
R2/RRR2-13/2	962.267	963.116	-1926.709	0.367	774.705	0.318	12	0.115	K.AQLLQSFR.D
R2/RRR2-13/2	963.050	963.116	-68.349	0.443	739.415	0.294	12	0.114	K.AQLLQSFR.D
R2/RRR2-13/2	963.082	963.116	-34.784	0.436	816.155	0.260	13	0.113	K.AQLLQSFR.D
R2/RRR2-6/2	1206.212	1205.432	-182.771	0.253	527.903	0.367	13	0.106	R.ILVVGGTGYIGR.H
R2/RRR2-13/3	1065.420	1065.251	159.482	0.520	964.411	0.336	20	0.082	R.LGHPTTALVR.D
R2/RRR2-12/3	1065.493	1065.251	227.900	0.482	952.324	0.349	20	0.082	-.LGHPTTALVR.-
R2/RRR2-12/3	1065.454	1065.251	190.848	0.502	828.721	0.341	21	0.081	R.LGHPTTALVR.D
R2/RRR2-12/3	1065.647	1065.251	372.634	0.483	752.555	0.349	18	0.080	R.LGHPTTALVR.D
R2/RRR2-13/3	1065.034	1065.251	-204.137	0.512	823.762	0.333	20	0.080	R.LGHPTTALVR.D
R2/RRR2-13/3	1065.406	1065.251	145.693	0.498	904.194	0.330	19	0.078	-.LGHPTTALVR.-
R2/RRR2-14/2	1609.421	1609.850	-267.830	0.378	952.628	0.369	20	0.123	K.STSSIFPLQNVFIR.K
R2/RRR2-14/2	1610.105	1609.850	158.426	0.395	720.024	0.406	18	0.117	K.STSSIFPLQNVFIR.K
R2/RRR2-4/2	1936.665	1936.194	244.055	0.559	1622.016	0.516	23	0.206	R.IVLEADGYQPYLISPEK.G
R2/RRR2-4/2	1937.389	1936.194	100.887	0.538	1548.359	0.488	22	0.189	R.IVLEADGYQPYLISPEK.G
R2/RRR2-4/2	1645.461	1645.881	-255.862	0.359	1292.989	0.252	20	0.124	R.GYVEAVLNSLAANVPK.A
R2/RRR2-4/2	1140.142	1140.358	-190.033	0.447	929.678	0.366	16	0.123	R.LPNLLSGLQGK.S
R2/RRR2-4/3	1143.250	1143.280	-26.904	0.498	1061.651	0.355	19	0.085	-.HFDINNVKR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1142.446	1143.280	-1610.904	0.478	1002.004	0.358	19	0.085	R.HFDINNVKR.I
R2/RRR2-4/3	1782.248	1782.035	120.378	0.324	915.355	0.365	23	0.079	R.VLLDIVNASANATPGLGR.Y
R2/RRR2-17/2	1897.762	1898.104	-180.620	0.619	2606.413	0.544	26	0.385	K.LGWAIDEDFGSFEALVK.K
R2/RRR2-17/2	1897.370	1898.104	-916.618	0.564	2596.274	0.522	26	0.376	K.LGWAIDEDFGSFEALVK.K
R2/RRR2-17/2	1897.369	1898.104	-917.393	0.582	2517.814	0.545	26	0.367	K.LGWAIDEDFGSFEALVK.K
R2/RRR2-17/2	1616.418	1616.795	-233.721	0.464	1934.943	0.542	21	0.258	K.LSVETTANQDPLVTK.G
R2/RRR2-17/2	1616.458	1616.795	-208.947	0.511	1698.267	0.548	20	0.223	K.LSVETTANQDPLVTK.G
R2/RRR2-17/2	1744.436	1744.968	-880.607	0.557	1593.842	0.576	25	0.219	K.KLSVETTANQDPLVTK.G
R2/RRR2-17/2	1744.697	1744.968	-155.764	0.592	1509.346	0.599	24	0.214	K.KLSVETTANQDPLVTK.G
R2/RRR2-17/2	1743.961	1744.968	-1154.159	0.565	1455.604	0.572	24	0.201	K.KLSVETTANQDPLVTK.G
R2/RRR2-17/2	1617.475	1616.795	-198.597	0.521	1357.312	0.559	18	0.183	K.LSVETTANQDPLVTK.G
R2/RRR2-17/3	1744.756	1744.968	-121.943	0.476	1722.650	0.391	28	0.161	K.KLSVETTANQDPLVTK.G
R2/RRR2-17/2	1504.749	1505.702	-1301.999	0.394	830.243	0.404	15	0.120	K.NVRPDYLSNIWK.V
R2/RRR2-17/2	1504.788	1505.702	-1275.847	0.385	792.059	0.377	15	0.116	K.NVRPDYLSNIWK.V
R2/RRR2-17/3	1506.868	1505.702	109.917	0.576	935.972	0.423	26	0.095	K.NVRPDYLSNIWK.V
R2/RRR2-17/3	1505.960	1505.702	171.853	0.526	1018.075	0.394	24	0.092	K.NVRPDYLSNIWK.V
R2/RRR2-17/3	1505.678	1505.702	-16.200	0.535	937.096	0.363	27	0.085	K.NVRPDYLSNIWK.V
R2/RRR2-4/2	1643.179	1643.608	-261.732	0.501	1335.225	0.565	24	0.186	R.SAFDSASNGPSSGSESR.S
R2/RRR2-5/2	1513.399	1513.764	-242.188	0.516	1546.080	0.600	22	0.218	K.GLLLQTLSSPVASAR.S
R2/RRR2-5/2	1336.987	1337.452	-348.871	0.505	1734.895	0.453	19	0.206	R.VVCEATQSTDVK.I
R2/RRR2-5/2	1337.057	1337.452	-296.748	0.492	1659.551	0.431	19	0.192	R.VVCEATQSTDVK.I
R2/RRR2-5/2	1366.758	1366.502	188.336	0.552	1556.341	0.471	18	0.188	R.TAAYETLNEVVR.C
R2/RRR2-5/2	1514.528	1513.764	-156.477	0.501	1410.207	0.539	20	0.186	K.GLLLQTLSSPVASAR.S
R2/RRR2-5/2	1512.772	1513.764	-1321.074	0.341	1090.120	0.473	20	0.142	K.GLLLQTLSSPVASAR.S
R2/RRR2-5/2	1336.449	1337.452	-1503.247	0.379	1164.358	0.405	18	0.140	R.VVCEATQSTDVK.I
R2/RRR2-2/2	1610.914	1610.835	49.128	0.416	823.234	0.399	17	0.117	R.NGILEAYSGILQGFK.S
R2/RRR2-5/2	1021.058	1021.109	-50.196	0.368	813.364	0.300	14	0.113	-.DTTAWTLGR.-
R2/RRR2-5/2	1365.445	1366.502	-1510.509	0.324	951.083	0.280	16	0.112	R.TAAYETLNEVVR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1020.402	1021.109	-1677.873	0.309	706.657	0.301	14	0.111	K.DTTAWTLGR.I
R2/RRR2-5/2	1365.576	1366.502	-1414.340	0.317	922.194	0.252	16	0.109	R.TAAYETLNEVVR.C
R2/RRR2-5/2	1020.995	1021.109	-111.838	0.312	748.906	0.221	14	0.106	-.DTTAWTLGR.-
R2/RRR2-8/3	1170.391	1170.303	75.820	0.487	1662.704	0.486	22	0.176	K.FGAAVVSPEHR.Y
R2/RRR2-8/3	1170.582	1170.303	239.289	0.478	1571.642	0.447	22	0.152	K.FGAAVVSPEHR.Y
R2/RRR2-8/3	1170.592	1170.303	248.073	0.469	1203.735	0.498	19	0.128	K.FGAAVVSPEHR.Y
R2/RRR2-8/2	1482.121	1481.590	-317.269	0.452	878.152	0.393	18	0.123	K.SSPFESLTTENLR.F
R2/RRR2-8/2	1332.443	1332.441	1.690	0.492	797.905	0.361	13	0.118	R.YYEFLDYYR.A
R2/RRR2-7/3	1170.930	1170.303	-319.203	0.424	1147.953	0.445	20	0.110	K.FGAAVVSPEHR.Y
R2/RRR2-8/2	1481.060	1481.590	-1036.048	0.350	831.967	0.286	18	0.110	K.SSPFESLTTENLR.F
R2/RRR2-8/3	1298.073	1298.475	-310.622	0.472	1161.599	0.367	22	0.095	K.KFGAAVVSPEHR.Y
R2/RRR2-8/3	1298.454	1298.475	-16.617	0.511	1130.869	0.337	22	0.087	-.KFGAAVVSPEHR.-
R2/RRR2-16/3	1298.616	1298.475	108.404	0.497	909.089	0.375	21	0.085	K.KFGAAVVSPEHR.Y
R2/RRR2-8/3	1297.452	1298.475	-1563.963	0.491	853.977	0.375	20	0.083	K.KFGAAVVSPEHR.Y
R2/RRR2-16/2	1673.340	1672.857	289.265	0.613	1882.913	0.587	22	0.260	R.AKDVALVYNECYAR.L
R2/RRR2-16/3	1673.134	1672.857	166.025	0.634	2234.554	0.464	32	0.253	R.AKDVALVYNECYAR.L
R2/RRR2-15/2	1672.120	1672.857	-1041.632	0.561	1773.534	0.598	21	0.247	R.AKDVALVYNECYAR.L
R2/RRR2-15/2	1672.462	1672.857	-236.651	0.617	1778.727	0.592	21	0.245	R.AKDVALVYNECYAR.L
R2/RRR2-16/2	1672.124	1672.857	-1039.360	0.585	1788.243	0.566	21	0.240	R.AKDVALVYNECYAR.L
R2/RRR2-15/2	1673.359	1672.857	-298.717	0.632	1725.940	0.572	21	0.232	R.AKDVALVYNECYAR.L
R2/RRR2-16/2	1672.329	1672.857	-916.308	0.573	1690.285	0.586	21	0.232	R.AKDVALVYNECYAR.L
R2/RRR2-15/2	1446.042	1446.534	-341.357	0.464	1863.682	0.474	18	0.226	R.AACYDCGTSVWR.D
R2/RRR2-15/2	1446.114	1446.534	-291.302	0.443	1802.151	0.478	18	0.219	R.AACYDCGTSVWR.D
R2/RRR2-16/3	1672.435	1672.857	-253.281	0.573	1978.142	0.465	29	0.216	-.AKDVALVYNECYAR.-
R2/RRR2-15/2	1446.095	1446.534	-304.175	0.452	1665.746	0.491	18	0.204	R.AACYDCGTSVWR.D
R2/RRR2-15/3	1672.957	1672.857	59.777	0.572	1968.819	0.446	30	0.203	R.AKDVALVYNECYAR.L
R2/RRR2-16/3	1673.871	1672.857	8.140	0.576	1969.098	0.437	29	0.201	R.AKDVALVYNECYAR.L
R2/RRR2-16/2	1445.942	1446.534	-1104.226	0.478	1730.975	0.441	18	0.201	R.AACYDCGTSVWR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1446.011	1446.534	-1056.334	0.434	1632.245	0.479	18	0.197	R.AACYDCGTSVWR.D
R2/RRR2-15/3	1673.488	1672.857	-221.003	0.586	1908.665	0.413	29	0.182	R.AKDVALVYNECYAR.L
R2/RRR2-15/2	1474.275	1473.606	-225.029	0.552	1317.843	0.538	19	0.179	K.DVALVYNECYAR.L
R2/RRR2-1/3	1674.125	1672.857	160.843	0.543	1713.306	0.435	27	0.165	R.AKDVALVYNECYAR.L
R2/RRR2-16/2	1445.266	1446.534	-1573.982	0.285	1602.200	0.338	18	0.163	R.AACYDCGTSVWR.D
R2/RRR2-16/2	1473.193	1473.606	-280.961	0.437	1329.695	0.451	19	0.162	K.DVALVYNECYAR.L
R2/RRR2-15/3	1673.465	1672.857	-234.615	0.569	1725.780	0.424	28	0.161	R.AKDVALVYNECYAR.L
R2/RRR2-16/2	1473.294	1473.606	-212.215	0.452	1238.552	0.448	19	0.154	K.DVALVYNECYAR.L
R2/RRR2-16/2	1473.104	1473.606	-1022.444	0.426	1311.515	0.416	19	0.154	K.DVALVYNECYAR.L
R2/RRR2-15/2	1473.057	1473.606	-1054.560	0.421	1352.405	0.383	19	0.151	K.DVALVYNECYAR.L
R2/RRR2-16/2	1266.522	1267.367	-1461.151	0.445	1376.779	0.340	18	0.146	R.LSDKDDFLADK.V
R2/RRR2-1/3	1673.680	1672.857	-105.760	0.468	1511.240	0.443	27	0.144	R.AKDVALVYNECYAR.L
R2/RRR2-15/2	1267.117	1267.367	-197.756	0.532	1193.380	0.387	18	0.141	R.LSDKDDFLADK.V
R2/RRR2-16/2	1266.512	1267.367	-1468.606	0.432	1316.601	0.315	18	0.138	R.LSDKDDFLADK.V
R2/RRR2-15/2	1266.961	1267.367	-321.090	0.522	1124.082	0.371	18	0.135	R.LSDKDDFLADK.V
R2/RRR2-18/2	1474.169	1473.606	-297.552	0.465	946.661	0.427	16	0.130	K.DVALVYNECYAR.L
R2/RRR2-15/2	1267.173	1267.367	-153.591	0.517	1025.688	0.371	17	0.129	R.LSDKDDFLADK.V
R2/RRR2-16/2	1266.576	1267.367	-1417.975	0.462	1176.044	0.318	17	0.129	R.LSDKDDFLADK.V
R2/RRR2-16/3	1268.557	1267.367	150.448	0.508	1390.793	0.322	24	0.101	R.LSDKDDFLADK.V
R2/RRR2-14/2	1446.412	1446.534	-84.277	0.384	905.891	0.089	14	0.088	-.AACYDCGTSVWR.-
R2/RRR2-19/2	1429.222	1429.604	-268.017	0.469	1381.725	0.525	18	0.182	R.DNFFFAGIDKVR.F
R2/RRR2-19/2	1175.187	1174.286	-84.974	0.489	1503.295	0.446	15	0.178	R.DNFFFAGIDK.V
R2/RRR2-19/2	1174.048	1174.286	-203.629	0.424	1346.605	0.399	15	0.154	R.DNFFFAGIDK.V
R2/RRR2-19/2	1428.949	1429.604	-1162.256	0.444	951.679	0.514	16	0.142	R.DNFFFAGIDKVR.F
R2/RRR2-19/2	1428.947	1429.604	-1163.543	0.472	948.746	0.468	16	0.136	R.DNFFFAGIDKVR.F
R2/RRR2-19/2	893.915	894.007	-103.151	0.406	1007.449	0.391	13	0.130	-.GGEYAVGIK.-
R2/RRR2-19/2	893.770	894.007	-265.362	0.333	1068.962	0.258	13	0.115	K.GGEYAVGIK.N
R2/RRR2-19/2	1173.454	1174.286	-1566.395	0.270	465.553	0.290	12	0.106	R.DNFFFAGIDK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/3	1633.276	1633.983	-1048.468	0.428	951.768	0.459	25	0.100	R.FRKPVIAGDTLIM*R.M
R2/RRR2-19/3	1618.747	1617.984	-146.979	0.423	1050.418	0.409	22	0.097	R.FRKPVIAGDTLIMR.M
R2/RRR2-19/3	1632.367	1633.983	-2222.101	0.357	1155.579	0.292	24	0.083	R.FRKPVIAGDTLIM*R.M
R2/RRR2-19/3	1617.795	1617.984	-116.944	0.308	783.269	0.228	22	0.066	R.FRKPVIAGDTLIMR.M
R2/RRR2-19/2	1735.348	1735.790	-255.874	0.553	2432.574	0.608	22	0.374	R.WSEYDFDQVFADGR.D
R2/RRR2-19/2	1735.144	1735.790	-951.652	0.545	2368.039	0.606	22	0.359	R.WSEYDFDQVFADGR.D
R2/RRR2-19/2	1734.982	1735.790	-1045.316	0.532	2166.770	0.589	22	0.313	R.WSEYDFDQVFADGR.D
R2/RRR2-19/2	1516.997	1517.668	-1104.886	0.504	1760.217	0.421	21	0.202	K.VSDTEVIGYHQLR.V
R2/RRR2-19/2	1517.258	1517.668	-271.187	0.439	1575.988	0.403	20	0.176	K.VSDTEVIGYHQLR.V
R2/RRR2-19/2	1517.108	1517.668	-1031.364	0.524	1011.009	0.422	18	0.133	K.VSDTEVIGYHQLR.V
R2/RRR2-19/2	1016.982	1017.123	-139.307	0.374	721.319	0.411	13	0.120	K.TQHFIGGTR.W
R2/RRR2-19/2	1017.033	1017.123	-88.738	0.240	644.889	0.300	12	0.106	K.TQHFIGGTR.W
R2/RRR2-19/2	1016.887	1017.123	-233.234	0.210	450.224	0.295	11	0.104	K.TQHFIGGTR.W
R2/RRR2-19/3	1517.285	1517.668	-253.197	0.409	628.881	0.497	23	0.091	K.VSDTEVIGYHQLR.V
R2/RRR2-19/3	1437.268	1437.507	-166.517	0.442	427.214	0.524	21	0.091	K.GHAHSANTHWYR.K
R2/RRR2-19/3	1519.075	1517.668	268.620	0.409	581.576	0.396	22	0.080	K.VSDTEVIGYHQLR.V
R2/RRR2-19/3	1517.653	1517.668	-10.263	0.379	603.934	0.390	22	0.079	K.VSDTEVIGYHQLR.V
R2/RRR2-19/3	1436.746	1437.507	-1229.373	0.391	405.961	0.395	18	0.078	K.GHAHSANTHWYR.K
R2/RRR2-9/2	1887.255	1887.141	60.295	0.553	2536.118	0.577	25	0.390	R.AVCMISNSTSVVEVFSR.I
R2/RRR2-8/2	1601.368	1599.804	-273.382	0.554	1254.207	0.571	17	0.177	R.TIQFVDWCPTGFK.C
R2/RRR2-9/2	1599.590	1599.804	-134.608	0.478	1156.959	0.520	17	0.158	R.TIQFVDWCPTGFK.C
R2/RRR2-13/2	1600.469	1599.804	-209.964	0.273	509.804	0.308	14	0.104	R.TIQFVDWCPTGFK.C
R2/RRR2-3/2	1177.537	1178.403	-1589.036	0.348	1665.703	0.400	18	0.185	K.LPTAILSTYAK.A
R2/RRR2-3/2	1229.051	1229.413	-295.231	0.429	1000.834	0.497	17	0.144	K.FSATAGLGVIHR.G
R2/RRR2-3/2	1177.418	1178.403	-1690.897	0.342	1052.655	0.440	15	0.136	K.LPTAILSTYAK.A
R2/RRR2-3/2	1229.315	1229.413	-80.137	0.431	839.623	0.480	16	0.132	K.FSATAGLGVIHR.G
R2/RRR2-4/2	1177.551	1178.403	-1577.373	0.305	975.219	0.371	15	0.122	K.LPTAILSTYAK.A
R2/RRR2-3/3	1910.603	1910.163	231.260	0.484	1748.686	0.267	32	0.122	K.KAPEPEPTFQILTNPAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1228.649	1229.413	-1439.923	0.374	633.690	0.359	15	0.112	K.FSATAGLGVIHR.G
R2/RRR2-3/3	1615.216	1614.827	241.337	0.438	804.021	0.573	29	0.109	R.IVSLLSESYNPHVR.Y
R2/RRR2-3/3	1614.417	1614.827	-254.761	0.447	685.084	0.547	28	0.100	R.IVSLLSESYNPHVR.Y
R2/RRR2-3/3	1229.073	1229.413	-277.555	0.467	607.199	0.518	22	0.096	K.FSATAGLGVIHR.G
R2/RRR2-3/3	1229.725	1229.413	254.116	0.425	621.579	0.526	23	0.096	K.FSATAGLGVIHR.G
R2/RRR2-3/3	1229.285	1229.413	-104.502	0.420	375.920	0.497	19	0.090	K.FSATAGLGVIHR.G
R2/RRR2-4/3	1229.017	1229.413	-323.144	0.383	321.167	0.492	18	0.087	K.FSATAGLGVIHR.G
R2/RRR2-4/3	1331.666	1330.516	113.161	0.403	936.179	0.383	21	0.085	K.RLDKLEEAISR.S
R2/RRR2-4/3	1910.337	1910.163	91.220	0.419	1287.518	0.264	27	0.085	K.KAPEPEPTFQILTNPAR.V
R2/RRR2-3/3	1909.903	1910.163	-136.560	0.415	1005.620	0.271	27	0.073	-.KAPEPEPTFQILTNPAR.-
R2/RRR2-3/3	1909.859	1910.163	-159.354	0.357	1283.839	0.161	27	0.071	-.KAPEPEPTFQILTNPAR.-
R2/RRR2-4/3	1910.483	1910.163	167.925	0.332	835.312	0.257	24	0.068	-.KAPEPEPTFQILTNPAR.-
R2/RRR2-4/3	1331.281	1330.516	-176.509	0.376	819.553	0.242	19	0.067	K.RLDKLEEAISR.S
R2/RRR2-21/2	1693.080	1693.966	-1117.107	0.475	1459.026	0.417	22	0.166	K.INGTPIELVEPEILR.V
R2/RRR2-22/2	1692.892	1693.966	-1228.393	0.410	963.550	0.499	19	0.139	K.INGTPIELVEPEILR.V
R2/RRR2-22/2	1694.071	1693.966	62.328	0.447	763.002	0.459	16	0.122	K.INGTPIELVEPEILR.V
R2/RRR2-21/2	1693.328	1693.966	-970.309	0.427	792.474	0.411	18	0.120	K.INGTPIELVEPEILR.V
R2/RRR2-22/2	1417.236	1417.635	-282.379	0.412	812.644	0.357	14	0.114	-.TYEPVLLLGQQR.-
R2/RRR2-22/2	1417.049	1417.635	-1122.507	0.206	545.793	0.252	13	0.099	K.TYEPVLLLGQQR.F
R2/RRR2-22/2	1694.808	1693.966	-93.164	0.318	303.238	0.342	11	0.098	-.INGTPIELVEPEILR.-
R2/RRR2-20/2	1420.870	1421.619	-1234.439	0.453	1528.252	0.617	19	0.217	K.CHFVAIDIFNGK.K
R2/RRR2-20/2	1422.023	1421.619	284.853	0.518	1570.820	0.567	19	0.212	K.CHFVAIDIFNGK.K
R2/RRR2-20/2	1421.409	1421.619	-147.951	0.521	1437.567	0.569	18	0.196	K.CHFVAIDIFNGK.K
R2/RRR2-20/2	1420.317	1421.619	-1625.768	0.461	1345.053	0.539	18	0.179	K.CHFVAIDIFNGK.K
R2/RRR2-20/2	1422.165	1421.619	-320.227	0.486	1172.048	0.567	18	0.169	K.CHFVAIDIFNGK.K
R2/RRR2-22/2	1421.357	1421.619	-184.824	0.472	1235.660	0.536	18	0.169	K.CHFVAIDIFNGK.K
R2/RRR2-20/2	1421.132	1421.619	-343.463	0.406	1070.046	0.541	17	0.154	K.CHFVAIDIFNGK.K
R2/RRR2-20/2	1300.182	1300.483	-232.466	0.448	1149.652	0.459	19	0.149	R.LPTDDSLLGQIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1300.368	1300.483	-89.034	0.456	1066.413	0.459	18	0.143	R.LPTDDSLLGQIK.T
R2/RRR2-20/3	1800.639	1800.004	-203.051	0.546	1203.402	0.525	30	0.134	K.DDLRLPTDDSLLGQIK.T
R2/RRR2-20/2	1299.645	1300.483	-1418.919	0.418	1027.328	0.368	19	0.129	R.LPTDDSLLGQIK.T
R2/RRR2-20/2	1300.348	1300.483	-104.477	0.459	894.525	0.389	18	0.126	R.LPTDDSLLGQIK.T
R2/RRR2-20/2	1135.878	1135.255	-332.491	0.354	219.512	0.494	12	0.122	K.TYPQQAGTIR.K
R2/RRR2-20/3	1799.540	1800.004	-258.456	0.517	1123.821	0.498	27	0.120	-.DDLRLPTDDSLLGQIK.-
R2/RRR2-22/2	1135.975	1135.255	-247.208	0.274	233.211	0.548	14	0.120	K.TYPQQAGTIR.K
R2/RRR2-21/2	1134.815	1135.255	-389.337	0.317	322.714	0.324	15	0.120	K.TYPQQAGTIR.K
R2/RRR2-22/2	1799.764	1800.004	-133.379	0.524	437.483	0.471	19	0.119	K.DDLRLPTDDSLLGQIK.T
R2/RRR2-20/3	1800.601	1800.004	-223.965	0.511	1066.168	0.510	29	0.119	K.DDLRLPTDDSLLGQIK.T
R2/RRR2-21/2	1135.057	1135.255	-174.812	0.260	276.269	0.435	15	0.118	K.TYPQQAGTIR.K
R2/RRR2-20/2	1134.956	1135.255	-263.827	0.256	281.348	0.409	15	0.118	K.TYPQQAGTIR.K
R2/RRR2-19/2	1135.023	1135.255	-204.590	0.224	173.452	0.319	12	0.117	K.TYPQQAGTIR.K
R2/RRR2-20/2	1135.997	1135.255	-228.234	0.262	328.085	0.337	15	0.117	K.TYPQQAGTIR.K
R2/RRR2-20/2	1134.941	1135.255	-277.639	0.229	290.868	0.357	15	0.116	K.TYPQQAGTIR.K
R2/RRR2-22/2	1136.166	1135.255	-78.840	0.225	247.884	0.521	15	0.116	K.TYPQQAGTIR.K
R2/RRR2-22/2	1135.802	1135.255	-400.210	0.235	215.023	0.447	13	0.115	K.TYPQQAGTIR.K
R2/RRR2-20/2	1135.308	1135.255	46.631	0.293	192.224	0.468	12	0.115	-.TYPQQAGTIR.-
R2/RRR2-21/2	1135.078	1135.255	-156.364	0.221	239.888	0.305	14	0.114	-.TYPQQAGTIR.-
R2/RRR2-20/2	1134.918	1135.255	-298.250	0.205	203.540	0.424	13	0.114	K.TYPQQAGTIR.K
R2/RRR2-22/3	1800.193	1800.004	105.337	0.444	1176.748	0.444	29	0.113	K.DDLRLPTDDSLLGQIK.T
R2/RRR2-19/2	1134.467	1135.255	-1580.941	0.232	285.329	0.328	14	0.112	-.TYPQQAGTIR.-
R2/RRR2-20/2	1134.927	1135.255	-290.157	0.190	331.179	0.453	16	0.111	K.TYPQQAGTIR.K
R2/RRR2-21/2	1799.429	1800.004	-877.782	0.421	456.815	0.373	19	0.111	K.DDLRLPTDDSLLGQIK.T
R2/RRR2-20/2	1301.218	1300.483	-204.523	0.344	682.269	0.301	16	0.110	R.LPTDDSLLGQIK.T
R2/RRR2-21/2	1800.581	1800.004	-235.112	0.480	406.496	0.348	18	0.109	K.DDLRLPTDDSLLGQIK.T
R2/RRR2-22/3	1800.228	1800.004	125.126	0.528	1007.458	0.463	28	0.105	K.DDLRLPTDDSLLGQIK.T
R2/RRR2-20/2	1134.455	1135.255	-1591.534	0.120	170.702	0.364	12	0.103	-.TYPQQAGTIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/3	1421.474	1421.619	-102.475	0.469	1190.340	0.359	24	0.095	K.CHFVAIDIFNGK.K
R2/RRR2-20/3	1421.359	1421.619	-183.627	0.422	1183.537	0.252	24	0.077	K.CHFVAIDIFNGK.K
R2/RRR2-20/3	1420.625	1421.619	-1407.635	0.287	668.197	0.203	19	0.061	-.CHFVAIDIFNGK.-
R2/RRR2-22/2	1697.403	1697.848	-263.492	0.531	2150.472	0.570	23	0.305	K.GQTWSEDM*IAAGSTVK.I
R2/RRR2-22/2	1681.025	1681.849	-1088.410	0.480	2065.288	0.535	23	0.279	K.GQTWSEDMIAAGSTVK.I
R2/RRR2-22/2	1549.141	1549.706	-1013.279	0.458	1500.361	0.523	21	0.190	R.TLSDPLFFGYSSSK.N
R2/RRR2-22/2	1550.146	1549.706	284.768	0.509	1301.257	0.583	20	0.182	R.TLSDPLFFGYSSSK.N
R2/RRR2-19/2	1549.347	1549.706	-232.302	0.394	1379.791	0.517	20	0.175	R.TLSDPLFFGYSSSK.N
R2/RRR2-22/2	1549.204	1549.706	-971.982	0.402	1384.428	0.480	20	0.169	R.TLSDPLFFGYSSSK.N
R2/RRR2-22/2	1549.213	1549.706	-318.782	0.456	1259.237	0.527	19	0.166	R.TLSDPLFFGYSSSK.N
R2/RRR2-19/2	1549.461	1549.706	-158.007	0.432	1262.652	0.492	19	0.160	R.TLSDPLFFGYSSSK.N
R2/RRR2-23/2	1549.335	1549.706	-239.574	0.420	1240.832	0.486	19	0.157	R.TLSDPLFFGYSSSK.N
R2/RRR2-22/2	1549.508	1549.706	-127.897	0.471	1114.701	0.527	18	0.154	R.TLSDPLFFGYSSSK.N
R2/RRR2-20/2	1548.749	1549.706	-1267.064	0.325	1302.078	0.448	19	0.154	R.TLSDPLFFGYSSSK.N
R2/RRR2-21/2	1549.182	1549.706	-986.697	0.445	1233.443	0.463	19	0.153	R.TLSDPLFFGYSSSK.N
R2/RRR2-21/2	1549.299	1549.706	-263.129	0.388	1105.857	0.515	18	0.150	R.TLSDPLFFGYSSSK.N
R2/RRR2-21/2	1549.460	1549.706	-158.718	0.419	1051.835	0.538	17	0.149	R.TLSDPLFFGYSSSK.N
R2/RRR2-22/2	1549.279	1549.706	-276.093	0.407	1100.722	0.479	18	0.144	R.TLSDPLFFGYSSSK.N
R2/RRR2-22/2	1825.497	1826.021	-837.536	0.554	719.731	0.576	24	0.143	K.KGQTWSEDM*IAAGSTVK.I
R2/RRR2-22/2	1551.089	1549.706	247.732	0.486	995.715	0.470	17	0.136	R.TLSDPLFFGYSSSK.N
R2/RRR2-21/2	1549.093	1549.706	-1044.293	0.399	1176.750	0.383	19	0.136	R.TLSDPLFFGYSSSK.N
R2/RRR2-20/2	1548.726	1549.706	-1281.867	0.274	1091.280	0.355	17	0.125	R.TLSDPLFFGYSSSK.N
R2/RRR2-20/2	1548.838	1549.706	-1209.680	0.264	728.163	0.429	15	0.115	R.TLSDPLFFGYSSSK.N
R2/RRR2-22/2	1737.252	1736.931	185.453	0.419	1112.637	0.467	19	0.078	K.VFGCPEPVDVTATLCA.-
R2/RRR2-22/2	1736.817	1736.931	-65.674	0.295	1065.461	0.295	18	0.067	K.VFGCPEPVDVTATLCA.-
R2/RRR2-22/2	1736.939	1736.931	4.257	0.273	933.009	0.400	18	0.052	K.VFGCPEPVDVTATLCA.-
R2/RRR2-17/2	1552.372	1551.685	-201.878	0.577	2546.927	0.529	21	0.365	K.LQIWDTAGQESFR.S
R2/RRR2-17/2	1551.218	1551.685	-301.716	0.492	2552.030	0.503	21	0.359	K.LQIWDTAGQESFR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1550.804	1551.685	-1216.199	0.408	2609.451	0.462	21	0.357	K.LQIWDTAGQESFR.S
R2/RRR2-17/2	1551.056	1551.685	-1053.549	0.539	2472.842	0.524	21	0.349	K.LQIWDTAGQESFR.S
R2/RRR2-17/2	1358.006	1358.435	-317.054	0.421	1113.621	0.460	16	0.144	R.AVSYEEGEQFAK.E
R2/RRR2-17/2	1357.925	1358.435	-1115.570	0.397	1036.812	0.467	16	0.140	R.AVSYEEGEQFAK.E
R2/RRR2-17/2	1691.182	1689.809	221.056	0.544	711.656	0.549	20	0.139	R.ETFNHLASWLEDAR.Q
R2/RRR2-17/2	1357.538	1358.435	-1401.339	0.286	1106.094	0.394	16	0.131	R.AVSYEEGEQFAK.E
R2/RRR2-17/2	1689.414	1689.809	-235.001	0.470	781.962	0.455	19	0.127	R.ETFNHLASWLEDAR.Q
R2/RRR2-17/2	1552.952	1551.685	172.772	0.379	1187.122	0.288	20	0.125	K.LQIWDTAGQESFR.S
R2/RRR2-17/2	1320.313	1320.519	-156.590	0.373	922.552	0.414	15	0.124	R.GAAGALLVYDITR.R
R2/RRR2-17/2	1320.153	1320.519	-278.011	0.336	1099.176	0.313	16	0.121	R.GAAGALLVYDITR.R
R2/RRR2-17/2	1689.240	1689.809	-932.068	0.444	614.327	0.415	17	0.116	R.ETFNHLASWLEDAR.Q
R2/RRR2-18/2	1691.030	1689.809	130.789	0.326	233.104	0.397	14	0.111	R.ETFNHLASWLEDAR.Q
R2/RRR2-17/2	1320.141	1320.519	-287.381	0.323	826.666	0.311	14	0.108	R.GAAGALLVYDITR.R
R2/RRR2-17/3	1689.850	1689.809	23.930	0.453	1199.111	0.369	26	0.098	R.ETFNHLASWLEDAR.Q
R2/RRR2-19/2	1377.585	1376.528	41.452	0.541	1554.111	0.471	18	0.185	K.CCDSIVQLPQR.I
R2/RRR2-21/2	1377.381	1376.528	-107.257	0.523	1525.385	0.453	18	0.178	K.CCDSIVQLPQR.I
R2/RRR2-20/2	1376.001	1376.528	-1112.926	0.432	1581.235	0.385	18	0.170	K.CCDSIVQLPQR.I
R2/RRR2-18/2	1376.205	1376.528	-235.905	0.473	1522.616	0.407	18	0.169	K.CCDSIVQLPQR.I
R2/RRR2-22/2	1376.167	1376.528	-263.047	0.474	1550.285	0.386	18	0.167	K.CCDSIVQLPQR.I
R2/RRR2-18/2	1377.270	1376.528	-188.251	0.547	1399.735	0.462	17	0.167	K.CCDSIVQLPQR.I
R2/RRR2-22/2	1377.240	1376.528	-210.036	0.537	1382.615	0.462	17	0.166	K.CCDSIVQLPQR.I
R2/RRR2-21/2	1375.690	1376.528	-1340.039	0.433	1521.691	0.382	18	0.164	K.CCDSIVQLPQR.I
R2/RRR2-21/2	1376.037	1376.528	-358.367	0.489	1377.401	0.448	17	0.163	K.CCDSIVQLPQR.I
R2/RRR2-17/2	1376.033	1376.528	-361.127	0.506	1391.115	0.435	17	0.162	K.CCDSIVQLPQR.I
R2/RRR2-17/2	1376.182	1376.528	-252.635	0.461	1575.168	0.345	18	0.162	K.CCDSIVQLPQR.I
R2/RRR2-20/2	1375.212	1376.528	-1689.596	0.341	1525.129	0.354	17	0.158	K.CCDSIVQLPQR.I
R2/RRR2-25/2	1376.353	1376.528	-127.797	0.474	1403.865	0.401	17	0.157	K.CCDSIVQLPQR.I
R2/RRR2-19/2	1375.954	1376.528	-1147.757	0.462	1305.020	0.411	17	0.151	K.CCDSIVQLPQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1376.163	1376.528	-266.073	0.448	1428.745	0.339	17	0.148	K.CCDSIVQLPQR.I
R2/RRR2-17/2	1377.266	1376.528	-191.097	0.448	1508.487	0.289	18	0.146	K.CCDSIVQLPQR.I
R2/RRR2-22/2	1376.082	1376.528	-324.990	0.445	1239.810	0.406	16	0.145	K.CCDSIVQLPQR.I
R2/RRR2-16/2	1376.263	1376.528	-193.549	0.473	1585.066	0.236	17	0.140	K.CCDSIVQLPQR.I
R2/RRR2-17/2	1375.576	1376.528	-1423.372	0.380	1344.126	0.320	17	0.139	K.CCDSIVQLPQR.I
R2/RRR2-20/2	1376.189	1376.528	-247.563	0.452	1196.241	0.349	16	0.133	K.CCDSIVQLPQR.I
R2/RRR2-16/2	1376.282	1376.528	-179.490	0.402	1256.341	0.308	16	0.132	-.CCDSIVQLPQR.-
R2/RRR2-17/2	1376.842	1376.528	228.840	0.456	1348.145	0.280	17	0.132	K.CCDSIVQLPQR.I
R2/RRR2-18/2	1377.144	1376.528	-280.109	0.415	1380.659	0.261	17	0.132	K.CCDSIVQLPQR.I
R2/RRR2-2/2	1376.128	1376.528	-291.971	0.413	1162.930	0.342	16	0.131	K.CCDSIVQLPQR.I
R2/RRR2-1/2	1277.967	1277.359	-307.307	0.325	820.180	0.492	16	0.130	K.ECVEAPGDFPR.G
R2/RRR2-16/2	1277.980	1277.359	-297.149	0.318	868.921	0.437	17	0.127	K.ECVEAPGDFPR.G
R2/RRR2-16/2	1278.121	1277.359	-186.666	0.324	792.135	0.462	16	0.126	K.ECVEAPGDFPR.G
R2/RRR2-17/2	1754.122	1754.855	-991.193	0.498	731.958	0.449	21	0.126	R.CDDELEPGKCTAACK.S
R2/RRR2-18/2	1377.081	1376.528	-325.377	0.420	1136.271	0.325	15	0.126	K.CCDSIVQLPQR.I
R2/RRR2-18/2	1062.730	1063.091	-341.090	0.357	941.319	0.368	14	0.125	R.CDDELEPGK.C
R2/RRR2-1/2	1278.482	1277.359	96.571	0.348	750.384	0.447	16	0.125	K.ECVEAPGDFPR.G
R2/RRR2-19/2	1375.335	1376.528	-1599.532	0.290	1236.272	0.259	16	0.124	K.CCDSIVQLPQR.I
R2/RRR2-18/2	1376.268	1376.528	-189.367	0.369	1280.588	0.236	17	0.124	K.CCDSIVQLPQR.I
R2/RRR2-18/2	1062.311	1063.091	-1680.948	0.312	1013.075	0.331	14	0.123	R.CDDELEPGK.C
R2/RRR2-17/2	1063.937	1063.091	-144.839	0.435	961.567	0.329	14	0.123	R.CDDELEPGK.C
R2/RRR2-19/2	1278.038	1277.359	-251.822	0.299	776.173	0.449	15	0.123	K.ECVEAPGDFPR.G
R2/RRR2-17/2	1062.526	1063.091	-1477.570	0.326	1005.656	0.316	14	0.122	R.CDDELEPGK.C
R2/RRR2-14/2	1375.754	1376.528	-1293.254	0.368	1113.794	0.276	17	0.122	K.CCDSIVQLPQR.I
R2/RRR2-17/2	1755.333	1754.855	272.754	0.536	647.915	0.437	20	0.122	R.CDDELEPGKCTAACK.S
R2/RRR2-18/2	1754.487	1754.855	-210.653	0.475	647.903	0.435	20	0.121	R.CDDELEPGKCTAACK.S
R2/RRR2-19/2	1062.999	1063.091	-86.686	0.398	943.995	0.315	14	0.121	R.CDDELEPGK.C
R2/RRR2-18/2	1754.049	1754.855	-1033.116	0.468	552.117	0.446	19	0.120	R.CDDELEPGKCTAACK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1754.367	1754.855	-279.131	0.521	532.383	0.458	18	0.120	R.CDDELEPGKCTAACK.S
R2/RRR2-17/2	1376.154	1376.528	-272.748	0.427	1148.918	0.269	15	0.119	K.CCDSIVQLPQR.I
R2/RRR2-20/2	1062.792	1063.091	-282.317	0.422	929.204	0.297	14	0.119	R.CDDELEPGK.C
R2/RRR2-17/2	1754.278	1754.855	-901.770	0.495	669.776	0.398	20	0.118	R.CDDELEPGKCTAACK.S
R2/RRR2-1/2	1375.983	1376.528	-1126.110	0.373	1025.868	0.279	16	0.118	K.CCDSIVQLPQR.I
R2/RRR2-21/2	1062.712	1063.091	-357.802	0.424	939.669	0.288	14	0.118	R.CDDELEPGK.C
R2/RRR2-24/2	1063.369	1063.091	262.564	0.321	897.710	0.319	13	0.118	R.CDDELEPGK.C
R2/RRR2-4/2	1375.996	1376.528	-1116.668	0.403	911.816	0.331	14	0.118	K.CCDSIVQLPQR.I
R2/RRR2-16/2	1375.449	1376.528	-1516.437	0.313	1209.531	0.201	16	0.116	K.CCDSIVQLPQR.I
R2/RRR2-17/2	1376.977	1376.528	327.071	0.407	1001.675	0.285	15	0.116	K.CCDSIVQLPQR.I
R2/RRR2-17/2	1062.936	1063.091	-146.704	0.416	906.764	0.289	14	0.116	-.CDDELEPGK.-
R2/RRR2-19/2	1277.823	1277.359	364.523	0.294	710.338	0.382	15	0.116	K.ECVEAPGDFPR.G
R2/RRR2-16/2	1063.194	1063.091	97.239	0.346	833.014	0.299	13	0.115	R.CDDELEPGK.C
R2/RRR2-26/2	1277.126	1277.359	-182.976	0.323	679.113	0.358	15	0.115	K.ECVEAPGDFPR.G
R2/RRR2-19/2	1063.116	1063.091	23.769	0.454	953.761	0.262	14	0.115	R.CDDELEPGK.C
R2/RRR2-22/2	1062.995	1063.091	-91.063	0.367	953.317	0.252	14	0.114	-.CDDELEPGK.-
R2/RRR2-25/2	1062.260	1063.091	-1728.861	0.331	896.250	0.257	14	0.113	-.CDDELEPGK.-
R2/RRR2-18/2	1062.114	1063.091	-1867.316	0.292	1097.434	0.192	14	0.113	R.CDDELEPGK.C
R2/RRR2-17/2	1062.361	1063.091	-1633.732	0.288	954.220	0.233	14	0.113	R.CDDELEPGK.C
R2/RRR2-1/2	1062.889	1063.091	-190.944	0.312	889.463	0.228	14	0.112	R.CDDELEPGK.C
R2/RRR2-19/2	1277.337	1277.359	-16.833	0.299	421.691	0.359	12	0.111	K.ECVEAPGDFPR.G
R2/RRR2-21/2	1062.708	1063.091	-361.144	0.374	918.328	0.210	14	0.111	R.CDDELEPGK.C
R2/RRR2-25/2	1063.011	1063.091	-75.628	0.313	760.048	0.253	13	0.110	-.CDDELEPGK.-
R2/RRR2-18/2	1276.958	1277.359	-314.262	0.291	701.567	0.280	15	0.110	K.ECVEAPGDFPR.G
R2/RRR2-18/2	1277.039	1277.359	-250.772	0.271	683.950	0.289	15	0.110	K.ECVEAPGDFPR.G
R2/RRR2-17/2	1062.216	1063.091	-1770.890	0.272	962.753	0.180	14	0.109	R.CDDELEPGK.C
R2/RRR2-18/2	1062.378	1063.091	-1617.340	0.296	948.551	0.173	14	0.108	-.CDDELEPGK.-
R2/RRR2-17/2	1062.244	1063.091	-1743.756	0.294	919.122	0.172	14	0.108	-.CDDELEPGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1277.143	1277.359	-169.552	0.274	700.489	0.232	15	0.108	K.ECVEAPGDFPR.G
R2/RRR2-4/2	1376.075	1376.528	-330.597	0.355	612.064	0.232	13	0.108	K.CCDSIVQLPQR.I
R2/RRR2-26/2	1276.928	1277.359	-338.240	0.207	742.678	0.265	16	0.108	K.ECVEAPGDFPR.G
R2/RRR2-1/2	1376.327	1376.528	-146.659	0.362	882.991	0.222	14	0.108	K.CCDSIVQLPQR.I
R2/RRR2-18/2	1062.217	1063.091	-1769.851	0.258	1064.571	0.140	14	0.108	R.CDDELEPGK.C
R2/RRR2-2/2	1277.098	1277.359	-204.743	0.245	819.729	0.208	16	0.107	K.ECVEAPGDFPR.G
R2/RRR2-20/2	1277.904	1277.359	-356.569	0.244	631.159	0.227	14	0.107	K.ECVEAPGDFPR.G
R2/RRR2-13/2	1277.072	1277.359	-225.264	0.248	738.016	0.204	15	0.106	K.ECVEAPGDFPR.G
R2/RRR2-13/2	1276.922	1277.359	-342.652	0.232	735.121	0.202	15	0.106	K.ECVEAPGDFPR.G
R2/RRR2-17/2	1276.985	1277.359	-293.545	0.235	673.036	0.173	15	0.106	K.ECVEAPGDFPR.G
R2/RRR2-25/2	1062.249	1063.091	-1739.483	0.214	971.495	0.128	14	0.105	R.CDDELEPGK.C
R2/RRR2-22/2	1062.306	1063.091	-1685.566	0.255	943.237	0.109	14	0.105	R.CDDELEPGK.C
R2/RRR2-2/2	1375.637	1376.528	-1378.986	0.285	717.321	0.128	14	0.105	K.CCDSIVQLPQR.I
R2/RRR2-1/2	1376.308	1376.528	-160.627	0.334	650.221	0.189	12	0.104	K.CCDSIVQLPQR.I
R2/RRR2-18/3	1755.993	1754.855	78.669	0.419	859.925	0.451	27	0.097	R.CDDELEPGKCTAACK.S
R2/RRR2-18/3	1754.405	1754.855	-257.568	0.424	1097.184	0.384	30	0.096	R.CDDELEPGKCTAACK.S
R2/RRR2-22/3	1754.000	1754.855	-1060.864	0.405	996.179	0.386	29	0.092	R.CDDELEPGKCTAACK.S
R2/RRR2-17/3	1754.578	1754.855	-158.733	0.441	695.881	0.434	26	0.090	R.CDDELEPGKCTAACK.S
R2/RRR2-18/3	1754.370	1754.855	-277.254	0.459	748.100	0.424	26	0.090	R.CDDELEPGKCTAACK.S
R2/RRR2-21/3	1754.282	1754.855	-899.263	0.415	709.656	0.429	25	0.089	R.CDDELEPGKCTAACK.S
R2/RRR2-17/3	1754.738	1754.855	-67.139	0.379	832.860	0.377	27	0.085	R.CDDELEPGKCTAACK.S
R2/RRR2-21/3	1754.488	1754.855	-209.928	0.377	617.299	0.393	24	0.084	R.CDDELEPGKCTAACK.S
R2/RRR2-14/3	1755.235	1754.855	216.958	0.379	448.501	0.356	21	0.082	R.CDDELEPGKCTAACK.S
R2/RRR2-22/3	1754.508	1754.855	-198.306	0.349	465.426	0.350	22	0.081	R.CDDELEPGKCTAACK.S
R2/RRR2-13/3	1754.368	1754.855	-278.720	0.382	523.021	0.328	23	0.080	R.CDDELEPGKCTAACK.S
R2/RRR2-22/3	1753.709	1754.855	-1227.341	0.348	669.451	0.315	24	0.077	R.CDDELEPGKCTAACK.S
R2/RRR2-16/2	1624.163	1624.726	-965.192	0.507	1824.541	0.589	21	0.254	K.GCVFTYDAVGSYER.T
R2/RRR2-16/2	1623.568	1624.726	-1332.878	0.341	1858.681	0.472	21	0.226	K.GCVFTYDAVGSYER.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1687.232	1687.870	-973.524	0.453	1494.884	0.498	25	0.188	R.DAVTPLSETEAVDLVK.D
R2/RRR2-16/2	1688.165	1687.870	175.542	0.524	1266.757	0.545	23	0.174	R.DAVTPLSETEAVDLVK.D
R2/RRR2-16/2	1687.427	1687.870	-263.575	0.479	1217.879	0.517	23	0.164	R.DAVTPLSETEAVDLVK.D
R2/RRR2-16/2	1051.015	1051.264	-237.718	0.492	1115.284	0.454	16	0.148	K.SPSPLLLPAR.D
R2/RRR2-16/2	995.373	996.056	-1695.831	0.334	920.481	0.455	14	0.131	K.DVFASATER.D
R2/RRR2-16/2	1050.581	1051.264	-1607.182	0.419	810.699	0.474	14	0.130	K.SPSPLLLPAR.D
R2/RRR2-16/2	995.768	996.056	-290.130	0.384	922.092	0.417	15	0.130	K.DVFASATER.D
R2/RRR2-16/2	995.901	996.056	-156.455	0.384	901.541	0.399	14	0.126	K.DVFASATER.D
R2/RRR2-16/2	1623.525	1624.726	-1359.761	0.224	487.038	0.267	12	0.099	K.GCVFTYDAVGSYER.T
R2/RRR2-3/2	1266.401	1267.415	-1595.484	0.279	755.811	0.348	14	0.110	R.FTWTIENLSR.V
R2/RRR2-3/2	1281.596	1282.513	-1500.140	0.298	1041.973	0.238	13	0.110	K.TREDILLFFK.L
R2/RRR2-2/2	1322.102	1322.449	-263.062	0.483	1888.864	0.415	18	0.215	K.GVADFLQEVTSR.K
R2/RRR2-3/2	1322.064	1322.449	-292.149	0.492	1680.830	0.443	17	0.194	K.GVADFLQEVTSR.K
R2/RRR2-2/2	1450.510	1450.622	-77.286	0.449	1316.375	0.501	18	0.169	R.KGVADFLQEVTSR.K
R2/RRR2-2/2	1321.548	1322.449	-1443.116	0.388	1632.441	0.343	18	0.169	K.GVADFLQEVTSR.K
R2/RRR2-2/2	1449.488	1450.622	-1476.820	0.464	997.480	0.558	16	0.151	R.KGVADFLQEVTSR.K
R2/RRR2-1/2	1322.172	1322.449	-209.801	0.340	1415.098	0.328	16	0.145	K.GVADFLQEVTSR.K
R2/RRR2-2/2	1641.370	1641.851	-293.722	0.375	743.589	0.499	20	0.125	R.GALVGLPGVSGLSTEQR.K
R2/RRR2-1/2	1001.005	1001.245	-240.971	0.378	869.743	0.395	16	0.124	K.TTLLLALAGK.L
R2/RRR2-2/2	1321.644	1322.449	-1369.454	0.280	557.498	0.447	14	0.113	K.GVADFLQEVTSR.K
R2/RRR2-2/3	1727.237	1726.870	213.173	0.511	743.852	0.549	31	0.105	K.HANLTGEVVEGQKDTK.S
R2/RRR2-3/2	1321.985	1322.449	-352.181	0.265	790.127	0.199	16	0.104	K.GVADFLQEVTSR.K
R2/RRR2-2/3	1451.778	1450.622	108.100	0.470	1035.841	0.349	20	0.085	-.KGVADFLQEVTSR.-
R2/RRR2-1/3	1450.497	1450.622	-86.497	0.366	1025.849	0.276	21	0.074	-.KGVADFLQEVTSR.-
R2/RRR2-15/2	1560.237	1560.650	-265.365	0.493	1296.803	0.575	20	0.182	R.TLDAHIEEQFGSGR.L
R2/RRR2-14/2	1560.160	1560.650	-315.133	0.487	1261.244	0.570	20	0.177	R.TLDAHIEEQFGSGR.L
R2/RRR2-15/2	1561.044	1560.650	253.054	0.526	1137.857	0.590	19	0.170	R.TLDAHIEEQFGSGR.L
R2/RRR2-14/2	1560.651	1560.650	0.815	0.490	1168.078	0.555	19	0.165	R.TLDAHIEEQFGSGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1560.636	1560.650	-9.227	0.491	1131.364	0.564	19	0.164	R.TLDAHIEEQFGSGR.L
R2/RRR2-15/2	1559.492	1560.650	-1387.721	0.394	1014.424	0.461	18	0.137	R.TLDAHIEEQFGSGR.L
R2/RRR2-14/3	1561.985	1560.650	215.346	0.480	965.767	0.504	28	0.108	R.TLDAHIEEQFGSGR.L
R2/RRR2-13/2	1897.448	1898.214	-933.550	0.524	1812.400	0.550	29	0.240	K.VM*VGLPTTGGVTPVPGAAEK.A
R2/RRR2-13/2	1898.358	1898.214	76.454	0.568	1600.735	0.620	28	0.229	K.VM*VGLPTTGGVTPVPGAAEK.A
R2/RRR2-13/2	1898.474	1898.214	137.394	0.564	1385.717	0.646	27	0.207	K.VM*VGLPTTGGVTPVPGAAEK.A
R2/RRR2-13/2	1595.203	1594.853	220.115	0.535	1700.003	0.480	18	0.202	K.FASFETIVEM*IYK.H
R2/RRR2-13/2	1579.919	1578.853	41.645	0.474	1548.943	0.464	19	0.183	K.FASFETIVEMIYK.H
R2/RRR2-14/2	1579.921	1578.853	43.195	0.465	1556.800	0.456	19	0.182	K.FASFETIVEMIYK.H
R2/RRR2-13/2	1594.124	1594.853	-1087.493	0.450	1478.611	0.430	17	0.167	K.FASFETIVEM*IYK.H
R2/RRR2-13/2	1594.141	1594.853	-1077.267	0.395	1461.146	0.351	17	0.151	K.FASFETIVEM*IYK.H
R2/RRR2-13/2	1594.000	1594.853	-1166.155	0.413	1175.621	0.428	18	0.143	K.FASFETIVEM*IYK.H
R2/RRR2-13/2	1881.422	1882.214	-955.755	0.490	765.023	0.554	21	0.133	K.VMVGLPTTGGVTPVPGAAEK.A
R2/RRR2-14/2	1580.239	1578.853	244.789	0.425	961.437	0.396	17	0.126	K.FASFETIVEMIYK.H
R2/RRR2-13/2	1593.896	1594.853	-1231.525	0.362	1019.607	0.348	18	0.124	K.FASFETIVEM*IYK.H
R2/RRR2-14/2	1594.129	1594.853	-1084.417	0.384	1002.109	0.320	16	0.118	K.FASFETIVEM*IYK.H
R2/RRR2-13/2	1593.543	1594.853	-1453.767	0.315	1042.304	0.293	17	0.117	K.FASFETIVEM*IYK.H
R2/RRR2-13/2	1594.373	1594.853	-301.578	0.309	306.624	0.332	13	0.111	K.FASFETIVEM*IYK.H
R2/RRR2-14/2	1594.026	1594.853	-1149.468	0.331	944.773	0.270	15	0.110	K.FASFETIVEM*IYK.H
R2/RRR2-14/2	1593.992	1594.853	-1170.692	0.283	552.951	0.339	14	0.108	K.FASFETIVEM*IYK.H
R2/RRR2-11/2	1580.303	1578.853	285.144	0.267	396.266	0.322	13	0.108	K.FASFETIVEMIYK.H
R2/RRR2-3/2	1315.157	1315.458	-229.447	0.291	882.084	0.433	13	0.122	R.FTWTIENFTR.I
R2/RRR2-14/2	1595.489	1595.779	-182.072	0.509	2448.070	0.621	25	0.382	K.VPGVDDVTGEPLIQR.K
R2/RRR2-14/2	1635.459	1634.812	-216.402	0.615	2490.749	0.418	22	0.310	K.VLNFAIDDSILEER.I
R2/RRR2-14/2	1634.420	1634.812	-240.811	0.567	2303.316	0.428	22	0.282	K.VLNFAIDDSILEER.I
R2/RRR2-14/2	1594.989	1595.779	-1125.703	0.483	1925.885	0.574	23	0.266	K.VPGVDDVTGEPLIQR.K
R2/RRR2-14/2	1595.491	1595.779	-180.921	0.518	1671.628	0.589	22	0.232	K.VPGVDDVTGEPLIQR.K
R2/RRR2-14/2	1633.400	1634.812	-1481.067	0.425	2090.216	0.350	22	0.228	K.VLNFAIDDSILEER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1634.759	1634.812	-32.401	0.465	1838.672	0.282	20	0.176	K.VLNFAIDDSILEER.I
R2/RRR2-14/2	1021.810	1022.181	-364.276	0.464	1215.976	0.463	14	0.156	K.GFILDGFPR.T
R2/RRR2-14/2	1022.034	1022.181	-144.968	0.496	1156.723	0.481	14	0.155	K.GFILDGFPR.T
R2/RRR2-14/2	1021.961	1022.181	-216.741	0.457	1145.939	0.451	14	0.148	K.GFILDGFPR.T
R2/RRR2-14/2	1038.129	1038.266	-132.282	0.441	742.039	0.332	15	0.112	-.LILVGPPGSGK.-
R2/RRR2-14/2	1038.190	1038.266	-73.190	0.377	580.374	0.270	13	0.104	R.LILVGPPGSGK.G
R2/RRR2-10/2	1635.940	1634.812	78.763	0.391	843.706	0.251	16	0.104	K.VLNFAIDDSILEER.I
R2/RRR2-16/2	1398.134	1397.561	-306.115	0.524	1854.346	0.489	20	0.229	K.LYGSTLSWNVTR.C
R2/RRR2-16/2	1398.177	1397.561	-275.282	0.542	1611.319	0.529	19	0.207	K.LYGSTLSWNVTR.C
R2/RRR2-16/2	1397.121	1397.561	-315.977	0.499	1733.091	0.429	20	0.198	K.LYGSTLSWNVTR.C
R2/RRR2-15/2	1397.436	1397.561	-89.684	0.460	1427.945	0.476	18	0.174	K.LYGSTLSWNVTR.C
R2/RRR2-16/2	1106.933	1107.285	-318.842	0.502	1375.585	0.415	15	0.161	K.KVLEVYEAR.L
R2/RRR2-16/2	1107.174	1107.285	-100.478	0.526	1320.254	0.383	15	0.150	K.KVLEVYEAR.L
R2/RRR2-15/2	1396.616	1397.561	-1396.318	0.377	1298.396	0.360	17	0.141	K.LYGSTLSWNVTR.C
R2/RRR2-15/2	978.942	979.112	-173.486	0.543	763.950	0.453	13	0.134	K.VLEVYEAR.L
R2/RRR2-15/2	1106.977	1107.285	-279.012	0.442	1051.844	0.389	14	0.133	K.KVLEVYEAR.L
R2/RRR2-15/2	1397.099	1397.561	-331.581	0.403	1077.629	0.398	16	0.132	K.LYGSTLSWNVTR.C
R2/RRR2-17/2	978.928	979.112	-188.497	0.442	868.825	0.428	13	0.132	K.VLEVYEAR.L
R2/RRR2-14/2	979.162	979.112	51.879	0.474	918.758	0.396	13	0.130	K.VLEVYEAR.L
R2/RRR2-15/2	978.881	979.112	-236.411	0.436	928.579	0.394	13	0.130	K.VLEVYEAR.L
R2/RRR2-17/2	979.157	979.112	46.502	0.420	976.047	0.362	13	0.128	K.VLEVYEAR.L
R2/RRR2-15/2	978.861	979.112	-257.054	0.443	731.827	0.418	13	0.128	K.VLEVYEAR.L
R2/RRR2-16/2	978.859	979.112	-259.306	0.501	775.480	0.398	13	0.127	K.VLEVYEAR.L
R2/RRR2-16/2	978.846	979.112	-271.818	0.402	736.947	0.402	13	0.125	K.VLEVYEAR.L
R2/RRR2-16/2	978.364	979.112	-1792.078	0.424	786.609	0.372	13	0.124	K.VLEVYEAR.L
R2/RRR2-13/2	978.880	979.112	-237.537	0.400	611.628	0.422	12	0.123	K.VLEVYEAR.L
R2/RRR2-16/2	1693.222	1693.908	-998.570	0.425	524.217	0.451	19	0.121	K.AWWTDLM*ARPSSQK.V
R2/RRR2-16/2	978.393	979.112	-1761.740	0.395	635.990	0.367	12	0.119	K.VLEVYEAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1693.294	1693.908	-956.084	0.440	602.437	0.406	19	0.118	K.AWWTDLM*ARPSSQK.V
R2/RRR2-16/2	978.421	979.112	-1733.660	0.344	738.543	0.335	13	0.118	K.VLEVYEAR.L
R2/RRR2-16/2	1397.054	1397.561	-1081.958	0.361	767.855	0.388	15	0.117	K.LYGSTLSWNVTR.C
R2/RRR2-16/2	1677.401	1677.908	-901.493	0.517	1199.345	0.268	18	0.116	K.AWWTDLMARPSSQK.V
R2/RRR2-16/2	1693.437	1693.908	-279.125	0.461	440.386	0.383	18	0.115	K.AWWTDLM*ARPSSQK.V
R2/RRR2-15/2	978.670	979.112	-453.144	0.367	552.886	0.313	11	0.112	-.VLEVYEAR.-
R2/RRR2-3/2	1397.430	1397.561	-93.714	0.320	427.317	0.334	12	0.108	K.LYGSTLSWNVTR.C
R2/RRR2-16/2	1398.606	1397.561	32.600	0.319	358.425	0.364	11	0.102	-.LYGSTLSWNVTR.-
R2/RRR2-23/2	1654.577	1653.905	-198.658	0.516	1640.048	0.563	23	0.217	R.TLLGATNPLASAPGTIR.G
R2/RRR2-22/2	1655.144	1653.905	145.238	0.527	1710.385	0.521	23	0.215	R.TLLGATNPLASAPGTIR.G
R2/RRR2-22/2	1392.114	1391.468	-255.373	0.576	1370.080	0.579	19	0.193	K.AGEVVNWSSENAK.W
R2/RRR2-23/2	1654.324	1653.905	253.957	0.489	1616.582	0.472	22	0.191	R.TLLGATNPLASAPGTIR.G
R2/RRR2-22/2	1392.224	1391.468	-175.676	0.568	1367.859	0.578	18	0.191	K.AGEVVNWSSENAK.W
R2/RRR2-22/2	1390.928	1391.468	-1110.754	0.511	1497.559	0.482	19	0.184	K.AGEVVNWSSENAK.W
R2/RRR2-23/2	1655.188	1653.905	171.716	0.416	1254.734	0.449	19	0.149	R.TLLGATNPLASAPGTIR.G
R2/RRR2-22/2	949.444	950.031	-1675.604	0.441	1186.641	0.434	14	0.148	-.GDFAIDVGR.-
R2/RRR2-22/2	949.867	950.031	-172.287	0.452	1091.932	0.431	14	0.142	R.GDFAIDVGR.N
R2/RRR2-23/2	950.979	950.031	-53.895	0.492	1056.251	0.430	14	0.140	R.GDFAIDVGR.N
R2/RRR2-23/2	912.197	912.112	93.605	0.398	919.914	0.425	13	0.130	R.GLVGPIISR.F
R2/RRR2-22/2	912.050	912.112	-68.277	0.360	989.213	0.380	14	0.127	R.GLVGPIISR.F
R2/RRR2-22/2	911.829	912.112	-311.333	0.356	854.284	0.424	13	0.125	R.GLVGPIISR.F
R2/RRR2-22/2	949.385	950.031	-1738.514	0.403	1001.769	0.322	14	0.122	R.GDFAIDVGR.N
R2/RRR2-23/2	949.367	950.031	-1756.988	0.369	982.144	0.268	14	0.116	-.GDFAIDVGR.-
R2/RRR2-22/2	911.549	912.112	-1719.205	0.296	872.633	0.322	13	0.114	R.GLVGPIISR.F
R2/RRR2-22/2	1653.096	1653.905	-1097.244	0.358	713.621	0.359	16	0.108	-.TLLGATNPLASAPGTIR.-
R2/RRR2-24/2	1654.116	1653.905	128.156	0.303	501.275	0.228	16	0.101	-.TLLGATNPLASAPGTIR.-
R2/RRR2-23/2	949.426	950.031	-1694.851	0.341	757.640	0.192	13	0.098	-.GDFAIDVGR.-
R2/RRR2-22/2	1653.768	1653.905	-82.964	0.245	190.239	0.379	11	0.081	-.TLLGATNPLASAPGTIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/3	1817.252	1818.021	-976.070	0.518	2418.904	0.513	34	0.340	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/3	1817.460	1818.021	-861.165	0.561	2133.632	0.536	32	0.284	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-11/3	1090.975	1091.249	-251.020	0.475	2327.518	0.399	28	0.244	K.HNPGVGAALVR.L
R2/RRR2-11/2	1818.027	1818.021	3.697	0.581	1597.196	0.576	25	0.215	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/2	1572.422	1572.825	-256.924	0.520	1526.845	0.576	23	0.210	K.LGAAVSCADIVVLAGR.D
R2/RRR2-16/2	1817.583	1818.021	-241.535	0.515	1576.894	0.532	25	0.202	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/3	1091.397	1091.249	136.615	0.556	2095.094	0.391	26	0.200	K.HNPGVGAALVR.L
R2/RRR2-12/2	947.727	947.028	-319.177	0.558	1636.406	0.434	17	0.191	R.DASAILSGGR.I
R2/RRR2-12/2	1817.519	1818.021	-828.694	0.513	1466.292	0.533	23	0.188	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/2	947.004	947.028	-25.549	0.468	1662.611	0.398	17	0.186	R.DASAILSGGR.I
R2/RRR2-12/3	1091.056	1091.249	-177.105	0.500	1947.553	0.393	25	0.181	K.HNPGVGAALVR.L
R2/RRR2-12/2	1817.694	1818.021	-180.292	0.538	1272.504	0.572	23	0.176	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/2	1817.391	1818.021	-899.355	0.499	1259.922	0.539	23	0.168	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/3	1818.168	1818.021	81.232	0.528	1579.576	0.459	30	0.160	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-11/2	1817.497	1818.021	-840.695	0.490	1177.171	0.519	23	0.158	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/2	1572.221	1572.825	-1023.557	0.427	1005.990	0.460	19	0.135	K.LGAAVSCADIVVLAGR.D
R2/RRR2-12/2	1090.959	1091.249	-266.274	0.362	489.420	0.581	16	0.128	K.HNPGVGAALVR.L
R2/RRR2-12/2	1090.435	1091.249	-1668.359	0.334	478.619	0.548	16	0.124	K.HNPGVGAALVR.L
R2/RRR2-12/3	1091.327	1091.249	72.422	0.487	1598.282	0.348	24	0.124	K.HNPGVGAALVR.L
R2/RRR2-16/2	1090.769	1091.249	-440.529	0.358	506.900	0.519	15	0.123	K.HNPGVGAALVR.L
R2/RRR2-1/2	1817.618	1818.021	-222.400	0.442	644.628	0.510	18	0.122	K.AAANNIGLDGFDVIDAIK.S
R2/RRR2-12/2	1090.630	1091.249	-1488.666	0.263	511.084	0.545	16	0.118	K.HNPGVGAALVR.L
R2/RRR2-11/2	946.335	947.028	-1794.964	0.379	714.253	0.369	13	0.115	R.DASAILSGGR.I
R2/RRR2-11/2	1090.935	1091.249	-288.502	0.285	495.528	0.414	15	0.113	K.HNPGVGAALVR.L
R2/RRR2-11/3	1091.509	1091.249	239.070	0.464	1343.572	0.351	23	0.103	K.HNPGVGAALVR.L
R2/RRR2-11/3	1091.036	1091.249	-194.952	0.328	714.966	0.276	21	0.072	K.HNPGVGAALVR.L
R2/RRR2-15/2	1533.053	1533.580	-999.074	0.502	2551.423	0.553	24	0.376	R.AAGGASGGEELTVEER.N
R2/RRR2-14/2	1533.046	1533.580	-1003.631	0.527	2495.012	0.556	24	0.365	R.AAGGASGGEELTVEER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1533.013	1533.580	-1025.216	0.526	2454.938	0.553	23	0.355	R.AAGGASGGEELTVEER.N
R2/RRR2-14/2	1532.651	1533.580	-1262.399	0.461	2220.792	0.531	23	0.302	R.AAGGASGGEELTVEER.N
R2/RRR2-15/2	1533.121	1533.580	-300.086	0.476	2215.744	0.516	23	0.296	R.AAGGASGGEELTVEER.N
R2/RRR2-14/2	1389.222	1389.537	-227.437	0.478	1174.573	0.531	18	0.164	R.IISSIEQKEEGR.G
R2/RRR2-14/2	1389.208	1389.537	-237.575	0.448	1182.673	0.511	18	0.160	R.IISSIEQKEEGR.G
R2/RRR2-14/2	1389.100	1389.537	-315.246	0.473	1211.607	0.471	18	0.156	R.IISSIEQKEEGR.G
R2/RRR2-17/2	1732.432	1733.002	-908.688	0.450	2313.027	0.408	23	0.287	K.ILFEQILVTEGNSLR.D
R2/RRR2-17/2	990.028	990.090	-62.652	0.409	1128.439	0.389	15	0.138	K.VDDLLEASK.S
R2/RRR2-17/2	1331.035	1331.561	-1149.904	0.487	1194.309	0.295	16	0.125	K.LPEM*VELDIQK.G
R2/RRR2-17/2	1363.942	1364.526	-1164.598	0.386	626.119	0.445	14	0.115	R.IAASFDELEAVAK.Q
R2/RRR2-17/2	1332.114	1331.561	-336.291	0.462	663.801	0.340	14	0.112	K.LPEM*VELDIQK.G
R2/RRR2-17/2	1331.832	1331.561	204.008	0.496	947.333	0.247	16	0.109	-.LPEM*VELDIQK.-
R2/RRR2-17/2	1312.904	1313.502	-1220.625	0.458	1963.728	0.476	20	0.245	K.FM*EVISGTGDIK.A
R2/RRR2-17/2	1313.058	1313.502	-339.594	0.475	1691.142	0.455	19	0.202	K.FM*EVISGTGDIK.A
R2/RRR2-17/2	1313.164	1313.502	-258.170	0.428	1485.897	0.472	18	0.181	K.FM*EVISGTGDIK.A
R2/RRR2-17/2	1257.397	1257.484	-69.380	0.463	1434.118	0.476	15	0.177	R.AM*DFLVELFR.N
R2/RRR2-17/2	1257.065	1257.484	-334.128	0.464	1407.612	0.472	15	0.173	R.AM*DFLVELFR.N
R2/RRR2-17/2	1256.674	1257.484	-1444.046	0.460	1233.047	0.505	15	0.164	R.AM*DFLVELFR.N
R2/RRR2-17/2	1673.195	1673.805	-965.080	0.480	1172.129	0.494	22	0.157	K.ENHDFLASVGLDDLK.A
R2/RRR2-17/2	1672.869	1673.805	-1160.758	0.408	1039.849	0.410	21	0.133	K.ENHDFLASVGLDDLK.A
R2/RRR2-17/2	1552.222	1552.708	-313.905	0.383	905.116	0.251	16	0.104	K.GSSSCTNGLLWLTR.A
R2/RRR2-9/2	1984.491	1984.152	171.417	0.621	3187.399	0.565	26	0.544	R.ELQDEGFDVQTAGYGLLK.T
R2/RRR2-9/2	1983.619	1984.152	-775.227	0.555	1788.769	0.519	22	0.227	R.ELQDEGFDVQTAGYGLLK.T
R2/RRR2-9/2	1488.249	1488.670	-283.878	0.476	1831.607	0.479	22	0.226	R.SNVIVEYPGTVPGR.A
R2/RRR2-9/2	1488.283	1488.670	-260.836	0.430	1685.504	0.541	22	0.221	R.SNVIVEYPGTVPGR.A
R2/RRR2-9/2	1488.041	1488.670	-1097.999	0.345	1708.474	0.387	21	0.187	R.SNVIVEYPGTVPGR.A
R2/RRR2-9/2	1760.600	1759.984	-218.754	0.543	982.790	0.487	20	0.137	R.DAVGGLDRDPFVSLLGK.L
R2/RRR2-9/2	1759.558	1759.984	-242.959	0.503	669.335	0.502	18	0.123	R.DAVGGLDRDPFVSLLGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1759.426	1759.984	-888.345	0.460	712.727	0.454	18	0.119	R.DAVGGLDRDPFVSLLGK.L
R2/RRR2-3/2	1761.411	1759.984	243.105	0.414	335.138	0.424	13	0.106	R.DAVGGLDRDPFVSLLGK.L
R2/RRR2-9/3	1872.519	1873.056	-823.584	0.391	1301.717	0.288	29	0.089	K.KLQEYVHDINENIEK.L
R2/RRR2-16/2	1451.943	1452.613	-1153.913	0.488	1876.297	0.498	21	0.235	R.EAGTTM*EVVAAQTK.A
R2/RRR2-15/2	1390.373	1389.573	-144.561	0.501	1597.240	0.496	19	0.198	K.VIACIGETLEQR.E
R2/RRR2-15/2	1452.143	1452.613	-324.943	0.493	1618.837	0.483	20	0.196	R.EAGTTM*EVVAAQTK.A
R2/RRR2-16/2	1390.317	1389.573	-184.811	0.556	1524.601	0.482	19	0.187	K.VIACIGETLEQR.E
R2/RRR2-16/2	1388.654	1389.573	-1386.250	0.405	1641.244	0.416	19	0.185	K.VIACIGETLEQR.E
R2/RRR2-16/2	1452.190	1452.613	-292.388	0.487	1436.768	0.519	19	0.183	R.EAGTTM*EVVAAQTK.A
R2/RRR2-16/2	1388.575	1389.573	-1443.289	0.385	1685.795	0.372	19	0.181	K.VIACIGETLEQR.E
R2/RRR2-15/2	1451.683	1452.613	-1333.344	0.424	1487.392	0.456	20	0.176	R.EAGTTM*EVVAAQTK.A
R2/RRR2-16/2	1451.953	1452.613	-1147.074	0.481	1382.143	0.457	19	0.165	R.EAGTTM*EVVAAQTK.A
R2/RRR2-16/2	1602.262	1602.773	-945.832	0.495	1124.445	0.550	22	0.163	K.WLATNVSPAVAESTR.I
R2/RRR2-16/2	1602.384	1602.773	-243.868	0.543	1046.401	0.569	21	0.160	K.WLATNVSPAVAESTR.I
R2/RRR2-16/2	1049.496	1050.233	-1660.408	0.367	1589.584	0.298	17	0.157	K.VAYALSQGIK.V
R2/RRR2-16/2	1603.212	1602.773	274.655	0.568	1060.685	0.545	21	0.157	K.WLATNVSPAVAESTR.I
R2/RRR2-16/2	1049.903	1050.233	-315.287	0.467	1333.903	0.403	16	0.155	K.VAYALSQGIK.V
R2/RRR2-16/2	1049.895	1050.233	-323.219	0.441	1294.619	0.419	16	0.154	K.VAYALSQGIK.V
R2/RRR2-15/2	1452.027	1452.613	-1096.002	0.438	1228.993	0.456	18	0.151	R.EAGTTM*EVVAAQTK.A
R2/RRR2-16/2	1389.032	1389.573	-1112.975	0.433	1223.248	0.400	18	0.144	K.VIACIGETLEQR.E
R2/RRR2-16/2	1389.188	1389.573	-278.209	0.374	1167.298	0.362	17	0.133	K.VIACIGETLEQR.E
R2/RRR2-16/2	1751.507	1751.956	-257.008	0.560	2049.795	0.524	25	0.272	R.IIYGGSVNAANCAELAK.K
R2/RRR2-16/2	1551.276	1549.750	-306.756	0.591	2031.934	0.521	24	0.271	K.KEDIDGFLVGGASLK.G
R2/RRR2-16/2	1450.534	1450.619	-58.546	0.544	1790.579	0.565	22	0.243	K.GPDFATIINSVTSK.K
R2/RRR2-16/2	1752.342	1751.956	221.027	0.585	1828.395	0.525	24	0.236	R.IIYGGSVNAANCAELAK.K
R2/RRR2-16/2	1451.236	1450.619	-264.795	0.529	1610.364	0.594	21	0.225	K.GPDFATIINSVTSK.K
R2/RRR2-16/2	1229.550	1230.353	-1471.032	0.348	1518.545	0.417	21	0.172	K.TNVSPEVASGIR.I
R2/RRR2-16/2	1229.724	1230.353	-1328.546	0.395	1402.091	0.396	20	0.158	K.TNVSPEVASGIR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1229.546	1230.353	-1474.123	0.407	1040.050	0.430	17	0.136	K.TNVSPEVASGIR.I
R2/RRR2-16/2	1449.976	1450.619	-1136.450	0.328	486.937	0.505	16	0.116	K.GPDFATIINSVTSK.K
R2/RRR2-16/2	1662.476	1662.908	-260.682	0.576	2044.282	0.490	22	0.260	K.LQQVLNVYDEILSK.N
R2/RRR2-16/2	1663.381	1662.908	284.741	0.610	1892.952	0.493	21	0.235	K.LQQVLNVYDEILSK.N
R2/RRR2-16/2	1663.392	1662.908	291.437	0.608	1826.025	0.483	21	0.223	K.LQQVLNVYDEILSK.N
R2/RRR2-16/2	1343.964	1343.460	-370.381	0.529	1552.910	0.554	17	0.208	R.YVCTQFPEGNK.T
R2/RRR2-16/2	1343.168	1343.460	-218.372	0.489	1562.430	0.441	17	0.183	R.YVCTQFPEGNK.T
R2/RRR2-16/2	1342.916	1343.460	-1153.292	0.463	1488.536	0.425	17	0.172	R.YVCTQFPEGNK.T
R2/RRR2-16/2	1097.037	1097.203	-151.965	0.392	1030.786	0.495	16	0.145	K.TLYGTGSLER.A
R2/RRR2-16/2	1275.080	1275.439	-281.981	0.421	991.468	0.496	16	0.143	K.LRDPNGQVTFK.H
R2/RRR2-16/2	1097.016	1097.203	-171.053	0.380	945.501	0.487	16	0.139	K.TLYGTGSLER.A
R2/RRR2-16/2	1275.124	1275.439	-247.404	0.434	1028.973	0.430	16	0.136	K.LRDPNGQVTFK.H
R2/RRR2-16/2	1097.905	1097.203	-273.065	0.382	829.992	0.471	17	0.133	K.TLYGTGSLER.A
R2/RRR2-16/2	1096.976	1097.203	-208.003	0.334	958.351	0.413	16	0.129	K.TLYGTGSLER.A
R2/RRR2-16/2	1274.514	1275.439	-1514.912	0.400	975.271	0.398	16	0.129	K.LRDPNGQVTFK.H
R2/RRR2-16/2	1096.994	1097.203	-191.816	0.267	642.547	0.369	15	0.113	K.TLYGTGSLER.A
R2/RRR2-16/2	1096.488	1097.203	-1568.813	0.230	499.393	0.351	13	0.108	K.TLYGTGSLER.A
R2/RRR2-16/3	1275.075	1275.439	-285.786	0.389	851.992	0.422	23	0.087	K.LRDPNGQVTFK.H
R2/RRR2-16/3	1275.488	1275.439	39.000	0.397	842.977	0.414	24	0.085	K.LRDPNGQVTFK.H
R2/RRR2-16/3	1275.440	1275.439	0.699	0.385	555.961	0.313	21	0.076	K.LRDPNGQVTFK.H
R2/RRR2-3/2	1664.024	1662.913	66.544	0.465	879.099	0.470	18	0.130	K.VSAYLLGEYGHLLAR.R
R2/RRR2-3/2	1479.535	1479.750	-145.696	0.463	766.680	0.492	17	0.130	R.AQVQIPLEVVNLR.A
R2/RRR2-3/2	1561.628	1560.884	-164.324	0.494	1130.659	0.347	18	0.128	R.M*LLVTDVQDIIKR.H
R2/RRR2-3/2	1479.384	1479.750	-247.591	0.428	769.186	0.479	17	0.128	R.AQVQIPLEVVNLR.A
R2/RRR2-2/2	1578.861	1577.629	147.293	0.437	997.542	0.354	20	0.122	K.AEDAEVDTAEQSAIK.L
R2/RRR2-13/2	1479.884	1479.750	91.288	0.340	733.205	0.409	17	0.118	R.AQVQIPLEVVNLR.A
R2/RRR2-3/2	1478.389	1479.750	-1601.659	0.307	407.601	0.347	12	0.105	R.AQVQIPLEVVNLR.A
R2/RRR2-3/3	1937.095	1936.202	-55.351	0.399	809.931	0.469	25	0.091	R.HQAQIITSLKDPDISIR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/3	1492.158	1491.760	267.189	0.552	1685.258	0.442	29	0.162	R.KTDLLLAANPVHAK.V
R2/RRR2-16/2	1389.648	1389.582	47.788	0.492	1046.727	0.480	20	0.146	K.LLGSTNPSPFVTR.V
R2/RRR2-15/2	1491.509	1491.760	-168.989	0.389	815.211	0.505	19	0.132	R.KTDLLLAANPVHAK.V
R2/RRR2-15/2	1389.151	1389.582	-310.651	0.459	799.093	0.468	17	0.129	K.LLGSTNPSPFVTR.V
R2/RRR2-15/2	1446.648	1446.630	12.390	0.376	745.352	0.494	17	0.127	R.GLPYDLVAVDLDR.K
R2/RRR2-16/2	885.011	885.086	-85.374	0.404	802.981	0.395	13	0.124	R.VELALALR.G
R2/RRR2-15/2	885.108	885.086	24.746	0.469	813.058	0.345	13	0.121	R.VELALALR.G
R2/RRR2-16/2	1390.209	1389.582	-269.109	0.310	845.796	0.417	16	0.120	K.LLGSTNPSPFVTR.V
R2/RRR2-15/2	884.973	885.086	-128.128	0.487	795.713	0.304	13	0.117	R.VELALALR.G
R2/RRR2-15/2	1445.319	1446.630	-1603.573	0.328	675.718	0.408	17	0.115	R.GLPYDLVAVDLDR.K
R2/RRR2-16/3	1492.256	1491.760	333.507	0.550	1271.518	0.421	26	0.114	R.KTDLLLAANPVHAK.V
R2/RRR2-16/2	1389.267	1389.582	-227.166	0.312	421.809	0.461	14	0.112	K.LLGSTNPSPFVTR.V
R2/RRR2-15/2	884.940	885.086	-166.319	0.482	846.602	0.248	13	0.111	R.VELALALR.G
R2/RRR2-15/3	1492.241	1491.760	323.295	0.549	1162.802	0.443	27	0.110	R.KTDLLLAANPVHAK.V
R2/RRR2-15/3	1492.143	1491.760	257.345	0.594	1101.005	0.411	25	0.099	R.KTDLLLAANPVHAK.V
R2/RRR2-16/3	1491.263	1491.760	-334.134	0.468	1059.206	0.370	24	0.091	R.KTDLLLAANPVHAK.V
R2/RRR2-16/3	1491.990	1491.760	154.219	0.486	818.697	0.391	23	0.085	R.KTDLLLAANPVHAK.V
R2/RRR2-5/3	1951.388	1951.255	68.282	0.586	1908.456	0.582	33	0.255	K.SKLDAQPELFIHIVPDK.A
R2/RRR2-5/2	1610.262	1610.812	-965.365	0.495	1770.710	0.558	23	0.237	K.ASNTLSIIDSGVGM*TK.S
R2/RRR2-5/3	1952.135	1951.255	-61.792	0.598	1769.323	0.589	33	0.231	K.SKLDAQPELFIHIVPDK.A
R2/RRR2-5/2	1610.281	1610.812	-953.797	0.494	1565.115	0.598	22	0.219	K.ASNTLSIIDSGVGM*TK.S
R2/RRR2-5/2	1610.249	1610.812	-973.585	0.448	1596.101	0.554	22	0.211	K.ASNTLSIIDSGVGM*TK.S
R2/RRR2-5/3	1951.680	1951.255	218.645	0.542	1576.806	0.535	31	0.183	K.SKLDAQPELFIHIVPDK.A
R2/RRR2-5/2	1735.596	1736.004	-235.732	0.541	1052.492	0.575	21	0.161	K.LDAQPELFIHIVPDK.A
R2/RRR2-5/2	1735.582	1736.004	-244.129	0.572	1061.188	0.554	20	0.157	K.LDAQPELFIHIVPDK.A
R2/RRR2-5/2	1735.530	1736.004	-273.977	0.483	1098.410	0.515	21	0.153	K.LDAQPELFIHIVPDK.A
R2/RRR2-5/2	1737.205	1736.004	115.965	0.438	690.672	0.442	16	0.117	K.LDAQPELFIHIVPDK.A
R2/RRR2-5/3	1736.958	1736.004	-26.696	0.366	801.468	0.414	29	0.086	K.LDAQPELFIHIVPDK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1737.155	1736.004	87.064	0.382	640.554	0.437	27	0.086	K.LDAQPELFIHIVPDK.A
R2/RRR2-4/3	1736.165	1736.004	92.861	0.355	736.128	0.420	27	0.085	K.LDAQPELFIHIVPDK.A
R2/RRR2-5/3	1735.972	1736.004	-18.847	0.343	547.936	0.415	25	0.082	K.LDAQPELFIHIVPDK.A
R2/RRR2-1/3	1736.976	1736.004	-16.439	0.385	585.154	0.374	21	0.078	K.LDAQPELFIHIVPDK.A
R2/RRR2-4/3	1735.716	1736.004	-166.453	0.339	762.037	0.280	22	0.071	K.LDAQPELFIHIVPDK.A
R2/RRR2-8/2	1494.339	1494.716	-253.389	0.477	3126.621	0.496	22	0.494	K.VADFFDAAVNLALK.V
R2/RRR2-8/2	1493.605	1494.716	-1417.869	0.411	3047.283	0.471	22	0.464	K.VADFFDAAVNLALK.V
R2/RRR2-8/2	1494.294	1494.716	-283.549	0.470	3031.890	0.471	22	0.459	K.VADFFDAAVNLALK.V
R2/RRR2-8/2	1208.287	1208.392	-87.105	0.550	1941.896	0.471	18	0.241	K.VLENVHIAANK.N
R2/RRR2-8/2	1091.624	1092.273	-1515.013	0.476	1708.552	0.555	19	0.229	K.LIVAGASAYAR.L
R2/RRR2-8/2	1091.499	1092.273	-1629.939	0.429	1648.051	0.517	19	0.211	K.LIVAGASAYAR.L
R2/RRR2-8/2	1092.013	1092.273	-238.884	0.553	1562.829	0.548	19	0.210	K.LIVAGASAYAR.L
R2/RRR2-8/2	1208.083	1208.392	-256.370	0.545	1723.359	0.456	18	0.207	K.VLENVHIAANK.N
R2/RRR2-9/2	1493.658	1494.716	-1382.490	0.333	1600.438	0.413	20	0.178	K.VADFFDAAVNLALK.V
R2/RRR2-9/2	1494.162	1494.716	-1043.188	0.432	1438.334	0.473	19	0.174	K.VADFFDAAVNLALK.V
R2/RRR2-8/3	1260.426	1260.381	35.823	0.523	1724.039	0.380	24	0.143	K.LRHDVEEYAK.Q
R2/RRR2-9/2	1493.406	1494.716	-1551.858	0.357	989.009	0.311	16	0.115	K.VADFFDAAVNLALK.V
R2/RRR2-9/3	1259.999	1260.381	-303.927	0.436	1190.418	0.451	20	0.113	K.LRHDVEEYAK.Q
R2/RRR2-8/3	1260.054	1260.381	-260.042	0.447	1079.004	0.446	20	0.105	K.LRHDVEEYAK.Q
R2/RRR2-9/3	1260.427	1260.381	36.551	0.481	1284.275	0.362	21	0.101	K.LRHDVEEYAK.Q
R2/RRR2-9/3	1260.436	1260.381	43.837	0.476	1208.183	0.369	21	0.097	K.LRHDVEEYAK.Q
R2/RRR2-8/3	1260.151	1260.381	-182.780	0.466	1158.922	0.355	21	0.092	K.LRHDVEEYAK.Q
R2/RRR2-9/2	1286.928	1287.488	-1215.644	0.392	1739.163	0.399	18	0.195	K.DASLVEIVTAIR.E
R2/RRR2-9/2	1405.355	1404.550	-138.925	0.527	1321.604	0.492	20	0.170	R.TLAIDFAPDADVR.L
R2/RRR2-9/2	1404.261	1404.550	-206.779	0.484	1161.652	0.525	19	0.161	R.TLAIDFAPDADVR.L
R2/RRR2-9/2	1403.945	1404.550	-1146.851	0.393	1070.217	0.434	18	0.137	R.TLAIDFAPDADVR.L
R2/RRR2-9/2	1360.192	1360.582	-287.380	0.396	1055.838	0.413	16	0.133	K.SVIEISLDSIKR.V
R2/RRR2-8/2	822.784	822.932	-180.297	0.299	942.431	0.375	12	0.121	R.LGFAASTR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1360.209	1360.582	-274.865	0.349	760.716	0.409	14	0.116	K.SVIEISLDSIKR.V
R2/RRR2-9/2	1287.125	1287.488	-282.957	0.313	976.426	0.287	16	0.113	K.DASLVEIVTAIR.E
R2/RRR2-8/2	822.327	822.932	-1957.104	0.141	823.820	0.027	12	0.095	R.LGFAASTR.H
R2/RRR2-13/2	1752.421	1752.092	188.459	0.592	1715.434	0.540	26	0.221	K.AVVAGASGGIGQPLSLLLK.L
R2/RRR2-12/2	1751.735	1752.092	-204.134	0.494	1646.678	0.448	24	0.189	K.AVVAGASGGIGQPLSLLLK.L
R2/RRR2-13/2	1751.449	1752.092	-940.556	0.511	1388.051	0.496	23	0.171	K.AVVAGASGGIGQPLSLLLK.L
R2/RRR2-13/2	1751.022	1752.092	-1185.515	0.395	1517.460	0.418	25	0.170	K.AVVAGASGGIGQPLSLLLK.L
R2/RRR2-12/2	1751.376	1752.092	-982.750	0.461	1489.181	0.398	23	0.162	K.AVVAGASGGIGQPLSLLLK.L
R2/RRR2-13/2	1234.514	1234.470	36.139	0.397	844.444	0.342	17	0.118	R.LFGVTTLDIVR.A
R2/RRR2-13/2	1234.215	1234.470	-207.293	0.334	827.436	0.338	16	0.115	R.LFGVTTLDIVR.A
R2/RRR2-13/2	1234.203	1234.470	-216.620	0.362	727.652	0.248	15	0.106	R.LFGVTTLDIVR.A
R2/RRR2-13/2	1211.158	1211.433	-227.717	0.241	780.044	0.262	14	0.102	K.GLIEIAAEVAPK.A
R2/RRR2-3/3	1908.778	1909.022	-128.227	0.523	2710.190	0.509	37	0.405	K.TQEKDADAM*QVDNAVEK.K
R2/RRR2-3/3	1908.641	1909.022	-200.210	0.515	2542.883	0.505	35	0.362	K.TQEKDADAM*QVDNAVEK.K
R2/RRR2-3/3	1908.241	1909.022	-936.062	0.508	2525.835	0.496	35	0.353	K.TQEKDADAM*QVDNAVEK.K
R2/RRR2-3/2	1402.278	1402.645	-262.602	0.500	1886.720	0.521	20	0.243	K.MGAILASGILDAGGR.N
R2/RRR2-3/2	1402.161	1402.645	-346.713	0.334	1272.695	0.396	18	0.143	K.MGAILASGILDAGGR.N
R2/RRR2-3/2	1417.459	1418.645	-1546.755	0.258	695.906	0.321	16	0.105	K.M*GAILASGILDAGGR.N
R2/RRR2-17/2	1432.004	1431.702	211.561	0.516	1642.435	0.557	20	0.189	K.LGSQIDILAPIKY.-
R2/RRR2-17/3	1538.811	1538.759	33.731	0.457	1710.779	0.425	29	0.158	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1538.458	1538.759	-196.179	0.469	1114.632	0.507	24	0.123	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1538.205	1538.759	-1013.155	0.490	1193.530	0.482	25	0.123	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1538.724	1538.759	-22.961	0.464	1277.985	0.439	26	0.119	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1538.212	1538.759	-1009.091	0.451	1097.205	0.485	24	0.117	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/2	886.672	887.016	-388.795	0.359	872.468	0.333	12	0.116	R.GEAALANLK.A
R2/RRR2-17/3	1538.625	1538.759	-87.657	0.434	1361.135	0.392	28	0.114	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/2	886.428	887.016	-1797.071	0.387	842.874	0.305	12	0.113	R.GEAALANLK.A
R2/RRR2-17/2	1428.221	1427.594	-262.139	0.432	700.376	0.358	15	0.112	-.CEEM*CISGGLVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1427.144	1427.594	-315.871	0.358	702.600	0.363	14	0.111	-.CEEM*CISGGLVR.-
R2/RRR2-17/3	1538.418	1538.759	-222.567	0.457	1135.256	0.429	25	0.107	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/2	886.345	887.016	-1890.342	0.285	817.295	0.208	12	0.104	R.GEAALANLK.A
R2/RRR2-17/2	1426.427	1427.594	-1523.290	0.311	459.305	0.291	12	0.104	R.CEEM*CISGGLVR.Q
R2/RRR2-16/3	1538.883	1538.759	80.631	0.498	906.647	0.459	23	0.101	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1538.473	1538.759	-186.627	0.415	1210.017	0.366	26	0.100	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1521.941	1522.760	-1198.808	0.398	1374.918	0.302	26	0.097	R.MNTKPSHGPIHFR.A
R2/RRR2-15/3	1537.705	1538.759	-1340.018	0.391	979.308	0.389	23	0.093	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1537.839	1538.759	-1252.244	0.393	380.543	0.403	21	0.091	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1538.284	1538.759	-309.502	0.397	531.826	0.413	23	0.089	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1538.585	1538.759	-113.562	0.386	487.557	0.388	21	0.087	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1539.442	1538.759	-206.353	0.348	773.212	0.380	21	0.086	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1522.856	1522.760	63.176	0.393	724.608	0.369	21	0.084	R.MNTKPSHGPIHFR.A
R2/RRR2-15/3	1538.075	1538.759	-1098.138	0.320	699.257	0.366	18	0.083	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/3	1522.229	1522.760	-1008.680	0.412	796.151	0.343	21	0.082	R.MNTKPSHGPIHFR.A
R2/RRR2-17/3	1538.147	1538.759	-1050.924	0.306	648.834	0.332	22	0.081	R.M*NTKPSHGPIHFR.A
R2/RRR2-17/2	1430.826	1431.702	-1314.758	0.363	1093.117	0.541	18	0.076	K.LGSQIDILAPIKY.-
R2/RRR2-17/3	1539.722	1538.759	-24.298	0.385	876.083	0.277	21	0.074	-.M*NTKPSHGPIHFR.-
R2/RRR2-17/2	1431.388	1431.702	-219.711	0.436	1038.149	0.547	17	0.066	K.LGSQIDILAPIKY.-
R2/RRR2-5/2	1624.108	1623.811	183.624	0.360	945.223	0.480	17	0.131	K.ANGTLTIQDSGIGM*TK.A
R2/RRR2-5/2	1624.360	1623.811	-278.455	0.357	802.045	0.446	17	0.120	K.ANGTLTIQDSGIGM*TK.A
R2/RRR2-5/2	1292.042	1292.375	-258.663	0.438	801.035	0.375	16	0.118	R.EIISNSSDALDK.I
R2/RRR2-5/2	1561.247	1561.719	-303.542	0.456	788.334	0.348	20	0.116	R.EIISNSSDALDKIR.Y
R2/RRR2-5/2	1560.726	1561.719	-1281.347	0.419	844.129	0.333	20	0.116	R.EIISNSSDALDKIR.Y
R2/RRR2-5/2	1561.163	1561.719	-1000.064	0.419	905.196	0.305	21	0.116	R.EIISNSSDALDKIR.Y
R2/RRR2-5/2	1292.028	1292.375	-269.185	0.441	693.125	0.369	15	0.114	R.EIISNSSDALDK.I
R2/RRR2-5/2	1291.586	1292.375	-1388.811	0.318	795.086	0.351	16	0.114	R.EIISNSSDALDK.I
R2/RRR2-15/2	1750.433	1750.953	-870.736	0.537	2064.192	0.564	19	0.290	K.DLVVDMTNFYNQYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1789.657	1791.093	-1365.582	0.383	1458.012	0.276	19	0.139	K.VDLSDCGPM*VLDVLLK.I
R2/RRR2-15/2	1508.144	1508.660	-1008.025	0.377	799.964	0.386	20	0.120	R.WDPDSPSTKPHLK.D
R2/RRR2-15/3	1079.575	1079.278	276.530	0.439	667.513	0.243	18	0.066	-.RKDAPPLPGK.-
R2/RRR2-15/3	1078.783	1079.278	-459.907	0.367	820.162	0.186	19	0.065	K.RKDAPPLPGK.E
R2/RRR2-15/3	1079.610	1079.278	308.842	0.409	1113.357	0.171	20	0.064	K.RKDAPPLPGK.E
R2/RRR2-9/2	1998.602	1999.212	-807.703	0.593	2748.479	0.558	28	0.425	K.TQDIQIVGDDLTVTNPIR.I
R2/RRR2-9/2	1998.544	1999.212	-836.704	0.573	2141.877	0.575	26	0.303	K.TQDIQIVGDDLTVTNPIR.I
R2/RRR2-9/2	1574.262	1573.773	311.126	0.557	1952.050	0.617	23	0.284	K.VNQIGTLTESIQAAK.D
R2/RRR2-9/2	1776.390	1776.924	-865.870	0.505	2150.280	0.481	25	0.276	R.SGETEDVTISDVVVGIR.A
R2/RRR2-9/2	1776.452	1776.924	-266.219	0.502	2210.928	0.440	23	0.272	R.SGETEDVTISDVVVGIR.A
R2/RRR2-9/2	1574.350	1573.773	-269.519	0.540	1808.487	0.550	23	0.241	K.VNQIGTLTESIQAAK.D
R2/RRR2-9/2	1573.337	1573.773	-278.253	0.531	1783.473	0.564	22	0.241	K.VNQIGTLTESIQAAK.D
R2/RRR2-9/2	1777.245	1776.924	181.486	0.557	1856.434	0.518	23	0.237	R.SGETEDVTISDVVVGIR.A
R2/RRR2-9/2	1998.018	1999.212	-1101.037	0.530	1872.015	0.501	24	0.235	K.TQDIQIVGDDLTVTNPIR.I
R2/RRR2-9/2	1898.007	1899.007	-1057.389	0.470	990.816	0.505	22	0.143	R.IEEELGSNAVYAGENFR.K
R2/RRR2-16/3	1787.592	1788.082	-275.046	0.528	2481.772	0.420	33	0.303	R.NKFDPLWNSLVIGGVK.K
R2/RRR2-16/3	1788.051	1788.082	-17.887	0.515	2411.064	0.416	31	0.289	R.NKFDPLWNSLVIGGVK.K
R2/RRR2-16/3	1788.479	1788.082	222.612	0.577	1833.658	0.478	30	0.201	R.NKFDPLWNSLVIGGVK.K
R2/RRR2-16/2	1787.284	1788.082	-1009.452	0.517	1316.695	0.531	24	0.177	R.NKFDPLWNSLVIGGVK.K
R2/RRR2-16/2	1642.494	1641.889	-241.640	0.463	1219.586	0.562	24	0.174	R.TQYPYVTGSSIIALK.Y
R2/RRR2-16/2	1641.397	1641.889	-300.580	0.466	1179.618	0.564	23	0.170	R.TQYPYVTGSSIIALK.Y
R2/RRR2-16/2	1787.407	1788.082	-940.061	0.522	1105.034	0.572	22	0.165	R.NKFDPLWNSLVIGGVK.K
R2/RRR2-16/2	1787.966	1788.082	-65.096	0.534	1073.681	0.585	22	0.164	R.NKFDPLWNSLVIGGVK.K
R2/RRR2-16/2	1640.979	1641.889	-1167.796	0.385	1047.073	0.526	22	0.149	R.TQYPYVTGSSIIALK.Y
R2/RRR2-16/2	1050.022	1050.313	-277.821	0.467	1168.570	0.354	13	0.136	K.CLLVLLYR.D
R2/RRR2-16/2	1050.076	1050.313	-226.038	0.443	971.096	0.287	12	0.116	K.CLLVLLYR.D
R2/RRR2-16/2	1654.443	1654.885	-267.572	0.472	825.090	0.354	19	0.115	K.ITTEGATIYPPYSLK.T
R2/RRR2-16/2	1654.331	1654.885	-942.189	0.403	762.446	0.366	19	0.115	K.ITTEGATIYPPYSLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1654.315	1654.885	-951.819	0.406	783.008	0.272	18	0.105	K.ITTEGATIYPPYSLK.T
R2/RRR2-6/2	1374.989	1375.492	-1096.560	0.455	1625.633	0.411	17	0.183	K.NSLENYAYNMR.N
R2/RRR2-6/2	1391.172	1391.492	-230.424	0.541	1374.072	0.502	17	0.176	K.NSLENYAYNM*R.N
R2/RRR2-6/2	1391.056	1391.492	-314.412	0.486	1361.492	0.416	17	0.158	K.NSLENYAYNM*R.N
R2/RRR2-6/2	1390.336	1391.492	-1555.200	0.310	1246.280	0.285	17	0.128	K.NSLENYAYNM*R.N
R2/RRR2-6/2	1374.828	1375.492	-1214.153	0.270	595.128	0.218	13	0.103	K.NSLENYAYNMR.N
R2/RRR2-12/2	1595.333	1595.862	-961.606	0.514	2209.352	0.501	22	0.292	R.LTNLAEIDPLASLPK.L
R2/RRR2-12/2	1492.412	1492.742	-221.392	0.524	2122.595	0.470	21	0.267	K.LQFLSLLDNTVTK.Q
R2/RRR2-12/2	1595.622	1595.862	-151.057	0.500	1921.088	0.535	21	0.253	R.LTNLAEIDPLASLPK.L
R2/RRR2-12/2	1595.343	1595.862	-954.769	0.476	1927.525	0.497	21	0.244	R.LTNLAEIDPLASLPK.L
R2/RRR2-12/2	1492.109	1492.742	-1097.796	0.453	2111.049	0.381	21	0.240	K.LQFLSLLDNTVTK.Q
R2/RRR2-12/2	1492.058	1492.742	-1132.052	0.435	1799.602	0.447	20	0.212	K.LQFLSLLDNTVTK.Q
R2/RRR2-12/2	1501.222	1501.667	-297.328	0.420	1473.622	0.475	20	0.181	K.AAIVNSQTLEEVAR.L
R2/RRR2-11/2	1493.859	1492.742	78.631	0.436	1272.102	0.510	18	0.166	K.LQFLSLLDNTVTK.Q
R2/RRR2-12/2	1368.195	1367.616	-308.250	0.398	523.050	0.502	18	0.122	K.VVAPTPEQITAIK.A
R2/RRR2-9/2	1420.976	1421.624	-1163.004	0.445	1466.161	0.517	18	0.187	R.VLISGSLDLFSNR.F
R2/RRR2-9/2	1039.052	1039.207	-149.369	0.481	1581.155	0.430	17	0.185	R.LGYTGLSLSK.Q
R2/RRR2-9/2	1039.281	1039.207	71.202	0.449	1391.748	0.520	16	0.183	R.LGYTGLSLSK.Q
R2/RRR2-9/2	1310.596	1311.380	-1364.836	0.544	1389.704	0.484	18	0.175	K.AGNEQFVTETSK.W
R2/RRR2-9/2	1310.997	1311.380	-292.560	0.563	1355.325	0.478	18	0.170	K.AGNEQFVTETSK.W
R2/RRR2-9/2	1421.761	1421.624	96.656	0.372	1296.834	0.496	16	0.163	R.VLISGSLDLFSNR.F
R2/RRR2-9/2	1298.964	1299.499	-1184.774	0.435	1098.216	0.489	16	0.150	K.VPDVYGVFQFK.V
R2/RRR2-9/2	1300.195	1299.499	-233.970	0.362	1057.774	0.400	14	0.130	K.VPDVYGVFQFK.V
R2/RRR2-9/2	1421.395	1421.624	-161.045	0.294	909.971	0.470	15	0.127	R.VLISGSLDLFSNR.F
R2/RRR2-11/2	1512.613	1512.861	-164.365	0.443	1174.982	0.484	19	0.155	K.WLQTITSLPILVK.G
R2/RRR2-11/2	1992.317	1993.240	-968.128	0.474	330.315	0.532	17	0.118	R.QLDYVPATISCLEEVVR.E
R2/RRR2-11/2	1007.071	1007.122	-50.833	0.424	797.467	0.305	15	0.116	K.NFEALDLGK.M
R2/RRR2-11/2	1008.016	1007.122	-105.079	0.422	752.049	0.273	14	0.111	K.NFEALDLGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	891.652	892.037	-433.722	0.373	893.656	0.223	13	0.108	R.RAELAGFK.A
R2/RRR2-11/2	1993.530	1993.240	145.889	0.418	213.162	0.408	14	0.108	R.QLDYVPATISCLEEVVR.E
R2/RRR2-10/2	1791.395	1791.940	-865.042	0.507	1642.180	0.576	25	0.224	K.SYELPDGQVITIGNER.-
R2/RRR2-12/2	1792.736	1791.940	-114.232	0.531	1453.391	0.560	24	0.196	K.SYELPDGQVITIGNER.-
R2/RRR2-10/2	1791.512	1791.940	-239.446	0.515	1422.618	0.566	23	0.194	K.SYELPDGQVITIGNER.-
R2/RRR2-10/2	1792.411	1791.940	263.628	0.542	1338.255	0.557	23	0.183	K.SYELPDGQVITIGNER.-
R2/RRR2-12/2	1791.509	1791.940	-241.155	0.483	1330.505	0.508	22	0.171	K.SYELPDGQVITIGNER.-
R2/RRR2-10/2	1954.610	1955.244	-838.473	0.498	1103.964	0.586	23	0.164	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/2	1955.603	1955.244	184.155	0.552	1054.376	0.592	23	0.162	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-12/2	1954.007	1955.244	-1147.829	0.402	957.228	0.531	21	0.141	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-12/2	1954.514	1955.244	-887.752	0.468	782.111	0.593	20	0.140	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/2	1955.434	1955.244	97.764	0.509	715.004	0.611	19	0.139	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/2	1133.958	1133.193	-207.589	0.509	630.034	0.538	16	0.137	R.GYTFSTTAER.E
R2/RRR2-10/2	1133.027	1133.193	-146.813	0.469	690.995	0.404	16	0.123	R.GYTFSTTAER.E
R2/RRR2-12/2	1954.312	1955.244	-991.340	0.406	518.575	0.516	16	0.117	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/2	1132.900	1133.193	-259.334	0.311	478.500	0.325	15	0.111	R.GYTFSTTAER.E
R2/RRR2-10/3	1792.433	1791.940	275.674	0.404	1151.195	0.386	27	0.099	K.SYELPDGQVITIGNER.-
R2/RRR2-10/3	1955.691	1955.244	229.247	0.426	733.292	0.403	29	0.085	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/3	1954.554	1955.244	-866.818	0.384	822.982	0.382	28	0.084	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/3	1791.579	1791.940	-201.994	0.314	812.273	0.402	25	0.082	K.SYELPDGQVITIGNER.-
R2/RRR2-12/3	1955.185	1955.244	-30.229	0.402	788.940	0.366	27	0.081	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-11/3	1954.582	1955.244	-852.805	0.397	449.356	0.370	23	0.080	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/3	1955.890	1955.244	-181.331	0.414	740.484	0.351	27	0.079	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-10/3	1955.064	1955.244	-92.230	0.404	532.951	0.355	25	0.079	R.VAPEEHPVLLTEAPINPK.S
R2/RRR2-11/3	1955.485	1955.244	123.613	0.379	405.182	0.369	22	0.077	-.VAPEEHPVLLTEAPINPK.-
R2/RRR2-11/3	1955.643	1955.244	204.930	0.402	504.551	0.349	24	0.076	-.VAPEEHPVLLTEAPINPK.-
R2/RRR2-10/3	1955.595	1955.244	180.236	0.436	408.962	0.385	22	0.069	-.VAPEEHPVLLTEAPINPK.-
R2/RRR2-10/3	1791.965	1791.940	13.889	0.316	627.405	0.269	23	0.067	-.SYELPDGQVITIGNER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1274.798	1275.352	-1222.985	0.469	1419.899	0.459	17	0.171	K.AQIWDTAGQER.F
R2/RRR2-16/2	1274.941	1275.352	-323.978	0.507	1310.424	0.490	17	0.168	K.AQIWDTAGQER.F
R2/RRR2-17/2	1274.284	1275.352	-1628.179	0.331	1561.103	0.378	17	0.168	K.AQIWDTAGQER.F
R2/RRR2-17/2	1274.206	1275.352	-1689.197	0.368	1461.018	0.416	17	0.166	K.AQIWDTAGQER.F
R2/RRR2-16/2	1274.352	1275.352	-1574.480	0.362	1387.898	0.430	17	0.161	K.AQIWDTAGQER.F
R2/RRR2-16/3	1471.496	1471.598	-69.578	0.504	1645.626	0.424	34	0.156	K.KPVASDEGGAGAAGGVK.E
R2/RRR2-17/2	1081.017	1081.204	-173.471	0.462	1082.972	0.520	16	0.155	K.STIGVEFATR.S
R2/RRR2-16/2	1274.763	1275.352	-1250.680	0.447	1317.960	0.417	17	0.154	K.AQIWDTAGQER.F
R2/RRR2-16/2	1080.575	1081.204	-1511.695	0.423	1135.651	0.491	16	0.153	K.STIGVEFATR.S
R2/RRR2-17/2	1630.367	1629.842	-292.250	0.376	1487.691	0.324	18	0.152	K.IIKAQIWDTAGQER.Y
R2/RRR2-16/2	1081.170	1081.204	-31.551	0.408	962.621	0.513	15	0.144	K.STIGVEFATR.S
R2/RRR2-17/2	1081.164	1081.204	-37.327	0.461	975.052	0.469	15	0.140	K.STIGVEFATR.S
R2/RRR2-16/2	1080.572	1081.204	-1514.986	0.359	917.834	0.455	15	0.132	K.STIGVEFATR.S
R2/RRR2-18/2	1081.300	1081.204	88.704	0.418	758.685	0.477	14	0.130	K.STIGVEFATR.S
R2/RRR2-16/3	1472.423	1471.598	-119.343	0.528	1325.946	0.415	31	0.119	K.KPVASDEGGAGAAGGVK.E
R2/RRR2-19/2	1081.485	1081.204	260.204	0.292	493.950	0.297	13	0.110	K.STIGVEFATR.S
R2/RRR2-18/2	1081.484	1081.204	259.978	0.274	546.698	0.307	13	0.109	K.STIGVEFATR.S
R2/RRR2-19/2	1081.346	1081.204	131.952	0.258	456.756	0.334	12	0.109	K.STIGVEFATR.S
R2/RRR2-3/2	1585.215	1585.658	-280.416	0.453	849.655	0.522	23	0.140	K.TSPIPQDDAQGQATR.Y
R2/RRR2-3/2	1809.226	1809.909	-933.258	0.463	670.585	0.535	21	0.130	K.EGDATPFTDVTVDNISK.A
R2/RRR2-3/2	1586.178	1585.658	-303.557	0.391	722.962	0.490	22	0.128	K.TSPIPQDDAQGQATR.Y
R2/RRR2-2/2	1585.374	1585.658	-179.681	0.376	808.122	0.422	22	0.124	K.TSPIPQDDAQGQATR.Y
R2/RRR2-3/2	1585.235	1585.658	-267.359	0.391	750.111	0.429	22	0.123	K.TSPIPQDDAQGQATR.Y
R2/RRR2-3/2	944.092	944.071	22.227	0.462	1030.479	0.272	13	0.116	-.AGVSQVLNR.-
R2/RRR2-3/2	1017.079	1017.158	-78.080	0.364	630.560	0.394	14	0.116	R.VSGEDVIIGK.T
R2/RRR2-3/2	1017.971	1017.158	-184.455	0.355	518.327	0.361	15	0.114	R.VSGEDVIIGK.T
R2/RRR2-3/3	1915.636	1915.010	-195.816	0.516	796.014	0.539	28	0.106	R.HGSYDKLDDDGLAPPGTR.V
R2/RRR2-3/3	1914.985	1915.010	-13.153	0.450	602.767	0.482	23	0.086	R.HGSYDKLDDDGLAPPGTR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1213.270	1213.323	-43.253	0.556	1816.983	0.549	21	0.241	R.AGGVDDAPLVGNK.A
R2/RRR2-17/2	1212.837	1213.323	-401.794	0.528	1818.438	0.517	21	0.233	R.AGGVDDAPLVGNK.A
R2/RRR2-18/2	1213.082	1213.323	-199.197	0.481	1408.924	0.462	19	0.170	R.AGGVDDAPLVGNK.A
R2/RRR2-17/2	1763.372	1764.013	-933.155	0.501	1064.937	0.540	21	0.153	K.SGGLGDLKYPLISDVTK.S
R2/RRR2-17/3	1763.831	1764.013	-103.409	0.430	1344.789	0.505	30	0.145	K.SGGLGDLKYPLISDVTK.S
R2/RRR2-17/3	1763.302	1764.013	-973.160	0.413	1501.527	0.438	31	0.144	K.SGGLGDLKYPLISDVTK.S
R2/RRR2-17/2	1486.356	1486.740	-259.198	0.475	843.089	0.470	22	0.134	K.SFGVLIPDQGIALR.G
R2/RRR2-17/2	1214.391	1213.323	56.802	0.495	687.066	0.513	17	0.131	R.AGGVDDAPLVGNK.A
R2/RRR2-18/2	1762.762	1764.013	-1280.764	0.411	869.766	0.430	19	0.123	K.SGGLGDLKYPLISDVTK.S
R2/RRR2-18/2	1213.340	1213.323	14.267	0.385	671.759	0.456	18	0.123	R.AGGVDDAPLVGNK.A
R2/RRR2-17/2	1036.489	1036.203	276.343	0.371	916.981	0.342	14	0.120	K.YPLISDVTK.S
R2/RRR2-18/2	1763.146	1764.013	-1061.742	0.362	712.965	0.389	18	0.112	K.SGGLGDLKYPLISDVTK.S
R2/RRR2-17/3	1763.790	1764.013	-126.631	0.429	1252.469	0.410	29	0.112	K.SGGLGDLKYPLISDVTK.S
R2/RRR2-17/2	1487.978	1486.740	160.239	0.435	459.965	0.396	17	0.112	-.SFGVLIPDQGIALR.-
R2/RRR2-19/2	1487.156	1486.740	280.363	0.376	560.998	0.293	18	0.108	K.SFGVLIPDQGIALR.G
R2/RRR2-18/2	1763.393	1764.013	-921.132	0.321	616.355	0.309	18	0.105	K.SGGLGDLKYPLISDVTK.S
R2/RRR2-17/2	1036.219	1036.203	15.406	0.192	704.970	0.135	12	0.098	K.YPLISDVTK.S
R2/RRR2-15/2	1831.008	1831.063	-29.931	0.451	2280.348	0.529	25	0.317	K.NAGVLALFDVDGTLTAPR.K
R2/RRR2-15/2	1830.633	1831.063	-235.064	0.418	2132.917	0.427	24	0.258	K.NAGVLALFDVDGTLTAPR.K
R2/RRR2-15/3	1888.880	1888.964	-44.837	0.548	1934.730	0.569	32	0.256	R.TIGHTVTSPDDTAEQCR.S
R2/RRR2-15/3	1888.838	1888.964	-66.910	0.580	1808.115	0.546	32	0.222	R.TIGHTVTSPDDTAEQCR.S
R2/RRR2-15/3	1888.528	1888.964	-231.755	0.554	1476.207	0.558	29	0.177	R.TIGHTVTSPDDTAEQCR.S
R2/RRR2-15/2	1146.774	1147.331	-1361.224	0.432	1074.615	0.398	17	0.135	R.SGM*LNVSPIGR.N
R2/RRR2-15/2	1402.087	1402.405	-227.010	0.478	1202.157	0.290	16	0.123	K.GGNDYEIFESDR.T
R2/RRR2-15/2	1402.291	1402.405	-81.515	0.461	1393.802	0.198	17	0.121	K.GGNDYEIFESDR.T
R2/RRR2-11/1	837.609	837.900	-348.259	-2.022	9.904	0.018	4	0.168	-.DRISYSP.-
R2/RRR2-15/2	1030.237	1031.145	-1857.709	0.406	1598.435	0.607	21	0.224	K.VAAATAAAGEAK.G
R2/RRR2-15/2	1031.088	1031.145	-55.883	0.385	1463.876	0.504	20	0.184	K.VAAATAAAGEAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1140.588	1141.303	-1507.512	0.409	1260.563	0.585	19	0.180	R.VPSPVTAGSAVR.L
R2/RRR2-15/2	1141.057	1141.303	-215.848	0.410	1140.876	0.609	18	0.172	R.VPSPVTAGSAVR.L
R2/RRR2-15/2	1141.113	1141.303	-167.018	0.461	1158.350	0.552	18	0.166	R.VPSPVTAGSAVR.L
R2/RRR2-15/3	1643.979	1643.829	91.812	0.456	1362.518	0.529	28	0.154	R.SPAAEALGPTHVLHSR.Y
R2/RRR2-15/2	1212.038	1211.308	-223.511	0.484	1167.515	0.461	18	0.153	R.VSFGENFSPAR.A
R2/RRR2-15/2	1211.112	1211.308	-162.621	0.491	1229.463	0.378	18	0.143	R.VSFGENFSPAR.A
R2/RRR2-15/2	1211.223	1211.308	-71.023	0.453	1318.197	0.329	18	0.140	R.VSFGENFSPAR.A
R2/RRR2-15/3	1644.763	1643.829	-40.028	0.495	1204.600	0.533	28	0.137	R.SPAAEALGPTHVLHSR.Y
R2/RRR2-15/3	1643.844	1643.829	9.592	0.416	933.683	0.523	28	0.110	R.SPAAEALGPTHVLHSR.Y
R2/RRR2-16/2	1030.901	1031.145	-237.130	0.244	461.192	0.392	17	0.109	K.VAAATAAAGEAK.G
R2/RRR2-14/2	1346.227	1346.517	-216.239	0.484	1860.668	0.595	21	0.262	R.TLTGIQIWGSGGR.G
R2/RRR2-14/2	1347.413	1346.517	-77.111	0.540	1342.157	0.613	20	0.198	R.TLTGIQIWGSGGR.G
R2/RRR2-14/2	1043.186	1043.202	-15.682	0.519	1621.341	0.429	16	0.187	R.GLVAQAQSLR.S
R2/RRR2-14/2	1042.629	1043.202	-1513.635	0.484	1669.247	0.380	16	0.182	R.GLVAQAQSLR.S
R2/RRR2-14/2	1043.300	1043.202	93.695	0.515	1637.706	0.392	16	0.181	R.GLVAQAQSLR.S
R2/RRR2-14/2	1072.504	1073.228	-1612.458	0.505	1242.522	0.451	18	0.157	R.SLATAAQAAIR.A
R2/RRR2-14/2	1073.036	1073.228	-179.382	0.487	1310.413	0.413	18	0.155	R.SLATAAQAAIR.A
R2/RRR2-14/2	1346.048	1346.517	-349.706	0.311	925.887	0.501	16	0.133	R.TLTGIQIWGSGGR.G
R2/RRR2-14/3	1543.421	1543.798	-245.379	0.459	751.051	0.444	27	0.089	R.GSKPAIVIHGTVHAR.E
R2/RRR2-14/3	1543.184	1543.798	-1049.490	0.447	487.325	0.466	23	0.086	R.GSKPAIVIHGTVHAR.E
R2/RRR2-14/3	1543.543	1543.798	-165.879	0.455	581.517	0.426	25	0.084	R.GSKPAIVIHGTVHAR.E
R2/RRR2-9/2	1930.587	1931.043	-236.656	0.628	2421.316	0.601	24	0.363	R.YYGGNDVIDEIENLCR.D
R2/RRR2-9/2	1816.392	1816.986	-880.167	0.536	2427.805	0.537	23	0.344	K.VSAATGYIDYEKLEEK.A
R2/RRR2-9/2	1816.356	1816.986	-899.935	0.559	2259.785	0.541	23	0.312	K.VSAATGYIDYEKLEEK.A
R2/RRR2-9/2	1930.496	1931.043	-803.599	0.586	2148.175	0.597	23	0.309	R.YYGGNDVIDEIENLCR.D
R2/RRR2-9/2	1620.233	1619.839	243.658	0.505	2254.015	0.488	22	0.294	K.ISATSIYFESLPYK.V
R2/RRR2-8/2	1930.126	1931.043	-996.087	0.543	2100.282	0.551	23	0.286	R.YYGGNDVIDEIENLCR.D
R2/RRR2-8/2	1930.375	1931.043	-866.759	0.563	2023.167	0.593	23	0.285	R.YYGGNDVIDEIENLCR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1816.452	1816.986	-847.245	0.588	2095.221	0.536	22	0.279	K.VSAATGYIDYEKLEEK.A
R2/RRR2-9/2	1930.198	1931.043	-958.434	0.573	1918.755	0.579	23	0.264	R.YYGGNDVIDEIENLCR.D
R2/RRR2-8/2	1620.381	1619.839	-283.322	0.539	1981.620	0.481	21	0.245	K.ISATSIYFESLPYK.V
R2/RRR2-9/2	1620.401	1619.839	-271.380	0.532	1774.639	0.504	21	0.222	K.ISATSIYFESLPYK.V
R2/RRR2-8/2	1816.604	1816.986	-210.999	0.528	1706.510	0.537	21	0.220	K.VSAATGYIDYEKLEEK.A
R2/RRR2-8/2	1619.398	1619.839	-273.287	0.456	1777.770	0.472	21	0.214	K.ISATSIYFESLPYK.V
R2/RRR2-9/2	1207.147	1207.398	-208.392	0.477	1656.918	0.494	19	0.206	K.LIICGGSAYPR.D
R2/RRR2-8/2	1207.060	1207.398	-280.830	0.481	1681.071	0.471	19	0.203	K.LIICGGSAYPR.D
R2/RRR2-9/2	1620.126	1619.839	177.624	0.506	1707.083	0.456	21	0.201	K.ISATSIYFESLPYK.V
R2/RRR2-8/2	1206.833	1207.398	-1300.686	0.441	1731.007	0.436	19	0.201	K.LIICGGSAYPR.D
R2/RRR2-8/2	1207.100	1207.398	-247.349	0.492	1548.747	0.467	19	0.187	K.LIICGGSAYPR.D
R2/RRR2-9/2	1207.030	1207.398	-305.182	0.512	1398.537	0.499	17	0.178	K.LIICGGSAYPR.D
R2/RRR2-9/3	1929.623	1931.043	-1257.962	0.403	1998.492	0.284	30	0.168	R.YYGGNDVIDEIENLCR.D
R2/RRR2-9/2	1207.179	1207.398	-181.915	0.448	1361.612	0.399	18	0.155	K.LIICGGSAYPR.D
R2/RRR2-8/2	1618.741	1619.839	-1300.169	0.267	1305.614	0.305	19	0.132	K.ISATSIYFESLPYK.V
R2/RRR2-8/2	1206.228	1207.398	-1804.493	0.319	593.938	0.346	12	0.109	K.LIICGGSAYPR.D
R2/RRR2-10/3	1941.191	1941.217	-13.165	0.424	800.119	0.424	27	0.086	-.VAPEDHPVLLTEAPLNPK.-
R2/RRR2-10/3	1941.243	1941.217	13.704	0.391	637.723	0.351	25	0.074	R.VAPEDHPVLLTEAPLNPK.A
R2/RRR2-10/3	1940.992	1941.217	-115.922	0.295	589.076	0.308	23	0.066	-.VAPEDHPVLLTEAPLNPK.-
R2/RRR2-11/2	1375.263	1375.550	-209.180	0.497	2329.077	0.579	22	0.342	R.IAAVQALSGTGACR.L
R2/RRR2-11/2	1375.140	1375.550	-299.214	0.508	1950.981	0.601	22	0.279	R.IAAVQALSGTGACR.L
R2/RRR2-11/2	1375.022	1375.550	-1114.966	0.514	1833.865	0.608	22	0.262	R.IAAVQALSGTGACR.L
R2/RRR2-11/2	1301.105	1301.388	-218.374	0.413	992.263	0.426	14	0.133	K.TFTYYHPESR.G
R2/RRR2-11/2	1344.415	1344.488	-54.242	0.367	925.522	0.345	17	0.120	K.LAYGENCEFIK.D
R2/RRR2-11/3	1938.448	1938.123	167.966	0.537	643.101	0.575	31	0.107	R.IFLEDGHQIGCAQSYAK.N
R2/RRR2-11/3	1937.406	1938.123	-889.025	0.456	605.899	0.581	29	0.104	R.IFLEDGHQIGCAQSYAK.N
R2/RRR2-11/3	1937.595	1938.123	-791.120	0.422	645.427	0.507	31	0.093	R.IFLEDGHQIGCAQSYAK.N
R2/RRR2-14/2	1101.862	1102.263	-364.979	0.463	1838.326	0.514	18	0.236	R.ALLEVVESGGK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1102.150	1102.263	-103.158	0.528	1839.808	0.481	17	0.227	R.ALLEVVESGGK.N
R2/RRR2-14/2	1102.047	1102.263	-196.936	0.458	1739.601	0.497	17	0.218	R.ALLEVVESGGK.N
R2/RRR2-14/2	1609.665	1609.802	-85.542	0.480	1641.471	0.458	21	0.198	R.LTVEDAVTVEYITR.Y
R2/RRR2-14/2	920.379	921.075	-1848.244	0.415	763.331	0.373	13	0.121	R.YIAGLQQK.Y
R2/RRR2-14/2	920.524	921.075	-1689.940	0.376	800.223	0.287	13	0.114	R.YIAGLQQK.Y
R2/RRR2-14/2	920.424	921.075	-1799.201	0.275	845.621	0.234	14	0.108	R.YIAGLQQK.Y
R2/RRR2-14/3	1782.542	1783.099	-876.386	0.409	909.198	0.447	28	0.093	R.KIASLDTHIALACAGLK.A
R2/RRR2-9/2	1730.237	1730.813	-914.016	0.548	2755.190	0.536	27	0.419	K.VFFTNSGSEANDSQVK.L
R2/RRR2-9/3	1663.968	1663.769	120.068	0.539	2710.431	0.411	31	0.350	R.FHLPGETEEEFATR.L
R2/RRR2-9/2	1730.359	1730.813	-263.616	0.535	1918.658	0.601	22	0.272	K.VFFTNSGSEANDSQVK.L
R2/RRR2-9/2	1730.194	1730.813	-938.948	0.508	1742.640	0.564	22	0.234	K.VFFTNSGSEANDSQVK.L
R2/RRR2-9/3	1663.458	1663.769	-187.153	0.523	2124.289	0.337	29	0.195	R.FHLPGETEEEFATR.L
R2/RRR2-9/3	1663.529	1663.769	-144.531	0.493	1983.400	0.330	29	0.171	R.FHLPGETEEEFATR.L
R2/RRR2-9/2	1270.211	1270.500	-228.023	0.490	1642.707	0.329	17	0.168	R.LANNLEELILK.E
R2/RRR2-9/2	1270.083	1270.500	-329.748	0.496	1470.356	0.390	18	0.164	R.LANNLEELILK.E
R2/RRR2-9/2	1663.316	1663.769	-273.211	0.387	729.151	0.453	20	0.124	R.FHLPGETEEEFATR.L
R2/RRR2-9/2	1663.252	1663.769	-914.904	0.386	730.795	0.377	20	0.117	R.FHLPGETEEEFATR.L
R2/RRR2-9/3	1367.619	1367.538	59.783	0.459	738.431	0.424	21	0.086	K.LPFYHSFWNR.T
R2/RRR2-9/3	1367.708	1367.538	124.905	0.327	432.762	0.346	18	0.066	-.LPFYHSFWNR.-
R2/RRR2-10/2	1425.398	1424.542	-101.238	0.601	2082.068	0.588	18	0.298	K.YAFEYAYLNNR.K
R2/RRR2-10/2	1281.135	1281.433	-233.437	0.483	1548.800	0.509	18	0.198	K.LADGLFLESCR.E
R2/RRR2-10/2	1423.976	1424.542	-1102.602	0.418	1537.480	0.436	16	0.178	K.YAFEYAYLNNR.K
R2/RRR2-10/2	1280.932	1281.433	-1175.932	0.388	1313.157	0.516	17	0.171	K.LADGLFLESCR.E
R2/RRR2-10/2	1280.488	1281.433	-1523.621	0.357	1027.908	0.506	16	0.144	K.LADGLFLESCR.E
R2/RRR2-10/2	1194.209	1194.366	-131.602	0.514	955.823	0.431	16	0.136	R.HQDVDIVVIR.E
R2/RRR2-10/2	1194.264	1194.366	-85.667	0.412	904.276	0.425	16	0.130	R.HQDVDIVVIR.E
R2/RRR2-10/2	1423.290	1424.542	-1586.327	0.276	1055.340	0.340	14	0.121	K.YAFEYAYLNNR.K
R2/RRR2-10/3	1832.646	1831.087	-241.810	0.346	876.275	0.342	29	0.075	K.GGLATPVGGGVSSLNM*QLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1995.570	1995.288	141.752	0.534	1851.804	0.585	25	0.260	K.GYINAGFAGIMLEDQVAPK.A
R2/RRR2-11/2	1288.222	1288.476	-197.557	0.502	1045.943	0.472	17	0.144	R.KESGSDIVIIAR.S
R2/RRR2-11/2	1254.213	1254.458	-195.398	0.427	576.991	0.505	17	0.127	K.INEGIPAGILEK.I
R2/RRR2-11/2	880.322	880.017	347.967	0.383	800.359	0.342	12	0.117	K.AFCAVSPK.V
R2/RRR2-11/2	1254.206	1254.458	-201.061	0.393	431.944	0.431	15	0.114	-.INEGIPAGILEK.-
R2/RRR2-11/2	880.073	880.017	64.537	0.323	644.912	0.361	11	0.113	K.AFCAVSPK.V
R2/RRR2-11/2	1253.574	1254.458	-1507.009	0.308	398.785	0.347	14	0.109	K.INEGIPAGILEK.I
R2/RRR2-11/2	880.149	880.017	150.500	0.269	691.206	0.296	11	0.108	K.AFCAVSPK.V
R2/RRR2-8/2	1644.449	1644.762	-191.096	0.500	1708.512	0.418	23	0.193	R.LDSDNPVADAESIVAK.A
R2/RRR2-8/2	962.878	963.112	-244.410	0.496	1356.555	0.374	13	0.152	R.IGDLELFR.A
R2/RRR2-8/2	962.965	963.112	-153.860	0.537	1383.940	0.343	13	0.147	R.IGDLELFR.A
R2/RRR2-8/2	963.032	963.112	-84.178	0.547	1297.927	0.357	13	0.144	R.IGDLELFR.A
R2/RRR2-8/2	1643.864	1644.762	-1158.150	0.418	1251.576	0.249	20	0.119	R.LDSDNPVADAESIVAK.A
R2/RRR2-8/2	1646.254	1644.762	299.974	0.407	998.855	0.316	20	0.116	R.LDSDNPVADAESIVAK.A
R2/RRR2-8/2	1040.147	1040.238	-88.473	0.416	749.556	0.319	14	0.115	R.LLLGEIPER.T
R2/RRR2-8/2	1039.700	1040.238	-1483.629	0.353	631.474	0.289	13	0.109	R.LLLGEIPER.T
R2/RRR2-8/3	1424.253	1424.497	-171.606	0.479	709.322	0.502	19	0.097	R.FEAHSNQQFCR.Y
R2/RRR2-8/3	1425.382	1424.497	-80.805	0.473	806.593	0.383	20	0.083	R.FEAHSNQQFCR.Y
R2/RRR2-8/3	1424.625	1424.497	90.651	0.456	691.096	0.417	19	0.082	-.FEAHSNQQFCR.-
R2/RRR2-11/2	1677.358	1677.832	-283.625	0.488	1299.972	0.522	24	0.175	K.ILQSLEESVTDTDVK.Y
R2/RRR2-11/2	1329.292	1329.486	-146.690	0.483	1368.805	0.447	20	0.168	K.IPATWQGIEASR.L
R2/RRR2-11/2	1677.171	1677.832	-993.526	0.469	981.926	0.536	24	0.151	K.ILQSLEESVTDTDVK.Y
R2/RRR2-11/2	1277.776	1278.439	-1305.990	0.383	1412.793	0.288	17	0.141	R.LAYDTQGIIQR.V
R2/RRR2-11/2	977.854	978.127	-280.483	0.536	1216.857	0.299	14	0.130	R.RVEELFGK.I
R2/RRR2-11/2	977.946	978.127	-185.932	0.481	1183.546	0.267	14	0.124	R.RVEELFGK.I
R2/RRR2-11/2	977.911	978.127	-221.622	0.455	1005.050	0.209	13	0.110	R.RVEELFGK.I
R2/RRR2-17/2	1966.262	1967.226	-1001.914	0.514	1151.935	0.613	24	0.175	R.VCPSVTM*GLEPGEAFTVR.N
R2/RRR2-17/2	1966.378	1967.226	-943.015	0.494	1152.419	0.594	25	0.172	R.VCPSVTM*GLEPGEAFTVR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1966.439	1967.226	-911.854	0.489	1055.194	0.567	23	0.158	R.VCPSVTM*GLEPGEAFTVR.N
R2/RRR2-17/2	1778.158	1777.874	160.254	0.576	1149.399	0.521	20	0.158	K.DGAPDSFHFVEDWVR.T
R2/RRR2-17/2	1777.438	1777.874	-245.819	0.517	1076.703	0.475	19	0.143	K.DGAPDSFHFVEDWVR.T
R2/RRR2-17/2	1777.390	1777.874	-272.829	0.517	1054.275	0.477	19	0.142	K.DGAPDSFHFVEDWVR.T
R2/RRR2-17/2	1245.007	1245.365	-287.612	0.423	956.371	0.445	16	0.134	K.EAVNQSLENLK.T
R2/RRR2-17/2	1244.609	1245.365	-1414.671	0.390	956.704	0.438	16	0.132	K.EAVNQSLENLK.T
R2/RRR2-17/2	1244.891	1245.365	-381.663	0.442	944.259	0.414	16	0.130	K.EAVNQSLENLK.T
R2/RRR2-17/2	1245.335	1245.365	-23.754	0.316	652.161	0.221	14	0.100	-.EAVNQSLENLK.-
R2/RRR2-17/3	1967.270	1967.226	22.294	0.352	891.750	0.304	26	0.071	R.VCPSVTM*GLEPGEAFTVR.N
R2/RRR2-17/3	1078.337	1078.199	128.448	0.452	1000.499	0.219	18	0.065	-.FKTEFYDK.-
R2/RRR2-17/3	1078.004	1078.199	-181.067	0.400	819.719	0.254	16	0.062	-.FKTEFYDK.-
R2/RRR2-16/2	1598.868	1598.849	11.663	0.595	3755.029	0.661	31	0.784	R.SPPVAGGAVAAGGAGALM*K.G
R2/RRR2-15/2	1023.929	1024.199	-264.693	0.499	568.924	0.610	15	0.142	R.GPLPASQVVR.D
R2/RRR2-16/2	1025.169	1024.199	-29.572	0.480	527.823	0.523	15	0.131	R.GPLPASQVVR.D
R2/RRR2-15/2	1023.276	1024.199	-1884.344	0.416	376.916	0.586	12	0.126	R.GPLPASQVVR.D
R2/RRR2-16/3	1295.290	1295.473	-141.902	0.392	1440.084	0.380	23	0.120	R.DRGPLPASQVVR.D
R2/RRR2-16/2	1294.583	1295.473	-1464.662	0.358	751.821	0.359	16	0.114	R.DRGPLPASQVVR.D
R2/RRR2-16/2	1295.077	1295.473	-306.556	0.291	541.732	0.326	15	0.107	R.DRGPLPASQVVR.D
R2/RRR2-16/3	1295.463	1295.473	-8.054	0.402	1024.370	0.343	21	0.084	R.DRGPLPASQVVR.D
R2/RRR2-15/3	1296.746	1295.473	211.287	0.241	354.820	0.330	21	0.068	-.DRGPLPASQVVR.-
R2/RRR2-9/2	1423.165	1423.550	-271.051	0.527	2436.848	0.501	23	0.336	K.FIASEGDTVTPGTK.V
R2/RRR2-9/2	1423.011	1423.550	-1084.506	0.486	2150.555	0.506	22	0.284	K.FIASEGDTVTPGTK.V
R2/RRR2-9/2	1423.040	1423.550	-1064.437	0.505	2156.475	0.457	22	0.270	K.FIASEGDTVTPGTK.V
R2/RRR2-9/2	1795.517	1795.885	-206.044	0.507	1416.302	0.633	22	0.206	K.SAAPAETHVAPSEDSTPK.E
R2/RRR2-9/2	1795.231	1795.885	-924.301	0.492	1404.152	0.636	22	0.205	K.SAAPAETHVAPSEDSTPK.E
R2/RRR2-9/2	1795.401	1795.885	-270.637	0.487	1180.851	0.640	21	0.181	K.SAAPAETHVAPSEDSTPK.E
R2/RRR2-9/2	1398.986	1399.466	-343.749	0.501	1599.040	0.391	18	0.175	R.DADNM*NFADIEK.G
R2/RRR2-9/2	1399.203	1399.466	-188.638	0.462	1485.762	0.393	17	0.164	R.DADNM*NFADIEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1399.035	1399.466	-308.468	0.498	1260.561	0.422	17	0.150	R.DADNM*NFADIEK.G
R2/RRR2-9/2	852.732	853.087	-417.479	0.246	600.814	0.387	11	0.106	-.GLVVPVIR.-
R2/RRR2-9/2	852.540	853.087	-1820.105	0.198	403.256	0.363	9	0.089	-.GLVVPVIR.-
R2/RRR2-17/1	1071.603	1072.280	-1570.214	0.203	1123.494	0.140	16	1.000	K.LLLIGDSGVGK.S
R2/RRR2-16/2	1639.331	1638.849	294.968	0.587	2162.386	0.556	22	0.298	K.TNLNVEQVFFSIAR.D
R2/RRR2-16/2	1638.289	1638.849	-955.076	0.536	2087.136	0.574	22	0.291	K.TNLNVEQVFFSIAR.D
R2/RRR2-17/2	1638.469	1638.849	-232.519	0.540	2075.805	0.541	22	0.279	K.TNLNVEQVFFSIAR.D
R2/RRR2-16/2	1638.269	1638.849	-967.120	0.532	2040.806	0.557	22	0.278	K.TNLNVEQVFFSIAR.D
R2/RRR2-17/2	1638.740	1638.849	-66.317	0.525	1743.658	0.575	21	0.237	K.TNLNVEQVFFSIAR.D
R2/RRR2-17/2	1165.046	1165.278	-199.738	0.411	1492.447	0.435	17	0.174	K.GQALADEYGIK.F
R2/RRR2-16/2	1165.126	1165.278	-130.369	0.452	1564.909	0.385	17	0.171	K.GQALADEYGIK.F
R2/RRR2-16/2	1165.152	1165.278	-108.299	0.414	1550.336	0.383	17	0.169	K.GQALADEYGIK.F
R2/RRR2-18/2	1558.430	1558.764	-214.528	0.450	1124.681	0.421	17	0.139	R.IKLQIWDTAGQER.F
R2/RRR2-17/2	1164.983	1165.278	-253.769	0.310	1017.584	0.320	14	0.118	K.GQALADEYGIK.F
R2/RRR2-2/2	1638.856	1638.849	4.138	0.327	455.318	0.375	13	0.106	-.TNLNVEQVFFSIAR.-
R2/RRR2-17/3	1559.512	1558.764	-162.022	0.404	878.248	0.379	22	0.082	R.IKLQIWDTAGQER.F
R2/RRR2-10/2	1453.225	1452.593	-253.901	0.516	2082.223	0.529	21	0.281	K.NIDSFISDWGIGK.V
R2/RRR2-10/2	1689.303	1689.883	-938.121	0.508	2099.670	0.508	22	0.275	R.SQDEALQIAELICAK.L
R2/RRR2-10/2	1689.211	1689.883	-992.606	0.547	1716.901	0.519	21	0.219	R.SQDEALQIAELICAK.L
R2/RRR2-10/2	1689.217	1689.883	-988.833	0.408	1838.786	0.444	20	0.217	R.SQDEALQIAELICAK.L
R2/RRR2-10/2	1134.701	1135.360	-1466.022	0.333	888.712	0.291	15	0.112	R.LMSLLDLSSR.C
R2/RRR2-10/2	1452.255	1452.593	-233.837	0.355	601.021	0.340	14	0.106	K.NIDSFISDWGIGK.V
R2/RRR2-10/2	877.164	877.023	161.412	0.387	1044.731	0.152	13	0.105	R.DLFLAAAR.I
R2/RRR2-14/2	1354.289	1354.536	-182.405	0.514	1826.078	0.523	21	0.237	R.IPSGEVWVGNPAK.F
R2/RRR2-14/2	1354.250	1354.536	-211.432	0.517	1528.637	0.550	20	0.204	R.IPSGEVWVGNPAK.F
R2/RRR2-14/2	1354.239	1354.536	-220.113	0.519	1351.411	0.512	20	0.177	R.IPSGEVWVGNPAK.F
R2/RRR2-14/2	1001.538	1002.150	-1613.937	0.469	713.685	0.434	16	0.127	R.LGSTIQGGLR.V
R2/RRR2-14/2	1815.691	1816.131	-242.933	0.420	356.048	0.550	18	0.122	R.EIPPELILPDNILPNK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1125.091	1124.223	-117.052	0.514	611.334	0.390	14	0.122	K.TFDEIELEK.M
R2/RRR2-14/2	1001.300	1002.150	-1852.885	0.453	574.290	0.397	15	0.119	R.LGSTIQGGLR.V
R2/RRR2-14/2	1816.299	1816.131	92.985	0.473	398.305	0.473	19	0.119	R.EIPPELILPDNILPNK.A
R2/RRR2-14/2	1124.144	1124.223	-70.317	0.508	710.720	0.329	14	0.116	K.TFDEIELEK.M
R2/RRR2-14/2	1123.956	1124.223	-237.433	0.495	502.806	0.323	13	0.114	K.TFDEIELEK.M
R2/RRR2-14/2	1815.212	1816.131	-1060.292	0.367	229.945	0.508	15	0.112	-.EIPPELILPDNILPNK.-
R2/RRR2-15/2	1817.907	1816.131	-123.696	0.325	148.167	0.353	13	0.085	-.EIPPELILPDNILPNK.-
R2/RRR2-15/2	1056.987	1057.139	-144.286	0.474	1060.528	0.499	17	0.152	R.APIGEEVEGR.R
R2/RRR2-14/2	1056.715	1057.139	-402.470	0.462	1008.386	0.499	16	0.147	R.APIGEEVEGR.R
R2/RRR2-14/2	1057.132	1057.139	-7.483	0.467	920.152	0.483	16	0.141	R.APIGEEVEGR.R
R2/RRR2-15/2	1057.057	1057.139	-77.907	0.508	957.444	0.456	16	0.139	R.APIGEEVEGR.R
R2/RRR2-15/2	1056.303	1057.139	-1743.595	0.359	1168.487	0.372	17	0.136	R.APIGEEVEGR.R
R2/RRR2-14/2	1057.226	1057.139	82.617	0.323	762.408	0.491	15	0.127	R.APIGEEVEGR.R
R2/RRR2-15/2	1046.141	1046.200	-56.366	0.318	806.383	0.238	15	0.106	R.SQGELTGILK.E
R2/RRR2-14/3	1261.371	1260.384	-10.262	0.422	718.338	0.447	22	0.089	K.ATVSHNSQLFR.F
R2/RRR2-15/3	1260.530	1260.384	115.807	0.398	741.718	0.448	22	0.089	K.ATVSHNSQLFR.F
R2/RRR2-15/3	1260.120	1260.384	-210.476	0.388	466.377	0.433	18	0.085	K.ATVSHNSQLFR.F
R2/RRR2-14/3	1735.971	1735.961	5.838	0.371	784.539	0.420	25	0.084	K.FVIRPYTPISDPDSK.G
R2/RRR2-15/3	1260.536	1260.384	121.052	0.346	530.312	0.356	19	0.066	-.ATVSHNSQLFR.-
R2/RRR2-14/3	1259.954	1260.384	-342.273	0.346	554.421	0.344	19	0.066	-.ATVSHNSQLFR.-
R2/RRR2-15/3	1737.018	1735.961	32.549	0.287	777.800	0.215	23	0.062	-.FVIRPYTPISDPDSK.-
R2/RRR2-10/2	1980.370	1981.107	-879.747	0.503	2174.866	0.591	25	0.316	R.ELGLEAVESGDADLVSYGR.L
R2/RRR2-10/2	1980.652	1981.107	-230.118	0.489	1763.363	0.591	23	0.244	R.ELGLEAVESGDADLVSYGR.L
R2/RRR2-10/2	1733.609	1733.948	-196.522	0.453	732.674	0.549	23	0.136	R.AIGGVPGPALAEYYAQR.T
R2/RRR2-10/3	1869.114	1869.885	-950.265	0.478	1359.177	0.433	29	0.128	K.DGINDRTDEYGGSLSNR.C
R2/RRR2-10/2	1303.319	1303.489	-130.731	0.456	1027.669	0.363	17	0.128	R.LFISNPDLVER.F
R2/RRR2-10/2	1733.447	1733.948	-868.815	0.410	471.221	0.548	19	0.122	R.AIGGVPGPALAEYYAQR.T
R2/RRR2-10/2	1303.490	1303.489	0.788	0.409	685.344	0.326	15	0.112	R.LFISNPDLVER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1302.528	1303.489	-1509.966	0.283	600.332	0.256	14	0.105	R.LFISNPDLVER.F
R2/RRR2-8/2	1767.326	1768.025	-964.409	0.483	1749.112	0.443	24	0.203	K.AGM*VVTFAPSNVTTEVK.S
R2/RRR2-8/2	1767.291	1768.025	-984.311	0.464	1662.271	0.422	24	0.188	K.AGM*VVTFAPSNVTTEVK.S
R2/RRR2-3/2	1025.747	1026.215	-457.592	0.429	1358.316	0.457	19	0.164	K.IGGIGTVPVGR.V
R2/RRR2-8/2	1026.029	1026.215	-181.455	0.461	1249.336	0.473	19	0.159	K.IGGIGTVPVGR.V
R2/RRR2-6/2	1025.557	1026.215	-1621.087	0.417	1305.934	0.451	19	0.159	K.IGGIGTVPVGR.V
R2/RRR2-9/2	1026.017	1026.215	-193.629	0.432	1188.618	0.467	19	0.153	K.IGGIGTVPVGR.V
R2/RRR2-5/2	1026.111	1026.215	-101.257	0.490	1253.598	0.435	19	0.153	K.IGGIGTVPVGR.V
R2/RRR2-6/2	1026.038	1026.215	-173.101	0.490	1130.180	0.489	17	0.152	K.IGGIGTVPVGR.V
R2/RRR2-3/2	1026.027	1026.215	-183.365	0.485	1102.830	0.477	18	0.150	K.IGGIGTVPVGR.V
R2/RRR2-1/2	1026.012	1026.215	-197.926	0.442	1103.814	0.482	17	0.149	K.IGGIGTVPVGR.V
R2/RRR2-8/2	1025.833	1026.215	-373.768	0.480	1034.575	0.484	18	0.147	K.IGGIGTVPVGR.V
R2/RRR2-15/2	1026.056	1026.215	-155.079	0.464	1109.245	0.447	18	0.145	K.IGGIGTVPVGR.V
R2/RRR2-11/2	1025.686	1026.215	-1495.187	0.406	1076.465	0.463	18	0.145	K.IGGIGTVPVGR.V
R2/RRR2-14/2	1025.915	1026.215	-292.704	0.455	1016.098	0.475	18	0.144	K.IGGIGTVPVGR.V
R2/RRR2-10/2	1026.184	1026.215	-30.617	0.468	1111.642	0.436	18	0.144	K.IGGIGTVPVGR.V
R2/RRR2-15/2	1026.185	1026.215	-28.708	0.383	1042.751	0.474	18	0.143	K.IGGIGTVPVGR.V
R2/RRR2-4/2	1026.166	1026.215	-47.679	0.463	1033.759	0.467	17	0.143	K.IGGIGTVPVGR.V
R2/RRR2-1/2	1025.854	1026.215	-353.113	0.419	954.945	0.496	17	0.142	K.IGGIGTVPVGR.V
R2/RRR2-4/2	1026.098	1026.215	-113.787	0.477	936.571	0.491	17	0.142	K.IGGIGTVPVGR.V
R2/RRR2-8/2	1261.116	1261.411	-234.133	0.453	958.185	0.493	16	0.142	K.ANISPNAPWYK.G
R2/RRR2-3/2	1025.986	1026.215	-223.469	0.468	918.361	0.504	16	0.141	K.IGGIGTVPVGR.V
R2/RRR2-9/2	1025.725	1026.215	-479.446	0.378	1043.104	0.453	18	0.141	K.IGGIGTVPVGR.V
R2/RRR2-13/2	1026.114	1026.215	-98.393	0.451	926.422	0.481	17	0.140	K.IGGIGTVPVGR.V
R2/RRR2-12/2	1025.995	1026.215	-214.755	0.463	1081.029	0.426	17	0.140	K.IGGIGTVPVGR.V
R2/RRR2-9/2	1026.131	1026.215	-81.567	0.461	926.062	0.472	17	0.139	K.IGGIGTVPVGR.V
R2/RRR2-13/2	1025.994	1026.215	-216.068	0.455	1133.303	0.391	18	0.138	K.IGGIGTVPVGR.V
R2/RRR2-13/2	1026.132	1026.215	-81.329	0.414	1083.302	0.407	18	0.138	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1025.743	1026.215	-461.055	0.397	956.104	0.456	17	0.137	K.IGGIGTVPVGR.V
R2/RRR2-6/2	1026.081	1026.215	-130.972	0.503	814.258	0.495	16	0.136	K.IGGIGTVPVGR.V
R2/RRR2-10/2	1026.023	1026.215	-187.065	0.450	963.601	0.440	17	0.136	K.IGGIGTVPVGR.V
R2/RRR2-12/2	1026.031	1026.215	-179.784	0.491	948.252	0.441	17	0.136	K.IGGIGTVPVGR.V
R2/RRR2-8/2	1260.779	1261.411	-1298.250	0.418	911.555	0.477	16	0.136	K.ANISPNAPWYK.G
R2/RRR2-10/2	1025.426	1026.215	-1749.770	0.408	831.577	0.476	17	0.134	K.IGGIGTVPVGR.V
R2/RRR2-5/2	1025.612	1026.215	-1567.878	0.397	928.531	0.446	17	0.134	K.IGGIGTVPVGR.V
R2/RRR2-2/2	1026.156	1026.215	-57.583	0.493	1049.509	0.399	17	0.134	K.IGGIGTVPVGR.V
R2/RRR2-14/2	1026.070	1026.215	-141.951	0.425	868.106	0.449	17	0.133	K.IGGIGTVPVGR.V
R2/RRR2-11/2	1025.980	1026.215	-229.914	0.459	806.778	0.469	16	0.133	K.IGGIGTVPVGR.V
R2/RRR2-8/2	1109.018	1109.254	-213.472	0.319	1301.547	0.294	14	0.133	R.FDEIVKETK.N
R2/RRR2-1/2	1025.491	1026.215	-1686.501	0.422	807.715	0.470	16	0.132	K.IGGIGTVPVGR.V
R2/RRR2-14/2	1025.985	1026.215	-224.543	0.457	908.150	0.423	17	0.132	K.IGGIGTVPVGR.V
R2/RRR2-9/2	1025.357	1026.215	-1817.712	0.387	725.587	0.490	16	0.131	K.IGGIGTVPVGR.V
R2/RRR2-11/2	1026.020	1026.215	-190.168	0.486	719.731	0.483	15	0.131	K.IGGIGTVPVGR.V
R2/RRR2-9/2	1025.581	1026.215	-1597.770	0.372	755.653	0.479	16	0.130	K.IGGIGTVPVGR.V
R2/RRR2-2/2	1026.122	1026.215	-90.875	0.490	775.366	0.446	16	0.129	K.IGGIGTVPVGR.V
R2/RRR2-5/2	1026.006	1026.215	-203.774	0.435	778.808	0.416	16	0.126	K.IGGIGTVPVGR.V
R2/RRR2-2/2	1025.571	1026.215	-1607.934	0.365	794.605	0.410	16	0.125	K.IGGIGTVPVGR.V
R2/RRR2-12/2	1026.045	1026.215	-165.701	0.377	833.054	0.395	16	0.124	K.IGGIGTVPVGR.V
R2/RRR2-8/2	1751.478	1752.026	-885.945	0.439	791.823	0.434	20	0.121	K.AGMVVTFAPSNVTTEVK.S
R2/RRR2-8/2	1027.183	1026.215	-31.302	0.341	386.321	0.433	14	0.120	K.IGGIGTVPVGR.V
R2/RRR2-8/2	1751.001	1752.026	-1159.658	0.429	682.450	0.450	19	0.119	K.AGMVVTFAPSNVTTEVK.S
R2/RRR2-21/2	1026.354	1026.215	136.279	0.321	605.153	0.342	14	0.115	K.IGGIGTVPVGR.V
R2/RRR2-9/2	1026.193	1026.215	-21.549	0.305	548.898	0.284	15	0.114	K.IGGIGTVPVGR.V
R2/RRR2-21/2	1026.351	1026.215	133.058	0.280	714.643	0.232	15	0.110	K.IGGIGTVPVGR.V
R2/RRR2-9/2	1026.390	1026.215	171.106	0.210	388.996	0.352	12	0.109	-.IGGIGTVPVGR.-
R2/RRR2-21/2	1025.993	1026.215	-216.665	0.244	477.228	0.286	12	0.104	-.IGGIGTVPVGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1026.539	1026.215	316.473	0.295	491.168	0.260	13	0.098	-.IGGIGTVPVGR.-
R2/RRR2-8/2	1108.973	1109.254	-254.662	0.234	703.869	0.063	13	0.097	-.FDEIVKETK.-
R2/RRR2-5/2	1682.208	1682.769	-930.651	0.539	2054.380	0.504	23	0.270	R.NQAFEDGVDPDFLSK.W
R2/RRR2-5/2	1121.516	1121.268	221.440	0.412	1386.842	0.528	16	0.182	R.FSLAIDAIDR.M
R2/RRR2-5/2	1121.416	1121.268	131.932	0.432	1371.174	0.447	16	0.165	R.FSLAIDAIDR.M
R2/RRR2-5/2	1254.179	1254.461	-225.568	0.317	1104.451	0.350	17	0.127	K.GNIDTPLALAIR.N
R2/RRR2-5/3	1243.559	1243.403	125.904	0.535	1360.479	0.417	23	0.121	K.RPGAAEHLHVR.G
R2/RRR2-5/3	1243.390	1243.403	-10.410	0.520	1148.833	0.458	22	0.113	K.RPGAAEHLHVR.G
R2/RRR2-5/2	1120.929	1121.268	-303.173	0.323	704.746	0.351	12	0.111	R.FSLAIDAIDR.M
R2/RRR2-5/2	1254.047	1254.461	-330.841	0.228	625.378	0.205	14	0.100	K.GNIDTPLALAIR.N
R2/RRR2-5/2	1253.993	1254.461	-374.596	0.186	685.500	0.230	14	0.100	K.GNIDTPLALAIR.N
R2/RRR2-8/2	1607.684	1607.833	-92.653	0.560	2519.207	0.527	23	0.359	R.SPPIEEVINTGVVPR.F
R2/RRR2-8/2	1607.285	1607.833	-966.034	0.504	2334.919	0.506	22	0.315	R.SPPIEEVINTGVVPR.F
R2/RRR2-8/2	1607.321	1607.833	-943.312	0.499	2289.155	0.452	22	0.289	R.SPPIEEVINTGVVPR.F
R2/RRR2-8/2	1344.241	1344.624	-286.145	0.457	1602.230	0.574	19	0.219	K.VVVESGAVPIFVK.L
R2/RRR2-8/2	1344.218	1344.624	-302.818	0.499	1510.284	0.605	19	0.215	K.VVVESGAVPIFVK.L
R2/RRR2-8/2	1601.458	1601.903	-278.718	0.483	1743.734	0.429	21	0.200	R.IVTVCLEGLENILK.V
R2/RRR2-8/2	1601.536	1601.903	-230.083	0.475	1601.334	0.420	20	0.181	R.IVTVCLEGLENILK.V
R2/RRR2-9/2	1602.091	1601.903	117.339	0.523	1482.365	0.473	21	0.180	R.IVTVCLEGLENILK.V
R2/RRR2-7/2	1607.311	1607.833	-949.641	0.448	1457.475	0.466	19	0.173	R.SPPIEEVINTGVVPR.F
R2/RRR2-9/2	1602.559	1601.903	-215.114	0.527	1351.669	0.486	21	0.170	R.IVTVCLEGLENILK.V
R2/RRR2-7/2	1608.285	1607.833	281.858	0.504	1423.142	0.465	19	0.169	R.SPPIEEVINTGVVPR.F
R2/RRR2-8/3	1976.970	1976.416	-225.827	0.311	835.077	0.315	24	0.071	R.LVELLM*HPSASVLIPALR.T
R2/RRR2-8/3	1960.318	1960.416	-50.386	0.255	1207.829	0.151	27	0.064	R.LVELLMHPSASVLIPALR.T
R2/RRR2-14/2	1455.023	1454.561	318.447	0.564	1660.848	0.590	21	0.232	R.DLVGVAYTEEETK.A
R2/RRR2-14/2	1453.978	1454.561	-1091.639	0.497	1570.069	0.554	21	0.210	R.DLVGVAYTEEETK.A
R2/RRR2-13/2	1454.032	1454.561	-1054.548	0.473	1550.193	0.547	20	0.205	R.DLVGVAYTEEETK.A
R2/RRR2-14/2	1453.778	1454.561	-1230.247	0.477	1564.729	0.524	21	0.202	R.DLVGVAYTEEETK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1665.541	1664.883	-205.657	0.492	672.948	0.530	22	0.133	R.FANGGAYPPDLSLITK.A
R2/RRR2-14/2	1666.400	1664.883	-290.927	0.499	676.332	0.507	22	0.131	R.FANGGAYPPDLSLITK.A
R2/RRR2-14/2	1665.211	1664.883	197.373	0.444	610.939	0.467	21	0.123	R.FANGGAYPPDLSLITK.A
R2/RRR2-14/2	1664.821	1664.883	-37.258	0.459	554.635	0.483	20	0.123	R.FANGGAYPPDLSLITK.A
R2/RRR2-14/2	1663.966	1664.883	-1155.490	0.320	725.849	0.472	21	0.122	R.FANGGAYPPDLSLITK.A
R2/RRR2-14/2	1665.359	1664.883	286.829	0.414	514.596	0.483	20	0.121	R.FANGGAYPPDLSLITK.A
R2/RRR2-13/2	1665.461	1664.883	-253.892	0.405	533.209	0.460	18	0.117	R.FANGGAYPPDLSLITK.A
R2/RRR2-14/2	1889.497	1890.049	-823.563	0.506	569.616	0.454	18	0.116	K.LSDRFPQPYPNEQAAR.F
R2/RRR2-14/3	1979.465	1979.247	110.287	0.398	972.659	0.380	27	0.087	-.EGLHYNPYFPGGAIAM*PK.-
R2/RRR2-13/3	1889.913	1890.049	-71.957	0.476	911.098	0.370	27	0.084	K.LSDRFPQPYPNEQAAR.F
R2/RRR2-13/3	1889.815	1890.049	-124.050	0.438	762.257	0.404	23	0.083	K.LSDRFPQPYPNEQAAR.F
R2/RRR2-14/3	1889.546	1890.049	-797.468	0.431	859.438	0.355	28	0.081	K.LSDRFPQPYPNEQAAR.F
R2/RRR2-13/3	1889.480	1890.049	-832.779	0.405	876.060	0.302	25	0.074	K.LSDRFPQPYPNEQAAR.F
R2/RRR2-13/3	1978.789	1979.247	-232.337	0.363	752.365	0.311	24	0.069	R.EGLHYNPYFPGGAIAM*PK.M
R2/RRR2-10/2	1770.324	1770.064	147.339	0.499	2175.371	0.542	24	0.300	R.VVALAAGSNVTLLADQVK.T
R2/RRR2-10/2	1769.556	1770.064	-854.822	0.443	1895.827	0.515	23	0.244	R.VVALAAGSNVTLLADQVK.T
R2/RRR2-10/2	1656.044	1654.974	42.393	0.515	1375.860	0.482	19	0.170	K.ETLIAGGPFVLPLAQK.H
R2/RRR2-10/2	1423.209	1423.575	-258.322	0.420	1071.815	0.503	19	0.147	R.AGGTM*TGVLSAANEK.A
R2/RRR2-10/2	1423.081	1423.575	-348.080	0.439	1139.991	0.446	19	0.143	R.AGGTM*TGVLSAANEK.A
R2/RRR2-10/2	1423.956	1423.575	268.548	0.457	891.257	0.504	19	0.136	R.AGGTM*TGVLSAANEK.A
R2/RRR2-10/2	1337.408	1337.547	-103.779	0.478	888.196	0.402	17	0.125	K.KITVDSATLFNK.G
R2/RRR2-8/2	1539.978	1538.597	248.485	0.486	1286.875	0.586	21	0.184	R.DAFNTFFSETSSGK.H
R2/RRR2-8/2	1539.840	1538.597	158.261	0.521	1049.615	0.535	19	0.153	R.DAFNTFFSETSSGK.H
R2/RRR2-9/2	1689.434	1688.943	291.800	0.510	1171.313	0.466	22	0.151	R.ALFVDLEPTVIDEVK.T
R2/RRR2-9/2	1688.504	1688.943	-260.579	0.454	1169.855	0.333	21	0.128	R.ALFVDLEPTVIDEVK.T
R2/RRR2-9/2	1688.227	1688.943	-1019.220	0.434	1001.105	0.373	20	0.125	R.ALFVDLEPTVIDEVK.T
R2/RRR2-8/2	1688.507	1688.943	-258.693	0.485	1061.921	0.334	21	0.123	R.ALFVDLEPTVIDEVK.T
R2/RRR2-9/2	1539.413	1538.597	-119.669	0.275	554.077	0.489	18	0.115	R.DAFNTFFSETSSGK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1688.107	1688.943	-1090.516	0.339	726.109	0.334	18	0.111	R.ALFVDLEPTVIDEVK.T
R2/RRR2-8/2	1539.103	1538.597	-321.672	0.328	690.749	0.342	17	0.110	R.DAFNTFFSETSSGK.H
R2/RRR2-1/2	1690.066	1688.943	73.415	0.364	590.893	0.380	15	0.109	R.ALFVDLEPTVIDEVK.T
R2/RRR2-8/2	1687.549	1688.943	-1422.734	0.286	814.758	0.264	18	0.107	R.ALFVDLEPTVIDEVK.T
R2/RRR2-10/2	1224.005	1224.262	-210.523	0.493	1864.450	0.378	18	0.205	R.GDSVDQFSNVR.H
R2/RRR2-10/2	1224.040	1224.262	-181.909	0.505	1726.986	0.362	18	0.184	R.GDSVDQFSNVR.H
R2/RRR2-10/2	1223.969	1224.262	-239.939	0.472	1572.017	0.350	17	0.165	R.GDSVDQFSNVR.H
R2/RRR2-10/2	1274.084	1273.503	-329.578	0.484	1081.750	0.452	16	0.143	K.FKDEIVPVPTK.I
R2/RRR2-10/2	1273.354	1273.503	-116.692	0.453	971.506	0.410	16	0.131	K.FKDEIVPVPTK.I
R2/RRR2-10/2	1272.886	1273.503	-1273.686	0.277	462.956	0.359	11	0.105	K.FKDEIVPVPTK.I
R2/RRR2-10/3	1845.976	1846.084	-58.713	0.424	770.601	0.513	30	0.100	K.VNVNGGAIALGHPLGATGAR.C
R2/RRR2-10/3	1846.060	1846.084	-12.749	0.397	644.413	0.519	27	0.093	-.VNVNGGAIALGHPLGATGAR.-
R2/RRR2-10/3	1846.667	1846.084	-226.401	0.452	503.352	0.506	24	0.087	-.VNVNGGAIALGHPLGATGAR.-
R2/RRR2-10/3	1957.016	1957.218	-103.399	0.316	731.330	0.450	29	0.085	K.VVISVDDGIRPGTTASGLAK.L
R2/RRR2-10/3	1957.927	1957.218	-149.063	0.372	579.475	0.447	28	0.082	K.VVISVDDGIRPGTTASGLAK.L
R2/RRR2-10/3	1846.606	1846.084	-259.228	0.362	425.043	0.448	24	0.079	-.VNVNGGAIALGHPLGATGAR.-
R2/RRR2-10/3	1846.505	1846.084	229.043	0.357	395.219	0.421	24	0.077	-.VNVNGGAIALGHPLGATGAR.-
R2/RRR2-10/3	1956.296	1957.218	-985.366	0.304	587.328	0.342	25	0.070	K.VVISVDDGIRPGTTASGLAK.L
R2/RRR2-11/2	1558.397	1558.868	-303.395	0.529	1746.531	0.537	21	0.228	K.GAALNAVQIAEM*LLK.-
R2/RRR2-11/2	1557.793	1558.868	-1336.188	0.409	1714.150	0.470	21	0.206	K.GAALNAVQIAEM*LLK.-
R2/RRR2-11/2	1161.001	1160.260	-223.740	0.530	1559.848	0.513	18	0.200	R.AAEGVTIIDDR.A
R2/RRR2-11/2	1558.604	1558.868	-169.890	0.499	1435.411	0.573	20	0.196	K.GAALNAVQIAEM*LLK.-
R2/RRR2-11/2	1161.047	1160.260	-183.553	0.536	1172.406	0.515	18	0.163	R.AAEGVTIIDDR.A
R2/RRR2-11/2	1161.118	1160.260	-122.594	0.548	1129.855	0.456	17	0.148	R.AAEGVTIIDDR.A
R2/RRR2-11/2	1087.055	1087.252	-181.743	0.339	453.337	0.470	16	0.118	K.LQTQEVLAGK.A
R2/RRR2-11/3	1997.422	1998.189	-887.322	0.371	1115.554	0.437	26	0.107	R.AHAPAAVASGAVVVDNSSAFR.M
R2/RRR2-7/2	1494.221	1494.628	-273.156	0.440	1730.080	0.457	21	0.209	R.ELGEGGIDNYLSVK.Q
R2/RRR2-7/2	1463.344	1462.626	-193.410	0.559	1472.755	0.551	20	0.198	K.SPIVVFDDVDVEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1463.227	1462.626	-273.503	0.526	1477.885	0.543	20	0.196	K.SPIVVFDDVDVEK.A
R2/RRR2-7/2	1307.160	1306.446	-219.329	0.537	1331.300	0.582	19	0.190	R.LGPVVSEGQYEK.I
R2/RRR2-7/2	1305.766	1306.446	-1291.029	0.474	1344.038	0.574	19	0.189	R.LGPVVSEGQYEK.I
R2/RRR2-7/2	1462.483	1462.626	-98.253	0.502	1450.081	0.513	20	0.186	K.SPIVVFDDVDVEK.A
R2/RRR2-7/2	1306.182	1306.446	-203.277	0.471	1296.980	0.541	19	0.177	R.LGPVVSEGQYEK.I
R2/RRR2-3/2	1463.267	1462.626	-246.553	0.429	1193.474	0.473	18	0.153	K.SPIVVFDDVDVEK.A
R2/RRR2-7/2	1161.837	1162.226	-336.022	0.389	1022.426	0.384	16	0.130	K.VSDPLEEGCR.L
R2/RRR2-7/2	1161.226	1162.226	-1726.916	0.278	761.870	0.281	15	0.108	K.VSDPLEEGCR.L
R2/RRR2-5/2	1532.584	1532.809	-147.524	0.504	2270.223	0.564	23	0.326	R.IGAILGLGIAYAGSQK.E
R2/RRR2-5/2	1122.950	1123.284	-298.267	0.521	1814.445	0.461	17	0.218	K.LSEGYLTLAR.D
R2/RRR2-5/2	1123.011	1123.284	-244.174	0.480	1613.593	0.390	17	0.178	K.LSEGYLTLAR.D
R2/RRR2-5/2	1122.453	1123.284	-1636.476	0.417	1558.269	0.410	16	0.175	K.LSEGYLTLAR.D
R2/RRR2-5/2	1370.599	1370.748	-109.127	0.377	1229.102	0.585	18	0.173	R.LLPVALGLLYLGK.Q
R2/RRR2-4/2	1122.864	1123.284	-375.271	0.442	1430.702	0.418	16	0.165	K.LSEGYLTLAR.D
R2/RRR2-4/2	1370.417	1370.748	-242.262	0.444	1126.710	0.562	20	0.164	R.LLPVALGLLYLGK.Q
R2/RRR2-5/2	1370.163	1370.748	-1159.846	0.444	1126.200	0.566	19	0.164	R.LLPVALGLLYLGK.Q
R2/RRR2-4/2	1122.668	1123.284	-1444.111	0.402	1384.850	0.384	16	0.154	K.LSEGYLTLAR.D
R2/RRR2-4/2	1348.171	1348.486	-234.908	0.432	1326.725	0.406	17	0.153	R.NLAGEIAQEFQK.R
R2/RRR2-4/2	1122.552	1123.284	-1547.767	0.393	800.015	0.450	14	0.127	K.LSEGYLTLAR.D
R2/RRR2-5/2	1531.798	1532.809	-1316.734	0.292	1183.541	0.311	20	0.125	R.IGAILGLGIAYAGSQK.E
R2/RRR2-5/2	1347.384	1348.486	-1564.742	0.335	582.582	0.379	13	0.107	-.NLAGEIAQEFQK.-
R2/RRR2-5/2	1369.976	1370.748	-1297.279	0.192	402.859	0.369	13	0.102	R.LLPVALGLLYLGK.Q
R2/RRR2-3/2	1498.218	1497.725	330.186	0.562	2602.613	0.469	21	0.357	R.SALLQGQALQALQR.F
R2/RRR2-3/2	1497.974	1497.725	166.934	0.517	2452.555	0.481	21	0.332	R.SALLQGQALQALQR.F
R2/RRR2-3/2	1148.152	1148.377	-196.492	0.373	825.388	0.408	14	0.122	K.ATFEVVQLLK.N
R2/RRR2-3/2	1056.882	1057.229	-329.076	0.386	924.091	0.296	15	0.115	K.SIQNVGLAVR.Y
R2/RRR2-1/2	1497.383	1497.725	-228.752	0.313	847.925	0.342	16	0.112	R.SALLQGQALQALQR.F
R2/RRR2-3/2	1148.252	1148.377	-109.253	0.365	646.680	0.256	13	0.105	-.ATFEVVQLLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1056.321	1057.229	-1811.604	0.283	870.111	0.165	14	0.101	K.SIQNVGLAVR.Y
R2/RRR2-3/3	1102.664	1102.271	357.598	0.479	412.425	0.547	16	0.098	R.VLRPNFEAR.T
R2/RRR2-3/3	1102.464	1102.271	175.668	0.480	288.021	0.507	14	0.095	R.VLRPNFEAR.T
R2/RRR2-1/3	1102.042	1102.271	-208.559	0.464	307.994	0.427	14	0.089	R.VLRPNFEAR.T
R2/RRR2-3/3	1102.059	1102.271	-192.890	0.436	328.338	0.413	15	0.088	R.VLRPNFEAR.T
R2/RRR2-1/3	1101.668	1102.271	-1459.564	0.356	286.132	0.448	14	0.082	-.VLRPNFEAR.-
R2/RRR2-11/3	1505.322	1504.756	-288.760	0.634	3217.188	0.429	32	0.474	K.KVSPQLIAEYTVR.A
R2/RRR2-16/3	1505.522	1504.756	-155.877	0.552	2838.081	0.441	30	0.385	K.KVSPQLIAEYTVR.A
R2/RRR2-10/3	1504.129	1504.756	-1085.084	0.511	2425.893	0.385	28	0.265	K.KVSPQLIAEYTVR.A
R2/RRR2-11/2	1504.358	1504.756	-265.130	0.552	2023.099	0.517	22	0.263	K.KVSPQLIAEYTVR.A
R2/RRR2-10/2	1505.271	1504.756	-322.964	0.556	1933.706	0.494	22	0.242	K.KVSPQLIAEYTVR.A
R2/RRR2-9/3	1505.004	1504.756	165.169	0.472	2377.478	0.366	32	0.241	K.KVSPQLIAEYTVR.A
R2/RRR2-10/3	1504.313	1504.756	-295.017	0.472	2283.136	0.380	27	0.238	K.KVSPQLIAEYTVR.A
R2/RRR2-2/3	1505.696	1504.756	-39.741	0.471	2146.855	0.400	28	0.219	K.KVSPQLIAEYTVR.A
R2/RRR2-14/2	1504.039	1504.756	-1144.606	0.469	1789.859	0.480	21	0.218	K.KVSPQLIAEYTVR.A
R2/RRR2-11/2	1503.786	1504.756	-1313.824	0.518	1749.602	0.490	21	0.216	K.KVSPQLIAEYTVR.A
R2/RRR2-10/2	1504.365	1504.756	-260.408	0.529	1687.491	0.495	21	0.209	K.KVSPQLIAEYTVR.A
R2/RRR2-11/2	1504.288	1504.756	-311.617	0.493	1534.779	0.502	20	0.192	K.KVSPQLIAEYTVR.A
R2/RRR2-12/3	1503.936	1504.756	-1213.934	0.452	2001.529	0.356	28	0.179	K.KVSPQLIAEYTVR.A
R2/RRR2-11/3	1296.663	1296.501	125.422	0.556	1672.296	0.449	24	0.162	K.KPWALSFSFGR.A
R2/RRR2-16/2	1504.579	1504.756	-118.045	0.402	1080.651	0.444	18	0.139	K.KVSPQLIAEYTVR.A
R2/RRR2-11/2	1376.244	1376.583	-246.663	0.479	642.245	0.563	17	0.137	K.VSPQLIAEYTVR.A
R2/RRR2-10/2	1377.391	1376.583	-139.701	0.447	613.857	0.547	17	0.133	K.VSPQLIAEYTVR.A
R2/RRR2-2/3	1504.664	1504.756	-61.453	0.468	1883.792	0.263	27	0.133	K.KVSPQLIAEYTVR.A
R2/RRR2-10/2	1377.244	1376.583	-246.929	0.454	610.377	0.540	17	0.133	K.VSPQLIAEYTVR.A
R2/RRR2-11/3	1296.228	1296.501	-211.035	0.532	1351.393	0.449	24	0.126	K.KPWALSFSFGR.A
R2/RRR2-11/2	1296.324	1296.501	-137.198	0.383	628.998	0.430	17	0.121	K.KPWALSFSFGR.A
R2/RRR2-11/2	1295.783	1296.501	-1329.888	0.337	738.334	0.407	18	0.120	K.KPWALSFSFGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1297.190	1296.501	-240.647	0.391	570.851	0.401	17	0.119	K.KPWALSFSFGR.A
R2/RRR2-11/2	1375.700	1376.583	-1372.871	0.308	590.837	0.431	17	0.117	K.VSPQLIAEYTVR.A
R2/RRR2-2/2	1376.979	1376.583	288.570	0.341	856.938	0.313	16	0.114	K.VSPQLIAEYTVR.A
R2/RRR2-11/2	1375.570	1376.583	-1467.972	0.257	250.694	0.306	12	0.110	K.VSPQLIAEYTVR.A
R2/RRR2-15/2	1377.123	1376.583	-335.058	0.340	499.696	0.326	13	0.107	-.VSPQLIAEYTVR.-
R2/RRR2-1/3	1505.310	1504.756	-297.181	0.440	1264.580	0.336	25	0.097	K.KVSPQLIAEYTVR.A
R2/RRR2-11/3	1504.393	1504.756	-241.897	0.424	1155.228	0.375	28	0.096	K.KVSPQLIAEYTVR.A
R2/RRR2-11/3	1296.149	1296.501	-272.401	0.500	980.270	0.392	20	0.090	K.KPWALSFSFGR.A
R2/RRR2-1/3	1504.553	1504.756	-135.308	0.337	1466.531	0.212	26	0.087	K.KVSPQLIAEYTVR.A
R2/RRR2-1/3	1504.759	1504.756	2.260	0.353	1264.899	0.170	25	0.071	-.KVSPQLIAEYTVR.-
R2/RRR2-2/3	1504.362	1504.756	-262.290	0.344	857.090	0.228	22	0.071	K.KVSPQLIAEYTVR.A
R2/RRR2-3/3	1505.786	1504.756	19.781	0.299	788.457	0.112	21	0.066	K.KVSPQLIAEYTVR.A
R2/RRR2-3/3	1505.242	1504.756	323.878	0.286	1097.693	0.055	24	0.058	K.KVSPQLIAEYTVR.A
R2/RRR2-12/2	1059.177	1059.243	-62.377	0.494	567.207	0.570	16	0.139	K.LGPQNAIFAK.A
R2/RRR2-12/2	1541.643	1540.848	-133.273	0.483	1050.645	0.400	18	0.132	K.VM*DVVLPFFESLK.L
R2/RRR2-12/2	1059.059	1059.243	-174.755	0.438	534.845	0.499	16	0.129	K.LGPQNAIFAK.A
R2/RRR2-12/2	1388.667	1389.578	-1380.771	0.401	1030.871	0.389	15	0.128	K.ALESLKEWEGVK.V
R2/RRR2-12/2	1540.639	1540.848	-136.220	0.446	930.389	0.394	17	0.124	K.VM*DVVLPFFESLK.L
R2/RRR2-12/2	1541.755	1540.848	-60.996	0.474	966.061	0.369	17	0.122	K.VM*DVVLPFFESLK.L
R2/RRR2-12/2	1425.040	1425.558	-1067.926	0.357	698.351	0.426	16	0.116	K.LSSTSVTVEDCVK.E
R2/RRR2-12/2	1058.761	1059.243	-456.738	0.385	391.104	0.442	11	0.114	K.LGPQNAIFAK.A
R2/RRR2-12/2	1523.795	1524.849	-1352.094	0.255	552.958	0.204	13	0.100	-.VMDVVLPFFESLK.-
R2/RRR2-11/2	1411.321	1411.689	-261.700	0.565	1488.702	0.556	18	0.204	K.LSISDVEYLLMK.S
R2/RRR2-11/3	1997.984	1996.249	-133.328	0.534	1662.762	0.503	29	0.190	R.QYPDKDAAISFLEGVITK.L
R2/RRR2-11/2	1088.905	1089.309	-372.020	0.425	901.655	0.380	14	0.125	R.INEPILYVK.M
R2/RRR2-11/2	1089.160	1089.309	-137.888	0.372	769.618	0.326	13	0.114	R.INEPILYVK.M
R2/RRR2-11/2	1148.276	1147.371	-82.905	0.317	1286.698	0.130	15	0.110	K.M*QIAAINLEK.G
R2/RRR2-13/2	1212.894	1212.358	-383.528	0.150	231.786	0.378	17	0.105	R.AIPGYGGGM*SSAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1211.903	1212.358	-376.568	0.157	197.523	0.603	17	0.104	R.AIPGYGGGM*SSAK.A
R2/RRR2-12/2	1211.882	1212.358	-393.749	0.067	258.560	0.316	19	0.099	R.AIPGYGGGM*SSAK.A
R2/RRR2-13/2	1212.104	1212.358	-210.341	0.037	152.106	0.333	16	0.098	R.AIPGYGGGM*SSAK.A
R2/RRR2-12/2	1211.938	1212.358	-347.765	0.039	169.639	0.401	16	0.094	R.AIPGYGGGM*SSAK.A
R2/RRR2-10/2	1255.141	1255.316	-139.846	0.469	1595.807	0.503	18	0.202	K.SIESSDLNFSR.Y
R2/RRR2-10/2	1255.097	1255.316	-175.555	0.362	1112.561	0.383	17	0.134	K.SIESSDLNFSR.Y
R2/RRR2-10/3	1406.651	1406.526	88.850	0.555	1359.577	0.436	25	0.124	K.RTSEALSEHFTK.E
R2/RRR2-10/2	1640.228	1639.960	164.176	0.427	651.771	0.461	21	0.123	K.LSGLPPETVFQPLLK.D
R2/RRR2-10/2	1374.194	1374.650	-332.921	0.414	641.322	0.400	17	0.118	R.EAILPSVLYIQK.T
R2/RRR2-10/2	1639.055	1639.960	-1165.207	0.375	559.174	0.435	19	0.116	K.LSGLPPETVFQPLLK.D
R2/RRR2-10/2	1374.008	1374.650	-1198.838	0.329	629.266	0.315	17	0.109	R.EAILPSVLYIQK.T
R2/RRR2-10/3	1406.521	1406.526	-3.719	0.532	1152.373	0.397	22	0.101	K.RTSEALSEHFTK.E
R2/RRR2-10/3	1406.291	1406.526	-167.355	0.527	1255.571	0.349	24	0.097	K.RTSEALSEHFTK.E
R2/RRR2-6/2	1641.899	1642.792	-1156.553	0.518	2215.912	0.562	25	0.313	K.LAGLSAGGGEEPQQLSK.N
R2/RRR2-6/2	1643.445	1642.792	-212.370	0.574	1780.658	0.590	22	0.246	K.LAGLSAGGGEEPQQLSK.N
R2/RRR2-6/2	1642.319	1642.792	-289.080	0.556	1762.941	0.579	23	0.241	K.LAGLSAGGGEEPQQLSK.N
R2/RRR2-6/2	1375.172	1375.550	-275.613	0.441	1184.620	0.460	19	0.152	K.LLFYDLYGGGEK.V
R2/RRR2-6/2	1496.493	1497.717	-1490.485	0.366	1075.709	0.364	19	0.128	K.FLANITVADYIEK.Y
R2/RRR2-6/2	1325.050	1325.403	-267.189	0.430	1061.222	0.349	15	0.125	R.TSELEDNEFIK.F
R2/RRR2-6/2	1375.302	1375.550	-181.221	0.377	637.781	0.337	15	0.111	K.LLFYDLYGGGEK.V
R2/RRR2-6/2	1324.425	1325.403	-1497.943	0.329	892.268	0.292	14	0.111	R.TSELEDNEFIK.F
R2/RRR2-1/2	1375.699	1375.550	108.347	0.369	464.806	0.351	13	0.107	-.LLFYDLYGGGEK.-
R2/RRR2-6/2	1375.106	1375.550	-323.885	0.226	665.606	0.321	14	0.105	K.LLFYDLYGGGEK.V
R2/RRR2-8/2	1259.965	1260.404	-350.028	0.515	2039.855	0.537	19	0.274	R.AFATGGYAAM*QR.V
R2/RRR2-8/2	1421.638	1420.639	-0.828	0.543	1679.158	0.523	21	0.217	R.AYAQSVATLNLLR.A
R2/RRR2-8/2	1260.105	1260.404	-238.445	0.516	1664.300	0.519	19	0.214	R.AFATGGYAAM*QR.V
R2/RRR2-8/2	1260.214	1260.404	-151.276	0.489	1485.163	0.495	19	0.187	R.AFATGGYAAM*QR.V
R2/RRR2-8/2	1420.303	1420.639	-237.029	0.452	1441.677	0.400	19	0.162	R.AYAQSVATLNLLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1450.754	1451.696	-1342.862	0.426	842.778	0.388	17	0.120	K.LIEILNPSNKPGR.I
R2/RRR2-8/2	1450.913	1451.696	-1232.338	0.373	663.241	0.443	15	0.117	K.LIEILNPSNKPGR.I
R2/RRR2-8/2	1404.412	1404.596	-131.346	0.463	744.842	0.400	15	0.116	-.TRPFDSILAEVR.-
R2/RRR2-8/2	1404.483	1404.596	-80.865	0.493	878.359	0.333	16	0.115	K.TRPFDSILAEVR.A
R2/RRR2-8/2	1450.471	1451.696	-1538.621	0.409	594.622	0.381	14	0.110	-.LIEILNPSNKPGR.-
R2/RRR2-8/2	1404.361	1404.596	-167.793	0.464	773.601	0.280	15	0.106	-.TRPFDSILAEVR.-
R2/RRR2-8/2	1419.522	1420.639	-1495.920	0.288	684.408	0.222	15	0.101	R.AYAQSVATLNLLR.A
R2/RRR2-8/3	1404.724	1404.596	91.412	0.422	1146.364	0.130	22	0.056	-.TRPFDSILAEVR.-
R2/RRR2-8/3	1404.439	1404.596	-112.043	0.426	1065.604	0.153	20	0.051	-.TRPFDSILAEVR.-
R2/RRR2-14/2	1093.239	1093.218	19.307	0.475	1025.246	0.492	16	0.148	R.NINASFASLR.Q
R2/RRR2-13/2	1346.143	1346.496	-262.870	0.505	894.831	0.518	19	0.143	R.DM*TALSGAHTIGR.A
R2/RRR2-14/2	991.989	992.150	-163.429	0.455	1249.625	0.367	14	0.141	R.GFEVIDAIK.T
R2/RRR2-14/2	1093.050	1093.218	-154.311	0.460	1101.645	0.416	17	0.141	R.NINASFASLR.Q
R2/RRR2-13/2	991.482	992.150	-1687.606	0.385	1332.592	0.322	14	0.141	-.GFEVIDAIK.-
R2/RRR2-13/2	1346.229	1346.496	-198.735	0.492	954.587	0.453	19	0.136	R.DM*TALSGAHTIGR.A
R2/RRR2-13/2	992.022	992.150	-129.482	0.449	1272.127	0.315	14	0.136	-.GFEVIDAIK.-
R2/RRR2-14/2	1549.314	1549.732	-270.432	0.491	823.204	0.485	23	0.135	K.M*GNLLPSSGTATEVR.L
R2/RRR2-14/2	991.491	992.150	-1678.700	0.383	1324.037	0.280	14	0.134	-.GFEVIDAIK.-
R2/RRR2-14/2	1093.155	1093.218	-57.638	0.434	891.178	0.446	16	0.133	R.NINASFASLR.Q
R2/RRR2-13/2	991.966	992.150	-186.267	0.427	1276.597	0.296	14	0.133	-.GFEVIDAIK.-
R2/RRR2-14/2	1345.435	1346.496	-1536.119	0.397	865.952	0.466	18	0.131	R.DM*TALSGAHTIGR.A
R2/RRR2-14/2	991.460	992.150	-1710.119	0.401	1240.615	0.289	14	0.130	-.GFEVIDAIK.-
R2/RRR2-13/2	1345.702	1346.496	-1336.742	0.450	834.925	0.457	18	0.130	R.DM*TALSGAHTIGR.A
R2/RRR2-14/2	1549.051	1549.732	-1088.776	0.442	675.645	0.432	22	0.123	K.M*GNLLPSSGTATEVR.L
R2/RRR2-14/2	1345.913	1346.496	-1179.338	0.399	756.594	0.372	17	0.117	R.DM*TALSGAHTIGR.A
R2/RRR2-14/2	1548.664	1549.732	-1339.271	0.353	649.482	0.394	21	0.116	K.M*GNLLPSSGTATEVR.L
R2/RRR2-13/2	1533.148	1533.733	-1037.025	0.400	499.845	0.384	20	0.115	K.MGNLLPSSGTATEVR.L
R2/RRR2-14/2	1345.358	1346.496	-1593.723	0.334	774.214	0.326	18	0.113	R.DM*TALSGAHTIGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1533.239	1533.733	-322.982	0.415	309.598	0.351	16	0.106	-.MGNLLPSSGTATEVR.-
R2/RRR2-10/2	1730.092	1729.822	156.427	0.575	1736.415	0.590	22	0.241	K.EAFVSSSEEPFTVDGK.E
R2/RRR2-10/2	1729.547	1729.822	-159.748	0.519	1264.476	0.527	20	0.168	K.EAFVSSSEEPFTVDGK.E
R2/RRR2-10/2	1697.955	1696.923	19.065	0.561	743.646	0.579	20	0.143	R.NLEVGIPELLENDIK.V
R2/RRR2-10/2	1665.256	1665.871	-972.917	0.465	1051.646	0.468	19	0.140	K.GFAIGNGLTDPAIQYK.A
R2/RRR2-9/2	1696.317	1696.923	-949.760	0.457	889.903	0.445	22	0.132	R.NLEVGIPELLENDIK.V
R2/RRR2-10/2	1696.616	1696.923	-181.395	0.493	712.377	0.509	20	0.131	R.NLEVGIPELLENDIK.V
R2/RRR2-10/2	1697.143	1696.923	130.029	0.497	632.929	0.514	19	0.128	R.NLEVGIPELLENDIK.V
R2/RRR2-9/2	1696.196	1696.923	-1021.578	0.424	567.953	0.497	18	0.123	R.NLEVGIPELLENDIK.V
R2/RRR2-9/2	1696.254	1696.923	-986.824	0.354	604.177	0.312	18	0.108	R.NLEVGIPELLENDIK.V
R2/RRR2-9/3	1594.444	1594.798	-222.636	0.405	1048.407	0.314	26	0.080	K.VHDAGHM*VPM*DQPK.A
R2/RRR2-10/3	1595.024	1594.798	142.331	0.382	780.153	0.341	23	0.074	-.VHDAGHM*VPM*DQPK.-
R2/RRR2-8/2	1399.366	1399.660	-210.390	0.466	1577.053	0.509	18	0.200	K.VLWLIENVDAVK.N
R2/RRR2-8/2	1399.473	1399.660	-133.559	0.485	1357.536	0.488	18	0.172	K.VLWLIENVDAVK.N
R2/RRR2-8/2	1463.257	1463.613	-243.542	0.406	1547.004	0.360	20	0.164	R.DSLGIISTASEIEK.L
R2/RRR2-8/2	1114.004	1114.237	-209.659	0.487	994.111	0.381	16	0.130	R.RLESELPGGR.T
R2/RRR2-8/2	1113.731	1114.237	-1356.318	0.503	995.009	0.356	16	0.127	R.RLESELPGGR.T
R2/RRR2-8/2	1463.019	1463.613	-1092.760	0.388	1088.537	0.318	19	0.122	R.DSLGIISTASEIEK.L
R2/RRR2-8/2	1398.648	1399.660	-1442.875	0.251	556.744	0.394	13	0.107	K.VLWLIENVDAVK.N
R2/RRR2-8/3	1578.361	1578.662	-191.659	0.477	713.880	0.537	27	0.101	K.VFGQHVTDCSNASR.T
R2/RRR2-8/3	1577.935	1578.662	-1097.957	0.422	789.638	0.501	25	0.097	K.VFGQHVTDCSNASR.T
R2/RRR2-9/2	1791.793	1792.023	-128.779	0.513	1622.464	0.535	26	0.215	K.TEAIFPATLETISNVGK.V
R2/RRR2-9/2	1373.156	1373.494	-247.129	0.491	1497.169	0.511	20	0.192	R.VLQDPSSSAEALR.T
R2/RRR2-9/2	1373.157	1373.494	-246.415	0.515	1384.628	0.541	21	0.188	R.VLQDPSSSAEALR.T
R2/RRR2-9/2	1445.575	1446.665	-1450.327	0.495	909.407	0.604	19	0.157	K.IPGTSELQISLCK.E
R2/RRR2-9/2	1447.228	1446.665	-302.584	0.486	646.596	0.622	18	0.143	K.IPGTSELQISLCK.E
R2/RRR2-9/2	1491.161	1491.706	-1039.047	0.391	689.121	0.412	16	0.116	K.ELAITNLTNCLTK.E
R2/RRR2-6/2	1434.572	1434.662	-63.465	0.530	2093.071	0.621	22	0.315	R.NVLGGLSLEGFLSK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1106.380	1106.300	72.749	0.492	1730.673	0.495	17	0.217	K.TALLQSFLGR.Q
R2/RRR2-6/2	1106.027	1106.300	-247.259	0.497	1570.341	0.517	17	0.203	K.TALLQSFLGR.Q
R2/RRR2-6/2	1107.084	1106.300	-195.708	0.513	1500.657	0.478	16	0.186	K.TALLQSFLGR.Q
R2/RRR2-6/2	1887.987	1889.099	-1122.015	0.488	1047.063	0.571	18	0.154	R.APDQTLELTGQAIDFLR.G
R2/RRR2-6/2	1331.531	1332.533	-1507.971	0.442	1002.597	0.416	15	0.132	K.GRLETTWTVLR.K
R2/RRR2-6/2	1888.495	1889.099	-851.879	0.444	795.516	0.500	17	0.126	R.APDQTLELTGQAIDFLR.G
R2/RRR2-6/2	1331.685	1332.533	-1392.044	0.392	887.973	0.364	16	0.121	K.GRLETTWTVLR.K
R2/RRR2-6/2	1888.220	1889.099	-997.898	0.374	652.936	0.379	15	0.107	R.APDQTLELTGQAIDFLR.G
R2/RRR2-7/2	1613.632	1612.810	-110.674	0.471	1222.934	0.554	20	0.172	K.VLEPLFSYWNSTR.Q
R2/RRR2-7/2	1614.013	1612.810	126.182	0.521	918.774	0.589	18	0.154	K.VLEPLFSYWNSTR.Q
R2/RRR2-6/2	1613.231	1612.810	261.868	0.491	1174.983	0.476	19	0.153	K.VLEPLFSYWNSTR.Q
R2/RRR2-6/3	1244.503	1244.385	95.704	0.549	1530.439	0.484	24	0.151	R.THRVETTFPR.L
R2/RRR2-7/3	1338.809	1338.538	202.729	0.575	1457.481	0.463	26	0.140	K.VGIKDHESVVVR.I
R2/RRR2-6/3	1244.516	1244.385	105.590	0.487	1106.870	0.561	22	0.130	R.THRVETTFPR.L
R2/RRR2-7/2	1171.071	1171.374	-258.827	0.401	531.391	0.501	15	0.124	R.NVLAPAAPYVR.K
R2/RRR2-6/3	1244.435	1244.385	40.514	0.502	982.760	0.539	21	0.117	R.THRVETTFPR.L
R2/RRR2-7/3	1337.763	1338.538	-1330.907	0.605	1058.855	0.503	24	0.116	K.VGIKDHESVVVR.I
R2/RRR2-7/2	1170.978	1171.374	-338.522	0.359	515.528	0.443	14	0.116	R.NVLAPAAPYVR.K
R2/RRR2-7/2	1170.480	1171.374	-1622.991	0.294	484.041	0.436	13	0.111	R.NVLAPAAPYVR.K
R2/RRR2-7/2	1611.648	1612.810	-1345.091	0.266	863.265	0.279	16	0.108	K.VLEPLFSYWNSTR.Q
R2/RRR2-1/2	1614.349	1612.810	-286.276	0.327	475.956	0.302	12	0.103	K.VLEPLFSYWNSTR.Q
R2/RRR2-6/3	1338.877	1338.538	254.294	0.562	766.239	0.442	20	0.091	K.VGIKDHESVVVR.I
R2/RRR2-7/3	1338.233	1338.538	-228.382	0.481	917.935	0.350	22	0.082	K.VGIKDHESVVVR.I
R2/RRR2-7/3	1244.399	1244.385	11.588	0.374	812.757	0.382	20	0.081	R.THRVETTFPR.L
R2/RRR2-8/2	1103.106	1103.253	-133.814	0.419	759.507	0.380	15	0.122	R.VLATDEWLR.V
R2/RRR2-8/2	1060.053	1060.226	-164.081	0.371	774.948	0.353	15	0.117	K.ALSLVDSQVK.N
R2/RRR2-8/2	1059.367	1060.226	-1760.280	0.327	654.496	0.394	15	0.116	K.ALSLVDSQVK.N
R2/RRR2-8/3	1973.804	1974.313	-767.117	0.426	1101.819	0.489	31	0.116	K.ISLIEAADHILTMFDKR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1102.471	1103.253	-1621.270	0.348	665.410	0.362	14	0.115	R.VLATDEWLR.V
R2/RRR2-8/2	1059.998	1060.226	-216.414	0.350	528.884	0.357	13	0.112	K.ALSLVDSQVK.N
R2/RRR2-8/3	1502.665	1502.632	22.116	0.451	859.410	0.357	24	0.081	K.M*KDAEENPEGPIR.I
R2/RRR2-8/3	1991.797	1990.313	243.929	0.307	685.705	0.406	22	0.077	K.ISLIEAADHILTM*FDKR.I
R2/RRR2-8/3	1502.383	1502.632	-166.622	0.445	707.806	0.354	21	0.073	-.M*KDAEENPEGPIR.-
R2/RRR2-8/3	1502.373	1502.632	-172.980	0.399	961.496	0.248	23	0.070	K.M*KDAEENPEGPIR.I
R2/RRR2-4/2	1502.277	1502.740	-309.182	0.500	1454.801	0.492	22	0.183	K.FSVSPVVQQGVQVK.N
R2/RRR2-4/2	1482.326	1481.722	-267.997	0.489	1507.994	0.441	18	0.176	R.AFNQFILDPIFR.I
R2/RRR2-4/2	1502.351	1502.740	-259.943	0.490	1311.737	0.485	22	0.168	K.FSVSPVVQQGVQVK.N
R2/RRR2-4/2	1502.091	1502.740	-1101.097	0.441	1333.297	0.463	21	0.164	K.FSVSPVVQQGVQVK.N
R2/RRR2-8/2	1481.814	1481.722	62.084	0.457	1327.784	0.407	17	0.152	R.AFNQFILDPIFR.I
R2/RRR2-4/2	1460.245	1460.572	-224.508	0.462	1150.559	0.477	19	0.151	K.SGTLTTSETAHNLK.V
R2/RRR2-13/2	1147.591	1147.284	267.605	0.388	728.473	0.375	14	0.117	R.EGVIAEEPM*R.G
R2/RRR2-8/2	1482.259	1481.722	-313.605	0.266	920.861	0.304	17	0.113	R.AFNQFILDPIFR.I
R2/RRR2-4/2	1147.121	1147.284	-142.570	0.323	920.710	0.274	14	0.112	R.EGVIAEEPM*R.G
R2/RRR2-4/2	1481.312	1481.722	-278.182	0.320	786.205	0.284	14	0.107	R.AFNQFILDPIFR.I
R2/RRR2-4/2	1480.888	1481.722	-1242.201	0.231	554.162	0.199	14	0.103	R.AFNQFILDPIFR.I
R2/RRR2-4/2	1146.763	1147.284	-1330.184	0.342	715.279	0.200	13	0.103	R.EGVIAEEPM*R.G
R2/RRR2-8/2	1482.605	1481.722	-79.329	0.172	533.665	0.233	15	0.102	R.AFNQFILDPIFR.I
R2/RRR2-24/3	1365.393	1365.565	-126.591	0.543	2983.221	0.435	31	0.415	R.HHVIGQYVVGQK.G
R2/RRR2-24/3	1365.551	1365.565	-10.107	0.534	2633.058	0.396	29	0.310	R.HHVIGQYVVGQK.G
R2/RRR2-24/3	1365.487	1365.565	-57.316	0.536	2183.350	0.437	27	0.237	R.HHVIGQYVVGQK.G
R2/RRR2-23/3	1365.518	1365.565	-34.316	0.497	2264.514	0.342	29	0.211	R.HHVIGQYVVGQK.G
R2/RRR2-23/3	1365.478	1365.565	-64.310	0.517	2045.959	0.393	26	0.197	R.HHVIGQYVVGQK.G
R2/RRR2-23/3	1365.828	1365.565	192.802	0.478	1854.955	0.344	26	0.153	R.HHVIGQYVVGQK.G
R2/RRR2-24/3	1365.840	1365.565	201.540	0.315	1851.222	0.315	26	0.148	R.HHVIGQYVVGQK.G
R2/RRR2-24/3	1649.708	1649.881	-105.479	0.414	1577.077	0.382	27	0.136	K.QRHHVIGQYVVGQK.G
R2/RRR2-24/2	1270.127	1270.374	-195.167	0.431	564.426	0.599	17	0.136	K.VPPNSASLEEAR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1270.106	1270.374	-211.943	0.406	653.705	0.561	18	0.135	K.VPPNSASLEEAR.H
R2/RRR2-24/2	1270.034	1270.374	-268.448	0.454	552.214	0.561	18	0.134	K.VPPNSASLEEAR.H
R2/RRR2-24/2	1270.130	1270.374	-192.853	0.456	609.214	0.538	18	0.134	K.VPPNSASLEEAR.H
R2/RRR2-24/2	1270.333	1270.374	-32.636	0.397	394.117	0.555	15	0.125	K.VPPNSASLEEAR.H
R2/RRR2-24/2	1269.475	1270.374	-1500.382	0.316	552.657	0.538	17	0.123	K.VPPNSASLEEAR.H
R2/RRR2-24/3	1650.274	1649.881	238.436	0.485	1230.299	0.403	25	0.108	K.QRHHVIGQYVVGQK.G
R2/RRR2-24/3	1365.828	1365.565	193.340	0.344	1193.151	0.287	22	0.084	R.HHVIGQYVVGQK.G
R2/RRR2-23/3	1649.065	1649.881	-1104.426	0.390	636.847	0.313	19	0.067	-.QRHHVIGQYVVGQK.-
R2/RRR2-24/3	1365.946	1365.565	280.045	0.259	829.401	0.178	19	0.065	R.HHVIGQYVVGQK.G
R2/RRR2-8/3	1705.033	1704.907	74.091	0.492	1572.775	0.425	27	0.151	K.LTPHSYIGEAEFLAR.N
R2/RRR2-8/2	1459.311	1459.629	-218.695	0.440	776.352	0.430	18	0.124	R.QFIEGLDLPEAAR.S
R2/RRR2-8/2	1296.256	1295.427	-132.104	0.347	681.483	0.515	16	0.123	R.THGQPASPTTLGK.E
R2/RRR2-8/2	1020.305	1020.119	182.747	0.312	775.827	0.306	14	0.110	R.DLTDSTVLR.N
R2/RRR2-8/2	1459.095	1459.629	-1054.246	0.374	846.580	0.269	19	0.110	R.QFIEGLDLPEAAR.S
R2/RRR2-8/2	1660.443	1659.861	-252.743	0.510	1470.433	0.561	21	0.199	K.ELQGVVFDDVPEALK.H
R2/RRR2-8/2	1659.425	1659.861	-263.965	0.480	1359.253	0.494	21	0.173	K.ELQGVVFDDVPEALK.H
R2/RRR2-8/3	1855.450	1854.950	-269.936	0.553	981.653	0.577	33	0.127	K.HLTSTYSSDETKEDIK.L
R2/RRR2-8/3	1855.892	1854.950	-30.988	0.541	851.440	0.555	31	0.115	K.HLTSTYSSDETKEDIK.L
R2/RRR2-8/2	1340.495	1340.509	-10.925	0.290	648.744	0.390	14	0.110	R.LLFGNTAYGDLR.Q
R2/RRR2-15/2	1341.784	1340.509	205.164	0.271	406.008	0.346	13	0.104	-.LLFGNTAYGDLR.-
R2/RRR2-2/3	1856.112	1854.950	87.652	0.511	646.668	0.523	28	0.101	K.HLTSTYSSDETKEDIK.L
R2/RRR2-8/3	1855.785	1854.950	-88.983	0.512	721.089	0.497	30	0.100	K.HLTSTYSSDETKEDIK.L
R2/RRR2-8/2	1031.880	1032.132	-244.855	0.209	908.071	0.138	14	0.098	K.VYIYSSGSR.E
R2/RRR2-15/3	1854.434	1854.950	-819.533	0.509	897.233	0.449	33	0.098	K.HLTSTYSSDETKEDIK.L
R2/RRR2-7/3	1854.653	1854.950	-160.598	0.536	727.443	0.440	31	0.092	K.HLTSTYSSDETKEDIK.L
R2/RRR2-15/3	1853.945	1854.950	-1084.442	0.471	539.779	0.468	27	0.092	K.HLTSTYSSDETKEDIK.L
R2/RRR2-7/3	1854.013	1854.950	-1047.751	0.511	553.255	0.424	27	0.088	K.HLTSTYSSDETKEDIK.L
R2/RRR2-1/3	1854.132	1854.950	-983.201	0.435	326.558	0.416	22	0.084	-.HLTSTYSSDETKEDIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/3	1854.685	1854.950	-143.366	0.469	529.456	0.374	26	0.083	K.HLTSTYSSDETKEDIK.L
R2/RRR2-3/2	1616.463	1616.883	-260.831	0.468	2391.322	0.535	22	0.338	K.SQPDLAILAVNTFVK.D
R2/RRR2-3/2	1616.320	1616.883	-970.179	0.462	1863.931	0.505	20	0.235	K.SQPDLAILAVNTFVK.D
R2/RRR2-5/2	1616.118	1616.883	-1095.152	0.379	1668.171	0.410	20	0.186	K.SQPDLAILAVNTFVK.D
R2/RRR2-3/2	982.111	982.114	-3.193	0.356	740.935	0.350	13	0.116	R.TSFLEAWK.S
R2/RRR2-3/2	981.846	982.114	-273.793	0.310	649.235	0.402	12	0.115	R.TSFLEAWK.S
R2/RRR2-5/2	1450.503	1450.576	-50.360	0.358	694.895	0.359	13	0.109	K.LYDINAELVEDR.G
R2/RRR2-5/2	1617.127	1616.883	151.303	0.205	605.202	0.095	16	0.098	K.SQPDLAILAVNTFVK.D
R2/RRR2-3/3	1509.900	1510.757	-1233.911	0.427	839.012	0.409	26	0.085	-.LQHANCAVVLSAVK.-
R2/RRR2-3/3	1510.563	1510.757	-129.136	0.404	1074.412	0.250	26	0.073	R.LQHANCAVVLSAVK.I
R2/RRR2-3/3	1510.143	1510.757	-1071.966	0.438	603.520	0.344	22	0.065	-.LQHANCAVVLSAVK.-
R2/RRR2-5/2	1457.967	1458.513	-1063.543	0.520	1977.183	0.527	23	0.263	R.VYGSSSNDVSSVTR.Q
R2/RRR2-5/2	1458.092	1458.513	-289.749	0.493	1885.631	0.539	22	0.251	R.VYGSSSNDVSSVTR.Q
R2/RRR2-5/2	1595.226	1595.842	-1016.472	0.499	1175.233	0.463	21	0.153	R.MTLVNNDLYLEAAK.A
R2/RRR2-5/3	1666.850	1666.821	17.980	0.486	991.849	0.459	25	0.103	R.NNLQAHGVTEQSVLR.A
R2/RRR2-5/3	1666.528	1666.821	-176.303	0.455	932.155	0.435	24	0.093	-.NNLQAHGVTEQSVLR.-
R2/RRR2-6/3	1366.857	1366.591	195.120	0.371	879.967	0.435	26	0.091	R.TAILAEAIASHLR.Q
R2/RRR2-5/3	1366.836	1366.591	179.537	0.331	982.872	0.398	27	0.088	R.TAILAEAIASHLR.Q
R2/RRR2-6/3	1367.121	1366.591	-344.997	0.327	812.470	0.351	25	0.078	R.TAILAEAIASHLR.Q
R2/RRR2-5/3	1367.781	1366.591	138.952	0.331	956.427	0.305	27	0.075	R.TAILAEAIASHLR.Q
R2/RRR2-5/3	1366.271	1366.591	-234.942	0.240	643.702	0.332	23	0.072	R.TAILAEAIASHLR.Q
R2/RRR2-7/2	973.734	974.137	-414.324	0.445	1130.065	0.527	16	0.160	K.AGANVVLTTK.G
R2/RRR2-7/2	974.016	974.137	-123.957	0.496	1035.217	0.517	16	0.153	K.AGANVVLTTK.G
R2/RRR2-7/2	1102.113	1101.275	-148.043	0.396	986.914	0.340	16	0.123	R.IADDDVILVK.G
R2/RRR2-8/2	1285.503	1285.472	24.610	0.435	489.674	0.465	13	0.119	K.VLVELAELQDR.E
R2/RRR2-8/2	1285.727	1285.472	199.158	0.419	788.397	0.328	14	0.112	K.VLVELAELQDR.E
R2/RRR2-7/2	1561.268	1560.863	260.624	0.327	1072.177	0.233	16	0.109	K.IIQFATEAAITILR.I
R2/RRR2-8/2	1285.927	1285.472	355.180	0.315	507.958	0.348	13	0.108	K.VLVELAELQDR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	974.994	974.137	-146.436	0.259	443.714	0.307	12	0.106	K.AGANVVLTTK.G
R2/RRR2-7/2	1562.257	1560.863	253.562	0.298	759.893	0.188	17	0.100	K.IIQFATEAAITILR.I
R2/RRR2-17/2	1850.188	1850.066	66.201	0.598	3267.665	0.586	25	0.576	R.NVQAILDSYTTIVNAAR.S
R2/RRR2-17/2	1849.966	1850.066	-54.244	0.532	3087.407	0.534	25	0.503	R.NVQAILDSYTTIVNAAR.S
R2/RRR2-17/2	1849.688	1850.066	-204.908	0.545	2971.243	0.541	25	0.475	R.NVQAILDSYTTIVNAAR.S
R2/RRR2-17/2	1382.148	1381.578	-312.039	0.579	1299.257	0.601	21	0.192	R.VDLVGSM*TSLQSK.C
R2/RRR2-17/2	1381.082	1381.578	-359.975	0.485	1383.852	0.490	21	0.176	R.VDLVGSM*TSLQSK.C
R2/RRR2-17/2	1375.292	1375.515	-162.705	0.425	1404.475	0.449	19	0.168	K.VWSQLSSAGLGNR.V
R2/RRR2-17/2	1380.503	1381.578	-1507.506	0.394	1383.501	0.352	20	0.148	R.VDLVGSM*TSLQSK.C
R2/RRR2-17/2	1374.965	1375.515	-1130.952	0.292	1102.963	0.310	18	0.121	K.VWSQLSSAGLGNR.V
R2/RRR2-10/2	1355.765	1356.467	-1259.040	0.480	1019.165	0.575	19	0.159	K.TLEAEAAHGTVTR.H
R2/RRR2-9/2	1078.312	1077.302	9.468	0.411	1449.421	0.370	15	0.158	K.DLALLIHGPK.V
R2/RRR2-10/2	1355.695	1356.467	-1310.764	0.513	932.343	0.584	18	0.154	K.TLEAEAAHGTVTR.H
R2/RRR2-10/2	1356.161	1356.467	-226.301	0.527	969.991	0.550	19	0.152	K.TLEAEAAHGTVTR.H
R2/RRR2-10/2	1776.336	1775.079	145.531	0.514	1078.877	0.456	18	0.139	R.NILNGTVFREPILCK.N
R2/RRR2-10/2	1775.803	1775.079	-155.725	0.525	665.384	0.386	18	0.113	R.NILNGTVFREPILCK.N
R2/RRR2-7/2	1356.177	1356.467	-214.291	0.226	904.053	0.072	16	0.096	K.TLEAEAAHGTVTR.H
R2/RRR2-7/2	1629.505	1628.804	-184.057	0.561	1463.482	0.484	19	0.183	R.LSQLYDQIEDYLK.K
R2/RRR2-7/2	1688.358	1688.866	-895.643	0.379	1403.581	0.411	20	0.160	R.STQGILNDLWNSLAR.Y
R2/RRR2-7/2	1129.054	1128.262	-185.502	0.463	702.061	0.450	16	0.127	K.GFTASYVQVR.G
R2/RRR2-7/2	1240.650	1241.378	-1396.388	0.354	758.791	0.368	13	0.112	K.AGLLENYASFR.L
R2/RRR2-22/3	1774.867	1774.911	-25.125	0.463	2269.698	0.388	30	0.247	R.HGTHAEFTTCLWTGR.V
R2/RRR2-23/2	987.916	988.123	-211.012	0.423	1317.637	0.460	15	0.163	K.VTIQNLSGR.D
R2/RRR2-22/2	988.184	988.123	61.627	0.429	1138.072	0.456	14	0.148	K.VTIQNLSGR.D
R2/RRR2-23/2	1115.535	1116.296	-1583.625	0.466	1112.375	0.452	16	0.147	R.KVTIQNLSGR.D
R2/RRR2-23/2	987.923	988.123	-203.078	0.449	1090.357	0.442	14	0.143	K.VTIQNLSGR.D
R2/RRR2-22/2	987.905	988.123	-221.796	0.436	1030.590	0.444	13	0.139	K.VTIQNLSGR.D
R2/RRR2-23/2	1116.104	1116.296	-173.173	0.463	782.164	0.518	15	0.138	R.KVTIQNLSGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1115.966	1116.296	-296.952	0.474	805.020	0.483	14	0.133	R.KVTIQNLSGR.D
R2/RRR2-23/2	987.338	988.123	-1813.798	0.380	967.622	0.403	14	0.130	K.VTIQNLSGR.D
R2/RRR2-22/2	1116.077	1116.296	-197.422	0.414	609.780	0.467	13	0.123	R.KVTIQNLSGR.D
R2/RRR2-22/2	1116.192	1116.296	-94.182	0.431	670.338	0.435	13	0.121	R.KVTIQNLSGR.D
R2/RRR2-22/2	988.084	988.123	-39.852	0.286	292.237	0.306	10	0.100	-.VTIQNLSGR.-
R2/RRR2-22/3	1116.702	1116.296	364.313	0.357	910.333	0.318	19	0.073	R.KVTIQNLSGR.D
R2/RRR2-23/3	1774.595	1774.911	-178.503	0.362	809.655	0.274	24	0.069	R.HGTHAEFTTCLWTGR.V
R2/RRR2-23/3	1775.745	1774.911	-94.028	0.281	1166.751	0.176	26	0.066	R.HGTHAEFTTCLWTGR.V
R2/RRR2-6/2	1559.374	1558.759	-247.532	0.509	2345.228	0.463	23	0.301	K.TFGSSADIFAGIFPK.N
R2/RRR2-9/2	1558.337	1558.759	-271.346	0.432	1704.943	0.416	20	0.190	K.TFGSSADIFAGIFPK.N
R2/RRR2-9/3	1365.221	1364.574	-259.382	0.536	1828.919	0.457	27	0.182	R.FIKEEFGQIPR.I
R2/RRR2-5/2	1560.037	1558.759	178.737	0.444	1286.072	0.468	20	0.158	K.TFGSSADIFAGIFPK.N
R2/RRR2-6/2	1191.113	1191.363	-210.477	0.343	1195.771	0.510	16	0.157	K.HAENVPWPLK.T
R2/RRR2-6/2	1558.436	1558.759	-208.006	0.420	1253.646	0.460	19	0.153	K.TFGSSADIFAGIFPK.N
R2/RRR2-6/2	1190.579	1191.363	-1503.243	0.346	1015.120	0.509	14	0.143	K.HAENVPWPLK.T
R2/RRR2-6/3	1364.649	1364.574	55.338	0.488	1613.547	0.399	24	0.140	R.FIKEEFGQIPR.I
R2/RRR2-9/2	1559.727	1558.759	-20.144	0.452	1025.831	0.424	19	0.132	K.TFGSSADIFAGIFPK.N
R2/RRR2-9/2	1559.564	1558.759	-125.031	0.401	766.046	0.413	17	0.118	K.TFGSSADIFAGIFPK.N
R2/RRR2-9/2	1191.067	1191.363	-249.856	0.342	533.945	0.435	13	0.116	K.HAENVPWPLK.T
R2/RRR2-3/2	1559.891	1558.759	84.879	0.349	606.626	0.328	15	0.106	K.TFGSSADIFAGIFPK.N
R2/RRR2-6/3	1723.323	1723.909	-923.020	0.413	603.187	0.535	24	0.094	R.IPVISDSIVVHDSEGR.E
R2/RRR2-6/3	1364.179	1364.574	-290.499	0.442	591.239	0.345	19	0.079	R.FIKEEFGQIPR.I
R2/RRR2-6/3	1723.889	1723.909	-11.273	0.352	615.175	0.385	24	0.075	R.IPVISDSIVVHDSEGR.E
R2/RRR2-6/3	1364.278	1364.574	-217.785	0.476	754.531	0.332	21	0.075	-.FIKEEFGQIPR.-
R2/RRR2-2/2	1924.016	1922.169	-79.584	0.545	1396.455	0.572	21	0.192	K.AISVGGQETNIITDYVLK.I
R2/RRR2-4/2	1608.218	1607.833	239.997	0.501	2331.688	0.444	22	0.301	R.SVEQLGYITVLTQR.N
R2/RRR2-4/3	1989.388	1990.205	-915.831	0.565	1400.532	0.429	25	0.129	R.DLNKEELIEFFNNHVK.V
R2/RRR2-4/3	1989.400	1990.205	-909.917	0.497	1166.368	0.455	24	0.115	R.DLNKEELIEFFNNHVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/3	1054.781	1055.211	-409.083	0.313	1277.760	0.336	20	0.090	R.SRPLYGSFK.G
R2/RRR2-4/3	1611.367	1611.697	-205.475	0.420	773.527	0.442	27	0.089	K.YIAEHGGSTNAFTSR.E
R2/RRR2-4/3	1989.469	1990.205	-875.084	0.492	1028.938	0.376	23	0.089	R.DLNKEELIEFFNNHVK.V
R2/RRR2-4/3	1612.561	1611.697	-84.751	0.461	571.619	0.450	26	0.087	K.YIAEHGGSTNAFTSR.E
R2/RRR2-4/3	1612.522	1611.697	-108.898	0.386	631.466	0.441	24	0.084	K.YIAEHGGSTNAFTSR.E
R2/RRR2-23/2	1259.544	1259.439	83.344	0.260	920.763	0.087	15	0.098	R.FPGQLNADLRK.L
R2/RRR2-23/2	1260.131	1259.439	-245.490	0.331	815.133	0.068	14	0.096	-.FPGQLNADLRK.-
R2/RRR2-23/2	1260.124	1259.439	-251.224	0.351	926.608	0.084	14	0.095	R.FPGQLNADLRK.L
R2/RRR2-6/2	1231.159	1231.464	-248.482	0.465	1354.053	0.487	20	0.172	R.ITVGTTILDAVK.A
R2/RRR2-1/2	1001.095	1001.162	-67.708	0.462	1516.314	0.378	17	0.168	R.IGAATALEVR.A
R2/RRR2-6/2	1231.065	1231.464	-325.182	0.397	1030.104	0.503	18	0.146	R.ITVGTTILDAVK.A
R2/RRR2-6/2	1395.447	1396.486	-1465.750	0.290	1478.417	0.287	18	0.144	K.GFTISDWEGIDR.I
R2/RRR2-6/2	1231.418	1231.464	-37.843	0.312	969.366	0.429	18	0.129	R.ITVGTTILDAVK.A
R2/RRR2-5/2	1396.051	1396.486	-312.624	0.377	917.940	0.345	16	0.118	K.GFTISDWEGIDR.I
R2/RRR2-5/2	1397.108	1396.486	-271.549	0.265	1007.861	0.278	15	0.113	K.GFTISDWEGIDR.I
R2/RRR2-5/2	1232.372	1231.464	-74.474	0.290	434.009	0.336	14	0.108	R.ITVGTTILDAVK.A
R2/RRR2-5/2	1396.321	1396.486	-118.691	0.309	614.112	0.221	14	0.103	K.GFTISDWEGIDR.I
R2/RRR2-6/3	1484.299	1483.720	-284.477	0.391	1064.585	0.395	23	0.094	K.MHANHDLVTGFLK.N
R2/RRR2-6/3	1483.760	1483.720	27.006	0.367	637.116	0.370	19	0.074	-.MHANHDLVTGFLK.-
R2/RRR2-6/3	1499.440	1499.720	-187.139	0.323	568.623	0.341	23	0.071	-.M*HANHDLVTGFLK.-
R2/RRR2-5/2	1910.612	1909.090	-251.050	0.525	1175.451	0.553	21	0.167	K.IEGPAAWDVLYNFEQR.W
R2/RRR2-4/2	1843.812	1844.098	-155.293	0.502	2021.740	0.421	23	0.236	K.NSPAIIFIDEIDSIAPK.R
R2/RRR2-4/2	1843.515	1844.098	-861.174	0.495	1768.523	0.493	22	0.218	K.NSPAIIFIDEIDSIAPK.R
R2/RRR2-4/2	1232.175	1232.414	-194.023	0.428	1363.656	0.332	20	0.145	R.FALGVSNPSALR.E
R2/RRR2-4/2	1578.871	1577.760	70.055	0.453	435.591	0.639	19	0.134	K.TPVSGDVDLQFIASK.T
R2/RRR2-4/2	1579.096	1577.760	213.176	0.478	509.908	0.584	20	0.133	K.TPVSGDVDLQFIASK.T
R2/RRR2-4/2	1844.369	1844.098	147.531	0.482	904.549	0.449	17	0.125	K.NSPAIIFIDEIDSIAPK.R
R2/RRR2-5/2	1578.550	1577.760	-133.455	0.339	385.888	0.363	13	0.104	K.TPVSGDVDLQFIASK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1868.643	1868.124	-258.588	0.597	2957.194	0.637	30	0.512	R.LQAQSALAEAAAASGVALPK.G
R2/RRR2-15/2	1868.679	1868.124	-238.796	0.580	2729.562	0.633	29	0.451	R.LQAQSALAEAAAASGVALPK.G
R2/RRR2-15/2	1868.590	1868.124	250.129	0.544	2352.386	0.615	28	0.358	R.LQAQSALAEAAAASGVALPK.G
R2/RRR2-15/3	1868.792	1868.124	-178.350	0.543	1981.522	0.487	36	0.233	R.LQAQSALAEAAAASGVALPK.G
R2/RRR2-15/3	1867.254	1868.124	-1004.585	0.409	1603.878	0.459	33	0.167	R.LQAQSALAEAAAASGVALPK.G
R2/RRR2-15/3	1867.509	1868.124	-867.753	0.354	1808.848	0.349	33	0.163	R.LQAQSALAEAAAASGVALPK.G
R2/RRR2-15/2	1480.074	1480.565	-332.432	0.475	1074.016	0.513	22	0.154	K.QYLAGGQDTSNLGR.G
R2/RRR2-15/2	1480.174	1480.565	-264.747	0.470	868.433	0.490	21	0.137	K.QYLAGGQDTSNLGR.G
R2/RRR2-15/2	1480.160	1480.565	-274.510	0.447	810.833	0.481	20	0.132	K.QYLAGGQDTSNLGR.G
R2/RRR2-15/2	1101.977	1102.222	-222.502	0.359	562.265	0.440	12	0.114	R.YSGSVDAFKK.I
R2/RRR2-23/3	1900.538	1901.012	-250.118	0.519	2568.433	0.383	39	0.312	R.RASTAGGSGGFSGGGGSNM*LR.F
R2/RRR2-23/3	1901.079	1901.012	35.712	0.504	2071.423	0.426	37	0.228	R.RASTAGGSGGFSGGGGSNM*LR.F
R2/RRR2-23/2	1744.242	1744.825	-910.234	0.493	1478.445	0.567	24	0.198	R.ASTAGGSGGFSGGGGSNM*LR.F
R2/RRR2-23/3	1900.308	1901.012	-899.344	0.500	1973.300	0.373	35	0.191	R.RASTAGGSGGFSGGGGSNM*LR.F
R2/RRR2-23/2	1744.216	1744.825	-925.480	0.474	1420.440	0.553	24	0.188	R.ASTAGGSGGFSGGGGSNM*LR.F
R2/RRR2-23/2	1744.346	1744.825	-275.517	0.511	1331.119	0.585	24	0.185	R.ASTAGGSGGFSGGGGSNM*LR.F
R2/RRR2-24/2	1169.372	1169.268	89.457	0.433	623.087	0.429	15	0.123	R.FYTDEAPGLR.L
R2/RRR2-24/2	1169.039	1169.268	-196.438	0.350	488.974	0.390	14	0.115	R.FYTDEAPGLR.L
R2/RRR2-24/2	1169.264	1169.268	-3.415	0.290	433.723	0.419	14	0.111	-.FYTDEAPGLR.-
R2/RRR2-23/2	1170.317	1169.268	41.783	0.308	381.173	0.275	13	0.110	R.FYTDEAPGLR.L
R2/RRR2-4/2	1085.876	1086.219	-316.568	0.431	1168.125	0.397	14	0.141	R.LSDFLDFTK.G
R2/RRR2-4/2	1668.485	1668.955	-282.565	0.348	638.044	0.501	20	0.123	R.FDPLPIVPVEDVLSK.Y
R2/RRR2-4/2	1085.914	1086.219	-282.056	0.343	727.924	0.420	13	0.120	R.LSDFLDFTK.G
R2/RRR2-4/2	1202.079	1201.395	-263.864	0.429	583.911	0.452	15	0.120	K.TLSGDSPLVIAK.G
R2/RRR2-4/2	1201.231	1201.395	-137.051	0.316	683.572	0.415	16	0.116	K.TLSGDSPLVIAK.G
R2/RRR2-3/2	1669.602	1668.955	-211.903	0.332	532.396	0.426	19	0.115	R.FDPLPIVPVEDVLSK.Y
R2/RRR2-4/2	1668.323	1668.955	-980.668	0.300	413.761	0.445	16	0.111	R.FDPLPIVPVEDVLSK.Y
R2/RRR2-3/2	1670.182	1668.955	136.527	0.343	324.653	0.408	15	0.110	R.FDPLPIVPVEDVLSK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1201.868	1201.395	395.201	0.263	452.460	0.391	14	0.108	K.TLSGDSPLVIAK.G
R2/RRR2-4/2	1667.858	1668.955	-1260.705	0.242	420.855	0.321	17	0.106	R.FDPLPIVPVEDVLSK.Y
R2/RRR2-23/2	1086.556	1086.219	310.824	0.249	269.730	0.321	10	0.105	-.LSDFLDFTK.-
R2/RRR2-22/2	1086.614	1086.219	364.216	0.172	247.642	0.384	10	0.100	-.LSDFLDFTK.-
R2/RRR2-25/3	1671.765	1671.814	-29.528	0.526	2326.887	0.416	32	0.264	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-25/2	1671.246	1671.814	-941.441	0.504	1557.486	0.479	21	0.188	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-26/2	1671.347	1671.814	-280.466	0.482	1471.397	0.460	21	0.175	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-25/3	1671.644	1671.814	-102.370	0.441	1873.839	0.361	30	0.168	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-25/2	1672.209	1671.814	237.040	0.559	1203.219	0.533	21	0.165	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-26/2	1671.483	1671.814	-198.989	0.493	1233.609	0.507	20	0.161	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-25/3	1827.523	1828.001	-261.839	0.509	1698.201	0.414	29	0.161	R.RVTSGEQQVVSGM*NYR.L
R2/RRR2-26/2	1671.042	1671.814	-1063.916	0.493	1312.410	0.450	20	0.157	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-25/2	1672.157	1671.814	205.855	0.587	1049.244	0.558	20	0.156	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-26/3	1672.153	1671.814	203.102	0.487	1713.380	0.362	29	0.145	R.VTSGEQQVVSGM*NYR.L
R2/RRR2-26/2	1042.671	1043.116	-427.736	0.436	548.725	0.539	15	0.132	R.HASLSSDGLR.F
R2/RRR2-26/2	1042.315	1043.116	-1732.576	0.377	546.797	0.587	14	0.131	R.HASLSSDGLR.F
R2/RRR2-26/2	1043.008	1043.116	-103.960	0.387	464.467	0.579	13	0.128	R.HASLSSDGLR.F
R2/RRR2-25/2	1042.470	1043.116	-1583.982	0.348	521.292	0.507	14	0.123	R.HASLSSDGLR.F
R2/RRR2-25/2	1042.163	1043.116	-1879.566	0.365	360.951	0.561	12	0.123	R.HASLSSDGLR.F
R2/RRR2-25/2	1042.367	1043.116	-1683.393	0.269	198.912	0.442	10	0.109	-.HASLSSDGLR.-
R2/RRR2-25/3	1826.648	1828.001	-1291.749	0.436	948.330	0.331	25	0.079	R.RVTSGEQQVVSGM*NYR.L
R2/RRR2-25/3	1827.203	1828.001	-986.706	0.439	962.300	0.328	23	0.078	R.RVTSGEQQVVSGM*NYR.L
R2/RRR2-26/3	1671.660	1671.814	-92.701	0.331	753.855	0.151	22	0.060	-.VTSGEQQVVSGM*NYR.-
R2/RRR2-4/2	1729.524	1729.912	-224.666	0.420	1585.635	0.366	20	0.167	R.ISEAFSGSSLISDFIR.S
R2/RRR2-4/2	1227.899	1228.336	-356.432	0.456	1311.435	0.342	16	0.142	K.LNIDETGFYR.V
R2/RRR2-4/2	1429.325	1429.598	-191.161	0.365	1090.213	0.405	19	0.134	K.ISIDATPDLAGDIK.Q
R2/RRR2-4/2	1729.603	1729.912	-179.068	0.340	1375.438	0.212	20	0.123	R.ISEAFSGSSLISDFIR.S
R2/RRR2-4/2	995.880	996.182	-304.113	0.368	665.328	0.399	14	0.119	R.SIVTLFTSK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	995.936	996.182	-248.406	0.361	541.344	0.444	13	0.119	R.SIVTLFTSK.E
R2/RRR2-4/2	1227.911	1228.336	-346.757	0.386	1069.195	0.230	16	0.114	K.LNIDETGFYR.V
R2/RRR2-4/2	1729.798	1729.912	-66.011	0.388	980.012	0.293	18	0.111	R.ISEAFSGSSLISDFIR.S
R2/RRR2-22/2	1779.621	1780.062	-248.751	0.578	2239.207	0.608	26	0.335	R.KLIGATNPLQAEPGTIR.G
R2/RRR2-22/2	1779.581	1780.062	-271.048	0.544	1994.437	0.616	24	0.291	R.KLIGATNPLQAEPGTIR.G
R2/RRR2-22/2	943.422	944.111	-1794.990	0.452	1163.041	0.393	14	0.141	R.GLVGEIISR.F
R2/RRR2-23/2	1349.163	1348.573	-304.975	0.351	817.324	0.222	15	0.102	R.GLVGEIISRFEK.K
R2/RRR2-17/2	1759.434	1759.979	-880.825	0.561	2612.438	0.538	26	0.393	K.IAELKEALESVTAEQK.Y
R2/RRR2-17/3	1759.917	1759.979	-35.287	0.510	1161.379	0.547	30	0.136	K.IAELKEALESVTAEQK.Y
R2/RRR2-17/2	1205.196	1205.297	-84.484	0.509	956.881	0.406	16	0.130	K.EALESVTAEQK.Y
R2/RRR2-17/2	1179.729	1180.292	-1329.532	0.433	752.368	0.406	14	0.122	K.DEHLDPINVK.I
R2/RRR2-17/2	1180.014	1180.292	-236.840	0.412	744.671	0.347	14	0.115	K.DEHLDPINVK.I
R2/RRR2-17/2	1180.039	1180.292	-215.461	0.399	633.012	0.330	13	0.111	K.DEHLDPINVK.I
R2/RRR2-17/3	1760.365	1759.979	219.699	0.463	661.727	0.519	25	0.096	K.IAELKEALESVTAEQK.Y
R2/RRR2-17/3	1180.374	1180.292	69.422	0.463	851.549	0.403	20	0.087	K.DEHLDPINVK.I
R2/RRR2-17/3	1180.426	1180.292	113.138	0.481	1045.019	0.328	21	0.083	K.DEHLDPINVK.I
R2/RRR2-17/3	1180.273	1180.292	-16.776	0.478	1179.171	0.238	22	0.074	K.DEHLDPINVK.I
R2/RRR2-10/2	1870.478	1871.037	-836.061	0.550	2973.065	0.527	24	0.469	K.LAYVALDYEQELDTAR.S
R2/RRR2-10/2	1871.300	1871.037	141.024	0.623	2700.377	0.583	24	0.422	K.LAYVALDYEQELDTAR.S
R2/RRR2-10/2	1871.310	1871.037	146.519	0.591	2640.797	0.532	24	0.389	K.LAYVALDYEQELDTAR.S
R2/RRR2-13/2	1894.588	1894.969	-201.926	0.565	2951.913	0.578	27	0.488	K.TEGKETEEDSSAAGLLEK.L
R2/RRR2-13/2	1609.360	1608.814	-283.360	0.565	2408.754	0.493	23	0.329	K.FKDLVEEISESLAK.T
R2/RRR2-13/2	1894.797	1894.969	-90.891	0.594	2149.923	0.547	26	0.296	K.TEGKETEEDSSAAGLLEK.L
R2/RRR2-13/2	1607.639	1608.814	-1357.509	0.462	2184.449	0.368	23	0.250	K.FKDLVEEISESLAK.T
R2/RRR2-13/3	1765.353	1765.898	-877.602	0.443	1068.702	0.397	30	0.095	K.KSEEVATKEESTEAVK.E
R2/RRR2-13/3	1765.970	1765.898	41.133	0.436	639.648	0.459	25	0.086	K.KSEEVATKEESTEAVK.E
R2/RRR2-16/3	1608.481	1608.814	-207.937	0.346	963.177	0.210	25	0.063	-.FKDLVEEISESLAK.-
R2/RRR2-14/2	1878.535	1879.019	-258.400	0.587	2523.862	0.526	24	0.361	R.AWDVLNEIFNEDGSLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1878.504	1879.019	-809.156	0.578	2113.217	0.483	24	0.268	R.AWDVLNEIFNEDGSLR.Q
R2/RRR2-14/2	1293.747	1294.485	-1347.122	0.539	1772.719	0.584	19	0.246	K.VIQDHVATVVGR.W
R2/RRR2-14/2	1879.034	1879.019	7.714	0.598	1808.056	0.437	23	0.207	R.AWDVLNEIFNEDGSLR.Q
R2/RRR2-14/2	1295.122	1294.485	-281.588	0.529	1437.000	0.579	19	0.201	K.VIQDHVATVVGR.W
R2/RRR2-14/2	1295.099	1294.485	-299.366	0.540	1323.067	0.575	19	0.188	K.VIQDHVATVVGR.W
R2/RRR2-14/2	934.907	935.059	-163.585	0.463	443.168	0.419	13	0.124	R.VLGEDFVR.I
R2/RRR2-14/2	934.462	935.059	-1714.064	0.439	484.204	0.413	13	0.123	R.VLGEDFVR.I
R2/RRR2-14/2	934.892	935.059	-179.696	0.348	606.504	0.268	13	0.111	R.VLGEDFVR.I
R2/RRR2-4/2	1561.301	1560.692	-250.834	0.439	1427.701	0.535	21	0.188	R.TYINPYATFADAGR.K
R2/RRR2-4/2	1332.219	1331.500	-211.803	0.457	926.510	0.555	20	0.150	R.QADTGAIVSLLSR.I
R2/RRR2-4/2	1561.179	1560.692	312.792	0.455	1100.807	0.458	19	0.144	R.TYINPYATFADAGR.K
R2/RRR2-4/2	1562.227	1560.692	-298.336	0.509	959.893	0.478	21	0.141	R.TYINPYATFADAGR.K
R2/RRR2-5/2	1587.244	1587.888	-1039.094	0.378	664.485	0.476	18	0.121	K.LLVFQSTLPSLGVGR.L
R2/RRR2-5/3	1582.201	1581.799	254.885	0.429	1496.901	0.352	30	0.119	R.LTTHAIPASQSLVSR.W
R2/RRR2-5/2	1587.274	1587.888	-1020.098	0.443	716.553	0.405	18	0.117	K.LLVFQSTLPSLGVGR.L
R2/RRR2-4/2	1587.252	1587.888	-1033.843	0.309	663.129	0.385	18	0.112	K.LLVFQSTLPSLGVGR.L
R2/RRR2-4/2	1586.749	1587.888	-1351.846	0.305	637.208	0.355	17	0.109	K.LLVFQSTLPSLGVGR.L
R2/RRR2-4/3	1581.741	1581.799	-36.824	0.418	1087.561	0.345	26	0.087	R.LTTHAIPASQSLVSR.W
R2/RRR2-4/3	1581.986	1581.799	118.744	0.268	738.363	0.176	20	0.058	-.LTTHAIPASQSLVSR.-
R2/RRR2-9/3	1867.550	1866.102	240.492	0.564	2359.984	0.543	30	0.340	K.TKELILNYANQLCER.L
R2/RRR2-9/2	1636.460	1636.825	-223.377	0.501	1507.643	0.486	19	0.189	K.ELILNYANQLCER.L
R2/RRR2-9/3	1559.870	1559.710	103.042	0.449	802.357	0.477	26	0.099	K.HYKGDHTYVPVSR.K
R2/RRR2-9/3	1559.223	1559.710	-313.407	0.488	681.806	0.469	25	0.096	K.HYKGDHTYVPVSR.K
R2/RRR2-9/3	1559.867	1559.710	100.923	0.450	684.005	0.471	24	0.095	K.HYKGDHTYVPVSR.K
R2/RRR2-14/3	1560.732	1559.710	14.103	0.449	671.814	0.469	25	0.095	K.HYKGDHTYVPVSR.K
R2/RRR2-14/3	1559.777	1559.710	42.763	0.422	857.501	0.431	27	0.093	K.HYKGDHTYVPVSR.K
R2/RRR2-8/3	1560.625	1559.710	-54.503	0.448	527.162	0.435	23	0.090	K.HYKGDHTYVPVSR.K
R2/RRR2-14/3	1559.318	1559.710	-252.496	0.419	679.561	0.419	24	0.089	K.HYKGDHTYVPVSR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1559.289	1559.710	-270.639	0.433	564.412	0.415	23	0.088	K.HYKGDHTYVPVSR.K
R2/RRR2-13/3	1561.002	1559.710	187.637	0.421	399.895	0.397	20	0.088	K.HYKGDHTYVPVSR.K
R2/RRR2-8/3	1560.068	1559.710	229.934	0.371	499.243	0.424	22	0.087	K.HYKGDHTYVPVSR.K
R2/RRR2-10/3	1559.020	1559.710	-1087.207	0.446	494.289	0.407	21	0.087	K.HYKGDHTYVPVSR.K
R2/RRR2-13/3	1560.824	1559.710	73.523	0.494	676.819	0.388	24	0.086	K.HYKGDHTYVPVSR.K
R2/RRR2-10/3	1559.949	1559.710	153.308	0.360	457.722	0.328	21	0.083	K.HYKGDHTYVPVSR.K
R2/RRR2-23/2	1234.184	1234.383	-161.962	0.408	990.212	0.433	17	0.133	R.VALINYGPDSGK.I
R2/RRR2-23/2	938.014	937.977	39.535	0.449	953.565	0.408	13	0.132	R.ASLNDFDR.F
R2/RRR2-23/2	1233.536	1234.383	-1501.712	0.403	1007.179	0.380	17	0.127	R.VALINYGPDSGK.I
R2/RRR2-23/2	937.917	937.977	-63.327	0.335	935.753	0.374	12	0.123	R.ASLNDFDR.F
R2/RRR2-23/2	937.923	937.977	-57.321	0.373	865.357	0.357	13	0.122	R.ASLNDFDR.F
R2/RRR2-22/2	937.676	937.977	-321.489	0.377	771.998	0.299	13	0.115	R.ASLNDFDR.F
R2/RRR2-23/2	1214.202	1213.324	-101.302	0.386	729.549	0.335	14	0.115	R.ASLNDFDRFK.-
R2/RRR2-22/2	937.830	937.977	-156.547	0.306	749.277	0.337	12	0.114	R.ASLNDFDR.F
R2/RRR2-23/2	1213.111	1213.324	-176.079	0.363	602.471	0.330	13	0.112	R.ASLNDFDRFK.-
R2/RRR2-23/2	1233.271	1234.383	-1718.164	0.279	629.167	0.403	14	0.110	R.VALINYGPDSGK.I
R2/RRR2-23/2	1212.973	1213.324	-290.666	0.334	655.030	0.310	13	0.110	R.ASLNDFDRFK.-
R2/RRR2-22/2	1212.498	1213.324	-1510.906	0.347	658.547	0.290	13	0.109	R.ASLNDFDRFK.-
R2/RRR2-22/2	1212.979	1213.324	-285.314	0.334	590.210	0.271	13	0.108	R.ASLNDFDRFK.-
R2/RRR2-22/2	1213.054	1213.324	-223.324	0.345	597.227	0.241	12	0.105	R.ASLNDFDRFK.-
R2/RRR2-2/2	1630.712	1630.910	-121.828	0.513	2545.865	0.417	24	0.327	R.LDQPIILTGFSALNK.L
R2/RRR2-2/2	1631.594	1630.910	-194.027	0.468	1666.345	0.444	20	0.193	R.LDQPIILTGFSALNK.L
R2/RRR2-1/3	1989.300	1989.218	41.008	0.484	1479.524	0.533	32	0.172	R.DLFEGILQAGSNIVENLR.T
R2/RRR2-1/2	1017.501	1018.148	-1623.152	0.384	875.217	0.424	14	0.126	R.GGAWVVVDSK.I
R2/RRR2-2/2	990.411	991.169	-1780.107	0.257	1085.542	0.319	16	0.120	R.AVGIGAYLAR.L
R2/RRR2-3/2	1631.842	1630.910	-41.312	0.419	658.323	0.298	17	0.105	R.LDQPIILTGFSALNK.L
R2/RRR2-3/2	1632.001	1630.910	56.371	0.313	454.009	0.291	15	0.104	R.LDQPIILTGFSALNK.L
R2/RRR2-16/2	1518.191	1518.782	-1051.435	0.360	2554.551	0.418	21	0.332	K.ASILLLQDAAAYLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1518.688	1518.782	-62.368	0.421	2337.545	0.458	21	0.301	K.ASILLLQDAAAYLR.K
R2/RRR2-16/2	1518.607	1518.782	-115.826	0.424	2313.187	0.435	21	0.290	K.ASILLLQDAAAYLR.K
R2/RRR2-17/2	1518.754	1518.782	-18.994	0.479	2273.532	0.444	20	0.284	K.ASILLLQDAAAYLR.K
R2/RRR2-16/2	1101.475	1102.180	-1552.930	0.423	1014.502	0.415	17	0.135	K.NVDEAVEGLR.A
R2/RRR2-16/2	1146.864	1147.288	-370.365	0.432	972.729	0.405	16	0.130	K.ALAAEM*GPNTR.V
R2/RRR2-16/2	1102.006	1102.180	-158.390	0.493	958.512	0.382	16	0.129	K.NVDEAVEGLR.A
R2/RRR2-17/2	1517.444	1518.782	-1545.994	0.305	683.738	0.290	16	0.106	K.ASILLLQDAAAYLR.K
R2/RRR2-16/2	1582.307	1582.734	-270.408	0.527	2624.329	0.492	21	0.372	R.SNVGELLEYSLETK.K
R2/RRR2-16/2	1582.084	1582.734	-1046.042	0.434	1887.787	0.448	20	0.225	R.SNVGELLEYSLETK.K
R2/RRR2-16/2	1581.667	1582.734	-1310.983	0.397	1875.480	0.428	21	0.219	R.SNVGELLEYSLETK.K
R2/RRR2-16/2	1471.193	1471.679	-331.943	0.532	1617.427	0.508	19	0.207	R.KYDAFIASDSLIK.Q
R2/RRR2-16/3	1490.294	1490.622	-220.487	0.557	1459.594	0.498	31	0.151	K.HGGIDSM*SADDLKK.L
R2/RRR2-16/3	1490.530	1490.622	-61.506	0.556	1292.909	0.510	30	0.137	K.HGGIDSM*SADDLKK.L
R2/RRR2-16/3	1582.838	1582.734	66.197	0.489	1424.260	0.411	27	0.128	R.SNVGELLEYSLETK.K
R2/RRR2-16/3	1490.166	1490.622	-306.654	0.510	925.312	0.480	26	0.103	K.HGGIDSM*SADDLKK.L
R2/RRR2-21/2	1245.157	1245.385	-183.639	0.464	1204.658	0.558	18	0.172	R.IGVAM*DYSASSK.R
R2/RRR2-21/2	1256.350	1256.479	-102.776	0.428	1331.443	0.362	15	0.147	-.ALDWAIANLLR.-
R2/RRR2-22/2	1255.947	1256.479	-1223.112	0.377	667.058	0.291	14	0.107	R.ALDWAIANLLR.R
R2/RRR2-22/3	1401.657	1401.571	61.557	0.450	826.525	0.477	25	0.095	R.IGVAM*DYSASSKR.A
R2/RRR2-17/3	1403.764	1403.520	173.767	0.547	2184.414	0.381	30	0.221	K.IKSEGEAEAAAAQK.S
R2/RRR2-16/3	1403.405	1403.520	-82.289	0.523	1980.396	0.344	29	0.175	K.IKSEGEAEAAAAQK.S
R2/RRR2-16/3	1403.272	1403.520	-177.574	0.567	1766.065	0.407	29	0.163	K.IKSEGEAEAAAAQK.S
R2/RRR2-13/2	1745.510	1746.001	-281.810	0.553	2322.850	0.489	23	0.313	K.GVDVILDNIGGLYLQR.N
R2/RRR2-13/2	942.914	943.126	-225.562	0.403	943.135	0.325	14	0.119	R.LTIQAAGLR.N
R2/RRR2-13/2	988.224	988.160	65.031	0.326	1015.041	0.301	14	0.119	K.ALIVSEVEK.N
R2/RRR2-13/2	988.309	988.160	150.630	0.369	822.681	0.288	14	0.113	K.ALIVSEVEK.N
R2/RRR2-13/2	989.145	988.160	-15.362	0.412	798.181	0.246	14	0.110	K.ALIVSEVEK.N
R2/RRR2-20/2	1324.015	1324.593	-1195.581	0.505	1685.090	0.398	17	0.186	R.VLQAM*QLM*TEK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1324.073	1324.593	-1151.235	0.469	1600.148	0.392	17	0.176	R.VLQAM*QLM*TEK.R
R2/RRR2-20/2	1324.080	1324.593	-1146.144	0.487	1543.062	0.387	17	0.169	R.VLQAM*QLM*TEK.R
R2/RRR2-20/2	945.864	946.083	-233.014	0.483	951.301	0.427	15	0.136	K.SIAGIVTER.D
R2/RRR2-20/2	945.508	946.083	-1671.509	0.449	998.280	0.388	15	0.132	K.SIAGIVTER.D
R2/RRR2-20/2	945.669	946.083	-439.050	0.413	848.446	0.336	14	0.119	K.SIAGIVTER.D
R2/RRR2-21/2	945.408	946.083	-1776.973	0.398	769.168	0.308	13	0.113	K.SIAGIVTER.D
R2/RRR2-20/2	1292.166	1292.594	-332.641	0.242	490.467	0.248	13	0.103	-.VLQAMQLMTEK.-
R2/RRR2-20/2	998.947	999.102	-154.875	0.362	1107.604	0.527	15	0.071	R.LNAYIQGGY.-
R2/RRR2-20/2	999.321	999.102	220.216	0.295	1064.618	0.504	15	0.065	R.LNAYIQGGY.-
R2/RRR2-20/2	998.279	999.102	-1831.326	0.261	841.155	0.479	13	0.038	R.LNAYIQGGY.-
R2/RRR2-6/2	1774.227	1775.041	-1025.369	0.514	3023.182	0.529	25	0.484	K.IPIDYSWAQELGLIR.K
R2/RRR2-6/2	1774.443	1775.041	-902.769	0.549	2748.158	0.570	24	0.431	K.IPIDYSWAQELGLIR.K
R2/RRR2-6/2	1775.306	1775.041	149.822	0.583	2412.270	0.551	23	0.347	K.IPIDYSWAQELGLIR.K
R2/RRR2-6/2	1413.081	1413.514	-307.123	0.525	1535.042	0.485	21	0.189	R.FGGALDGAAEEFTK.A
R2/RRR2-6/2	1414.281	1413.514	-165.145	0.569	1335.605	0.555	22	0.185	R.FGGALDGAAEEFTK.A
R2/RRR2-6/2	1414.432	1413.514	-58.136	0.547	1299.179	0.561	22	0.183	R.FGGALDGAAEEFTK.A
R2/RRR2-6/2	1620.006	1618.896	68.352	0.337	1076.128	0.433	18	0.134	K.ILVLLGEVGGVEEYK.V
R2/RRR2-11/2	1494.611	1494.781	-114.327	0.535	2791.820	0.520	23	0.415	K.MVGYALQAAEILSK.E
R2/RRR2-11/2	1510.083	1510.781	-1127.282	0.450	2447.366	0.488	24	0.330	K.M*VGYALQAAEILSK.E
R2/RRR2-11/2	1494.844	1494.781	41.886	0.497	2474.880	0.456	23	0.324	K.MVGYALQAAEILSK.E
R2/RRR2-11/2	1510.917	1510.781	90.641	0.487	2359.917	0.467	23	0.306	K.M*VGYALQAAEILSK.E
R2/RRR2-12/2	1510.533	1510.781	-164.579	0.437	2275.693	0.400	23	0.270	K.M*VGYALQAAEILSK.E
R2/RRR2-11/2	1510.389	1510.781	-260.249	0.490	2129.466	0.459	23	0.263	K.M*VGYALQAAEILSK.E
R2/RRR2-12/2	1511.290	1510.781	-325.391	0.493	1941.978	0.481	24	0.240	K.M*VGYALQAAEILSK.E
R2/RRR2-12/2	1201.164	1201.355	-158.973	0.419	1675.889	0.399	18	0.186	K.EGISAEVINLR.S
R2/RRR2-11/2	1495.512	1494.781	-180.817	0.495	1424.377	0.506	20	0.180	K.MVGYALQAAEILSK.E
R2/RRR2-11/2	1202.070	1201.355	-237.995	0.483	1393.615	0.390	18	0.157	K.EGISAEVINLR.S
R2/RRR2-12/2	1201.266	1201.355	-73.956	0.406	1412.610	0.294	17	0.141	K.EGISAEVINLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1705.265	1704.929	197.489	0.464	776.187	0.480	20	0.128	R.IAGADVPM*PYAANLER.M
R2/RRR2-11/2	1201.453	1201.355	82.177	0.362	993.350	0.319	18	0.121	K.EGISAEVINLR.S
R2/RRR2-11/2	1688.336	1688.930	-946.490	0.405	680.196	0.446	20	0.120	R.IAGADVPMPYAANLER.M
R2/RRR2-11/2	1704.430	1704.929	-293.545	0.460	662.643	0.436	19	0.119	R.IAGADVPM*PYAANLER.M
R2/RRR2-11/2	1704.173	1704.929	-1033.307	0.424	596.900	0.459	18	0.118	R.IAGADVPM*PYAANLER.M
R2/RRR2-11/2	1688.252	1688.930	-996.433	0.389	631.680	0.437	19	0.117	R.IAGADVPMPYAANLER.M
R2/RRR2-11/2	1202.222	1201.355	-110.764	0.378	784.535	0.310	16	0.114	K.EGISAEVINLR.S
R2/RRR2-13/2	1438.287	1438.522	-163.325	0.497	1957.199	0.530	21	0.259	R.ELAEEGYSGVEVR.V
R2/RRR2-13/2	1438.058	1438.522	-323.159	0.490	1996.913	0.507	21	0.259	R.ELAEEGYSGVEVR.V
R2/RRR2-13/2	1438.535	1438.522	9.055	0.483	1927.556	0.504	21	0.247	R.ELAEEGYSGVEVR.V
R2/RRR2-13/2	1228.219	1228.463	-199.234	0.391	564.842	0.492	17	0.125	R.VTPTVTDIIIR.A
R2/RRR2-13/2	1228.358	1228.463	-85.781	0.272	419.625	0.325	15	0.108	R.VTPTVTDIIIR.A
R2/RRR2-13/3	1582.502	1582.704	-128.024	0.400	597.344	0.521	23	0.093	R.ATHTQEVLGEQGRR.I
R2/RRR2-13/3	1583.049	1582.704	218.784	0.317	443.158	0.331	21	0.074	R.ATHTQEVLGEQGRR.I
R2/RRR2-13/3	1582.405	1582.704	-189.428	0.229	478.693	0.350	22	0.070	R.ATHTQEVLGEQGRR.I
R2/RRR2-13/2	1846.162	1847.104	-1055.378	0.502	2114.934	0.541	21	0.289	R.IM*YADFYSGVYDMVR.N
R2/RRR2-13/2	1863.405	1863.104	162.121	0.532	1953.854	0.504	20	0.250	R.IM*YADFYSGVYDM*VR.N
R2/RRR2-13/2	1545.226	1545.639	-268.022	0.534	1263.647	0.505	19	0.166	K.FNDLSTNHNNQLK.T
R2/RRR2-13/2	1544.918	1545.639	-1117.173	0.563	1331.121	0.461	20	0.164	K.FNDLSTNHNNQLK.T
R2/RRR2-13/2	1545.190	1545.639	-290.928	0.489	1242.840	0.400	20	0.146	K.FNDLSTNHNNQLK.T
R2/RRR2-13/3	1673.513	1673.812	-178.640	0.476	981.851	0.482	26	0.106	K.KFNDLSTNHNNQLK.T
R2/RRR2-13/3	1673.543	1673.812	-160.968	0.462	877.409	0.481	27	0.100	K.KFNDLSTNHNNQLK.T
R2/RRR2-13/3	1674.070	1673.812	154.925	0.430	969.960	0.336	26	0.081	K.KFNDLSTNHNNQLK.T
R2/RRR2-16/3	1976.276	1975.066	106.887	0.522	1954.707	0.628	35	0.286	R.ASGDYAIVISHNPDNGTSR.I
R2/RRR2-16/3	1974.527	1975.066	-781.563	0.481	1395.716	0.589	32	0.177	R.ASGDYAIVISHNPDNGTSR.I
R2/RRR2-14/3	1975.894	1975.066	-87.261	0.439	1464.620	0.511	30	0.163	R.ASGDYAIVISHNPDNGTSR.I
R2/RRR2-15/2	1254.433	1254.504	-56.474	0.397	1089.296	0.365	18	0.130	R.ATLSIGNVLPIR.S
R2/RRR2-14/2	1033.104	1033.188	-81.308	0.400	1064.324	0.367	16	0.129	R.AM*IGQVAGGGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1254.221	1254.504	-226.439	0.426	1006.345	0.364	18	0.127	R.ATLSIGNVLPIR.S
R2/RRR2-13/2	1255.411	1254.504	-74.278	0.398	928.244	0.400	17	0.127	R.ATLSIGNVLPIR.S
R2/RRR2-14/2	1254.222	1254.504	-225.854	0.389	1009.799	0.370	17	0.126	R.ATLSIGNVLPIR.S
R2/RRR2-16/2	1254.247	1254.504	-205.154	0.292	1130.667	0.321	17	0.125	R.ATLSIGNVLPIR.S
R2/RRR2-14/2	1032.733	1033.188	-441.628	0.368	961.829	0.381	15	0.124	R.AM*IGQVAGGGR.T
R2/RRR2-1/3	1975.272	1975.066	105.019	0.455	834.317	0.586	26	0.119	R.ASGDYAIVISHNPDNGTSR.I
R2/RRR2-15/2	1254.278	1254.504	-180.940	0.353	906.465	0.334	16	0.117	R.ATLSIGNVLPIR.S
R2/RRR2-14/2	1032.451	1033.188	-1687.043	0.316	686.162	0.403	14	0.114	R.AM*IGQVAGGGR.T
R2/RRR2-15/2	1253.807	1254.504	-1357.908	0.179	729.535	0.237	14	0.102	R.ATLSIGNVLPIR.S
R2/RRR2-17/2	1255.672	1254.504	134.500	0.260	548.010	0.180	13	0.101	-.ATLSIGNVLPIR.-
R2/RRR2-1/2	1254.279	1254.504	-180.159	0.262	533.906	0.145	12	0.096	-.ATLSIGNVLPIR.-
R2/RRR2-15/3	1976.910	1975.066	-78.700	0.331	1030.510	0.382	27	0.092	R.ASGDYAIVISHNPDNGTSR.I
R2/RRR2-14/3	1975.632	1975.066	-220.019	0.354	792.856	0.418	25	0.086	R.ASGDYAIVISHNPDNGTSR.I
R2/RRR2-21/2	1737.176	1737.720	-891.195	0.570	2152.962	0.568	25	0.302	K.DATDDFEDVGHSTTAR.A
R2/RRR2-21/2	1737.216	1737.720	-867.916	0.586	1956.934	0.559	24	0.265	K.DATDDFEDVGHSTTAR.A
R2/RRR2-22/2	1737.181	1737.720	-888.443	0.534	1960.242	0.511	23	0.251	K.DATDDFEDVGHSTTAR.A
R2/RRR2-21/2	1737.284	1737.720	-251.501	0.565	1740.654	0.605	23	0.245	K.DATDDFEDVGHSTTAR.A
R2/RRR2-22/2	1901.582	1902.051	-247.220	0.562	1282.258	0.617	26	0.192	K.FLEDHPGGDDVLLSSTAK.D
R2/RRR2-22/2	1901.365	1902.051	-889.643	0.554	1291.846	0.584	26	0.186	K.FLEDHPGGDDVLLSSTAK.D
R2/RRR2-22/2	1017.623	1018.186	-1540.903	0.339	327.664	0.453	13	0.118	K.VLTLEEVSK.H
R2/RRR2-22/2	1017.872	1018.186	-309.150	0.336	427.649	0.414	15	0.118	K.VLTLEEVSK.H
R2/RRR2-22/2	1018.057	1018.186	-126.893	0.270	415.629	0.367	15	0.112	K.VLTLEEVSK.H
R2/RRR2-21/3	1737.114	1737.720	-927.110	0.310	1030.492	0.477	29	0.107	K.DATDDFEDVGHSTTAR.A
R2/RRR2-21/3	1738.677	1737.720	-24.838	0.366	911.557	0.460	29	0.098	K.DATDDFEDVGHSTTAR.A
R2/RRR2-22/3	1737.206	1737.720	-873.779	0.359	648.575	0.503	23	0.094	K.DATDDFEDVGHSTTAR.A
R2/RRR2-22/3	1737.888	1737.720	96.926	0.353	587.027	0.487	25	0.090	K.DATDDFEDVGHSTTAR.A
R2/RRR2-20/3	1737.324	1737.720	-228.528	0.363	631.904	0.476	24	0.090	K.DATDDFEDVGHSTTAR.A
R2/RRR2-22/3	1902.028	1902.051	-12.019	0.442	995.104	0.378	30	0.089	K.FLEDHPGGDDVLLSSTAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/3	1737.173	1737.720	-892.878	0.327	673.976	0.454	24	0.088	K.DATDDFEDVGHSTTAR.A
R2/RRR2-21/3	1737.534	1737.720	-107.159	0.313	732.910	0.430	27	0.086	K.DATDDFEDVGHSTTAR.A
R2/RRR2-22/3	1903.066	1902.051	7.738	0.457	763.214	0.400	28	0.083	K.FLEDHPGGDDVLLSSTAK.D
R2/RRR2-22/3	1902.062	1902.051	5.940	0.411	587.375	0.385	23	0.073	-.FLEDHPGGDDVLLSSTAK.-
R2/RRR2-21/3	1901.835	1902.051	-114.092	0.351	789.998	0.200	24	0.062	K.FLEDHPGGDDVLLSSTAK.D
R2/RRR2-24/2	1465.510	1465.720	-143.331	0.455	1559.627	0.511	19	0.198	K.TVTSLDVVYALKR.Q
R2/RRR2-24/2	1228.874	1229.385	-1233.482	0.457	1593.574	0.455	17	0.193	R.ISAM*IYEETR.G
R2/RRR2-24/2	1465.258	1465.720	-316.074	0.464	1338.528	0.534	18	0.178	K.TVTSLDVVYALKR.Q
R2/RRR2-23/2	1326.181	1326.527	-261.699	0.423	1254.616	0.406	18	0.147	R.DNIQGITKPAIR.R
R2/RRR2-23/2	1325.605	1326.527	-1454.030	0.434	1064.616	0.486	17	0.146	R.DNIQGITKPAIR.R
R2/RRR2-24/2	1326.226	1326.527	-227.901	0.464	995.277	0.463	17	0.139	R.DNIQGITKPAIR.R
R2/RRR2-24/2	1326.261	1326.527	-201.123	0.470	1185.429	0.380	18	0.138	R.DNIQGITKPAIR.R
R2/RRR2-23/2	1326.227	1326.527	-226.700	0.434	992.023	0.437	17	0.135	R.DNIQGITKPAIR.R
R2/RRR2-24/2	1466.360	1465.720	-246.283	0.460	898.787	0.465	17	0.132	K.TVTSLDVVYALKR.Q
R2/RRR2-24/2	1326.305	1326.527	-167.606	0.475	968.297	0.411	16	0.129	R.DNIQGITKPAIR.R
R2/RRR2-14/2	1618.209	1618.813	-993.712	0.575	2488.362	0.439	22	0.319	K.VLNFAIDDAILEER.I
R2/RRR2-15/2	1619.532	1618.813	-173.699	0.603	2353.589	0.485	22	0.308	K.VLNFAIDDAILEER.I
R2/RRR2-14/2	1619.341	1618.813	-291.972	0.610	2384.898	0.458	22	0.304	K.VLNFAIDDAILEER.I
R2/RRR2-14/2	1618.488	1618.813	-200.969	0.580	2362.237	0.447	22	0.297	K.VLNFAIDDAILEER.I
R2/RRR2-15/2	1618.255	1618.813	-965.160	0.529	2460.009	0.317	22	0.274	K.VLNFAIDDAILEER.I
R2/RRR2-14/2	1611.411	1611.778	-228.673	0.526	1752.449	0.500	23	0.218	K.TPGLDDVTGEPLIQR.K
R2/RRR2-15/2	1618.390	1618.813	-262.034	0.471	1938.000	0.290	22	0.190	K.VLNFAIDDAILEER.I
R2/RRR2-15/2	1612.502	1611.778	-171.647	0.537	1329.372	0.587	21	0.188	K.TPGLDDVTGEPLIQR.K
R2/RRR2-14/2	1612.466	1611.778	-194.051	0.550	1381.606	0.537	21	0.182	K.TPGLDDVTGEPLIQR.K
R2/RRR2-14/2	1612.440	1611.778	-210.455	0.540	1337.817	0.531	21	0.176	K.TPGLDDVTGEPLIQR.K
R2/RRR2-15/2	1611.586	1611.778	-119.475	0.503	1327.873	0.521	21	0.173	K.TPGLDDVTGEPLIQR.K
R2/RRR2-15/2	1612.368	1611.778	-255.267	0.532	1235.658	0.545	20	0.169	K.TPGLDDVTGEPLIQR.K
R2/RRR2-14/3	1619.198	1618.813	238.815	0.430	1567.245	0.339	27	0.124	K.VLNFAIDDAILEER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/3	1618.641	1618.813	-106.596	0.304	858.753	0.200	23	0.062	K.VLNFAIDDAILEER.I
R2/RRR2-16/2	1610.096	1610.752	-1031.569	0.466	2283.692	0.502	21	0.312	R.FALENQAVNEATFR.C
R2/RRR2-16/2	1210.557	1211.393	-1521.318	0.320	669.894	0.452	19	0.120	R.VPIVPSDGAISR.T
R2/RRR2-16/2	1211.092	1211.393	-248.960	0.331	398.004	0.468	15	0.113	-.VPIVPSDGAISR.-
R2/RRR2-16/2	1211.145	1211.393	-205.480	0.296	500.443	0.383	17	0.110	-.VPIVPSDGAISR.-
R2/RRR2-16/3	1502.789	1502.695	62.594	0.323	1173.733	0.137	26	0.060	R.TRETTLPVNELTK.S
R2/RRR2-18/2	1521.122	1520.840	186.287	0.514	1973.958	0.435	20	0.232	K.NILFVISKPDVFK.S
R2/RRR2-15/2	1528.388	1528.645	-168.677	0.528	1296.885	0.595	20	0.186	K.SPNSDTYVIFGEAK.I
R2/RRR2-15/2	1520.004	1520.840	-1211.765	0.526	1675.621	0.406	18	0.184	K.NILFVISKPDVFK.S
R2/RRR2-18/2	1528.602	1528.645	-28.243	0.497	1384.231	0.528	20	0.181	K.SPNSDTYVIFGEAK.I
R2/RRR2-15/2	1528.460	1528.645	-121.327	0.539	1314.587	0.559	20	0.181	K.SPNSDTYVIFGEAK.I
R2/RRR2-15/2	1528.429	1528.645	-141.356	0.525	1270.823	0.578	20	0.180	K.SPNSDTYVIFGEAK.I
R2/RRR2-18/2	1529.193	1528.645	-296.614	0.537	1310.986	0.519	20	0.172	K.SPNSDTYVIFGEAK.I
R2/RRR2-18/2	1528.163	1528.645	-316.363	0.460	1325.597	0.487	20	0.167	K.SPNSDTYVIFGEAK.I
R2/RRR2-15/2	1044.197	1044.184	12.944	0.483	1026.366	0.450	16	0.142	K.APDLSNVISK.A
R2/RRR2-15/2	1043.889	1044.184	-283.207	0.499	869.605	0.465	15	0.135	K.APDLSNVISK.A
R2/RRR2-15/2	1043.564	1044.184	-1556.509	0.455	723.460	0.479	14	0.129	K.APDLSNVISK.A
R2/RRR2-18/2	1519.454	1520.840	-1574.810	0.357	1069.615	0.322	17	0.122	K.NILFVISKPDVFK.S
R2/RRR2-15/2	1520.392	1520.840	-295.754	0.345	935.586	0.236	16	0.107	K.NILFVISKPDVFK.S
R2/RRR2-15/2	1519.377	1520.840	-1625.657	0.380	1004.596	0.222	15	0.106	K.NILFVISKPDVFK.S
R2/RRR2-9/2	1556.387	1556.786	-257.526	0.578	2716.198	0.471	22	0.377	K.MFVLDEADEMLSR.G
R2/RRR2-9/2	1572.269	1572.786	-967.885	0.445	2423.390	0.425	21	0.305	K.MFVLDEADEM*LSR.G
R2/RRR2-9/2	1556.512	1556.786	-176.799	0.562	2332.114	0.475	21	0.301	K.MFVLDEADEMLSR.G
R2/RRR2-9/2	1556.325	1556.786	-297.658	0.572	2284.161	0.496	21	0.299	K.MFVLDEADEMLSR.G
R2/RRR2-9/2	1588.145	1588.785	-1035.927	0.530	2163.048	0.500	22	0.281	K.M*FVLDEADEM*LSR.G
R2/RRR2-9/2	1588.294	1588.785	-310.057	0.530	1878.239	0.503	21	0.236	K.M*FVLDEADEM*LSR.G
R2/RRR2-9/2	1572.251	1572.786	-979.032	0.505	1695.394	0.427	20	0.192	K.MFVLDEADEM*LSR.G
R2/RRR2-9/2	1572.242	1572.786	-984.722	0.460	1451.125	0.382	18	0.157	K.MFVLDEADEM*LSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1369.399	1369.466	-49.140	0.425	1027.696	0.519	19	0.148	K.GHDVIAQAQSGTGK.T
R2/RRR2-10/2	1084.885	1085.322	-404.096	0.326	1197.237	0.434	17	0.145	R.VLIATDLLAR.G
R2/RRR2-23/2	1319.994	1320.493	-379.017	0.410	1766.661	0.469	17	0.215	K.SEIEYYAM*LGK.V
R2/RRR2-23/2	1395.064	1394.681	275.350	0.362	842.804	0.414	16	0.122	K.LIILANNCPPLR.K
R2/RRR2-23/2	1395.292	1394.681	-279.449	0.368	687.884	0.408	16	0.117	K.LIILANNCPPLR.K
R2/RRR2-23/2	1319.749	1320.493	-1325.832	0.333	1027.153	0.266	15	0.114	K.SEIEYYAM*LGK.V
R2/RRR2-23/2	1394.341	1394.681	-244.867	0.350	367.860	0.398	14	0.112	K.LIILANNCPPLR.K
R2/RRR2-5/2	1571.283	1571.718	-277.370	0.499	2296.410	0.553	22	0.326	R.GLEGLTVQQAIDGNR.L
R2/RRR2-5/2	1572.124	1571.718	259.603	0.494	1920.092	0.560	21	0.260	R.GLEGLTVQQAIDGNR.L
R2/RRR2-5/2	1649.391	1649.744	-214.351	0.522	1716.888	0.554	20	0.227	R.YGDQTSTITAAHVER.G
R2/RRR2-5/3	1648.100	1649.744	-2217.744	0.521	1464.088	0.667	27	0.210	R.YGDQTSTITAAHVER.G
R2/RRR2-5/3	1649.738	1649.744	-3.579	0.542	1402.238	0.665	28	0.199	R.YGDQTSTITAAHVER.G
R2/RRR2-5/2	1650.201	1649.744	277.889	0.515	1459.124	0.539	19	0.190	R.YGDQTSTITAAHVER.G
R2/RRR2-4/3	1650.729	1649.744	-8.954	0.526	1291.653	0.646	28	0.179	R.YGDQTSTITAAHVER.G
R2/RRR2-5/2	1648.817	1649.744	-1171.898	0.492	1193.572	0.564	19	0.169	R.YGDQTSTITAAHVER.G
R2/RRR2-6/3	1649.935	1649.744	116.303	0.503	1167.499	0.636	26	0.162	R.YGDQTSTITAAHVER.G
R2/RRR2-3/3	1649.033	1649.744	-1040.595	0.492	1254.906	0.599	26	0.161	R.YGDQTSTITAAHVER.G
R2/RRR2-4/3	1649.612	1649.744	-80.287	0.505	1197.225	0.607	25	0.158	R.YGDQTSTITAAHVER.G
R2/RRR2-5/2	1570.614	1571.718	-1343.204	0.393	1294.067	0.457	18	0.156	R.GLEGLTVQQAIDGNR.L
R2/RRR2-3/3	1650.387	1649.744	-216.827	0.506	1220.307	0.595	27	0.156	R.YGDQTSTITAAHVER.G
R2/RRR2-5/3	1649.834	1649.744	55.086	0.523	1116.330	0.613	25	0.151	R.YGDQTSTITAAHVER.G
R2/RRR2-2/3	1650.880	1649.744	82.714	0.457	1047.877	0.621	25	0.146	R.YGDQTSTITAAHVER.G
R2/RRR2-4/3	1648.898	1649.744	-1122.879	0.495	935.745	0.618	24	0.136	R.YGDQTSTITAAHVER.G
R2/RRR2-2/3	1649.713	1649.744	-18.608	0.472	923.282	0.585	23	0.128	R.YGDQTSTITAAHVER.G
R2/RRR2-5/2	1399.300	1399.685	-275.720	0.439	978.912	0.398	16	0.126	R.EILAGVNPM*VIAR.L
R2/RRR2-1/3	1650.280	1649.744	-282.055	0.502	951.265	0.565	24	0.125	R.YGDQTSTITAAHVER.G
R2/RRR2-7/3	1649.997	1649.744	154.031	0.430	835.489	0.595	25	0.123	R.YGDQTSTITAAHVER.G
R2/RRR2-3/3	1649.035	1649.744	-1039.368	0.401	870.662	0.574	24	0.121	R.YGDQTSTITAAHVER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/3	1649.971	1649.744	138.117	0.458	589.245	0.605	21	0.112	R.YGDQTSTITAAHVER.G
R2/RRR2-7/3	1649.963	1649.744	133.109	0.450	755.638	0.551	23	0.111	R.YGDQTSTITAAHVER.G
R2/RRR2-5/2	1384.354	1383.685	-239.823	0.327	723.943	0.323	15	0.108	R.EILAGVNPMVIAR.L
R2/RRR2-2/3	1649.602	1649.744	-86.077	0.376	490.086	0.529	19	0.097	R.YGDQTSTITAAHVER.G
R2/RRR2-1/3	1650.972	1649.744	138.552	0.406	731.015	0.469	23	0.096	R.YGDQTSTITAAHVER.G
R2/RRR2-1/3	1648.404	1649.744	-1423.698	0.284	521.783	0.405	21	0.085	R.YGDQTSTITAAHVER.G
R2/RRR2-22/2	1225.297	1225.420	-100.684	0.500	1588.014	0.492	20	0.197	R.VLLINEGPNAGK.L
R2/RRR2-21/2	1224.944	1225.420	-389.577	0.502	1525.879	0.495	18	0.189	R.VLLINEGPNAGK.L
R2/RRR2-21/2	1225.142	1225.420	-226.917	0.465	1422.609	0.484	18	0.176	R.VLLINEGPNAGK.L
R2/RRR2-22/2	1225.154	1225.420	-217.221	0.494	1325.306	0.496	19	0.170	R.VLLINEGPNAGK.L
R2/RRR2-22/2	1225.179	1225.420	-196.830	0.548	1259.800	0.498	18	0.164	R.VLLINEGPNAGK.L
R2/RRR2-21/2	1224.925	1225.420	-404.876	0.478	1168.689	0.523	18	0.161	R.VLLINEGPNAGK.L
R2/RRR2-22/2	1131.909	1132.206	-263.131	0.416	1457.664	0.387	18	0.161	R.VLVDGPSSDSR.L
R2/RRR2-22/2	1243.366	1243.350	12.544	0.468	1138.484	0.450	16	0.148	R.SNLTDFDRFK.V
R2/RRR2-22/2	1131.930	1132.206	-245.171	0.401	1286.923	0.383	17	0.146	R.VLVDGPSSDSR.L
R2/RRR2-21/2	1132.045	1132.206	-142.831	0.398	1309.435	0.363	18	0.145	R.VLVDGPSSDSR.L
R2/RRR2-21/2	1131.406	1132.206	-1596.256	0.273	1339.493	0.333	17	0.139	R.VLVDGPSSDSR.L
R2/RRR2-22/2	1242.990	1243.350	-290.738	0.454	949.806	0.460	14	0.136	R.SNLTDFDRFK.V
R2/RRR2-22/2	1131.861	1132.206	-306.411	0.378	1052.593	0.416	16	0.134	R.VLVDGPSSDSR.L
R2/RRR2-21/2	1131.812	1132.206	-349.479	0.418	1049.806	0.377	16	0.130	R.VLVDGPSSDSR.L
R2/RRR2-22/2	1243.283	1243.350	-53.928	0.387	645.788	0.372	13	0.114	R.SNLTDFDRFK.V
R2/RRR2-19/2	1688.354	1687.985	219.379	0.581	2097.034	0.672	24	0.330	R.HVVFGQVIEGM*DIVK.M
R2/RRR2-19/2	1409.970	1409.611	255.419	0.495	1597.428	0.568	19	0.217	K.VYFDISIGNPVGK.N
R2/RRR2-19/2	1994.443	1994.193	125.380	0.631	1303.819	0.658	26	0.203	R.VVIGLYGDDVPQTAENFR.A
R2/RRR2-19/2	1993.502	1994.193	-850.981	0.544	1162.122	0.635	26	0.183	R.VVIGLYGDDVPQTAENFR.A
R2/RRR2-19/2	1410.272	1409.611	-241.493	0.484	1323.836	0.541	19	0.179	K.VYFDISIGNPVGK.N
R2/RRR2-19/2	1993.396	1994.193	-904.340	0.554	1140.453	0.610	25	0.175	R.VVIGLYGDDVPQTAENFR.A
R2/RRR2-20/2	1993.418	1994.193	-893.397	0.507	1032.139	0.605	24	0.163	R.VVIGLYGDDVPQTAENFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/2	1673.503	1671.985	-288.741	0.475	855.898	0.462	20	0.130	R.HVVFGQVIEGMDIVK.M
R2/RRR2-20/3	1996.174	1994.193	-9.766	0.317	869.400	0.321	26	0.071	R.VVIGLYGDDVPQTAENFR.A
R2/RRR2-12/2	1157.945	1158.244	-258.589	0.473	1518.503	0.469	19	0.186	K.VASDDLDPAVR.E
R2/RRR2-12/2	1157.458	1158.244	-1547.528	0.340	1395.812	0.427	19	0.161	K.VASDDLDPAVR.E
R2/RRR2-12/2	1157.403	1158.244	-1594.993	0.419	1393.530	0.401	19	0.159	K.VASDDLDPAVR.E
R2/RRR2-12/2	1108.050	1108.229	-162.498	0.495	920.355	0.487	16	0.140	R.VAEEGLPHGAK.I
R2/RRR2-12/2	1563.212	1563.888	-1075.589	0.382	865.250	0.484	16	0.129	R.GLVMIHPYFLGTSK.V
R2/RRR2-9/2	1584.165	1584.672	-953.623	0.525	1922.057	0.542	25	0.260	K.GFAFVGSGVSGGEEGAR.-
R2/RRR2-9/2	1121.164	1121.225	-54.560	0.492	1199.162	0.407	16	0.146	K.VDNFLANEAK.G
R2/RRR2-9/2	1490.692	1491.628	-1302.367	0.368	979.244	0.396	18	0.126	K.SIVGAHSTEEFVSK.L
R2/RRR2-9/2	1121.060	1121.225	-147.725	0.424	1068.970	0.326	15	0.125	K.VDNFLANEAK.G
R2/RRR2-9/2	1490.505	1491.628	-1428.705	0.311	523.160	0.382	15	0.107	K.SIVGAHSTEEFVSK.L
R2/RRR2-17/2	1298.782	1299.585	-1392.146	0.452	1853.080	0.522	19	0.240	R.TLINNLIIGVTK.G
R2/RRR2-17/2	1299.316	1299.585	-207.084	0.532	1809.291	0.481	19	0.223	R.TLINNLIIGVTK.G
R2/RRR2-17/3	1501.773	1501.669	69.240	0.553	1687.775	0.493	28	0.182	K.SLSHVAVNFSQPSK.N
R2/RRR2-17/2	1501.267	1501.669	-268.775	0.497	1366.600	0.534	20	0.181	K.SLSHVAVNFSQPSK.N
R2/RRR2-17/3	1500.985	1501.669	-1125.573	0.568	1646.981	0.476	28	0.170	K.SLSHVAVNFSQPSK.N
R2/RRR2-17/2	1501.037	1501.669	-1090.450	0.408	1400.842	0.449	20	0.167	K.SLSHVAVNFSQPSK.N
R2/RRR2-17/3	1501.537	1501.669	-88.408	0.567	1667.965	0.440	28	0.161	K.SLSHVAVNFSQPSK.N
R2/RRR2-17/2	1501.127	1501.669	-1030.599	0.434	1293.267	0.469	19	0.160	K.SLSHVAVNFSQPSK.N
R2/RRR2-17/2	870.899	871.016	-134.838	0.350	497.275	0.488	12	0.122	R.LVTVEGPR.G
R2/RRR2-17/2	1298.683	1299.585	-1468.900	0.401	695.731	0.440	15	0.120	R.TLINNLIIGVTK.G
R2/RRR2-17/2	870.501	871.016	-1746.053	0.243	391.524	0.239	12	0.109	R.LVTVEGPR.G
R2/RRR2-17/2	870.262	871.016	-2021.861	0.257	353.646	0.413	11	0.103	-.LVTVEGPR.-
R2/RRR2-15/2	1743.455	1743.942	-279.684	0.493	809.664	0.573	20	0.144	R.ELNAGLAEKDWLLDR.M
R2/RRR2-15/2	983.801	984.133	-338.525	0.344	729.447	0.343	11	0.114	R.GFYQSLLR.E
R2/RRR2-15/2	984.112	984.133	-22.035	0.381	801.257	0.310	11	0.113	R.GFYQSLLR.E
R2/RRR2-15/2	1042.336	1043.114	-1711.634	0.283	781.051	0.330	13	0.111	K.YAASPYTNR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	983.299	984.133	-1871.242	0.313	825.655	0.290	11	0.111	R.GFYQSLLR.E
R2/RRR2-15/2	1042.555	1043.114	-1500.001	0.226	595.513	0.302	12	0.104	K.YAASPYTNR.G
R2/RRR2-9/2	1470.568	1469.712	-97.712	0.563	2392.415	0.538	21	0.339	K.SGLVALNLDLAQVR.Q
R2/RRR2-9/2	1469.971	1469.712	177.194	0.525	2302.299	0.503	21	0.310	K.SGLVALNLDLAQVR.Q
R2/RRR2-9/2	1469.345	1469.712	-250.116	0.455	1632.922	0.451	20	0.192	K.SGLVALNLDLAQVR.Q
R2/RRR2-9/2	1433.275	1432.653	-264.526	0.563	1605.754	0.454	20	0.190	K.WGNIQFPLPFGR.V
R2/RRR2-9/2	1433.230	1432.653	-295.800	0.512	1390.005	0.455	19	0.168	K.WGNIQFPLPFGR.V
R2/RRR2-9/2	1433.354	1432.653	-209.330	0.531	1387.029	0.448	19	0.166	K.WGNIQFPLPFGR.V
R2/RRR2-9/2	1433.330	1432.653	-225.820	0.575	1333.002	0.469	18	0.164	K.WGNIQFPLPFGR.V
R2/RRR2-9/2	1433.117	1432.653	324.340	0.420	930.103	0.348	15	0.118	K.WGNIQFPLPFGR.V
R2/RRR2-9/2	1067.057	1067.131	-69.374	0.405	455.411	0.467	12	0.118	R.GELDDTAAFK.N
R2/RRR2-9/2	1066.931	1067.131	-188.384	0.333	704.889	0.371	14	0.114	R.GELDDTAAFK.N
R2/RRR2-9/2	1432.359	1432.653	-205.629	0.391	893.184	0.262	15	0.108	K.WGNIQFPLPFGR.V
R2/RRR2-15/2	1138.930	1138.169	-211.091	0.419	726.959	0.443	14	0.124	R.AVSAEDNFER.A
R2/RRR2-15/2	1137.917	1138.169	-222.576	0.416	703.194	0.340	14	0.114	R.AVSAEDNFER.A
R2/RRR2-15/2	1137.441	1138.169	-1524.386	0.267	595.971	0.195	13	0.103	R.AVSAEDNFER.A
R2/RRR2-15/3	1145.568	1145.336	203.313	0.489	877.516	0.434	20	0.093	K.LSHPDHVLVK.R
R2/RRR2-15/3	1301.095	1301.522	-329.615	0.494	862.424	0.419	22	0.090	K.LSHPDHVLVKR.A
R2/RRR2-15/3	1301.584	1301.522	47.530	0.523	609.495	0.453	19	0.089	K.LSHPDHVLVKR.A
R2/RRR2-15/3	1145.208	1145.336	-112.549	0.411	739.280	0.423	18	0.085	K.LSHPDHVLVK.R
R2/RRR2-15/3	1145.749	1145.336	361.649	0.457	795.348	0.416	19	0.084	-.LSHPDHVLVK.-
R2/RRR2-15/3	1301.874	1301.522	270.692	0.463	673.988	0.347	20	0.078	K.LSHPDHVLVKR.A
R2/RRR2-23/2	1079.868	1080.176	-286.470	0.548	1737.860	0.574	19	0.238	R.LAGSSAAAFER.C
R2/RRR2-24/2	1080.847	1080.176	-305.128	0.507	1699.173	0.538	19	0.223	R.LAGSSAAAFER.C
R2/RRR2-24/2	1080.059	1080.176	-108.556	0.515	1592.754	0.589	19	0.222	R.LAGSSAAAFER.C
R2/RRR2-23/2	1079.988	1080.176	-174.430	0.500	1650.880	0.546	19	0.219	R.LAGSSAAAFER.C
R2/RRR2-23/2	1079.326	1080.176	-1719.221	0.427	1458.103	0.540	18	0.192	R.LAGSSAAAFER.C
R2/RRR2-24/2	1734.362	1734.963	-926.032	0.520	1120.044	0.467	19	0.145	R.VGGPCGYGVCYLYLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1733.506	1734.963	-1421.743	0.489	1152.621	0.413	19	0.138	R.VGGPCGYGVCYLYLR.R
R2/RRR2-24/2	1734.408	1734.963	-899.606	0.509	1058.712	0.440	19	0.136	R.VGGPCGYGVCYLYLR.R
R2/RRR2-23/2	1733.794	1734.963	-1254.637	0.422	1210.552	0.336	18	0.129	R.VGGPCGYGVCYLYLR.R
R2/RRR2-24/2	1198.382	1199.374	-1667.243	0.330	898.741	0.288	14	0.114	R.TCWYTVQIK.T
R2/RRR2-24/2	1198.604	1199.374	-1481.227	0.343	824.363	0.246	14	0.109	R.TCWYTVQIK.T
R2/RRR2-24/2	1198.466	1199.374	-1597.249	0.285	691.108	0.235	13	0.106	R.TCWYTVQIK.T
R2/RRR2-21/2	1888.289	1888.025	140.533	0.579	1774.837	0.629	28	0.259	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-21/2	1887.660	1888.025	-193.586	0.564	1681.113	0.584	27	0.232	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-21/2	1887.189	1888.025	-975.606	0.533	1476.175	0.644	26	0.220	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-21/3	1887.974	1888.025	-26.603	0.520	1651.417	0.451	34	0.164	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-21/3	1887.507	1888.025	-806.601	0.488	1390.509	0.467	31	0.139	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-21/3	1644.545	1643.819	-167.082	0.561	1130.616	0.524	25	0.128	K.HNSKDDCWLIIGGK.V
R2/RRR2-21/3	1887.951	1888.025	-39.055	0.470	1273.831	0.420	31	0.116	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-20/3	1887.110	1888.025	-1017.567	0.373	1275.087	0.340	31	0.099	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-20/3	1887.694	1888.025	-175.462	0.352	743.677	0.319	27	0.074	K.FLEDHPGGDDVLLSSTGK.D
R2/RRR2-21/3	1642.924	1643.819	-1156.995	0.372	576.716	0.286	19	0.058	-.HNSKDDCWLIIGGK.-
R2/RRR2-24/2	1031.921	1032.173	-244.727	0.444	1323.032	0.489	16	0.170	K.AVQASELVSK.H
R2/RRR2-24/2	1032.068	1032.173	-102.333	0.441	1028.259	0.468	15	0.142	K.AVQASELVSK.H
R2/RRR2-24/3	1530.768	1531.709	-1271.411	0.425	921.827	0.404	26	0.088	K.HGCAYYKEVM*EK.N
R2/RRR2-24/3	1531.598	1531.709	-72.776	0.455	470.081	0.416	21	0.084	K.HGCAYYKEVM*EK.N
R2/RRR2-24/3	1531.014	1531.709	-1109.986	0.412	363.949	0.343	19	0.081	K.HGCAYYKEVM*EK.N
R2/RRR2-24/3	1504.099	1504.716	-1078.390	0.459	765.944	0.373	23	0.080	-.NKQHVVQPPTVEK.-
R2/RRR2-24/3	1504.473	1504.716	-161.683	0.444	801.935	0.344	24	0.080	K.NKQHVVQPPTVEK.C
R2/RRR2-24/3	1504.289	1504.716	-284.767	0.427	720.487	0.329	23	0.078	K.NKQHVVQPPTVEK.C
R2/RRR2-24/3	1504.581	1504.716	-89.775	0.496	957.425	0.300	25	0.077	K.NKQHVVQPPTVEK.C
R2/RRR2-24/3	1505.680	1504.716	-23.762	0.301	660.374	0.246	21	0.069	-.NKQHVVQPPTVEK.-
R2/RRR2-23/3	1503.672	1504.716	-1363.399	0.373	663.821	0.252	20	0.064	-.NKQHVVQPPTVEK.-
R2/RRR2-24/3	1504.598	1504.716	-78.667	0.470	525.429	0.287	20	0.061	-.NKQHVVQPPTVEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1260.101	1260.374	-217.512	0.465	1103.948	0.466	16	0.149	K.SKFDNLYGCR.H
R2/RRR2-8/2	1260.014	1260.374	-286.616	0.506	1041.567	0.481	15	0.146	K.SKFDNLYGCR.H
R2/RRR2-8/2	905.533	906.083	-1715.821	0.357	968.639	0.417	15	0.131	R.ATDVMLAGK.V
R2/RRR2-8/2	1260.010	1260.374	-290.115	0.470	686.452	0.474	13	0.126	K.SKFDNLYGCR.H
R2/RRR2-8/2	1130.065	1130.367	-267.569	0.365	884.697	0.414	13	0.125	K.DIIMVDHMR.K
R2/RRR2-8/2	905.323	906.083	-1948.968	0.320	937.290	0.375	15	0.123	R.ATDVMLAGK.V
R2/RRR2-11/2	1273.164	1273.418	-199.798	0.455	1326.264	0.513	18	0.173	K.GLIDINQDSLGK.A
R2/RRR2-11/2	1272.640	1273.418	-1401.310	0.387	1461.893	0.445	18	0.172	K.GLIDINQDSLGK.A
R2/RRR2-11/2	1073.088	1072.283	-182.854	0.543	1416.458	0.359	17	0.153	K.ISQATLALVR.N
R2/RRR2-11/2	1072.945	1072.283	-316.618	0.458	1232.632	0.383	17	0.144	K.ISQATLALVR.N
R2/RRR2-11/2	1273.239	1273.418	-140.935	0.447	1083.532	0.454	17	0.143	K.GLIDINQDSLGK.A
R2/RRR2-11/2	1157.116	1157.342	-196.134	0.379	745.225	0.337	15	0.113	K.SPIILGNDLSK.I
R2/RRR2-11/2	1156.525	1157.342	-1575.666	0.338	688.455	0.330	14	0.109	K.SPIILGNDLSK.I
R2/RRR2-11/2	1072.943	1072.283	-318.673	0.320	553.399	0.322	13	0.109	K.ISQATLALVR.N
R2/RRR2-24/3	1934.300	1934.877	-817.756	0.456	2354.782	0.440	37	0.299	R.GGGGYGGGGGYGNQGGYGDGNR.G
R2/RRR2-24/3	1934.150	1934.877	-895.681	0.486	2068.313	0.444	35	0.239	R.GGGGYGGGGGYGNQGGYGDGNR.G
R2/RRR2-24/2	1431.925	1432.519	-1116.147	0.365	754.308	0.423	16	0.117	R.GFGFVSFANGDDAK.S
R2/RRR2-24/3	1542.642	1542.675	-21.306	0.380	331.183	0.574	19	0.091	K.SAM*DAM*DGKELEGR.S
R2/RRR2-24/3	1542.530	1542.675	-94.173	0.408	337.063	0.566	21	0.089	-.SAM*DAM*DGKELEGR.-
R2/RRR2-24/3	1542.285	1542.675	-253.516	0.359	438.663	0.534	23	0.086	-.SAM*DAM*DGKELEGR.-
R2/RRR2-2/2	1117.917	1118.219	-271.462	0.383	988.877	0.351	16	0.124	R.ELSEIAEQAK.R
R2/RRR2-3/2	1060.906	1061.133	-214.959	0.354	1174.344	0.252	15	0.121	R.EAQWATAQR.T
R2/RRR2-2/2	1274.173	1274.406	-183.016	0.440	559.908	0.422	16	0.121	R.ELSEIAEQAKR.R
R2/RRR2-2/2	1273.556	1274.406	-1457.023	0.422	562.213	0.417	16	0.120	R.ELSEIAEQAKR.R
R2/RRR2-3/2	1274.171	1274.406	-185.034	0.415	474.000	0.431	15	0.119	R.ELSEIAEQAKR.R
R2/RRR2-2/2	1117.964	1118.219	-229.506	0.481	942.239	0.318	15	0.118	R.ELSEIAEQAK.R
R2/RRR2-3/2	1060.762	1061.133	-351.072	0.362	952.684	0.288	15	0.117	R.EAQWATAQR.T
R2/RRR2-3/2	1060.808	1061.133	-306.967	0.329	1091.385	0.217	15	0.114	R.EAQWATAQR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1060.905	1061.133	-215.306	0.296	1192.561	0.158	15	0.111	R.EAQWATAQR.T
R2/RRR2-11/2	1650.752	1651.932	-1324.576	0.460	2352.506	0.553	24	0.337	R.VPQVGSIAINDGVILR.N
R2/RRR2-11/2	1651.503	1651.932	-260.783	0.527	2237.355	0.528	25	0.306	R.VPQVGSIAINDGVILR.N
R2/RRR2-11/2	1650.819	1651.932	-1283.656	0.446	2159.028	0.526	23	0.291	R.VPQVGSIAINDGVILR.N
R2/RRR2-11/2	1108.152	1107.281	-116.963	0.517	1269.003	0.540	16	0.176	K.YGAVEDILVK.M
R2/RRR2-11/2	1922.557	1922.258	156.051	0.585	955.327	0.596	22	0.155	K.LIANIEAQPSIAVQNVLK.S
R2/RRR2-11/2	1922.823	1922.258	-226.851	0.585	876.616	0.574	22	0.146	K.LIANIEAQPSIAVQNVLK.S
R2/RRR2-11/2	1922.350	1922.258	47.921	0.521	949.564	0.546	22	0.146	K.LIANIEAQPSIAVQNVLK.S
R2/RRR2-11/2	1106.982	1107.281	-271.600	0.258	433.933	0.382	11	0.106	K.YGAVEDILVK.M
R2/RRR2-11/3	1923.005	1922.258	-132.287	0.454	836.815	0.469	24	0.093	K.LIANIEAQPSIAVQNVLK.S
R2/RRR2-17/2	1712.924	1712.926	-1.402	0.623	1871.826	0.544	25	0.247	R.NQDTGLAELPATVAALK.N
R2/RRR2-17/2	1712.368	1712.926	-912.328	0.531	1769.350	0.521	25	0.227	R.NQDTGLAELPATVAALK.N
R2/RRR2-17/2	1712.429	1712.926	-290.900	0.572	1665.816	0.533	24	0.215	R.NQDTGLAELPATVAALK.N
R2/RRR2-17/2	1187.965	1188.359	-332.857	0.382	1682.902	0.330	17	0.174	R.AFAYFVLSGGR.F
R2/RRR2-17/2	1323.940	1324.380	-333.535	0.445	921.322	0.523	16	0.145	K.VVYDEYNHER.H
R2/RRR2-17/2	1324.031	1324.380	-264.435	0.440	774.198	0.525	15	0.137	K.VVYDEYNHER.H
R2/RRR2-17/2	1323.953	1324.380	-324.007	0.402	743.827	0.461	15	0.127	K.VVYDEYNHER.H
R2/RRR2-23/2	1491.786	1490.753	22.474	0.518	1456.083	0.527	19	0.191	K.M*LSSLSAWLVNPR.R
R2/RRR2-23/2	1490.372	1490.753	-255.999	0.321	1535.818	0.381	18	0.166	K.M*LSSLSAWLVNPR.R
R2/RRR2-23/2	1242.048	1242.366	-256.457	0.488	1026.523	0.566	16	0.158	K.HQYLPADAQAK.Q
R2/RRR2-23/2	1242.025	1242.366	-275.192	0.512	882.264	0.525	15	0.142	K.HQYLPADAQAK.Q
R2/RRR2-23/2	1241.719	1242.366	-1330.306	0.494	812.893	0.543	15	0.141	K.HQYLPADAQAK.Q
R2/RRR2-23/2	1232.231	1231.426	-158.841	0.486	701.486	0.345	17	0.117	R.EALGALPLYQR.T
R2/RRR2-23/2	1230.491	1231.426	-1577.270	0.249	450.265	0.354	12	0.104	R.EALGALPLYQR.T
R2/RRR2-13/2	1700.409	1700.782	-220.305	0.498	2050.812	0.576	25	0.289	R.ASGYDVESSASSDAILK.A
R2/RRR2-13/2	1700.386	1700.782	-233.989	0.549	1988.765	0.526	24	0.262	R.ASGYDVESSASSDAILK.A
R2/RRR2-13/2	1625.624	1624.819	-120.101	0.516	1341.266	0.628	23	0.200	K.VYQGQLVGPSTFEAK.L
R2/RRR2-13/2	1625.475	1624.819	-212.308	0.563	1277.992	0.539	23	0.175	K.VYQGQLVGPSTFEAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1427.590	1426.647	-39.933	0.381	761.135	0.493	16	0.127	K.VWVLDGGLPQWR.A
R2/RRR2-13/2	1624.427	1624.819	-241.840	0.525	823.404	0.444	19	0.126	K.VYQGQLVGPSTFEAK.L
R2/RRR2-20/2	1215.964	1215.342	-311.901	0.595	1732.479	0.416	18	0.192	R.SLEGLQANVQR.L
R2/RRR2-19/2	1214.485	1215.342	-1533.334	0.468	1810.406	0.339	18	0.186	R.SLEGLQANVQR.L
R2/RRR2-19/2	1214.893	1215.342	-370.427	0.545	1751.034	0.369	18	0.185	R.SLEGLQANVQR.L
R2/RRR2-15/2	1215.184	1215.342	-130.540	0.569	1679.501	0.398	18	0.183	R.SLEGLQANVQR.L
R2/RRR2-15/2	1214.990	1215.342	-290.485	0.576	1698.230	0.375	18	0.179	R.SLEGLQANVQR.L
R2/RRR2-20/2	1215.208	1215.342	-110.286	0.511	1683.026	0.356	18	0.175	R.SLEGLQANVQR.L
R2/RRR2-15/2	1214.693	1215.342	-1361.214	0.513	1644.177	0.370	18	0.174	R.SLEGLQANVQR.L
R2/RRR2-20/2	1214.483	1215.342	-1535.152	0.444	1633.739	0.352	18	0.171	R.SLEGLQANVQR.L
R2/RRR2-19/2	1214.493	1215.342	-1526.772	0.401	1405.198	0.261	17	0.134	R.SLEGLQANVQR.L
R2/RRR2-15/3	1456.660	1457.659	-1376.511	0.492	1333.728	0.473	27	0.132	K.KYAPTIGISVDHR.R
R2/RRR2-15/3	1458.035	1457.659	258.788	0.508	1371.593	0.460	30	0.130	K.KYAPTIGISVDHR.R
R2/RRR2-15/2	975.107	975.085	22.462	0.435	722.467	0.382	11	0.122	K.HWQNYVK.T
R2/RRR2-15/2	974.863	975.085	-227.840	0.473	752.141	0.345	11	0.119	K.HWQNYVK.T
R2/RRR2-15/2	974.415	975.085	-1718.546	0.400	702.017	0.357	10	0.117	K.HWQNYVK.T
R2/RRR2-15/3	1457.938	1457.659	191.790	0.491	701.307	0.354	25	0.080	K.KYAPTIGISVDHR.R
R2/RRR2-15/2	1669.541	1669.904	-218.511	0.570	1329.188	0.557	22	0.184	R.RVEPYVAYGYPNLK.S
R2/RRR2-15/2	1514.349	1513.718	-244.381	0.496	1137.564	0.534	21	0.163	R.VEPYVAYGYPNLK.S
R2/RRR2-15/2	1670.521	1669.904	-230.036	0.597	1113.218	0.543	21	0.162	R.RVEPYVAYGYPNLK.S
R2/RRR2-15/2	1669.647	1669.904	-154.773	0.558	1166.294	0.518	20	0.160	R.RVEPYVAYGYPNLK.S
R2/RRR2-15/2	1513.247	1513.718	-312.523	0.370	1178.200	0.445	21	0.147	R.VEPYVAYGYPNLK.S
R2/RRR2-15/2	1267.166	1266.429	-208.183	0.393	992.992	0.395	15	0.129	K.EANNFLWPFK.L
R2/RRR2-15/2	1513.024	1513.718	-1122.838	0.313	1062.428	0.383	21	0.129	R.VEPYVAYGYPNLK.S
R2/RRR2-15/2	1266.266	1266.429	-129.238	0.343	997.872	0.326	15	0.120	K.EANNFLWPFK.L
R2/RRR2-16/2	1668.449	1669.904	-1475.932	0.419	595.965	0.451	15	0.116	R.RVEPYVAYGYPNLK.S
R2/RRR2-15/2	1265.667	1266.429	-1395.777	0.292	685.014	0.324	13	0.109	K.EANNFLWPFK.L
R2/RRR2-15/3	1670.420	1669.904	-290.821	0.407	890.593	0.435	22	0.091	-.RVEPYVAYGYPNLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/3	1669.821	1669.904	-50.133	0.435	1102.911	0.328	24	0.085	R.RVEPYVAYGYPNLK.S
R2/RRR2-15/3	1671.172	1669.904	160.871	0.411	1295.646	0.250	26	0.082	R.RVEPYVAYGYPNLK.S
R2/RRR2-12/2	1280.015	1279.421	-317.911	0.540	994.184	0.588	20	0.164	R.LVGDVDFAEVSK.V
R2/RRR2-12/2	1278.783	1279.421	-1285.047	0.451	1044.716	0.514	20	0.152	R.LVGDVDFAEVSK.V
R2/RRR2-12/2	1280.061	1279.421	-281.840	0.377	859.444	0.493	17	0.133	R.LVGDVDFAEVSK.V
R2/RRR2-12/2	1013.350	1013.130	218.254	0.376	731.644	0.348	14	0.117	R.TPNPESIVR.E
R2/RRR2-12/2	1012.894	1013.130	-233.005	0.351	531.209	0.308	13	0.111	R.TPNPESIVR.E
R2/RRR2-12/2	1466.077	1466.834	-1202.054	0.260	706.239	0.343	16	0.107	R.SNIVGLPVSLLLLK.A
R2/RRR2-12/2	1012.972	1013.130	-156.357	0.336	654.373	0.199	14	0.106	R.TPNPESIVR.E
R2/RRR2-2/2	1466.807	1466.834	-18.164	0.322	422.553	0.311	12	0.097	-.SNIVGLPVSLLLLK.-
R2/RRR2-18/2	1466.079	1465.633	304.938	0.546	1713.226	0.530	20	0.221	R.DSSVAVIVFDVASR.Q
R2/RRR2-18/2	1465.186	1465.633	-306.145	0.369	1788.936	0.462	20	0.214	R.DSSVAVIVFDVASR.Q
R2/RRR2-18/2	1465.183	1465.633	-308.569	0.379	1544.011	0.467	19	0.184	R.DSSVAVIVFDVASR.Q
R2/RRR2-18/2	1461.877	1460.722	106.650	0.446	498.753	0.524	19	0.125	K.IAAALPGMETLSSAK.Q
R2/RRR2-17/2	1318.244	1317.432	-143.461	0.490	896.563	0.376	16	0.124	R.LQLWDTAGQER.F
R2/RRR2-16/2	1317.033	1317.432	-304.049	0.426	854.069	0.356	15	0.119	-.LQLWDTAGQER.-
R2/RRR2-19/2	1317.967	1317.432	-354.463	0.416	823.977	0.355	15	0.118	R.LQLWDTAGQER.F
R2/RRR2-16/2	1316.542	1317.432	-1440.512	0.315	911.121	0.326	15	0.117	R.LQLWDTAGQER.F
R2/RRR2-17/2	1317.261	1317.432	-130.555	0.431	824.187	0.322	15	0.115	R.LQLWDTAGQER.F
R2/RRR2-18/2	1316.920	1317.432	-1151.699	0.347	856.826	0.336	15	0.115	-.LQLWDTAGQER.-
R2/RRR2-17/2	1317.131	1317.432	-229.475	0.434	836.055	0.325	15	0.115	-.LQLWDTAGQER.-
R2/RRR2-16/2	1317.162	1317.432	-205.952	0.417	822.355	0.316	15	0.115	R.LQLWDTAGQER.F
R2/RRR2-18/2	1316.957	1317.432	-361.986	0.336	871.605	0.291	15	0.113	R.LQLWDTAGQER.F
R2/RRR2-18/2	1316.920	1317.432	-1151.885	0.371	860.828	0.280	15	0.112	-.LQLWDTAGQER.-
R2/RRR2-18/2	1475.948	1476.721	-1204.942	0.290	485.786	0.439	19	0.112	K.IAAALPGM*ETLSSAK.Q
R2/RRR2-18/2	1317.045	1317.432	-294.750	0.311	804.402	0.240	15	0.108	-.LQLWDTAGQER.-
R2/RRR2-19/2	1317.381	1317.432	-39.184	0.296	333.774	0.380	11	0.107	-.LQLWDTAGQER.-
R2/RRR2-19/2	1317.056	1317.432	-286.752	0.285	574.993	0.237	13	0.106	R.LQLWDTAGQER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1475.753	1476.721	-1337.597	0.173	387.677	0.322	17	0.101	K.IAAALPGM*ETLSSAK.Q
R2/RRR2-15/2	1948.672	1949.071	-205.369	0.621	2410.660	0.693	24	0.401	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-16/3	1949.172	1949.071	51.902	0.560	2505.623	0.523	32	0.357	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-15/3	1949.440	1949.071	189.629	0.554	2471.625	0.510	31	0.343	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-15/2	1948.611	1949.071	-236.981	0.621	2160.769	0.664	23	0.337	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-14/3	1948.834	1949.071	-121.958	0.538	2319.105	0.530	32	0.317	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-16/3	1948.307	1949.071	-908.277	0.466	2433.355	0.458	31	0.315	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-15/3	1948.829	1949.071	-124.880	0.518	2178.840	0.519	29	0.285	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-14/3	1949.323	1949.071	129.720	0.533	2124.944	0.508	31	0.266	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-16/3	1948.414	1949.071	-853.274	0.498	2047.376	0.483	31	0.241	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-14/3	1948.707	1949.071	-187.655	0.493	1954.651	0.459	29	0.217	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-15/3	1948.941	1949.071	-67.108	0.484	1741.362	0.454	29	0.181	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-17/2	1974.533	1974.204	167.321	0.521	1255.211	0.529	22	0.168	R.IYDADPTVLNALANQNIK.V
R2/RRR2-13/3	1949.411	1949.071	174.935	0.450	1217.143	0.455	28	0.120	K.VAHATYAFNDYYQTAGR.A
R2/RRR2-16/2	1681.535	1681.912	-224.816	0.424	865.199	0.365	19	0.116	R.DGNNLIDPPSVVSLLK.A
R2/RRR2-16/2	1681.268	1681.912	-980.327	0.347	983.471	0.318	19	0.115	R.DGNNLIDPPSVVSLLK.A
R2/RRR2-16/2	1680.961	1681.912	-1164.202	0.247	634.416	0.289	16	0.101	R.DGNNLIDPPSVVSLLK.A
R2/RRR2-16/2	1289.052	1289.467	-322.806	0.505	1574.304	0.584	19	0.218	R.VVGGWASPFVNR.V
R2/RRR2-16/2	1290.008	1289.467	-356.545	0.471	1319.232	0.559	19	0.183	R.VVGGWASPFVNR.V
R2/RRR2-16/2	1289.059	1289.467	-317.295	0.455	1369.307	0.530	18	0.181	R.VVGGWASPFVNR.V
R2/RRR2-16/2	1113.171	1113.251	-72.330	0.384	1314.837	0.414	17	0.155	K.VPNLAAWADR.F
R2/RRR2-16/2	1158.079	1158.327	-214.578	0.477	1128.467	0.462	17	0.149	K.IAGVELLDEAK.V
R2/RRR2-16/2	1157.554	1158.327	-1535.870	0.427	1250.602	0.398	17	0.146	K.IAGVELLDEAK.V
R2/RRR2-16/2	1158.063	1158.327	-228.643	0.464	1099.416	0.454	17	0.145	K.IAGVELLDEAK.V
R2/RRR2-21/2	1686.436	1685.902	-276.944	0.526	568.237	0.643	24	0.146	R.LDPGVTASHAFVLETK.V
R2/RRR2-21/2	1344.458	1343.485	-20.617	0.530	1042.331	0.469	18	0.145	K.EAFELVSGEM*SK.T
R2/RRR2-21/2	1687.180	1685.902	165.267	0.514	597.993	0.600	23	0.141	R.LDPGVTASHAFVLETK.V
R2/RRR2-21/2	1685.304	1685.902	-951.245	0.459	671.625	0.510	24	0.132	R.LDPGVTASHAFVLETK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1238.357	1239.405	-1658.409	0.313	943.857	0.365	16	0.121	R.FQGSPAVITYR.V
R2/RRR2-21/2	1239.300	1239.405	-84.728	0.393	781.023	0.386	16	0.120	R.FQGSPAVITYR.V
R2/RRR2-21/2	1239.017	1239.405	-313.905	0.378	762.126	0.362	17	0.118	R.FQGSPAVITYR.V
R2/RRR2-21/2	1684.731	1685.902	-1292.847	0.320	640.459	0.359	20	0.111	R.LDPGVTASHAFVLETK.V
R2/RRR2-13/3	1561.830	1561.786	28.557	0.550	1622.769	0.445	30	0.154	K.RGEEVLKAEEMAAK.Y
R2/RRR2-13/3	1561.877	1561.786	58.188	0.476	1429.974	0.473	28	0.142	K.RGEEVLKAEEMAAK.Y
R2/RRR2-13/2	1263.536	1262.437	78.624	0.381	1070.549	0.354	15	0.128	-.LSAILSWENTK.-
R2/RRR2-13/3	1577.803	1577.785	11.354	0.419	1045.072	0.403	29	0.095	K.RGEEVLKAEEM*AAK.Y
R2/RRR2-14/3	1577.587	1577.785	-125.898	0.429	957.574	0.378	28	0.088	K.RGEEVLKAEEM*AAK.Y
R2/RRR2-13/3	1561.862	1561.786	48.781	0.454	1205.049	0.269	25	0.081	K.RGEEVLKAEEMAAK.Y
R2/RRR2-13/3	1577.632	1577.785	-97.606	0.330	1071.847	0.293	30	0.078	K.RGEEVLKAEEM*AAK.Y
R2/RRR2-13/3	1577.359	1577.785	-270.990	0.356	879.766	0.316	27	0.078	K.RGEEVLKAEEM*AAK.Y
R2/RRR2-14/3	1577.834	1577.785	30.559	0.400	831.509	0.295	28	0.076	K.RGEEVLKAEEM*AAK.Y
R2/RRR2-13/2	865.691	866.033	-396.733	0.370	1151.681	0.378	12	0.073	K.KLIGCFGA.-
R2/RRR2-23/3	1577.841	1577.785	35.564	0.365	1058.104	0.179	28	0.066	K.RGEEVLKAEEM*AAK.Y
R2/RRR2-13/2	865.796	866.033	-275.209	0.338	740.452	0.224	11	0.021	-.KLIGCFGA.-
R2/RRR2-19/3	1761.112	1761.017	54.282	0.502	1239.789	0.520	29	0.137	K.VYFHDVVGGTKPTAIR.V
R2/RRR2-19/2	1215.896	1216.282	-318.061	0.518	791.430	0.455	16	0.130	R.AQGSYTFADQK.T
R2/RRR2-19/2	1217.133	1216.282	-122.887	0.544	689.991	0.468	15	0.127	R.AQGSYTFADQK.T
R2/RRR2-19/2	1215.520	1216.282	-1454.066	0.463	697.429	0.438	15	0.123	R.AQGSYTFADQK.T
R2/RRR2-19/2	887.703	888.004	-340.415	0.369	1146.519	0.244	13	0.120	-.NEVLSAVR.-
R2/RRR2-19/3	1760.239	1761.017	-1013.179	0.476	902.271	0.556	29	0.116	K.VYFHDVVGGTKPTAIR.V
R2/RRR2-19/3	1761.060	1761.017	24.562	0.466	840.721	0.549	29	0.110	K.VYFHDVVGGTKPTAIR.V
R2/RRR2-19/2	887.978	888.004	-29.384	0.331	998.817	0.131	12	0.103	-.NEVLSAVR.-
R2/RRR2-19/2	887.872	888.004	-149.360	0.397	1129.218	0.112	13	0.103	R.NEVLSAVR.E
R2/RRR2-9/2	1585.281	1585.824	-976.122	0.438	2565.689	0.356	21	0.316	R.FELTFYALNPELK.V
R2/RRR2-9/2	1585.675	1585.824	-94.094	0.511	2484.563	0.405	21	0.314	R.FELTFYALNPELK.V
R2/RRR2-9/2	1042.120	1042.170	-47.302	0.490	1348.091	0.470	15	0.169	K.YAELVYAGR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1041.924	1042.170	-235.914	0.477	1209.029	0.501	14	0.162	K.YAELVYAGR.W
R2/RRR2-9/2	1042.067	1042.170	-98.414	0.532	1207.043	0.469	14	0.157	K.YAELVYAGR.W
R2/RRR2-9/2	959.973	960.110	-143.435	0.479	1015.877	0.411	17	0.136	K.ASGASQLVVK.D
R2/RRR2-9/2	959.975	960.110	-141.394	0.478	1033.354	0.403	17	0.136	K.ASGASQLVVK.D
R2/RRR2-9/2	959.542	960.110	-1639.086	0.433	660.138	0.415	16	0.123	K.ASGASQLVVK.D
R2/RRR2-17/2	1629.168	1629.749	-973.425	0.506	1829.921	0.497	20	0.230	R.VNIYYDELDSELR.F
R2/RRR2-17/2	1629.874	1629.749	77.178	0.569	1783.181	0.513	20	0.227	R.VNIYYDELDSELR.F
R2/RRR2-17/2	1629.044	1629.749	-1049.484	0.457	1797.547	0.442	20	0.212	R.VNIYYDELDSELR.F
R2/RRR2-17/2	1063.065	1063.232	-157.858	0.393	1457.532	0.367	15	0.159	R.LSLYNPSLR.V
R2/RRR2-17/2	1062.503	1063.232	-1632.246	0.384	1012.870	0.340	13	0.123	R.LSLYNPSLR.V
R2/RRR2-17/3	1619.643	1619.762	-74.062	0.311	1029.240	0.269	24	0.071	R.LGHATGATPAEFYQR.R
R2/RRR2-7/2	1317.289	1316.486	-150.071	0.573	2486.259	0.524	20	0.350	K.SIQVIVVTDGER.I
R2/RRR2-6/2	1315.763	1316.486	-1313.462	0.494	2339.890	0.541	19	0.328	K.SIQVIVVTDGER.I
R2/RRR2-7/2	1317.396	1316.486	-68.645	0.607	2341.484	0.537	19	0.324	K.SIQVIVVTDGER.I
R2/RRR2-7/2	1316.157	1316.486	-250.575	0.452	2281.774	0.493	19	0.301	K.SIQVIVVTDGER.I
R2/RRR2-6/2	1316.037	1316.486	-342.051	0.475	2132.197	0.540	19	0.289	K.SIQVIVVTDGER.I
R2/RRR2-7/2	1317.139	1316.486	-264.425	0.493	2070.572	0.512	19	0.269	K.SIQVIVVTDGER.I
R2/RRR2-7/2	1802.351	1802.123	127.349	0.493	764.289	0.546	20	0.133	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-7/2	1802.285	1802.123	90.534	0.456	706.610	0.540	20	0.130	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-2/2	1786.267	1785.934	187.081	0.460	953.028	0.435	20	0.129	R.AVFASGSPFDPVEYNGK.I
R2/RRR2-6/2	1801.242	1802.123	-1047.357	0.371	780.726	0.516	20	0.128	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-7/2	1802.313	1802.123	105.885	0.467	760.458	0.495	21	0.128	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-6/2	1801.440	1802.123	-937.137	0.426	508.014	0.525	18	0.120	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-6/2	1800.579	1802.123	-1973.812	0.289	590.469	0.376	18	0.108	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-6/2	1785.346	1786.123	-998.615	0.331	607.286	0.368	17	0.107	R.ILGLGDLGCQGMGIPVGK.L
R2/RRR2-6/3	1801.614	1802.123	-839.872	0.357	1019.141	0.401	27	0.093	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-6/3	1801.631	1802.123	-273.870	0.290	720.939	0.195	24	0.060	R.ILGLGDLGCQGM*GIPVGK.L
R2/RRR2-21/2	1381.126	1381.475	-253.149	0.524	1297.984	0.519	20	0.173	R.WVGAAVDFSEGSR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1381.153	1381.475	-233.819	0.528	1333.810	0.501	20	0.172	R.WVGAAVDFSEGSR.A
R2/RRR2-21/3	1981.703	1982.204	-760.104	0.473	1762.568	0.411	30	0.172	K.YGAKPDAETLDM*LNTVAR.Q
R2/RRR2-21/2	1381.006	1381.475	-340.321	0.529	1245.893	0.511	20	0.167	R.WVGAAVDFSEGSR.A
R2/RRR2-21/3	1981.443	1982.204	-891.634	0.429	1638.575	0.342	29	0.135	K.YGAKPDAETLDM*LNTVAR.Q
R2/RRR2-21/2	958.450	959.084	-1710.256	0.370	872.946	0.337	14	0.121	R.WAADNLLR.A
R2/RRR2-20/2	1380.803	1381.475	-1214.308	0.369	836.596	0.414	15	0.120	R.WVGAAVDFSEGSR.A
R2/RRR2-21/3	1981.860	1982.204	-174.259	0.471	1380.286	0.381	27	0.117	K.YGAKPDAETLDM*LNTVAR.Q
R2/RRR2-20/2	958.583	959.084	-1570.540	0.403	574.852	0.333	12	0.116	R.WAADNLLR.A
R2/RRR2-20/2	958.434	959.084	-1726.379	0.381	589.068	0.290	12	0.113	R.WAADNLLR.A
R2/RRR2-21/2	958.374	959.084	-1788.959	0.391	634.278	0.319	12	0.113	-.WAADNLLR.-
R2/RRR2-20/2	958.396	959.084	-1766.690	0.385	522.141	0.294	11	0.112	R.WAADNLLR.A
R2/RRR2-21/2	958.933	959.084	-157.571	0.445	622.377	0.256	12	0.111	R.WAADNLLR.A
R2/RRR2-14/2	1859.769	1859.285	261.190	0.534	1401.395	0.632	24	0.206	R.LPLVGPLLTPPVSVASVAK.V
R2/RRR2-14/2	1586.475	1586.772	-187.892	0.450	1280.424	0.571	22	0.180	K.INGTANINAISVAAEK.G
R2/RRR2-14/2	962.023	962.080	-58.558	0.430	825.357	0.441	15	0.130	R.ATEAELLSK.F
R2/RRR2-16/2	1860.491	1859.285	110.913	0.423	699.346	0.508	16	0.120	R.LPLVGPLLTPPVSVASVAK.V
R2/RRR2-14/2	961.249	962.080	-1909.962	0.370	501.528	0.425	12	0.109	-.ATEAELLSK.-
R2/RRR2-17/2	1522.481	1522.773	-192.009	0.454	1929.835	0.472	20	0.241	K.FVNDLHALISPPAK.G
R2/RRR2-17/2	1559.280	1558.677	-255.791	0.512	967.020	0.569	22	0.155	K.FVSNGQPGPAQNVDK.S
R2/RRR2-17/2	1559.238	1558.677	-282.418	0.487	962.582	0.521	22	0.146	K.FVSNGQPGPAQNVDK.S
R2/RRR2-17/2	1560.080	1558.677	258.547	0.519	921.619	0.538	21	0.146	K.FVSNGQPGPAQNVDK.S
R2/RRR2-17/2	1558.217	1558.677	-296.511	0.548	820.540	0.509	22	0.138	K.FVSNGQPGPAQNVDK.S
R2/RRR2-17/2	1557.996	1558.677	-1082.254	0.515	778.845	0.510	22	0.136	K.FVSNGQPGPAQNVDK.S
R2/RRR2-17/2	1557.761	1558.677	-1234.033	0.447	706.223	0.446	21	0.125	K.FVSNGQPGPAQNVDK.S
R2/RRR2-17/3	1522.824	1522.773	33.510	0.459	641.635	0.484	27	0.092	K.FVNDLHALISPPAK.G
R2/RRR2-17/3	1705.288	1705.917	-958.231	0.464	893.631	0.423	26	0.091	K.HQELLKNEQYQM*K.L
R2/RRR2-17/3	1705.620	1705.917	-174.340	0.452	760.606	0.442	25	0.089	K.HQELLKNEQYQM*K.L
R2/RRR2-17/3	1705.571	1705.917	-203.419	0.438	788.025	0.435	25	0.089	K.HQELLKNEQYQM*K.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/3	1522.641	1522.773	-86.741	0.440	728.778	0.425	28	0.086	K.FVNDLHALISPPAK.G
R2/RRR2-17/3	1522.591	1522.773	-119.793	0.409	664.085	0.401	27	0.082	K.FVNDLHALISPPAK.G
R2/RRR2-12/2	1591.887	1592.780	-1192.811	0.494	2002.072	0.368	21	0.220	R.NLSDVFWEAVQKR.Q
R2/RRR2-12/2	1592.561	1592.780	-138.201	0.514	1269.675	0.449	19	0.156	R.NLSDVFWEAVQKR.Q
R2/RRR2-12/2	1594.340	1592.780	-276.814	0.523	925.621	0.459	17	0.133	R.NLSDVFWEAVQKR.Q
R2/RRR2-12/2	1348.952	1347.628	241.014	0.381	689.982	0.441	16	0.120	K.SVATILTYPLIR.C
R2/RRR2-12/3	1455.498	1455.600	-70.427	0.487	679.248	0.446	24	0.088	K.FQAELQTQPGAHK.Y
R2/RRR2-12/3	1455.064	1455.600	-1058.901	0.450	804.639	0.406	26	0.085	K.FQAELQTQPGAHK.Y
R2/RRR2-12/2	1450.182	1449.588	-280.185	0.578	1409.080	0.551	19	0.190	K.DGTTLLWDLTEGK.M
R2/RRR2-12/2	1449.132	1449.588	-315.536	0.501	1477.231	0.479	19	0.181	K.DGTTLLWDLTEGK.M
R2/RRR2-12/2	1448.679	1449.588	-1321.628	0.402	1446.170	0.330	19	0.149	K.DGTTLLWDLTEGK.M
R2/RRR2-12/3	1773.111	1771.992	67.241	0.556	1106.104	0.601	29	0.145	K.LDAGAIIHSLCFSPNR.Y
R2/RRR2-12/2	1772.534	1771.992	-259.209	0.493	971.965	0.494	19	0.139	K.LDAGAIIHSLCFSPNR.Y
R2/RRR2-12/3	1771.879	1771.992	-63.691	0.508	803.812	0.628	25	0.125	K.LDAGAIIHSLCFSPNR.Y
R2/RRR2-12/3	1662.413	1662.975	-942.659	0.373	1096.400	0.365	27	0.090	K.LVM*QDLKPEVQAFK.S
R2/RRR2-12/3	1772.052	1771.992	34.048	0.394	710.535	0.477	23	0.089	-.LDAGAIIHSLCFSPNR.-
R2/RRR2-12/3	1663.238	1662.975	158.512	0.321	681.583	0.318	24	0.072	K.LVM*QDLKPEVQAFK.S
R2/RRR2-12/3	1662.843	1662.975	-79.793	0.372	747.792	0.283	25	0.071	K.LVM*QDLKPEVQAFK.S
R2/RRR2-9/2	1388.877	1389.487	-1162.819	0.454	2215.892	0.447	21	0.282	R.VVLDCATADPDGR.K
R2/RRR2-9/2	1441.480	1441.698	-151.751	0.345	791.941	0.350	17	0.112	K.SGLVALNLDIAQVK.E
R2/RRR2-9/2	1441.581	1441.698	-81.417	0.390	618.483	0.301	15	0.104	K.SGLVALNLDIAQVK.E
R2/RRR2-10/2	1594.509	1594.836	-205.450	0.559	1870.898	0.520	24	0.242	R.LPGYLGEYLALTGAR.L
R2/RRR2-10/2	1594.409	1594.836	-268.432	0.542	1648.608	0.501	23	0.207	R.LPGYLGEYLALTGAR.L
R2/RRR2-10/2	1595.313	1594.836	300.190	0.559	1536.890	0.536	22	0.201	R.LPGYLGEYLALTGAR.L
R2/RRR2-10/2	1295.004	1295.424	-324.726	0.397	1428.077	0.373	19	0.156	R.SVVTGDVYEGIR.A
R2/RRR2-10/2	1295.195	1295.424	-177.399	0.301	1339.015	0.261	18	0.130	R.SVVTGDVYEGIR.A
R2/RRR2-11/2	1296.713	1295.424	223.719	0.435	929.952	0.399	16	0.126	R.SVVTGDVYEGIR.A
R2/RRR2-10/3	1009.212	1009.100	112.133	0.493	295.091	0.504	14	0.095	K.FEHTVYGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1009.581	1009.100	477.917	0.486	299.657	0.501	14	0.094	K.FEHTVYGR.T
R2/RRR2-10/3	1009.108	1009.100	8.770	0.455	207.297	0.433	12	0.090	K.FEHTVYGR.T
R2/RRR2-14/3	1693.269	1692.896	220.884	0.395	1679.378	0.407	29	0.156	K.KVNEILSHYPSNYK.Q
R2/RRR2-14/2	1480.338	1480.688	-237.341	0.408	800.948	0.454	20	0.128	R.EIEEALLEHLGVK.R
R2/RRR2-14/3	1564.160	1564.724	-1002.853	0.442	609.414	0.524	21	0.094	K.VNEILSHYPSNYK.Q
R2/RRR2-14/3	1564.355	1564.724	-236.186	0.295	385.293	0.387	16	0.072	K.VNEILSHYPSNYK.Q
R2/RRR2-15/2	1295.150	1295.430	-216.826	0.487	1174.078	0.658	21	0.190	R.HSGLAVAGLAADGR.Q
R2/RRR2-21/2	1090.466	1091.247	-1637.771	0.433	1653.242	0.350	15	0.174	K.FGVLANWQR.E
R2/RRR2-21/2	1090.970	1091.247	-254.712	0.439	1602.613	0.271	15	0.153	K.FGVLANWQR.E
R2/RRR2-21/2	1091.047	1091.247	-183.659	0.434	1469.476	0.321	15	0.151	K.FGVLANWQR.E
R2/RRR2-21/2	1216.173	1216.366	-159.831	0.495	1589.977	0.271	16	0.150	R.LLEELERGEK.G
R2/RRR2-21/2	1216.026	1216.366	-280.572	0.456	1547.023	0.266	16	0.146	R.LLEELERGEK.G
R2/RRR2-21/2	1216.419	1216.366	43.219	0.526	1564.723	0.264	16	0.145	R.LLEELERGEK.G
R2/RRR2-21/3	1806.477	1806.930	-251.316	0.487	1082.194	0.481	26	0.114	R.INM*SCVNHETGAVDSR.K
R2/RRR2-21/3	1806.209	1806.930	-955.417	0.500	1090.589	0.474	26	0.113	R.INM*SCVNHETGAVDSR.K
R2/RRR2-21/3	1806.730	1806.930	-111.206	0.512	1021.827	0.453	26	0.104	R.INM*SCVNHETGAVDSR.K
R2/RRR2-22/2	1432.141	1432.567	-298.163	0.470	1230.797	0.527	22	0.168	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/2	1432.205	1432.567	-253.182	0.484	1164.401	0.501	22	0.158	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/2	1432.064	1432.567	-1052.344	0.468	936.191	0.524	20	0.145	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/3	1432.516	1432.567	-35.403	0.422	633.786	0.508	27	0.096	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/2	1058.081	1058.217	-129.094	0.412	902.160	0.114	13	0.096	R.TLLVADNRR.C
R2/RRR2-23/3	1433.255	1432.567	-218.281	0.439	946.299	0.413	27	0.093	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/3	1432.382	1432.567	-129.004	0.408	601.434	0.484	26	0.093	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/3	1623.236	1622.894	211.595	0.477	962.455	0.391	27	0.089	K.VNGRPLSLVEPATLR.Y
R2/RRR2-22/3	1432.905	1432.567	236.839	0.400	501.281	0.425	25	0.087	R.VTGGGHTSQVYAVR.Q
R2/RRR2-23/3	1432.543	1432.567	-16.429	0.400	550.380	0.413	25	0.085	R.VTGGGHTSQVYAVR.Q
R2/RRR2-23/3	1433.356	1432.567	-147.282	0.365	427.476	0.411	23	0.085	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/3	1622.664	1622.894	-141.908	0.453	935.665	0.362	27	0.084	K.VNGRPLSLVEPATLR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1433.473	1432.567	-65.530	0.387	375.566	0.294	22	0.083	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/3	1432.774	1432.567	145.339	0.310	398.626	0.364	21	0.081	R.VTGGGHTSQVYAVR.Q
R2/RRR2-22/3	1622.896	1622.894	1.153	0.410	764.623	0.323	25	0.073	-.VNGRPLSLVEPATLR.-
R2/RRR2-9/3	1978.118	1978.192	-37.708	0.561	3508.123	0.563	41	0.710	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-9/2	1978.169	1978.192	-11.798	0.545	3738.657	0.539	29	0.698	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-9/2	1977.780	1978.192	-209.218	0.586	3231.923	0.548	28	0.542	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-9/2	1977.803	1978.192	-197.516	0.578	2818.836	0.549	27	0.433	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-9/3	1977.513	1978.192	-851.956	0.352	2216.853	0.332	31	0.229	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-11/2	1979.849	1978.192	-173.812	0.488	1206.976	0.508	21	0.154	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-10/2	1979.834	1978.192	-181.605	0.415	758.090	0.499	18	0.122	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-9/2	1978.942	1978.192	-126.685	0.382	756.291	0.452	18	0.117	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-9/3	1600.653	1601.736	-1305.193	0.356	928.913	0.332	25	0.076	R.VCAYLDPSEPNHAK.I
R2/RRR2-9/3	1977.599	1978.192	-808.271	0.291	1337.741	0.173	28	0.074	R.SNFGALLDTVELQLASGGGK.S
R2/RRR2-11/2	1532.265	1532.592	-213.716	0.549	1889.125	0.503	22	0.240	K.IADAEENLGESEVR.E
R2/RRR2-11/2	1532.162	1532.592	-281.415	0.566	1894.263	0.495	22	0.238	K.IADAEENLGESEVR.E
R2/RRR2-11/2	1325.228	1324.591	-274.637	0.540	1638.334	0.621	22	0.238	K.VVDAPEILAVIGK.V
R2/RRR2-11/2	1532.207	1532.592	-251.761	0.542	1844.162	0.472	22	0.225	K.IADAEENLGESEVR.E
R2/RRR2-11/2	1324.333	1324.591	-195.776	0.529	1442.694	0.563	21	0.198	K.VVDAPEILAVIGK.V
R2/RRR2-11/2	1323.784	1324.591	-1368.905	0.507	1384.450	0.570	20	0.192	K.VVDAPEILAVIGK.V
R2/RRR2-11/2	1584.226	1583.810	263.803	0.457	1352.388	0.308	19	0.136	K.LFLLSHPDVDDLAK.V
R2/RRR2-11/2	1583.022	1583.810	-1132.511	0.352	1214.322	0.298	18	0.126	K.LFLLSHPDVDDLAK.V
R2/RRR2-6/2	1002.417	1003.135	-1718.847	0.373	656.513	0.383	12	0.116	R.VAVTNTLER.R
R2/RRR2-6/2	1002.265	1003.135	-1871.564	0.299	654.232	0.357	12	0.111	R.VAVTNTLER.R
R2/RRR2-6/2	1002.276	1003.135	-1860.304	0.309	739.543	0.295	12	0.109	R.VAVTNTLER.R
R2/RRR2-17/2	1728.434	1728.967	-889.398	0.500	1081.408	0.560	24	0.163	K.IWQVPETLSEEVLGK.M
R2/RRR2-17/2	1728.478	1728.967	-283.595	0.510	977.564	0.579	23	0.158	K.IWQVPETLSEEVLGK.M
R2/RRR2-17/2	1874.425	1874.126	160.124	0.513	1180.328	0.482	22	0.152	K.LAEEIKKGASSVEGVEVK.I
R2/RRR2-16/2	1728.442	1728.967	-884.860	0.488	971.780	0.495	23	0.144	K.IWQVPETLSEEVLGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1729.128	1728.967	93.424	0.509	781.892	0.554	21	0.141	K.IWQVPETLSEEVLGK.M
R2/RRR2-17/2	1046.712	1047.298	-1520.041	0.378	1028.127	0.418	14	0.134	R.FGM*M*AAQMK.A
R2/RRR2-17/2	1729.701	1728.967	-153.929	0.370	241.884	0.366	11	0.099	-.IWQVPETLSEEVLGK.-
R2/RRR2-9/1	1298.735	1299.543	-1396.665	0.296	810.305	0.364	16	0.632	R.EHALLAFTLGVK.Q
R2/RRR2-9/1	1298.848	1299.543	-1309.159	0.392	781.607	0.423	16	0.619	R.EHALLAFTLGVK.Q
R2/RRR2-9/1	1298.606	1299.543	-1496.649	0.298	769.624	0.366	16	0.581	R.EHALLAFTLGVK.Q
R2/RRR2-9/2	1299.265	1299.543	-214.631	0.433	1197.514	0.526	19	0.164	R.EHALLAFTLGVK.Q
R2/RRR2-9/2	1299.362	1299.543	-140.175	0.473	1142.910	0.541	19	0.163	R.EHALLAFTLGVK.Q
R2/RRR2-9/2	1299.443	1299.543	-77.320	0.430	968.594	0.531	19	0.148	R.EHALLAFTLGVK.Q
R2/RRR2-1/2	1299.712	1299.543	130.037	0.364	489.244	0.488	16	0.120	R.EHALLAFTLGVK.Q
R2/RRR2-9/2	1956.365	1957.220	-950.997	0.408	586.599	0.459	17	0.116	K.YYFTIIDAPGHRDFIK.N
R2/RRR2-9/2	1955.584	1957.220	-1864.650	0.395	595.460	0.384	17	0.109	K.YYFTIIDAPGHRDFIK.N
R2/RRR2-9/3	1299.633	1299.543	69.175	0.512	754.920	0.420	23	0.088	R.EHALLAFTLGVK.Q
R2/RRR2-9/3	1299.364	1299.543	-138.583	0.437	1214.609	0.316	26	0.088	R.EHALLAFTLGVK.Q
R2/RRR2-3/3	1454.181	1453.626	-306.703	0.411	920.263	0.327	23	0.079	K.YYFTIIDAPGHR.D
R2/RRR2-9/3	1452.529	1453.626	-1448.281	0.451	522.094	0.297	19	0.076	K.YYFTIIDAPGHR.D
R2/RRR2-9/3	1298.755	1299.543	-1381.250	0.393	872.529	0.316	25	0.075	R.EHALLAFTLGVK.Q
R2/RRR2-3/3	1453.328	1453.626	-205.494	0.334	955.331	0.216	22	0.067	K.YYFTIIDAPGHR.D
R2/RRR2-10/3	1452.984	1453.626	-1133.475	0.338	784.155	0.208	22	0.067	K.YYFTIIDAPGHR.D
R2/RRR2-9/3	1452.570	1453.626	-1419.539	0.395	863.649	0.195	21	0.065	K.YYFTIIDAPGHR.D
R2/RRR2-12/2	1657.280	1657.850	-950.190	0.552	1800.900	0.691	30	0.280	K.GLPLGSGLGSSAASAAAAAK.A
R2/RRR2-12/2	1657.199	1657.850	-999.737	0.534	1831.042	0.659	30	0.276	K.GLPLGSGLGSSAASAAAAAK.A
R2/RRR2-12/2	1657.226	1657.850	-983.024	0.549	1449.022	0.671	29	0.223	K.GLPLGSGLGSSAASAAAAAK.A
R2/RRR2-12/2	1162.233	1162.364	-112.784	0.517	1870.080	0.420	18	0.215	K.AVDALFGSLLR.Q
R2/RRR2-12/2	1162.054	1162.364	-267.157	0.474	1890.492	0.385	17	0.209	K.AVDALFGSLLR.Q
R2/RRR2-12/2	1161.549	1162.364	-1567.165	0.481	1806.414	0.340	18	0.188	K.AVDALFGSLLR.Q
R2/RRR2-13/2	1163.288	1162.364	-65.425	0.391	972.218	0.340	16	0.121	K.AVDALFGSLLR.Q
R2/RRR2-12/2	1417.182	1417.544	-256.039	0.410	628.659	0.398	17	0.115	R.QDDLVLAGLESEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/2	1720.331	1719.902	249.875	0.520	1335.184	0.516	19	0.172	R.TGGTITM*SNFFNAWR.N
R2/RRR2-19/2	1718.580	1719.902	-1354.971	0.420	1212.758	0.512	18	0.159	R.TGGTITM*SNFFNAWR.N
R2/RRR2-19/2	1199.331	1199.342	-9.148	0.426	1029.605	0.376	14	0.130	K.TFNQYWAIR.T
R2/RRR2-19/2	1718.472	1719.902	-1418.110	0.341	894.813	0.423	16	0.121	R.TGGTITM*SNFFNAWR.N
R2/RRR2-19/2	1199.333	1199.342	-7.719	0.358	849.582	0.313	14	0.116	K.TFNQYWAIR.T
R2/RRR2-19/2	1079.492	1080.173	-1562.324	0.283	745.939	0.403	14	0.116	R.YNAPSIEGTK.T
R2/RRR2-19/2	1079.893	1080.173	-260.159	0.348	710.359	0.374	14	0.116	R.YNAPSIEGTK.T
R2/RRR2-19/2	1198.857	1199.342	-406.020	0.311	687.139	0.295	13	0.111	K.TFNQYWAIR.T
R2/RRR2-19/2	1199.179	1199.342	-136.775	0.404	609.703	0.294	13	0.111	-.TFNQYWAIR.-
R2/RRR2-19/2	1198.572	1199.342	-1481.471	0.359	581.862	0.286	12	0.110	K.TFNQYWAIR.T
R2/RRR2-19/2	1198.670	1199.342	-1399.328	0.303	619.228	0.309	11	0.109	K.TFNQYWAIR.T
R2/RRR2-18/2	1199.768	1199.342	355.787	0.264	606.693	0.253	12	0.107	K.TFNQYWAIR.T
R2/RRR2-19/2	1079.424	1080.173	-1625.033	0.159	573.976	0.248	12	0.097	-.YNAPSIEGTK.-
R2/RRR2-6/2	1857.364	1858.166	-973.210	0.556	1950.486	0.502	25	0.248	K.QIVVSCGTLSSPLVLQR.S
R2/RRR2-6/2	1858.792	1858.166	-201.994	0.505	1168.338	0.499	21	0.154	K.QIVVSCGTLSSPLVLQR.S
R2/RRR2-6/2	1949.619	1950.184	-804.949	0.514	822.882	0.587	20	0.146	K.VSFGNYTYPIAWDFLR.A
R2/RRR2-6/2	1951.556	1950.184	191.124	0.564	769.785	0.575	19	0.140	K.VSFGNYTYPIAWDFLR.A
R2/RRR2-6/2	1114.074	1113.248	-156.345	0.412	547.777	0.442	14	0.120	R.DLHGFEGPIK.V
R2/RRR2-5/2	1858.188	1858.166	11.952	0.470	689.359	0.479	17	0.120	K.QIVVSCGTLSSPLVLQR.S
R2/RRR2-6/2	1113.100	1113.248	-132.942	0.264	388.117	0.461	12	0.109	R.DLHGFEGPIK.V
R2/RRR2-6/3	1113.783	1113.248	-418.467	0.463	1079.466	0.216	20	0.063	-.DLHGFEGPIK.-
R2/RRR2-10/2	1186.253	1185.304	-43.412	0.497	1522.558	0.509	16	0.196	K.FGCTDFVNPK.D
R2/RRR2-10/2	1186.025	1185.304	-236.259	0.543	1474.836	0.513	15	0.191	K.FGCTDFVNPK.D
R2/RRR2-10/2	1313.156	1313.477	-245.274	0.466	1023.073	0.477	16	0.144	K.KFGCTDFVNPK.D
R2/RRR2-10/2	1643.617	1643.908	-178.007	0.502	962.343	0.479	18	0.136	R.IIGVDLNPAKFEQAK.K
R2/RRR2-11/2	1948.419	1949.189	-911.517	0.526	1780.081	0.552	20	0.238	R.SILEELCGNVHSIYWK.S
R2/RRR2-11/2	1274.968	1275.434	-366.417	0.373	1133.093	0.465	18	0.147	K.EIVGSIQSQVSK.I
R2/RRR2-11/2	1776.382	1776.068	177.163	0.454	912.502	0.526	21	0.140	R.YGLPPSFLSAVLAPSQK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1775.669	1776.068	-225.447	0.399	889.191	0.496	25	0.136	R.YGLPPSFLSAVLAPSQK.G
R2/RRR2-11/2	1274.607	1275.434	-1437.763	0.372	968.792	0.381	17	0.125	K.EIVGSIQSQVSK.I
R2/RRR2-11/2	1775.668	1776.068	-226.413	0.424	650.897	0.475	23	0.125	R.YGLPPSFLSAVLAPSQK.G
R2/RRR2-10/2	1775.102	1776.068	-1110.874	0.424	530.706	0.525	20	0.124	R.YGLPPSFLSAVLAPSQK.G
R2/RRR2-11/2	1775.196	1776.068	-1057.708	0.402	544.718	0.498	21	0.122	R.YGLPPSFLSAVLAPSQK.G
R2/RRR2-10/2	1775.631	1776.068	-246.897	0.378	536.741	0.454	21	0.118	R.YGLPPSFLSAVLAPSQK.G
R2/RRR2-10/2	1774.787	1776.068	-1289.264	0.352	538.033	0.385	20	0.112	R.YGLPPSFLSAVLAPSQK.G
R2/RRR2-23/2	1404.265	1404.596	-236.946	0.427	1093.171	0.465	19	0.145	R.STYQVAALPLNAR.I
R2/RRR2-24/2	1404.048	1404.596	-1106.392	0.432	1012.780	0.470	18	0.140	R.STYQVAALPLNAR.I
R2/RRR2-24/2	1288.151	1287.489	-263.247	0.507	639.780	0.584	17	0.138	K.APAALGPYSQAIK.A
R2/RRR2-23/2	1286.985	1287.489	-1172.399	0.426	878.845	0.514	17	0.137	K.APAALGPYSQAIK.A
R2/RRR2-23/2	1056.036	1056.151	-109.402	0.463	863.769	0.463	17	0.134	K.ASGASYSSVVK.T
R2/RRR2-23/2	1403.991	1404.596	-1147.075	0.436	1055.713	0.407	19	0.134	R.STYQVAALPLNAR.I
R2/RRR2-23/2	1055.945	1056.151	-196.374	0.454	688.605	0.526	16	0.134	K.ASGASYSSVVK.T
R2/RRR2-23/2	1287.235	1287.489	-197.994	0.448	797.642	0.498	18	0.133	K.APAALGPYSQAIK.A
R2/RRR2-23/2	1288.337	1287.489	-118.566	0.499	623.874	0.560	16	0.133	K.APAALGPYSQAIK.A
R2/RRR2-23/2	1055.952	1056.151	-188.952	0.424	736.366	0.506	16	0.132	K.ASGASYSSVVK.T
R2/RRR2-24/2	1055.473	1056.151	-1595.093	0.368	895.990	0.448	17	0.131	K.ASGASYSSVVK.T
R2/RRR2-24/2	1287.304	1287.489	-144.626	0.436	694.926	0.523	16	0.130	K.APAALGPYSQAIK.A
R2/RRR2-24/2	1404.405	1404.596	-136.403	0.427	1148.067	0.317	20	0.127	R.STYQVAALPLNAR.I
R2/RRR2-24/2	1287.352	1287.489	-106.863	0.436	628.487	0.508	16	0.126	K.APAALGPYSQAIK.A
R2/RRR2-23/2	1403.691	1404.596	-1361.107	0.346	955.784	0.375	18	0.123	R.STYQVAALPLNAR.I
R2/RRR2-24/2	1055.454	1056.151	-1613.102	0.359	648.632	0.415	16	0.119	K.ASGASYSSVVK.T
R2/RRR2-7/2	1752.382	1752.904	-871.235	0.543	2242.358	0.517	23	0.303	R.SFGTDLDTATNELVIR.V
R2/RRR2-7/2	1753.556	1752.904	-198.756	0.580	1971.374	0.512	22	0.253	R.SFGTDLDTATNELVIR.V
R2/RRR2-7/2	1752.668	1752.904	-135.077	0.496	1479.886	0.450	20	0.172	R.SFGTDLDTATNELVIR.V
R2/RRR2-7/2	1879.438	1880.094	-883.475	0.440	1096.039	0.420	21	0.134	K.DSVTPTFAAAALFINNAR.W
R2/RRR2-7/2	1879.359	1880.094	-925.532	0.349	553.695	0.387	17	0.106	K.DSVTPTFAAAALFINNAR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1171.635	1172.357	-1474.254	0.376	783.383	0.234	13	0.103	-.ELVENLSVLR.-
R2/RRR2-11/2	1932.635	1933.152	-786.999	0.493	1663.605	0.562	24	0.222	R.SFLQAVSTVTEEAPSPLR.V
R2/RRR2-11/2	1932.494	1933.152	-860.487	0.521	1622.493	0.583	24	0.222	R.SFLQAVSTVTEEAPSPLR.V
R2/RRR2-11/2	1590.647	1589.856	-131.516	0.578	1810.781	0.406	19	0.204	K.LSWVDIFEEIPIK.V
R2/RRR2-11/2	1931.978	1933.152	-1128.216	0.321	1411.344	0.461	22	0.167	R.SFLQAVSTVTEEAPSPLR.V
R2/RRR2-11/2	1276.839	1277.428	-1248.347	0.416	1097.533	0.418	16	0.140	K.LTDSFM*DLYR.N
R2/RRR2-15/2	1427.122	1427.542	-294.836	0.574	1694.410	0.583	19	0.205	K.NLKDEPVAAEQNV.-
R2/RRR2-15/2	1885.388	1886.138	-931.145	0.501	990.201	0.586	23	0.156	K.SGATVLPDLVAAQEWLSK.N
R2/RRR2-15/2	1885.443	1886.138	-901.961	0.506	933.797	0.600	22	0.154	K.SGATVLPDLVAAQEWLSK.N
R2/RRR2-15/2	1885.198	1886.138	-1032.295	0.494	939.039	0.571	22	0.149	K.SGATVLPDLVAAQEWLSK.N
R2/RRR2-15/2	1482.294	1481.499	-138.487	0.491	1057.112	0.482	16	0.145	K.AGYEYDEETFEK.I
R2/RRR2-15/2	1481.286	1481.499	-143.871	0.444	1052.932	0.450	16	0.139	K.AGYEYDEETFEK.I
R2/RRR2-15/2	1427.161	1427.542	-267.718	0.571	1292.848	0.546	19	0.105	K.NLKDEPVAAEQNV.-
R2/RRR2-15/2	1480.323	1481.499	-1474.013	0.172	594.686	0.206	15	0.100	K.AGYEYDEETFEK.I
R2/RRR2-15/3	1782.754	1782.844	-50.631	0.477	1478.525	0.562	31	0.178	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-20/2	1412.291	1412.610	-227.017	0.487	1308.907	0.528	20	0.174	K.VVEVVESSPPEIK.A
R2/RRR2-15/2	1413.151	1412.610	-326.342	0.538	1218.369	0.562	20	0.173	K.VVEVVESSPPEIK.A
R2/RRR2-15/3	1782.747	1782.844	-54.443	0.468	1409.630	0.556	31	0.167	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-15/3	1782.408	1782.844	-244.969	0.393	1411.916	0.525	29	0.160	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-15/2	1412.274	1412.610	-238.897	0.478	1114.860	0.535	19	0.158	K.VVEVVESSPPEIK.A
R2/RRR2-21/2	1659.273	1659.948	-1012.655	0.399	1152.684	0.511	23	0.154	K.SGTTPLSPAIVFILDK.V
R2/RRR2-20/2	1412.264	1412.610	-246.267	0.418	1202.487	0.480	19	0.154	K.VVEVVESSPPEIK.A
R2/RRR2-20/2	1412.236	1412.610	-266.213	0.433	1093.443	0.505	19	0.151	K.VVEVVESSPPEIK.A
R2/RRR2-20/2	1659.098	1659.948	-1118.366	0.431	1039.392	0.534	22	0.150	K.SGTTPLSPAIVFILDK.V
R2/RRR2-15/2	1412.163	1412.610	-317.553	0.445	1048.926	0.514	19	0.149	K.VVEVVESSPPEIK.A
R2/RRR2-14/2	1660.407	1659.948	277.582	0.476	981.157	0.540	21	0.147	K.SGTTPLSPAIVFILDK.V
R2/RRR2-15/2	1660.279	1659.948	200.319	0.485	922.985	0.551	21	0.146	K.SGTTPLSPAIVFILDK.V
R2/RRR2-18/2	1411.900	1412.610	-1214.792	0.377	1228.185	0.411	19	0.145	K.VVEVVESSPPEIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1659.564	1659.948	-232.145	0.406	1028.599	0.501	22	0.144	K.SGTTPLSPAIVFILDK.V
R2/RRR2-21/2	1658.857	1659.948	-1264.077	0.386	1063.433	0.489	22	0.144	K.SGTTPLSPAIVFILDK.V
R2/RRR2-19/2	1660.283	1659.948	202.605	0.486	928.954	0.525	21	0.142	K.SGTTPLSPAIVFILDK.V
R2/RRR2-18/2	1411.989	1412.610	-1151.937	0.387	1071.823	0.460	18	0.141	K.VVEVVESSPPEIK.A
R2/RRR2-19/2	1659.409	1659.948	-929.861	0.424	942.031	0.504	21	0.139	K.SGTTPLSPAIVFILDK.V
R2/RRR2-19/2	1660.404	1659.948	275.886	0.462	979.026	0.476	22	0.139	K.SGTTPLSPAIVFILDK.V
R2/RRR2-21/2	1659.066	1659.948	-1137.427	0.394	920.973	0.487	21	0.135	K.SGTTPLSPAIVFILDK.V
R2/RRR2-20/2	1659.298	1659.948	-997.513	0.383	918.903	0.489	21	0.135	K.SGTTPLSPAIVFILDK.V
R2/RRR2-20/3	1782.989	1782.844	81.736	0.492	1098.896	0.556	29	0.133	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-19/2	1783.121	1782.844	155.894	0.349	650.093	0.585	25	0.133	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-19/2	1782.337	1782.844	-848.074	0.332	682.903	0.582	25	0.133	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-15/2	1783.276	1782.844	243.214	0.330	714.864	0.554	26	0.132	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-20/2	1782.345	1782.844	-280.795	0.352	634.747	0.571	24	0.131	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-15/2	1658.891	1659.948	-1243.385	0.313	948.981	0.439	21	0.129	K.SGTTPLSPAIVFILDK.V
R2/RRR2-15/2	1782.388	1782.844	-256.265	0.309	701.020	0.531	25	0.127	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-20/3	1782.546	1782.844	-167.266	0.447	1206.862	0.491	30	0.127	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-19/2	1782.194	1782.844	-928.521	0.328	717.528	0.499	25	0.126	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-14/2	1659.692	1659.948	-154.594	0.397	743.540	0.472	19	0.125	K.SGTTPLSPAIVFILDK.V
R2/RRR2-20/2	1782.394	1782.844	-253.035	0.310	520.774	0.543	23	0.122	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-14/2	1659.638	1659.948	-187.060	0.377	690.390	0.464	19	0.122	K.SGTTPLSPAIVFILDK.V
R2/RRR2-21/2	1412.215	1412.610	-280.608	0.343	661.802	0.433	18	0.120	K.VVEVVESSPPEIK.A
R2/RRR2-10/2	1659.789	1659.948	-96.163	0.265	1061.538	0.296	20	0.117	K.SGTTPLSPAIVFILDK.V
R2/RRR2-19/3	1784.408	1782.844	-244.866	0.448	822.957	0.577	25	0.117	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-15/2	1782.403	1782.844	-247.951	0.271	814.313	0.348	27	0.115	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-20/2	1782.240	1782.844	-902.392	0.242	536.895	0.478	23	0.114	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-20/3	1782.456	1782.844	-217.865	0.427	949.885	0.522	29	0.113	K.AEPEPEPEAPAAETTSR.E
R2/RRR2-21/2	1411.524	1412.610	-1482.277	0.262	458.486	0.317	17	0.110	K.VVEVVESSPPEIK.A
R2/RRR2-21/2	1412.327	1412.610	-201.090	0.275	424.043	0.326	16	0.109	-.VVEVVESSPPEIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1659.132	1659.948	-1097.975	0.299	409.989	0.349	15	0.108	K.SGTTPLSPAIVFILDK.V
R2/RRR2-10/2	1660.404	1659.948	275.886	0.341	974.431	0.214	19	0.106	K.SGTTPLSPAIVFILDK.V
R2/RRR2-12/2	1660.239	1659.948	175.766	0.250	364.095	0.377	12	0.105	K.SGTTPLSPAIVFILDK.V
R2/RRR2-20/2	1934.346	1935.169	-945.239	0.579	1844.905	0.528	30	0.241	R.IWVFSGDADSVVPLTATR.Y
R2/RRR2-20/2	1934.056	1935.169	-1095.858	0.525	1423.745	0.538	26	0.188	R.IWVFSGDADSVVPLTATR.Y
R2/RRR2-20/2	1933.916	1935.169	-1168.364	0.481	1412.470	0.527	27	0.185	R.IWVFSGDADSVVPLTATR.Y
R2/RRR2-20/2	1154.162	1154.297	-116.862	0.391	727.126	0.368	13	0.117	K.YYNLPEVQK.A
R2/RRR2-20/3	1326.699	1326.492	156.267	0.478	1180.995	0.436	26	0.109	R.GAGHEVPLHRPR.Q
R2/RRR2-20/2	1155.093	1154.297	-177.186	0.418	474.519	0.320	11	0.108	-.YYNLPEVQK.-
R2/RRR2-20/2	1153.614	1154.297	-1462.896	0.290	695.503	0.270	13	0.107	K.YYNLPEVQK.A
R2/RRR2-20/3	1326.345	1326.492	-111.209	0.455	958.362	0.448	23	0.099	R.GAGHEVPLHRPR.Q
R2/RRR2-20/3	1326.728	1326.492	178.135	0.439	827.031	0.445	22	0.093	R.GAGHEVPLHRPR.Q
R2/RRR2-19/3	1326.717	1326.492	170.108	0.491	565.968	0.440	21	0.088	R.GAGHEVPLHRPR.Q
R2/RRR2-18/3	1326.656	1326.492	123.740	0.412	701.288	0.427	21	0.086	R.GAGHEVPLHRPR.Q
R2/RRR2-12/1	963.606	964.183	-1642.197	0.262	859.232	0.253	12	0.641	R.TALAFVTLK.S
R2/RRR2-12/1	963.596	964.183	-1652.697	0.229	771.925	0.357	12	0.578	R.TALAFVTLK.S
R2/RRR2-12/1	963.554	964.183	-1696.353	0.169	667.295	0.273	11	0.446	-.TALAFVTLK.-
R2/RRR2-12/2	1690.190	1689.761	254.508	0.468	1360.486	0.540	21	0.182	K.NGVNAEGCLFDEHAR.T
R2/RRR2-12/2	1690.270	1689.761	-291.237	0.475	1093.370	0.522	19	0.153	K.NGVNAEGCLFDEHAR.T
R2/RRR2-12/2	964.088	964.183	-99.580	0.463	936.679	0.495	15	0.144	R.TALAFVTLK.S
R2/RRR2-12/2	964.041	964.183	-147.846	0.496	975.661	0.452	15	0.140	R.TALAFVTLK.S
R2/RRR2-12/2	1795.564	1794.037	-264.612	0.331	1099.270	0.092	20	0.097	K.IFHYGSISLITEPCR.-
R2/RRR2-12/3	1793.886	1794.037	-84.511	0.491	1343.476	0.241	28	0.082	K.IFHYGSISLITEPCR.-
R2/RRR2-12/3	1793.597	1794.037	-246.308	0.390	1084.154	0.173	23	0.062	K.IFHYGSISLITEPCR.-
R2/RRR2-12/3	1792.962	1794.037	-1160.626	0.310	765.953	0.070	21	0.047	-.IFHYGSISLITEPCR.-
R2/RRR2-17/2	1771.537	1770.965	-242.491	0.568	896.525	0.571	21	0.148	R.VGDLGQLTPTDQVLASR.H
R2/RRR2-17/2	1291.360	1291.438	-60.358	0.427	967.007	0.332	15	0.121	R.LNEQVQEFKR.L
R2/RRR2-17/2	1291.474	1291.438	27.720	0.309	336.971	0.314	13	0.110	R.LNEQVQEFKR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/3	1446.637	1446.547	62.654	0.510	1136.898	0.401	24	0.101	K.HGSVEEIQQYQK.E
R2/RRR2-23/2	1786.710	1786.963	-142.302	0.439	854.220	0.571	23	0.144	K.EAALAAVPNDNPTIFDK.I
R2/RRR2-23/2	1656.215	1656.950	-1050.822	0.449	962.305	0.383	19	0.123	R.DINPQAPTHIVIIPK.V
R2/RRR2-23/2	1787.475	1786.963	-273.892	0.461	357.152	0.542	16	0.118	K.EAALAAVPNDNPTIFDK.I
R2/RRR2-23/2	1656.615	1656.950	-203.069	0.459	797.618	0.367	17	0.113	R.DINPQAPTHIVIIPK.V
R2/RRR2-23/3	1464.751	1464.605	99.452	0.484	1034.190	0.472	29	0.106	K.VVAKQEGLEDGYR.I
R2/RRR2-23/3	1464.140	1464.605	-318.582	0.465	1104.345	0.450	30	0.105	K.VVAKQEGLEDGYR.I
R2/RRR2-23/2	1785.754	1786.963	-1241.168	0.270	356.371	0.361	16	0.104	K.EAALAAVPNDNPTIFDK.I
R2/RRR2-23/3	1464.206	1464.605	-273.789	0.457	991.236	0.455	28	0.100	K.VVAKQEGLEDGYR.I
R2/RRR2-2/2	1873.574	1873.998	-226.802	0.493	1929.996	0.375	21	0.211	K.SSSSEADFEQQLYILR.R
R2/RRR2-2/2	1873.950	1873.998	-25.390	0.471	1583.721	0.377	19	0.168	K.SSSSEADFEQQLYILR.R
R2/RRR2-2/2	1436.502	1437.671	-1514.803	0.332	684.733	0.464	15	0.117	K.VAESLGHVILGWR.W
R2/RRR2-2/2	958.008	958.184	-183.859	0.550	900.832	0.283	14	0.116	R.RLSILSIR.A
R2/RRR2-2/3	1438.006	1437.671	233.274	0.534	972.894	0.508	27	0.111	K.VAESLGHVILGWR.W
R2/RRR2-2/3	1437.664	1437.671	-4.788	0.498	744.945	0.515	23	0.100	K.VAESLGHVILGWR.W
R2/RRR2-9/3	1848.946	1848.048	-55.573	0.504	1800.519	0.421	27	0.180	R.ELDHLANFLQAAVDYK.K
R2/RRR2-9/2	1069.927	1070.223	-277.459	0.470	1126.691	0.438	16	0.146	K.VYAYGAAQVK.K
R2/RRR2-9/2	1070.053	1070.223	-159.344	0.467	993.371	0.461	16	0.141	K.VYAYGAAQVK.K
R2/RRR2-9/3	1847.333	1848.048	-931.578	0.425	1338.020	0.429	24	0.126	R.ELDHLANFLQAAVDYK.K
R2/RRR2-9/3	1848.569	1848.048	-260.145	0.369	1171.167	0.376	25	0.099	R.ELDHLANFLQAAVDYK.K
R2/RRR2-9/2	1070.060	1070.223	-152.363	0.322	582.313	0.231	12	0.096	-.VYAYGAAQVK.-
R2/RRR2-9/3	1932.429	1932.162	138.457	0.330	1156.703	0.275	28	0.078	K.TLTETNKNLDEIVELAK.K
R2/RRR2-6/2	1462.274	1462.633	-245.715	0.471	1326.446	0.440	21	0.160	K.QFAAEEISAQVLR.K
R2/RRR2-6/2	1462.309	1462.633	-221.931	0.504	1339.421	0.407	21	0.156	K.QFAAEEISAQVLR.K
R2/RRR2-6/2	1462.419	1462.633	-146.816	0.537	1194.711	0.457	21	0.154	K.QFAAEEISAQVLR.K
R2/RRR2-6/2	1581.370	1580.766	-251.444	0.473	542.092	0.528	16	0.125	R.QAVVNPENTFFSVK.R
R2/RRR2-6/2	1580.472	1580.766	-186.281	0.444	596.770	0.464	17	0.120	R.QAVVNPENTFFSVK.R
R2/RRR2-6/2	1580.230	1580.766	-974.825	0.422	452.709	0.484	15	0.117	R.QAVVNPENTFFSVK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1858.360	1859.008	-889.723	0.462	1136.004	0.314	26	0.084	R.KM*NEVDEESKQVSYR.V
R2/RRR2-4/2	1623.563	1623.833	-166.632	0.419	1682.744	0.406	18	0.187	R.VINTALFSEYYFR.V
R2/RRR2-5/2	1624.686	1623.833	-90.177	0.461	1417.115	0.449	18	0.168	R.VINTALFSEYYFR.V
R2/RRR2-4/2	974.962	975.083	-124.967	0.489	747.910	0.487	12	0.133	K.HGESYLLR.V
R2/RRR2-4/2	1623.858	1623.833	15.637	0.355	1125.193	0.340	17	0.127	R.VINTALFSEYYFR.V
R2/RRR2-4/2	1326.425	1326.541	-87.581	0.414	1014.650	0.331	16	0.122	R.M*VEESFILDVK.H
R2/RRR2-5/2	1623.470	1623.833	-224.033	0.355	568.727	0.405	15	0.113	R.VINTALFSEYYFR.V
R2/RRR2-1/2	1624.549	1623.833	-174.972	0.325	566.185	0.310	14	0.106	R.VINTALFSEYYFR.V
R2/RRR2-4/2	1326.898	1326.541	269.823	0.358	676.431	0.254	14	0.105	R.M*VEESFILDVK.H
R2/RRR2-11/2	1287.241	1287.445	-158.520	0.414	990.008	0.523	16	0.147	K.TFASWGVDYLK.Y
R2/RRR2-11/2	1287.947	1287.445	-387.251	0.475	867.460	0.510	16	0.140	K.TFASWGVDYLK.Y
R2/RRR2-10/2	1113.994	1114.314	-287.695	0.367	1225.016	0.339	16	0.135	K.APLLIGCDVR.S
R2/RRR2-10/2	1113.972	1114.314	-307.375	0.349	1285.403	0.314	16	0.135	K.APLLIGCDVR.S
R2/RRR2-10/3	1502.106	1501.601	-330.975	0.372	1142.214	0.297	25	0.082	-.M*PGSLDHEEQDVK.T
R2/RRR2-10/3	1501.974	1501.601	248.745	0.357	1191.298	0.277	25	0.081	-.M*PGSLDHEEQDVK.T
R2/RRR2-11/3	1501.243	1501.601	-239.006	0.339	705.631	0.303	21	0.072	-.M*PGSLDHEEQDVK.T
R2/RRR2-10/3	1501.508	1501.601	-61.976	0.335	720.076	0.216	22	0.067	-.M*PGSLDHEEQDVK.T
R2/RRR2-17/2	1502.616	1501.579	24.476	0.457	517.687	0.545	16	0.128	R.QNYEDLLSSFER.W
R2/RRR2-18/2	947.543	948.058	-1603.246	0.363	1100.624	0.337	14	0.127	R.SPAAEAVFR.N
R2/RRR2-18/3	1233.226	1233.359	-107.494	0.515	1305.192	0.452	23	0.123	R.HREPLPDSGPK.K
R2/RRR2-18/3	1232.880	1233.359	-389.662	0.480	1554.193	0.339	22	0.120	R.HREPLPDSGPK.K
R2/RRR2-17/3	1233.003	1233.359	-289.083	0.403	1223.906	0.319	22	0.089	R.HREPLPDSGPK.K
R2/RRR2-17/3	1232.991	1233.359	-299.065	0.450	1176.444	0.323	23	0.087	R.HREPLPDSGPK.K
R2/RRR2-4/2	1395.429	1395.690	-187.257	0.536	1893.303	0.518	18	0.242	R.VTIDLLEM*VFAK.G
R2/RRR2-4/2	1395.509	1395.690	-129.955	0.470	1837.260	0.405	18	0.205	R.VTIDLLEM*VFAK.G
R2/RRR2-4/2	1395.660	1395.690	-21.335	0.463	1567.398	0.413	16	0.174	R.VTIDLLEM*VFAK.G
R2/RRR2-3/2	1395.144	1395.690	-1111.311	0.460	1359.839	0.483	16	0.168	R.VTIDLLEM*VFAK.G
R2/RRR2-3/2	1395.525	1395.690	-118.372	0.406	1336.209	0.350	17	0.143	R.VTIDLLEM*VFAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1395.104	1395.690	-1139.953	0.336	1521.668	0.214	17	0.135	R.VTIDLLEM*VFAK.G
R2/RRR2-4/2	1395.481	1395.690	-149.786	0.428	902.625	0.376	14	0.119	R.VTIDLLEM*VFAK.G
R2/RRR2-12/2	1715.228	1715.008	128.159	0.447	757.893	0.483	20	0.126	K.GIAVDSVLPSVAEMLGR.T
R2/RRR2-9/2	1936.682	1936.174	-255.051	0.520	1883.459	0.562	27	0.256	K.GVYAYDFGDTAGLTPLM*K.M
R2/RRR2-9/2	1936.426	1936.174	130.354	0.541	1828.505	0.561	27	0.247	K.GVYAYDFGDTAGLTPLM*K.M
R2/RRR2-9/2	1936.451	1936.174	143.503	0.581	1533.036	0.528	25	0.197	K.GVYAYDFGDTAGLTPLM*K.M
R2/RRR2-9/2	1259.081	1258.440	-285.564	0.400	508.054	0.521	15	0.122	K.AVEPAACPTLTK.G
R2/RRR2-9/2	1552.257	1552.749	-318.236	0.411	880.039	0.329	20	0.118	R.FIDIPEEVAEVYK.L
R2/RRR2-9/2	1552.524	1552.749	-145.314	0.367	669.095	0.328	18	0.111	R.FIDIPEEVAEVYK.L
R2/RRR2-9/2	1552.172	1552.749	-1019.109	0.313	662.941	0.231	18	0.105	R.FIDIPEEVAEVYK.L
R2/RRR2-14/2	1293.133	1293.491	-277.476	0.534	1375.536	0.485	18	0.175	R.KLTDDEIAFIK.E
R2/RRR2-13/2	1097.920	1098.304	-350.948	0.366	1108.327	0.432	18	0.141	K.HGM*VAAGALVR.Q
R2/RRR2-13/2	1293.066	1293.491	-329.190	0.440	1017.414	0.402	16	0.132	R.KLTDDEIAFIK.E
R2/RRR2-14/2	1098.167	1098.304	-125.879	0.345	832.973	0.471	16	0.129	K.HGM*VAAGALVR.Q
R2/RRR2-14/2	1098.013	1098.304	-266.619	0.369	858.897	0.449	16	0.128	K.HGM*VAAGALVR.Q
R2/RRR2-14/2	1098.085	1098.304	-200.928	0.369	864.571	0.438	16	0.128	K.HGM*VAAGALVR.Q
R2/RRR2-14/3	1098.302	1098.304	-2.693	0.444	1816.254	0.228	24	0.120	K.HGM*VAAGALVR.Q
R2/RRR2-13/3	1899.392	1900.082	-892.250	0.431	867.761	0.522	29	0.105	K.AHAAENAKPVEKTEFEK.L
R2/RRR2-12/2	1499.196	1499.693	-332.357	0.426	1339.807	0.428	20	0.158	R.SIGISNYDIFLTR.D
R2/RRR2-13/2	1499.270	1499.693	-283.098	0.458	1151.202	0.447	19	0.146	R.SIGISNYDIFLTR.D
R2/RRR2-13/2	897.606	898.085	-535.671	0.528	1236.913	0.358	13	0.139	K.TPAQLVLR.W
R2/RRR2-12/2	1499.522	1499.693	-114.279	0.495	967.516	0.460	18	0.137	R.SIGISNYDIFLTR.D
R2/RRR2-13/2	1498.594	1499.693	-1404.734	0.366	1186.536	0.374	18	0.136	R.SIGISNYDIFLTR.D
R2/RRR2-12/2	897.788	898.085	-332.227	0.496	1185.192	0.345	13	0.135	K.TPAQLVLR.W
R2/RRR2-12/2	897.570	898.085	-1692.712	0.535	1246.443	0.310	13	0.132	K.TPAQLVLR.W
R2/RRR2-13/2	897.965	898.085	-133.637	0.540	1196.690	0.324	13	0.131	K.TPAQLVLR.W
R2/RRR2-13/2	898.015	898.085	-78.548	0.533	1087.411	0.318	13	0.125	K.TPAQLVLR.W
R2/RRR2-12/2	897.574	898.085	-1688.203	0.557	1072.901	0.325	13	0.125	K.TPAQLVLR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1498.455	1499.693	-1497.930	0.362	1014.736	0.327	18	0.121	R.SIGISNYDIFLTR.D
R2/RRR2-13/2	1124.362	1123.284	69.517	0.427	686.016	0.388	13	0.119	K.REDLFITTK.L
R2/RRR2-13/2	1123.042	1123.284	-216.476	0.381	548.408	0.322	12	0.110	K.REDLFITTK.L
R2/RRR2-13/2	898.046	898.085	-44.052	0.192	610.903	0.232	11	0.104	K.TPAQLVLR.W
R2/RRR2-12/2	1557.328	1557.767	-282.921	0.426	1373.251	0.583	20	0.191	R.VPTPNVSVVDLTCR.I
R2/RRR2-11/2	1557.513	1557.767	-163.872	0.412	1329.004	0.557	19	0.180	R.VPTPNVSVVDLTCR.I
R2/RRR2-12/2	1556.707	1557.767	-1327.677	0.304	1028.547	0.551	18	0.146	R.VPTPNVSVVDLTCR.I
R2/RRR2-11/2	1509.203	1508.854	231.810	0.383	686.410	0.473	15	0.119	R.VLDLIAHMALVNAK.-
R2/RRR2-12/2	1525.512	1524.854	-224.711	0.378	391.548	0.366	15	0.107	-.VLDLIAHM*ALVNAK.-
R2/RRR2-10/2	1747.358	1747.925	-899.665	0.488	1766.613	0.454	23	0.212	R.QCSSGLQAVANVASNIK.A
R2/RRR2-10/2	1664.707	1664.896	-114.037	0.399	1082.307	0.415	23	0.137	R.DCLLPM*GLTSENVAK.R
R2/RRR2-10/2	949.360	950.074	-1810.847	0.413	688.014	0.267	12	0.110	K.VELFSQAR.D
R2/RRR2-10/2	949.325	950.074	-1848.058	0.436	699.033	0.247	12	0.109	K.VELFSQAR.D
R2/RRR2-10/2	949.269	950.074	-1907.239	0.324	783.597	0.257	12	0.108	-.VELFSQAR.-
R2/RRR2-14/2	1515.320	1515.737	-276.059	0.471	1520.726	0.376	20	0.164	R.AGDGVFHFVVEIPK.E
R2/RRR2-14/2	1515.334	1515.737	-266.765	0.415	1327.323	0.328	19	0.139	R.AGDGVFHFVVEIPK.E
R2/RRR2-14/2	1070.982	1071.249	-250.206	0.443	898.337	0.467	15	0.135	K.IVAISLDDPK.A
R2/RRR2-14/2	1070.339	1071.249	-1789.822	0.405	824.899	0.460	15	0.130	K.IVAISLDDPK.A
R2/RRR2-14/2	1364.099	1364.439	-250.116	0.406	432.386	0.503	16	0.122	K.VIEETNESWEK.L
R2/RRR2-14/2	1071.035	1071.249	-200.466	0.324	728.750	0.388	14	0.116	K.IVAISLDDPK.A
R2/RRR2-14/3	1515.691	1515.737	-30.310	0.434	1197.899	0.433	27	0.111	R.AGDGVFHFVVEIPK.E
R2/RRR2-14/3	1515.371	1515.737	-242.043	0.377	955.881	0.286	25	0.074	R.AGDGVFHFVVEIPK.E
R2/RRR2-14/3	1515.944	1515.737	136.880	0.350	914.094	0.297	24	0.073	R.AGDGVFHFVVEIPK.E
R2/RRR2-20/2	1674.549	1672.880	-198.490	0.489	576.425	0.532	21	0.134	R.IIPNFM*CQGGDFTR.X
R2/RRR2-21/2	1657.227	1656.881	209.406	0.487	367.206	0.524	19	0.129	R.IIPNFMCQGGDFTR.X
R2/RRR2-20/2	1657.017	1656.881	82.416	0.436	411.390	0.507	19	0.127	R.IIPNFMCQGGDFTR.X
R2/RRR2-21/2	1658.137	1656.881	155.166	0.448	326.408	0.497	18	0.125	R.IIPNFMCQGGDFTR.X
R2/RRR2-20/2	1657.089	1656.881	125.636	0.447	293.926	0.488	18	0.125	R.IIPNFMCQGGDFTR.X

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1348.792	1349.621	-1360.046	0.323	932.870	0.411	16	0.124	R.VVMELFADTVPK.T
R2/RRR2-20/2	1673.630	1672.880	-149.950	0.392	403.675	0.492	19	0.124	R.IIPNFM*CQGGDFTR.X
R2/RRR2-20/2	1673.160	1672.880	167.668	0.420	366.651	0.484	18	0.124	R.IIPNFM*CQGGDFTR.X
R2/RRR2-20/2	1656.920	1656.881	23.379	0.423	233.875	0.469	17	0.123	R.IIPNFMCQGGDFTR.X
R2/RRR2-20/2	1657.237	1656.881	215.610	0.427	282.382	0.450	18	0.123	R.IIPNFMCQGGDFTR.X
R2/RRR2-21/2	1673.172	1672.880	174.984	0.314	420.847	0.521	19	0.121	R.IIPNFM*CQGGDFTR.X
R2/RRR2-21/2	1674.160	1672.880	167.275	0.313	363.790	0.490	18	0.119	R.IIPNFM*CQGGDFTR.X
R2/RRR2-21/2	1656.734	1656.881	-88.728	0.318	343.898	0.434	18	0.118	R.IIPNFMCQGGDFTR.X
R2/RRR2-20/2	1051.643	1052.291	-1571.096	0.365	644.996	0.402	14	0.117	R.VFFDILIGK.A
R2/RRR2-21/2	1674.186	1672.880	183.069	0.293	360.469	0.440	18	0.116	R.IIPNFM*CQGGDFTR.X
R2/RRR2-21/2	1674.216	1672.880	201.349	0.318	228.395	0.345	15	0.116	R.IIPNFM*CQGGDFTR.X
R2/RRR2-20/2	1673.154	1672.880	164.156	0.263	365.993	0.484	18	0.116	R.IIPNFM*CQGGDFTR.X
R2/RRR2-20/2	1672.318	1672.880	-936.822	0.177	269.828	0.302	18	0.112	R.IIPNFM*CQGGDFTR.X
R2/RRR2-20/2	1673.337	1672.880	273.745	0.162	418.342	0.438	19	0.107	R.IIPNFM*CQGGDFTR.X
R2/RRR2-19/2	1365.539	1365.620	-59.802	0.312	669.321	0.307	14	0.106	R.VVM*ELFADTVPK.T
R2/RRR2-4/2	1489.505	1489.698	-129.761	0.475	2331.970	0.512	22	0.325	K.AFVQQAEVILADGK.L
R2/RRR2-4/2	1197.416	1197.406	8.322	0.455	1037.023	0.476	18	0.146	K.IPADLIINAEK.A
R2/RRR2-4/2	1196.960	1197.406	-373.726	0.437	1138.231	0.423	18	0.144	K.IPADLIINAEK.A
R2/RRR2-4/2	1198.373	1197.406	-27.954	0.475	996.632	0.433	18	0.138	K.IPADLIINAEK.A
R2/RRR2-4/3	1665.681	1666.005	-194.879	0.441	1077.101	0.349	25	0.087	-.IRLDNALVQAVALLR.-
R2/RRR2-16/2	1606.264	1606.798	-957.882	0.521	3502.018	0.420	25	0.577	R.FQAQADAVNLICGAK.T
R2/RRR2-16/2	1130.123	1130.317	-171.350	0.340	531.366	0.455	13	0.115	R.VLVTPTSDLGK.I
R2/RRR2-16/2	1129.924	1130.317	-348.004	0.297	527.247	0.388	13	0.110	R.VLVTPTSDLGK.I
R2/RRR2-16/2	1129.407	1130.317	-1695.998	0.252	506.945	0.294	13	0.104	R.VLVTPTSDLGK.I
R2/RRR2-15/2	1442.301	1441.620	-221.784	0.602	1250.854	0.551	19	0.177	R.IYNQNLINHVGR.G
R2/RRR2-15/2	1397.197	1396.533	-241.299	0.511	1294.405	0.514	18	0.171	R.NNIQAYPSVSFR.Y
R2/RRR2-15/2	1440.667	1441.620	-1359.318	0.540	1346.928	0.477	19	0.170	R.IYNQNLINHVGR.G
R2/RRR2-15/2	1441.255	1441.620	-253.801	0.544	1291.283	0.478	19	0.165	R.IYNQNLINHVGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1397.065	1396.533	-335.971	0.499	1252.983	0.467	18	0.158	R.NNIQAYPSVSFR.Y
R2/RRR2-15/2	1396.129	1396.533	-290.243	0.475	1150.136	0.467	17	0.149	R.NNIQAYPSVSFR.Y
R2/RRR2-15/2	1122.443	1123.330	-1686.340	0.433	805.180	0.449	17	0.127	R.GALVSAGLGHIK.V
R2/RRR2-15/2	1122.393	1123.330	-1730.922	0.433	810.022	0.445	16	0.126	R.GALVSAGLGHIK.V
R2/RRR2-15/2	1396.574	1396.533	29.403	0.326	831.556	0.271	16	0.109	R.NNIQAYPSVSFR.Y
R2/RRR2-15/2	1397.167	1396.533	-262.862	0.368	671.913	0.275	14	0.106	R.NNIQAYPSVSFR.Y
R2/RRR2-6/2	1830.613	1832.130	-1927.202	0.480	2513.811	0.381	24	0.313	R.FKDVDLVIEAVIENVK.L
R2/RRR2-6/2	1209.211	1209.420	-173.407	0.420	1389.097	0.590	21	0.194	K.VPGATDLGLIPR.K
R2/RRR2-5/2	1209.412	1209.420	-6.541	0.454	1163.914	0.512	20	0.160	K.VPGATDLGLIPR.K
R2/RRR2-6/2	1208.773	1209.420	-1367.172	0.392	1037.536	0.492	19	0.145	K.VPGATDLGLIPR.K
R2/RRR2-5/2	1209.193	1209.420	-188.092	0.436	896.999	0.529	18	0.143	K.VPGATDLGLIPR.K
R2/RRR2-5/2	1685.117	1685.852	-1032.654	0.458	960.018	0.516	17	0.141	K.EANAFQGLLFADTCK.N
R2/RRR2-5/2	1209.371	1209.420	-40.760	0.380	736.395	0.506	17	0.130	K.VPGATDLGLIPR.K
R2/RRR2-6/2	1831.571	1832.130	-853.620	0.476	578.160	0.399	20	0.114	R.FKDVDLVIEAVIENVK.L
R2/RRR2-12/2	1614.330	1614.744	-257.611	0.501	1468.843	0.388	20	0.161	K.TWQGRPENVEAAQK.A
R2/RRR2-12/2	1614.294	1614.744	-279.764	0.489	1422.488	0.394	19	0.157	K.TWQGRPENVEAAQK.A
R2/RRR2-12/2	1614.297	1614.744	-277.639	0.501	1157.116	0.405	18	0.137	K.TWQGRPENVEAAQK.A
R2/RRR2-12/3	1129.547	1129.295	223.973	0.432	1813.396	0.261	23	0.129	R.AKANSLAQLGR.Y
R2/RRR2-12/2	1500.343	1499.771	-285.833	0.406	708.590	0.477	21	0.126	R.TVVSIPCGPSALAVK.E
R2/RRR2-12/2	1499.311	1499.771	-307.425	0.224	504.853	0.369	18	0.105	R.TVVSIPCGPSALAVK.E
R2/RRR2-12/2	1499.374	1499.771	-265.521	0.244	531.063	0.288	18	0.104	R.TVVSIPCGPSALAVK.E
R2/RRR2-12/3	1129.284	1129.295	-9.998	0.398	1586.001	0.247	22	0.102	R.AKANSLAQLGR.Y
R2/RRR2-9/2	1399.540	1398.607	-48.140	0.514	1151.133	0.513	20	0.160	K.IGM*DVAASEFLTK.D
R2/RRR2-9/2	1398.799	1398.607	137.923	0.495	1069.223	0.482	19	0.147	K.IGM*DVAASEFLTK.D
R2/RRR2-9/2	1058.563	1059.155	-1508.778	0.456	1133.877	0.379	15	0.137	R.IEEELGNVR.Y
R2/RRR2-9/2	1058.920	1059.155	-222.647	0.492	1061.774	0.333	15	0.127	R.IEEELGNVR.Y
R2/RRR2-9/2	1059.051	1059.155	-99.148	0.535	963.761	0.332	14	0.121	-.IEEELGNVR.-
R2/RRR2-8/2	1970.522	1970.255	135.974	0.477	849.406	0.444	22	0.126	K.ALQLPEYPNAAELEAVLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1969.501	1970.255	-893.243	0.414	783.546	0.402	22	0.118	K.ALQLPEYPNAAELEAVLK.T
R2/RRR2-9/2	1969.936	1970.255	-162.318	0.344	464.991	0.321	17	0.103	K.ALQLPEYPNAAELEAVLK.T
R2/RRR2-15/2	1712.763	1711.896	-77.891	0.536	1174.800	0.514	25	0.161	K.TEGVFSFLPASQATGAK.F
R2/RRR2-15/2	1711.368	1711.896	-895.906	0.503	1213.238	0.470	26	0.156	K.TEGVFSFLPASQATGAK.F
R2/RRR2-15/2	1711.363	1711.896	-898.484	0.455	1003.445	0.470	22	0.138	K.TEGVFSFLPASQATGAK.F
R2/RRR2-15/2	1132.000	1132.249	-220.819	0.449	713.521	0.433	17	0.123	K.AGNSVGLEVASK.Y
R2/RRR2-15/2	1131.929	1132.249	-283.570	0.467	633.898	0.424	16	0.120	K.AGNSVGLEVASK.Y
R2/RRR2-15/2	1131.502	1132.249	-1549.050	0.335	726.437	0.342	16	0.112	K.AGNSVGLEVASK.Y
R2/RRR2-15/3	1177.717	1177.292	362.177	0.394	758.865	0.425	19	0.084	K.NKTPNNVDFK.V
R2/RRR2-15/3	1177.418	1177.292	107.240	0.387	585.490	0.252	17	0.063	-.NKTPNNVDFK.-
R2/RRR2-9/2	1590.526	1589.821	-185.950	0.653	2993.225	0.666	24	0.525	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1589.069	1589.821	-1105.549	0.581	2935.960	0.680	25	0.518	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1589.422	1589.821	-251.942	0.601	2829.483	0.641	24	0.473	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1589.248	1589.821	-992.483	0.584	2801.953	0.627	24	0.460	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.267	1589.821	-980.731	0.508	2703.414	0.576	36	0.420	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1589.170	1589.821	-1041.686	0.594	2353.942	0.661	23	0.370	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.821	1589.821	-0.055	0.544	2317.064	0.545	33	0.310	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.741	1589.821	-50.193	0.583	2231.162	0.589	34	0.309	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.580	1589.821	-151.871	0.584	2176.695	0.584	34	0.294	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.400	1589.821	-265.358	0.480	2196.053	0.551	32	0.292	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.538	1589.821	-178.564	0.551	2169.026	0.563	32	0.288	K.THINIVVIGHVDSGK.S
R2/RRR2-11/3	1589.641	1589.821	-113.739	0.515	2246.048	0.503	32	0.279	K.THINIVVIGHVDSGK.S
R2/RRR2-2/3	1589.838	1589.821	10.919	0.536	2222.544	0.506	33	0.272	K.THINIVVIGHVDSGK.S
R2/RRR2-10/3	1590.053	1589.821	146.748	0.542	2105.531	0.544	31	0.268	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.903	1589.821	51.810	0.542	2086.038	0.542	31	0.263	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.727	1589.821	-59.436	0.564	1985.789	0.558	31	0.250	K.THINIVVIGHVDSGK.S
R2/RRR2-10/3	1589.785	1589.821	-22.813	0.533	2078.551	0.514	32	0.249	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.938	1589.821	73.987	0.553	1871.570	0.597	31	0.246	K.THINIVVIGHVDSGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/3	1589.923	1589.821	64.400	0.567	1916.720	0.564	31	0.240	K.THINIVVIGHVDSGK.S
R2/RRR2-2/3	1588.526	1589.821	-1448.729	0.459	1879.390	0.550	31	0.232	K.THINIVVIGHVDSGK.S
R2/RRR2-10/3	1589.824	1589.821	2.139	0.543	1892.420	0.540	32	0.225	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.834	1589.821	8.608	0.524	1930.255	0.518	31	0.225	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.896	1589.821	47.536	0.504	1703.560	0.576	30	0.212	K.THINIVVIGHVDSGK.S
R2/RRR2-10/3	1589.058	1589.821	-1112.384	0.487	1716.596	0.565	30	0.210	K.THINIVVIGHVDSGK.S
R2/RRR2-10/3	1590.212	1589.821	246.979	0.476	1812.436	0.521	31	0.208	K.THINIVVIGHVDSGK.S
R2/RRR2-2/3	1589.773	1589.821	-30.091	0.492	1718.591	0.537	29	0.201	K.THINIVVIGHVDSGK.S
R2/RRR2-1/3	1590.800	1589.821	-13.140	0.524	1744.936	0.520	29	0.198	K.THINIVVIGHVDSGK.S
R2/RRR2-1/3	1589.489	1589.821	-209.420	0.518	1689.062	0.534	29	0.195	K.THINIVVIGHVDSGK.S
R2/RRR2-10/3	1589.521	1589.821	-188.965	0.496	1546.261	0.564	28	0.186	K.THINIVVIGHVDSGK.S
R2/RRR2-11/3	1589.842	1589.821	13.576	0.492	1559.390	0.542	30	0.179	K.THINIVVIGHVDSGK.S
R2/RRR2-7/3	1591.011	1589.821	120.187	0.549	1653.664	0.501	29	0.177	K.THINIVVIGHVDSGK.S
R2/RRR2-4/3	1590.175	1589.821	223.540	0.442	1516.201	0.538	28	0.175	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.704	1589.821	-73.531	0.485	1522.252	0.500	28	0.163	K.THINIVVIGHVDSGK.S
R2/RRR2-2/2	1121.178	1121.268	-80.768	0.517	1032.634	0.532	15	0.153	K.STTTGHLIYK.L
R2/RRR2-2/2	1120.960	1121.268	-276.078	0.451	929.196	0.543	15	0.148	K.STTTGHLIYK.L
R2/RRR2-2/2	1122.073	1121.268	-174.435	0.497	1000.119	0.505	15	0.147	K.STTTGHLIYK.L
R2/RRR2-8/2	1121.054	1121.268	-191.412	0.430	882.680	0.527	14	0.141	K.STTTGHLIYK.L
R2/RRR2-13/3	1589.646	1589.821	-110.388	0.335	1341.718	0.483	28	0.139	K.THINIVVIGHVDSGK.S
R2/RRR2-8/2	1120.996	1121.268	-243.739	0.425	883.100	0.507	14	0.139	K.STTTGHLIYK.L
R2/RRR2-6/2	1121.223	1121.268	-40.689	0.482	900.789	0.488	14	0.138	K.STTTGHLIYK.L
R2/RRR2-4/2	1120.416	1121.268	-1658.466	0.354	934.972	0.469	14	0.134	K.STTTGHLIYK.L
R2/RRR2-10/3	1589.896	1589.821	47.421	0.452	1177.826	0.523	26	0.134	K.THINIVVIGHVDSGK.S
R2/RRR2-4/2	1121.159	1121.268	-98.024	0.407	855.476	0.474	14	0.133	K.STTTGHLIYK.L
R2/RRR2-9/2	1120.950	1121.268	-284.600	0.380	736.241	0.531	13	0.132	K.STTTGHLIYK.L
R2/RRR2-3/2	1121.000	1121.268	-239.588	0.477	769.602	0.489	13	0.131	K.STTTGHLIYK.L
R2/RRR2-5/2	1121.070	1121.268	-177.102	0.407	852.364	0.452	14	0.131	K.STTTGHLIYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1120.419	1121.268	-1655.182	0.357	847.294	0.461	14	0.130	K.STTTGHLIYK.L
R2/RRR2-6/2	1121.277	1121.268	7.795	0.432	756.405	0.461	14	0.129	K.STTTGHLIYK.L
R2/RRR2-9/2	1121.019	1121.268	-222.764	0.379	778.690	0.469	14	0.129	K.STTTGHLIYK.L
R2/RRR2-3/2	1121.112	1121.268	-139.309	0.414	723.000	0.481	13	0.128	K.STTTGHLIYK.L
R2/RRR2-8/2	1121.005	1121.268	-235.873	0.353	738.137	0.486	13	0.127	K.STTTGHLIYK.L
R2/RRR2-9/2	1589.619	1589.821	-127.442	0.364	669.957	0.551	16	0.127	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1121.148	1121.268	-107.417	0.365	783.524	0.442	14	0.126	K.STTTGHLIYK.L
R2/RRR2-3/2	1120.940	1121.268	-293.996	0.412	671.411	0.460	13	0.125	K.STTTGHLIYK.L
R2/RRR2-1/2	1120.945	1121.268	-288.751	0.387	756.356	0.443	13	0.125	K.STTTGHLIYK.L
R2/RRR2-6/2	1120.954	1121.268	-281.103	0.364	759.457	0.428	14	0.124	K.STTTGHLIYK.L
R2/RRR2-1/2	1120.825	1121.268	-396.819	0.362	612.097	0.476	13	0.124	K.STTTGHLIYK.L
R2/RRR2-4/2	1120.888	1121.268	-339.886	0.401	653.546	0.441	12	0.121	K.STTTGHLIYK.L
R2/RRR2-3/3	1588.471	1589.821	-1483.811	0.468	1269.466	0.440	27	0.121	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1120.901	1121.268	-328.741	0.330	728.804	0.416	13	0.120	K.STTTGHLIYK.L
R2/RRR2-11/2	1121.111	1121.268	-140.620	0.418	630.355	0.385	13	0.118	K.STTTGHLIYK.L
R2/RRR2-1/2	1120.397	1121.268	-1675.323	0.312	683.167	0.387	13	0.117	K.STTTGHLIYK.L
R2/RRR2-11/2	1120.246	1121.268	-1810.856	0.317	506.536	0.339	13	0.115	K.STTTGHLIYK.L
R2/RRR2-9/2	1120.960	1121.268	-275.313	0.297	622.094	0.315	13	0.112	K.STTTGHLIYK.L
R2/RRR2-13/3	1589.278	1589.821	-973.675	0.340	972.344	0.489	28	0.110	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1589.641	1589.821	-113.269	0.280	472.403	0.427	14	0.108	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1588.845	1589.821	-1247.187	0.295	359.704	0.474	12	0.108	K.THINIVVIGHVDSGK.S
R2/RRR2-9/2	1589.103	1589.821	-1083.952	0.286	357.138	0.348	12	0.105	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.298	1589.821	-961.068	0.303	834.767	0.485	28	0.102	K.THINIVVIGHVDSGK.S
R2/RRR2-8/3	1588.581	1589.821	-1414.343	0.354	579.706	0.483	24	0.096	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1588.804	1589.821	-1273.468	0.346	332.121	0.458	21	0.094	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.065	1589.821	-1108.450	0.383	302.634	0.424	21	0.094	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.170	1589.821	-1042.157	0.318	348.555	0.445	25	0.094	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1588.922	1589.821	-1198.358	0.296	359.844	0.469	22	0.093	K.THINIVVIGHVDSGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/3	1589.019	1589.821	-1137.029	0.336	408.683	0.430	26	0.092	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1589.297	1589.821	-961.530	0.334	403.717	0.363	25	0.089	K.THINIVVIGHVDSGK.S
R2/RRR2-3/3	1589.846	1589.821	15.655	0.352	1022.707	0.337	25	0.088	K.THINIVVIGHVDSGK.S
R2/RRR2-15/3	1590.483	1589.821	-212.907	0.395	748.915	0.369	23	0.085	K.THINIVVIGHVDSGK.S
R2/RRR2-9/3	1588.949	1589.821	-1181.348	0.236	479.785	0.362	27	0.085	K.THINIVVIGHVDSGK.S
R2/RRR2-13/3	1588.801	1589.821	-1275.204	0.191	952.501	0.342	29	0.084	K.THINIVVIGHVDSGK.S
R2/RRR2-8/2	1711.891	1712.969	-1217.263	0.410	1580.042	0.465	24	0.189	K.QTLDLGSTGLLPLEVR.F
R2/RRR2-8/2	1712.490	1712.969	-280.380	0.527	1251.405	0.563	23	0.176	K.QTLDLGSTGLLPLEVR.F
R2/RRR2-8/2	1712.741	1712.969	-133.579	0.517	1128.473	0.539	22	0.160	K.QTLDLGSTGLLPLEVR.F
R2/RRR2-8/2	1529.037	1528.646	256.429	0.356	685.689	0.351	16	0.111	R.WDEQFYGQDLVK.K
R2/RRR2-8/3	1552.829	1551.730	64.440	0.454	1410.516	0.335	27	0.106	R.HLHVYDWPGGELK.Q
R2/RRR2-8/3	1551.646	1551.730	-54.069	0.301	971.682	0.211	20	0.065	R.HLHVYDWPGGELK.Q
R2/RRR2-8/3	1551.423	1551.730	-198.143	0.326	971.174	0.197	22	0.064	R.HLHVYDWPGGELK.Q
R2/RRR2-8/2	1536.364	1536.756	-255.941	0.464	1132.718	0.496	21	0.154	K.AALAPYFELTNAVR.V
R2/RRR2-8/2	1535.518	1536.756	-1461.854	0.363	868.513	0.467	19	0.129	K.AALAPYFELTNAVR.V
R2/RRR2-8/2	1536.104	1536.756	-1078.788	0.309	773.320	0.411	18	0.117	K.AALAPYFELTNAVR.V
R2/RRR2-22/2	1832.523	1832.006	-264.153	0.552	3213.507	0.554	29	0.537	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-22/2	1830.916	1832.006	-1144.751	0.424	2988.021	0.477	29	0.448	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-22/2	1831.467	1832.006	-842.772	0.474	2578.090	0.587	29	0.392	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-21/2	1831.391	1832.006	-884.123	0.483	2295.672	0.533	28	0.313	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-21/2	1831.562	1832.006	-243.101	0.466	1750.521	0.504	27	0.216	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-22/2	978.976	979.072	-98.441	0.484	1039.194	0.523	14	0.153	R.GNLDIFSGR.G
R2/RRR2-23/2	978.754	979.072	-326.135	0.470	1072.939	0.510	14	0.153	R.GNLDIFSGR.G
R2/RRR2-22/2	978.941	979.072	-134.214	0.490	1027.704	0.521	14	0.152	R.GNLDIFSGR.G
R2/RRR2-23/2	1831.950	1832.006	-30.517	0.463	1126.890	0.504	27	0.152	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-24/2	978.920	979.072	-155.730	0.406	1027.459	0.533	14	0.151	R.GNLDIFSGR.G
R2/RRR2-24/2	978.360	979.072	-1755.419	0.408	1147.667	0.477	14	0.151	R.GNLDIFSGR.G
R2/RRR2-23/2	978.636	979.072	-447.030	0.446	1050.556	0.511	14	0.151	R.GNLDIFSGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	978.384	979.072	-1729.970	0.439	984.935	0.531	14	0.150	R.GNLDIFSGR.G
R2/RRR2-26/2	978.884	979.072	-192.633	0.471	1019.667	0.511	14	0.150	R.GNLDIFSGR.G
R2/RRR2-22/2	978.388	979.072	-1725.834	0.402	1004.903	0.527	14	0.149	R.GNLDIFSGR.G
R2/RRR2-21/2	978.753	979.072	-326.760	0.421	1107.462	0.468	14	0.147	R.GNLDIFSGR.G
R2/RRR2-26/2	979.844	979.072	-232.805	0.468	1035.158	0.475	14	0.145	R.GNLDIFSGR.G
R2/RRR2-21/2	978.781	979.072	-297.605	0.441	1037.604	0.464	14	0.143	R.GNLDIFSGR.G
R2/RRR2-21/2	978.638	979.072	-445.027	0.380	1065.811	0.461	14	0.142	R.GNLDIFSGR.G
R2/RRR2-26/2	978.340	979.072	-1775.853	0.427	997.552	0.474	14	0.142	R.GNLDIFSGR.G
R2/RRR2-24/2	978.549	979.072	-1560.892	0.441	918.145	0.503	13	0.141	R.GNLDIFSGR.G
R2/RRR2-21/2	1832.182	1832.006	96.455	0.455	960.941	0.507	26	0.141	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-24/2	1831.957	1832.006	-26.574	0.348	283.651	0.511	21	0.117	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-24/2	1831.787	1832.006	-119.952	0.331	163.653	0.358	16	0.110	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-24/2	1832.108	1832.006	56.095	0.282	213.735	0.421	18	0.110	K.GGTDSVIGVTLLGADGSGVR.I
R2/RRR2-13/2	1254.220	1254.504	-227.025	0.563	1725.636	0.580	20	0.238	K.INNAVAQVLLAK.R
R2/RRR2-9/2	1253.442	1254.504	-1649.781	0.448	1496.314	0.546	18	0.197	K.INNAVAQVLLAK.R
R2/RRR2-13/2	1254.408	1254.504	-76.875	0.534	1194.620	0.537	17	0.166	K.INNAVAQVLLAK.R
R2/RRR2-9/2	1253.718	1254.504	-1428.905	0.432	1253.194	0.476	17	0.158	K.INNAVAQVLLAK.R
R2/RRR2-9/3	1984.042	1984.197	-78.232	0.491	1408.418	0.441	33	0.134	R.IIAETGAGQHGVATATVCAR.F
R2/RRR2-9/3	1984.411	1984.197	108.361	0.508	1104.237	0.539	31	0.130	R.IIAETGAGQHGVATATVCAR.F
R2/RRR2-9/2	1934.397	1933.235	84.143	0.461	588.271	0.489	15	0.116	R.FGLQCIIYMGAQDMER.Q
R2/RRR2-10/2	1253.331	1254.504	-1738.922	0.322	798.382	0.372	16	0.116	K.INNAVAQVLLAK.R
R2/RRR2-13/3	1984.117	1984.197	-40.463	0.456	1198.277	0.442	31	0.115	R.IIAETGAGQHGVATATVCAR.F
R2/RRR2-9/3	1984.030	1984.197	-84.434	0.516	995.435	0.486	30	0.109	R.IIAETGAGQHGVATATVCAR.F
R2/RRR2-6/2	1687.645	1687.870	-133.897	0.504	2333.084	0.416	23	0.287	R.VVDSLDDLSLDIPSAK.S
R2/RRR2-6/2	1686.948	1687.870	-1142.506	0.421	1883.266	0.399	21	0.211	R.VVDSLDDLSLDIPSAK.S
R2/RRR2-6/2	1755.585	1755.946	-206.267	0.525	1154.697	0.582	21	0.171	K.SVAPIIEEYFSTGDVK.L
R2/RRR2-12/2	902.753	901.908	-171.242	0.345	876.052	0.184	16	0.102	-.GGGGGGGGGGVR.-
R2/RRR2-7/2	1688.338	1687.870	278.283	0.296	708.118	0.095	15	0.092	R.VVDSLDDLSLDIPSAK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	902.448	901.908	-510.343	0.261	633.654	0.173	15	0.089	-.GGGGGGGGGGVR.-
R2/RRR2-3/3	1822.708	1822.938	-126.578	0.540	1525.786	0.507	34	0.167	K.SSLAGEHAAAGNFDTAM*R.L
R2/RRR2-3/2	1722.241	1721.958	164.635	0.513	922.183	0.542	17	0.142	R.GPPALVFTFPQM*EDR.L
R2/RRR2-3/3	1822.808	1822.938	-71.559	0.509	1222.470	0.505	30	0.132	K.SSLAGEHAAAGNFDTAM*R.L
R2/RRR2-3/2	1190.062	1190.248	-156.238	0.435	985.376	0.312	17	0.120	K.GWSESASPNVR.G
R2/RRR2-3/2	1705.710	1705.958	-146.045	0.416	686.227	0.419	15	0.113	R.GPPALVFTFPQMEDR.L
R2/RRR2-2/2	1189.881	1190.248	-309.375	0.390	853.396	0.281	16	0.112	K.GWSESASPNVR.G
R2/RRR2-3/2	1190.018	1190.248	-193.077	0.427	853.784	0.239	16	0.104	-.GWSESASPNVR.-
R2/RRR2-3/2	1189.392	1190.248	-1565.067	0.326	687.816	0.200	15	0.104	K.GWSESASPNVR.G
R2/RRR2-11/2	1722.245	1721.958	167.194	0.267	389.187	0.340	11	0.100	-.GPPALVFTFPQM*EDR.-
R2/RRR2-9/2	1305.990	1306.406	-319.932	0.367	997.321	0.455	18	0.136	K.LGVSYNQPDGQK.L
R2/RRR2-9/2	1171.467	1170.381	73.620	0.532	801.883	0.437	14	0.124	-.LDVLSGLPEVK.-
R2/RRR2-9/2	1305.592	1306.406	-1393.888	0.350	866.954	0.404	17	0.122	K.LGVSYNQPDGQK.L
R2/RRR2-9/2	1170.635	1170.381	218.111	0.461	1032.645	0.279	15	0.115	K.LDVLSGLPEVK.L
R2/RRR2-9/3	1892.438	1892.191	131.290	0.411	1170.776	0.450	32	0.113	R.IEELVGVPVHYIGVGPGR.D
R2/RRR2-9/3	1891.979	1892.191	-112.324	0.334	866.848	0.483	29	0.096	R.IEELVGVPVHYIGVGPGR.D
R2/RRR2-9/2	1092.714	1093.215	-1378.036	0.492	1716.274	0.490	18	0.215	K.IGYDNAAAVAK.K
R2/RRR2-9/2	1092.888	1093.215	-300.197	0.489	1601.153	0.497	17	0.201	K.IGYDNAAAVAK.K
R2/RRR2-9/2	1235.948	1236.316	-298.438	0.403	1507.066	0.375	18	0.166	R.SLQNFDIGGER.E
R2/RRR2-9/2	1165.529	1166.306	-1528.617	0.394	717.606	0.444	17	0.124	R.LLGDASVSFEK.N
R2/RRR2-9/2	1166.050	1166.306	-220.041	0.471	574.394	0.407	16	0.120	R.LLGDASVSFEK.N
R2/RRR2-4/2	1869.626	1870.006	-204.033	0.467	949.804	0.426	21	0.129	K.TYEPSEEPFDISLVSR.E
R2/RRR2-12/2	1166.230	1166.349	-101.899	0.405	1095.530	0.493	18	0.150	R.LPTSVYSALSK.A
R2/RRR2-11/2	1594.845	1594.858	-8.001	0.474	975.857	0.501	24	0.143	R.VSAPAVTM*SFAGGAALK.L
R2/RRR2-11/2	1165.970	1166.349	-325.800	0.409	957.835	0.487	17	0.140	R.LPTSVYSALSK.A
R2/RRR2-11/2	858.055	858.021	39.581	0.482	1131.315	0.386	15	0.138	-.SAGLIGLAR.-
R2/RRR2-11/2	1166.118	1166.349	-198.925	0.429	919.123	0.468	16	0.136	R.LPTSVYSALSK.A
R2/RRR2-12/2	1165.559	1166.349	-1539.818	0.340	898.891	0.497	18	0.136	R.LPTSVYSALSK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	858.143	858.021	142.732	0.468	1088.929	0.345	15	0.130	R.SAGLIGLAR.N
R2/RRR2-11/2	857.835	858.021	-217.033	0.409	1114.881	0.335	15	0.130	R.SAGLIGLAR.N
R2/RRR2-12/2	857.736	858.021	-332.680	0.393	1097.411	0.338	15	0.129	R.SAGLIGLAR.N
R2/RRR2-11/2	858.043	858.021	25.883	0.389	1133.184	0.317	15	0.128	R.SAGLIGLAR.N
R2/RRR2-12/2	1165.635	1166.349	-1474.489	0.387	648.555	0.487	15	0.125	R.LPTSVYSALSK.A
R2/RRR2-11/2	1577.509	1578.858	-1493.415	0.283	512.180	0.343	17	0.103	R.VSAPAVTMSFAGGAALK.L
R2/RRR2-9/2	993.010	993.138	-129.292	0.417	620.595	0.479	15	0.128	R.VVGSEFVQK.Y
R2/RRR2-9/2	992.965	993.138	-175.167	0.372	451.328	0.423	14	0.119	R.VVGSEFVQK.Y
R2/RRR2-9/2	1067.044	1066.269	-211.198	0.313	720.916	0.363	14	0.114	R.LVFQVCTAK.M
R2/RRR2-9/2	1066.852	1066.269	-391.990	0.360	540.519	0.382	12	0.113	R.LVFQVCTAK.M
R2/RRR2-13/2	1290.288	1290.493	-159.475	0.454	1384.077	0.427	15	0.161	R.YQILAGVIEQR.M
R2/RRR2-13/2	1216.925	1217.442	-1250.560	0.391	1274.706	0.453	16	0.156	R.EALFVLAQLGR.K
R2/RRR2-13/2	1216.519	1217.442	-1586.025	0.394	1274.739	0.364	15	0.141	R.EALFVLAQLGR.K
R2/RRR2-13/2	1290.319	1290.493	-135.559	0.507	1236.003	0.378	16	0.141	R.YQILAGVIEQR.M
R2/RRR2-13/2	1290.267	1290.493	-175.894	0.439	1104.474	0.371	15	0.132	-.YQILAGVIEQR.-
R2/RRR2-13/2	1120.090	1119.335	-219.779	0.537	604.551	0.445	16	0.127	R.LLADDLFLAK.L
R2/RRR2-13/2	1118.563	1119.335	-1589.299	0.322	494.219	0.305	13	0.108	R.LLADDLFLAK.L
R2/RRR2-11/3	1513.875	1513.812	41.472	0.592	3635.450	0.565	39	0.730	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-11/3	1513.332	1513.812	-318.704	0.574	3176.016	0.523	37	0.541	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-10/3	1513.420	1513.812	-260.194	0.526	2810.908	0.562	36	0.456	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-11/2	1513.470	1513.812	-227.211	0.501	2741.739	0.539	26	0.425	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-11/3	1513.460	1513.812	-233.491	0.562	2486.149	0.534	34	0.353	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-16/3	1515.239	1513.812	282.229	0.489	2338.561	0.482	32	0.300	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-11/3	1513.455	1513.812	-236.646	0.526	1915.523	0.463	31	0.207	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-11/3	1512.825	1513.812	-1317.718	0.406	742.812	0.385	25	0.082	K.HLGVVGLGGLGHLGVK.F
R2/RRR2-14/2	950.979	950.117	-145.692	0.481	657.736	0.396	14	0.122	K.YLSGLGIAR.Q
R2/RRR2-13/2	950.165	950.117	51.207	0.415	747.545	0.331	14	0.117	K.YLSGLGIAR.Q
R2/RRR2-13/2	1592.448	1592.775	-206.254	0.380	721.644	0.440	17	0.116	R.DSVLGFSVNVPGTTAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	950.138	950.117	22.859	0.488	708.492	0.317	14	0.116	K.YLSGLGIAR.Q
R2/RRR2-13/2	949.874	950.117	-256.585	0.437	640.812	0.319	14	0.115	K.YLSGLGIAR.Q
R2/RRR2-13/2	1329.007	1329.398	-295.229	0.351	1080.966	0.377	18	0.066	R.DGLLQGQATTTSH.-
R2/RRR2-9/2	1447.236	1447.533	-206.392	0.570	1611.589	0.567	25	0.221	R.EVEAIGGNVSASASR.E
R2/RRR2-9/2	1447.085	1447.533	-310.990	0.504	1504.507	0.514	24	0.194	R.EVEAIGGNVSASASR.E
R2/RRR2-9/2	1720.392	1721.011	-944.369	0.420	1396.324	0.431	21	0.163	K.AYVPEMVEVLIDSVR.N
R2/RRR2-9/2	1509.615	1509.688	-48.144	0.469	511.736	0.493	18	0.122	K.QSSGGLFSWLLGEK.S
R2/RRR2-9/2	1736.411	1737.011	-924.219	0.306	440.696	0.276	17	0.105	K.AYVPEM*VEVLIDSVR.N
R2/RRR2-9/2	1736.690	1737.011	-185.231	0.336	337.026	0.339	14	0.104	-.AYVPEM*VEVLIDSVR.-
R2/RRR2-8/2	1606.871	1607.833	-1224.662	0.429	2025.949	0.387	23	0.231	R.SPPIEEVIQSGVVPR.F
R2/RRR2-8/2	1607.449	1607.833	-239.443	0.477	1706.450	0.448	22	0.202	R.SPPIEEVIQSGVVPR.F
R2/RRR2-8/3	1968.499	1968.415	43.058	0.346	1259.896	0.342	29	0.098	R.LVELLLHPSPSVLIPALR.T
R2/RRR2-10/2	1298.157	1298.471	-241.977	0.453	1269.159	0.539	19	0.174	R.LLAGESGIGPIDR.F
R2/RRR2-10/2	1122.807	1123.233	-380.197	0.384	947.730	0.444	16	0.132	R.SDGLGVSSCIK.Q
R2/RRR2-9/2	1054.916	1055.125	-199.003	0.445	715.627	0.352	13	0.116	R.FDASNFPTR.F
R2/RRR2-10/2	1056.047	1055.125	-74.155	0.413	614.388	0.327	13	0.111	-.FDASNFPTR.-
R2/RRR2-8/2	1331.158	1331.414	-192.841	0.475	1078.595	0.462	16	0.143	R.GSNQLVIDEAER.S
R2/RRR2-8/2	1328.614	1327.597	12.753	0.270	698.365	0.353	13	0.106	K.IAVIQFQVSPPK.T
R2/RRR2-8/2	930.437	931.069	-1759.378	0.402	1102.296	0.147	13	0.105	K.IDDIVTVR.-
R2/RRR2-12/2	1205.958	1206.288	-274.386	0.455	1179.985	0.520	21	0.164	R.VIGSGTNLDSSR.F
R2/RRR2-12/2	1205.961	1206.288	-272.558	0.447	994.822	0.575	20	0.158	R.VIGSGTNLDSSR.F
R2/RRR2-12/2	1206.992	1206.288	-246.661	0.440	866.204	0.576	19	0.149	R.VIGSGTNLDSSR.F
R2/RRR2-12/2	1904.601	1904.026	-223.621	0.411	862.621	0.497	20	0.131	K.ASSLSELGFDADGPSFFR.H
R2/RRR2-12/3	1685.890	1685.929	-23.372	0.390	1110.320	0.373	25	0.093	R.GEM*LDLQHAAAFLPR.V
R2/RRR2-6/2	1498.202	1497.679	-318.930	0.433	1333.091	0.475	18	0.166	R.SFASVSAAQFPWAK.M
R2/RRR2-6/2	913.516	913.100	457.422	0.407	872.366	0.354	12	0.118	R.GILLNGAVR.K
R2/RRR2-6/3	1506.586	1506.598	-7.373	0.440	1182.870	0.402	27	0.104	R.TKNEAALEAATDSGK.Q
R2/RRR2-6/3	1506.343	1506.598	-169.285	0.427	1167.101	0.390	26	0.101	R.TKNEAALEAATDSGK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1506.507	1506.598	-60.037	0.457	1018.334	0.390	25	0.092	R.TKNEAALEAATDSGK.Q
R2/RRR2-7/3	1506.968	1506.598	246.363	0.377	737.966	0.312	23	0.072	-.TKNEAALEAATDSGK.-
R2/RRR2-17/2	1676.367	1675.904	277.130	0.508	866.941	0.598	21	0.151	K.ALADEIGIPFLETSAK.D
R2/RRR2-17/2	1676.226	1675.904	192.497	0.464	748.573	0.479	20	0.127	K.ALADEIGIPFLETSAK.D
R2/RRR2-17/2	1675.447	1675.904	-273.645	0.445	661.886	0.485	19	0.123	K.ALADEIGIPFLETSAK.D
R2/RRR2-17/3	1923.027	1922.177	-78.624	0.439	1112.530	0.499	34	0.119	R.M*ASQPATNASKPATVQM*R.G
R2/RRR2-17/3	1922.313	1922.177	70.610	0.427	1011.641	0.408	30	0.095	R.M*ASQPATNASKPATVQM*R.G
R2/RRR2-17/3	1921.934	1922.177	-126.798	0.384	859.600	0.411	31	0.088	R.M*ASQPATNASKPATVQM*R.G
R2/RRR2-17/3	1921.452	1922.177	-900.783	0.368	783.894	0.420	30	0.086	R.M*ASQPATNASKPATVQM*R.G
R2/RRR2-17/3	1905.870	1906.178	-161.781	0.311	416.087	0.391	25	0.078	R.MASQPATNASKPATVQM*R.G
R2/RRR2-6/2	1702.472	1702.803	-195.298	0.525	1851.100	0.510	21	0.239	R.FTTEVSNYLAQGESR.E
R2/RRR2-6/2	1293.395	1293.539	-111.287	0.527	803.908	0.537	16	0.140	R.FAAFLSPLTLGR.V
R2/RRR2-6/2	1458.930	1457.671	177.780	0.348	773.248	0.263	13	0.102	K.SSSFQMDLLCLR.E
R2/RRR2-18/2	1877.462	1878.113	-881.535	0.576	2895.574	0.608	26	0.481	R.IVNAGGECLTFDQLALR.A
R2/RRR2-18/2	1878.562	1878.113	239.742	0.657	2781.779	0.600	24	0.445	R.IVNAGGECLTFDQLALR.A
R2/RRR2-20/2	1878.090	1878.113	-12.100	0.610	2710.872	0.597	24	0.428	R.IVNAGGECLTFDQLALR.A
R2/RRR2-18/2	1878.373	1878.113	138.864	0.654	2737.131	0.581	25	0.426	R.IVNAGGECLTFDQLALR.A
R2/RRR2-18/2	1183.123	1182.398	-232.699	0.480	1650.652	0.536	19	0.212	R.APLGQNTVLLR.G
R2/RRR2-17/2	1183.525	1182.398	107.422	0.480	1568.507	0.508	19	0.196	R.APLGQNTVLLR.G
R2/RRR2-18/2	1181.664	1182.398	-1471.999	0.513	1457.147	0.513	19	0.186	R.APLGQNTVLLR.G
R2/RRR2-20/2	1182.475	1182.398	65.686	0.435	1475.527	0.510	19	0.186	R.APLGQNTVLLR.G
R2/RRR2-18/2	1182.684	1182.398	242.391	0.502	1392.950	0.537	19	0.185	R.APLGQNTVLLR.G
R2/RRR2-18/2	1181.939	1182.398	-389.145	0.462	1455.624	0.509	18	0.184	R.APLGQNTVLLR.G
R2/RRR2-18/2	1182.673	1182.398	233.076	0.486	1401.751	0.483	18	0.174	R.APLGQNTVLLR.G
R2/RRR2-18/2	1182.135	1182.398	-223.158	0.504	1290.074	0.528	18	0.173	R.APLGQNTVLLR.G
R2/RRR2-20/2	1183.091	1182.398	-260.027	0.495	1301.385	0.514	18	0.171	R.APLGQNTVLLR.G
R2/RRR2-18/2	1182.629	1182.398	195.710	0.450	1361.813	0.483	19	0.170	R.APLGQNTVLLR.G
R2/RRR2-20/2	1182.117	1182.398	-238.180	0.467	1189.324	0.503	18	0.160	R.APLGQNTVLLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1182.696	1182.398	252.844	0.480	1178.250	0.491	18	0.157	R.APLGQNTVLLR.G
R2/RRR2-19/2	1183.074	1182.398	-275.037	0.401	1241.629	0.448	17	0.152	R.APLGQNTVLLR.G
R2/RRR2-20/2	1183.352	1182.398	-39.070	0.450	1122.123	0.483	17	0.151	R.APLGQNTVLLR.G
R2/RRR2-17/2	1182.492	1182.398	80.078	0.427	1057.495	0.470	17	0.144	R.APLGQNTVLLR.G
R2/RRR2-20/2	1182.205	1182.398	-163.905	0.441	997.674	0.479	17	0.143	R.APLGQNTVLLR.G
R2/RRR2-20/2	1182.089	1182.398	-262.111	0.379	644.594	0.494	15	0.127	R.APLGQNTVLLR.G
R2/RRR2-17/2	1183.233	1182.398	-139.963	0.374	547.754	0.429	13	0.118	R.APLGQNTVLLR.G
R2/RRR2-18/3	1877.447	1878.113	-889.701	0.474	1289.673	0.419	28	0.118	R.IVNAGGECLTFDQLALR.A
R2/RRR2-18/2	1181.802	1182.398	-1354.757	0.256	469.209	0.429	12	0.112	R.APLGQNTVLLR.G
R2/RRR2-9/2	1183.458	1182.398	51.251	0.243	480.403	0.297	13	0.110	R.APLGQNTVLLR.G
R2/RRR2-18/2	1181.512	1182.398	-1601.412	0.181	334.416	0.468	12	0.108	R.APLGQNTVLLR.G
R2/RRR2-18/2	1182.000	1182.398	-337.851	0.245	329.294	0.370	10	0.105	-.APLGQNTVLLR.-
R2/RRR2-18/3	1877.639	1878.113	-252.922	0.445	941.483	0.347	26	0.080	R.IVNAGGECLTFDQLALR.A
R2/RRR2-8/2	1951.374	1952.120	-897.148	0.531	1349.380	0.576	22	0.187	K.GLHSSLNHLANEFDQIR.S
R2/RRR2-8/2	1426.314	1426.561	-173.452	0.497	1236.402	0.487	19	0.160	R.SSGGFWTWLTGAR.S
R2/RRR2-8/2	1951.539	1952.120	-812.250	0.435	680.434	0.555	20	0.131	K.GLHSSLNHLANEFDQIR.S
R2/RRR2-8/2	1426.313	1426.561	-173.967	0.458	891.470	0.444	17	0.129	R.SSGGFWTWLTGAR.S
R2/RRR2-8/2	1951.432	1952.120	-867.445	0.482	793.286	0.495	20	0.129	K.GLHSSLNHLANEFDQIR.S
R2/RRR2-8/2	1426.183	1426.561	-265.498	0.469	793.752	0.443	15	0.123	R.SSGGFWTWLTGAR.S
R2/RRR2-8/3	1644.853	1644.891	-23.650	0.345	964.163	0.445	30	0.094	K.AVDGVTLKDITALAEK.I
R2/RRR2-8/3	1644.218	1644.891	-1021.042	0.380	612.253	0.408	25	0.079	K.AVDGVTLKDITALAEK.I
R2/RRR2-8/2	1039.274	1039.210	61.660	0.483	855.140	0.420	15	0.128	K.SPELAGPVLR.L
R2/RRR2-8/3	1319.755	1319.495	197.492	0.460	707.252	0.555	21	0.103	K.IGVLTHSHGEIR.H
R2/RRR2-7/2	1601.252	1600.839	258.857	0.371	809.541	0.230	16	0.098	R.GLLATDAALLLNADTK.A
R2/RRR2-1/2	1040.222	1039.210	10.875	0.216	406.495	0.268	10	0.091	-.SPELAGPVLR.-
R2/RRR2-8/3	1319.145	1319.495	-265.889	0.420	745.565	0.420	21	0.084	K.IGVLTHSHGEIR.H
R2/RRR2-6/2	1651.278	1650.856	256.205	0.520	1130.988	0.452	19	0.144	R.QFLTLNALNEFDPK.I
R2/RRR2-6/2	1650.571	1650.856	-173.103	0.464	936.165	0.367	18	0.121	R.QFLTLNALNEFDPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1650.108	1650.856	-1062.353	0.384	975.400	0.266	17	0.110	R.QFLTLNALNEFDPK.I
R2/RRR2-7/2	1651.061	1650.856	124.463	0.419	662.109	0.212	17	0.099	-.QFLTLNALNEFDPK.-
R2/RRR2-6/3	1340.438	1340.512	-55.327	0.414	1264.498	0.323	22	0.093	R.SIHSWDIVVQR.V
R2/RRR2-6/3	1439.491	1439.510	-13.075	0.463	731.279	0.439	23	0.088	R.CEVHAVNADPGGGR.Q
R2/RRR2-6/3	1439.555	1439.510	31.961	0.442	747.875	0.426	23	0.086	R.CEVHAVNADPGGGR.Q
R2/RRR2-6/3	1439.121	1439.510	-270.607	0.396	572.837	0.386	21	0.078	R.CEVHAVNADPGGGR.Q
R2/RRR2-6/3	1340.234	1340.512	-208.263	0.408	1259.572	0.223	23	0.075	R.SIHSWDIVVQR.V
R2/RRR2-10/2	1562.165	1562.774	-1033.342	0.497	2877.550	0.483	25	0.425	K.M*GQIGVLSGTQGEIR.L
R2/RRR2-10/2	1562.337	1562.774	-280.508	0.475	2517.005	0.423	24	0.324	K.M*GQIGVLSGTQGEIR.L
R2/RRR2-11/2	1562.340	1562.774	-278.705	0.488	2335.170	0.422	24	0.288	K.M*GQIGVLSGTQGEIR.L
R2/RRR2-11/2	1561.781	1562.774	-1279.757	0.447	1943.277	0.455	22	0.234	K.M*GQIGVLSGTQGEIR.L
R2/RRR2-10/2	1562.289	1562.774	-311.237	0.480	1854.436	0.405	22	0.208	K.M*GQIGVLSGTQGEIR.L
R2/RRR2-11/2	893.899	894.010	-124.588	0.316	865.479	0.350	13	0.118	K.ATVNSFVR.S
R2/RRR2-10/2	894.093	894.010	92.898	0.351	614.953	0.393	12	0.118	K.ATVNSFVR.S
R2/RRR2-11/2	893.551	894.010	-515.151	0.345	672.471	0.370	12	0.116	K.ATVNSFVR.S
R2/RRR2-10/2	894.032	894.010	24.841	0.329	724.751	0.348	12	0.114	-.ATVNSFVR.-
R2/RRR2-10/3	1562.703	1562.755	-33.942	0.447	1831.555	0.285	32	0.139	K.AVAHQPVSVAIEAGGR.E
R2/RRR2-10/3	1562.825	1562.755	44.795	0.423	1829.109	0.260	30	0.134	K.AVAHQPVSVAIEAGGR.E
R2/RRR2-10/2	1791.423	1791.894	-263.310	0.498	943.650	0.445	23	0.134	K.VVSIDGFEDVPQNDEK.S
R2/RRR2-10/2	1791.400	1791.894	-276.095	0.493	910.969	0.447	23	0.132	K.VVSIDGFEDVPQNDEK.S
R2/RRR2-10/2	1791.401	1791.894	-275.889	0.442	837.757	0.470	21	0.130	K.VVSIDGFEDVPQNDEK.S
R2/RRR2-10/2	1526.993	1527.665	-1098.455	0.511	629.495	0.417	19	0.121	R.EFQLYHSGVFSGR.C
R2/RRR2-6/2	1488.495	1488.622	-85.925	0.502	1710.766	0.595	22	0.237	K.IDSPSGVDVTVSPSK.L
R2/RRR2-5/2	1488.176	1488.622	-300.346	0.448	1738.301	0.566	23	0.233	K.IDSPSGVDVTVSPSK.L
R2/RRR2-5/2	1488.234	1488.622	-261.339	0.429	1704.271	0.555	23	0.225	K.IDSPSGVDVTVSPSK.L
R2/RRR2-5/2	1338.162	1337.421	-194.027	0.526	1496.997	0.566	21	0.204	R.NVGSNANAVYEAK.I
R2/RRR2-5/2	1337.058	1337.421	-271.932	0.481	1486.437	0.509	21	0.189	R.NVGSNANAVYEAK.I
R2/RRR2-5/2	1488.365	1488.622	-173.213	0.407	1500.497	0.507	22	0.188	K.IDSPSGVDVTVSPSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1338.044	1337.421	-282.621	0.535	1333.605	0.552	20	0.183	R.NVGSNANAVYEAK.I
R2/RRR2-6/2	1488.058	1488.622	-1054.214	0.411	1308.556	0.542	21	0.174	K.IDSPSGVDVTVSPSK.L
R2/RRR2-6/2	1337.175	1337.421	-183.915	0.500	1238.689	0.528	20	0.169	R.NVGSNANAVYEAK.I
R2/RRR2-6/2	1338.567	1337.421	109.798	0.527	1124.851	0.518	19	0.157	R.NVGSNANAVYEAK.I
R2/RRR2-6/2	1847.869	1846.072	-110.625	0.561	778.420	0.581	22	0.144	R.TGDLNYPAFAVVLSSYK.D
R2/RRR2-3/2	1046.531	1047.146	-1548.354	0.238	979.833	0.252	13	0.108	R.AFADPELQR.D
R2/RRR2-7/2	1504.142	1503.597	-303.507	0.491	1368.719	0.460	21	0.167	R.ASQPTDTTTSPLAGR.L
R2/RRR2-7/2	1332.671	1332.525	109.548	0.390	812.123	0.414	18	0.122	K.IATTATEIVDVAK.M
R2/RRR2-7/2	1332.502	1332.525	-17.238	0.292	509.597	0.378	16	0.108	K.IATTATEIVDVAK.M
R2/RRR2-7/2	1072.257	1072.240	15.117	0.316	937.274	0.221	15	0.108	K.DIGAVNTIIR.K
R2/RRR2-7/2	1071.940	1072.240	-280.821	0.266	938.900	0.200	14	0.105	K.DIGAVNTIIR.K
R2/RRR2-16/3	1981.658	1981.147	-247.215	0.533	2920.292	0.560	37	0.502	K.DLSVIATEVGEEGQEYLK.L
R2/RRR2-16/3	1981.166	1981.147	9.720	0.572	1896.843	0.606	34	0.264	K.DLSVIATEVGEEGQEYLK.L
R2/RRR2-16/2	1980.527	1981.147	-820.268	0.550	1854.967	0.561	23	0.248	K.DLSVIATEVGEEGQEYLK.L
R2/RRR2-16/2	1980.904	1981.147	-122.604	0.529	1711.705	0.536	22	0.220	K.DLSVIATEVGEEGQEYLK.L
R2/RRR2-16/2	1981.237	1981.147	46.002	0.551	1567.964	0.595	22	0.216	K.DLSVIATEVGEEGQEYLK.L
R2/RRR2-16/3	1980.633	1981.147	-766.605	0.491	1442.937	0.497	31	0.155	K.DLSVIATEVGEEGQEYLK.L
R2/RRR2-16/3	1245.472	1245.408	51.785	0.527	1338.221	0.273	22	0.087	-.AREVLLEASEK.-
R2/RRR2-16/3	1245.372	1245.408	-28.582	0.473	840.337	0.255	18	0.056	-.AREVLLEASEK.-
R2/RRR2-7/2	1196.839	1197.453	-1352.160	0.393	1501.495	0.341	16	0.156	K.ELVQNLLVLR.F
R2/RRR2-8/2	1197.305	1197.453	-123.797	0.511	1530.283	0.318	16	0.153	K.ELVQNLLVLR.F
R2/RRR2-7/2	1197.323	1197.453	-108.559	0.447	1446.911	0.341	16	0.152	K.ELVQNLLVLR.F
R2/RRR2-8/2	1197.365	1197.453	-73.481	0.532	1480.348	0.330	16	0.151	K.ELVQNLLVLR.F
R2/RRR2-7/2	1198.382	1197.453	-59.013	0.506	1421.540	0.343	16	0.149	K.ELVQNLLVLR.F
R2/RRR2-8/2	1197.175	1197.453	-232.525	0.484	1485.194	0.305	16	0.147	K.ELVQNLLVLR.F
R2/RRR2-8/2	1290.354	1289.465	-86.689	0.295	549.462	0.438	16	0.114	R.DNIANVQIVFR.E
R2/RRR2-7/3	1702.384	1701.950	255.986	0.450	1095.889	0.438	25	0.105	R.VNNERWEGVPFILK.A
R2/RRR2-8/2	1289.592	1289.465	98.492	0.242	446.541	0.256	11	0.097	-.DNIANVQIVFR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/3	1701.816	1701.950	-78.687	0.363	652.392	0.257	22	0.067	R.VNNERWEGVPFILK.A
R2/RRR2-5/2	1325.442	1325.561	-89.968	0.478	1293.454	0.396	17	0.150	R.FPM*FLEAINAR.Y
R2/RRR2-5/2	1887.658	1887.128	-249.692	0.475	1029.433	0.521	20	0.147	R.IDLAEALEQLHPSFFR.F
R2/RRR2-5/2	1886.995	1887.128	-70.634	0.487	996.641	0.421	20	0.130	R.IDLAEALEQLHPSFFR.F
R2/RRR2-5/2	1325.201	1325.561	-272.364	0.393	759.725	0.442	14	0.122	R.FPM*FLEAINAR.Y
R2/RRR2-5/2	1886.364	1887.128	-937.543	0.411	633.672	0.393	17	0.111	R.IDLAEALEQLHPSFFR.F
R2/RRR2-5/3	1405.413	1404.593	-128.823	0.396	1215.325	0.157	23	0.064	R.KPDQLVVNEFSK.F
R2/RRR2-3/2	1761.441	1762.040	-910.753	0.464	2205.372	0.410	22	0.264	K.LVENYAELLASQGLLK.T
R2/RRR2-3/2	1761.549	1762.040	-279.731	0.480	2079.412	0.413	22	0.243	K.LVENYAELLASQGLLK.T
R2/RRR2-3/2	1762.179	1762.040	78.887	0.533	2009.242	0.439	22	0.238	K.LVENYAELLASQGLLK.T
R2/RRR2-3/2	1939.474	1939.115	186.002	0.488	1368.142	0.457	19	0.161	K.SVGSSAQAEISYLTWNPK.F
R2/RRR2-4/3	1494.850	1494.592	173.417	0.483	1091.377	0.464	25	0.110	R.NQKPLTSFSDSNR.T
R2/RRR2-4/2	1938.412	1939.115	-881.104	0.419	777.769	0.309	18	0.104	K.SVGSSAQAEISYLTWNPK.F
R2/RRR2-4/3	1494.788	1494.592	131.528	0.441	1054.252	0.421	24	0.099	R.NQKPLTSFSDSNR.T
R2/RRR2-3/3	1494.508	1494.592	-56.095	0.377	495.980	0.402	19	0.080	R.NQKPLTSFSDSNR.T
R2/RRR2-7/3	1493.928	1494.592	-1116.957	0.267	673.795	0.275	21	0.068	R.NQKPLTSFSDSNR.T
R2/RRR2-4/3	1761.526	1762.040	-861.854	0.396	1036.218	0.121	23	0.051	-.LVENYAELLASQGLLK.-
R2/RRR2-8/3	1711.363	1711.857	-289.158	0.452	769.553	0.515	25	0.100	K.GASEEHLSDFLQHIK.Y
R2/RRR2-8/3	1954.468	1955.202	-889.909	0.363	1184.833	0.378	28	0.100	K.AAWQIFTPLLHDIDEGK.V
R2/RRR2-8/3	1711.747	1711.857	-64.211	0.491	519.869	0.506	22	0.090	K.GASEEHLSDFLQHIK.Y
R2/RRR2-8/3	1954.531	1955.202	-857.557	0.317	835.370	0.441	27	0.087	K.AAWQIFTPLLHDIDEGK.V
R2/RRR2-6/2	1789.063	1789.966	-1066.550	0.520	1887.170	0.427	23	0.217	R.ASSGDLDNTNIISQILK.L
R2/RRR2-6/2	1790.299	1789.966	186.728	0.581	1578.123	0.498	20	0.191	R.ASSGDLDNTNIISQILK.L
R2/RRR2-6/3	1706.990	1706.969	12.393	0.486	1557.681	0.499	28	0.169	R.LGQSKPIYQAFNAIR.N
R2/RRR2-5/2	1789.503	1789.966	-259.351	0.428	891.145	0.342	18	0.112	R.ASSGDLDNTNIISQILK.L
R2/RRR2-6/3	1750.029	1748.958	40.668	0.345	1035.240	0.231	24	0.068	-.FNQIEQELEKLTQK.-
R2/RRR2-5/3	1707.393	1706.969	248.709	0.292	636.776	0.273	18	0.056	-.LGQSKPIYQAFNAIR.-
R2/RRR2-12/2	1608.541	1608.731	-118.788	0.571	2993.543	0.473	24	0.453	R.VEEEGDVATAFTLAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1608.041	1608.731	-1054.512	0.451	2587.822	0.425	24	0.344	R.VEEEGDVATAFTLAR.I
R2/RRR2-12/2	1421.242	1421.767	-1075.830	0.412	713.761	0.441	14	0.119	K.LLLNFPM*VVCAK.V
R2/RRR2-3/2	1103.131	1103.210	-71.323	0.437	1062.749	0.601	16	0.166	R.TSGYSVSFVR.L
R2/RRR2-3/2	1542.196	1542.718	-989.658	0.477	1224.014	0.405	19	0.144	R.FGPIIEQNVDPANK.G
R2/RRR2-3/2	1103.136	1103.210	-67.327	0.341	1041.660	0.480	16	0.141	R.TSGYSVSFVR.L
R2/RRR2-3/2	1103.039	1103.210	-155.134	0.292	585.504	0.384	14	0.112	R.TSGYSVSFVR.L
R2/RRR2-3/2	1200.332	1200.453	-100.942	0.309	721.387	0.316	16	0.109	K.LLDSIVALLSR.T
R2/RRR2-5/2	1208.952	1209.379	-353.714	0.532	2745.551	0.656	21	0.468	R.VPAGAAALYYGR.G
R2/RRR2-5/2	1209.227	1209.379	-125.918	0.522	2883.701	0.561	21	0.463	R.VPAGAAALYYGR.G
R2/RRR2-5/2	1731.655	1730.948	-169.452	0.402	442.848	0.452	17	0.111	R.TPAFLGLSAGAGAWPASR.Y
R2/RRR2-5/2	1731.535	1730.948	-239.184	0.365	699.370	0.363	19	0.109	R.TPAFLGLSAGAGAWPASR.Y
R2/RRR2-2/2	1860.513	1861.044	-825.272	0.487	1935.065	0.508	22	0.252	R.LDIDFAEVYANSALYR.S
R2/RRR2-6/2	1304.126	1304.386	-199.749	0.476	897.928	0.480	17	0.138	K.TIDEIEAELDR.L
R2/RRR2-6/3	1319.856	1319.540	240.241	0.499	1210.205	0.262	23	0.079	R.LQHPWVGIVNR.S
R2/RRR2-6/3	1104.796	1104.374	383.976	0.560	635.465	0.311	18	0.079	R.RPLVLQLHK.T
R2/RRR2-6/3	1104.270	1104.374	-93.659	0.538	612.326	0.322	17	0.079	R.RPLVLQLHK.T
R2/RRR2-6/3	1104.078	1104.374	-268.168	0.537	922.786	0.304	21	0.078	R.RPLVLQLHK.T
R2/RRR2-3/2	1687.590	1687.920	-195.932	0.506	1692.814	0.577	22	0.232	R.AVSDEIKNVIIASATR.K
R2/RRR2-3/2	1687.374	1687.920	-918.659	0.474	1721.871	0.521	21	0.221	R.AVSDEIKNVIIASATR.K
R2/RRR2-3/2	1486.340	1486.653	-211.176	0.379	1321.544	0.359	19	0.142	R.LASSLSSPATPADLR.A
R2/RRR2-3/2	1237.037	1236.402	-295.997	0.497	1024.159	0.442	18	0.141	K.LNNVITHPEAK.H
R2/RRR2-3/2	1236.219	1236.402	-148.523	0.462	1118.726	0.377	16	0.134	K.LNNVITHPEAK.H
R2/RRR2-3/2	1486.209	1486.653	-299.590	0.398	1215.822	0.329	19	0.132	-.LASSLSSPATPADLR.-
R2/RRR2-3/2	1236.465	1236.402	50.342	0.449	625.537	0.441	13	0.119	K.LNNVITHPEAK.H
R2/RRR2-3/2	1486.109	1486.653	-1041.920	0.355	799.963	0.273	17	0.106	-.LASSLSSPATPADLR.-
R2/RRR2-1/3	1236.483	1236.402	65.183	0.378	1100.683	0.301	22	0.079	K.LNNVITHPEAK.H
R2/RRR2-1/3	1236.599	1236.402	159.039	0.295	846.852	0.186	20	0.062	K.LNNVITHPEAK.H
R2/RRR2-5/3	1747.726	1746.986	-148.707	0.480	2565.468	0.506	31	0.364	R.FLEKPELFYDAFAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/3	1747.378	1746.986	225.361	0.531	2286.653	0.539	30	0.312	R.FLEKPELFYDAFAR.A
R2/RRR2-5/2	1746.559	1746.986	-244.767	0.475	1050.273	0.488	22	0.148	R.FLEKPELFYDAFAR.A
R2/RRR2-5/3	1746.937	1746.986	-27.840	0.453	1331.476	0.464	28	0.130	R.FLEKPELFYDAFAR.A
R2/RRR2-5/2	1746.277	1746.986	-981.483	0.407	768.075	0.439	20	0.124	R.FLEKPELFYDAFAR.A
R2/RRR2-5/3	1903.239	1903.172	35.336	0.505	1018.957	0.383	23	0.090	R.RFLEKPELFYDAFAR.A
R2/RRR2-4/2	1859.567	1860.061	-266.171	0.568	1107.248	0.593	25	0.171	R.GVVPASGFSFSSQQFWK.V
R2/RRR2-3/2	1296.343	1295.510	-128.695	0.359	1045.540	0.354	16	0.125	K.TPLENLEPILR.E
R2/RRR2-4/2	1100.907	1101.283	-342.830	0.352	841.010	0.282	13	0.110	K.STLLNHLFR.T
R2/RRR2-4/2	1858.383	1860.061	-1984.974	0.279	372.404	0.342	16	0.103	R.GVVPASGFSFSSQQFWK.V
R2/RRR2-12/2	1825.257	1826.237	-1088.047	0.480	2401.430	0.549	26	0.340	K.VAILGAAGGIGQPLSLLM*K.L
R2/RRR2-12/2	1825.597	1826.237	-900.997	0.544	2340.727	0.539	26	0.323	K.VAILGAAGGIGQPLSLLM*K.L
R2/RRR2-12/3	1810.936	1810.238	-167.010	0.527	2318.629	0.530	37	0.320	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/3	1810.141	1810.238	-53.416	0.451	2389.436	0.461	33	0.313	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/3	1809.962	1810.238	-152.861	0.458	1981.684	0.484	35	0.233	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/3	1809.441	1810.238	-995.779	0.405	1812.066	0.472	33	0.202	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/2	1809.556	1810.238	-931.937	0.431	1410.359	0.405	21	0.154	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/2	1809.738	1810.238	-277.018	0.440	1455.279	0.359	22	0.150	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/2	1826.659	1826.237	231.823	0.532	993.398	0.533	22	0.144	K.VAILGAAGGIGQPLSLLM*K.L
R2/RRR2-12/2	1808.988	1810.238	-1247.088	0.273	1358.148	0.349	21	0.141	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/2	1810.470	1810.238	128.788	0.387	1254.092	0.392	20	0.139	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-12/2	1810.241	1810.238	1.785	0.374	698.248	0.395	17	0.110	K.VAILGAAGGIGQPLSLLMK.L
R2/RRR2-3/2	1826.655	1826.237	229.679	0.440	697.612	0.378	18	0.109	K.VAILGAAGGIGQPLSLLM*K.L
R2/RRR2-12/3	1953.742	1954.410	-856.417	0.300	1321.925	0.298	30	0.096	R.KVAILGAAGGIGQPLSLLM*K.L
R2/RRR2-12/3	1953.853	1954.410	-799.500	0.387	594.876	0.401	26	0.078	R.KVAILGAAGGIGQPLSLLM*K.L
R2/RRR2-12/3	1937.671	1938.411	-900.467	0.343	824.365	0.297	26	0.071	-.KVAILGAAGGIGQPLSLLMK.-
R2/RRR2-12/3	1953.738	1954.410	-858.392	0.281	782.759	0.212	26	0.063	R.KVAILGAAGGIGQPLSLLM*K.L
R2/RRR2-20/2	1544.116	1544.817	-1104.749	0.405	2506.664	0.507	22	0.354	K.VIGEVLDIFNPTVK.M
R2/RRR2-20/2	1544.456	1544.817	-233.988	0.494	2187.749	0.486	20	0.283	K.VIGEVLDIFNPTVK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1545.398	1544.817	-271.478	0.584	1955.296	0.560	19	0.264	K.VIGEVLDIFNPTVK.M
R2/RRR2-20/2	972.216	973.066	-1907.810	0.305	971.096	0.298	13	0.115	R.VEVQGGDLR.S
R2/RRR2-20/2	972.844	973.066	-228.943	0.389	762.094	0.341	12	0.114	R.VEVQGGDLR.S
R2/RRR2-19/2	972.926	973.066	-144.105	0.344	594.636	0.250	11	0.076	-.VEVQGGDLR.-
R2/RRR2-22/2	1811.602	1811.885	-156.567	0.583	2523.210	0.655	29	0.418	K.SQNADPLTGISSEGYSGK.G
R2/RRR2-22/2	1212.303	1211.370	-55.417	0.421	658.138	0.480	15	0.123	R.SFAGPAPSTM*TK.E
R2/RRR2-22/2	1210.826	1211.370	-1279.116	0.363	779.706	0.401	15	0.118	R.SFAGPAPSTM*TK.E
R2/RRR2-6/2	1251.218	1251.454	-188.820	0.467	1315.268	0.427	17	0.158	K.AKEYILGELSK.V
R2/RRR2-6/2	1969.232	1969.179	26.946	0.474	314.346	0.600	20	0.126	R.GGFPPPVAGLDSCYDIFR.M
R2/RRR2-6/2	1968.527	1969.179	-841.564	0.470	422.077	0.570	21	0.126	R.GGFPPPVAGLDSCYDIFR.M
R2/RRR2-6/3	1417.668	1418.540	-1324.163	0.395	543.318	0.575	25	0.100	R.AAADGRPSVGPTYR.S
R2/RRR2-6/3	1417.803	1418.540	-1228.570	0.356	537.435	0.492	26	0.088	R.AAADGRPSVGPTYR.S
R2/RRR2-6/3	1417.734	1418.540	-1277.596	0.364	541.304	0.459	24	0.086	R.AAADGRPSVGPTYR.S
R2/RRR2-5/3	1418.752	1418.540	149.623	0.299	294.871	0.531	19	0.083	-.AAADGRPSVGPTYR.-
R2/RRR2-5/3	1418.772	1418.540	163.860	0.283	217.222	0.426	17	0.075	-.AAADGRPSVGPTYR.-
R2/RRR2-5/3	1447.859	1447.573	197.819	0.505	1757.012	0.318	26	0.135	K.SKDREEIAEIEK.M
R2/RRR2-5/2	1501.572	1501.664	-61.530	0.458	815.636	0.451	17	0.127	K.LPADTPYSQFAYK.F
R2/RRR2-5/2	1329.192	1329.569	-284.503	0.287	925.501	0.374	16	0.119	R.ALVEGPFLDVLR.S
R2/RRR2-5/2	1501.439	1501.664	-150.665	0.420	862.922	0.354	17	0.117	K.LPADTPYSQFAYK.F
R2/RRR2-5/2	1329.012	1329.569	-1175.399	0.260	480.814	0.389	13	0.106	R.ALVEGPFLDVLR.S
R2/RRR2-5/2	1329.353	1329.569	-163.077	0.243	708.131	0.274	14	0.103	R.ALVEGPFLDVLR.S
R2/RRR2-5/3	1446.986	1447.573	-1100.012	0.518	1126.468	0.336	26	0.087	K.SKDREEIAEIEK.M
R2/RRR2-5/3	1447.580	1447.573	4.887	0.528	1194.484	0.305	26	0.085	K.SKDREEIAEIEK.M
R2/RRR2-5/2	1817.329	1817.933	-885.238	0.567	2703.273	0.602	24	0.433	R.NPQDITQEEYAAFYK.S
R2/RRR2-5/2	1817.323	1817.933	-888.609	0.575	2426.772	0.536	24	0.345	R.NPQDITQEEYAAFYK.S
R2/RRR2-5/2	1817.140	1817.933	-989.430	0.590	2274.201	0.560	23	0.323	R.NPQDITQEEYAAFYK.S
R2/RRR2-5/2	1258.133	1257.422	-229.822	0.446	1053.004	0.417	16	0.134	K.ADLVNNLGTIAR.S
R2/RRR2-5/2	1257.155	1257.422	-212.471	0.431	895.855	0.466	16	0.132	K.ADLVNNLGTIAR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1257.129	1257.422	-233.317	0.350	908.974	0.415	16	0.125	K.ADLVNNLGTIAR.S
R2/RRR2-25/2	1631.261	1631.683	-259.741	0.547	2076.730	0.593	26	0.298	K.GSPAADEEQSTAAAAVR.F
R2/RRR2-25/2	1631.242	1631.683	-271.228	0.543	1899.132	0.589	25	0.266	K.GSPAADEEQSTAAAAVR.F
R2/RRR2-25/2	1631.131	1631.683	-954.689	0.525	1892.460	0.580	25	0.262	K.GSPAADEEQSTAAAAVR.F
R2/RRR2-25/3	1760.343	1759.856	277.291	0.475	962.532	0.408	31	0.092	R.KGSPAADEEQSTAAAAVR.F
R2/RRR2-25/3	1759.600	1759.856	-146.242	0.459	735.845	0.462	31	0.090	R.KGSPAADEEQSTAAAAVR.F
R2/RRR2-5/2	1675.335	1676.038	-1020.048	0.459	1156.775	0.495	17	0.151	K.RLPFTVPSLVFSALK.L
R2/RRR2-5/2	1675.760	1676.038	-166.775	0.469	1130.228	0.446	17	0.141	K.RLPFTVPSLVFSALK.L
R2/RRR2-1/2	1404.896	1404.578	226.896	0.441	859.801	0.445	16	0.126	R.IANAAQQM*ANVTR.G
R2/RRR2-5/2	1283.210	1282.554	-269.222	0.392	604.036	0.448	15	0.118	K.QIVALLSAPLEK.Y
R2/RRR2-5/2	1282.343	1282.554	-165.237	0.314	533.356	0.326	15	0.107	K.QIVALLSAPLEK.Y
R2/RRR2-20/2	1815.419	1816.003	-875.041	0.574	2564.498	0.573	24	0.388	R.GIDLDQLLDLTSDQLR.D
R2/RRR2-20/2	1814.662	1816.003	-1293.724	0.479	2651.203	0.492	23	0.379	R.GIDLDQLLDLTSDQLR.D
R2/RRR2-20/2	1816.238	1816.003	129.929	0.600	2440.534	0.552	23	0.352	R.GIDLDQLLDLTSDQLR.D
R2/RRR2-20/3	1333.924	1333.442	363.088	0.539	1415.432	0.484	30	0.143	K.HGRPGIGATHSSR.F
R2/RRR2-25/2	1115.500	1116.290	-1609.028	0.491	2433.275	0.628	21	0.371	R.VVGAGGAVVACR.G
R2/RRR2-25/2	1115.752	1116.290	-1382.503	0.529	2379.529	0.631	21	0.361	R.VVGAGGAVVACR.G
R2/RRR2-18/2	1115.548	1116.290	-1565.826	0.548	2258.614	0.664	21	0.348	R.VVGAGGAVVACR.G
R2/RRR2-18/2	1116.025	1116.290	-237.694	0.535	2267.361	0.643	21	0.343	R.VVGAGGAVVACR.G
R2/RRR2-19/2	1115.775	1116.290	-1361.680	0.542	2246.842	0.630	21	0.334	R.VVGAGGAVVACR.G
R2/RRR2-26/2	1115.549	1116.290	-1564.946	0.513	2199.940	0.644	21	0.330	R.VVGAGGAVVACR.G
R2/RRR2-26/2	1116.102	1116.290	-168.566	0.547	2232.976	0.620	21	0.329	R.VVGAGGAVVACR.G
R2/RRR2-25/2	1116.108	1116.290	-163.080	0.550	2147.415	0.652	21	0.323	R.VVGAGGAVVACR.G
R2/RRR2-14/2	1116.415	1116.290	112.564	0.439	2158.563	0.590	20	0.304	R.VVGAGGAVVACR.G
R2/RRR2-19/2	1115.439	1116.290	-1664.549	0.462	2062.159	0.612	20	0.293	R.VVGAGGAVVACR.G
R2/RRR2-17/2	1115.303	1116.290	-1786.605	0.463	2145.275	0.559	20	0.292	R.VVGAGGAVVACR.G
R2/RRR2-18/2	1115.968	1116.290	-289.271	0.570	2012.408	0.617	20	0.288	R.VVGAGGAVVACR.G
R2/RRR2-26/2	1116.145	1116.290	-130.057	0.517	1986.602	0.592	20	0.276	R.VVGAGGAVVACR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1116.151	1116.290	-124.461	0.533	1858.387	0.639	20	0.269	R.VVGAGGAVVACR.G
R2/RRR2-16/2	1115.923	1116.290	-329.769	0.435	1753.983	0.644	20	0.252	R.VVGAGGAVVACR.G
R2/RRR2-18/2	1674.218	1673.852	219.493	0.592	1495.221	0.584	21	0.203	R.GLVSYDFPASFWAGR.V
R2/RRR2-18/2	1116.148	1116.290	-127.862	0.407	1409.864	0.608	18	0.197	R.VVGAGGAVVACR.G
R2/RRR2-18/2	1674.300	1673.852	268.916	0.548	1370.797	0.556	21	0.184	R.GLVSYDFPASFWAGR.V
R2/RRR2-17/2	1115.464	1116.290	-1641.790	0.370	1422.677	0.511	18	0.178	R.VVGAGGAVVACR.G
R2/RRR2-17/2	1674.314	1673.852	276.958	0.480	1221.610	0.520	19	0.161	R.GLVSYDFPASFWAGR.V
R2/RRR2-18/2	1673.185	1673.852	-999.186	0.496	1121.862	0.541	20	0.158	R.GLVSYDFPASFWAGR.V
R2/RRR2-19/2	1673.439	1673.852	-247.268	0.507	1151.100	0.500	18	0.150	R.GLVSYDFPASFWAGR.V
R2/RRR2-19/2	1673.176	1673.852	-1004.680	0.511	1014.017	0.542	19	0.149	R.GLVSYDFPASFWAGR.V
R2/RRR2-18/2	1673.217	1673.852	-979.849	0.497	1074.093	0.517	19	0.149	R.GLVSYDFPASFWAGR.V
R2/RRR2-13/2	1116.142	1116.290	-133.128	0.348	981.998	0.494	18	0.140	R.VVGAGGAVVACR.G
R2/RRR2-18/2	1672.563	1673.852	-1372.160	0.338	1172.778	0.374	18	0.132	R.GLVSYDFPASFWAGR.V
R2/RRR2-4/2	1674.872	1673.852	12.383	0.428	722.205	0.478	15	0.121	R.GLVSYDFPASFWAGR.V
R2/RRR2-16/2	1673.461	1673.852	-234.168	0.413	807.664	0.390	16	0.116	R.GLVSYDFPASFWAGR.V
R2/RRR2-18/3	1674.404	1673.852	-267.937	0.458	935.217	0.532	26	0.113	R.GLVSYDFPASFWAGR.V
R2/RRR2-13/2	1674.433	1673.852	-250.777	0.404	349.505	0.346	15	0.111	R.GLVSYDFPASFWAGR.V
R2/RRR2-19/2	1672.818	1673.852	-1219.273	0.312	592.693	0.362	15	0.109	R.GLVSYDFPASFWAGR.V
R2/RRR2-17/2	1115.316	1116.290	-1775.168	0.141	740.728	0.329	16	0.106	R.VVGAGGAVVACR.G
R2/RRR2-16/2	1673.116	1673.852	-1040.500	0.286	256.947	0.387	12	0.104	-.GLVSYDFPASFWAGR.-
R2/RRR2-18/3	1673.763	1673.852	-53.160	0.411	911.237	0.436	26	0.093	R.GLVSYDFPASFWAGR.V
R2/RRR2-18/2	1116.540	1116.290	225.059	0.212	144.782	0.365	12	0.084	-.VVGAGGAVVACR.-
R2/RRR2-23/3	1717.202	1717.776	-919.393	0.622	2447.055	0.512	32	0.329	K.HGYIGEFEELDDHR.S
R2/RRR2-23/3	1716.477	1717.776	-1343.483	0.538	2228.207	0.489	30	0.276	K.HGYIGEFEELDDHR.S
R2/RRR2-23/2	898.833	899.073	-267.886	0.463	756.845	0.392	13	0.124	K.IVVQLNGR.L
R2/RRR2-23/2	898.354	899.073	-1919.727	0.415	717.122	0.394	12	0.121	K.IVVQLNGR.L
R2/RRR2-23/2	898.972	899.073	-112.309	0.458	579.210	0.392	11	0.118	K.IVVQLNGR.L
R2/RRR2-23/3	1717.715	1717.776	-35.833	0.471	851.261	0.382	22	0.083	K.HGYIGEFEELDDHR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1556.647	1556.743	-61.870	0.456	2777.170	0.489	24	0.410	R.NDAGLAAAELALAVEK.H
R2/RRR2-9/2	1556.553	1556.743	-122.362	0.455	2301.706	0.472	23	0.302	R.NDAGLAAAELALAVEK.H
R2/RRR2-9/2	1311.152	1311.466	-239.952	0.541	1015.143	0.500	18	0.148	K.IINQDPPALSDK.S
R2/RRR2-9/2	1311.227	1311.466	-183.073	0.530	969.086	0.489	18	0.143	K.IINQDPPALSDK.S
R2/RRR2-11/2	1615.308	1615.641	-206.443	0.518	2707.820	0.500	26	0.394	R.LDFSSGQSTGTASNSR.L
R2/RRR2-11/2	1758.313	1758.918	-915.786	0.551	2539.888	0.581	24	0.393	R.APQQSSGWVAWGINTR.G
R2/RRR2-11/2	1616.254	1615.641	-240.336	0.545	2198.546	0.513	24	0.293	R.LDFSSGQSTGTASNSR.L
R2/RRR2-11/2	1615.083	1615.641	-967.586	0.472	2340.903	0.407	24	0.287	R.LDFSSGQSTGTASNSR.L
R2/RRR2-3/2	1357.255	1357.580	-240.011	0.486	1390.225	0.580	18	0.195	K.IPSVNDIPLNFK.V
R2/RRR2-3/2	1357.297	1357.580	-208.521	0.510	1306.336	0.472	18	0.164	K.IPSVNDIPLNFK.V
R2/RRR2-3/2	1357.225	1357.580	-262.298	0.439	1143.362	0.515	17	0.157	K.IPSVNDIPLNFK.V
R2/RRR2-3/2	1104.249	1103.299	-45.527	0.398	818.002	0.240	13	0.106	R.LAQLQNFLR.K
R2/RRR2-3/3	1517.377	1517.617	-158.573	0.367	1294.862	0.240	23	0.081	R.DSHEISSCEAILR.Q
R2/RRR2-2/2	1910.277	1911.144	-980.543	0.542	1395.424	0.579	25	0.197	R.YEAVGVDPSTTLLEFLR.T
R2/RRR2-2/2	1267.257	1267.543	-225.946	0.366	1039.706	0.557	18	0.153	K.LVSAPVILEAVR.L
R2/RRR2-2/2	1155.016	1155.371	-308.431	0.469	1075.891	0.470	15	0.147	R.VSLAVSYLFR.F
R2/RRR2-2/2	1058.272	1057.229	40.770	0.446	1827.310	0.479	17	0.226	K.VLLNAVASNR.F
R2/RRR2-2/2	1600.811	1600.799	7.755	0.459	1898.021	0.286	21	0.185	K.VSGGIDLDTVNIIQR.D
R2/RRR2-2/2	1057.453	1057.229	212.741	0.378	1402.471	0.492	16	0.175	K.VLLNAVASNR.F
R2/RRR2-2/2	1600.268	1600.799	-959.329	0.431	1672.380	0.299	20	0.163	K.VSGGIDLDTVNIIQR.D
R2/RRR2-2/2	1667.777	1666.943	-99.960	0.470	1015.148	0.423	17	0.129	R.VLEGTQAELVLQPLR.L
R2/RRR2-2/2	1056.955	1057.229	-260.129	0.331	710.682	0.431	14	0.119	K.VLLNAVASNR.F
R2/RRR2-2/2	1668.250	1666.943	184.243	0.427	962.301	0.357	17	0.118	R.VLEGTQAELVLQPLR.L
R2/RRR2-1/2	1601.590	1600.799	-130.541	0.346	891.619	0.311	18	0.112	K.VSGGIDLDTVNIIQR.D
R2/RRR2-2/2	1668.184	1666.943	144.617	0.322	592.742	0.154	14	0.095	-.VLEGTQAELVLQPLR.-
R2/RRR2-9/2	1934.442	1934.223	113.636	0.606	2989.225	0.679	26	0.543	K.KALSFYDVVFDAVYAPK.V
R2/RRR2-9/2	1935.495	1934.223	141.154	0.577	1272.624	0.664	23	0.201	K.KALSFYDVVFDAVYAPK.V
R2/RRR2-5/3	1714.050	1713.871	104.952	0.471	2765.037	0.390	33	0.370	R.ALHTIVQEQGSLDSSK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1785.467	1784.987	269.728	0.495	761.478	0.529	17	0.130	K.QSGVELGNSILFFGCR.N
R2/RRR2-5/2	1784.132	1784.987	-1042.734	0.379	678.023	0.514	16	0.122	K.QSGVELGNSILFFGCR.N
R2/RRR2-2/2	1204.500	1203.416	70.178	0.425	1792.100	0.485	19	0.223	K.ILLENAGAVFR.T
R2/RRR2-2/2	1204.411	1203.416	-3.620	0.458	1720.954	0.433	18	0.201	K.ILLENAGAVFR.T
R2/RRR2-3/2	1390.023	1390.563	-1111.477	0.500	908.098	0.438	18	0.131	K.VGESPEEIAAFLK.S
R2/RRR2-3/2	1390.384	1390.563	-129.149	0.351	467.718	0.438	14	0.111	K.VGESPEEIAAFLK.S
R2/RRR2-2/3	1849.561	1849.848	-155.976	0.480	773.878	0.564	30	0.109	K.TEDESRPLEDGTGEASR.S
R2/RRR2-2/3	1849.271	1849.848	-855.488	0.485	641.969	0.550	28	0.100	K.TEDESRPLEDGTGEASR.S
R2/RRR2-5/2	1459.056	1458.752	209.149	0.295	843.526	0.207	16	0.099	R.MQAKAIADAAVAVAK.E
R2/RRR2-1/2	1294.268	1294.436	-130.226	0.464	1302.687	0.497	17	0.167	K.GVADFLQEVTSK.K
R2/RRR2-2/2	1294.066	1294.436	-286.170	0.305	1195.366	0.352	15	0.131	K.GVADFLQEVTSK.K
R2/RRR2-2/2	1294.943	1294.436	-381.850	0.313	926.833	0.423	15	0.124	K.GVADFLQEVTSK.K
R2/RRR2-2/2	1287.450	1288.474	-1577.102	0.306	1029.755	0.353	18	0.123	R.AIANELAVPFDK.S
R2/RRR2-2/2	1029.050	1029.259	-203.291	0.481	929.592	0.347	16	0.123	K.TTLLLALAGR.L
R2/RRR2-2/2	1287.920	1288.474	-1209.954	0.248	490.477	0.362	14	0.105	R.AIANELAVPFDK.S
R2/RRR2-3/2	1356.466	1356.509	-31.827	0.392	1107.990	0.348	17	0.128	R.FLAVGSYDNTIR.I
R2/RRR2-3/2	984.493	985.206	-1744.793	0.425	885.895	0.316	16	0.117	R.LLAGVGSVLR.L
R2/RRR2-2/2	1356.115	1356.509	-291.314	0.426	753.427	0.341	16	0.113	R.FLAVGSYDNTIR.I
R2/RRR2-3/2	1461.379	1461.645	-182.024	0.378	851.299	0.289	17	0.110	R.LGETFNETAIPLR.Y
R2/RRR2-3/2	1461.371	1461.645	-187.806	0.380	726.756	0.309	16	0.108	R.LGETFNETAIPLR.Y
R2/RRR2-8/2	1851.282	1852.017	-939.974	0.587	2723.113	0.596	23	0.430	R.M*TNFYTNFQVDEIGR.V
R2/RRR2-8/2	1851.338	1852.017	-909.921	0.563	2411.854	0.569	22	0.350	R.M*TNFYTNFQVDEIGR.V
R2/RRR2-8/2	1836.329	1836.018	169.980	0.600	2567.134	0.480	23	0.348	R.MTNFYTNFQVDEIGR.V
R2/RRR2-8/2	1835.384	1836.018	-892.806	0.562	2427.345	0.510	23	0.332	R.MTNFYTNFQVDEIGR.V
R2/RRR2-8/2	1836.724	1836.018	-160.625	0.597	2369.092	0.503	23	0.317	R.MTNFYTNFQVDEIGR.V
R2/RRR2-8/2	1851.352	1852.017	-901.978	0.535	2248.010	0.535	22	0.307	R.M*TNFYTNFQVDEIGR.V
R2/RRR2-8/2	1204.174	1204.356	-150.849	0.533	1974.011	0.394	18	0.223	R.AAELTTLLESR.M
R2/RRR2-8/2	1204.040	1204.356	-262.519	0.488	1812.657	0.348	17	0.190	R.AAELTTLLESR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1203.564	1204.356	-1492.925	0.417	1604.433	0.406	17	0.180	R.AAELTTLLESR.M
R2/RRR2-8/3	1851.439	1852.017	-855.123	0.476	1317.704	0.348	25	0.104	R.M*TNFYTNFQVDEIGR.V
R2/RRR2-15/2	1910.321	1910.068	132.503	0.543	2213.670	0.549	25	0.304	R.ASGSCDFAGAATIVTQQPK.I
R2/RRR2-15/2	1910.503	1910.068	228.427	0.553	2147.593	0.558	25	0.294	R.ASGSCDFAGAATIVTQQPK.I
R2/RRR2-14/2	1909.465	1910.068	-842.010	0.528	2086.861	0.554	25	0.283	R.ASGSCDFAGAATIVTQQPK.I
R2/RRR2-14/2	1909.492	1910.068	-828.084	0.554	2083.447	0.541	24	0.276	R.ASGSCDFAGAATIVTQQPK.I
R2/RRR2-14/2	1909.557	1910.068	-794.010	0.524	2010.367	0.534	24	0.263	R.ASGSCDFAGAATIVTQQPK.I
R2/RRR2-15/2	1910.364	1910.068	155.124	0.528	1657.418	0.542	23	0.212	R.ASGSCDFAGAATIVTQQPK.I
R2/RRR2-15/3	1909.714	1910.068	-185.908	0.397	836.391	0.442	24	0.090	-.ASGSCDFAGAATIVTQQPK.-
R2/RRR2-14/3	1909.729	1910.068	-178.213	0.348	1173.183	0.299	28	0.085	R.ASGSCDFAGAATIVTQQPK.I
R2/RRR2-14/3	1910.125	1910.068	29.696	0.391	715.392	0.377	23	0.075	-.ASGSCDFAGAATIVTQQPK.-
R2/RRR2-15/2	1750.298	1750.974	-960.621	0.472	2480.971	0.585	24	0.382	R.IAVSAEVDGVASTLVYR.S
R2/RRR2-20/3	1310.490	1309.455	26.747	0.565	1149.231	0.457	24	0.112	R.RLDYGHVYASK.S
R2/RRR2-20/3	1309.543	1309.455	67.063	0.493	1183.801	0.383	23	0.099	R.RLDYGHVYASK.S
R2/RRR2-20/3	1309.644	1309.455	144.326	0.507	1189.994	0.377	23	0.098	R.RLDYGHVYASK.S
R2/RRR2-11/3	1309.663	1309.455	159.468	0.517	937.316	0.432	21	0.096	R.RLDYGHVYASK.S
R2/RRR2-21/2	1495.459	1495.659	-134.157	0.532	1939.257	0.610	23	0.280	K.ITLISDFGEISGSR.G
R2/RRR2-21/2	1495.365	1495.659	-197.538	0.516	1856.010	0.626	22	0.270	K.ITLISDFGEISGSR.G
R2/RRR2-21/2	1494.676	1495.659	-1330.678	0.409	1967.186	0.552	22	0.265	K.ITLISDFGEISGSR.G
R2/RRR2-21/2	1624.002	1623.832	104.598	0.429	933.288	0.484	18	0.136	-.KITLISDFGEISGSR.-
R2/RRR2-21/3	1496.649	1495.659	-7.258	0.427	1448.303	0.430	27	0.134	K.ITLISDFGEISGSR.G
R2/RRR2-21/3	1623.861	1623.832	17.853	0.449	1096.104	0.535	26	0.127	R.KITLISDFGEISGSR.G
R2/RRR2-21/3	1495.531	1495.659	-86.062	0.434	1229.683	0.443	24	0.117	K.ITLISDFGEISGSR.G
R2/RRR2-21/3	1495.243	1495.659	-279.161	0.430	1195.393	0.361	26	0.096	-.ITLISDFGEISGSR.-
R2/RRR2-21/3	1623.160	1623.832	-1033.308	0.315	883.844	0.264	22	0.067	R.KITLISDFGEISGSR.G
R2/RRR2-10/3	1755.892	1755.873	10.758	0.533	2565.753	0.556	35	0.387	R.TAVHQGIGHQTYAESR.G
R2/RRR2-10/3	1755.690	1755.873	-104.516	0.529	2095.293	0.535	31	0.272	R.TAVHQGIGHQTYAESR.G
R2/RRR2-9/3	1755.678	1755.873	-111.316	0.505	1811.898	0.510	29	0.211	R.TAVHQGIGHQTYAESR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/3	1756.037	1755.873	93.797	0.482	1735.507	0.529	28	0.207	R.TAVHQGIGHQTYAESR.G
R2/RRR2-10/3	1756.605	1755.873	-152.695	0.540	1532.922	0.492	29	0.162	R.TAVHQGIGHQTYAESR.G
R2/RRR2-10/3	1774.379	1774.094	160.864	0.426	896.047	0.519	28	0.107	R.APEYLALNDKVISLVK.G
R2/RRR2-10/3	1773.875	1774.094	-123.703	0.394	993.630	0.483	29	0.106	R.APEYLALNDKVISLVK.G
R2/RRR2-10/3	1773.639	1774.094	-257.191	0.403	826.288	0.495	26	0.099	R.APEYLALNDKVISLVK.G
R2/RRR2-12/2	1945.267	1946.197	-994.817	0.504	2539.666	0.525	28	0.372	R.GINSLVDVGGGYGAVAAAVVR.A
R2/RRR2-12/2	1126.986	1127.187	-178.237	0.418	825.867	0.471	16	0.132	R.DGEATYTLTR.V
R2/RRR2-12/3	1945.020	1946.197	-1122.232	0.378	1166.424	0.461	29	0.117	R.GINSLVDVGGGYGAVAAAVVR.A
R2/RRR2-16/2	1130.029	1130.320	-258.151	0.447	2295.557	0.530	22	0.313	K.VAVITGGASGIGK.A
R2/RRR2-16/2	1131.383	1130.320	56.424	0.544	2175.829	0.582	22	0.308	K.VAVITGGASGIGK.A
R2/RRR2-13/2	1129.571	1130.320	-1552.457	0.433	2217.248	0.526	22	0.297	K.VAVITGGASGIGK.A
R2/RRR2-14/2	1130.096	1130.320	-199.090	0.524	2201.081	0.526	22	0.294	K.VAVITGGASGIGK.A
R2/RRR2-15/2	1130.157	1130.320	-144.586	0.521	2142.152	0.549	22	0.291	K.VAVITGGASGIGK.A
R2/RRR2-13/2	1130.013	1130.320	-272.457	0.534	2154.409	0.538	22	0.290	K.VAVITGGASGIGK.A
R2/RRR2-15/2	1130.056	1130.320	-233.876	0.521	2128.343	0.526	22	0.282	K.VAVITGGASGIGK.A
R2/RRR2-14/2	1130.022	1130.320	-264.220	0.498	2133.185	0.511	22	0.278	K.VAVITGGASGIGK.A
R2/RRR2-15/2	1327.988	1328.497	-1139.519	0.489	2107.241	0.506	20	0.275	K.VIIADVQDELGR.S
R2/RRR2-13/2	1130.114	1130.320	-182.511	0.539	2126.116	0.498	22	0.272	K.VAVITGGASGIGK.A
R2/RRR2-16/2	1131.004	1130.320	-280.121	0.559	1886.455	0.587	21	0.260	K.VAVITGGASGIGK.A
R2/RRR2-15/2	1129.546	1130.320	-1574.712	0.422	1692.144	0.536	20	0.217	K.VAVITGGASGIGK.A
R2/RRR2-15/2	1328.272	1328.497	-169.570	0.415	751.450	0.370	14	0.112	-.VIIADVQDELGR.-
R2/RRR2-15/2	1329.427	1328.497	-52.920	0.345	681.222	0.350	14	0.109	-.VIIADVQDELGR.-
R2/RRR2-15/2	1328.132	1328.497	-275.696	0.377	651.396	0.349	13	0.107	-.VIIADVQDELGR.-
R2/RRR2-15/2	1329.276	1328.497	-166.679	0.299	405.514	0.371	12	0.106	-.VIIADVQDELGR.-
R2/RRR2-11/2	1604.151	1603.708	276.860	0.562	1489.415	0.624	23	0.218	K.AGDTVGVGYFVDSCR.A
R2/RRR2-11/2	1603.237	1603.708	-294.599	0.514	1356.705	0.637	22	0.204	K.AGDTVGVGYFVDSCR.A
R2/RRR2-11/2	1602.709	1603.708	-1250.990	0.413	1337.225	0.570	22	0.184	K.AGDTVGVGYFVDSCR.A
R2/RRR2-11/3	1880.565	1879.056	-262.067	0.417	831.584	0.383	23	0.077	-.FKAGDTVGVGYFVDSCR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-2/2	1158.201	1158.373	-149.119	0.437	1780.462	0.505	19	0.228	R.IVALSASLANAK.D
R2/RRR2-1/2	1687.772	1686.844	-42.627	0.454	1175.776	0.359	19	0.133	R.YYDLSSQEIGELIR.F
R2/RRR2-2/2	1687.650	1686.844	-115.396	0.411	870.084	0.359	18	0.117	R.YYDLSSQEIGELIR.F
R2/RRR2-2/2	1256.153	1257.377	-1775.758	0.371	684.164	0.389	13	0.113	K.TGYFQVTDLGR.I
R2/RRR2-3/2	1310.133	1310.481	-266.960	0.401	1000.160	0.418	16	0.130	R.LSGSVGFVLSTSR.A
R2/RRR2-3/2	1020.952	1021.152	-196.329	0.368	687.375	0.501	13	0.125	R.ALGSTPGVYR.V
R2/RRR2-3/2	1021.166	1021.152	13.535	0.341	658.326	0.504	13	0.123	R.ALGSTPGVYR.V
R2/RRR2-3/3	1786.960	1787.048	-49.587	0.365	1229.091	0.391	23	0.106	K.LIDKYDLYGQVAYPK.H
R2/RRR2-3/2	1020.335	1021.152	-1785.559	0.199	395.465	0.391	12	0.103	-.ALGSTPGVYR.-
R2/RRR2-19/2	1663.307	1662.860	269.074	0.528	2388.811	0.517	25	0.331	K.AITSGVLAGCSDAIAQK.I
R2/RRR2-19/2	1662.343	1662.860	-915.404	0.483	1987.876	0.488	23	0.250	K.AITSGVLAGCSDAIAQK.I
R2/RRR2-19/2	1662.548	1662.860	-188.352	0.508	1978.888	0.485	23	0.247	K.AITSGVLAGCSDAIAQK.I
R2/RRR2-19/2	983.959	984.135	-179.259	0.429	468.384	0.463	14	0.125	K.ISGVPNLQR.R
R2/RRR2-19/2	983.426	984.135	-1743.076	0.350	408.073	0.421	13	0.117	K.ISGVPNLQR.R
R2/RRR2-19/2	983.790	984.135	-351.907	0.372	473.303	0.365	14	0.114	-.ISGVPNLQR.-
R2/RRR2-19/3	1662.749	1662.860	-67.135	0.259	1127.786	0.162	27	0.061	K.AITSGVLAGCSDAIAQK.I
R2/RRR2-2/3	1329.789	1330.428	-1236.504	0.336	1223.543	0.198	21	0.069	R.FEHLEAEAEVR.V
R2/RRR2-11/2	1616.390	1616.868	-296.747	0.533	2452.647	0.504	23	0.342	K.MGQIQVLTGSQGQIR.A
R2/RRR2-11/2	1632.393	1632.867	-291.469	0.545	2375.468	0.535	23	0.337	K.M*GQIQVLTGSQGQIR.A
R2/RRR2-12/3	1986.603	1987.161	-786.642	0.432	867.970	0.529	24	0.109	R.TPNVFDNKYYVDLQNR.Q
R2/RRR2-11/3	1987.150	1987.161	-5.528	0.450	988.643	0.477	25	0.106	R.TPNVFDNKYYVDLQNR.Q
R2/RRR2-11/3	1988.633	1987.161	237.978	0.446	790.725	0.493	26	0.098	R.TPNVFDNKYYVDLQNR.Q
R2/RRR2-11/3	1987.600	1987.161	221.778	0.464	923.131	0.434	27	0.095	R.TPNVFDNKYYVDLQNR.Q
R2/RRR2-19/3	1582.637	1582.651	-8.875	0.520	2060.197	0.599	29	0.292	R.SGAEVHTGHELCER.K
R2/RRR2-19/3	1582.731	1582.651	51.000	0.483	1574.474	0.568	26	0.194	R.SGAEVHTGHELCER.K
R2/RRR2-19/3	1582.348	1582.651	-192.143	0.451	1213.495	0.530	25	0.136	R.SGAEVHTGHELCER.K
R2/RRR2-19/2	920.063	920.092	-32.152	0.386	1050.510	0.345	13	0.127	R.AAGFVWLR.Q
R2/RRR2-14/3	1756.551	1756.896	-196.647	0.598	2414.965	0.529	32	0.335	K.KGDNDLPGLTDTEKPR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/3	1756.986	1756.896	51.866	0.573	2267.964	0.541	32	0.308	K.KGDNDLPGLTDTEKPR.M
R2/RRR2-14/3	1756.286	1756.896	-919.081	0.583	2173.005	0.547	31	0.290	K.KGDNDLPGLTDTEKPR.M
R2/RRR2-20/3	1756.795	1756.896	-57.582	0.530	2297.673	0.447	31	0.274	K.KGDNDLPGLTDTEKPR.M
R2/RRR2-14/3	1756.572	1756.896	-184.935	0.589	2013.779	0.516	29	0.246	K.KGDNDLPGLTDTEKPR.M
R2/RRR2-2/3	1756.856	1756.896	-22.560	0.471	1546.377	0.456	28	0.154	K.KGDNDLPGLTDTEKPR.M
R2/RRR2-14/2	1374.219	1373.537	-232.415	0.554	1257.742	0.379	18	0.144	K.KLEIDDDQKLR.A
R2/RRR2-14/2	1372.991	1373.537	-1129.634	0.512	1237.125	0.353	18	0.139	K.KLEIDDDQKLR.A
R2/RRR2-13/3	1373.239	1373.537	-218.281	0.454	817.610	0.439	21	0.092	K.KLEIDDDQKLR.A
R2/RRR2-14/3	1373.488	1373.537	-36.256	0.486	1158.854	0.325	24	0.087	K.KLEIDDDQKLR.A
R2/RRR2-14/3	1373.974	1373.537	318.642	0.432	1043.507	0.339	22	0.085	K.KLEIDDDQKLR.A
R2/RRR2-13/3	1373.601	1373.537	46.108	0.411	655.496	0.341	19	0.079	K.KLEIDDDQKLR.A
R2/RRR2-19/3	1373.648	1373.537	80.868	0.401	653.070	0.294	20	0.076	K.KLEIDDDQKLR.A
R2/RRR2-24/3	1372.421	1373.537	-1547.136	0.405	814.768	0.258	19	0.071	K.KLEIDDDQKLR.A
R2/RRR2-14/3	1374.571	1373.537	24.653	0.368	734.725	0.217	19	0.068	-.KLEIDDDQKLR.-
R2/RRR2-12/2	1577.275	1576.843	275.134	0.556	2120.367	0.585	24	0.301	R.MFYGPGGPYALFAGK.D
R2/RRR2-12/2	1593.214	1592.842	234.521	0.567	1907.329	0.587	23	0.265	R.M*FYGPGGPYALFAGK.D
R2/RRR2-12/2	1576.539	1576.843	-193.347	0.518	1925.715	0.527	23	0.250	R.MFYGPGGPYALFAGK.D
R2/RRR2-12/2	1591.820	1592.842	-1274.213	0.473	1516.420	0.538	22	0.197	R.M*FYGPGGPYALFAGK.D
R2/RRR2-12/2	1592.412	1592.842	-270.819	0.528	1446.454	0.560	22	0.195	R.M*FYGPGGPYALFAGK.D
R2/RRR2-12/2	1576.349	1576.843	-313.838	0.510	1657.530	0.454	22	0.194	R.MFYGPGGPYALFAGK.D
R2/RRR2-12/2	1168.098	1167.254	-133.810	0.527	1276.525	0.503	16	0.169	K.GQIYDVTQSR.M
R2/RRR2-12/2	1168.015	1167.254	-205.101	0.519	1244.970	0.487	16	0.163	K.GQIYDVTQSR.M
R2/RRR2-12/2	1167.026	1167.254	-196.147	0.463	1214.348	0.415	16	0.148	K.GQIYDVTQSR.M
R2/RRR2-13/2	1773.391	1772.962	242.567	0.533	2147.430	0.605	29	0.315	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-13/2	1772.445	1772.962	-858.541	0.533	1552.634	0.601	27	0.218	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-13/2	1772.232	1772.962	-978.992	0.523	1441.210	0.610	25	0.205	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-13/3	1772.764	1772.962	-111.867	0.450	1160.461	0.502	33	0.126	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-14/3	1772.786	1772.962	-99.123	0.455	847.257	0.571	33	0.118	R.GM*GDAADLVALSGGHTVGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/3	1772.125	1772.962	-1039.582	0.419	863.567	0.543	32	0.113	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-13/3	1772.712	1772.962	-140.982	0.442	680.144	0.577	30	0.109	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-14/3	1772.649	1772.962	-177.145	0.424	859.264	0.527	33	0.109	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-12/3	1773.848	1772.962	-64.103	0.446	769.982	0.547	32	0.109	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-12/3	1773.665	1772.962	-167.655	0.419	690.005	0.515	30	0.100	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-14/3	1772.324	1772.962	-926.515	0.391	662.381	0.505	28	0.097	R.GM*GDAADLVALSGGHTVGK.-
R2/RRR2-13/3	1756.602	1756.962	-205.737	0.259	341.809	0.510	27	0.087	R.GMGDAADLVALSGGHTVGK.-
R2/RRR2-13/3	1757.044	1756.962	46.429	0.162	238.609	0.427	23	0.079	R.GMGDAADLVALSGGHTVGK.-
R2/RRR2-18/2	1625.180	1625.757	-973.026	0.535	2076.078	0.618	22	0.300	R.YVCQDQFTGQPGPK.C
R2/RRR2-21/2	1625.956	1625.757	122.996	0.613	1929.960	0.645	22	0.284	R.YVCQDQFTGQPGPK.C
R2/RRR2-21/2	1625.307	1625.757	-277.868	0.520	1919.494	0.621	22	0.275	R.YVCQDQFTGQPGPK.C
R2/RRR2-19/2	1625.300	1625.757	-282.012	0.521	1888.958	0.637	22	0.274	R.YVCQDQFTGQPGPK.C
R2/RRR2-20/2	1625.336	1625.757	-259.859	0.527	1929.147	0.612	22	0.274	R.YVCQDQFTGQPGPK.C
R2/RRR2-20/2	1625.149	1625.757	-992.708	0.524	1876.120	0.612	22	0.265	R.YVCQDQFTGQPGPK.C
R2/RRR2-19/2	1625.205	1625.757	-957.718	0.571	1871.978	0.610	23	0.265	R.YVCQDQFTGQPGPK.C
R2/RRR2-20/2	1625.097	1625.757	-1024.458	0.534	1797.501	0.622	22	0.256	R.YVCQDQFTGQPGPK.C
R2/RRR2-21/2	1625.191	1625.757	-966.314	0.529	1809.645	0.606	22	0.253	R.YVCQDQFTGQPGPK.C
R2/RRR2-19/2	1625.304	1625.757	-279.601	0.532	1713.536	0.622	21	0.243	R.YVCQDQFTGQPGPK.C
R2/RRR2-21/2	1626.261	1625.757	-305.712	0.572	1700.188	0.618	22	0.241	R.YVCQDQFTGQPGPK.C
R2/RRR2-21/3	1406.546	1406.554	-5.634	0.515	1420.563	0.449	26	0.131	K.CCDNIERLPTK.T
R2/RRR2-21/3	1406.149	1406.554	-288.925	0.467	745.036	0.342	20	0.077	K.CCDNIERLPTK.T
R2/RRR2-4/2	1392.192	1392.625	-312.611	0.363	1166.695	0.293	17	0.124	R.SVEQLGYITLLR.Q
R2/RRR2-4/2	973.820	974.177	-367.517	0.372	570.478	0.428	14	0.118	R.TLLETVIGK.I
R2/RRR2-4/2	1392.494	1392.625	-94.398	0.383	1138.383	0.243	16	0.117	-.SVEQLGYITLLR.-
R2/RRR2-4/2	1392.115	1392.625	-1088.523	0.326	826.133	0.317	14	0.111	-.SVEQLGYITLLR.-
R2/RRR2-4/2	1524.674	1525.642	-1294.620	0.289	951.177	0.256	17	0.107	R.SSPESSVLTDVFTR.L
R2/RRR2-13/3	1844.486	1845.008	-827.339	0.563	2383.729	0.501	36	0.310	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/3	1844.347	1845.008	-903.279	0.564	1826.177	0.503	35	0.203	K.YVNGHNLVVDGGFTSHK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1151.986	1152.279	-254.825	0.542	1603.344	0.406	17	0.177	R.AALYLASDEAK.Y
R2/RRR2-13/2	1151.872	1152.279	-354.022	0.423	1566.588	0.411	17	0.176	R.AALYLASDEAK.Y
R2/RRR2-14/2	1152.061	1152.279	-189.768	0.494	1490.709	0.446	17	0.176	R.AALYLASDEAK.Y
R2/RRR2-13/3	1844.562	1845.008	-242.623	0.547	1586.003	0.504	33	0.170	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/2	1152.082	1152.279	-171.804	0.497	1469.991	0.421	17	0.168	R.AALYLASDEAK.Y
R2/RRR2-14/3	1844.647	1845.008	-196.316	0.568	1605.148	0.490	33	0.167	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-13/2	1151.495	1152.279	-1553.947	0.385	1490.998	0.401	17	0.166	R.AALYLASDEAK.Y
R2/RRR2-14/2	1151.983	1152.279	-258.121	0.510	1477.466	0.391	17	0.162	R.AALYLASDEAK.Y
R2/RRR2-13/3	1845.628	1845.008	-206.195	0.496	1693.167	0.426	33	0.160	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/3	1844.897	1845.008	-60.407	0.545	1423.211	0.486	32	0.145	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/2	1845.511	1845.008	-270.122	0.521	845.552	0.536	20	0.138	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/3	1845.597	1845.008	-223.115	0.481	1276.267	0.457	30	0.125	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/3	1845.575	1845.008	-235.159	0.495	892.820	0.503	35	0.107	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-13/3	1846.395	1845.008	210.258	0.490	710.593	0.499	32	0.100	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/3	1846.078	1845.008	38.187	0.505	594.995	0.500	30	0.098	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-14/3	1844.342	1845.008	-905.870	0.469	627.906	0.496	31	0.097	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-13/3	1845.244	1845.008	128.212	0.488	801.973	0.430	31	0.092	K.YVNGHNLVVDGGFTSHK.G
R2/RRR2-15/2	1479.439	1479.660	-149.844	0.446	2307.021	0.445	20	0.290	R.STNEALLVIEAYR.T
R2/RRR2-15/2	1479.081	1479.660	-1070.628	0.347	1868.722	0.374	20	0.203	R.STNEALLVIEAYR.T
R2/RRR2-15/2	1478.575	1479.660	-1414.479	0.335	1358.620	0.374	15	0.146	R.STNEALLVIEAYR.T
R2/RRR2-17/2	1478.905	1479.660	-1190.303	0.315	1348.527	0.332	17	0.140	R.STNEALLVIEAYR.T
R2/RRR2-17/2	1031.055	1031.188	-129.746	0.471	1184.599	0.371	15	0.139	R.LDNLSSLIR.Q
R2/RRR2-15/2	1030.522	1031.188	-1622.189	0.510	1106.671	0.368	15	0.134	R.LDNLSSLIR.Q
R2/RRR2-15/2	1030.938	1031.188	-243.891	0.523	1054.853	0.360	15	0.131	R.LDNLSSLIR.Q
R2/RRR2-17/2	1030.871	1031.188	-308.280	0.464	1202.064	0.307	15	0.130	R.LDNLSSLIR.Q
R2/RRR2-15/2	1031.015	1031.188	-168.227	0.539	1087.592	0.326	15	0.127	R.LDNLSSLIR.Q
R2/RRR2-17/2	1478.814	1479.660	-1252.389	0.316	1026.850	0.280	15	0.113	R.STNEALLVIEAYR.T
R2/RRR2-16/2	1030.984	1031.188	-198.990	0.406	902.345	0.218	14	0.109	R.LDNLSSLIR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1480.063	1479.660	273.269	0.268	619.209	0.295	15	0.106	R.STNEALLVIEAYR.T
R2/RRR2-16/2	1030.576	1031.188	-1568.641	0.227	651.369	0.101	13	0.103	R.LDNLSSLIR.Q
R2/RRR2-6/3	1661.223	1660.893	199.755	0.543	2537.106	0.352	36	0.281	R.IINEPTAAAIAYGIDK.K
R2/RRR2-6/2	1660.455	1660.893	-264.317	0.531	1948.018	0.565	26	0.266	R.IINEPTAAAIAYGIDK.K
R2/RRR2-6/3	1660.567	1660.893	-196.769	0.544	2388.902	0.347	33	0.251	R.IINEPTAAAIAYGIDK.K
R2/RRR2-6/2	1660.441	1660.893	-272.726	0.505	1544.660	0.577	25	0.211	R.IINEPTAAAIAYGIDK.K
R2/RRR2-6/2	1788.604	1789.066	-259.071	0.522	1401.939	0.579	25	0.195	R.IINEPTAAAIAYGIDKK.A
R2/RRR2-6/2	1788.532	1789.066	-859.786	0.556	1348.842	0.570	24	0.187	R.IINEPTAAAIAYGIDKK.A
R2/RRR2-6/2	1788.528	1789.066	-862.527	0.539	1287.117	0.576	24	0.182	R.IINEPTAAAIAYGIDKK.A
R2/RRR2-10/2	1660.134	1660.893	-1062.280	0.471	1225.395	0.504	23	0.161	R.IINEPTAAAIAYGIDK.K
R2/RRR2-6/2	1661.342	1660.893	271.456	0.405	724.409	0.523	22	0.131	R.IINEPTAAAIAYGIDK.K
R2/RRR2-5/2	1660.009	1660.893	-1138.108	0.341	1022.982	0.377	20	0.125	R.IINEPTAAAIAYGIDK.K
R2/RRR2-17/2	1585.118	1583.812	193.828	0.552	2164.928	0.568	21	0.307	R.FSAFFATHLDSVLK.T
R2/RRR2-17/2	1584.910	1583.812	62.526	0.576	1903.456	0.576	21	0.264	R.FSAFFATHLDSVLK.T
R2/RRR2-17/2	1486.212	1485.620	-275.534	0.479	474.711	0.521	17	0.126	R.QTVFDAVALDYDK.V
R2/RRR2-17/2	1484.913	1485.620	-1152.587	0.284	443.637	0.409	16	0.109	R.QTVFDAVALDYDK.V
R2/RRR2-20/2	1351.177	1351.449	-202.126	0.498	2189.104	0.514	20	0.294	K.YGVGDAHFEVTR.F
R2/RRR2-20/2	1652.181	1651.844	204.487	0.549	2133.335	0.490	23	0.275	K.SAWSEAYNQLVAAIK.Q
R2/RRR2-20/2	1351.031	1351.449	-310.535	0.524	2052.864	0.506	20	0.268	K.YGVGDAHFEVTR.F
R2/RRR2-20/2	1651.348	1651.844	-301.216	0.472	2068.662	0.449	23	0.253	K.SAWSEAYNQLVAAIK.Q
R2/RRR2-20/2	1352.003	1351.449	-330.869	0.548	1702.214	0.522	19	0.219	K.YGVGDAHFEVTR.F
R2/RRR2-20/2	1650.919	1651.844	-1169.813	0.345	1206.647	0.358	19	0.133	K.SAWSEAYNQLVAAIK.Q
R2/RRR2-20/3	1651.586	1651.844	-156.696	0.456	1163.040	0.472	25	0.118	K.SAWSEAYNQLVAAIK.Q
R2/RRR2-20/3	1351.788	1351.449	251.639	0.435	790.550	0.538	21	0.105	K.YGVGDAHFEVTR.F
R2/RRR2-20/3	1351.504	1351.449	40.928	0.416	843.507	0.504	21	0.101	K.YGVGDAHFEVTR.F
R2/RRR2-20/3	1351.593	1351.449	106.691	0.374	709.546	0.516	20	0.095	K.YGVGDAHFEVTR.F
R2/RRR2-23/2	1464.155	1464.562	-279.183	0.523	2445.008	0.401	23	0.308	R.FEALDANGDGVLSR.A
R2/RRR2-23/2	1184.165	1184.240	-62.927	0.380	1024.992	0.278	15	0.115	R.GFVADDDAFAR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1199.091	1199.425	-280.042	0.522	2221.505	0.472	19	0.279	R.VDIGQVLLSVR.C
R2/RRR2-23/2	1199.190	1199.425	-196.808	0.562	1983.881	0.444	19	0.233	R.VDIGQVLLSVR.C
R2/RRR2-23/2	1199.045	1199.425	-318.242	0.514	1829.328	0.459	18	0.216	R.VDIGQVLLSVR.C
R2/RRR2-24/2	1198.764	1199.425	-1390.231	0.441	1827.345	0.396	18	0.201	R.VDIGQVLLSVR.C
R2/RRR2-16/2	1199.314	1199.425	-92.861	0.484	1734.708	0.437	18	0.199	R.VDIGQVLLSVR.C
R2/RRR2-24/2	1199.130	1199.425	-247.155	0.445	1628.338	0.434	17	0.186	R.VDIGQVLLSVR.C
R2/RRR2-18/2	1199.323	1199.425	-85.612	0.443	1640.895	0.410	17	0.182	R.VDIGQVLLSVR.C
R2/RRR2-18/2	1199.308	1199.425	-98.068	0.532	1518.209	0.435	17	0.174	R.VDIGQVLLSVR.C
R2/RRR2-17/2	1199.128	1199.425	-248.993	0.464	1365.583	0.475	16	0.167	R.VDIGQVLLSVR.C
R2/RRR2-17/2	1199.218	1199.425	-173.117	0.497	1306.594	0.455	17	0.160	R.VDIGQVLLSVR.C
R2/RRR2-18/2	1198.758	1199.425	-1395.242	0.423	1293.390	0.446	16	0.156	R.VDIGQVLLSVR.C
R2/RRR2-1/2	1199.109	1199.425	-264.517	0.366	1130.783	0.486	14	0.147	R.VDIGQVLLSVR.C
R2/RRR2-17/2	1198.781	1199.425	-1375.810	0.345	1226.739	0.330	15	0.132	R.VDIGQVLLSVR.C
R2/RRR2-15/2	1199.220	1199.425	-172.095	0.359	929.012	0.382	16	0.125	R.VDIGQVLLSVR.C
R2/RRR2-25/2	1198.720	1199.425	-1426.950	0.341	522.678	0.450	16	0.121	R.VDIGQVLLSVR.C
R2/RRR2-16/3	1567.555	1567.726	-108.976	0.454	933.786	0.484	27	0.103	R.CKPNNAVHASEALR.R
R2/RRR2-16/3	1567.425	1567.726	-192.293	0.472	959.580	0.455	27	0.100	R.CKPNNAVHASEALR.R
R2/RRR2-15/2	1198.705	1199.425	-1439.019	0.193	324.387	0.335	10	0.099	-.VDIGQVLLSVR.-
R2/RRR2-16/3	1567.045	1567.726	-1075.818	0.397	997.010	0.406	27	0.092	R.CKPNNAVHASEALR.R
R2/RRR2-16/2	1502.381	1501.750	-246.817	0.595	2051.766	0.654	23	0.310	K.AVASINSVLTDLVAK.G
R2/RRR2-17/2	1501.308	1501.750	-295.680	0.520	2193.754	0.559	23	0.305	K.AVASINSVLTDLVAK.G
R2/RRR2-16/2	1501.461	1501.750	-193.148	0.557	1938.055	0.586	23	0.269	K.AVASINSVLTDLVAK.G
R2/RRR2-17/2	1501.029	1501.750	-1150.327	0.409	1989.826	0.516	23	0.257	K.AVASINSVLTDLVAK.G
R2/RRR2-17/2	1502.218	1501.750	312.110	0.574	1841.026	0.592	22	0.255	K.AVASINSVLTDLVAK.G
R2/RRR2-16/2	1380.132	1379.540	-296.979	0.559	1575.676	0.574	18	0.216	K.ANNVIYGLAQCR.G
R2/RRR2-16/2	1501.046	1501.750	-1138.895	0.414	1675.223	0.514	22	0.211	K.AVASINSVLTDLVAK.G
R2/RRR2-16/2	1379.154	1379.540	-281.032	0.490	1522.863	0.417	18	0.173	K.ANNVIYGLAQCR.G
R2/RRR2-16/2	1379.049	1379.540	-357.052	0.464	1538.396	0.374	18	0.166	K.ANNVIYGLAQCR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/3	1501.623	1501.750	-85.101	0.459	1351.605	0.419	30	0.121	K.AVASINSVLTDLVAK.G
R2/RRR2-16/3	1501.410	1501.750	-227.373	0.441	1514.552	0.326	30	0.114	K.AVASINSVLTDLVAK.G
R2/RRR2-16/3	1501.582	1501.750	-112.622	0.418	1043.358	0.304	26	0.079	K.AVASINSVLTDLVAK.G
R2/RRR2-20/2	1500.822	1499.734	58.524	0.616	1813.424	0.602	20	0.255	K.APLLDVTQFGYFK.V
R2/RRR2-20/2	1499.331	1499.734	-269.775	0.553	1747.549	0.620	20	0.251	K.APLLDVTQFGYFK.V
R2/RRR2-21/2	1499.362	1499.734	-248.947	0.575	1720.368	0.598	20	0.241	K.APLLDVTQFGYFK.V
R2/RRR2-21/2	1499.233	1499.734	-1004.298	0.549	1662.338	0.612	20	0.236	K.APLLDVTQFGYFK.V
R2/RRR2-21/2	1499.448	1499.734	-191.366	0.557	1569.586	0.585	20	0.217	K.APLLDVTQFGYFK.V
R2/RRR2-21/3	969.296	969.077	226.329	0.481	596.115	0.470	16	0.086	-.YHPGYFGK.-
R2/RRR2-21/3	968.920	969.077	-162.532	0.420	475.316	0.411	14	0.083	K.YHPGYFGK.V
R2/RRR2-21/3	969.030	969.077	-48.325	0.415	439.314	0.377	13	0.081	K.YHPGYFGK.V
R2/RRR2-15/2	1422.276	1421.622	-244.448	0.555	1877.392	0.660	22	0.283	K.LPGLFIWSADSSK.V
R2/RRR2-14/2	1422.369	1421.622	-178.667	0.555	1749.155	0.607	21	0.247	K.LPGLFIWSADSSK.V
R2/RRR2-14/2	1421.658	1421.622	25.095	0.519	1583.718	0.562	21	0.213	K.LPGLFIWSADSSK.V
R2/RRR2-15/2	1422.405	1421.622	-153.012	0.538	1497.622	0.577	20	0.206	K.LPGLFIWSADSSK.V
R2/RRR2-14/2	1421.282	1421.622	-240.053	0.507	1429.001	0.583	20	0.199	K.LPGLFIWSADSSK.V
R2/RRR2-15/2	1421.182	1421.622	-310.628	0.516	1370.172	0.602	19	0.196	K.LPGLFIWSADSSK.V
R2/RRR2-14/2	1338.083	1338.404	-240.430	0.484	1233.359	0.557	17	0.174	K.VSSYGFEYETR.G
R2/RRR2-14/2	1338.024	1338.404	-284.821	0.454	1131.707	0.524	17	0.159	K.VSSYGFEYETR.G
R2/RRR2-14/2	1339.033	1338.404	-277.383	0.504	980.219	0.573	16	0.157	K.VSSYGFEYETR.G
R2/RRR2-12/2	1543.199	1543.651	-294.080	0.512	2199.195	0.499	24	0.290	K.ITGCYVVGSAGSDEK.V
R2/RRR2-12/2	1543.024	1543.651	-1057.763	0.516	2167.908	0.508	25	0.288	K.ITGCYVVGSAGSDEK.V
R2/RRR2-12/2	1544.181	1543.651	-305.549	0.557	2066.185	0.479	24	0.260	K.ITGCYVVGSAGSDEK.V
R2/RRR2-12/2	1352.503	1352.475	20.766	0.491	1707.649	0.426	18	0.197	K.FGFDDAFNYKK.E
R2/RRR2-12/2	1351.982	1352.475	-366.193	0.492	1513.984	0.468	18	0.185	K.FGFDDAFNYKK.E
R2/RRR2-12/2	1352.105	1352.475	-274.882	0.484	1572.633	0.362	18	0.168	K.FGFDDAFNYKK.E
R2/RRR2-12/3	1352.876	1352.475	297.140	0.525	979.417	0.451	24	0.100	K.FGFDDAFNYKK.E
R2/RRR2-12/3	1352.298	1352.475	-131.076	0.539	1099.328	0.396	25	0.096	K.FGFDDAFNYKK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/3	1352.467	1352.475	-6.266	0.513	980.779	0.397	24	0.091	K.FGFDDAFNYKK.E
R2/RRR2-11/2	1344.143	1344.539	-295.912	0.535	1873.166	0.588	21	0.264	R.LVDIGTVTAQQAK.D
R2/RRR2-11/2	1343.559	1344.539	-1478.434	0.416	1397.918	0.469	20	0.172	R.LVDIGTVTAQQAK.D
R2/RRR2-11/2	1114.026	1114.314	-259.442	0.419	1079.512	0.316	15	0.125	R.LLNCEVPLR.A
R2/RRR2-11/2	1114.067	1114.314	-222.286	0.443	1022.375	0.258	15	0.116	R.LLNCEVPLR.A
R2/RRR2-15/2	1534.219	1534.721	-981.935	0.493	2051.947	0.599	22	0.292	K.AAAVGANSQAAQSM*LK.Q
R2/RRR2-16/2	1534.274	1534.721	-291.940	0.520	1988.053	0.527	22	0.259	K.AAAVGANSQAAQSM*LK.Q
R2/RRR2-16/2	1536.167	1534.721	291.205	0.525	1540.646	0.564	20	0.204	K.AAAVGANSQAAQSM*LK.Q
R2/RRR2-15/2	1534.167	1534.721	-1015.886	0.498	1606.247	0.476	20	0.191	K.AAAVGANSQAAQSM*LK.Q
R2/RRR2-15/2	1536.069	1534.721	227.457	0.561	1391.180	0.580	20	0.190	K.AAAVGANSQAAQSM*LK.Q
R2/RRR2-16/2	1536.143	1534.721	275.428	0.528	1004.234	0.564	21	0.154	K.AAAVGANSQAAQSM*LK.Q
R2/RRR2-15/2	1007.942	1008.110	-167.219	0.367	657.171	0.395	13	0.117	-.TTIFSPEGR.-
R2/RRR2-15/2	1007.521	1008.110	-1582.177	0.282	527.312	0.394	12	0.113	R.TTIFSPEGR.L
R2/RRR2-16/2	1007.974	1008.110	-135.025	0.325	564.191	0.376	11	0.112	R.TTIFSPEGR.L
R2/RRR2-15/2	1007.967	1008.110	-142.193	0.264	566.117	0.309	12	0.109	R.TTIFSPEGR.L
R2/RRR2-16/2	1007.367	1008.110	-1735.682	0.274	517.294	0.229	12	0.106	-.TTIFSPEGR.-
R2/RRR2-16/2	1007.576	1008.110	-1526.678	0.237	604.648	0.181	13	0.105	R.TTIFSPEGR.L
R2/RRR2-15/3	1534.158	1534.721	-1021.327	0.448	761.263	0.496	25	0.095	K.AAAVGANSQAAQSM*LK.Q
R2/RRR2-21/2	1794.319	1793.055	147.665	0.622	2873.633	0.574	23	0.444	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1793.400	1793.055	193.004	0.614	2877.550	0.560	23	0.439	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1792.219	1793.055	-1027.191	0.566	2691.949	0.549	23	0.394	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-19/2	1792.337	1793.055	-961.271	0.578	2636.465	0.554	23	0.383	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-18/2	1794.581	1793.055	-264.781	0.639	2540.943	0.586	23	0.372	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1794.023	1793.055	-17.673	0.632	2583.222	0.554	23	0.368	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-21/2	1793.467	1793.055	230.817	0.602	2534.696	0.544	22	0.355	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1793.489	1793.055	242.693	0.602	2441.600	0.559	22	0.342	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1776.391	1777.055	-939.568	0.566	2316.115	0.525	23	0.307	K.AM*SIMNSFINDIFEK.L
R2/RRR2-20/2	1794.135	1793.055	45.043	0.627	2205.231	0.580	22	0.303	K.AM*SIM*NSFINDIFEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/2	1792.469	1793.055	-887.157	0.593	2233.143	0.562	21	0.302	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-19/2	1792.177	1793.055	-1050.784	0.549	2121.988	0.546	21	0.279	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-15/2	1793.612	1793.055	-247.654	0.566	2137.500	0.534	22	0.278	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-15/2	1794.348	1793.055	163.697	0.603	2046.830	0.574	21	0.274	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1776.087	1777.055	-1111.517	0.569	2106.305	0.504	22	0.263	K.AM*SIMNSFINDIFEK.L
R2/RRR2-2/2	1794.426	1793.055	207.700	0.544	1978.567	0.543	21	0.255	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1793.019	1793.055	-20.142	0.585	1836.200	0.615	20	0.252	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-18/2	1793.733	1793.055	-179.925	0.592	1898.477	0.558	21	0.246	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1776.684	1777.055	-209.831	0.591	2006.396	0.498	21	0.244	K.AM*SIMNSFINDIFEK.L
R2/RRR2-17/2	1794.184	1793.055	72.133	0.590	1887.328	0.534	21	0.237	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-16/2	1793.449	1793.055	220.374	0.556	1708.720	0.534	21	0.214	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1792.478	1793.055	-882.439	0.547	1641.519	0.536	19	0.204	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-19/2	1794.695	1793.055	-200.773	0.563	1449.542	0.596	20	0.198	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-21/2	1791.717	1793.055	-1308.471	0.462	1660.177	0.489	19	0.197	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-12/2	1793.677	1793.055	-211.262	0.482	1559.728	0.524	20	0.194	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-16/2	1794.821	1793.055	-130.632	0.572	1425.975	0.586	18	0.190	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-22/2	1794.788	1793.055	-148.917	0.578	1257.350	0.603	19	0.178	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-22/2	1794.240	1793.055	103.452	0.597	1379.637	0.545	19	0.176	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-2/2	1794.261	1793.055	115.529	0.541	1194.043	0.538	19	0.160	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-11/2	1794.713	1793.055	-191.220	0.491	1027.083	0.535	18	0.147	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-3/2	1794.267	1793.055	118.463	0.482	998.500	0.492	17	0.138	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-12/2	1794.377	1793.055	180.344	0.483	649.314	0.519	16	0.126	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-12/2	1794.665	1793.055	-218.037	0.465	636.184	0.508	15	0.123	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-2/2	1793.629	1793.055	-238.027	0.484	656.670	0.488	16	0.123	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-20/2	1775.355	1777.055	-2090.721	0.393	961.575	0.347	18	0.119	K.AMSIM*NSFINDIFEK.L
R2/RRR2-14/2	1794.666	1793.055	-217.491	0.417	521.604	0.438	17	0.118	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-14/2	1794.397	1793.055	191.327	0.387	287.851	0.387	14	0.112	-.AM*SIM*NSFINDIFEK.-
R2/RRR2-18/2	1794.523	1793.055	261.657	0.390	248.298	0.326	12	0.111	K.AM*SIM*NSFINDIFEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	1794.431	1793.055	210.087	0.338	279.597	0.351	12	0.110	K.AM*SIM*NSFINDIFEK.L
R2/RRR2-14/3	1825.135	1825.058	42.147	0.537	2200.401	0.535	35	0.296	K.WGLVNHIVDDTQVLSK.A
R2/RRR2-14/2	1131.965	1132.286	-284.210	0.308	952.786	0.190	14	0.105	K.AIEVCEAIAR.N
R2/RRR2-14/2	1131.376	1132.286	-1693.262	0.214	600.695	0.208	13	0.101	K.AIEVCEAIAR.N
R2/RRR2-20/2	1964.875	1965.230	-181.430	0.560	2118.691	0.606	26	0.309	R.IAECLVGDETGIIVFTAR.N
R2/RRR2-20/2	1964.448	1965.230	-910.000	0.538	1925.948	0.576	25	0.266	R.IAECLVGDETGIIVFTAR.N
R2/RRR2-20/2	1964.774	1965.230	-233.037	0.524	1844.757	0.615	25	0.264	R.IAECLVGDETGIIVFTAR.N
R2/RRR2-20/3	1798.711	1799.070	-200.376	0.338	887.819	0.407	25	0.087	K.VDQLRPGTHGHNLLLK.V
R2/RRR2-20/3	1799.043	1799.070	-15.362	0.320	904.776	0.339	26	0.078	K.VDQLRPGTHGHNLLLK.V
R2/RRR2-20/3	1798.434	1799.070	-912.519	0.378	531.040	0.397	21	0.067	-.VDQLRPGTHGHNLLLK.-
R2/RRR2-26/2	1375.110	1375.507	-289.516	0.472	1815.581	0.486	18	0.225	R.EGDILTLLESER.E
R2/RRR2-26/2	1375.866	1375.507	262.017	0.487	1535.464	0.533	18	0.201	R.EGDILTLLESER.E
R2/RRR2-26/2	1375.071	1375.507	-317.749	0.460	1309.642	0.460	17	0.161	R.EGDILTLLESER.E
R2/RRR2-26/3	1134.900	1135.255	-313.964	0.517	914.984	0.272	18	0.061	-.VKFLDDQNR.-
R2/RRR2-26/3	1135.117	1135.255	-122.340	0.456	789.819	0.231	17	0.058	-.VKFLDDQNR.-
R2/RRR2-26/3	1135.806	1135.255	-396.879	0.557	1061.337	0.230	18	0.053	-.VKFLDDQNR.-
R2/RRR2-22/2	1647.033	1647.917	-1147.702	0.454	1222.892	0.460	20	0.153	R.SGKM*ELPEWVDIVK.T
R2/RRR2-22/2	1647.392	1647.917	-928.798	0.487	1096.751	0.512	20	0.153	R.SGKM*ELPEWVDIVK.T
R2/RRR2-21/2	1647.376	1647.917	-938.246	0.479	1083.268	0.509	20	0.151	R.SGKM*ELPEWVDIVK.T
R2/RRR2-21/2	1648.309	1647.917	238.510	0.542	1020.347	0.510	19	0.147	R.SGKM*ELPEWVDIVK.T
R2/RRR2-22/2	1647.623	1647.917	-179.019	0.505	959.703	0.517	19	0.144	R.SGKM*ELPEWVDIVK.T
R2/RRR2-21/2	1648.010	1647.917	56.608	0.560	846.113	0.542	18	0.141	R.SGKM*ELPEWVDIVK.T
R2/RRR2-22/2	1376.045	1375.615	313.015	0.446	735.370	0.465	17	0.130	K.M*ELPEWVDIVK.T
R2/RRR2-22/2	1375.361	1375.615	-185.171	0.476	757.042	0.445	17	0.129	K.M*ELPEWVDIVK.T
R2/RRR2-22/2	1374.555	1375.615	-1502.945	0.452	726.832	0.409	17	0.124	K.M*ELPEWVDIVK.T
R2/RRR2-22/2	1359.760	1359.616	106.646	0.435	941.651	0.328	18	0.122	K.MELPEWVDIVK.T
R2/RRR2-21/2	1375.285	1375.615	-240.734	0.344	691.074	0.374	14	0.114	-.M*ELPEWVDIVK.-
R2/RRR2-21/2	1647.240	1647.917	-1021.348	0.350	900.369	0.317	17	0.113	R.SGKM*ELPEWVDIVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1359.280	1359.616	-247.580	0.388	731.742	0.275	17	0.113	K.MELPEWVDIVK.T
R2/RRR2-22/2	1358.985	1359.616	-1203.622	0.344	749.695	0.260	17	0.111	K.MELPEWVDIVK.T
R2/RRR2-21/2	1358.491	1359.616	-1569.074	0.295	758.548	0.212	17	0.107	-.MELPEWVDIVK.-
R2/RRR2-22/2	1358.564	1359.616	-1514.465	0.280	608.018	0.219	15	0.106	-.MELPEWVDIVK.-
R2/RRR2-21/3	1647.748	1647.917	-103.296	0.359	1042.325	0.173	25	0.064	R.SGKM*ELPEWVDIVK.T
R2/RRR2-22/3	1647.569	1647.917	-211.879	0.345	822.666	0.177	23	0.063	R.SGKM*ELPEWVDIVK.T
R2/RRR2-21/3	1647.810	1647.917	-65.398	0.296	1145.117	0.095	25	0.058	R.SGKM*ELPEWVDIVK.T
R2/RRR2-21/3	1647.234	1647.917	-1025.077	0.304	1021.401	0.057	25	0.055	R.SGKM*ELPEWVDIVK.T
R2/RRR2-23/3	1914.913	1914.959	-23.895	0.502	931.570	0.511	30	0.109	K.KDGEEESSGVVDYDKEK.K
R2/RRR2-23/3	1786.908	1786.786	68.504	0.435	578.344	0.550	25	0.096	K.DGEEESSGVVDYDKEK.K
R2/RRR2-23/3	1914.806	1914.959	-80.006	0.492	565.655	0.492	24	0.089	K.KDGEEESSGVVDYDKEK.K
R2/RRR2-23/3	1786.809	1786.786	13.210	0.394	473.241	0.482	22	0.081	-.DGEEESSGVVDYDKEK.-
R2/RRR2-10/2	1630.460	1630.910	-276.689	0.537	2150.578	0.592	25	0.311	R.ELLGGNGILADFLVAK.A
R2/RRR2-10/2	1630.554	1630.910	-218.705	0.537	1635.756	0.582	22	0.224	R.ELLGGNGILADFLVAK.A
R2/RRR2-10/2	1629.882	1630.910	-1247.937	0.443	1338.642	0.473	21	0.165	R.ELLGGNGILADFLVAK.A
R2/RRR2-10/2	1691.352	1690.924	254.189	0.460	864.069	0.389	21	0.122	K.QFGVPLAAFQLNQEK.L
R2/RRR2-25/2	1189.008	1189.384	-317.119	0.479	1309.971	0.478	18	0.165	K.LSAGIASILESK.L
R2/RRR2-25/2	1317.996	1317.557	334.276	0.560	1158.559	0.484	20	0.156	K.KLSAGIASILESK.L
R2/RRR2-25/2	1189.222	1189.384	-136.375	0.528	1167.057	0.476	18	0.154	K.LSAGIASILESK.L
R2/RRR2-25/2	1188.610	1189.384	-1496.668	0.524	1145.777	0.428	18	0.144	K.LSAGIASILESK.L
R2/RRR2-13/2	1212.690	1212.424	220.037	0.471	2239.071	0.489	22	0.295	K.VLVIGGGDGGVLR.E
R2/RRR2-13/2	1213.235	1212.424	-156.181	0.545	1798.176	0.504	23	0.229	K.VLVIGGGDGGVLR.E
R2/RRR2-13/2	1212.210	1212.424	-177.422	0.513	1695.618	0.517	22	0.218	K.VLVIGGGDGGVLR.E
R2/RRR2-13/3	1356.413	1356.595	-134.831	0.441	1177.036	0.434	26	0.109	R.VSLHIGDGVAFLK.N
R2/RRR2-13/3	1356.513	1356.595	-60.764	0.484	991.466	0.477	26	0.105	R.VSLHIGDGVAFLK.N
R2/RRR2-12/3	1581.467	1581.752	-181.334	0.473	736.150	0.581	27	0.109	K.TKFGFDDAFNYKK.E
R2/RRR2-12/3	1581.172	1581.752	-1002.594	0.459	768.961	0.479	27	0.095	K.TKFGFDDAFNYKK.E
R2/RRR2-12/3	1581.881	1581.752	81.562	0.453	679.931	0.478	26	0.092	K.TKFGFDDAFNYKK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1603.260	1602.815	278.846	0.560	2202.453	0.536	23	0.302	R.AVNITINSIGTELTR.D
R2/RRR2-11/2	1603.368	1602.815	-279.150	0.559	2165.409	0.543	23	0.297	R.AVNITINSIGTELTR.D
R2/RRR2-11/2	1601.965	1602.815	-1158.098	0.421	1929.290	0.483	22	0.241	R.AVNITINSIGTELTR.D
R2/RRR2-11/2	1286.989	1287.422	-337.225	0.421	691.646	0.429	15	0.120	K.ISYGESQM*LDK.A
R2/RRR2-3/2	1824.496	1825.076	-868.982	0.532	2094.531	0.545	24	0.289	R.LTQM*NTDLFGGVDAVVK.Y
R2/RRR2-3/2	1531.445	1532.678	-1462.384	0.391	1507.236	0.413	21	0.171	K.EDLVVSASLDQTVR.V
R2/RRR2-3/2	1532.451	1532.678	-148.735	0.369	998.774	0.431	18	0.131	K.EDLVVSASLDQTVR.V
R2/RRR2-9/2	1782.721	1783.021	-168.650	0.459	2022.344	0.513	24	0.267	R.FAVEVIDAVVGEIGAHR.V
R2/RRR2-9/2	1157.180	1156.359	-155.388	0.484	1141.295	0.396	16	0.140	R.LFLANPDLPR.R
R2/RRR2-9/3	1783.030	1783.021	4.929	0.421	1122.542	0.524	35	0.123	R.FAVEVIDAVVGEIGAHR.V
R2/RRR2-9/3	1782.896	1783.021	-70.164	0.453	937.997	0.544	32	0.115	R.FAVEVIDAVVGEIGAHR.V
R2/RRR2-9/2	1155.904	1156.359	-394.733	0.351	245.710	0.432	12	0.115	R.LFLANPDLPR.R
R2/RRR2-9/3	1782.833	1783.021	-105.500	0.416	651.324	0.563	28	0.101	R.FAVEVIDAVVGEIGAHR.V
R2/RRR2-15/2	1439.012	1439.556	-1075.850	0.520	1604.648	0.582	23	0.225	R.RGADVVVNYGSSSK.A
R2/RRR2-15/2	843.834	843.994	-190.381	0.429	1426.035	0.435	15	0.169	K.VALVTGAGR.G
R2/RRR2-15/2	843.919	843.994	-89.096	0.404	1224.381	0.418	15	0.148	K.VALVTGAGR.G
R2/RRR2-15/2	844.155	843.994	191.147	0.445	1196.642	0.392	15	0.143	K.VALVTGAGR.G
R2/RRR2-8/2	1432.044	1432.514	-328.962	0.522	1851.621	0.576	19	0.256	R.VNVYYNEASCGR.F
R2/RRR2-8/2	1431.570	1432.514	-1362.055	0.432	1781.898	0.545	19	0.235	R.VNVYYNEASCGR.F
R2/RRR2-9/2	1431.825	1432.514	-1183.180	0.513	1766.304	0.514	19	0.226	R.VNVYYNEASCGR.F
R2/RRR2-8/3	1918.020	1918.049	-15.111	0.411	787.081	0.509	26	0.100	K.FWEVVCDEHGIDPTGR.Y
R2/RRR2-8/3	1917.365	1918.049	-881.140	0.356	788.229	0.430	26	0.087	K.FWEVVCDEHGIDPTGR.Y
R2/RRR2-8/3	1917.527	1918.049	-796.208	0.323	583.803	0.448	20	0.082	K.FWEVVCDEHGIDPTGR.Y
R2/RRR2-9/3	1917.854	1918.049	-101.967	0.271	681.140	0.397	21	0.077	K.FWEVVCDEHGIDPTGR.Y
R2/RRR2-26/2	1122.890	1123.284	-352.256	0.491	1055.254	0.438	16	0.142	R.VCGNPHGLIR.K
R2/RRR2-26/2	1122.543	1123.284	-1555.851	0.446	1058.011	0.434	16	0.140	R.VCGNPHGLIR.K
R2/RRR2-26/2	1122.970	1123.284	-280.490	0.453	1071.274	0.423	16	0.140	R.VCGNPHGLIR.K
R2/RRR2-26/2	975.430	976.120	-1737.958	0.385	965.954	0.333	11	0.122	K.YGLM*CCR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-26/2	975.902	976.120	-224.197	0.388	1175.938	0.252	12	0.122	K.YGLM*CCR.Q
R2/RRR2-26/2	975.532	976.120	-1632.475	0.402	939.634	0.315	11	0.120	K.YGLM*CCR.Q
R2/RRR2-26/2	959.875	960.120	-256.909	0.305	1023.791	0.287	11	0.118	K.YGLMCCR.Q
R2/RRR2-14/2	1456.331	1455.640	-213.090	0.477	2085.667	0.490	19	0.270	K.SQIQSYVFDVIR.A
R2/RRR2-14/2	1454.846	1455.640	-1237.170	0.364	1885.411	0.408	19	0.216	K.SQIQSYVFDVIR.A
R2/RRR2-26/2	1495.115	1495.605	-328.433	0.503	2831.047	0.500	23	0.421	R.VCACVDSAGAVTER.G
R2/RRR2-27/2	1495.295	1495.605	-207.946	0.498	2836.535	0.481	23	0.414	R.VCACVDSAGAVTER.G
R2/RRR2-26/2	1495.010	1495.605	-1070.114	0.512	2765.577	0.505	23	0.407	R.VCACVDSAGAVTER.G
R2/RRR2-27/2	1494.984	1495.605	-1087.577	0.517	2760.705	0.502	23	0.405	R.VCACVDSAGAVTER.G
R2/RRR2-27/2	1496.033	1495.605	286.966	0.534	2638.116	0.503	23	0.376	R.VCACVDSAGAVTER.G
R2/RRR2-12/2	1331.728	1332.517	-1347.593	0.327	1050.823	0.346	15	0.122	R.RGMQSGPAVSWR.G
R2/RRR2-17/2	1592.310	1591.779	-295.178	0.345	939.959	0.065	16	0.090	R.GM*QSGPAVSWRGWR.R
R2/RRR2-5/2	1554.450	1554.724	-176.797	0.519	1974.146	0.446	22	0.237	K.LSTSAQSEVEYVLK.F
R2/RRR2-5/2	1554.093	1554.724	-1052.672	0.467	1573.237	0.408	21	0.177	K.LSTSAQSEVEYVLK.F
R2/RRR2-5/2	1086.830	1086.226	-364.619	0.383	790.429	0.323	14	0.115	K.FPLHSTLDR.L
R2/RRR2-5/2	1086.934	1086.226	-268.837	0.306	629.308	0.350	13	0.111	K.FPLHSTLDR.L
R2/RRR2-5/2	1553.486	1554.724	-1444.394	0.244	945.743	0.242	19	0.107	K.LSTSAQSEVEYVLK.F
R2/RRR2-21/2	1205.849	1206.380	-1273.013	0.515	953.388	0.553	17	0.152	R.KGHAVGDIPGVR.F
R2/RRR2-21/2	1206.064	1206.380	-262.789	0.489	902.164	0.515	17	0.142	R.KGHAVGDIPGVR.F
R2/RRR2-21/2	1077.879	1078.207	-304.832	0.400	583.171	0.554	15	0.129	K.GHAVGDIPGVR.F
R2/RRR2-21/3	1206.558	1206.380	148.335	0.502	1332.872	0.408	26	0.114	R.KGHAVGDIPGVR.F
R2/RRR2-27/2	1078.010	1078.207	-182.927	0.310	259.439	0.515	12	0.114	K.GHAVGDIPGVR.F
R2/RRR2-20/3	1206.031	1206.380	-289.863	0.345	1203.129	0.337	23	0.094	R.KGHAVGDIPGVR.F
R2/RRR2-22/3	1206.322	1206.380	-48.334	0.412	1007.199	0.394	24	0.093	R.KGHAVGDIPGVR.F
R2/RRR2-21/3	1206.487	1206.380	89.434	0.465	975.705	0.401	25	0.093	R.KGHAVGDIPGVR.F
R2/RRR2-27/3	1206.944	1206.380	-362.125	0.471	816.208	0.367	21	0.084	R.KGHAVGDIPGVR.F
R2/RRR2-26/3	1206.355	1206.380	-20.169	0.443	741.404	0.375	21	0.082	-.KGHAVGDIPGVR.-
R2/RRR2-20/3	1206.444	1206.380	53.663	0.407	831.367	0.322	22	0.080	R.KGHAVGDIPGVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1206.816	1206.380	362.727	0.433	629.452	0.359	20	0.078	-.KGHAVGDIPGVR.-
R2/RRR2-27/3	1206.436	1206.380	46.813	0.431	983.827	0.278	23	0.077	R.KGHAVGDIPGVR.F
R2/RRR2-24/2	1077.556	1078.207	-1536.042	0.215	152.625	0.369	11	0.076	-.GHAVGDIPGVR.-
R2/RRR2-19/3	1206.773	1206.380	326.976	0.311	650.648	0.276	20	0.076	R.KGHAVGDIPGVR.F
R2/RRR2-22/3	1205.703	1206.380	-1394.629	0.314	788.807	0.298	21	0.075	-.KGHAVGDIPGVR.-
R2/RRR2-24/3	1206.298	1206.380	-67.518	0.350	733.187	0.266	22	0.075	R.KGHAVGDIPGVR.F
R2/RRR2-21/3	1206.056	1206.380	-268.842	0.358	838.571	0.272	21	0.075	R.KGHAVGDIPGVR.F
R2/RRR2-26/3	1205.363	1206.380	-1678.422	0.409	902.298	0.243	25	0.073	R.KGHAVGDIPGVR.F
R2/RRR2-27/3	1206.568	1206.380	156.554	0.384	737.063	0.257	23	0.071	-.KGHAVGDIPGVR.-
R2/RRR2-14/3	1770.066	1770.922	-1052.066	0.554	1985.848	0.549	29	0.259	K.KGENDLPGLTDTEKPR.M
R2/RRR2-14/3	1770.777	1770.922	-82.399	0.544	1788.907	0.502	29	0.204	K.KGENDLPGLTDTEKPR.M
R2/RRR2-14/3	1770.295	1770.922	-921.836	0.549	1743.756	0.520	29	0.204	K.KGENDLPGLTDTEKPR.M
R2/RRR2-22/2	1473.024	1472.624	271.832	0.529	1970.877	0.515	20	0.260	R.AFVVHELEDDLGK.G
R2/RRR2-22/2	1324.036	1324.511	-360.328	0.341	597.062	0.558	17	0.127	K.QIPLSGPNSVVGR.A
R2/RRR2-22/2	1324.254	1324.511	-194.493	0.355	585.130	0.508	17	0.123	K.QIPLSGPNSVVGR.A
R2/RRR2-22/2	1324.354	1324.511	-118.762	0.355	569.900	0.491	16	0.120	K.QIPLSGPNSVVGR.A
R2/RRR2-21/2	1324.165	1324.511	-262.005	0.321	481.554	0.490	15	0.116	K.QIPLSGPNSVVGR.A
R2/RRR2-21/2	1324.111	1324.511	-303.071	0.309	420.276	0.500	14	0.114	K.QIPLSGPNSVVGR.A
R2/RRR2-21/2	1324.020	1324.511	-372.169	0.302	482.977	0.408	15	0.111	K.QIPLSGPNSVVGR.A
R2/RRR2-3/3	1281.606	1281.443	127.421	0.569	1626.906	0.512	24	0.176	K.HVVDDGLELRK.A
R2/RRR2-3/3	1281.374	1281.443	-54.437	0.529	1200.295	0.483	22	0.122	K.HVVDDGLELRK.A
R2/RRR2-3/2	1152.986	1153.270	-247.489	0.332	637.032	0.414	13	0.114	K.HVVDDGLELR.K
R2/RRR2-3/3	1281.216	1281.443	-177.720	0.502	1037.460	0.479	21	0.109	K.HVVDDGLELRK.A
R2/RRR2-24/2	1275.110	1275.396	-224.650	0.412	986.580	0.569	19	0.152	R.HGGSGGPADPVPVK.L
R2/RRR2-24/2	1274.980	1275.396	-327.041	0.407	696.777	0.516	18	0.128	R.HGGSGGPADPVPVK.L
R2/RRR2-24/3	1544.583	1544.740	-101.996	0.455	860.076	0.459	28	0.096	R.LRHGGSGGPADPVPVK.L
R2/RRR2-24/3	1544.726	1544.740	-9.251	0.480	864.414	0.437	28	0.093	R.LRHGGSGGPADPVPVK.L
R2/RRR2-24/3	1544.608	1544.740	-85.943	0.472	862.733	0.394	28	0.086	R.LRHGGSGGPADPVPVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1275.408	1275.396	9.483	0.385	717.170	0.393	20	0.082	R.HGGSGGPADPVPVK.L
R2/RRR2-23/3	1275.788	1275.396	308.328	0.351	1113.442	0.287	23	0.081	R.HGGSGGPADPVPVK.L
R2/RRR2-24/3	1275.480	1275.396	66.070	0.377	861.883	0.334	22	0.078	R.HGGSGGPADPVPVK.L
R2/RRR2-25/3	1275.438	1275.396	33.097	0.326	854.569	0.258	22	0.070	-.HGGSGGPADPVPVK.-
R2/RRR2-23/3	1275.849	1275.396	356.248	0.306	1033.730	0.221	23	0.069	R.HGGSGGPADPVPVK.L
R2/RRR2-24/3	1274.788	1275.396	-1264.977	0.308	675.463	0.220	19	0.066	-.HGGSGGPADPVPVK.-
R2/RRR2-10/2	1693.443	1691.903	-272.978	0.587	2105.867	0.540	27	0.286	K.FVAPDVSILESDSAIK.S
R2/RRR2-10/2	1691.315	1691.903	-942.072	0.511	1961.051	0.526	25	0.258	K.FVAPDVSILESDSAIK.S
R2/RRR2-10/2	1691.343	1691.903	-925.262	0.456	1159.163	0.510	21	0.156	K.FVAPDVSILESDSAIK.S
R2/RRR2-10/2	1768.349	1768.088	148.265	0.487	489.372	0.516	16	0.119	R.QSLLPLTVPINTETLK.M
R2/RRR2-10/2	1767.664	1768.088	-240.598	0.411	516.621	0.488	17	0.117	R.QSLLPLTVPINTETLK.M
R2/RRR2-10/2	1768.007	1768.088	-46.094	0.408	540.628	0.445	18	0.115	R.QSLLPLTVPINTETLK.M
R2/RRR2-12/2	1678.319	1677.873	266.303	0.584	1761.970	0.597	23	0.248	K.VPNDVCADVVYNAIK.V
R2/RRR2-12/2	1678.418	1677.873	-272.358	0.564	1743.430	0.580	23	0.240	K.VPNDVCADVVYNAIK.V
R2/RRR2-12/2	1676.993	1677.873	-1124.465	0.535	1573.545	0.613	22	0.225	K.VPNDVCADVVYNAIK.V
R2/RRR2-12/2	1277.659	1277.560	77.755	0.312	679.061	0.415	14	0.114	K.EMPLVGFGLWK.V
R2/RRR2-15/2	1828.883	1827.067	-100.929	0.594	1892.354	0.616	23	0.269	R.SLGLGDLDFSAVYEVLK.G
R2/RRR2-15/2	1828.337	1827.067	147.820	0.564	1881.235	0.578	23	0.256	R.SLGLGDLDFSAVYEVLK.G
R2/RRR2-15/2	1828.885	1827.067	-99.857	0.587	1846.680	0.570	23	0.248	R.SLGLGDLDFSAVYEVLK.G
R2/RRR2-14/2	1828.288	1827.067	120.769	0.549	1395.951	0.550	20	0.183	R.SLGLGDLDFSAVYEVLK.G
R2/RRR2-15/2	1205.989	1206.330	-283.516	0.495	984.129	0.475	16	0.137	K.GGAFVEAPVSGSK.K
R2/RRR2-15/2	1206.052	1206.330	-231.524	0.432	918.065	0.417	17	0.127	K.GGAFVEAPVSGSK.K
R2/RRR2-15/2	1206.196	1206.330	-111.414	0.473	782.050	0.461	16	0.126	K.GGAFVEAPVSGSK.K
R2/RRR2-14/2	1828.333	1827.067	145.544	0.281	261.637	0.456	13	0.106	R.SLGLGDLDFSAVYEVLK.G
R2/RRR2-20/3	1866.904	1867.012	-57.891	0.520	1953.298	0.548	30	0.252	R.HDVESAIPYHAELTQR.G
R2/RRR2-20/3	1867.045	1867.012	17.659	0.536	1436.223	0.602	28	0.186	R.HDVESAIPYHAELTQR.G
R2/RRR2-21/3	1866.630	1867.012	-204.892	0.492	1561.214	0.511	27	0.175	R.HDVESAIPYHAELTQR.G
R2/RRR2-21/2	1466.044	1464.604	301.020	0.534	910.018	0.487	16	0.137	R.LSYLWADDPEVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1464.090	1464.604	-1036.850	0.403	788.736	0.436	15	0.123	R.LSYLWADDPEVR.A
R2/RRR2-21/2	1463.955	1464.604	-1129.864	0.311	687.487	0.349	14	0.110	R.LSYLWADDPEVR.A
R2/RRR2-21/2	1463.368	1464.604	-1532.591	0.288	832.760	0.280	15	0.108	R.LSYLWADDPEVR.A
R2/RRR2-16/2	1420.260	1419.648	-273.502	0.483	2000.750	0.534	19	0.265	K.GANEVLLVIEAYK.T
R2/RRR2-16/2	1419.329	1419.648	-225.373	0.393	1651.279	0.413	17	0.185	K.GANEVLLVIEAYK.T
R2/RRR2-16/2	1419.034	1419.648	-1140.609	0.333	1226.636	0.391	16	0.139	K.GANEVLLVIEAYK.T
R2/RRR2-15/2	1419.188	1419.648	-324.781	0.237	533.272	0.217	13	0.101	-.GANEVLLVIEAYK.-
R2/RRR2-16/3	1850.830	1851.084	-137.446	0.418	928.073	0.454	30	0.098	K.VTAVPAKEEEICGATFK.V
R2/RRR2-16/3	1849.576	1851.084	-1902.287	0.351	446.496	0.484	21	0.084	K.VTAVPAKEEEICGATFK.V
R2/RRR2-15/3	1849.771	1851.084	-1254.019	0.258	710.258	0.352	26	0.074	K.VTAVPAKEEEICGATFK.V
R2/RRR2-15/3	1850.873	1851.084	-114.224	0.286	688.368	0.331	26	0.072	K.VTAVPAKEEEICGATFK.V
R2/RRR2-16/2	1809.352	1809.143	116.078	0.529	2001.990	0.494	24	0.256	K.LIQNIVIEAIQSLPTR.A
R2/RRR2-16/2	1808.545	1809.143	-886.220	0.469	2008.744	0.456	23	0.247	K.LIQNIVIEAIQSLPTR.A
R2/RRR2-16/3	1809.580	1809.143	242.411	0.490	1450.537	0.548	28	0.171	K.LIQNIVIEAIQSLPTR.A
R2/RRR2-16/3	1809.767	1809.143	-208.319	0.498	1140.306	0.490	29	0.120	K.LIQNIVIEAIQSLPTR.A
R2/RRR2-16/2	1175.025	1175.317	-249.620	0.452	1070.278	0.260	18	0.117	K.AADSNTTILLR.L
R2/RRR2-24/2	1487.115	1487.596	-324.025	0.403	1843.299	0.424	20	0.214	K.ATLDITADYGYGAR.G
R2/RRR2-24/2	1486.582	1487.596	-1358.926	0.310	1651.235	0.404	21	0.183	K.ATLDITADYGYGAR.G
R2/RRR2-24/2	1167.969	1167.274	-261.858	0.505	1131.175	0.438	14	0.144	K.GWDEGVTQM*K.V
R2/RRR2-24/2	1168.199	1167.274	-64.139	0.501	1058.252	0.430	14	0.138	K.GWDEGVTQM*K.V
R2/RRR2-12/2	943.931	944.071	-148.077	0.513	1574.135	0.451	15	0.186	R.SAVQAALQR.E
R2/RRR2-1/2	943.882	944.071	-200.750	0.463	1611.688	0.385	15	0.176	R.SAVQAALQR.E
R2/RRR2-13/2	943.150	944.071	-2043.004	0.423	1480.538	0.396	15	0.165	R.SAVQAALQR.E
R2/RRR2-14/2	944.824	944.071	-261.455	0.529	1355.635	0.390	14	0.152	R.SAVQAALQR.E
R2/RRR2-12/2	943.554	944.071	-1612.620	0.418	1443.102	0.315	14	0.147	R.SAVQAALQR.E
R2/RRR2-12/2	944.050	944.071	-22.257	0.484	1328.605	0.366	14	0.146	R.SAVQAALQR.E
R2/RRR2-12/2	1027.061	1027.243	-177.100	0.380	1186.597	0.339	16	0.133	R.EIALAAGLIR.I
R2/RRR2-3/2	944.636	944.071	-461.240	0.352	567.331	0.246	12	0.105	-.SAVQAALQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/3	1794.562	1794.993	-240.957	0.509	1983.421	0.461	31	0.223	K.TQRPAQENISLGPQVR.E
R2/RRR2-22/2	1076.674	1077.215	-1435.865	0.367	1101.511	0.373	16	0.132	R.EGELVFGVAR.I
R2/RRR2-22/2	1077.228	1077.215	11.865	0.374	930.900	0.383	17	0.126	R.EGELVFGVAR.I
R2/RRR2-22/2	1076.990	1077.215	-209.589	0.372	852.628	0.355	16	0.120	R.EGELVFGVAR.I
R2/RRR2-22/3	1793.807	1794.993	-1222.430	0.444	1087.991	0.340	28	0.086	K.TQRPAQENISLGPQVR.E
R2/RRR2-14/2	1536.362	1536.841	-312.363	0.471	2569.810	0.596	23	0.400	R.ALALQENPGLVILGK.Q
R2/RRR2-14/2	1536.128	1536.841	-1118.305	0.427	1886.970	0.514	21	0.242	R.ALALQENPGLVILGK.Q
R2/RRR2-14/2	1535.839	1536.841	-1307.131	0.399	1698.514	0.462	19	0.202	R.ALALQENPGLVILGK.Q
R2/RRR2-26/2	1484.119	1484.624	-1017.083	0.441	1894.065	0.394	20	0.210	R.SPCSLYACEAGLR.A
R2/RRR2-27/2	1484.075	1484.624	-1046.648	0.469	1774.840	0.375	20	0.190	R.SPCSLYACEAGLR.A
R2/RRR2-27/2	1483.998	1484.624	-1098.350	0.409	1779.483	0.351	20	0.186	R.SPCSLYACEAGLR.A
R2/RRR2-27/2	1484.100	1484.624	-1029.636	0.451	1710.647	0.384	20	0.185	R.SPCSLYACEAGLR.A
R2/RRR2-26/2	1484.062	1484.624	-1055.237	0.431	1718.405	0.370	20	0.183	R.SPCSLYACEAGLR.A
R2/RRR2-26/2	1484.139	1484.624	-327.727	0.435	1764.642	0.339	20	0.181	R.SPCSLYACEAGLR.A
R2/RRR2-26/2	993.863	994.080	-218.988	0.381	743.729	0.296	14	0.114	R.AWCGSGVTR.C
R2/RRR2-26/2	993.771	994.080	-311.411	0.345	725.351	0.308	14	0.114	R.AWCGSGVTR.C
R2/RRR2-27/2	993.913	994.080	-168.471	0.344	710.946	0.299	14	0.114	R.AWCGSGVTR.C
R2/RRR2-26/2	993.880	994.080	-201.615	0.299	648.439	0.296	14	0.112	R.AWCGSGVTR.C
R2/RRR2-27/2	993.778	994.080	-305.126	0.274	683.815	0.248	14	0.109	R.AWCGSGVTR.C
R2/RRR2-27/2	993.904	994.080	-177.835	0.266	808.881	0.235	14	0.108	R.AWCGSGVTR.C
R2/RRR2-27/2	993.808	994.080	-274.440	0.254	670.047	0.228	13	0.107	R.AWCGSGVTR.C
R2/RRR2-1/2	1485.981	1484.624	241.448	0.229	659.410	0.160	15	0.101	-.SPCSLYACEAGLR.-
R2/RRR2-26/2	994.224	994.080	145.362	0.169	545.284	0.237	11	0.101	-.AWCGSGVTR.-
R2/RRR2-7/2	1161.137	1161.336	-171.519	0.454	1779.006	0.439	17	0.211	R.DALAFVAGLQR.E
R2/RRR2-7/2	1170.014	1170.298	-243.050	0.357	982.919	0.245	16	0.110	R.TVEITGPAEPR.K
R2/RRR2-9/2	1828.573	1829.048	-260.840	0.591	1323.643	0.619	24	0.197	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-9/3	1828.990	1829.048	-32.047	0.414	1597.989	0.564	31	0.194	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-9/2	1828.484	1829.048	-858.276	0.591	1254.788	0.571	24	0.179	R.GIYAYGFEKPSAIQQR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1828.815	1829.048	-127.753	0.501	1441.119	0.584	31	0.178	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-9/2	1828.431	1829.048	-887.229	0.571	1150.558	0.539	23	0.163	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-9/3	1829.195	1829.048	80.407	0.431	1316.897	0.563	29	0.157	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-9/3	1828.772	1829.048	-151.356	0.417	1078.117	0.508	27	0.120	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-10/2	926.087	926.138	-55.939	0.276	708.009	0.375	13	0.112	R.AVLPIISGR.-
R2/RRR2-10/3	1829.197	1829.048	81.612	0.391	912.270	0.520	24	0.110	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-10/3	1828.718	1829.048	-181.288	0.358	986.692	0.482	25	0.107	R.GIYAYGFEKPSAIQQR.A
R2/RRR2-10/2	926.223	926.138	91.725	0.230	476.704	0.331	12	0.105	R.AVLPIISGR.-
R2/RRR2-13/2	1581.075	1580.723	223.596	0.576	1939.897	0.531	23	0.256	R.QSDVEAFFAAELPR.Y
R2/RRR2-13/2	1580.197	1580.723	-968.570	0.398	1270.585	0.424	21	0.151	R.QSDVEAFFAAELPR.Y
R2/RRR2-13/2	1580.243	1580.723	-304.309	0.368	1239.453	0.411	20	0.146	R.QSDVEAFFAAELPR.Y
R2/RRR2-13/2	886.012	886.074	-70.215	0.460	1059.505	0.403	14	0.136	R.GLVGSAILR.H
R2/RRR2-13/2	885.996	886.074	-88.319	0.255	588.689	0.212	12	0.102	-.GLVGSAILR.-
R2/RRR2-24/2	1377.214	1377.546	-241.733	0.509	2205.701	0.554	22	0.306	K.GTDPVAIDLGSM*GK.G
R2/RRR2-23/2	1376.971	1377.546	-1147.398	0.466	1651.055	0.517	21	0.209	K.GTDPVAIDLGSM*GK.G
R2/RRR2-24/2	1377.093	1377.546	-330.219	0.482	1643.282	0.480	19	0.198	K.GTDPVAIDLGSM*GK.G
R2/RRR2-24/2	1376.484	1377.546	-1502.531	0.436	1483.679	0.498	20	0.184	K.GTDPVAIDLGSM*GK.G
R2/RRR2-26/2	1723.023	1723.866	-1072.610	0.461	1194.799	0.541	21	0.163	R.IGAQTSVFTVESGSPSR.S
R2/RRR2-26/2	1723.258	1723.866	-935.836	0.480	950.344	0.582	18	0.149	R.IGAQTSVFTVESGSPSR.S
R2/RRR2-26/2	1723.275	1723.866	-925.809	0.492	1054.767	0.519	20	0.148	R.IGAQTSVFTVESGSPSR.S
R2/RRR2-24/2	1362.505	1361.547	-30.967	0.345	681.724	0.427	19	0.119	K.GTDPVAIDLGSMGK.G
R2/RRR2-24/2	1361.418	1361.547	-94.934	0.292	295.597	0.386	13	0.108	K.GTDPVAIDLGSMGK.G
R2/RRR2-11/2	1325.167	1325.538	-280.470	0.550	1581.534	0.551	19	0.211	R.YSGNFLVNLLGK.W
R2/RRR2-11/2	1325.264	1325.538	-207.279	0.546	1465.122	0.587	18	0.205	R.YSGNFLVNLLGK.W
R2/RRR2-11/2	1325.092	1325.538	-336.941	0.496	1405.906	0.534	18	0.186	R.YSGNFLVNLLGK.W
R2/RRR2-11/2	1165.101	1165.278	-152.440	0.466	1241.178	0.418	17	0.149	K.TWIEVSGSSAK.D
R2/RRR2-11/2	1325.057	1325.538	-363.562	0.393	763.668	0.546	16	0.135	R.YSGNFLVNLLGK.W
R2/RRR2-11/2	1165.169	1165.278	-94.006	0.452	1005.729	0.334	18	0.124	K.TWIEVSGSSAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1165.264	1165.278	-11.937	0.355	866.607	0.287	17	0.113	K.TWIEVSGSSAK.D
R2/RRR2-17/2	1202.017	1202.383	-305.538	0.481	1717.304	0.358	18	0.185	K.INIKDDVSAVK.K
R2/RRR2-17/2	1197.094	1197.323	-192.243	0.511	1127.476	0.493	18	0.156	R.HLVAVQTDEGK.A
R2/RRR2-17/2	1196.996	1197.323	-273.781	0.502	1155.050	0.459	18	0.152	R.HLVAVQTDEGK.A
R2/RRR2-17/2	1196.460	1197.323	-1561.858	0.472	1153.093	0.407	18	0.142	R.HLVAVQTDEGK.A
R2/RRR2-5/2	1010.809	1011.116	-303.679	0.415	403.719	0.430	14	0.122	K.FGDFANALR.I
R2/RRR2-5/2	1010.929	1011.116	-184.710	0.386	413.184	0.422	14	0.120	K.FGDFANALR.I
R2/RRR2-5/2	1010.393	1011.116	-1710.429	0.276	414.683	0.326	13	0.110	K.FGDFANALR.I
R2/RRR2-15/3	1963.000	1963.098	-50.317	0.493	1990.889	0.506	30	0.244	K.VAHATYAFNDFYQTTGR.A
R2/RRR2-15/3	1962.252	1963.098	-943.346	0.513	1572.313	0.492	30	0.169	K.VAHATYAFNDFYQTTGR.A
R2/RRR2-15/3	1962.909	1963.098	-96.352	0.518	1411.558	0.533	28	0.161	K.VAHATYAFNDFYQTTGR.A
R2/RRR2-14/2	1286.033	1285.432	-311.568	0.444	1113.682	0.391	16	0.135	R.NFGLFYPNGQK.V
R2/RRR2-15/2	1286.397	1285.432	-27.089	0.371	940.970	0.330	14	0.117	R.NFGLFYPNGQK.V
R2/RRR2-15/2	1286.474	1285.432	32.586	0.433	668.693	0.400	13	0.113	-.NFGLFYPNGQK.-
R2/RRR2-15/2	1286.217	1285.432	-167.785	0.334	902.021	0.268	15	0.111	-.NFGLFYPNGQK.-
R2/RRR2-15/2	1285.974	1285.432	-357.569	0.318	750.573	0.233	14	0.105	R.NFGLFYPNGQK.V
R2/RRR2-15/2	1284.261	1285.432	-1695.612	0.309	626.848	0.221	13	0.100	-.NFGLFYPNGQK.-
R2/RRR2-19/3	1962.674	1963.098	-216.699	0.404	738.937	0.408	24	0.083	K.VAHATYAFNDFYQTTGR.A
R2/RRR2-23/2	1865.734	1867.118	-1281.807	0.439	1976.450	0.465	25	0.246	K.DM*PVLQDGPPPGGFAPVR.Y
R2/RRR2-22/2	1570.036	1570.726	-1080.116	0.441	803.888	0.535	22	0.140	R.TALVPVLQAEEDER.F
R2/RRR2-22/2	1570.188	1570.726	-982.698	0.419	707.882	0.494	21	0.130	R.TALVPVLQAEEDER.F
R2/RRR2-22/2	1570.133	1570.726	-1017.822	0.326	628.271	0.357	20	0.112	R.TALVPVLQAEEDER.F
R2/RRR2-18/3	1911.645	1912.136	-257.678	0.492	1701.640	0.596	36	0.227	R.GAAAAIVVYDITNAASFTR.A
R2/RRR2-18/2	1572.998	1571.759	152.590	0.426	1033.178	0.485	18	0.142	K.TAINVNDVFHEIAK.R
R2/RRR2-10/2	1506.221	1506.601	-253.097	0.485	1856.999	0.580	23	0.260	K.LASLSQGAAGESSTAR.E
R2/RRR2-10/2	1357.108	1356.553	-329.173	0.429	1213.608	0.533	18	0.164	R.GVAIGVGQSEILGR.I
R2/RRR2-10/2	1356.557	1356.553	3.014	0.300	494.952	0.266	13	0.097	-.GVAIGVGQSEILGR.-
R2/RRR2-16/2	1532.120	1532.672	-1015.745	0.456	1252.154	0.566	18	0.175	R.ATEGPIVADKNCEK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1532.185	1532.672	-318.329	0.455	751.026	0.551	17	0.135	R.ATEGPIVADKNCEK.I
R2/RRR2-16/2	973.501	974.220	-1771.286	0.416	717.810	0.373	15	0.121	R.VVTSLTLLK.S
R2/RRR2-16/2	973.989	974.220	-237.536	0.358	701.264	0.368	15	0.118	R.VVTSLTLLK.S
R2/RRR2-16/2	974.005	974.220	-221.568	0.411	678.954	0.328	15	0.117	R.VVTSLTLLK.S
R2/RRR2-15/2	973.892	974.220	-337.254	0.287	511.107	0.320	13	0.110	R.VVTSLTLLK.S
R2/RRR2-15/3	1532.743	1532.672	46.952	0.269	611.582	0.500	24	0.087	R.ATEGPIVADKNCEK.I
R2/RRR2-16/3	1532.684	1532.672	8.490	0.239	364.546	0.518	19	0.080	-.ATEGPIVADKNCEK.-
R2/RRR2-16/3	1532.554	1532.672	-77.192	0.228	416.826	0.483	22	0.077	-.ATEGPIVADKNCEK.-
R2/RRR2-15/3	1532.313	1532.672	-234.813	0.231	336.019	0.374	19	0.076	R.ATEGPIVADKNCEK.I
R2/RRR2-16/3	1531.890	1532.672	-1166.325	0.244	430.362	0.429	21	0.075	-.ATEGPIVADKNCEK.-
R2/RRR2-21/2	1925.761	1924.960	-103.735	0.593	2447.518	0.642	27	0.386	R.SLNDGDVVEFSVGSGNDGR.T
R2/RRR2-20/2	1925.509	1924.960	-234.800	0.602	2115.807	0.646	25	0.318	R.SLNDGDVVEFSVGSGNDGR.T
R2/RRR2-20/2	1924.272	1924.960	-880.070	0.525	2056.206	0.637	25	0.305	R.SLNDGDVVEFSVGSGNDGR.T
R2/RRR2-20/2	1924.185	1924.960	-925.160	0.539	1825.463	0.628	24	0.262	R.SLNDGDVVEFSVGSGNDGR.T
R2/RRR2-10/3	1926.074	1926.157	-43.145	0.486	1989.792	0.456	35	0.223	K.SIALDVEELADNLQLGPK.F
R2/RRR2-10/3	1926.595	1926.157	227.784	0.524	1696.555	0.512	35	0.193	K.SIALDVEELADNLQLGPK.F
R2/RRR2-10/2	1925.575	1926.157	-824.347	0.450	1052.409	0.449	18	0.133	K.SIALDVEELADNLQLGPK.F
R2/RRR2-10/2	1925.704	1926.157	-236.112	0.284	564.508	0.252	14	0.096	K.SIALDVEELADNLQLGPK.F
R2/RRR2-10/3	1381.573	1381.646	-52.971	0.407	464.629	0.557	20	0.093	K.LPWVVYHELPK.S
R2/RRR2-10/3	1382.058	1381.646	298.795	0.414	406.491	0.538	19	0.091	K.LPWVVYHELPK.S
R2/RRR2-7/2	1647.780	1647.806	-15.872	0.466	2579.368	0.532	24	0.377	R.TEEELIEAIATATGAK.K
R2/RRR2-7/2	1647.523	1647.806	-172.532	0.417	2227.867	0.466	22	0.284	R.TEEELIEAIATATGAK.K
R2/RRR2-7/2	1647.191	1647.806	-983.587	0.385	2119.906	0.448	22	0.260	R.TEEELIEAIATATGAK.K
R2/RRR2-2/2	1649.074	1647.806	162.775	0.348	628.235	0.339	15	0.105	R.TEEELIEAIATATGAK.K
R2/RRR2-4/2	1440.698	1441.652	-1360.138	0.436	1762.114	0.448	21	0.210	K.LLVSEDLQPLGEK.L
R2/RRR2-3/2	1441.110	1441.652	-1073.180	0.411	1484.291	0.362	20	0.159	K.LLVSEDLQPLGEK.L
R2/RRR2-4/2	1490.067	1490.705	-1102.575	0.394	729.655	0.355	20	0.114	K.EVM*DGSKPAAELVK.L
R2/RRR2-19/2	1139.933	1139.237	-267.401	0.397	828.365	0.463	15	0.130	R.EAIEGTYIDK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/2	1139.056	1138.292	-207.950	0.384	633.898	0.389	15	0.119	K.CPFTGTVSIR.G
R2/RRR2-19/2	1139.091	1139.237	-128.942	0.349	664.121	0.412	14	0.117	R.EAIEGTYIDK.K
R2/RRR2-17/2	1138.045	1138.292	-218.033	0.434	534.436	0.340	14	0.116	K.CPFTGTVSIR.G
R2/RRR2-19/2	1139.278	1138.292	-12.424	0.491	405.133	0.438	13	0.115	-.CPFTGTVSIR.-
R2/RRR2-16/2	1138.257	1138.292	-30.722	0.398	363.142	0.368	12	0.113	-.CPFTGTVSIR.-
R2/RRR2-16/2	1137.785	1138.292	-1328.613	0.271	335.842	0.305	11	0.110	K.CPFTGTVSIR.G
R2/RRR2-20/2	1137.405	1138.292	-1664.049	0.379	364.205	0.360	12	0.109	-.CPFTGTVSIR.-
R2/RRR2-17/2	1137.198	1138.292	-1847.384	0.314	263.225	0.392	11	0.108	-.CPFTGTVSIR.-
R2/RRR2-16/2	1138.576	1138.292	250.060	0.375	306.341	0.433	12	0.107	-.CPFTGTVSIR.-
R2/RRR2-15/2	1344.473	1343.513	-29.561	0.529	1321.414	0.513	18	0.173	R.LDEALATGLFHR.I
R2/RRR2-15/2	1344.346	1343.513	-124.282	0.472	1154.029	0.525	18	0.160	R.LDEALATGLFHR.I
R2/RRR2-24/2	1343.254	1343.513	-193.474	0.480	1256.883	0.478	18	0.160	R.LDEALATGLFHR.I
R2/RRR2-15/2	1208.956	1209.399	-366.968	0.438	1079.703	0.475	19	0.147	R.GTVGVM*VTATTR.C
R2/RRR2-15/2	1208.936	1209.399	-384.090	0.425	943.944	0.501	18	0.141	R.GTVGVM*VTATTR.C
R2/RRR2-24/2	1208.885	1209.399	-1256.131	0.449	833.467	0.518	17	0.138	R.GTVGVM*VTATTR.C
R2/RRR2-24/2	1209.064	1209.399	-277.720	0.443	913.886	0.475	18	0.137	R.GTVGVM*VTATTR.C
R2/RRR2-24/2	1342.751	1343.513	-1316.470	0.442	977.005	0.466	16	0.137	R.LDEALATGLFHR.I
R2/RRR2-24/2	1209.088	1209.399	-258.171	0.442	879.511	0.474	18	0.135	R.GTVGVM*VTATTR.C
R2/RRR2-15/2	1342.550	1343.513	-1466.229	0.367	1004.017	0.418	17	0.131	R.LDEALATGLFHR.I
R2/RRR2-15/2	1208.826	1209.399	-1305.114	0.426	853.456	0.454	18	0.131	R.GTVGVM*VTATTR.C
R2/RRR2-24/2	1342.610	1343.513	-1421.753	0.391	720.740	0.441	15	0.121	R.LDEALATGLFHR.I
R2/RRR2-15/2	1193.273	1193.399	-106.259	0.363	927.548	0.263	17	0.112	R.GTVGVMVTATTR.C
R2/RRR2-24/3	1343.158	1343.513	-265.374	0.495	876.880	0.522	24	0.109	R.LDEALATGLFHR.I
R2/RRR2-24/3	1343.509	1343.513	-3.392	0.481	792.729	0.503	24	0.101	R.LDEALATGLFHR.I
R2/RRR2-15/3	1343.064	1343.513	-335.132	0.485	956.550	0.431	25	0.096	R.LDEALATGLFHR.I
R2/RRR2-15/3	1343.523	1343.513	7.270	0.489	772.868	0.443	24	0.092	R.LDEALATGLFHR.I
R2/RRR2-15/3	1343.738	1343.513	167.589	0.511	909.812	0.404	24	0.091	R.LDEALATGLFHR.I
R2/RRR2-24/3	1343.090	1343.513	-315.982	0.517	690.519	0.412	23	0.087	R.LDEALATGLFHR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1446.184	1445.685	346.215	0.512	2319.053	0.307	20	0.252	R.LPDFSLDVAQIVK.V
R2/RRR2-10/2	1446.226	1445.685	-318.371	0.438	1788.243	0.279	21	0.174	R.LPDFSLDVAQIVK.V
R2/RRR2-10/2	1903.827	1902.225	-209.757	0.474	613.230	0.480	21	0.122	R.SLAPYQPILPFEVLSAR.L
R2/RRR2-15/2	1700.446	1698.942	-292.662	0.595	2489.678	0.603	24	0.385	R.NVQAALVNLDLADTIK.V
R2/RRR2-14/2	1698.965	1698.942	13.072	0.354	301.766	0.344	13	0.103	R.NVQAALVNLDLADTIK.V
R2/RRR2-19/2	1369.215	1369.546	-241.938	0.526	1514.994	0.500	20	0.192	K.HLLDETISDVVK.S
R2/RRR2-19/2	1370.016	1369.546	344.194	0.526	1407.429	0.544	20	0.191	K.HLLDETISDVVK.S
R2/RRR2-19/2	1369.051	1369.546	-362.253	0.440	1467.385	0.479	20	0.181	K.HLLDETISDVVK.S
R2/RRR2-19/2	1139.003	1139.197	-171.089	0.460	594.153	0.431	15	0.126	R.LIDDYNTER.K
R2/RRR2-19/2	1138.959	1139.197	-209.903	0.466	603.981	0.367	15	0.120	R.LIDDYNTER.K
R2/RRR2-19/2	1138.887	1139.197	-273.344	0.428	646.328	0.362	15	0.119	R.LIDDYNTER.K
R2/RRR2-9/3	1636.835	1636.793	25.528	0.507	1794.666	0.463	28	0.189	K.FVQKHEYGTNIGSR.M
R2/RRR2-9/2	1421.892	1422.469	-1112.312	0.476	999.350	0.560	19	0.156	K.YGTGYCDAQCAR.D
R2/RRR2-9/2	1421.950	1422.469	-1071.539	0.518	933.745	0.553	19	0.153	K.YGTGYCDAQCAR.D
R2/RRR2-9/3	1636.293	1636.793	-306.128	0.535	1181.138	0.484	27	0.122	K.FVQKHEYGTNIGSR.M
R2/RRR2-9/3	1635.673	1636.793	-1300.079	0.532	1008.233	0.493	26	0.111	K.FVQKHEYGTNIGSR.M
R2/RRR2-12/2	1359.286	1359.509	-164.620	0.492	1715.573	0.506	20	0.207	R.IGEVISGEGVHYV.-
R2/RRR2-12/2	1200.357	1200.327	25.030	0.426	1312.780	0.274	16	0.130	K.SGLSLNDQLPR.N
R2/RRR2-12/2	1200.103	1200.327	-187.170	0.354	1163.023	0.292	17	0.124	K.SGLSLNDQLPR.N
R2/RRR2-12/2	1359.260	1359.509	-184.170	0.354	1058.011	0.344	16	0.064	R.IGEVISGEGVHYV.-
R2/RRR2-12/2	1569.731	1569.657	47.063	0.529	1790.764	0.544	23	0.241	K.NFGDEALIGEGSFGR.V
R2/RRR2-6/2	1182.079	1181.372	-248.027	0.408	959.047	0.355	15	0.123	R.VYFGVLRNGR.S
R2/RRR2-6/2	1182.164	1181.372	-175.821	0.448	1158.005	0.262	16	0.121	R.VYFGVLRNGR.S
R2/RRR2-6/2	1181.046	1181.372	-276.545	0.386	958.723	0.283	15	0.115	R.VYFGVLRNGR.S
R2/RRR2-9/2	1399.479	1399.578	-70.918	0.487	818.015	0.445	13	0.125	K.LLQYVYWSNGR.E
R2/RRR2-9/2	870.141	870.075	76.038	0.270	1004.657	0.278	11	0.113	K.NLVVLVGR.L
R2/RRR2-1/2	1400.122	1399.578	-327.018	0.358	863.434	0.236	15	0.106	K.LLQYVYWSNGR.E
R2/RRR2-9/2	869.998	870.075	-88.325	0.225	740.089	0.247	12	0.104	K.NLVVLVGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-11/2	1088.045	1088.283	-219.275	0.462	1593.988	0.562	19	0.215	R.VVGVLLGTSSR.G
R2/RRR2-11/2	1088.031	1088.283	-232.444	0.469	1525.657	0.561	18	0.206	R.VVGVLLGTSSR.G
R2/RRR2-11/2	1087.982	1088.283	-277.581	0.479	1605.193	0.508	18	0.204	R.VVGVLLGTSSR.G
R2/RRR2-11/3	1974.103	1974.338	-119.374	0.421	565.885	0.553	24	0.093	K.VVVHPLVLLSIVDHYNR.V
R2/RRR2-25/3	1314.561	1314.561	0.026	0.532	1338.083	0.373	24	0.107	K.VREVPGYLKPR.L
R2/RRR2-25/3	1247.496	1247.385	88.997	0.541	1074.575	0.332	23	0.084	R.HLAHLEELER.Q
R2/RRR2-25/3	1314.254	1314.561	-234.179	0.451	1109.992	0.300	22	0.080	-.VREVPGYLKPR.-
R2/RRR2-24/3	1246.816	1247.385	-1262.325	0.443	335.841	0.372	18	0.080	-.HLAHLEELER.-
R2/RRR2-25/3	1247.413	1247.385	22.161	0.505	1056.332	0.298	22	0.079	R.HLAHLEELER.Q
R2/RRR2-25/3	1314.995	1314.561	330.746	0.458	1083.617	0.291	22	0.079	K.VREVPGYLKPR.L
R2/RRR2-25/3	1246.930	1247.385	-366.223	0.492	805.196	0.310	21	0.077	R.HLAHLEELER.Q
R2/RRR2-24/3	1247.010	1247.385	-301.839	0.376	410.180	0.300	19	0.072	-.HLAHLEELER.-
R2/RRR2-4/2	1705.584	1705.889	-179.364	0.496	2143.937	0.503	20	0.286	R.VPAWYVILEDDQEK.I
R2/RRR2-4/2	1906.421	1907.147	-908.348	0.488	836.368	0.548	20	0.138	K.IICDAELVDPTFGTGAVK.I
R2/RRR2-23/2	1170.062	1170.256	-166.338	0.396	908.042	0.458	16	0.134	K.LQGFAEDYAR.Q
R2/RRR2-22/2	1170.099	1170.256	-134.733	0.392	1028.421	0.371	17	0.130	K.LQGFAEDYAR.Q
R2/RRR2-23/2	1169.532	1170.256	-1478.579	0.387	870.247	0.435	16	0.130	K.LQGFAEDYAR.Q
R2/RRR2-23/2	1170.024	1170.256	-199.412	0.400	822.707	0.403	16	0.125	K.LQGFAEDYAR.Q
R2/RRR2-22/2	1169.954	1170.256	-258.760	0.295	664.218	0.452	14	0.118	K.LQGFAEDYAR.Q
R2/RRR2-10/2	1609.569	1610.920	-1464.657	0.366	1866.864	0.488	23	0.234	R.TPIGALLGALSSLPATK.L
R2/RRR2-10/2	1909.491	1909.045	233.871	0.571	1567.548	0.587	24	0.217	R.DSGAFSWEIAPVEISSGR.G
R2/RRR2-10/2	1908.694	1909.045	-184.910	0.462	1292.397	0.583	22	0.182	R.DSGAFSWEIAPVEISSGR.G
R2/RRR2-4/2	1965.686	1964.245	225.005	0.451	2525.047	0.523	23	0.369	K.VLTELLDQLDIGTYEIK.L
R2/RRR2-10/2	1775.173	1775.941	-998.958	0.489	1468.140	0.491	23	0.185	K.SYELPDGNVIVIGNER.F
R2/RRR2-11/2	1205.203	1204.357	-128.573	0.448	1419.085	0.484	17	0.176	R.YVDIGIPANNK.G
R2/RRR2-11/2	1204.130	1204.357	-189.493	0.469	1415.689	0.409	18	0.162	R.YVDIGIPANNK.G
R2/RRR2-11/2	1203.429	1204.357	-1607.143	0.450	1370.550	0.420	18	0.160	R.YVDIGIPANNK.G
R2/RRR2-16/2	1204.139	1204.357	-182.069	0.429	1345.486	0.413	17	0.156	R.YVDIGIPANNK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1203.980	1204.357	-313.887	0.334	1276.972	0.355	17	0.140	R.YVDIGIPANNK.G
R2/RRR2-16/2	1204.100	1204.357	-214.410	0.334	1183.924	0.389	17	0.138	R.YVDIGIPANNK.G
R2/RRR2-16/2	1465.338	1464.730	-268.263	0.428	947.245	0.468	17	0.136	K.QSIGCLFWLLAR.M
R2/RRR2-14/2	1465.449	1464.730	-192.547	0.475	915.419	0.423	17	0.130	K.QSIGCLFWLLAR.M
R2/RRR2-16/2	1465.979	1464.730	170.076	0.495	597.767	0.484	17	0.128	K.QSIGCLFWLLAR.M
R2/RRR2-15/2	1465.809	1464.730	54.409	0.397	584.786	0.512	17	0.128	K.QSIGCLFWLLAR.M
R2/RRR2-14/2	1465.613	1464.730	-80.332	0.485	412.472	0.448	15	0.121	K.QSIGCLFWLLAR.M
R2/RRR2-14/2	1465.991	1464.730	178.343	0.461	643.535	0.415	16	0.120	K.QSIGCLFWLLAR.M
R2/RRR2-10/2	1464.257	1464.730	-323.648	0.338	405.005	0.407	13	0.113	K.QSIGCLFWLLAR.M
R2/RRR2-13/2	1464.023	1464.730	-1169.787	0.369	588.293	0.370	14	0.113	K.QSIGCLFWLLAR.M
R2/RRR2-10/2	1464.413	1464.730	-216.930	0.318	487.489	0.281	15	0.110	K.QSIGCLFWLLAR.M
R2/RRR2-13/2	1464.217	1464.730	-1036.175	0.362	245.560	0.352	10	0.103	-.QSIGCLFWLLAR.-
R2/RRR2-12/2	1464.504	1464.730	-154.800	0.358	171.578	0.401	10	0.096	-.QSIGCLFWLLAR.-
R2/RRR2-1/2	1746.495	1746.982	-279.828	0.465	2246.192	0.382	26	0.264	K.NEILAESEFAAPTIIK.L
R2/RRR2-2/2	1747.528	1746.982	-260.676	0.577	1841.729	0.419	24	0.210	K.NEILAESEFAAPTIIK.L
R2/RRR2-1/2	1758.269	1758.010	147.722	0.409	744.200	0.430	17	0.117	K.GAIEILGPYGISYTFR.R
R2/RRR2-13/2	1384.318	1383.615	-215.772	0.485	1516.375	0.570	19	0.209	K.VIVIDVNDPLASK.L
R2/RRR2-13/2	1088.927	1089.138	-194.923	0.494	1128.806	0.409	15	0.143	K.LNDVEDVER.H
R2/RRR2-6/2	1950.727	1950.144	-214.254	0.545	1669.078	0.578	27	0.230	K.GAADFQPLALGLGNASYAGR.-
R2/RRR2-6/3	1668.159	1668.745	-953.543	0.518	1121.280	0.488	23	0.119	K.YGETYKAEHDDLAR.R
R2/RRR2-6/3	1668.044	1668.745	-1022.862	0.344	664.931	0.386	22	0.074	-.YGETYKAEHDDLAR.-
R2/RRR2-24/2	1586.336	1586.752	-263.007	0.527	2496.219	0.565	23	0.367	K.AGGAYTM*NTASAVTVR.S
R2/RRR2-24/2	1586.212	1586.752	-974.083	0.513	2394.279	0.582	23	0.352	K.AGGAYTM*NTASAVTVR.S
R2/RRR2-24/2	1570.166	1570.753	-1014.058	0.517	2170.460	0.536	23	0.293	K.AGGAYTMNTASAVTVR.S
R2/RRR2-24/2	1570.340	1570.753	-264.048	0.544	2021.535	0.537	22	0.267	K.AGGAYTMNTASAVTVR.S
R2/RRR2-24/2	1586.238	1586.752	-957.781	0.510	1989.662	0.503	22	0.252	K.AGGAYTM*NTASAVTVR.S
R2/RRR2-25/2	1586.349	1586.752	-255.055	0.484	1904.066	0.501	22	0.239	K.AGGAYTM*NTASAVTVR.S
R2/RRR2-15/2	1142.455	1142.332	107.640	0.440	1234.632	0.538	16	0.171	R.HAGIIDIQFK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1142.228	1142.332	-91.606	0.380	1274.887	0.464	16	0.159	R.HAGIIDIQFK.R
R2/RRR2-15/3	1298.259	1298.519	-200.662	0.501	1169.830	0.435	26	0.106	R.HAGIIDIQFKR.V
R2/RRR2-15/3	1298.536	1298.519	13.368	0.488	669.677	0.446	21	0.089	R.HAGIIDIQFKR.V
R2/RRR2-15/3	1298.097	1298.519	-325.613	0.439	638.850	0.336	20	0.074	-.HAGIIDIQFKR.-
R2/RRR2-8/3	1349.575	1349.518	42.937	0.488	2165.694	0.396	30	0.227	K.AREEAYAAGLLGK.N
R2/RRR2-8/2	1577.258	1576.841	265.650	0.376	259.416	0.411	19	0.115	K.AVQSGLGTAAVIVM*DK.S
R2/RRR2-8/2	1560.998	1560.841	100.584	0.358	172.053	0.587	17	0.112	-.AVQSGLGTAAVIVMDK.-
R2/RRR2-9/2	1561.035	1560.841	124.425	0.321	428.096	0.298	16	0.104	K.AVQSGLGTAAVIVMDK.S
R2/RRR2-9/2	1348.677	1349.518	-1369.150	0.350	1186.702	0.117	19	0.103	K.AREEAYAAGLLGK.N
R2/RRR2-16/2	1134.825	1135.204	-334.310	0.493	1800.744	0.352	20	0.194	R.CLAEASADAAR.S
R2/RRR2-16/2	1343.132	1343.553	-314.184	0.404	792.044	0.339	14	0.111	K.WSVNLAEVSPLK.S
R2/RRR2-24/2	1260.040	1260.466	-338.595	0.498	1411.810	0.507	19	0.182	R.FTTFALSGFIR.A
R2/RRR2-24/2	1259.846	1260.466	-1289.007	0.448	1282.477	0.564	18	0.179	R.FTTFALSGFIR.A
R2/RRR2-24/2	1259.924	1260.466	-1226.830	0.480	1306.870	0.534	18	0.177	R.FTTFALSGFIR.A
R2/RRR2-24/2	1674.088	1674.796	-1023.294	0.476	1399.666	0.405	20	0.157	R.AQGDADSALDRLWQK.R
R2/RRR2-25/2	1260.218	1260.466	-196.701	0.457	1112.870	0.504	17	0.154	R.FTTFALSGFIR.A
R2/RRR2-24/2	1674.336	1674.796	-275.654	0.534	1221.103	0.466	19	0.152	R.AQGDADSALDRLWQK.R
R2/RRR2-25/2	1260.161	1260.466	-242.181	0.387	860.304	0.460	16	0.131	R.FTTFALSGFIR.A
R2/RRR2-25/2	1259.519	1260.466	-1549.959	0.318	605.406	0.494	17	0.123	R.FTTFALSGFIR.A
R2/RRR2-25/2	1674.455	1674.796	-204.196	0.422	793.855	0.390	17	0.116	R.AQGDADSALDRLWQK.R
R2/RRR2-24/2	1674.272	1674.796	-912.904	0.460	884.955	0.374	16	0.115	R.AQGDADSALDRLWQK.R
R2/RRR2-15/2	1618.660	1617.659	1.013	0.542	1922.492	0.457	21	0.231	K.NSWGADWGDNGYFK.M
R2/RRR2-15/2	1618.131	1617.659	292.930	0.411	1104.310	0.396	17	0.132	K.NSWGADWGDNGYFK.M
R2/RRR2-15/2	1616.828	1617.659	-1135.487	0.419	956.120	0.411	19	0.128	K.NSWGADWGDNGYFK.M
R2/RRR2-15/2	1616.138	1617.659	-2184.775	0.302	985.356	0.312	18	0.116	K.NSWGADWGDNGYFK.M
R2/RRR2-15/3	1401.736	1401.549	133.621	0.514	1384.561	0.322	28	0.098	K.DWREDGIVSPVK.D
R2/RRR2-15/3	1401.693	1401.549	102.703	0.454	781.847	0.380	23	0.083	K.DWREDGIVSPVK.D
R2/RRR2-16/3	1401.479	1401.549	-50.078	0.494	1059.682	0.303	25	0.080	K.DWREDGIVSPVK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/3	1401.537	1401.549	-8.930	0.532	980.842	0.304	25	0.078	K.DWREDGIVSPVK.D
R2/RRR2-16/3	1401.111	1401.549	-313.820	0.450	973.057	0.297	24	0.077	K.DWREDGIVSPVK.D
R2/RRR2-8/2	1683.434	1682.893	-273.801	0.524	1749.020	0.523	21	0.226	K.TTITEDDIVGLTYLK.M
R2/RRR2-8/2	1682.308	1682.893	-945.297	0.411	1501.036	0.442	19	0.175	K.TTITEDDIVGLTYLK.M
R2/RRR2-8/2	1441.587	1442.560	-1372.464	0.446	628.396	0.466	15	0.119	K.GNNFEFLPFGSGR.R
R2/RRR2-9/2	1978.425	1979.049	-823.429	0.562	1713.073	0.693	25	0.263	K.TVGGGDDAFNTFFSETGAGK.H
R2/RRR2-9/2	1978.352	1979.049	-860.716	0.577	1613.804	0.670	25	0.242	K.TVGGGDDAFNTFFSETGAGK.H
R2/RRR2-9/2	1979.589	1979.049	-233.520	0.581	1563.072	0.671	26	0.236	K.TVGGGDDAFNTFFSETGAGK.H
R2/RRR2-9/2	1702.586	1702.929	-202.333	0.547	1468.491	0.517	23	0.186	R.AVFVDLEPTVIDEVR.T
R2/RRR2-9/2	1703.351	1702.929	248.445	0.590	1292.435	0.551	23	0.177	R.AVFVDLEPTVIDEVR.T
R2/RRR2-9/2	1702.406	1702.929	-897.314	0.540	1334.861	0.513	24	0.174	R.AVFVDLEPTVIDEVR.T
R2/RRR2-3/2	1703.731	1702.929	-117.110	0.576	1187.774	0.548	21	0.165	R.AVFVDLEPTVIDEVR.T
R2/RRR2-1/2	1703.682	1702.929	-145.500	0.562	1180.060	0.541	22	0.164	R.AVFVDLEPTVIDEVR.T
R2/RRR2-3/2	1703.828	1702.929	-59.616	0.563	1157.129	0.522	21	0.158	R.AVFVDLEPTVIDEVR.T
R2/RRR2-8/2	1702.135	1702.929	-1057.360	0.395	1171.216	0.389	22	0.138	R.AVFVDLEPTVIDEVR.T
R2/RRR2-2/2	1702.673	1702.929	-151.052	0.514	791.945	0.519	19	0.134	R.AVFVDLEPTVIDEVR.T
R2/RRR2-21/2	1703.133	1702.929	120.155	0.483	823.498	0.461	19	0.128	R.AVFVDLEPTVIDEVR.T
R2/RRR2-3/2	1703.096	1702.929	98.015	0.403	762.224	0.389	16	0.115	R.AVFVDLEPTVIDEVR.T
R2/RRR2-18/2	1702.311	1702.929	-953.752	0.350	716.009	0.378	17	0.114	R.AVFVDLEPTVIDEVR.T
R2/RRR2-13/2	1702.918	1702.929	-7.018	0.427	769.533	0.234	18	0.103	R.AVFVDLEPTVIDEVR.T
R2/RRR2-13/2	1702.391	1702.929	-906.528	0.446	684.121	0.174	17	0.097	R.AVFVDLEPTVIDEVR.T
R2/RRR2-20/2	1978.136	1979.049	-970.302	0.372	221.717	0.418	12	0.086	-.TVGGGDDAFNTFFSETGAGK.-
R2/RRR2-9/3	1701.861	1702.929	-1218.869	0.346	843.044	0.358	24	0.076	R.AVFVDLEPTVIDEVR.T
R2/RRR2-8/2	1466.578	1465.678	-68.759	0.528	1852.150	0.509	22	0.238	K.FLGNSLEVYPLGR.T
R2/RRR2-8/2	1466.399	1465.678	-190.753	0.568	1733.867	0.492	21	0.216	K.FLGNSLEVYPLGR.T
R2/RRR2-8/2	1466.074	1465.678	270.782	0.535	1723.740	0.482	21	0.212	K.FLGNSLEVYPLGR.T
R2/RRR2-8/2	932.561	933.089	-1643.707	0.514	938.347	0.375	13	0.128	K.VNNLIFGR.T
R2/RRR2-8/2	932.499	933.089	-1710.385	0.458	852.272	0.399	12	0.126	K.VNNLIFGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1472.613	1471.768	-105.392	0.645	2454.335	0.581	21	0.362	K.TNMVMVFGEITTK.A
R2/RRR2-10/2	1471.437	1471.768	-225.463	0.528	2410.602	0.487	21	0.323	K.TNMVMVFGEITTK.A
R2/RRR2-10/2	1503.165	1503.767	-1068.626	0.526	2375.521	0.466	21	0.309	K.TNM*VM*VFGEITTK.A
R2/RRR2-10/2	1503.309	1503.767	-305.387	0.531	2369.968	0.447	21	0.301	K.TNM*VM*VFGEITTK.A
R2/RRR2-10/2	1471.364	1471.768	-275.402	0.526	2073.514	0.534	21	0.276	K.TNMVMVFGEITTK.A
R2/RRR2-10/2	1503.034	1503.767	-1156.288	0.505	2245.713	0.413	21	0.269	K.TNM*VM*VFGEITTK.A
R2/RRR2-10/2	1174.105	1174.329	-192.149	0.443	1286.257	0.363	16	0.143	K.RDELTLEGLK.Q
R2/RRR2-9/2	1173.530	1174.329	-1538.228	0.459	1316.601	0.347	16	0.143	K.RDELTLEGLK.Q
R2/RRR2-9/2	1173.577	1174.329	-1497.582	0.472	1295.166	0.319	16	0.137	K.RDELTLEGLK.Q
R2/RRR2-10/2	1173.993	1174.329	-287.802	0.446	1256.628	0.312	16	0.133	K.RDELTLEGLK.Q
R2/RRR2-9/2	1173.508	1174.329	-1556.723	0.487	1216.922	0.267	16	0.124	K.RDELTLEGLK.Q
R2/RRR2-9/3	1308.317	1308.532	-165.063	0.458	1255.529	0.317	22	0.090	R.KVDWLTDKM*R.E
R2/RRR2-9/3	1308.836	1308.532	232.948	0.483	519.434	0.282	17	0.077	R.KVDWLTDKM*R.E
R2/RRR2-9/3	1308.164	1308.532	-281.888	0.422	767.989	0.265	19	0.071	R.KVDWLTDKM*R.E
R2/RRR2-6/2	1730.412	1730.986	-912.155	0.536	2327.850	0.626	28	0.358	R.IINEPTAAAIAYGLGAGK.S
R2/RRR2-6/2	1730.339	1730.986	-954.719	0.535	2225.467	0.637	28	0.341	R.IINEPTAAAIAYGLGAGK.S
R2/RRR2-14/2	1730.977	1730.986	-4.994	0.341	596.561	0.401	16	0.107	R.IINEPTAAAIAYGLGAGK.S
R2/RRR2-25/2	1500.179	1499.673	-330.692	0.508	1016.077	0.539	20	0.154	R.LM*GFFPNDSEVAR.Y
R2/RRR2-25/2	1499.188	1499.673	-324.622	0.459	964.406	0.481	20	0.141	R.LM*GFFPNDSEVAR.Y
R2/RRR2-24/2	1354.183	1354.536	-260.989	0.424	1005.893	0.484	16	0.141	K.VVGNFSALDYLR.L
R2/RRR2-25/2	1499.424	1499.673	-166.485	0.441	1009.875	0.469	19	0.141	R.LM*GFFPNDSEVAR.Y
R2/RRR2-24/2	1499.214	1499.673	-307.548	0.491	868.507	0.504	19	0.139	R.LM*GFFPNDSEVAR.Y
R2/RRR2-24/2	1499.057	1499.673	-1081.621	0.443	959.659	0.466	20	0.138	R.LM*GFFPNDSEVAR.Y
R2/RRR2-24/2	1353.550	1354.536	-1471.501	0.361	969.655	0.474	17	0.136	K.VVGNFSALDYLR.L
R2/RRR2-24/2	1499.114	1499.673	-1043.520	0.445	855.205	0.485	19	0.135	R.LM*GFFPNDSEVAR.Y
R2/RRR2-25/2	1353.788	1354.536	-1294.793	0.252	296.577	0.446	12	0.107	K.VVGNFSALDYLR.L
R2/RRR2-25/2	1354.251	1354.536	-210.618	0.260	306.822	0.470	10	0.106	K.VVGNFSALDYLR.L
R2/RRR2-24/2	1101.162	1101.322	-145.502	0.456	1036.219	0.510	17	0.152	R.LVTIATLVDR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/2	1100.648	1101.322	-1525.063	0.404	1005.576	0.540	17	0.151	R.LVTIATLVDR.L
R2/RRR2-24/2	1100.599	1101.322	-1570.074	0.365	1002.535	0.529	17	0.147	R.LVTIATLVDR.L
R2/RRR2-24/3	1691.423	1690.836	-244.502	0.506	964.893	0.539	26	0.117	K.STSDKLYKDVQSYR.L
R2/RRR2-7/2	1307.967	1307.434	-358.202	0.528	1867.027	0.535	20	0.247	R.VDAAEVFDTIAR.R
R2/RRR2-6/2	1307.045	1307.434	-299.066	0.377	1615.892	0.356	19	0.171	R.VDAAEVFDTIAR.R
R2/RRR2-7/2	1466.366	1466.835	-321.429	0.382	1421.789	0.432	20	0.165	K.LIFVDPALLPVLR.D
R2/RRR2-7/2	1466.426	1466.835	-279.920	0.383	1219.800	0.490	19	0.157	K.LIFVDPALLPVLR.D
R2/RRR2-7/2	1306.164	1307.434	-1743.481	0.287	1280.386	0.429	17	0.149	R.VDAAEVFDTIAR.R
R2/RRR2-7/2	1466.339	1466.835	-339.554	0.380	1215.608	0.405	18	0.143	K.LIFVDPALLPVLR.D
R2/RRR2-7/2	1466.237	1466.835	-1093.117	0.352	955.169	0.460	17	0.132	K.LIFVDPALLPVLR.D
R2/RRR2-7/2	1465.879	1466.835	-1338.528	0.309	684.770	0.447	14	0.116	K.LIFVDPALLPVLR.D
R2/RRR2-18/2	1590.210	1590.716	-950.229	0.487	1611.578	0.470	25	0.193	R.EYVAEGSAPALPETR.R
R2/RRR2-18/2	1590.217	1590.716	-315.028	0.466	1446.440	0.456	23	0.172	R.EYVAEGSAPALPETR.R
R2/RRR2-19/2	1590.245	1590.716	-297.391	0.484	1260.205	0.482	23	0.161	R.EYVAEGSAPALPETR.R
R2/RRR2-17/2	1590.351	1590.716	-230.546	0.472	1278.833	0.460	23	0.158	R.EYVAEGSAPALPETR.R
R2/RRR2-18/2	1541.848	1542.890	-1328.560	0.413	1379.617	0.408	21	0.157	R.LLELGVKPVFLTGR.T
R2/RRR2-19/2	1590.102	1590.716	-1017.822	0.352	1290.230	0.387	22	0.145	R.EYVAEGSAPALPETR.R
R2/RRR2-18/3	1542.299	1542.890	-1034.930	0.426	1505.244	0.433	28	0.140	R.LLELGVKPVFLTGR.T
R2/RRR2-21/2	1590.518	1590.716	-125.061	0.494	959.284	0.483	21	0.139	R.EYVAEGSAPALPETR.R
R2/RRR2-18/2	1542.402	1542.890	-317.888	0.414	1032.901	0.446	19	0.137	R.LLELGVKPVFLTGR.T
R2/RRR2-19/2	1590.246	1590.716	-296.390	0.455	994.724	0.451	21	0.136	R.EYVAEGSAPALPETR.R
R2/RRR2-18/2	1542.426	1542.890	-301.689	0.420	1004.298	0.438	19	0.134	R.LLELGVKPVFLTGR.T
R2/RRR2-18/2	1590.141	1590.716	-993.312	0.443	996.128	0.406	21	0.130	R.EYVAEGSAPALPETR.R
R2/RRR2-21/2	1541.495	1542.890	-1558.727	0.406	826.271	0.467	17	0.127	R.LLELGVKPVFLTGR.T
R2/RRR2-17/2	1589.627	1590.716	-1317.819	0.357	979.445	0.382	21	0.125	R.EYVAEGSAPALPETR.R
R2/RRR2-17/2	1542.913	1542.890	15.029	0.443	879.467	0.414	18	0.125	R.LLELGVKPVFLTGR.T
R2/RRR2-17/2	1589.659	1590.716	-1298.076	0.303	999.211	0.343	21	0.121	R.EYVAEGSAPALPETR.R
R2/RRR2-21/3	1541.621	1542.890	-1476.407	0.376	1551.724	0.332	28	0.119	R.LLELGVKPVFLTGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1541.593	1542.890	-1494.613	0.373	750.381	0.406	17	0.118	R.LLELGVKPVFLTGR.T
R2/RRR2-19/2	1541.447	1542.890	-1589.991	0.355	749.492	0.401	16	0.116	R.LLELGVKPVFLTGR.T
R2/RRR2-17/2	1541.603	1542.890	-1488.250	0.349	754.207	0.353	17	0.113	R.LLELGVKPVFLTGR.T
R2/RRR2-19/3	1541.593	1542.890	-1495.019	0.454	1078.601	0.475	26	0.113	R.LLELGVKPVFLTGR.T
R2/RRR2-18/3	1542.970	1542.890	52.037	0.417	995.313	0.499	24	0.113	R.LLELGVKPVFLTGR.T
R2/RRR2-21/2	1541.531	1542.890	-1534.862	0.325	938.372	0.277	18	0.112	R.LLELGVKPVFLTGR.T
R2/RRR2-17/3	1542.775	1542.890	-75.212	0.481	1271.624	0.407	26	0.112	R.LLELGVKPVFLTGR.T
R2/RRR2-19/2	1541.478	1542.890	-1569.784	0.343	687.900	0.289	16	0.107	R.LLELGVKPVFLTGR.T
R2/RRR2-21/3	1541.746	1542.890	-1395.286	0.375	1203.559	0.372	25	0.101	R.LLELGVKPVFLTGR.T
R2/RRR2-21/3	1541.868	1542.890	-1315.370	0.339	997.060	0.417	24	0.097	R.LLELGVKPVFLTGR.T
R2/RRR2-18/3	1542.700	1542.890	-124.025	0.430	1093.086	0.386	25	0.097	R.LLELGVKPVFLTGR.T
R2/RRR2-19/3	1542.017	1542.890	-1218.772	0.333	1015.587	0.356	24	0.088	R.LLELGVKPVFLTGR.T
R2/RRR2-17/3	1541.622	1542.890	-1475.930	0.311	1090.254	0.304	25	0.083	R.LLELGVKPVFLTGR.T
R2/RRR2-18/3	1543.028	1542.890	89.170	0.312	564.575	0.308	21	0.077	R.LLELGVKPVFLTGR.T
R2/RRR2-17/3	1542.083	1542.890	-1175.249	0.255	818.955	0.303	23	0.075	R.LLELGVKPVFLTGR.T
R2/RRR2-8/2	1585.439	1584.675	-149.402	0.505	1790.636	0.570	21	0.248	K.HQLDDKWDGVNTR.L
R2/RRR2-1/2	1812.261	1812.210	28.182	0.462	998.120	0.489	18	0.139	R.VNM*ILDNLPLVVSVLR.Q
R2/RRR2-7/3	1585.690	1584.675	9.750	0.466	1298.069	0.485	26	0.132	K.HQLDDKWDGVNTR.L
R2/RRR2-7/3	1583.869	1584.675	-1143.393	0.495	1115.014	0.538	22	0.130	K.HQLDDKWDGVNTR.L
R2/RRR2-8/3	1585.106	1584.675	272.570	0.444	1260.060	0.464	24	0.124	K.HQLDDKWDGVNTR.L
R2/RRR2-1/3	1585.530	1584.675	-91.717	0.483	1354.956	0.424	25	0.122	K.HQLDDKWDGVNTR.L
R2/RRR2-7/3	1584.420	1584.675	-161.175	0.509	1072.914	0.495	24	0.116	K.HQLDDKWDGVNTR.L
R2/RRR2-8/3	1586.080	1584.675	256.384	0.427	1105.985	0.461	24	0.111	K.HQLDDKWDGVNTR.L
R2/RRR2-2/3	1583.239	1584.675	-1543.235	0.371	1138.508	0.394	23	0.101	K.HQLDDKWDGVNTR.L
R2/RRR2-2/3	1584.483	1584.675	-121.296	0.426	646.811	0.493	18	0.094	K.HQLDDKWDGVNTR.L
R2/RRR2-2/3	1584.862	1584.675	118.490	0.312	558.664	0.310	18	0.068	-.HQLDDKWDGVNTR.-
R2/RRR2-17/2	1772.337	1772.978	-928.988	0.523	1569.417	0.549	24	0.207	R.NQDVSLTELPATVSAVK.N
R2/RRR2-17/2	1772.291	1772.978	-954.987	0.495	1440.776	0.571	24	0.197	R.NQDVSLTELPATVSAVK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1772.259	1772.978	-972.828	0.502	1308.947	0.575	23	0.183	R.NQDVSLTELPATVSAVK.N
R2/RRR2-24/2	1091.831	1092.252	-386.667	0.485	1394.140	0.379	15	0.156	K.SAQLLEQM*R.L
R2/RRR2-24/2	1091.465	1092.252	-1642.499	0.433	1068.138	0.338	14	0.127	K.SAQLLEQM*R.L
R2/RRR2-24/3	1387.636	1387.588	34.749	0.404	901.110	0.412	24	0.089	R.LHM*ATDAGKDIAK.K
R2/RRR2-24/3	1387.644	1387.588	40.572	0.366	817.869	0.347	23	0.077	R.LHM*ATDAGKDIAK.K
R2/RRR2-24/3	1387.509	1387.588	-56.975	0.370	544.398	0.332	21	0.075	R.LHM*ATDAGKDIAK.K
R2/RRR2-16/2	1156.274	1156.359	-73.975	0.569	1347.293	0.457	16	0.167	R.TPLLVAWAER.V
R2/RRR2-16/2	1448.851	1448.606	169.467	0.457	1004.185	0.489	17	0.139	R.AYGAAVGVEVLDAGR.T
R2/RRR2-16/2	1156.200	1156.359	-137.835	0.471	742.364	0.390	13	0.118	R.TPLLVAWAER.V
R2/RRR2-24/2	1518.479	1517.710	-152.442	0.459	391.011	0.567	18	0.127	K.GNPIPDLGVYSWAK.K
R2/RRR2-24/2	1104.186	1104.239	-48.413	0.461	569.313	0.456	15	0.124	R.GQTISTILDR.G
R2/RRR2-24/2	1104.112	1104.239	-115.395	0.401	543.303	0.434	15	0.120	R.GQTISTILDR.G
R2/RRR2-7/2	1860.712	1861.004	-157.238	0.573	1587.672	0.616	23	0.227	K.TPLTAHGADAFPFTEER.-
R2/RRR2-7/2	1860.424	1861.004	-851.635	0.565	1409.139	0.576	22	0.194	K.TPLTAHGADAFPFTEER.-
R2/RRR2-7/2	1226.137	1226.408	-221.241	0.360	1156.619	0.510	20	0.154	R.GIPSLVAIGADGR.T
R2/RRR2-7/2	1226.151	1226.408	-209.955	0.378	972.213	0.488	19	0.139	R.GIPSLVAIGADGR.T
R2/RRR2-7/2	1226.006	1226.408	-328.521	0.377	866.005	0.492	18	0.133	R.GIPSLVAIGADGR.T
R2/RRR2-6/2	1226.176	1226.408	-189.281	0.401	1107.497	0.397	16	0.133	R.GIPSLVAIGADGR.T
R2/RRR2-6/2	1225.953	1226.408	-372.278	0.366	906.586	0.368	16	0.119	R.GIPSLVAIGADGR.T
R2/RRR2-6/3	1860.829	1861.004	-94.203	0.464	1326.674	0.405	30	0.117	K.TPLTAHGADAFPFTEER.-
R2/RRR2-6/2	1226.063	1226.408	-281.670	0.319	807.790	0.379	15	0.115	R.GIPSLVAIGADGR.T
R2/RRR2-2/2	1225.833	1226.408	-1288.017	0.189	745.938	0.237	15	0.102	R.GIPSLVAIGADGR.T
R2/RRR2-6/3	1861.040	1861.004	19.295	0.462	1058.658	0.427	28	0.101	K.TPLTAHGADAFPFTEER.-
R2/RRR2-6/3	1860.490	1861.004	-816.142	0.458	1026.227	0.428	29	0.099	K.TPLTAHGADAFPFTEER.-
R2/RRR2-12/2	1372.566	1373.539	-1441.837	0.331	1865.332	0.372	20	0.204	R.AIQQDGLVWGASK.L
R2/RRR2-12/2	1373.324	1373.539	-157.499	0.450	1586.166	0.455	19	0.189	R.AIQQDGLVWGASK.L
R2/RRR2-12/2	1783.430	1784.003	-884.489	0.465	1270.841	0.561	26	0.178	R.SYIVGTAPSQADVVTFK.A
R2/RRR2-12/2	1784.160	1784.003	88.689	0.539	892.238	0.575	22	0.149	R.SYIVGTAPSQADVVTFK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1783.589	1784.003	-232.684	0.471	806.718	0.525	22	0.136	R.SYIVGTAPSQADVVTFK.A
R2/RRR2-20/2	945.019	945.100	-85.848	0.391	952.354	0.306	13	0.119	R.LAVDKWGR.I
R2/RRR2-20/2	944.995	945.100	-111.892	0.394	1021.517	0.271	13	0.117	R.LAVDKWGR.I
R2/RRR2-20/2	945.277	945.100	187.602	0.330	925.314	0.273	13	0.114	R.LAVDKWGR.I
R2/RRR2-19/2	1334.191	1334.500	-232.046	0.323	815.781	0.227	15	0.102	R.IEVTDPASFQVK.E
R2/RRR2-16/2	1308.131	1308.509	-289.458	0.449	1370.744	0.519	18	0.178	K.SELLLASNPVHK.K
R2/RRR2-15/2	1308.760	1308.509	192.846	0.470	1190.900	0.527	17	0.163	K.SELLLASNPVHK.K
R2/RRR2-15/2	1308.338	1308.509	-130.604	0.402	1288.277	0.401	18	0.149	K.SELLLASNPVHK.K
R2/RRR2-16/2	1308.133	1308.509	-287.679	0.430	1189.319	0.440	18	0.148	K.SELLLASNPVHK.K
R2/RRR2-16/2	1308.594	1308.509	65.624	0.389	454.449	0.445	16	0.119	K.SELLLASNPVHK.K
R2/RRR2-16/2	1679.965	1678.848	69.275	0.383	878.301	0.278	17	0.109	R.FWGQYIDDM*FSPR.I
R2/RRR2-14/3	1414.170	1413.606	-309.537	0.537	1206.953	0.585	28	0.149	R.LPAAGPPSPAEHLR.E
R2/RRR2-14/2	1525.139	1525.639	-328.791	0.399	1163.051	0.457	21	0.149	R.VDVAAPEQCPPEGR.L
R2/RRR2-14/3	1413.807	1413.606	142.093	0.495	1168.036	0.572	28	0.141	R.LPAAGPPSPAEHLR.E
R2/RRR2-14/3	1413.462	1413.606	-102.406	0.485	947.272	0.591	26	0.127	R.LPAAGPPSPAEHLR.E
R2/RRR2-15/3	1413.171	1413.606	-308.932	0.491	576.435	0.585	21	0.105	R.LPAAGPPSPAEHLR.E
R2/RRR2-12/2	1347.219	1347.414	-145.283	0.518	2394.104	0.577	21	0.354	K.APVTSAEVSQDSR.F
R2/RRR2-12/2	1347.015	1347.414	-296.827	0.515	2185.084	0.563	20	0.308	K.APVTSAEVSQDSR.F
R2/RRR2-12/2	1347.120	1347.414	-218.731	0.521	2026.038	0.583	20	0.286	K.APVTSAEVSQDSR.F
R2/RRR2-9/3	1469.403	1468.637	-159.709	0.512	1315.578	0.478	24	0.134	R.VTSHSLQELQPTK.S
R2/RRR2-9/2	1318.113	1318.547	-329.901	0.359	774.066	0.303	18	0.112	K.FTVLLLPSGSQR.V
R2/RRR2-9/2	1318.058	1318.547	-371.530	0.360	594.692	0.307	16	0.108	K.FTVLLLPSGSQR.V
R2/RRR2-22/2	1307.168	1307.502	-256.716	0.452	1243.754	0.475	19	0.160	R.LM*GSLTNTQGLR.F
R2/RRR2-22/2	1306.639	1307.502	-1430.643	0.408	1143.383	0.496	18	0.153	R.LM*GSLTNTQGLR.F
R2/RRR2-22/2	1306.551	1307.502	-1498.304	0.383	1057.263	0.467	18	0.142	R.LM*GSLTNTQGLR.F
R2/RRR2-22/2	747.504	747.908	-541.684	0.402	807.819	0.364	11	0.121	R.FGVVVAR.F
R2/RRR2-22/2	747.807	747.908	-135.421	0.385	776.267	0.363	11	0.120	R.FGVVVAR.F
R2/RRR2-22/2	747.568	747.908	-455.981	0.374	784.127	0.362	11	0.119	R.FGVVVAR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1186.212	1186.345	-112.466	0.468	769.051	0.542	16	0.141	R.HSGIIDIQFR.R
R2/RRR2-14/2	1048.067	1048.211	-137.920	0.382	340.728	0.479	14	0.123	R.VPCNYPGLK.I
R2/RRR2-14/2	1185.452	1186.345	-1601.355	0.366	566.077	0.472	16	0.123	R.HSGIIDIQFR.R
R2/RRR2-14/2	1186.110	1186.345	-198.978	0.300	439.993	0.430	15	0.115	R.HSGIIDIQFR.R
R2/RRR2-14/2	1047.870	1048.211	-326.181	0.379	273.458	0.509	12	0.112	-.VPCNYPGLK.-
R2/RRR2-14/2	1047.900	1048.211	-297.195	0.264	245.550	0.386	12	0.101	-.VPCNYPGLK.-
R2/RRR2-16/2	1298.102	1298.427	-251.608	0.413	1157.520	0.502	21	0.156	K.EAAAASAPLPSQGK.T
R2/RRR2-5/2	1675.387	1675.862	-284.689	0.387	1772.465	0.590	24	0.243	K.AAVAVLGDLADTLGSSSK.D
R2/RRR2-4/2	1675.554	1675.862	-184.552	0.331	902.681	0.369	20	0.116	K.AAVAVLGDLADTLGSSSK.D
R2/RRR2-2/2	1676.679	1675.862	-109.798	0.267	329.189	0.360	15	0.102	-.AAVAVLGDLADTLGSSSK.-
R2/RRR2-16/2	1760.092	1760.924	-1044.177	0.479	2540.814	0.472	24	0.350	K.LSEIQSGVEEAESLIR.K
R2/RRR2-24/2	1761.663	1760.924	-148.843	0.469	741.782	0.429	17	0.117	K.LSEIQSGVEEAESLIR.K
R2/RRR2-7/2	1297.919	1297.526	303.506	0.402	671.622	0.568	20	0.136	K.VVGVPVSLNGDLK.N
R2/RRR2-7/2	1296.699	1297.526	-1413.268	0.372	511.897	0.568	18	0.127	K.VVGVPVSLNGDLK.N
R2/RRR2-7/2	820.834	820.959	-152.534	0.378	773.714	0.396	12	0.121	R.VGVVFSGR.Q
R2/RRR2-7/2	820.566	820.959	-480.696	0.342	705.739	0.411	12	0.119	R.VGVVFSGR.Q
R2/RRR2-7/2	1297.439	1297.526	-66.964	0.285	453.044	0.469	16	0.112	K.VVGVPVSLNGDLK.N
R2/RRR2-4/2	1308.304	1308.492	-144.457	0.483	1164.891	0.473	18	0.152	R.NMSVIAHVDHGK.S
R2/RRR2-4/2	1308.040	1308.492	-346.669	0.483	954.724	0.500	17	0.142	R.NMSVIAHVDHGK.S
R2/RRR2-1/2	1324.693	1324.492	152.540	0.434	892.791	0.490	19	0.139	R.NM*SVIAHVDHGK.S
R2/RRR2-4/2	1324.335	1324.492	-118.394	0.417	933.427	0.428	19	0.132	R.NM*SVIAHVDHGK.S
R2/RRR2-3/2	1040.206	1040.285	-75.991	0.433	911.000	0.416	13	0.129	R.IRPVLTVNK.M
R2/RRR2-4/2	1308.066	1308.492	-327.100	0.447	748.642	0.461	18	0.129	R.NMSVIAHVDHGK.S
R2/RRR2-5/2	1039.935	1040.285	-336.911	0.489	768.716	0.428	12	0.125	R.IRPVLTVNK.M
R2/RRR2-3/2	1040.089	1040.285	-188.420	0.470	818.143	0.387	13	0.123	R.IRPVLTVNK.M
R2/RRR2-3/2	1039.730	1040.285	-1499.720	0.462	832.130	0.380	13	0.123	R.IRPVLTVNK.M
R2/RRR2-4/2	1041.119	1040.285	-159.539	0.440	722.486	0.405	12	0.121	R.IRPVLTVNK.M
R2/RRR2-2/2	1039.354	1040.285	-1863.442	0.340	602.278	0.357	14	0.117	R.IRPVLTVNK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-5/2	1040.020	1040.285	-255.300	0.470	587.438	0.392	11	0.116	R.IRPVLTVNK.M
R2/RRR2-2/2	1040.092	1040.285	-185.712	0.388	499.640	0.378	10	0.109	-.IRPVLTVNK.-
R2/RRR2-4/2	1041.161	1040.285	-119.432	0.427	616.548	0.306	11	0.100	-.IRPVLTVNK.-
R2/RRR2-17/2	1521.830	1522.685	-1222.540	0.363	1581.865	0.413	20	0.180	K.IAVSTAQQFSNDIK.E
R2/RRR2-17/2	1172.968	1173.295	-279.598	0.428	1251.746	0.504	17	0.165	R.AAGPELVEACR.K
R2/RRR2-17/2	1172.678	1173.295	-1382.629	0.407	1133.880	0.404	16	0.138	R.AAGPELVEACR.K
R2/RRR2-10/3	1314.232	1314.473	-184.109	0.499	1891.543	0.432	25	0.188	R.HLAYHEYGVPK.D
R2/RRR2-10/2	1819.734	1820.124	-215.211	0.451	986.495	0.356	21	0.120	K.LFPASSVISFNPAILSR.E
R2/RRR2-10/2	1819.489	1820.124	-901.683	0.406	683.754	0.382	19	0.112	K.LFPASSVISFNPAILSR.E
R2/RRR2-10/3	1313.940	1314.473	-1170.442	0.489	1096.415	0.379	21	0.094	R.HLAYHEYGVPK.D
R2/RRR2-10/3	1315.159	1314.473	-240.023	0.437	1131.449	0.342	21	0.089	R.HLAYHEYGVPK.D
R2/RRR2-15/2	1315.240	1315.410	-129.732	0.452	1729.737	0.354	18	0.185	K.YEDKIDAFGEK.A
R2/RRR2-15/2	981.128	981.128	0.673	0.452	890.507	0.504	15	0.142	K.SPPNIPEVK.I
R2/RRR2-15/2	980.744	981.128	-392.700	0.332	1014.091	0.364	15	0.126	K.SPPNIPEVK.I
R2/RRR2-15/2	980.875	981.128	-258.836	0.352	887.109	0.399	14	0.125	K.SPPNIPEVK.I
R2/RRR2-16/2	981.286	981.128	162.127	0.398	1159.177	0.276	15	0.124	K.SPPNIPEVK.I
R2/RRR2-17/2	981.412	981.128	290.729	0.304	724.106	0.297	13	0.111	K.SPPNIPEVK.I
R2/RRR2-7/2	1240.200	1240.388	-151.897	0.532	1482.721	0.579	19	0.206	K.YGVTESTLLTR.N
R2/RRR2-7/2	1240.174	1240.388	-172.829	0.558	1530.664	0.515	18	0.196	K.YGVTESTLLTR.N
R2/RRR2-8/2	1240.043	1240.388	-278.890	0.535	1265.445	0.610	18	0.189	K.YGVTESTLLTR.N
R2/RRR2-8/2	1240.642	1240.388	205.112	0.556	1235.075	0.601	18	0.185	K.YGVTESTLLTR.N
R2/RRR2-7/2	1240.008	1240.388	-307.236	0.514	1211.655	0.589	17	0.178	K.YGVTESTLLTR.N
R2/RRR2-7/2	1869.547	1869.154	210.838	0.577	1216.374	0.558	24	0.171	R.LPIYVVQPQDGLDAIAR.N
R2/RRR2-8/2	1868.497	1869.154	-889.500	0.544	1263.760	0.534	24	0.170	R.LPIYVVQPQDGLDAIAR.N
R2/RRR2-8/2	1868.567	1869.154	-851.725	0.524	1152.130	0.549	24	0.164	R.LPIYVVQPQDGLDAIAR.N
R2/RRR2-7/2	1869.704	1869.154	-241.285	0.571	1193.600	0.535	23	0.163	R.LPIYVVQPQDGLDAIAR.N
R2/RRR2-7/2	1868.309	1869.154	-990.249	0.513	1140.070	0.511	24	0.156	R.LPIYVVQPQDGLDAIAR.N
R2/RRR2-8/2	1867.764	1869.154	-1283.229	0.565	1069.856	0.535	23	0.154	R.LPIYVVQPQDGLDAIAR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1240.631	1240.388	196.232	0.360	1301.185	0.410	17	0.150	K.YGVTESTLLTR.N
R2/RRR2-12/2	1241.253	1240.388	-108.958	0.164	573.056	0.222	14	0.102	K.YGVTESTLLTR.N
R2/RRR2-20/3	1913.553	1913.077	249.171	0.394	1311.636	0.469	27	0.132	R.ELVFKEDGQEYAQVTR.M
R2/RRR2-20/2	1134.831	1135.252	-371.638	0.383	709.939	0.410	15	0.122	K.AYGELPDTLR.L
R2/RRR2-20/2	1135.055	1135.252	-173.518	0.342	806.673	0.388	15	0.121	K.AYGELPDTLR.L
R2/RRR2-20/2	1135.180	1135.252	-63.054	0.388	633.366	0.413	14	0.120	K.AYGELPDTLR.L
R2/RRR2-19/2	1135.286	1135.252	30.347	0.361	640.798	0.419	13	0.118	K.AYGELPDTLR.L
R2/RRR2-20/2	1134.141	1135.252	-1867.045	0.303	561.343	0.451	13	0.116	K.AYGELPDTLR.L
R2/RRR2-19/2	1135.163	1135.252	-78.694	0.301	551.385	0.164	12	0.089	-.AYGELPDTLR.-
R2/RRR2-15/2	1401.364	1401.676	-222.671	0.434	1150.836	0.444	18	0.146	K.AFEEAKPIIAALK.E
R2/RRR2-16/2	921.333	922.060	-1880.683	0.344	506.208	0.485	14	0.121	K.VVDSFGGIK.A
R2/RRR2-16/2	921.954	922.060	-115.751	0.346	430.071	0.412	14	0.118	K.VVDSFGGIK.A
R2/RRR2-15/2	921.815	922.060	-266.852	0.282	375.608	0.422	12	0.112	K.VVDSFGGIK.A
R2/RRR2-17/2	1778.569	1779.029	-259.775	0.573	1158.382	0.509	24	0.159	K.IWQVPETLHEEVLGK.M
R2/RRR2-17/2	1778.420	1779.029	-907.497	0.526	1059.690	0.533	24	0.157	K.IWQVPETLHEEVLGK.M
R2/RRR2-17/2	1778.445	1779.029	-893.302	0.512	1136.386	0.495	24	0.155	K.IWQVPETLHEEVLGK.M
R2/RRR2-16/2	1778.347	1779.029	-948.637	0.499	866.629	0.518	22	0.141	K.IWQVPETLHEEVLGK.M
R2/RRR2-17/2	1779.528	1779.029	281.293	0.506	877.665	0.483	21	0.136	K.IWQVPETLHEEVLGK.M
R2/RRR2-16/2	1777.886	1779.029	-1208.991	0.513	860.780	0.470	22	0.134	K.IWQVPETLHEEVLGK.M
R2/RRR2-16/2	1778.466	1779.029	-881.381	0.501	763.857	0.505	21	0.134	K.IWQVPETLHEEVLGK.M
R2/RRR2-17/3	1778.872	1779.029	-88.631	0.405	820.465	0.434	26	0.091	K.IWQVPETLHEEVLGK.M
R2/RRR2-16/3	1778.992	1779.029	-21.110	0.388	719.263	0.408	25	0.085	K.IWQVPETLHEEVLGK.M
R2/RRR2-16/3	1778.410	1779.029	-913.086	0.368	736.758	0.384	25	0.082	K.IWQVPETLHEEVLGK.M
R2/RRR2-17/3	1780.087	1779.029	32.622	0.379	572.082	0.321	24	0.077	K.IWQVPETLHEEVLGK.M
R2/RRR2-16/3	1779.824	1779.029	-115.757	0.337	706.072	0.336	25	0.077	K.IWQVPETLHEEVLGK.M
R2/RRR2-17/3	1778.316	1779.029	-966.321	0.334	583.111	0.338	23	0.076	K.IWQVPETLHEEVLGK.M
R2/RRR2-17/3	1778.895	1779.029	-75.519	0.300	528.840	0.344	22	0.074	-.IWQVPETLHEEVLGK.-
R2/RRR2-19/2	1902.886	1901.108	-117.078	0.341	554.786	0.490	16	0.113	K.TSQKPVSPEDGEEIKKK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/3	1772.367	1772.935	-887.427	0.457	776.449	0.480	25	0.094	K.TSQKPVSPEDGEEIKK.K
R2/RRR2-19/3	1773.060	1772.935	70.869	0.501	900.607	0.432	26	0.093	K.TSQKPVSPEDGEEIKK.K
R2/RRR2-13/2	1785.603	1786.020	-234.067	0.480	1367.169	0.516	20	0.175	R.TGNTFLGSLLWVDYAK.W
R2/RRR2-13/2	1787.677	1786.020	-192.702	0.516	1114.925	0.464	19	0.142	R.TGNTFLGSLLWVDYAK.W
R2/RRR2-13/2	1785.077	1786.020	-1091.909	0.430	1090.000	0.395	19	0.131	R.TGNTFLGSLLWVDYAK.W
R2/RRR2-14/2	1125.214	1125.383	-150.335	0.447	1610.024	0.412	16	0.182	K.IAIDLLEPIK.R
R2/RRR2-14/2	1125.110	1125.383	-243.174	0.453	1499.560	0.396	16	0.169	-.IAIDLLEPIK.-
R2/RRR2-14/2	1125.252	1125.383	-117.035	0.493	1344.106	0.440	15	0.162	-.IAIDLLEPIK.-
R2/RRR2-16/2	1125.284	1125.383	-87.872	0.399	596.773	0.375	12	0.112	-.IAIDLLEPIK.-
R2/RRR2-16/2	1125.850	1125.383	415.577	0.194	591.093	0.343	13	0.105	K.IAIDLLEPIK.R
R2/RRR2-14/3	1591.709	1591.706	1.945	0.431	1072.345	0.447	29	0.103	R.LAWHDAGTYDVNTK.T
R2/RRR2-14/3	1591.700	1591.706	-3.363	0.387	627.372	0.323	24	0.073	R.LAWHDAGTYDVNTK.T
R2/RRR2-18/2	1275.547	1275.434	88.922	0.433	1283.131	0.437	16	0.155	R.GFGFVTFDEKK.A
R2/RRR2-18/2	1275.035	1275.434	-313.968	0.474	1230.802	0.388	16	0.143	R.GFGFVTFDEKK.A
R2/RRR2-17/2	879.916	879.980	-73.693	0.481	1266.073	0.281	14	0.131	K.FGNLTEAK.V
R2/RRR2-18/2	879.519	879.980	-525.875	0.407	1048.323	0.270	14	0.120	K.FGNLTEAK.V
R2/RRR2-18/2	879.572	879.980	-465.849	0.499	1010.909	0.259	14	0.117	K.FGNLTEAK.V
R2/RRR2-17/2	879.368	879.980	-1838.648	0.305	576.259	0.222	12	0.109	K.FGNLTEAK.V
R2/RRR2-18/2	879.742	879.980	-271.751	0.362	767.107	0.258	11	0.108	-.FGNLTEAK.-
R2/RRR2-10/2	1419.070	1418.534	-327.742	0.551	1426.524	0.600	19	0.202	R.GPLLDEDGPSYVR.V
R2/RRR2-10/2	1418.120	1418.534	-292.477	0.487	1421.741	0.586	19	0.198	R.GPLLDEDGPSYVR.V
R2/RRR2-9/2	1418.219	1418.534	-222.355	0.472	1462.096	0.566	19	0.198	R.GPLLDEDGPSYVR.V
R2/RRR2-9/2	1418.183	1418.534	-247.916	0.503	1330.665	0.595	19	0.190	R.GPLLDEDGPSYVR.V
R2/RRR2-10/2	1417.303	1418.534	-1578.516	0.384	1470.451	0.530	19	0.189	R.GPLLDEDGPSYVR.V
R2/RRR2-9/2	1048.093	1048.217	-118.876	0.366	1101.527	0.362	15	0.130	R.ALFVQADGVK.L
R2/RRR2-13/3	1632.886	1632.755	81.001	0.513	578.416	0.558	26	0.102	K.IVASEDRDLTVEER.N
R2/RRR2-13/3	1633.581	1632.755	-106.595	0.539	661.669	0.506	28	0.098	K.IVASEDRDLTVEER.N
R2/RRR2-13/3	1632.268	1632.755	-299.044	0.448	496.431	0.454	25	0.087	K.IVASEDRDLTVEER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1354.067	1353.465	-294.829	0.505	940.548	0.629	17	0.162	R.DNVQAYPGVSFR.Y
R2/RRR2-12/2	1353.210	1353.465	-188.884	0.465	1059.721	0.498	18	0.149	R.DNVQAYPGVSFR.Y
R2/RRR2-12/2	1353.216	1353.465	-184.359	0.474	929.508	0.507	17	0.142	R.DNVQAYPGVSFR.Y
R2/RRR2-13/2	1353.268	1353.465	-145.991	0.353	630.539	0.405	14	0.114	R.DNVQAYPGVSFR.Y
R2/RRR2-13/2	1137.158	1137.314	-137.128	0.302	668.511	0.362	16	0.111	K.LISHVQGGTPK.R
R2/RRR2-9/2	1971.793	1970.170	-191.970	0.528	1606.351	0.529	21	0.209	R.KNPDLENLLFDDFFNK.A
R2/RRR2-9/3	1672.648	1672.782	-80.242	0.386	875.404	0.484	25	0.099	K.YPEGQDIHVNWTGR.G
R2/RRR2-9/3	1672.486	1672.782	-177.761	0.392	1006.712	0.399	27	0.091	K.YPEGQDIHVNWTGR.G
R2/RRR2-9/3	1672.341	1672.782	-264.753	0.419	801.775	0.385	25	0.082	K.YPEGQDIHVNWTGR.G
R2/RRR2-14/2	1497.208	1497.677	-313.908	0.286	1236.180	0.383	16	0.138	R.EQIQSYVFDVIR.A
R2/RRR2-14/2	934.054	934.117	-68.308	0.540	904.067	0.379	15	0.127	K.YLAGLGIAR.Q
R2/RRR2-14/2	1497.239	1497.677	-293.131	0.271	1057.275	0.363	16	0.124	R.EQIQSYVFDVIR.A
R2/RRR2-14/2	934.216	934.117	106.274	0.417	894.238	0.285	15	0.115	K.YLAGLGIAR.Q
R2/RRR2-14/2	1497.410	1497.677	-178.871	0.292	694.927	0.278	15	0.106	R.EQIQSYVFDVIR.A
R2/RRR2-10/2	1458.085	1458.596	-1039.273	0.417	1598.341	0.507	20	0.201	R.EADPLDSQVVTVGK.F
R2/RRR2-10/2	1459.276	1458.596	-220.127	0.468	1369.949	0.489	19	0.171	R.EADPLDSQVVTVGK.F
R2/RRR2-10/2	1458.264	1458.596	-228.088	0.385	1227.507	0.500	19	0.159	R.EADPLDSQVVTVGK.F
R2/RRR2-10/3	1744.014	1742.958	32.138	0.389	1159.572	0.308	29	0.084	K.QRIEEVIVSQASVQR.C
R2/RRR2-12/2	1859.264	1859.933	-900.503	0.494	1469.626	0.542	20	0.194	R.DAGVNFFDNAEVYANGR.A
R2/RRR2-12/2	1219.153	1219.330	-146.384	0.378	952.701	0.300	16	0.116	K.LFWGGQGPNDK.G
R2/RRR2-12/2	1219.076	1219.330	-209.064	0.377	758.604	0.304	15	0.111	K.LFWGGQGPNDK.G
R2/RRR2-12/2	1219.415	1219.330	69.520	0.376	889.530	0.200	16	0.105	K.LFWGGQGPNDK.G
R2/RRR2-12/2	1610.472	1610.905	-269.833	0.459	1038.847	0.433	20	0.137	R.M*PNLHFIPVNLGNK.E
R2/RRR2-12/2	1146.087	1146.321	-204.431	0.460	995.283	0.356	16	0.127	R.FPDIASVQLR.M
R2/RRR2-12/2	1146.523	1146.321	176.885	0.499	1127.743	0.315	16	0.127	R.FPDIASVQLR.M
R2/RRR2-12/3	1594.281	1594.906	-1021.959	0.321	907.995	0.296	23	0.072	R.MPNLHFIPVNLGNK.E
R2/RRR2-12/3	1610.424	1610.905	-299.690	0.410	439.323	0.363	21	0.059	-.M*PNLHFIPVNLGNK.-
R2/RRR2-21/2	1124.268	1124.229	34.347	0.436	913.307	0.497	17	0.140	K.GISSSAVPYSR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1124.066	1124.229	-145.587	0.491	758.667	0.527	16	0.138	K.GISSSAVPYSR.N
R2/RRR2-21/2	1123.972	1124.229	-229.259	0.463	808.912	0.505	17	0.137	K.GISSSAVPYSR.N
R2/RRR2-21/2	1326.399	1326.570	-129.379	0.454	900.364	0.441	18	0.130	K.KGATPSQIGVVLR.D
R2/RRR2-21/2	1326.728	1326.570	119.083	0.409	991.653	0.355	19	0.124	K.KGATPSQIGVVLR.D
R2/RRR2-17/2	1333.843	1334.546	-1280.467	0.346	788.044	0.339	14	0.109	R.GAVGALLVYDISR.R
R2/RRR2-17/2	1334.370	1334.546	-132.001	0.328	567.507	0.326	13	0.104	-.GAVGALLVYDISR.-
R2/RRR2-7/2	1965.153	1966.330	-1111.211	0.486	1102.233	0.632	21	0.171	R.YFELSGLPM*LVLIGPDGK.T
R2/RRR2-6/2	1952.002	1950.330	-168.451	0.560	1272.629	0.525	23	0.167	R.YFELSGLPMLVLIGPDGK.T
R2/RRR2-7/2	1965.569	1966.330	-898.690	0.355	987.159	0.521	21	0.140	R.YFELSGLPM*LVLIGPDGK.T
R2/RRR2-7/2	928.012	928.108	-103.781	0.404	717.059	0.553	14	0.137	K.VPVSELVGK.T
R2/RRR2-6/2	927.254	928.108	-2005.668	0.365	631.763	0.537	14	0.130	K.VPVSELVGK.T
R2/RRR2-7/2	928.084	928.108	-26.070	0.388	716.079	0.471	14	0.128	K.VPVSELVGK.T
R2/RRR2-7/2	1965.802	1966.330	-779.310	0.420	819.867	0.460	20	0.124	R.YFELSGLPM*LVLIGPDGK.T
R2/RRR2-6/2	927.560	928.108	-1673.954	0.380	524.873	0.486	13	0.121	-.VPVSELVGK.-
R2/RRR2-6/2	927.621	928.108	-526.588	0.282	542.718	0.462	13	0.117	K.VPVSELVGK.T
R2/RRR2-3/2	928.437	928.108	355.320	0.292	830.123	0.343	14	0.116	K.VPVSELVGK.T
R2/RRR2-6/2	1965.809	1966.330	-775.820	0.362	649.774	0.432	17	0.112	R.YFELSGLPM*LVLIGPDGK.T
R2/RRR2-1/2	928.028	928.108	-85.836	0.301	658.669	0.294	13	0.111	K.VPVSELVGK.T
R2/RRR2-24/2	1487.182	1486.719	312.360	0.446	1073.273	0.447	19	0.140	R.GIM*QPVPVSDALSR.F
R2/RRR2-24/2	1486.315	1486.719	-272.904	0.434	1101.063	0.430	19	0.139	R.GIM*QPVPVSDALSR.F
R2/RRR2-24/2	1486.248	1486.719	-317.730	0.403	1073.053	0.363	19	0.127	R.GIM*QPVPVSDALSR.F
R2/RRR2-24/2	1038.824	1039.148	-312.366	0.353	823.821	0.363	17	0.121	R.FAGGAPEM*SR.A
R2/RRR2-25/2	1038.766	1039.148	-368.489	0.340	624.825	0.406	15	0.118	R.FAGGAPEM*SR.A
R2/RRR2-24/2	1038.991	1039.148	-151.462	0.363	509.890	0.350	13	0.111	-.FAGGAPEM*SR.-
R2/RRR2-24/2	1038.839	1039.148	-297.747	0.269	506.833	0.258	14	0.109	R.FAGGAPEM*SR.A
R2/RRR2-25/2	1039.009	1039.148	-133.902	0.195	801.365	0.224	14	0.104	R.FAGGAPEM*SR.A
R2/RRR2-25/2	1039.177	1039.148	28.359	0.141	556.661	0.155	12	0.101	-.FAGGAPEM*SR.-
R2/RRR2-15/2	1730.421	1730.852	-249.456	0.539	2100.489	0.595	23	0.298	R.SGTALCSYIASTAQSGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1729.659	1730.852	-1271.227	0.451	2021.104	0.599	22	0.285	R.SGTALCSYIASTAQSGR.I
R2/RRR2-14/2	1730.361	1730.852	-284.136	0.509	2017.568	0.575	23	0.278	R.SGTALCSYIASTAQSGR.I
R2/RRR2-15/2	1730.367	1730.852	-280.809	0.521	1942.162	0.575	23	0.265	R.SGTALCSYIASTAQSGR.I
R2/RRR2-14/2	1731.284	1730.852	250.518	0.585	1807.770	0.608	22	0.252	R.SGTALCSYIASTAQSGR.I
R2/RRR2-15/2	1930.377	1930.151	117.300	0.498	1755.098	0.559	26	0.233	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-14/2	1730.259	1730.852	-923.416	0.514	1663.411	0.572	21	0.222	R.SGTALCSYIASTAQSGR.I
R2/RRR2-15/2	1931.735	1930.151	-215.980	0.519	1667.562	0.582	25	0.209	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-14/2	1932.031	1930.151	-62.397	0.478	1661.279	0.533	25	0.206	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-15/2	1930.391	1930.151	124.530	0.466	1603.898	0.584	26	0.192	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-15/2	1929.844	1930.151	-159.663	0.397	1563.378	0.541	24	0.185	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-15/2	1930.036	1930.151	-59.797	0.477	1511.017	0.526	25	0.164	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-15/2	1929.779	1930.151	-193.041	0.406	927.624	0.562	18	0.058	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-14/2	1929.449	1930.151	-884.562	0.318	925.832	0.397	20	0.052	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-14/2	1930.803	1930.151	-180.827	0.342	750.728	0.450	19	0.032	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-14/2	1929.627	1930.151	-792.096	0.292	702.980	0.430	17	0.028	R.ISGIPSGTVNLLAFNGNPSA.-
R2/RRR2-23/2	1562.125	1562.620	-317.871	0.368	628.297	0.493	20	0.123	R.QSGTTPGYSYSTANK.N
R2/RRR2-23/2	922.982	923.088	-114.959	0.374	907.114	0.340	13	0.121	R.ADLISYLK.E
R2/RRR2-23/2	1562.107	1562.620	-971.322	0.410	483.795	0.499	18	0.120	R.QSGTTPGYSYSTANK.N
R2/RRR2-23/2	922.563	923.088	-1658.602	0.374	890.124	0.309	13	0.117	R.ADLISYLK.E
R2/RRR2-23/2	1562.125	1562.620	-317.793	0.346	567.720	0.463	18	0.116	R.QSGTTPGYSYSTANK.N
R2/RRR2-23/2	922.894	923.088	-211.020	0.364	846.064	0.305	13	0.116	R.ADLISYLK.E
R2/RRR2-8/2	1486.242	1486.693	-304.032	0.454	1255.964	0.579	19	0.179	R.VADPTFLGYFIDK.G
R2/RRR2-8/2	1544.574	1544.684	-71.470	0.483	1364.081	0.500	19	0.176	K.YVDCYGVDNALVR.V
R2/RRR2-8/2	1486.323	1486.693	-249.318	0.452	1131.459	0.491	18	0.152	R.VADPTFLGYFIDK.G
R2/RRR2-8/2	1486.321	1486.693	-250.637	0.426	1012.721	0.513	18	0.146	R.VADPTFLGYFIDK.G
R2/RRR2-7/2	1588.550	1587.754	-128.299	0.548	1469.334	0.439	23	0.173	R.NCPEFAFSFLGAAR.L
R2/RRR2-7/2	1587.186	1587.754	-990.841	0.487	1433.636	0.441	23	0.171	R.NCPEFAFSFLGAAR.L
R2/RRR2-7/2	1587.877	1587.754	77.985	0.556	1448.510	0.429	23	0.169	R.NCPEFAFSFLGAAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/2	1269.189	1269.472	-223.769	0.301	881.184	0.389	16	0.118	K.VVIIQPVDSGNK.L
R2/RRR2-21/2	1066.132	1066.229	-92.058	0.314	638.924	0.423	13	0.116	R.YTLELEGLK.G
R2/RRR2-21/2	1066.210	1066.229	-17.754	0.328	595.169	0.367	13	0.113	R.YTLELEGLK.G
R2/RRR2-13/2	1633.346	1633.912	-961.715	0.449	1479.611	0.489	22	0.181	K.VGPALLSGPVFATFEK.V
R2/RRR2-14/2	1634.326	1633.912	254.368	0.547	1288.043	0.562	21	0.176	K.VGPALLSGPVFATFEK.V
R2/RRR2-13/2	1633.517	1633.912	-242.518	0.492	1230.953	0.514	21	0.162	K.VGPALLSGPVFATFEK.V
R2/RRR2-14/2	1633.598	1633.912	-192.815	0.501	1207.458	0.513	21	0.160	K.VGPALLSGPVFATFEK.V
R2/RRR2-13/2	1633.435	1633.912	-293.051	0.491	1181.049	0.517	20	0.157	K.VGPALLSGPVFATFEK.V
R2/RRR2-14/2	1633.436	1633.912	-292.301	0.491	1195.127	0.501	20	0.155	K.VGPALLSGPVFATFEK.V
R2/RRR2-19/2	1401.999	1400.644	253.728	0.436	840.779	0.476	16	0.129	K.VVEIYEAAPAPLK.V
R2/RRR2-16/2	1635.302	1633.912	239.017	0.400	664.259	0.401	16	0.112	K.VGPALLSGPVFATFEK.V
R2/RRR2-7/2	1755.434	1754.961	270.297	0.555	1539.981	0.528	22	0.198	K.EGVAFYNSLIDDVIAK.G
R2/RRR2-7/2	1754.702	1754.961	-148.457	0.485	1335.943	0.542	21	0.178	K.EGVAFYNSLIDDVIAK.G
R2/RRR2-7/2	1754.418	1754.961	-882.367	0.486	1213.753	0.542	20	0.166	K.EGVAFYNSLIDDVIAK.G
R2/RRR2-7/2	880.477	881.013	-1749.491	0.310	821.173	0.254	11	0.108	-.FSIAWTR.-
R2/RRR2-7/2	880.277	881.013	-1978.552	0.315	628.787	0.127	11	0.096	-.FSIAWTR.-
R2/RRR2-8/2	1103.896	1104.199	-275.687	0.515	849.789	0.432	16	0.131	R.RLESELSGGR.T
R2/RRR2-19/2	1117.096	1117.275	-160.306	0.485	765.684	0.386	16	0.123	K.LEVSDVVVEK.A
R2/RRR2-19/2	926.786	927.080	-318.529	0.494	746.791	0.378	12	0.121	R.HLDTIISK.T
R2/RRR2-19/2	1116.932	1117.275	-308.095	0.373	653.453	0.431	15	0.120	K.LEVSDVVVEK.A
R2/RRR2-19/2	927.009	927.080	-76.751	0.506	589.243	0.368	11	0.114	-.HLDTIISK.-
R2/RRR2-19/2	927.006	927.080	-80.582	0.527	569.499	0.343	11	0.112	-.HLDTIISK.-
R2/RRR2-10/2	1422.523	1421.620	-68.564	0.486	1804.435	0.413	19	0.207	R.FLDLDTGIIATNK.Q
R2/RRR2-10/2	1577.339	1577.760	-268.154	0.279	647.162	0.368	15	0.105	R.GDQYAIALALLDEGK.V
R2/RRR2-17/2	960.181	960.173	7.892	0.255	800.392	0.165	10	0.100	-.DMLLKDPK.-
R2/RRR2-20/2	1263.864	1264.371	-1195.881	0.430	446.664	0.574	15	0.129	K.GGAPAEFQPSFR.G
R2/RRR2-20/2	1263.512	1264.371	-1476.164	0.409	438.905	0.556	15	0.127	K.GGAPAEFQPSFR.G
R2/RRR2-20/2	1264.589	1264.371	173.005	0.378	503.563	0.533	16	0.126	K.GGAPAEFQPSFR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/2	1264.033	1264.371	-268.657	0.381	437.180	0.561	15	0.126	K.GGAPAEFQPSFR.G
R2/RRR2-20/2	1263.984	1264.371	-307.607	0.404	455.072	0.512	15	0.124	K.GGAPAEFQPSFR.G
R2/RRR2-19/2	1263.519	1264.371	-1470.535	0.416	434.695	0.505	15	0.124	K.GGAPAEFQPSFR.G
R2/RRR2-21/2	1264.101	1264.371	-214.403	0.369	527.207	0.481	16	0.122	K.GGAPAEFQPSFR.G
R2/RRR2-21/2	1264.079	1264.371	-231.841	0.383	373.226	0.467	15	0.120	K.GGAPAEFQPSFR.G
R2/RRR2-21/2	1263.866	1264.371	-1194.523	0.353	489.100	0.460	16	0.120	K.GGAPAEFQPSFR.G
R2/RRR2-20/2	1265.028	1264.371	-271.736	0.396	414.456	0.437	15	0.119	K.GGAPAEFQPSFR.G
R2/RRR2-19/2	1265.199	1264.371	-136.412	0.353	335.634	0.520	13	0.119	K.GGAPAEFQPSFR.G
R2/RRR2-19/2	1264.829	1264.371	362.847	0.339	404.467	0.434	14	0.116	K.GGAPAEFQPSFR.G
R2/RRR2-19/2	1263.435	1264.371	-1536.723	0.285	419.473	0.402	15	0.114	K.GGAPAEFQPSFR.G
R2/RRR2-20/2	1676.389	1674.919	280.924	0.498	640.486	0.400	17	0.113	R.SYLNLPSEVVPNTLK.K
R2/RRR2-19/2	1673.890	1674.919	-1216.225	0.326	436.100	0.309	13	0.101	R.SYLNLPSEVVPNTLK.K
R2/RRR2-21/2	1031.456	1032.136	-1634.489	0.333	850.901	0.342	13	0.116	K.HGWDYVVR.K
R2/RRR2-21/2	1033.166	1033.249	-80.894	0.351	825.928	0.323	14	0.115	R.KVVIYSPAR.T
R2/RRR2-21/2	1033.863	1033.249	-373.944	0.358	895.826	0.201	14	0.106	R.KVVIYSPAR.T
R2/RRR2-18/3	1529.765	1529.724	27.155	0.533	1281.160	0.499	30	0.134	R.GFGHIGVTVHDVYK.A
R2/RRR2-18/2	987.112	987.091	21.320	0.420	736.975	0.381	13	0.122	K.VSLDFYSR.V
R2/RRR2-18/2	986.554	987.091	-1562.002	0.345	780.177	0.292	12	0.112	K.VSLDFYSR.V
R2/RRR2-18/2	986.726	987.091	-371.272	0.255	773.323	0.263	12	0.107	K.VSLDFYSR.V
R2/RRR2-24/1	1531.814	1531.645	110.222	0.480	813.049	0.470	18	0.690	R.AGDCALIHSGSWEK.A
R2/RRR2-24/1	1530.775	1531.645	-1225.265	0.278	738.084	0.313	17	0.541	R.AGDCALIHSGSWEK.A
R2/RRR2-24/1	1530.727	1531.645	-1256.658	0.212	715.642	0.208	17	0.479	R.AGDCALIHSGSWEK.A
R2/RRR2-23/1	1530.760	1531.645	-1235.435	0.241	635.110	0.221	16	0.407	R.AGDCALIHSGSWEK.A
R2/RRR2-23/1	1530.823	1531.645	-1193.954	0.223	605.073	0.272	16	0.398	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	1531.141	1531.645	-985.448	0.480	1865.426	0.408	21	0.208	R.AGDCALIHSGSWEK.A
R2/RRR2-24/2	1531.414	1531.645	-151.154	0.518	1551.467	0.485	20	0.187	R.AGDCALIHSGSWEK.A
R2/RRR2-22/2	1531.226	1531.645	-274.951	0.509	1565.375	0.471	21	0.187	R.AGDCALIHSGSWEK.A
R2/RRR2-24/2	1531.124	1531.645	-996.814	0.510	1561.139	0.462	21	0.184	R.AGDCALIHSGSWEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/3	1531.876	1531.645	151.242	0.479	1783.425	0.434	31	0.171	R.AGDCALIHSGSWEK.A
R2/RRR2-24/2	1531.114	1531.645	-1003.138	0.501	1487.166	0.432	21	0.170	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	1531.288	1531.645	-233.842	0.467	1352.594	0.473	20	0.165	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	1530.570	1531.645	-1359.948	0.495	1388.155	0.435	20	0.161	R.AGDCALIHSGSWEK.A
R2/RRR2-24/3	1531.218	1531.645	-280.118	0.445	1610.909	0.423	30	0.147	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	1531.214	1531.645	-282.469	0.477	1266.982	0.388	20	0.143	R.AGDCALIHSGSWEK.A
R2/RRR2-16/3	1530.996	1531.645	-1080.557	0.493	1536.994	0.434	29	0.142	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	1530.914	1531.645	-1134.190	0.471	1162.750	0.404	18	0.137	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	1530.381	1531.645	-1483.802	0.353	1521.249	0.218	21	0.136	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	1531.115	1531.645	-1002.658	0.367	1510.893	0.145	20	0.123	R.AGDCALIHSGSWEK.A
R2/RRR2-24/2	1530.383	1531.645	-1482.840	0.318	1352.046	0.160	20	0.117	R.AGDCALIHSGSWEK.A
R2/RRR2-22/3	1531.065	1531.645	-1035.286	0.437	1152.621	0.457	25	0.116	R.AGDCALIHSGSWEK.A
R2/RRR2-23/3	1531.897	1531.645	164.548	0.475	1133.139	0.465	26	0.116	R.AGDCALIHSGSWEK.A
R2/RRR2-24/2	849.632	849.949	-374.185	0.327	631.625	0.377	12	0.114	-.TTAIGCAR.-
R2/RRR2-23/2	849.680	849.949	-317.966	0.292	499.559	0.360	11	0.111	R.TTAIGCAR.V
R2/RRR2-24/2	850.000	849.949	59.978	0.366	377.925	0.261	10	0.111	R.TTAIGCAR.V
R2/RRR2-25/3	1530.193	1531.645	-1607.294	0.347	1322.053	0.374	27	0.111	R.AGDCALIHSGSWEK.A
R2/RRR2-25/3	1531.802	1531.645	102.812	0.428	1249.160	0.403	27	0.111	R.AGDCALIHSGSWEK.A
R2/RRR2-21/3	1531.553	1531.645	-60.135	0.510	1137.927	0.426	27	0.107	R.AGDCALIHSGSWEK.A
R2/RRR2-23/2	849.886	849.949	-74.568	0.321	303.494	0.284	9	0.106	-.TTAIGCAR.-
R2/RRR2-24/3	1531.835	1531.645	124.390	0.453	1169.997	0.400	27	0.104	R.AGDCALIHSGSWEK.A
R2/RRR2-24/3	1531.893	1531.645	162.030	0.485	1276.029	0.373	29	0.104	R.AGDCALIHSGSWEK.A
R2/RRR2-23/3	1531.671	1531.645	17.089	0.401	1217.792	0.371	26	0.103	R.AGDCALIHSGSWEK.A
R2/RRR2-24/2	1530.897	1531.645	-1145.559	0.333	591.211	0.176	15	0.102	R.AGDCALIHSGSWEK.A
R2/RRR2-19/3	1530.392	1531.645	-1476.760	0.377	1181.603	0.351	26	0.097	R.AGDCALIHSGSWEK.A
R2/RRR2-26/3	1531.947	1531.645	197.870	0.409	1175.723	0.351	26	0.096	R.AGDCALIHSGSWEK.A
R2/RRR2-18/3	1531.531	1531.645	-74.885	0.438	1211.667	0.340	26	0.095	R.AGDCALIHSGSWEK.A
R2/RRR2-22/3	1531.930	1531.645	186.483	0.454	1097.222	0.370	26	0.095	R.AGDCALIHSGSWEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-24/3	1531.605	1531.645	-26.078	0.442	1047.077	0.379	24	0.094	R.AGDCALIHSGSWEK.A
R2/RRR2-22/3	1531.774	1531.645	84.350	0.455	1107.558	0.364	27	0.094	R.AGDCALIHSGSWEK.A
R2/RRR2-19/3	1531.507	1531.645	-90.236	0.451	1072.490	0.350	26	0.090	R.AGDCALIHSGSWEK.A
R2/RRR2-21/3	1531.647	1531.645	1.022	0.423	1015.153	0.356	26	0.090	R.AGDCALIHSGSWEK.A
R2/RRR2-1/3	1531.797	1531.645	99.096	0.476	815.033	0.391	23	0.088	R.AGDCALIHSGSWEK.A
R2/RRR2-26/3	1531.277	1531.645	-241.128	0.375	1021.925	0.331	24	0.087	R.AGDCALIHSGSWEK.A
R2/RRR2-23/3	1530.515	1531.645	-1396.124	0.385	1161.296	0.294	25	0.086	R.AGDCALIHSGSWEK.A
R2/RRR2-26/3	1531.954	1531.645	202.424	0.412	1056.848	0.319	26	0.085	R.AGDCALIHSGSWEK.A
R2/RRR2-21/3	1532.682	1531.645	23.748	0.430	1097.160	0.299	25	0.083	R.AGDCALIHSGSWEK.A
R2/RRR2-20/3	1531.310	1531.645	-219.895	0.389	975.164	0.313	25	0.083	R.AGDCALIHSGSWEK.A
R2/RRR2-3/3	1530.854	1531.645	-1173.633	0.366	749.640	0.337	22	0.082	R.AGDCALIHSGSWEK.A
R2/RRR2-18/3	1531.036	1531.645	-1054.018	0.369	954.891	0.306	24	0.081	R.AGDCALIHSGSWEK.A
R2/RRR2-25/3	1531.602	1531.645	-28.476	0.380	712.460	0.312	22	0.080	R.AGDCALIHSGSWEK.A
R2/RRR2-20/3	1531.191	1531.645	-297.635	0.394	882.719	0.303	23	0.080	R.AGDCALIHSGSWEK.A
R2/RRR2-23/3	1531.284	1531.645	-236.690	0.396	904.020	0.285	24	0.078	R.AGDCALIHSGSWEK.A
R2/RRR2-20/3	1531.340	1531.645	-199.742	0.421	973.644	0.274	25	0.077	R.AGDCALIHSGSWEK.A
R2/RRR2-24/3	1531.175	1531.645	-308.313	0.338	1045.706	0.251	23	0.077	R.AGDCALIHSGSWEK.A
R2/RRR2-18/3	1531.401	1531.645	-160.039	0.394	716.168	0.299	21	0.077	-.AGDCALIHSGSWEK.-
R2/RRR2-24/3	1531.458	1531.645	-122.857	0.383	705.022	0.259	21	0.074	-.AGDCALIHSGSWEK.-
R2/RRR2-19/3	1531.609	1531.645	-23.560	0.362	990.069	0.214	24	0.072	R.AGDCALIHSGSWEK.A
R2/RRR2-16/2	1885.353	1885.070	150.299	0.556	1210.922	0.590	26	0.176	R.LDPGQSWSISVAAGTPAAR.I
R2/RRR2-17/2	1884.573	1885.070	-264.458	0.498	1210.683	0.586	25	0.174	R.LDPGQSWSISVAAGTPAAR.I
R2/RRR2-16/2	1649.114	1649.825	-1040.498	0.431	1236.561	0.504	22	0.161	R.CSYTVWPGALPGGGAR.L
R2/RRR2-17/2	1884.523	1885.070	-823.398	0.494	1211.578	0.516	24	0.160	R.LDPGQSWSISVAAGTPAAR.I
R2/RRR2-16/2	1649.097	1649.825	-1051.126	0.388	1198.946	0.487	21	0.154	R.CSYTVWPGALPGGGAR.L
R2/RRR2-16/2	1884.462	1885.070	-856.203	0.470	1066.242	0.498	23	0.145	R.LDPGQSWSISVAAGTPAAR.I
R2/RRR2-17/2	1885.618	1885.070	-240.612	0.569	952.446	0.544	23	0.145	R.LDPGQSWSISVAAGTPAAR.I
R2/RRR2-17/2	1649.177	1649.825	-1002.596	0.372	1181.945	0.420	22	0.142	R.CSYTVWPGALPGGGAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1648.787	1649.825	-1239.792	0.263	810.404	0.388	18	0.114	-.CSYTVWPGALPGGGAR.-
R2/RRR2-4/2	1641.216	1641.853	-999.999	0.461	969.797	0.490	19	0.139	R.GVNGTVAHEFIIDLR.G
R2/RRR2-4/2	1641.922	1641.853	42.161	0.380	1093.013	0.390	20	0.132	R.GVNGTVAHEFIIDLR.G
R2/RRR2-4/2	1230.513	1231.335	-1484.507	0.375	990.019	0.343	17	0.122	K.TTAGIEPEDVAK.R
R2/RRR2-4/2	1231.154	1231.335	-147.046	0.454	699.165	0.426	16	0.120	-.TTAGIEPEDVAK.-
R2/RRR2-4/2	1230.933	1231.335	-327.504	0.471	597.498	0.435	15	0.119	K.TTAGIEPEDVAK.R
R2/RRR2-17/2	957.094	957.149	-57.836	0.514	1146.229	0.425	14	0.145	R.AAVLLLDNK.K
R2/RRR2-17/2	957.000	957.149	-156.482	0.529	1057.599	0.414	14	0.138	R.AAVLLLDNK.K
R2/RRR2-17/2	1348.038	1348.533	-367.809	0.430	1212.372	0.343	16	0.134	K.SREPVVQLYTR.D
R2/RRR2-17/2	1348.237	1348.533	-219.730	0.417	993.643	0.312	16	0.119	K.SREPVVQLYTR.D
R2/RRR2-17/2	1348.314	1348.533	-162.600	0.408	676.033	0.310	15	0.111	K.SREPVVQLYTR.D
R2/RRR2-16/2	1057.958	1058.254	-280.251	0.430	797.466	0.515	15	0.135	K.LSGIVGVPTSK.R
R2/RRR2-16/2	1059.113	1058.254	-133.014	0.456	738.895	0.459	15	0.126	K.LSGIVGVPTSK.R
R2/RRR2-16/2	1058.143	1058.254	-105.134	0.447	734.361	0.460	15	0.126	K.LSGIVGVPTSK.R
R2/RRR2-16/3	1085.841	1085.279	-404.767	0.444	842.084	0.438	21	0.092	K.TPIKDALAAGK.E
R2/RRR2-15/3	1085.855	1085.279	-391.739	0.421	770.280	0.453	21	0.091	K.TPIKDALAAGK.E
R2/RRR2-16/3	1085.220	1085.279	-54.377	0.438	883.275	0.422	21	0.091	K.TPIKDALAAGK.E
R2/RRR2-16/3	1084.901	1085.279	-349.368	0.408	535.436	0.397	18	0.082	K.TPIKDALAAGK.E
R2/RRR2-15/3	1085.303	1085.279	22.199	0.384	536.800	0.399	18	0.082	K.TPIKDALAAGK.E
R2/RRR2-4/2	1720.304	1720.822	-884.918	0.416	1223.517	0.566	23	0.172	R.TLSFAIADGSQPGNEGR.E
R2/RRR2-4/2	1268.260	1268.444	-145.929	0.367	802.868	0.400	18	0.121	R.EADGTLRPLPAK.H
R2/RRR2-4/2	1267.622	1268.444	-1442.111	0.384	411.374	0.377	15	0.112	R.EADGTLRPLPAK.H
R2/RRR2-13/2	1264.185	1264.326	-112.212	0.520	1454.213	0.480	20	0.181	K.FGDAVQEDVGAR.L
R2/RRR2-13/2	1264.122	1264.326	-162.097	0.561	1446.917	0.469	20	0.178	K.FGDAVQEDVGAR.L
R2/RRR2-13/2	1359.112	1359.421	-228.332	0.479	1251.433	0.518	20	0.167	K.AEEPSASGDPLASK.S
R2/RRR2-13/2	1263.466	1264.326	-1477.284	0.527	1305.620	0.480	19	0.167	K.FGDAVQEDVGAR.L
R2/RRR2-13/2	1359.048	1359.421	-275.370	0.462	1290.712	0.497	20	0.166	K.AEEPSASGDPLASK.S
R2/RRR2-13/2	1358.809	1359.421	-1189.721	0.355	1132.885	0.385	19	0.133	K.AEEPSASGDPLASK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1359.944	1360.541	-1177.475	0.394	1554.897	0.448	18	0.183	K.FVAYTSAWTWK.K
R2/RRR2-20/2	1360.293	1360.541	-182.410	0.356	1332.959	0.429	17	0.156	K.FVAYTSAWTWK.K
R2/RRR2-12/2	1292.315	1291.481	-128.907	0.413	982.052	0.447	16	0.134	R.GVNVIYALTGQR.R
R2/RRR2-20/2	1292.024	1291.481	-355.231	0.421	1014.939	0.433	16	0.134	R.GVNVIYALTGQR.R
R2/RRR2-13/2	1291.454	1291.481	-21.294	0.407	1054.748	0.397	16	0.131	R.GVNVIYALTGQR.R
R2/RRR2-20/2	1291.130	1291.481	-272.691	0.356	1047.020	0.397	16	0.130	R.GVNVIYALTGQR.R
R2/RRR2-20/2	1291.028	1291.481	-352.091	0.291	1051.432	0.369	16	0.125	R.GVNVIYALTGQR.R
R2/RRR2-20/2	1360.208	1360.541	-244.890	0.290	742.644	0.391	13	0.113	K.FVAYTSAWTWK.K
R2/RRR2-12/2	1291.022	1291.481	-356.502	0.319	757.923	0.348	15	0.113	R.GVNVIYALTGQR.R
R2/RRR2-6/2	1421.182	1421.581	-281.422	0.493	1179.320	0.524	20	0.163	R.IVTNVGQDNAVYK.A
R2/RRR2-6/2	1824.679	1823.127	-245.964	0.517	916.263	0.544	20	0.142	K.GSLVDLNLPSITIPNLR.M
R2/RRR2-6/2	1420.568	1421.581	-1421.300	0.383	1045.558	0.460	19	0.140	R.IVTNVGQDNAVYK.A
R2/RRR2-6/2	1421.100	1421.581	-338.905	0.465	984.007	0.453	19	0.137	R.IVTNVGQDNAVYK.A
R2/RRR2-6/3	1421.857	1421.581	194.978	0.449	1486.370	0.407	24	0.134	R.IVTNVGQDNAVYK.A
R2/RRR2-6/2	1824.511	1823.127	211.210	0.515	744.107	0.521	19	0.130	K.GSLVDLNLPSITIPNLR.M
R2/RRR2-5/2	1422.137	1421.581	-313.088	0.454	863.780	0.449	17	0.129	R.IVTNVGQDNAVYK.A
R2/RRR2-5/2	1822.607	1823.127	-835.986	0.418	711.230	0.503	18	0.124	K.GSLVDLNLPSITIPNLR.M
R2/RRR2-5/2	1823.846	1823.127	-154.509	0.484	681.251	0.502	17	0.122	K.GSLVDLNLPSITIPNLR.M
R2/RRR2-5/2	1421.213	1421.581	-259.362	0.390	870.698	0.381	17	0.120	R.IVTNVGQDNAVYK.A
R2/RRR2-5/2	1822.523	1823.127	-882.244	0.401	567.939	0.511	16	0.118	K.GSLVDLNLPSITIPNLR.M
R2/RRR2-6/2	1822.654	1823.127	-259.940	0.376	466.846	0.450	15	0.110	K.GSLVDLNLPSITIPNLR.M
R2/RRR2-6/2	1192.188	1191.362	-146.101	0.483	1835.145	0.462	19	0.223	R.FAATLGELVGGR.V
R2/RRR2-6/2	1191.205	1191.362	-131.626	0.382	1726.363	0.462	19	0.207	R.FAATLGELVGGR.V
R2/RRR2-6/2	1463.421	1463.621	-136.843	0.315	1431.636	0.327	23	0.147	R.ATGGADAAAALAAYLR.G
R2/RRR2-6/2	1463.047	1463.621	-1078.596	0.227	885.335	0.195	18	0.100	R.ATGGADAAAALAAYLR.G
R2/RRR2-21/2	1269.860	1269.300	-347.258	0.470	833.941	0.477	18	0.133	R.GNGTGGESIYGEK.-
R2/RRR2-21/2	1269.527	1269.300	179.132	0.434	680.519	0.534	16	0.131	R.GNGTGGESIYGEK.-
R2/RRR2-18/2	1595.553	1595.847	-184.827	0.456	571.544	0.457	21	0.125	R.VIPNFMLQGGDFTR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1595.075	1595.847	-1114.666	0.390	580.831	0.469	21	0.124	R.VIPNFMLQGGDFTR.G
R2/RRR2-20/2	1270.048	1269.300	-198.938	0.441	757.010	0.428	17	0.123	R.GNGTGGESIYGEK.-
R2/RRR2-18/2	1611.231	1611.847	-1005.800	0.331	426.980	0.515	21	0.122	R.VIPNFM*LQGGDFTR.G
R2/RRR2-18/2	1611.270	1611.847	-981.688	0.344	346.665	0.491	20	0.121	R.VIPNFM*LQGGDFTR.G
R2/RRR2-21/2	1269.996	1269.300	-239.919	0.463	642.860	0.428	16	0.120	R.GNGTGGESIYGEK.-
R2/RRR2-20/2	1268.955	1269.300	-272.343	0.374	432.316	0.464	16	0.120	R.GNGTGGESIYGEK.-
R2/RRR2-20/2	1269.975	1269.300	-256.602	0.348	709.254	0.419	17	0.120	R.GNGTGGESIYGEK.-
R2/RRR2-20/2	1268.976	1269.300	-256.322	0.387	541.011	0.424	17	0.119	R.GNGTGGESIYGEK.-
R2/RRR2-21/2	1269.459	1269.300	125.709	0.348	665.339	0.428	16	0.119	R.GNGTGGESIYGEK.-
R2/RRR2-21/2	1269.000	1269.300	-236.827	0.397	393.076	0.436	15	0.118	R.GNGTGGESIYGEK.-
R2/RRR2-21/2	1269.938	1269.300	-285.629	0.365	584.711	0.437	15	0.117	R.GNGTGGESIYGEK.-
R2/RRR2-18/2	1594.972	1595.847	-1179.143	0.340	586.702	0.394	21	0.117	R.VIPNFMLQGGDFTR.G
R2/RRR2-20/2	1269.332	1269.300	25.599	0.347	623.582	0.423	15	0.116	R.GNGTGGESIYGEK.-
R2/RRR2-21/2	1268.897	1269.300	-318.478	0.380	436.715	0.363	16	0.115	R.GNGTGGESIYGEK.-
R2/RRR2-21/2	1269.815	1269.300	-382.656	0.369	569.216	0.400	15	0.115	R.GNGTGGESIYGEK.-
R2/RRR2-18/2	1596.124	1595.847	173.775	0.423	422.748	0.375	17	0.114	R.VIPNFMLQGGDFTR.G
R2/RRR2-18/2	1610.475	1611.847	-1477.400	0.261	304.090	0.312	20	0.114	R.VIPNFM*LQGGDFTR.G
R2/RRR2-18/2	1612.056	1611.847	130.024	0.264	277.348	0.463	18	0.114	R.VIPNFM*LQGGDFTR.G
R2/RRR2-20/2	1268.986	1269.300	-248.312	0.410	417.397	0.360	15	0.114	R.GNGTGGESIYGEK.-
R2/RRR2-21/2	1268.600	1269.300	-1343.907	0.291	467.223	0.404	16	0.114	R.GNGTGGESIYGEK.-
R2/RRR2-20/2	1269.861	1269.300	-346.968	0.333	298.432	0.352	13	0.110	-.GNGTGGESIYGEK.-
R2/RRR2-13/2	1996.389	1995.261	64.113	0.598	1101.677	0.636	23	0.176	R.VQIANFLCPGNYAVSGGVK.G
R2/RRR2-13/3	1995.363	1995.261	51.376	0.484	1615.811	0.454	33	0.166	R.VQIANFLCPGNYAVSGGVK.G
R2/RRR2-13/2	1204.058	1204.352	-245.534	0.442	1220.076	0.394	18	0.144	R.LESALAETEIK.T
R2/RRR2-12/2	1203.659	1204.352	-1410.820	0.378	973.923	0.342	18	0.123	R.LESALAETEIK.T
R2/RRR2-13/2	1203.507	1204.352	-1537.452	0.257	926.465	0.174	17	0.104	R.LESALAETEIK.T
R2/RRR2-15/2	1595.288	1594.746	-288.469	0.538	1177.893	0.569	23	0.174	K.LAEAPYLDSVDWSK.W
R2/RRR2-15/2	1594.320	1594.746	-267.909	0.537	1057.221	0.579	22	0.165	K.LAEAPYLDSVDWSK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-15/2	1594.181	1594.746	-984.881	0.485	925.937	0.535	21	0.147	K.LAEAPYLDSVDWSK.W
R2/RRR2-15/2	1349.342	1349.601	-192.238	0.266	1019.784	0.274	16	0.111	R.GAFTVVLSGGSLIK.N
R2/RRR2-21/2	1772.231	1773.003	-1003.020	0.564	2329.758	0.541	23	0.328	R.AM*SILNSFVNDIFER.V
R2/RRR2-21/2	1772.370	1773.003	-924.466	0.569	2115.744	0.527	22	0.283	R.AM*SILNSFVNDIFER.V
R2/RRR2-21/2	1771.676	1773.003	-1317.567	0.517	1733.643	0.477	21	0.210	R.AM*SILNSFVNDIFER.V
R2/RRR2-13/2	1114.408	1115.267	-1673.340	0.355	808.161	0.586	17	0.140	R.AHAYAAAVAAAK.G
R2/RRR2-13/2	1134.004	1133.196	-170.008	0.388	720.774	0.483	14	0.126	R.DVHLGDYSAR.L
R2/RRR2-13/3	1115.191	1115.267	-68.149	0.467	1085.883	0.358	21	0.088	-.AHAYAAAVAAAK.-
R2/RRR2-13/3	1115.606	1115.267	304.584	0.472	697.343	0.322	18	0.055	-.AHAYAAAVAAAK.-
R2/RRR2-13/3	1115.017	1115.267	-224.469	0.439	695.384	0.238	18	0.049	-.AHAYAAAVAAAK.-
R2/RRR2-13/2	1589.064	1588.791	172.004	0.531	1461.566	0.457	20	0.173	R.DNVQAYWPNVIIR.Y
R2/RRR2-13/2	1589.736	1588.791	-34.936	0.549	1462.184	0.444	20	0.170	R.DNVQAYWPNVIIR.Y
R2/RRR2-14/2	1588.330	1588.791	-291.506	0.460	1477.181	0.418	20	0.168	R.DNVQAYWPNVIIR.Y
R2/RRR2-13/2	1589.319	1588.791	-298.412	0.566	1311.237	0.466	19	0.160	R.DNVQAYWPNVIIR.Y
R2/RRR2-14/2	1588.323	1588.791	-295.515	0.442	1264.116	0.471	19	0.158	R.DNVQAYWPNVIIR.Y
R2/RRR2-14/2	1808.348	1808.027	177.958	0.513	915.717	0.555	22	0.148	R.EIPLNYATFQPGTTVR.D
R2/RRR2-14/2	1589.140	1588.791	219.996	0.516	1068.463	0.490	18	0.147	R.DNVQAYWPNVIIR.Y
R2/RRR2-14/2	1808.174	1808.027	81.485	0.459	919.659	0.561	21	0.147	R.EIPLNYATFQPGTTVR.D
R2/RRR2-14/2	1807.484	1808.027	-856.190	0.447	914.091	0.527	22	0.142	R.EIPLNYATFQPGTTVR.D
R2/RRR2-14/2	1807.392	1808.027	-907.718	0.443	871.497	0.515	22	0.138	R.EIPLNYATFQPGTTVR.D
R2/RRR2-14/2	1588.405	1588.791	-243.701	0.480	1119.624	0.405	18	0.136	R.DNVQAYWPNVIIR.Y
R2/RRR2-14/2	1808.282	1808.027	141.131	0.508	435.871	0.580	17	0.127	R.EIPLNYATFQPGTTVR.D
R2/RRR2-13/2	1807.380	1808.027	-914.159	0.475	661.977	0.511	19	0.127	R.EIPLNYATFQPGTTVR.D
R2/RRR2-13/2	1807.622	1808.027	-225.187	0.480	768.247	0.474	19	0.126	R.EIPLNYATFQPGTTVR.D
R2/RRR2-13/2	1807.472	1808.027	-863.037	0.502	559.818	0.527	18	0.125	R.EIPLNYATFQPGTTVR.D
R2/RRR2-15/2	1589.776	1588.791	-9.443	0.471	1116.632	0.327	17	0.123	R.DNVQAYWPNVIIR.Y
R2/RRR2-14/2	1808.488	1808.027	255.733	0.505	523.505	0.507	18	0.123	R.EIPLNYATFQPGTTVR.D
R2/RRR2-14/2	1588.638	1588.791	-96.616	0.461	747.981	0.454	14	0.121	R.DNVQAYWPNVIIR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1588.800	1588.791	5.270	0.376	834.431	0.283	15	0.108	R.DNVQAYWPNVIIR.Y
R2/RRR2-14/3	1807.816	1808.027	-117.452	0.437	1059.571	0.351	29	0.087	R.EIPLNYATFQPGTTVR.D
R2/RRR2-14/3	1808.963	1808.027	-35.887	0.429	901.198	0.385	26	0.085	R.EIPLNYATFQPGTTVR.D
R2/RRR2-14/3	1808.114	1808.027	48.232	0.369	778.961	0.338	25	0.075	R.EIPLNYATFQPGTTVR.D
R2/RRR2-20/2	1422.997	1423.726	-1218.828	0.422	724.992	0.461	20	0.126	K.QSLAGIPLLVLGNK.I
R2/RRR2-20/2	1056.299	1056.195	99.149	0.329	922.700	0.349	13	0.118	K.SELHDLLTK.Q
R2/RRR2-19/2	1423.202	1423.726	-1073.865	0.325	431.684	0.426	16	0.111	K.QSLAGIPLLVLGNK.I
R2/RRR2-20/2	1423.779	1423.726	37.269	0.247	460.946	0.374	16	0.106	K.QSLAGIPLLVLGNK.I
R2/RRR2-8/2	1735.520	1736.004	-279.623	0.427	1623.180	0.499	20	0.202	K.SVADSLTALAWVGFLGK.D
R2/RRR2-15/3	1191.207	1190.335	-108.562	0.414	883.365	0.406	19	0.085	R.RPDYFNHIK.S
R2/RRR2-15/3	1190.524	1190.335	158.612	0.358	680.787	0.277	17	0.067	-.RPDYFNHIK.-
R2/RRR2-15/2	1143.930	1144.346	-364.828	0.533	2115.261	0.651	22	0.322	K.VAVITGAASGIGK.A
R2/RRR2-15/2	1144.229	1144.346	-103.003	0.528	2104.496	0.646	22	0.318	K.VAVITGAASGIGK.A
R2/RRR2-15/2	1143.553	1144.346	-1573.090	0.451	1942.166	0.635	22	0.284	K.VAVITGAASGIGK.A
R2/RRR2-13/2	1143.766	1144.346	-1385.786	0.421	1815.548	0.590	21	0.250	K.VAVITGAASGIGK.A
R2/RRR2-13/2	1144.108	1144.346	-208.958	0.395	1727.510	0.535	20	0.222	K.VAVITGAASGIGK.A
R2/RRR2-13/2	1143.524	1144.346	-1598.827	0.385	1640.220	0.584	20	0.221	K.VAVITGAASGIGK.A
R2/RRR2-8/1	994.516	995.113	-1610.670	0.354	799.336	0.345	12	0.597	R.DSAAVFAWK.G
R2/RRR2-8/1	994.442	995.113	-1685.710	0.267	795.282	0.306	12	0.581	R.DSAAVFAWK.G
R2/RRR2-8/1	994.465	995.113	-1662.278	0.252	758.674	0.169	11	0.502	R.DSAAVFAWK.G
R2/RRR2-9/2	994.900	995.113	-214.207	0.412	1469.428	0.441	15	0.173	R.DSAAVFAWK.G
R2/RRR2-8/2	994.405	995.113	-1722.229	0.484	1388.114	0.452	15	0.168	R.DSAAVFAWK.G
R2/RRR2-2/2	994.678	995.113	-438.897	0.348	1471.396	0.377	15	0.159	R.DSAAVFAWK.G
R2/RRR2-8/2	994.928	995.113	-186.389	0.472	1267.486	0.442	14	0.155	R.DSAAVFAWK.G
R2/RRR2-8/2	995.042	995.113	-71.688	0.479	1136.733	0.469	14	0.151	R.DSAAVFAWK.G
R2/RRR2-2/2	994.948	995.113	-166.696	0.468	1166.530	0.438	14	0.147	R.DSAAVFAWK.G
R2/RRR2-9/2	994.905	995.113	-209.406	0.451	1125.658	0.444	14	0.146	R.DSAAVFAWK.G
R2/RRR2-1/2	994.967	995.113	-147.004	0.413	1003.086	0.396	14	0.132	R.DSAAVFAWK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1762.794	1762.917	-70.063	0.418	1047.208	0.268	15	0.111	K.GM*SLQEYWWCTER.A
R2/RRR2-2/2	1762.383	1762.917	-872.899	0.324	747.331	0.265	14	0.103	K.GM*SLQEYWWCTER.A
R2/RRR2-11/2	1627.450	1625.862	-253.879	0.569	1225.778	0.552	18	0.170	K.EGLCGIAMEASYPVK.T
R2/RRR2-11/2	1139.177	1139.288	-98.193	0.453	783.727	0.359	13	0.117	-.FNVFKDNVR.-
R2/RRR2-14/2	1298.015	1298.467	-349.158	0.458	968.691	0.524	17	0.146	K.VVLNPDEVADVK.Y
R2/RRR2-14/2	1299.188	1298.467	-215.775	0.447	843.583	0.476	17	0.133	K.VVLNPDEVADVK.Y
R2/RRR2-14/2	1551.197	1550.695	-322.084	0.484	1110.128	0.296	17	0.118	R.ESELIQENYLGVR.N
R2/RRR2-14/2	1298.172	1298.467	-228.487	0.289	675.188	0.458	14	0.116	K.VVLNPDEVADVK.Y
R2/RRR2-14/2	1549.733	1550.695	-1269.894	0.355	1018.047	0.246	17	0.110	R.ESELIQENYLGVR.N
R2/RRR2-24/2	1430.224	1429.560	-235.299	0.541	1109.485	0.448	21	0.146	K.YSPAAHDVVEVNK.A
R2/RRR2-24/2	1430.123	1429.560	-306.288	0.555	1081.889	0.454	21	0.146	K.YSPAAHDVVEVNK.A
R2/RRR2-18/2	1558.788	1557.734	34.512	0.371	1140.714	0.421	18	0.140	R.TNYAQWVSAITFR.V
R2/RRR2-24/2	1429.153	1429.560	-285.250	0.511	1092.078	0.358	20	0.130	K.YSPAAHDVVEVNK.A
R2/RRR2-24/3	1429.721	1429.560	113.236	0.334	429.319	0.553	24	0.087	K.YSPAAHDVVEVNK.A
R2/RRR2-24/3	1429.332	1429.560	-160.032	0.139	369.976	0.389	22	0.064	K.YSPAAHDVVEVNK.A
R2/RRR2-8/3	1801.019	1800.992	15.145	0.482	1590.546	0.468	29	0.168	K.VTSGLAEGAAVIQEALDR.M
R2/RRR2-8/3	1903.477	1904.153	-883.163	0.257	1584.509	0.132	30	0.083	R.SALDYLELQPDLSALVR.G
R2/RRR2-19/3	1698.387	1698.904	-896.165	0.479	1892.311	0.411	29	0.194	R.ILVDHSIVEGFAQGGR.T
R2/RRR2-19/2	1831.251	1832.090	-1007.346	0.479	628.146	0.498	22	0.126	R.VYGSLVPVLDGENLSIR.I
R2/RRR2-14/2	1312.503	1312.540	-28.322	0.477	2248.000	0.542	22	0.314	K.LEAPVVIVTGASR.G
R2/RRR2-14/2	1313.485	1312.540	-42.563	0.529	1925.939	0.567	22	0.265	K.LEAPVVIVTGASR.G
R2/RRR2-14/2	1311.982	1312.540	-1191.029	0.468	1655.449	0.517	20	0.211	K.LEAPVVIVTGASR.G
R2/RRR2-8/2	1091.906	1092.230	-298.001	0.415	1157.840	0.345	14	0.132	K.SLFQLQAER.I
R2/RRR2-8/2	1091.988	1092.230	-222.520	0.393	967.305	0.181	13	0.104	K.SLFQLQAER.I
R2/RRR2-15/3	1567.552	1567.772	-141.000	0.453	1388.749	0.368	28	0.113	R.LPLRDVLDDAGVGAR.V
R2/RRR2-15/3	1567.265	1567.772	-964.384	0.461	1292.162	0.392	27	0.110	R.LPLRDVLDDAGVGAR.V
R2/RRR2-9/2	1088.697	1088.153	-420.562	0.311	976.770	0.128	16	0.100	R.DVLDDAGVGAR.V
R2/RRR2-15/3	1567.734	1567.772	-24.071	0.435	1190.495	0.313	24	0.088	R.LPLRDVLDDAGVGAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/3	1568.018	1567.772	157.595	0.217	666.430	0.157	21	0.061	-.LPLRDVLDDAGVGAR.-
R2/RRR2-20/1	1219.600	1220.357	-1445.025	0.167	820.893	0.253	15	0.620	K.LNPAADAGSIYK.T
R2/RRR2-21/1	1219.661	1220.357	-1394.659	0.194	640.709	0.256	15	0.414	K.LNPAADAGSIYK.T
R2/RRR2-20/1	1219.646	1220.357	-1407.024	0.124	561.660	0.217	13	0.352	K.LNPAADAGSIYK.T
R2/RRR2-20/1	1219.669	1220.357	-1387.723	0.211	586.176	0.181	14	0.349	K.LNPAADAGSIYK.T
R2/RRR2-21/1	1219.646	1220.357	-1407.225	0.217	528.767	0.246	14	0.322	K.LNPAADAGSIYK.T
R2/RRR2-20/2	1220.088	1220.357	-221.234	0.483	891.878	0.528	20	0.146	K.LNPAADAGSIYK.T
R2/RRR2-20/2	1220.034	1220.357	-265.300	0.468	895.716	0.529	20	0.146	K.LNPAADAGSIYK.T
R2/RRR2-20/2	1219.935	1220.357	-346.314	0.447	811.387	0.553	19	0.143	K.LNPAADAGSIYK.T
R2/RRR2-21/2	1219.931	1220.357	-350.129	0.447	655.572	0.512	18	0.132	K.LNPAADAGSIYK.T
R2/RRR2-19/2	1220.057	1220.357	-246.127	0.406	712.847	0.499	18	0.131	K.LNPAADAGSIYK.T
R2/RRR2-21/2	1219.391	1220.357	-1616.830	0.376	546.211	0.513	17	0.125	K.LNPAADAGSIYK.T
R2/RRR2-21/2	1219.422	1220.357	-1591.688	0.356	759.330	0.405	19	0.122	K.LNPAADAGSIYK.T
R2/RRR2-18/2	1219.884	1220.357	-388.282	0.375	498.990	0.417	16	0.118	K.LNPAADAGSIYK.T
R2/RRR2-13/2	1241.164	1240.476	-252.299	0.519	1267.396	0.501	19	0.168	R.DVAWAPVLGLAK.A
R2/RRR2-13/2	1463.818	1463.568	171.666	0.438	1270.117	0.444	19	0.155	K.YGTILASCSYDGR.V
R2/RRR2-13/2	1240.027	1240.476	-363.116	0.335	1139.714	0.506	17	0.151	R.DVAWAPVLGLAK.A
R2/RRR2-13/2	1240.126	1240.476	-283.117	0.370	952.123	0.517	16	0.140	R.DVAWAPVLGLAK.A
R2/RRR2-13/2	1463.018	1463.568	-1062.717	0.374	853.504	0.236	16	0.104	K.YGTILASCSYDGR.V
R2/RRR2-11/2	1192.131	1192.303	-145.389	0.447	890.439	0.528	18	0.145	K.VLAPYSAEDAR.G
R2/RRR2-11/2	1191.979	1192.303	-272.571	0.444	953.741	0.502	18	0.144	K.VLAPYSAEDAR.G
R2/RRR2-11/2	1770.447	1770.046	227.549	0.473	758.812	0.508	18	0.129	K.SNYMSAGQISVPIVFR.G
R2/RRR2-11/2	1770.297	1770.046	142.569	0.460	768.860	0.441	19	0.122	K.SNYMSAGQISVPIVFR.G
R2/RRR2-11/2	1769.377	1770.046	-946.250	0.376	666.270	0.453	17	0.117	K.SNYMSAGQISVPIVFR.G
R2/RRR2-11/2	1191.295	1192.303	-1691.242	0.268	934.642	0.309	17	0.114	K.VLAPYSAEDAR.G
R2/RRR2-18/2	1259.503	1260.376	-1491.750	0.448	1224.327	0.424	18	0.148	R.LGGGQQEVCGVR.E
R2/RRR2-18/2	1260.067	1260.376	-245.794	0.402	1086.581	0.456	16	0.141	R.LGGGQQEVCGVR.E
R2/RRR2-18/2	1259.271	1260.376	-1676.564	0.342	1171.355	0.393	16	0.137	R.LGGGQQEVCGVR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1919.245	1918.182	32.879	0.523	809.985	0.532	20	0.136	R.AENIWLATEGVYLPVNK.S
R2/RRR2-14/2	1441.338	1441.698	-250.559	0.503	1290.249	0.434	22	0.156	K.VTPTVLQSAGLNLK.Q
R2/RRR2-14/2	1441.382	1441.698	-219.547	0.463	1129.628	0.419	22	0.142	K.VTPTVLQSAGLNLK.Q
R2/RRR2-14/2	1441.475	1441.698	-155.489	0.517	1048.307	0.442	22	0.141	K.VTPTVLQSAGLNLK.Q
R2/RRR2-14/2	1102.955	1103.296	-310.334	0.239	829.197	0.291	15	0.107	K.VAVSFTHTIK.A
R2/RRR2-12/2	1306.009	1306.490	-368.770	0.501	1554.772	0.362	20	0.167	K.AFGAELVLTDAAK.G
R2/RRR2-12/2	1114.378	1115.310	-1738.867	0.311	732.501	0.299	14	0.106	K.IQGIGAGFVPR.N
R2/RRR2-4/2	1520.443	1520.755	-206.117	0.359	2162.983	0.275	21	0.225	R.TVEQLGYIAGLSLR.S
R2/RRR2-4/2	1612.449	1611.777	-203.848	0.459	821.138	0.514	17	0.134	K.FSTGSWETLETKPK.E
R2/RRR2-22/2	1540.160	1540.702	-1004.003	0.386	648.524	0.421	17	0.116	K.EAPAVIESYYNKR.I
R2/RRR2-22/3	1580.432	1580.789	-226.778	0.319	979.609	0.414	24	0.091	K.RFDM*DPPVGPFGTK.E
R2/RRR2-22/3	1581.175	1580.789	244.785	0.360	926.093	0.250	24	0.068	K.RFDM*DPPVGPFGTK.E
R2/RRR2-3/2	1011.240	1011.243	-3.585	0.467	638.099	0.428	15	0.123	R.LIGASLPAIR.A
R2/RRR2-3/2	1158.301	1159.280	-1713.731	0.448	878.897	0.354	16	0.120	R.RFPAAPTEGGR.L
R2/RRR2-3/2	1010.939	1011.243	-302.248	0.393	642.309	0.416	15	0.120	R.LIGASLPAIR.A
R2/RRR2-3/2	1158.374	1159.280	-1650.416	0.433	832.724	0.345	15	0.116	R.RFPAAPTEGGR.L
R2/RRR2-3/2	1158.677	1159.280	-1387.713	0.478	777.780	0.337	16	0.116	R.RFPAAPTEGGR.L
R2/RRR2-17/2	1294.363	1294.485	-94.461	0.454	769.658	0.422	16	0.125	R.TDINQALHLLR.E
R2/RRR2-17/2	923.908	924.033	-135.384	0.312	260.493	0.336	12	0.117	R.QYSVLDAK.V
R2/RRR2-17/2	923.864	924.033	-183.895	0.333	214.996	0.496	11	0.116	-.QYSVLDAK.-
R2/RRR2-17/2	1294.247	1294.485	-184.245	0.446	617.126	0.332	14	0.111	R.TDINQALHLLR.E
R2/RRR2-17/2	1293.643	1294.485	-1428.058	0.433	427.510	0.307	12	0.101	-.TDINQALHLLR.-
R2/RRR2-17/2	923.789	924.033	-264.360	0.252	142.880	0.337	9	0.084	-.QYSVLDAK.-
R2/RRR2-13/2	1260.887	1261.452	-1245.218	0.443	923.940	0.563	20	0.149	R.AFTVGIGGPVGTGK.T
R2/RRR2-13/2	1443.612	1443.626	-9.636	0.347	919.961	0.375	15	0.119	K.YSLAAVTNDIFTK.E
R2/RRR2-13/2	1443.854	1443.626	158.521	0.336	605.827	0.369	14	0.108	K.YSLAAVTNDIFTK.E
R2/RRR2-16/2	1382.976	1382.549	309.717	0.430	1159.570	0.402	17	0.139	R.IPTGELWAGNPAR.F
R2/RRR2-14/3	1461.307	1461.706	-273.836	0.411	1372.576	0.249	23	0.086	R.KLTNEEIM*EIPK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/3	1461.105	1461.706	-1099.109	0.447	1026.362	0.096	22	0.055	-.KLTNEEIM*EIPK.-
R2/RRR2-20/1	445.531	445.492	88.214	-0.402	36.006	0.358	4	0.000	P.AAAAAA.A
R2/RRR2-17/2	1636.310	1634.686	-230.356	0.527	2257.209	0.547	26	0.316	R.ASDFDSLGSDGGPGPVR.S
R2/RRR2-17/2	1636.218	1634.686	-286.566	0.553	2002.983	0.551	25	0.271	R.ASDFDSLGSDGGPGPVR.S
R2/RRR2-17/2	1636.010	1634.686	199.025	0.499	1406.866	0.557	22	0.189	R.ASDFDSLGSDGGPGPVR.S
R2/RRR2-16/2	1642.504	1643.908	-1468.237	0.345	1049.741	0.472	21	0.139	K.NLVAPVIGEANLAAYK.A
R2/RRR2-16/2	1448.456	1448.691	-162.854	0.430	525.182	0.502	16	0.123	K.INPSFVYPLLER.F
R2/RRR2-14/2	1304.083	1304.475	-301.247	0.289	805.068	0.447	17	0.119	K.ANTIVLSGLSGSGK.T
R2/RRR2-14/3	1510.672	1510.769	-64.289	0.441	706.213	0.476	28	0.090	K.VKPVHVVDVPGHAR.L
R2/RRR2-11/2	1557.365	1558.671	-1484.901	0.359	960.688	0.498	18	0.137	R.GCSANVFLDNAAYR.Q
R2/RRR2-11/2	1557.241	1558.671	-1565.138	0.356	798.966	0.493	17	0.127	R.GCSANVFLDNAAYR.Q
R2/RRR2-11/2	1314.091	1314.477	-294.294	0.335	335.555	0.594	14	0.122	R.QHAFWVPVSSR.Y
R2/RRR2-11/2	1558.429	1558.671	-155.762	0.413	517.258	0.487	18	0.121	R.GCSANVFLDNAAYR.Q
R2/RRR2-11/2	1314.242	1314.477	-179.299	0.198	261.597	0.519	13	0.106	R.QHAFWVPVSSR.Y
R2/RRR2-11/2	1313.496	1314.477	-1512.738	0.131	137.911	0.390	10	0.099	-.QHAFWVPVSSR.-
R2/RRR2-12/3	1553.388	1553.788	-258.307	0.414	1594.409	0.406	25	0.148	R.LPLRDVLADTGIGGR.A
R2/RRR2-17/2	1225.008	1224.345	-276.016	0.329	680.004	0.483	16	0.122	R.YEVEVTVASAR.D
R2/RRR2-20/3	1553.579	1553.788	-135.215	0.429	1468.163	0.319	24	0.110	R.LPLRDVLADTGIGGR.A
R2/RRR2-14/3	1553.171	1553.788	-1044.358	0.371	1281.029	0.284	24	0.089	R.LPLRDVLADTGIGGR.A
R2/RRR2-19/3	1553.988	1553.788	129.078	0.394	424.150	0.437	23	0.080	-.LPLRDVLADTGIGGR.-
R2/RRR2-14/3	1554.017	1553.788	147.275	0.380	760.104	0.361	21	0.078	-.LPLRDVLADTGIGGR.-
R2/RRR2-20/3	1553.650	1553.788	-89.462	0.347	636.004	0.291	22	0.071	-.LPLRDVLADTGIGGR.-
R2/RRR2-19/3	1553.260	1553.788	-986.952	0.382	716.517	0.285	23	0.069	-.LPLRDVLADTGIGGR.-
R2/RRR2-7/2	1065.172	1065.334	-152.373	0.378	607.706	0.500	17	0.126	K.AVKPVLVGGPK.M
R2/RRR2-7/2	1065.923	1065.334	-387.048	0.319	523.957	0.513	16	0.121	K.AVKPVLVGGPK.M
R2/RRR2-7/2	1065.056	1065.334	-261.714	0.318	534.446	0.495	16	0.120	K.AVKPVLVGGPK.M
R2/RRR2-7/2	1225.817	1226.452	-1338.174	0.356	703.879	0.422	13	0.117	R.VNVLFQHIQK.M
R2/RRR2-6/2	1064.404	1065.334	-1819.128	0.216	442.553	0.274	14	0.105	K.AVKPVLVGGPK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1183.165	1183.466	-255.147	0.395	621.542	0.475	13	0.120	K.TPIGILNITLK.Q
R2/RRR2-17/2	1182.882	1183.466	-1342.652	0.207	376.784	0.323	10	0.098	-.TPIGILNITLK.-
R2/RRR2-17/3	1409.532	1409.570	-26.686	0.429	1047.702	0.244	23	0.069	-.TSRPSYAVIDTAK.-
R2/RRR2-17/3	1409.430	1409.570	-99.659	0.450	728.186	0.281	19	0.056	-.TSRPSYAVIDTAK.-
R2/RRR2-7/2	1280.253	1280.538	-223.270	0.350	1175.246	0.466	18	0.148	R.GLPTLVLIGPDGK.T
R2/RRR2-6/2	1280.216	1280.538	-252.254	0.388	989.647	0.538	18	0.147	R.GLPTLVLIGPDGK.T
R2/RRR2-6/2	1280.138	1280.538	-313.864	0.360	1000.529	0.470	17	0.136	R.GLPTLVLIGPDGK.T
R2/RRR2-7/2	1516.174	1516.639	-307.801	0.316	1318.039	0.302	20	0.134	K.DNQTVQSVLGTPTR.D
R2/RRR2-7/2	1516.231	1516.639	-269.675	0.321	1167.990	0.322	19	0.127	K.DNQTVQSVLGTPTR.D
R2/RRR2-6/2	1280.393	1280.538	-113.660	0.359	794.603	0.465	16	0.125	R.GLPTLVLIGPDGK.T
R2/RRR2-6/2	1515.762	1516.639	-1241.974	0.321	882.599	0.407	17	0.121	K.DNQTVQSVLGTPTR.D
R2/RRR2-7/2	1279.559	1280.538	-1551.903	0.274	776.787	0.346	14	0.110	R.GLPTLVLIGPDGK.T
R2/RRR2-7/2	1279.663	1280.538	-1470.067	0.281	654.019	0.352	15	0.109	R.GLPTLVLIGPDGK.T
R2/RRR2-4/2	1280.423	1280.538	-90.708	0.339	625.874	0.277	14	0.105	R.GLPTLVLIGPDGK.T
R2/RRR2-7/2	1517.640	1516.639	0.516	0.409	601.484	0.260	16	0.103	K.DNQTVQSVLGTPTR.D
R2/RRR2-16/2	1591.867	1592.754	-1188.732	0.448	924.237	0.520	24	0.143	-.M*DGAASVPSSNEVALK.Q
R2/RRR2-16/2	1592.205	1592.754	-975.781	0.439	929.363	0.477	25	0.138	-.M*DGAASVPSSNEVALK.Q
R2/RRR2-16/2	1592.282	1592.754	-297.301	0.469	831.010	0.498	24	0.136	-.M*DGAASVPSSNEVALK.Q
R2/RRR2-16/2	1951.552	1951.212	175.001	0.489	849.676	0.510	20	0.134	K.QPVSVLIEANSNFQLYK.Q
R2/RRR2-15/2	1592.264	1592.754	-308.608	0.451	769.318	0.472	23	0.130	-.M*DGAASVPSSNEVALK.Q
R2/RRR2-16/2	1952.060	1951.212	-77.813	0.457	424.057	0.451	16	0.111	K.QPVSVLIEANSNFQLYK.Q
R2/RRR2-16/2	1576.069	1576.754	-1072.641	0.264	319.659	0.350	17	0.108	-.MDGAASVPSSNEVALK.Q
R2/RRR2-7/2	1550.132	1550.781	-1067.130	0.489	1227.067	0.418	20	0.148	R.LLSSTNQPSFLSKK.D
R2/RRR2-20/1	1186.703	1187.411	-1443.916	0.217	738.417	0.346	14	0.566	K.AVVVLGSSEVVK.G
R2/RRR2-20/1	1186.697	1187.411	-1448.669	0.207	713.344	0.340	14	0.534	K.AVVVLGSSEVVK.G
R2/RRR2-20/2	1336.244	1336.476	-173.873	0.494	1361.716	0.530	19	0.182	R.AVVVHADPDDLGK.G
R2/RRR2-10/2	1397.230	1397.473	-174.083	0.389	928.709	0.475	18	0.134	K.DGTGTLTVFTNDR.G
R2/RRR2-10/3	1884.844	1885.236	-208.823	0.416	1214.890	0.385	27	0.104	R.QAIPFLESLVVADVAALK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1884.658	1885.236	-839.847	0.353	1264.629	0.360	27	0.103	R.QAIPFLESLVVADVAALK.D
R2/RRR2-17/2	991.842	992.111	-271.343	0.476	1176.876	0.315	13	0.130	K.FAEEVLQR.E
R2/RRR2-17/2	991.867	992.111	-246.401	0.558	1276.807	0.271	13	0.126	K.FAEEVLQR.E
R2/RRR2-17/2	991.597	992.111	-1531.216	0.481	1197.931	0.252	13	0.122	K.FAEEVLQR.E
R2/RRR2-17/2	1278.221	1278.399	-140.194	0.485	720.114	0.377	16	0.116	-.RLEDAGYAVGAR.-
R2/RRR2-17/2	1278.040	1278.399	-282.286	0.491	698.910	0.369	16	0.114	-.RLEDAGYAVGAR.-
R2/RRR2-17/2	1278.025	1278.399	-294.169	0.384	717.059	0.335	16	0.112	-.RLEDAGYAVGAR.-
R2/RRR2-17/2	1641.111	1641.861	-1069.768	0.455	1336.008	0.317	20	0.138	R.M*EPVSYDQALICAK.E
R2/RRR2-17/2	1063.083	1063.181	-91.977	0.383	933.316	0.236	16	0.109	K.CVVTGDGAVGK.T
R2/RRR2-17/2	1063.223	1063.181	39.889	0.299	937.940	0.182	15	0.105	-.CVVTGDGAVGK.-
R2/RRR2-2/2	1789.360	1789.087	152.748	0.563	2118.268	0.401	24	0.243	R.M*LAISALNTLLQGSPDK.A
R2/RRR2-2/2	1789.070	1789.087	-9.488	0.471	1451.128	0.429	20	0.164	R.M*LAISALNTLLQGSPDK.A
R2/RRR2-2/2	1789.308	1789.087	123.603	0.512	1543.746	0.354	21	0.157	R.M*LAISALNTLLQGSPDK.A
R2/RRR2-2/2	1262.154	1262.354	-158.858	0.377	1257.205	0.426	18	0.150	R.EPAAFSGAVGEAR.A
R2/RRR2-13/2	1366.168	1365.514	-253.680	0.374	748.496	0.534	13	0.128	K.EPYTATIVSVER.L
R2/RRR2-13/2	1366.228	1365.514	-209.668	0.387	940.853	0.389	15	0.123	K.EPYTATIVSVER.L
R2/RRR2-13/2	1365.131	1365.514	-281.138	0.290	838.523	0.404	14	0.117	K.EPYTATIVSVER.L
R2/RRR2-13/2	911.144	911.037	117.296	0.340	893.566	0.285	13	0.113	R.LYSIASTR.Y
R2/RRR2-5/2	1780.497	1781.045	-871.987	0.430	1930.794	0.346	21	0.207	K.IVFQALYNTVNEIGAK.A
R2/RRR2-5/2	1176.334	1176.302	26.686	0.351	818.543	0.339	13	0.115	K.YPFYSTLER.L
R2/RRR2-10/2	1445.235	1445.642	-282.415	0.444	958.089	0.468	18	0.137	R.ENIDPSVIGPIYK.Y
R2/RRR2-10/3	1744.863	1744.845	10.335	0.487	1068.782	0.470	27	0.110	R.THDVGGHFAAYEQPSK.L
R2/RRR2-4/2	1144.164	1143.325	-141.425	0.351	858.918	0.097	12	0.090	-.RRLSVEQVR.-
R2/RRR2-3/2	1143.542	1143.325	190.622	0.333	744.596	0.109	11	0.081	-.RRLSVEQVR.-
R2/RRR2-15/3	1367.305	1366.598	-214.840	0.315	1034.558	0.181	24	0.061	K.ARLARDLGLQPR.Q
R2/RRR2-11/2	1808.500	1809.098	-886.445	0.489	1197.669	0.545	23	0.168	K.LETYSPGFALALISLGR.N
R2/RRR2-11/2	1985.464	1986.294	-924.603	0.441	843.388	0.494	22	0.130	R.NEGLAQLPFLTLGGCLPGK.I
R2/RRR2-14/2	1440.872	1441.698	-1270.836	0.415	902.144	0.436	21	0.130	K.ITPTVLQSAGLNVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1440.650	1441.698	-1425.538	0.367	761.210	0.478	19	0.126	K.ITPTVLQSAGLNVK.Q
R2/RRR2-14/2	1440.728	1441.698	-1371.753	0.349	727.091	0.478	19	0.124	K.ITPTVLQSAGLNVK.Q
R2/RRR2-15/3	1897.399	1897.081	167.922	0.508	1379.773	0.459	29	0.136	K.DPNRPFPSGQNETPLVK.W
R2/RRR2-16/2	964.912	965.045	-138.767	0.361	863.813	0.337	15	0.117	K.GGYSAISGPR.V
R2/RRR2-15/2	965.334	965.045	300.010	0.284	363.217	0.325	13	0.107	-.GGYSAISGPR.-
R2/RRR2-15/3	1896.232	1897.081	-977.869	0.508	582.843	0.415	29	0.084	K.DPNRPFPSGQNETPLVK.W
R2/RRR2-15/3	1896.933	1897.081	-78.145	0.392	891.421	0.371	28	0.083	K.DPNRPFPSGQNETPLVK.W
R2/RRR2-14/2	1705.415	1705.894	-281.328	0.557	2290.714	0.483	25	0.306	R.YVFTGASWVTNAFNK.V
R2/RRR2-3/3	1585.970	1584.799	108.063	0.395	1490.113	0.383	29	0.129	R.LAGDKLVDGEGALAVR.A
R2/RRR2-3/2	1620.337	1618.847	303.261	0.394	641.075	0.418	17	0.112	R.TVATEILAAPSSAVCK.R
R2/RRR2-12/2	784.865	784.970	-134.175	0.461	875.275	0.309	13	0.118	R.VGILGLGR.I
R2/RRR2-12/2	784.973	784.970	3.414	0.464	892.041	0.305	13	0.118	R.VGILGLGR.I
R2/RRR2-12/2	784.993	784.970	30.085	0.488	863.027	0.281	13	0.115	R.VGILGLGR.I
R2/RRR2-11/2	1650.381	1650.944	-949.933	0.334	892.231	0.340	17	0.112	K.VIDALGPEGVLINIAR.G
R2/RRR2-13/2	1912.447	1912.269	93.559	0.498	1351.163	0.409	21	0.151	R.AFGMIAGGSGITPMFQVAR.A
R2/RRR2-13/2	1228.348	1228.377	-24.083	0.429	985.059	0.299	15	0.115	R.AILENPNDITK.V
R2/RRR2-3/3	1747.761	1747.868	-61.195	0.360	688.705	0.459	24	0.085	K.ASEM*LAYAHDTQHEK.I
R2/RRR2-3/3	1747.422	1747.868	-255.643	0.386	541.120	0.483	23	0.085	K.ASEM*LAYAHDTQHEK.I
R2/RRR2-16/2	1595.477	1593.934	-287.053	0.459	624.471	0.452	19	0.122	K.IILITPPPIYEPAR.I
R2/RRR2-16/2	1593.992	1593.934	36.131	0.352	416.474	0.412	15	0.110	K.IILITPPPIYEPAR.I
R2/RRR2-16/2	1593.512	1593.934	-265.356	0.316	444.673	0.359	15	0.107	K.IILITPPPIYEPAR.I
R2/RRR2-16/3	1978.061	1978.157	-48.634	0.519	760.195	0.450	24	0.089	K.QVHQHVPLDEYQTNLR.A
R2/RRR2-7/2	958.172	958.054	123.359	0.456	1245.938	0.262	14	0.125	K.DLAGGLQQR.R
R2/RRR2-7/2	958.014	958.054	-41.742	0.449	1206.903	0.265	14	0.123	K.DLAGGLQQR.R
R2/RRR2-3/3	1640.717	1641.680	-1200.004	0.538	2187.289	0.516	30	0.281	R.FHEDEHGEVVAESR.R
R2/RRR2-3/3	1641.650	1641.680	-18.475	0.516	1667.108	0.461	26	0.172	R.FHEDEHGEVVAESR.R
R2/RRR2-14/2	993.784	994.088	-307.157	0.355	769.038	0.403	13	0.123	K.HFSVNAYR.V
R2/RRR2-14/2	994.144	994.088	56.146	0.425	636.026	0.348	13	0.120	K.HFSVNAYR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	993.987	994.088	-101.635	0.368	618.454	0.355	13	0.118	K.HFSVNAYR.V
R2/RRR2-23/2	994.059	994.088	-29.943	0.403	636.554	0.331	13	0.118	K.HFSVNAYR.V
R2/RRR2-23/2	993.943	994.088	-146.601	0.379	519.667	0.339	12	0.117	K.HFSVNAYR.V
R2/RRR2-23/2	994.003	994.088	-86.113	0.408	452.026	0.274	11	0.111	-.HFSVNAYR.-
R2/RRR2-13/2	993.812	994.088	-278.443	0.317	455.006	0.321	11	0.111	-.HFSVNAYR.-
R2/RRR2-13/2	993.334	994.088	-1771.357	0.297	387.890	0.308	10	0.107	-.HFSVNAYR.-
R2/RRR2-14/3	1297.662	1296.548	88.056	0.477	1069.510	0.440	24	0.104	K.HITGGMMGGHAVK.L
R2/RRR2-13/3	1296.272	1296.548	-213.720	0.429	954.313	0.469	22	0.103	K.HITGGMMGGHAVK.L
R2/RRR2-14/3	1296.770	1296.548	171.440	0.408	1311.141	0.356	26	0.103	K.HITGGMMGGHAVK.L
R2/RRR2-13/3	1296.284	1296.548	-204.368	0.405	798.170	0.470	21	0.096	K.HITGGMMGGHAVK.L
R2/RRR2-23/3	1328.265	1328.547	-213.106	0.388	471.573	0.388	19	0.081	K.HITGGM*M*GGHAVK.L
R2/RRR2-23/3	1295.977	1296.548	-1215.716	0.314	463.876	0.383	20	0.077	-.HITGGMMGGHAVK.-
R2/RRR2-23/3	1295.801	1296.548	-1352.084	0.329	793.569	0.267	21	0.071	K.HITGGMMGGHAVK.L
R2/RRR2-8/2	1386.514	1385.500	10.101	0.511	1274.451	0.455	17	0.160	K.FLENFCGDQVR.F
R2/RRR2-8/2	1022.995	1023.125	-127.058	0.471	882.762	0.348	14	0.121	K.SGNFELVTR.E
R2/RRR2-8/2	1023.027	1023.125	-95.339	0.444	860.530	0.322	14	0.118	K.SGNFELVTR.E
R2/RRR2-8/2	1022.468	1023.125	-1625.147	0.409	857.546	0.297	14	0.114	-.SGNFELVTR.-
R2/RRR2-11/2	1554.182	1554.770	-1024.723	0.431	1111.159	0.454	21	0.145	R.VLTDVGDVPIQEIR.D
R2/RRR2-11/2	1101.337	1101.322	14.384	0.429	905.363	0.476	17	0.138	R.VIDASLTLIR.E
R2/RRR2-11/2	1101.038	1101.322	-258.610	0.290	459.117	0.269	14	0.106	-.VIDASLTLIR.-
R2/RRR2-26/2	1304.051	1304.437	-297.029	0.573	2091.815	0.565	23	0.289	K.NVAAGAAGGPYISR.A
R2/RRR2-26/2	1305.061	1304.437	-288.825	0.581	2046.782	0.574	23	0.284	K.NVAAGAAGGPYISR.A
R2/RRR2-25/2	1303.894	1304.437	-1186.774	0.461	2135.957	0.513	23	0.281	K.NVAAGAAGGPYISR.A
R2/RRR2-25/2	1304.030	1304.437	-313.183	0.468	1992.633	0.550	22	0.268	K.NVAAGAAGGPYISR.A
R2/RRR2-26/2	1304.124	1304.437	-240.870	0.564	1871.932	0.573	22	0.255	K.NVAAGAAGGPYISR.A
R2/RRR2-25/2	1303.394	1304.437	-1572.088	0.456	1887.194	0.498	22	0.237	K.NVAAGAAGGPYISR.A
R2/RRR2-4/2	1464.565	1464.649	-57.066	0.435	1391.699	0.544	20	0.186	R.LPPISADGDVPNLR.A
R2/RRR2-4/2	1464.254	1464.649	-270.552	0.448	1263.949	0.610	19	0.185	R.LPPISADGDVPNLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-4/2	1118.836	1119.295	-411.969	0.315	1461.216	0.151	15	0.123	R.VFVQEVLER.E
R2/RRR2-4/2	1118.782	1119.295	-1357.200	0.381	1125.849	0.180	15	0.112	-.VFVQEVLER.-
R2/RRR2-14/3	1570.811	1570.729	51.972	0.470	2115.010	0.525	32	0.269	R.SPSGVIHLTDTSVTR.F
R2/RRR2-14/3	1570.795	1570.729	42.034	0.453	1332.219	0.519	31	0.144	R.SPSGVIHLTDTSVTR.F
R2/RRR2-13/3	1570.815	1570.729	54.427	0.335	1096.337	0.424	26	0.102	R.SPSGVIHLTDTSVTR.F
R2/RRR2-13/3	1571.745	1570.729	9.603	0.360	943.962	0.428	25	0.094	R.SPSGVIHLTDTSVTR.F
R2/RRR2-12/2	1221.237	1221.345	-88.186	0.432	1148.096	0.427	18	0.143	K.VFGSPTSAEVAR.V
R2/RRR2-12/2	1441.302	1441.572	-188.128	0.451	892.212	0.515	21	0.141	R.QGNPDLIGTGALER.A
R2/RRR2-12/2	1440.672	1441.572	-1322.855	0.395	927.686	0.480	21	0.136	R.QGNPDLIGTGALER.A
R2/RRR2-12/2	1220.470	1221.345	-1540.964	0.375	1036.454	0.423	19	0.135	K.VFGSPTSAEVAR.V
R2/RRR2-12/2	1441.459	1441.572	-78.621	0.423	678.516	0.496	20	0.128	R.QGNPDLIGTGALER.A
R2/RRR2-12/2	1220.980	1221.345	-299.589	0.457	907.108	0.397	18	0.127	K.VFGSPTSAEVAR.V
R2/RRR2-18/2	1588.533	1587.755	-140.170	0.522	1930.582	0.615	25	0.277	K.LAFGSLGDSFSATSVK.A
R2/RRR2-18/2	1587.246	1587.755	-954.087	0.479	1985.754	0.566	25	0.271	K.LAFGSLGDSFSATSVK.A
R2/RRR2-19/2	1587.345	1587.755	-259.368	0.495	1976.087	0.560	25	0.268	K.LAFGSLGDSFSATSVK.A
R2/RRR2-19/2	1588.226	1587.755	297.058	0.518	1945.902	0.566	25	0.265	K.LAFGSLGDSFSATSVK.A
R2/RRR2-19/2	1588.164	1587.755	258.138	0.532	1676.936	0.587	24	0.230	K.LAFGSLGDSFSATSVK.A
R2/RRR2-18/2	1586.712	1587.755	-1291.613	0.379	1724.908	0.513	24	0.216	K.LAFGSLGDSFSATSVK.A
R2/RRR2-13/2	1293.782	1293.408	289.997	0.428	1076.052	0.394	17	0.135	K.FYFNPGDTGFK.A
R2/RRR2-13/2	1293.802	1293.408	305.607	0.427	847.289	0.412	16	0.126	K.FYFNPGDTGFK.A
R2/RRR2-13/2	1293.932	1293.408	-368.617	0.449	813.489	0.397	16	0.123	K.FYFNPGDTGFK.A
R2/RRR2-13/2	1328.129	1328.412	-213.470	0.378	546.449	0.455	16	0.118	K.SHIPDGPGYQEK.F
R2/RRR2-13/2	1328.791	1328.412	286.135	0.352	508.203	0.346	16	0.111	K.SHIPDGPGYQEK.F
R2/RRR2-17/2	1292.815	1293.408	-1235.773	0.246	630.475	0.236	14	0.103	K.FYFNPGDTGFK.A
R2/RRR2-7/2	1369.385	1369.635	-182.898	0.429	650.654	0.554	19	0.136	K.QQQILLATQVVK.M
R2/RRR2-7/2	1369.119	1369.635	-1110.830	0.417	445.298	0.511	17	0.125	K.QQQILLATQVVK.M
R2/RRR2-7/2	1368.625	1369.635	-1472.916	0.308	250.934	0.436	14	0.113	K.QQQILLATQVVK.M
R2/RRR2-7/2	977.956	978.081	-127.964	0.417	1002.951	0.161	14	0.106	R.FQELSPEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	978.002	978.081	-81.012	0.410	992.848	0.160	14	0.106	R.FQELSPEK.L
R2/RRR2-21/2	1505.011	1505.698	-1124.098	0.382	1506.827	0.379	20	0.164	K.ALELFLNAGNDLSK.S
R2/RRR2-15/2	995.034	995.111	-77.349	0.386	1095.698	0.305	12	0.123	R.YDLVDLTR.Q
R2/RRR2-17/2	1505.206	1505.698	-327.695	0.320	329.340	0.328	14	0.106	K.ALELFLNAGNDLSK.S
R2/RRR2-7/2	1701.356	1699.974	225.779	0.505	1158.865	0.558	18	0.164	K.LALQGLNALLQQSTTK.T
R2/RRR2-7/2	1584.436	1583.770	-211.238	0.461	694.115	0.378	15	0.113	K.HNYLVLDVEDIPR.V
R2/RRR2-7/2	1584.325	1583.770	-281.346	0.432	402.037	0.324	13	0.105	K.HNYLVLDVEDIPR.V
R2/RRR2-7/2	1335.048	1334.458	-307.925	0.514	1023.720	0.460	15	0.140	K.ASSFLLDDFYR.T
R2/RRR2-7/2	1335.075	1334.458	-287.651	0.464	986.527	0.404	15	0.129	K.ASSFLLDDFYR.T
R2/RRR2-7/2	1891.699	1892.996	-1217.868	0.432	457.256	0.615	19	0.128	R.GSVPSNFDCDYAYALGR.I
R2/RRR2-7/2	1334.900	1334.458	332.244	0.401	1140.713	0.303	15	0.123	K.ASSFLLDDFYR.T
R2/RRR2-8/2	816.599	815.981	-468.562	0.424	838.027	0.296	13	0.112	-.SGLLALNK.-
R2/RRR2-9/3	1461.684	1461.774	-61.501	0.411	886.120	0.501	27	0.102	R.APLIKPSPLTAQPK.H
R2/RRR2-9/3	1461.003	1461.774	-1215.540	0.385	593.975	0.490	23	0.089	R.APLIKPSPLTAQPK.H
R2/RRR2-9/3	1462.059	1461.774	195.646	0.323	544.010	0.336	23	0.073	R.APLIKPSPLTAQPK.H
R2/RRR2-3/2	1431.484	1431.614	-90.459	0.367	1460.844	0.342	19	0.153	K.LVDNCAGLSLVNR.F
R2/RRR2-3/3	1165.427	1165.367	51.612	0.476	1163.472	0.342	19	0.091	R.HISILKDNPK.I
R2/RRR2-7/2	1235.281	1234.538	-208.855	0.489	1345.634	0.410	16	0.157	R.VVFM*LPWLGR.T
R2/RRR2-7/2	1150.617	1150.266	305.756	0.353	1072.487	0.298	17	0.120	R.LAFLDTDAAGR.A
R2/RRR2-7/2	1235.734	1234.538	159.006	0.287	588.107	0.303	12	0.105	R.VVFM*LPWLGR.T
R2/RRR2-17/2	1292.168	1292.420	-195.059	0.318	927.512	0.348	16	0.116	K.AVDVTGPDGSFVK.G
R2/RRR2-18/3	1495.177	1495.567	-261.567	0.375	690.825	0.480	24	0.088	R.SCYNCGEAGHIAR.D
R2/RRR2-18/3	1495.411	1495.567	-104.449	0.285	715.472	0.473	25	0.083	R.SCYNCGEAGHIAR.D
R2/RRR2-4/2	1935.430	1935.166	136.984	0.465	1447.714	0.497	20	0.180	K.GVPSLFSDLSPLYEQPGK.A
R2/RRR2-4/2	1836.816	1837.022	-112.624	0.460	1445.135	0.382	21	0.157	K.LLETIFGDQDVANSWK.A
R2/RRR2-4/2	1837.141	1837.022	64.605	0.429	880.632	0.381	17	0.116	K.LLETIFGDQDVANSWK.A
R2/RRR2-18/2	1679.331	1679.861	-913.799	0.456	745.846	0.491	20	0.129	R.EALGIHQGTVPSWQR.C
R2/RRR2-18/2	1680.350	1679.861	291.993	0.443	589.311	0.488	19	0.123	R.EALGIHQGTVPSWQR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-18/2	1679.257	1679.861	-957.878	0.334	727.947	0.438	20	0.119	R.EALGIHQGTVPSWQR.C
R2/RRR2-24/2	1265.694	1265.482	168.066	0.336	952.692	0.288	14	0.113	R.LLYKPESWTK.R
R2/RRR2-14/2	857.839	858.021	-212.179	0.451	933.644	0.269	13	0.112	-.VGGVLAVSR.-
R2/RRR2-14/2	1021.143	1021.195	-51.331	0.373	955.318	0.228	13	0.110	K.LLQEAYKR.E
R2/RRR2-16/2	1001.285	1001.076	209.696	0.342	991.579	0.173	14	0.105	K.ATNEPDVVR.R
R2/RRR2-23/2	1229.350	1228.384	-27.748	0.314	873.136	0.042	14	0.088	-.AKGSGRVQAEPK.-
R2/RRR2-13/2	1828.260	1828.016	134.299	0.452	617.788	0.468	20	0.120	R.AGAEEVLPLGPLNDFER.A
R2/RRR2-12/2	1829.485	1828.016	257.550	0.439	503.614	0.310	17	0.102	R.AGAEEVLPLGPLNDFER.A
R2/RRR2-22/2	1259.490	1259.439	40.381	0.496	2131.530	0.493	22	0.275	R.FPGVNGLGISAAR.V
R2/RRR2-23/2	1259.270	1259.439	-134.915	0.418	1913.147	0.432	21	0.224	R.FPGVNGLGISAAR.V
R2/RRR2-22/2	1259.082	1259.439	-284.883	0.479	1853.648	0.451	21	0.221	R.FPGVNGLGISAAR.V
R2/RRR2-22/2	1259.254	1259.439	-147.848	0.476	1710.014	0.488	20	0.210	R.FPGVNGLGISAAR.V
R2/RRR2-22/2	1260.220	1259.439	-174.452	0.394	1870.930	0.307	19	0.188	R.FPGVNGLGISAAR.V
R2/RRR2-8/2	1946.009	1945.335	-167.774	0.558	1823.676	0.639	23	0.270	R.LPAPVTTSAVELVALPLPR.V
R2/RRR2-10/2	1410.934	1411.672	-1235.757	0.472	1985.456	0.551	21	0.270	K.LGILGALEVIDAAR.K
R2/RRR2-10/2	1411.679	1411.672	5.238	0.225	585.297	0.159	15	0.097	K.LGILGALEVIDAAR.K
R2/RRR2-13/2	1494.978	1495.703	-1156.867	0.378	1000.956	0.408	15	0.128	R.SGYLYNLQYFVK.W
R2/RRR2-13/3	1228.435	1228.339	78.168	0.523	715.267	0.519	21	0.101	R.IPESGTPYAHR.S
R2/RRR2-13/3	1228.397	1228.339	47.372	0.497	594.763	0.426	21	0.087	R.IPESGTPYAHR.S
R2/RRR2-13/3	1228.269	1228.339	-57.140	0.421	455.620	0.414	17	0.082	R.IPESGTPYAHR.S
R2/RRR2-9/2	1168.178	1168.368	-163.043	0.530	1305.539	0.411	15	0.153	K.AEEIVLQPIR.E
R2/RRR2-9/2	1167.651	1168.368	-1475.194	0.426	1261.368	0.345	15	0.138	K.AEEIVLQPIR.E
R2/RRR2-9/3	1297.640	1296.541	76.500	0.450	826.660	0.371	22	0.080	-.ERPIGDLVVGLK.-
R2/RRR2-9/3	1295.956	1296.541	-1226.317	0.429	804.233	0.349	23	0.079	R.ERPIGDLVVGLK.Q
R2/RRR2-9/3	1296.446	1296.541	-73.684	0.395	630.256	0.284	20	0.070	-.ERPIGDLVVGLK.-
R2/RRR2-5/2	1494.279	1494.678	-267.574	0.483	998.837	0.561	22	0.156	R.LPATGEPIGQLQGGR.E
R2/RRR2-5/2	1145.166	1145.296	-113.717	0.380	437.646	0.476	14	0.120	R.SHPDVLAHLR.A
R2/RRR2-5/2	1145.733	1145.296	382.184	0.301	219.434	0.386	10	0.096	-.SHPDVLAHLR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1333.193	1332.527	-251.506	0.468	1178.892	0.468	17	0.153	K.YVEEQGAPIVVK.A
R2/RRR2-9/2	1559.383	1558.798	-266.924	0.332	705.069	0.340	15	0.106	R.LQSDLAQVLLAACR.G
R2/RRR2-20/2	1552.252	1552.713	-297.492	0.567	2022.733	0.545	22	0.273	K.DFNLAEHPDIPGVK.N
R2/RRR2-20/2	1552.453	1552.713	-168.034	0.500	1775.499	0.536	21	0.233	K.DFNLAEHPDIPGVK.N
R2/RRR2-20/2	1552.970	1552.713	165.989	0.568	1365.720	0.534	19	0.180	K.DFNLAEHPDIPGVK.N
R2/RRR2-4/2	1812.111	1813.046	-1071.093	0.477	2105.244	0.493	24	0.272	K.AYLPVLESFGFNADLR.A
R2/RRR2-4/2	1812.324	1813.046	-953.011	0.510	1872.764	0.535	24	0.246	K.AYLPVLESFGFNADLR.A
R2/RRR2-4/2	1813.284	1813.046	131.964	0.605	1597.407	0.563	24	0.215	K.AYLPVLESFGFNADLR.A
R2/RRR2-16/2	1130.412	1131.331	-1702.901	0.349	605.610	0.449	16	0.118	R.VAGM*VTPAAAAR.S
R2/RRR2-10/2	1098.524	1099.261	-1586.303	0.340	800.132	0.373	15	0.117	K.GFETFLGSLK.A
R2/RRR2-16/2	1130.299	1131.331	-1803.595	0.331	722.749	0.362	14	0.110	-.VAGM*VTPAAAAR.-
R2/RRR2-16/2	1130.253	1131.331	-1844.399	0.319	561.705	0.338	16	0.110	R.VAGM*VTPAAAAR.S
R2/RRR2-21/2	1355.087	1355.542	-337.248	0.515	2091.786	0.496	20	0.267	R.FSQVVSNALDM*K.L
R2/RRR2-21/2	1356.136	1355.542	-300.603	0.545	1657.643	0.534	19	0.214	R.FSQVVSNALDM*K.L
R2/RRR2-21/2	1355.099	1355.542	-328.300	0.520	1657.803	0.483	19	0.202	R.FSQVVSNALDM*K.L
R2/RRR2-21/2	1339.316	1339.543	-170.092	0.411	1422.819	0.489	18	0.176	R.FSQVVSNALDMK.L
R2/RRR2-21/2	1338.585	1339.543	-1467.189	0.382	1288.596	0.379	16	0.143	R.FSQVVSNALDMK.L
R2/RRR2-21/2	1338.439	1339.543	-1577.030	0.370	981.054	0.397	17	0.128	R.FSQVVSNALDMK.L
R2/RRR2-20/2	1355.008	1355.542	-1135.857	0.336	641.267	0.354	13	0.109	-.FSQVVSNALDM*K.-
R2/RRR2-21/2	1356.282	1355.542	-192.604	0.281	582.009	0.235	14	0.105	R.FSQVVSNALDM*K.L
R2/RRR2-21/3	1355.298	1355.542	-180.874	0.443	1123.852	0.369	25	0.092	R.FSQVVSNALDM*K.L
R2/RRR2-21/3	1355.316	1355.542	-167.592	0.441	987.306	0.317	23	0.079	R.FSQVVSNALDM*K.L
R2/RRR2-21/3	1355.842	1355.542	221.498	0.422	827.137	0.284	21	0.070	-.FSQVVSNALDM*K.-
R2/RRR2-6/2	1928.113	1929.204	-1087.933	0.442	1961.269	0.533	24	0.262	R.NLADPSSLAVATTNLISLK.G
R2/RRR2-4/2	1323.274	1323.439	-124.966	0.522	1491.796	0.468	17	0.182	R.INFVTWSQDGR.H
R2/RRR2-4/2	1322.234	1323.439	-1672.659	0.359	1442.009	0.436	17	0.168	R.INFVTWSQDGR.H
R2/RRR2-4/2	1474.264	1474.602	-230.097	0.490	1438.687	0.422	19	0.166	K.IQSNETSNVVQVR.T
R2/RRR2-4/2	1474.361	1474.602	-163.813	0.496	1430.337	0.404	19	0.162	K.IQSNETSNVVQVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1537.345	1536.926	273.281	0.410	1144.275	0.452	18	0.144	R.VAPLQVIVIPVPYK.D
R2/RRR2-8/2	1536.476	1536.926	-293.375	0.339	1116.715	0.371	19	0.130	R.VAPLQVIVIPVPYK.D
R2/RRR2-8/2	1394.297	1394.558	-187.972	0.422	1017.396	0.346	17	0.125	R.WEFSNPTPFIR.S
R2/RRR2-8/2	1395.146	1394.558	-296.591	0.436	803.129	0.388	16	0.122	R.WEFSNPTPFIR.S
R2/RRR2-8/2	1394.241	1394.558	-228.726	0.427	840.426	0.363	16	0.120	R.WEFSNPTPFIR.S
R2/RRR2-8/2	1536.503	1536.926	-275.680	0.240	799.452	0.331	16	0.108	R.VAPLQVIVIPVPYK.D
R2/RRR2-9/2	1891.343	1891.158	98.034	0.558	1813.156	0.610	23	0.256	R.FIQYNIFGNVFEVTAK.Y
R2/RRR2-9/2	1892.086	1891.158	-38.089	0.593	1160.189	0.620	23	0.179	R.FIQYNIFGNVFEVTAK.Y
R2/RRR2-9/2	1892.185	1891.158	14.584	0.563	966.435	0.567	23	0.155	R.FIQYNIFGNVFEVTAK.Y
R2/RRR2-10/2	1892.208	1891.158	26.360	0.291	140.757	0.389	12	0.108	R.FIQYNIFGNVFEVTAK.Y
R2/RRR2-11/2	1892.228	1891.158	36.972	0.207	139.033	0.462	13	0.104	R.FIQYNIFGNVFEVTAK.Y
R2/RRR2-10/2	1246.978	1247.425	-359.619	0.373	741.304	0.423	16	0.121	K.FTAEIIPVNSR.V
R2/RRR2-10/2	1246.364	1247.425	-1658.659	0.359	709.615	0.360	14	0.113	K.FTAEIIPVNSR.V
R2/RRR2-10/3	1959.673	1958.206	239.058	0.370	858.356	0.412	27	0.084	R.AGANVTVASVEDKLQVVTR.R
R2/RRR2-11/2	1275.093	1275.391	-234.159	0.339	1297.616	0.369	18	0.143	R.VSTVVDVDLGDR.S
R2/RRR2-11/2	1061.077	1061.213	-128.267	0.412	1111.357	0.282	14	0.121	R.LGWIDESIK.K
R2/RRR2-11/2	1275.036	1275.391	-278.822	0.231	805.304	0.248	16	0.103	R.VSTVVDVDLGDR.S
R2/RRR2-3/2	1427.282	1427.549	-187.231	0.432	1138.444	0.513	17	0.156	R.NPVYQNAGNFFR.L
R2/RRR2-3/2	1042.055	1042.209	-148.468	0.389	1072.386	0.414	14	0.137	R.LSDFLTFAK.D
R2/RRR2-3/2	1042.012	1042.209	-189.717	0.391	823.616	0.442	13	0.127	R.LSDFLTFAK.D
R2/RRR2-3/2	1427.153	1427.549	-277.757	0.395	845.338	0.414	16	0.123	R.NPVYQNAGNFFR.L
R2/RRR2-3/2	1427.302	1427.549	-172.988	0.384	728.697	0.447	15	0.121	R.NPVYQNAGNFFR.L
R2/RRR2-3/2	1042.135	1042.209	-71.973	0.296	646.895	0.300	12	0.108	R.LSDFLTFAK.D
R2/RRR2-4/2	1624.071	1622.891	111.605	0.451	1299.472	0.522	20	0.171	R.VLQIQLETPAPSLGR.T
R2/RRR2-4/2	1623.761	1622.891	-80.199	0.410	728.539	0.492	17	0.124	R.VLQIQLETPAPSLGR.T
R2/RRR2-4/2	1716.322	1715.802	-280.396	0.379	763.756	0.371	19	0.115	K.SLSDAYNSLEQANFR.L
R2/RRR2-4/2	1715.817	1715.802	8.876	0.262	686.449	0.178	17	0.098	K.SLSDAYNSLEQANFR.L
R2/RRR2-5/2	1745.362	1745.913	-891.294	0.414	2032.786	0.485	24	0.261	K.VAILTVSDTVSSGAGPDR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1212.664	1212.467	163.098	0.482	2122.183	0.459	19	0.269	R.VNIGQIILSVR.T
R2/RRR2-6/2	1442.771	1443.623	-1287.154	0.357	1405.836	0.381	17	0.155	K.SIDTETFLEFLK.T
R2/RRR2-6/2	1158.247	1158.287	-34.737	0.446	1178.781	0.404	17	0.144	R.IVEVVQGEER.A
R2/RRR2-6/2	1158.030	1158.287	-222.305	0.474	1032.019	0.386	17	0.134	R.IVEVVQGEER.A
R2/RRR2-6/2	1157.806	1158.287	-416.715	0.401	933.321	0.409	16	0.129	R.IVEVVQGEER.A
R2/RRR2-9/2	1891.449	1891.116	176.289	0.481	504.800	0.462	20	0.116	R.IDTAQPAPDYAAAVAFLR.G
R2/RRR2-9/2	1890.406	1891.116	-907.494	0.394	246.699	0.432	15	0.099	-.IDTAQPAPDYAAAVAFLR.-
R2/RRR2-9/3	1538.201	1536.927	178.559	0.379	911.189	0.415	28	0.088	R.TLELVAGKPLLLLR.W
R2/RRR2-9/3	1536.646	1536.927	-183.595	0.352	587.104	0.432	22	0.081	R.TLELVAGKPLLLLR.W
R2/RRR2-9/3	1536.848	1536.927	-51.761	0.295	631.790	0.304	23	0.070	R.TLELVAGKPLLLLR.W
R2/RRR2-13/2	1827.573	1828.059	-266.677	0.467	1983.289	0.523	25	0.260	R.ELGDFPLPIALVENSGR.C
R2/RRR2-13/2	1827.404	1828.059	-908.162	0.449	1349.635	0.493	22	0.169	R.ELGDFPLPIALVENSGR.C
R2/RRR2-13/2	1827.631	1828.059	-234.714	0.425	1060.737	0.453	20	0.137	R.ELGDFPLPIALVENSGR.C
R2/RRR2-6/2	1425.092	1425.633	-1083.953	0.528	1844.549	0.586	20	0.257	K.AAMLVAEDLGYSGK.A
R2/RRR2-6/2	1441.314	1441.632	-221.125	0.459	1881.669	0.477	21	0.233	K.AAM*LVAEDLGYSGK.A
R2/RRR2-6/2	1258.343	1258.526	-145.912	0.435	735.761	0.447	18	0.126	R.IPSSLCGIIGLK.T
R2/RRR2-6/2	1258.302	1258.526	-178.610	0.360	456.335	0.544	16	0.123	R.IPSSLCGIIGLK.T
R2/RRR2-1/2	1258.725	1258.526	158.199	0.328	634.144	0.340	15	0.110	R.IPSSLCGIIGLK.T
R2/RRR2-6/3	1234.186	1234.378	-156.616	0.480	516.643	0.436	20	0.087	R.SVEKDAVCVAR.L
R2/RRR2-6/3	1234.638	1234.378	210.710	0.445	751.914	0.409	23	0.082	-.SVEKDAVCVAR.-
R2/RRR2-6/3	1234.057	1234.378	-261.105	0.364	461.104	0.368	19	0.067	-.SVEKDAVCVAR.-
R2/RRR2-5/2	1352.510	1353.629	-1571.214	0.383	1301.837	0.469	18	0.161	R.CVVPLAAAISPVR.S
R2/RRR2-5/2	1369.880	1370.490	-1178.855	0.428	645.104	0.437	15	0.118	R.LVVCDQHGSQAR.F
R2/RRR2-16/2	1447.993	1448.520	-1057.255	0.521	1224.145	0.494	19	0.161	R.SPSAYLNNPAEER.S
R2/RRR2-16/2	1447.948	1448.520	-1088.575	0.514	1109.709	0.531	18	0.158	R.SPSAYLNNPAEER.S
R2/RRR2-19/2	1536.506	1536.708	-131.927	0.449	1207.021	0.446	20	0.150	R.NDLLTDGTFALVEK.L
R2/RRR2-16/2	1448.187	1448.520	-230.520	0.484	1126.771	0.433	18	0.142	R.SPSAYLNNPAEER.S
R2/RRR2-19/2	1535.973	1536.708	-1133.404	0.281	839.776	0.376	17	0.114	R.NDLLTDGTFALVEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1132.196	1132.246	-44.079	0.439	1355.068	0.280	17	0.134	K.TAEDAVADVLK.A
R2/RRR2-6/2	1131.924	1132.246	-285.410	0.429	1183.331	0.292	16	0.125	K.TAEDAVADVLK.A
R2/RRR2-6/3	1840.801	1840.976	-95.161	0.383	495.465	0.575	27	0.092	K.SQVSSIAVIGHNANDATR.L
R2/RRR2-8/3	1503.460	1503.547	-58.286	0.516	1377.922	0.366	25	0.110	R.VHCAESGEESLER.E
R2/RRR2-7/3	1502.970	1503.547	-1052.765	0.483	970.384	0.358	24	0.085	R.VHCAESGEESLER.E
R2/RRR2-8/3	1503.187	1503.547	-240.218	0.505	935.135	0.356	22	0.082	-.VHCAESGEESLER.-
R2/RRR2-10/3	1503.458	1503.547	-59.507	0.506	926.993	0.344	22	0.080	-.VHCAESGEESLER.-
R2/RRR2-10/3	1503.214	1503.547	-222.376	0.502	754.706	0.351	22	0.077	-.VHCAESGEESLER.-
R2/RRR2-8/3	1502.517	1503.547	-1355.116	0.460	827.674	0.311	22	0.076	R.VHCAESGEESLER.E
R2/RRR2-10/3	1503.803	1503.547	170.838	0.483	704.831	0.392	21	0.073	-.VHCAESGEESLER.-
R2/RRR2-8/3	1675.519	1675.864	-206.486	0.334	1210.994	0.156	25	0.064	K.GGILKDDADWSTLGVK.D
R2/RRR2-10/2	1146.008	1145.295	-251.133	0.392	776.180	0.395	14	0.118	-.VAGNFHFAPGK.-
R2/RRR2-10/2	1146.140	1145.295	-135.519	0.329	583.507	0.265	13	0.092	-.VAGNFHFAPGK.-
R2/RRR2-10/3	1708.061	1707.871	111.342	0.442	998.848	0.322	24	0.079	R.KINSNQFSVTEHFR.E
R2/RRR2-12/2	1672.684	1672.819	-80.928	0.563	1863.983	0.565	23	0.257	K.LIGLAGDTNVQGEEQK.K
R2/RRR2-13/2	1209.945	1210.365	-348.060	0.551	1616.474	0.645	21	0.241	K.APSAAVAQPAAAGK.V
R2/RRR2-13/2	1210.096	1210.365	-222.959	0.569	1412.741	0.618	20	0.207	K.APSAAVAQPAAAGK.V
R2/RRR2-18/2	1258.369	1258.490	-95.703	0.448	1860.722	0.537	19	0.245	R.SIVGATLEVIQK.K
R2/RRR2-17/2	1258.080	1258.490	-326.861	0.449	976.816	0.470	16	0.137	R.SIVGATLEVIQK.K
R2/RRR2-18/2	1258.212	1258.490	-221.440	0.337	1054.521	0.377	16	0.127	R.SIVGATLEVIQK.K
R2/RRR2-8/2	1359.302	1358.520	-160.655	0.485	630.990	0.422	17	0.119	K.TVLEATAPGLEEK.L
R2/RRR2-8/2	1433.398	1433.502	-72.913	0.301	1114.142	0.274	18	0.118	R.EVEEFDPPSEVR.A
R2/RRR2-8/2	1358.107	1358.520	-304.860	0.323	575.290	0.371	15	0.109	K.TVLEATAPGLEEK.L
R2/RRR2-14/2	1794.484	1794.001	269.874	0.570	1802.521	0.579	26	0.247	R.DIPLNYATFQPGTTVR.D
R2/RRR2-13/2	1793.467	1794.001	-857.625	0.515	1444.371	0.547	23	0.191	R.DIPLNYATFQPGTTVR.D
R2/RRR2-14/2	1793.364	1794.001	-915.159	0.442	1448.457	0.501	24	0.182	R.DIPLNYATFQPGTTVR.D
R2/RRR2-14/2	1793.276	1794.001	-964.772	0.452	1278.572	0.525	23	0.169	R.DIPLNYATFQPGTTVR.D
R2/RRR2-13/2	1793.432	1794.001	-877.508	0.472	990.323	0.509	20	0.142	R.DIPLNYATFQPGTTVR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	1793.539	1794.001	-258.426	0.467	904.246	0.467	20	0.132	R.DIPLNYATFQPGTTVR.D
R2/RRR2-8/2	1972.784	1971.238	-230.974	0.540	1650.893	0.616	24	0.234	K.TPTGSAVADLELLEIIAEK.V
R2/RRR2-8/2	1971.939	1971.238	-152.343	0.385	239.488	0.522	12	0.106	-.TPTGSAVADLELLEIIAEK.-
R2/RRR2-8/2	1972.968	1971.238	-137.060	0.372	196.549	0.432	11	0.088	-.TPTGSAVADLELLEIIAEK.-
R2/RRR2-16/2	1524.271	1524.703	-283.675	0.467	1921.209	0.508	22	0.248	K.GVNPWIEVDGGVGPK.N
R2/RRR2-16/2	1524.360	1524.703	-225.346	0.422	1812.460	0.526	22	0.235	K.GVNPWIEVDGGVGPK.N
R2/RRR2-2/2	1714.130	1714.987	-1086.317	0.345	1592.424	0.387	21	0.174	K.VQLVQFGILSPDEIR.Q
R2/RRR2-2/2	1716.499	1714.987	-285.075	0.493	1010.258	0.388	18	0.125	K.VQLVQFGILSPDEIR.Q
R2/RRR2-2/2	1084.996	1085.194	-183.442	0.307	883.126	0.203	13	0.105	R.GFVENSYLR.G
R2/RRR2-2/2	1085.108	1085.194	-79.842	0.281	775.541	0.205	12	0.103	-.GFVENSYLR.-
R2/RRR2-3/2	1626.567	1626.876	-190.863	0.469	2067.347	0.427	20	0.250	R.ELIQQEVINILEGK.H
R2/RRR2-10/2	1933.597	1934.179	-820.990	0.541	1743.657	0.584	26	0.240	K.LITELIGSPDDSSLGFLR.S
R2/RRR2-10/2	1933.625	1934.179	-806.478	0.491	1730.874	0.461	26	0.206	K.LITELIGSPDDSSLGFLR.S
R2/RRR2-10/2	1933.092	1934.179	-1083.104	0.472	1512.874	0.509	25	0.191	K.LITELIGSPDDSSLGFLR.S
R2/RRR2-4/2	1659.090	1659.908	-1099.258	0.343	887.164	0.383	18	0.118	R.ETLAGINPYAIELVR.-
R2/RRR2-4/3	1685.195	1683.848	206.649	0.331	1139.093	0.223	23	0.070	K.DKFAWLRDEEFAR.E
R2/RRR2-6/2	1121.143	1121.271	-114.625	0.260	577.272	0.422	13	0.109	R.HADAIPVLER.A
R2/RRR2-7/3	1557.918	1557.688	148.478	0.404	605.522	0.493	24	0.092	K.LGTANPDVEDEKLR.L
R2/RRR2-7/3	1557.650	1557.688	-24.463	0.413	464.929	0.483	21	0.088	K.LGTANPDVEDEKLR.L
R2/RRR2-7/3	1557.075	1557.688	-1038.987	0.421	554.772	0.426	22	0.084	K.LGTANPDVEDEKLR.L
R2/RRR2-6/3	1557.655	1557.688	-20.690	0.344	455.116	0.449	20	0.080	-.LGTANPDVEDEKLR.-
R2/RRR2-6/3	1557.866	1557.688	114.531	0.366	632.032	0.365	23	0.078	K.LGTANPDVEDEKLR.L
R2/RRR2-9/2	1285.438	1284.482	-34.729	0.415	1075.480	0.359	15	0.129	R.YFEVELKEVK.L
R2/RRR2-9/2	1284.805	1284.482	251.713	0.394	1016.040	0.387	14	0.129	R.YFEVELKEVK.L
R2/RRR2-9/2	1285.408	1284.482	-57.876	0.351	696.276	0.356	13	0.113	R.YFEVELKEVK.L
R2/RRR2-9/2	1626.242	1626.838	-984.060	0.353	1001.790	0.240	17	0.108	K.GSSQVIAQYYQLIR.H
R2/RRR2-7/1	949.480	950.070	-1680.298	0.247	810.966	0.204	11	0.580	-.GFEVIDAAK.-
R2/RRR2-9/1	949.464	950.070	-1696.638	0.287	817.690	0.165	12	0.551	-.GFEVIDAAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/1	949.470	950.070	-1690.696	0.265	800.646	0.165	12	0.533	R.GFEVIDAAK.A
R2/RRR2-8/1	949.511	950.070	-1647.232	0.280	685.643	0.182	11	0.426	-.GFEVIDAAK.-
R2/RRR2-8/1	949.517	950.070	-1640.516	0.286	544.467	0.175	10	0.310	-.GFEVIDAAK.-
R2/RRR2-8/2	1393.087	1393.607	-1094.091	0.475	2374.092	0.471	21	0.307	R.VVSCADILAFAAR.D
R2/RRR2-8/2	1393.079	1393.607	-1100.426	0.454	2430.614	0.430	22	0.305	R.VVSCADILAFAAR.D
R2/RRR2-7/1	949.478	950.070	-1682.236	0.284	533.343	0.182	10	0.303	-.GFEVIDAAK.-
R2/RRR2-9/1	949.434	950.070	-1728.738	0.234	559.028	0.048	10	0.300	-.GFEVIDAAK.-
R2/RRR2-8/2	1394.191	1393.607	-299.253	0.571	2217.005	0.517	21	0.292	R.VVSCADILAFAAR.D
R2/RRR2-9/2	1394.279	1393.607	-236.008	0.561	2078.479	0.510	21	0.266	R.VVSCADILAFAAR.D
R2/RRR2-8/1	949.482	950.070	-1677.973	0.256	467.265	0.152	9	0.262	-.GFEVIDAAK.-
R2/RRR2-7/1	949.486	950.070	-1673.452	0.186	483.987	0.061	10	0.254	-.GFEVIDAAK.-
R2/RRR2-9/2	1394.467	1393.607	-100.850	0.564	1996.736	0.511	20	0.253	R.VVSCADILAFAAR.D
R2/RRR2-7/2	1393.437	1393.607	-122.628	0.417	1354.036	0.439	17	0.158	R.VVSCADILAFAAR.D
R2/RRR2-7/2	1393.529	1393.607	-56.285	0.426	1348.127	0.425	18	0.156	R.VVSCADILAFAAR.D
R2/RRR2-10/2	949.542	950.070	-1614.183	0.399	1315.206	0.417	15	0.154	R.GFEVIDAAK.A
R2/RRR2-8/2	1394.778	1393.607	123.280	0.372	1286.216	0.442	17	0.152	R.VVSCADILAFAAR.D
R2/RRR2-2/2	950.101	950.070	32.009	0.415	1138.695	0.463	15	0.149	R.GFEVIDAAK.A
R2/RRR2-10/2	949.921	950.070	-157.455	0.461	1211.196	0.408	15	0.146	R.GFEVIDAAK.A
R2/RRR2-2/2	949.927	950.070	-151.396	0.425	1056.166	0.465	14	0.144	R.GFEVIDAAK.A
R2/RRR2-7/2	949.424	950.070	-1739.862	0.367	1131.916	0.424	14	0.141	R.GFEVIDAAK.A
R2/RRR2-2/2	949.949	950.070	-128.064	0.417	1084.813	0.420	14	0.139	R.GFEVIDAAK.A
R2/RRR2-8/2	949.447	950.070	-1715.447	0.340	1209.255	0.376	14	0.138	R.GFEVIDAAK.A
R2/RRR2-8/2	949.862	950.070	-220.110	0.456	1072.721	0.392	14	0.135	R.GFEVIDAAK.A
R2/RRR2-9/2	949.513	950.070	-1645.309	0.408	1110.569	0.380	14	0.135	R.GFEVIDAAK.A
R2/RRR2-9/2	949.930	950.070	-148.431	0.458	1104.949	0.379	14	0.135	R.GFEVIDAAK.A
R2/RRR2-8/2	949.951	950.070	-126.259	0.443	1009.279	0.410	14	0.134	R.GFEVIDAAK.A
R2/RRR2-9/2	949.868	950.070	-214.179	0.447	1101.997	0.376	14	0.134	R.GFEVIDAAK.A
R2/RRR2-3/2	949.898	950.070	-181.949	0.337	1064.885	0.402	14	0.134	R.GFEVIDAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-7/2	949.833	950.070	-250.924	0.373	1105.489	0.370	14	0.133	R.GFEVIDAAK.A
R2/RRR2-7/2	950.996	950.070	-78.098	0.479	1060.650	0.376	14	0.132	R.GFEVIDAAK.A
R2/RRR2-10/2	949.516	950.070	-1642.468	0.337	981.969	0.402	14	0.130	R.GFEVIDAAK.A
R2/RRR2-5/2	950.089	950.070	19.638	0.289	1245.298	0.298	14	0.130	R.GFEVIDAAK.A
R2/RRR2-7/2	1393.091	1393.607	-1091.628	0.339	1094.891	0.357	17	0.127	R.VVSCADILAFAAR.D
R2/RRR2-7/2	1394.790	1393.607	131.618	0.343	1106.873	0.351	16	0.126	R.VVSCADILAFAAR.D
R2/RRR2-11/2	949.736	950.070	-352.794	0.383	886.503	0.394	13	0.126	R.GFEVIDAAK.A
R2/RRR2-1/2	949.682	950.070	-410.185	0.319	944.170	0.391	13	0.126	R.GFEVIDAAK.A
R2/RRR2-7/2	1394.531	1393.607	-54.839	0.285	955.747	0.404	15	0.123	R.VVSCADILAFAAR.D
R2/RRR2-3/2	949.988	950.070	-87.203	0.386	921.323	0.344	13	0.122	R.GFEVIDAAK.A
R2/RRR2-1/2	949.881	950.070	-200.384	0.310	859.206	0.328	13	0.117	R.GFEVIDAAK.A
R2/RRR2-9/2	1394.773	1393.607	119.769	0.260	781.118	0.316	16	0.110	R.VVSCADILAFAAR.D
R2/RRR2-4/2	1392.461	1393.607	-1545.390	0.356	908.082	0.191	15	0.102	R.VVSCADILAFAAR.D
R2/RRR2-6/2	1394.455	1393.607	-109.280	0.279	1052.266	0.134	15	0.102	R.VVSCADILAFAAR.D
R2/RRR2-6/2	949.871	950.070	-210.956	0.184	540.385	0.044	11	0.049	-.GFEVIDAAK.-
R2/RRR2-6/2	1337.197	1337.460	-197.281	0.323	1164.661	0.268	17	0.120	R.YLNISDNALGEK.G
R2/RRR2-6/3	1673.894	1673.851	25.475	0.526	984.470	0.492	29	0.109	R.KYGLLGKEEAHDNAK.R
R2/RRR2-6/3	1673.645	1673.851	-123.539	0.538	826.527	0.497	27	0.102	R.KYGLLGKEEAHDNAK.R
R2/RRR2-6/3	1673.065	1673.851	-1070.946	0.477	700.820	0.465	26	0.091	R.KYGLLGKEEAHDNAK.R
R2/RRR2-4/2	1416.666	1416.607	41.777	0.332	1170.221	0.395	17	0.136	R.GADPAIVLNNLYR.H
R2/RRR2-4/2	1416.827	1416.607	155.928	0.194	548.898	0.363	16	0.103	R.GADPAIVLNNLYR.H
R2/RRR2-17/2	1146.440	1147.307	-1633.207	0.243	859.473	0.123	13	0.099	R.CSVIERRAR.F
R2/RRR2-16/2	1146.968	1147.307	-296.825	0.299	914.425	0.056	13	0.096	R.CSVIERRAR.F
R2/RRR2-10/2	1048.090	1048.220	-124.834	0.393	958.257	0.292	15	0.115	K.VFLGNLSAAR.D
R2/RRR2-10/3	1797.595	1797.946	-196.005	0.313	1106.544	0.034	26	0.050	K.YFRPAEVDSLQGDATK.A
R2/RRR2-23/2	1523.311	1523.713	-264.242	0.484	1992.550	0.461	22	0.243	R.LSYGAISDLSGIQAK.K
R2/RRR2-23/2	1525.139	1523.713	280.365	0.514	2009.764	0.452	22	0.242	R.LSYGAISDLSGIQAK.K
R2/RRR2-23/2	1522.902	1523.713	-1192.736	0.373	1995.325	0.351	21	0.215	R.LSYGAISDLSGIQAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-23/2	1523.230	1523.713	-317.629	0.479	1845.863	0.406	21	0.207	R.LSYGAISDLSGIQAK.K
R2/RRR2-23/3	1523.416	1523.713	-195.718	0.435	1585.968	0.278	28	0.112	R.LSYGAISDLSGIQAK.K
R2/RRR2-9/2	1097.349	1096.305	40.210	0.389	930.528	0.327	16	0.117	-.AGPGILGVNLGK.-
R2/RRR2-9/2	1097.290	1096.305	-13.793	0.289	789.287	0.314	15	0.109	K.AGPGILGVNLGK.N
R2/RRR2-9/2	1499.055	1498.706	233.380	0.309	870.157	0.235	17	0.103	K.QDLEDIAAVALALR.L
R2/RRR2-4/2	1860.625	1861.125	-808.903	0.419	1220.213	0.462	18	0.150	K.AISLYADEPEVTTPLLK.F
R2/RRR2-4/3	1764.475	1765.007	-870.857	0.374	971.088	0.422	26	0.092	R.VLQLINVTDTGVHAQR.Y
R2/RRR2-4/2	1033.143	1033.246	-99.975	0.456	1191.718	0.354	16	0.136	K.TFASGIIVPK.K
R2/RRR2-3/2	1034.143	1033.246	-99.760	0.495	879.583	0.423	15	0.130	K.TFASGIIVPK.K
R2/RRR2-4/2	1032.788	1033.246	-444.870	0.412	959.611	0.368	15	0.125	K.TFASGIIVPK.K
R2/RRR2-4/2	1032.988	1033.246	-250.282	0.297	948.894	0.341	15	0.119	K.TFASGIIVPK.K
R2/RRR2-12/2	1188.016	1188.268	-212.984	0.537	1819.751	0.529	18	0.232	R.FDDSFSAASLK.A
R2/RRR2-18/2	1189.124	1188.268	-121.766	0.537	1697.712	0.575	18	0.228	R.FDDSFSAASLK.A
R2/RRR2-18/2	1188.984	1188.268	-240.099	0.486	1802.254	0.509	18	0.225	R.FDDSFSAASLK.A
R2/RRR2-14/2	1187.988	1188.268	-236.281	0.456	1839.794	0.487	18	0.224	R.FDDSFSAASLK.A
R2/RRR2-17/2	1187.751	1188.268	-1281.380	0.466	1760.567	0.521	18	0.222	R.FDDSFSAASLK.A
R2/RRR2-14/2	1188.089	1188.268	-151.551	0.472	1790.281	0.502	18	0.221	R.FDDSFSAASLK.A
R2/RRR2-12/2	1188.110	1188.268	-133.618	0.493	1697.010	0.548	18	0.221	R.FDDSFSAASLK.A
R2/RRR2-4/2	1187.951	1188.268	-268.136	0.465	1705.294	0.534	18	0.218	R.FDDSFSAASLK.A
R2/RRR2-12/2	1188.099	1188.268	-142.791	0.476	1686.336	0.527	18	0.214	R.FDDSFSAASLK.A
R2/RRR2-14/2	1187.950	1188.268	-268.651	0.425	1548.122	0.496	17	0.190	R.FDDSFSAASLK.A
R2/RRR2-19/2	1189.065	1188.268	-171.712	0.512	1394.416	0.560	17	0.188	R.FDDSFSAASLK.A
R2/RRR2-7/2	1188.132	1188.268	-114.963	0.483	1436.031	0.510	18	0.182	R.FDDSFSAASLK.A
R2/RRR2-4/2	1188.081	1188.268	-158.148	0.400	1471.706	0.494	17	0.181	R.FDDSFSAASLK.A
R2/RRR2-15/2	1188.204	1188.268	-54.058	0.414	1412.526	0.511	17	0.178	R.FDDSFSAASLK.A
R2/RRR2-13/2	1188.154	1188.268	-96.309	0.462	1461.940	0.474	17	0.177	R.FDDSFSAASLK.A
R2/RRR2-4/2	1187.663	1188.268	-1355.700	0.430	1201.616	0.560	16	0.168	R.FDDSFSAASLK.A
R2/RRR2-16/2	1187.859	1188.268	-345.565	0.398	1329.018	0.488	17	0.166	R.FDDSFSAASLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1187.893	1188.268	-317.314	0.420	1258.759	0.474	16	0.157	R.FDDSFSAASLK.A
R2/RRR2-13/2	1189.132	1188.268	-115.381	0.407	1255.333	0.440	16	0.151	R.FDDSFSAASLK.A
R2/RRR2-5/2	1188.048	1188.268	-185.771	0.439	684.696	0.470	16	0.129	R.FDDSFSAASLK.A
R2/RRR2-5/2	1187.737	1188.268	-1293.147	0.374	630.075	0.472	16	0.126	R.FDDSFSAASLK.A
R2/RRR2-17/2	1187.936	1188.268	-280.816	0.347	961.831	0.356	16	0.123	R.FDDSFSAASLK.A
R2/RRR2-15/2	1187.892	1188.268	-317.829	0.248	651.064	0.385	14	0.113	R.FDDSFSAASLK.A
R2/RRR2-5/2	1075.154	1075.286	-123.058	0.391	747.995	0.393	13	0.120	R.VVLNIFDVR.T
R2/RRR2-5/2	1075.136	1075.286	-139.914	0.369	772.004	0.377	13	0.118	R.VVLNIFDVR.T
R2/RRR2-5/2	1075.169	1075.286	-109.277	0.408	682.478	0.347	13	0.115	R.VVLNIFDVR.T
R2/RRR2-5/2	1071.093	1070.172	-73.114	0.291	687.820	0.365	13	0.111	K.NLFSVSDCK.M
R2/RRR2-3/2	1712.164	1711.041	72.253	0.528	876.194	0.495	21	0.137	R.ENILGFVTQLPPLLR.A
R2/RRR2-3/2	1711.383	1711.041	200.204	0.483	855.225	0.475	21	0.133	R.ENILGFVTQLPPLLR.A
R2/RRR2-3/2	1339.895	1339.543	263.660	0.407	802.406	0.355	14	0.113	R.TAAMDFVSELVR.K
R2/RRR2-2/2	1712.231	1711.041	111.150	0.395	386.481	0.414	14	0.109	R.ENILGFVTQLPPLLR.A
R2/RRR2-25/2	1539.195	1539.711	-987.610	0.491	1763.042	0.575	20	0.241	R.FLFCQSSPASAPAR.E
R2/RRR2-25/2	1539.415	1539.711	-192.283	0.523	1456.417	0.601	20	0.207	R.FLFCQSSPASAPAR.E
R2/RRR2-25/2	1539.207	1539.711	-980.046	0.448	1439.039	0.554	19	0.192	R.FLFCQSSPASAPAR.E
R2/RRR2-4/2	1848.871	1848.108	-128.975	0.493	1242.007	0.441	21	0.150	K.IMQAADTDISALVEIEK.N
R2/RRR2-4/2	958.021	957.109	-92.415	0.422	703.861	0.294	12	0.110	R.AVAIENALR.L
R2/RRR2-1/2	956.792	957.109	-332.981	0.305	862.239	0.200	12	0.105	-.AVAIENALR.-
R2/RRR2-4/2	957.161	957.109	54.606	0.318	733.579	0.158	12	0.102	R.AVAIENALR.L
R2/RRR2-3/2	957.467	957.109	375.172	0.374	715.738	0.158	12	0.101	R.AVAIENALR.L
R2/RRR2-2/2	1049.326	1049.248	74.255	0.494	1168.994	0.397	14	0.142	K.STLIQALFR.I
R2/RRR2-9/2	935.296	935.081	230.970	0.174	895.031	0.055	13	0.095	-.DGMIVQSGK.-
R2/RRR2-10/2	1199.118	1198.418	-250.527	0.271	1106.673	0.354	17	0.126	K.FGTITSAVVM*R.E
R2/RRR2-10/2	1182.136	1182.418	-239.522	0.177	708.897	0.238	13	0.100	K.FGTITSAVVMR.E
R2/RRR2-10/2	1181.681	1182.418	-1474.879	0.143	540.338	0.065	12	0.097	-.FGTITSAVVMR.-
R2/RRR2-6/3	1549.587	1549.863	-178.701	0.413	868.428	0.303	23	0.072	-.M*VGSKPLYVALAQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1550.330	1549.863	302.103	0.347	954.426	0.281	23	0.071	-.M*VGSKPLYVALAQR.-
R2/RRR2-5/2	1244.115	1244.423	-247.863	0.466	864.078	0.465	19	0.135	R.QSALALLGDLSR.V
R2/RRR2-5/2	1244.050	1244.423	-300.825	0.310	356.484	0.458	13	0.110	R.QSALALLGDLSR.V
R2/RRR2-4/2	1274.243	1274.449	-162.155	0.297	901.178	0.125	14	0.098	-.SLLENSAITLGR.-
R2/RRR2-5/3	1752.315	1752.130	106.014	0.514	2063.453	0.409	34	0.217	K.SFALLSLLSSILPVYK.E
R2/RRR2-5/2	1752.481	1752.130	201.168	0.358	866.968	0.454	20	0.126	K.SFALLSLLSSILPVYK.E
R2/RRR2-5/2	1751.423	1752.130	-977.621	0.290	769.753	0.397	19	0.114	K.SFALLSLLSSILPVYK.E
R2/RRR2-5/2	1240.308	1240.434	-102.230	0.524	1492.184	0.621	20	0.218	R.VPATNILLGEGR.G
R2/RRR2-5/2	1240.290	1240.434	-116.348	0.486	1496.082	0.584	20	0.209	R.VPATNILLGEGR.G
R2/RRR2-5/2	1240.309	1240.434	-101.144	0.376	587.365	0.519	14	0.122	R.VPATNILLGEGR.G
R2/RRR2-26/2	963.868	964.165	-308.848	0.366	1107.895	0.196	13	0.111	R.M*ITKIEGR.G
R2/RRR2-22/2	1110.109	1109.147	-34.368	0.294	754.073	0.283	13	0.109	K.EGEAADEEMK.K
R2/RRR2-19/2	1109.758	1109.147	-350.797	0.342	456.746	0.278	11	0.107	-.EGEAADEEMK.-
R2/RRR2-25/2	1109.800	1109.147	-312.833	0.248	602.299	0.238	12	0.105	-.EGEAADEEMK.-
R2/RRR2-26/2	1109.876	1109.147	-244.637	0.274	552.240	0.240	11	0.105	-.EGEAADEEMK.-
R2/RRR2-26/2	1109.746	1109.147	-362.055	0.299	437.577	0.326	10	0.104	-.EGEAADEEMK.-
R2/RRR2-28/2	1109.706	1109.147	-398.478	0.223	596.303	0.215	12	0.104	K.EGEAADEEMK.K
R2/RRR2-28/2	1109.943	1109.147	-184.173	0.306	472.220	0.268	11	0.104	-.EGEAADEEMK.-
R2/RRR2-18/2	1109.813	1109.147	-301.797	0.231	632.145	0.149	12	0.103	-.EGEAADEEMK.-
R2/RRR2-24/2	1109.855	1109.147	-263.616	0.216	580.268	0.263	11	0.102	-.EGEAADEEMK.-
R2/RRR2-1/2	1109.471	1109.147	293.258	0.283	480.222	0.190	11	0.088	-.EGEAADEEMK.-
R2/RRR2-13/2	1460.019	1459.669	240.710	0.421	1945.331	0.437	20	0.231	R.SPWSTLDIIAEVK.Q
R2/RRR2-13/2	1460.380	1459.669	-198.246	0.427	1621.223	0.480	20	0.198	R.SPWSTLDIIAEVK.Q
R2/RRR2-13/2	1460.484	1459.669	-126.555	0.367	1031.199	0.414	17	0.131	R.SPWSTLDIIAEVK.Q
R2/RRR2-26/2	1298.680	1299.502	-1407.058	0.488	1592.181	0.580	20	0.222	R.LLAQAALTVGADR.A
R2/RRR2-21/2	1247.200	1246.392	-155.069	0.560	1948.180	0.442	18	0.231	K.SGDVTELQIGVK.H
R2/RRR2-21/2	1245.606	1246.392	-1438.604	0.437	1686.891	0.322	18	0.171	K.SGDVTELQIGVK.H
R2/RRR2-21/2	1245.422	1246.392	-1587.067	0.429	1656.965	0.262	18	0.155	K.SGDVTELQIGVK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1620.165	1618.813	217.975	0.551	1551.964	0.607	22	0.224	K.VPVENTAQAVYDAIK.L
R2/RRR2-15/2	1488.239	1488.710	-317.446	0.474	1682.234	0.537	21	0.220	K.AQDTFTPISAVIPK.S
R2/RRR2-15/2	1488.254	1488.710	-307.076	0.441	1522.982	0.507	21	0.192	K.AQDTFTPISAVIPK.S
R2/RRR2-15/2	1488.225	1488.710	-326.910	0.440	1314.524	0.536	19	0.175	K.AQDTFTPISAVIPK.S
R2/RRR2-6/2	1891.616	1892.187	-833.126	0.533	1492.858	0.584	28	0.209	R.FIVSGGAPLSVAVEEFLR.V
R2/RRR2-6/2	1893.214	1892.187	14.253	0.566	1013.830	0.568	23	0.156	R.FIVSGGAPLSVAVEEFLR.V
R2/RRR2-2/2	1957.942	1957.087	-74.515	0.510	1522.816	0.562	20	0.206	R.FLVNYVDYAFDDFGDR.Q
R2/RRR2-9/2	1529.278	1529.752	-311.249	0.507	1803.977	0.475	20	0.225	K.YNIDVICEYIVK.K
R2/RRR2-17/2	1567.658	1567.727	-44.409	0.428	1734.167	0.492	20	0.218	K.LQLNDFTGAVFEGR.L
R2/RRR2-6/2	1171.150	1170.344	-166.079	0.449	1943.388	0.396	20	0.221	K.DAGAIAGLNVLR.I
R2/RRR2-6/2	1170.834	1170.344	420.107	0.406	1176.329	0.322	16	0.127	K.DAGAIAGLNVLR.I
R2/RRR2-10/2	1171.286	1170.344	-49.403	0.314	1087.382	0.312	16	0.121	K.DAGAIAGLNVLR.I
R2/RRR2-13/2	1385.245	1385.593	-252.131	0.536	1436.705	0.592	21	0.203	R.DVGVSPAIVGAFPR.K
R2/RRR2-13/2	1385.215	1385.593	-273.880	0.374	1046.549	0.414	20	0.133	R.DVGVSPAIVGAFPR.K
R2/RRR2-12/2	1386.738	1385.593	105.189	0.331	422.201	0.392	14	0.108	R.DVGVSPAIVGAFPR.K
R2/RRR2-12/2	1267.903	1268.491	-1255.708	0.445	1765.793	0.469	19	0.212	R.IVVAGNQIAVQR.T
R2/RRR2-13/2	1267.612	1268.491	-1486.456	0.360	1670.300	0.410	18	0.186	R.IVVAGNQIAVQR.T
R2/RRR2-13/2	1267.677	1268.491	-1434.805	0.409	1452.508	0.506	18	0.182	R.IVVAGNQIAVQR.T
R2/RRR2-19/2	1268.293	1268.491	-156.738	0.428	1145.991	0.477	16	0.149	R.IVVAGNQIAVQR.T
R2/RRR2-12/2	1267.535	1268.491	-1547.981	0.386	1178.171	0.395	16	0.138	R.IVVAGNQIAVQR.T
R2/RRR2-13/2	1267.401	1268.491	-1653.733	0.344	991.128	0.351	15	0.121	R.IVVAGNQIAVQR.T
R2/RRR2-24/2	1268.196	1268.491	-233.405	0.344	1046.319	0.256	16	0.115	-.IVVAGNQIAVQR.-
R2/RRR2-17/2	1269.148	1268.491	-270.854	0.361	508.124	0.361	14	0.112	R.IVVAGNQIAVQR.T
R2/RRR2-13/2	1504.363	1503.685	-214.587	0.434	1601.501	0.528	20	0.204	R.ALEWITANGGITTR.D
R2/RRR2-15/2	1503.384	1503.685	-200.719	0.372	1762.313	0.299	19	0.173	R.ALEWITANGGITTR.D
R2/RRR2-15/2	1503.433	1503.685	-168.138	0.397	1559.064	0.356	18	0.162	R.ALEWITANGGITTR.D
R2/RRR2-19/2	1503.073	1503.685	-1075.533	0.335	1242.245	0.302	19	0.129	R.ALEWITANGGITTR.D
R2/RRR2-19/2	1502.503	1503.685	-1456.736	0.352	763.788	0.314	17	0.110	R.ALEWITANGGITTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-19/2	1503.432	1503.685	-168.626	0.299	647.511	0.285	14	0.103	R.ALEWITANGGITTR.D
R2/RRR2-8/2	1712.165	1710.867	174.941	0.485	1821.753	0.449	21	0.218	K.SNFATLDESTGIIVSR.R
R2/RRR2-13/2	1963.578	1964.189	-822.921	0.542	1456.600	0.574	25	0.203	K.NVNYLPNVLSIMDAEDR.G
R2/RRR2-23/2	1366.124	1366.519	-289.786	0.535	1776.453	0.470	17	0.217	K.SELEYYSM*LSK.T
R2/RRR2-23/2	1366.014	1366.519	-1104.640	0.450	1343.058	0.462	16	0.165	K.SELEYYSM*LSK.T
R2/RRR2-20/2	1867.511	1869.018	-1883.289	0.471	1598.427	0.537	22	0.210	K.LPDATLSYFDSPDGELK.T
R2/RRR2-16/2	1700.517	1700.920	-237.931	0.541	1550.793	0.554	24	0.206	R.NLAGNSAIFVAPNGLNK.G
R2/RRR2-16/2	1700.369	1700.920	-914.734	0.514	1492.577	0.555	24	0.200	R.NLAGNSAIFVAPNGLNK.G
R2/RRR2-15/2	1701.420	1700.920	-294.726	0.609	1392.110	0.590	23	0.195	R.NLAGNSAIFVAPNGLNK.G
R2/RRR2-14/3	1738.194	1737.725	270.787	0.266	211.720	0.604	19	0.079	R.GYGDSYQNDRDYQR.K
R2/RRR2-11/2	1215.071	1215.298	-187.988	0.523	1641.402	0.512	21	0.208	R.AVAGGGAAGEEAVR.A
R2/RRR2-11/2	1214.346	1215.298	-1612.355	0.406	1669.826	0.437	21	0.194	R.AVAGGGAAGEEAVR.A
R2/RRR2-11/2	1214.332	1215.298	-1623.968	0.404	1381.802	0.419	21	0.160	R.AVAGGGAAGEEAVR.A
R2/RRR2-8/2	1197.928	1198.351	-354.005	0.471	1315.407	0.595	19	0.191	R.VVDALGNPIDGK.G
R2/RRR2-8/2	1197.941	1198.351	-343.576	0.454	1061.776	0.515	17	0.151	R.VVDALGNPIDGK.G
R2/RRR2-25/2	1206.445	1206.245	166.070	0.540	1385.855	0.587	21	0.197	R.NSADAAATAAGSAK.L
R2/RRR2-25/2	1205.629	1206.245	-1344.740	0.436	943.440	0.570	17	0.148	R.NSADAAATAAGSAK.L
R2/RRR2-10/2	1683.310	1683.843	-913.749	0.538	1452.060	0.563	24	0.201	R.VFFANTGTEANEAAIK.F
R2/RRR2-12/2	1867.066	1867.990	-1033.664	0.480	1511.694	0.546	22	0.201	R.APCPASGDAPWPEDIQR.L
R2/RRR2-9/2	1996.956	1997.149	-97.094	0.535	1430.367	0.567	23	0.194	K.GFIDFDSDPWPVISDSAK.D
R2/RRR2-9/2	1997.085	1997.149	-32.530	0.572	1269.813	0.625	22	0.189	K.GFIDFDSDPWPVISDSAK.D
R2/RRR2-2/2	922.185	922.063	132.023	0.349	808.628	0.408	11	0.120	R.VSINVFSR.H
R2/RRR2-3/3	1312.598	1312.373	172.124	0.405	1456.536	0.186	25	0.079	R.HDDTQVFAHGGK.S
R2/RRR2-3/3	1313.570	1312.373	150.698	0.440	1262.887	0.197	24	0.071	R.HDDTQVFAHGGK.S
R2/RRR2-3/3	1311.807	1312.373	-1196.752	0.373	565.881	0.288	21	0.071	-.HDDTQVFAHGGK.-
R2/RRR2-20/2	1854.242	1854.959	-928.759	0.479	1158.130	0.627	25	0.175	R.AGGGGGAASSAAGPVVPAASDAR.A
R2/RRR2-20/2	1855.105	1854.959	78.697	0.504	1033.416	0.535	24	0.147	R.AGGGGGAASSAAGPVVPAASDAR.A
R2/RRR2-20/3	1854.600	1854.959	-194.536	0.351	829.001	0.356	29	0.076	R.AGGGGGAASSAAGPVVPAASDAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/3	1854.559	1854.959	-216.426	0.371	605.734	0.281	27	0.065	R.AGGGGGAASSAAGPVVPAASDAR.A
R2/RRR2-7/2	1376.241	1376.536	-215.437	0.521	1480.218	0.554	20	0.200	R.YGALEGLDVVDPK.T
R2/RRR2-7/2	1377.158	1376.536	-275.394	0.518	1535.003	0.493	21	0.192	R.YGALEGLDVVDPK.T
R2/RRR2-7/2	1376.119	1376.536	-304.429	0.508	1402.884	0.521	20	0.184	R.YGALEGLDVVDPK.T
R2/RRR2-24/2	1740.345	1740.888	-889.220	0.524	1811.258	0.438	24	0.213	K.IYIFDVTDTSPPDEK.S
R2/RRR2-24/2	1741.639	1740.888	-143.454	0.560	1656.603	0.469	24	0.201	K.IYIFDVTDTSPPDEK.S
R2/RRR2-23/2	1832.453	1833.121	-913.344	0.392	1386.974	0.564	23	0.187	K.DAPSAVNVVVVPNVNLPK.E
R2/RRR2-23/2	1833.472	1833.121	191.814	0.486	1075.163	0.554	21	0.155	K.DAPSAVNVVVVPNVNLPK.E
R2/RRR2-17/2	1173.569	1174.374	-1542.662	0.488	1524.525	0.529	16	0.200	K.LSELGILSWR.L
R2/RRR2-17/2	1174.016	1174.374	-306.464	0.364	1488.010	0.269	17	0.144	K.LSELGILSWR.L
R2/RRR2-18/2	1828.452	1828.960	-827.556	0.504	1347.739	0.575	23	0.189	R.VVGNSVSEFQSGFSDIR.T
R2/RRR2-3/2	1273.124	1272.436	-246.158	0.462	1429.390	0.534	19	0.187	K.AAVVGGNVLTSQR.V
R2/RRR2-3/2	1272.175	1272.436	-206.113	0.406	1320.489	0.518	17	0.170	K.AAVVGGNVLTSQR.V
R2/RRR2-2/2	1273.364	1272.436	-56.596	0.265	831.798	0.312	16	0.109	K.AAVVGGNVLTSQR.V
R2/RRR2-2/2	1273.688	1272.436	198.349	0.333	519.936	0.229	13	0.083	-.AAVVGGNVLTSQR.-
R2/RRR2-15/3	1468.055	1468.556	-1025.553	0.552	1914.248	0.368	27	0.169	R.HYNDISELSPHR.L
R2/RRR2-15/3	1468.573	1468.556	11.820	0.549	1767.796	0.384	27	0.154	R.HYNDISELSPHR.L
R2/RRR2-15/3	1468.339	1468.556	-147.901	0.558	1766.826	0.345	26	0.142	R.HYNDISELSPHR.L
R2/RRR2-3/2	1892.308	1891.158	79.674	0.301	116.605	0.532	14	0.107	K.EIGQLSNLIFLSLNSNK.F
R2/RRR2-4/2	1988.488	1987.201	145.089	0.528	1219.662	0.585	22	0.173	R.SADVLSAGLLEVANPSLSSR.F
R2/RRR2-4/2	1987.790	1987.201	-207.179	0.396	674.205	0.426	17	0.110	R.SADVLSAGLLEVANPSLSSR.F
R2/RRR2-5/2	1289.235	1288.346	-86.859	0.394	1124.636	0.254	18	0.118	-.EAAAADDDLAAVR.-
R2/RRR2-6/2	828.917	828.976	-71.876	0.180	1159.625	0.157	11	0.107	-.KDDILPK.-
R2/RRR2-21/3	1428.983	1429.511	-1072.701	0.524	1715.309	0.450	29	0.163	K.DCRPVESSEPPR.Y
R2/RRR2-20/3	1429.077	1429.511	-304.723	0.553	1587.893	0.480	28	0.157	K.DCRPVESSEPPR.Y
R2/RRR2-21/3	1429.197	1429.511	-220.785	0.523	1283.409	0.458	27	0.121	K.DCRPVESSEPPR.Y
R2/RRR2-21/3	1429.705	1429.511	136.016	0.544	1155.282	0.472	26	0.115	K.DCRPVESSEPPR.Y
R2/RRR2-20/3	1429.134	1429.511	-264.745	0.477	1289.087	0.412	26	0.112	K.DCRPVESSEPPR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-21/3	1429.177	1429.511	-234.410	0.512	1167.264	0.437	28	0.107	K.DCRPVESSEPPR.Y
R2/RRR2-20/3	1429.243	1429.511	-188.525	0.501	1091.451	0.427	25	0.103	K.DCRPVESSEPPR.Y
R2/RRR2-21/3	1429.291	1429.511	-154.982	0.491	884.138	0.435	22	0.095	K.DCRPVESSEPPR.Y
R2/RRR2-21/3	1429.516	1429.511	2.936	0.500	634.477	0.473	23	0.095	K.DCRPVESSEPPR.Y
R2/RRR2-22/3	1429.111	1429.511	-280.813	0.510	830.793	0.425	24	0.092	K.DCRPVESSEPPR.Y
R2/RRR2-18/2	1535.312	1533.831	314.474	0.483	1669.785	0.465	21	0.199	K.ALLYCGLAPTVLGGK.I
R2/RRR2-18/2	1533.595	1533.831	-153.973	0.423	1671.126	0.359	21	0.176	K.ALLYCGLAPTVLGGK.I
R2/RRR2-17/2	1534.041	1533.831	137.389	0.385	697.937	0.427	16	0.116	K.ALLYCGLAPTVLGGK.I
R2/RRR2-17/2	1533.362	1533.831	-306.587	0.265	502.677	0.248	14	0.100	K.ALLYCGLAPTVLGGK.I
R2/RRR2-8/3	1626.518	1626.883	-225.052	0.423	1403.324	0.531	32	0.158	K.VAQGVVGAVADKGSVLR.F
R2/RRR2-8/3	1627.379	1626.883	305.703	0.385	1075.539	0.523	31	0.120	K.VAQGVVGAVADKGSVLR.F
R2/RRR2-15/3	1581.854	1581.717	86.498	0.563	1519.818	0.513	29	0.164	K.NHAVHISQIGEGYR.A
R2/RRR2-15/3	1581.418	1581.717	-189.817	0.510	1192.812	0.535	27	0.135	K.NHAVHISQIGEGYR.A
R2/RRR2-16/3	1581.432	1581.717	-180.641	0.330	645.467	0.282	21	0.068	-.NHAVHISQIGEGYR.-
R2/RRR2-3/2	1491.213	1490.689	-320.097	0.436	1665.291	0.444	21	0.194	K.AVSVFNASAVGAGLAR.S
R2/RRR2-3/2	1491.667	1490.689	-14.907	0.293	677.962	0.393	17	0.109	K.AVSVFNASAVGAGLAR.S
R2/RRR2-19/2	1475.311	1475.663	-239.312	0.483	1479.730	0.524	20	0.193	R.TNVGICLADPSLSK.I
R2/RRR2-8/2	1449.252	1449.677	-294.389	0.512	1374.380	0.548	20	0.185	R.ASASAVAFGLGLLSGK.G
R2/RRR2-8/2	1375.264	1374.569	-222.445	0.504	1290.831	0.559	17	0.178	R.YATNAVTAFIFR.E
R2/RRR2-8/2	1374.299	1374.569	-196.765	0.419	1363.784	0.491	17	0.171	R.YATNAVTAFIFR.E
R2/RRR2-8/2	1374.104	1374.569	-338.912	0.504	1101.811	0.437	16	0.140	R.YATNAVTAFIFR.E
R2/RRR2-9/2	1375.710	1374.569	102.739	0.285	650.840	0.369	16	0.112	R.YATNAVTAFIFR.E
R2/RRR2-9/2	1374.434	1374.569	-98.222	0.280	371.874	0.365	11	0.106	R.YATNAVTAFIFR.E
R2/RRR2-17/2	1909.807	1910.025	-114.474	0.551	1203.617	0.580	23	0.175	R.GQFVCLDETPEGISGGSR.D
R2/RRR2-3/2	1398.776	1397.607	121.440	0.452	1595.382	0.471	18	0.193	R.AGLIDFLHGLGQR.Y
R2/RRR2-3/2	1398.933	1397.607	233.629	0.413	1303.007	0.439	17	0.155	R.AGLIDFLHGLGQR.Y
R2/RRR2-10/2	1754.761	1754.018	-146.777	0.563	1224.244	0.566	24	0.176	K.IQLLDLPGIIEGASEGK.G
R2/RRR2-9/2	1386.213	1386.490	-200.109	0.494	1523.482	0.502	20	0.191	K.TYGASTSGNSLSLK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-9/2	1385.984	1386.490	-1090.070	0.490	1387.743	0.493	19	0.174	K.TYGASTSGNSLSLK.F
R2/RRR2-9/2	1385.498	1386.490	-1441.634	0.333	1270.587	0.424	17	0.148	K.TYGASTSGNSLSLK.F
R2/RRR2-11/2	1319.328	1319.491	-124.133	0.428	1591.736	0.466	18	0.191	R.AAIFNQVEASLR.R
R2/RRR2-11/2	1318.929	1319.491	-1188.098	0.382	1336.297	0.401	16	0.151	R.AAIFNQVEASLR.R
R2/RRR2-11/2	1318.849	1319.491	-1249.071	0.279	1199.172	0.172	16	0.110	R.AAIFNQVEASLR.R
R2/RRR2-9/2	1738.368	1738.882	-873.680	0.507	1275.325	0.561	23	0.178	K.AIGAAQAAGTAPDAYYAR.R
R2/RRR2-16/2	1050.225	1050.233	-7.999	0.553	1519.374	0.495	16	0.191	R.SLGAAIIYNK.D
R2/RRR2-16/2	1049.343	1050.233	-1806.499	0.420	1286.180	0.529	16	0.172	R.SLGAAIIYNK.D
R2/RRR2-16/2	1050.063	1050.233	-162.844	0.527	1182.152	0.547	16	0.170	R.SLGAAIIYNK.D
R2/RRR2-17/2	1049.762	1050.233	-450.390	0.285	610.720	0.318	14	0.108	-.SLGAAIIYNK.-
R2/RRR2-12/2	1394.876	1394.595	202.182	0.458	1595.326	0.469	19	0.192	R.AVVDSAYEVISLK.G
R2/RRR2-12/2	1394.477	1394.595	-84.518	0.420	1324.273	0.440	18	0.158	R.AVVDSAYEVISLK.G
R2/RRR2-12/2	1394.224	1394.595	-266.666	0.394	854.997	0.352	15	0.114	R.AVVDSAYEVISLK.G
R2/RRR2-10/2	1533.741	1534.696	-1278.345	0.459	1447.672	0.518	21	0.188	K.LPSVGLDGSSPYSVR.D
R2/RRR2-8/2	1419.452	1419.694	-171.357	0.485	1265.359	0.558	18	0.177	R.KLSIQELLTAFR.V
R2/RRR2-8/2	1419.623	1419.694	-50.248	0.479	1358.434	0.506	18	0.176	R.KLSIQELLTAFR.V
R2/RRR2-8/2	1418.889	1419.694	-1275.856	0.377	1121.708	0.400	17	0.136	R.KLSIQELLTAFR.V
R2/RRR2-14/2	1236.003	1236.399	-321.703	0.564	1837.963	0.368	18	0.200	R.VYVLSVEGDVR.E
R2/RRR2-14/3	1819.848	1819.141	-161.651	0.558	1257.884	0.553	31	0.147	K.LPNNAVAPSLFFFRPK.N
R2/RRR2-14/3	1819.633	1819.141	270.746	0.366	619.508	0.456	24	0.085	K.LPNNAVAPSLFFFRPK.N
R2/RRR2-15/3	1817.716	1819.141	-1338.304	0.366	664.422	0.374	22	0.077	K.LPNNAVAPSLFFFRPK.N
R2/RRR2-14/3	1819.918	1819.141	-123.298	0.355	615.142	0.309	25	0.073	K.LPNNAVAPSLFFFRPK.N
R2/RRR2-6/3	1538.435	1538.773	-220.467	0.434	2041.916	0.216	27	0.151	R.EAM*QGGLAM*SLLER.A
R2/RRR2-20/2	1586.549	1585.739	-120.203	0.515	1294.898	0.555	22	0.178	K.STGFGLIYDNLDAAK.K
R2/RRR2-21/2	1585.218	1585.739	-962.567	0.485	1244.134	0.554	22	0.173	K.STGFGLIYDNLDAAK.K
R2/RRR2-21/2	1585.237	1585.739	-950.739	0.491	1178.639	0.512	21	0.159	K.STGFGLIYDNLDAAK.K
R2/RRR2-20/2	1584.785	1585.739	-1237.172	0.346	1169.071	0.469	21	0.148	K.STGFGLIYDNLDAAK.K
R2/RRR2-21/2	1585.342	1585.739	-251.586	0.470	1050.828	0.507	20	0.147	K.STGFGLIYDNLDAAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1585.481	1585.739	-163.529	0.469	991.582	0.524	20	0.146	K.STGFGLIYDNLDAAK.K
R2/RRR2-10/2	1226.274	1226.404	-106.894	0.525	1268.846	0.551	19	0.181	R.IPAEALDVIER.S
R2/RRR2-20/2	1846.266	1847.127	-1011.239	0.568	1419.381	0.526	26	0.186	K.IFEVAPSASQM*FSFLR.N
R2/RRR2-20/2	1830.479	1831.128	-903.560	0.589	1397.140	0.526	27	0.185	K.IFEVAPSASQMFSFLR.N
R2/RRR2-20/2	1830.478	1831.128	-903.828	0.587	1256.640	0.537	26	0.173	K.IFEVAPSASQMFSFLR.N
R2/RRR2-20/2	1847.394	1847.127	144.821	0.605	1245.773	0.535	25	0.171	K.IFEVAPSASQM*FSFLR.N
R2/RRR2-20/2	1847.174	1847.127	25.396	0.609	1262.688	0.520	25	0.169	K.IFEVAPSASQM*FSFLR.N
R2/RRR2-20/3	1846.910	1847.127	-117.866	0.439	1659.606	0.402	31	0.152	K.IFEVAPSASQM*FSFLR.N
R2/RRR2-20/2	1830.662	1831.128	-254.924	0.506	1162.504	0.457	25	0.150	K.IFEVAPSASQMFSFLR.N
R2/RRR2-20/3	1847.242	1847.127	62.704	0.479	1287.020	0.458	30	0.125	K.IFEVAPSASQM*FSFLR.N
R2/RRR2-20/3	1847.323	1847.127	106.246	0.311	613.706	0.304	24	0.070	K.IFEVAPSASQM*FSFLR.N
R2/RRR2-13/3	1607.472	1606.808	-210.086	0.510	1657.797	0.437	28	0.163	K.ALAHQPVSVAIEASGR.N
R2/RRR2-13/3	1607.243	1606.808	271.215	0.396	1370.303	0.372	26	0.115	K.ALAHQPVSVAIEASGR.N
R2/RRR2-14/3	1606.815	1606.808	4.288	0.434	1002.617	0.361	24	0.086	K.ALAHQPVSVAIEASGR.N
R2/RRR2-13/3	1606.324	1606.808	-302.121	0.318	953.096	0.254	25	0.070	K.ALAHQPVSVAIEASGR.N
R2/RRR2-16/2	1295.239	1295.467	-176.353	0.463	1013.852	0.588	16	0.158	R.VNQSFVIATSTK.L
R2/RRR2-16/2	1295.021	1295.467	-345.333	0.393	1113.169	0.492	16	0.148	R.VNQSFVIATSTK.L
R2/RRR2-16/2	1294.698	1295.467	-1369.869	0.387	1083.625	0.502	15	0.147	R.VNQSFVIATSTK.L
R2/RRR2-15/2	1295.131	1295.467	-260.126	0.398	524.371	0.487	17	0.123	R.VNQSFVIATSTK.L
R2/RRR2-6/2	1596.673	1596.807	-84.244	0.446	1454.980	0.495	23	0.184	R.DGEAILQLIGGDVAPK.D
R2/RRR2-16/2	1659.368	1659.866	-301.457	0.477	1451.165	0.516	22	0.186	R.FDPATTPLLAAWAER.F
R2/RRR2-16/2	1659.904	1659.866	23.042	0.472	1403.548	0.479	21	0.173	R.FDPATTPLLAAWAER.F
R2/RRR2-16/2	1659.340	1659.866	-922.890	0.474	1227.451	0.479	20	0.156	R.FDPATTPLLAAWAER.F
R2/RRR2-10/2	1253.647	1252.400	197.320	0.247	332.188	0.535	14	0.109	R.FFPALQGENTK.M
R2/RRR2-14/2	1728.125	1726.997	73.853	0.474	1418.402	0.505	22	0.179	K.QGPGTAILLGPNFLAEK.G
R2/RRR2-14/2	1727.194	1726.997	114.298	0.491	1072.686	0.432	22	0.136	K.QGPGTAILLGPNFLAEK.G
R2/RRR2-14/2	1725.652	1726.997	-1363.365	0.318	729.479	0.319	17	0.105	K.QGPGTAILLGPNFLAEK.G
R2/RRR2-14/2	1488.334	1487.642	-207.767	0.384	365.228	0.548	16	0.119	R.GAGIPIPAAANTDYR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1487.123	1487.642	-1024.579	0.319	410.277	0.537	17	0.116	R.GAGIPIPAAANTDYR.H
R2/RRR2-14/2	1487.228	1487.642	-279.462	0.350	326.999	0.436	15	0.111	R.GAGIPIPAAANTDYR.H
R2/RRR2-11/2	1415.086	1415.531	-315.254	0.503	1487.025	0.483	21	0.186	R.SPNELLNSEGGLGK.Q
R2/RRR2-1/2	1557.859	1557.665	124.797	0.437	1220.290	0.536	22	0.167	R.VM*GTGDATDGFPSTGK.D
R2/RRR2-5/2	1233.841	1234.347	-1223.988	0.493	1751.412	0.382	21	0.192	R.AAGGFGGITVNNR.A
R2/RRR2-5/2	1234.021	1234.347	-265.071	0.414	1274.390	0.313	19	0.133	R.AAGGFGGITVNNR.A
R2/RRR2-14/2	1659.238	1659.735	-300.816	0.485	1244.119	0.543	21	0.171	K.SGGLESEKDYPYTGR.D
R2/RRR2-20/3	1659.556	1659.735	-108.616	0.459	1285.770	0.544	28	0.148	K.SGGLESEKDYPYTGR.D
R2/RRR2-14/2	1658.993	1659.735	-1053.417	0.466	962.470	0.511	19	0.142	K.SGGLESEKDYPYTGR.D
R2/RRR2-14/2	1659.285	1659.735	-272.252	0.564	831.094	0.556	18	0.141	K.SGGLESEKDYPYTGR.D
R2/RRR2-13/3	1659.670	1659.735	-39.447	0.433	1282.515	0.465	27	0.127	K.SGGLESEKDYPYTGR.D
R2/RRR2-20/3	1659.337	1659.735	-240.449	0.459	1168.966	0.487	26	0.123	K.SGGLESEKDYPYTGR.D
R2/RRR2-13/3	1659.944	1659.735	126.186	0.457	1163.063	0.474	27	0.119	K.SGGLESEKDYPYTGR.D
R2/RRR2-14/3	1658.764	1659.735	-1192.189	0.417	1153.019	0.475	26	0.119	K.SGGLESEKDYPYTGR.D
R2/RRR2-13/3	1659.834	1659.735	59.807	0.487	1024.682	0.496	25	0.114	K.SGGLESEKDYPYTGR.D
R2/RRR2-14/3	1658.942	1659.735	-1084.123	0.437	1151.623	0.448	27	0.112	K.SGGLESEKDYPYTGR.D
R2/RRR2-14/3	1660.635	1659.735	-60.806	0.506	890.393	0.498	24	0.106	K.SGGLESEKDYPYTGR.D
R2/RRR2-14/2	1678.449	1677.840	-233.910	0.514	1407.964	0.506	19	0.180	K.EFTSVFYSLQNWR.S
R2/RRR2-14/2	1678.447	1677.840	-235.005	0.502	1157.569	0.477	18	0.151	K.EFTSVFYSLQNWR.S
R2/RRR2-14/2	1678.842	1677.840	0.977	0.486	1050.613	0.424	17	0.135	K.EFTSVFYSLQNWR.S
R2/RRR2-19/2	1617.259	1616.760	309.289	0.530	1414.510	0.503	22	0.181	K.GQQPLQGDITAANFR.T
R2/RRR2-19/2	1616.803	1616.760	26.458	0.493	1370.640	0.495	22	0.175	K.GQQPLQGDITAANFR.T
R2/RRR2-1/2	1452.779	1452.638	97.205	0.384	929.879	0.486	17	0.134	R.AIISGTSSIYNLGR.K
R2/RRR2-2/2	1453.073	1452.638	300.421	0.345	770.862	0.421	17	0.118	R.AIISGTSSIYNLGR.K
R2/RRR2-1/2	1545.071	1544.732	219.931	0.337	1334.958	0.123	19	0.110	R.SNQEELGSVLNLLK.Y
R2/RRR2-2/2	1453.109	1452.638	325.270	0.292	376.503	0.329	13	0.104	R.AIISGTSSIYNLGR.K
R2/RRR2-9/2	1435.448	1434.623	-121.853	0.429	1087.901	0.563	18	0.161	R.HWGIFTYDGLPK.Y
R2/RRR2-22/2	1745.521	1745.956	-250.033	0.417	1139.785	0.556	19	0.088	R.TGDSYLSAIGVYVRPF.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1745.165	1745.956	-1029.535	0.369	1033.854	0.444	18	0.066	R.TGDSYLSAIGVYVRPF.-
R2/RRR2-3/2	1157.148	1157.259	-96.351	0.441	1188.984	0.293	17	0.128	R.ISQDDVPQVR.K
R2/RRR2-3/2	1089.973	1090.297	-298.529	0.376	722.674	0.362	12	0.114	K.ALEQIFLQK.Q
R2/RRR2-3/2	1156.806	1157.259	-392.732	0.382	962.799	0.161	16	0.104	R.ISQDDVPQVR.K
R2/RRR2-21/2	1597.118	1597.684	-983.268	0.481	1482.190	0.482	20	0.180	K.VSDSGELNSLM*DDAK.Y
R2/RRR2-22/2	1598.211	1597.684	-297.103	0.522	1414.200	0.490	20	0.174	K.VSDSGELNSLM*DDAK.Y
R2/RRR2-21/2	1596.636	1597.684	-1286.467	0.401	1387.731	0.380	20	0.151	K.VSDSGELNSLM*DDAK.Y
R2/RRR2-21/2	1597.066	1597.684	-1015.882	0.480	1204.227	0.455	19	0.149	K.VSDSGELNSLM*DDAK.Y
R2/RRR2-22/2	1596.421	1597.684	-1421.929	0.283	1379.013	0.279	20	0.134	K.VSDSGELNSLM*DDAK.Y
R2/RRR2-20/2	1332.345	1331.497	-114.834	0.444	492.990	0.564	17	0.131	R.QALTLQSVVEDK.T
R2/RRR2-20/2	1332.324	1331.497	-130.825	0.406	502.279	0.541	17	0.127	R.QALTLQSVVEDK.T
R2/RRR2-20/2	1332.604	1331.497	80.061	0.379	228.622	0.400	13	0.114	R.QALTLQSVVEDK.T
R2/RRR2-7/2	1457.138	1456.542	-278.175	0.484	1206.292	0.543	18	0.170	-.SFGFNTAVEEAQR.-
R2/RRR2-6/2	1360.101	1360.535	-320.707	0.498	1606.854	0.431	19	0.185	R.NLSQQCLNALAK.A
R2/RRR2-6/2	1360.193	1360.535	-252.454	0.499	1488.447	0.400	19	0.167	R.NLSQQCLNALAK.A
R2/RRR2-6/2	1360.050	1360.535	-357.718	0.462	1423.878	0.404	19	0.162	R.NLSQQCLNALAK.A
R2/RRR2-1/2	1360.159	1360.535	-277.485	0.405	1052.203	0.359	18	0.128	R.NLSQQCLNALAK.A
R2/RRR2-16/2	1586.372	1586.726	-223.329	0.499	1090.868	0.559	24	0.163	K.DLALPVSGVSAEENGK.A
R2/RRR2-16/2	1586.352	1586.726	-235.990	0.430	801.460	0.504	21	0.132	K.DLALPVSGVSAEENGK.A
R2/RRR2-9/2	1291.077	1291.438	-280.384	0.441	683.464	0.578	19	0.139	R.GIAAAPVTNSYAR.R
R2/RRR2-9/2	1290.552	1291.438	-1465.727	0.327	589.081	0.474	17	0.118	R.GIAAAPVTNSYAR.R
R2/RRR2-9/2	1290.544	1291.438	-1471.997	0.252	386.983	0.302	14	0.104	-.GIAAAPVTNSYAR.-
R2/RRR2-10/2	1586.391	1586.689	-188.442	0.502	1268.414	0.542	21	0.172	K.GGLGNDAVILNSQDGR.S
R2/RRR2-10/2	1587.249	1586.689	-278.282	0.520	975.256	0.585	20	0.155	K.GGLGNDAVILNSQDGR.S
R2/RRR2-10/2	1586.352	1586.689	-212.990	0.479	702.004	0.598	18	0.138	K.GGLGNDAVILNSQDGR.S
R2/RRR2-15/2	1213.169	1213.319	-124.399	0.497	1079.129	0.556	16	0.159	K.SAAAVDPVEPEK.V
R2/RRR2-15/2	1213.042	1213.319	-228.979	0.435	923.796	0.498	15	0.137	-.SAAAVDPVEPEK.-
R2/RRR2-3/2	1637.050	1637.902	-1134.549	0.462	715.104	0.553	19	0.133	R.IPGTELLPGDIVSIGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1638.403	1637.902	-305.613	0.459	670.763	0.471	20	0.123	R.IPGTELLPGDIVSIGR.S
R2/RRR2-3/2	1636.832	1637.902	-1268.744	0.428	606.738	0.487	18	0.121	R.IPGTELLPGDIVSIGR.S
R2/RRR2-5/2	1393.958	1393.529	308.506	0.597	1510.585	0.453	19	0.178	R.GFVISDWQGLDR.I
R2/RRR2-5/2	1392.750	1393.529	-1281.165	0.454	1524.246	0.373	19	0.164	R.GFVISDWQGLDR.I
R2/RRR2-5/2	1392.444	1393.529	-1502.061	0.389	1564.078	0.321	19	0.158	R.GFVISDWQGLDR.I
R2/RRR2-3/2	1392.922	1393.529	-1157.421	0.400	775.938	0.404	15	0.119	R.GFVISDWQGLDR.I
R2/RRR2-2/2	1393.650	1393.529	87.097	0.362	468.447	0.354	13	0.109	R.GFVISDWQGLDR.I
R2/RRR2-6/2	1394.121	1393.529	-293.647	0.261	415.488	0.365	12	0.103	-.GFVISDWQGLDR.-
R2/RRR2-5/2	1536.635	1535.681	-29.450	0.530	1683.423	0.400	19	0.189	R.SWDFLGLNYYEK.S
R2/RRR2-8/2	1592.158	1590.764	248.339	0.482	846.851	0.574	17	0.146	K.YQTSFFPFGWGPR.I
R2/RRR2-6/2	1686.140	1686.028	66.252	0.558	1700.630	0.390	26	0.187	R.KDDFLLPGVVEVIIK.S
R2/RRR2-5/2	1687.584	1686.028	-263.841	0.580	942.004	0.506	18	0.138	R.KDDFLLPGVVEVIIK.S
R2/RRR2-1/2	1686.698	1686.028	-196.471	0.242	546.852	0.295	15	0.101	R.KDDFLLPGVVEVIIK.S
R2/RRR2-13/2	1523.289	1523.630	-224.138	0.512	1588.526	0.436	20	0.185	K.VLSDNFEQLNTSR.A
R2/RRR2-13/2	1524.164	1523.630	-306.509	0.595	1322.376	0.481	20	0.167	K.VLSDNFEQLNTSR.A
R2/RRR2-13/2	1524.448	1523.630	-119.639	0.588	1085.832	0.540	19	0.159	K.VLSDNFEQLNTSR.A
R2/RRR2-2/2	1542.650	1541.620	18.927	0.501	509.842	0.534	20	0.131	R.ISAEDETSGM*DLTR.H
R2/RRR2-2/2	1542.934	1541.620	204.133	0.451	267.301	0.512	18	0.124	R.ISAEDETSGM*DLTR.H
R2/RRR2-2/2	1542.937	1541.620	205.720	0.451	315.836	0.517	17	0.123	R.ISAEDETSGM*DLTR.H
R2/RRR2-1/2	1542.620	1541.620	-0.280	0.178	159.678	0.311	16	0.107	-.ISAEDETSGM*DLTR.-
R2/RRR2-4/2	1544.411	1544.732	-208.309	0.438	1539.348	0.434	18	0.179	R.GSLLQLLETDEIGR.V
R2/RRR2-22/3	1716.954	1716.868	50.008	0.432	814.911	0.575	28	0.112	R.VPDEVIDKVQEETSK.S
R2/RRR2-22/3	1717.082	1716.868	125.196	0.451	762.092	0.568	28	0.109	R.VPDEVIDKVQEETSK.S
R2/RRR2-22/3	1716.729	1716.868	-81.035	0.489	722.474	0.546	27	0.104	R.VPDEVIDKVQEETSK.S
R2/RRR2-1/2	1727.072	1726.913	92.613	0.500	1351.562	0.494	27	0.175	K.DAIVGLPGVNGLSTEQR.K
R2/RRR2-4/2	1487.799	1486.698	68.089	0.410	1501.582	0.438	17	0.176	R.WIELGAFYPFSR.D
R2/RRR2-17/2	1824.502	1825.078	-866.688	0.567	936.309	0.542	22	0.149	K.AFM*IDKDQVDWIQAK.F
R2/RRR2-17/2	1824.422	1825.078	-910.548	0.558	764.710	0.573	20	0.143	K.AFM*IDKDQVDWIQAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/3	1824.931	1825.078	-81.157	0.515	1269.808	0.521	26	0.141	K.AFM*IDKDQVDWIQAK.F
R2/RRR2-17/2	1824.550	1825.078	-839.890	0.496	645.973	0.550	20	0.134	K.AFM*IDKDQVDWIQAK.F
R2/RRR2-17/3	1824.733	1825.078	-189.966	0.545	1096.410	0.447	27	0.107	K.AFM*IDKDQVDWIQAK.F
R2/RRR2-17/3	1807.469	1809.079	-2003.301	0.357	742.693	0.261	24	0.068	K.AFMIDKDQVDWIQAK.F
R2/RRR2-9/2	1818.028	1819.181	-1187.953	0.336	462.732	0.539	14	0.110	K.VPGVTGPIPAALATLTALR.E
R2/RRR2-27/3	1116.381	1116.295	77.295	0.406	2020.627	0.161	25	0.120	R.GGWVSLVAAQK.G
R2/RRR2-26/3	1115.402	1116.295	-1701.607	0.300	796.491	0.183	21	0.060	-.GGWVSLVAAQK.-
R2/RRR2-26/3	1116.324	1116.295	26.628	0.338	1090.949	0.120	20	0.060	-.GGWVSLVAAQK.-
R2/RRR2-28/3	1116.587	1116.295	262.648	0.360	1021.018	0.116	20	0.057	-.GGWVSLVAAQK.-
R2/RRR2-25/3	1116.443	1116.295	132.727	0.338	1128.930	0.074	19	0.054	-.GGWVSLVAAQK.-
R2/RRR2-27/3	1117.234	1116.295	-54.161	0.382	1190.960	0.066	21	0.053	-.GGWVSLVAAQK.-
R2/RRR2-24/3	1116.676	1116.295	342.722	0.395	850.728	0.172	18	0.052	-.GGWVSLVAAQK.-
R2/RRR2-10/3	1299.451	1299.420	23.959	0.547	1110.146	0.532	23	0.126	R.HLSTLTGYHNR.T
R2/RRR2-10/3	1298.799	1299.420	-1251.961	0.463	924.876	0.541	21	0.114	R.HLSTLTGYHNR.T
R2/RRR2-11/3	1298.791	1299.420	-1258.615	0.491	855.399	0.510	20	0.106	R.HLSTLTGYHNR.T
R2/RRR2-10/3	1299.518	1299.420	75.541	0.502	677.279	0.530	19	0.102	R.HLSTLTGYHNR.T
R2/RRR2-11/3	1299.546	1299.420	97.162	0.424	691.017	0.440	18	0.088	R.HLSTLTGYHNR.T
R2/RRR2-11/3	1298.864	1299.420	-1201.419	0.347	665.634	0.343	18	0.077	R.HLSTLTGYHNR.T
R2/RRR2-6/2	1334.266	1334.543	-207.991	0.438	1387.748	0.467	17	0.171	R.AYELQALLGLDK.Q
R2/RRR2-6/2	1971.478	1971.301	89.928	0.538	1254.907	0.517	21	0.164	K.LM*STTYLVALCQAVDLR.H
R2/RRR2-6/2	1970.716	1971.301	-806.916	0.460	1025.312	0.457	19	0.135	K.LM*STTYLVALCQAVDLR.H
R2/RRR2-6/2	1972.133	1971.301	-85.487	0.499	1001.687	0.424	20	0.129	K.LM*STTYLVALCQAVDLR.H
R2/RRR2-6/2	1956.409	1955.302	54.972	0.471	1111.574	0.393	18	0.129	K.LMSTTYLVALCQAVDLR.H
R2/RRR2-2/3	1970.800	1971.301	-763.866	0.346	1074.333	0.219	23	0.068	-.LM*STTYLVALCQAVDLR.-
R2/RRR2-5/2	1853.540	1853.065	257.180	0.461	1345.149	0.478	21	0.166	R.EAATFAFGSILEGPSVQK.L
R2/RRR2-9/2	1762.450	1762.985	-873.274	0.396	752.771	0.555	22	0.133	K.LLEATGISTVPGSGFGQK.E
R2/RRR2-9/2	1762.592	1762.985	-223.508	0.466	562.253	0.603	21	0.133	K.LLEATGISTVPGSGFGQK.E
R2/RRR2-9/2	1762.618	1762.985	-208.848	0.450	713.348	0.534	23	0.132	K.LLEATGISTVPGSGFGQK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-16/2	1283.144	1283.416	-212.843	0.395	444.900	0.534	15	0.121	R.APQPSQIESAVR.W
R2/RRR2-2/2	1513.692	1513.764	-47.853	0.398	572.845	0.509	17	0.119	K.VPTGVSGTALAASLLR.D
R2/RRR2-18/2	1498.840	1498.624	145.027	0.509	1573.383	0.421	17	0.178	K.GDWLLFEYQNGR.S
R2/RRR2-18/2	1498.768	1498.624	96.673	0.484	1616.141	0.373	18	0.173	K.GDWLLFEYQNGR.S
R2/RRR2-19/2	1499.903	1498.624	186.719	0.377	636.058	0.321	14	0.108	K.GDWLLFEYQNGR.S
R2/RRR2-8/2	1850.257	1851.007	-949.156	0.478	1286.007	0.494	21	0.162	K.GFSINGTVGEDVVAELSR.A
R2/RRR2-8/2	1850.618	1851.007	-211.024	0.489	978.095	0.523	18	0.140	K.GFSINGTVGEDVVAELSR.A
R2/RRR2-5/2	1360.208	1360.580	-274.685	0.499	1001.875	0.541	19	0.154	K.FTEQALPVDLVK.R
R2/RRR2-5/2	1361.320	1360.580	-191.986	0.537	812.847	0.537	18	0.143	K.FTEQALPVDLVK.R
R2/RRR2-8/2	995.006	995.241	-236.210	0.412	580.430	0.538	16	0.130	K.VGPLTIPLGK.I
R2/RRR2-13/2	1595.490	1594.877	-243.310	0.431	1365.790	0.471	20	0.168	R.NIEGVSLPVLTPNLK.G
R2/RRR2-12/2	1524.285	1523.758	-311.063	0.537	829.390	0.536	18	0.141	R.ILGVQYSIPDYVR.V
R2/RRR2-12/2	1524.674	1523.758	-55.217	0.299	264.563	0.412	15	0.110	R.ILGVQYSIPDYVR.V
R2/RRR2-12/2	1342.884	1343.384	-373.415	0.447	1333.125	0.483	19	0.169	R.AAAAAYNYEGDAR.W
R2/RRR2-9/3	1187.270	1187.328	-49.265	0.403	2021.717	0.143	25	0.119	R.AKEEAEAVALR.A
R2/RRR2-9/3	1187.213	1187.328	-97.686	0.342	2044.067	0.104	25	0.113	R.AKEEAEAVALR.A
R2/RRR2-20/2	1147.971	1147.304	-291.126	0.481	1023.209	0.536	18	0.155	K.IGSLVDVQTSK.D
R2/RRR2-20/2	1147.044	1147.304	-227.210	0.425	1095.881	0.423	18	0.141	K.IGSLVDVQTSK.D
R2/RRR2-20/2	1146.451	1147.304	-1621.338	0.288	600.162	0.376	15	0.111	K.IGSLVDVQTSK.D
R2/RRR2-12/2	1088.839	1089.181	-315.820	0.508	1598.271	0.398	17	0.178	K.LGGELTVDER.N
R2/RRR2-12/2	1089.127	1089.181	-50.431	0.560	1592.176	0.386	17	0.174	K.LGGELTVDER.N
R2/RRR2-12/2	1088.929	1089.181	-232.702	0.459	1290.180	0.357	16	0.143	K.LGGELTVDER.N
R2/RRR2-13/2	1089.678	1089.181	457.238	0.376	982.883	0.299	16	0.119	K.LGGELTVDER.N
R2/RRR2-11/2	989.389	989.105	288.261	0.489	1447.680	0.451	17	0.177	K.AAEEILAGSK.K
R2/RRR2-9/2	1711.343	1710.995	204.286	0.421	1496.653	0.428	20	0.171	R.VIYGADLAAFLQTLSK.I
R2/RRR2-9/2	1710.396	1710.995	-937.719	0.339	1218.286	0.278	22	0.124	R.VIYGADLAAFLQTLSK.I
R2/RRR2-14/3	1925.807	1926.061	-132.537	0.456	800.022	0.544	30	0.107	K.GGRPIQM*STDHDPNVER.G
R2/RRR2-14/3	1926.824	1926.061	-123.349	0.424	486.693	0.524	27	0.092	K.GGRPIQM*STDHDPNVER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/3	1925.556	1926.061	-784.206	0.448	610.464	0.466	29	0.088	K.GGRPIQM*STDHDPNVER.G
R2/RRR2-13/2	1218.084	1217.266	-150.131	0.477	1387.151	0.466	16	0.171	R.DLGYLDDSYR.A
R2/RRR2-13/2	1216.971	1217.266	-243.934	0.365	1248.180	0.370	16	0.141	R.DLGYLDDSYR.A
R2/RRR2-13/2	1217.147	1217.266	-98.743	0.286	1083.055	0.340	15	0.124	R.DLGYLDDSYR.A
R2/RRR2-16/2	1476.209	1474.788	286.175	0.359	1992.236	0.137	18	0.164	K.KMEEELILLEVK.Y
R2/RRR2-29/2	1475.674	1474.788	-77.627	0.290	1324.342	0.226	16	0.124	K.KMEEELILLEVK.Y
R2/RRR2-30/2	1476.237	1474.788	305.245	0.349	1436.557	0.168	16	0.121	K.KMEEELILLEVK.Y
R2/RRR2-24/2	1475.606	1474.788	-123.764	0.294	1345.606	0.177	17	0.119	K.KMEEELILLEVK.Y
R2/RRR2-5/2	1475.708	1474.788	-54.229	0.276	1131.638	0.221	16	0.114	K.KMEEELILLEVK.Y
R2/RRR2-13/2	1476.096	1474.788	209.388	0.405	1074.811	0.240	16	0.113	-.KMEEELILLEVK.-
R2/RRR2-15/2	1476.158	1474.788	251.432	0.333	1276.715	0.138	17	0.111	K.KMEEELILLEVK.Y
R2/RRR2-3/2	1476.091	1474.788	206.071	0.320	988.107	0.163	15	0.105	-.KMEEELILLEVK.-
R2/RRR2-19/2	1476.242	1474.788	308.479	0.349	1053.947	0.128	15	0.103	-.KMEEELILLEVK.-
R2/RRR2-28/2	1475.925	1474.788	92.694	0.310	914.573	0.148	15	0.102	K.KMEEELILLEVK.Y
R2/RRR2-11/2	1476.147	1474.788	243.803	0.336	1109.398	0.102	15	0.100	K.KMEEELILLEVK.Y
R2/RRR2-23/2	1476.038	1474.788	169.581	0.325	915.736	0.108	15	0.100	-.KMEEELILLEVK.-
R2/RRR2-2/2	1475.774	1474.788	-9.757	0.286	747.724	0.165	13	0.099	-.KMEEELILLEVK.-
R2/RRR2-10/2	1476.128	1474.788	231.115	0.321	886.985	0.085	15	0.099	-.KMEEELILLEVK.-
R2/RRR2-19/2	1476.146	1474.788	243.388	0.335	825.645	0.139	14	0.095	-.KMEEELILLEVK.-
R2/RRR2-14/3	1918.783	1918.183	-209.469	0.416	582.354	0.535	24	0.094	R.VATNPAIIVGLHPCGGNAR.Q
R2/RRR2-14/3	1918.015	1918.183	-88.011	0.358	536.943	0.491	25	0.086	R.VATNPAIIVGLHPCGGNAR.Q
R2/RRR2-14/3	1917.716	1918.183	-244.125	0.328	480.415	0.492	22	0.082	-.VATNPAIIVGLHPCGGNAR.-
R2/RRR2-13/3	1918.973	1918.183	-110.106	0.256	385.128	0.392	19	0.065	-.VATNPAIIVGLHPCGGNAR.-
R2/RRR2-6/2	1418.380	1417.589	-147.490	0.411	468.248	0.518	12	0.114	-.WVADELAVVAESK.-
R2/RRR2-3/2	1560.696	1559.744	-30.800	0.507	1254.572	0.480	16	0.159	R.IIEETADQFFAFK.V
R2/RRR2-23/2	1343.261	1343.551	-216.807	0.518	1166.839	0.510	19	0.161	R.TPEGTIIELTIR.G
R2/RRR2-23/2	1343.353	1343.551	-148.344	0.508	1139.086	0.525	18	0.161	R.TPEGTIIELTIR.G
R2/RRR2-6/2	1149.948	1149.235	-250.699	0.435	311.844	0.452	13	0.120	R.HSTVVDSFEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/2	1149.108	1149.235	-111.302	0.398	338.862	0.451	14	0.120	R.HSTVVDSFEK.K
R2/RRR2-11/2	1302.923	1302.461	355.903	0.370	379.627	0.493	14	0.119	R.QALSLDEALWR.V
R2/RRR2-11/2	1302.330	1302.461	-100.934	0.353	503.712	0.374	16	0.114	R.QALSLDEALWR.V
R2/RRR2-11/2	1302.317	1302.461	-110.900	0.367	336.600	0.410	13	0.114	R.QALSLDEALWR.V
R2/RRR2-20/2	723.662	722.944	-390.510	-0.108	809.073	0.179	10	0.069	R.MSVVMR.L
R2/RRR2-10/2	1253.514	1252.400	90.778	0.456	1447.989	0.441	18	0.172	K.NFGVTEFVNPK.D
R2/RRR2-10/2	1252.115	1252.400	-228.483	0.489	1126.167	0.494	17	0.154	K.NFGVTEFVNPK.D
R2/RRR2-1/2	1252.949	1252.400	-361.228	0.317	430.528	0.367	13	0.110	K.NFGVTEFVNPK.D
R2/RRR2-20/2	1771.101	1770.924	100.058	0.276	449.905	0.504	20	0.113	R.EALNEHADVVAELFGR.V
R2/RRR2-20/2	1771.286	1770.924	204.907	0.291	246.383	0.400	17	0.108	R.EALNEHADVVAELFGR.V
R2/RRR2-8/2	1158.948	1159.230	-244.315	0.419	1200.649	0.495	15	0.158	R.SAVDYFEATR.A
R2/RRR2-8/2	1159.105	1159.230	-108.652	0.426	1205.938	0.478	15	0.156	R.SAVDYFEATR.A
R2/RRR2-8/2	1158.934	1159.230	-256.678	0.468	1143.439	0.462	15	0.149	R.SAVDYFEATR.A
R2/RRR2-9/3	1599.077	1598.869	130.338	0.483	1317.390	0.475	26	0.131	R.TPFYLYSKPQVVR.N
R2/RRR2-9/3	1598.624	1598.869	-153.845	0.356	914.567	0.387	23	0.084	R.TPFYLYSKPQVVR.N
R2/RRR2-8/2	1572.222	1572.656	-276.893	0.454	1144.759	0.509	23	0.158	K.TFTTAETTTNANTAK.T
R2/RRR2-1/2	1876.796	1875.067	-145.127	0.433	858.341	0.519	21	0.136	K.ILLLDEATSALDVESER.I
R2/RRR2-3/2	1874.142	1875.067	-1030.219	0.415	1193.627	0.299	20	0.122	K.ILLLDEATSALDVESER.I
R2/RRR2-1/2	1874.912	1875.067	-83.105	0.412	562.618	0.446	21	0.118	K.ILLLDEATSALDVESER.I
R2/RRR2-19/2	1184.237	1184.371	-112.860	0.372	445.488	0.510	14	0.120	K.NNPTLAAINKK.F
R2/RRR2-19/2	1183.535	1184.371	-1555.535	0.384	427.058	0.422	14	0.116	K.NNPTLAAINKK.F
R2/RRR2-20/2	1184.075	1184.371	-250.608	0.402	431.745	0.335	14	0.112	K.NNPTLAAINKK.F
R2/RRR2-1/2	1991.755	1990.329	214.314	0.385	552.376	0.487	17	0.113	R.IETLPAGFLLVATNLTSTK.L
R2/RRR2-6/2	1949.029	1950.209	-1121.930	0.509	474.090	0.471	18	0.115	K.FPGGNYVM*GNYLLNAFR.W
R2/RRR2-2/2	1253.569	1253.387	145.860	0.381	1400.957	0.412	18	0.160	K.ALAAEVTSTFSR.R
R2/RRR2-2/2	1254.342	1253.387	-35.785	0.284	687.288	0.411	16	0.113	K.ALAAEVTSTFSR.R
R2/RRR2-12/2	1798.190	1798.971	-993.525	0.511	910.639	0.540	22	0.146	R.VGFYQSSCPNAEALVR.Q
R2/RRR2-12/2	1798.380	1798.971	-887.281	0.524	696.193	0.508	20	0.129	R.VGFYQSSCPNAEALVR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1343.144	1342.437	-218.832	0.400	1332.141	0.473	18	0.165	R.TSFSDLVVGSSSR.T
R2/RRR2-5/2	1591.422	1591.790	-232.392	0.533	709.180	0.511	20	0.132	K.LISGDLQPTSGTVFR.S
R2/RRR2-1/3	1913.361	1914.066	-893.808	0.457	1333.133	0.461	32	0.132	R.LGM*EKGEGM*SAVADSGEGR.G
R2/RRR2-9/3	1913.651	1914.066	-217.430	0.337	884.115	0.343	27	0.077	R.LGM*EKGEGM*SAVADSGEGR.G
R2/RRR2-5/3	1311.465	1310.401	48.619	0.400	1361.776	0.443	26	0.129	R.HGVPSAVGSANASR.G
R2/RRR2-5/3	1310.096	1310.401	-233.754	0.356	1091.892	0.316	25	0.082	R.HGVPSAVGSANASR.G
R2/RRR2-8/2	1232.149	1232.409	-211.616	0.454	1183.651	0.510	18	0.161	K.NTVEGITGIISK.T
R2/RRR2-8/2	1231.978	1232.409	-350.482	0.396	836.417	0.477	18	0.132	K.NTVEGITGIISK.T
R2/RRR2-11/2	1516.309	1516.679	-244.549	0.376	1382.863	0.440	20	0.163	K.IDTNGVVSALLEER.L
R2/RRR2-11/2	1516.169	1516.679	-998.975	0.400	1319.503	0.397	20	0.150	K.IDTNGVVSALLEER.L
R2/RRR2-19/3	1773.890	1772.938	-27.348	0.445	1239.558	0.494	28	0.130	R.KENLSKPDDVLSAAER.Y
R2/RRR2-10/2	1080.200	1080.259	-54.589	0.467	1011.259	0.517	15	0.150	K.AILQSYLSGK.H
R2/RRR2-10/2	1079.608	1080.259	-1534.144	0.329	1254.269	0.409	15	0.146	K.AILQSYLSGK.H
R2/RRR2-10/2	1079.613	1080.259	-1529.714	0.327	1037.545	0.496	15	0.142	K.AILQSYLSGK.H
R2/RRR2-11/2	1444.151	1444.608	-317.387	0.442	1207.825	0.493	17	0.159	R.APTYSILDTCFR.G
R2/RRR2-8/2	1622.858	1622.803	34.357	0.396	383.046	0.480	17	0.117	R.ELGQWGLDNYLSVK.Q
R2/RRR2-8/2	1622.262	1622.803	-952.361	0.287	365.751	0.355	17	0.108	R.ELGQWGLDNYLSVK.Q
R2/RRR2-8/2	1097.816	1097.242	-388.964	0.347	429.372	0.490	12	0.120	R.SHCASFLFK.N
R2/RRR2-8/2	1096.989	1097.242	-231.439	0.388	379.257	0.480	11	0.120	R.SHCASFLFK.N
R2/RRR2-8/2	1096.481	1097.242	-1610.586	0.320	388.208	0.414	11	0.114	R.SHCASFLFK.N
R2/RRR2-7/2	1096.888	1097.242	-323.325	0.259	474.890	0.393	12	0.111	R.SHCASFLFK.N
R2/RRR2-9/2	1096.294	1097.242	-1781.957	0.208	405.473	0.387	11	0.107	R.SHCASFLFK.N
R2/RRR2-11/2	1548.645	1548.766	-78.081	0.511	1432.261	0.438	19	0.168	R.IPSFTKEQSELIR.G
R2/RRR2-11/2	1549.559	1548.766	-133.977	0.524	1276.292	0.478	19	0.162	R.IPSFTKEQSELIR.G
R2/RRR2-11/2	1549.267	1548.766	-322.564	0.554	1110.501	0.440	18	0.142	-.IPSFTKEQSELIR.-
R2/RRR2-6/2	1182.193	1182.395	-170.846	0.483	626.848	0.490	16	0.129	R.VPVNDANLIVK.T
R2/RRR2-6/2	1182.059	1182.395	-284.595	0.420	592.037	0.503	15	0.126	R.VPVNDANLIVK.T
R2/RRR2-6/2	1182.211	1182.395	-155.930	0.401	589.311	0.464	15	0.122	R.VPVNDANLIVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-1/2	1838.829	1838.053	-122.555	0.397	769.977	0.409	17	0.115	R.ILYLLSFDTQNEPAGR.A
R2/RRR2-2/2	1686.872	1685.861	6.488	0.401	727.951	0.382	18	0.113	R.VLTQDNEDNALLAIR.I
R2/RRR2-11/2	1978.106	1978.275	-85.702	0.405	654.362	0.516	17	0.119	R.APTVEIIGLTTIFGNTTTK.N
R2/RRR2-11/2	1550.422	1550.783	-233.483	0.442	1624.708	0.363	19	0.174	K.TLFVINFDPINTR.T
R2/RRR2-23/3	1736.554	1736.732	-102.530	0.495	1116.194	0.503	28	0.121	K.DAKEEFDDAGHSESAK.E
R2/RRR2-23/3	1736.417	1736.732	-181.969	0.466	1002.396	0.416	27	0.095	K.DAKEEFDDAGHSESAK.E
R2/RRR2-23/3	1735.398	1736.732	-1349.084	0.369	585.839	0.337	21	0.072	K.DAKEEFDDAGHSESAK.E
R2/RRR2-3/2	1518.958	1518.819	91.599	0.435	1169.195	0.476	18	0.152	R.LLEVELYPTLLSK.A
R2/RRR2-7/2	1585.388	1585.784	-250.652	0.413	1538.059	0.385	20	0.169	R.VLGDVTEGNALEVLR.Q
R2/RRR2-22/2	934.954	935.102	-158.600	0.540	1316.502	0.451	15	0.164	-.SGLFVGINK.-
R2/RRR2-22/2	935.062	935.102	-42.701	0.466	1324.449	0.406	15	0.155	K.SGLFVGINK.X
R2/RRR2-15/2	1635.274	1635.886	-989.182	0.409	1139.377	0.492	17	0.150	K.VVEPWVAYGYPNLK.S
R2/RRR2-5/2	1120.926	1120.280	-317.046	0.415	1447.671	0.418	16	0.168	R.TSGLEVVWTK.T
R2/RRR2-10/3	1306.350	1305.594	-187.375	0.378	1567.603	0.365	24	0.130	R.HVVLITNVKPGK.L
R2/RRR2-10/3	1305.363	1305.594	-177.621	0.409	1251.686	0.476	22	0.126	R.HVVLITNVKPGK.L
R2/RRR2-9/2	1407.114	1407.512	-283.714	0.479	694.266	0.509	14	0.130	R.HNEFEISDFLR.R
R2/RRR2-8/2	1408.132	1407.512	-271.162	0.337	561.432	0.353	14	0.110	R.HNEFEISDFLR.R
R2/RRR2-10/2	1684.567	1684.831	-157.254	0.403	1426.942	0.418	20	0.163	K.ALNLGSFFTSGADEVR.Q
R2/RRR2-13/3	1596.335	1596.764	-269.497	0.455	1178.676	0.489	28	0.123	K.TAGKDLASDKTTYPK.L
R2/RRR2-13/3	1596.803	1596.764	24.788	0.435	776.262	0.502	26	0.098	K.TAGKDLASDKTTYPK.L
R2/RRR2-13/3	1596.410	1596.764	-222.547	0.417	1010.944	0.413	26	0.095	K.TAGKDLASDKTTYPK.L
R2/RRR2-7/3	1676.519	1677.754	-1337.017	0.407	942.529	0.514	28	0.107	R.HGEILSDHAEESQPK.G
R2/RRR2-6/2	1508.807	1507.715	61.217	0.447	566.774	0.499	19	0.125	K.FTPSVIEPSFGIGR.I
R2/RRR2-6/2	1507.106	1507.715	-1070.623	0.312	700.124	0.372	21	0.114	K.FTPSVIEPSFGIGR.I
R2/RRR2-13/2	1847.648	1846.074	-231.309	0.395	528.835	0.500	15	0.115	K.HSVISDEVTTLVIFER.R
R2/RRR2-3/2	1759.667	1760.027	-205.302	0.463	544.978	0.476	22	0.120	K.SFASSGIPAPTLLSAALR.V
R2/RRR2-3/2	1759.435	1760.027	-907.825	0.330	254.528	0.416	15	0.106	K.SFASSGIPAPTLLSAALR.V
R2/RRR2-16/2	1279.378	1279.427	-38.338	0.470	979.961	0.511	18	0.146	K.GVVTDIIHDPGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1279.202	1279.427	-176.841	0.442	848.676	0.556	17	0.143	K.GVVTDIIHDPGR.G
R2/RRR2-14/2	1279.278	1279.427	-117.396	0.376	761.068	0.450	16	0.123	K.GVVTDIIHDPGR.G
R2/RRR2-26/2	1109.304	1109.257	42.316	0.542	1200.289	0.468	17	0.158	R.YIEATGIVSR.A
R2/RRR2-26/2	1109.892	1109.257	-330.678	0.528	1203.018	0.418	17	0.149	R.YIEATGIVSR.A
R2/RRR2-26/2	1108.967	1109.257	-262.833	0.522	1084.000	0.460	17	0.148	R.YIEATGIVSR.A
R2/RRR2-19/2	1033.278	1033.154	120.198	0.403	1468.035	0.400	14	0.165	R.GLEECGLVR.E
R2/RRR2-19/2	1032.897	1033.154	-250.304	0.336	1146.982	0.253	13	0.118	R.GLEECGLVR.E
R2/RRR2-3/2	1698.711	1697.913	-119.186	0.413	1203.403	0.457	18	0.149	K.YAQFSLAVINQLDSK.Y
R2/RRR2-3/2	1697.979	1697.913	39.182	0.300	791.031	0.300	15	0.105	K.YAQFSLAVINQLDSK.Y
R2/RRR2-12/3	1505.523	1504.676	-101.959	0.420	717.628	0.515	24	0.098	R.LAAALSSPAHPAGGAGR.N
R2/RRR2-11/3	1504.425	1504.676	-167.181	0.413	665.812	0.530	23	0.097	R.LAAALSSPAHPAGGAGR.N
R2/RRR2-12/3	1504.170	1504.676	-1004.104	0.354	538.406	0.432	23	0.081	R.LAAALSSPAHPAGGAGR.N
R2/RRR2-12/3	1504.727	1504.676	33.994	0.326	613.117	0.363	22	0.074	R.LAAALSSPAHPAGGAGR.N
R2/RRR2-11/2	1368.455	1368.518	-46.221	0.455	1433.925	0.421	19	0.166	K.YIGLSEASASTIR.R
R2/RRR2-12/2	1368.080	1368.518	-320.537	0.370	1403.501	0.347	17	0.148	K.YIGLSEASASTIR.R
R2/RRR2-24/3	1232.985	1233.424	-356.508	0.505	674.623	0.489	21	0.096	K.LLRPNM*ESTR.D
R2/RRR2-23/3	1233.666	1233.424	197.184	0.498	451.198	0.441	18	0.090	K.LLRPNM*ESTR.D
R2/RRR2-24/3	1233.195	1233.424	-186.225	0.439	588.443	0.420	18	0.085	K.LLRPNM*ESTR.D
R2/RRR2-23/3	1233.944	1233.424	-390.216	0.350	435.729	0.286	17	0.079	K.LLRPNM*ESTR.D
R2/RRR2-23/3	1232.971	1233.424	-368.429	0.363	303.608	0.432	14	0.069	-.LLRPNM*ESTR.-
R2/RRR2-11/2	1366.291	1365.519	-167.361	0.392	622.247	0.503	13	0.122	K.IISWNTTSWTR.I
R2/RRR2-11/3	1849.969	1851.180	-1198.754	0.432	1289.506	0.453	27	0.126	K.LLVDKDPGLVGNLLVER.L
R2/RRR2-17/2	1183.934	1184.329	-334.817	0.447	518.782	0.483	15	0.123	R.SPVYIPHSAGR.Y
R2/RRR2-19/3	1184.833	1184.329	-419.776	0.393	628.104	0.498	17	0.089	R.SPVYIPHSAGR.Y
R2/RRR2-19/3	1184.733	1184.329	341.998	0.399	485.978	0.482	16	0.084	R.SPVYIPHSAGR.Y
R2/RRR2-6/2	1742.137	1740.981	89.634	0.476	512.398	0.470	17	0.120	K.QLLQWPVDEIETLR.T
R2/RRR2-6/2	1740.292	1740.981	-973.320	0.406	407.026	0.364	15	0.108	K.QLLQWPVDEIETLR.T
R2/RRR2-6/2	1340.883	1341.452	-1173.668	0.429	921.717	0.508	16	0.140	R.TQVEHGIQDSVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1142.092	1142.292	-176.201	0.385	1037.431	0.491	16	0.145	K.TIFHLNPSGR.F
R2/RRR2-9/2	1142.216	1142.292	-67.382	0.358	881.999	0.392	15	0.124	K.TIFHLNPSGR.F
R2/RRR2-10/2	1142.159	1142.292	-117.232	0.368	802.978	0.413	14	0.123	K.TIFHLNPSGR.F
R2/RRR2-10/2	1142.085	1142.292	-182.313	0.380	995.444	0.315	16	0.121	K.TIFHLNPSGR.F
R2/RRR2-9/2	1143.088	1142.292	-179.368	0.401	946.903	0.315	16	0.120	K.TIFHLNPSGR.F
R2/RRR2-9/2	1142.077	1142.292	-188.961	0.338	786.830	0.385	15	0.120	K.TIFHLNPSGR.F
R2/RRR2-8/2	1143.423	1142.292	114.509	0.338	752.566	0.315	14	0.113	K.TIFHLNPSGR.F
R2/RRR2-16/2	1410.016	1410.684	-1186.719	0.374	703.432	0.508	16	0.124	R.SIGPVEGLALNLVK.D
R2/RRR2-16/2	1410.782	1410.684	69.723	0.370	784.994	0.471	15	0.122	R.SIGPVEGLALNLVK.D
R2/RRR2-9/2	1229.678	1230.436	-1434.038	0.409	1385.228	0.424	18	0.162	K.TLNDQIVVLSK.R
R2/RRR2-9/2	1231.132	1230.436	-248.189	0.577	987.709	0.495	17	0.146	K.TLNDQIVVLSK.R
R2/RRR2-9/2	1229.601	1230.436	-1496.760	0.450	1036.885	0.477	17	0.145	K.TLNDQIVVLSK.R
R2/RRR2-5/2	1898.887	1899.178	-153.755	0.438	941.051	0.492	20	0.134	K.LALGTLALEDALSTGSPIR.T
R2/RRR2-11/2	1085.067	1085.234	-154.431	0.316	785.640	0.498	14	0.127	K.YGVSGYPTLK.F
R2/RRR2-11/2	1085.093	1085.234	-130.506	0.357	578.847	0.510	13	0.123	K.YGVSGYPTLK.F
R2/RRR2-11/2	1084.632	1085.234	-1482.110	0.320	470.763	0.478	10	0.112	K.YGVSGYPTLK.F
R2/RRR2-9/2	1361.117	1361.528	-303.016	0.474	1434.218	0.413	17	0.166	R.LIQENQAEFLR.L
R2/RRR2-21/2	1259.300	1258.472	-136.618	0.484	1331.039	0.440	16	0.161	K.FNLFM*QQVSK.S
R2/RRR2-21/2	1258.200	1258.472	-216.435	0.508	1275.984	0.415	16	0.152	K.FNLFM*QQVSK.S
R2/RRR2-21/2	1258.104	1258.472	-292.846	0.408	1218.655	0.345	16	0.136	K.FNLFM*QQVSK.S
R2/RRR2-2/2	1144.456	1143.362	82.846	0.543	1576.510	0.354	15	0.166	K.KRELVVEAAK.K
R2/RRR2-8/2	1314.215	1314.427	-161.509	0.374	570.987	0.493	17	0.120	R.LGPGDDVDAVLSR.M
R2/RRR2-14/2	1535.471	1534.734	-171.646	0.450	1116.008	0.483	21	0.150	R.VSTTVTVDEALTGLK.T
R2/RRR2-11/3	1624.098	1624.772	-1033.992	0.461	785.557	0.507	24	0.100	K.LVLHHWSDDDCVK.I
R2/RRR2-11/3	1624.637	1624.772	-83.254	0.463	664.628	0.483	24	0.093	K.LVLHHWSDDDCVK.I
R2/RRR2-11/3	1624.974	1624.772	124.268	0.443	614.558	0.482	23	0.090	K.LVLHHWSDDDCVK.I
R2/RRR2-10/2	1086.047	1086.224	-163.085	0.437	1231.185	0.457	17	0.155	K.EAAIQAINAGK.N
R2/RRR2-10/2	1085.873	1086.224	-324.011	0.429	724.130	0.466	14	0.125	K.EAAIQAINAGK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/2	1085.832	1086.224	-361.910	0.296	992.187	0.238	14	0.109	K.EAAIQAINAGK.N
R2/RRR2-7/3	1675.864	1676.812	-1165.924	0.362	1181.183	0.454	25	0.115	R.HGEILSDHAKESQPK.G
R2/RRR2-7/3	1676.027	1676.812	-1068.287	0.390	866.841	0.477	25	0.097	R.HGEILSDHAKESQPK.G
R2/RRR2-19/3	1464.883	1464.645	162.630	0.475	735.305	0.496	22	0.095	K.KGEEVPLSEYKGK.V
R2/RRR2-24/2	1338.088	1338.535	-334.675	0.505	1151.974	0.473	20	0.152	K.VSGVEIVPDPVAR.G
R2/RRR2-23/2	1338.331	1338.535	-152.652	0.519	1116.813	0.465	20	0.148	K.VSGVEIVPDPVAR.G
R2/RRR2-24/2	1338.146	1338.535	-291.566	0.471	1111.822	0.429	20	0.142	K.VSGVEIVPDPVAR.G
R2/RRR2-23/2	1339.122	1338.535	-308.725	0.484	944.612	0.490	19	0.141	K.VSGVEIVPDPVAR.G
R2/RRR2-23/2	1337.712	1338.535	-1366.460	0.360	856.823	0.356	18	0.118	K.VSGVEIVPDPVAR.G
R2/RRR2-24/2	1338.254	1338.535	-210.665	0.469	832.191	0.352	18	0.118	K.VSGVEIVPDPVAR.G
R2/RRR2-1/2	1339.516	1338.535	-13.949	0.389	555.437	0.281	15	0.107	K.VSGVEIVPDPVAR.G
R2/RRR2-18/2	935.983	936.136	-164.770	0.456	712.383	0.495	14	0.135	R.HVVIIAQR.T
R2/RRR2-18/2	935.920	936.136	-232.284	0.426	698.377	0.507	14	0.135	R.HVVIIAQR.T
R2/RRR2-18/2	936.230	936.136	100.487	0.451	706.423	0.376	14	0.123	R.HVVIIAQR.T
R2/RRR2-18/2	935.272	936.136	-1999.601	0.351	506.835	0.468	11	0.120	R.HVVIIAQR.T
R2/RRR2-20/2	1448.349	1447.616	-185.268	0.402	723.537	0.502	18	0.127	K.TVTLQSELVGNASK.V
R2/RRR2-20/2	1446.561	1447.616	-1424.961	0.339	705.963	0.499	17	0.123	K.TVTLQSELVGNASK.V
R2/RRR2-21/2	1345.320	1345.529	-155.954	0.380	492.383	0.475	17	0.120	R.NSPVPSFSGLLAR.A
R2/RRR2-20/2	1346.210	1345.529	-237.342	0.373	493.793	0.444	17	0.117	R.NSPVPSFSGLLAR.A
R2/RRR2-21/2	1345.792	1345.529	196.364	0.335	576.589	0.365	18	0.113	R.NSPVPSFSGLLAR.A
R2/RRR2-21/2	1345.119	1345.529	-305.801	0.270	234.520	0.348	13	0.102	-.NSPVPSFSGLLAR.-
R2/RRR2-13/2	1030.964	1031.187	-216.452	0.399	612.476	0.491	12	0.124	K.FTDVPINPK.V
R2/RRR2-13/2	1030.924	1031.187	-255.534	0.337	662.831	0.492	12	0.122	K.FTDVPINPK.V
R2/RRR2-10/2	1638.669	1637.814	-88.660	0.445	720.208	0.489	15	0.124	K.FAFVDVSPEELQQK.E
R2/RRR2-10/2	1637.502	1637.814	-191.084	0.321	875.395	0.265	18	0.108	K.FAFVDVSPEELQQK.E
R2/RRR2-21/2	1394.629	1395.573	-1398.420	0.408	852.049	0.511	21	0.136	R.GAAAAAAPAVQHM*GR.-
R2/RRR2-21/2	1395.107	1395.573	-335.326	0.423	670.811	0.524	19	0.128	R.GAAAAAAPAVQHM*GR.-
R2/RRR2-21/2	1395.178	1395.573	-283.883	0.385	680.235	0.418	19	0.117	R.GAAAAAAPAVQHM*GR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1497.416	1497.719	-202.828	0.357	579.304	0.492	14	0.116	R.VPTPDVSVVDLTVR.L
R2/RRR2-12/2	1497.229	1497.719	-328.133	0.386	612.663	0.410	15	0.112	R.VPTPDVSVVDLTVR.L
R2/RRR2-9/2	1146.019	1146.321	-263.951	0.370	842.395	0.493	14	0.132	R.ITEGVNLPFR.V
R2/RRR2-9/2	1504.683	1504.826	-95.172	0.432	1004.838	0.488	19	0.141	R.SMHLLAPAIAGVAPR.A
R2/RRR2-2/2	1822.967	1821.965	1.571	0.484	1054.203	0.487	19	0.143	R.AQAYAEDVDIPEVWSK.V
R2/RRR2-8/2	1178.792	1178.320	401.898	0.355	797.383	0.473	14	0.126	K.YTSDPGLVLGR.Q
R2/RRR2-8/2	1178.692	1178.320	316.340	0.306	684.236	0.474	14	0.120	K.YTSDPGLVLGR.Q
R2/RRR2-8/2	1177.969	1178.320	-298.575	0.320	797.506	0.373	14	0.116	K.YTSDPGLVLGR.Q
R2/RRR2-4/2	1178.675	1178.320	301.905	0.265	960.784	0.320	15	0.116	K.YTSDPGLVLGR.Q
R2/RRR2-3/2	1178.270	1178.320	-42.667	0.225	560.023	0.345	13	0.106	K.YTSDPGLVLGR.Q
R2/RRR2-21/2	1898.634	1898.064	-227.419	0.479	751.709	0.489	23	0.131	K.IFTQFWDEEGIANAQK.S
R2/RRR2-19/2	1031.730	1032.216	-472.739	0.381	854.937	0.495	16	0.135	R.ILNGTVVSTK.M
R2/RRR2-16/2	1652.970	1651.997	-16.415	0.468	1133.180	0.473	18	0.146	K.IGVYVGGIVPVMYQR.V
R2/RRR2-16/2	1652.528	1651.997	-284.478	0.424	808.496	0.459	17	0.124	K.IGVYVGGIVPVMYQR.V
R2/RRR2-17/2	1579.490	1578.855	-231.653	0.442	848.450	0.492	15	0.129	K.EYGLIDGVIM*NPLK.A
R2/RRR2-17/2	1579.856	1578.855	0.974	0.365	566.761	0.400	15	0.110	K.EYGLIDGVIM*NPLK.A
R2/RRR2-8/2	1894.982	1894.192	-110.718	0.274	768.955	0.462	19	0.116	-.MAEVEVAAAAAAAGVLHRR.I
R2/RRR2-9/2	1895.590	1894.192	210.912	0.250	727.372	0.317	17	0.102	-.MAEVEVAAAAAAAGVLHRR.I
R2/RRR2-10/2	826.043	826.021	27.330	0.409	281.115	0.380	9	0.122	R.IVRFYK.K
R2/RRR2-10/2	826.091	826.021	86.169	0.324	283.381	0.270	9	0.117	R.IVRFYK.K
R2/RRR2-10/2	825.950	826.021	-85.327	0.182	285.212	0.312	9	0.108	R.IVRFYK.K
R2/RRR2-9/2	1198.960	1199.382	-352.985	0.462	1476.809	0.388	19	0.165	K.TPLELGATAGLR.L
R2/RRR2-9/2	1969.898	1970.214	-160.643	0.430	526.825	0.457	18	0.114	K.FTVIFDTGSSNLWVPSAK.C
R2/RRR2-9/2	1969.485	1970.214	-880.506	0.360	368.276	0.360	15	0.104	K.FTVIFDTGSSNLWVPSAK.C
R2/RRR2-9/2	1969.598	1970.214	-822.768	0.318	380.427	0.326	16	0.103	K.FTVIFDTGSSNLWVPSAK.C
R2/RRR2-11/3	1618.966	1617.805	99.841	0.410	636.044	0.483	21	0.088	R.HQADVCHAYQIM*K.K
R2/RRR2-11/3	1618.125	1617.805	198.448	0.395	499.508	0.436	20	0.081	R.HQADVCHAYQIM*K.K
R2/RRR2-22/2	1082.434	1082.232	186.679	0.402	971.802	0.484	17	0.140	R.YGSLTGLSGVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1082.464	1082.232	214.838	0.353	771.027	0.488	16	0.128	R.YGSLTGLSGVK.V
R2/RRR2-20/2	1081.927	1082.232	-283.095	0.417	749.806	0.476	15	0.128	R.YGSLTGLSGVK.V
R2/RRR2-20/2	1081.607	1082.232	-1506.744	0.385	673.212	0.510	15	0.128	R.YGSLTGLSGVK.V
R2/RRR2-24/2	1248.005	1248.368	-292.317	0.354	824.685	0.478	17	0.127	R.GGVIVDSGTSVTR.L
R2/RRR2-14/3	1458.950	1458.690	178.272	0.457	1371.735	0.411	28	0.119	K.YSVRPNTGVVLPR.S
R2/RRR2-14/3	1458.059	1458.690	-1122.056	0.437	1268.900	0.439	27	0.117	K.YSVRPNTGVVLPR.S
R2/RRR2-18/2	1160.932	1161.375	-382.899	0.541	1376.338	0.401	18	0.156	K.LLFLGLDNAGK.T
R2/RRR2-17/2	1161.119	1161.375	-221.503	0.513	1381.653	0.395	18	0.156	K.LLFLGLDNAGK.T
R2/RRR2-17/2	1161.206	1161.375	-146.308	0.412	1287.707	0.404	18	0.150	K.LLFLGLDNAGK.T
R2/RRR2-18/2	1161.087	1161.375	-249.032	0.539	1294.706	0.393	18	0.149	K.LLFLGLDNAGK.T
R2/RRR2-18/2	1160.847	1161.375	-1320.359	0.488	1337.256	0.376	17	0.148	K.LLFLGLDNAGK.T
R2/RRR2-18/2	1161.241	1161.375	-116.044	0.499	1262.566	0.378	18	0.144	K.LLFLGLDNAGK.T
R2/RRR2-17/2	1160.736	1161.375	-1417.002	0.493	1206.627	0.390	17	0.142	K.LLFLGLDNAGK.T
R2/RRR2-11/2	1218.307	1218.384	-63.174	0.374	999.638	0.473	16	0.139	R.YIDIGIPANNK.G
R2/RRR2-11/2	1218.457	1218.384	59.928	0.274	527.966	0.197	13	0.098	-.YIDIGIPANNK.-
R2/RRR2-6/2	1733.678	1732.916	-137.757	0.414	741.306	0.489	20	0.127	K.DGAPGLWPFGPVDFEK.M
R2/RRR2-6/2	1732.108	1732.916	-1046.697	0.346	573.196	0.426	19	0.114	K.DGAPGLWPFGPVDFEK.M
R2/RRR2-6/2	1732.696	1732.916	-127.448	0.389	579.934	0.420	18	0.113	K.DGAPGLWPFGPVDFEK.M
R2/RRR2-19/2	867.898	868.056	-182.563	0.426	498.501	0.446	14	0.123	K.VGPLGLSPK.K
R2/RRR2-19/2	867.829	868.056	-262.008	0.369	686.696	0.433	15	0.123	K.VGPLGLSPK.K
R2/RRR2-19/2	867.850	868.056	-237.595	0.351	655.035	0.431	15	0.121	K.VGPLGLSPK.K
R2/RRR2-7/2	1978.564	1978.234	167.166	0.415	716.031	0.466	18	0.118	R.ELTAPFVDDGLIEVVGFR.D
R2/RRR2-12/3	1731.680	1730.946	-154.044	0.453	928.318	0.480	31	0.102	R.VLSIQSHTVQGYVGNK.S
R2/RRR2-12/3	1730.877	1730.946	-40.017	0.408	768.511	0.511	28	0.098	R.VLSIQSHTVQGYVGNK.S
R2/RRR2-12/3	1731.848	1730.946	-57.103	0.465	744.784	0.476	28	0.094	R.VLSIQSHTVQGYVGNK.S
R2/RRR2-21/2	1389.808	1389.625	132.178	0.490	1214.902	0.444	17	0.150	K.NVSNFLVQAGIVK.K
R2/RRR2-17/2	1043.971	1044.227	-245.890	0.392	827.227	0.484	15	0.131	K.VLVLGDAATGK.T
R2/RRR2-17/2	1043.795	1044.227	-414.960	0.295	852.814	0.389	14	0.117	K.VLVLGDAATGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-17/2	1043.663	1044.227	-1502.984	0.219	757.115	0.291	14	0.105	K.VLVLGDAATGK.T
R2/RRR2-6/2	1336.088	1335.579	-368.349	0.438	535.826	0.436	17	0.121	K.SLHPKWSPAALK.S
R2/RRR2-6/2	1335.108	1335.579	-353.488	0.372	365.159	0.341	14	0.111	K.SLHPKWSPAALK.S
R2/RRR2-6/2	1334.538	1335.579	-1534.024	0.330	456.670	0.357	15	0.110	K.SLHPKWSPAALK.S
R2/RRR2-6/3	1335.590	1335.579	8.735	0.436	1057.847	0.346	25	0.086	K.SLHPKWSPAALK.S
R2/RRR2-6/3	1334.535	1335.579	-1535.918	0.416	826.401	0.329	23	0.077	K.SLHPKWSPAALK.S
R2/RRR2-6/3	1334.479	1335.579	-1578.509	0.412	914.828	0.298	23	0.075	K.SLHPKWSPAALK.S
R2/RRR2-5/3	1335.712	1335.579	100.168	0.390	1011.275	0.219	24	0.068	K.SLHPKWSPAALK.S
R2/RRR2-8/2	1699.422	1697.916	-291.830	0.485	588.987	0.439	18	0.114	-.VVWEDGILNVVPGSGR.-
R2/RRR2-3/2	1144.382	1144.305	67.873	0.416	679.538	0.469	14	0.125	K.HQATLLEFGK.V
R2/RRR2-16/2	1249.592	1250.426	-1471.639	0.441	1471.978	0.370	17	0.161	K.ALEVYQAQLSK.S
R2/RRR2-11/2	1593.874	1592.885	-6.960	0.404	566.659	0.459	15	0.113	R.GIGEVLAMQFASLGAK.L
R2/RRR2-11/2	1593.978	1592.885	58.868	0.294	643.111	0.137	16	0.095	R.GIGEVLAMQFASLGAK.L
R2/RRR2-16/2	1547.841	1546.697	93.766	0.435	631.461	0.468	21	0.126	R.FGTICVFCGSNAGR.R
R2/RRR2-16/2	1548.140	1546.697	287.509	0.432	362.170	0.579	16	0.125	R.FGTICVFCGSNAGR.R
R2/RRR2-16/2	1548.084	1546.697	251.218	0.281	235.104	0.549	16	0.113	R.FGTICVFCGSNAGR.R
R2/RRR2-19/2	1565.975	1566.784	-1158.757	0.390	868.048	0.480	17	0.130	K.IFFVSWSPAAADVR.S
R2/RRR2-17/2	1237.283	1237.518	-190.650	0.454	704.572	0.470	17	0.129	K.LPFAPVPLVQR.M
R2/RRR2-17/2	1237.310	1237.518	-168.876	0.401	648.428	0.498	17	0.128	K.LPFAPVPLVQR.M
R2/RRR2-17/2	1236.567	1237.518	-1582.688	0.369	505.016	0.528	15	0.124	K.LPFAPVPLVQR.M
R2/RRR2-12/2	1507.950	1507.674	184.098	0.456	1216.598	0.439	19	0.151	R.GWLEWNGADFALK.T
R2/RRR2-8/2	1247.267	1246.480	-171.258	0.234	886.303	0.440	17	0.120	R.ALLVGINYPGTK.A
R2/RRR2-8/2	1247.443	1246.480	-30.192	0.254	795.678	0.358	17	0.112	R.ALLVGINYPGTK.A
R2/RRR2-6/2	1039.222	1039.124	94.652	0.410	761.424	0.469	13	0.129	K.ANITESFTR.Q
R2/RRR2-5/2	1040.054	1039.124	-67.291	0.339	692.390	0.443	13	0.121	K.ANITESFTR.Q
R2/RRR2-6/2	1039.885	1039.124	-230.843	0.365	559.389	0.434	12	0.118	K.ANITESFTR.Q
R2/RRR2-23/2	1307.387	1308.470	-1598.566	0.369	1173.680	0.436	17	0.145	K.GVAFVNNFNIGR.F
R2/RRR2-8/2	1616.647	1615.918	-168.632	0.523	949.927	0.459	21	0.137	R.DFPLGDLPMLEVLR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/2	1616.658	1615.918	-161.663	0.439	679.138	0.412	19	0.119	R.DFPLGDLPMLEVLR.C
R2/RRR2-8/2	1615.885	1615.918	-20.504	0.395	632.584	0.365	18	0.113	R.DFPLGDLPMLEVLR.C
R2/RRR2-12/2	1248.859	1249.357	-399.568	0.458	894.247	0.473	17	0.137	K.TGFTGGLNYYR.C
R2/RRR2-12/2	1248.472	1249.357	-1513.952	0.411	781.846	0.431	16	0.125	K.TGFTGGLNYYR.C
R2/RRR2-12/2	1249.230	1249.357	-101.892	0.402	697.206	0.422	15	0.120	K.TGFTGGLNYYR.C
R2/RRR2-8/3	1727.316	1727.927	-935.624	0.479	1054.142	0.458	26	0.107	R.RVQEHM*TLASNPTAR.R
R2/RRR2-8/3	1727.929	1727.927	1.229	0.462	877.029	0.469	23	0.098	R.RVQEHM*TLASNPTAR.R
R2/RRR2-8/3	1728.018	1727.927	52.457	0.447	731.265	0.452	22	0.089	R.RVQEHM*TLASNPTAR.R
R2/RRR2-26/3	1707.318	1707.819	-881.683	0.362	721.014	0.480	24	0.087	K.CM*SYCSGHSGPCCK.W
R2/RRR2-19/2	1370.601	1370.621	-15.151	0.394	1079.672	0.455	19	0.143	K.VHLVAIDIFTNK.K
R2/RRR2-21/2	1888.980	1889.061	-42.559	0.510	900.407	0.459	18	0.130	R.LTWWEQIDNGQQLTR.N
R2/RRR2-1/2	1732.434	1731.934	289.151	0.486	1132.718	0.432	19	0.140	K.LNSELLNNLGNFINR.V
R2/RRR2-4/2	1731.390	1731.934	-894.314	0.441	883.288	0.440	18	0.126	K.LNSELLNNLGNFINR.V
R2/RRR2-5/3	1731.709	1731.934	-130.497	0.409	1067.313	0.349	22	0.086	K.LNSELLNNLGNFINR.V
R2/RRR2-5/2	1972.708	1971.206	-253.202	0.429	890.966	0.461	15	0.124	R.GVWLNDFQYAIFGLGNR.Q
R2/RRR2-5/2	1973.112	1971.206	-48.067	0.332	355.975	0.375	12	0.101	R.GVWLNDFQYAIFGLGNR.Q
R2/RRR2-13/2	1614.433	1613.794	-224.225	0.519	1020.044	0.451	20	0.139	K.ILNENDLITPDLSR.V
R2/RRR2-13/2	1613.219	1613.794	-979.481	0.426	917.887	0.413	19	0.127	K.ILNENDLITPDLSR.V
R2/RRR2-12/2	1656.627	1655.914	-173.727	0.423	593.061	0.454	16	0.114	R.AVITPESIEGVVDVVK.A
R2/RRR2-13/2	1567.056	1567.769	-1096.077	0.486	809.349	0.462	20	0.128	R.SRPSELALPVSDPAK.A
R2/RRR2-5/2	1200.452	1199.425	22.376	0.445	1531.991	0.333	16	0.159	R.LLNLQTLDIR.N
R2/RRR2-4/2	1200.283	1199.425	-119.206	0.443	921.520	0.322	14	0.117	R.LLNLQTLDIR.N
R2/RRR2-14/3	1319.847	1320.433	-1205.000	0.450	1179.706	0.438	21	0.110	K.FSEIQKEDPAR.E
R2/RRR2-14/3	1319.732	1320.433	-1292.916	0.390	814.003	0.417	20	0.086	K.FSEIQKEDPAR.E
R2/RRR2-14/3	1320.335	1320.433	-74.484	0.360	769.623	0.364	19	0.078	K.FSEIQKEDPAR.E
R2/RRR2-12/2	1245.382	1245.408	-20.706	0.430	1141.604	0.444	18	0.144	K.NSLSGTIPASLGK.I
R2/RRR2-11/2	1245.141	1245.408	-214.619	0.430	990.209	0.424	18	0.132	K.NSLSGTIPASLGK.I
R2/RRR2-23/2	1293.846	1293.494	272.950	0.468	1200.370	0.430	15	0.149	K.NFAFLDYFKK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1512.741	1513.593	-1228.437	0.462	977.397	0.453	21	0.100	-.VLYHEDPNSPDAR.-
R2/RRR2-8/3	1513.715	1513.593	80.301	0.464	1057.163	0.425	22	0.100	-.VLYHEDPNSPDAR.-
R2/RRR2-1/3	1513.321	1513.593	-180.357	0.412	982.358	0.354	22	0.084	K.VLYHEDPNSPDAR.I
R2/RRR2-8/3	1513.431	1513.593	-107.898	0.412	765.930	0.350	21	0.078	K.VLYHEDPNSPDAR.I
R2/RRR2-12/3	1565.055	1565.740	-1079.694	0.484	1095.467	0.443	29	0.105	K.AM*GNEHALVISNHR.S
R2/RRR2-12/3	1565.093	1565.740	-1055.142	0.460	1064.918	0.391	29	0.093	K.AM*GNEHALVISNHR.S
R2/RRR2-12/3	1565.514	1565.740	-144.707	0.372	836.339	0.336	28	0.076	K.AM*GNEHALVISNHR.S
R2/RRR2-9/2	1171.243	1170.301	-49.614	0.447	739.918	0.460	13	0.128	K.SPNYTWFVR.L
R2/RRR2-9/2	1171.235	1170.301	-56.932	0.419	711.068	0.438	13	0.124	K.SPNYTWFVR.L
R2/RRR2-9/2	1171.117	1170.301	-157.720	0.384	683.687	0.416	12	0.119	K.SPNYTWFVR.L
R2/RRR2-20/2	712.966	712.734	325.664	0.063	787.183	0.318	10	0.092	R.LHGDDR.V
R2/RRR2-21/2	712.724	712.734	-14.020	-0.020	747.981	0.276	10	0.081	R.LHGDDR.V
R2/RRR2-21/3	1384.027	1382.670	258.561	0.498	1070.125	0.442	24	0.104	R.CKQLGITALHIK.I
R2/RRR2-21/3	1383.965	1382.670	213.188	0.475	969.465	0.396	22	0.090	R.CKQLGITALHIK.I
R2/RRR2-5/3	1397.987	1398.549	-1120.613	0.491	1339.748	0.385	25	0.112	R.VGHYLHISSEQK.L
R2/RRR2-22/3	1442.433	1442.517	-58.163	0.460	1262.803	0.415	25	0.114	R.ALAADHDASASAVSR.R
R2/RRR2-22/3	1442.142	1442.517	-260.404	0.477	948.569	0.517	25	0.112	R.ALAADHDASASAVSR.R
R2/RRR2-22/3	1443.960	1442.517	308.158	0.492	1052.135	0.451	26	0.105	R.ALAADHDASASAVSR.R
R2/RRR2-21/3	1442.171	1442.517	-240.278	0.379	452.289	0.360	21	0.056	-.ALAADHDASASAVSR.-
R2/RRR2-3/2	1242.247	1242.407	-129.569	0.438	984.511	0.437	17	0.133	K.LPGGLAASLTGER.S
R2/RRR2-13/2	1101.754	1102.268	-1378.397	0.424	768.716	0.462	13	0.129	R.ILDITHAYR.A
R2/RRR2-13/2	1101.567	1102.268	-1548.576	0.365	806.815	0.354	13	0.117	R.ILDITHAYR.A
R2/RRR2-13/2	1101.445	1102.268	-1659.796	0.238	717.487	0.206	12	0.102	R.ILDITHAYR.A
R2/RRR2-18/2	1111.104	1111.234	-116.762	0.375	654.646	0.453	12	0.120	R.YGNFPAQWK.A
R2/RRR2-16/2	1058.106	1058.254	-140.199	0.316	1131.956	0.419	17	0.138	K.VVLLGDTGVGK.S
R2/RRR2-16/2	1058.085	1058.254	-159.295	0.267	945.771	0.325	16	0.115	K.VVLLGDTGVGK.S
R2/RRR2-16/2	1058.048	1058.254	-194.942	0.265	656.186	0.375	13	0.109	-.VVLLGDTGVGK.-
R2/RRR2-21/2	1384.481	1384.691	-152.074	0.469	988.704	0.453	18	0.138	R.LVAIIQNPLQFK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-20/2	1386.006	1384.691	227.857	0.226	463.266	0.346	13	0.102	-.LVAIIQNPLQFK.-
R2/RRR2-4/2	1878.886	1877.070	-98.373	0.396	632.105	0.441	17	0.113	R.NNTASDILNQMASVLER.I
R2/RRR2-4/3	1931.553	1932.984	-1262.093	0.382	849.141	0.459	24	0.091	R.HDFSFEDAHDLDLGTGR.S
R2/RRR2-10/2	1426.739	1426.660	54.896	0.469	1214.189	0.420	18	0.148	R.ILIGSIM*EEYNK.A
R2/RRR2-10/2	1426.045	1426.660	-1135.919	0.387	745.004	0.324	15	0.110	R.ILIGSIM*EEYNK.A
R2/RRR2-14/2	1058.882	1059.198	-299.547	0.434	1422.984	0.365	16	0.156	K.ILESAAELGR.G
R2/RRR2-3/2	1440.732	1439.677	38.360	0.316	888.257	0.423	15	0.122	K.LPACFFILTNSR.S
R2/RRR2-6/2	1496.907	1495.703	136.626	0.310	565.450	0.438	13	0.109	R.LPVTWYPASFADK.V
R2/RRR2-12/2	1189.571	1189.348	188.599	0.450	1063.144	0.442	14	0.142	K.HQQWYVLSK.T
R2/RRR2-3/2	1655.283	1653.898	232.803	0.473	892.972	0.424	20	0.127	K.LPSSDIPDILIDVQK.R
R2/RRR2-13/3	1551.496	1551.768	-175.485	0.329	759.286	0.461	23	0.087	R.YGEITAWTGKPTVK.V
R2/RRR2-13/3	1551.872	1551.768	67.636	0.329	460.104	0.413	18	0.075	R.YGEITAWTGKPTVK.V
R2/RRR2-10/3	1119.069	1119.252	-163.974	0.514	1229.919	0.404	24	0.104	R.ILHDTSGTFK.Y
R2/RRR2-10/3	1118.929	1119.252	-289.721	0.491	1132.324	0.428	23	0.103	R.ILHDTSGTFK.Y
R2/RRR2-10/3	1119.013	1119.252	-214.860	0.317	953.618	0.239	21	0.067	R.ILHDTSGTFK.Y
R2/RRR2-17/3	1538.407	1538.734	-213.429	0.440	952.890	0.451	25	0.099	R.KIENVATGPNNRPK.L
R2/RRR2-17/3	1538.288	1538.734	-290.929	0.449	974.480	0.419	25	0.094	R.KIENVATGPNNRPK.L
R2/RRR2-17/3	1538.781	1538.734	30.815	0.438	664.605	0.418	22	0.083	R.KIENVATGPNNRPK.L
R2/RRR2-5/2	1561.286	1560.768	-309.730	0.367	641.198	0.427	15	0.113	K.LPLEIGSVSEISCR.R
R2/RRR2-4/2	1561.839	1560.768	45.733	0.299	191.613	0.367	12	0.106	K.LPLEIGSVSEISCR.R
R2/RRR2-15/2	940.956	941.151	-208.661	0.412	628.625	0.413	13	0.123	K.IPFPLTPR.F
R2/RRR2-15/2	941.053	941.151	-105.075	0.370	564.795	0.462	12	0.122	K.IPFPLTPR.F
R2/RRR2-15/2	940.634	941.151	-1618.407	0.270	476.107	0.390	11	0.111	K.IPFPLTPR.F
R2/RRR2-24/2	931.025	931.072	-50.448	0.377	936.617	0.446	15	0.132	R.VAGGSITGLR.G
R2/RRR2-12/2	1022.177	1023.165	-1950.334	0.340	1466.882	0.317	17	0.150	K.VAFETASAVK.K
R2/RRR2-9/2	864.092	863.981	129.493	0.467	1192.455	0.399	14	0.143	K.GGFEAAIAK.A
R2/RRR2-9/2	864.150	863.981	196.784	0.397	928.050	0.253	13	0.111	-.GGFEAAIAK.-
R2/RRR2-22/3	1320.132	1319.531	-303.299	0.435	1305.685	0.385	22	0.108	K.YSDRIPVIVEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/3	1319.736	1319.531	155.190	0.397	969.375	0.338	20	0.078	-.YSDRIPVIVEK.-
R2/RRR2-22/3	1319.834	1319.531	230.041	0.323	722.193	0.223	19	0.066	K.YSDRIPVIVEK.A
R2/RRR2-12/2	1555.956	1555.843	73.290	0.403	1101.456	0.427	17	0.137	K.FLSDLQGQPLPLVK.L
R2/RRR2-11/2	941.118	941.150	-34.230	0.521	1121.845	0.381	13	0.137	R.ILLITDPR.T
R2/RRR2-17/2	941.089	941.150	-64.544	0.492	1085.112	0.389	13	0.136	R.ILLITDPR.T
R2/RRR2-12/2	940.424	941.150	-1840.942	0.451	1101.727	0.383	13	0.136	R.ILLITDPR.T
R2/RRR2-15/2	940.954	941.150	-208.596	0.471	1051.583	0.398	13	0.136	R.ILLITDPR.T
R2/RRR2-11/2	940.981	941.150	-180.355	0.502	1067.607	0.391	13	0.136	R.ILLITDPR.T
R2/RRR2-15/2	940.642	941.150	-1607.393	0.437	1156.619	0.355	13	0.135	R.ILLITDPR.T
R2/RRR2-13/2	940.511	941.150	-1747.692	0.439	1060.736	0.384	13	0.134	R.ILLITDPR.T
R2/RRR2-15/2	941.001	941.150	-158.882	0.519	1133.088	0.360	13	0.134	R.ILLITDPR.T
R2/RRR2-14/2	941.042	941.150	-115.290	0.464	1061.278	0.380	13	0.134	R.ILLITDPR.T
R2/RRR2-16/2	941.148	941.150	-1.445	0.480	1110.775	0.356	13	0.133	R.ILLITDPR.T
R2/RRR2-16/2	940.898	941.150	-268.467	0.487	1068.165	0.368	13	0.133	R.ILLITDPR.T
R2/RRR2-17/2	941.069	941.150	-85.753	0.462	960.171	0.397	12	0.130	R.ILLITDPR.T
R2/RRR2-11/2	940.995	941.150	-165.389	0.440	1018.493	0.364	13	0.130	R.ILLITDPR.T
R2/RRR2-13/2	940.477	941.150	-1784.208	0.351	1036.748	0.365	13	0.129	R.ILLITDPR.T
R2/RRR2-12/2	940.549	941.150	-1707.528	0.429	1036.182	0.355	12	0.128	R.ILLITDPR.T
R2/RRR2-14/2	940.476	941.150	-1785.512	0.428	949.144	0.365	12	0.126	R.ILLITDPR.T
R2/RRR2-13/2	941.007	941.150	-152.116	0.508	877.546	0.371	12	0.125	R.ILLITDPR.T
R2/RRR2-17/2	940.783	941.150	-391.485	0.447	952.607	0.343	12	0.124	R.ILLITDPR.T
R2/RRR2-14/2	941.086	941.150	-68.448	0.483	894.251	0.355	12	0.123	R.ILLITDPR.T
R2/RRR2-12/2	941.114	941.150	-38.523	0.513	926.599	0.351	12	0.123	R.ILLITDPR.T
R2/RRR2-16/2	940.443	941.150	-1820.595	0.415	811.388	0.390	11	0.123	R.ILLITDPR.T
R2/RRR2-11/2	1274.636	1273.380	201.371	0.383	1272.013	0.389	17	0.145	K.AVAEQAAWEAAR.R
R2/RRR2-2/2	1552.462	1551.809	-224.185	0.347	681.348	0.388	15	0.110	R.SIYTVGSLINVLGSK.A
R2/RRR2-2/2	1552.382	1551.809	-275.778	0.311	332.492	0.364	12	0.102	R.SIYTVGSLINVLGSK.A
R2/RRR2-26/2	1086.958	1087.210	-232.786	0.479	955.929	0.431	14	0.135	R.GYISYQSLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-26/2	1086.946	1087.210	-244.053	0.469	943.362	0.403	14	0.130	R.GYISYQSLR.R
R2/RRR2-26/2	1087.783	1087.210	-393.902	0.493	937.962	0.357	14	0.124	R.GYISYQSLR.R
R2/RRR2-7/3	1480.728	1480.610	80.064	0.482	742.877	0.417	22	0.087	R.LHDRNETLYYR.V
R2/RRR2-7/3	1479.764	1480.610	-1251.014	0.409	739.741	0.386	22	0.081	R.LHDRNETLYYR.V
R2/RRR2-7/3	1480.522	1480.610	-59.106	0.446	1009.041	0.301	23	0.077	R.LHDRNETLYYR.V
R2/RRR2-22/2	901.923	902.031	-119.272	0.496	1304.360	0.373	15	0.148	R.SAIADVVAR.E
R2/RRR2-22/2	901.754	902.031	-307.480	0.340	1217.163	0.305	14	0.129	R.SAIADVVAR.E
R2/RRR2-18/2	1197.075	1197.234	-132.617	0.467	1064.788	0.427	18	0.140	R.FEDGSISDQAK.R
R2/RRR2-18/2	1197.843	1197.234	-327.352	0.474	949.333	0.472	17	0.140	R.FEDGSISDQAK.R
R2/RRR2-18/2	1197.257	1197.234	19.777	0.395	769.056	0.329	15	0.113	R.FEDGSISDQAK.R
R2/RRR2-23/2	1369.545	1370.577	-1488.019	0.304	1095.938	0.404	18	0.133	K.TPIQNLKDAIEK.L
R2/RRR2-23/2	1370.281	1370.577	-216.642	0.429	953.423	0.439	17	0.133	K.TPIQNLKDAIEK.L
R2/RRR2-23/2	1369.807	1370.577	-1295.562	0.335	866.062	0.374	17	0.119	K.TPIQNLKDAIEK.L
R2/RRR2-10/2	1388.034	1388.509	-343.185	0.369	1463.351	0.319	20	0.150	K.LADQIDQSAGITR.L
R2/RRR2-11/3	1483.667	1483.741	-50.522	0.436	1778.926	0.166	29	0.100	K.GQLKDGQVIAAKVR.K
R2/RRR2-11/3	1483.629	1483.741	-75.776	0.407	1055.681	0.191	26	0.065	K.GQLKDGQVIAAKVR.K
R2/RRR2-11/3	1483.561	1483.741	-121.583	0.415	942.354	0.109	25	0.057	-.GQLKDGQVIAAKVR.-
R2/RRR2-5/2	1530.592	1530.709	-76.682	0.500	851.861	0.425	20	0.129	R.SPQFPEAIDWIAR.N
R2/RRR2-14/2	1347.058	1347.366	-229.557	0.486	1192.375	0.402	18	0.144	K.YEDQIDSYGEK.G
R2/RRR2-14/2	1346.894	1347.366	-351.122	0.521	1236.425	0.377	18	0.143	K.YEDQIDSYGEK.G
R2/RRR2-12/3	1132.258	1132.297	-34.897	0.426	1091.918	0.421	21	0.099	R.LQQAPPPPQR.Q
R2/RRR2-12/3	1132.669	1132.297	328.965	0.397	715.731	0.331	17	0.074	R.LQQAPPPPQR.Q
R2/RRR2-10/2	979.869	980.140	-276.970	0.379	1056.883	0.415	14	0.135	R.DGIYTALVK.R
R2/RRR2-10/2	980.130	980.140	-9.445	0.281	910.874	0.332	14	0.115	R.DGIYTALVK.R
R2/RRR2-16/2	1324.239	1324.508	-203.464	0.482	1096.225	0.416	17	0.138	K.SELLLSSNPVHK.K
R2/RRR2-16/2	1323.585	1324.508	-1457.175	0.423	1116.021	0.384	17	0.134	K.SELLLSSNPVHK.K
R2/RRR2-11/2	1295.118	1295.468	-271.001	0.448	826.882	0.434	15	0.126	R.HWILDPIDGTK.G
R2/RRR2-11/2	1294.413	1295.468	-1592.738	0.358	666.548	0.421	13	0.115	R.HWILDPIDGTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-14/2	1610.578	1610.883	-190.021	0.414	705.372	0.424	16	0.115	K.IAIVGFGNFGQFLAR.T
R2/RRR2-13/2	1610.897	1610.883	8.770	0.421	426.526	0.417	14	0.108	K.IAIVGFGNFGQFLAR.T
R2/RRR2-7/2	1502.564	1502.719	-102.935	0.369	916.620	0.429	21	0.127	K.M*GEGLPETLGGVLGR.L
R2/RRR2-13/2	1739.686	1737.977	-167.966	0.395	615.760	0.414	18	0.111	R.LVSEPTFANGLVGGFTK.I
R2/RRR2-17/2	1097.211	1097.205	5.065	0.388	717.959	0.433	13	0.122	K.HFQAYTTTK.K
R2/RRR2-17/2	1097.133	1097.205	-65.575	0.308	694.702	0.311	13	0.110	K.HFQAYTTTK.K
R2/RRR2-17/2	1112.138	1111.275	-123.479	0.466	1023.235	0.423	15	0.138	R.FFLQDATLR.Q
R2/RRR2-8/3	1995.844	1994.381	232.702	0.322	1068.935	0.169	23	0.060	-.MNIAGCKLDFTLILLDR.K
R2/RRR2-22/2	1308.233	1308.590	-273.618	0.456	1001.333	0.426	18	0.136	K.IPYDFLISLVK.D
R2/RRR2-22/2	1308.237	1308.590	-270.342	0.458	866.605	0.420	18	0.130	K.IPYDFLISLVK.D
R2/RRR2-22/2	1308.320	1308.590	-206.876	0.391	776.787	0.250	17	0.109	K.IPYDFLISLVK.D
R2/RRR2-13/2	1621.389	1621.773	-237.611	0.391	962.585	0.428	16	0.127	K.SLAEFFTDFGYAPR.E
R2/RRR2-13/2	1621.731	1621.773	-26.470	0.292	1080.796	0.295	18	0.118	K.SLAEFFTDFGYAPR.E
R2/RRR2-13/2	1622.845	1621.773	44.090	0.307	865.928	0.145	18	0.099	K.SLAEFFTDFGYAPR.E
R2/RRR2-6/2	1541.950	1541.731	142.243	0.321	1371.990	0.336	18	0.141	R.ESDLAAAVAVAPVATR.K
R2/RRR2-6/2	1541.665	1541.731	-43.252	0.286	1327.731	0.269	18	0.131	-.ESDLAAAVAVAPVATR.-
R2/RRR2-6/2	1542.497	1541.731	-152.688	0.331	1222.812	0.287	18	0.126	-.ESDLAAAVAVAPVATR.-
R2/RRR2-7/2	1542.450	1541.731	-183.173	0.360	1106.906	0.361	16	0.124	R.ESDLAAAVAVAPVATR.K
R2/RRR2-7/2	1542.017	1541.731	185.589	0.309	1039.450	0.288	16	0.115	-.ESDLAAAVAVAPVATR.-
R2/RRR2-7/2	1542.249	1541.731	-313.394	0.303	978.259	0.308	16	0.112	R.ESDLAAAVAVAPVATR.K
R2/RRR2-13/3	1986.157	1986.259	-51.518	0.393	721.359	0.428	22	0.081	-.AYALILENNPFDQIVHK.-
R2/RRR2-13/3	1986.229	1986.259	-15.085	0.368	381.617	0.375	19	0.045	-.AYALILENNPFDQIVHK.-
R2/RRR2-6/2	1142.814	1143.272	-402.468	0.380	776.441	0.433	16	0.123	K.NPEDAAAITIK.S
R2/RRR2-10/2	1744.643	1743.123	-275.985	0.363	610.773	0.416	17	0.111	R.SFTAEIKPLVPLVISK.I
R2/RRR2-4/2	1418.106	1417.575	-331.956	0.415	1013.169	0.389	17	0.127	-.M*AAVANGGAAPEWR.-
R2/RRR2-4/2	1416.811	1417.575	-1249.144	0.336	1123.675	0.323	17	0.125	-.M*AAVANGGAAPEWR.-
R2/RRR2-4/2	1416.730	1417.575	-1306.513	0.301	832.333	0.307	15	0.109	-.M*AAVANGGAAPEWR.-
R2/RRR2-12/3	1669.395	1669.869	-284.913	0.354	1349.994	0.353	30	0.108	R.DVAGHVLGVPAGHGGAVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1131.222	1132.209	-1762.547	0.327	1031.132	0.406	17	0.131	R.NITVNEAQSR.R
R2/RRR2-25/2	1131.931	1132.209	-246.901	0.448	984.667	0.374	17	0.130	R.NITVNEAQSR.R
R2/RRR2-23/2	1132.058	1132.209	-133.961	0.419	841.027	0.365	16	0.122	R.NITVNEAQSR.R
R2/RRR2-22/2	1132.902	1132.209	-272.627	0.412	794.786	0.374	16	0.122	R.NITVNEAQSR.R
R2/RRR2-8/2	1466.072	1464.649	289.657	0.344	621.161	0.417	15	0.111	R.TILDGGTVLQYGAR.T
R2/RRR2-11/2	1776.314	1775.039	155.596	0.453	829.405	0.428	16	0.119	K.STLINTIFASHLIESK.G
R2/RRR2-18/2	1272.052	1272.390	-266.578	0.410	953.768	0.426	18	0.133	K.VLTPISQDDQR.Q
R2/RRR2-18/2	1272.080	1272.390	-244.628	0.351	762.599	0.377	17	0.119	K.VLTPISQDDQR.Q
R2/RRR2-18/2	1271.928	1272.390	-364.405	0.289	694.185	0.399	16	0.115	K.VLTPISQDDQR.Q
R2/RRR2-17/2	1272.115	1272.390	-216.998	0.325	575.497	0.360	15	0.112	K.VLTPISQDDQR.Q
R2/RRR2-13/2	1700.812	1701.905	-1233.974	0.362	669.409	0.419	17	0.112	R.GWAPTFLGYSAQGAFK.Y
R2/RRR2-9/3	1785.473	1785.979	-845.563	0.398	791.191	0.421	29	0.084	R.LEYQSRPSISGVSSFK.N
R2/RRR2-13/2	1406.204	1405.581	-269.009	0.333	808.229	0.430	17	0.120	K.GLLASDQVLFADR.R
R2/RRR2-11/3	1246.360	1246.397	-29.689	0.450	861.800	0.424	19	0.091	R.HDDVILATHPK.S
R2/RRR2-12/3	1246.201	1246.397	-158.053	0.443	1018.125	0.382	21	0.090	R.HDDVILATHPK.S
R2/RRR2-11/3	1245.878	1246.397	-1223.180	0.407	685.405	0.426	17	0.085	R.HDDVILATHPK.S
R2/RRR2-12/3	1246.965	1246.397	-347.999	0.442	900.751	0.352	20	0.082	R.HDDVILATHPK.S
R2/RRR2-9/3	1836.756	1836.186	-234.355	0.397	1527.602	0.278	29	0.108	K.GMTPISTFILEKGALEK.K
R2/RRR2-2/2	1280.243	1279.426	-143.320	0.270	662.414	0.389	13	0.109	R.LSAFEVGDWVR.L
R2/RRR2-3/2	1279.996	1279.426	-336.760	0.269	643.386	0.053	13	0.097	-.LSAFEVGDWVR.-
R2/RRR2-11/2	1619.239	1619.819	-978.650	0.381	1030.724	0.414	20	0.130	K.GILDEIESGGPSAM*VK.Y
R2/RRR2-9/2	1342.312	1342.563	-187.407	0.369	1463.042	0.310	18	0.148	R.IAEELSEVPVKK.A
R2/RRR2-14/2	963.977	964.100	-128.232	0.413	999.782	0.421	14	0.134	R.AVATGIFER.I
R2/RRR2-13/2	965.029	964.100	-74.298	0.475	722.441	0.499	14	0.134	R.AVATGIFER.I
R2/RRR2-14/2	963.908	964.100	-199.627	0.418	880.281	0.445	14	0.132	R.AVATGIFER.I
R2/RRR2-7/3	1373.248	1373.542	-215.025	0.478	1359.765	0.348	24	0.105	K.IYAHSSIGQLQR.A
R2/RRR2-7/3	1373.101	1373.542	-322.317	0.499	1233.643	0.299	24	0.086	K.IYAHSSIGQLQR.A
R2/RRR2-7/3	1373.332	1373.542	-153.363	0.448	599.888	0.258	22	0.074	K.IYAHSSIGQLQR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-8/3	1648.585	1648.827	-147.387	0.490	905.011	0.403	28	0.089	R.LRPNSSGSQTVQM*AR.A
R2/RRR2-7/3	1648.452	1648.827	-228.060	0.427	628.101	0.388	24	0.079	R.LRPNSSGSQTVQM*AR.A
R2/RRR2-6/3	1649.062	1648.827	142.884	0.510	598.606	0.366	24	0.079	R.LRPNSSGSQTVQM*AR.A
R2/RRR2-22/2	1103.899	1104.322	-384.824	0.351	834.012	0.424	13	0.124	R.IAVYSYLFK.E
R2/RRR2-22/2	1105.218	1104.322	-95.117	0.298	513.283	0.476	12	0.115	R.IAVYSYLFK.E
R2/RRR2-24/2	980.727	981.045	-324.854	0.489	1263.158	0.374	15	0.146	R.SNVDVFSGR.G
R2/RRR2-21/2	1647.460	1647.860	-243.512	0.416	802.818	0.429	19	0.121	R.TVNRPYGGVLSGTAVR.E
R2/RRR2-21/2	1647.096	1647.860	-1074.704	0.395	772.465	0.367	18	0.112	R.TVNRPYGGVLSGTAVR.E
R2/RRR2-21/3	1648.828	1647.860	-19.732	0.490	1026.823	0.411	27	0.096	R.TVNRPYGGVLSGTAVR.E
R2/RRR2-21/3	1648.639	1647.860	-134.696	0.504	1026.185	0.395	28	0.093	R.TVNRPYGGVLSGTAVR.E
R2/RRR2-22/3	1545.050	1545.682	-1059.555	0.420	938.322	0.424	23	0.092	K.YSAQRHDVVEVNK.A
R2/RRR2-22/3	1544.549	1545.682	-1385.223	0.409	1006.930	0.379	23	0.088	K.YSAQRHDVVEVNK.A
R2/RRR2-13/2	1712.798	1712.840	-24.205	0.440	851.137	0.422	18	0.121	R.SANTLATFDESTSVLR.K
R2/RRR2-9/2	1242.381	1242.490	-87.967	0.488	731.091	0.399	18	0.124	R.LATNLENLILK.E
R2/RRR2-9/2	1242.305	1242.490	-148.978	0.459	771.335	0.321	18	0.117	R.LATNLENLILK.E
R2/RRR2-9/2	1241.863	1242.490	-1314.180	0.370	479.808	0.350	15	0.113	R.LATNLENLILK.E
R2/RRR2-23/2	924.357	924.003	384.505	0.195	623.376	0.373	12	0.102	-.RAGAAAGHGR.-
R2/RRR2-7/2	943.947	944.152	-217.533	0.324	616.746	0.405	13	0.116	K.SVVFGPLPK.T
R2/RRR2-7/2	944.360	944.152	220.780	0.323	516.635	0.423	12	0.115	K.SVVFGPLPK.T
R2/RRR2-7/2	943.605	944.152	-1644.127	0.236	560.538	0.359	12	0.107	K.SVVFGPLPK.T
R2/RRR2-26/2	976.217	976.070	150.991	0.396	667.508	0.385	11	0.118	R.FYQAQYR.N
R2/RRR2-12/2	1344.232	1344.408	-131.579	0.381	1120.534	0.407	16	0.137	K.TFLSDSPEYER.L
R2/RRR2-12/2	1344.006	1344.408	-300.224	0.309	734.353	0.355	14	0.111	K.TFLSDSPEYER.L
R2/RRR2-4/2	1356.469	1356.505	-27.043	0.504	952.552	0.382	16	0.126	K.LLSEEIFDFSR.G
R2/RRR2-4/2	1355.802	1356.505	-1260.360	0.336	575.367	0.450	13	0.115	K.LLSEEIFDFSR.G
R2/RRR2-17/2	1032.526	1033.311	-1734.026	0.489	922.528	0.409	16	0.131	K.VGLSGILM*VK.G
R2/RRR2-8/2	1192.165	1192.386	-186.568	0.512	881.360	0.396	15	0.126	R.ILVQEGIYEK.F
R2/RRR2-9/2	1192.388	1192.386	1.067	0.297	629.339	0.344	13	0.109	R.ILVQEGIYEK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1920.126	1920.068	30.186	0.354	680.777	0.413	17	0.110	K.GPYTFSIGDVSGLGTYER.G
R2/RRR2-18/2	1437.085	1437.661	-1100.638	0.396	1134.989	0.398	18	0.137	R.VVFELYDDIVPK.T
R2/RRR2-18/2	1436.956	1437.661	-1190.202	0.450	1067.630	0.402	17	0.134	R.VVFELYDDIVPK.T
R2/RRR2-18/2	1437.119	1437.661	-1076.757	0.290	996.577	0.239	15	0.109	R.VVFELYDDIVPK.T
R2/RRR2-18/2	1437.288	1437.661	-260.294	0.395	517.557	0.271	13	0.103	-.VVFELYDDIVPK.-
R2/RRR2-3/2	1254.541	1254.418	98.609	0.442	974.956	0.397	17	0.128	R.SPNSVIVEVGPR.M
R2/RRR2-4/2	1786.523	1787.050	-857.052	0.448	903.532	0.428	20	0.128	R.LDQLIYIPLPDDKSR.M
R2/RRR2-4/2	1786.493	1787.050	-873.720	0.457	844.319	0.411	20	0.124	R.LDQLIYIPLPDDKSR.M
R2/RRR2-3/2	1788.146	1787.050	53.845	0.413	564.585	0.492	16	0.119	R.LDQLIYIPLPDDKSR.M
R2/RRR2-2/2	1788.423	1787.050	209.174	0.403	476.264	0.381	15	0.109	R.LDQLIYIPLPDDKSR.M
R2/RRR2-1/2	1788.323	1787.050	153.524	0.341	419.998	0.391	13	0.107	R.LDQLIYIPLPDDKSR.M
R2/RRR2-1/2	1787.318	1787.050	150.596	0.410	469.394	0.306	15	0.105	R.LDQLIYIPLPDDKSR.M
R2/RRR2-3/2	1306.338	1306.490	-116.276	0.353	858.468	0.408	16	0.120	R.FSVGGLADVAEIK.G
R2/RRR2-12/2	1123.715	1123.287	381.610	0.279	620.618	0.396	13	0.110	R.AHQLVQEGLK.Y
R2/RRR2-11/2	1176.867	1177.289	-359.300	0.264	807.834	0.398	14	0.115	K.GYDPEVIDIR.S
R2/RRR2-8/2	1516.879	1517.665	-1180.764	0.311	1346.472	0.314	18	0.138	R.EVAIEDPFNVDIR.Q
R2/RRR2-7/2	1087.931	1088.241	-285.809	0.387	767.891	0.412	14	0.121	R.LEGIQGAPFR.G
R2/RRR2-6/2	1088.174	1088.241	-62.065	0.401	678.240	0.310	13	0.110	R.LEGIQGAPFR.G
R2/RRR2-6/2	1088.019	1088.241	-204.989	0.258	752.850	0.298	14	0.108	R.LEGIQGAPFR.G
R2/RRR2-25/2	1334.125	1333.497	-279.192	0.477	927.524	0.408	18	0.127	R.NLNM*GNAASIPSK.C
R2/RRR2-25/2	1334.138	1333.497	-269.921	0.467	1048.085	0.360	19	0.127	R.NLNM*GNAASIPSK.C
R2/RRR2-25/2	1333.141	1333.497	-267.827	0.414	971.062	0.378	19	0.126	R.NLNM*GNAASIPSK.C
R2/RRR2-26/2	1333.051	1333.497	-335.444	0.419	932.227	0.384	19	0.125	R.NLNM*GNAASIPSK.C
R2/RRR2-25/2	1333.044	1333.497	-340.865	0.410	866.925	0.396	18	0.123	R.NLNM*GNAASIPSK.C
R2/RRR2-26/2	1333.054	1333.497	-332.871	0.386	885.501	0.357	18	0.120	R.NLNM*GNAASIPSK.C
R2/RRR2-26/2	1332.679	1333.497	-1367.816	0.299	947.629	0.302	19	0.115	R.NLNM*GNAASIPSK.C
R2/RRR2-6/2	1787.477	1787.993	-850.293	0.431	884.865	0.409	18	0.120	K.LSVDNLDEVILVGGSTR.I
R2/RRR2-6/2	1787.597	1787.993	-221.888	0.410	755.724	0.410	17	0.114	K.LSVDNLDEVILVGGSTR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-12/2	1844.516	1843.138	205.335	0.401	586.749	0.378	14	0.101	-.SSRTAGYLSMISASVIAK.-
R2/RRR2-12/2	1844.355	1843.138	118.124	0.381	572.010	0.313	14	0.098	-.SSRTAGYLSMISASVIAK.-
R2/RRR2-12/2	1843.360	1843.138	120.911	0.282	477.090	0.192	13	0.089	-.SSRTAGYLSMISASVIAK.-
R2/RRR2-11/2	1563.346	1562.877	301.238	0.439	908.619	0.409	16	0.123	K.SLVLVNYFPSVPVK.V
R2/RRR2-11/2	1563.757	1562.877	-76.778	0.325	533.477	0.441	16	0.113	K.SLVLVNYFPSVPVK.V
R2/RRR2-11/2	1563.568	1562.877	-198.083	0.182	528.879	0.278	17	0.101	K.SLVLVNYFPSVPVK.V
R2/RRR2-11/2	1598.546	1597.842	-185.592	0.253	639.416	0.381	15	0.106	R.NKMVNMGGELFNDK.V
R2/RRR2-11/2	1599.079	1597.842	148.799	0.259	486.882	0.381	13	0.103	R.NKMVNMGGELFNDK.V
R2/RRR2-5/2	944.487	944.111	399.385	0.441	766.991	0.405	13	0.122	R.LTVVGIDAR.Y
R2/RRR2-12/3	1417.210	1416.523	-221.400	0.439	1158.380	0.381	25	0.096	R.YHELGQHAFGEK.L
R2/RRR2-12/3	1416.640	1416.523	83.211	0.379	596.994	0.306	20	0.072	R.YHELGQHAFGEK.L
R2/RRR2-9/2	882.991	883.070	-90.284	0.304	497.743	0.366	10	0.104	-.LVDVLPAR.-
R2/RRR2-9/2	882.893	883.070	-201.790	0.298	684.887	0.309	11	0.098	-.LVDVLPAR.-
R2/RRR2-24/2	1086.873	1087.207	-308.618	0.337	621.660	0.392	15	0.114	R.AYSEGVYIGK.E
R2/RRR2-22/2	1536.043	1536.665	-1059.542	0.374	814.122	0.411	17	0.120	K.ELELVNDEANVYK.L
R2/RRR2-23/3	1926.941	1925.291	-181.959	0.474	1615.427	0.231	27	0.103	-.RYLQMIQKNSIFNLR.-
R2/RRR2-23/3	1926.856	1925.291	-226.383	0.476	1577.817	0.223	27	0.095	R.RYLQMIQKNSIFNLR.S
R2/RRR2-23/3	1926.854	1925.291	-227.146	0.476	1478.064	0.228	27	0.089	R.RYLQMIQKNSIFNLR.S
R2/RRR2-7/3	1586.655	1585.910	-161.256	0.278	807.120	0.381	21	0.075	K.VGLTLIDTGVKDLLK.N
R2/RRR2-24/2	982.013	982.244	-234.971	0.499	1034.465	0.383	13	0.133	K.LAVLKFYK.V
R2/RRR2-23/2	982.173	982.244	-72.503	0.444	948.966	0.377	13	0.128	K.LAVLKFYK.V
R2/RRR2-24/2	982.124	982.244	-122.497	0.460	919.317	0.383	13	0.128	K.LAVLKFYK.V
R2/RRR2-23/2	981.596	982.244	-1683.211	0.399	789.671	0.389	13	0.124	K.LAVLKFYK.V
R2/RRR2-24/2	982.053	982.244	-194.817	0.467	787.526	0.336	13	0.120	K.LAVLKFYK.V
R2/RRR2-23/2	981.980	982.244	-269.517	0.462	766.292	0.327	13	0.119	K.LAVLKFYK.V
R2/RRR2-10/2	1763.118	1763.927	-1028.774	0.375	665.165	0.390	18	0.111	R.ITFAIEPSSLEDGIDR.L
R2/RRR2-15/2	925.899	926.138	-259.196	0.411	1034.289	0.391	12	0.132	R.SQLIVLPR.N
R2/RRR2-8/3	1231.206	1231.381	-143.023	0.412	951.602	0.392	20	0.088	R.LHFHDCFVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-10/3	1231.081	1231.381	-244.779	0.319	406.553	0.374	17	0.085	R.LHFHDCFVR.-
R2/RRR2-9/3	1230.515	1231.381	-1521.331	0.337	852.175	0.381	19	0.083	R.LHFHDCFVR.-
R2/RRR2-8/3	1231.636	1231.381	207.595	0.430	868.746	0.354	20	0.083	R.LHFHDCFVR.-
R2/RRR2-9/3	1230.874	1231.381	-1227.994	0.340	776.448	0.373	18	0.082	R.LHFHDCFVR.-
R2/RRR2-12/3	1230.744	1231.381	-1333.773	0.359	537.242	0.344	14	0.080	R.LHFHDCFVR.-
R2/RRR2-10/3	1231.515	1231.381	109.339	0.374	704.663	0.325	18	0.079	R.LHFHDCFVR.-
R2/RRR2-3/3	1232.535	1231.381	125.143	0.294	486.749	0.329	15	0.075	-.LHFHDCFVR.-
R2/RRR2-9/3	1230.896	1231.381	-395.065	0.282	691.365	0.288	18	0.074	R.LHFHDCFVR.-
R2/RRR2-6/3	1231.370	1231.381	-9.219	0.357	486.381	0.312	16	0.073	-.LHFHDCFVR.-
R2/RRR2-7/3	1231.464	1231.381	67.437	0.353	759.209	0.244	18	0.073	R.LHFHDCFVR.-
R2/RRR2-5/3	1887.823	1886.317	-262.584	0.272	1660.613	0.137	25	0.091	R.TRLLFPFHFQIPKIK.V
R2/RRR2-8/3	1796.521	1797.006	-270.749	0.406	926.608	0.402	26	0.088	K.EVLKENDQLLADRPR.N
R2/RRR2-8/3	1796.665	1797.006	-190.178	0.397	645.499	0.341	23	0.073	K.EVLKENDQLLADRPR.N
R2/RRR2-5/2	1617.791	1616.840	-30.470	0.496	815.757	0.376	17	0.116	K.FQQLSPEIVQIEGK.D
R2/RRR2-11/2	1126.170	1127.276	-1875.585	0.347	618.381	0.389	15	0.112	-.TPADAAQLIAR.-
R2/RRR2-8/2	1258.682	1257.462	175.714	0.380	742.116	0.399	14	0.115	R.ELALGLELSGVR.F
R2/RRR2-9/2	1502.122	1500.639	322.156	0.396	927.483	0.398	19	0.124	-.QAEVDALVNAGGSIR.-
R2/RRR2-13/3	1678.325	1676.988	201.549	0.467	890.220	0.333	25	0.074	-.VEALHVVILDAKGRR.-
R2/RRR2-4/2	1186.526	1186.343	153.998	0.506	1259.195	0.347	15	0.137	K.GNINIEELRK.A
R2/RRR2-4/2	1186.378	1186.343	29.040	0.410	1102.907	0.293	15	0.123	-.GNINIEELRK.-
R2/RRR2-4/2	1186.348	1186.343	4.272	0.425	919.941	0.309	15	0.117	-.GNINIEELRK.-
R2/RRR2-5/2	1186.920	1186.343	-357.494	0.334	994.900	0.200	14	0.108	-.GNINIEELRK.-
R2/RRR2-9/2	1020.993	1021.066	-71.005	0.459	758.144	0.383	14	0.122	K.FGDPTEQAR.A
R2/RRR2-9/2	1020.656	1021.066	-402.835	0.411	772.634	0.358	14	0.119	K.FGDPTEQAR.A
R2/RRR2-9/2	1021.073	1021.066	6.822	0.463	771.287	0.331	14	0.117	K.FGDPTEQAR.A
R2/RRR2-10/2	1021.395	1021.066	323.880	0.307	327.027	0.267	11	0.109	-.FGDPTEQAR.-
R2/RRR2-13/2	1774.399	1774.996	-902.791	0.379	732.584	0.397	19	0.114	K.VDALPVASPTGLDLYSR.F
R2/RRR2-13/2	1773.461	1774.996	-1999.043	0.267	490.467	0.337	15	0.101	K.VDALPVASPTGLDLYSR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/2	969.611	970.191	-1634.566	0.437	1152.108	0.374	15	0.138	R.ALLDVGLIR.T
R2/RRR2-13/2	970.123	970.191	-70.753	0.487	950.212	0.398	14	0.130	R.ALLDVGLIR.T
R2/RRR2-13/2	970.129	970.191	-64.442	0.519	982.060	0.353	14	0.125	R.ALLDVGLIR.T
R2/RRR2-6/2	1208.650	1208.346	252.682	0.259	776.076	0.360	16	0.109	R.GADLLGYAAGTAK.G
R2/RRR2-9/2	1438.269	1438.693	-295.190	0.400	773.963	0.398	16	0.120	K.TFVLTPEQYIVK.L
R2/RRR2-19/2	1438.493	1438.693	-139.469	0.405	508.668	0.433	13	0.114	K.TFVLTPEQYIVK.L
R2/RRR2-9/2	1437.688	1438.693	-1398.584	0.304	502.954	0.411	14	0.111	K.TFVLTPEQYIVK.L
R2/RRR2-3/2	1439.303	1438.693	-271.584	0.365	430.990	0.288	11	0.098	-.TFVLTPEQYIVK.-
R2/RRR2-1/2	1741.513	1739.943	-247.515	0.388	903.526	0.319	15	0.110	K.SDDIILCEPVFFQR.E
R2/RRR2-10/2	1480.242	1480.774	-1037.944	0.424	1104.169	0.378	19	0.132	K.IQLLDLPGIIEGAK.D
R2/RRR2-4/2	1594.733	1593.760	-17.168	0.377	1278.846	0.341	18	0.136	R.SVFGEDALANLSIEK.E
R2/RRR2-7/2	1129.379	1130.234	-1647.255	0.341	1454.689	0.268	18	0.140	K.NAGEEGAVVVGK.L
R2/RRR2-17/2	1514.713	1513.633	53.057	0.460	947.598	0.388	19	0.127	K.FSFEDISAQNQVK.A
R2/RRR2-17/2	1513.661	1513.633	18.393	0.316	623.815	0.260	16	0.104	K.FSFEDISAQNQVK.A
R2/RRR2-6/3	997.394	998.160	-1776.252	0.431	876.007	0.392	20	0.083	K.LFHVDPAAK.R
R2/RRR2-13/2	1562.957	1562.834	78.837	0.496	976.119	0.376	18	0.122	-.LFNIIEPDVAVFGK.-
R2/RRR2-13/2	1562.463	1562.834	-237.874	0.425	770.556	0.314	16	0.107	-.LFNIIEPDVAVFGK.-
R2/RRR2-13/2	1561.672	1562.834	-1388.528	0.241	789.716	0.074	16	0.096	-.LFNIIEPDVAVFGK.-
R2/RRR2-12/2	1566.733	1565.622	71.067	0.321	775.428	0.381	15	0.110	R.SVDTASGQLSSQEQK.T
R2/RRR2-12/2	1205.562	1205.432	108.201	0.350	648.787	0.381	16	0.112	R.VLVIGGTGYIGR.Y
R2/RRR2-6/3	1688.774	1688.845	-42.016	0.483	1013.583	0.387	29	0.091	K.AAQEM*TGSHLDEVKR.M
R2/RRR2-6/3	1688.108	1688.845	-1032.088	0.433	693.521	0.346	27	0.078	K.AAQEM*TGSHLDEVKR.M
R2/RRR2-5/3	1688.792	1688.845	-31.249	0.449	515.124	0.295	23	0.075	K.AAQEM*TGSHLDEVKR.M
R2/RRR2-6/3	1688.524	1688.845	-190.271	0.416	909.786	0.211	28	0.066	K.AAQEM*TGSHLDEVKR.M
R2/RRR2-22/2	1384.143	1384.596	-327.785	0.362	712.417	0.390	14	0.115	R.TCMESTAVEMPK.I
R2/RRR2-29/2	1384.148	1384.596	-324.069	0.350	543.543	0.304	14	0.108	R.TCMESTAVEMPK.I
R2/RRR2-3/2	1383.776	1384.596	-1319.114	0.255	598.879	0.063	14	0.100	-.TCMESTAVEMPK.-
R2/RRR2-28/2	1383.577	1384.596	-1463.724	0.286	637.448	0.122	14	0.100	-.TCMESTAVEMPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-22/2	1384.184	1384.596	-298.321	0.331	760.488	0.142	15	0.099	-.TCMESTAVEMPK.-
R2/RRR2-2/2	1384.251	1384.596	-249.836	0.358	712.501	0.172	14	0.099	-.TCMESTAVEMPK.-
R2/RRR2-4/2	1385.311	1384.596	-205.984	0.312	747.181	0.100	15	0.099	R.TCMESTAVEMPK.I
R2/RRR2-28/2	1384.968	1384.596	269.489	0.365	529.022	0.199	13	0.093	-.TCMESTAVEMPK.-
R2/RRR2-9/2	1628.220	1628.764	-951.508	0.410	881.471	0.392	20	0.122	R.GDELLTSYPGLGSYR.V
R2/RRR2-6/2	885.892	885.988	-109.199	0.370	830.715	0.391	13	0.122	R.TPVDNALR.D
R2/RRR2-17/2	1347.957	1347.540	310.406	0.301	769.937	0.382	15	0.114	R.VFFGSDFVTVTK.S
R2/RRR2-17/2	1347.834	1347.540	218.686	0.284	860.333	0.256	14	0.105	R.VFFGSDFVTVTK.S
R2/RRR2-10/3	1218.833	1219.503	-1374.382	0.390	1061.510	0.377	22	0.089	R.FPAPPPLVRPK.A
R2/RRR2-6/2	964.891	965.088	-205.578	0.449	897.084	0.366	14	0.124	R.AGVANYTLR.A
R2/RRR2-6/2	964.468	965.088	-1685.239	0.341	953.063	0.363	13	0.122	R.AGVANYTLR.A
R2/RRR2-6/2	964.416	965.088	-1739.666	0.375	686.604	0.326	12	0.109	-.AGVANYTLR.-
R2/RRR2-12/2	1448.424	1448.620	-135.599	0.444	1086.678	0.370	16	0.131	K.NLYISCDPYM*R.N
R2/RRR2-12/2	1448.044	1448.620	-1091.676	0.421	878.063	0.370	15	0.121	K.NLYISCDPYM*R.N
R2/RRR2-12/2	1448.155	1448.620	-321.880	0.421	798.941	0.371	14	0.117	K.NLYISCDPYM*R.N
R2/RRR2-5/2	997.929	997.173	-245.333	0.337	661.379	0.363	12	0.110	R.LPAVLVGDGR.L
R2/RRR2-10/2	1872.854	1872.967	-60.250	0.424	799.109	0.383	16	0.112	R.YTEQGDAIVFESELDR.I
R2/RRR2-10/2	1232.361	1231.376	-12.181	0.364	959.888	0.385	14	0.125	R.CSGLYLSQFR.H
R2/RRR2-26/2	1335.900	1336.469	-1178.137	0.427	1331.866	0.323	17	0.137	K.AGGFGPVCTVDQK.N
R2/RRR2-26/2	1336.825	1336.469	267.105	0.396	1358.502	0.298	18	0.136	K.AGGFGPVCTVDQK.N
R2/RRR2-26/2	1335.731	1336.469	-1305.239	0.405	1050.236	0.320	16	0.119	K.AGGFGPVCTVDQK.N
R2/RRR2-15/3	1237.321	1237.347	-21.544	0.412	1326.894	0.317	23	0.095	K.VRDGEAYVATR.K
R2/RRR2-2/3	1609.946	1610.867	-1196.893	0.442	1463.621	0.324	23	0.110	R.RHEMDQKVVVNVR.R
R2/RRR2-2/3	1609.553	1610.867	-1441.822	0.440	1537.066	0.274	24	0.105	R.RHEMDQKVVVNVR.R
R2/RRR2-2/3	1609.578	1610.867	-1426.053	0.449	1284.400	0.347	24	0.100	R.RHEMDQKVVVNVR.R
R2/RRR2-27/3	1202.557	1202.385	143.738	0.514	1520.601	0.217	23	0.084	-.KVWGEDNLIK.-
R2/RRR2-27/3	1202.379	1202.385	-4.401	0.483	1305.546	0.147	22	0.063	-.KVWGEDNLIK.-
R2/RRR2-1/3	1201.870	1202.385	-1263.587	0.525	1293.542	0.151	22	0.063	-.KVWGEDNLIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-28/3	1202.475	1202.385	75.172	0.480	1256.230	0.157	22	0.061	-.KVWGEDNLIK.-
R2/RRR2-28/3	1202.298	1202.385	-72.377	0.490	1310.672	0.135	22	0.061	-.KVWGEDNLIK.-
R2/RRR2-17/3	1201.869	1202.385	-1265.117	0.510	1132.523	0.218	21	0.057	-.KVWGEDNLIK.-
R2/RRR2-26/3	1202.651	1202.385	222.372	0.401	1499.801	0.045	24	0.057	-.KVWGEDNLIK.-
R2/RRR2-27/3	1202.616	1202.385	193.210	0.452	1356.432	0.073	22	0.055	-.KVWGEDNLIK.-
R2/RRR2-25/3	1202.429	1202.385	37.143	0.410	1279.407	0.041	21	0.050	-.KVWGEDNLIK.-
R2/RRR2-28/3	1202.180	1202.385	-170.461	0.442	1056.368	0.115	20	0.049	-.KVWGEDNLIK.-
R2/RRR2-25/3	1201.984	1202.385	-334.436	0.429	1056.360	0.090	20	0.047	-.KVWGEDNLIK.-
R2/RRR2-1/3	1202.140	1202.385	-204.382	0.451	1124.478	0.089	21	0.045	-.KVWGEDNLIK.-
R2/RRR2-22/2	1131.631	1131.225	359.898	0.355	748.057	0.382	15	0.118	R.NITVNQAQSR.G
R2/RRR2-23/2	1131.606	1131.225	338.266	0.402	668.390	0.379	14	0.115	-.NITVNQAQSR.-
R2/RRR2-23/2	1131.563	1131.225	299.868	0.340	908.151	0.288	16	0.114	R.NITVNQAQSR.G
R2/RRR2-16/2	1164.385	1164.336	42.417	0.378	1333.902	0.311	15	0.140	-.SIGAAVIYNQK.-
R2/RRR2-22/2	1468.530	1467.661	-89.575	0.404	755.460	0.354	14	0.113	R.CM*VVTNLIDEEK.G
R2/RRR2-22/2	1468.047	1467.661	263.599	0.364	648.693	0.336	13	0.108	-.CM*VVTNLIDEEK.-
R2/RRR2-22/2	1468.057	1467.661	270.603	0.310	703.549	0.248	13	0.103	R.CM*VVTNLIDEEK.G
R2/RRR2-23/2	1468.226	1467.661	-297.153	0.285	569.325	0.186	12	0.099	-.CM*VVTNLIDEEK.-
R2/RRR2-23/2	1467.228	1467.661	-296.187	0.185	615.985	0.048	12	0.099	-.CM*VVTNLIDEEK.-
R2/RRR2-23/2	1468.709	1467.661	32.564	0.339	469.447	0.243	11	0.096	-.CM*VVTNLIDEEK.-
R2/RRR2-5/2	1307.708	1306.450	198.244	0.323	708.913	0.353	15	0.112	K.HYALWEDPFK.K
R2/RRR2-14/2	976.996	977.058	-63.425	0.397	758.814	0.381	14	0.122	R.WWADVSGR.E
R2/RRR2-14/2	976.963	977.058	-97.140	0.397	652.717	0.337	13	0.117	R.WWADVSGR.E
R2/RRR2-14/2	976.327	977.058	-1777.633	0.300	531.356	0.278	11	0.108	R.WWADVSGR.E
R2/RRR2-9/2	1230.979	1231.381	-327.890	0.385	973.608	0.379	16	0.126	R.SIVQELLGDTR.I
R2/RRR2-9/2	1230.226	1231.381	-1756.951	0.268	788.545	0.275	16	0.108	R.SIVQELLGDTR.I
R2/RRR2-9/2	1230.661	1231.381	-1401.554	0.241	294.908	0.349	11	0.104	-.SIVQELLGDTR.-
R2/RRR2-9/2	1577.583	1576.693	-69.431	0.428	755.217	0.360	16	0.110	R.TTGAGSNWLAQDLNK.G
R2/RRR2-6/3	1089.039	1088.238	-183.814	0.544	1169.253	0.311	22	0.078	-.ADGWAVDLLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-6/3	1088.242	1088.238	3.013	0.432	973.520	0.248	20	0.053	-.ADGWAVDLLK.-
R2/RRR2-16/2	1423.896	1424.691	-1264.147	0.404	780.319	0.377	16	0.117	R.SINTLFLTEMVR.G
R2/RRR2-23/2	964.628	965.104	-494.594	0.376	1368.693	0.284	14	0.102	R.M*GELEKLE.-
R2/RRR2-7/2	1464.306	1464.645	-232.582	0.366	689.075	0.357	17	0.111	R.SVGLQLTLDDFQK.V
R2/RRR2-19/2	977.271	978.149	-1927.057	0.299	915.473	0.366	16	0.119	K.GLLSM*ANAGK.D
R2/RRR2-8/2	1237.405	1237.429	-18.959	0.322	1561.704	0.186	17	0.136	K.YVAVGNEPFLK.A
R2/RRR2-21/2	1157.874	1158.285	-356.628	0.377	1062.628	0.362	15	0.128	K.AVYSFQEVSK.H
R2/RRR2-21/2	1157.900	1158.285	-334.098	0.259	1077.744	0.261	15	0.115	K.AVYSFQEVSK.H
R2/RRR2-21/2	1157.257	1158.285	-1758.019	0.167	1040.655	0.180	15	0.104	K.AVYSFQEVSK.H
R2/RRR2-7/2	1055.009	1055.250	-228.346	0.311	947.211	0.359	14	0.120	K.APSSEILPIK.F
R2/RRR2-7/2	1054.991	1055.250	-245.990	0.239	400.856	0.360	10	0.102	-.APSSEILPIK.-
R2/RRR2-9/2	1253.533	1252.443	71.340	0.198	726.803	0.321	14	0.104	R.ALVEYYPLAGR.L
R2/RRR2-10/2	1253.495	1252.443	40.867	0.208	636.210	0.277	13	0.101	R.ALVEYYPLAGR.L
R2/RRR2-12/3	1317.505	1317.458	36.352	0.460	1017.832	0.363	22	0.086	K.FEHHEM*FPAR.T
R2/RRR2-12/3	1317.623	1317.458	125.833	0.454	994.190	0.348	21	0.083	K.FEHHEM*FPAR.T
R2/RRR2-25/2	1415.070	1415.579	-1069.740	0.468	1087.227	0.356	18	0.129	K.WADGKQEKPTVR.T
R2/RRR2-25/2	1415.828	1415.579	176.533	0.378	542.650	0.220	15	0.103	K.WADGKQEKPTVR.T
R2/RRR2-25/3	1415.093	1415.579	-344.852	0.464	942.622	0.354	24	0.083	K.WADGKQEKPTVR.T
R2/RRR2-25/3	1415.506	1415.579	-51.658	0.464	616.499	0.349	22	0.076	-.WADGKQEKPTVR.-
R2/RRR2-25/3	1415.398	1415.579	-128.217	0.401	1044.173	0.226	23	0.069	K.WADGKQEKPTVR.T
R2/RRR2-25/3	1414.920	1415.579	-1175.908	0.399	500.469	0.332	17	0.063	-.WADGKQEKPTVR.-
R2/RRR2-17/3	1760.322	1761.977	-2082.969	0.349	1377.093	0.270	27	0.093	K.DEGLGMGDKPDWITVK.A
R2/RRR2-24/2	1502.159	1500.716	295.984	0.244	1352.096	0.244	19	0.127	K.CGAKPILASSPPSSK.V
R2/RRR2-24/2	1501.479	1500.716	-158.408	0.195	833.124	0.183	17	0.098	K.CGAKPILASSPPSSK.V
R2/RRR2-12/3	1076.142	1076.234	-85.355	0.484	1369.487	0.286	24	0.091	K.HVGHLGGALSK.N
R2/RRR2-12/3	1076.575	1076.234	317.958	0.493	1100.847	0.278	23	0.077	K.HVGHLGGALSK.N
R2/RRR2-3/2	1165.132	1165.343	-181.446	0.389	1079.271	0.364	16	0.129	-.M*AVKDIDATGK.M
R2/RRR2-3/2	1165.977	1165.343	-314.884	0.359	800.896	0.350	16	0.116	-.M*AVKDIDATGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-3/2	1166.016	1165.343	-280.852	0.357	840.608	0.285	16	0.111	-.M*AVKDIDATGK.M
R2/RRR2-12/2	1484.287	1483.733	-301.958	0.409	795.564	0.370	15	0.116	K.KFEDKFVDTLLK.Y
R2/RRR2-12/2	1484.216	1483.733	325.960	0.404	1010.202	0.269	16	0.113	K.KFEDKFVDTLLK.Y
R2/RRR2-12/2	1484.062	1483.733	221.795	0.362	611.405	0.291	14	0.105	-.KFEDKFVDTLLK.-
R2/RRR2-13/2	1708.486	1706.976	-288.137	0.310	726.478	0.361	17	0.108	R.GRREAAMAVAGSNLM*R.L
R2/RRR2-15/2	809.206	809.893	-2091.272	0.087	882.953	0.150	11	0.093	-.EASHLPR.-
R2/RRR2-15/2	1572.384	1570.861	-303.806	0.383	678.665	0.365	16	0.110	R.AVLVLQQNLTPFAR.S
R2/RRR2-9/2	1199.747	1200.410	-1390.520	0.414	706.616	0.353	14	0.112	R.LLAAELTEIAR.A
R2/RRR2-23/2	1060.160	1060.231	-67.054	0.352	1038.660	0.358	15	0.126	R.AAFNLSPLAR.E
R2/RRR2-1/2	1195.121	1195.503	-321.171	0.371	1502.889	0.212	16	0.135	R.FM*KIKVVGTR.-
R2/RRR2-17/2	1433.303	1432.607	-212.413	0.407	883.751	0.372	16	0.117	K.DEKTFIGALGPAGR.S
R2/RRR2-17/2	1433.054	1432.607	313.247	0.375	763.551	0.363	15	0.112	-.DEKTFIGALGPAGR.-
R2/RRR2-17/2	1432.650	1432.607	30.116	0.368	686.709	0.312	15	0.106	K.DEKTFIGALGPAGR.S
R2/RRR2-10/3	1317.254	1316.403	-113.046	0.337	970.903	0.363	19	0.081	R.TNHPWFSPDSK.S
R2/RRR2-5/2	1134.183	1133.261	-69.047	0.444	905.767	0.364	17	0.125	K.NNAVEMIADR.S
R2/RRR2-5/2	1134.102	1133.261	-140.089	0.355	718.183	0.236	17	0.108	K.NNAVEMIADR.S
R2/RRR2-8/2	1389.857	1390.528	-1206.310	0.419	1117.693	0.351	17	0.129	K.IVFANGSQDPWR.H
R2/RRR2-8/2	1390.976	1390.528	323.251	0.399	838.383	0.330	17	0.115	K.IVFANGSQDPWR.H
R2/RRR2-9/2	1365.068	1364.446	-277.833	0.367	768.918	0.367	15	0.112	R.EGGGNNIYGIDVR.E
R2/RRR2-2/2	1492.308	1492.569	-175.791	0.278	1400.787	0.209	17	0.127	R.LTLEDLEDSWDR.G
R2/RRR2-7/2	1101.524	1102.266	-1586.205	0.349	1255.356	0.308	17	0.132	K.AALLSSLGVDR.V
R2/RRR2-7/2	1101.729	1102.266	-1399.543	0.347	428.159	0.376	11	0.083	-.AALLSSLGVDR.-
R2/RRR2-3/2	1655.975	1654.759	131.118	0.419	809.835	0.340	16	0.109	K.EGSETDQFWSLLGGK.S
R2/RRR2-9/3	1445.452	1445.479	-18.993	0.410	882.643	0.367	24	0.085	K.AGHQTSAESWGTGR.A
R2/RRR2-10/3	1445.477	1445.479	-1.586	0.429	921.963	0.342	25	0.082	K.AGHQTSAESWGTGR.A
R2/RRR2-9/3	1445.073	1445.479	-282.202	0.402	698.613	0.348	20	0.078	K.AGHQTSAESWGTGR.A
R2/RRR2-25/3	1444.811	1445.479	-1157.979	0.429	608.811	0.354	20	0.077	-.AGHQTSAESWGTGR.-
R2/RRR2-9/3	1445.336	1445.479	-99.046	0.390	636.935	0.344	21	0.077	-.AGHQTSAESWGTGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R2/RRR2-13/3	1445.422	1445.479	-39.577	0.348	626.123	0.284	20	0.074	K.AGHQTSAESWGTGR.A
R2/RRR2-24/3	1444.738	1445.479	-1208.504	0.345	788.778	0.292	22	0.074	-.AGHQTSAESWGTGR.-
R2/RRR2-13/3	1445.822	1445.479	238.110	0.349	622.292	0.266	21	0.072	-.AGHQTSAESWGTGR.-
R2/RRR2-10/3	1444.395	1445.479	-1447.197	0.317	770.882	0.236	22	0.070	K.AGHQTSAESWGTGR.A
R2/RRR2-25/3	1445.298	1445.479	-125.480	0.362	820.541	0.219	22	0.068	K.AGHQTSAESWGTGR.A
R2/RRR2-6/2	1372.400	1371.520	-87.484	0.364	929.382	0.359	17	0.119	R.GYNYATALEGALK.V
R2/RRR2-14/3	1580.799	1580.768	20.004	0.303	843.255	0.363	25	0.075	R.HTLDITDVLRPDGK.N
R2/RRR2-11/2	1420.198	1420.712	-1069.067	0.315	718.809	0.354	14	0.109	K.TILEPYLAVLCK.Q
R2/RRR2-13/2	1221.418	1220.348	57.076	0.270	687.542	0.345	16	0.108	R.CAGNDDIITIK.A
R2/RRR2-5/2	1233.564	1234.387	-1481.927	0.427	1284.172	0.335	17	0.140	R.LLQYGEQNIR.R
R2/RRR2-5/2	1234.085	1234.387	-244.817	0.442	1290.613	0.322	17	0.138	R.LLQYGEQNIR.R
R2/RRR2-9/2	1402.268	1403.517	-1608.799	0.288	1311.194	0.269	17	0.128	K.CHSIQEAKSGASK.R
R2/RRR2-9/2	1402.169	1403.517	-1679.904	0.309	1316.201	0.222	17	0.122	K.CHSIQEAKSGASK.R
R2/RRR2-11/2	1402.183	1403.517	-1669.671	0.310	1176.262	0.263	17	0.119	K.CHSIQEAKSGASK.R
R2/RRR2-9/2	1402.248	1403.517	-1622.705	0.305	1248.503	0.197	17	0.115	K.CHSIQEAKSGASK.R
R3/RRR3-2/2	1847.816	1847.062	-133.223	0.670	3752.394	0.637	29	0.799	K.YKEAAELAAESPQGLLR.T
R3/RRR3-1/2	1846.663	1847.062	-216.913	0.657	3624.106	0.602	29	0.736	K.YKEAAELAAESPQGLLR.T
R3/RRR3-2/2	1846.341	1847.062	-934.988	0.614	3379.010	0.592	29	0.654	K.YKEAAELAAESPQGLLR.T
R3/RRR3-3/2	1846.063	1847.062	-1085.948	0.589	3299.696	0.627	28	0.647	K.YKEAAELAAESPQGLLR.T
R3/RRR3-3/2	1846.490	1847.062	-853.951	0.618	3314.909	0.612	28	0.643	K.YKEAAELAAESPQGLLR.T
R3/RRR3-2/2	1847.558	1847.062	269.477	0.651	3181.423	0.606	27	0.598	K.YKEAAELAAESPQGLLR.T
R3/RRR3-3/2	1846.449	1847.062	-876.051	0.631	3092.913	0.627	28	0.583	K.YKEAAELAAESPQGLLR.T
R3/RRR3-2/2	1842.517	1843.120	-872.272	0.581	3085.726	0.499	26	0.528	K.FNLNVQAVNVLLDNIR.S
R3/RRR3-1/2	1842.485	1843.120	-889.698	0.553	3020.877	0.449	25	0.490	K.FNLNVQAVNVLLDNIR.S
R3/RRR3-2/2	1564.980	1565.711	-1109.579	0.525	2690.781	0.592	24	0.462	R.SQALEAHAASFASFK.V
R3/RRR3-3/2	1565.985	1565.711	175.009	0.579	2648.746	0.552	24	0.435	R.SQALEAHAASFASFK.V
R3/RRR3-3/2	1564.479	1565.711	-1431.115	0.483	2553.698	0.528	24	0.406	R.SQALEAHAASFASFK.V
R3/RRR3-2/2	1564.643	1565.711	-1325.637	0.498	2535.809	0.533	24	0.404	R.SQALEAHAASFASFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1565.240	1565.711	-302.220	0.561	2548.649	0.519	24	0.400	R.SQALEAHAASFASFK.V
R3/RRR3-2/2	1842.086	1843.120	-1107.501	0.543	2648.891	0.431	24	0.393	K.FNLNVQAVNVLLDNIR.S
R3/RRR3-3/2	1564.660	1565.711	-1314.746	0.536	2488.404	0.511	24	0.385	R.SQALEAHAASFASFK.V
R3/RRR3-2/2	1842.458	1843.120	-904.796	0.581	2401.095	0.509	24	0.367	K.FNLNVQAVNVLLDNIR.S
R3/RRR3-2/2	1694.540	1694.979	-259.792	0.488	2275.805	0.537	23	0.352	R.AHM*GIFTELGVLYAR.Y
R3/RRR3-1/2	1564.805	1565.711	-1222.062	0.481	2346.919	0.460	22	0.339	R.SQALEAHAASFASFK.V
R3/RRR3-3/3	1673.734	1673.876	-85.202	0.540	2732.739	0.345	34	0.331	R.RPITADSALM*NPNTR.I
R3/RRR3-1/2	1566.342	1565.711	-236.347	0.489	2262.824	0.458	22	0.322	R.SQALEAHAASFASFK.V
R3/RRR3-3/3	1673.209	1673.876	-999.692	0.553	2588.030	0.394	34	0.319	R.RPITADSALM*NPNTR.I
R3/RRR3-3/2	1633.279	1632.740	-283.183	0.535	2147.579	0.488	20	0.313	K.EVCFACVDAEEFR.L
R3/RRR3-3/3	1304.914	1304.480	333.817	0.535	2515.114	0.424	30	0.308	K.LKQFQGAVDAAR.K
R3/RRR3-1/2	1565.528	1565.711	-117.829	0.490	1991.775	0.493	22	0.286	R.SQALEAHAASFASFK.V
R3/RRR3-2/2	1227.261	1226.403	-116.286	0.608	1847.252	0.564	18	0.284	K.VDGELIFAYAK.I
R3/RRR3-2/2	1632.143	1632.740	-981.628	0.368	2095.087	0.388	20	0.277	K.EVCFACVDAEEFR.L
R3/RRR3-2/2	1632.131	1632.740	-988.837	0.374	1953.810	0.474	20	0.276	K.EVCFACVDAEEFR.L
R3/RRR3-3/2	1506.157	1506.591	-288.875	0.510	2045.213	0.411	20	0.273	R.GQCDDELINVTNK.N
R3/RRR3-2/3	1516.389	1516.749	-238.005	0.484	2827.370	0.154	27	0.272	K.SHQMPEQVVFWK.W
R3/RRR3-3/2	1437.097	1437.534	-304.973	0.505	1912.077	0.486	20	0.272	R.AAEEANVYDDLVK.Y
R3/RRR3-2/2	1304.134	1304.480	-266.123	0.456	1897.070	0.483	19	0.271	K.LKQFQGAVDAAR.K
R3/RRR3-2/2	1295.433	1295.424	7.503	0.485	1967.113	0.428	18	0.269	K.LNAYESLELSR.L
R3/RRR3-3/2	1226.075	1226.403	-268.486	0.542	1802.788	0.520	18	0.265	K.VDGELIFAYAK.I
R3/RRR3-2/3	1674.603	1673.876	-163.608	0.545	2422.378	0.345	33	0.265	R.RPITADSALM*NPNTR.I
R3/RRR3-3/3	1846.607	1847.062	-246.829	0.574	2034.991	0.522	34	0.265	K.YKEAAELAAESPQGLLR.T
R3/RRR3-3/2	1225.688	1226.403	-1403.645	0.501	1861.462	0.482	18	0.264	K.VDGELIFAYAK.I
R3/RRR3-3/2	1304.103	1304.480	-289.976	0.429	1909.259	0.449	19	0.263	K.LKQFQGAVDAAR.K
R3/RRR3-2/2	1693.911	1694.979	-1224.181	0.482	1784.175	0.527	21	0.263	R.AHM*GIFTELGVLYAR.Y
R3/RRR3-2/2	1480.574	1480.648	-49.916	0.522	1699.258	0.555	20	0.262	R.GKLNAYESLELSR.L
R3/RRR3-3/3	1847.171	1847.062	58.978	0.564	2174.457	0.439	33	0.260	K.YKEAAELAAESPQGLLR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1226.313	1226.403	-73.344	0.574	1784.680	0.506	18	0.258	K.VDGELIFAYAK.I
R3/RRR3-2/2	1437.080	1437.534	-316.648	0.461	1814.332	0.486	20	0.258	R.AAEEANVYDDLVK.Y
R3/RRR3-3/2	1507.016	1506.591	282.681	0.537	1979.180	0.397	20	0.258	R.GQCDDELINVTNK.N
R3/RRR3-2/2	1226.213	1226.403	-155.626	0.583	1781.182	0.501	18	0.256	K.VDGELIFAYAK.I
R3/RRR3-1/3	1847.267	1847.062	111.369	0.549	2066.421	0.473	33	0.254	K.YKEAAELAAESPQGLLR.T
R3/RRR3-1/2	1226.196	1226.403	-169.408	0.399	1715.244	0.523	18	0.252	K.VDGELIFAYAK.I
R3/RRR3-1/2	1437.241	1437.534	-204.505	0.528	1630.789	0.544	20	0.247	R.AAEEANVYDDLVK.Y
R3/RRR3-3/2	1778.652	1779.076	-238.630	0.533	1589.810	0.556	24	0.245	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-3/2	1141.199	1141.346	-128.918	0.602	1635.176	0.528	17	0.243	R.GNLQIVVQAAK.E
R3/RRR3-2/2	1226.151	1226.403	-206.260	0.482	1722.019	0.472	18	0.242	K.VDGELIFAYAK.I
R3/RRR3-1/2	1140.765	1141.346	-1389.969	0.415	1736.835	0.464	17	0.241	R.GNLQIVVQAAK.E
R3/RRR3-1/2	1438.188	1437.534	-240.721	0.552	1645.512	0.515	20	0.241	R.AAEEANVYDDLVK.Y
R3/RRR3-1/2	1451.295	1450.619	-223.699	0.532	1566.117	0.558	19	0.241	R.EGLVSEAIESFIR.A
R3/RRR3-2/2	1450.213	1450.619	-280.770	0.518	1688.182	0.487	20	0.240	R.EGLVSEAIESFIR.A
R3/RRR3-2/3	1846.922	1847.062	-75.952	0.556	1969.256	0.476	32	0.238	K.YKEAAELAAESPQGLLR.T
R3/RRR3-3/2	1450.276	1450.619	-236.942	0.498	1695.405	0.451	20	0.232	R.EGLVSEAIESFIR.A
R3/RRR3-3/2	1325.813	1326.567	-1327.101	0.468	1821.640	0.370	17	0.231	K.IIYAFISNWAK.L
R3/RRR3-3/3	1673.347	1673.876	-916.636	0.496	2282.910	0.317	32	0.231	R.RPITADSALM*NPNTR.I
R3/RRR3-2/2	1140.621	1141.346	-1516.593	0.447	1507.546	0.536	17	0.229	R.GNLQIVVQAAK.E
R3/RRR3-2/2	1555.380	1555.715	-216.050	0.440	1780.867	0.384	22	0.229	K.EAAELAAESPQGLLR.T
R3/RRR3-2/2	1736.430	1736.941	-872.540	0.494	1423.965	0.580	23	0.229	K.VVGNENPSTLICFASK.T
R3/RRR3-3/2	1506.198	1506.591	-261.636	0.487	1723.262	0.410	19	0.227	R.GQCDDELINVTNK.N
R3/RRR3-2/2	1555.240	1555.715	-306.446	0.437	1841.802	0.336	22	0.225	K.EAAELAAESPQGLLR.T
R3/RRR3-2/2	1584.388	1584.801	-261.320	0.507	1544.718	0.496	18	0.225	R.ALQHYTELPDIKR.V
R3/RRR3-2/2	1437.209	1437.534	-226.744	0.509	1595.514	0.462	20	0.223	R.AAEEANVYDDLVK.Y
R3/RRR3-2/2	1437.001	1437.534	-1069.773	0.475	1539.508	0.490	20	0.223	R.AAEEANVYDDLVK.Y
R3/RRR3-2/2	1678.870	1678.979	-65.534	0.424	1474.749	0.532	20	0.222	R.AHMGIFTELGVLYAR.Y
R3/RRR3-2/2	1505.743	1506.591	-1231.211	0.345	1776.282	0.351	19	0.221	R.GQCDDELINVTNK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1736.433	1736.941	-871.128	0.522	1355.321	0.573	22	0.219	K.VVGNENPSTLICFASK.T
R3/RRR3-2/2	1450.101	1450.619	-1049.724	0.494	1514.190	0.485	19	0.218	R.EGLVSEAIESFIR.A
R3/RRR3-3/2	1439.019	1439.579	-1087.654	0.479	1589.348	0.436	18	0.216	K.GNM*QLFSVDQQR.S
R3/RRR3-1/2	1437.276	1437.534	-179.710	0.472	1530.071	0.464	20	0.216	R.AAEEANVYDDLVK.Y
R3/RRR3-3/2	1361.695	1361.482	157.296	0.513	1530.134	0.450	19	0.215	R.VEEDAVWSQVAK.A
R3/RRR3-2/2	1141.050	1141.346	-260.379	0.500	1379.891	0.530	17	0.214	R.GNLQIVVQAAK.E
R3/RRR3-3/2	1737.269	1736.941	189.609	0.579	1305.602	0.576	22	0.214	K.VVGNENPSTLICFASK.T
R3/RRR3-3/3	1846.608	1847.062	-246.630	0.550	1824.480	0.474	33	0.213	K.YKEAAELAAESPQGLLR.T
R3/RRR3-2/2	1506.043	1506.591	-1030.649	0.465	1656.231	0.382	19	0.212	R.GQCDDELINVTNK.N
R3/RRR3-1/2	1141.118	1141.346	-200.386	0.432	1458.227	0.477	17	0.211	R.GNLQIVVQAAK.E
R3/RRR3-1/2	1226.046	1226.403	-292.260	0.486	1397.972	0.505	17	0.211	K.VDGELIFAYAK.I
R3/RRR3-2/2	1141.231	1141.346	-101.020	0.526	1376.320	0.503	17	0.208	R.GNLQIVVQAAK.E
R3/RRR3-1/2	1450.131	1450.619	-337.101	0.408	1459.595	0.446	19	0.204	R.EGLVSEAIESFIR.A
R3/RRR3-3/2	1450.154	1450.619	-321.646	0.489	1501.963	0.425	19	0.204	R.EGLVSEAIESFIR.A
R3/RRR3-1/2	1736.463	1736.941	-276.086	0.498	1185.440	0.583	21	0.203	K.VVGNENPSTLICFASK.T
R3/RRR3-2/2	1304.153	1304.480	-251.661	0.429	1580.154	0.365	18	0.201	K.LKQFQGAVDAAR.K
R3/RRR3-1/2	1628.459	1628.849	-239.963	0.442	1363.702	0.470	21	0.198	R.QLIDQVVSTALPESK.S
R3/RRR3-2/2	1439.048	1439.579	-1067.553	0.485	1390.867	0.446	17	0.197	K.GNM*QLFSVDQQR.S
R3/RRR3-1/2	1628.449	1628.849	-246.054	0.433	1345.187	0.465	22	0.196	R.QLIDQVVSTALPESK.S
R3/RRR3-2/2	1362.079	1361.482	-296.510	0.396	1317.546	0.475	18	0.195	R.VEEDAVWSQVAK.A
R3/RRR3-2/2	1345.238	1344.448	-156.965	0.527	1190.958	0.513	18	0.194	R.LYDEELYEAAK.I
R3/RRR3-3/2	1436.861	1437.534	-1167.700	0.411	1336.432	0.457	19	0.194	R.AAEEANVYDDLVK.Y
R3/RRR3-3/2	1344.440	1344.448	-6.430	0.532	1188.670	0.510	18	0.194	R.LYDEELYEAAK.I
R3/RRR3-1/3	1847.097	1847.062	19.109	0.547	1761.398	0.440	32	0.193	K.YKEAAELAAESPQGLLR.T
R3/RRR3-2/2	1736.180	1736.941	-1017.515	0.478	1138.696	0.556	21	0.193	K.VVGNENPSTLICFASK.T
R3/RRR3-2/2	1343.439	1344.448	-1500.165	0.337	1358.255	0.440	18	0.192	R.LYDEELYEAAK.I
R3/RRR3-3/2	1735.962	1736.941	-1143.467	0.542	1154.663	0.541	21	0.192	K.VVGNENPSTLICFASK.T
R3/RRR3-2/3	1846.392	1847.062	-906.854	0.540	1595.645	0.502	30	0.192	K.YKEAAELAAESPQGLLR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/3	1673.964	1673.876	52.719	0.511	2051.605	0.306	30	0.192	R.RPITADSALM*NPNTR.I
R3/RRR3-3/2	1439.242	1439.579	-235.082	0.438	1366.802	0.429	17	0.191	K.GNM*QLFSVDQQR.S
R3/RRR3-1/2	1735.696	1736.941	-1297.491	0.426	1218.781	0.493	21	0.188	K.VVGNENPSTLICFASK.T
R3/RRR3-3/2	1373.347	1373.496	-108.998	0.436	1372.198	0.410	17	0.188	R.ADDATHFLDVIR.A
R3/RRR3-3/2	1344.155	1344.448	-218.849	0.466	1215.168	0.467	18	0.187	R.LYDEELYEAAK.I
R3/RRR3-1/2	1628.362	1628.849	-300.129	0.436	1346.157	0.419	21	0.187	R.QLIDQVVSTALPESK.S
R3/RRR3-1/2	1555.941	1555.715	146.000	0.456	1573.328	0.306	21	0.187	K.EAAELAAESPQGLLR.T
R3/RRR3-2/2	1628.569	1628.849	-172.359	0.466	1157.290	0.503	20	0.185	R.QLIDQVVSTALPESK.S
R3/RRR3-3/2	1736.057	1736.941	-1088.465	0.489	1063.728	0.551	20	0.185	K.VVGNENPSTLICFASK.T
R3/RRR3-3/2	1304.226	1304.480	-195.603	0.452	1297.256	0.428	17	0.185	K.LKQFQGAVDAAR.K
R3/RRR3-2/2	1449.988	1450.619	-1128.081	0.451	1302.079	0.429	18	0.185	R.EGLVSEAIESFIR.A
R3/RRR3-1/2	1373.229	1373.496	-195.314	0.446	1282.366	0.434	17	0.185	R.ADDATHFLDVIR.A
R3/RRR3-2/2	1099.057	1099.261	-185.774	0.443	1150.186	0.481	14	0.184	K.VANVELYYK.A
R3/RRR3-1/2	1344.149	1344.448	-223.314	0.431	1198.277	0.456	18	0.184	R.LYDEELYEAAK.I
R3/RRR3-2/2	1438.885	1439.579	-1180.844	0.439	1376.595	0.374	17	0.182	K.GNM*QLFSVDQQR.S
R3/RRR3-3/2	1016.109	1016.130	-20.979	0.358	1342.578	0.368	17	0.179	K.SPEQVSAAVK.A
R3/RRR3-3/2	1304.138	1304.480	-263.306	0.401	1429.198	0.327	17	0.179	K.LKQFQGAVDAAR.K
R3/RRR3-2/2	1373.430	1373.496	-48.461	0.439	1303.429	0.388	17	0.178	R.ADDATHFLDVIR.A
R3/RRR3-2/2	1345.546	1344.448	73.104	0.500	1069.773	0.469	17	0.176	R.LYDEELYEAAK.I
R3/RRR3-3/2	1449.643	1450.619	-1367.287	0.442	1286.158	0.381	18	0.175	R.EGLVSEAIESFIR.A
R3/RRR3-3/2	1099.092	1099.261	-154.354	0.509	934.932	0.501	14	0.174	K.VANVELYYK.A
R3/RRR3-3/2	1374.193	1373.496	-221.015	0.500	1118.962	0.448	16	0.173	R.ADDATHFLDVIR.A
R3/RRR3-3/2	1372.695	1373.496	-1316.116	0.389	1285.284	0.358	18	0.173	R.ADDATHFLDVIR.A
R3/RRR3-3/2	1537.326	1537.749	-275.851	0.500	955.712	0.495	21	0.172	K.RANLPGAENLVVQR.F
R3/RRR3-1/2	1373.183	1373.496	-228.935	0.464	1284.172	0.357	17	0.171	R.ADDATHFLDVIR.A
R3/RRR3-3/2	1439.273	1439.579	-213.810	0.482	1276.697	0.361	17	0.171	K.GNM*QLFSVDQQR.S
R3/RRR3-2/2	1100.001	1099.261	-237.261	0.580	882.608	0.499	14	0.171	K.VANVELYYK.A
R3/RRR3-1/2	1326.784	1326.567	163.742	0.349	1173.738	0.405	15	0.170	K.IIYAFISNWAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1372.940	1373.496	-1136.811	0.457	1059.279	0.439	17	0.169	R.ADDATHFLDVIR.A
R3/RRR3-2/2	1327.554	1326.567	-10.017	0.468	1112.361	0.411	16	0.168	K.IIYAFISNWAK.L
R3/RRR3-2/2	1071.275	1070.306	-29.214	0.473	960.618	0.457	14	0.168	K.YGLIYVITK.L
R3/RRR3-2/2	1627.848	1628.849	-1232.648	0.344	1307.493	0.324	21	0.168	R.QLIDQVVSTALPESK.S
R3/RRR3-3/2	1098.582	1099.261	-1532.723	0.412	941.853	0.468	14	0.167	K.VANVELYYK.A
R3/RRR3-3/2	1098.264	1099.261	-1824.135	0.361	939.665	0.482	14	0.167	K.VANVELYYK.A
R3/RRR3-2/2	1098.624	1099.261	-1494.104	0.437	928.609	0.460	14	0.166	K.VANVELYYK.A
R3/RRR3-2/2	1537.289	1537.749	-300.069	0.588	794.033	0.522	20	0.166	K.RANLPGAENLVVQR.F
R3/RRR3-2/2	1422.944	1423.580	-1153.135	0.362	1436.532	0.235	16	0.163	K.GNMQLFSVDQQR.S
R3/RRR3-3/2	1345.268	1344.448	-134.754	0.523	892.617	0.455	16	0.163	R.LYDEELYEAAK.I
R3/RRR3-1/2	1450.306	1450.619	-216.339	0.425	1044.802	0.416	16	0.162	R.EGLVSEAIESFIR.A
R3/RRR3-2/2	1070.435	1070.306	120.944	0.375	810.796	0.500	13	0.162	K.YGLIYVITK.L
R3/RRR3-3/2	1423.101	1423.580	-337.998	0.325	1430.723	0.217	17	0.161	K.GNMQLFSVDQQR.S
R3/RRR3-4/2	1451.422	1450.619	-135.696	0.376	745.067	0.542	15	0.161	R.EGLVSEAIESFIR.A
R3/RRR3-3/2	1436.318	1437.534	-1547.389	0.279	1130.743	0.367	18	0.160	R.AAEEANVYDDLVK.Y
R3/RRR3-2/2	1381.289	1381.563	-199.049	0.400	826.869	0.463	19	0.160	R.ANLPGAENLVVQR.F
R3/RRR3-1/2	1381.038	1381.563	-1107.360	0.424	933.828	0.410	20	0.159	R.ANLPGAENLVVQR.F
R3/RRR3-1/2	1372.755	1373.496	-1271.730	0.420	1031.270	0.385	16	0.159	R.ADDATHFLDVIR.A
R3/RRR3-3/2	863.846	862.996	-173.640	0.467	623.388	0.474	13	0.158	K.VVAAFAER.R
R3/RRR3-2/2	1069.642	1070.306	-1559.998	0.311	986.810	0.402	14	0.158	K.YGLIYVITK.L
R3/RRR3-3/2	1381.192	1381.563	-269.182	0.441	940.886	0.393	20	0.158	R.ANLPGAENLVVQR.F
R3/RRR3-2/2	1373.325	1373.496	-124.691	0.407	1034.592	0.373	16	0.157	R.ADDATHFLDVIR.A
R3/RRR3-3/2	1695.591	1694.979	-229.737	0.379	841.283	0.458	19	0.157	R.AHM*GIFTELGVLYAR.Y
R3/RRR3-3/3	1778.588	1779.076	-274.959	0.504	1448.560	0.444	32	0.157	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-3/3	1480.442	1480.648	-139.579	0.518	1685.234	0.362	29	0.156	R.GKLNAYESLELSR.L
R3/RRR3-2/2	862.145	862.996	-2153.514	0.337	643.370	0.499	13	0.155	K.VVAAFAER.R
R3/RRR3-3/2	1111.854	1112.260	-366.324	0.490	955.826	0.363	14	0.155	R.FQELFAQTK.Y
R3/RRR3-3/2	863.034	862.996	43.680	0.414	647.388	0.446	13	0.154	K.VVAAFAER.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	862.609	862.996	-450.099	0.369	641.728	0.463	13	0.154	K.VVAAFAER.R
R3/RRR3-2/2	1381.172	1381.563	-284.079	0.423	731.360	0.444	18	0.154	R.ANLPGAENLVVQR.F
R3/RRR3-3/2	1381.160	1381.563	-292.769	0.450	779.107	0.411	19	0.153	R.ANLPGAENLVVQR.F
R3/RRR3-1/2	1382.320	1381.563	-176.315	0.466	667.213	0.445	18	0.153	R.ANLPGAENLVVQR.F
R3/RRR3-1/2	1381.586	1381.563	17.050	0.418	798.253	0.406	19	0.153	R.ANLPGAENLVVQR.F
R3/RRR3-1/2	1111.997	1112.260	-237.454	0.359	876.266	0.381	14	0.152	R.FQELFAQTK.Y
R3/RRR3-3/2	1140.415	1141.346	-1697.878	0.373	680.549	0.470	14	0.152	R.GNLQIVVQAAK.E
R3/RRR3-3/2	1112.049	1112.260	-190.100	0.485	785.628	0.390	14	0.152	R.FQELFAQTK.Y
R3/RRR3-2/2	1555.185	1555.715	-986.351	0.388	1175.351	0.282	20	0.152	K.EAAELAAESPQGLLR.T
R3/RRR3-3/2	1381.273	1381.563	-210.043	0.364	687.796	0.454	18	0.152	R.ANLPGAENLVVQR.F
R3/RRR3-2/3	1846.352	1847.062	-928.657	0.523	1412.038	0.434	29	0.151	K.YKEAAELAAESPQGLLR.T
R3/RRR3-3/2	969.902	970.190	-297.173	0.404	800.537	0.406	13	0.151	R.IAAYIYKK.A
R3/RRR3-3/2	1016.286	1016.130	153.592	0.358	883.794	0.364	16	0.151	K.SPEQVSAAVK.A
R3/RRR3-1/2	862.490	862.996	-1751.197	0.327	778.020	0.409	13	0.151	K.VVAAFAER.R
R3/RRR3-2/2	1111.496	1112.260	-1591.362	0.363	882.959	0.360	14	0.151	R.FQELFAQTK.Y
R3/RRR3-1/2	862.562	862.996	-504.489	0.353	694.433	0.417	13	0.151	K.VVAAFAER.R
R3/RRR3-2/3	1673.747	1673.876	-77.849	0.482	1660.919	0.335	30	0.150	R.RPITADSALM*NPNTR.I
R3/RRR3-2/2	1627.779	1628.849	-1275.424	0.317	1138.132	0.275	20	0.150	R.QLIDQVVSTALPESK.S
R3/RRR3-2/2	1785.426	1785.026	224.817	0.479	693.641	0.457	18	0.149	R.SLLPVEPLVDECEKR.N
R3/RRR3-1/2	1631.353	1632.740	-1467.240	0.216	1254.026	0.226	17	0.149	K.EVCFACVDAEEFR.L
R3/RRR3-3/2	1017.032	1016.130	-96.804	0.458	853.126	0.341	16	0.149	K.SPEQVSAAVK.A
R3/RRR3-3/2	1112.000	1112.260	-234.701	0.475	780.873	0.353	14	0.148	R.FQELFAQTK.Y
R3/RRR3-3/2	1537.150	1537.749	-1043.724	0.495	535.418	0.468	17	0.148	K.RANLPGAENLVVQR.F
R3/RRR3-1/3	1673.870	1673.876	-3.674	0.496	1741.797	0.295	30	0.148	R.RPITADSALM*NPNTR.I
R3/RRR3-3/2	1261.101	1261.455	-281.709	0.393	694.182	0.387	16	0.147	K.RDPTLAVVAYR.R
R3/RRR3-2/2	1516.066	1516.749	-1113.075	0.351	845.327	0.405	15	0.147	K.SHQMPEQVVFWK.W
R3/RRR3-1/2	1015.904	1016.130	-223.939	0.364	748.151	0.369	15	0.147	K.SPEQVSAAVK.A
R3/RRR3-2/2	1380.605	1381.563	-1422.090	0.307	771.956	0.381	19	0.147	R.ANLPGAENLVVQR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1140.842	1141.346	-1321.725	0.354	803.266	0.371	14	0.146	R.GNLQIVVQAAK.E
R3/RRR3-2/2	1673.449	1673.876	-256.412	0.319	294.508	0.532	18	0.146	R.RPITADSALM*NPNTR.I
R3/RRR3-2/2	1262.144	1261.455	-247.135	0.443	625.070	0.377	16	0.146	K.RDPTLAVVAYR.R
R3/RRR3-2/2	1673.495	1673.876	-228.677	0.311	241.579	0.532	17	0.145	R.RPITADSALM*NPNTR.I
R3/RRR3-1/3	1673.453	1673.876	-253.566	0.507	1607.154	0.327	27	0.143	R.RPITADSALM*NPNTR.I
R3/RRR3-2/2	1673.287	1673.876	-952.515	0.291	300.392	0.479	18	0.142	R.RPITADSALM*NPNTR.I
R3/RRR3-2/2	1785.359	1785.026	187.519	0.458	604.475	0.412	18	0.142	R.SLLPVEPLVDECEKR.N
R3/RRR3-1/2	1016.896	1016.130	-231.185	0.414	545.014	0.325	15	0.142	K.SPEQVSAAVK.A
R3/RRR3-3/2	1673.378	1673.876	-298.567	0.279	285.889	0.481	18	0.142	R.RPITADSALM*NPNTR.I
R3/RRR3-3/2	1694.095	1694.979	-1115.133	0.299	144.485	0.490	14	0.142	R.AHM*GIFTELGVLYAR.Y
R3/RRR3-2/2	1147.768	1148.250	-421.426	0.384	709.242	0.333	14	0.140	K.VLQPENEYR.R
R3/RRR3-3/2	1673.315	1673.876	-936.109	0.268	222.880	0.469	16	0.140	R.RPITADSALM*NPNTR.I
R3/RRR3-3/2	999.576	1000.129	-1559.047	0.406	771.340	0.278	13	0.140	-.YIEGYVQK.-
R3/RRR3-3/2	999.879	1000.129	-251.284	0.442	708.021	0.287	13	0.140	-.YIEGYVQK.-
R3/RRR3-3/2	1070.140	1070.306	-155.212	0.262	432.327	0.428	11	0.139	K.YGLIYVITK.L
R3/RRR3-3/2	1695.323	1694.979	203.331	0.461	726.101	0.335	18	0.139	R.AHM*GIFTELGVLYAR.Y
R3/RRR3-1/2	999.932	1000.129	-197.762	0.424	752.932	0.269	13	0.139	-.YIEGYVQK.-
R3/RRR3-2/2	1261.153	1261.455	-239.951	0.385	487.754	0.376	13	0.139	-.RDPTLAVVAYR.-
R3/RRR3-2/2	1261.437	1261.455	-14.133	0.386	538.462	0.316	14	0.138	K.RDPTLAVVAYR.R
R3/RRR3-3/2	1069.487	1070.306	-1705.845	0.257	740.194	0.312	13	0.138	K.YGLIYVITK.L
R3/RRR3-3/2	1261.307	1261.455	-118.001	0.409	601.548	0.319	15	0.138	-.RDPTLAVVAYR.-
R3/RRR3-1/2	1226.196	1226.403	-169.508	0.316	564.049	0.340	12	0.138	K.VDGELIFAYAK.I
R3/RRR3-1/2	999.934	1000.129	-195.925	0.404	717.167	0.252	13	0.137	-.YIEGYVQK.-
R3/RRR3-3/2	1673.194	1673.876	-1008.401	0.227	331.729	0.377	18	0.136	R.RPITADSALM*NPNTR.I
R3/RRR3-3/2	1261.336	1261.455	-95.090	0.379	694.355	0.243	16	0.136	K.RDPTLAVVAYR.R
R3/RRR3-3/2	1628.665	1628.849	-113.411	0.352	298.087	0.386	13	0.135	-.QLIDQVVSTALPESK.-
R3/RRR3-1/2	999.230	1000.129	-1907.085	0.331	535.312	0.250	11	0.135	-.YIEGYVQK.-
R3/RRR3-1/2	1439.525	1439.579	-37.797	0.308	518.107	0.280	13	0.135	K.GNM*QLFSVDQQR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1677.890	1678.979	-1249.300	0.281	402.094	0.348	14	0.135	R.AHMGIFTELGVLYAR.Y
R3/RRR3-3/2	999.497	1000.129	-1638.427	0.373	710.553	0.202	13	0.134	-.YIEGYVQK.-
R3/RRR3-3/2	1423.174	1423.580	-286.362	0.276	1298.479	0.062	16	0.134	K.GNMQLFSVDQQR.S
R3/RRR3-3/2	1627.586	1628.849	-1394.357	0.276	732.979	0.263	16	0.133	R.QLIDQVVSTALPESK.S
R3/RRR3-2/3	1480.061	1480.648	-1075.140	0.458	1503.183	0.335	28	0.132	R.GKLNAYESLELSR.L
R3/RRR3-2/2	758.007	757.944	82.440	0.301	584.593	0.182	9	0.131	-.GLILSVR.-
R3/RRR3-3/2	1295.224	1295.424	-154.329	0.243	536.441	0.311	13	0.131	K.LNAYESLELSR.L
R3/RRR3-3/3	1929.655	1930.109	-236.206	0.467	894.835	0.532	25	0.131	K.VDELVKDRIESQNEVR.A
R3/RRR3-2/3	1673.351	1673.876	-914.110	0.516	1647.820	0.265	27	0.131	R.RPITADSALM*NPNTR.I
R3/RRR3-2/2	1227.499	1226.403	78.737	0.266	765.345	0.172	14	0.131	K.VDGELIFAYAK.I
R3/RRR3-1/2	1111.330	1112.260	-1741.763	0.354	488.798	0.248	12	0.130	-.FQELFAQTK.-
R3/RRR3-3/3	1585.029	1584.801	144.278	0.505	1195.757	0.433	26	0.130	R.ALQHYTELPDIKR.V
R3/RRR3-1/3	1585.715	1584.801	-54.567	0.564	1166.354	0.441	25	0.130	R.ALQHYTELPDIKR.V
R3/RRR3-2/3	1778.390	1779.076	-950.721	0.426	982.457	0.496	30	0.130	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-3/2	757.835	757.944	-145.180	0.289	718.915	0.108	10	0.129	K.GLILSVR.S
R3/RRR3-3/3	1305.319	1304.480	-123.459	0.529	1286.089	0.403	26	0.129	K.LKQFQGAVDAAR.K
R3/RRR3-2/2	757.755	757.944	-250.544	0.272	819.395	0.108	10	0.128	K.GLILSVR.S
R3/RRR3-2/3	1516.485	1516.749	-174.410	0.468	1742.687	0.228	27	0.128	K.SHQMPEQVVFWK.W
R3/RRR3-1/2	757.829	757.944	-153.260	0.278	893.801	0.089	11	0.128	K.GLILSVR.S
R3/RRR3-3/2	757.910	757.944	-45.654	0.192	760.700	0.079	10	0.127	-.GLILSVR.-
R3/RRR3-2/3	1304.300	1304.480	-138.152	0.552	1290.710	0.386	26	0.125	K.LKQFQGAVDAAR.K
R3/RRR3-3/3	1584.449	1584.801	-222.643	0.505	1221.238	0.397	27	0.124	R.ALQHYTELPDIKR.V
R3/RRR3-2/3	1585.115	1584.801	198.609	0.508	1139.287	0.417	25	0.123	R.ALQHYTELPDIKR.V
R3/RRR3-3/3	1930.065	1930.109	-23.200	0.451	968.115	0.451	24	0.120	K.VDELVKDRIESQNEVR.A
R3/RRR3-2/3	1532.377	1532.748	-242.968	0.466	1258.173	0.361	23	0.120	K.SHQM*PEQVVFWK.W
R3/RRR3-2/3	1480.657	1480.648	5.936	0.521	1294.105	0.346	26	0.119	R.GKLNAYESLELSR.L
R3/RRR3-1/2	1016.792	1016.130	-334.164	0.182	285.157	0.342	14	0.119	-.SPEQVSAAVK.-
R3/RRR3-2/3	1930.216	1930.109	55.393	0.441	1016.604	0.420	26	0.118	K.VDELVKDRIESQNEVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1779.004	1779.076	-40.242	0.458	928.315	0.443	30	0.117	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-1/3	1845.267	1847.062	-2062.655	0.426	1022.588	0.401	26	0.116	K.YKEAAELAAESPQGLLR.T
R3/RRR3-3/3	1479.840	1480.648	-1225.467	0.481	1143.246	0.371	25	0.115	R.GKLNAYESLELSR.L
R3/RRR3-1/3	1584.636	1584.801	-104.402	0.513	1034.672	0.402	24	0.115	R.ALQHYTELPDIKR.V
R3/RRR3-1/3	1584.475	1584.801	-206.180	0.514	1153.167	0.369	26	0.115	R.ALQHYTELPDIKR.V
R3/RRR3-1/3	1373.230	1373.496	-194.387	0.442	885.417	0.450	26	0.114	R.ADDATHFLDVIR.A
R3/RRR3-1/3	1480.099	1480.648	-1049.427	0.471	1152.859	0.358	25	0.113	R.GKLNAYESLELSR.L
R3/RRR3-3/3	1479.875	1480.648	-1201.735	0.477	1103.962	0.372	25	0.113	R.GKLNAYESLELSR.L
R3/RRR3-1/3	1779.074	1779.076	-0.807	0.432	843.751	0.438	29	0.113	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-2/3	1480.222	1480.648	-288.363	0.498	1118.994	0.366	25	0.113	R.GKLNAYESLELSR.L
R3/RRR3-2/3	1779.917	1779.076	-89.164	0.451	737.876	0.460	28	0.113	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-3/3	1778.857	1779.076	-123.150	0.432	828.978	0.432	25	0.111	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-1/3	1778.959	1779.076	-65.949	0.430	655.531	0.462	27	0.111	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-3/3	1929.890	1930.109	-113.988	0.436	837.432	0.423	24	0.110	K.VDELVKDRIESQNEVR.A
R3/RRR3-2/3	1584.650	1584.801	-95.825	0.461	1065.260	0.360	25	0.109	R.ALQHYTELPDIKR.V
R3/RRR3-1/3	1480.615	1480.648	-22.221	0.521	1025.271	0.365	23	0.108	R.GKLNAYESLELSR.L
R3/RRR3-3/3	1539.810	1539.755	35.804	0.443	677.644	0.442	26	0.108	K.LPDARPLINVCDR.F
R3/RRR3-3/3	1373.584	1373.496	64.382	0.446	577.596	0.438	22	0.108	R.ADDATHFLDVIR.A
R3/RRR3-3/3	1539.323	1539.755	-281.666	0.447	850.875	0.406	27	0.107	K.LPDARPLINVCDR.F
R3/RRR3-2/3	1373.644	1373.496	107.965	0.439	633.448	0.424	22	0.106	R.ADDATHFLDVIR.A
R3/RRR3-1/3	1373.219	1373.496	-202.280	0.481	618.064	0.413	24	0.106	R.ADDATHFLDVIR.A
R3/RRR3-3/3	1451.015	1450.619	274.132	0.487	1158.437	0.317	24	0.106	R.EGLVSEAIESFIR.A
R3/RRR3-2/3	1930.804	1930.109	-158.386	0.433	913.491	0.379	24	0.106	K.VDELVKDRIESQNEVR.A
R3/RRR3-2/3	1778.935	1779.076	-79.062	0.430	729.855	0.407	28	0.105	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-3/3	1373.346	1373.496	-109.855	0.428	670.924	0.409	24	0.105	R.ADDATHFLDVIR.A
R3/RRR3-2/3	1373.559	1373.496	46.332	0.464	651.708	0.391	24	0.104	R.ADDATHFLDVIR.A
R3/RRR3-1/3	1304.388	1304.480	-70.842	0.490	944.639	0.351	24	0.103	K.LKQFQGAVDAAR.K
R3/RRR3-1/3	1373.712	1373.496	157.693	0.424	703.729	0.390	24	0.103	R.ADDATHFLDVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1373.283	1373.496	-155.731	0.414	542.809	0.439	22	0.103	-.ADDATHFLDVIR.-
R3/RRR3-1/3	1304.595	1304.480	88.245	0.441	691.154	0.377	23	0.102	K.LKQFQGAVDAAR.K
R3/RRR3-1/3	1778.717	1779.076	-201.940	0.395	725.812	0.380	26	0.102	K.LHVIELGAQPGKPGFSK.K
R3/RRR3-2/3	1532.225	1532.748	-996.901	0.453	1070.649	0.309	21	0.101	K.SHQM*PEQVVFWK.W
R3/RRR3-2/3	1929.815	1930.109	-153.201	0.424	761.285	0.391	23	0.101	-.VDELVKDRIESQNEVR.-
R3/RRR3-2/3	1305.252	1304.480	-174.822	0.505	629.860	0.434	22	0.101	-.LKQFQGAVDAAR.-
R3/RRR3-2/3	1539.144	1539.755	-1050.177	0.356	797.553	0.398	29	0.101	K.LPDARPLINVCDR.F
R3/RRR3-2/3	1540.841	1539.755	55.645	0.416	721.577	0.373	27	0.100	K.LPDARPLINVCDR.F
R3/RRR3-2/3	1373.719	1373.496	162.639	0.455	518.142	0.394	21	0.100	-.ADDATHFLDVIR.-
R3/RRR3-1/3	1304.734	1304.480	195.355	0.507	887.962	0.329	23	0.099	K.LKQFQGAVDAAR.K
R3/RRR3-3/3	1382.169	1381.563	-285.699	0.436	912.701	0.346	22	0.099	R.ANLPGAENLVVQR.F
R3/RRR3-3/3	1539.697	1539.755	-38.028	0.399	662.973	0.342	27	0.097	K.LPDARPLINVCDR.F
R3/RRR3-2/3	1304.971	1304.480	377.571	0.494	766.566	0.336	22	0.096	-.LKQFQGAVDAAR.-
R3/RRR3-3/3	1450.954	1450.619	231.867	0.387	609.939	0.309	24	0.094	R.EGLVSEAIESFIR.A
R3/RRR3-1/3	1480.327	1480.648	-217.626	0.486	1057.912	0.257	24	0.093	R.GKLNAYESLELSR.L
R3/RRR3-3/3	1583.901	1584.801	-1203.124	0.341	579.341	0.268	21	0.091	-.ALQHYTELPDIKR.-
R3/RRR3-3/3	1304.851	1304.480	285.275	0.490	724.401	0.328	22	0.090	-.LKQFQGAVDAAR.-
R3/RRR3-2/3	1450.059	1450.619	-1078.514	0.370	1022.355	0.231	23	0.089	R.EGLVSEAIESFIR.A
R3/RRR3-3/3	1532.962	1532.748	139.658	0.276	793.928	0.156	21	0.082	K.SHQM*PEQVVFWK.W
R3/RRR3-3/3	1449.854	1450.619	-1220.538	0.413	199.938	0.315	19	0.075	-.EGLVSEAIESFIR.-
R3/RRR3-1/3	1304.442	1304.480	-29.587	0.350	636.459	0.235	19	0.063	-.LKQFQGAVDAAR.-
R3/RRR3-7/2	1446.096	1446.542	-309.255	0.533	2174.861	0.353	20	0.277	K.SPEDATNLIDDKK.I
R3/RRR3-7/2	1489.333	1489.700	-246.841	0.517	1753.017	0.540	21	0.265	K.VVVADNVHDFVFK.S
R3/RRR3-7/2	1489.159	1489.700	-1037.484	0.539	1562.386	0.582	20	0.249	K.VVVADNVHDFVFK.S
R3/RRR3-7/2	1489.045	1489.700	-1114.608	0.508	1602.884	0.547	20	0.246	K.VVVADNVHDFVFK.S
R3/RRR3-7/3	1523.595	1522.730	-88.615	0.527	2404.901	0.308	31	0.245	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	1446.118	1446.542	-293.926	0.541	1661.027	0.453	20	0.230	K.SPEDATNLIDDKK.I
R3/RRR3-7/2	1523.300	1522.730	-282.731	0.526	1405.131	0.577	20	0.227	K.AHVEPDQIVSWLK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1522.522	1522.730	-136.677	0.497	1484.047	0.529	20	0.225	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	1446.098	1446.542	-307.646	0.548	1580.137	0.458	20	0.221	K.SPEDATNLIDDKK.I
R3/RRR3-7/2	1900.606	1901.154	-817.333	0.554	1533.620	0.472	21	0.216	K.VVTFDKNPDNHPYLLK.F
R3/RRR3-7/2	1524.149	1522.730	275.808	0.532	1273.237	0.587	19	0.215	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	1878.513	1878.071	236.033	0.548	1387.812	0.527	20	0.211	K.SVYYGAAEEFKDKEIK.F
R3/RRR3-7/3	1522.790	1522.730	39.701	0.470	2239.915	0.254	30	0.200	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	1196.189	1196.377	-157.383	0.441	1316.626	0.460	16	0.194	K.YEIQGFPTLK.I
R3/RRR3-7/2	1279.203	1279.464	-204.693	0.460	1377.870	0.427	16	0.193	R.TADEIVDFIKK.N
R3/RRR3-7/2	1279.244	1279.464	-172.815	0.449	1396.436	0.407	17	0.192	R.TADEIVDFIKK.N
R3/RRR3-7/2	1196.231	1196.377	-121.861	0.360	1490.245	0.347	16	0.189	K.YEIQGFPTLK.I
R3/RRR3-7/2	1196.092	1196.377	-239.082	0.414	1301.288	0.434	16	0.188	K.YEIQGFPTLK.I
R3/RRR3-7/2	1278.393	1279.464	-1624.669	0.440	1331.377	0.408	16	0.185	R.TADEIVDFIKK.N
R3/RRR3-7/2	1878.512	1878.071	235.381	0.495	1234.107	0.472	19	0.184	K.SVYYGAAEEFKDKEIK.F
R3/RRR3-7/3	1523.076	1522.730	228.283	0.417	2070.577	0.263	29	0.180	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	1150.404	1151.291	-1645.353	0.405	1253.250	0.396	16	0.177	R.TADEIVDFIK.K
R3/RRR3-7/3	1880.979	1881.000	-11.568	0.517	1274.255	0.591	30	0.176	R.SDYDFGHTLHANHLPR.G
R3/RRR3-7/2	1151.018	1151.291	-237.594	0.519	1154.613	0.429	16	0.176	R.TADEIVDFIK.K
R3/RRR3-7/2	1877.519	1878.071	-829.274	0.516	1082.259	0.490	18	0.174	K.SVYYGAAEEFKDKEIK.F
R3/RRR3-7/2	975.935	976.063	-131.115	0.492	1352.756	0.317	15	0.172	K.SDEDVVIAK.M
R3/RRR3-7/3	1446.290	1446.542	-174.875	0.552	1614.373	0.446	29	0.170	K.SPEDATNLIDDKK.I
R3/RRR3-7/2	1507.299	1507.625	-217.094	0.413	943.919	0.491	17	0.166	K.SVYYGAAEEFKDK.E
R3/RRR3-7/2	1151.073	1151.291	-190.250	0.477	1114.761	0.386	16	0.166	R.TADEIVDFIK.K
R3/RRR3-7/2	975.919	976.063	-147.677	0.467	1220.287	0.335	15	0.166	K.SDEDVVIAK.M
R3/RRR3-7/2	1506.691	1507.625	-1287.725	0.393	942.412	0.489	17	0.165	K.SVYYGAAEEFKDK.E
R3/RRR3-7/2	989.997	990.181	-186.328	0.469	536.818	0.542	14	0.161	K.HDPPIVLAK.V
R3/RRR3-7/2	975.984	976.063	-81.430	0.483	1157.370	0.316	15	0.159	K.SDEDVVIAK.M
R3/RRR3-7/2	1104.997	1105.229	-210.703	0.341	937.168	0.398	15	0.156	K.NIQEYKGPR.E
R3/RRR3-7/2	1451.943	1452.591	-1138.536	0.391	485.823	0.536	18	0.154	K.SEPIPEVNNEPVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1453.028	1452.591	301.357	0.415	476.164	0.507	18	0.153	K.SEPIPEVNNEPVK.V
R3/RRR3-2/2	1523.888	1522.730	103.917	0.345	650.073	0.499	15	0.151	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	1717.506	1717.990	-283.054	0.449	484.516	0.543	17	0.150	K.AAQELSKHDPPIVLAK.V
R3/RRR3-7/2	1453.107	1452.591	-334.305	0.339	486.918	0.520	18	0.150	K.SEPIPEVNNEPVK.V
R3/RRR3-7/2	1717.560	1717.990	-251.395	0.503	549.017	0.504	18	0.150	K.AAQELSKHDPPIVLAK.V
R3/RRR3-7/2	1453.099	1452.591	-340.036	0.464	354.689	0.488	16	0.149	K.SEPIPEVNNEPVK.V
R3/RRR3-7/2	1104.916	1105.229	-284.186	0.349	809.257	0.377	15	0.149	K.NIQEYKGPR.E
R3/RRR3-7/2	1524.001	1522.730	178.625	0.425	879.120	0.355	17	0.148	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	965.955	966.070	-119.034	0.401	726.302	0.352	16	0.148	K.FIDASSTPK.V
R3/RRR3-7/2	989.694	990.181	-493.189	0.446	439.874	0.418	13	0.148	K.HDPPIVLAK.V
R3/RRR3-7/2	1717.733	1717.990	-150.369	0.466	507.303	0.498	17	0.147	K.AAQELSKHDPPIVLAK.V
R3/RRR3-7/2	965.852	966.070	-226.290	0.398	629.306	0.346	16	0.146	K.FIDASSTPK.V
R3/RRR3-7/2	1279.205	1279.464	-202.778	0.343	358.440	0.434	16	0.145	R.EAEGIVEYLKK.Q
R3/RRR3-7/2	1537.321	1537.781	-300.302	0.440	687.361	0.380	19	0.145	R.LFKPFDELVVDSK.D
R3/RRR3-7/2	1037.316	1038.133	-1756.388	0.333	792.069	0.363	13	0.144	K.DFDVTALEK.F
R3/RRR3-7/2	1537.707	1537.781	-48.220	0.463	694.440	0.364	19	0.143	R.LFKPFDELVVDSK.D
R3/RRR3-7/2	1151.306	1151.291	12.803	0.384	494.789	0.444	14	0.143	R.EAEGIVEYLK.K
R3/RRR3-7/2	1104.601	1105.229	-1478.150	0.321	889.921	0.304	14	0.143	K.NIQEYKGPR.E
R3/RRR3-7/2	965.913	966.070	-163.024	0.397	601.780	0.338	14	0.143	K.FIDASSTPK.V
R3/RRR3-7/2	1279.217	1279.464	-193.684	0.356	317.477	0.381	15	0.143	R.EAEGIVEYLKK.Q
R3/RRR3-7/2	989.565	990.181	-1637.982	0.340	363.642	0.410	12	0.143	K.HDPPIVLAK.V
R3/RRR3-7/3	1446.463	1446.542	-54.488	0.543	1250.780	0.463	27	0.140	K.SPEDATNLIDDKK.I
R3/RRR3-2/2	966.252	966.070	189.168	0.330	614.128	0.292	15	0.140	K.FIDASSTPK.V
R3/RRR3-7/2	1278.552	1279.464	-1499.689	0.243	340.422	0.388	16	0.138	R.EAEGIVEYLKK.Q
R3/RRR3-7/3	1881.294	1881.000	156.538	0.496	1027.259	0.525	27	0.138	R.SDYDFGHTLHANHLPR.G
R3/RRR3-7/2	1453.291	1452.591	-207.385	0.289	344.719	0.310	15	0.137	K.SEPIPEVNNEPVK.V
R3/RRR3-1/2	1523.094	1522.730	239.664	0.291	458.807	0.313	15	0.137	K.AHVEPDQIVSWLK.Q
R3/RRR3-2/2	990.268	990.181	88.451	0.259	360.400	0.278	11	0.136	K.HDPPIVLAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/3	1880.398	1881.000	-854.773	0.484	923.589	0.542	27	0.134	R.SDYDFGHTLHANHLPR.G
R3/RRR3-7/2	1038.183	1038.133	48.399	0.292	719.466	0.255	12	0.133	K.DFDVTALEK.F
R3/RRR3-7/2	1627.219	1627.775	-958.790	0.460	988.690	0.542	22	0.132	K.EKAESAPAEPLKDEL.-
R3/RRR3-2/3	1446.807	1446.542	183.914	0.496	1057.763	0.486	25	0.132	K.SPEDATNLIDDKK.I
R3/RRR3-7/2	966.947	966.070	-127.775	0.235	553.664	0.272	14	0.131	-.FIDASSTPK.-
R3/RRR3-2/3	1446.804	1446.542	181.757	0.509	991.570	0.501	24	0.131	K.SPEDATNLIDDKK.I
R3/RRR3-7/2	1522.251	1522.730	-315.339	0.222	756.978	0.204	16	0.131	K.AHVEPDQIVSWLK.Q
R3/RRR3-7/2	1278.757	1279.464	-1339.170	0.175	623.080	0.287	13	0.130	R.EAEGIVEYLKK.Q
R3/RRR3-7/3	1446.721	1446.542	124.261	0.561	1149.172	0.417	26	0.123	K.SPEDATNLIDDKK.I
R3/RRR3-7/3	1719.073	1717.990	48.380	0.455	930.551	0.478	31	0.121	K.AAQELSKHDPPIVLAK.V
R3/RRR3-6/3	1445.839	1446.542	-1181.120	0.388	1262.327	0.354	24	0.121	K.SPEDATNLIDDKK.I
R3/RRR3-7/2	1523.384	1522.730	-227.822	0.173	198.566	0.355	12	0.116	-.AHVEPDQIVSWLK.-
R3/RRR3-3/3	1445.931	1446.542	-1117.538	0.482	841.589	0.427	22	0.111	K.SPEDATNLIDDKK.I
R3/RRR3-3/3	1446.389	1446.542	-105.789	0.491	695.613	0.452	21	0.111	K.SPEDATNLIDDKK.I
R3/RRR3-6/3	1446.829	1446.542	199.017	0.427	986.932	0.374	23	0.109	K.SPEDATNLIDDKK.I
R3/RRR3-7/3	1538.293	1537.781	-317.950	0.476	1122.170	0.350	23	0.109	-.LFKPFDELVVDSK.-
R3/RRR3-7/3	1717.348	1717.990	-959.383	0.393	710.166	0.425	27	0.104	K.AAQELSKHDPPIVLAK.V
R3/RRR3-7/2	1370.239	1370.487	-181.533	0.444	915.399	0.451	17	0.104	K.AESAPAEPLKDEL.-
R3/RRR3-7/2	1369.517	1370.487	-1443.170	0.343	940.917	0.318	17	0.103	K.AESAPAEPLKDEL.-
R3/RRR3-7/2	1371.263	1370.487	-163.808	0.500	892.371	0.508	17	0.101	K.AESAPAEPLKDEL.-
R3/RRR3-7/3	1717.188	1717.990	-1052.733	0.358	589.585	0.351	25	0.092	-.AAQELSKHDPPIVLAK.-
R3/RRR3-7/2	1627.552	1627.775	-137.486	0.439	787.096	0.607	21	0.085	K.EKAESAPAEPLKDEL.-
R3/RRR3-7/2	1627.407	1627.775	-226.651	0.393	692.272	0.558	19	0.063	K.EKAESAPAEPLKDEL.-
R3/RRR3-5/1	963.554	964.097	-1605.816	0.341	829.447	0.172	11	0.879	-.FQELGLEK.-
R3/RRR3-5/1	963.532	964.097	-1629.489	0.335	803.128	0.164	11	0.878	-.FQELGLEK.-
R3/RRR3-5/1	963.561	964.097	-1598.498	0.337	719.914	0.155	11	0.876	R.FQELGLEK.G
R3/RRR3-1/3	1927.913	1927.150	-123.313	0.531	2776.948	0.607	37	0.483	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/3	1928.183	1927.150	17.004	0.573	2792.424	0.589	37	0.476	R.IGDSLSAHPNELVAVFTR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/3	1926.670	1927.150	-250.235	0.520	2448.969	0.604	36	0.394	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-2/3	1927.176	1927.150	13.423	0.516	2318.385	0.587	36	0.355	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/3	1928.018	1927.150	-68.820	0.553	2305.770	0.554	36	0.335	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1863.405	1864.118	-921.893	0.569	2061.220	0.554	24	0.318	K.MFDLIEQYNLNGHIR.W
R3/RRR3-5/3	1928.086	1927.150	-33.384	0.571	2177.521	0.546	35	0.304	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-2/3	1928.968	1927.150	-94.810	0.543	1987.877	0.614	34	0.296	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1863.501	1864.118	-870.137	0.608	1802.488	0.582	23	0.282	K.MFDLIEQYNLNGHIR.W
R3/RRR3-4/3	1927.015	1927.150	-70.635	0.541	1880.264	0.605	32	0.274	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1878.533	1880.117	-1913.496	0.558	1731.394	0.578	25	0.272	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-6/3	1927.147	1927.150	-1.539	0.550	1923.350	0.548	36	0.255	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1880.562	1880.117	237.143	0.609	1703.151	0.518	25	0.251	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-1/3	1926.642	1927.150	-785.132	0.494	1882.398	0.520	32	0.244	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-4/3	1927.145	1927.150	-2.968	0.522	1872.518	0.525	33	0.242	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1863.428	1864.118	-909.594	0.559	1435.209	0.574	21	0.229	K.MFDLIEQYNLNGHIR.W
R3/RRR3-5/2	1267.733	1268.491	-1390.895	0.428	1467.409	0.523	16	0.221	R.IKQQGLNITPR.I
R3/RRR3-5/2	1927.532	1927.150	198.461	0.551	1221.001	0.613	25	0.214	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1144.182	1144.350	-146.773	0.469	1743.671	0.328	18	0.212	R.SLSALQGALRK.A
R3/RRR3-1/2	1235.090	1235.414	-263.850	0.537	1294.195	0.552	16	0.210	K.NLTGLVELYGR.N
R3/RRR3-5/2	1268.255	1268.491	-186.573	0.447	1399.467	0.492	17	0.208	R.IKQQGLNITPR.I
R3/RRR3-5/2	1268.231	1268.491	-205.209	0.437	1351.401	0.501	16	0.204	R.IKQQGLNITPR.I
R3/RRR3-5/2	1144.160	1144.350	-166.038	0.433	1528.911	0.341	17	0.192	R.SLSALQGALRK.A
R3/RRR3-5/2	1748.347	1747.949	228.445	0.514	1005.552	0.589	24	0.190	R.TM*ASTVPLAVEGEPSNK.-
R3/RRR3-5/2	1145.105	1144.350	-214.550	0.472	1451.288	0.369	17	0.189	R.SLSALQGALRK.A
R3/RRR3-5/2	1416.238	1416.712	-336.092	0.509	1010.315	0.551	18	0.185	R.LMTLTGVYGFWK.Y
R3/RRR3-2/2	1234.864	1235.414	-1259.164	0.456	1130.853	0.490	16	0.183	K.NLTGLVELYGR.N
R3/RRR3-5/2	1205.537	1205.349	156.749	0.452	1343.993	0.382	17	0.181	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1926.603	1927.150	-805.287	0.531	912.120	0.590	22	0.180	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1416.320	1416.712	-277.547	0.504	961.447	0.531	19	0.180	R.LMTLTGVYGFWK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1416.335	1416.712	-266.825	0.500	980.170	0.512	19	0.178	R.LMTLTGVYGFWK.Y
R3/RRR3-5/2	1021.953	1022.094	-138.330	0.448	1462.549	0.286	15	0.176	K.DGAFEDVLR.S
R3/RRR3-4/2	1268.113	1268.491	-298.978	0.419	1095.734	0.460	16	0.175	R.IKQQGLNITPR.I
R3/RRR3-5/2	1417.467	1416.712	-173.670	0.543	828.361	0.548	18	0.174	R.LMTLTGVYGFWK.Y
R3/RRR3-1/3	1927.083	1927.150	-35.085	0.463	1249.987	0.576	29	0.174	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-1/2	1268.184	1268.491	-242.483	0.397	1219.949	0.392	16	0.173	R.IKQQGLNITPR.I
R3/RRR3-5/2	1926.496	1927.150	-861.450	0.526	768.952	0.605	21	0.172	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1225.615	1226.406	-1465.465	0.381	881.826	0.542	17	0.172	R.VVHGIDVFDPK.F
R3/RRR3-2/2	1204.478	1205.349	-1557.255	0.367	1119.468	0.428	18	0.172	K.SIGNGVQFLNR.H
R3/RRR3-4/3	1927.341	1927.150	99.182	0.479	1304.285	0.543	28	0.171	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-4/2	1432.288	1432.712	-296.510	0.409	1182.607	0.397	18	0.171	R.LM*TLTGVYGFWK.Y
R3/RRR3-5/2	1747.315	1747.949	-937.861	0.479	849.891	0.546	23	0.171	R.TM*ASTVPLAVEGEPSNK.-
R3/RRR3-5/2	1205.621	1205.349	226.304	0.487	965.721	0.470	18	0.171	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1226.158	1226.406	-202.864	0.435	858.803	0.528	17	0.171	R.VVHGIDVFDPK.F
R3/RRR3-5/2	1206.005	1205.349	-285.949	0.459	1049.260	0.432	17	0.169	K.SIGNGVQFLNR.H
R3/RRR3-4/2	1205.229	1205.349	-99.212	0.461	972.175	0.445	18	0.168	K.SIGNGVQFLNR.H
R3/RRR3-1/2	1016.083	1016.177	-92.978	0.419	1501.184	0.223	16	0.166	R.SLSALQGALR.K
R3/RRR3-6/2	1015.434	1016.177	-1720.927	0.385	1474.969	0.228	16	0.166	R.SLSALQGALR.K
R3/RRR3-1/2	1205.199	1205.349	-124.713	0.495	892.594	0.462	17	0.166	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1015.511	1016.177	-1645.082	0.404	1490.303	0.221	16	0.165	R.SLSALQGALR.K
R3/RRR3-6/2	1016.022	1016.177	-152.393	0.456	1503.184	0.220	16	0.165	R.SLSALQGALR.K
R3/RRR3-5/2	1205.097	1205.349	-209.661	0.437	878.850	0.459	17	0.164	K.SIGNGVQFLNR.H
R3/RRR3-1/2	1016.045	1016.177	-130.337	0.405	1457.908	0.225	16	0.164	R.SLSALQGALR.K
R3/RRR3-5/2	1206.016	1205.349	-276.708	0.479	981.726	0.417	17	0.163	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1015.994	1016.177	-180.596	0.472	1489.722	0.218	16	0.163	R.SLSALQGALR.K
R3/RRR3-5/2	1206.179	1205.349	-140.549	0.465	985.292	0.417	16	0.162	K.SIGNGVQFLNR.H
R3/RRR3-1/2	1205.073	1205.349	-228.969	0.412	893.866	0.440	17	0.162	K.SIGNGVQFLNR.H
R3/RRR3-3/2	1015.983	1016.177	-190.841	0.413	1549.424	0.176	16	0.162	R.SLSALQGALR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1016.074	1016.177	-101.052	0.417	1485.612	0.203	16	0.162	R.SLSALQGALR.K
R3/RRR3-5/2	1015.988	1016.177	-186.502	0.478	1492.024	0.213	16	0.161	R.SLSALQGALR.K
R3/RRR3-5/2	1433.147	1432.712	304.767	0.554	827.098	0.465	17	0.161	R.LM*TLTGVYGFWK.Y
R3/RRR3-5/2	1225.604	1226.406	-1474.969	0.391	768.947	0.495	16	0.160	R.VVHGIDVFDPK.F
R3/RRR3-6/2	1015.988	1016.177	-186.261	0.407	1400.095	0.229	16	0.160	R.SLSALQGALR.K
R3/RRR3-5/2	1160.062	1160.408	-298.666	0.379	871.370	0.446	14	0.160	R.YLEM*LYALK.Y
R3/RRR3-2/2	1205.925	1205.349	-352.571	0.429	868.467	0.425	17	0.159	K.SIGNGVQFLNR.H
R3/RRR3-2/2	1016.296	1016.177	117.629	0.422	1446.224	0.205	16	0.159	R.SLSALQGALR.K
R3/RRR3-1/2	1205.479	1205.349	108.411	0.420	844.463	0.432	16	0.158	K.SIGNGVQFLNR.H
R3/RRR3-2/2	1234.410	1235.414	-1628.600	0.369	950.807	0.415	15	0.158	K.NLTGLVELYGR.N
R3/RRR3-1/2	1205.152	1205.349	-163.222	0.462	779.853	0.440	16	0.157	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1192.975	1193.444	-394.351	0.344	689.319	0.501	16	0.157	R.NKPIIFSM*AR.L
R3/RRR3-1/2	1205.873	1205.349	-395.738	0.451	850.965	0.418	16	0.157	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1205.128	1205.349	-183.240	0.450	686.809	0.459	16	0.157	K.SIGNGVQFLNR.H
R3/RRR3-2/2	1206.337	1205.349	-9.298	0.421	817.029	0.428	16	0.157	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1731.271	1731.949	-972.168	0.436	768.832	0.472	22	0.156	R.TMASTVPLAVEGEPSNK.-
R3/RRR3-3/3	1927.001	1927.150	-77.879	0.455	1130.889	0.549	27	0.156	R.IGDSLSAHPNELVAVFTR.L
R3/RRR3-5/2	1205.138	1205.349	-175.009	0.455	730.683	0.441	16	0.156	K.SIGNGVQFLNR.H
R3/RRR3-2/2	1204.643	1205.349	-1420.442	0.385	819.049	0.419	16	0.155	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1160.080	1160.408	-283.358	0.324	1006.308	0.355	15	0.155	R.YLEM*LYALK.Y
R3/RRR3-1/2	1206.043	1205.349	-253.758	0.449	764.150	0.423	16	0.155	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1159.696	1160.408	-1480.794	0.344	784.802	0.438	14	0.154	R.YLEM*LYALK.Y
R3/RRR3-5/2	1415.099	1415.574	-336.968	0.435	739.127	0.440	16	0.153	K.TKYPNSDLYWK.K
R3/RRR3-5/2	1262.638	1263.425	-1419.198	0.466	782.229	0.421	16	0.153	K.LKDGAFEDVLR.S
R3/RRR3-5/2	1021.514	1022.094	-1550.915	0.387	1259.531	0.231	15	0.153	K.DGAFEDVLR.S
R3/RRR3-5/2	1193.018	1193.444	-357.904	0.300	657.967	0.498	15	0.152	R.NKPIIFSM*AR.L
R3/RRR3-5/2	1192.513	1193.444	-1623.886	0.296	641.727	0.506	15	0.152	R.NKPIIFSM*AR.L
R3/RRR3-5/2	1005.872	1006.164	-291.598	0.420	515.527	0.427	13	0.152	R.WISAQMNR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1584.363	1584.816	-286.975	0.504	652.186	0.469	19	0.152	K.M*GVTHCTIAHALEK.T
R3/RRR3-6/2	1204.946	1205.349	-335.076	0.408	633.011	0.433	15	0.151	K.SIGNGVQFLNR.H
R3/RRR3-2/2	1416.794	1416.712	57.761	0.380	629.689	0.454	16	0.151	R.LMTLTGVYGFWK.Y
R3/RRR3-2/2	1015.996	1016.177	-178.306	0.411	1272.753	0.216	16	0.150	R.SLSALQGALR.K
R3/RRR3-5/2	1732.465	1731.949	-280.610	0.514	481.382	0.523	18	0.150	R.TMASTVPLAVEGEPSNK.-
R3/RRR3-1/2	1234.847	1235.414	-1273.459	0.411	628.488	0.470	13	0.150	K.NLTGLVELYGR.N
R3/RRR3-5/2	1096.590	1097.245	-1513.735	0.388	840.114	0.374	12	0.150	R.IEEKYTWK.L
R3/RRR3-5/2	1206.089	1205.349	-215.884	0.463	930.658	0.347	15	0.150	K.SIGNGVQFLNR.H
R3/RRR3-1/2	1016.054	1016.177	-120.696	0.410	1216.000	0.230	16	0.150	R.SLSALQGALR.K
R3/RRR3-6/2	1205.074	1205.349	-228.766	0.340	530.568	0.464	14	0.149	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1287.981	1288.341	-280.773	0.452	402.519	0.465	14	0.149	K.CQEDPSHWTK.I
R3/RRR3-1/2	1204.544	1205.349	-1502.485	0.417	743.431	0.375	16	0.149	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1415.160	1415.574	-294.040	0.443	728.738	0.402	16	0.149	K.TKYPNSDLYWK.K
R3/RRR3-5/2	1227.300	1226.406	-86.254	0.323	698.218	0.436	15	0.149	R.VVHGIDVFDPK.F
R3/RRR3-3/2	1016.101	1016.177	-74.299	0.413	1275.577	0.196	16	0.148	R.SLSALQGALR.K
R3/RRR3-3/2	1204.700	1205.349	-1372.099	0.386	629.548	0.393	15	0.148	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1263.212	1263.425	-168.805	0.432	756.119	0.377	16	0.147	K.LKDGAFEDVLR.S
R3/RRR3-5/2	1144.128	1144.408	-246.088	0.518	684.351	0.387	14	0.147	-.YLEMLYALK.-
R3/RRR3-5/2	1731.351	1731.949	-925.945	0.415	622.561	0.434	21	0.147	R.TMASTVPLAVEGEPSNK.-
R3/RRR3-5/2	1390.039	1390.518	-345.509	0.265	475.005	0.556	21	0.147	R.LLPDATGTTCGQR.L
R3/RRR3-5/2	1144.108	1144.408	-262.894	0.439	846.407	0.326	14	0.147	R.YLEMLYALK.Y
R3/RRR3-5/2	1005.472	1006.164	-1687.565	0.400	469.267	0.349	13	0.147	R.WISAQMNR.V
R3/RRR3-5/2	1005.858	1006.164	-305.479	0.390	454.088	0.364	12	0.146	R.WISAQMNR.V
R3/RRR3-5/2	1236.486	1235.414	58.262	0.411	628.908	0.387	15	0.145	K.NLTGLVELYGR.N
R3/RRR3-3/2	1015.588	1016.177	-1568.885	0.369	1166.597	0.209	16	0.145	R.SLSALQGALR.K
R3/RRR3-5/2	1021.948	1022.163	-211.435	0.416	484.038	0.320	13	0.145	R.WISAQM*NR.V
R3/RRR3-5/2	1177.143	1177.445	-257.596	0.327	576.370	0.388	15	0.144	R.NKPIIFSMAR.L
R3/RRR3-1/2	1021.979	1022.163	-181.238	0.354	358.643	0.273	12	0.144	R.WISAQM*NR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1021.811	1022.163	-346.264	0.317	303.189	0.193	11	0.143	R.WISAQM*NR.V
R3/RRR3-5/2	1021.161	1022.094	-1897.719	0.351	989.815	0.255	14	0.142	K.DGAFEDVLR.S
R3/RRR3-5/2	1287.965	1288.341	-293.134	0.484	299.180	0.447	12	0.142	-.CQEDPSHWTK.-
R3/RRR3-5/2	1415.146	1415.574	-303.560	0.460	535.893	0.389	14	0.142	K.TKYPNSDLYWK.K
R3/RRR3-2/2	1226.244	1226.406	-132.857	0.267	729.379	0.357	16	0.142	R.VVHGIDVFDPK.F
R3/RRR3-5/2	1177.140	1177.445	-260.093	0.344	592.535	0.329	15	0.142	R.NKPIIFSMAR.L
R3/RRR3-5/2	1431.659	1432.712	-1437.914	0.403	898.131	0.276	17	0.142	R.LM*TLTGVYGFWK.Y
R3/RRR3-5/2	1287.375	1288.341	-1532.209	0.390	340.360	0.356	13	0.141	K.CQEDPSHWTK.I
R3/RRR3-1/2	1235.436	1235.414	17.382	0.277	645.403	0.398	13	0.141	K.NLTGLVELYGR.N
R3/RRR3-5/2	1021.889	1022.163	-268.838	0.329	448.100	0.268	12	0.141	R.WISAQM*NR.V
R3/RRR3-16/2	1205.146	1205.349	-168.913	0.362	466.698	0.266	15	0.141	K.SIGNGVQFLNR.H
R3/RRR3-1/2	1021.909	1022.163	-249.543	0.389	484.582	0.248	12	0.140	R.WISAQM*NR.V
R3/RRR3-5/2	1177.268	1177.445	-150.760	0.307	623.852	0.314	15	0.140	R.NKPIIFSMAR.L
R3/RRR3-3/2	1206.132	1205.349	-179.636	0.355	476.757	0.264	14	0.139	K.SIGNGVQFLNR.H
R3/RRR3-5/2	1138.841	1139.329	-429.516	0.451	804.410	0.273	14	0.139	R.AM*ENEM*LLR.I
R3/RRR3-5/2	1021.827	1022.163	-330.202	0.324	486.472	0.203	13	0.139	R.WISAQM*NR.V
R3/RRR3-5/2	1096.589	1097.245	-1514.629	0.438	673.072	0.290	12	0.139	R.IEEKYTWK.L
R3/RRR3-5/2	1391.174	1390.518	-248.064	0.276	631.824	0.352	20	0.139	R.LLPDATGTTCGQR.L
R3/RRR3-4/2	1226.139	1226.406	-218.145	0.307	746.406	0.286	16	0.138	R.VVHGIDVFDPK.F
R3/RRR3-5/2	1138.387	1139.329	-1710.962	0.344	847.221	0.250	14	0.138	R.AM*ENEM*LLR.I
R3/RRR3-5/3	1568.041	1568.817	-1136.039	0.554	949.169	0.550	28	0.138	K.MGVTHCTIAHALEK.T
R3/RRR3-1/2	1389.935	1390.518	-1142.290	0.292	437.431	0.301	20	0.137	R.LLPDATGTTCGQR.L
R3/RRR3-4/2	1263.371	1263.425	-42.701	0.389	726.962	0.277	16	0.137	K.LKDGAFEDVLR.S
R3/RRR3-24/2	1432.200	1432.712	-1058.572	0.349	409.504	0.299	13	0.137	R.LM*TLTGVYGFWK.Y
R3/RRR3-3/2	1021.926	1022.163	-232.885	0.368	317.497	0.233	11	0.137	-.WISAQM*NR.-
R3/RRR3-4/2	1144.043	1144.408	-320.165	0.305	459.725	0.314	12	0.137	-.YLEMLYALK.-
R3/RRR3-2/2	1584.531	1584.816	-180.389	0.460	542.942	0.346	17	0.136	K.M*GVTHCTIAHALEK.T
R3/RRR3-5/2	1138.396	1139.329	-1702.990	0.386	900.343	0.217	14	0.136	R.AM*ENEM*LLR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1880.224	1880.117	56.834	0.472	967.485	0.528	26	0.135	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-5/2	1097.054	1097.245	-174.841	0.345	603.913	0.265	11	0.135	R.IEEKYTWK.L
R3/RRR3-5/2	1015.755	1016.177	-416.289	0.265	942.818	0.169	16	0.135	R.SLSALQGALR.K
R3/RRR3-4/2	1431.375	1432.712	-1637.160	0.277	485.054	0.257	13	0.134	R.LM*TLTGVYGFWK.Y
R3/RRR3-16/2	1205.006	1205.349	-284.967	0.358	311.877	0.324	12	0.134	-.SIGNGVQFLNR.-
R3/RRR3-24/2	1733.086	1731.949	79.081	0.274	304.723	0.346	14	0.134	R.TMASTVPLAVEGEPSNK.-
R3/RRR3-1/2	1194.021	1193.444	-355.553	0.185	722.203	0.265	15	0.133	R.NKPIIFSM*AR.L
R3/RRR3-5/3	1585.633	1584.816	-115.990	0.546	734.650	0.587	25	0.133	K.M*GVTHCTIAHALEK.T
R3/RRR3-5/3	1415.202	1415.574	-264.107	0.506	1101.203	0.483	23	0.133	K.TKYPNSDLYWK.K
R3/RRR3-5/2	964.063	964.097	-35.955	0.334	948.609	0.133	14	0.133	R.FQELGLEK.G
R3/RRR3-11/2	1016.820	1016.177	-352.276	0.236	621.786	0.131	13	0.132	R.SLSALQGALR.K
R3/RRR3-5/3	1880.928	1880.117	-101.007	0.531	1065.670	0.484	30	0.132	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-5/3	1415.833	1415.574	183.398	0.555	1037.480	0.494	23	0.132	K.TKYPNSDLYWK.K
R3/RRR3-6/2	964.100	964.097	2.907	0.387	795.209	0.151	13	0.131	-.FQELGLEK.-
R3/RRR3-5/3	1415.445	1415.574	-91.493	0.522	1023.017	0.502	24	0.131	K.TKYPNSDLYWK.K
R3/RRR3-5/2	1015.404	1016.177	-1751.365	0.208	677.918	0.072	15	0.131	R.SLSALQGALR.K
R3/RRR3-5/3	1584.649	1584.816	-106.057	0.484	926.940	0.517	27	0.129	K.M*GVTHCTIAHALEK.T
R3/RRR3-5/3	1568.635	1568.817	-116.511	0.483	846.437	0.541	27	0.129	K.MGVTHCTIAHALEK.T
R3/RRR3-6/2	963.841	964.097	-266.523	0.352	780.828	0.135	13	0.129	-.FQELGLEK.-
R3/RRR3-4/2	963.943	964.097	-160.055	0.288	788.052	0.103	13	0.128	-.FQELGLEK.-
R3/RRR3-5/2	963.940	964.097	-163.230	0.237	779.368	0.104	13	0.128	-.FQELGLEK.-
R3/RRR3-2/2	963.867	964.097	-239.078	0.353	821.972	0.108	13	0.127	-.FQELGLEK.-
R3/RRR3-1/2	963.907	964.097	-197.405	0.280	779.065	0.086	13	0.127	-.FQELGLEK.-
R3/RRR3-5/3	1568.597	1568.817	-140.867	0.520	887.613	0.513	28	0.127	K.MGVTHCTIAHALEK.T
R3/RRR3-6/2	963.968	964.097	-134.140	0.279	799.285	0.068	13	0.127	-.FQELGLEK.-
R3/RRR3-1/2	963.505	964.097	-1657.696	0.193	924.599	0.048	14	0.126	R.FQELGLEK.G
R3/RRR3-2/3	1263.142	1263.425	-224.705	0.496	1596.345	0.268	23	0.124	K.LKDGAFEDVLR.S
R3/RRR3-6/3	1926.774	1927.150	-195.891	0.359	962.909	0.426	26	0.119	R.IGDSLSAHPNELVAVFTR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1143.277	1144.408	-1870.117	0.169	435.199	0.231	11	0.118	-.YLEMLYALK.-
R3/RRR3-5/3	1864.576	1864.118	246.720	0.419	624.966	0.512	24	0.116	K.MFDLIEQYNLNGHIR.W
R3/RRR3-5/3	1863.841	1864.118	-148.902	0.416	511.448	0.528	25	0.116	K.MFDLIEQYNLNGHIR.W
R3/RRR3-6/3	1263.423	1263.425	-1.233	0.412	1534.988	0.236	22	0.115	K.LKDGAFEDVLR.S
R3/RRR3-1/3	1263.686	1263.425	207.610	0.469	1441.910	0.280	24	0.114	K.LKDGAFEDVLR.S
R3/RRR3-5/3	1880.699	1880.117	-222.890	0.385	1087.399	0.370	25	0.114	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-5/3	1177.225	1177.445	-187.023	0.418	1217.126	0.352	21	0.113	R.NKPIIFSMAR.L
R3/RRR3-5/3	1263.779	1263.425	280.983	0.519	1517.005	0.245	24	0.112	-.LKDGAFEDVLR.-
R3/RRR3-5/3	1268.394	1268.491	-76.810	0.492	1407.372	0.280	24	0.112	R.IKQQGLNITPR.I
R3/RRR3-5/3	1879.454	1880.117	-887.318	0.426	940.864	0.401	26	0.111	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-5/3	1864.259	1864.118	75.841	0.386	685.086	0.464	25	0.111	K.MFDLIEQYNLNGHIR.W
R3/RRR3-2/3	1268.511	1268.491	16.146	0.466	1249.710	0.307	23	0.108	R.IKQQGLNITPR.I
R3/RRR3-5/3	1863.655	1864.118	-249.236	0.480	398.747	0.426	21	0.105	K.MFDLIEQYNLNGHIR.W
R3/RRR3-5/3	1462.921	1462.719	138.326	0.450	1054.637	0.338	22	0.103	R.VKNLTGLVELYGR.N
R3/RRR3-1/3	1263.995	1263.425	-340.694	0.483	1214.419	0.262	21	0.100	-.LKDGAFEDVLR.-
R3/RRR3-5/3	1177.547	1177.445	86.745	0.400	1229.567	0.258	20	0.099	R.NKPIIFSMAR.L
R3/RRR3-5/3	1263.702	1263.425	220.252	0.540	1334.673	0.238	23	0.099	-.LKDGAFEDVLR.-
R3/RRR3-5/3	1880.616	1880.117	266.198	0.390	705.962	0.351	23	0.099	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-5/3	1881.305	1880.117	100.112	0.357	827.327	0.326	23	0.098	K.M*FDLIEQYNLNGHIR.W
R3/RRR3-5/3	1268.628	1268.491	108.795	0.451	1166.722	0.230	21	0.093	R.IKQQGLNITPR.I
R3/RRR3-5/3	1267.467	1268.491	-1601.542	0.385	681.001	0.268	18	0.091	-.IKQQGLNITPR.-
R3/RRR3-1/3	1268.747	1268.491	202.585	0.453	943.768	0.245	21	0.091	R.IKQQGLNITPR.I
R3/RRR3-1/3	1415.987	1415.574	292.067	0.336	619.454	0.275	17	0.090	K.TKYPNSDLYWK.K
R3/RRR3-1/3	1264.412	1263.425	-9.995	0.497	1120.625	0.228	21	0.089	-.LKDGAFEDVLR.-
R3/RRR3-2/3	1268.238	1268.491	-200.198	0.416	762.502	0.225	20	0.089	R.IKQQGLNITPR.I
R3/RRR3-3/3	1268.655	1268.491	129.783	0.457	978.809	0.220	20	0.088	R.IKQQGLNITPR.I
R3/RRR3-5/3	1263.466	1263.425	32.490	0.513	1101.193	0.254	22	0.088	-.LKDGAFEDVLR.-
R3/RRR3-6/3	1263.803	1263.425	300.595	0.437	1074.729	0.250	20	0.087	-.LKDGAFEDVLR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1263.641	1263.425	172.010	0.507	1327.613	0.165	24	0.087	K.LKDGAFEDVLR.S
R3/RRR3-5/3	1178.425	1177.445	-17.166	0.375	972.304	0.205	20	0.085	R.NKPIIFSMAR.L
R3/RRR3-4/3	1263.229	1263.425	-155.196	0.457	1137.423	0.148	21	0.082	K.LKDGAFEDVLR.S
R3/RRR3-5/3	1269.026	1268.491	-367.130	0.445	1022.418	0.207	22	0.082	-.IKQQGLNITPR.-
R3/RRR3-2/3	1268.379	1268.491	-88.829	0.422	919.994	0.151	21	0.081	-.IKQQGLNITPR.-
R3/RRR3-4/3	1263.674	1263.425	197.730	0.491	1089.093	0.201	21	0.075	-.LKDGAFEDVLR.-
R3/RRR3-6/3	1268.530	1268.491	30.768	0.454	694.531	0.259	18	0.075	-.IKQQGLNITPR.-
R3/RRR3-4/2	1434.239	1434.684	-311.093	0.528	2513.355	0.474	23	0.381	K.TNM*ASVLLEAGLAK.L
R3/RRR3-4/2	1420.131	1419.565	-306.288	0.572	1805.536	0.484	18	0.256	K.AALQNLEQFQEK.A
R3/RRR3-4/2	1273.989	1274.359	-291.352	0.358	1951.162	0.387	17	0.256	R.DVEIEVEAVDR.T
R3/RRR3-4/2	1434.032	1434.684	-1155.282	0.441	1761.769	0.473	22	0.248	K.TNM*ASVLLEAGLAK.L
R3/RRR3-4/2	1212.543	1213.324	-1473.489	0.509	1767.570	0.387	17	0.230	K.FYVQTVGDQR.V
R3/RRR3-4/2	1418.676	1419.565	-1335.166	0.453	1830.095	0.305	18	0.217	K.AALQNLEQFQEK.A
R3/RRR3-4/2	1420.220	1419.565	-243.422	0.574	1517.230	0.437	17	0.207	K.AALQNLEQFQEK.A
R3/RRR3-4/2	1213.115	1213.324	-172.647	0.476	1465.241	0.430	16	0.204	K.FYVQTVGDQR.V
R3/RRR3-4/2	1286.274	1286.503	-178.629	0.372	1302.048	0.449	17	0.188	R.VASIQQQLASLK.L
R3/RRR3-4/3	1547.988	1547.738	162.204	0.530	1893.444	0.354	28	0.183	R.KAALQNLEQFQEK.A
R3/RRR3-4/2	1286.105	1286.503	-310.504	0.341	1380.764	0.375	18	0.183	R.VASIQQQLASLK.L
R3/RRR3-4/2	1058.141	1058.254	-106.986	0.446	949.060	0.547	16	0.178	K.VVVTEVLGGGK.F
R3/RRR3-4/2	1385.181	1385.588	-294.659	0.381	1159.121	0.449	17	0.174	K.DLALELVENGLAK.Y
R3/RRR3-4/2	1058.072	1058.254	-172.026	0.414	764.588	0.550	16	0.166	K.VVVTEVLGGGK.F
R3/RRR3-4/2	1057.562	1058.254	-1604.097	0.423	830.298	0.473	16	0.161	K.VVVTEVLGGGK.F
R3/RRR3-4/2	1647.201	1647.726	-928.502	0.463	715.666	0.502	21	0.158	R.ISTVDGQPTTNTADAR.V
R3/RRR3-4/2	1045.208	1045.238	-29.555	0.474	694.178	0.449	15	0.156	R.IPDANVLM*R.A
R3/RRR3-4/2	1469.607	1469.753	-99.609	0.406	965.575	0.400	18	0.154	K.LKDAPVIGAFNPVK.G
R3/RRR3-4/2	1262.630	1263.473	-1463.619	0.458	1109.473	0.316	14	0.153	K.ARDFLPFLQR.N
R3/RRR3-4/2	1647.218	1647.726	-918.235	0.459	625.028	0.484	20	0.152	R.ISTVDGQPTTNTADAR.V
R3/RRR3-4/2	1264.142	1263.473	-262.241	0.481	891.652	0.393	13	0.151	-.ARDFLPFLQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1326.332	1326.479	-111.292	0.459	792.890	0.392	17	0.150	R.TGTFLGSLWESK.T
R3/RRR3-4/2	1327.176	1326.479	-228.845	0.510	615.878	0.438	16	0.149	R.TGTFLGSLWESK.T
R3/RRR3-4/2	1045.013	1045.238	-216.317	0.479	691.359	0.380	15	0.149	R.IPDANVLM*R.A
R3/RRR3-5/2	1286.469	1286.503	-26.326	0.276	1078.326	0.292	17	0.148	R.VASIQQQLASLK.L
R3/RRR3-4/2	858.265	858.044	257.549	0.354	798.494	0.389	12	0.147	R.AMIVNGPR.G
R3/RRR3-4/2	1647.262	1647.726	-282.340	0.426	631.733	0.427	20	0.146	R.ISTVDGQPTTNTADAR.V
R3/RRR3-1/2	1647.913	1647.726	113.853	0.446	587.258	0.423	19	0.144	R.ISTVDGQPTTNTADAR.V
R3/RRR3-4/2	1325.768	1326.479	-1294.638	0.429	695.657	0.365	16	0.144	R.TGTFLGSLWESK.T
R3/RRR3-4/2	1044.471	1045.238	-1697.079	0.400	511.704	0.338	14	0.142	R.IPDANVLM*R.A
R3/RRR3-4/2	1263.464	1263.473	-6.939	0.440	918.439	0.284	13	0.140	-.ARDFLPFLQR.-
R3/RRR3-5/2	1325.478	1326.479	-1514.211	0.342	511.714	0.302	14	0.136	R.TGTFLGSLWESK.T
R3/RRR3-4/2	1417.824	1418.685	-1316.539	0.422	687.762	0.313	15	0.134	K.TNMASVLLEAGLAK.L
R3/RRR3-4/2	1461.010	1461.595	-1087.977	0.305	818.148	0.285	16	0.134	K.ETCSIAFSFSGVR.C
R3/RRR3-4/3	1470.226	1469.753	322.348	0.479	1397.525	0.358	27	0.130	K.LKDAPVIGAFNPVK.G
R3/RRR3-5/2	1286.030	1286.503	-368.692	0.229	754.348	0.168	14	0.129	-.VASIQQQLASLK.-
R3/RRR3-4/2	1417.594	1418.685	-1479.558	0.307	708.416	0.175	14	0.126	K.TNMASVLLEAGLAK.L
R3/RRR3-4/3	1922.540	1921.211	171.648	0.360	1008.840	0.434	27	0.114	K.LSSFGLDRIPDANVLM*R.A
R3/RRR3-4/3	1803.965	1803.912	29.034	0.417	1056.074	0.366	31	0.107	R.RISTVDGQPTTNTADAR.V
R3/RRR3-5/3	1502.528	1502.659	-86.965	0.457	1132.716	0.330	24	0.107	R.HSAIVEYVFSGHR.F
R3/RRR3-4/3	1469.626	1469.753	-86.912	0.425	1077.884	0.316	24	0.102	-.LKDAPVIGAFNPVK.-
R3/RRR3-5/2	1325.754	1326.479	-1305.180	0.349	333.413	0.350	10	0.100	-.TGTFLGSLWESK.-
R3/RRR3-4/3	1248.329	1248.330	-0.659	0.441	937.676	0.334	17	0.098	R.RDEKPDNFAR.E
R3/RRR3-2/3	1502.473	1502.659	-124.127	0.450	667.091	0.338	19	0.094	R.HSAIVEYVFSGHR.F
R3/RRR3-4/3	1469.044	1469.753	-1166.631	0.322	720.479	0.276	26	0.087	-.LKDAPVIGAFNPVK.-
R3/RRR3-2/3	1503.542	1502.659	-78.030	0.407	823.601	0.253	20	0.085	-.HSAIVEYVFSGHR.-
R3/RRR3-4/3	1547.051	1547.738	-1093.719	0.420	813.283	0.256	23	0.083	-.KAALQNLEQFQEK.-
R3/RRR3-6/2	1968.685	1969.179	-251.667	0.632	3290.740	0.598	26	0.631	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1556.067	1556.618	-1000.192	0.474	3350.111	0.520	25	0.619	K.DEAYFAANAAAQASR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1556.106	1556.618	-974.831	0.475	3253.538	0.517	24	0.589	K.DEAYFAANAAAQASR.R
R3/RRR3-5/2	1969.580	1969.179	204.232	0.653	3136.086	0.574	25	0.571	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1968.606	1969.179	-801.601	0.615	2933.232	0.544	25	0.504	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1807.518	1808.137	-898.599	0.569	2795.030	0.623	25	0.494	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-5/2	1968.545	1969.179	-832.538	0.610	2787.846	0.579	25	0.482	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1807.369	1808.137	-981.184	0.575	2763.858	0.609	25	0.481	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-5/2	1808.526	1808.137	215.899	0.612	2518.916	0.612	24	0.422	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-5/3	1978.094	1978.201	-54.173	0.540	2563.045	0.552	32	0.398	R.KAEHAFYLDWAVHSFR.I
R3/RRR3-6/2	1807.551	1808.137	-880.226	0.554	2421.902	0.598	24	0.397	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-1/2	1807.886	1808.137	-139.506	0.543	2399.686	0.586	24	0.388	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-5/2	1792.470	1792.138	186.161	0.610	2326.710	0.604	23	0.376	K.GMLTGPVTILNWSFVR.N
R3/RRR3-6/2	1792.554	1792.138	232.803	0.582	2334.980	0.594	23	0.376	K.GMLTGPVTILNWSFVR.N
R3/RRR3-5/2	1555.549	1556.618	-1334.174	0.426	2460.226	0.452	23	0.364	K.DEAYFAANAAAQASR.R
R3/RRR3-6/2	1807.492	1808.137	-912.769	0.552	2253.100	0.591	23	0.359	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-4/2	1807.858	1808.137	-154.949	0.574	2233.218	0.569	23	0.347	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-6/2	1793.760	1792.138	-211.024	0.620	2147.685	0.598	23	0.339	K.GMLTGPVTILNWSFVR.N
R3/RRR3-10/2	1808.617	1808.137	265.916	0.547	2166.431	0.582	22	0.338	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-6/2	1793.356	1792.138	122.302	0.597	2090.769	0.582	22	0.323	K.GMLTGPVTILNWSFVR.N
R3/RRR3-5/3	1968.586	1969.179	-811.380	0.575	2154.448	0.594	36	0.316	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1792.287	1792.138	83.300	0.562	2038.197	0.584	22	0.315	K.GMLTGPVTILNWSFVR.N
R3/RRR3-4/2	1806.893	1808.137	-1245.438	0.514	1973.125	0.612	22	0.313	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-5/3	1977.941	1978.201	-131.894	0.572	2291.535	0.494	32	0.306	R.KAEHAFYLDWAVHSFR.I
R3/RRR3-6/2	1790.728	1792.138	-1349.646	0.478	2028.052	0.511	22	0.293	K.GMLTGPVTILNWSFVR.N
R3/RRR3-6/3	1851.007	1850.028	-10.962	0.533	2075.916	0.529	31	0.276	K.AEHAFYLDWAVHSFR.I
R3/RRR3-6/2	1791.109	1792.138	-1135.877	0.493	1918.509	0.508	22	0.275	K.GMLTGPVTILNWSFVR.N
R3/RRR3-6/2	1807.870	1808.137	-148.040	0.533	1829.664	0.532	21	0.266	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-6/3	1849.830	1850.028	-107.239	0.471	2046.152	0.492	29	0.260	K.AEHAFYLDWAVHSFR.I
R3/RRR3-6/3	1970.172	1969.179	-3.649	0.600	1837.361	0.598	35	0.256	K.KISEDEYVSAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1792.260	1792.138	68.614	0.541	1718.605	0.543	21	0.253	K.GMLTGPVTILNWSFVR.N
R3/RRR3-5/2	1739.572	1740.015	-255.015	0.563	1597.520	0.576	26	0.253	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-5/2	1791.530	1792.138	-899.967	0.507	1771.278	0.509	21	0.252	K.GMLTGPVTILNWSFVR.N
R3/RRR3-5/3	1977.935	1978.201	-134.773	0.546	1974.893	0.499	31	0.248	R.KAEHAFYLDWAVHSFR.I
R3/RRR3-1/3	1969.648	1969.179	238.811	0.603	1787.971	0.596	35	0.247	K.KISEDEYVSAIKEEISK.V
R3/RRR3-2/3	1969.186	1969.179	3.748	0.587	1765.131	0.571	35	0.234	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1707.644	1707.951	-180.008	0.550	1551.221	0.528	21	0.232	K.LDSEIKSWLAFAAQK.V
R3/RRR3-4/2	1792.477	1792.138	189.848	0.551	1485.840	0.556	20	0.226	K.GMLTGPVTILNWSFVR.N
R3/RRR3-6/3	1968.617	1969.179	-795.882	0.603	1640.994	0.591	34	0.223	K.KISEDEYVSAIKEEISK.V
R3/RRR3-6/3	1739.372	1740.015	-947.526	0.516	1677.520	0.553	33	0.216	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-4/2	1809.609	1808.137	261.710	0.506	1505.864	0.486	22	0.214	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-5/2	1485.672	1486.653	-1336.848	0.465	1641.328	0.399	18	0.214	R.IPSTEEIADRINK.M
R3/RRR3-5/2	1486.332	1486.653	-216.120	0.501	1657.681	0.384	20	0.213	R.IPSTEEIADRINK.M
R3/RRR3-5/2	1707.538	1707.951	-242.473	0.536	1446.177	0.490	21	0.211	K.LDSEIKSWLAFAAQK.V
R3/RRR3-5/2	1659.488	1659.826	-204.710	0.498	1351.819	0.536	22	0.210	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-5/2	1708.826	1707.951	-73.270	0.480	1416.663	0.476	20	0.205	K.LDSEIKSWLAFAAQK.V
R3/RRR3-6/2	1706.859	1707.951	-1229.388	0.456	1403.015	0.466	21	0.202	K.LDSEIKSWLAFAAQK.V
R3/RRR3-5/3	1807.992	1808.137	-80.521	0.522	1901.371	0.400	32	0.201	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-6/2	1659.301	1659.826	-922.100	0.458	1275.849	0.527	22	0.200	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/2	1486.380	1486.653	-184.152	0.481	1443.468	0.428	19	0.199	R.IPSTEEIADRINK.M
R3/RRR3-6/2	1659.312	1659.826	-915.453	0.444	1197.097	0.529	21	0.193	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-7/2	1809.339	1808.137	112.065	0.542	1070.149	0.600	18	0.192	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-5/2	1660.253	1659.826	257.475	0.538	1145.233	0.525	20	0.186	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-5/2	1740.226	1740.015	121.911	0.533	1059.903	0.549	22	0.186	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-5/3	1969.185	1969.179	3.002	0.472	1468.009	0.537	32	0.185	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1867.638	1868.188	-832.163	0.512	969.520	0.578	25	0.185	R.KYTEVKPALTNM*VSAAK.L
R3/RRR3-6/2	1840.337	1841.006	-909.764	0.550	1272.045	0.463	20	0.185	K.ISEDEYVSAIKEEISK.V
R3/RRR3-6/2	1486.211	1486.653	-297.778	0.512	1354.333	0.409	18	0.185	R.IPSTEEIADRINK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1659.290	1659.826	-928.895	0.484	1153.501	0.511	20	0.185	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1849.551	1850.028	-258.683	0.368	1723.816	0.418	28	0.185	K.AEHAFYLDWAVHSFR.I
R3/RRR3-5/2	1486.308	1486.653	-232.846	0.473	1454.085	0.342	19	0.183	R.IPSTEEIADRINK.M
R3/RRR3-6/3	1968.988	1969.179	-97.174	0.527	1455.036	0.529	32	0.181	K.KISEDEYVSAIKEEISK.V
R3/RRR3-6/3	1724.935	1724.015	-46.969	0.500	1391.584	0.555	32	0.179	K.YTEVKPALTNMVSAAK.L
R3/RRR3-5/3	1741.056	1740.015	24.061	0.529	1455.989	0.527	33	0.178	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-5/2	1840.567	1841.006	-239.117	0.551	1280.500	0.419	20	0.177	K.ISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1723.360	1724.015	-963.203	0.525	988.532	0.512	24	0.177	K.YTEVKPALTNMVSAAK.L
R3/RRR3-4/3	1968.597	1969.179	-805.778	0.483	1480.006	0.499	32	0.176	K.KISEDEYVSAIKEEISK.V
R3/RRR3-2/3	1968.377	1969.179	-918.018	0.500	1390.911	0.535	31	0.176	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/3	1968.551	1969.179	-829.681	0.524	1436.243	0.517	31	0.176	K.KISEDEYVSAIKEEISK.V
R3/RRR3-6/2	1193.556	1194.362	-1518.266	0.472	1147.817	0.428	16	0.176	R.SDEKLLSVFR.E
R3/RRR3-6/2	1021.298	1022.181	-1850.172	0.420	1267.795	0.370	15	0.175	K.SWLAFAAQK.V
R3/RRR3-5/2	1022.035	1022.181	-143.290	0.440	1290.578	0.347	15	0.173	K.SWLAFAAQK.V
R3/RRR3-5/2	1194.121	1194.362	-202.565	0.536	1143.346	0.408	16	0.171	R.SDEKLLSVFR.E
R3/RRR3-5/3	1723.780	1724.015	-137.100	0.520	1392.752	0.522	31	0.171	K.YTEVKPALTNMVSAAK.L
R3/RRR3-5/2	1194.101	1194.362	-219.076	0.554	1141.272	0.407	16	0.171	R.SDEKLLSVFR.E
R3/RRR3-5/3	1849.312	1850.028	-930.481	0.423	1440.966	0.493	27	0.170	K.AEHAFYLDWAVHSFR.I
R3/RRR3-4/2	1659.403	1659.826	-255.926	0.420	1028.904	0.480	19	0.170	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/2	1659.281	1659.826	-933.991	0.455	977.688	0.490	19	0.168	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/2	1193.479	1194.362	-1582.995	0.519	1113.489	0.396	16	0.168	R.SDEKLLSVFR.E
R3/RRR3-6/2	1193.562	1194.362	-1512.513	0.503	1139.242	0.385	16	0.168	R.SDEKLLSVFR.E
R3/RRR3-2/3	1969.154	1969.179	-12.480	0.485	1327.853	0.521	31	0.165	K.KISEDEYVSAIKEEISK.V
R3/RRR3-2/2	1130.945	1131.218	-242.569	0.481	861.347	0.453	17	0.165	R.IPSTEEIADR.I
R3/RRR3-5/2	1021.707	1022.181	-465.693	0.432	1127.026	0.370	14	0.165	K.SWLAFAAQK.V
R3/RRR3-5/2	1130.977	1131.218	-214.199	0.494	690.006	0.505	16	0.164	R.IPSTEEIADR.I
R3/RRR3-5/2	1867.565	1868.188	-871.531	0.504	708.651	0.563	22	0.164	R.KYTEVKPALTNM*VSAAK.L
R3/RRR3-5/2	1195.359	1194.362	-3.135	0.516	1122.781	0.370	16	0.164	R.SDEKLLSVFR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1841.400	1841.006	214.326	0.518	981.825	0.465	19	0.164	K.ISEDEYVSAIKEEISK.V
R3/RRR3-6/3	1739.287	1740.015	-996.250	0.439	1491.538	0.458	33	0.164	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-3/3	1969.419	1969.179	122.366	0.482	1303.289	0.524	31	0.163	K.KISEDEYVSAIKEEISK.V
R3/RRR3-5/2	1841.281	1841.006	149.574	0.501	1046.104	0.432	19	0.163	K.ISEDEYVSAIKEEISK.V
R3/RRR3-2/2	1659.778	1659.826	-29.404	0.438	817.187	0.525	17	0.162	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-5/3	1723.960	1724.015	-32.259	0.499	1417.781	0.483	33	0.162	K.YTEVKPALTNMVSAAK.L
R3/RRR3-6/3	1739.300	1740.015	-988.745	0.469	1399.092	0.480	32	0.160	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-4/2	1130.778	1131.218	-390.511	0.494	748.264	0.451	16	0.160	R.IPSTEEIADR.I
R3/RRR3-6/2	1021.557	1022.181	-1594.895	0.411	1131.039	0.334	14	0.160	K.SWLAFAAQK.V
R3/RRR3-5/3	1739.867	1740.015	-85.244	0.476	1435.306	0.470	34	0.159	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-2/2	1130.911	1131.218	-272.457	0.474	827.500	0.420	17	0.159	R.IPSTEEIADR.I
R3/RRR3-5/2	1021.555	1022.181	-1596.576	0.377	1213.453	0.289	15	0.159	K.SWLAFAAQK.V
R3/RRR3-4/2	1131.092	1131.218	-111.884	0.488	880.597	0.398	17	0.158	R.IPSTEEIADR.I
R3/RRR3-6/2	1840.552	1841.006	-247.368	0.530	971.525	0.439	18	0.158	K.ISEDEYVSAIKEEISK.V
R3/RRR3-5/2	943.010	943.123	-120.048	0.431	662.744	0.458	15	0.158	K.VVEVNALAK.A
R3/RRR3-2/2	1130.372	1131.218	-1638.551	0.407	808.502	0.428	16	0.158	R.IPSTEEIADR.I
R3/RRR3-4/2	1131.085	1131.218	-118.488	0.463	720.377	0.438	16	0.157	R.IPSTEEIADR.I
R3/RRR3-6/2	1021.558	1022.181	-1593.815	0.440	1097.084	0.324	14	0.156	K.SWLAFAAQK.V
R3/RRR3-5/2	1131.626	1131.218	361.739	0.468	739.018	0.420	16	0.156	R.IPSTEEIADR.I
R3/RRR3-1/2	1131.090	1131.218	-113.833	0.462	773.508	0.403	16	0.155	R.IPSTEEIADR.I
R3/RRR3-2/2	1659.397	1659.826	-259.616	0.375	858.789	0.451	17	0.155	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-3/2	1659.382	1659.826	-268.768	0.424	877.925	0.426	18	0.154	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-5/2	1458.661	1457.689	-19.357	0.500	911.156	0.391	18	0.153	R.FETCYQIALAIK.K
R3/RRR3-5/2	1808.934	1808.137	-112.825	0.435	914.450	0.414	17	0.153	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-6/2	1131.201	1131.218	-15.652	0.443	743.686	0.375	16	0.151	R.IPSTEEIADR.I
R3/RRR3-1/3	1968.747	1969.179	-220.229	0.486	1138.224	0.531	30	0.150	K.KISEDEYVSAIKEEISK.V
R3/RRR3-7/2	943.173	943.123	53.144	0.435	379.284	0.437	12	0.150	K.VVEVNALAK.A
R3/RRR3-2/2	1194.214	1194.362	-124.835	0.418	909.875	0.349	14	0.150	R.SDEKLLSVFR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1659.419	1659.826	-246.414	0.420	900.595	0.615	29	0.149	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-1/2	942.972	943.123	-159.654	0.382	717.718	0.366	15	0.149	K.VVEVNALAK.A
R3/RRR3-3/3	1968.913	1969.179	-135.235	0.531	1213.737	0.502	31	0.149	K.KISEDEYVSAIKEEISK.V
R3/RRR3-1/2	942.871	943.123	-267.840	0.359	497.879	0.412	14	0.148	K.VVEVNALAK.A
R3/RRR3-1/2	1194.278	1194.362	-71.211	0.412	1020.035	0.281	15	0.147	R.SDEKLLSVFR.E
R3/RRR3-2/2	942.329	943.123	-1908.876	0.349	540.973	0.389	14	0.147	K.VVEVNALAK.A
R3/RRR3-5/3	1740.149	1740.015	77.512	0.472	1294.897	0.469	32	0.147	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-5/2	943.012	943.123	-117.061	0.320	716.242	0.361	15	0.146	K.VVEVNALAK.A
R3/RRR3-14/2	1131.844	1131.218	-331.729	0.370	635.094	0.360	15	0.146	R.IPSTEEIADR.I
R3/RRR3-6/3	1723.964	1724.015	-30.022	0.445	1375.993	0.427	30	0.146	K.YTEVKPALTNMVSAAK.L
R3/RRR3-1/2	942.506	943.123	-1720.155	0.337	490.294	0.398	13	0.146	K.VVEVNALAK.A
R3/RRR3-3/2	1131.413	1131.218	172.646	0.401	644.876	0.347	15	0.146	R.IPSTEEIADR.I
R3/RRR3-2/2	1659.341	1659.826	-293.641	0.393	614.787	0.446	15	0.144	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-24/2	1132.036	1131.218	-161.651	0.398	732.727	0.307	16	0.144	R.IPSTEEIADR.I
R3/RRR3-5/2	943.102	943.123	-22.019	0.428	508.542	0.310	14	0.144	K.VVEVNALAK.A
R3/RRR3-4/2	942.909	943.123	-227.186	0.304	296.198	0.349	11	0.143	K.VVEVNALAK.A
R3/RRR3-5/3	1194.681	1194.362	267.360	0.465	1557.866	0.364	22	0.143	R.SDEKLLSVFR.E
R3/RRR3-2/3	1660.689	1659.826	-82.700	0.479	789.444	0.616	28	0.143	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1659.401	1659.826	-257.041	0.455	760.620	0.624	28	0.142	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-24/2	1131.560	1131.218	303.331	0.321	591.940	0.331	14	0.142	R.IPSTEEIADR.I
R3/RRR3-4/2	942.389	943.123	-1845.484	0.288	453.558	0.341	13	0.142	K.VVEVNALAK.A
R3/RRR3-12/2	1130.524	1131.218	-1503.063	0.312	369.066	0.314	12	0.142	R.IPSTEEIADR.I
R3/RRR3-16/2	1131.169	1131.218	-43.795	0.422	576.238	0.357	13	0.141	-.IPSTEEIADR.-
R3/RRR3-7/2	942.538	943.123	-1686.063	0.268	324.858	0.305	11	0.141	K.VVEVNALAK.A
R3/RRR3-7/2	1807.431	1808.137	-946.602	0.318	715.149	0.355	16	0.140	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-25/2	1131.158	1131.218	-53.753	0.261	683.360	0.258	15	0.138	R.IPSTEEIADR.I
R3/RRR3-10/3	1659.550	1659.826	-167.047	0.445	778.662	0.592	28	0.137	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/2	1807.197	1808.137	-1076.804	0.401	678.577	0.344	15	0.137	K.GM*LTGPVTILNWSFVR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1659.744	1659.826	-50.068	0.426	818.419	0.576	29	0.136	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-4/2	942.963	943.123	-169.653	0.275	292.509	0.316	11	0.136	-.VVEVNALAK.-
R3/RRR3-7/2	1660.135	1659.826	186.545	0.274	461.280	0.378	14	0.136	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-1/3	1659.421	1659.826	-245.085	0.492	614.037	0.619	26	0.135	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1659.577	1659.826	-150.998	0.435	648.362	0.610	26	0.134	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1659.505	1659.826	-194.276	0.420	899.860	0.532	29	0.133	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-7/2	1660.066	1659.826	144.513	0.298	399.961	0.337	13	0.133	-.YGAGIGPGVYDIHSPR.-
R3/RRR3-5/3	1850.311	1850.028	153.535	0.366	1169.074	0.443	25	0.132	K.AEHAFYLDWAVHSFR.I
R3/RRR3-5/3	1660.506	1659.826	-193.754	0.451	816.431	0.546	26	0.132	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-1/2	1660.210	1659.826	231.670	0.292	632.743	0.263	15	0.131	-.YGAGIGPGVYDIHSPR.-
R3/RRR3-1/3	1658.845	1659.826	-1198.110	0.414	610.500	0.601	24	0.131	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-7/2	942.707	943.123	-442.053	0.305	298.983	0.324	10	0.131	-.VVEVNALAK.-
R3/RRR3-6/3	1976.936	1978.201	-1148.861	0.465	1242.906	0.406	24	0.130	R.KAEHAFYLDWAVHSFR.I
R3/RRR3-26/2	1131.329	1131.218	97.768	0.211	642.367	0.086	14	0.129	-.IPSTEEIADR.-
R3/RRR3-10/3	1659.657	1659.826	-102.301	0.408	679.368	0.568	25	0.129	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-3/3	1659.767	1659.826	-35.793	0.458	532.471	0.599	21	0.128	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-26/2	1131.207	1131.218	-9.807	0.199	597.444	0.103	14	0.128	-.IPSTEEIADR.-
R3/RRR3-2/3	1659.708	1659.826	-71.536	0.411	638.624	0.571	26	0.128	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-26/2	1131.974	1131.218	-216.606	0.252	635.206	0.021	14	0.127	-.IPSTEEIADR.-
R3/RRR3-7/3	1659.895	1659.826	41.548	0.387	672.861	0.559	26	0.127	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-12/2	1130.508	1131.218	-1517.489	0.352	440.561	0.330	12	0.127	-.IPSTEEIADR.-
R3/RRR3-5/3	1708.852	1707.951	-58.015	0.408	1248.144	0.403	28	0.126	K.LDSEIKSWLAFAAQK.V
R3/RRR3-6/3	1867.867	1868.188	-172.319	0.531	828.074	0.516	29	0.125	R.KYTEVKPALTNM*VSAAK.L
R3/RRR3-8/2	1659.850	1659.826	14.302	0.201	167.179	0.362	12	0.125	-.YGAGIGPGVYDIHSPR.-
R3/RRR3-5/3	1853.062	1852.188	-68.168	0.510	668.106	0.539	27	0.122	R.KYTEVKPALTNMVSAAK.L
R3/RRR3-6/3	1808.158	1808.137	11.306	0.426	1399.563	0.310	28	0.122	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-4/3	1659.831	1659.826	2.602	0.419	564.900	0.539	26	0.121	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1194.246	1194.362	-97.316	0.456	1302.952	0.351	21	0.120	R.SDEKLLSVFR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1659.640	1659.826	-112.704	0.406	596.872	0.512	24	0.118	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-3/3	1659.373	1659.826	-274.311	0.392	405.764	0.543	22	0.118	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1991.672	1992.176	-757.161	0.480	576.144	0.542	27	0.117	K.IQEELDIDVLVHGEPER.N
R3/RRR3-5/3	1658.929	1659.826	-1146.902	0.343	659.202	0.493	25	0.117	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-1/3	1659.382	1659.826	-268.665	0.360	467.811	0.521	22	0.116	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1868.246	1868.188	31.401	0.537	651.038	0.500	27	0.116	R.KYTEVKPALTNM*VSAAK.L
R3/RRR3-7/3	1659.456	1659.826	-223.721	0.401	503.434	0.491	22	0.114	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-5/3	1194.191	1194.362	-143.919	0.509	1243.831	0.337	21	0.113	R.SDEKLLSVFR.E
R3/RRR3-6/3	1991.978	1992.176	-99.740	0.503	493.343	0.499	28	0.112	K.IQEELDIDVLVHGEPER.N
R3/RRR3-4/3	1658.832	1659.826	-1206.090	0.337	467.332	0.476	22	0.111	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-7/3	1659.858	1659.826	18.978	0.385	708.870	0.437	23	0.111	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-3/3	1659.898	1659.826	43.429	0.387	489.162	0.462	24	0.111	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1194.683	1194.362	269.358	0.446	1184.126	0.333	20	0.110	R.SDEKLLSVFR.E
R3/RRR3-5/3	1867.111	1868.188	-1115.724	0.432	627.212	0.454	27	0.108	R.KYTEVKPALTNM*VSAAK.L
R3/RRR3-6/3	1194.560	1194.362	166.224	0.538	1152.346	0.335	20	0.108	R.SDEKLLSVFR.E
R3/RRR3-6/3	1867.972	1868.188	-115.875	0.475	622.673	0.445	28	0.108	R.KYTEVKPALTNM*VSAAK.L
R3/RRR3-2/3	1194.154	1194.362	-174.682	0.405	1135.868	0.317	20	0.105	R.SDEKLLSVFR.E
R3/RRR3-6/3	1660.065	1659.826	144.099	0.270	664.193	0.391	24	0.105	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-6/3	1992.428	1992.176	126.668	0.411	328.590	0.460	22	0.103	K.IQEELDIDVLVHGEPER.N
R3/RRR3-5/3	1868.053	1868.188	-72.317	0.458	576.522	0.401	26	0.102	R.KYTEVKPALTNM*VSAAK.L
R3/RRR3-5/3	1194.471	1194.362	91.512	0.399	1040.960	0.316	19	0.102	R.SDEKLLSVFR.E
R3/RRR3-4/3	1194.213	1194.362	-125.308	0.314	1084.080	0.286	19	0.099	R.SDEKLLSVFR.E
R3/RRR3-13/3	1660.268	1659.826	266.756	0.347	523.166	0.393	21	0.099	-.YGAGIGPGVYDIHSPR.-
R3/RRR3-8/3	1661.253	1659.826	257.828	0.270	585.404	0.302	25	0.098	K.YGAGIGPGVYDIHSPR.I
R3/RRR3-5/3	1850.096	1850.028	37.211	0.373	833.461	0.331	23	0.097	K.AEHAFYLDWAVHSFR.I
R3/RRR3-2/3	1194.367	1194.362	4.027	0.473	955.236	0.307	18	0.097	-.SDEKLLSVFR.-
R3/RRR3-5/3	1867.854	1868.188	-179.006	0.425	609.193	0.361	26	0.096	-.KYTEVKPALTNM*VSAAK.-
R3/RRR3-4/3	1194.712	1194.362	293.640	0.266	815.203	0.267	18	0.091	R.SDEKLLSVFR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/3	1740.957	1740.015	-33.430	0.321	847.965	0.230	25	0.089	K.YTEVKPALTNM*VSAAK.L
R3/RRR3-6/3	1807.592	1808.137	-857.319	0.315	803.657	0.209	23	0.083	K.GM*LTGPVTILNWSFVR.N
R3/RRR3-4/2	1569.342	1569.746	-258.755	0.610	2498.234	0.560	22	0.410	R.KYQAFAQTLQQSR.G
R3/RRR3-4/2	1569.379	1569.746	-235.110	0.620	2431.149	0.530	22	0.384	R.KYQAFAQTLQQSR.G
R3/RRR3-4/2	1441.346	1441.574	-158.561	0.567	2029.260	0.536	19	0.307	K.YQAFAQTLQQSR.G
R3/RRR3-4/2	1431.157	1431.767	-1128.210	0.516	1982.644	0.562	20	0.304	R.IVSQLLTLMDGLK.Q
R3/RRR3-4/2	1441.214	1441.574	-250.581	0.561	1994.528	0.515	19	0.295	K.YQAFAQTLQQSR.G
R3/RRR3-4/2	1431.397	1431.767	-259.056	0.543	1926.610	0.555	19	0.292	R.IVSQLLTLMDGLK.Q
R3/RRR3-5/2	1431.236	1431.767	-1072.628	0.534	1966.105	0.513	21	0.288	R.IVSQLLTLMDGLK.Q
R3/RRR3-4/2	1441.086	1441.574	-339.132	0.553	1939.245	0.520	19	0.287	K.YQAFAQTLQQSR.G
R3/RRR3-5/2	1431.201	1431.767	-1097.292	0.480	1920.641	0.532	20	0.285	R.IVSQLLTLMDGLK.Q
R3/RRR3-4/2	1353.191	1353.503	-230.960	0.482	1964.040	0.485	19	0.283	K.LAEDVDLEHIAK.D
R3/RRR3-5/2	1442.295	1441.574	-193.856	0.564	1816.729	0.516	19	0.267	K.YQAFAQTLQQSR.G
R3/RRR3-4/2	1448.382	1447.766	-266.233	0.533	1695.384	0.577	20	0.264	R.IVSQLLTLM*DGLK.Q
R3/RRR3-5/2	1440.518	1441.574	-1431.620	0.456	1910.590	0.418	19	0.255	K.YQAFAQTLQQSR.G
R3/RRR3-4/2	1846.393	1846.969	-856.118	0.519	1662.321	0.533	21	0.247	K.YTQGFSGADITEICQR.A
R3/RRR3-4/2	1447.370	1447.766	-274.540	0.408	1751.414	0.475	20	0.245	R.IVSQLLTLM*DGLK.Q
R3/RRR3-4/2	1431.440	1431.767	-228.513	0.471	1599.207	0.542	19	0.241	R.IVSQLLTLMDGLK.Q
R3/RRR3-4/2	1847.449	1846.969	260.347	0.555	1540.635	0.570	21	0.240	K.YTQGFSGADITEICQR.A
R3/RRR3-5/2	1430.840	1431.767	-1350.342	0.419	1610.794	0.523	18	0.237	R.IVSQLLTLMDGLK.Q
R3/RRR3-4/2	1677.389	1677.969	-944.638	0.460	1613.554	0.501	21	0.235	R.VLNQLLTEMDGMNAK.K
R3/RRR3-4/2	1352.606	1353.503	-1406.902	0.493	1681.182	0.438	19	0.230	K.LAEDVDLEHIAK.D
R3/RRR3-5/2	1565.397	1565.746	-224.054	0.503	1499.039	0.486	19	0.216	K.AIANECQANFISVK.G
R3/RRR3-4/2	1252.214	1252.437	-178.305	0.419	1330.579	0.535	19	0.209	K.GVLFYGPPGCGK.T
R3/RRR3-4/2	1251.943	1252.437	-395.943	0.445	1225.562	0.580	18	0.207	K.GVLFYGPPGCGK.T
R3/RRR3-4/2	1565.195	1565.746	-993.811	0.464	1546.247	0.421	19	0.207	K.AIANECQANFISVK.G
R3/RRR3-4/2	1846.413	1846.969	-845.433	0.508	1303.864	0.550	19	0.206	K.YTQGFSGADITEICQR.A
R3/RRR3-4/2	1565.386	1565.746	-230.625	0.511	1508.355	0.438	19	0.206	K.AIANECQANFISVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1447.540	1447.766	-156.600	0.458	1412.116	0.461	18	0.201	R.IVSQLLTLM*DGLK.Q
R3/RRR3-5/2	1952.680	1953.165	-249.226	0.497	1304.984	0.499	22	0.197	K.GPELLTM*WFGESEANVR.E
R3/RRR3-4/2	1951.877	1953.165	-1175.690	0.497	1290.175	0.510	20	0.196	K.GPELLTM*WFGESEANVR.E
R3/RRR3-4/2	1187.735	1188.316	-1335.311	0.480	1328.581	0.461	20	0.196	K.TALGTSNPSALR.E
R3/RRR3-5/2	1565.498	1565.746	-158.813	0.490	1335.956	0.467	18	0.194	K.AIANECQANFISVK.G
R3/RRR3-4/2	1188.048	1188.316	-226.582	0.492	1253.275	0.480	19	0.192	K.TALGTSNPSALR.E
R3/RRR3-5/2	1566.366	1565.746	-243.457	0.566	1271.340	0.486	18	0.190	K.AIANECQANFISVK.G
R3/RRR3-4/2	1565.222	1565.746	-976.898	0.462	1299.985	0.444	18	0.186	K.AIANECQANFISVK.G
R3/RRR3-4/2	1446.910	1447.766	-1286.675	0.475	1125.990	0.512	17	0.184	R.IVSQLLTLM*DGLK.Q
R3/RRR3-1/2	1187.845	1188.316	-397.930	0.480	1240.667	0.437	20	0.184	K.TALGTSNPSALR.E
R3/RRR3-4/2	1187.632	1188.316	-1422.747	0.413	1162.008	0.456	19	0.180	K.TALGTSNPSALR.E
R3/RRR3-5/2	1952.812	1953.165	-181.245	0.513	1059.076	0.525	20	0.179	K.GPELLTM*WFGESEANVR.E
R3/RRR3-4/2	1160.431	1159.360	61.975	0.496	1009.100	0.507	17	0.177	K.GILLYGPPGSGK.T
R3/RRR3-5/2	1252.131	1252.437	-244.809	0.322	1099.851	0.473	17	0.173	K.GVLFYGPPGCGK.T
R3/RRR3-2/2	1187.793	1188.316	-1286.283	0.508	1191.300	0.399	19	0.173	K.TALGTSNPSALR.E
R3/RRR3-5/2	1447.466	1447.766	-207.614	0.436	1152.745	0.423	18	0.172	R.IVSQLLTLM*DGLK.Q
R3/RRR3-4/2	1953.428	1953.165	134.959	0.552	949.701	0.533	19	0.171	K.GPELLTM*WFGESEANVR.E
R3/RRR3-2/2	1187.908	1188.316	-344.726	0.466	1049.962	0.432	19	0.169	K.TALGTSNPSALR.E
R3/RRR3-5/2	1952.408	1953.165	-902.579	0.485	1054.053	0.473	19	0.169	K.GPELLTM*WFGESEANVR.E
R3/RRR3-5/2	1160.076	1159.360	-245.555	0.454	998.746	0.446	17	0.166	K.GILLYGPPGSGK.T
R3/RRR3-1/2	1188.145	1188.316	-144.640	0.469	1163.097	0.358	19	0.165	K.TALGTSNPSALR.E
R3/RRR3-4/2	1952.564	1953.165	-822.118	0.495	898.040	0.495	19	0.163	K.GPELLTM*WFGESEANVR.E
R3/RRR3-5/2	1252.144	1252.437	-234.442	0.383	858.856	0.463	16	0.159	K.GVLFYGPPGCGK.T
R3/RRR3-3/2	1188.056	1188.316	-219.366	0.458	971.059	0.376	18	0.156	K.TALGTSNPSALR.E
R3/RRR3-2/2	1187.957	1188.316	-303.073	0.447	787.165	0.415	17	0.153	K.TALGTSNPSALR.E
R3/RRR3-4/2	1300.221	1299.412	-147.521	0.446	560.232	0.491	16	0.153	R.EIDIGVPDEVGR.L
R3/RRR3-5/2	1300.188	1299.412	-172.762	0.401	535.193	0.512	16	0.153	R.EIDIGVPDEVGR.L
R3/RRR3-5/2	1300.038	1299.412	-288.340	0.392	603.555	0.485	17	0.153	R.EIDIGVPDEVGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1159.149	1159.360	-182.270	0.416	817.744	0.425	15	0.153	K.GILLYGPPGSGK.T
R3/RRR3-5/2	1299.955	1299.412	-352.781	0.473	478.150	0.493	15	0.151	R.EIDIGVPDEVGR.L
R3/RRR3-1/2	1188.297	1188.316	-15.930	0.489	811.695	0.387	17	0.151	K.TALGTSNPSALR.E
R3/RRR3-3/2	1187.941	1188.316	-316.373	0.501	808.397	0.367	18	0.149	K.TALGTSNPSALR.E
R3/RRR3-5/2	969.094	969.160	-68.428	0.364	860.023	0.347	13	0.149	R.ELVELPLR.H
R3/RRR3-2/2	1160.342	1159.360	-15.259	0.377	842.547	0.373	15	0.148	K.GILLYGPPGSGK.T
R3/RRR3-4/2	958.940	959.079	-144.738	0.393	824.631	0.349	14	0.147	K.DVDLNALAK.Y
R3/RRR3-4/2	958.882	959.079	-205.781	0.409	797.693	0.340	14	0.146	K.DVDLNALAK.Y
R3/RRR3-4/2	958.914	959.079	-172.832	0.351	817.936	0.345	14	0.146	K.DVDLNALAK.Y
R3/RRR3-4/2	968.517	969.160	-1701.263	0.303	751.795	0.340	13	0.144	R.ELVELPLR.H
R3/RRR3-4/2	968.437	969.160	-1784.593	0.340	728.199	0.325	12	0.143	R.ELVELPLR.H
R3/RRR3-5/2	1159.116	1159.360	-210.478	0.398	614.479	0.420	13	0.142	-.GILLYGPPGSGK.-
R3/RRR3-4/2	1052.040	1052.163	-117.149	0.368	725.014	0.349	13	0.142	K.DFSTAILER.K
R3/RRR3-4/2	968.487	969.160	-1732.162	0.335	556.798	0.360	11	0.142	R.ELVELPLR.H
R3/RRR3-5/2	968.615	969.160	-1599.716	0.329	747.222	0.315	12	0.142	R.ELVELPLR.H
R3/RRR3-4/2	1299.114	1299.412	-230.489	0.411	414.112	0.441	14	0.142	-.EIDIGVPDEVGR.-
R3/RRR3-5/2	968.531	969.160	-1686.701	0.312	742.166	0.313	12	0.141	R.ELVELPLR.H
R3/RRR3-3/2	1075.674	1076.143	-437.150	0.369	884.742	0.242	15	0.137	K.LAGESESNLR.K
R3/RRR3-4/2	1075.293	1076.143	-1725.556	0.290	575.103	0.315	12	0.133	K.LAGESESNLR.K
R3/RRR3-2/2	1158.950	1159.360	-354.924	0.227	429.178	0.351	12	0.132	-.GILLYGPPGSGK.-
R3/RRR3-4/2	1051.979	1052.163	-175.233	0.380	601.985	0.308	12	0.132	-.DFSTAILER.-
R3/RRR3-4/3	1553.606	1553.736	-83.711	0.397	727.853	0.494	23	0.115	R.LGDVVSVHQCPDVK.Y
R3/RRR3-4/3	1552.918	1553.736	-1174.185	0.407	761.177	0.445	23	0.109	R.LGDVVSVHQCPDVK.Y
R3/RRR3-4/3	1553.518	1553.736	-140.698	0.367	593.477	0.440	21	0.104	R.LGDVVSVHQCPDVK.Y
R3/RRR3-5/3	1553.694	1553.736	-26.614	0.395	731.827	0.408	23	0.104	R.LGDVVSVHQCPDVK.Y
R3/RRR3-5/3	1554.223	1553.736	314.420	0.371	549.817	0.410	21	0.101	R.LGDVVSVHQCPDVK.Y
R3/RRR3-4/3	1603.693	1603.952	-162.097	0.379	965.437	0.332	24	0.097	R.RIVSQLLTLM*DGLK.Q
R3/RRR3-7/2	1160.437	1159.360	66.617	0.190	323.283	0.336	9	0.092	-.GILLYGPPGSGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1886.226	1885.881	183.853	0.583	2551.414	0.616	28	0.435	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1887.300	1885.881	222.932	0.593	2222.226	0.583	27	0.351	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1885.414	1885.881	-248.431	0.639	2062.181	0.673	28	0.351	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1799.414	1800.047	-910.041	0.565	2223.213	0.541	24	0.343	R.LFHETTATALAYGIYK.T
R3/RRR3-4/2	1886.270	1885.881	207.086	0.573	2102.734	0.622	27	0.342	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1885.427	1885.881	-241.221	0.608	2036.917	0.638	28	0.335	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1469.005	1469.645	-1120.025	0.460	2282.155	0.460	24	0.331	R.FIGTAGAASSTM*NPK.N
R3/RRR3-4/2	1470.153	1469.645	-335.971	0.566	2033.931	0.603	22	0.328	R.FIGTAGAASSTM*NPK.N
R3/RRR3-4/2	1799.516	1800.047	-853.518	0.539	1937.939	0.550	23	0.295	R.LFHETTATALAYGIYK.T
R3/RRR3-4/2	1885.373	1885.881	-802.246	0.574	1672.145	0.643	26	0.275	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1469.222	1469.645	-288.934	0.498	1830.196	0.504	21	0.265	R.FIGTAGAASSTM*NPK.N
R3/RRR3-4/3	1422.861	1422.655	145.577	0.549	2483.637	0.320	30	0.264	K.HANPVLLSSDLKK.K
R3/RRR3-4/2	1567.311	1567.796	-310.179	0.503	1674.856	0.518	21	0.247	R.GCALECAILSPTFK.V
R3/RRR3-4/3	1422.665	1422.655	7.339	0.558	2205.637	0.358	28	0.230	K.HANPVLLSSDLKK.K
R3/RRR3-4/2	1542.341	1541.811	-305.358	0.381	1719.265	0.399	21	0.224	R.AVLDAATIAGLCPLR.L
R3/RRR3-4/2	1567.125	1567.796	-1069.466	0.372	1619.431	0.421	21	0.217	R.GCALECAILSPTFK.V
R3/RRR3-4/2	1567.391	1567.796	-259.077	0.498	1518.883	0.463	20	0.214	R.GCALECAILSPTFK.V
R3/RRR3-4/2	1294.084	1294.482	-308.305	0.426	1401.180	0.471	19	0.204	K.HANPVLLSSDLK.K
R3/RRR3-4/2	1884.054	1885.881	-2037.406	0.413	1153.318	0.628	23	0.204	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-3/2	1887.348	1885.881	248.162	0.527	1221.523	0.573	21	0.199	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1422.349	1422.655	-215.598	0.482	1294.423	0.493	20	0.198	K.HANPVLLSSDLKK.K
R3/RRR3-4/3	1886.293	1885.881	219.020	0.444	1671.138	0.474	33	0.198	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-1/2	1884.354	1885.881	-1877.177	0.496	1063.588	0.608	24	0.194	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1541.391	1541.811	-273.455	0.307	1486.270	0.376	20	0.191	R.AVLDAATIAGLCPLR.L
R3/RRR3-4/3	1886.988	1885.881	56.954	0.494	1686.668	0.457	36	0.191	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-2/2	1542.426	1541.811	-250.252	0.361	1305.287	0.395	18	0.177	R.AVLDAATIAGLCPLR.L
R3/RRR3-4/3	1423.261	1422.655	-277.623	0.543	1789.648	0.351	26	0.168	K.HANPVLLSSDLKK.K
R3/RRR3-1/2	1743.033	1741.919	65.424	0.437	971.369	0.460	17	0.162	R.GPSIDQLAYCINSFR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1567.355	1567.796	-282.049	0.401	956.836	0.424	17	0.158	R.GCALECAILSPTFK.V
R3/RRR3-4/2	1680.710	1681.870	-1289.164	0.465	549.201	0.544	17	0.152	K.ISTYTVGPFNPGKGDK.A
R3/RRR3-4/2	1681.382	1681.870	-291.320	0.471	571.908	0.519	18	0.152	K.ISTYTVGPFNPGKGDK.A
R3/RRR3-4/2	899.026	899.070	-49.179	0.387	656.774	0.459	13	0.152	-.ISAPILER.-
R3/RRR3-4/2	1481.162	1481.638	-322.021	0.426	809.855	0.416	18	0.151	R.VSEGPDGFPLVHAR.Y
R3/RRR3-4/2	1347.238	1347.479	-178.907	0.352	933.681	0.372	15	0.150	K.NAVESYVYDMR.N
R3/RRR3-4/2	1681.381	1681.870	-291.685	0.463	604.073	0.488	18	0.149	K.ISTYTVGPFNPGKGDK.A
R3/RRR3-4/2	1008.003	1008.067	-63.661	0.386	685.486	0.404	12	0.149	K.YSDPELQR.D
R3/RRR3-4/2	936.788	937.077	-308.462	0.335	533.519	0.513	10	0.149	R.DIAAFPFR.V
R3/RRR3-2/2	1542.714	1541.811	-63.064	0.351	907.784	0.395	15	0.148	R.AVLDAATIAGLCPLR.L
R3/RRR3-4/2	1346.751	1347.479	-1286.831	0.293	916.296	0.372	14	0.147	K.NAVESYVYDMR.N
R3/RRR3-4/2	1481.317	1481.638	-217.182	0.434	654.576	0.427	17	0.146	R.VSEGPDGFPLVHAR.Y
R3/RRR3-4/2	1041.080	1041.183	-99.566	0.475	974.461	0.287	15	0.146	K.IQQQDALPK.H
R3/RRR3-4/3	1885.274	1885.881	-854.705	0.510	1096.121	0.525	32	0.145	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	1480.770	1481.638	-1265.370	0.338	816.417	0.375	18	0.145	R.VSEGPDGFPLVHAR.Y
R3/RRR3-4/2	1040.984	1041.183	-191.904	0.445	941.837	0.288	15	0.145	K.IQQQDALPK.H
R3/RRR3-4/2	1604.276	1604.783	-941.668	0.366	1274.119	0.177	19	0.145	K.VINQCSEAEVWLR.E
R3/RRR3-4/2	936.353	937.077	-1845.938	0.331	506.622	0.456	10	0.144	R.DIAAFPFR.V
R3/RRR3-4/3	1541.736	1541.811	-48.738	0.428	1459.415	0.394	29	0.144	R.AVLDAATIAGLCPLR.L
R3/RRR3-4/2	1007.942	1008.067	-124.158	0.357	542.779	0.379	11	0.143	K.YSDPELQR.D
R3/RRR3-10/3	1422.646	1422.655	-6.086	0.447	1595.624	0.323	24	0.142	K.HANPVLLSSDLKK.K
R3/RRR3-2/2	1801.308	1800.047	145.212	0.396	643.935	0.408	17	0.142	R.LFHETTATALAYGIYK.T
R3/RRR3-4/2	1008.433	1008.067	363.739	0.334	559.478	0.368	11	0.140	-.YSDPELQR.-
R3/RRR3-4/3	1886.167	1885.881	152.044	0.523	1205.198	0.465	33	0.140	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	898.630	899.070	-491.053	0.335	474.654	0.378	11	0.140	-.ISAPILER.-
R3/RRR3-4/3	1886.843	1885.881	-20.033	0.468	1184.461	0.459	33	0.138	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-4/2	898.463	899.070	-1793.508	0.273	533.451	0.385	11	0.138	-.ISAPILER.-
R3/RRR3-4/2	1381.293	1381.558	-192.312	0.299	790.074	0.317	19	0.137	K.ISTYTVGPFNPGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1008.346	1008.067	278.167	0.206	230.149	0.262	10	0.137	-.YSDPELQR.-
R3/RRR3-2/3	1885.906	1885.881	13.197	0.445	1311.898	0.401	32	0.136	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-3/2	898.992	899.070	-86.361	0.223	610.050	0.274	12	0.133	K.ISAPILER.V
R3/RRR3-2/2	1740.994	1741.919	-1109.008	0.328	198.383	0.395	11	0.132	R.GPSIDQLAYCINSFR.D
R3/RRR3-4/2	1604.092	1604.783	-1056.879	0.326	1000.171	0.165	18	0.132	K.VINQCSEAEVWLR.E
R3/RRR3-2/2	1801.542	1800.047	275.477	0.373	616.444	0.265	18	0.132	R.LFHETTATALAYGIYK.T
R3/RRR3-1/2	1885.894	1885.881	7.102	0.251	196.346	0.500	14	0.131	-.APADAAADGAENGAPNSEEK.-
R3/RRR3-4/3	1789.941	1789.969	-15.371	0.561	1079.129	0.463	28	0.130	K.FKDEYKIDVYQNAR.A
R3/RRR3-3/3	1885.712	1885.881	-89.940	0.507	913.597	0.511	31	0.129	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-8/2	936.798	937.077	-297.872	0.153	480.047	0.338	10	0.129	R.DIAAFPFR.V
R3/RRR3-2/2	1007.934	1008.067	-131.690	0.240	250.726	0.320	9	0.129	-.YSDPELQR.-
R3/RRR3-2/3	1421.898	1422.655	-1239.240	0.475	1560.287	0.285	25	0.128	K.HANPVLLSSDLKK.K
R3/RRR3-2/3	1481.482	1481.638	-105.679	0.389	830.526	0.471	24	0.118	R.VSEGPDGFPLVHAR.Y
R3/RRR3-4/3	1481.617	1481.638	-14.190	0.416	738.690	0.490	24	0.117	R.VSEGPDGFPLVHAR.Y
R3/RRR3-2/3	1481.715	1481.638	51.998	0.366	917.155	0.445	25	0.117	R.VSEGPDGFPLVHAR.Y
R3/RRR3-4/3	1483.014	1481.638	254.636	0.421	634.311	0.497	22	0.115	R.VSEGPDGFPLVHAR.Y
R3/RRR3-7/3	1481.895	1481.638	173.942	0.403	781.590	0.464	24	0.115	R.VSEGPDGFPLVHAR.Y
R3/RRR3-4/3	1481.811	1481.638	117.311	0.362	752.980	0.435	23	0.110	R.VSEGPDGFPLVHAR.Y
R3/RRR3-2/3	1422.267	1422.655	-273.254	0.482	1344.587	0.264	24	0.107	K.HANPVLLSSDLKK.K
R3/RRR3-4/3	1886.139	1885.881	137.246	0.416	745.619	0.413	26	0.106	K.APADAAADGAENGAPNSEEK.S
R3/RRR3-1/3	1482.891	1481.638	171.554	0.347	814.098	0.378	25	0.104	R.VSEGPDGFPLVHAR.Y
R3/RRR3-2/3	1481.370	1481.638	-181.437	0.345	795.212	0.380	25	0.103	R.VSEGPDGFPLVHAR.Y
R3/RRR3-3/3	1481.552	1481.638	-58.321	0.344	703.148	0.386	23	0.103	R.VSEGPDGFPLVHAR.Y
R3/RRR3-5/3	1481.551	1481.638	-58.569	0.327	850.669	0.356	22	0.103	R.VSEGPDGFPLVHAR.Y
R3/RRR3-1/3	1481.323	1481.638	-212.810	0.371	766.362	0.346	23	0.100	R.VSEGPDGFPLVHAR.Y
R3/RRR3-3/3	1422.262	1422.655	-277.000	0.397	862.212	0.321	21	0.098	K.HANPVLLSSDLKK.K
R3/RRR3-1/3	1422.011	1422.655	-1159.196	0.442	1280.267	0.201	24	0.095	-.HANPVLLSSDLKK.-
R3/RRR3-4/3	1887.489	1885.881	-208.044	0.401	775.893	0.293	26	0.092	K.APADAAADGAENGAPNSEEK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1886.133	1885.881	134.325	0.384	700.390	0.295	28	0.091	-.APADAAADGAENGAPNSEEK.-
R3/RRR3-6/1	1412.826	1413.562	-1231.969	0.325	656.489	0.518	18	0.943	K.SSVHDVVLVGGSTR.I
R3/RRR3-6/1	1412.814	1413.562	-1240.645	0.294	702.628	0.409	18	0.910	K.SSVHDVVLVGGSTR.I
R3/RRR3-6/2	1967.430	1968.236	-920.756	0.619	2443.338	0.572	25	0.399	R.VQQLLQDFFNGKELCK.S
R3/RRR3-6/2	1437.323	1437.625	-210.626	0.584	2088.845	0.508	18	0.307	-.VQQLLQDFFNGK.-
R3/RRR3-6/2	1676.242	1676.683	-263.946	0.484	2039.733	0.526	24	0.306	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/2	1438.190	1437.625	-303.123	0.647	2026.418	0.533	19	0.300	R.VQQLLQDFFNGK.E
R3/RRR3-6/2	1412.620	1413.562	-1378.593	0.470	1882.165	0.571	22	0.294	K.SSVHDVVLVGGSTR.I
R3/RRR3-6/2	1436.798	1437.625	-1275.378	0.540	2079.358	0.462	19	0.290	R.VQQLLQDFFNGK.E
R3/RRR3-6/2	1437.314	1437.625	-216.590	0.537	2037.183	0.450	18	0.279	R.VQQLLQDFFNGK.E
R3/RRR3-6/2	1309.102	1309.490	-297.380	0.387	1844.502	0.504	19	0.268	R.EIAEAYLGTTIK.N
R3/RRR3-6/2	1232.213	1232.436	-181.331	0.526	1869.861	0.430	20	0.252	K.DAGVIAGLNVM*R.I
R3/RRR3-6/2	1216.390	1216.436	-37.707	0.573	1704.446	0.499	20	0.247	K.DAGVIAGLNVMR.I
R3/RRR3-6/2	1676.091	1676.683	-952.382	0.469	1655.050	0.530	22	0.246	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/2	1968.582	1968.236	176.410	0.631	1555.515	0.577	22	0.243	R.VQQLLQDFFNGKELCK.S
R3/RRR3-6/2	1308.916	1309.490	-1206.167	0.338	1753.977	0.461	19	0.243	R.EIAEAYLGTTIK.N
R3/RRR3-6/2	1309.065	1309.490	-325.728	0.370	1659.904	0.512	18	0.242	R.EIAEAYLGTTIK.N
R3/RRR3-6/2	1196.674	1197.277	-1343.548	0.520	1679.071	0.482	18	0.240	R.FSDASVQSDIK.L
R3/RRR3-6/2	1216.592	1216.436	128.706	0.539	1641.722	0.486	20	0.236	K.DAGVIAGLNVMR.I
R3/RRR3-6/2	1375.057	1375.492	-317.595	0.481	1521.147	0.513	16	0.226	K.NALENYAYNM*R.N
R3/RRR3-6/2	1232.208	1232.436	-185.306	0.544	1645.338	0.443	19	0.225	K.DAGVIAGLNVM*R.I
R3/RRR3-6/2	1412.653	1413.562	-1355.420	0.426	1498.862	0.504	19	0.220	K.SSVHDVVLVGGSTR.I
R3/RRR3-6/2	1374.987	1375.492	-1097.918	0.456	1471.599	0.503	16	0.218	K.NALENYAYNM*R.N
R3/RRR3-6/2	1197.240	1197.277	-30.742	0.568	1356.380	0.493	18	0.205	R.FSDASVQSDIK.L
R3/RRR3-6/2	1567.423	1566.844	-269.382	0.593	1516.961	0.429	22	0.205	K.QFAAEEISSMVLIK.M
R3/RRR3-6/2	1437.674	1437.625	34.695	0.538	1321.201	0.527	16	0.205	R.VQQLLQDFFNGK.E
R3/RRR3-6/2	1233.306	1232.436	-105.026	0.464	1587.310	0.368	19	0.202	K.DAGVIAGLNVM*R.I
R3/RRR3-6/2	1968.058	1968.236	-90.743	0.577	1391.945	0.469	20	0.197	R.VQQLLQDFFNGKELCK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1197.101	1197.277	-147.444	0.556	1311.196	0.473	18	0.197	R.FSDASVQSDIK.L
R3/RRR3-1/2	1436.358	1437.625	-1583.147	0.462	1324.873	0.425	18	0.187	R.VQQLLQDFFNGK.E
R3/RRR3-6/2	1359.088	1359.493	-298.694	0.457	1283.640	0.444	16	0.187	K.NALENYAYNMR.N
R3/RRR3-6/2	1677.190	1676.683	-294.530	0.518	1095.886	0.540	20	0.186	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/2	1359.172	1359.493	-236.880	0.413	1253.141	0.442	16	0.184	K.NALENYAYNMR.N
R3/RRR3-6/2	1375.081	1375.492	-300.138	0.442	1279.490	0.417	16	0.182	K.NALENYAYNM*R.N
R3/RRR3-6/2	1359.268	1359.493	-165.703	0.452	1217.348	0.409	16	0.176	K.NALENYAYNMR.N
R3/RRR3-6/2	1541.244	1541.757	-984.231	0.477	1128.563	0.438	19	0.175	R.ARFEELNMDLFR.K
R3/RRR3-2/2	1437.385	1437.625	-167.260	0.423	1196.680	0.425	16	0.175	R.VQQLLQDFFNGK.E
R3/RRR3-6/2	1331.135	1330.491	-268.650	0.473	984.695	0.504	14	0.174	R.FEELNM*DLFR.K
R3/RRR3-6/2	1353.348	1353.463	-85.639	0.477	1309.667	0.339	20	0.172	R.RFSDASVQSDIK.L
R3/RRR3-6/2	1566.273	1566.844	-1005.869	0.530	1178.064	0.396	22	0.171	K.QFAAEEISSMVLIK.M
R3/RRR3-6/2	1596.154	1596.874	-1080.698	0.523	1167.979	0.388	20	0.167	K.MREIAEAYLGTTIK.N
R3/RRR3-6/2	1541.054	1541.757	-1108.374	0.489	986.755	0.435	18	0.165	R.ARFEELNMDLFR.K
R3/RRR3-6/2	1540.679	1541.757	-1352.376	0.475	1018.117	0.413	18	0.163	R.ARFEELNMDLFR.K
R3/RRR3-6/2	1682.238	1681.830	243.193	0.417	642.349	0.551	21	0.161	K.NAVVTVPAYFNDSQR.Q
R3/RRR3-6/3	1566.636	1566.844	-133.150	0.490	1600.138	0.412	32	0.161	K.QFAAEEISSMVLIK.M
R3/RRR3-6/2	1868.447	1869.109	-892.276	0.514	821.051	0.509	18	0.160	R.FSDASVQSDIKLWPFK.V
R3/RRR3-6/2	1356.581	1357.571	-1471.371	0.358	1194.835	0.296	18	0.156	K.ELEGICNPIIAK.M
R3/RRR3-6/2	1582.289	1582.844	-985.151	0.474	1005.934	0.379	19	0.156	K.QFAAEEISSM*VLIK.M
R3/RRR3-6/2	1583.387	1582.844	-289.465	0.520	828.361	0.425	19	0.154	K.QFAAEEISSM*VLIK.M
R3/RRR3-6/2	1681.385	1681.830	-265.542	0.387	653.934	0.484	21	0.154	K.NAVVTVPAYFNDSQR.Q
R3/RRR3-6/2	1612.397	1612.873	-296.278	0.491	626.387	0.470	20	0.153	K.M*REIAEAYLGTTIK.N
R3/RRR3-6/2	1613.294	1612.873	261.695	0.600	530.271	0.465	21	0.152	K.M*REIAEAYLGTTIK.N
R3/RRR3-6/2	1869.392	1869.109	151.778	0.483	602.778	0.518	16	0.150	R.FSDASVQSDIKLWPFK.V
R3/RRR3-6/2	1331.678	1330.491	140.508	0.405	551.006	0.461	14	0.150	R.FEELNM*DLFR.K
R3/RRR3-6/2	1681.470	1681.830	-215.213	0.344	564.907	0.498	20	0.150	K.NAVVTVPAYFNDSQR.Q
R3/RRR3-6/2	1357.004	1357.571	-1158.823	0.380	805.048	0.397	16	0.148	K.ELEGICNPIIAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1197.841	1197.277	-364.456	0.336	695.352	0.416	15	0.147	R.FSDASVQSDIK.L
R3/RRR3-6/2	1582.239	1582.844	-1017.064	0.433	891.660	0.342	19	0.147	K.QFAAEEISSM*VLIK.M
R3/RRR3-6/2	1558.026	1557.756	173.577	0.361	491.232	0.413	18	0.145	R.ARFEELNM*DLFR.K
R3/RRR3-6/3	1541.319	1541.757	-284.518	0.567	1535.943	0.369	24	0.145	R.ARFEELNMDLFR.K
R3/RRR3-5/2	1681.392	1681.830	-261.827	0.405	493.573	0.428	19	0.145	K.NAVVTVPAYFNDSQR.Q
R3/RRR3-1/2	1437.316	1437.625	-215.568	0.459	565.237	0.410	14	0.145	R.VQQLLQDFFNGK.E
R3/RRR3-6/2	1868.416	1869.109	-908.673	0.469	527.239	0.494	15	0.144	R.FSDASVQSDIKLWPFK.V
R3/RRR3-2/2	1682.190	1681.830	214.159	0.462	387.287	0.451	16	0.143	K.NAVVTVPAYFNDSQR.Q
R3/RRR3-2/2	1438.584	1437.625	-28.649	0.375	430.433	0.461	12	0.142	-.VQQLLQDFFNGK.-
R3/RRR3-6/2	1313.955	1314.492	-1173.121	0.364	416.582	0.328	15	0.142	R.FEELNMDLFR.K
R3/RRR3-6/2	1437.316	1437.625	-215.568	0.353	485.749	0.386	13	0.141	R.VQQLLQDFFNGK.E
R3/RRR3-1/2	1232.135	1232.436	-244.939	0.357	736.984	0.323	16	0.141	K.DAGVIAGLNVM*R.I
R3/RRR3-10/2	1436.953	1437.625	-1166.858	0.271	236.615	0.345	11	0.137	-.VQQLLQDFFNGK.-
R3/RRR3-6/2	1314.059	1314.492	-330.826	0.340	278.298	0.362	13	0.134	-.FEELNMDLFR.-
R3/RRR3-6/2	1566.112	1566.844	-1109.090	0.378	504.944	0.261	17	0.133	-.QFAAEEISSMVLIK.-
R3/RRR3-1/2	1438.967	1437.625	238.615	0.339	681.934	0.184	14	0.130	R.VQQLLQDFFNGK.E
R3/RRR3-6/3	1677.289	1676.683	-235.613	0.443	799.801	0.543	30	0.127	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/3	1676.591	1676.683	-55.042	0.421	669.737	0.565	27	0.125	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/3	1968.526	1968.236	147.735	0.513	800.658	0.525	27	0.124	R.VQQLLQDFFNGKELCK.S
R3/RRR3-6/2	1353.491	1353.463	20.479	0.258	503.418	0.209	10	0.123	-.RFSDASVQSDIK.-
R3/RRR3-6/3	1968.621	1968.236	196.146	0.512	793.476	0.518	29	0.123	R.VQQLLQDFFNGKELCK.S
R3/RRR3-6/3	1869.239	1869.109	69.744	0.477	791.810	0.522	27	0.122	R.FSDASVQSDIKLWPFK.V
R3/RRR3-6/3	1677.699	1676.683	9.873	0.407	585.643	0.564	25	0.122	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-15/3	1676.124	1676.683	-932.868	0.388	655.011	0.539	26	0.120	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-17/2	1197.442	1197.277	138.689	0.224	217.954	0.400	11	0.119	-.FSDASVQSDIK.-
R3/RRR3-8/3	1676.210	1676.683	-282.732	0.424	796.601	0.485	27	0.118	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/3	1869.928	1869.109	-96.985	0.424	622.103	0.548	25	0.118	R.FSDASVQSDIKLWPFK.V
R3/RRR3-6/3	1868.325	1869.109	-957.874	0.389	708.241	0.514	26	0.115	R.FSDASVQSDIKLWPFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1279.092	1279.492	-313.700	0.415	546.328	0.520	19	0.114	R.MVNHFVQEFK.R
R3/RRR3-6/3	1295.381	1295.492	-85.901	0.479	612.737	0.478	22	0.112	R.M*VNHFVQEFK.R
R3/RRR3-6/3	1278.654	1279.492	-1442.080	0.395	611.078	0.477	20	0.110	R.MVNHFVQEFK.R
R3/RRR3-6/3	1279.446	1279.492	-36.146	0.408	498.082	0.429	19	0.106	R.MVNHFVQEFK.R
R3/RRR3-15/3	1675.812	1676.683	-1119.566	0.331	472.227	0.453	22	0.105	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/3	1294.946	1295.492	-1197.454	0.397	394.692	0.369	19	0.104	R.M*VNHFVQEFK.R
R3/RRR3-13/3	1678.133	1676.683	269.243	0.357	395.116	0.408	22	0.103	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-6/3	1681.435	1681.830	-236.124	0.317	970.268	0.369	25	0.101	K.NAVVTVPAYFNDSQR.Q
R3/RRR3-6/3	1295.198	1295.492	-227.568	0.374	557.436	0.375	22	0.100	R.M*VNHFVQEFK.R
R3/RRR3-5/3	1675.350	1676.683	-1396.451	0.323	508.521	0.309	25	0.096	K.ATAGDTHLGGEDFDNR.M
R3/RRR3-5/3	1295.791	1295.492	231.605	0.435	416.856	0.373	18	0.096	-.M*VNHFVQEFK.-
R3/RRR3-6/3	1437.796	1437.625	119.540	0.465	1139.061	0.252	22	0.095	R.VQQLLQDFFNGK.E
R3/RRR3-6/3	1968.981	1968.236	-129.540	0.371	395.920	0.363	23	0.094	-.VQQLLQDFFNGKELCK.-
R3/RRR3-6/3	1556.799	1557.756	-1261.079	0.350	1028.815	0.250	21	0.089	-.ARFEELNM*DLFR.-
R3/RRR3-5/3	1675.275	1676.683	-1441.570	0.287	640.090	0.249	27	0.088	-.ATAGDTHLGGEDFDNR.-
R3/RRR3-6/3	1566.529	1566.844	-201.743	0.373	1056.854	0.216	25	0.087	K.QFAAEEISSMVLIK.M
R3/RRR3-4/2	1993.500	1994.066	-787.660	0.588	2643.576	0.614	28	0.466	K.SEGHDTIVLAGAEYGSGSSR.D
R3/RRR3-6/2	1569.222	1569.783	-997.659	0.539	2214.643	0.459	21	0.315	K.YLLQSGLQEYLNK.Q
R3/RRR3-1/2	1569.474	1569.783	-197.416	0.575	2194.981	0.427	21	0.300	K.YLLQSGLQEYLNK.Q
R3/RRR3-4/2	1528.151	1528.563	-270.296	0.444	1853.969	0.509	21	0.270	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/2	1545.129	1545.656	-990.873	0.523	1761.133	0.547	20	0.269	K.M*FVDYNEPQTER.V
R3/RRR3-1/2	1569.409	1569.783	-239.396	0.552	2008.219	0.418	21	0.267	K.YLLQSGLQEYLNK.Q
R3/RRR3-4/2	1499.292	1498.684	-262.024	0.536	1773.960	0.532	20	0.265	R.SDETVAMIEAYLR.A
R3/RRR3-4/2	1498.218	1498.684	-311.408	0.424	2001.906	0.398	20	0.264	R.SDETVAMIEAYLR.A
R3/RRR3-4/2	1528.160	1528.563	-264.606	0.458	1771.437	0.500	22	0.256	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/3	1995.930	1994.066	-68.135	0.532	1800.580	0.591	34	0.256	K.SEGHDTIVLAGAEYGSGSSR.D
R3/RRR3-4/2	1724.279	1724.761	-280.451	0.628	1898.673	0.428	23	0.253	R.NCDNFQVNQNDVEK.I
R3/RRR3-2/2	1570.464	1569.783	-204.152	0.599	1748.072	0.469	19	0.241	K.YLLQSGLQEYLNK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1545.088	1545.656	-1017.366	0.515	1450.960	0.562	19	0.230	K.M*FVDYNEPQTER.V
R3/RRR3-4/2	1528.152	1528.563	-269.735	0.444	1611.356	0.466	21	0.226	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/3	1993.416	1994.066	-829.927	0.445	1703.849	0.532	33	0.220	K.SEGHDTIVLAGAEYGSGSSR.D
R3/RRR3-4/2	1725.073	1724.761	181.510	0.656	1625.189	0.429	23	0.216	R.NCDNFQVNQNDVEK.I
R3/RRR3-4/2	1545.215	1545.656	-285.856	0.482	1388.904	0.531	18	0.215	K.M*FVDYNEPQTER.V
R3/RRR3-4/2	1498.028	1498.684	-1108.333	0.401	1639.651	0.376	19	0.210	R.SDETVAMIEAYLR.A
R3/RRR3-4/2	1724.205	1724.761	-904.929	0.609	1500.216	0.428	23	0.204	R.NCDNFQVNQNDVEK.I
R3/RRR3-4/2	1264.159	1264.431	-215.846	0.415	1276.971	0.523	18	0.202	K.FVEFYGEGMGK.L
R3/RRR3-4/2	1264.097	1264.431	-265.350	0.379	1263.190	0.410	18	0.180	K.FVEFYGEGMGK.L
R3/RRR3-4/2	1279.914	1280.431	-1188.932	0.317	1305.761	0.386	17	0.178	K.FVEFYGEGM*GK.L
R3/RRR3-4/2	1514.398	1514.683	-188.595	0.412	1215.362	0.388	18	0.171	R.SDETVAM*IEAYLR.A
R3/RRR3-4/2	1529.381	1529.656	-180.255	0.521	794.978	0.534	16	0.167	K.MFVDYNEPQTER.V
R3/RRR3-4/2	1566.245	1565.896	223.753	0.442	686.604	0.571	17	0.164	R.SNLVGM*GIIPLCFK.A
R3/RRR3-4/2	1117.111	1117.278	-149.563	0.350	827.742	0.488	20	0.161	K.TSLAPGSGVVTK.Y
R3/RRR3-4/2	1548.795	1549.897	-1361.100	0.311	1016.612	0.406	18	0.158	R.SNLVGMGIIPLCFK.A
R3/RRR3-4/2	1118.218	1117.278	-53.718	0.422	686.105	0.484	18	0.157	K.TSLAPGSGVVTK.Y
R3/RRR3-4/2	1565.328	1565.896	-1004.604	0.449	590.707	0.538	17	0.156	R.SNLVGM*GIIPLCFK.A
R3/RRR3-4/2	1202.926	1203.326	-333.908	0.484	724.190	0.413	16	0.153	K.IIDWENTSPK.L
R3/RRR3-4/2	1202.464	1203.326	-1553.041	0.465	733.305	0.412	16	0.153	K.IIDWENTSPK.L
R3/RRR3-4/2	1118.144	1117.278	-119.641	0.424	666.598	0.446	18	0.152	K.TSLAPGSGVVTK.Y
R3/RRR3-4/2	1766.336	1766.957	-920.275	0.540	438.219	0.534	18	0.151	R.SPNAVQSNM*ELEFKR.N
R3/RRR3-4/2	914.984	915.112	-140.384	0.526	579.895	0.393	13	0.151	R.ILLESAIR.N
R3/RRR3-4/2	914.613	915.112	-547.531	0.442	567.045	0.400	13	0.151	R.ILLESAIR.N
R3/RRR3-4/2	1202.466	1203.326	-1551.308	0.386	755.900	0.389	16	0.150	K.IIDWENTSPK.L
R3/RRR3-4/2	814.544	815.059	-1865.776	0.519	1040.780	0.312	12	0.149	-.GPMLLGVK.-
R3/RRR3-4/2	1645.585	1645.881	-180.324	0.439	486.044	0.512	17	0.147	K.NILTTLPKPGGGEYGK.F
R3/RRR3-4/2	1767.397	1766.957	249.363	0.548	432.812	0.505	17	0.147	R.SPNAVQSNM*ELEFKR.N
R3/RRR3-4/3	1724.468	1724.761	-170.415	0.502	1515.148	0.378	27	0.147	R.NCDNFQVNQNDVEK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1993.780	1994.066	-143.680	0.458	1209.548	0.494	32	0.146	K.SEGHDTIVLAGAEYGSGSSR.D
R3/RRR3-4/2	814.851	815.059	-256.279	0.487	948.085	0.312	12	0.146	-.GPMLLGVK.-
R3/RRR3-4/2	1263.911	1264.431	-1206.202	0.329	907.677	0.330	16	0.146	K.FVEFYGEGMGK.L
R3/RRR3-1/2	1292.987	1293.453	-360.742	0.364	674.065	0.388	15	0.145	K.FYSLPALNDPR.I
R3/RRR3-3/2	1293.423	1293.453	-23.155	0.358	698.437	0.395	14	0.145	K.FYSLPALNDPR.I
R3/RRR3-4/2	814.878	815.059	-222.914	0.508	937.159	0.311	12	0.145	-.GPMLLGVK.-
R3/RRR3-4/3	1528.818	1528.563	167.281	0.500	1117.475	0.523	29	0.145	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/2	914.468	915.112	-1804.026	0.449	467.518	0.373	12	0.144	-.ILLESAIR.-
R3/RRR3-4/2	1289.162	1289.421	-201.592	0.357	1012.311	0.281	15	0.144	K.FDFHGQPAELK.H
R3/RRR3-2/2	914.977	915.112	-148.548	0.466	481.137	0.307	12	0.143	R.ILLESAIR.N
R3/RRR3-4/2	1288.922	1289.421	-387.908	0.348	1107.517	0.229	16	0.143	K.FDFHGQPAELK.H
R3/RRR3-4/2	1564.474	1565.896	-1552.741	0.309	575.685	0.439	16	0.142	R.SNLVGM*GIIPLCFK.A
R3/RRR3-5/2	915.030	915.112	-90.468	0.369	696.783	0.288	13	0.142	R.ILLESAIR.N
R3/RRR3-5/2	915.099	915.112	-14.465	0.443	606.164	0.280	13	0.142	R.ILLESAIR.N
R3/RRR3-4/2	1645.569	1645.881	-190.519	0.428	305.572	0.510	14	0.142	K.NILTTLPKPGGGEYGK.F
R3/RRR3-1/2	915.040	915.112	-79.361	0.343	607.396	0.294	13	0.141	R.ILLESAIR.N
R3/RRR3-4/2	1293.012	1293.453	-341.987	0.289	492.293	0.437	13	0.141	K.FYSLPALNDPR.I
R3/RRR3-4/3	1751.864	1750.958	-53.620	0.489	1203.466	0.479	30	0.141	R.SPNAVQSNMELEFKR.N
R3/RRR3-4/2	1292.499	1293.453	-1516.093	0.272	778.550	0.330	15	0.141	K.FYSLPALNDPR.I
R3/RRR3-7/2	1569.179	1569.783	-1025.307	0.420	609.011	0.329	17	0.140	K.YLLQSGLQEYLNK.Q
R3/RRR3-1/2	915.172	915.112	65.808	0.406	476.020	0.297	12	0.140	-.ILLESAIR.-
R3/RRR3-1/3	1528.555	1528.563	-5.705	0.442	1060.619	0.508	27	0.138	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/3	1750.921	1750.958	-21.308	0.534	912.112	0.547	26	0.135	R.SPNAVQSNMELEFKR.N
R3/RRR3-4/2	1646.492	1645.881	-237.186	0.433	384.496	0.378	15	0.135	K.NILTTLPKPGGGEYGK.F
R3/RRR3-5/2	915.018	915.112	-103.314	0.354	646.439	0.189	12	0.135	R.ILLESAIR.N
R3/RRR3-1/2	1292.379	1293.453	-1609.456	0.211	733.995	0.281	15	0.134	K.FYSLPALNDPR.I
R3/RRR3-2/2	1571.278	1569.783	315.925	0.396	610.427	0.268	15	0.133	K.YLLQSGLQEYLNK.Q
R3/RRR3-4/3	1528.590	1528.563	17.604	0.492	954.984	0.517	27	0.133	K.AGEDADSLGLTGHER.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	914.499	915.112	-1769.288	0.212	624.241	0.165	11	0.132	R.ILLESAIR.N
R3/RRR3-12/2	1571.200	1569.783	266.068	0.390	333.051	0.367	11	0.131	-.YLLQSGLQEYLNK.-
R3/RRR3-5/2	1117.262	1117.278	-14.532	0.314	410.628	0.323	15	0.131	-.TSLAPGSGVVTK.-
R3/RRR3-4/3	1751.792	1750.958	-95.034	0.539	910.564	0.523	26	0.131	R.SPNAVQSNMELEFKR.N
R3/RRR3-2/2	1202.950	1203.326	-313.443	0.343	713.334	0.148	15	0.130	K.IIDWENTSPK.L
R3/RRR3-4/2	1548.893	1549.897	-1297.617	0.200	579.339	0.152	15	0.128	R.SNLVGMGIIPLCFK.A
R3/RRR3-4/2	1513.720	1514.683	-1300.437	0.279	765.714	0.149	15	0.127	R.SDETVAM*IEAYLR.A
R3/RRR3-17/2	1293.174	1293.453	-216.021	0.271	641.529	0.167	13	0.123	-.FYSLPALNDPR.-
R3/RRR3-2/3	1529.469	1528.563	-61.577	0.434	1092.264	0.416	27	0.122	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/3	1658.212	1657.972	145.294	0.416	1368.552	0.323	27	0.121	K.KACELGLEVKPWVK.T
R3/RRR3-4/3	1528.567	1528.563	2.225	0.478	744.195	0.484	24	0.117	K.AGEDADSLGLTGHER.Y
R3/RRR3-1/3	1528.953	1528.563	255.794	0.435	788.923	0.471	25	0.117	K.AGEDADSLGLTGHER.Y
R3/RRR3-1/3	1528.412	1528.563	-99.551	0.442	883.671	0.447	27	0.117	K.AGEDADSLGLTGHER.Y
R3/RRR3-2/3	1528.383	1528.563	-118.058	0.429	722.937	0.449	24	0.112	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/3	1766.288	1766.957	-948.105	0.456	701.717	0.456	25	0.110	R.SPNAVQSNM*ELEFKR.N
R3/RRR3-5/3	1528.878	1528.563	206.676	0.402	765.479	0.424	25	0.109	K.AGEDADSLGLTGHER.Y
R3/RRR3-5/3	1528.124	1528.563	-288.497	0.436	519.825	0.455	21	0.108	K.AGEDADSLGLTGHER.Y
R3/RRR3-4/3	1767.067	1766.957	62.359	0.465	559.078	0.459	24	0.108	R.SPNAVQSNM*ELEFKR.N
R3/RRR3-4/3	1767.749	1766.957	-117.952	0.443	701.999	0.430	26	0.107	R.SPNAVQSNM*ELEFKR.N
R3/RRR3-25/3	1528.449	1528.563	-75.156	0.391	669.466	0.416	22	0.106	K.AGEDADSLGLTGHER.Y
R3/RRR3-5/3	1105.304	1105.312	-7.612	0.469	569.983	0.395	19	0.105	R.IDKLPYSIR.I
R3/RRR3-4/3	1105.618	1105.312	277.270	0.539	907.055	0.373	21	0.104	R.IDKLPYSIR.I
R3/RRR3-1/3	1105.445	1105.312	120.812	0.441	428.085	0.344	16	0.104	R.IDKLPYSIR.I
R3/RRR3-5/3	1105.369	1105.312	52.201	0.439	485.787	0.354	17	0.103	R.IDKLPYSIR.I
R3/RRR3-2/3	1527.857	1528.563	-1120.281	0.378	582.834	0.414	21	0.103	-.AGEDADSLGLTGHER.-
R3/RRR3-1/3	1104.585	1105.312	-1567.745	0.389	426.947	0.336	16	0.103	R.IDKLPYSIR.I
R3/RRR3-6/3	1528.270	1528.563	-192.573	0.448	623.739	0.388	22	0.102	K.AGEDADSLGLTGHER.Y
R3/RRR3-5/3	1105.159	1105.312	-138.313	0.520	554.976	0.295	19	0.100	R.IDKLPYSIR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1105.366	1105.312	48.712	0.432	415.491	0.345	18	0.100	-.IDKLPYSIR.-
R3/RRR3-4/3	1105.575	1105.312	238.741	0.502	519.494	0.361	19	0.099	-.IDKLPYSIR.-
R3/RRR3-2/3	1105.254	1105.312	-52.145	0.425	545.835	0.319	19	0.095	-.IDKLPYSIR.-
R3/RRR3-2/3	1105.158	1105.312	-139.726	0.461	533.321	0.363	18	0.095	-.IDKLPYSIR.-
R3/RRR3-2/3	1105.579	1105.312	242.395	0.470	347.436	0.324	15	0.094	-.IDKLPYSIR.-
R3/RRR3-4/3	1659.517	1657.972	-274.878	0.346	847.477	0.290	22	0.092	K.KACELGLEVKPWVK.T
R3/RRR3-4/3	1658.332	1657.972	217.933	0.438	745.652	0.290	21	0.091	K.KACELGLEVKPWVK.T
R3/RRR3-4/3	1289.400	1289.421	-16.116	0.438	1183.454	0.209	23	0.090	K.FDFHGQPAELK.H
R3/RRR3-4/3	1289.528	1289.421	83.152	0.424	1158.395	0.200	23	0.088	K.FDFHGQPAELK.H
R3/RRR3-2/3	1658.134	1657.972	98.006	0.322	1051.869	0.189	23	0.086	K.KACELGLEVKPWVK.T
R3/RRR3-6/3	1658.774	1657.972	-119.628	0.313	1043.764	0.129	24	0.080	K.KACELGLEVKPWVK.T
R3/RRR3-2/2	1559.196	1559.743	-995.279	0.460	2244.837	0.514	23	0.337	K.IDQSALTGESLPVTK.G
R3/RRR3-3/2	1990.538	1991.233	-854.094	0.459	2102.704	0.473	25	0.300	R.TENQDAIDAAMVGMLADPK.E
R3/RRR3-3/2	1633.701	1633.746	-27.625	0.512	1952.206	0.554	22	0.298	R.TALTYIDADGNWHR.A
R3/RRR3-2/2	1559.450	1559.743	-188.478	0.456	2035.851	0.473	22	0.288	K.IDQSALTGESLPVTK.G
R3/RRR3-3/2	1560.184	1559.743	282.936	0.523	1872.046	0.537	22	0.279	K.IDQSALTGESLPVTK.G
R3/RRR3-2/2	1634.137	1633.746	239.937	0.531	1865.460	0.526	21	0.275	R.TALTYIDADGNWHR.A
R3/RRR3-2/2	1493.198	1492.742	306.206	0.535	1876.322	0.515	20	0.273	K.LSVDKNLVEVFTK.G
R3/RRR3-3/2	1633.425	1633.746	-197.108	0.466	1868.792	0.506	21	0.271	R.TALTYIDADGNWHR.A
R3/RRR3-2/2	1492.692	1492.742	-33.680	0.536	1813.613	0.541	19	0.270	K.LSVDKNLVEVFTK.G
R3/RRR3-5/2	1492.940	1492.742	132.971	0.532	1897.058	0.495	19	0.270	K.LSVDKNLVEVFTK.G
R3/RRR3-3/2	1407.448	1407.643	-139.501	0.523	1858.860	0.500	20	0.268	K.GVDKDHVLLLAAR.A
R3/RRR3-1/2	1559.510	1559.743	-150.001	0.468	1836.568	0.483	22	0.259	K.IDQSALTGESLPVTK.G
R3/RRR3-3/2	1492.263	1492.742	-322.087	0.506	1813.572	0.492	20	0.258	K.LSVDKNLVEVFTK.G
R3/RRR3-3/2	1398.069	1398.451	-273.814	0.517	1531.266	0.595	21	0.248	K.NPGDEVFSGSTCK.Q
R3/RRR3-3/2	1397.986	1398.451	-333.911	0.514	1522.319	0.585	21	0.244	K.NPGDEVFSGSTCK.Q
R3/RRR3-2/2	1940.736	1940.229	-254.850	0.569	1765.995	0.470	26	0.242	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-3/2	1399.094	1398.451	-256.199	0.577	1508.351	0.572	22	0.240	K.NPGDEVFSGSTCK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1398.079	1398.451	-266.631	0.547	1481.672	0.580	21	0.238	K.NPGDEVFSGSTCK.Q
R3/RRR3-2/2	1633.499	1633.746	-151.602	0.494	1605.725	0.525	20	0.238	R.TALTYIDADGNWHR.A
R3/RRR3-1/2	1398.068	1398.451	-274.515	0.514	1452.030	0.594	21	0.238	K.NPGDEVFSGSTCK.Q
R3/RRR3-1/2	1559.334	1559.743	-263.085	0.403	1786.854	0.421	21	0.237	K.IDQSALTGESLPVTK.G
R3/RRR3-3/2	1406.951	1407.643	-1206.621	0.472	1628.858	0.496	19	0.235	K.GVDKDHVLLLAAR.A
R3/RRR3-3/2	1559.477	1559.743	-171.360	0.469	1592.708	0.519	21	0.234	K.IDQSALTGESLPVTK.G
R3/RRR3-3/2	1559.339	1559.743	-260.257	0.428	1712.088	0.435	21	0.230	K.IDQSALTGESLPVTK.G
R3/RRR3-3/2	1407.393	1407.643	-178.306	0.498	1529.058	0.515	19	0.227	K.GVDKDHVLLLAAR.A
R3/RRR3-2/2	1633.180	1633.746	-961.888	0.464	1550.257	0.499	20	0.225	R.TALTYIDADGNWHR.A
R3/RRR3-2/2	1491.771	1492.742	-1325.391	0.524	1518.005	0.512	20	0.225	K.LSVDKNLVEVFTK.G
R3/RRR3-1/2	1491.566	1492.742	-1462.902	0.413	1634.370	0.453	19	0.224	K.LSVDKNLVEVFTK.G
R3/RRR3-3/2	1492.148	1492.742	-1071.428	0.511	1511.738	0.517	19	0.224	K.LSVDKNLVEVFTK.G
R3/RRR3-1/2	1939.550	1940.229	-868.214	0.514	1487.768	0.535	25	0.224	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-1/2	1632.710	1633.746	-1250.575	0.460	1463.281	0.532	19	0.221	R.TALTYIDADGNWHR.A
R3/RRR3-2/2	1407.129	1407.643	-1079.432	0.521	1457.421	0.507	19	0.217	K.GVDKDHVLLLAAR.A
R3/RRR3-2/2	1406.931	1407.643	-1220.736	0.513	1471.072	0.491	19	0.215	K.GVDKDHVLLLAAR.A
R3/RRR3-4/2	1492.323	1492.742	-281.544	0.529	1463.439	0.497	19	0.214	K.LSVDKNLVEVFTK.G
R3/RRR3-3/2	1633.326	1633.746	-257.988	0.457	1528.551	0.460	20	0.214	R.TALTYIDADGNWHR.A
R3/RRR3-1/2	1492.629	1492.742	-75.679	0.479	1435.796	0.491	20	0.211	K.LSVDKNLVEVFTK.G
R3/RRR3-3/2	1492.487	1492.742	-171.422	0.500	1406.176	0.506	20	0.211	K.LSVDKNLVEVFTK.G
R3/RRR3-2/2	1397.340	1398.451	-1515.023	0.467	1280.955	0.561	21	0.211	K.NPGDEVFSGSTCK.Q
R3/RRR3-2/2	1558.639	1559.743	-1354.310	0.326	1621.091	0.389	21	0.209	K.IDQSALTGESLPVTK.G
R3/RRR3-4/2	1633.806	1633.746	36.750	0.512	1392.075	0.509	19	0.208	R.TALTYIDADGNWHR.A
R3/RRR3-4/2	1940.559	1940.229	170.629	0.540	1534.048	0.439	25	0.207	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-2/3	1429.398	1429.649	-176.170	0.575	2076.955	0.380	30	0.206	R.KVHAVIDKYAER.G
R3/RRR3-1/2	1558.566	1559.743	-1401.036	0.327	1566.540	0.405	20	0.205	K.IDQSALTGESLPVTK.G
R3/RRR3-2/2	1399.211	1398.451	-171.649	0.574	1176.926	0.574	20	0.204	K.NPGDEVFSGSTCK.Q
R3/RRR3-2/2	1914.394	1915.182	-936.662	0.541	1373.084	0.493	24	0.203	R.LGM*GTNM*YPSSALLGQNK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1493.036	1492.742	197.746	0.544	1269.265	0.530	19	0.202	K.LSVDKNLVEVFTK.G
R3/RRR3-3/2	1939.705	1940.229	-787.981	0.547	1363.796	0.467	25	0.196	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-1/2	1633.467	1633.746	-171.093	0.465	1229.887	0.521	18	0.194	R.TALTYIDADGNWHR.A
R3/RRR3-2/2	1407.179	1407.643	-331.033	0.491	1291.824	0.466	18	0.191	K.GVDKDHVLLLAAR.A
R3/RRR3-1/2	1398.183	1398.451	-191.916	0.483	1232.384	0.467	21	0.189	K.NPGDEVFSGSTCK.Q
R3/RRR3-5/2	1493.513	1492.742	-153.842	0.509	1228.536	0.477	19	0.188	K.LSVDKNLVEVFTK.G
R3/RRR3-2/2	1914.471	1915.182	-896.078	0.538	1164.704	0.516	22	0.186	R.LGM*GTNM*YPSSALLGQNK.D
R3/RRR3-2/2	1939.519	1940.229	-884.388	0.531	1188.641	0.497	24	0.186	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-4/2	1491.371	1492.742	-1594.778	0.350	1372.644	0.400	18	0.185	K.LSVDKNLVEVFTK.G
R3/RRR3-5/3	1429.641	1429.649	-5.671	0.616	1938.403	0.369	28	0.184	R.KVHAVIDKYAER.G
R3/RRR3-3/2	1990.256	1991.233	-996.198	0.420	1274.976	0.436	21	0.180	R.TENQDAIDAAMVGMLADPK.E
R3/RRR3-1/2	1940.489	1940.229	134.608	0.538	1172.574	0.452	22	0.174	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-4/2	1642.383	1642.829	-272.519	0.436	1180.810	0.411	23	0.174	K.DASLEALPVDELIEK.A
R3/RRR3-2/2	1643.028	1642.829	121.644	0.489	1159.507	0.419	23	0.173	K.DASLEALPVDELIEK.A
R3/RRR3-4/3	1407.841	1407.643	140.999	0.550	1615.960	0.445	27	0.172	K.GVDKDHVLLLAAR.A
R3/RRR3-4/2	1162.986	1163.370	-331.294	0.440	1209.189	0.373	18	0.171	K.M*ITGDQLAIGK.E
R3/RRR3-1/2	1162.600	1163.370	-1526.913	0.375	1320.792	0.324	18	0.170	K.M*ITGDQLAIGK.E
R3/RRR3-4/3	1408.101	1407.643	326.179	0.563	1635.580	0.429	27	0.170	K.GVDKDHVLLLAAR.A
R3/RRR3-3/2	1163.022	1163.370	-299.807	0.428	1046.469	0.436	17	0.169	K.M*ITGDQLAIGK.E
R3/RRR3-2/2	1163.218	1163.370	-131.135	0.442	1159.151	0.379	18	0.168	K.M*ITGDQLAIGK.E
R3/RRR3-3/2	1643.322	1642.829	300.957	0.458	1202.031	0.363	23	0.167	K.DASLEALPVDELIEK.A
R3/RRR3-3/2	1162.963	1163.370	-351.199	0.485	1197.161	0.351	18	0.166	K.M*ITGDQLAIGK.E
R3/RRR3-2/2	1642.382	1642.829	-273.041	0.409	1047.758	0.425	21	0.166	K.DASLEALPVDELIEK.A
R3/RRR3-3/2	1940.116	1940.229	-58.161	0.559	1022.590	0.447	23	0.164	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-5/2	1939.618	1940.229	-833.213	0.541	962.934	0.468	22	0.164	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-1/3	1429.593	1429.649	-39.073	0.603	1569.568	0.446	27	0.163	R.KVHAVIDKYAER.G
R3/RRR3-4/2	1163.121	1163.370	-214.621	0.480	1008.287	0.402	17	0.162	K.M*ITGDQLAIGK.E
R3/RRR3-3/3	1406.840	1407.643	-1286.054	0.512	1694.256	0.372	27	0.161	K.GVDKDHVLLLAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/3	1407.675	1407.643	22.552	0.531	1892.469	0.295	28	0.161	K.GVDKDHVLLLAAR.A
R3/RRR3-5/2	1939.662	1940.229	-810.091	0.509	971.033	0.446	22	0.161	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-1/3	1407.772	1407.643	91.954	0.526	1674.635	0.376	26	0.161	K.GVDKDHVLLLAAR.A
R3/RRR3-4/2	1939.575	1940.229	-855.452	0.480	1018.929	0.417	23	0.161	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-4/2	1163.001	1163.370	-318.130	0.420	1037.314	0.381	17	0.161	K.M*ITGDQLAIGK.E
R3/RRR3-2/3	1408.852	1407.643	148.415	0.529	1649.508	0.388	27	0.160	K.GVDKDHVLLLAAR.A
R3/RRR3-4/3	1839.044	1840.094	-1118.307	0.520	1355.022	0.495	33	0.160	K.HIVGM*TGDGVNDAPALKK.A
R3/RRR3-2/2	1914.485	1915.182	-888.908	0.553	901.362	0.484	20	0.160	R.LGM*GTNM*YPSSALLGQNK.D
R3/RRR3-3/2	1027.121	1027.156	-34.761	0.504	771.866	0.446	16	0.160	K.LGDIVPADAR.L
R3/RRR3-2/2	1147.278	1147.371	-81.065	0.324	1021.233	0.392	17	0.160	K.MITGDQLAIGK.E
R3/RRR3-4/2	1027.113	1027.156	-42.390	0.484	769.279	0.442	16	0.159	K.LGDIVPADAR.L
R3/RRR3-2/2	1148.109	1147.371	-228.812	0.503	741.596	0.462	16	0.158	K.MITGDQLAIGK.E
R3/RRR3-1/3	1839.470	1840.094	-885.918	0.524	1001.997	0.620	31	0.158	K.HIVGM*TGDGVNDAPALKK.A
R3/RRR3-3/2	1643.319	1642.829	299.020	0.451	944.889	0.404	21	0.158	K.DASLEALPVDELIEK.A
R3/RRR3-5/2	1939.674	1940.229	-804.153	0.504	943.406	0.427	22	0.157	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-2/2	1939.549	1940.229	-868.593	0.526	802.311	0.478	21	0.157	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-1/2	1162.847	1163.370	-1313.798	0.384	846.416	0.422	15	0.155	K.M*ITGDQLAIGK.E
R3/RRR3-4/2	1026.848	1027.156	-300.784	0.438	686.149	0.435	15	0.154	K.LGDIVPADAR.L
R3/RRR3-1/3	1429.834	1429.649	129.710	0.582	1648.951	0.381	27	0.154	R.KVHAVIDKYAER.G
R3/RRR3-2/2	1026.523	1027.156	-1596.066	0.321	804.466	0.420	16	0.153	K.LGDIVPADAR.L
R3/RRR3-3/2	1940.567	1940.229	174.540	0.497	995.813	0.382	22	0.153	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-2/2	1162.921	1163.370	-387.429	0.400	1024.339	0.317	17	0.152	K.M*ITGDQLAIGK.E
R3/RRR3-5/2	1642.349	1642.829	-293.249	0.399	1031.378	0.320	22	0.152	K.DASLEALPVDELIEK.A
R3/RRR3-1/2	1938.648	1940.229	-1852.646	0.343	819.929	0.430	21	0.151	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-3/3	1429.787	1429.649	96.832	0.543	1688.800	0.356	28	0.151	R.KVHAVIDKYAER.G
R3/RRR3-5/2	1642.208	1642.829	-990.075	0.307	998.084	0.339	21	0.151	K.DASLEALPVDELIEK.A
R3/RRR3-4/2	1026.995	1027.156	-158.037	0.500	620.187	0.436	15	0.150	-.LGDIVPADAR.-
R3/RRR3-4/2	1642.618	1642.829	-129.144	0.451	976.370	0.337	21	0.150	K.DASLEALPVDELIEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1643.397	1642.829	-263.708	0.463	923.260	0.350	21	0.150	K.DASLEALPVDELIEK.A
R3/RRR3-2/3	1839.527	1840.094	-854.341	0.498	1515.770	0.391	35	0.150	K.KHIVGM*TGDGVNDAPALK.K
R3/RRR3-3/2	1147.182	1147.371	-164.747	0.363	863.380	0.349	16	0.149	K.MITGDQLAIGK.E
R3/RRR3-1/2	1026.973	1027.156	-179.023	0.400	665.611	0.384	15	0.149	K.LGDIVPADAR.L
R3/RRR3-2/2	1027.024	1027.156	-128.944	0.508	567.496	0.439	14	0.148	-.LGDIVPADAR.-
R3/RRR3-2/3	1429.874	1429.649	157.450	0.551	1720.725	0.331	28	0.148	R.KVHAVIDKYAER.G
R3/RRR3-4/2	1599.317	1598.829	305.639	0.429	642.508	0.414	17	0.147	R.EVHFLPFNPVDKR.T
R3/RRR3-5/2	1642.283	1642.829	-944.553	0.394	831.665	0.351	20	0.147	K.DASLEALPVDELIEK.A
R3/RRR3-4/3	1429.501	1429.649	-103.569	0.553	1591.705	0.372	27	0.146	R.KVHAVIDKYAER.G
R3/RRR3-3/2	1027.384	1027.156	221.947	0.498	687.046	0.376	15	0.146	-.LGDIVPADAR.-
R3/RRR3-1/2	1162.286	1163.370	-1798.580	0.317	869.904	0.319	16	0.145	K.M*ITGDQLAIGK.E
R3/RRR3-4/3	1839.254	1840.094	-1003.449	0.505	1172.517	0.500	31	0.145	K.HIVGM*TGDGVNDAPALKK.A
R3/RRR3-3/2	1026.883	1027.156	-266.674	0.352	560.517	0.365	14	0.144	K.LGDIVPADAR.L
R3/RRR3-3/2	1642.585	1642.829	-149.198	0.438	827.002	0.331	20	0.144	K.DASLEALPVDELIEK.A
R3/RRR3-1/2	949.909	950.114	-216.039	0.317	718.746	0.339	13	0.144	K.NLVEVFTK.G
R3/RRR3-5/2	1026.440	1027.156	-1677.426	0.340	724.766	0.329	15	0.144	K.LGDIVPADAR.L
R3/RRR3-4/2	1940.835	1940.229	-203.486	0.550	788.569	0.395	20	0.144	R.WGEQEAAILVPGDIISIK.L
R3/RRR3-4/3	1429.184	1429.649	-326.674	0.561	1325.959	0.452	25	0.143	R.KVHAVIDKYAER.G
R3/RRR3-1/2	1026.854	1027.156	-295.775	0.373	582.704	0.339	14	0.143	K.LGDIVPADAR.L
R3/RRR3-2/2	1598.276	1598.829	-975.003	0.383	491.421	0.416	15	0.143	R.EVHFLPFNPVDKR.T
R3/RRR3-1/2	1642.193	1642.829	-999.628	0.326	778.242	0.330	19	0.142	K.DASLEALPVDELIEK.A
R3/RRR3-3/2	1147.445	1147.371	65.024	0.347	564.815	0.349	14	0.142	K.MITGDQLAIGK.E
R3/RRR3-2/2	950.106	950.114	-7.746	0.344	596.708	0.297	13	0.141	K.NLVEVFTK.G
R3/RRR3-12/2	1026.999	1027.156	-153.268	0.421	745.078	0.284	15	0.141	K.LGDIVPADAR.L
R3/RRR3-2/2	1027.078	1027.156	-76.724	0.405	579.415	0.455	14	0.141	-.LGDIVPADAR.-
R3/RRR3-3/2	949.880	950.114	-246.852	0.291	531.080	0.344	12	0.141	K.NLVEVFTK.G
R3/RRR3-2/3	1429.385	1429.649	-185.552	0.604	1427.383	0.410	26	0.140	R.KVHAVIDKYAER.G
R3/RRR3-1/2	950.031	950.114	-86.877	0.285	562.326	0.330	12	0.140	K.NLVEVFTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1407.189	1407.643	-323.819	0.523	1338.122	0.424	25	0.140	K.GVDKDHVLLLAAR.A
R3/RRR3-2/2	949.616	950.114	-525.802	0.267	560.590	0.346	12	0.140	K.NLVEVFTK.G
R3/RRR3-4/2	949.440	950.114	-1767.750	0.255	445.410	0.372	11	0.140	K.NLVEVFTK.G
R3/RRR3-1/2	1642.090	1642.829	-1062.322	0.313	727.885	0.295	19	0.138	K.DASLEALPVDELIEK.A
R3/RRR3-5/2	1026.317	1027.156	-1797.520	0.354	539.372	0.270	13	0.138	K.LGDIVPADAR.L
R3/RRR3-5/2	1027.030	1027.156	-123.102	0.392	501.037	0.412	13	0.138	-.LGDIVPADAR.-
R3/RRR3-3/2	1599.418	1598.829	-258.252	0.404	405.097	0.379	14	0.137	-.EVHFLPFNPVDKR.-
R3/RRR3-4/3	1839.103	1840.094	-1085.816	0.521	1004.553	0.526	29	0.137	K.HIVGM*TGDGVNDAPALKK.A
R3/RRR3-5/3	1407.582	1407.643	-43.989	0.498	1509.325	0.353	27	0.137	K.GVDKDHVLLLAAR.A
R3/RRR3-3/3	1429.371	1429.649	-194.804	0.568	1430.973	0.392	26	0.137	R.KVHAVIDKYAER.G
R3/RRR3-4/2	950.002	950.114	-117.295	0.308	625.925	0.228	13	0.137	K.NLVEVFTK.G
R3/RRR3-1/3	1407.399	1407.643	-174.226	0.508	1412.100	0.385	26	0.137	K.GVDKDHVLLLAAR.A
R3/RRR3-2/2	1642.257	1642.829	-960.000	0.377	511.623	0.311	16	0.137	K.DASLEALPVDELIEK.A
R3/RRR3-4/3	1407.828	1407.643	131.216	0.542	1507.054	0.353	26	0.137	K.GVDKDHVLLLAAR.A
R3/RRR3-4/2	1641.668	1642.829	-1320.196	0.270	702.565	0.290	18	0.137	K.DASLEALPVDELIEK.A
R3/RRR3-5/3	1430.089	1429.649	308.579	0.578	1543.765	0.352	27	0.136	R.KVHAVIDKYAER.G
R3/RRR3-2/2	949.585	950.114	-1614.691	0.236	524.202	0.242	12	0.135	K.NLVEVFTK.G
R3/RRR3-2/2	1597.752	1598.829	-1303.838	0.389	458.483	0.274	15	0.135	R.EVHFLPFNPVDKR.T
R3/RRR3-3/2	1598.663	1598.829	-104.588	0.442	419.765	0.333	14	0.135	-.EVHFLPFNPVDKR.-
R3/RRR3-1/2	1147.116	1147.371	-222.499	0.181	699.171	0.237	15	0.133	K.MITGDQLAIGK.E
R3/RRR3-4/2	1990.122	1991.233	-1064.001	0.341	234.860	0.360	14	0.132	R.TENQDAIDAAMVGMLADPK.E
R3/RRR3-1/3	1429.608	1429.649	-28.667	0.553	1300.717	0.410	25	0.132	R.KVHAVIDKYAER.G
R3/RRR3-3/2	1599.504	1598.829	-204.196	0.438	323.564	0.324	13	0.131	-.EVHFLPFNPVDKR.-
R3/RRR3-2/2	1882.492	1883.183	-901.033	0.426	495.741	0.352	16	0.131	-.LGMGTNMYPSSALLGQNK.-
R3/RRR3-3/3	1840.220	1840.094	68.669	0.488	1164.850	0.439	31	0.131	K.KHIVGM*TGDGVNDAPALK.K
R3/RRR3-3/3	1429.926	1429.649	193.920	0.574	1321.008	0.390	26	0.127	R.KVHAVIDKYAER.G
R3/RRR3-2/3	1407.623	1407.643	-14.893	0.524	1295.522	0.383	25	0.127	K.GVDKDHVLLLAAR.A
R3/RRR3-3/3	1492.665	1492.742	-51.776	0.492	1078.921	0.450	26	0.126	K.LSVDKNLVEVFTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1492.559	1492.742	-122.778	0.439	1176.677	0.413	26	0.125	K.LSVDKNLVEVFTK.G
R3/RRR3-2/3	1839.562	1840.094	-835.256	0.467	1120.387	0.428	31	0.125	K.KHIVGM*TGDGVNDAPALK.K
R3/RRR3-4/2	884.768	885.040	-308.678	0.216	884.216	0.123	12	0.125	R.LLEGDPLK.I
R3/RRR3-7/2	1026.987	1027.156	-165.787	0.305	499.015	0.255	11	0.124	-.LGDIVPADAR.-
R3/RRR3-5/3	1493.018	1492.742	185.644	0.457	1160.566	0.405	26	0.123	K.LSVDKNLVEVFTK.G
R3/RRR3-7/3	1407.434	1407.643	-149.038	0.474	1373.917	0.314	26	0.119	K.GVDKDHVLLLAAR.A
R3/RRR3-3/3	1839.740	1840.094	-193.058	0.498	1091.630	0.401	31	0.118	K.KHIVGM*TGDGVNDAPALK.K
R3/RRR3-2/3	1839.781	1840.094	-170.993	0.509	1071.837	0.402	32	0.117	K.KHIVGM*TGDGVNDAPALK.K
R3/RRR3-4/3	1492.340	1492.742	-269.858	0.451	870.881	0.449	24	0.116	K.LSVDKNLVEVFTK.G
R3/RRR3-5/3	1492.703	1492.742	-26.060	0.460	882.515	0.443	24	0.116	K.LSVDKNLVEVFTK.G
R3/RRR3-2/3	1407.818	1407.643	124.173	0.513	1227.139	0.343	24	0.115	K.GVDKDHVLLLAAR.A
R3/RRR3-4/3	1492.713	1492.742	-19.663	0.468	953.524	0.405	25	0.112	K.LSVDKNLVEVFTK.G
R3/RRR3-1/3	1493.092	1492.742	235.451	0.454	671.626	0.448	23	0.111	K.LSVDKNLVEVFTK.G
R3/RRR3-3/3	1840.431	1840.094	183.618	0.509	998.097	0.386	30	0.110	K.KHIVGM*TGDGVNDAPALK.K
R3/RRR3-3/3	1492.662	1492.742	-53.868	0.452	851.040	0.413	24	0.110	K.LSVDKNLVEVFTK.G
R3/RRR3-2/3	1492.769	1492.742	17.985	0.456	1064.466	0.360	26	0.110	K.LSVDKNLVEVFTK.G
R3/RRR3-1/3	1492.330	1492.742	-276.629	0.466	776.646	0.407	23	0.108	K.LSVDKNLVEVFTK.G
R3/RRR3-2/3	1492.510	1492.742	-156.006	0.425	895.792	0.369	25	0.105	K.LSVDKNLVEVFTK.G
R3/RRR3-4/3	1430.511	1429.649	-96.606	0.480	460.031	0.359	18	0.102	R.KVHAVIDKYAER.G
R3/RRR3-3/3	1492.281	1492.742	-309.498	0.403	548.721	0.357	20	0.101	K.LSVDKNLVEVFTK.G
R3/RRR3-2/3	1492.520	1492.742	-149.237	0.410	866.504	0.322	25	0.099	K.LSVDKNLVEVFTK.G
R3/RRR3-1/3	1491.810	1492.742	-1298.938	0.340	560.039	0.323	21	0.098	K.LSVDKNLVEVFTK.G
R3/RRR3-5/3	1492.827	1492.742	57.229	0.369	745.597	0.292	23	0.095	K.LSVDKNLVEVFTK.G
R3/RRR3-7/3	1408.745	1407.643	72.422	0.391	678.773	0.264	26	0.094	K.GVDKDHVLLLAAR.A
R3/RRR3-5/3	1839.761	1840.094	-181.676	0.398	432.304	0.368	23	0.092	-.HIVGM*TGDGVNDAPALKK.-
R3/RRR3-6/2	1465.359	1465.683	-221.552	0.513	2386.537	0.583	25	0.394	K.KVLTTGPAGGLHSAR.F
R3/RRR3-6/2	1465.384	1465.683	-204.504	0.520	1959.936	0.564	24	0.305	K.KVLTTGPAGGLHSAR.F
R3/RRR3-6/2	1465.379	1465.683	-208.265	0.492	1898.591	0.579	23	0.298	K.KVLTTGPAGGLHSAR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1707.343	1707.826	-283.735	0.529	1695.552	0.577	23	0.264	R.EVNSVNDNPVIDVHR.G
R3/RRR3-6/2	1707.332	1707.826	-290.478	0.531	1712.152	0.557	23	0.261	R.EVNSVNDNPVIDVHR.G
R3/RRR3-6/2	1398.033	1398.534	-1076.734	0.439	1595.946	0.507	18	0.234	R.EELGCVYLTGEK.L
R3/RRR3-8/2	1707.364	1707.826	-271.398	0.517	1490.421	0.554	22	0.230	R.EVNSVNDNPVIDVHR.G
R3/RRR3-1/2	1707.400	1707.826	-250.525	0.516	1447.584	0.566	22	0.228	R.EVNSVNDNPVIDVHR.G
R3/RRR3-6/2	1377.097	1377.528	-313.459	0.481	1462.013	0.554	20	0.228	R.VAFETGTAPITNR.I
R3/RRR3-3/2	1707.265	1707.826	-917.063	0.496	1510.710	0.534	21	0.228	R.EVNSVNDNPVIDVHR.G
R3/RRR3-1/2	1707.334	1707.826	-288.972	0.537	1405.520	0.580	22	0.227	R.EVNSVNDNPVIDVHR.G
R3/RRR3-2/2	1708.375	1707.826	-265.002	0.549	1364.374	0.588	22	0.224	R.EVNSVNDNPVIDVHR.G
R3/RRR3-2/2	1707.328	1707.826	-292.845	0.490	1405.738	0.567	21	0.223	R.EVNSVNDNPVIDVHR.G
R3/RRR3-1/2	1377.032	1377.528	-361.487	0.435	1554.214	0.475	20	0.220	R.VAFETGTAPITNR.I
R3/RRR3-6/2	1337.194	1337.510	-236.927	0.423	1547.747	0.461	21	0.218	K.VLTTGPAGGLHSAR.F
R3/RRR3-6/2	1957.822	1957.275	-231.916	0.522	1494.995	0.477	22	0.213	K.LM*SSTYLVALCQAVDLR.H
R3/RRR3-8/2	1708.168	1707.826	200.580	0.505	1312.042	0.547	22	0.210	R.EVNSVNDNPVIDVHR.G
R3/RRR3-2/2	1377.204	1377.528	-235.912	0.442	1461.745	0.456	20	0.206	R.VAFETGTAPITNR.I
R3/RRR3-2/2	1708.293	1707.826	274.173	0.544	1232.135	0.562	21	0.204	R.EVNSVNDNPVIDVHR.G
R3/RRR3-6/3	1464.691	1465.683	-1364.199	0.525	1591.540	0.538	30	0.199	K.KVLTTGPAGGLHSAR.F
R3/RRR3-6/2	1707.343	1707.826	-284.022	0.536	1155.408	0.574	20	0.199	R.EVNSVNDNPVIDVHR.G
R3/RRR3-2/2	1377.113	1377.528	-301.986	0.468	1282.256	0.500	19	0.197	R.VAFETGTAPITNR.I
R3/RRR3-6/2	1398.281	1398.534	-181.132	0.390	1266.480	0.515	17	0.197	R.EELGCVYLTGEK.L
R3/RRR3-6/3	1800.704	1801.027	-179.484	0.494	1646.817	0.485	29	0.192	R.FVREELGCVYLTGEK.L
R3/RRR3-2/2	1377.159	1377.528	-268.726	0.465	1321.731	0.452	19	0.191	R.VAFETGTAPITNR.I
R3/RRR3-6/2	1337.003	1337.510	-1130.737	0.425	1242.445	0.490	20	0.191	K.VLTTGPAGGLHSAR.F
R3/RRR3-5/3	1465.465	1465.683	-149.319	0.496	1570.768	0.512	29	0.190	K.KVLTTGPAGGLHSAR.F
R3/RRR3-3/2	1377.155	1377.528	-271.749	0.419	1251.287	0.434	19	0.182	R.VAFETGTAPITNR.I
R3/RRR3-5/2	1377.128	1377.528	-291.403	0.413	1211.403	0.444	19	0.181	R.VAFETGTAPITNR.I
R3/RRR3-6/2	1376.606	1377.528	-1400.250	0.326	1268.632	0.390	19	0.175	R.VAFETGTAPITNR.I
R3/RRR3-3/2	1377.093	1377.528	-316.839	0.444	1106.702	0.433	19	0.172	R.VAFETGTAPITNR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1625.586	1624.865	-172.450	0.509	1080.248	0.450	19	0.170	R.TSPQWLGPQIEVIR.A
R3/RRR3-2/2	1625.289	1624.865	261.507	0.519	944.972	0.476	20	0.168	R.TSPQWLGPQIEVIR.A
R3/RRR3-2/3	1465.573	1465.683	-75.498	0.528	1323.977	0.538	29	0.167	K.KVLTTGPAGGLHSAR.F
R3/RRR3-6/2	1623.818	1624.865	-1264.435	0.306	977.237	0.467	20	0.165	R.TSPQWLGPQIEVIR.A
R3/RRR3-1/2	1624.297	1624.865	-968.429	0.440	961.796	0.439	20	0.164	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	1376.680	1377.528	-1346.547	0.366	1126.362	0.375	18	0.163	R.VAFETGTAPITNR.I
R3/RRR3-6/2	1624.665	1624.865	-123.412	0.456	851.610	0.472	19	0.162	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	934.991	935.102	-119.047	0.467	895.496	0.433	13	0.162	K.VFLAISER.K
R3/RRR3-6/2	1397.651	1398.534	-1351.572	0.338	1039.864	0.418	16	0.162	R.EELGCVYLTGEK.L
R3/RRR3-2/2	1625.426	1624.865	-270.842	0.479	786.343	0.482	18	0.160	R.TSPQWLGPQIEVIR.A
R3/RRR3-4/2	1624.450	1624.865	-256.081	0.483	810.856	0.460	19	0.159	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	959.422	960.107	-1761.738	0.403	980.729	0.388	15	0.159	K.TAEAVDILK.L
R3/RRR3-5/2	1624.580	1624.865	-176.023	0.457	914.592	0.435	18	0.159	R.TSPQWLGPQIEVIR.A
R3/RRR3-5/2	1625.054	1624.865	116.886	0.487	845.576	0.443	19	0.158	R.TSPQWLGPQIEVIR.A
R3/RRR3-2/3	1465.335	1465.683	-237.942	0.463	1219.547	0.540	28	0.158	K.KVLTTGPAGGLHSAR.F
R3/RRR3-6/2	1624.422	1624.865	-273.422	0.412	687.420	0.499	18	0.158	R.TSPQWLGPQIEVIR.A
R3/RRR3-2/2	1624.464	1624.865	-247.789	0.471	793.902	0.453	19	0.158	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/3	1465.761	1465.683	53.692	0.531	1239.468	0.531	28	0.158	K.KVLTTGPAGGLHSAR.F
R3/RRR3-2/3	1465.797	1465.683	77.747	0.532	1264.245	0.520	29	0.157	K.KVLTTGPAGGLHSAR.F
R3/RRR3-6/2	1252.253	1252.485	-185.633	0.544	874.976	0.419	16	0.156	K.VNEVDPLLKPK.Q
R3/RRR3-2/2	1109.100	1108.226	-113.882	0.353	1012.683	0.373	14	0.156	K.ITAFEEELR.E
R3/RRR3-5/3	1465.656	1465.683	-18.355	0.499	1153.931	0.557	28	0.156	K.KVLTTGPAGGLHSAR.F
R3/RRR3-3/3	1466.180	1465.683	340.148	0.524	1201.141	0.537	27	0.156	K.KVLTTGPAGGLHSAR.F
R3/RRR3-1/2	1626.304	1624.865	270.755	0.469	769.014	0.455	18	0.156	R.TSPQWLGPQIEVIR.A
R3/RRR3-7/2	1625.263	1624.865	245.465	0.492	734.784	0.452	19	0.156	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	1624.666	1624.865	-122.658	0.434	672.316	0.477	18	0.155	R.TSPQWLGPQIEVIR.A
R3/RRR3-3/3	1465.798	1465.683	78.749	0.512	1268.484	0.509	28	0.155	K.KVLTTGPAGGLHSAR.F
R3/RRR3-2/2	1625.483	1624.865	-235.657	0.501	745.707	0.442	19	0.155	R.TSPQWLGPQIEVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1376.470	1377.528	-1499.478	0.331	1053.694	0.345	18	0.155	R.VAFETGTAPITNR.I
R3/RRR3-6/2	1624.667	1624.865	-122.583	0.433	683.010	0.461	18	0.154	R.TSPQWLGPQIEVIR.A
R3/RRR3-5/2	1376.785	1377.528	-1269.520	0.328	1083.776	0.324	18	0.154	R.VAFETGTAPITNR.I
R3/RRR3-6/2	934.583	935.102	-1630.260	0.471	933.686	0.355	13	0.154	K.VFLAISER.K
R3/RRR3-7/2	1624.626	1624.865	-147.607	0.438	650.313	0.461	18	0.153	R.TSPQWLGPQIEVIR.A
R3/RRR3-1/2	1251.935	1252.485	-1241.603	0.480	791.205	0.428	15	0.153	K.VNEVDPLLKPK.Q
R3/RRR3-6/2	1626.268	1624.865	248.250	0.535	849.685	0.411	19	0.153	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	1624.440	1624.865	-262.565	0.457	723.502	0.451	17	0.153	R.TSPQWLGPQIEVIR.A
R3/RRR3-3/2	1624.471	1624.865	-243.567	0.447	793.539	0.405	19	0.152	R.TSPQWLGPQIEVIR.A
R3/RRR3-2/2	1625.501	1624.865	-224.883	0.437	743.356	0.424	18	0.152	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	1251.620	1252.485	-1494.689	0.503	850.013	0.398	15	0.152	K.VNEVDPLLKPK.Q
R3/RRR3-2/2	934.969	935.102	-142.622	0.482	958.091	0.331	13	0.151	K.VFLAISER.K
R3/RRR3-5/2	1376.969	1377.528	-1135.352	0.332	892.202	0.378	18	0.151	R.VAFETGTAPITNR.I
R3/RRR3-6/2	872.479	873.032	-1785.667	0.324	952.539	0.352	13	0.151	-.ALLTAIDR.-
R3/RRR3-4/2	1625.324	1624.865	283.272	0.503	807.389	0.397	19	0.151	R.TSPQWLGPQIEVIR.A
R3/RRR3-3/2	1624.159	1624.865	-1053.621	0.431	665.279	0.431	18	0.151	R.TSPQWLGPQIEVIR.A
R3/RRR3-4/2	1624.195	1624.865	-1031.586	0.464	713.133	0.421	18	0.151	R.TSPQWLGPQIEVIR.A
R3/RRR3-5/2	1623.649	1624.865	-1368.705	0.354	653.211	0.447	18	0.151	R.TSPQWLGPQIEVIR.A
R3/RRR3-8/2	1624.402	1624.865	-285.937	0.403	596.547	0.445	17	0.150	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/3	1088.629	1088.280	322.198	0.455	1751.634	0.327	26	0.148	R.KTAEAVDILK.L
R3/RRR3-3/2	1624.362	1624.865	-928.291	0.459	715.038	0.390	18	0.147	R.TSPQWLGPQIEVIR.A
R3/RRR3-2/2	960.233	960.107	131.573	0.403	886.689	0.323	15	0.147	K.TAEAVDILK.L
R3/RRR3-6/2	1942.275	1941.275	-0.228	0.489	661.431	0.454	20	0.147	K.LMSSTYLVALCQAVDLR.H
R3/RRR3-6/2	1624.756	1624.865	-67.189	0.445	380.629	0.472	14	0.147	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	1624.431	1624.865	-267.767	0.422	792.474	0.356	19	0.147	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	1252.206	1252.485	-223.479	0.507	876.366	0.337	16	0.146	K.VNEVDPLLKPK.Q
R3/RRR3-6/2	959.888	960.107	-228.079	0.436	874.806	0.300	15	0.145	K.TAEAVDILK.L
R3/RRR3-6/2	1040.937	1041.138	-193.912	0.337	334.707	0.441	11	0.145	R.NPSLDYGFK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	872.582	873.032	-518.130	0.304	797.085	0.350	12	0.144	K.ALLTAIDR.E
R3/RRR3-6/2	1107.971	1108.226	-230.692	0.463	846.284	0.316	14	0.144	K.ITAFEEELR.E
R3/RRR3-1/3	1466.379	1465.683	-207.756	0.515	1130.714	0.513	28	0.144	K.KVLTTGPAGGLHSAR.F
R3/RRR3-1/2	1376.445	1377.528	-1517.384	0.286	1127.327	0.220	18	0.144	R.VAFETGTAPITNR.I
R3/RRR3-6/2	1040.676	1041.138	-445.381	0.270	453.635	0.453	13	0.143	R.NPSLDYGFK.G
R3/RRR3-6/2	1040.752	1041.138	-372.881	0.323	372.018	0.380	12	0.143	R.NPSLDYGFK.G
R3/RRR3-1/2	1623.328	1624.865	-2185.734	0.319	560.982	0.376	17	0.143	R.TSPQWLGPQIEVIR.A
R3/RRR3-6/2	934.857	935.102	-262.475	0.390	838.311	0.288	13	0.143	K.VFLAISER.K
R3/RRR3-8/2	1623.816	1624.865	-1265.945	0.381	462.716	0.385	15	0.142	R.TSPQWLGPQIEVIR.A
R3/RRR3-5/2	1040.348	1041.138	-1726.202	0.307	316.786	0.349	12	0.142	R.NPSLDYGFK.G
R3/RRR3-5/2	872.936	873.032	-110.890	0.287	910.757	0.265	13	0.140	K.ALLTAIDR.E
R3/RRR3-9/2	1041.108	1041.138	-29.002	0.235	367.267	0.460	12	0.140	R.NPSLDYGFK.G
R3/RRR3-9/2	1625.612	1624.865	-156.028	0.380	637.269	0.308	16	0.138	R.TSPQWLGPQIEVIR.A
R3/RRR3-8/2	1623.714	1624.865	-1328.761	0.289	553.489	0.292	17	0.138	R.TSPQWLGPQIEVIR.A
R3/RRR3-9/2	1041.092	1041.138	-44.996	0.189	265.506	0.303	10	0.136	R.NPSLDYGFK.G
R3/RRR3-3/3	1465.509	1465.683	-119.112	0.470	1026.777	0.509	26	0.136	K.KVLTTGPAGGLHSAR.F
R3/RRR3-6/2	1336.258	1337.510	-1690.380	0.247	705.662	0.297	18	0.134	K.VLTTGPAGGLHSAR.F
R3/RRR3-2/2	872.674	873.032	-412.148	0.203	820.927	0.233	12	0.133	K.ALLTAIDR.E
R3/RRR3-9/2	1626.309	1624.865	273.690	0.404	606.436	0.238	15	0.131	-.TSPQWLGPQIEVIR.-
R3/RRR3-10/2	1042.091	1041.138	-45.658	0.168	294.539	0.355	10	0.125	-.NPSLDYGFK.-
R3/RRR3-6/3	1252.127	1252.485	-286.916	0.373	1007.758	0.397	21	0.112	K.VNEVDPLLKPK.Q
R3/RRR3-6/3	1252.723	1252.485	190.564	0.461	845.110	0.391	20	0.106	K.VNEVDPLLKPK.Q
R3/RRR3-6/3	1252.420	1252.485	-52.079	0.413	822.644	0.368	21	0.102	K.VNEVDPLLKPK.Q
R3/RRR3-5/3	1252.852	1252.485	293.597	0.385	642.259	0.413	19	0.101	-.VNEVDPLLKPK.-
R3/RRR3-2/3	1252.213	1252.485	-217.818	0.362	610.633	0.360	19	0.099	K.VNEVDPLLKPK.Q
R3/RRR3-3/3	1253.152	1252.485	-266.799	0.256	483.152	0.368	17	0.088	-.VNEVDPLLKPK.-
R3/RRR3-2/3	1252.734	1252.485	199.652	0.330	468.992	0.334	17	0.088	-.VNEVDPLLKPK.-
R3/RRR3-6/3	1088.320	1088.280	37.269	0.486	961.019	0.231	22	0.082	-.KTAEAVDILK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/3	1407.439	1406.647	-148.515	0.430	985.699	0.181	22	0.074	-.SAVKNCVTTVAKK.-
R3/RRR3-13/3	1407.250	1406.647	-282.956	0.431	1043.973	0.099	23	0.071	-.SAVKNCVTTVAKK.-
R3/RRR3-13/3	1407.315	1406.647	-236.616	0.387	723.261	0.139	20	0.062	-.SAVKNCVTTVAKK.-
R3/RRR3-8/2	1997.273	1997.392	-59.868	0.556	3256.754	0.538	29	0.592	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/2	1996.679	1997.392	-860.297	0.573	3207.796	0.565	29	0.589	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/2	1683.372	1682.880	293.214	0.600	3158.109	0.492	26	0.541	R.GLLYLGM*GVSGGEEGAR.N
R3/RRR3-9/2	1996.656	1997.392	-872.081	0.597	2868.126	0.591	27	0.505	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/2	1682.322	1682.880	-928.915	0.566	2964.165	0.514	26	0.500	R.GLLYLGM*GVSGGEEGAR.N
R3/RRR3-9/2	1666.365	1666.881	-912.092	0.572	3026.341	0.443	27	0.486	R.GLLYLGMGVSGGEEGAR.N
R3/RRR3-9/2	1682.302	1682.880	-940.934	0.546	2913.304	0.500	26	0.481	R.GLLYLGM*GVSGGEEGAR.N
R3/RRR3-9/2	1667.294	1666.881	248.383	0.595	2883.340	0.514	26	0.478	R.GLLYLGMGVSGGEEGAR.N
R3/RRR3-9/2	1666.514	1666.881	-220.818	0.560	2908.395	0.496	25	0.477	R.GLLYLGMGVSGGEEGAR.N
R3/RRR3-9/2	1997.762	1997.392	185.723	0.596	2543.067	0.563	26	0.413	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/3	1998.081	1997.392	-156.117	0.519	2563.962	0.462	41	0.354	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-8/2	1996.325	1997.392	-1038.309	0.520	2192.851	0.580	25	0.347	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/3	1997.346	1997.392	-22.909	0.498	2164.213	0.531	39	0.299	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/2	1110.057	1110.292	-212.500	0.558	1497.490	0.533	17	0.231	R.LPANLVQAQR.D
R3/RRR3-9/2	1110.367	1110.292	67.857	0.467	1383.815	0.521	17	0.215	R.LPANLVQAQR.D
R3/RRR3-9/2	1823.772	1823.984	-116.451	0.504	1504.373	0.467	19	0.211	K.LTNSELQQVFSEWNK.G
R3/RRR3-9/2	1110.914	1110.292	-341.285	0.534	1394.736	0.485	17	0.209	R.LPANLVQAQR.D
R3/RRR3-9/2	1563.306	1563.780	-304.160	0.521	1514.810	0.436	21	0.208	R.FLSGLKDERVEAAK.V
R3/RRR3-9/2	1553.308	1553.697	-251.415	0.493	1360.046	0.443	21	0.194	K.VFQGDFSSNLPVDK.A
R3/RRR3-9/2	1554.167	1553.697	303.253	0.524	1313.264	0.463	21	0.194	K.VFQGDFSSNLPVDK.A
R3/RRR3-9/2	1823.496	1823.984	-268.348	0.499	1262.981	0.494	17	0.190	K.LTNSELQQVFSEWNK.G
R3/RRR3-9/2	1554.224	1553.697	-305.465	0.502	1288.766	0.441	21	0.187	K.VFQGDFSSNLPVDK.A
R3/RRR3-9/2	1398.224	1398.647	-303.556	0.463	1324.551	0.418	19	0.187	K.ICSYAQGMNIIK.A
R3/RRR3-9/2	1398.319	1398.647	-234.976	0.477	1261.066	0.446	19	0.187	K.ICSYAQGMNIIK.A
R3/RRR3-9/2	1398.453	1398.647	-139.260	0.506	1204.119	0.463	18	0.184	K.ICSYAQGMNIIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1217.059	1216.371	-257.296	0.410	1503.650	0.317	17	0.184	K.GWSLNLGELAR.I
R3/RRR3-9/2	1998.629	1997.392	118.869	0.359	1564.358	0.296	23	0.183	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/2	1415.220	1414.646	-302.263	0.531	1190.148	0.461	18	0.183	K.ICSYAQGM*NIIK.A
R3/RRR3-9/2	1563.348	1563.780	-276.976	0.545	1354.200	0.395	20	0.182	R.FLSGLKDERVEAAK.V
R3/RRR3-9/2	1562.700	1563.780	-1335.199	0.469	1328.038	0.372	20	0.177	R.FLSGLKDERVEAAK.V
R3/RRR3-9/2	1823.585	1823.984	-219.053	0.471	1070.466	0.465	16	0.168	K.LTNSELQQVFSEWNK.G
R3/RRR3-9/2	1216.283	1216.371	-72.943	0.336	1277.946	0.320	17	0.166	K.GWSLNLGELAR.I
R3/RRR3-9/2	1259.082	1259.308	-180.347	0.383	1046.477	0.380	15	0.160	R.DYFGAHTYER.V
R3/RRR3-9/2	1258.929	1259.308	-302.132	0.333	994.799	0.409	16	0.160	R.DYFGAHTYER.V
R3/RRR3-9/2	1259.134	1259.308	-139.111	0.392	882.830	0.428	15	0.157	R.DYFGAHTYER.V
R3/RRR3-9/2	1762.477	1762.978	-854.296	0.452	723.059	0.490	22	0.156	K.VAAQVPDSGPCVTYIGK.G
R3/RRR3-9/2	1598.164	1597.775	244.116	0.463	595.671	0.490	16	0.152	R.VDM*PGSFHTEWFK.I
R3/RRR3-9/2	1763.329	1762.978	199.305	0.477	503.981	0.528	20	0.152	K.VAAQVPDSGPCVTYIGK.G
R3/RRR3-9/2	1762.293	1762.978	-959.085	0.488	690.241	0.460	22	0.152	K.VAAQVPDSGPCVTYIGK.G
R3/RRR3-9/2	1582.498	1581.776	-176.062	0.446	513.326	0.471	17	0.149	R.VDMPGSFHTEWFK.I
R3/RRR3-9/2	801.947	802.104	-196.203	0.388	382.046	0.407	11	0.149	R.VVIMLVK.A
R3/RRR3-9/2	943.355	944.067	-1821.206	0.364	793.560	0.378	12	0.148	K.AQLIEDVR.Q
R3/RRR3-9/2	1381.262	1381.566	-220.859	0.485	579.525	0.402	19	0.148	R.DRLPANLVQAQR.D
R3/RRR3-8/2	1052.769	1053.196	-406.538	0.349	318.247	0.552	12	0.148	K.GFPISVYNR.T
R3/RRR3-9/2	801.557	802.104	-1936.103	0.440	400.564	0.341	11	0.146	R.VVIMLVK.A
R3/RRR3-9/2	1571.252	1571.736	-309.188	0.390	546.820	0.452	18	0.146	R.NGPSLM*PGGSFEAYK.Y
R3/RRR3-9/2	1596.705	1597.775	-1300.701	0.384	598.797	0.432	16	0.145	R.VDM*PGSFHTEWFK.I
R3/RRR3-9/2	802.076	802.104	-35.126	0.361	322.326	0.320	10	0.144	R.VVIMLVK.A
R3/RRR3-9/2	1381.208	1381.566	-259.871	0.480	432.818	0.387	17	0.144	R.DRLPANLVQAQR.D
R3/RRR3-9/2	1571.249	1571.736	-311.292	0.373	507.762	0.437	18	0.144	R.NGPSLM*PGGSFEAYK.Y
R3/RRR3-8/2	1216.041	1216.371	-272.010	0.314	787.968	0.347	15	0.143	K.GWSLNLGELAR.I
R3/RRR3-9/2	1381.184	1381.566	-277.605	0.430	524.735	0.351	18	0.142	R.DRLPANLVQAQR.D
R3/RRR3-9/2	1555.242	1555.737	-318.884	0.360	332.115	0.478	15	0.142	R.NGPSLMPGGSFEAYK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	943.923	944.067	-153.332	0.440	759.149	0.311	12	0.142	K.AQLIEDVR.Q
R3/RRR3-9/2	818.117	818.103	17.206	0.395	476.535	0.262	11	0.141	R.VVIM*LVK.A
R3/RRR3-8/2	1053.144	1053.196	-49.481	0.330	394.720	0.366	14	0.141	K.GFPISVYNR.T
R3/RRR3-17/2	1217.156	1216.371	-177.104	0.344	715.218	0.329	14	0.140	K.GWSLNLGELAR.I
R3/RRR3-9/2	944.368	944.067	319.182	0.472	809.490	0.279	13	0.139	-.AQLIEDVR.-
R3/RRR3-9/2	1570.785	1571.736	-1246.192	0.290	440.813	0.410	17	0.138	R.NGPSLM*PGGSFEAYK.Y
R3/RRR3-9/2	817.935	818.103	-205.678	0.315	458.423	0.217	11	0.138	R.VVIM*LVK.A
R3/RRR3-9/2	817.571	818.103	-1879.597	0.417	403.354	0.238	10	0.137	-.VVIM*LVK.-
R3/RRR3-9/2	1580.489	1581.776	-1451.091	0.271	418.920	0.379	15	0.136	R.VDMPGSFHTEWFK.I
R3/RRR3-9/2	1216.114	1216.371	-212.392	0.272	555.187	0.224	13	0.132	K.GWSLNLGELAR.I
R3/RRR3-9/2	1555.063	1555.737	-1079.808	0.290	249.202	0.331	13	0.131	-.NGPSLMPGGSFEAYK.-
R3/RRR3-9/2	1217.348	1216.371	-19.171	0.293	825.138	0.135	14	0.128	K.GWSLNLGELAR.I
R3/RRR3-8/3	1996.944	1997.392	-224.783	0.463	1219.053	0.394	30	0.127	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-20/2	1555.065	1553.697	237.335	0.383	459.112	0.266	13	0.121	-.VFQGDFSSNLPVDK.-
R3/RRR3-9/3	1762.580	1762.978	-226.817	0.396	716.040	0.479	30	0.110	K.VAAQVPDSGPCVTYIGK.G
R3/RRR3-8/3	1996.515	1997.392	-942.918	0.372	1057.838	0.335	29	0.106	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/3	1998.807	1997.392	208.528	0.334	911.756	0.307	29	0.097	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-9/3	1381.510	1381.566	-40.787	0.477	928.713	0.330	22	0.094	-.DRLPANLVQAQR.-
R3/RRR3-9/3	1762.757	1762.978	-125.837	0.318	563.575	0.377	26	0.093	K.VAAQVPDSGPCVTYIGK.G
R3/RRR3-9/3	1997.006	1997.392	-193.600	0.401	721.990	0.311	25	0.092	-.IGLAGLAVMGQNLALNIAEK.-
R3/RRR3-8/3	1381.581	1381.566	10.792	0.496	925.845	0.271	22	0.089	-.DRLPANLVQAQR.-
R3/RRR3-8/3	1998.205	1997.392	-93.976	0.285	680.389	0.242	25	0.087	R.IGLAGLAVMGQNLALNIAEK.G
R3/RRR3-1/3	1381.866	1381.566	217.854	0.372	792.598	0.183	21	0.084	R.DRLPANLVQAQR.D
R3/RRR3-8/3	1381.842	1381.566	200.048	0.443	754.308	0.270	20	0.083	-.DRLPANLVQAQR.-
R3/RRR3-9/3	1380.465	1381.566	-1526.901	0.371	833.237	0.179	21	0.072	-.DRLPANLVQAQR.-
R3/RRR3-4/2	1646.344	1646.869	-929.060	0.479	3263.831	0.551	24	0.607	K.LLVAGDLQSFGEQLR.N
R3/RRR3-4/2	1646.512	1646.869	-217.552	0.558	2846.367	0.561	24	0.493	K.LLVAGDLQSFGEQLR.N
R3/RRR3-4/2	1645.517	1646.869	-1433.926	0.365	2522.627	0.497	23	0.392	K.LLVAGDLQSFGEQLR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1979.514	1980.162	-835.099	0.597	2115.076	0.553	24	0.325	K.VSEDDKLVEYDALLVDR.F
R3/RRR3-4/2	1979.535	1980.162	-824.142	0.593	2062.697	0.546	24	0.313	K.VSEDDKLVEYDALLVDR.F
R3/RRR3-4/2	1979.394	1980.162	-895.830	0.582	2064.064	0.533	24	0.310	K.VSEDDKLVEYDALLVDR.F
R3/RRR3-1/2	1981.783	1980.162	-191.621	0.550	1912.608	0.556	22	0.290	K.VSEDDKLVEYDALLVDR.F
R3/RRR3-4/2	1269.102	1268.444	-270.671	0.534	1783.261	0.530	22	0.269	K.LADLEAAPAAVAR.L
R3/RRR3-4/2	1860.370	1860.958	-856.136	0.580	1742.323	0.502	23	0.251	K.DITADDKQELDEALQR.E
R3/RRR3-4/2	1860.531	1860.958	-229.708	0.618	1543.654	0.508	22	0.224	K.DITADDKQELDEALQR.E
R3/RRR3-4/2	1860.388	1860.958	-845.992	0.575	1304.118	0.477	20	0.191	K.DITADDKQELDEALQR.E
R3/RRR3-4/2	1187.942	1188.293	-296.453	0.413	959.348	0.580	16	0.184	R.TPPTPQDEM*R.A
R3/RRR3-2/2	1268.069	1268.444	-297.347	0.457	1236.547	0.445	18	0.182	K.LADLEAAPAAVAR.L
R3/RRR3-4/2	1187.871	1188.293	-356.253	0.387	819.585	0.592	15	0.174	R.TPPTPQDEM*R.A
R3/RRR3-4/2	1316.357	1316.491	-102.277	0.480	1392.679	0.291	16	0.170	K.RQDWLLSELR.G
R3/RRR3-4/2	1113.553	1114.299	-1572.887	0.392	1175.479	0.358	14	0.166	R.LSAAWQM*YK.A
R3/RRR3-4/2	1067.813	1068.169	-334.536	0.445	748.331	0.496	14	0.161	R.HQSIDAQLR.L
R3/RRR3-4/2	1120.201	1120.237	-32.201	0.413	681.875	0.528	17	0.161	K.GDPGIAALYDK.L
R3/RRR3-4/2	1469.961	1470.677	-1170.975	0.432	1133.484	0.368	15	0.161	R.AGMSYFHETIWK.G
R3/RRR3-4/2	1120.141	1120.237	-86.199	0.441	550.806	0.533	17	0.158	K.GDPGIAALYDK.L
R3/RRR3-4/2	1490.447	1490.733	-191.865	0.482	687.525	0.473	18	0.158	R.AIPWIFAWTQTR.F
R3/RRR3-4/2	1673.852	1674.927	-1243.536	0.429	1071.571	0.374	18	0.157	R.FLDILQDLHGPHLR.E
R3/RRR3-4/2	1113.930	1114.299	-332.525	0.398	1136.336	0.312	14	0.157	R.LSAAWQM*YK.A
R3/RRR3-4/3	1742.886	1742.932	-26.408	0.479	1330.394	0.491	29	0.156	R.INGKQEVM*IGYSDSGK.D
R3/RRR3-4/2	1491.280	1490.733	-304.647	0.482	598.415	0.490	17	0.156	R.AIPWIFAWTQTR.F
R3/RRR3-4/2	1113.926	1114.299	-336.153	0.422	989.494	0.344	14	0.153	R.LSAAWQM*YK.A
R3/RRR3-4/2	1119.888	1120.237	-312.858	0.388	448.967	0.563	16	0.152	-.GDPGIAALYDK.-
R3/RRR3-4/2	1022.406	1023.168	-1728.773	0.486	878.195	0.346	11	0.150	K.HYIEFWK.K
R3/RRR3-4/2	1316.166	1316.491	-247.411	0.394	1162.408	0.252	15	0.149	K.RQDWLLSELR.G
R3/RRR3-4/2	975.421	976.154	-1782.423	0.396	922.148	0.319	13	0.148	R.SIVFKEPR.F
R3/RRR3-4/2	1316.166	1316.491	-247.597	0.467	1086.655	0.270	15	0.147	K.RQDWLLSELR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1486.074	1486.676	-1081.671	0.435	571.637	0.434	15	0.146	R.AGM*SYFHETIWK.G
R3/RRR3-4/2	976.030	976.154	-127.339	0.449	798.531	0.346	12	0.146	R.SIVFKEPR.F
R3/RRR3-4/2	1486.558	1486.676	-80.038	0.498	576.897	0.429	15	0.146	R.AGM*SYFHETIWK.G
R3/RRR3-4/2	1067.353	1068.169	-1706.618	0.400	536.975	0.441	12	0.146	R.HQSIDAQLR.L
R3/RRR3-4/2	1490.393	1490.733	-228.675	0.423	710.823	0.368	17	0.146	R.AIPWIFAWTQTR.F
R3/RRR3-4/2	1022.392	1023.168	-1742.089	0.432	874.456	0.304	11	0.146	K.HYIEFWK.K
R3/RRR3-4/3	1860.366	1860.958	-857.856	0.539	1439.517	0.404	32	0.144	K.DITADDKQELDEALQR.E
R3/RRR3-4/2	1486.326	1486.676	-236.399	0.425	537.943	0.402	15	0.143	R.AGM*SYFHETIWK.G
R3/RRR3-4/2	1022.424	1023.168	-1710.659	0.357	812.647	0.295	11	0.143	K.HYIEFWK.K
R3/RRR3-4/2	1490.025	1490.733	-1149.537	0.304	611.666	0.367	18	0.142	R.AIPWIFAWTQTR.F
R3/RRR3-4/2	1490.124	1490.733	-1082.825	0.295	648.949	0.349	18	0.141	R.AIPWIFAWTQTR.F
R3/RRR3-4/2	1490.078	1490.733	-1113.589	0.322	628.845	0.328	18	0.141	R.AIPWIFAWTQTR.F
R3/RRR3-4/2	1097.836	1098.300	-423.418	0.327	789.822	0.296	13	0.139	-.LSAAWQMYK.-
R3/RRR3-4/2	1199.665	1200.373	-1427.866	0.392	764.604	0.294	17	0.139	K.RKPSGGIESLR.A
R3/RRR3-4/2	1200.075	1200.373	-249.715	0.347	714.998	0.274	15	0.135	K.RKPSGGIESLR.A
R3/RRR3-4/2	976.864	976.154	-298.440	0.435	674.390	0.319	11	0.134	-.SIVFKEPR.-
R3/RRR3-1/2	1022.748	1023.168	-411.587	0.277	594.586	0.185	10	0.133	K.HYIEFWK.K
R3/RRR3-4/3	1832.372	1832.114	141.361	0.517	976.667	0.516	25	0.133	R.IRDPSFEVM*PQPALSK.E
R3/RRR3-1/2	1187.328	1188.293	-1660.154	0.250	529.437	0.281	12	0.132	R.TPPTPQDEM*R.A
R3/RRR3-4/2	1023.434	1023.168	260.906	0.239	706.309	0.161	10	0.130	K.HYIEFWK.K
R3/RRR3-4/3	1860.346	1860.958	-868.823	0.560	1276.324	0.397	31	0.129	K.DITADDKQELDEALQR.E
R3/RRR3-4/3	1860.276	1860.958	-906.766	0.530	1217.518	0.383	30	0.122	K.DITADDKQELDEALQR.E
R3/RRR3-4/3	1742.396	1742.932	-884.541	0.462	783.094	0.439	23	0.106	-.INGKQEVM*IGYSDSGK.-
R3/RRR3-4/3	1831.640	1832.114	-259.253	0.415	632.920	0.367	22	0.090	-.IRDPSFEVM*PQPALSK.-
R3/RRR3-4/3	1831.781	1832.114	-182.434	0.414	563.579	0.333	21	0.084	-.IRDPSFEVM*PQPALSK.-
R3/RRR3-7/2	1619.307	1619.792	-300.598	0.514	2229.742	0.505	23	0.334	K.IGDTAGTIDNIIQCK.L
R3/RRR3-7/2	1619.293	1619.792	-309.069	0.488	2161.924	0.509	23	0.323	K.IGDTAGTIDNIIQCK.L
R3/RRR3-7/2	1619.331	1619.792	-285.925	0.513	2048.111	0.527	23	0.308	K.IGDTAGTIDNIIQCK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1600.660	1599.899	-149.740	0.557	1989.083	0.540	26	0.301	K.VILGPATVGGIQAGAFK.I
R3/RRR3-7/2	1600.403	1599.899	-310.957	0.540	1731.753	0.548	25	0.262	K.VILGPATVGGIQAGAFK.I
R3/RRR3-7/2	1529.541	1528.729	-123.563	0.547	1519.237	0.639	24	0.258	R.VVAIIAEGVPESDTK.Q
R3/RRR3-7/2	1528.318	1528.729	-269.946	0.447	1499.678	0.638	24	0.252	R.VVAIIAEGVPESDTK.Q
R3/RRR3-7/2	1817.436	1817.977	-850.693	0.473	1563.224	0.572	25	0.244	R.ETPSVAGIINPGSDGFQK.L
R3/RRR3-6/2	1599.388	1599.899	-947.302	0.391	1831.435	0.412	24	0.242	K.VILGPATVGGIQAGAFK.I
R3/RRR3-7/2	1818.166	1817.977	104.135	0.524	1494.611	0.591	24	0.240	R.ETPSVAGIINPGSDGFQK.L
R3/RRR3-7/2	1817.126	1817.977	-1021.982	0.465	1319.911	0.567	24	0.213	R.ETPSVAGIINPGSDGFQK.L
R3/RRR3-7/2	1598.895	1599.899	-1257.037	0.347	1602.872	0.399	24	0.209	K.VILGPATVGGIQAGAFK.I
R3/RRR3-7/2	1527.631	1528.729	-1378.033	0.409	1321.112	0.527	22	0.205	R.VVAIIAEGVPESDTK.Q
R3/RRR3-7/2	1248.774	1249.396	-1302.887	0.509	1385.272	0.450	16	0.199	K.TTQALFYNYK.Q
R3/RRR3-7/2	1249.040	1249.396	-286.487	0.431	1395.834	0.427	15	0.195	K.TTQALFYNYK.Q
R3/RRR3-7/2	1563.081	1563.696	-1036.315	0.468	1269.618	0.438	18	0.183	K.SGGM*SNEM*YNTIAR.V
R3/RRR3-7/2	1658.519	1658.920	-242.258	0.413	1101.596	0.513	22	0.183	K.VQKPVVAWVSGTCAR.L
R3/RRR3-7/2	1250.237	1249.396	-127.663	0.538	1128.448	0.459	15	0.178	K.TTQALFYNYK.Q
R3/RRR3-2/2	1619.198	1619.792	-987.509	0.436	1061.480	0.499	19	0.176	K.IGDTAGTIDNIIQCK.L
R3/RRR3-7/2	1290.389	1290.464	-58.085	0.425	1290.836	0.359	15	0.173	R.M*LDFDFLCGR.E
R3/RRR3-7/2	1274.303	1274.464	-127.366	0.393	1212.649	0.373	16	0.170	R.MLDFDFLCGR.E
R3/RRR3-7/2	1563.171	1563.696	-978.529	0.477	1161.861	0.414	18	0.170	K.SGGM*SNEM*YNTIAR.V
R3/RRR3-7/2	1846.637	1847.142	-817.483	0.475	878.814	0.538	21	0.169	K.ISPVTEITPPPIPEDLK.T
R3/RRR3-7/2	992.410	993.055	-1663.204	0.459	1292.294	0.319	17	0.168	R.FGGAIDDAAR.Y
R3/RRR3-7/2	1187.262	1187.332	-58.638	0.425	881.500	0.494	16	0.167	K.YAHTHFPSVK.Y
R3/RRR3-7/2	1836.255	1836.033	121.645	0.514	847.789	0.533	24	0.167	K.DAGAVVPTSYEALETAIK.E
R3/RRR3-7/2	1658.534	1658.920	-233.249	0.451	1001.350	0.456	21	0.167	K.VQKPVVAWVSGTCAR.L
R3/RRR3-7/2	1563.325	1563.696	-238.093	0.480	1015.508	0.448	17	0.164	K.SGGM*SNEM*YNTIAR.V
R3/RRR3-7/2	1310.112	1310.526	-316.963	0.438	1122.145	0.359	18	0.161	K.LYRPGSVGFVSK.S
R3/RRR3-1/2	1529.454	1528.729	-180.327	0.400	970.771	0.426	19	0.159	R.VVAIIAEGVPESDTK.Q
R3/RRR3-7/2	1290.135	1290.464	-255.967	0.370	1147.844	0.336	14	0.159	R.M*LDFDFLCGR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1627.503	1627.907	-248.906	0.242	1243.390	0.319	19	0.158	K.DLVSSLVSGLLTIGPR.F
R3/RRR3-7/2	1847.547	1847.142	219.776	0.486	647.200	0.530	19	0.154	K.ISPVTEITPPPIPEDLK.T
R3/RRR3-7/2	1187.996	1187.332	-283.585	0.410	683.179	0.445	15	0.152	K.YAHTHFPSVK.Y
R3/RRR3-7/2	1187.038	1187.332	-247.816	0.428	854.634	0.377	16	0.152	K.YAHTHFPSVK.Y
R3/RRR3-7/2	1309.697	1310.526	-1401.018	0.407	1009.386	0.301	17	0.147	K.LYRPGSVGFVSK.S
R3/RRR3-7/2	1310.334	1310.526	-147.411	0.428	762.503	0.323	15	0.139	K.LYRPGSVGFVSK.S
R3/RRR3-7/3	1659.945	1658.920	15.436	0.471	1379.194	0.388	30	0.135	K.VQKPVVAWVSGTCAR.L
R3/RRR3-6/2	992.879	993.055	-177.895	0.367	603.295	0.264	14	0.132	-.FGGAIDDAAR.-
R3/RRR3-7/3	1883.520	1884.210	-899.801	0.404	1424.339	0.297	29	0.120	R.AGKDLVSSLVSGLLTIGPR.F
R3/RRR3-7/3	1659.904	1658.920	-9.568	0.432	1338.012	0.326	30	0.118	K.VQKPVVAWVSGTCAR.L
R3/RRR3-7/3	1636.561	1635.868	-188.494	0.505	880.141	0.454	29	0.116	R.SAAASSM*SALKQPTIR.V
R3/RRR3-7/3	1599.428	1599.899	-295.194	0.372	863.768	0.435	26	0.107	K.VILGPATVGGIQAGAFK.I
R3/RRR3-7/3	1635.020	1635.868	-1133.667	0.426	411.447	0.440	22	0.102	R.SAAASSM*SALKQPTIR.V
R3/RRR3-7/3	1635.447	1635.868	-258.545	0.358	666.778	0.388	27	0.098	R.SAAASSM*SALKQPTIR.V
R3/RRR3-7/3	1658.178	1658.920	-1053.795	0.349	651.999	0.327	24	0.093	K.VQKPVVAWVSGTCAR.L
R3/RRR3-4/2	1814.540	1815.062	-840.985	0.537	2127.661	0.531	25	0.319	K.AYLPVIESFGFSSQLR.A
R3/RRR3-4/2	1814.463	1815.062	-883.667	0.537	2127.556	0.516	25	0.314	K.AYLPVIESFGFSSQLR.A
R3/RRR3-2/2	1814.376	1815.062	-931.553	0.511	2059.440	0.516	25	0.303	K.AYLPVIESFGFSSQLR.A
R3/RRR3-4/2	1814.613	1815.062	-247.733	0.547	1936.720	0.553	24	0.293	K.AYLPVIESFGFSSQLR.A
R3/RRR3-5/2	1814.417	1815.062	-909.062	0.532	1961.924	0.528	24	0.290	K.AYLPVIESFGFSSQLR.A
R3/RRR3-2/2	1814.431	1815.062	-901.227	0.542	1979.633	0.519	24	0.290	K.AYLPVIESFGFSSQLR.A
R3/RRR3-3/2	1814.696	1815.062	-201.842	0.515	1958.636	0.520	24	0.287	K.AYLPVIESFGFSSQLR.A
R3/RRR3-5/2	1813.999	1815.062	-1140.646	0.468	1986.079	0.497	24	0.285	K.AYLPVIESFGFSSQLR.A
R3/RRR3-5/2	1814.394	1815.062	-921.827	0.512	1906.548	0.521	24	0.279	K.AYLPVIESFGFSSQLR.A
R3/RRR3-1/2	1813.964	1815.062	-1159.836	0.440	1944.628	0.480	24	0.274	K.AYLPVIESFGFSSQLR.A
R3/RRR3-5/2	1819.216	1819.945	-953.641	0.532	1870.060	0.516	22	0.272	K.NATLTNEKESDACPIR.A
R3/RRR3-2/2	1816.569	1815.062	-271.932	0.596	1711.740	0.605	23	0.271	K.AYLPVIESFGFSSQLR.A
R3/RRR3-4/2	1820.370	1819.945	233.954	0.549	1762.035	0.553	21	0.265	K.NATLTNEKESDACPIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1819.453	1819.945	-271.232	0.550	1853.042	0.501	22	0.265	K.NATLTNEKESDACPIR.A
R3/RRR3-5/3	1820.533	1819.945	-227.364	0.459	2064.217	0.468	33	0.252	K.NATLTNEKESDACPIR.A
R3/RRR3-4/2	1819.459	1819.945	-268.270	0.549	1709.911	0.530	21	0.252	K.NATLTNEKESDACPIR.A
R3/RRR3-4/2	1819.353	1819.945	-877.927	0.535	1686.241	0.534	21	0.250	K.NATLTNEKESDACPIR.A
R3/RRR3-4/2	1389.122	1388.586	-334.367	0.526	1638.890	0.534	17	0.246	R.GFVQFCYEPIK.Q
R3/RRR3-4/3	1814.585	1815.062	-263.668	0.417	2063.993	0.417	29	0.239	K.AYLPVIESFGFSSQLR.A
R3/RRR3-6/2	1814.586	1815.062	-262.648	0.489	1677.682	0.496	22	0.239	K.AYLPVIESFGFSSQLR.A
R3/RRR3-4/3	1819.533	1819.945	-227.152	0.446	1851.338	0.534	36	0.234	K.NATLTNEKESDACPIR.A
R3/RRR3-1/2	1813.883	1815.062	-1204.641	0.419	1656.882	0.453	23	0.227	K.AYLPVIESFGFSSQLR.A
R3/RRR3-4/2	1388.239	1388.586	-250.353	0.467	1606.099	0.462	17	0.225	R.GFVQFCYEPIK.Q
R3/RRR3-4/2	1425.290	1425.569	-196.255	0.506	1489.353	0.501	20	0.220	R.LWGENFFDPATK.K
R3/RRR3-5/2	1347.301	1347.588	-213.613	0.472	1391.172	0.554	18	0.219	R.VIYASQLTAKPR.L
R3/RRR3-5/2	1650.801	1651.841	-1239.689	0.467	1736.317	0.376	19	0.218	K.ILSEEFGWDKDLAK.K
R3/RRR3-4/2	1424.916	1425.569	-1163.913	0.487	1468.587	0.493	20	0.216	R.LWGENFFDPATK.K
R3/RRR3-4/2	1388.075	1388.586	-1091.868	0.411	1594.691	0.429	17	0.216	R.GFVQFCYEPIK.Q
R3/RRR3-4/2	1347.252	1347.588	-249.881	0.442	1319.416	0.563	19	0.214	R.VIYASQLTAKPR.L
R3/RRR3-4/2	1424.501	1425.569	-1456.655	0.449	1476.834	0.475	20	0.213	R.LWGENFFDPATK.K
R3/RRR3-4/2	1347.250	1347.588	-251.881	0.473	1277.925	0.570	18	0.211	R.VIYASQLTAKPR.L
R3/RRR3-4/2	1624.068	1623.846	137.312	0.578	1274.489	0.562	22	0.210	R.NCDPEGPLMLYVSK.M
R3/RRR3-5/2	1425.251	1425.569	-224.093	0.516	1440.541	0.471	20	0.209	R.LWGENFFDPATK.K
R3/RRR3-5/2	1425.237	1425.569	-234.061	0.446	1441.438	0.459	20	0.206	R.LWGENFFDPATK.K
R3/RRR3-5/3	1815.517	1815.062	251.768	0.501	1703.571	0.503	31	0.206	K.AYLPVIESFGFSSQLR.A
R3/RRR3-5/2	1426.156	1425.569	-290.915	0.543	1357.537	0.492	20	0.205	R.LWGENFFDPATK.K
R3/RRR3-5/2	1388.050	1388.586	-1109.794	0.412	1676.194	0.332	16	0.204	R.GFVQFCYEPIK.Q
R3/RRR3-4/2	1650.814	1651.841	-1231.669	0.468	1674.727	0.333	20	0.202	K.ILSEEFGWDKDLAK.K
R3/RRR3-4/2	1652.310	1651.841	284.722	0.513	1642.804	0.355	19	0.201	K.ILSEEFGWDKDLAK.K
R3/RRR3-4/2	1347.254	1347.588	-248.699	0.503	1140.555	0.586	17	0.201	R.VIYASQLTAKPR.L
R3/RRR3-4/2	1387.439	1388.586	-1552.044	0.349	1358.592	0.433	16	0.190	R.GFVQFCYEPIK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1426.544	1425.569	-17.733	0.392	1348.171	0.433	18	0.190	R.LWGENFFDPATK.K
R3/RRR3-3/3	1820.032	1819.945	47.782	0.484	1561.719	0.519	33	0.189	K.NATLTNEKESDACPIR.A
R3/RRR3-2/2	1347.378	1347.588	-156.443	0.454	1105.964	0.538	17	0.188	R.VIYASQLTAKPR.L
R3/RRR3-4/2	1651.331	1651.841	-917.060	0.502	1484.217	0.367	18	0.187	K.ILSEEFGWDKDLAK.K
R3/RRR3-2/2	1651.341	1651.841	-303.664	0.474	1515.686	0.331	18	0.183	K.ILSEEFGWDKDLAK.K
R3/RRR3-4/3	1819.763	1819.945	-100.365	0.434	1579.277	0.478	33	0.180	K.NATLTNEKESDACPIR.A
R3/RRR3-1/3	1819.312	1819.945	-900.230	0.477	1438.569	0.533	31	0.180	K.NATLTNEKESDACPIR.A
R3/RRR3-1/2	1625.140	1623.846	181.145	0.534	1093.393	0.490	20	0.179	R.NCDPEGPLMLYVSK.M
R3/RRR3-4/2	1624.288	1623.846	273.201	0.564	1096.170	0.481	21	0.179	R.NCDPEGPLMLYVSK.M
R3/RRR3-5/2	1652.306	1651.841	281.981	0.489	1445.392	0.333	18	0.177	K.ILSEEFGWDKDLAK.K
R3/RRR3-5/2	1650.798	1651.841	-1241.100	0.460	1513.506	0.295	18	0.177	K.ILSEEFGWDKDLAK.K
R3/RRR3-3/2	1651.672	1651.841	-102.565	0.496	1378.978	0.357	18	0.176	K.ILSEEFGWDKDLAK.K
R3/RRR3-4/3	1819.892	1819.945	-29.516	0.475	1433.237	0.515	33	0.172	K.NATLTNEKESDACPIR.A
R3/RRR3-3/2	1347.272	1347.588	-235.155	0.432	789.227	0.576	15	0.171	R.VIYASQLTAKPR.L
R3/RRR3-2/2	1425.346	1425.569	-156.905	0.392	1148.533	0.410	17	0.170	R.LWGENFFDPATK.K
R3/RRR3-5/2	1639.012	1639.845	-1121.845	0.471	1120.681	0.407	21	0.169	R.NCDPEGPLM*LYVSK.M
R3/RRR3-5/2	1639.498	1639.845	-212.367	0.481	1179.637	0.384	21	0.169	R.NCDPEGPLM*LYVSK.M
R3/RRR3-4/2	1120.947	1120.219	-243.641	0.479	937.963	0.471	16	0.169	K.EGALAEENMR.G
R3/RRR3-4/3	1814.312	1815.062	-966.955	0.403	1443.527	0.485	29	0.168	K.AYLPVIESFGFSSQLR.A
R3/RRR3-1/2	1425.546	1425.569	-16.199	0.422	929.800	0.481	15	0.165	R.LWGENFFDPATK.K
R3/RRR3-2/2	1348.425	1347.588	-120.819	0.418	824.361	0.518	15	0.165	R.VIYASQLTAKPR.L
R3/RRR3-4/2	1640.605	1639.845	-146.774	0.542	980.236	0.430	20	0.162	R.NCDPEGPLM*LYVSK.M
R3/RRR3-4/2	1553.227	1553.742	-978.767	0.408	895.133	0.439	18	0.159	R.LWGENFFDPATKK.W
R3/RRR3-4/2	1553.283	1553.742	-296.349	0.403	955.507	0.413	18	0.159	R.LWGENFFDPATKK.W
R3/RRR3-4/2	1867.713	1868.098	-206.858	0.520	1059.767	0.570	20	0.159	K.GLKEQM*TPLSDFEDKL.-
R3/RRR3-4/2	1639.023	1639.845	-1115.339	0.480	1020.692	0.383	20	0.158	R.NCDPEGPLM*LYVSK.M
R3/RRR3-4/2	1640.059	1639.845	130.292	0.494	973.406	0.387	20	0.157	R.NCDPEGPLM*LYVSK.M
R3/RRR3-5/2	1639.390	1639.845	-278.476	0.456	1024.227	0.365	20	0.156	R.NCDPEGPLM*LYVSK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1425.608	1425.569	26.915	0.470	835.395	0.439	15	0.156	R.LWGENFFDPATK.K
R3/RRR3-4/2	1119.252	1120.219	-1762.252	0.331	1072.876	0.335	16	0.155	K.EGALAEENMR.G
R3/RRR3-1/2	1553.134	1553.742	-1038.659	0.406	915.511	0.392	18	0.154	R.LWGENFFDPATKK.W
R3/RRR3-3/2	891.018	891.049	-35.880	0.364	824.964	0.400	13	0.154	K.FSVSPVVR.V
R3/RRR3-13/2	955.886	956.081	-205.145	0.391	920.650	0.353	16	0.152	R.GGGQVIPTAR.R
R3/RRR3-3/3	1820.646	1819.945	-164.808	0.453	1432.031	0.427	32	0.150	K.NATLTNEKESDACPIR.A
R3/RRR3-3/2	890.884	891.049	-186.236	0.363	669.589	0.403	12	0.150	K.FSVSPVVR.V
R3/RRR3-1/2	1820.414	1819.945	258.295	0.476	501.368	0.510	17	0.149	K.NATLTNEKESDACPIR.A
R3/RRR3-5/2	891.000	891.049	-55.806	0.347	629.014	0.391	12	0.148	K.FSVSPVVR.V
R3/RRR3-5/2	1346.810	1347.588	-1323.865	0.366	650.381	0.451	13	0.148	R.VIYASQLTAKPR.L
R3/RRR3-4/2	1553.860	1553.742	75.910	0.402	926.891	0.326	18	0.147	R.LWGENFFDPATKK.W
R3/RRR3-1/2	1425.139	1425.569	-302.806	0.305	616.254	0.444	14	0.146	R.LWGENFFDPATK.K
R3/RRR3-13/2	1348.320	1347.588	-199.376	0.322	695.954	0.401	15	0.146	R.VIYASQLTAKPR.L
R3/RRR3-5/2	1387.985	1388.586	-1156.509	0.357	941.151	0.316	14	0.146	R.GFVQFCYEPIK.Q
R3/RRR3-5/2	1553.420	1553.742	-207.811	0.435	674.317	0.394	16	0.145	R.LWGENFFDPATKK.W
R3/RRR3-1/2	890.738	891.049	-350.526	0.323	511.147	0.403	10	0.144	K.FSVSPVVR.V
R3/RRR3-1/2	1652.474	1651.841	-222.917	0.471	840.339	0.375	15	0.144	K.ILSEEFGWDKDLAK.K
R3/RRR3-5/2	1553.045	1553.742	-1095.874	0.451	686.313	0.369	17	0.144	R.LWGENFFDPATKK.W
R3/RRR3-8/2	744.692	744.863	-229.620	0.334	353.170	0.397	9	0.144	-.FFAFGR.-
R3/RRR3-8/2	744.798	744.863	-87.391	0.340	340.255	0.378	9	0.144	-.FFAFGR.-
R3/RRR3-4/2	744.878	744.863	20.446	0.409	289.668	0.438	8	0.143	-.FFAFGR.-
R3/RRR3-5/2	890.519	891.049	-1723.163	0.303	443.866	0.389	10	0.143	K.FSVSPVVR.V
R3/RRR3-4/2	890.918	891.049	-147.887	0.318	459.945	0.373	10	0.143	K.FSVSPVVR.V
R3/RRR3-13/2	955.465	956.081	-1696.696	0.353	619.745	0.342	14	0.142	R.GGGQVIPTAR.R
R3/RRR3-5/2	744.787	744.863	-102.681	0.324	349.678	0.329	9	0.142	-.FFAFGR.-
R3/RRR3-1/2	956.059	956.081	-23.898	0.373	671.158	0.329	14	0.142	R.GGGQVIPTAR.R
R3/RRR3-7/2	890.692	891.049	-402.780	0.310	484.309	0.354	10	0.142	K.FSVSPVVR.V
R3/RRR3-4/2	744.382	744.863	-647.167	0.289	406.263	0.388	10	0.142	-.FFAFGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1819.942	1819.945	-1.562	0.408	1439.463	0.375	29	0.142	K.NATLTNEKESDACPIR.A
R3/RRR3-4/2	1426.037	1425.569	328.783	0.336	569.236	0.389	13	0.141	R.LWGENFFDPATK.K
R3/RRR3-5/2	890.930	891.049	-134.142	0.333	510.741	0.363	11	0.141	-.FSVSPVVR.-
R3/RRR3-8/2	744.778	744.863	-114.025	0.371	288.852	0.398	8	0.141	-.FFAFGR.-
R3/RRR3-4/2	1554.520	1553.742	-143.237	0.402	631.307	0.366	15	0.141	R.LWGENFFDPATKK.W
R3/RRR3-5/2	1119.542	1120.219	-1502.004	0.369	703.910	0.357	13	0.141	-.EGALAEENMR.-
R3/RRR3-3/2	890.336	891.049	-1930.207	0.261	492.548	0.370	10	0.141	K.FSVSPVVR.V
R3/RRR3-2/2	1424.999	1425.569	-1105.333	0.314	601.092	0.376	13	0.140	R.LWGENFFDPATK.K
R3/RRR3-6/2	891.026	891.049	-26.123	0.279	541.033	0.325	11	0.140	K.FSVSPVVR.V
R3/RRR3-1/2	890.476	891.049	-1772.334	0.279	456.008	0.408	10	0.140	-.FSVSPVVR.-
R3/RRR3-1/3	1819.843	1819.945	-56.462	0.420	1150.009	0.483	29	0.140	K.NATLTNEKESDACPIR.A
R3/RRR3-3/2	1425.344	1425.569	-158.795	0.388	536.685	0.359	13	0.140	R.LWGENFFDPATK.K
R3/RRR3-4/2	842.023	841.930	110.712	0.364	707.505	0.334	10	0.140	-.FGVDEFK.-
R3/RRR3-23/2	1814.861	1815.062	-110.816	0.315	263.345	0.356	15	0.140	K.AYLPVIESFGFSSQLR.A
R3/RRR3-13/2	1348.076	1347.588	363.328	0.253	570.069	0.381	15	0.140	R.VIYASQLTAKPR.L
R3/RRR3-5/2	955.411	956.081	-1753.820	0.338	689.878	0.301	14	0.140	R.GGGQVIPTAR.R
R3/RRR3-1/2	890.594	891.049	-512.668	0.271	499.535	0.327	10	0.139	K.FSVSPVVR.V
R3/RRR3-11/2	1426.063	1425.569	346.893	0.303	323.825	0.335	12	0.139	R.LWGENFFDPATK.K
R3/RRR3-1/2	1389.062	1388.586	343.970	0.381	600.410	0.336	13	0.139	R.GFVQFCYEPIK.Q
R3/RRR3-8/2	891.124	891.049	83.934	0.312	457.721	0.340	10	0.139	-.FSVSPVVR.-
R3/RRR3-7/2	891.893	891.049	-175.455	0.286	708.574	0.295	12	0.139	-.FSVSPVVR.-
R3/RRR3-8/2	891.048	891.049	-1.114	0.308	536.457	0.317	11	0.139	-.FSVSPVVR.-
R3/RRR3-3/2	744.282	744.863	-2130.907	0.197	350.933	0.311	9	0.139	R.FFAFGR.V
R3/RRR3-1/2	956.663	956.081	-438.932	0.378	546.350	0.297	13	0.138	R.GGGQVIPTAR.R
R3/RRR3-1/2	956.895	956.081	-195.205	0.432	634.658	0.283	14	0.138	R.GGGQVIPTAR.R
R3/RRR3-13/2	955.483	956.081	-1678.213	0.290	590.165	0.293	14	0.138	R.GGGQVIPTAR.R
R3/RRR3-2/2	744.175	744.863	-2275.339	0.214	340.753	0.262	9	0.137	-.FFAFGR.-
R3/RRR3-13/2	1348.359	1347.588	-170.586	0.278	426.552	0.328	13	0.137	R.VIYASQLTAKPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	842.075	841.930	171.627	0.289	642.517	0.287	10	0.137	-.FGVDEFK.-
R3/RRR3-5/2	1553.260	1553.742	-311.488	0.313	771.553	0.258	17	0.136	R.LWGENFFDPATKK.W
R3/RRR3-4/2	842.733	841.930	-235.305	0.280	707.285	0.241	10	0.136	K.FGVDEFK.M
R3/RRR3-4/2	744.349	744.863	-2039.258	0.228	356.938	0.359	9	0.134	-.FFAFGR.-
R3/RRR3-11/2	955.926	956.081	-162.742	0.390	526.665	0.245	13	0.134	-.GGGQVIPTAR.-
R3/RRR3-2/2	744.308	744.863	-2095.136	0.193	288.530	0.292	8	0.134	-.FFAFGR.-
R3/RRR3-5/2	744.305	744.863	-2099.586	0.173	348.133	0.340	9	0.134	-.FFAFGR.-
R3/RRR3-2/2	1624.559	1623.846	-177.382	0.330	746.141	0.256	16	0.134	-.NCDPEGPLMLYVSK.-
R3/RRR3-7/2	890.478	891.049	-1770.130	0.236	678.686	0.286	10	0.134	-.FSVSPVVR.-
R3/RRR3-3/2	1388.948	1388.586	261.841	0.365	534.524	0.296	12	0.132	-.GFVQFCYEPIK.-
R3/RRR3-2/2	744.777	744.863	-115.669	0.120	336.753	0.281	9	0.131	-.FFAFGR.-
R3/RRR3-5/2	1347.386	1347.588	-150.627	0.196	582.394	0.167	14	0.131	R.VIYASQLTAKPR.L
R3/RRR3-2/3	1819.611	1819.945	-183.944	0.404	1004.204	0.487	28	0.131	K.NATLTNEKESDACPIR.A
R3/RRR3-2/2	842.080	841.930	178.605	0.191	698.188	0.203	10	0.128	-.FGVDEFK.-
R3/RRR3-1/2	842.273	841.930	407.513	0.211	612.379	0.276	9	0.128	-.FGVDEFK.-
R3/RRR3-8/2	891.109	891.049	67.447	0.290	389.293	0.382	9	0.127	-.FSVSPVVR.-
R3/RRR3-3/3	1820.249	1819.945	167.539	0.385	1203.097	0.396	30	0.126	K.NATLTNEKESDACPIR.A
R3/RRR3-1/2	841.987	841.930	67.819	0.226	737.535	0.183	10	0.125	-.FGVDEFK.-
R3/RRR3-6/3	1502.563	1503.774	-1476.162	0.469	1226.990	0.388	25	0.124	R.RVIYASQLTAKPR.L
R3/RRR3-2/2	841.871	841.930	-71.351	0.158	590.019	0.143	9	0.123	-.FGVDEFK.-
R3/RRR3-3/2	841.946	841.930	18.380	0.161	507.265	0.131	8	0.118	-.FGVDEFK.-
R3/RRR3-5/3	1502.864	1503.774	-1274.719	0.435	1173.482	0.358	25	0.115	R.RVIYASQLTAKPR.L
R3/RRR3-5/3	1815.495	1815.062	239.228	0.373	1050.857	0.384	25	0.114	K.AYLPVIESFGFSSQLR.A
R3/RRR3-2/3	1819.848	1819.945	-53.737	0.403	846.524	0.427	27	0.113	K.NATLTNEKESDACPIR.A
R3/RRR3-5/3	1502.756	1503.774	-1347.283	0.439	1288.332	0.305	25	0.113	-.RVIYASQLTAKPR.-
R3/RRR3-8/3	1819.210	1819.945	-956.915	0.434	771.883	0.437	24	0.112	K.NATLTNEKESDACPIR.A
R3/RRR3-1/3	1504.524	1503.774	-167.007	0.451	1042.414	0.376	24	0.112	R.RVIYASQLTAKPR.L
R3/RRR3-4/2	1851.727	1852.099	-201.112	0.498	926.025	0.485	18	0.110	K.GLKEQMTPLSDFEDKL.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1503.237	1503.774	-1025.415	0.450	1040.143	0.362	24	0.109	R.RVIYASQLTAKPR.L
R3/RRR3-3/3	1503.638	1503.774	-90.850	0.490	789.315	0.411	22	0.108	R.RVIYASQLTAKPR.L
R3/RRR3-4/3	1421.271	1421.624	-249.540	0.427	780.502	0.424	20	0.108	K.FGVDEFKM*M*ER.L
R3/RRR3-5/3	1818.169	1819.945	-2083.161	0.332	827.407	0.386	25	0.107	K.NATLTNEKESDACPIR.A
R3/RRR3-3/3	1503.975	1503.774	133.614	0.416	756.904	0.394	22	0.105	R.RVIYASQLTAKPR.L
R3/RRR3-5/3	1503.518	1503.774	-170.987	0.458	926.667	0.341	22	0.102	R.RVIYASQLTAKPR.L
R3/RRR3-6/3	1820.024	1819.945	43.241	0.296	625.811	0.351	24	0.100	K.NATLTNEKESDACPIR.A
R3/RRR3-1/3	1504.156	1503.774	254.231	0.428	720.797	0.348	22	0.099	R.RVIYASQLTAKPR.L
R3/RRR3-6/3	1502.480	1503.774	-1531.371	0.411	943.442	0.309	23	0.098	R.RVIYASQLTAKPR.L
R3/RRR3-4/3	1421.392	1421.624	-163.983	0.351	791.484	0.331	21	0.096	K.FGVDEFKM*M*ER.L
R3/RRR3-5/3	1421.456	1421.624	-118.755	0.384	592.600	0.318	18	0.095	K.FGVDEFKM*M*ER.L
R3/RRR3-4/3	1421.418	1421.624	-145.633	0.422	656.808	0.293	19	0.093	K.FGVDEFKM*M*ER.L
R3/RRR3-5/3	1814.247	1815.062	-1003.129	0.332	658.554	0.293	22	0.092	K.AYLPVIESFGFSSQLR.A
R3/RRR3-2/3	1814.457	1815.062	-886.916	0.323	709.084	0.295	21	0.092	-.AYLPVIESFGFSSQLR.-
R3/RRR3-5/3	1420.986	1421.624	-1156.672	0.301	644.958	0.282	19	0.091	K.FGVDEFKM*M*ER.L
R3/RRR3-4/3	1814.390	1815.062	-923.793	0.304	587.278	0.215	21	0.077	-.AYLPVIESFGFSSQLR.-
R3/RRR3-5/2	1970.735	1971.200	-236.681	0.660	3511.501	0.669	27	0.740	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/2	1970.755	1971.200	-226.179	0.645	3277.786	0.661	27	0.660	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/2	1970.324	1971.200	-954.761	0.604	3245.317	0.667	26	0.654	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/3	1961.933	1961.210	-141.644	0.596	2730.959	0.534	37	0.427	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1969.318	1969.312	2.946	0.656	2310.606	0.510	25	0.344	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/3	1961.615	1961.210	206.927	0.574	2415.068	0.510	35	0.340	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/3	1970.940	1971.200	-131.989	0.581	2284.970	0.567	37	0.331	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/2	1969.576	1969.312	134.733	0.638	2183.166	0.477	24	0.309	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/2	1969.964	1969.312	-177.170	0.604	2144.177	0.460	24	0.298	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/3	1960.614	1961.210	-816.272	0.547	2101.901	0.524	33	0.283	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/3	1972.084	1971.200	-58.839	0.611	1959.583	0.608	36	0.282	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/3	1971.350	1971.200	76.628	0.585	1944.463	0.565	35	0.264	R.HQLLAEFDALIEADKEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/3	1970.564	1971.200	-832.437	0.576	1765.188	0.608	34	0.250	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/3	1971.013	1971.200	-95.086	0.585	1769.614	0.563	33	0.235	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-2/3	1961.337	1961.210	65.283	0.495	1777.264	0.533	31	0.231	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1840.341	1841.009	-908.963	0.549	1381.272	0.571	22	0.220	R.DLANLVIVCGDHGNQSK.D
R3/RRR3-5/2	1840.251	1841.009	-958.375	0.547	1342.813	0.555	21	0.212	R.DLANLVIVCGDHGNQSK.D
R3/RRR3-2/3	1961.572	1961.210	185.023	0.507	1570.361	0.568	30	0.212	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1840.399	1841.009	-877.600	0.548	1205.552	0.583	20	0.203	R.DLANLVIVCGDHGNQSK.D
R3/RRR3-1/3	1970.751	1971.200	-228.361	0.542	1600.766	0.530	32	0.200	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/2	1541.419	1541.768	-226.824	0.493	1604.063	0.359	19	0.199	K.LGVTQCTIAHALEK.T
R3/RRR3-5/2	1240.688	1241.462	-1434.339	0.489	1466.405	0.400	18	0.197	R.IKQQGLDITPK.I
R3/RRR3-5/2	1241.254	1241.462	-167.944	0.491	1510.423	0.379	18	0.197	R.IKQQGLDITPK.I
R3/RRR3-5/2	1254.089	1254.418	-263.270	0.545	1171.052	0.494	19	0.190	K.VIGTEHTDILR.V
R3/RRR3-5/3	1970.714	1971.200	-247.097	0.554	1567.122	0.502	30	0.188	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-2/2	1241.139	1241.462	-260.887	0.510	1293.818	0.406	17	0.182	R.IKQQGLDITPK.I
R3/RRR3-5/2	1389.105	1388.546	-317.889	0.429	961.370	0.545	21	0.180	R.LLPDAVGTTCGQR.V
R3/RRR3-5/2	1969.108	1969.312	-103.814	0.427	1332.602	0.382	21	0.178	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/3	1961.168	1961.210	-21.334	0.473	1425.244	0.514	29	0.177	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/3	1969.413	1969.312	51.369	0.447	1781.126	0.358	32	0.172	K.LFQDKESLYPLLNFLK.A
R3/RRR3-4/2	1960.692	1961.210	-776.674	0.452	845.570	0.569	20	0.171	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1541.362	1541.768	-264.008	0.471	1324.057	0.311	18	0.164	K.LGVTQCTIAHALEK.T
R3/RRR3-4/3	1961.273	1961.210	32.417	0.481	1274.889	0.526	28	0.164	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-4/3	1961.450	1961.210	123.050	0.511	1190.530	0.557	28	0.162	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-2/2	1388.284	1388.546	-189.227	0.471	681.165	0.511	20	0.162	R.LLPDAVGTTCGQR.V
R3/RRR3-5/2	1241.254	1241.462	-167.944	0.455	1272.746	0.297	17	0.162	R.IKQQGLDITPK.I
R3/RRR3-2/2	1388.123	1388.546	-305.501	0.419	743.301	0.490	21	0.162	R.LLPDAVGTTCGQR.V
R3/RRR3-5/2	1540.320	1541.768	-1594.016	0.383	1345.317	0.273	17	0.161	K.LGVTQCTIAHALEK.T
R3/RRR3-1/2	1388.139	1388.546	-293.590	0.406	612.936	0.513	20	0.158	R.LLPDAVGTTCGQR.V
R3/RRR3-5/2	1274.992	1275.477	-382.013	0.438	845.560	0.437	16	0.158	K.NM*TGLVEM*YGK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1540.418	1541.768	-1530.090	0.368	1379.649	0.233	17	0.157	K.LGVTQCTIAHALEK.T
R3/RRR3-2/2	1254.008	1254.418	-327.629	0.447	860.747	0.412	18	0.157	K.VIGTEHTDILR.V
R3/RRR3-5/3	1960.403	1961.210	-924.376	0.460	1222.539	0.517	26	0.157	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/3	1969.905	1969.312	-207.296	0.380	1873.630	0.242	29	0.155	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/2	1253.648	1254.418	-1415.604	0.449	889.541	0.394	17	0.155	K.VIGTEHTDILR.V
R3/RRR3-6/2	1967.748	1969.312	-1816.724	0.389	825.432	0.465	17	0.154	K.LFQDKESLYPLLNFLK.A
R3/RRR3-1/2	1387.832	1388.546	-1238.065	0.370	663.466	0.470	19	0.154	R.LLPDAVGTTCGQR.V
R3/RRR3-5/2	1541.511	1541.768	-166.923	0.465	1104.124	0.341	16	0.153	K.LGVTQCTIAHALEK.T
R3/RRR3-5/2	1254.065	1254.418	-282.508	0.453	911.807	0.358	18	0.153	K.VIGTEHTDILR.V
R3/RRR3-5/2	1961.072	1961.210	-70.338	0.441	613.670	0.512	19	0.152	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/3	1457.507	1457.610	-70.834	0.492	1560.442	0.395	26	0.152	K.TKYPNSDIYLDK.F
R3/RRR3-5/2	1388.019	1388.546	-1102.938	0.383	606.534	0.448	20	0.152	R.LLPDAVGTTCGQR.V
R3/RRR3-4/2	1388.098	1388.546	-323.412	0.376	677.032	0.410	20	0.150	R.LLPDAVGTTCGQR.V
R3/RRR3-5/2	1259.275	1259.478	-161.690	0.402	591.133	0.444	15	0.150	K.NM*TGLVEMYGK.N
R3/RRR3-2/2	1961.701	1961.210	251.238	0.412	618.406	0.460	19	0.147	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1337.195	1337.588	-295.344	0.376	560.266	0.442	16	0.146	K.ESLYPLLNFLK.A
R3/RRR3-4/2	1960.348	1961.210	-952.750	0.366	641.692	0.446	19	0.146	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1259.381	1259.478	-77.096	0.383	472.639	0.408	15	0.145	K.NM*TGLVEMYGK.N
R3/RRR3-5/2	1275.053	1275.477	-333.598	0.435	518.730	0.386	14	0.144	K.NM*TGLVEM*YGK.N
R3/RRR3-5/2	1336.819	1337.588	-1327.715	0.373	590.990	0.377	17	0.143	K.ESLYPLLNFLK.A
R3/RRR3-4/3	1961.193	1961.210	-8.598	0.494	1069.299	0.518	27	0.142	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-1/2	1970.483	1969.312	87.324	0.366	696.920	0.375	18	0.142	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/3	1969.202	1969.312	-56.158	0.448	1435.918	0.384	29	0.142	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/2	1960.770	1961.210	-224.896	0.320	231.926	0.527	14	0.141	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1389.371	1388.546	-126.335	0.283	242.641	0.405	17	0.140	-.LLPDAVGTTCGQR.-
R3/RRR3-5/3	1961.712	1961.210	-254.285	0.508	1031.653	0.521	27	0.140	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-1/2	1960.342	1961.210	-955.563	0.356	401.616	0.442	16	0.140	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1970.060	1969.312	-128.188	0.408	745.612	0.323	18	0.138	K.LFQDKESLYPLLNFLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1274.979	1275.477	-392.004	0.365	383.636	0.261	13	0.137	K.NM*TGLVEM*YGK.N
R3/RRR3-6/2	1960.568	1961.210	-840.172	0.336	303.758	0.422	14	0.137	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-12/2	1962.661	1961.210	230.716	0.265	347.438	0.425	16	0.137	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1389.524	1388.546	-15.297	0.202	290.509	0.358	18	0.136	-.LLPDAVGTTCGQR.-
R3/RRR3-5/2	1106.023	1105.291	-242.653	0.435	724.407	0.314	12	0.135	-.ALENEM*LLR.-
R3/RRR3-12/2	1960.653	1961.210	-796.485	0.267	512.636	0.359	16	0.134	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-5/2	1242.406	1243.479	-1673.601	0.266	576.080	0.231	15	0.134	K.NMTGLVEMYGK.N
R3/RRR3-3/2	1961.734	1961.210	-243.072	0.296	232.936	0.373	13	0.134	-.LGATFSSHPNELIALFSR.-
R3/RRR3-5/3	1969.141	1969.312	-87.125	0.411	1451.463	0.337	30	0.132	K.LFQDKESLYPLLNFLK.A
R3/RRR3-4/2	1968.588	1969.312	-878.482	0.248	523.942	0.238	17	0.132	K.LFQDKESLYPLLNFLK.A
R3/RRR3-1/3	1970.479	1971.200	-875.999	0.448	883.287	0.515	26	0.128	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-2/3	1970.124	1971.200	-1057.003	0.447	948.812	0.455	28	0.121	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-5/3	1457.237	1457.610	-256.615	0.448	1332.276	0.334	24	0.119	K.TKYPNSDIYLDK.F
R3/RRR3-5/3	1960.852	1961.210	-182.902	0.393	872.708	0.457	22	0.119	-.LGATFSSHPNELIALFSR.-
R3/RRR3-5/3	1968.433	1969.312	-957.116	0.357	1270.128	0.332	28	0.118	K.LFQDKESLYPLLNFLK.A
R3/RRR3-2/3	1971.344	1971.200	73.367	0.464	813.245	0.447	25	0.113	R.HQLLAEFDALIEADKEK.Y
R3/RRR3-4/2	1244.214	1243.479	-213.303	0.356	272.748	0.356	10	0.108	-.NMTGLVEMYGK.-
R3/RRR3-5/3	1960.108	1961.210	-1075.553	0.444	675.336	0.410	23	0.104	R.LGATFSSHPNELIALFSR.Y
R3/RRR3-1/3	1241.629	1241.462	134.925	0.516	1262.636	0.269	24	0.101	R.IKQQGLDITPK.I
R3/RRR3-3/3	1241.853	1241.462	315.620	0.554	1252.028	0.270	23	0.100	R.IKQQGLDITPK.I
R3/RRR3-5/3	1241.709	1241.462	199.108	0.498	1133.880	0.288	22	0.100	R.IKQQGLDITPK.I
R3/RRR3-5/3	1457.277	1457.610	-228.756	0.423	755.008	0.348	19	0.097	K.TKYPNSDIYLDK.F
R3/RRR3-5/3	1961.488	1961.210	142.336	0.361	772.953	0.296	22	0.095	-.LGATFSSHPNELIALFSR.-
R3/RRR3-5/3	1241.894	1241.462	348.587	0.508	1223.374	0.239	25	0.094	R.IKQQGLDITPK.I
R3/RRR3-5/3	1241.613	1241.462	121.467	0.484	976.881	0.270	22	0.094	R.IKQQGLDITPK.I
R3/RRR3-3/3	1241.645	1241.462	147.496	0.491	945.313	0.271	22	0.093	R.IKQQGLDITPK.I
R3/RRR3-1/3	1241.729	1241.462	215.817	0.519	1295.748	0.209	24	0.092	R.IKQQGLDITPK.I
R3/RRR3-5/3	1242.166	1241.462	-239.244	0.479	1035.403	0.239	22	0.091	R.IKQQGLDITPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1242.064	1241.462	-321.475	0.493	1407.587	0.165	24	0.090	R.IKQQGLDITPK.I
R3/RRR3-4/3	1241.821	1241.462	290.191	0.443	890.923	0.237	21	0.090	R.IKQQGLDITPK.I
R3/RRR3-3/3	1242.153	1241.462	-249.596	0.513	880.328	0.282	21	0.089	-.IKQQGLDITPK.-
R3/RRR3-5/3	1242.080	1241.462	-308.607	0.450	1219.752	0.176	23	0.087	R.IKQQGLDITPK.I
R3/RRR3-6/3	1968.768	1969.312	-786.617	0.317	810.978	0.210	24	0.086	K.LFQDKESLYPLLNFLK.A
R3/RRR3-5/3	1969.245	1969.312	-34.147	0.267	665.059	0.186	19	0.086	-.LFQDKESLYPLLNFLK.-
R3/RRR3-2/3	1241.667	1241.462	165.687	0.393	1096.299	0.169	22	0.085	-.IKQQGLDITPK.-
R3/RRR3-4/3	1241.480	1241.462	14.525	0.476	832.127	0.245	21	0.084	-.IKQQGLDITPK.-
R3/RRR3-4/3	1241.675	1241.462	171.750	0.432	873.708	0.204	21	0.084	-.IKQQGLDITPK.-
R3/RRR3-4/3	1969.410	1969.312	49.877	0.322	867.696	0.142	26	0.082	-.LFQDKESLYPLLNFLK.-
R3/RRR3-2/2	1592.227	1592.644	-262.879	0.548	2565.773	0.526	22	0.412	R.TQDLENELSTANEK.F
R3/RRR3-2/2	1592.331	1592.644	-197.427	0.542	2475.211	0.533	22	0.394	R.TQDLENELSTANEK.F
R3/RRR3-2/2	1612.281	1611.732	-280.341	0.572	2395.535	0.558	21	0.388	K.VSQLSDELEAYQTK.A
R3/RRR3-2/2	1592.225	1592.644	-263.956	0.545	2391.101	0.552	22	0.383	R.TQDLENELSTANEK.F
R3/RRR3-2/2	1203.189	1203.328	-115.661	0.533	1818.531	0.375	18	0.232	K.TAALEEQALTR.E
R3/RRR3-2/2	1507.398	1507.625	-150.963	0.509	1550.315	0.506	20	0.228	K.INELQASLDSTTSK.N
R3/RRR3-2/2	1162.197	1162.315	-101.832	0.449	1569.955	0.470	17	0.223	R.TSLEASLLEAK.Q
R3/RRR3-2/2	1160.842	1161.248	-350.654	0.424	1632.657	0.403	18	0.217	R.GLELQSAAESR.S
R3/RRR3-2/2	1202.636	1203.328	-1410.697	0.424	1737.521	0.342	18	0.216	K.TAALEEQALTR.E
R3/RRR3-2/2	1388.248	1388.509	-188.703	0.468	1495.909	0.458	18	0.212	R.TIANQEEQISVR.E
R3/RRR3-2/2	1388.153	1388.509	-257.072	0.435	1544.451	0.414	19	0.209	R.TIANQEEQISVR.E
R3/RRR3-2/2	1357.014	1357.535	-1123.807	0.472	1399.701	0.419	19	0.194	R.SLELESLLHTSK.S
R3/RRR3-2/2	1202.908	1203.328	-349.689	0.412	1673.777	0.255	18	0.190	K.TAALEEQALTR.E
R3/RRR3-2/2	1162.054	1162.315	-225.750	0.367	1123.168	0.518	16	0.184	R.TSLEASLLEAK.Q
R3/RRR3-2/2	1101.949	1101.318	-336.506	0.511	935.923	0.515	16	0.175	K.VLALEESLVK.L
R3/RRR3-2/2	1425.009	1425.529	-1069.840	0.444	1062.675	0.462	17	0.171	K.AIDHQQVEESLR.S
R3/RRR3-3/2	1161.749	1162.315	-1352.532	0.359	891.688	0.408	15	0.153	R.TSLEASLLEAK.Q
R3/RRR3-2/2	1543.411	1543.701	-188.612	0.444	577.123	0.508	17	0.151	K.VVEEEKASPIEQGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1544.252	1543.701	-291.422	0.460	421.364	0.512	17	0.149	K.VVEEEKASPIEQGK.T
R3/RRR3-2/2	1073.978	1074.253	-257.146	0.327	749.268	0.323	13	0.138	K.LALVNTEVSK.L
R3/RRR3-2/2	1010.197	1010.123	74.283	0.367	906.884	0.226	12	0.135	-.YNITLEEK.-
R3/RRR3-2/2	1160.401	1161.248	-1595.937	0.261	446.900	0.324	14	0.133	R.GLELQSAAESR.S
R3/RRR3-2/2	1101.362	1101.318	39.619	0.256	336.731	0.323	11	0.130	-.VLALEESLVK.-
R3/RRR3-2/2	1075.020	1074.253	-217.034	0.351	461.577	0.270	11	0.119	-.LALVNTEVSK.-
R3/RRR3-10/3	1318.006	1318.502	-377.500	0.455	1119.057	0.402	27	0.117	K.RTSLEASLLEAK.Q
R3/RRR3-2/3	1322.452	1322.452	0.026	0.519	603.137	0.486	19	0.112	K.TIEHLTEVHSR.G
R3/RRR3-1/3	1317.379	1318.502	-1616.238	0.373	1109.373	0.351	27	0.107	K.RTSLEASLLEAK.Q
R3/RRR3-3/3	1528.088	1527.660	281.137	0.467	1083.069	0.342	24	0.106	K.FKEVEADLEQYR.S
R3/RRR3-2/3	1588.432	1588.707	-173.409	0.489	1016.554	0.351	25	0.105	R.QNLHYTSLQEAQR.S
R3/RRR3-2/3	1543.870	1543.701	110.177	0.398	895.720	0.378	28	0.103	K.VVEEEKASPIEQGK.T
R3/RRR3-4/3	1317.763	1318.502	-1323.790	0.356	865.624	0.348	25	0.100	K.RTSLEASLLEAK.Q
R3/RRR3-2/3	1321.447	1322.452	-1521.852	0.409	410.463	0.462	15	0.099	-.TIEHLTEVHSR.-
R3/RRR3-2/3	1589.736	1588.707	18.583	0.517	785.623	0.337	23	0.098	R.QNLHYTSLQEAQR.S
R3/RRR3-3/3	1317.978	1318.502	-1159.843	0.358	627.138	0.331	22	0.097	K.RTSLEASLLEAK.Q
R3/RRR3-2/3	1543.678	1543.701	-14.968	0.390	616.150	0.363	24	0.097	K.VVEEEKASPIEQGK.T
R3/RRR3-8/3	1317.759	1318.502	-1326.163	0.350	606.009	0.318	21	0.097	K.RTSLEASLLEAK.Q
R3/RRR3-1/3	1317.935	1318.502	-1192.488	0.364	809.292	0.304	24	0.095	K.RTSLEASLLEAK.Q
R3/RRR3-9/3	1318.000	1318.502	-1142.963	0.351	640.842	0.278	22	0.094	K.RTSLEASLLEAK.Q
R3/RRR3-2/3	1317.888	1318.502	-1228.485	0.316	640.457	0.259	22	0.092	K.RTSLEASLLEAK.Q
R3/RRR3-3/3	1317.876	1318.502	-1237.694	0.312	646.182	0.258	21	0.091	-.RTSLEASLLEAK.-
R3/RRR3-2/3	1543.050	1543.701	-1072.750	0.319	594.796	0.271	25	0.090	K.VVEEEKASPIEQGK.T
R3/RRR3-2/3	1416.656	1416.602	37.879	0.489	1129.243	0.208	21	0.089	R.RIEELELEKEK.L
R3/RRR3-2/3	1416.333	1416.602	-190.460	0.485	1099.960	0.192	21	0.085	-.RIEELELEKEK.-
R3/RRR3-3/3	1528.217	1527.660	-291.084	0.426	794.051	0.172	20	0.081	-.FKEVEADLEQYR.-
R3/RRR3-10/3	1317.825	1318.502	-1276.205	0.441	1188.628	0.101	24	0.078	-.RTSLEASLLEAK.-
R3/RRR3-4/2	1843.652	1844.098	-242.370	0.500	2228.726	0.419	25	0.302	K.NAPSIIFIDEIDSIAPK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1844.407	1844.098	167.907	0.540	2114.270	0.472	24	0.296	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-4/2	1843.527	1844.098	-854.925	0.497	1967.033	0.482	24	0.277	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-5/2	1843.448	1844.098	-897.602	0.490	1949.321	0.442	23	0.262	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-5/2	1843.937	1844.098	-87.621	0.511	1923.530	0.431	24	0.255	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-4/2	1584.851	1584.750	64.151	0.505	1702.807	0.518	20	0.251	R.LGDVVSVHQCQDVK.Y
R3/RRR3-4/2	1843.468	1844.098	-886.699	0.503	1921.993	0.412	24	0.250	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-4/2	1843.573	1844.098	-829.734	0.480	1814.341	0.445	23	0.244	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-5/2	1843.249	1844.098	-1006.037	0.471	1796.095	0.420	23	0.235	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-5/2	1843.549	1844.098	-842.828	0.467	1852.260	0.366	23	0.229	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-5/2	1843.662	1844.098	-237.056	0.498	1606.757	0.426	22	0.212	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-4/2	1843.898	1844.098	-108.672	0.473	1497.819	0.418	22	0.199	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-2/2	1843.525	1844.098	-855.590	0.425	1461.108	0.422	22	0.197	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-1/2	1845.369	1844.098	147.517	0.500	1206.222	0.539	20	0.194	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-5/2	1800.393	1801.033	-913.763	0.475	729.216	0.455	19	0.153	R.LDQLIYIPLPDEQSR.L
R3/RRR3-5/2	1800.879	1801.033	-85.909	0.450	814.016	0.418	19	0.152	R.LDQLIYIPLPDEQSR.L
R3/RRR3-4/2	1800.488	1801.033	-860.605	0.439	605.928	0.439	18	0.147	R.LDQLIYIPLPDEQSR.L
R3/RRR3-4/2	1800.877	1801.033	-87.201	0.451	430.107	0.466	15	0.144	R.LDQLIYIPLPDEQSR.L
R3/RRR3-3/2	1801.739	1801.033	-163.812	0.467	524.544	0.430	16	0.143	R.LDQLIYIPLPDEQSR.L
R3/RRR3-5/2	1845.085	1844.098	-7.074	0.370	637.449	0.401	17	0.142	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-1/2	1801.839	1801.033	-108.355	0.444	444.825	0.392	15	0.138	R.LDQLIYIPLPDEQSR.L
R3/RRR3-5/2	1845.671	1844.098	-232.221	0.329	349.178	0.355	14	0.136	K.NAPSIIFIDEIDSIAPK.R
R3/RRR3-5/2	1584.144	1584.750	-1016.317	0.317	491.080	0.322	16	0.133	R.LGDVVSVHQCQDVK.Y
R3/RRR3-5/3	1583.999	1584.750	-1108.710	0.375	943.150	0.459	25	0.118	R.LGDVVSVHQCQDVK.Y
R3/RRR3-5/3	1584.180	1584.750	-994.044	0.370	779.267	0.435	22	0.108	R.LGDVVSVHQCQDVK.Y
R3/RRR3-4/3	1584.499	1584.750	-158.578	0.410	844.824	0.398	23	0.106	R.LGDVVSVHQCQDVK.Y
R3/RRR3-4/3	1585.650	1584.750	-62.832	0.429	822.163	0.381	23	0.103	R.LGDVVSVHQCQDVK.Y
R3/RRR3-5/3	1585.484	1584.750	-168.248	0.363	772.074	0.211	22	0.085	R.LGDVVSVHQCQDVK.Y
R3/RRR3-15/2	1367.137	1367.556	-307.657	0.540	1996.263	0.578	22	0.313	K.FDVGNVVM*VTGGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1367.209	1367.556	-254.715	0.550	1921.078	0.567	22	0.297	K.FDVGNVVM*VTGGR.N
R3/RRR3-15/2	1367.258	1367.556	-218.528	0.558	1906.862	0.570	21	0.295	K.FDVGNVVM*VTGGR.N
R3/RRR3-15/2	1351.412	1351.557	-107.324	0.542	2025.837	0.471	21	0.285	K.FDVGNVVMVTGGR.N
R3/RRR3-15/3	1885.820	1884.186	-194.497	0.542	2161.363	0.487	32	0.280	R.TDKTYPAGFMDVISIPK.T
R3/RRR3-14/3	1483.922	1483.818	70.527	0.538	1985.483	0.389	27	0.204	K.SRECLPLILIIR.N
R3/RRR3-15/2	949.081	949.129	-50.778	0.555	1168.842	0.536	15	0.198	R.LGNVFTIGK.G
R3/RRR3-15/2	949.151	949.129	23.915	0.479	1053.147	0.575	15	0.194	R.LGNVFTIGK.G
R3/RRR3-14/2	1368.713	1367.556	114.472	0.426	1401.800	0.422	20	0.194	K.FDVGNVVM*VTGGR.N
R3/RRR3-14/2	1368.687	1367.556	95.688	0.409	1323.949	0.418	20	0.186	K.FDVGNVVM*VTGGR.N
R3/RRR3-14/3	1483.445	1483.818	-252.081	0.567	1812.355	0.411	27	0.186	K.SRECLPLILIIR.N
R3/RRR3-14/2	949.083	949.129	-48.843	0.458	1031.577	0.518	15	0.183	R.LGNVFTIGK.G
R3/RRR3-15/2	949.078	949.129	-53.616	0.462	1036.076	0.510	15	0.182	R.LGNVFTIGK.G
R3/RRR3-16/2	949.397	949.129	282.994	0.479	903.231	0.529	14	0.176	R.LGNVFTIGK.G
R3/RRR3-15/2	1350.565	1351.557	-1479.013	0.412	1177.295	0.417	17	0.172	K.FDVGNVVMVTGGR.N
R3/RRR3-16/2	949.046	949.129	-87.161	0.417	1070.937	0.422	15	0.170	R.LGNVFTIGK.G
R3/RRR3-15/3	1884.108	1884.186	-41.084	0.422	1610.700	0.389	28	0.163	R.TDKTYPAGFMDVISIPK.T
R3/RRR3-16/2	949.476	949.129	367.304	0.412	892.102	0.452	14	0.163	R.LGNVFTIGK.G
R3/RRR3-15/2	1482.689	1483.818	-1440.448	0.520	1139.447	0.369	17	0.162	K.SRECLPLILIIR.N
R3/RRR3-15/2	1883.028	1884.186	-1149.092	0.428	806.617	0.526	20	0.161	R.TDKTYPAGFMDVISIPK.T
R3/RRR3-15/2	1105.013	1105.334	-291.005	0.452	1021.506	0.384	14	0.160	R.EVISILM*QR.H
R3/RRR3-15/2	1127.008	1126.333	-288.936	0.462	600.918	0.515	15	0.159	K.GNKPWVSLPK.G
R3/RRR3-15/2	1105.185	1105.334	-134.754	0.358	1166.333	0.310	15	0.158	R.EVISILM*QR.H
R3/RRR3-15/2	1483.555	1483.818	-177.818	0.535	1115.455	0.357	17	0.158	K.SRECLPLILIIR.N
R3/RRR3-14/2	1483.861	1483.818	29.159	0.498	1078.342	0.363	16	0.157	K.SRECLPLILIIR.N
R3/RRR3-15/2	1883.435	1884.186	-932.110	0.409	804.740	0.490	20	0.156	R.TDKTYPAGFMDVISIPK.T
R3/RRR3-14/2	1483.382	1483.818	-294.549	0.402	1114.904	0.324	16	0.155	K.SRECLPLILIIR.N
R3/RRR3-14/2	1368.265	1367.556	-213.267	0.383	668.141	0.500	14	0.152	K.FDVGNVVM*VTGGR.N
R3/RRR3-15/2	1539.172	1539.820	-1074.172	0.334	528.496	0.497	19	0.149	K.TYPAGFMDVISIPK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1483.537	1483.818	-189.870	0.532	992.312	0.339	16	0.148	K.SRECLPLILIIR.N
R3/RRR3-15/2	1556.183	1555.820	233.763	0.468	334.147	0.392	20	0.147	K.TYPAGFM*DVISIPK.T
R3/RRR3-15/2	987.332	988.120	-1816.475	0.438	1018.674	0.267	13	0.146	K.LSIIEEQR.K
R3/RRR3-15/2	1126.047	1126.333	-254.497	0.425	512.598	0.390	14	0.145	K.GNKPWVSLPK.G
R3/RRR3-15/2	1539.106	1539.820	-1117.494	0.325	488.046	0.431	19	0.144	K.TYPAGFMDVISIPK.T
R3/RRR3-15/2	1548.750	1548.805	-35.781	0.483	937.281	0.306	19	0.144	K.IDLETNKIVDFIK.F
R3/RRR3-15/2	987.544	988.120	-1601.227	0.459	948.459	0.259	13	0.143	K.LSIIEEQR.K
R3/RRR3-15/2	1125.468	1126.333	-1661.791	0.357	464.778	0.409	13	0.143	K.GNKPWVSLPK.G
R3/RRR3-15/2	1555.262	1555.820	-1004.743	0.341	226.431	0.384	16	0.143	K.TYPAGFM*DVISIPK.T
R3/RRR3-15/2	1105.202	1105.334	-119.464	0.396	987.206	0.248	14	0.142	R.EVISILM*QR.H
R3/RRR3-15/2	1555.084	1555.820	-1119.336	0.294	220.384	0.366	17	0.142	K.TYPAGFM*DVISIPK.T
R3/RRR3-14/2	987.309	988.120	-1840.452	0.377	1025.353	0.224	13	0.142	K.LSIIEEQR.K
R3/RRR3-14/2	987.998	988.120	-124.185	0.497	972.373	0.247	13	0.141	K.LSIIEEQR.K
R3/RRR3-1/2	1106.135	1105.334	-180.242	0.349	793.582	0.290	13	0.140	R.EVISILM*QR.H
R3/RRR3-15/2	1538.784	1539.820	-1327.625	0.296	389.832	0.375	17	0.139	K.TYPAGFMDVISIPK.T
R3/RRR3-15/2	988.175	988.120	55.247	0.459	1021.620	0.205	13	0.138	K.LSIIEEQR.K
R3/RRR3-15/2	1269.067	1269.388	-253.216	0.212	328.307	0.560	15	0.138	K.GIPYLNTYDGR.T
R3/RRR3-2/2	948.882	949.129	-260.337	0.245	863.388	0.256	14	0.138	R.LGNVFTIGK.G
R3/RRR3-14/2	1125.486	1126.333	-1645.446	0.287	456.869	0.311	14	0.137	K.GNKPWVSLPK.G
R3/RRR3-15/2	1547.578	1548.805	-1443.579	0.358	765.139	0.292	17	0.136	K.IDLETNKIVDFIK.F
R3/RRR3-14/2	988.064	988.120	-57.511	0.508	943.183	0.216	13	0.136	K.LSIIEEQR.K
R3/RRR3-14/2	1268.208	1269.388	-1724.220	0.192	226.950	0.383	15	0.135	K.GIPYLNTYDGR.T
R3/RRR3-14/2	1268.955	1269.388	-342.102	0.187	178.606	0.317	12	0.135	K.GIPYLNTYDGR.T
R3/RRR3-15/2	988.423	988.120	307.557	0.359	842.837	0.159	12	0.131	-.LSIIEEQR.-
R3/RRR3-15/3	1483.315	1483.818	-1016.075	0.551	1582.612	0.291	25	0.130	-.SRECLPLILIIR.-
R3/RRR3-14/2	846.232	846.005	268.591	0.283	721.696	0.105	10	0.129	R.YPDPIIK.A
R3/RRR3-15/2	845.974	846.005	-37.284	0.367	760.964	0.122	10	0.129	R.YPDPIIK.A
R3/RRR3-15/2	845.898	846.005	-127.027	0.284	770.853	0.173	10	0.129	-.YPDPIIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	845.820	846.005	-219.971	0.295	978.721	0.074	11	0.129	-.YPDPIIK.-
R3/RRR3-15/2	846.157	846.005	179.626	0.238	707.552	0.032	10	0.128	-.YPDPIIK.-
R3/RRR3-15/2	845.997	846.005	-10.074	0.319	726.106	0.152	10	0.127	-.YPDPIIK.-
R3/RRR3-15/2	845.893	846.005	-133.541	0.296	757.302	0.131	10	0.127	-.YPDPIIK.-
R3/RRR3-15/3	1475.790	1475.626	111.111	0.465	877.328	0.521	23	0.126	K.ANDTIKIDLETNK.I
R3/RRR3-15/3	1475.618	1475.626	-5.619	0.479	1014.786	0.457	25	0.122	K.ANDTIKIDLETNK.I
R3/RRR3-15/3	1883.705	1884.186	-255.975	0.360	1591.400	0.215	28	0.119	R.TDKTYPAGFMDVISIPK.T
R3/RRR3-15/3	1216.988	1216.454	-384.589	0.485	1313.559	0.363	24	0.119	R.TIRYPDPIIK.A
R3/RRR3-15/3	1452.639	1451.655	-10.807	0.337	700.592	0.474	24	0.110	K.LGGAFAPKPSSGPHK.A
R3/RRR3-14/2	1351.260	1351.557	-220.417	0.266	376.048	0.277	12	0.107	-.FDVGNVVMVTGGR.-
R3/RRR3-15/3	1216.794	1216.454	280.412	0.469	1071.858	0.332	22	0.103	R.TIRYPDPIIK.A
R3/RRR3-15/3	1216.469	1216.454	12.056	0.494	1145.915	0.294	22	0.101	R.TIRYPDPIIK.A
R3/RRR3-14/3	1450.711	1451.655	-1344.135	0.264	667.669	0.408	24	0.100	K.LGGAFAPKPSSGPHK.A
R3/RRR3-15/3	1451.947	1451.655	202.237	0.321	561.913	0.391	23	0.099	K.LGGAFAPKPSSGPHK.A
R3/RRR3-15/3	1451.346	1451.655	-213.493	0.299	485.642	0.391	21	0.098	K.LGGAFAPKPSSGPHK.A
R3/RRR3-14/3	1216.400	1216.454	-44.562	0.476	1261.637	0.248	23	0.097	R.TIRYPDPIIK.A
R3/RRR3-14/3	1451.354	1451.655	-207.798	0.308	705.963	0.348	24	0.096	K.LGGAFAPKPSSGPHK.A
R3/RRR3-14/3	1452.692	1451.655	25.983	0.300	589.639	0.364	21	0.096	K.LGGAFAPKPSSGPHK.A
R3/RRR3-15/3	1216.231	1216.454	-184.246	0.515	1036.928	0.282	22	0.096	R.TIRYPDPIIK.A
R3/RRR3-15/3	1216.458	1216.454	3.299	0.468	857.023	0.291	20	0.095	R.TIRYPDPIIK.A
R3/RRR3-15/3	1482.537	1483.818	-1542.845	0.439	1035.544	0.284	22	0.091	-.SRECLPLILIIR.-
R3/RRR3-15/3	1216.120	1216.454	-275.477	0.387	841.696	0.207	20	0.087	R.TIRYPDPIIK.A
R3/RRR3-14/3	1215.739	1216.454	-1415.395	0.303	968.495	0.110	20	0.079	R.TIRYPDPIIK.A
R3/RRR3-8/2	1842.573	1842.085	265.289	0.662	2973.955	0.631	27	0.555	K.HVAEADIIFVSVNTPTK.T
R3/RRR3-8/2	1842.576	1842.085	267.216	0.665	2859.808	0.657	27	0.535	K.HVAEADIIFVSVNTPTK.T
R3/RRR3-8/2	1842.316	1842.085	125.631	0.654	2878.466	0.642	27	0.534	K.HVAEADIIFVSVNTPTK.T
R3/RRR3-8/2	1682.192	1682.979	-1066.038	0.556	2523.297	0.610	24	0.433	K.CPAIEVVVVDISKPR.I
R3/RRR3-8/3	1681.970	1682.979	-1198.307	0.551	2579.771	0.530	34	0.382	K.CPAIEVVVVDISKPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1682.534	1682.979	-265.506	0.543	2173.329	0.571	23	0.344	K.CPAIEVVVVDISKPR.I
R3/RRR3-8/3	1682.899	1682.979	-48.252	0.613	2339.372	0.519	33	0.319	K.CPAIEVVVVDISKPR.I
R3/RRR3-9/3	1683.150	1682.979	101.787	0.514	2107.549	0.574	32	0.298	K.CPAIEVVVVDISKPR.I
R3/RRR3-9/2	1619.937	1619.796	87.401	0.594	1938.688	0.538	25	0.293	K.FLNASVGFGGSCFQK.D
R3/RRR3-8/2	1682.425	1682.979	-926.528	0.521	1982.002	0.514	23	0.292	K.CPAIEVVVVDISKPR.I
R3/RRR3-9/3	1683.108	1682.979	76.584	0.584	2054.589	0.566	31	0.285	K.CPAIEVVVVDISKPR.I
R3/RRR3-8/2	1476.377	1476.699	-218.904	0.577	1798.926	0.518	21	0.261	R.IITTNLWSAELSK.L
R3/RRR3-8/2	1620.290	1619.796	306.217	0.597	1725.391	0.537	24	0.259	K.FLNASVGFGGSCFQK.D
R3/RRR3-8/2	1354.177	1354.450	-202.130	0.540	1788.459	0.506	19	0.259	K.AADLTYWESAAR.M
R3/RRR3-8/2	1620.316	1619.796	-296.859	0.596	1677.974	0.555	24	0.258	K.FLNASVGFGGSCFQK.D
R3/RRR3-8/3	1683.271	1682.979	173.571	0.594	1989.683	0.518	31	0.253	K.CPAIEVVVVDISKPR.I
R3/RRR3-9/2	1476.350	1476.699	-237.402	0.507	1813.362	0.474	21	0.252	R.IITTNLWSAELSK.L
R3/RRR3-4/2	1477.459	1476.699	-162.972	0.562	1648.132	0.537	21	0.246	R.IITTNLWSAELSK.L
R3/RRR3-8/2	1076.003	1075.246	-226.736	0.547	1805.882	0.447	17	0.245	K.LAANAFLAQR.I
R3/RRR3-8/2	1477.213	1476.699	-329.844	0.567	1673.984	0.519	21	0.245	R.IITTNLWSAELSK.L
R3/RRR3-8/2	1476.270	1476.699	-291.489	0.488	1807.289	0.445	21	0.244	R.IITTNLWSAELSK.L
R3/RRR3-9/2	1355.180	1354.450	-199.541	0.572	1628.276	0.536	18	0.244	K.AADLTYWESAAR.M
R3/RRR3-2/2	1477.167	1476.699	317.734	0.563	1706.391	0.493	21	0.242	R.IITTNLWSAELSK.L
R3/RRR3-9/3	1682.779	1682.979	-119.522	0.573	1857.747	0.544	30	0.242	K.CPAIEVVVVDISKPR.I
R3/RRR3-6/2	1477.296	1476.699	-273.882	0.544	1697.609	0.486	21	0.239	R.IITTNLWSAELSK.L
R3/RRR3-8/2	1355.133	1354.450	-234.243	0.572	1649.882	0.499	18	0.237	K.AADLTYWESAAR.M
R3/RRR3-9/2	1475.441	1476.699	-1535.319	0.409	1826.698	0.399	21	0.236	R.IITTNLWSAELSK.L
R3/RRR3-4/2	1476.336	1476.699	-246.858	0.498	1681.289	0.478	21	0.236	R.IITTNLWSAELSK.L
R3/RRR3-10/2	1477.297	1476.699	-273.385	0.521	1692.388	0.462	21	0.233	R.IITTNLWSAELSK.L
R3/RRR3-7/2	1476.351	1476.699	-236.240	0.548	1695.793	0.458	21	0.232	R.IITTNLWSAELSK.L
R3/RRR3-2/2	1355.280	1354.450	-125.538	0.556	1581.249	0.489	18	0.226	K.AADLTYWESAAR.M
R3/RRR3-9/2	1074.456	1075.246	-1670.721	0.438	1627.663	0.460	17	0.226	K.LAANAFLAQR.I
R3/RRR3-9/2	1476.193	1476.699	-1023.456	0.419	1677.765	0.429	20	0.224	R.IITTNLWSAELSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1354.107	1354.450	-254.041	0.505	1628.183	0.446	18	0.223	K.AADLTYWESAAR.M
R3/RRR3-8/2	1075.123	1075.246	-114.976	0.557	1598.804	0.458	17	0.222	K.LAANAFLAQR.I
R3/RRR3-7/2	1475.546	1476.699	-1463.518	0.384	1657.191	0.430	20	0.221	R.IITTNLWSAELSK.L
R3/RRR3-8/2	1620.297	1619.796	-308.575	0.578	1494.391	0.503	22	0.219	K.FLNASVGFGGSCFQK.D
R3/RRR3-4/2	1075.255	1075.246	8.243	0.441	1660.804	0.411	17	0.219	K.LAANAFLAQR.I
R3/RRR3-7/3	1682.828	1682.979	-90.489	0.542	1594.273	0.587	29	0.216	K.CPAIEVVVVDISKPR.I
R3/RRR3-6/2	1477.339	1476.699	-244.868	0.552	1436.639	0.520	20	0.216	R.IITTNLWSAELSK.L
R3/RRR3-9/2	1353.617	1354.450	-1358.183	0.447	1683.798	0.381	18	0.215	K.AADLTYWESAAR.M
R3/RRR3-2/2	1075.037	1075.246	-195.050	0.434	1737.685	0.351	17	0.215	K.LAANAFLAQR.I
R3/RRR3-8/2	1074.568	1075.246	-1565.950	0.487	1513.990	0.463	17	0.214	K.LAANAFLAQR.I
R3/RRR3-10/2	1076.256	1075.246	9.373	0.583	1553.586	0.450	17	0.214	K.LAANAFLAQR.I
R3/RRR3-7/2	1074.984	1075.246	-244.832	0.499	1622.647	0.405	17	0.213	K.LAANAFLAQR.I
R3/RRR3-8/2	1271.983	1272.453	-371.013	0.425	1288.807	0.567	20	0.212	R.VVSSM*FNTVSGK.K
R3/RRR3-5/2	1074.831	1075.246	-387.486	0.449	1543.923	0.435	17	0.211	K.LAANAFLAQR.I
R3/RRR3-5/2	1074.986	1075.246	-242.098	0.509	1499.644	0.455	17	0.211	K.LAANAFLAQR.I
R3/RRR3-9/2	1272.002	1272.453	-355.799	0.454	1203.352	0.605	19	0.211	R.VVSSM*FNTVSGK.K
R3/RRR3-8/2	1256.166	1256.454	-229.695	0.471	1277.618	0.556	20	0.210	R.VVSSMFNTVSGK.K
R3/RRR3-6/2	1075.171	1075.246	-70.217	0.463	1442.413	0.469	17	0.208	K.LAANAFLAQR.I
R3/RRR3-5/2	1074.920	1075.246	-304.304	0.449	1464.990	0.452	17	0.207	K.LAANAFLAQR.I
R3/RRR3-10/2	1477.209	1476.699	-332.746	0.512	1454.807	0.467	20	0.207	R.IITTNLWSAELSK.L
R3/RRR3-9/2	1353.704	1354.450	-1293.246	0.469	1517.513	0.419	18	0.205	K.AADLTYWESAAR.M
R3/RRR3-9/2	1074.527	1075.246	-1604.865	0.474	1461.710	0.436	17	0.203	K.LAANAFLAQR.I
R3/RRR3-2/2	1355.319	1354.450	-96.536	0.495	1321.928	0.507	18	0.203	K.AADLTYWESAAR.M
R3/RRR3-4/2	1074.322	1075.246	-1796.521	0.455	1419.535	0.449	17	0.202	K.LAANAFLAQR.I
R3/RRR3-9/2	1074.598	1075.246	-1537.877	0.475	1489.666	0.413	17	0.201	K.LAANAFLAQR.I
R3/RRR3-7/2	1476.117	1476.699	-1075.101	0.410	1435.706	0.423	20	0.196	R.IITTNLWSAELSK.L
R3/RRR3-2/2	1476.172	1476.699	-1037.986	0.436	1325.225	0.450	19	0.191	R.IITTNLWSAELSK.L
R3/RRR3-8/2	1256.194	1256.454	-207.565	0.482	1070.918	0.548	19	0.190	R.VVSSMFNTVSGK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1354.418	1354.450	-23.649	0.447	1459.291	0.372	18	0.190	K.AADLTYWESAAR.M
R3/RRR3-8/2	1271.507	1272.453	-1535.521	0.263	1341.463	0.445	20	0.188	R.VVSSM*FNTVSGK.K
R3/RRR3-8/2	1255.602	1256.454	-1479.027	0.412	1277.472	0.441	20	0.187	R.VVSSMFNTVSGK.K
R3/RRR3-10/2	1476.181	1476.699	-1031.261	0.413	1334.277	0.424	19	0.187	R.IITTNLWSAELSK.L
R3/RRR3-9/2	1353.356	1354.450	-1551.324	0.356	1460.451	0.348	18	0.185	K.AADLTYWESAAR.M
R3/RRR3-6/2	1076.155	1075.246	-85.171	0.525	1159.667	0.474	16	0.184	K.LAANAFLAQR.I
R3/RRR3-6/2	1075.274	1075.246	25.892	0.515	1177.461	0.461	16	0.183	K.LAANAFLAQR.I
R3/RRR3-6/2	1476.043	1476.699	-1125.256	0.418	1315.095	0.408	19	0.182	R.IITTNLWSAELSK.L
R3/RRR3-8/2	981.139	980.228	-90.674	0.470	1207.922	0.439	15	0.182	K.IAILGFAFK.K
R3/RRR3-4/2	1075.143	1075.246	-96.184	0.392	1326.511	0.386	17	0.181	K.LAANAFLAQR.I
R3/RRR3-1/2	1476.384	1476.699	-213.844	0.418	1181.093	0.461	18	0.180	R.IITTNLWSAELSK.L
R3/RRR3-8/2	1271.982	1272.453	-371.302	0.415	990.983	0.535	18	0.179	R.VVSSM*FNTVSGK.K
R3/RRR3-8/2	1076.183	1075.246	-58.661	0.422	1106.241	0.473	15	0.178	K.LAANAFLAQR.I
R3/RRR3-8/2	980.044	980.228	-187.720	0.467	1054.070	0.459	15	0.174	K.IAILGFAFK.K
R3/RRR3-3/2	1476.122	1476.699	-1071.613	0.329	1264.756	0.340	19	0.167	R.IITTNLWSAELSK.L
R3/RRR3-3/2	1475.936	1476.699	-1198.421	0.377	1173.072	0.383	17	0.166	R.IITTNLWSAELSK.L
R3/RRR3-8/3	1801.956	1802.046	-50.521	0.540	1181.181	0.570	28	0.162	R.IFDNM*QKPAFVFDGR.N
R3/RRR3-9/2	1626.322	1625.799	-293.730	0.451	579.325	0.536	22	0.160	R.ETPAIDVCHGLLGDK.A
R3/RRR3-2/3	1682.478	1682.979	-895.033	0.495	1400.259	0.464	26	0.158	K.CPAIEVVVVDISKPR.I
R3/RRR3-8/2	1625.361	1625.799	-270.326	0.422	559.567	0.535	21	0.157	R.ETPAIDVCHGLLGDK.A
R3/RRR3-8/2	1201.236	1200.322	-72.327	0.463	1040.796	0.358	15	0.157	R.NLFFSTDVEK.H
R3/RRR3-9/3	1785.922	1786.047	-70.388	0.506	1119.845	0.576	29	0.157	R.IFDNMQKPAFVFDGR.N
R3/RRR3-8/2	1625.383	1625.799	-256.311	0.420	565.474	0.508	22	0.156	R.ETPAIDVCHGLLGDK.A
R3/RRR3-8/2	1400.018	1400.626	-1152.195	0.328	748.701	0.494	19	0.154	R.VVSSM*FNTVSGKK.I
R3/RRR3-8/2	1624.770	1625.799	-1252.165	0.409	493.683	0.511	20	0.153	R.ETPAIDVCHGLLGDK.A
R3/RRR3-8/2	1400.297	1400.626	-236.159	0.435	536.516	0.516	17	0.152	R.VVSSM*FNTVSGKK.I
R3/RRR3-8/3	1841.354	1842.085	-943.180	0.464	1521.920	0.388	26	0.152	K.HVAEADIIFVSVNTPTK.T
R3/RRR3-4/2	1075.296	1075.246	46.614	0.403	499.414	0.428	15	0.151	K.LAANAFLAQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1801.475	1802.046	-874.767	0.436	785.607	0.452	17	0.151	R.IFDNM*QKPAFVFDGR.N
R3/RRR3-9/2	1625.374	1625.799	-262.188	0.420	475.184	0.485	20	0.151	R.ETPAIDVCHGLLGDK.A
R3/RRR3-8/3	1802.444	1802.046	221.341	0.544	971.509	0.594	27	0.150	R.IFDNM*QKPAFVFDGR.N
R3/RRR3-9/2	1496.655	1496.646	6.004	0.478	700.284	0.410	18	0.149	K.QVSVVWDAYEATK.G
R3/RRR3-9/2	1496.257	1496.646	-260.592	0.397	737.580	0.385	19	0.148	K.QVSVVWDAYEATK.G
R3/RRR3-8/2	1227.037	1227.394	-291.724	0.407	956.922	0.313	17	0.148	R.HLQPTSPTAFK.Q
R3/RRR3-8/2	1496.262	1496.646	-257.236	0.395	563.650	0.443	17	0.147	K.QVSVVWDAYEATK.G
R3/RRR3-9/2	1201.037	1200.322	-238.301	0.402	824.917	0.356	14	0.147	R.NLFFSTDVEK.H
R3/RRR3-1/2	1475.432	1476.699	-1541.553	0.292	759.428	0.399	15	0.146	R.IITTNLWSAELSK.L
R3/RRR3-9/2	1496.381	1496.646	-177.439	0.425	424.587	0.408	15	0.142	K.QVSVVWDAYEATK.G
R3/RRR3-8/2	1070.127	1070.224	-91.257	0.384	736.722	0.370	12	0.142	R.NVVDPEKLR.E
R3/RRR3-4/2	1476.167	1476.699	-1041.307	0.320	679.861	0.341	15	0.141	R.IITTNLWSAELSK.L
R3/RRR3-9/2	1199.971	1200.322	-293.509	0.382	730.913	0.318	13	0.140	R.NLFFSTDVEK.H
R3/RRR3-8/2	1199.617	1200.322	-1425.883	0.350	854.036	0.273	14	0.140	R.NLFFSTDVEK.H
R3/RRR3-9/2	1199.358	1200.322	-1642.815	0.318	866.633	0.272	14	0.139	R.NLFFSTDVEK.H
R3/RRR3-9/3	1801.387	1802.046	-924.095	0.508	946.796	0.556	28	0.139	R.IFDNM*QKPAFVFDGR.N
R3/RRR3-8/2	1226.328	1227.394	-1689.752	0.327	796.161	0.287	16	0.139	R.HLQPTSPTAFK.Q
R3/RRR3-9/3	1801.858	1802.046	-104.646	0.513	958.243	0.545	27	0.138	R.IFDNM*QKPAFVFDGR.N
R3/RRR3-8/2	1496.250	1496.646	-265.421	0.288	378.758	0.278	15	0.136	K.QVSVVWDAYEATK.G
R3/RRR3-4/2	1625.714	1625.799	-52.388	0.260	461.191	0.370	16	0.136	R.ETPAIDVCHGLLGDK.A
R3/RRR3-8/2	1226.842	1227.394	-1269.194	0.333	607.438	0.236	14	0.132	R.HLQPTSPTAFK.Q
R3/RRR3-3/2	1682.524	1682.979	-271.329	0.251	404.797	0.300	14	0.130	-.CPAIEVVVVDISKPR.-
R3/RRR3-8/2	1800.722	1802.046	-1294.786	0.303	563.896	0.285	14	0.128	R.IFDNM*QKPAFVFDGR.N
R3/RRR3-9/3	1785.151	1786.047	-1065.088	0.482	969.556	0.484	29	0.126	R.IFDNMQKPAFVFDGR.N
R3/RRR3-8/3	1801.173	1802.046	-1043.400	0.469	780.528	0.522	25	0.124	R.IFDNM*QKPAFVFDGR.N
R3/RRR3-1/2	1075.350	1075.246	96.937	0.369	575.513	0.165	12	0.122	-.LAANAFLAQR.-
R3/RRR3-9/3	1785.317	1786.047	-971.687	0.478	858.247	0.490	27	0.122	R.IFDNMQKPAFVFDGR.N
R3/RRR3-8/3	1476.762	1476.699	42.680	0.439	1189.723	0.364	26	0.115	R.IITTNLWSAELSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/3	1785.908	1786.047	-78.102	0.416	739.468	0.460	24	0.113	R.IFDNMQKPAFVFDGR.N
R3/RRR3-8/3	1476.632	1476.699	-45.373	0.388	1067.544	0.377	23	0.111	R.IITTNLWSAELSK.L
R3/RRR3-8/3	1786.020	1786.047	-15.165	0.379	553.930	0.334	23	0.098	R.IFDNMQKPAFVFDGR.N
R3/RRR3-1/3	1682.197	1682.979	-1062.549	0.381	667.964	0.322	22	0.094	-.CPAIEVVVVDISKPR.-
R3/RRR3-8/3	1476.665	1476.699	-23.110	0.399	809.371	0.287	22	0.091	R.IITTNLWSAELSK.L
R3/RRR3-3/2	1458.610	1459.670	-1416.800	0.413	2322.716	0.527	25	0.361	K.LVAEAGIGTVASGVSK.G
R3/RRR3-2/2	1906.460	1907.199	-915.073	0.510	1739.170	0.512	25	0.254	R.FGVTPTFLVNAEQIEIK.I
R3/RRR3-2/2	1963.578	1964.191	-824.043	0.451	1646.444	0.538	22	0.245	K.GQMEAWDGPALLLFSDGR.T
R3/RRR3-3/2	1906.227	1907.199	-1037.543	0.475	1638.450	0.477	25	0.232	R.FGVTPTFLVNAEQIEIK.I
R3/RRR3-3/2	1676.154	1676.807	-989.162	0.488	1787.216	0.398	21	0.230	K.ASDSANLDSTAELLLR.S
R3/RRR3-3/2	1908.596	1907.199	208.833	0.504	1605.617	0.480	25	0.228	R.FGVTPTFLVNAEQIEIK.I
R3/RRR3-2/2	1906.246	1907.199	-1027.448	0.511	1580.736	0.486	25	0.226	R.FGVTPTFLVNAEQIEIK.I
R3/RRR3-3/2	1201.995	1202.343	-290.366	0.404	1671.432	0.421	19	0.226	R.NGSQLLVLSDR.S
R3/RRR3-2/2	1906.714	1907.199	-255.030	0.510	1438.742	0.495	24	0.212	R.FGVTPTFLVNAEQIEIK.I
R3/RRR3-3/2	1218.986	1219.321	-275.371	0.504	1441.236	0.440	18	0.204	K.VLCDEADAAVR.N
R3/RRR3-3/2	1143.775	1144.303	-1340.496	0.502	1411.167	0.455	16	0.202	K.IGGLTLDELGR.E
R3/RRR3-3/2	1677.458	1676.807	-208.648	0.555	1441.901	0.419	22	0.194	K.ASDSANLDSTAELLLR.S
R3/RRR3-3/2	1219.150	1219.321	-139.957	0.536	1381.497	0.406	18	0.190	K.VLCDEADAAVR.N
R3/RRR3-3/2	1458.709	1459.670	-1348.633	0.393	1158.317	0.508	21	0.184	K.LVAEAGIGTVASGVSK.G
R3/RRR3-2/2	1616.031	1615.762	166.482	0.515	1438.881	0.357	18	0.184	K.YPEVIDFYDYYK.G
R3/RRR3-3/2	1276.172	1276.379	-162.198	0.452	1155.483	0.475	19	0.182	K.GLQNGDTATSAIK.Q
R3/RRR3-3/2	1276.014	1276.379	-286.860	0.404	1104.855	0.469	19	0.176	K.GLQNGDTATSAIK.Q
R3/RRR3-3/2	1521.229	1521.699	-309.434	0.393	1317.348	0.346	18	0.172	K.VFTDEGLEVLGWR.T
R3/RRR3-2/2	1676.496	1676.807	-186.347	0.470	1383.157	0.331	20	0.172	K.ASDSANLDSTAELLLR.S
R3/RRR3-2/2	1881.583	1879.998	-221.151	0.478	904.215	0.544	18	0.170	K.SASWADELYFCSLSSR.T
R3/RRR3-3/2	1880.144	1879.998	77.910	0.509	844.864	0.480	17	0.156	K.SASWADELYFCSLSSR.T
R3/RRR3-3/2	1022.310	1022.177	131.009	0.345	996.383	0.356	14	0.154	K.GLIEAYVEK.T
R3/RRR3-1/2	1676.303	1676.807	-900.258	0.420	1134.697	0.307	20	0.152	K.ASDSANLDSTAELLLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1520.821	1521.699	-1238.083	0.257	1226.399	0.244	18	0.150	K.VFTDEGLEVLGWR.T
R3/RRR3-3/2	1277.114	1276.379	-207.520	0.351	573.160	0.494	16	0.148	K.GLQNGDTATSAIK.Q
R3/RRR3-3/2	1022.182	1022.177	5.616	0.311	921.934	0.340	14	0.148	K.GLIEAYVEK.T
R3/RRR3-3/2	1164.882	1165.278	-340.609	0.405	590.853	0.413	16	0.148	R.LVGEANDYVGK.G
R3/RRR3-3/2	1049.176	1049.245	-66.472	0.453	631.258	0.436	14	0.146	-.YLLSSAGLPK.-
R3/RRR3-2/2	1520.956	1521.699	-1149.344	0.271	1005.025	0.302	17	0.145	K.VFTDEGLEVLGWR.T
R3/RRR3-3/2	1165.105	1165.278	-148.446	0.408	697.459	0.323	16	0.142	R.LVGEANDYVGK.G
R3/RRR3-3/2	1049.148	1049.245	-93.082	0.296	869.980	0.276	15	0.140	K.YLLSSAGLPK.W
R3/RRR3-3/2	1049.796	1049.245	-429.382	0.293	819.194	0.267	15	0.138	K.YLLSSAGLPK.W
R3/RRR3-2/2	1165.976	1165.278	-260.063	0.373	614.710	0.274	16	0.137	R.LVGEANDYVGK.G
R3/RRR3-2/2	1165.982	1165.278	-254.497	0.396	637.698	0.237	16	0.135	R.LVGEANDYVGK.G
R3/RRR3-3/2	1522.525	1521.699	-114.563	0.298	894.051	0.230	16	0.134	K.VFTDEGLEVLGWR.T
R3/RRR3-1/2	1964.996	1964.191	-99.358	0.292	358.545	0.423	15	0.133	K.GQMEAWDGPALLLFSDGR.T
R3/RRR3-3/2	1165.353	1165.278	65.075	0.323	555.613	0.225	15	0.133	-.LVGEANDYVGK.-
R3/RRR3-3/2	1980.065	1980.190	-63.643	0.338	426.493	0.306	17	0.131	K.GQM*EAWDGPALLLFSDGR.T
R3/RRR3-3/2	1021.646	1022.177	-1502.357	0.188	543.961	0.229	12	0.129	K.GLIEAYVEK.T
R3/RRR3-2/3	1713.783	1713.864	-47.418	0.511	1101.526	0.436	28	0.125	R.ICHTNNCPVGVASQR.E
R3/RRR3-2/3	1636.665	1636.877	-130.445	0.451	819.239	0.514	30	0.122	K.IAQGAKPGEGGQLPGKK.V
R3/RRR3-2/3	1508.824	1508.705	79.628	0.353	1312.910	0.333	31	0.119	K.IAQGAKPGEGGQLPGK.K
R3/RRR3-2/3	1508.777	1508.705	48.104	0.384	1261.976	0.347	31	0.118	K.IAQGAKPGEGGQLPGK.K
R3/RRR3-2/3	1713.796	1713.864	-39.702	0.483	807.722	0.456	26	0.114	R.ICHTNNCPVGVASQR.E
R3/RRR3-2/2	1048.848	1049.245	-379.925	0.255	518.801	0.136	12	0.113	-.YLLSSAGLPK.-
R3/RRR3-3/3	1636.474	1636.877	-247.400	0.462	810.073	0.450	28	0.112	K.IAQGAKPGEGGQLPGKK.V
R3/RRR3-3/3	1637.042	1636.877	100.578	0.425	666.074	0.491	26	0.112	K.IAQGAKPGEGGQLPGKK.V
R3/RRR3-2/3	1508.630	1508.705	-49.646	0.346	1278.114	0.289	31	0.109	K.IAQGAKPGEGGQLPGK.K
R3/RRR3-3/3	1713.997	1713.864	77.954	0.460	690.298	0.432	23	0.106	R.ICHTNNCPVGVASQR.E
R3/RRR3-3/3	1713.572	1713.864	-170.784	0.492	806.295	0.398	25	0.105	R.ICHTNNCPVGVASQR.E
R3/RRR3-2/3	1636.957	1636.877	48.526	0.436	824.030	0.387	29	0.104	K.IAQGAKPGEGGQLPGKK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1510.082	1508.705	250.639	0.368	987.212	0.321	28	0.100	K.IAQGAKPGEGGQLPGK.K
R3/RRR3-3/3	1713.220	1713.864	-962.516	0.382	527.251	0.368	21	0.097	R.ICHTNNCPVGVASQR.E
R3/RRR3-3/3	1508.250	1508.705	-302.081	0.277	1044.105	0.269	29	0.095	K.IAQGAKPGEGGQLPGK.K
R3/RRR3-3/3	1508.770	1508.705	43.600	0.355	959.820	0.278	26	0.094	K.IAQGAKPGEGGQLPGK.K
R3/RRR3-7/2	1403.791	1404.570	-1271.381	0.521	2253.843	0.487	20	0.334	R.YAGM*LQYDGELK.L
R3/RRR3-7/2	1434.170	1434.578	-285.362	0.501	2292.646	0.443	21	0.327	R.GWDAQVLGEAPYK.F
R3/RRR3-7/2	1434.401	1434.578	-123.393	0.532	2170.743	0.487	21	0.318	R.GWDAQVLGEAPYK.F
R3/RRR3-7/2	1780.465	1779.974	276.606	0.574	1970.296	0.596	24	0.314	K.SVGPVVDGDAVVTFNFR.A
R3/RRR3-7/2	1435.027	1434.578	314.181	0.564	2089.666	0.482	21	0.302	R.GWDAQVLGEAPYK.F
R3/RRR3-7/2	1404.104	1404.570	-333.011	0.506	1979.866	0.509	20	0.292	R.YAGM*LQYDGELK.L
R3/RRR3-7/2	1780.692	1779.974	-158.666	0.570	1857.373	0.577	23	0.288	K.SVGPVVDGDAVVTFNFR.A
R3/RRR3-7/2	1491.053	1490.598	305.825	0.500	1654.661	0.547	18	0.253	K.ALEYADFDKFDR.V
R3/RRR3-7/2	1779.565	1779.974	-230.733	0.486	1661.759	0.534	22	0.247	K.SVGPVVDGDAVVTFNFR.A
R3/RRR3-7/2	1489.835	1490.598	-1186.747	0.444	1480.939	0.523	17	0.223	K.ALEYADFDKFDR.V
R3/RRR3-7/2	1590.240	1590.764	-961.298	0.480	1214.069	0.510	19	0.192	K.RGWDAQVLGEAPYK.F
R3/RRR3-7/2	1069.988	1070.307	-299.871	0.504	1492.958	0.340	14	0.187	R.LDQVQLLLK.G
R3/RRR3-7/2	1591.306	1590.764	-288.729	0.452	1239.285	0.425	20	0.180	K.RGWDAQVLGEAPYK.F
R3/RRR3-7/2	1070.105	1070.307	-189.427	0.531	1579.283	0.259	14	0.177	R.LDQVQLLLK.G
R3/RRR3-7/2	1590.137	1590.764	-1026.500	0.451	1111.377	0.461	18	0.174	K.RGWDAQVLGEAPYK.F
R3/RRR3-7/3	1732.655	1732.965	-179.644	0.415	1541.355	0.468	30	0.174	K.GTLHLIGLLSDGGVHSR.L
R3/RRR3-7/2	910.466	911.041	-1734.294	0.391	1053.878	0.450	13	0.171	R.VHILTDGR.D
R3/RRR3-7/2	1070.249	1070.307	-54.639	0.506	1405.008	0.287	14	0.169	R.LDQVQLLLK.G
R3/RRR3-7/2	911.018	911.041	-24.676	0.405	1092.841	0.398	13	0.167	R.VHILTDGR.D
R3/RRR3-7/2	910.340	911.041	-1873.468	0.355	1022.946	0.417	13	0.163	R.VHILTDGR.D
R3/RRR3-7/2	1349.259	1349.518	-192.341	0.433	884.790	0.434	16	0.157	R.DAILSGKFDQVR.V
R3/RRR3-7/2	1388.231	1388.571	-245.415	0.362	859.633	0.445	16	0.156	R.YAGMLQYDGELK.L
R3/RRR3-7/2	1348.764	1349.518	-1304.156	0.402	889.981	0.425	16	0.156	R.DAILSGKFDQVR.V
R3/RRR3-7/2	1387.991	1388.571	-1141.508	0.399	1014.661	0.352	17	0.154	R.YAGMLQYDGELK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1349.159	1349.518	-266.317	0.353	918.363	0.387	16	0.152	R.DAILSGKFDQVR.V
R3/RRR3-7/2	1005.429	1006.137	-1703.712	0.395	818.492	0.369	16	0.151	K.FQNAVEAVK.T
R3/RRR3-7/2	1865.454	1866.060	-863.713	0.418	639.773	0.432	23	0.148	K.ASDQYLPPFVIVDESGK.S
R3/RRR3-7/2	1005.949	1006.137	-187.390	0.433	856.042	0.321	16	0.147	K.FQNAVEAVK.T
R3/RRR3-7/2	1483.522	1482.629	-72.100	0.387	938.960	0.358	15	0.147	K.FGHVTFFWNGNR.S
R3/RRR3-7/2	1005.893	1006.137	-243.269	0.451	831.122	0.317	16	0.145	-.FQNAVEAVK.-
R3/RRR3-7/2	1865.435	1866.060	-874.158	0.327	580.480	0.453	22	0.144	K.ASDQYLPPFVIVDESGK.S
R3/RRR3-7/2	1319.440	1319.444	-2.840	0.383	778.262	0.330	16	0.143	K.IYDGEGFNYIK.E
R3/RRR3-7/2	986.268	987.175	-1940.218	0.342	795.024	0.331	15	0.141	K.LVDLALASGK.I
R3/RRR3-7/3	1576.384	1576.782	-253.258	0.569	1040.639	0.526	24	0.140	K.ARDAILSGKFDQVR.V
R3/RRR3-7/2	1319.988	1319.444	-345.850	0.388	676.497	0.319	16	0.139	-.IYDGEGFNYIK.-
R3/RRR3-7/2	1319.560	1319.444	88.183	0.383	664.806	0.315	15	0.138	K.IYDGEGFNYIK.E
R3/RRR3-7/2	1864.803	1866.060	-1214.095	0.262	603.843	0.333	21	0.135	K.ASDQYLPPFVIVDESGK.S
R3/RRR3-7/3	1482.615	1482.629	-9.226	0.522	1267.361	0.383	23	0.125	K.FGHVTFFWNGNR.S
R3/RRR3-7/3	1576.965	1576.782	116.017	0.478	985.718	0.451	25	0.120	K.ARDAILSGKFDQVR.V
R3/RRR3-7/3	1577.312	1576.782	-298.906	0.498	838.250	0.486	22	0.119	K.ARDAILSGKFDQVR.V
R3/RRR3-7/3	1482.544	1482.629	-57.291	0.452	1102.363	0.333	23	0.106	K.FGHVTFFWNGNR.S
R3/RRR3-7/3	1483.344	1482.629	-192.627	0.400	1015.875	0.298	20	0.098	-.FGHVTFFWNGNR.-
R3/RRR3-7/3	1482.362	1482.629	-180.448	0.420	989.067	0.239	21	0.090	K.FGHVTFFWNGNR.S
R3/RRR3-7/3	1483.565	1482.629	-43.552	0.345	851.621	0.208	19	0.085	-.FGHVTFFWNGNR.-
R3/RRR3-5/2	1846.388	1847.057	-906.782	0.593	2483.229	0.578	25	0.412	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1846.489	1847.057	-851.564	0.628	2392.170	0.584	25	0.394	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1846.548	1847.057	-819.512	0.614	2338.235	0.589	24	0.384	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1569.396	1569.786	-249.384	0.595	2140.019	0.518	21	0.324	K.IKEVSHEWSLVNK.Q
R3/RRR3-5/2	1837.568	1838.052	-264.294	0.546	1694.306	0.518	22	0.248	K.HSEFISYPISLWTEK.T
R3/RRR3-5/3	1321.061	1321.463	-304.754	0.583	1743.852	0.505	25	0.206	K.HFSVEGQLEFK.A
R3/RRR3-5/2	1838.377	1838.052	177.116	0.549	1201.582	0.570	20	0.202	K.HSEFISYPISLWTEK.T
R3/RRR3-5/3	1848.028	1847.057	-15.716	0.576	1534.126	0.566	32	0.197	R.KPEEITKEEYAAFYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1584.343	1584.710	-231.962	0.520	1380.560	0.446	19	0.194	K.SGDELTSLKDYVTR.M
R3/RRR3-5/2	1543.220	1542.675	-295.504	0.565	1254.815	0.491	19	0.193	K.SLTNDWEEHLAVK.H
R3/RRR3-5/2	1542.387	1542.675	-187.071	0.533	1307.831	0.463	19	0.192	K.SLTNDWEEHLAVK.H
R3/RRR3-5/2	1357.334	1357.621	-211.943	0.464	1406.140	0.403	18	0.191	K.VIKEVLGDKVEK.V
R3/RRR3-6/2	1274.329	1273.421	-72.502	0.496	1201.948	0.497	17	0.189	K.SDLVNNLGTIAR.S
R3/RRR3-5/2	1541.997	1542.675	-1091.419	0.506	1299.202	0.448	19	0.189	K.SLTNDWEEHLAVK.H
R3/RRR3-2/2	1529.361	1528.689	-215.323	0.551	1269.244	0.433	22	0.183	K.GIVDSEDLPLNISR.Q
R3/RRR3-6/2	1528.337	1528.689	-231.089	0.488	1319.840	0.405	22	0.183	K.GIVDSEDLPLNISR.Q
R3/RRR3-1/2	1529.301	1528.689	-254.481	0.544	1335.076	0.407	21	0.183	K.GIVDSEDLPLNISR.Q
R3/RRR3-6/2	1543.390	1542.675	-184.966	0.533	1016.685	0.522	19	0.180	K.SLTNDWEEHLAVK.H
R3/RRR3-5/2	1528.226	1528.689	-304.012	0.488	1283.796	0.407	21	0.180	K.GIVDSEDLPLNISR.Q
R3/RRR3-6/2	1528.403	1528.689	-188.141	0.524	1228.518	0.428	21	0.179	K.GIVDSEDLPLNISR.Q
R3/RRR3-6/2	1272.302	1273.421	-1670.266	0.404	1175.644	0.433	18	0.176	K.SDLVNNLGTIAR.S
R3/RRR3-5/2	1528.293	1528.689	-259.936	0.495	1300.620	0.377	22	0.176	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/2	1273.200	1273.421	-174.597	0.498	1142.133	0.446	17	0.176	K.SDLVNNLGTIAR.S
R3/RRR3-2/2	1529.463	1528.689	-148.225	0.547	1131.433	0.452	20	0.175	K.GIVDSEDLPLNISR.Q
R3/RRR3-6/2	1273.464	1273.421	33.400	0.480	1173.926	0.424	17	0.174	K.SDLVNNLGTIAR.S
R3/RRR3-5/3	1321.388	1321.463	-56.449	0.568	1620.449	0.441	23	0.173	K.HFSVEGQLEFK.A
R3/RRR3-6/3	1846.973	1847.057	-45.722	0.559	1334.627	0.554	30	0.172	R.KPEEITKEEYAAFYK.S
R3/RRR3-4/2	1528.361	1528.689	-215.384	0.480	1209.464	0.393	20	0.171	K.GIVDSEDLPLNISR.Q
R3/RRR3-7/2	1528.371	1528.689	-209.054	0.466	1204.563	0.389	20	0.170	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/2	1528.394	1528.689	-194.070	0.516	1214.127	0.383	20	0.169	K.GIVDSEDLPLNISR.Q
R3/RRR3-6/2	1543.316	1542.675	-232.971	0.548	940.528	0.480	19	0.169	K.SLTNDWEEHLAVK.H
R3/RRR3-5/2	1585.153	1584.710	280.101	0.501	980.770	0.481	18	0.168	K.SGDELTSLKDYVTR.M
R3/RRR3-5/2	1528.406	1528.689	-186.058	0.500	1212.958	0.370	21	0.168	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/2	1583.790	1584.710	-1215.530	0.536	964.148	0.492	17	0.168	K.SGDELTSLKDYVTR.M
R3/RRR3-5/2	1134.100	1134.264	-144.839	0.458	916.425	0.470	16	0.167	K.AVENSPFLEK.L
R3/RRR3-6/2	1585.477	1584.710	-147.158	0.535	1100.728	0.425	18	0.166	K.SGDELTSLKDYVTR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1528.324	1528.689	-239.903	0.512	1222.647	0.364	20	0.166	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/2	1357.358	1357.621	-194.350	0.475	1207.245	0.358	17	0.166	K.VIKEVLGDKVEK.V
R3/RRR3-5/2	1837.634	1838.052	-228.172	0.519	822.833	0.509	18	0.163	K.HSEFISYPISLWTEK.T
R3/RRR3-5/2	1321.173	1321.463	-219.876	0.480	843.687	0.472	16	0.162	K.HFSVEGQLEFK.A
R3/RRR3-3/2	1527.528	1528.689	-1419.405	0.337	1342.432	0.269	20	0.162	K.GIVDSEDLPLNISR.Q
R3/RRR3-3/3	1847.447	1847.057	211.762	0.502	1431.100	0.469	29	0.161	R.KPEEITKEEYAAFYK.S
R3/RRR3-6/2	1527.559	1528.689	-1399.178	0.377	1254.711	0.285	21	0.159	K.GIVDSEDLPLNISR.Q
R3/RRR3-1/2	1528.204	1528.689	-318.437	0.408	1113.219	0.328	20	0.156	K.GIVDSEDLPLNISR.Q
R3/RRR3-1/2	1528.419	1528.689	-177.485	0.496	1106.666	0.338	20	0.156	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/2	1357.196	1357.621	-314.086	0.429	1173.195	0.300	17	0.155	K.VIKEVLGDKVEK.V
R3/RRR3-5/2	1274.186	1273.421	-184.936	0.432	1028.266	0.354	16	0.154	K.SDLVNNLGTIAR.S
R3/RRR3-2/2	1528.015	1528.689	-1099.082	0.347	1123.758	0.305	20	0.154	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/2	1321.189	1321.463	-208.011	0.423	702.549	0.452	16	0.154	K.HFSVEGQLEFK.A
R3/RRR3-4/2	1528.795	1528.689	69.226	0.492	1040.637	0.345	19	0.153	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/2	1262.236	1262.437	-159.042	0.542	896.288	0.397	15	0.152	K.KAVENSPFLEK.L
R3/RRR3-5/2	1262.176	1262.437	-207.163	0.533	901.675	0.380	16	0.152	K.KAVENSPFLEK.L
R3/RRR3-5/3	1528.158	1528.689	-1005.087	0.447	1549.396	0.391	29	0.152	K.GIVDSEDLPLNISR.Q
R3/RRR3-2/3	1847.334	1847.057	150.336	0.563	1175.578	0.523	29	0.149	R.KPEEITKEEYAAFYK.S
R3/RRR3-3/2	1528.209	1528.689	-315.232	0.404	1040.316	0.297	19	0.148	K.GIVDSEDLPLNISR.Q
R3/RRR3-6/3	1846.982	1847.057	-41.048	0.571	1096.569	0.547	30	0.148	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1321.300	1321.463	-123.299	0.394	809.090	0.361	16	0.147	K.HFSVEGQLEFK.A
R3/RRR3-5/2	1261.690	1262.437	-1388.920	0.473	770.089	0.390	14	0.146	K.KAVENSPFLEK.L
R3/RRR3-5/2	1133.866	1134.264	-351.978	0.420	564.217	0.398	14	0.145	K.AVENSPFLEK.L
R3/RRR3-5/3	1966.997	1966.225	-116.039	0.549	1196.914	0.491	27	0.144	K.KHSEFISYPISLWTEK.T
R3/RRR3-5/3	1321.596	1321.463	101.285	0.526	1169.872	0.515	24	0.144	K.HFSVEGQLEFK.A
R3/RRR3-4/2	1273.207	1273.421	-168.826	0.430	740.885	0.338	17	0.144	K.SDLVNNLGTIAR.S
R3/RRR3-7/2	1322.316	1321.463	-111.167	0.384	599.467	0.377	15	0.143	K.HFSVEGQLEFK.A
R3/RRR3-2/2	1839.633	1838.052	-228.590	0.395	619.670	0.394	17	0.142	K.HSEFISYPISLWTEK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1272.207	1273.421	-1745.747	0.292	352.275	0.353	15	0.141	K.SDLVNNLGTIAR.S
R3/RRR3-1/3	1846.757	1847.057	-163.075	0.505	907.273	0.571	28	0.140	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1133.515	1134.264	-1547.704	0.350	683.211	0.326	14	0.140	K.AVENSPFLEK.L
R3/RRR3-1/2	1839.608	1838.052	-242.037	0.351	414.833	0.442	14	0.140	K.HSEFISYPISLWTEK.T
R3/RRR3-4/2	1272.301	1273.421	-1671.037	0.329	326.315	0.375	14	0.139	-.SDLVNNLGTIAR.-
R3/RRR3-7/3	1847.105	1847.057	26.069	0.499	998.045	0.527	26	0.138	R.KPEEITKEEYAAFYK.S
R3/RRR3-2/3	1846.385	1847.057	-908.449	0.493	920.327	0.554	27	0.138	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1081.391	1082.191	-1668.838	0.319	892.419	0.230	14	0.137	R.APFDLFDTR.K
R3/RRR3-5/3	1846.869	1847.057	-102.008	0.551	936.076	0.540	28	0.136	R.KPEEITKEEYAAFYK.S
R3/RRR3-2/2	1839.176	1838.052	67.796	0.324	289.221	0.360	13	0.134	-.HSEFISYPISLWTEK.-
R3/RRR3-2/3	1847.075	1847.057	9.663	0.548	976.118	0.513	28	0.133	R.KPEEITKEEYAAFYK.S
R3/RRR3-6/3	1846.787	1847.057	-146.863	0.546	915.881	0.526	28	0.132	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1272.982	1273.421	-346.118	0.213	656.986	0.232	14	0.131	K.SDLVNNLGTIAR.S
R3/RRR3-4/3	1584.506	1584.710	-129.098	0.442	1267.311	0.409	27	0.131	K.SGDELTSLKDYVTR.M
R3/RRR3-5/3	1837.763	1838.052	-157.777	0.512	1164.360	0.432	28	0.128	K.HSEFISYPISLWTEK.T
R3/RRR3-1/3	1584.668	1584.710	-26.634	0.479	905.772	0.509	24	0.128	K.SGDELTSLKDYVTR.M
R3/RRR3-5/2	1081.212	1082.191	-1835.010	0.183	585.108	0.143	11	0.127	R.APFDLFDTR.K
R3/RRR3-5/3	1569.669	1569.786	-75.094	0.481	849.806	0.528	26	0.126	K.IKEVSHEWSLVNK.Q
R3/RRR3-4/3	1846.856	1847.057	-109.467	0.531	881.082	0.500	24	0.126	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/3	1569.254	1569.786	-979.585	0.493	835.421	0.522	24	0.125	K.IKEVSHEWSLVNK.Q
R3/RRR3-4/3	1584.812	1584.710	64.685	0.457	1048.765	0.449	26	0.124	K.SGDELTSLKDYVTR.M
R3/RRR3-5/3	1584.479	1584.710	-146.255	0.446	981.118	0.468	26	0.124	K.SGDELTSLKDYVTR.M
R3/RRR3-1/3	1584.831	1584.710	76.852	0.418	871.159	0.478	24	0.120	K.SGDELTSLKDYVTR.M
R3/RRR3-4/3	1847.318	1847.057	141.588	0.461	887.593	0.459	27	0.119	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/2	1083.085	1082.191	-97.513	0.300	520.778	0.269	11	0.117	-.APFDLFDTR.-
R3/RRR3-7/3	1846.980	1847.057	-42.142	0.516	734.476	0.476	25	0.116	R.KPEEITKEEYAAFYK.S
R3/RRR3-5/3	1367.353	1366.550	-144.587	0.550	1126.489	0.379	24	0.115	K.RAPFDLFDTRK.K
R3/RRR3-5/3	1366.258	1366.550	-214.422	0.544	1000.340	0.403	22	0.114	K.RAPFDLFDTRK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1528.245	1528.689	-291.639	0.465	1217.004	0.336	26	0.113	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/3	1142.106	1142.204	-86.643	0.449	462.606	0.505	19	0.112	K.LGIHEDSTNR.N
R3/RRR3-5/3	1357.416	1357.621	-151.463	0.455	984.153	0.404	25	0.111	K.VIKEVLGDKVEK.V
R3/RRR3-5/3	1142.115	1142.204	-78.281	0.457	444.444	0.489	19	0.111	K.LGIHEDSTNR.N
R3/RRR3-5/3	1142.085	1142.204	-104.494	0.437	538.752	0.485	20	0.110	K.LGIHEDSTNR.N
R3/RRR3-5/3	1966.068	1966.225	-80.099	0.444	685.906	0.478	23	0.109	K.KHSEFISYPISLWTEK.T
R3/RRR3-5/3	1584.528	1584.710	-115.072	0.470	856.389	0.407	25	0.109	K.SGDELTSLKDYVTR.M
R3/RRR3-5/3	1569.516	1569.786	-172.573	0.436	869.617	0.404	22	0.107	K.IKEVSHEWSLVNK.Q
R3/RRR3-5/3	1585.379	1584.710	-209.577	0.471	832.433	0.395	24	0.106	K.SGDELTSLKDYVTR.M
R3/RRR3-5/3	1528.904	1528.689	140.685	0.484	997.136	0.355	25	0.105	K.GIVDSEDLPLNISR.Q
R3/RRR3-5/3	1357.731	1357.621	81.095	0.453	670.414	0.399	22	0.103	K.VIKEVLGDKVEK.V
R3/RRR3-5/3	1584.924	1584.710	135.481	0.382	861.923	0.360	22	0.102	K.SGDELTSLKDYVTR.M
R3/RRR3-5/3	1366.467	1366.550	-61.038	0.530	836.195	0.334	21	0.099	K.RAPFDLFDTRK.K
R3/RRR3-5/3	1357.659	1357.621	27.666	0.443	758.988	0.345	23	0.098	K.VIKEVLGDKVEK.V
R3/RRR3-5/3	1838.637	1838.052	-226.357	0.446	608.127	0.388	22	0.092	-.HSEFISYPISLWTEK.-
R3/RRR3-5/3	1836.887	1838.052	-1182.297	0.338	719.060	0.284	22	0.090	K.HSEFISYPISLWTEK.T
R3/RRR3-5/3	1837.694	1838.052	-195.459	0.307	759.773	0.231	20	0.085	-.HSEFISYPISLWTEK.-
R3/RRR3-1/3	1356.532	1357.621	-1544.724	0.296	242.830	0.387	18	0.077	-.VIKEVLGDKVEK.-
R3/RRR3-10/2	1760.592	1760.969	-214.582	0.642	2888.156	0.551	24	0.498	R.FKDIFQEVYEAGWK.S
R3/RRR3-10/2	1760.588	1760.969	-216.947	0.643	2700.987	0.543	24	0.448	R.FKDIFQEVYEAGWK.S
R3/RRR3-10/3	1778.248	1777.908	191.360	0.551	2804.294	0.489	35	0.429	R.DATDDKVTVEAAEATLK.Y
R3/RRR3-10/2	1760.555	1760.969	-235.798	0.634	2575.289	0.537	23	0.416	R.FKDIFQEVYEAGWK.S
R3/RRR3-10/2	1321.039	1321.453	-313.970	0.546	2241.524	0.633	21	0.379	K.LEAACVGTVESGK.M
R3/RRR3-10/2	1436.085	1436.569	-338.354	0.517	2168.289	0.596	20	0.350	R.AFAEASM*TTAYEK.K
R3/RRR3-10/2	1436.063	1436.569	-1052.144	0.539	2195.860	0.551	20	0.341	R.AFAEASM*TTAYEK.K
R3/RRR3-10/2	1321.059	1321.453	-299.230	0.548	2027.633	0.623	22	0.335	K.LEAACVGTVESGK.M
R3/RRR3-10/2	1436.977	1436.569	284.528	0.544	2088.185	0.565	20	0.325	R.AFAEASM*TTAYEK.K
R3/RRR3-10/3	1778.143	1777.908	132.499	0.597	2320.127	0.504	33	0.317	R.DATDDKVTVEAAEATLK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1777.328	1777.908	-891.701	0.585	2452.900	0.427	33	0.313	R.DATDDKVTVEAAEATLK.Y
R3/RRR3-10/2	1321.118	1321.453	-253.897	0.543	1947.424	0.555	22	0.300	K.LEAACVGTVESGK.M
R3/RRR3-10/2	1485.404	1485.622	-147.017	0.478	1964.939	0.408	18	0.262	K.DIFQEVYEAGWK.S
R3/RRR3-10/2	1798.507	1798.934	-238.038	0.523	1745.134	0.489	22	0.245	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	1799.313	1798.934	211.378	0.545	1718.059	0.486	22	0.240	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	1594.755	1594.755	0.030	0.567	1485.372	0.584	19	0.239	K.SKFEAAGIWYEHR.L
R3/RRR3-10/2	1420.132	1420.570	-308.961	0.504	1588.655	0.506	19	0.232	R.AFAEASMTTAYEK.K
R3/RRR3-10/2	1420.082	1420.570	-344.666	0.489	1612.175	0.482	19	0.229	R.AFAEASMTTAYEK.K
R3/RRR3-10/2	1777.390	1777.908	-857.048	0.567	1615.026	0.477	24	0.227	R.DATDDKVTVEAAEATLK.Y
R3/RRR3-10/2	1798.262	1798.934	-932.548	0.500	1687.867	0.446	22	0.227	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	1420.067	1420.570	-1061.148	0.484	1607.457	0.474	19	0.227	R.AFAEASMTTAYEK.K
R3/RRR3-10/2	1496.236	1496.694	-307.157	0.528	1621.006	0.454	23	0.226	K.DLALLIHGSSNVTR.S
R3/RRR3-10/2	1485.070	1485.622	-1048.256	0.379	1769.871	0.368	18	0.225	K.DIFQEVYEAGWK.S
R3/RRR3-10/2	1496.395	1496.694	-200.102	0.513	1548.831	0.485	23	0.225	K.DLALLIHGSSNVTR.S
R3/RRR3-10/2	1778.346	1777.908	246.987	0.571	1539.288	0.501	23	0.223	R.DATDDKVTVEAAEATLK.Y
R3/RRR3-10/2	1776.879	1777.908	-1145.525	0.534	1551.968	0.488	23	0.222	R.DATDDKVTVEAAEATLK.Y
R3/RRR3-10/2	1057.033	1057.226	-182.735	0.485	1674.246	0.402	18	0.221	R.ATDAVLKGPGK.L
R3/RRR3-10/3	1760.805	1760.969	-93.400	0.573	2025.977	0.410	32	0.217	R.FKDIFQEVYEAGWK.S
R3/RRR3-9/2	1799.365	1798.934	239.951	0.507	1496.954	0.473	21	0.210	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	1594.279	1594.755	-299.173	0.541	1382.654	0.495	19	0.207	K.SKFEAAGIWYEHR.L
R3/RRR3-10/2	1594.186	1594.755	-987.028	0.532	1372.548	0.495	19	0.206	K.SKFEAAGIWYEHR.L
R3/RRR3-10/2	1057.094	1057.226	-124.697	0.471	1489.423	0.418	17	0.203	R.ATDAVLKGPGK.L
R3/RRR3-10/2	1136.019	1136.285	-234.049	0.517	1365.431	0.415	15	0.191	K.YYDLGVLHR.D
R3/RRR3-10/2	1578.388	1577.888	317.604	0.580	1408.643	0.394	20	0.187	K.DKLIFPFLDLDIK.Y
R3/RRR3-10/2	1056.902	1057.226	-307.407	0.471	1317.582	0.426	16	0.187	R.ATDAVLKGPGK.L
R3/RRR3-10/2	1252.120	1252.505	-308.566	0.568	1065.040	0.522	18	0.186	R.LIDDMVAYALK.S
R3/RRR3-10/3	1761.394	1760.969	241.849	0.546	1771.942	0.407	30	0.181	R.FKDIFQEVYEAGWK.S
R3/RRR3-10/2	1252.113	1252.505	-313.946	0.557	1059.368	0.493	18	0.181	R.LIDDMVAYALK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1252.198	1252.505	-246.459	0.550	1062.149	0.491	18	0.181	R.LIDDMVAYALK.S
R3/RRR3-10/2	1136.044	1136.285	-211.950	0.515	1139.428	0.450	14	0.178	K.YYDLGVLHR.D
R3/RRR3-10/2	1268.225	1268.505	-220.919	0.458	1077.003	0.465	18	0.177	R.LIDDM*VAYALK.S
R3/RRR3-26/2	1321.673	1321.453	167.339	0.495	919.178	0.532	20	0.176	K.LEAACVGTVESGK.M
R3/RRR3-10/2	1577.161	1577.888	-1098.759	0.515	1299.518	0.360	19	0.172	K.DKLIFPFLDLDIK.Y
R3/RRR3-10/2	1577.132	1577.888	-1116.945	0.505	1376.412	0.319	19	0.171	K.DKLIFPFLDLDIK.Y
R3/RRR3-10/3	1760.370	1760.969	-911.385	0.509	1732.077	0.381	29	0.170	R.FKDIFQEVYEAGWK.S
R3/RRR3-10/2	1268.277	1268.505	-180.171	0.455	1117.892	0.400	18	0.169	R.LIDDM*VAYALK.S
R3/RRR3-10/2	1268.072	1268.505	-342.024	0.408	1024.359	0.439	18	0.169	R.LIDDM*VAYALK.S
R3/RRR3-3/2	1799.895	1798.934	-22.081	0.423	1042.906	0.424	19	0.162	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	993.347	994.045	-1715.006	0.327	937.486	0.448	13	0.160	R.HAFGDQYR.C
R3/RRR3-2/2	1798.070	1798.934	-1039.622	0.423	1101.775	0.377	18	0.157	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	1798.327	1798.934	-896.498	0.401	866.547	0.432	18	0.153	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	1799.293	1798.934	200.017	0.403	772.519	0.456	18	0.151	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/2	993.425	994.045	-1635.870	0.356	641.988	0.472	12	0.151	R.HAFGDQYR.C
R3/RRR3-10/3	1760.006	1760.969	-1118.497	0.463	1695.930	0.310	28	0.148	R.FKDIFQEVYEAGWK.S
R3/RRR3-10/2	1334.256	1334.628	-279.294	0.373	1017.805	0.276	17	0.146	-.LIFPFLDLDIK.-
R3/RRR3-10/2	1497.848	1496.694	103.517	0.335	665.708	0.422	16	0.144	K.DLALLIHGSSNVTR.S
R3/RRR3-2/2	1799.526	1798.934	-227.357	0.402	603.637	0.396	18	0.141	K.GGETSTNSIASIFAWTR.G
R3/RRR3-26/2	1321.723	1321.453	204.757	0.361	288.965	0.413	14	0.141	K.LEAACVGTVESGK.M
R3/RRR3-10/2	1333.666	1334.628	-1475.446	0.403	953.613	0.263	16	0.141	K.LIFPFLDLDIK.Y
R3/RRR3-1/2	1799.641	1798.934	-163.255	0.386	961.717	0.284	19	0.140	K.GGETSTNSIASIFAWTR.G
R3/RRR3-17/2	1268.337	1268.505	-132.765	0.315	857.000	0.277	15	0.140	R.LIDDM*VAYALK.S
R3/RRR3-10/2	1334.242	1334.628	-289.941	0.428	984.846	0.221	17	0.138	-.LIFPFLDLDIK.-
R3/RRR3-10/2	1497.506	1496.694	-126.124	0.267	492.796	0.403	14	0.135	K.DLALLIHGSSNVTR.S
R3/RRR3-10/3	1595.365	1594.755	-245.026	0.593	934.796	0.505	27	0.129	K.SKFEAAGIWYEHR.L
R3/RRR3-10/3	1596.133	1594.755	238.009	0.583	818.860	0.492	25	0.121	K.SKFEAAGIWYEHR.L
R3/RRR3-10/3	1799.458	1798.934	-265.340	0.396	1111.723	0.415	25	0.121	K.GGETSTNSIASIFAWTR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1496.823	1496.694	86.851	0.365	765.310	0.529	25	0.118	K.DLALLIHGSSNVTR.S
R3/RRR3-9/3	1777.770	1777.908	-77.805	0.310	1238.902	0.279	26	0.106	R.DATDDKVTVEAAEATLK.Y
R3/RRR3-10/3	1496.804	1496.694	74.092	0.324	614.579	0.466	24	0.104	K.DLALLIHGSSNVTR.S
R3/RRR3-10/3	1577.791	1577.888	-61.942	0.317	1138.718	0.252	22	0.095	K.DKLIFPFLDLDIK.Y
R3/RRR3-10/3	1496.469	1496.694	-150.848	0.361	535.899	0.330	22	0.094	K.DLALLIHGSSNVTR.S
R3/RRR3-10/3	1798.806	1798.934	-71.518	0.339	638.073	0.265	25	0.086	K.GGETSTNSIASIFAWTR.G
R3/RRR3-10/3	1577.288	1577.888	-1017.483	0.210	1082.055	0.147	20	0.080	K.DKLIFPFLDLDIK.Y
R3/RRR3-10/3	1576.909	1577.888	-1259.160	0.248	1170.240	0.102	21	0.078	K.DKLIFPFLDLDIK.Y
R3/RRR3-8/2	1094.138	1094.374	-215.816	0.401	1312.769	0.430	16	0.188	K.IAVLGFAFKK.D
R3/RRR3-8/2	1094.181	1094.374	-176.755	0.406	1189.813	0.417	16	0.176	K.IAVLGFAFKK.D
R3/RRR3-8/2	1094.209	1094.374	-151.238	0.446	1119.105	0.444	16	0.176	K.KIAVLGFAFK.K
R3/RRR3-8/2	1094.202	1094.374	-157.953	0.381	1165.011	0.414	16	0.173	K.IAVLGFAFKK.D
R3/RRR3-8/2	966.028	966.201	-179.481	0.501	1036.863	0.418	15	0.168	K.IAVLGFAFK.K
R3/RRR3-7/2	965.549	966.201	-1716.575	0.413	1032.326	0.404	15	0.165	K.IAVLGFAFK.K
R3/RRR3-2/2	966.117	966.201	-86.698	0.473	988.676	0.388	15	0.161	K.IAVLGFAFK.K
R3/RRR3-8/2	965.967	966.201	-242.614	0.471	1008.289	0.381	15	0.161	K.IAVLGFAFK.K
R3/RRR3-9/2	965.629	966.201	-1633.129	0.393	1014.063	0.380	15	0.160	K.IAVLGFAFK.K
R3/RRR3-7/2	965.956	966.201	-254.151	0.449	972.441	0.381	15	0.159	K.IAVLGFAFK.K
R3/RRR3-8/2	966.046	966.201	-160.847	0.514	989.437	0.372	15	0.159	K.IAVLGFAFK.K
R3/RRR3-9/2	965.940	966.201	-271.394	0.470	960.282	0.379	15	0.159	K.IAVLGFAFK.K
R3/RRR3-9/2	966.123	966.201	-81.121	0.448	941.295	0.381	15	0.158	K.IAVLGFAFK.K
R3/RRR3-8/3	1842.179	1841.100	42.787	0.485	1411.217	0.406	26	0.144	K.HVAEANIIFVSVNTPTK.T
R3/RRR3-9/2	1094.719	1094.374	316.112	0.407	920.256	0.256	15	0.140	K.KIAVLGFAFK.K
R3/RRR3-9/2	1095.043	1094.374	-303.296	0.338	620.092	0.304	13	0.135	-.KIAVLGFAFK.-
R3/RRR3-8/3	1094.578	1094.374	187.196	0.477	1005.231	0.360	21	0.101	-.KIAVLGFAFK.-
R3/RRR3-2/2	1647.687	1646.909	-134.915	0.587	2005.402	0.566	24	0.312	R.LDQPIILTGYSALNK.L
R3/RRR3-2/2	1281.144	1281.483	-265.547	0.480	1808.502	0.523	18	0.268	K.IIEEGPVTVAPR.E
R3/RRR3-2/2	1281.217	1281.483	-208.385	0.453	1870.061	0.486	18	0.267	K.IIEEGPVTVAPR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1281.218	1281.483	-207.811	0.486	1848.037	0.492	18	0.265	K.IIEEGPVTVAPR.E
R3/RRR3-2/2	1646.374	1646.909	-934.917	0.522	1756.189	0.501	22	0.253	R.LDQPIILTGYSALNK.L
R3/RRR3-2/2	1545.949	1546.679	-1122.232	0.423	1675.926	0.461	19	0.234	R.SLSELEM*FTEESK.G
R3/RRR3-2/2	1645.680	1646.909	-1358.641	0.366	1749.458	0.411	22	0.231	R.LDQPIILTGYSALNK.L
R3/RRR3-1/2	1281.249	1281.483	-183.343	0.451	1657.802	0.431	18	0.224	K.IIEEGPVTVAPR.E
R3/RRR3-1/2	1646.825	1646.909	-51.494	0.496	1507.884	0.508	21	0.222	R.LDQPIILTGYSALNK.L
R3/RRR3-1/3	1803.846	1803.135	-160.845	0.444	1919.717	0.448	31	0.222	R.HVEPPLSALLELDKLK.V
R3/RRR3-2/3	1803.192	1803.135	31.321	0.548	1856.640	0.407	31	0.196	R.HVEPPLSALLELDKLK.V
R3/RRR3-2/2	1905.655	1905.095	-231.657	0.564	957.126	0.596	21	0.184	K.TVTANTATVSDYVGYLTK.G
R3/RRR3-2/2	1204.181	1205.216	-1695.208	0.272	1612.252	0.213	18	0.176	R.VGWSDDGSPER.G
R3/RRR3-2/2	1956.542	1955.149	201.463	0.499	1005.492	0.532	19	0.175	R.TTYCYDFPLAFETAVR.K
R3/RRR3-2/2	1182.026	1181.357	-281.288	0.370	964.569	0.531	17	0.174	K.VVEFCTALGGK.T
R3/RRR3-2/2	1181.240	1181.357	-99.672	0.320	1102.488	0.459	18	0.172	K.VVEFCTALGGK.T
R3/RRR3-2/2	1905.481	1905.095	202.942	0.505	844.459	0.559	21	0.170	K.TVTANTATVSDYVGYLTK.G
R3/RRR3-2/2	1711.575	1710.935	-211.356	0.447	1152.906	0.415	20	0.170	K.FDSGIINDFPANMLR.V
R3/RRR3-2/2	1905.813	1905.095	-148.185	0.501	738.665	0.547	23	0.165	K.TVTANTATVSDYVGYLTK.G
R3/RRR3-2/2	1204.340	1205.216	-1562.416	0.316	1444.230	0.225	17	0.164	R.VGWSDDGSPER.G
R3/RRR3-2/2	1204.136	1205.216	-1732.282	0.284	1508.006	0.178	18	0.162	R.VGWSDDGSPER.G
R3/RRR3-1/3	1802.997	1803.135	-76.750	0.520	1315.729	0.502	30	0.158	R.HVEPPLSALLELDKLK.V
R3/RRR3-2/2	1149.201	1149.282	-70.595	0.386	1035.252	0.379	15	0.157	K.TAQALLDFNR.E
R3/RRR3-1/2	1905.457	1905.095	190.543	0.493	586.772	0.553	20	0.157	K.TVTANTATVSDYVGYLTK.G
R3/RRR3-1/2	1906.376	1905.095	147.935	0.415	360.923	0.577	20	0.153	K.TVTANTATVSDYVGYLTK.G
R3/RRR3-2/2	1107.206	1107.307	-90.855	0.367	1138.227	0.303	14	0.153	K.SLESLSMAIR.F
R3/RRR3-2/3	1802.578	1803.135	-866.509	0.489	1682.746	0.326	30	0.151	R.HVEPPLSALLELDKLK.V
R3/RRR3-1/2	1430.851	1429.691	112.642	0.426	724.150	0.445	14	0.149	R.EGLPLFILANWR.-
R3/RRR3-1/2	1430.851	1429.691	112.642	0.402	794.344	0.404	15	0.148	R.EGLPLFILANWR.-
R3/RRR3-2/2	994.100	994.123	-23.168	0.354	794.726	0.397	14	0.148	K.ATELVFADK.H
R3/RRR3-1/2	1906.679	1905.095	-219.011	0.349	223.589	0.576	17	0.146	K.TVTANTATVSDYVGYLTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1021.227	1021.195	31.039	0.418	666.871	0.387	14	0.143	R.TVGIGAYLAR.L
R3/RRR3-2/2	1308.539	1307.436	78.820	0.432	605.300	0.420	14	0.141	R.AGQVWFPDSATK.T
R3/RRR3-1/2	1430.949	1429.691	180.828	0.357	658.182	0.386	13	0.140	R.EGLPLFILANWR.-
R3/RRR3-1/2	1389.540	1390.610	-1493.657	0.202	744.431	0.310	13	0.129	R.EIIVVANDITFR.A
R3/RRR3-4/2	1906.116	1905.095	10.945	0.185	97.194	0.428	14	0.120	-.TVTANTATVSDYVGYLTK.-
R3/RRR3-2/3	1555.308	1554.792	-312.110	0.520	1107.284	0.361	24	0.112	R.MHHLSVCQWEVK.L
R3/RRR3-2/2	1726.212	1726.935	-1000.923	0.355	209.302	0.336	12	0.111	-.FDSGIINDFPANM*LR.-
R3/RRR3-2/3	1646.454	1646.909	-277.356	0.331	966.721	0.302	24	0.092	R.LDQPIILTGYSALNK.L
R3/RRR3-8/2	1243.011	1242.447	-351.705	0.509	2157.043	0.585	19	0.350	R.NLVVVSSPDLAK.E
R3/RRR3-8/2	1157.550	1157.302	214.759	0.589	2067.280	0.520	20	0.310	R.DPAAATSGVVIR.R
R3/RRR3-8/2	1501.128	1501.754	-1086.469	0.443	2111.105	0.486	20	0.308	K.ILVNAWFLANDPK.R
R3/RRR3-8/2	1156.738	1157.302	-1356.274	0.489	1886.103	0.557	20	0.291	R.DPAAATSGVVIR.R
R3/RRR3-8/2	1501.392	1501.754	-241.923	0.513	1888.269	0.543	19	0.287	K.ILVNAWFLANDPK.R
R3/RRR3-8/2	1158.002	1157.302	-259.634	0.591	1884.614	0.506	20	0.276	R.DPAAATSGVVIR.R
R3/RRR3-8/2	1713.354	1711.882	276.507	0.526	1144.354	0.580	19	0.199	K.GQDMVFTVYGDHWR.K
R3/RRR3-8/2	1163.494	1164.290	-1548.023	0.353	1239.269	0.391	17	0.174	K.LAGYDIPAESK.I
R3/RRR3-8/2	1164.180	1164.290	-94.822	0.468	1085.720	0.438	17	0.172	K.LAGYDIPAESK.I
R3/RRR3-8/2	1163.516	1164.290	-1529.158	0.402	1005.138	0.472	16	0.170	K.LAGYDIPAESK.I
R3/RRR3-8/2	1313.245	1313.488	-185.589	0.422	930.728	0.470	20	0.165	R.RDPAAATSGVVIR.R
R3/RRR3-8/2	1713.124	1711.882	141.967	0.468	940.862	0.472	18	0.164	K.GQDMVFTVYGDHWR.K
R3/RRR3-8/2	1312.560	1313.488	-1473.239	0.432	858.508	0.486	20	0.164	R.RDPAAATSGVVIR.R
R3/RRR3-8/2	1102.513	1103.342	-1663.963	0.447	1146.368	0.335	16	0.162	R.RFGDILLLR.M
R3/RRR3-8/2	1102.745	1103.342	-1452.880	0.500	1151.485	0.316	16	0.159	R.RFGDILLLR.M
R3/RRR3-8/2	1103.153	1103.342	-171.766	0.498	1085.730	0.325	16	0.157	R.RFGDILLLR.M
R3/RRR3-8/2	1298.249	1297.395	-112.380	0.379	1087.819	0.315	16	0.152	R.FDSVDDPLFNK.L
R3/RRR3-8/3	1453.774	1453.581	133.428	0.477	1884.685	0.248	27	0.151	R.RFDSVDDPLFNK.L
R3/RRR3-8/2	1459.055	1459.589	-1054.191	0.368	420.423	0.497	18	0.147	K.EVLHTQGVEFGSR.T
R3/RRR3-8/2	1459.332	1459.589	-176.575	0.358	465.850	0.459	17	0.144	K.EVLHTQGVEFGSR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	946.912	947.156	-258.616	0.566	1101.134	0.231	13	0.140	R.FGDILLLR.M
R3/RRR3-8/2	1198.140	1198.459	-267.491	0.291	423.075	0.382	13	0.137	R.IMTVPFFTNK.V
R3/RRR3-8/2	947.051	947.156	-111.714	0.553	1094.417	0.207	13	0.137	R.FGDILLLR.M
R3/RRR3-8/2	946.910	947.156	-260.168	0.556	1049.926	0.206	13	0.135	R.FGDILLLR.M
R3/RRR3-8/3	1469.366	1469.675	-211.000	0.518	1158.110	0.436	28	0.128	R.RDPAAATSGVVIRR.R
R3/RRR3-8/2	1214.184	1214.459	-226.557	0.249	845.878	0.082	14	0.124	R.IM*TVPFFTNK.V
R3/RRR3-8/3	1891.724	1892.018	-155.962	0.518	1083.167	0.417	32	0.120	R.FLEEEKAVEAHGNDFR.F
R3/RRR3-8/3	1468.996	1469.675	-1145.999	0.477	773.621	0.384	25	0.103	R.RDPAAATSGVVIRR.R
R3/RRR3-8/3	1459.427	1459.589	-111.429	0.339	821.305	0.389	23	0.100	K.EVLHTQGVEFGSR.T
R3/RRR3-8/3	1468.518	1469.675	-1473.032	0.454	701.190	0.332	23	0.095	R.RDPAAATSGVVIRR.R
R3/RRR3-8/3	1460.337	1459.589	-173.151	0.311	560.597	0.339	19	0.091	K.EVLHTQGVEFGSR.T
R3/RRR3-2/2	1558.538	1558.757	-141.296	0.505	1994.418	0.520	20	0.296	K.LVYELFTDTLTSR.L
R3/RRR3-3/2	1558.529	1558.757	-146.560	0.503	1961.898	0.438	20	0.267	K.LVYELFTDTLTSR.L
R3/RRR3-3/2	1559.168	1558.757	264.509	0.551	1800.089	0.490	20	0.257	K.LVYELFTDTLTSR.L
R3/RRR3-3/2	1558.321	1558.757	-280.855	0.462	1825.304	0.433	19	0.246	K.LVYELFTDTLTSR.L
R3/RRR3-3/2	1227.216	1227.392	-144.525	0.508	1431.665	0.469	19	0.207	K.IIGLDGSEAPVR.V
R3/RRR3-3/2	1227.062	1227.392	-269.667	0.500	1385.021	0.473	19	0.204	K.IIGLDGSEAPVR.V
R3/RRR3-3/2	1674.279	1674.788	-904.345	0.409	1441.709	0.436	23	0.200	K.AIENTAASISDVPEEK.L
R3/RRR3-3/2	1095.978	1096.219	-220.369	0.490	1267.868	0.484	14	0.195	R.HDNVQLLEK.L
R3/RRR3-3/2	1095.914	1096.219	-278.924	0.397	1339.988	0.422	14	0.189	R.HDNVQLLEK.L
R3/RRR3-26/2	1648.161	1648.774	-981.674	0.489	1523.460	0.322	19	0.184	K.VLNDM*IQDDSEQPK.K
R3/RRR3-2/2	1558.756	1558.757	-0.833	0.401	1237.222	0.444	17	0.181	K.LVYELFTDTLTSR.L
R3/RRR3-3/2	1507.790	1508.761	-1311.405	0.348	1076.635	0.517	19	0.179	R.LTEPSFLESLM*PK.K
R3/RRR3-3/2	1673.480	1674.788	-1383.554	0.291	1268.482	0.350	21	0.167	K.AIENTAASISDVPEEK.L
R3/RRR3-1/2	1227.122	1227.392	-220.764	0.348	1258.088	0.334	18	0.167	K.IIGLDGSEAPVR.V
R3/RRR3-2/2	1227.262	1227.392	-106.210	0.418	1049.464	0.401	17	0.163	K.IIGLDGSEAPVR.V
R3/RRR3-3/2	1507.768	1508.761	-1326.122	0.319	983.899	0.444	19	0.162	R.LTEPSFLESLM*PK.K
R3/RRR3-3/2	1508.017	1508.761	-1160.112	0.413	806.798	0.489	18	0.161	R.LTEPSFLESLM*PK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1311.040	1310.485	-339.992	0.455	724.523	0.514	17	0.160	K.LTTGHGLLQVDR.A
R3/RRR3-3/2	1309.145	1309.495	-268.097	0.405	574.015	0.544	16	0.158	K.LADFVPLTNYR.L
R3/RRR3-3/2	1237.066	1237.409	-278.326	0.409	934.320	0.392	18	0.156	R.LGSM*ETGTGLVR.A
R3/RRR3-26/2	908.987	909.065	-85.749	0.395	483.759	0.493	12	0.153	K.YGSLTVLR.E
R3/RRR3-3/2	1310.298	1309.495	-151.059	0.384	748.114	0.433	17	0.153	K.LADFVPLTNYR.L
R3/RRR3-3/2	1236.497	1237.409	-1550.946	0.432	840.127	0.389	19	0.153	R.LGSM*ETGTGLVR.A
R3/RRR3-2/2	1236.899	1237.409	-1224.578	0.440	829.758	0.397	18	0.153	R.LGSM*ETGTGLVR.A
R3/RRR3-26/2	909.013	909.065	-57.461	0.364	552.074	0.470	13	0.152	K.YGSLTVLR.E
R3/RRR3-3/2	1055.438	1056.153	-1629.831	0.335	1227.871	0.250	13	0.152	R.AFEYAQQAK.E
R3/RRR3-2/2	1227.287	1227.392	-85.956	0.357	887.435	0.364	18	0.150	K.IIGLDGSEAPVR.V
R3/RRR3-1/2	1227.288	1227.392	-84.958	0.447	906.335	0.358	17	0.150	K.IIGLDGSEAPVR.V
R3/RRR3-2/2	1310.036	1309.495	-351.655	0.366	648.485	0.430	16	0.148	K.LADFVPLTNYR.L
R3/RRR3-26/2	908.301	909.065	-1947.229	0.316	502.259	0.418	13	0.146	K.YGSLTVLR.E
R3/RRR3-3/2	1309.352	1309.495	-109.182	0.348	506.174	0.427	15	0.144	K.LADFVPLTNYR.L
R3/RRR3-3/2	1491.747	1492.762	-1354.795	0.294	945.188	0.302	19	0.144	R.LTEPSFLESLMPK.K
R3/RRR3-3/2	1236.264	1237.409	-1740.201	0.378	722.286	0.336	18	0.143	R.LGSM*ETGTGLVR.A
R3/RRR3-3/2	908.493	909.065	-1735.366	0.274	520.178	0.405	13	0.143	K.YGSLTVLR.E
R3/RRR3-3/2	1310.296	1310.485	-144.612	0.375	601.968	0.401	16	0.143	K.LTTGHGLLQVDR.A
R3/RRR3-3/2	1432.210	1432.560	-245.488	0.385	666.022	0.368	16	0.142	R.QTSEWTVQLDPK.F
R3/RRR3-2/2	1508.229	1508.761	-1019.348	0.300	385.755	0.352	17	0.139	R.LTEPSFLESLM*PK.K
R3/RRR3-3/2	908.383	909.065	-1857.152	0.280	408.005	0.368	12	0.139	-.YGSLTVLR.-
R3/RRR3-3/2	908.400	909.065	-1837.708	0.245	342.217	0.382	12	0.137	-.YGSLTVLR.-
R3/RRR3-3/2	1432.374	1432.560	-130.577	0.400	633.709	0.300	16	0.137	R.QTSEWTVQLDPK.F
R3/RRR3-3/2	1055.269	1056.153	-1790.785	0.292	1120.823	0.151	13	0.135	R.AFEYAQQAK.E
R3/RRR3-3/2	1432.118	1432.560	-309.452	0.370	522.334	0.228	15	0.131	-.QTSEWTVQLDPK.-
R3/RRR3-3/3	1626.668	1626.750	-50.333	0.504	518.774	0.532	22	0.117	R.IYDNKFESQYYR.I
R3/RRR3-3/3	1929.353	1929.075	144.357	0.498	752.612	0.466	28	0.113	K.SLSLKPDPEDEEAQKNK.K
R3/RRR3-3/3	1626.872	1626.750	75.205	0.492	552.794	0.471	23	0.111	R.IYDNKFESQYYR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1403.920	1403.608	222.455	0.462	721.560	0.443	23	0.109	K.FKLEDGAEIKPR.V
R3/RRR3-3/3	1929.822	1929.075	-131.598	0.500	651.807	0.455	27	0.108	K.SLSLKPDPEDEEAQKNK.K
R3/RRR3-3/3	1672.027	1670.761	159.361	0.510	987.246	0.352	25	0.104	K.WDEHNQEAISEALK.Q
R3/RRR3-3/3	1929.202	1929.075	66.212	0.462	598.442	0.436	26	0.104	K.SLSLKPDPEDEEAQKNK.K
R3/RRR3-3/3	1403.647	1403.608	27.545	0.480	632.159	0.399	22	0.103	K.FKLEDGAEIKPR.V
R3/RRR3-3/3	1403.639	1403.608	21.788	0.472	699.692	0.383	23	0.102	K.FKLEDGAEIKPR.V
R3/RRR3-3/3	1625.999	1626.750	-1080.373	0.391	534.502	0.400	22	0.097	-.IYDNKFESQYYR.-
R3/RRR3-3/3	1670.907	1670.761	87.511	0.427	736.893	0.306	23	0.092	K.WDEHNQEAISEALK.Q
R3/RRR3-2/3	1627.141	1626.750	240.772	0.461	547.856	0.418	19	0.092	-.IYDNKFESQYYR.-
R3/RRR3-2/2	1954.767	1954.172	-208.174	0.608	3631.047	0.537	27	0.707	R.SPVYAQFSEALNGLSTIR.A
R3/RRR3-1/2	1953.465	1954.172	-876.947	0.569	3533.479	0.564	27	0.691	R.SPVYAQFSEALNGLSTIR.A
R3/RRR3-1/2	1953.583	1954.172	-816.101	0.545	3554.481	0.545	27	0.689	R.SPVYAQFSEALNGLSTIR.A
R3/RRR3-2/2	1953.380	1954.172	-920.233	0.600	3392.520	0.568	26	0.646	R.SPVYAQFSEALNGLSTIR.A
R3/RRR3-2/2	1954.518	1954.172	177.053	0.624	3362.148	0.535	26	0.619	R.SPVYAQFSEALNGLSTIR.A
R3/RRR3-1/2	1486.101	1485.708	265.403	0.522	2670.242	0.496	22	0.424	K.ILVLDEATAAVDVR.T
R3/RRR3-2/2	1488.353	1487.641	-193.862	0.571	2556.891	0.555	22	0.417	R.LASLAENSLNAVER.V
R3/RRR3-1/2	1952.865	1954.172	-1185.241	0.424	2690.234	0.440	25	0.407	R.SPVYAQFSEALNGLSTIR.A
R3/RRR3-2/2	1487.068	1487.641	-1060.762	0.475	2538.030	0.501	22	0.395	R.LASLAENSLNAVER.V
R3/RRR3-1/2	1488.189	1487.641	-304.540	0.557	2487.861	0.526	22	0.392	R.LASLAENSLNAVER.V
R3/RRR3-1/2	1487.298	1487.641	-231.044	0.521	2492.473	0.495	22	0.382	R.LASLAENSLNAVER.V
R3/RRR3-1/2	1487.168	1487.641	-318.744	0.500	2259.528	0.488	21	0.333	R.LASLAENSLNAVER.V
R3/RRR3-1/2	1484.860	1485.708	-1248.031	0.390	2265.106	0.466	23	0.329	K.ILVLDEATAAVDVR.T
R3/RRR3-2/2	1486.730	1487.641	-1289.120	0.390	2237.449	0.417	21	0.308	R.LASLAENSLNAVER.V
R3/RRR3-1/2	1484.681	1485.708	-1369.243	0.392	1955.299	0.473	22	0.277	K.ILVLDEATAAVDVR.T
R3/RRR3-2/2	1357.593	1357.538	40.709	0.467	1523.644	0.441	18	0.212	K.RLEDLLLAEER.L
R3/RRR3-1/2	1850.510	1851.007	-269.657	0.530	1199.434	0.591	24	0.207	R.HDLDLLPGGDLTEIGER.G
R3/RRR3-2/2	1357.624	1357.538	63.345	0.517	1461.409	0.449	18	0.207	K.RLEDLLLAEER.L
R3/RRR3-2/2	1486.499	1485.708	-140.731	0.386	1415.768	0.396	18	0.188	K.ILVLDEATAAVDVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1357.584	1357.538	33.946	0.427	1327.649	0.410	17	0.186	K.RLEDLLLAEER.L
R3/RRR3-2/2	1357.519	1357.538	-13.674	0.440	1280.248	0.420	17	0.183	K.RLEDLLLAEER.L
R3/RRR3-1/2	1200.351	1201.352	-1671.750	0.417	1389.137	0.364	15	0.182	R.LEDLLLAEER.L
R3/RRR3-1/2	1357.773	1357.538	173.260	0.454	1168.847	0.410	16	0.172	K.RLEDLLLAEER.L
R3/RRR3-2/2	1850.403	1851.007	-869.481	0.503	767.368	0.562	21	0.167	R.HDLDLLPGGDLTEIGER.G
R3/RRR3-1/2	1504.881	1503.753	85.022	0.460	730.101	0.567	19	0.166	R.APM*VFFHTNPLGR.I
R3/RRR3-2/2	1850.290	1851.007	-931.008	0.499	582.084	0.591	20	0.161	R.HDLDLLPGGDLTEIGER.G
R3/RRR3-1/2	1400.315	1400.603	-206.225	0.331	1175.084	0.349	16	0.160	K.DAVITLQNVLEGK.H
R3/RRR3-1/2	844.315	844.941	-1931.515	0.368	806.678	0.463	12	0.159	R.HANIFSR.I
R3/RRR3-2/2	1754.670	1754.109	-250.823	0.420	544.831	0.535	21	0.154	K.VLGIIPQAPVLFSGSVR.F
R3/RRR3-1/2	1753.600	1754.109	-863.368	0.398	511.660	0.553	20	0.153	K.VLGIIPQAPVLFSGSVR.F
R3/RRR3-2/2	1754.503	1754.109	225.011	0.413	585.964	0.495	22	0.152	K.VLGIIPQAPVLFSGSVR.F
R3/RRR3-2/2	1642.180	1642.705	-930.968	0.410	797.958	0.439	16	0.150	K.LDSWDETETLYNR.F
R3/RRR3-2/2	1940.727	1941.343	-835.134	0.351	477.821	0.521	21	0.148	R.LLLPNPPLDPELPAISIK.N
R3/RRR3-1/2	844.379	844.941	-1855.533	0.334	863.906	0.351	12	0.148	R.HANIFSR.I
R3/RRR3-2/2	1753.081	1754.109	-1160.307	0.386	574.667	0.459	21	0.147	K.VLGIIPQAPVLFSGSVR.F
R3/RRR3-2/2	1940.467	1941.343	-969.767	0.325	370.006	0.586	18	0.147	R.LLLPNPPLDPELPAISIK.N
R3/RRR3-2/2	1941.826	1941.343	249.585	0.402	252.042	0.548	17	0.146	R.LLLPNPPLDPELPAISIK.N
R3/RRR3-2/2	1892.840	1894.249	-1276.159	0.370	903.962	0.372	17	0.145	R.IFFSWM*TPLM*QQGFK.R
R3/RRR3-1/2	844.820	844.941	-143.565	0.299	692.801	0.400	11	0.145	R.HANIFSR.I
R3/RRR3-2/3	1503.032	1503.753	-1148.386	0.441	1196.725	0.500	26	0.144	R.APM*VFFHTNPLGR.I
R3/RRR3-1/2	1939.975	1941.343	-1224.167	0.334	340.679	0.535	18	0.144	R.LLLPNPPLDPELPAISIK.N
R3/RRR3-1/2	1122.321	1123.198	-1677.032	0.277	881.403	0.341	14	0.144	K.TLVFGDGEER.L
R3/RRR3-1/2	1941.575	1941.343	119.902	0.385	341.427	0.477	18	0.143	R.LLLPNPPLDPELPAISIK.N
R3/RRR3-1/2	1753.340	1754.109	-1012.095	0.357	362.844	0.454	17	0.141	K.VLGIIPQAPVLFSGSVR.F
R3/RRR3-1/2	1400.130	1400.603	-338.909	0.415	554.443	0.419	14	0.140	-.DAVITLQNVLEGK.-
R3/RRR3-1/2	1357.741	1357.538	150.089	0.284	871.752	0.285	15	0.140	K.RLEDLLLAEER.L
R3/RRR3-1/2	1942.027	1941.343	-163.453	0.380	235.376	0.423	16	0.140	R.LLLPNPPLDPELPAISIK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	875.042	875.005	42.381	0.271	722.871	0.347	13	0.138	K.AIDVTSLR.H
R3/RRR3-1/2	1400.260	1400.603	-245.580	0.354	545.862	0.362	13	0.136	K.DAVITLQNVLEGK.H
R3/RRR3-1/2	1122.768	1123.198	-384.355	0.196	843.428	0.270	15	0.134	K.TLVFGDGEER.L
R3/RRR3-2/2	1400.246	1400.603	-255.376	0.275	783.883	0.264	15	0.134	K.DAVITLQNVLEGK.H
R3/RRR3-1/2	1122.407	1123.198	-1600.655	0.160	575.755	0.158	12	0.127	-.TLVFGDGEER.-
R3/RRR3-2/3	1503.062	1503.753	-1128.691	0.450	893.066	0.485	25	0.122	R.APM*VFFHTNPLGR.I
R3/RRR3-1/3	1503.719	1503.753	-22.480	0.469	862.658	0.487	23	0.121	R.APM*VFFHTNPLGR.I
R3/RRR3-2/3	1487.887	1487.754	90.006	0.456	733.530	0.510	21	0.120	R.APMVFFHTNPLGR.I
R3/RRR3-2/3	1851.750	1851.007	-139.559	0.451	948.444	0.455	27	0.119	R.HDLDLLPGGDLTEIGER.G
R3/RRR3-2/3	1488.032	1487.754	187.623	0.446	887.206	0.443	23	0.115	R.APMVFFHTNPLGR.I
R3/RRR3-1/3	1940.506	1941.343	-949.533	0.424	869.296	0.461	27	0.115	R.LLLPNPPLDPELPAISIK.N
R3/RRR3-2/3	1503.884	1503.753	87.308	0.384	807.586	0.458	24	0.113	R.APM*VFFHTNPLGR.I
R3/RRR3-1/3	1504.410	1503.753	-229.066	0.414	610.652	0.493	21	0.113	R.APM*VFFHTNPLGR.I
R3/RRR3-1/3	1503.432	1503.753	-214.027	0.427	711.892	0.464	22	0.112	R.APM*VFFHTNPLGR.I
R3/RRR3-1/3	952.045	952.136	-95.935	0.449	900.385	0.391	16	0.106	R.AHLKDVIR.R
R3/RRR3-1/3	952.491	952.136	374.097	0.475	698.661	0.392	15	0.103	R.AHLKDVIR.R
R3/RRR3-2/3	1940.950	1941.343	-203.102	0.406	738.647	0.427	26	0.103	-.LLLPNPPLDPELPAISIK.-
R3/RRR3-2/3	1851.928	1851.007	-43.153	0.416	778.688	0.382	25	0.100	R.HDLDLLPGGDLTEIGER.G
R3/RRR3-1/3	1851.918	1851.007	-48.707	0.383	663.824	0.404	24	0.099	R.HDLDLLPGGDLTEIGER.G
R3/RRR3-1/3	952.162	952.136	27.715	0.428	671.528	0.341	15	0.097	R.AHLKDVIR.R
R3/RRR3-2/3	1940.185	1941.343	-1115.437	0.326	678.355	0.320	24	0.090	R.LLLPNPPLDPELPAISIK.N
R3/RRR3-4/2	1832.572	1833.143	-859.835	0.544	2804.210	0.541	25	0.472	R.NGVTATDLVLTVTQMLR.K
R3/RRR3-4/2	1833.199	1833.143	30.281	0.575	2733.182	0.584	24	0.471	R.NGVTATDLVLTVTQMLR.K
R3/RRR3-4/2	1850.497	1849.143	192.154	0.544	1755.311	0.545	22	0.262	R.NGVTATDLVLTVTQM*LR.K
R3/RRR3-4/2	1558.121	1558.589	-301.322	0.513	1623.592	0.575	22	0.254	K.SGEDADTLGLTGHER.F
R3/RRR3-4/2	1515.224	1515.630	-268.255	0.509	1665.636	0.539	20	0.254	K.M*FVDYNQPEAER.V
R3/RRR3-4/2	1656.308	1656.768	-278.729	0.512	1778.828	0.480	21	0.252	K.SDWLSCLDNDVGFK.G
R3/RRR3-4/2	1515.132	1515.630	-329.040	0.493	1639.156	0.546	20	0.252	K.M*FVDYNQPEAER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1501.287	1500.656	-246.915	0.544	1795.093	0.470	20	0.249	R.SDDTVAMIESYLR.A
R3/RRR3-4/2	1501.206	1500.656	-300.675	0.514	1751.084	0.394	20	0.225	R.SDDTVAMIESYLR.A
R3/RRR3-4/2	1517.467	1516.656	-124.861	0.568	1456.331	0.519	20	0.219	R.SDDTVAM*IESYLR.A
R3/RRR3-4/2	1522.614	1521.843	-150.822	0.579	1193.442	0.621	21	0.215	R.SNLAGMGIIPLCFK.S
R3/RRR3-4/2	1501.109	1500.656	302.390	0.550	1554.722	0.443	19	0.212	R.SDDTVAMIESYLR.A
R3/RRR3-4/2	1517.356	1516.656	-197.815	0.516	1468.741	0.469	20	0.210	R.SDDTVAM*IESYLR.A
R3/RRR3-4/2	1656.360	1656.768	-246.861	0.494	1425.142	0.492	20	0.210	K.SDWLSCLDNDVGFK.G
R3/RRR3-4/2	1880.333	1879.083	133.510	0.427	1638.853	0.346	24	0.203	K.FVEFYGGGMSELSLADR.A
R3/RRR3-4/2	1656.251	1656.768	-918.475	0.442	1475.520	0.390	20	0.194	K.SDWLSCLDNDVGFK.G
R3/RRR3-4/2	1558.328	1558.589	-168.500	0.503	1171.813	0.530	22	0.194	K.SGEDADTLGLTGHER.F
R3/RRR3-4/2	1283.239	1282.426	-146.516	0.409	1121.286	0.560	17	0.193	K.YYSLPALSDPR.I
R3/RRR3-4/2	1521.356	1521.843	-321.400	0.485	1077.893	0.568	20	0.192	R.SNLAGMGIIPLCFK.S
R3/RRR3-4/2	1558.291	1558.589	-191.918	0.505	1113.710	0.530	20	0.187	K.SGEDADTLGLTGHER.F
R3/RRR3-4/2	1516.149	1516.656	-996.558	0.474	1297.087	0.436	19	0.187	R.SDDTVAM*IESYLR.A
R3/RRR3-1/2	1517.588	1516.656	-45.060	0.462	1173.824	0.487	19	0.185	R.SDDTVAM*IESYLR.A
R3/RRR3-1/2	1517.862	1516.656	136.280	0.415	1215.340	0.395	18	0.172	R.SDDTVAM*IESYLR.A
R3/RRR3-1/2	1557.655	1558.589	-1245.750	0.481	923.127	0.515	20	0.171	K.SGEDADTLGLTGHER.F
R3/RRR3-4/2	1521.170	1521.843	-1103.223	0.437	967.279	0.480	19	0.168	R.SNLAGMGIIPLCFK.S
R3/RRR3-4/2	1618.004	1616.793	130.411	0.467	788.677	0.509	21	0.165	R.DIWPSTEEIAEVVK.S
R3/RRR3-5/2	1502.046	1500.656	260.222	0.456	1271.370	0.310	17	0.161	R.SDDTVAMIESYLR.A
R3/RRR3-4/2	1537.414	1537.843	-279.501	0.441	588.148	0.576	17	0.160	R.SNLAGM*GIIPLCFK.S
R3/RRR3-4/2	1537.383	1537.843	-299.736	0.413	607.000	0.542	18	0.158	R.SNLAGM*GIIPLCFK.S
R3/RRR3-4/2	1174.162	1173.300	-117.895	0.570	815.686	0.427	16	0.157	K.ILDWENSAPK.Q
R3/RRR3-4/2	1537.212	1537.843	-1064.155	0.422	674.425	0.509	18	0.157	R.SNLAGM*GIIPLCFK.S
R3/RRR3-4/2	1880.154	1879.083	37.991	0.330	1377.220	0.224	22	0.157	K.FVEFYGGGMSELSLADR.A
R3/RRR3-4/2	1173.165	1173.300	-115.282	0.524	834.605	0.411	16	0.156	K.ILDWENSAPK.Q
R3/RRR3-4/2	1282.203	1282.426	-174.995	0.374	818.005	0.461	14	0.156	K.YYSLPALSDPR.I
R3/RRR3-5/2	1283.316	1282.426	-86.306	0.354	849.172	0.442	15	0.155	K.YYSLPALSDPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1173.018	1173.300	-240.967	0.478	818.226	0.363	16	0.150	K.ILDWENSAPK.Q
R3/RRR3-4/2	1281.302	1282.426	-1662.642	0.303	919.286	0.373	15	0.150	K.YYSLPALSDPR.I
R3/RRR3-4/2	1197.912	1198.258	-290.027	0.338	935.930	0.324	16	0.147	R.NCDEFQVTGK.D
R3/RRR3-4/2	951.888	952.086	-208.965	0.284	931.935	0.325	15	0.147	K.LSVFDAATK.Y
R3/RRR3-4/2	1616.336	1616.793	-284.107	0.420	756.293	0.370	21	0.147	R.DIWPSTEEIAEVVK.S
R3/RRR3-4/2	1197.876	1198.258	-319.882	0.350	1029.729	0.283	15	0.147	R.NCDEFQVTGK.D
R3/RRR3-4/2	1172.583	1173.300	-1469.094	0.390	844.362	0.325	16	0.146	K.ILDWENSAPK.Q
R3/RRR3-4/2	951.904	952.086	-192.498	0.280	675.125	0.371	14	0.143	K.LSVFDAATK.Y
R3/RRR3-4/2	951.954	952.086	-139.498	0.302	801.152	0.320	14	0.143	K.LSVFDAATK.Y
R3/RRR3-4/2	1847.860	1849.143	-1238.888	0.348	839.687	0.373	16	0.142	-.NGVTATDLVLTVTQM*LR.-
R3/RRR3-4/2	1616.227	1616.793	-972.280	0.336	742.415	0.348	19	0.142	R.DIWPSTEEIAEVVK.S
R3/RRR3-4/2	1616.363	1616.793	-267.362	0.357	600.304	0.378	18	0.141	R.DIWPSTEEIAEVVK.S
R3/RRR3-4/2	1197.585	1198.258	-1401.721	0.274	936.957	0.270	15	0.140	R.NCDEFQVTGK.D
R3/RRR3-1/2	952.050	952.086	-38.145	0.265	500.161	0.342	11	0.137	K.LSVFDAATK.Y
R3/RRR3-5/2	1516.227	1516.656	-283.315	0.297	494.763	0.313	15	0.137	R.SDDTVAM*IESYLR.A
R3/RRR3-1/2	1657.257	1656.768	296.136	0.353	637.100	0.304	16	0.135	K.SDWLSCLDNDVGFK.G
R3/RRR3-2/2	952.255	952.086	177.870	0.213	575.183	0.309	12	0.135	K.LSVFDAATK.Y
R3/RRR3-1/2	951.826	952.086	-274.711	0.187	580.405	0.334	12	0.134	K.LSVFDAATK.Y
R3/RRR3-4/2	974.856	975.166	-319.463	0.302	742.060	0.258	14	0.133	-.FLKGEVGPK.-
R3/RRR3-4/2	974.855	975.166	-320.469	0.315	1027.901	0.145	16	0.133	K.FLKGEVGPK.T
R3/RRR3-3/2	952.064	952.086	-23.355	0.116	634.785	0.162	12	0.127	K.LSVFDAATK.Y
R3/RRR3-4/3	1558.825	1558.589	151.377	0.478	879.714	0.497	26	0.123	K.SGEDADTLGLTGHER.F
R3/RRR3-4/3	1558.180	1558.589	-263.799	0.480	691.329	0.472	24	0.112	K.SGEDADTLGLTGHER.F
R3/RRR3-4/3	1148.340	1147.352	-10.632	0.408	947.853	0.399	18	0.108	R.IERLPYSIR.I
R3/RRR3-4/3	1558.978	1558.589	249.964	0.410	546.090	0.430	23	0.104	K.SGEDADTLGLTGHER.F
R3/RRR3-4/3	1148.392	1147.352	34.467	0.368	687.028	0.368	18	0.097	R.IERLPYSIR.I
R3/RRR3-2/3	1558.291	1558.589	-192.359	0.306	481.488	0.411	21	0.097	-.SGEDADTLGLTGHER.-
R3/RRR3-1/3	1558.629	1558.589	25.199	0.367	560.516	0.348	22	0.096	K.SGEDADTLGLTGHER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1147.508	1147.352	136.336	0.379	723.424	0.306	19	0.093	R.IERLPYSIR.I
R3/RRR3-19/2	1844.581	1844.996	-225.853	0.471	2162.710	0.496	25	0.780	K.FLDGIYVSDKGTITEDA.-
R3/RRR3-19/2	1845.439	1844.996	240.263	0.542	1925.935	0.565	25	0.606	K.FLDGIYVSDKGTITEDA.-
R3/RRR3-19/2	1843.848	1844.996	-1168.928	0.410	1673.552	0.456	23	0.439	K.FLDGIYVSDKGTITEDA.-
R3/RRR3-19/2	1914.652	1915.135	-252.758	0.648	2493.231	0.572	26	0.409	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/2	1914.531	1915.135	-840.166	0.638	2470.914	0.560	26	0.400	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/2	1914.490	1915.135	-861.672	0.630	2446.174	0.564	26	0.396	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/2	1583.477	1582.827	-221.495	0.581	2225.990	0.616	22	0.364	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1915.258	1915.135	64.616	0.563	2601.136	0.465	34	0.364	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/2	1582.454	1582.827	-236.339	0.525	2242.510	0.597	22	0.362	R.TAISHVQNLITGVTK.G
R3/RRR3-19/2	1582.362	1582.827	-294.540	0.529	2139.172	0.634	22	0.354	R.TAISHVQNLITGVTK.G
R3/RRR3-18/2	1582.368	1582.827	-290.437	0.496	2198.813	0.593	23	0.353	R.TAISHVQNLITGVTK.G
R3/RRR3-21/2	1582.329	1582.827	-315.515	0.496	2102.885	0.591	22	0.333	R.TAISHVQNLITGVTK.G
R3/RRR3-24/2	1582.288	1582.827	-975.415	0.531	2058.267	0.588	22	0.324	R.TAISHVQNLITGVTK.G
R3/RRR3-18/2	1583.297	1582.827	298.138	0.506	1866.839	0.633	21	0.304	R.TAISHVQNLITGVTK.G
R3/RRR3-20/2	1582.187	1582.827	-1039.087	0.497	1951.827	0.571	22	0.301	R.TAISHVQNLITGVTK.G
R3/RRR3-19/2	1374.106	1374.675	-1145.380	0.537	1977.607	0.489	20	0.284	R.KVDMLEGVTILR.S
R3/RRR3-21/2	1583.946	1582.827	75.937	0.563	1649.306	0.622	20	0.266	R.TAISHVQNLITGVTK.G
R3/RRR3-20/2	1583.264	1582.827	277.264	0.554	1653.839	0.619	20	0.266	R.TAISHVQNLITGVTK.G
R3/RRR3-24/2	1581.776	1582.827	-1299.977	0.469	1722.824	0.564	21	0.262	R.TAISHVQNLITGVTK.G
R3/RRR3-19/2	1513.293	1512.695	-266.720	0.583	1673.505	0.572	22	0.262	K.HLNLDFQLLEGGR.K
R3/RRR3-19/2	1583.587	1582.827	-151.509	0.545	1495.739	0.646	20	0.252	R.TAISHVQNLITGVTK.G
R3/RRR3-21/2	1583.295	1582.827	297.055	0.568	1579.012	0.604	19	0.251	R.TAISHVQNLITGVTK.G
R3/RRR3-19/2	1261.973	1262.502	-1215.049	0.478	1800.416	0.441	18	0.246	K.VDM*LEGVTILR.S
R3/RRR3-19/2	1374.374	1374.675	-220.006	0.528	1774.579	0.453	19	0.244	R.KVDMLEGVTILR.S
R3/RRR3-19/2	1511.694	1512.695	-1327.929	0.501	1586.698	0.522	21	0.237	K.HLNLDFQLLEGGR.K
R3/RRR3-19/2	1512.422	1512.695	-181.143	0.511	1479.586	0.541	21	0.229	K.HLNLDFQLLEGGR.K
R3/RRR3-19/2	1262.084	1262.502	-332.138	0.553	1648.775	0.383	18	0.212	K.VDM*LEGVTILR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1512.671	1512.695	-15.671	0.468	1498.259	0.436	21	0.208	K.HLNLDFQLLEGGR.K
R3/RRR3-21/3	1913.907	1915.135	-1167.472	0.511	2061.404	0.341	33	0.206	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/2	1261.931	1262.502	-1248.465	0.460	1564.953	0.375	17	0.202	K.VDM*LEGVTILR.S
R3/RRR3-19/2	1321.108	1321.509	-304.594	0.489	1452.473	0.395	17	0.194	R.KLQVDAWFGTR.R
R3/RRR3-19/2	1512.532	1512.695	-107.953	0.439	1282.840	0.423	18	0.182	K.HLNLDFQLLEGGR.K
R3/RRR3-19/2	1390.246	1390.675	-309.139	0.506	1040.373	0.484	19	0.177	R.KVDM*LEGVTILR.S
R3/RRR3-19/3	1915.656	1915.135	-250.556	0.504	1700.931	0.397	31	0.174	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/2	1321.149	1321.509	-272.982	0.461	1243.651	0.380	16	0.173	R.KLQVDAWFGTR.R
R3/RRR3-19/2	1389.644	1390.675	-1465.757	0.458	1006.100	0.465	19	0.172	R.KVDM*LEGVTILR.S
R3/RRR3-19/2	1284.949	1285.470	-1187.692	0.400	1328.565	0.324	18	0.171	R.KFLDGIYVSDK.G
R3/RRR3-19/2	1156.477	1157.297	-1578.802	0.443	1100.476	0.420	16	0.170	K.FLDGIYVSDK.G
R3/RRR3-19/2	1157.203	1157.297	-81.745	0.572	1032.703	0.442	16	0.170	K.FLDGIYVSDK.G
R3/RRR3-19/2	1156.500	1157.297	-1558.973	0.490	1085.451	0.411	16	0.168	K.FLDGIYVSDK.G
R3/RRR3-19/2	1390.300	1390.675	-269.850	0.467	1032.399	0.430	19	0.168	R.KVDM*LEGVTILR.S
R3/RRR3-19/2	1286.112	1285.470	-279.658	0.472	1156.879	0.374	17	0.166	R.KFLDGIYVSDK.G
R3/RRR3-19/2	1192.538	1193.336	-1512.375	0.348	950.867	0.425	17	0.160	K.LQVDAWFGTR.R
R3/RRR3-19/2	1284.447	1285.470	-1579.549	0.344	1133.898	0.331	17	0.158	R.KFLDGIYVSDK.G
R3/RRR3-19/2	856.588	856.990	-470.201	0.383	490.611	0.510	12	0.156	K.VVTVEGPR.G
R3/RRR3-24/2	857.249	856.990	302.845	0.353	615.132	0.468	13	0.154	K.VVTVEGPR.G
R3/RRR3-19/2	1321.482	1321.509	-20.532	0.462	906.434	0.408	14	0.154	R.KLQVDAWFGTR.R
R3/RRR3-25/2	856.287	856.990	-1994.734	0.347	624.596	0.447	13	0.153	K.VVTVEGPR.G
R3/RRR3-18/2	857.092	856.990	119.908	0.350	330.928	0.508	10	0.151	K.VVTVEGPR.G
R3/RRR3-19/2	857.027	856.990	43.200	0.335	500.543	0.460	12	0.151	K.VVTVEGPR.G
R3/RRR3-18/2	856.872	856.990	-137.545	0.345	402.146	0.456	11	0.149	K.VVTVEGPR.G
R3/RRR3-20/2	856.879	856.990	-129.828	0.335	448.551	0.435	12	0.149	K.VVTVEGPR.G
R3/RRR3-25/2	856.158	856.990	-2145.333	0.323	321.607	0.470	10	0.148	K.VVTVEGPR.G
R3/RRR3-19/2	856.644	856.990	-404.853	0.336	310.451	0.450	10	0.148	K.VVTVEGPR.G
R3/RRR3-19/2	1193.284	1193.336	-43.772	0.371	757.875	0.382	14	0.146	K.LQVDAWFGTR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1375.628	1374.675	-34.588	0.388	760.988	0.403	14	0.146	-.KVDMLEGVTILR.-
R3/RRR3-21/2	856.996	856.990	6.770	0.319	521.934	0.387	12	0.146	K.VVTVEGPR.G
R3/RRR3-18/2	856.458	856.990	-1793.910	0.309	500.055	0.383	12	0.145	K.VVTVEGPR.G
R3/RRR3-20/2	856.783	856.990	-242.307	0.322	512.680	0.361	12	0.145	K.VVTVEGPR.G
R3/RRR3-19/2	856.695	856.990	-345.661	0.291	331.613	0.412	10	0.144	K.VVTVEGPR.G
R3/RRR3-25/2	856.346	856.990	-1925.539	0.257	531.608	0.328	11	0.140	K.VVTVEGPR.G
R3/RRR3-19/2	1375.160	1374.675	353.501	0.381	556.872	0.355	14	0.140	R.KVDMLEGVTILR.S
R3/RRR3-21/2	856.240	856.990	-2049.609	0.289	492.893	0.226	12	0.139	K.VVTVEGPR.G
R3/RRR3-19/2	856.839	856.990	-176.846	0.268	311.540	0.395	9	0.139	-.VVTVEGPR.-
R3/RRR3-20/2	856.540	856.990	-526.118	0.199	415.111	0.267	11	0.137	K.VVTVEGPR.G
R3/RRR3-19/2	1246.012	1246.502	-394.683	0.327	382.594	0.329	11	0.135	K.VDMLEGVTILR.S
R3/RRR3-25/3	1583.145	1582.827	201.563	0.490	1229.592	0.436	31	0.133	R.TAISHVQNLITGVTK.G
R3/RRR3-19/2	1192.485	1193.336	-1556.900	0.267	639.483	0.254	13	0.132	K.LQVDAWFGTR.R
R3/RRR3-24/2	1511.371	1512.695	-1542.160	0.237	525.439	0.256	14	0.131	K.HLNLDFQLLEGGR.K
R3/RRR3-19/3	1641.122	1640.868	155.536	0.458	955.878	0.517	25	0.130	K.HLNLDFQLLEGGRK.L
R3/RRR3-19/3	1914.446	1915.135	-884.722	0.495	1048.642	0.467	25	0.129	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/3	1640.774	1640.868	-57.437	0.468	925.621	0.500	24	0.126	K.HLNLDFQLLEGGRK.L
R3/RRR3-19/3	1582.447	1582.827	-240.759	0.446	1071.567	0.400	29	0.117	R.TAISHVQNLITGVTK.G
R3/RRR3-25/3	1583.425	1582.827	-254.103	0.490	878.186	0.452	29	0.117	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1582.311	1582.827	-960.436	0.478	925.784	0.437	29	0.116	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1640.548	1640.868	-195.588	0.438	803.199	0.481	23	0.116	K.HLNLDFQLLEGGRK.L
R3/RRR3-19/3	1583.016	1582.827	119.905	0.464	600.984	0.482	26	0.114	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1582.433	1582.827	-249.349	0.483	1002.496	0.399	27	0.114	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1512.182	1512.695	-1003.763	0.381	1275.176	0.314	22	0.113	K.HLNLDFQLLEGGR.K
R3/RRR3-20/3	1582.633	1582.827	-122.482	0.459	1011.729	0.387	28	0.112	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1374.710	1374.675	25.586	0.499	1463.386	0.260	26	0.112	R.KVDMLEGVTILR.S
R3/RRR3-21/3	1582.875	1582.827	30.923	0.382	607.981	0.428	23	0.107	R.TAISHVQNLITGVTK.G
R3/RRR3-20/3	1582.302	1582.827	-966.594	0.400	670.990	0.395	26	0.105	R.TAISHVQNLITGVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/3	1582.963	1582.827	86.379	0.448	775.594	0.373	28	0.104	R.TAISHVQNLITGVTK.G
R3/RRR3-24/3	1582.961	1582.827	85.103	0.406	675.203	0.378	26	0.103	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1583.922	1582.827	60.663	0.359	547.612	0.407	23	0.103	-.TAISHVQNLITGVTK.-
R3/RRR3-26/3	1913.419	1915.135	-1947.660	0.445	589.246	0.402	26	0.102	K.VKDELVLDGNDIELVSR.S
R3/RRR3-21/3	1582.810	1582.827	-10.382	0.416	853.021	0.348	27	0.102	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1374.157	1374.675	-1108.461	0.432	1630.661	0.146	27	0.101	R.KVDMLEGVTILR.S
R3/RRR3-19/3	1322.032	1321.509	-361.996	0.392	916.988	0.363	21	0.100	R.KLQVDAWFGTR.R
R3/RRR3-25/3	1582.926	1582.827	63.292	0.410	701.385	0.346	25	0.100	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1390.714	1390.675	28.364	0.428	1518.718	0.169	25	0.100	R.KVDM*LEGVTILR.S
R3/RRR3-24/3	1582.092	1582.827	-1099.870	0.308	524.007	0.318	23	0.097	-.TAISHVQNLITGVTK.-
R3/RRR3-19/3	1390.911	1390.675	170.302	0.439	1215.867	0.222	24	0.094	R.KVDM*LEGVTILR.S
R3/RRR3-19/3	1915.364	1915.135	120.226	0.267	511.511	0.326	21	0.093	-.VKDELVLDGNDIELVSR.-
R3/RRR3-20/3	1582.193	1582.827	-1035.609	0.333	690.021	0.243	22	0.092	R.TAISHVQNLITGVTK.G
R3/RRR3-19/3	1390.987	1390.675	225.482	0.465	1274.432	0.192	24	0.092	-.KVDM*LEGVTILR.-
R3/RRR3-19/3	1512.191	1512.695	-997.563	0.382	983.337	0.256	22	0.091	-.HLNLDFQLLEGGR.-
R3/RRR3-19/3	1373.716	1374.675	-1430.345	0.443	1230.513	0.190	24	0.090	-.KVDMLEGVTILR.-
R3/RRR3-17/3	1915.288	1915.135	80.437	0.326	696.581	0.202	24	0.086	K.VKDELVLDGNDIELVSR.S
R3/RRR3-19/3	1512.258	1512.695	-289.702	0.373	997.440	0.171	21	0.082	-.HLNLDFQLLEGGR.-
R3/RRR3-15/2	1803.159	1804.124	-1093.054	0.566	3753.236	0.612	28	0.789	K.NFMIDFLM*GGVSAAVSK.T
R3/RRR3-15/2	1803.422	1804.124	-946.793	0.611	3741.216	0.620	28	0.788	K.NFMIDFLM*GGVSAAVSK.T
R3/RRR3-15/2	1819.357	1820.123	-973.499	0.586	3713.651	0.604	27	0.770	K.NFM*IDFLM*GGVSAAVSK.T
R3/RRR3-15/2	1803.295	1804.124	-1017.267	0.604	3652.070	0.584	27	0.737	K.NFMIDFLM*GGVSAAVSK.T
R3/RRR3-15/2	1820.554	1820.123	237.145	0.635	3502.451	0.620	27	0.705	K.NFM*IDFLM*GGVSAAVSK.T
R3/RRR3-15/2	1820.093	1820.123	-16.468	0.615	3040.853	0.622	26	0.565	K.NFM*IDFLM*GGVSAAVSK.T
R3/RRR3-2/2	1820.760	1820.123	-200.175	0.570	2880.642	0.582	25	0.505	K.NFM*IDFLM*GGVSAAVSK.T
R3/RRR3-15/2	1498.235	1498.745	-1010.687	0.438	2055.190	0.401	20	0.272	R.GFNISCVGIIVYR.G
R3/RRR3-15/2	1498.072	1498.745	-1119.742	0.353	1797.877	0.436	19	0.242	R.GFNISCVGIIVYR.G
R3/RRR3-15/2	1497.571	1498.745	-1455.810	0.325	2058.619	0.250	20	0.235	R.GFNISCVGIIVYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1294.206	1294.482	-213.483	0.435	1396.460	0.507	20	0.212	K.TLKSDGIAGLYR.G
R3/RRR3-15/2	1228.071	1227.413	-278.917	0.540	1504.657	0.449	17	0.209	K.SSMDAFSQILK.N
R3/RRR3-15/2	1226.972	1227.413	-359.795	0.523	1495.925	0.431	17	0.204	K.SSMDAFSQILK.N
R3/RRR3-16/2	1243.003	1243.412	-329.756	0.375	1393.426	0.438	17	0.195	K.SSM*DAFSQILK.N
R3/RRR3-15/2	1345.140	1345.591	-336.107	0.544	1380.346	0.431	17	0.192	K.LLIQNQDEMIK.S
R3/RRR3-15/2	1243.004	1243.412	-329.559	0.462	1317.918	0.446	16	0.190	K.SSM*DAFSQILK.N
R3/RRR3-15/2	1243.079	1243.412	-268.866	0.462	1262.292	0.462	16	0.188	K.SSM*DAFSQILK.N
R3/RRR3-15/2	1599.700	1599.763	-39.157	0.411	1224.721	0.481	21	0.188	R.LSEPYKGIGDCFGR.T
R3/RRR3-15/2	1498.483	1498.745	-175.230	0.409	1450.009	0.375	17	0.188	R.GFNISCVGIIVYR.G
R3/RRR3-15/2	1227.007	1227.413	-331.546	0.449	1369.189	0.408	16	0.188	K.SSMDAFSQILK.N
R3/RRR3-16/2	1242.616	1243.412	-1449.371	0.377	1349.803	0.415	16	0.187	K.SSM*DAFSQILK.N
R3/RRR3-15/2	1345.042	1345.591	-1154.928	0.481	1483.725	0.338	18	0.185	K.LLIQNQDEMIK.S
R3/RRR3-16/2	1345.430	1345.591	-119.996	0.486	1508.570	0.326	18	0.184	K.LLIQNQDEMIK.S
R3/RRR3-15/2	1243.040	1243.412	-299.803	0.454	1252.740	0.434	16	0.182	K.SSM*DAFSQILK.N
R3/RRR3-15/2	1345.168	1345.591	-315.165	0.513	1280.579	0.419	17	0.182	K.LLIQNQDEMIK.S
R3/RRR3-13/2	1361.199	1361.590	-287.847	0.478	1453.971	0.337	18	0.182	K.LLIQNQDEM*IK.S
R3/RRR3-16/2	1242.546	1243.412	-1506.506	0.361	1328.802	0.399	16	0.182	K.SSM*DAFSQILK.N
R3/RRR3-15/2	1362.325	1361.590	-195.219	0.533	1359.942	0.352	17	0.175	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	1361.091	1361.590	-368.109	0.498	1265.303	0.380	17	0.174	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	1423.164	1423.598	-306.066	0.448	1171.007	0.411	19	0.174	R.TIKDEGFASLWR.G
R3/RRR3-14/2	1361.235	1361.590	-261.575	0.510	1319.335	0.353	17	0.173	K.LLIQNQDEM*IK.S
R3/RRR3-16/2	1227.105	1227.413	-251.498	0.459	1057.513	0.461	15	0.172	K.SSMDAFSQILK.N
R3/RRR3-15/2	1361.186	1361.590	-297.564	0.544	1256.452	0.374	17	0.171	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	1448.155	1447.661	341.939	0.469	756.389	0.542	19	0.170	R.YFPTQALNFAFK.D
R3/RRR3-15/2	1362.252	1361.590	-248.617	0.540	1219.622	0.376	17	0.169	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	1448.103	1447.661	305.680	0.487	762.938	0.506	20	0.167	R.YFPTQALNFAFK.D
R3/RRR3-2/2	1361.194	1361.590	-291.806	0.504	1281.136	0.321	17	0.165	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	1423.250	1423.598	-245.055	0.464	991.558	0.423	18	0.164	R.TIKDEGFASLWR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1423.214	1423.598	-270.439	0.419	1083.754	0.372	19	0.162	R.TIKDEGFASLWR.G
R3/RRR3-15/2	1422.699	1423.598	-1338.705	0.447	930.243	0.431	18	0.162	R.TIKDEGFASLWR.G
R3/RRR3-15/2	1422.727	1423.598	-1319.230	0.448	994.871	0.399	18	0.161	R.TIKDEGFASLWR.G
R3/RRR3-2/2	1361.010	1361.590	-1164.638	0.460	1282.739	0.287	17	0.160	K.LLIQNQDEM*IK.S
R3/RRR3-3/2	1361.014	1361.590	-1161.125	0.444	1269.041	0.287	17	0.160	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	1447.248	1447.661	-286.421	0.409	699.697	0.485	19	0.159	R.YFPTQALNFAFK.D
R3/RRR3-15/2	1422.731	1423.598	-1316.128	0.427	972.375	0.389	18	0.158	R.TIKDEGFASLWR.G
R3/RRR3-16/2	1423.191	1423.598	-287.047	0.411	934.657	0.403	18	0.158	R.TIKDEGFASLWR.G
R3/RRR3-1/2	1361.968	1361.590	278.485	0.517	1263.290	0.290	17	0.158	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	951.432	952.046	-1702.281	0.417	727.695	0.458	14	0.157	K.SDGIAGLYR.G
R3/RRR3-14/2	1360.996	1361.590	-1175.085	0.458	1237.578	0.280	17	0.156	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	951.495	952.046	-1634.997	0.424	862.013	0.386	15	0.155	K.SDGIAGLYR.G
R3/RRR3-15/2	1360.622	1361.590	-1450.854	0.412	1302.973	0.239	17	0.155	K.LLIQNQDEM*IK.S
R3/RRR3-2/2	1360.965	1361.590	-1197.512	0.425	1298.252	0.234	17	0.154	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	952.060	952.046	13.875	0.469	767.449	0.405	14	0.154	K.SDGIAGLYR.G
R3/RRR3-16/2	1345.105	1345.591	-361.966	0.448	1159.012	0.293	16	0.153	K.LLIQNQDEMIK.S
R3/RRR3-16/2	1423.379	1423.598	-154.283	0.378	905.443	0.376	18	0.153	R.TIKDEGFASLWR.G
R3/RRR3-16/2	1212.450	1211.351	81.936	0.387	431.516	0.508	16	0.153	R.QFNGLVDVYR.K
R3/RRR3-1/2	1362.210	1361.590	-279.814	0.552	1146.041	0.305	17	0.152	K.LLIQNQDEM*IK.S
R3/RRR3-15/2	1446.528	1447.661	-1479.249	0.377	562.390	0.468	18	0.152	R.YFPTQALNFAFK.D
R3/RRR3-15/2	1447.653	1447.661	-5.972	0.418	755.645	0.406	18	0.152	R.YFPTQALNFAFK.D
R3/RRR3-15/2	1498.972	1498.745	152.284	0.376	861.329	0.407	16	0.151	R.GFNISCVGIIVYR.G
R3/RRR3-15/2	1361.132	1361.590	-337.875	0.459	1275.175	0.235	17	0.151	K.LLIQNQDEM*IK.S
R3/RRR3-14/2	1360.577	1361.590	-1483.748	0.388	1166.024	0.261	17	0.151	K.LLIQNQDEM*IK.S
R3/RRR3-16/2	1447.022	1447.661	-1136.147	0.374	649.462	0.427	18	0.150	R.YFPTQALNFAFK.D
R3/RRR3-16/2	1226.213	1227.413	-1799.346	0.304	962.143	0.341	14	0.149	K.SSMDAFSQILK.N
R3/RRR3-16/2	1423.370	1423.598	-160.563	0.386	792.147	0.384	16	0.149	R.TIKDEGFASLWR.G
R3/RRR3-15/2	1599.151	1599.763	-1011.221	0.390	920.594	0.359	19	0.149	R.LSEPYKGIGDCFGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	952.058	952.046	11.817	0.425	681.481	0.380	13	0.147	K.SDGIAGLYR.G
R3/RRR3-15/2	881.458	881.950	-559.097	0.286	635.273	0.449	12	0.147	K.GIGDCFGR.T
R3/RRR3-16/2	1227.290	1227.413	-100.421	0.315	938.488	0.320	15	0.147	K.SSMDAFSQILK.N
R3/RRR3-15/2	1424.488	1423.598	-77.495	0.415	684.103	0.369	15	0.144	R.TIKDEGFASLWR.G
R3/RRR3-16/2	771.213	771.888	-2179.136	0.408	1022.560	0.242	13	0.144	K.GAGANILR.A
R3/RRR3-16/2	1210.424	1211.351	-1596.944	0.317	281.656	0.448	13	0.143	R.QFNGLVDVYR.K
R3/RRR3-16/2	881.555	881.950	-449.454	0.283	708.080	0.371	12	0.143	K.GIGDCFGR.T
R3/RRR3-3/2	1361.333	1361.590	-189.336	0.457	1090.128	0.241	16	0.143	K.LLIQNQDEM*IK.S
R3/RRR3-1/2	771.154	771.888	-2255.830	0.340	553.609	0.341	12	0.143	K.GAGANILR.A
R3/RRR3-15/2	1424.202	1423.598	-278.934	0.382	771.342	0.311	16	0.141	R.TIKDEGFASLWR.G
R3/RRR3-2/2	951.862	952.046	-194.114	0.373	250.967	0.441	12	0.141	-.SDGIAGLYR.-
R3/RRR3-16/2	1447.231	1447.661	-297.930	0.361	358.946	0.347	14	0.141	R.YFPTQALNFAFK.D
R3/RRR3-15/2	1423.331	1423.598	-188.009	0.394	622.428	0.339	14	0.140	R.TIKDEGFASLWR.G
R3/RRR3-15/2	881.755	881.950	-221.906	0.241	637.959	0.316	12	0.137	K.GIGDCFGR.T
R3/RRR3-16/2	771.413	771.888	-617.268	0.343	755.118	0.233	12	0.137	K.GAGANILR.A
R3/RRR3-15/2	771.650	771.888	-309.897	0.395	910.433	0.199	13	0.137	K.GAGANILR.A
R3/RRR3-15/2	1211.916	1211.351	-360.224	0.229	308.036	0.321	13	0.136	R.QFNGLVDVYR.K
R3/RRR3-16/2	881.865	881.950	-96.091	0.213	638.788	0.306	12	0.135	K.GIGDCFGR.T
R3/RRR3-16/2	771.289	771.888	-2080.025	0.366	688.498	0.199	12	0.135	K.GAGANILR.A
R3/RRR3-15/2	828.625	828.936	-376.431	0.241	517.609	0.433	10	0.135	-.TAAAPIER.-
R3/RRR3-15/2	1446.603	1447.661	-1427.375	0.191	466.295	0.318	16	0.134	R.YFPTQALNFAFK.D
R3/RRR3-15/2	1499.395	1498.745	-233.835	0.260	392.990	0.315	13	0.134	R.GFNISCVGIIVYR.G
R3/RRR3-1/2	771.683	771.888	-266.728	0.387	700.799	0.207	12	0.134	-.GAGANILR.-
R3/RRR3-15/2	828.409	828.936	-1849.773	0.256	436.289	0.430	9	0.133	-.TAAAPIER.-
R3/RRR3-1/2	1803.258	1804.124	-1037.657	0.201	189.856	0.378	12	0.133	K.NFMIDFLM*GGVSAAVSK.T
R3/RRR3-1/2	1243.371	1243.412	-32.866	0.301	676.802	0.207	13	0.132	K.SSM*DAFSQILK.N
R3/RRR3-16/2	1446.934	1447.661	-1197.649	0.138	478.148	0.285	16	0.131	R.YFPTQALNFAFK.D
R3/RRR3-15/2	951.616	952.046	-453.804	0.362	307.116	0.369	12	0.131	-.SDGIAGLYR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	771.794	771.888	-122.645	0.384	742.093	0.126	12	0.130	K.GAGANILR.A
R3/RRR3-15/2	828.738	828.936	-239.574	0.156	422.947	0.382	9	0.129	K.TAAAPIER.V
R3/RRR3-15/2	881.140	881.950	-2059.985	0.171	766.674	0.160	13	0.129	K.GIGDCFGR.T
R3/RRR3-15/2	771.746	771.888	-184.685	0.393	775.990	0.104	12	0.128	K.GAGANILR.A
R3/RRR3-2/2	951.511	952.046	-1618.757	0.142	159.747	0.353	12	0.126	-.SDGIAGLYR.-
R3/RRR3-15/2	1212.201	1211.351	-124.801	0.181	142.856	0.404	9	0.124	-.QFNGLVDVYR.-
R3/RRR3-15/3	1498.217	1498.745	-1022.722	0.473	1029.800	0.416	25	0.116	R.GFNISCVGIIVYR.G
R3/RRR3-12/2	881.140	881.950	-2059.706	0.234	321.457	0.337	9	0.105	-.GIGDCFGR.-
R3/RRR3-15/3	1293.524	1294.482	-1518.025	0.388	1065.079	0.314	22	0.100	K.TLKSDGIAGLYR.G
R3/RRR3-15/3	1497.700	1498.745	-1369.612	0.425	762.207	0.365	23	0.099	R.GFNISCVGIIVYR.G
R3/RRR3-15/3	1803.629	1804.124	-275.358	0.349	1033.282	0.328	27	0.099	K.NFMIDFLM*GGVSAAVSK.T
R3/RRR3-15/3	1498.480	1498.745	-177.200	0.379	545.262	0.297	22	0.093	R.GFNISCVGIIVYR.G
R3/RRR3-16/3	1423.214	1423.598	-270.879	0.428	729.270	0.298	19	0.093	-.TIKDEGFASLWR.-
R3/RRR3-15/3	1423.550	1423.598	-33.820	0.412	1094.479	0.204	23	0.089	-.TIKDEGFASLWR.-
R3/RRR3-15/3	1424.637	1423.598	27.010	0.445	871.732	0.264	21	0.086	-.TIKDEGFASLWR.-
R3/RRR3-15/3	1294.183	1294.482	-231.946	0.363	739.236	0.256	19	0.085	-.TLKSDGIAGLYR.-
R3/RRR3-15/3	1423.245	1423.598	-248.936	0.412	834.799	0.220	20	0.084	-.TIKDEGFASLWR.-
R3/RRR3-2/3	1423.236	1423.598	-255.132	0.385	836.711	0.204	20	0.082	-.TIKDEGFASLWR.-
R3/RRR3-15/3	1423.741	1423.598	100.726	0.467	872.025	0.269	21	0.081	-.TIKDEGFASLWR.-
R3/RRR3-16/3	1423.441	1423.598	-110.591	0.402	755.346	0.207	20	0.079	-.TIKDEGFASLWR.-
R3/RRR3-2/3	1423.766	1423.598	118.525	0.423	844.485	0.165	21	0.077	-.TIKDEGFASLWR.-
R3/RRR3-15/3	1423.652	1423.598	38.037	0.459	766.808	0.225	20	0.075	-.TIKDEGFASLWR.-
R3/RRR3-14/3	1423.574	1423.598	-16.919	0.412	782.245	0.215	19	0.075	-.TIKDEGFASLWR.-
R3/RRR3-15/3	1423.368	1423.598	-161.949	0.375	704.612	0.185	19	0.074	-.TIKDEGFASLWR.-
R3/RRR3-6/2	1496.296	1496.694	-266.640	0.569	2740.774	0.576	23	0.473	K.SQIHEIVLVGGSTR.I
R3/RRR3-6/2	1496.290	1496.694	-270.487	0.572	2561.135	0.617	22	0.445	K.SQIHEIVLVGGSTR.I
R3/RRR3-6/2	1496.085	1496.694	-1078.756	0.540	2557.443	0.543	22	0.417	K.SQIHEIVLVGGSTR.I
R3/RRR3-6/2	1508.366	1507.777	-273.354	0.502	1754.705	0.562	22	0.270	K.VFSPEEVSAMILGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1507.304	1507.777	-314.902	0.525	2236.979	0.428	32	0.263	K.VFSPEEVSAMILGK.M
R3/RRR3-6/2	1507.466	1507.777	-206.998	0.495	1856.238	0.451	22	0.256	K.VFSPEEVSAMILGK.M
R3/RRR3-6/2	1537.046	1537.620	-1026.668	0.472	1660.934	0.536	20	0.249	K.NGHVEIIANDQGNR.I
R3/RRR3-6/2	1156.138	1156.317	-155.845	0.529	1710.548	0.457	19	0.239	K.DAGVIAGLNVAR.I
R3/RRR3-6/2	1537.253	1537.620	-239.226	0.489	1557.088	0.506	20	0.229	K.NGHVEIIANDQGNR.I
R3/RRR3-6/2	1536.661	1537.620	-1278.625	0.478	1519.511	0.519	19	0.226	K.NGHVEIIANDQGNR.I
R3/RRR3-6/2	1524.045	1523.776	176.665	0.436	1445.680	0.452	20	0.204	K.VFSPEEVSAM*ILGK.M
R3/RRR3-6/2	1298.108	1297.398	-223.877	0.529	1413.018	0.450	16	0.202	R.FEELNNDLFR.K
R3/RRR3-6/2	1524.498	1524.663	-108.070	0.543	1258.989	0.466	19	0.190	R.ARFEELNNDLFR.K
R3/RRR3-6/2	1404.022	1403.585	312.138	0.510	1415.150	0.387	17	0.189	R.NQLETYVYNMK.N
R3/RRR3-6/2	1524.257	1523.776	316.567	0.445	1338.368	0.428	20	0.189	K.VFSPEEVSAM*ILGK.M
R3/RRR3-6/2	1507.882	1507.777	70.105	0.416	1295.645	0.440	19	0.186	K.VFSPEEVSAMILGK.M
R3/RRR3-6/2	1524.315	1524.663	-228.486	0.485	1260.397	0.427	19	0.183	R.ARFEELNNDLFR.K
R3/RRR3-6/2	1144.146	1144.305	-139.501	0.501	976.955	0.534	19	0.182	K.FDLSGIPAAPR.G
R3/RRR3-6/2	1403.286	1403.585	-214.252	0.490	1416.599	0.316	17	0.175	R.NQLETYVYNMK.N
R3/RRR3-6/2	1524.457	1524.663	-134.978	0.496	1221.276	0.386	19	0.173	R.ARFEELNNDLFR.K
R3/RRR3-6/2	1143.623	1144.305	-1475.034	0.449	851.923	0.499	18	0.165	-.FDLSGIPAAPR.-
R3/RRR3-6/3	1652.230	1652.835	-974.815	0.541	1692.504	0.377	26	0.164	R.ARFEELNNDLFRK.T
R3/RRR3-6/2	1297.052	1297.398	-267.670	0.421	1202.368	0.322	15	0.161	R.FEELNNDLFR.K
R3/RRR3-6/3	1385.771	1385.612	115.442	0.498	1705.063	0.373	27	0.161	K.M*KETAEAYLGKK.I
R3/RRR3-6/3	1537.487	1537.620	-86.739	0.503	1644.222	0.377	28	0.159	K.NGHVEIIANDQGNR.I
R3/RRR3-6/2	1509.370	1509.645	-182.645	0.369	504.668	0.534	18	0.153	R.ITPSWVAFTDSER.L
R3/RRR3-6/3	1536.695	1537.620	-1256.137	0.439	1624.529	0.361	29	0.152	K.NGHVEIIANDQGNR.I
R3/RRR3-6/3	1652.821	1652.835	-8.720	0.525	1623.161	0.354	25	0.151	R.ARFEELNNDLFRK.T
R3/RRR3-6/3	1524.633	1524.663	-19.612	0.611	1479.079	0.414	27	0.148	R.ARFEELNNDLFR.K
R3/RRR3-6/2	1509.185	1509.645	-305.333	0.340	532.930	0.469	18	0.147	R.ITPSWVAFTDSER.L
R3/RRR3-6/3	1369.520	1369.612	-67.562	0.510	1478.855	0.403	25	0.146	K.MKETAEAYLGKK.I
R3/RRR3-6/2	1509.117	1509.645	-1015.082	0.352	428.614	0.470	16	0.145	R.ITPSWVAFTDSER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1652.331	1652.835	-913.401	0.559	1703.404	0.301	26	0.144	R.ARFEELNNDLFRK.T
R3/RRR3-6/2	1227.115	1227.305	-154.614	0.412	762.971	0.363	13	0.144	R.DYFEGKEPNK.G
R3/RRR3-6/2	1226.591	1227.305	-1401.514	0.377	750.049	0.367	13	0.144	R.DYFEGKEPNK.G
R3/RRR3-6/3	1385.469	1385.612	-102.988	0.518	1565.566	0.360	26	0.143	K.M*KETAEAYLGKK.I
R3/RRR3-6/2	1226.486	1227.305	-1486.785	0.385	809.380	0.336	13	0.143	R.DYFEGKEPNK.G
R3/RRR3-6/2	1509.618	1509.645	-17.811	0.305	247.248	0.454	13	0.139	R.ITPSWVAFTDSER.L
R3/RRR3-6/3	1385.201	1385.612	-297.508	0.483	1555.410	0.337	26	0.137	K.M*KETAEAYLGKK.I
R3/RRR3-6/3	1369.449	1369.612	-119.600	0.515	1432.771	0.341	27	0.126	K.MKETAEAYLGKK.I
R3/RRR3-6/2	1971.015	1970.856	80.716	0.499	955.955	0.530	23	0.125	R.TGGAPGGGADGEGGGDDEHDEL.-
R3/RRR3-6/3	1507.299	1507.777	-317.705	0.471	1292.719	0.364	25	0.124	K.VFSPEEVSAMILGK.M
R3/RRR3-6/3	1506.883	1507.777	-1260.676	0.455	1293.285	0.334	27	0.117	K.VFSPEEVSAMILGK.M
R3/RRR3-6/3	1537.059	1537.620	-1018.663	0.475	1325.475	0.301	25	0.114	K.NGHVEIIANDQGNR.I
R3/RRR3-6/3	1502.866	1502.783	55.177	0.390	963.238	0.396	22	0.109	K.IVNKDGKPYIQVK.I
R3/RRR3-6/3	1369.614	1369.612	1.500	0.481	981.647	0.380	25	0.108	K.MKETAEAYLGKK.I
R3/RRR3-6/3	1524.719	1524.663	37.242	0.551	1149.542	0.322	24	0.106	R.ARFEELNNDLFR.K
R3/RRR3-6/3	1502.572	1502.783	-140.742	0.423	973.129	0.374	23	0.106	K.IVNKDGKPYIQVK.I
R3/RRR3-6/3	1524.158	1524.663	-990.012	0.520	1042.046	0.321	23	0.102	R.ARFEELNNDLFR.K
R3/RRR3-6/3	1538.464	1537.620	-101.646	0.392	1153.392	0.207	23	0.090	K.NGHVEIIANDQGNR.I
R3/RRR3-6/3	1502.822	1502.783	25.971	0.338	894.572	0.246	22	0.087	K.IVNKDGKPYIQVK.I
R3/RRR3-6/3	1538.599	1537.620	-13.307	0.327	928.288	0.151	22	0.077	-.NGHVEIIANDQGNR.-
R3/RRR3-6/2	1970.371	1970.856	-246.853	0.463	740.707	0.553	22	0.072	R.TGGAPGGGADGEGGGDDEHDEL.-
R3/RRR3-6/2	1970.242	1970.856	-821.815	0.445	553.299	0.506	22	0.036	R.TGGAPGGGADGEGGGDDEHDEL.-
R3/RRR3-4/3	1802.783	1803.946	-1203.100	0.456	2163.195	0.448	34	0.261	K.NATLTNEKEADACPIR.A
R3/RRR3-1/3	1804.471	1803.946	-263.992	0.413	2222.820	0.381	35	0.247	K.NATLTNEKEADACPIR.A
R3/RRR3-4/2	1803.322	1803.946	-903.316	0.531	1647.547	0.526	22	0.245	K.NATLTNEKEADACPIR.A
R3/RRR3-5/3	1805.043	1803.946	54.046	0.451	1721.604	0.529	33	0.215	K.NATLTNEKEADACPIR.A
R3/RRR3-2/3	1803.788	1803.946	-87.916	0.457	1580.641	0.397	30	0.159	K.NATLTNEKEADACPIR.A
R3/RRR3-1/3	1803.928	1803.946	-10.026	0.429	1309.373	0.385	31	0.129	K.NATLTNEKEADACPIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/1	1546.949	1546.705	158.136	0.362	734.012	0.451	19	0.953	K.GATTIIGGGDSVAAVEK.A
R3/RRR3-10/3	1450.968	1450.816	104.532	0.563	3223.074	0.430	32	0.497	K.FLKPAVAGFLMQK.E
R3/RRR3-11/2	1917.633	1918.175	-806.372	0.612	2823.519	0.557	25	0.478	K.SLVEEDKLELATSLIEK.A
R3/RRR3-11/2	1917.729	1918.175	-233.518	0.656	2726.008	0.561	25	0.454	K.SLVEEDKLELATSLIEK.A
R3/RRR3-11/2	1918.464	1918.175	151.151	0.634	2648.096	0.572	23	0.439	K.SLVEEDKLELATSLIEK.A
R3/RRR3-10/2	1918.642	1918.175	244.050	0.637	2601.712	0.584	24	0.434	K.SLVEEDKLELATSLIEK.A
R3/RRR3-10/2	1918.481	1918.175	160.084	0.652	2531.036	0.597	24	0.422	K.SLVEEDKLELATSLIEK.A
R3/RRR3-10/3	1450.544	1450.816	-188.669	0.563	2942.656	0.420	29	0.420	K.FLKPAVAGFLMQK.E
R3/RRR3-10/2	1917.715	1918.175	-240.671	0.620	2419.188	0.565	23	0.386	K.SLVEEDKLELATSLIEK.A
R3/RRR3-11/2	1804.459	1804.016	246.505	0.526	2277.528	0.592	28	0.373	K.M*SHISTGGGASLELLEGK.T
R3/RRR3-11/3	1450.538	1450.816	-192.468	0.560	2818.776	0.396	30	0.372	K.FLKPAVAGFLMQK.E
R3/RRR3-11/3	1450.812	1450.816	-3.183	0.547	2727.730	0.424	29	0.367	K.FLKPAVAGFLMQK.E
R3/RRR3-11/3	1467.038	1466.816	151.574	0.552	2600.894	0.425	28	0.339	K.FLKPAVAGFLM*QK.E
R3/RRR3-10/2	1389.068	1389.578	-1090.823	0.404	2323.084	0.459	22	0.338	K.ELDYLVGAVANPK.K
R3/RRR3-11/2	1547.184	1546.705	310.557	0.536	2221.802	0.529	24	0.337	K.GATTIIGGGDSVAAVEK.A
R3/RRR3-11/2	1547.177	1546.705	306.127	0.538	2136.633	0.545	24	0.326	K.GATTIIGGGDSVAAVEK.A
R3/RRR3-11/3	1450.850	1450.816	23.020	0.529	2571.445	0.403	29	0.320	K.FLKPAVAGFLMQK.E
R3/RRR3-10/2	1546.203	1546.705	-973.869	0.463	2192.598	0.479	24	0.317	K.GATTIIGGGDSVAAVEK.A
R3/RRR3-11/2	1389.201	1389.578	-272.477	0.441	2145.748	0.493	22	0.316	K.ELDYLVGAVANPK.K
R3/RRR3-11/3	1467.005	1466.816	129.293	0.534	2349.758	0.484	27	0.312	K.FLKPAVAGFLM*QK.E
R3/RRR3-10/2	1546.241	1546.705	-300.866	0.502	2064.224	0.536	24	0.311	K.GATTIIGGGDSVAAVEK.A
R3/RRR3-10/3	1467.115	1466.816	204.517	0.569	2289.538	0.510	27	0.308	K.FLKPAVAGFLM*QK.E
R3/RRR3-10/2	1547.262	1546.705	-286.661	0.540	2004.807	0.533	24	0.299	K.GATTIIGGGDSVAAVEK.A
R3/RRR3-10/3	1467.244	1466.816	292.369	0.585	2342.673	0.450	27	0.293	K.FLKPAVAGFLM*QK.E
R3/RRR3-11/2	1546.186	1546.705	-985.203	0.474	1943.227	0.502	24	0.281	K.GATTIIGGGDSVAAVEK.A
R3/RRR3-11/3	1466.905	1466.816	60.818	0.538	2205.612	0.483	27	0.281	K.FLKPAVAGFLM*QK.E
R3/RRR3-11/2	1390.435	1389.578	-103.344	0.515	1952.763	0.484	21	0.280	K.ELDYLVGAVANPK.K
R3/RRR3-11/2	1921.354	1921.103	131.105	0.537	1768.896	0.579	24	0.275	K.LASVADLYVNDAFGTAHR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1921.570	1921.103	243.997	0.556	1723.330	0.605	23	0.274	K.LASVADLYVNDAFGTAHR.A
R3/RRR3-10/3	1466.621	1466.816	-133.140	0.573	2206.544	0.471	28	0.273	K.FLKPAVAGFLM*QK.E
R3/RRR3-10/3	1450.601	1450.816	-148.781	0.546	2341.369	0.400	28	0.271	K.FLKPAVAGFLMQK.E
R3/RRR3-11/2	1791.731	1790.158	-239.092	0.575	1602.208	0.567	21	0.248	K.VDVLILGGGM*IFTFYK.A
R3/RRR3-11/3	1735.797	1736.049	-145.496	0.563	2148.832	0.412	33	0.245	K.LAAALPEGGVLLLENVR.F
R3/RRR3-15/2	1917.527	1918.175	-862.223	0.500	1687.198	0.516	22	0.245	K.SLVEEDKLELATSLIEK.A
R3/RRR3-11/2	1920.215	1921.103	-985.925	0.517	1516.249	0.604	22	0.244	K.LASVADLYVNDAFGTAHR.A
R3/RRR3-11/2	1390.371	1389.578	-149.756	0.523	1729.510	0.445	20	0.236	K.ELDYLVGAVANPK.K
R3/RRR3-11/2	1735.514	1736.049	-887.039	0.545	1419.385	0.557	28	0.225	K.LAAALPEGGVLLLENVR.F
R3/RRR3-11/2	1735.512	1736.049	-888.098	0.527	1400.909	0.555	28	0.223	K.LAAALPEGGVLLLENVR.F
R3/RRR3-10/3	1735.442	1736.049	-928.673	0.519	2049.051	0.367	32	0.214	K.LAAALPEGGVLLLENVR.F
R3/RRR3-10/3	1736.365	1736.049	182.754	0.600	1961.980	0.412	31	0.213	K.LAAALPEGGVLLLENVR.F
R3/RRR3-10/2	1736.545	1736.049	286.634	0.572	1207.104	0.589	26	0.209	K.LAAALPEGGVLLLENVR.F
R3/RRR3-10/2	1735.610	1736.049	-253.436	0.532	1325.259	0.526	27	0.208	K.LAAALPEGGVLLLENVR.F
R3/RRR3-11/2	1093.081	1093.258	-162.372	0.364	1518.085	0.415	18	0.205	K.FAAGTDAIAKK.L
R3/RRR3-10/2	1042.687	1043.282	-1534.099	0.457	1283.486	0.509	17	0.202	K.IGVIESLLAK.V
R3/RRR3-11/2	1735.474	1736.049	-910.129	0.526	1181.735	0.530	26	0.195	K.LAAALPEGGVLLLENVR.F
R3/RRR3-11/2	1043.155	1043.282	-121.786	0.524	1190.536	0.477	17	0.188	K.IGVIESLLAK.V
R3/RRR3-11/2	1042.672	1043.282	-1548.682	0.442	1141.630	0.506	16	0.188	K.IGVIESLLAK.V
R3/RRR3-11/2	1043.063	1043.282	-210.302	0.516	1251.204	0.421	17	0.183	K.IGVIESLLAK.V
R3/RRR3-10/2	1787.386	1788.016	-915.001	0.445	1345.159	0.410	21	0.182	K.MSHISTGGGASLELLEGK.T
R3/RRR3-10/2	1042.588	1043.282	-1629.955	0.419	1157.170	0.465	16	0.181	K.IGVIESLLAK.V
R3/RRR3-11/2	1774.509	1774.908	-225.526	0.560	1019.371	0.523	21	0.181	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/2	1092.551	1093.258	-1567.407	0.439	1263.514	0.413	17	0.181	K.FAAGTDAIAKK.L
R3/RRR3-10/3	1736.345	1736.049	170.805	0.529	1674.950	0.426	29	0.180	K.LAAALPEGGVLLLENVR.F
R3/RRR3-10/2	1735.558	1736.049	-283.708	0.539	1015.173	0.505	24	0.176	K.LAAALPEGGVLLLENVR.F
R3/RRR3-10/2	1734.798	1736.049	-1301.480	0.375	990.626	0.526	24	0.175	K.LAAALPEGGVLLLENVR.F
R3/RRR3-11/2	1774.372	1774.908	-867.889	0.519	914.488	0.532	20	0.175	R.FYKEEEKNDPEFAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1774.385	1774.908	-860.914	0.507	922.532	0.502	20	0.170	R.FYKEEEKNDPEFAK.K
R3/RRR3-10/2	1774.350	1774.908	-880.735	0.508	885.857	0.512	20	0.170	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/2	1787.497	1788.016	-852.613	0.423	1166.219	0.395	22	0.166	K.MSHISTGGGASLELLEGK.T
R3/RRR3-10/2	1075.161	1075.286	-116.224	0.398	822.147	0.478	18	0.162	K.KPFAAIVGGSK.V
R3/RRR3-10/2	1043.167	1043.282	-110.399	0.450	1007.813	0.377	15	0.158	K.IGVIESLLAK.V
R3/RRR3-10/3	1774.448	1774.908	-260.041	0.458	1228.192	0.525	23	0.157	R.FYKEEEKNDPEFAK.K
R3/RRR3-10/2	964.783	965.085	-314.042	0.307	1136.186	0.321	17	0.157	K.FAAGTDAIAK.K
R3/RRR3-11/2	1466.426	1466.816	-266.822	0.494	663.645	0.475	20	0.157	K.FLKPAVAGFLM*QK.E
R3/RRR3-11/2	1075.284	1075.286	-1.436	0.357	799.924	0.436	18	0.155	K.KPFAAIVGGSK.V
R3/RRR3-11/2	1074.667	1075.286	-1511.006	0.422	613.481	0.477	17	0.155	K.KPFAAIVGGSK.V
R3/RRR3-10/2	964.906	965.085	-186.605	0.418	926.977	0.352	16	0.152	K.FAAGTDAIAK.K
R3/RRR3-11/2	1074.649	1075.286	-1527.437	0.370	535.043	0.482	17	0.152	K.KPFAAIVGGSK.V
R3/RRR3-10/2	1075.232	1075.286	-49.717	0.396	530.683	0.464	17	0.152	K.KPFAAIVGGSK.V
R3/RRR3-10/2	1075.144	1075.286	-131.942	0.375	636.487	0.436	18	0.151	K.KPFAAIVGGSK.V
R3/RRR3-11/2	964.868	965.085	-225.950	0.362	1003.365	0.307	16	0.149	K.FAAGTDAIAK.K
R3/RRR3-11/2	964.351	965.085	-1803.709	0.300	891.024	0.271	15	0.140	K.FAAGTDAIAK.K
R3/RRR3-10/2	1737.685	1736.049	-209.872	0.424	259.180	0.473	13	0.140	K.LAAALPEGGVLLLENVR.F
R3/RRR3-10/3	1774.809	1774.908	-55.618	0.458	1019.912	0.531	24	0.139	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/2	1450.718	1450.816	-67.907	0.436	549.003	0.333	18	0.139	K.FLKPAVAGFLMQK.E
R3/RRR3-10/2	964.293	965.085	-1864.510	0.316	836.947	0.236	15	0.137	K.FAAGTDAIAK.K
R3/RRR3-11/3	1775.116	1774.908	117.792	0.447	1179.078	0.462	27	0.136	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/2	1449.739	1450.816	-1437.462	0.302	260.211	0.287	14	0.132	-.FLKPAVAGFLMQK.-
R3/RRR3-11/3	1075.095	1075.286	-177.685	0.371	1588.046	0.302	25	0.130	K.KPFAAIVGGSK.V
R3/RRR3-10/3	1774.869	1774.908	-21.676	0.435	907.988	0.513	24	0.128	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/3	1774.789	1774.908	-67.312	0.443	959.546	0.480	24	0.125	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/3	1774.954	1774.908	26.232	0.415	906.433	0.495	24	0.125	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/3	1775.084	1774.908	99.792	0.498	833.779	0.486	23	0.120	R.FYKEEEKNDPEFAK.K
R3/RRR3-11/3	1921.050	1921.103	-27.675	0.409	868.839	0.465	32	0.116	K.LASVADLYVNDAFGTAHR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1075.502	1075.286	201.303	0.377	1093.342	0.396	21	0.116	K.KPFAAIVGGSK.V
R3/RRR3-11/3	1918.909	1918.175	-139.205	0.429	1062.940	0.395	24	0.114	K.SLVEEDKLELATSLIEK.A
R3/RRR3-10/3	1920.564	1921.103	-803.619	0.344	667.823	0.503	29	0.112	K.LASVADLYVNDAFGTAHR.A
R3/RRR3-11/3	1920.925	1921.103	-92.785	0.409	620.107	0.480	29	0.109	K.LASVADLYVNDAFGTAHR.A
R3/RRR3-10/3	1918.049	1918.175	-66.082	0.336	1083.779	0.350	26	0.107	K.SLVEEDKLELATSLIEK.A
R3/RRR3-11/3	1075.489	1075.286	189.523	0.363	1207.516	0.297	21	0.106	K.KPFAAIVGGSK.V
R3/RRR3-10/3	1921.719	1921.103	-200.388	0.367	646.598	0.446	27	0.105	K.LASVADLYVNDAFGTAHR.A
R3/RRR3-10/3	1075.254	1075.286	-29.232	0.338	1048.025	0.294	22	0.097	K.KPFAAIVGGSK.V
R3/RRR3-11/3	1735.320	1736.049	-999.330	0.351	1052.926	0.263	25	0.096	K.LAAALPEGGVLLLENVR.F
R3/RRR3-11/3	1075.104	1075.286	-169.654	0.375	1113.130	0.255	22	0.095	K.KPFAAIVGGSK.V
R3/RRR3-11/3	1735.750	1736.049	-172.799	0.294	842.659	0.284	23	0.093	-.LAAALPEGGVLLLENVR.-
R3/RRR3-11/3	1389.606	1389.578	19.893	0.247	1001.136	0.298	22	0.093	K.ELDYLVGAVANPK.K
R3/RRR3-10/3	1074.617	1075.286	-1557.517	0.315	958.801	0.252	21	0.090	K.KPFAAIVGGSK.V
R3/RRR3-15/3	1736.323	1736.049	158.220	0.472	742.816	0.274	26	0.090	K.LAAALPEGGVLLLENVR.F
R3/RRR3-15/3	1774.055	1774.908	-1047.422	0.351	409.949	0.385	18	0.089	-.FYKEEEKNDPEFAK.-
R3/RRR3-11/3	1389.110	1389.578	-338.522	0.261	1085.621	0.201	24	0.084	K.ELDYLVGAVANPK.K
R3/RRR3-11/3	1751.854	1752.048	-111.105	0.462	2672.447	0.436	34	0.373	K.LAATLPDGGVLLLENVR.F
R3/RRR3-10/2	1574.182	1574.758	-1004.004	0.437	2077.686	0.514	25	0.309	K.GVTTIIGGGDSVAAVEK.A
R3/RRR3-11/2	1573.865	1574.758	-1206.625	0.438	1744.971	0.494	22	0.249	K.GVTTIIGGGDSVAAVEK.A
R3/RRR3-11/2	1150.180	1150.261	-71.173	0.457	1041.314	0.496	17	0.178	R.SVGTLTESDLK.G
R3/RRR3-11/2	1751.552	1752.048	-284.403	0.506	863.096	0.578	24	0.178	K.LAATLPDGGVLLLENVR.F
R3/RRR3-11/2	1752.406	1752.048	204.739	0.535	816.032	0.568	24	0.174	K.LAATLPDGGVLLLENVR.F
R3/RRR3-11/2	1150.169	1150.261	-80.861	0.469	952.983	0.493	17	0.172	R.SVGTLTESDLK.G
R3/RRR3-11/2	1752.484	1752.048	249.304	0.503	653.715	0.568	22	0.163	K.LAATLPDGGVLLLENVR.F
R3/RRR3-11/2	1573.413	1574.758	-1495.046	0.265	1233.844	0.353	20	0.163	K.GVTTIIGGGDSVAAVEK.A
R3/RRR3-10/2	1073.060	1073.313	-236.714	0.413	494.478	0.437	15	0.152	K.YSLKPLVPR.L
R3/RRR3-11/2	1073.019	1073.313	-275.290	0.394	434.394	0.449	14	0.151	K.YSLKPLVPR.L
R3/RRR3-10/2	1072.715	1073.313	-1494.581	0.398	427.092	0.414	14	0.149	K.YSLKPLVPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1073.021	1073.313	-273.350	0.383	369.682	0.385	13	0.146	K.YSLKPLVPR.L
R3/RRR3-11/2	1072.256	1073.313	-1923.873	0.325	371.425	0.367	13	0.143	K.YSLKPLVPR.L
R3/RRR3-11/2	1149.258	1150.261	-1748.629	0.315	646.408	0.398	15	0.143	R.SVGTLTESDLK.G
R3/RRR3-10/2	1072.547	1073.313	-1651.435	0.301	371.827	0.265	13	0.140	K.YSLKPLVPR.L
R3/RRR3-11/3	1751.509	1752.048	-881.533	0.375	1234.382	0.410	25	0.130	K.LAATLPDGGVLLLENVR.F
R3/RRR3-11/2	1573.538	1574.758	-1415.406	0.254	623.108	0.272	16	0.129	K.GVTTIIGGGDSVAAVEK.A
R3/RRR3-4/2	1074.058	1073.313	-238.432	0.122	627.297	0.092	13	0.128	-.YSLKPLVPR.-
R3/RRR3-11/3	1751.608	1752.048	-252.248	0.389	972.705	0.460	26	0.120	K.LAATLPDGGVLLLENVR.F
R3/RRR3-14/2	1477.033	1477.666	-1108.501	0.491	2194.206	0.486	20	0.325	K.VLQAQDDLVNSM*K.E
R3/RRR3-14/2	1782.447	1782.884	-245.472	0.505	1617.828	0.493	22	0.232	K.ASEISVSAEEEFNIEK.L
R3/RRR3-14/2	1782.296	1782.884	-893.639	0.499	1465.862	0.506	21	0.216	K.ASEISVSAEEEFNIEK.L
R3/RRR3-14/2	1782.295	1782.884	-894.189	0.482	1526.825	0.460	21	0.213	K.ASEISVSAEEEFNIEK.L
R3/RRR3-14/2	1152.659	1153.307	-1434.154	0.481	1356.447	0.502	19	0.208	R.FCSGGVVLASR.D
R3/RRR3-13/2	1191.172	1191.310	-116.212	0.512	1254.468	0.425	17	0.184	K.IVCENTLDAR.L
R3/RRR3-14/3	1584.752	1584.823	-44.833	0.577	1679.529	0.445	28	0.181	R.KKIEYSM*QLNASR.I
R3/RRR3-13/2	1153.232	1153.307	-65.040	0.413	1090.080	0.466	16	0.175	R.FCSGGVVLASR.D
R3/RRR3-14/2	1153.119	1153.307	-163.792	0.464	990.476	0.484	18	0.174	R.FCSGGVVLASR.D
R3/RRR3-14/2	1192.108	1191.310	-170.349	0.477	1132.477	0.393	17	0.169	-.IVCENTLDAR.-
R3/RRR3-14/2	1152.475	1153.307	-1594.271	0.377	1011.759	0.454	18	0.169	R.FCSGGVVLASR.D
R3/RRR3-13/2	1191.155	1191.310	-130.398	0.429	1118.865	0.374	17	0.166	K.IVCENTLDAR.L
R3/RRR3-14/2	1190.650	1191.310	-1398.779	0.473	1027.781	0.411	17	0.165	-.IVCENTLDAR.-
R3/RRR3-13/2	1154.163	1153.307	-124.606	0.382	964.655	0.432	17	0.163	R.FCSGGVVLASR.D
R3/RRR3-14/2	1027.094	1027.243	-145.505	0.385	1036.696	0.354	14	0.157	K.ELVVQGLLR.L
R3/RRR3-14/2	1026.590	1027.243	-1614.327	0.399	1079.355	0.327	14	0.155	K.ELVVQGLLR.L
R3/RRR3-14/2	1190.564	1191.310	-1471.485	0.329	1051.241	0.332	17	0.154	-.IVCENTLDAR.-
R3/RRR3-14/2	1038.972	1039.297	-313.537	0.444	794.726	0.378	15	0.150	R.LKEPAVLLR.C
R3/RRR3-14/2	1027.053	1027.243	-185.566	0.424	923.326	0.331	13	0.148	K.ELVVQGLLR.L
R3/RRR3-14/3	1584.260	1584.823	-989.208	0.527	1469.794	0.406	27	0.147	R.KKIEYSM*QLNASR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1026.968	1027.243	-267.963	0.306	570.925	0.287	12	0.136	K.ELVVQGLLR.L
R3/RRR3-14/3	1455.946	1456.650	-1173.642	0.590	1216.072	0.453	25	0.135	K.KIEYSM*QLNASR.I
R3/RRR3-14/3	1753.918	1753.900	10.351	0.483	867.917	0.571	28	0.135	R.KEDHHHVESVLHSAK.N
R3/RRR3-14/2	1038.550	1039.297	-1686.868	0.229	626.831	0.331	13	0.134	R.LKEPAVLLR.C
R3/RRR3-14/3	1456.317	1456.650	-228.996	0.529	1334.362	0.385	26	0.129	K.KIEYSM*QLNASR.I
R3/RRR3-14/3	1584.489	1584.823	-211.516	0.533	1261.116	0.393	26	0.127	R.KKIEYSM*QLNASR.I
R3/RRR3-14/3	1753.923	1753.900	13.283	0.487	779.386	0.513	27	0.120	R.KEDHHHVESVLHSAK.N
R3/RRR3-14/3	1456.785	1456.650	92.930	0.563	1047.480	0.390	24	0.113	K.KIEYSM*QLNASR.I
R3/RRR3-14/3	1440.314	1440.651	-234.595	0.509	1105.113	0.354	22	0.110	K.KIEYSMQLNASR.I
R3/RRR3-14/3	1150.691	1150.266	370.151	0.545	795.436	0.374	19	0.104	R.FIRQEAEEK.A
R3/RRR3-14/3	1619.773	1619.809	-21.824	0.522	821.287	0.376	24	0.104	R.VSHNHHEYKNLLK.E
R3/RRR3-14/3	1440.668	1440.651	11.879	0.477	971.419	0.367	22	0.103	-.KIEYSMQLNASR.-
R3/RRR3-14/3	1619.791	1619.809	-10.826	0.507	918.300	0.346	25	0.102	R.VSHNHHEYKNLLK.E
R3/RRR3-14/3	1150.390	1150.266	107.471	0.557	1001.068	0.320	20	0.098	-.FIRQEAEEK.-
R3/RRR3-14/3	1619.801	1619.809	-5.043	0.473	741.777	0.343	23	0.098	R.VSHNHHEYKNLLK.E
R3/RRR3-14/3	1619.861	1619.809	32.258	0.474	580.971	0.299	22	0.095	R.VSHNHHEYKNLLK.E
R3/RRR3-14/2	977.090	977.182	-94.433	0.389	816.473	0.540	13	0.087	R.KLLFGQVTA.-
R3/RRR3-14/3	1150.692	1150.266	370.630	0.489	516.841	0.313	17	0.075	-.FIRQEAEEK.-
R3/RRR3-14/2	976.617	977.182	-1607.169	0.312	731.401	0.515	12	0.069	R.KLLFGQVTA.-
R3/RRR3-14/2	977.046	977.182	-139.800	0.392	674.627	0.602	12	0.062	R.KLLFGQVTA.-
R3/RRR3-8/2	1911.439	1911.020	219.732	0.639	3236.417	0.503	28	0.570	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-8/3	1911.023	1911.020	1.716	0.543	3082.185	0.455	34	0.496	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-8/2	1910.341	1911.020	-881.296	0.597	2941.561	0.500	27	0.490	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-8/2	1481.123	1481.550	-288.881	0.500	2440.121	0.568	25	0.400	K.YGVDSGANLVTGGDR.L
R3/RRR3-8/2	1910.540	1911.020	-251.892	0.597	2523.388	0.519	26	0.396	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-8/2	1481.113	1481.550	-295.413	0.521	2379.510	0.587	25	0.394	K.YGVDSGANLVTGGDR.L
R3/RRR3-9/3	1911.073	1911.020	27.759	0.512	2594.033	0.468	35	0.368	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-8/2	1481.213	1481.550	-227.778	0.508	2319.101	0.521	25	0.358	K.YGVDSGANLVTGGDR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/3	1910.311	1911.020	-897.116	0.496	2370.830	0.417	33	0.297	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-9/3	1910.991	1911.020	-14.910	0.426	2229.678	0.422	32	0.274	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-8/2	1819.306	1818.879	235.504	0.602	1642.217	0.574	23	0.255	K.NGVEQGPQIDDEQFNK.I
R3/RRR3-8/2	1818.297	1818.879	-872.781	0.548	1585.811	0.566	22	0.246	K.NGVEQGPQIDDEQFNK.I
R3/RRR3-8/2	1818.216	1818.879	-917.533	0.558	1586.899	0.551	23	0.242	K.NGVEQGPQIDDEQFNK.I
R3/RRR3-8/2	1464.926	1464.645	192.013	0.530	1338.420	0.588	21	0.222	K.TAEQTPLSALFASK.L
R3/RRR3-9/2	1673.625	1672.947	-192.666	0.515	1850.260	0.342	21	0.222	K.IAQEEIFGPVQSILK.F
R3/RRR3-8/2	1464.407	1464.645	-163.338	0.558	1287.811	0.579	21	0.215	K.TAEQTPLSALFASK.L
R3/RRR3-8/2	1378.323	1378.599	-200.899	0.491	1789.605	0.313	18	0.212	K.GIDSLKNYLQVK.A
R3/RRR3-9/2	1674.468	1672.947	-286.454	0.563	1614.076	0.410	21	0.208	K.IAQEEIFGPVQSILK.F
R3/RRR3-8/2	1400.203	1399.655	-323.851	0.532	1257.543	0.559	20	0.207	K.VGPALACGNTVVLK.T
R3/RRR3-8/2	1248.113	1248.413	-240.889	0.459	1549.935	0.335	17	0.193	K.FNDLNEVIKR.A
R3/RRR3-8/2	1399.219	1399.655	-312.003	0.512	1141.733	0.527	20	0.190	K.VGPALACGNTVVLK.T
R3/RRR3-9/2	1465.480	1464.645	-113.090	0.444	993.853	0.575	19	0.185	K.TAEQTPLSALFASK.L
R3/RRR3-8/2	1399.332	1399.655	-231.044	0.479	1122.213	0.500	19	0.183	K.VGPALACGNTVVLK.T
R3/RRR3-9/2	1398.788	1399.655	-1338.481	0.447	986.388	0.523	18	0.175	K.VGPALACGNTVVLK.T
R3/RRR3-8/2	1819.316	1818.879	240.819	0.533	1145.312	0.459	20	0.175	K.NGVEQGPQIDDEQFNK.I
R3/RRR3-9/2	1464.547	1464.645	-67.600	0.384	1052.653	0.489	18	0.174	K.TAEQTPLSALFASK.L
R3/RRR3-2/2	1674.301	1672.947	212.243	0.525	1237.916	0.409	19	0.173	K.IAQEEIFGPVQSILK.F
R3/RRR3-9/2	1399.383	1399.655	-194.901	0.476	957.714	0.509	18	0.172	K.VGPALACGNTVVLK.T
R3/RRR3-8/2	1463.658	1464.645	-1362.141	0.320	1004.005	0.446	19	0.163	K.TAEQTPLSALFASK.L
R3/RRR3-8/2	1174.593	1175.318	-1473.043	0.429	801.236	0.502	14	0.162	R.KAFDEGPWPK.M
R3/RRR3-9/2	1399.333	1399.655	-230.344	0.395	1046.156	0.409	18	0.162	K.VGPALACGNTVVLK.T
R3/RRR3-8/2	1248.137	1248.413	-222.050	0.435	1164.594	0.325	16	0.160	K.FNDLNEVIKR.A
R3/RRR3-8/2	1098.138	1098.188	-45.558	0.362	1096.929	0.358	18	0.160	K.IAFTGSTDTGK.I
R3/RRR3-8/2	1091.917	1092.227	-284.766	0.428	1330.441	0.253	14	0.159	K.FNDLNEVIK.R
R3/RRR3-8/2	1378.260	1378.599	-246.569	0.500	1210.667	0.325	16	0.159	K.GIDSLKNYLQVK.A
R3/RRR3-8/3	1464.786	1464.645	96.190	0.486	1322.438	0.497	24	0.157	K.TAEQTPLSALFASK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1671.666	1672.947	-1368.576	0.362	1273.114	0.274	19	0.157	K.IAQEEIFGPVQSILK.F
R3/RRR3-8/2	1378.413	1378.599	-134.889	0.490	1160.338	0.329	16	0.156	K.GIDSLKNYLQVK.A
R3/RRR3-8/2	1672.488	1672.947	-275.080	0.511	900.920	0.434	18	0.156	K.IAQEEIFGPVQSILK.F
R3/RRR3-2/2	1463.764	1464.645	-1289.439	0.340	930.624	0.391	18	0.153	K.TAEQTPLSALFASK.L
R3/RRR3-8/2	1248.155	1248.413	-207.823	0.472	1038.578	0.319	16	0.152	K.FNDLNEVIKR.A
R3/RRR3-8/2	1174.976	1175.318	-291.625	0.421	652.102	0.464	13	0.151	R.KAFDEGPWPK.M
R3/RRR3-8/2	1672.508	1672.947	-262.852	0.479	874.518	0.400	18	0.151	K.IAQEEIFGPVQSILK.F
R3/RRR3-8/3	1910.570	1911.020	-236.195	0.451	1570.589	0.354	29	0.150	R.TGELIAHVAEGDAEDINR.A
R3/RRR3-8/2	884.522	885.086	-1774.298	0.393	638.925	0.410	13	0.149	K.IVLELAAR.S
R3/RRR3-8/2	1091.974	1092.227	-232.053	0.455	1192.526	0.236	14	0.148	K.FNDLNEVIK.R
R3/RRR3-8/2	1091.873	1092.227	-324.810	0.429	1154.286	0.231	14	0.146	K.FNDLNEVIK.R
R3/RRR3-8/2	1097.322	1098.188	-1705.754	0.327	717.336	0.416	15	0.145	K.IAFTGSTDTGK.I
R3/RRR3-8/2	884.924	885.086	-183.755	0.473	619.931	0.349	13	0.145	K.IVLELAAR.S
R3/RRR3-8/2	884.493	885.086	-1806.747	0.402	584.956	0.354	13	0.144	K.IVLELAAR.S
R3/RRR3-1/2	1674.565	1672.947	-228.750	0.506	920.318	0.342	17	0.143	K.IAQEEIFGPVQSILK.F
R3/RRR3-7/2	1464.945	1464.645	204.965	0.378	396.355	0.399	17	0.143	K.TAEQTPLSALFASK.L
R3/RRR3-3/2	1674.276	1672.947	197.255	0.476	753.561	0.366	17	0.142	K.IAQEEIFGPVQSILK.F
R3/RRR3-7/2	1674.593	1672.947	-211.783	0.513	1000.808	0.302	18	0.141	K.IAQEEIFGPVQSILK.F
R3/RRR3-8/2	1043.900	1043.151	-241.215	0.354	403.735	0.377	10	0.138	-.IYDEFVEK.-
R3/RRR3-8/2	1174.579	1175.318	-1484.630	0.378	627.426	0.324	13	0.138	R.KAFDEGPWPK.M
R3/RRR3-8/2	1673.828	1672.947	-70.852	0.490	872.661	0.312	17	0.138	-.IAQEEIFGPVQSILK.-
R3/RRR3-8/2	1043.035	1043.151	-111.235	0.356	470.130	0.290	10	0.135	-.IYDEFVEK.-
R3/RRR3-2/2	1673.996	1672.947	29.723	0.518	784.690	0.291	17	0.133	K.IAQEEIFGPVQSILK.F
R3/RRR3-3/2	1673.803	1672.947	-86.068	0.412	517.570	0.297	14	0.133	K.IAQEEIFGPVQSILK.F
R3/RRR3-4/2	1674.569	1672.947	-226.409	0.489	502.105	0.337	14	0.131	-.IAQEEIFGPVQSILK.-
R3/RRR3-8/2	1673.484	1672.947	-277.258	0.398	540.877	0.283	16	0.131	-.IAQEEIFGPVQSILK.-
R3/RRR3-1/2	1043.617	1043.151	448.088	0.183	916.916	0.128	12	0.128	R.IYDEFVEK.A
R3/RRR3-8/3	1175.207	1175.318	-94.621	0.530	1125.413	0.417	20	0.122	R.KAFDEGPWPK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/3	1378.484	1378.599	-83.199	0.548	929.694	0.453	28	0.118	K.GIDSLKNYLQVK.A
R3/RRR3-8/3	1175.116	1175.318	-172.303	0.558	913.219	0.448	19	0.117	R.KAFDEGPWPK.M
R3/RRR3-8/3	1378.530	1378.599	-49.757	0.508	1056.395	0.420	28	0.117	K.GIDSLKNYLQVK.A
R3/RRR3-8/3	1175.335	1175.318	15.238	0.502	1083.085	0.400	20	0.116	R.KAFDEGPWPK.M
R3/RRR3-8/3	1672.807	1672.947	-83.638	0.356	1052.149	0.325	26	0.099	K.IAQEEIFGPVQSILK.F
R3/RRR3-8/3	1818.797	1818.879	-45.286	0.402	909.143	0.351	26	0.098	K.NGVEQGPQIDDEQFNK.I
R3/RRR3-8/3	1378.615	1378.599	11.926	0.499	909.048	0.303	26	0.094	-.GIDSLKNYLQVK.-
R3/RRR3-7/2	1688.599	1689.011	-244.685	0.474	2432.470	0.553	23	0.388	K.SALGILMNLGLIEESK.I
R3/RRR3-7/2	1704.986	1705.010	-14.281	0.555	2383.102	0.527	23	0.367	K.SALGILM*NLGLIEESK.I
R3/RRR3-8/2	1705.057	1705.010	27.439	0.461	2171.055	0.499	22	0.318	K.SALGILM*NLGLIEESK.I
R3/RRR3-7/2	1688.584	1689.011	-253.389	0.480	1863.113	0.508	20	0.268	K.SALGILMNLGLIEESK.I
R3/RRR3-7/2	1604.410	1603.761	-219.674	0.508	1679.510	0.530	22	0.250	K.GFLTINSQPAVNGER.S
R3/RRR3-7/2	1604.301	1603.761	-287.612	0.510	1722.485	0.484	22	0.244	K.GFLTINSQPAVNGER.S
R3/RRR3-7/2	1845.290	1845.946	-900.355	0.508	1464.714	0.588	24	0.235	R.SDSTSVGWGGPGGYVYQK.A
R3/RRR3-7/2	1703.710	1705.010	-1353.993	0.393	1561.527	0.449	21	0.214	K.SALGILM*NLGLIEESK.I
R3/RRR3-7/2	1845.289	1845.946	-900.953	0.506	1373.608	0.540	23	0.213	R.SDSTSVGWGGPGGYVYQK.A
R3/RRR3-8/2	1704.278	1705.010	-1019.554	0.439	1441.278	0.470	19	0.204	K.SALGILM*NLGLIEESK.I
R3/RRR3-7/2	1846.197	1845.946	136.442	0.546	1187.150	0.578	22	0.200	R.SDSTSVGWGGPGGYVYQK.A
R3/RRR3-7/2	1329.937	1330.433	-373.735	0.464	1218.508	0.458	17	0.185	R.TLGWDQYPHGR.W
R3/RRR3-7/2	1889.328	1889.052	146.159	0.517	1134.836	0.512	20	0.183	K.LTSSPWSELDGLQPETK.I
R3/RRR3-7/2	1689.241	1689.011	136.726	0.466	1362.458	0.396	19	0.181	K.SALGILMNLGLIEESK.I
R3/RRR3-7/2	1200.135	1199.381	-205.528	0.482	1295.540	0.397	15	0.180	K.LQEEWAVPVK.S
R3/RRR3-7/2	1166.063	1165.313	-214.999	0.520	1180.499	0.438	14	0.179	K.AYLEFFCSK.E
R3/RRR3-7/2	1888.495	1889.052	-827.307	0.484	1215.040	0.442	19	0.176	K.LTSSPWSELDGLQPETK.I
R3/RRR3-7/2	1889.045	1889.052	-3.993	0.501	1187.754	0.437	20	0.173	K.LTSSPWSELDGLQPETK.I
R3/RRR3-7/2	1327.163	1327.553	-294.716	0.529	1043.833	0.440	17	0.168	K.KLQEEWAVPVK.S
R3/RRR3-7/2	1199.180	1199.381	-167.507	0.435	1066.799	0.392	15	0.163	K.LQEEWAVPVK.S
R3/RRR3-7/2	989.508	990.133	-1647.419	0.381	970.865	0.421	14	0.162	K.IDDALTTIK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1325.288	1324.550	-197.575	0.497	743.432	0.476	19	0.160	K.AFPSLTYIAVNK.D
R3/RRR3-7/2	989.479	990.133	-1676.669	0.378	839.590	0.449	14	0.159	K.IDDALTTIK.S
R3/RRR3-7/2	1165.062	1165.313	-216.235	0.445	1145.101	0.308	14	0.156	K.AYLEFFCSK.E
R3/RRR3-7/2	1198.630	1199.381	-1464.749	0.369	1049.308	0.353	14	0.155	K.LQEEWAVPVK.S
R3/RRR3-7/2	1324.110	1324.550	-333.308	0.409	712.340	0.445	19	0.154	K.AFPSLTYIAVNK.D
R3/RRR3-7/2	1378.466	1379.607	-1557.968	0.358	792.823	0.461	15	0.154	K.TLHLYTLNM*EK.S
R3/RRR3-26/2	989.926	990.133	-209.655	0.422	883.618	0.369	15	0.154	K.IDDALTTIK.S
R3/RRR3-26/2	989.930	990.133	-205.821	0.439	880.485	0.368	14	0.153	K.IDDALTTIK.S
R3/RRR3-7/2	1324.139	1324.550	-311.016	0.414	710.795	0.415	19	0.151	K.AFPSLTYIAVNK.D
R3/RRR3-7/2	990.055	990.133	-79.284	0.483	797.644	0.375	14	0.151	K.IDDALTTIK.S
R3/RRR3-26/2	989.463	990.133	-1692.658	0.312	741.199	0.410	13	0.148	K.IDDALTTIK.S
R3/RRR3-7/2	1603.197	1603.761	-978.578	0.456	784.942	0.405	18	0.148	K.GFLTINSQPAVNGER.S
R3/RRR3-26/2	1185.853	1185.359	417.987	0.391	860.454	0.365	15	0.147	K.SNGIQNVLALR.G
R3/RRR3-7/2	1164.963	1165.313	-301.068	0.398	1019.384	0.280	13	0.146	K.AYLEFFCSK.E
R3/RRR3-7/2	1379.212	1379.607	-287.407	0.369	792.724	0.373	15	0.145	K.TLHLYTLNM*EK.S
R3/RRR3-14/2	990.068	990.133	-65.556	0.412	917.019	0.285	13	0.143	-.IDDALTTIK.-
R3/RRR3-7/2	1602.657	1603.761	-1317.190	0.310	993.547	0.273	19	0.142	K.GFLTINSQPAVNGER.S
R3/RRR3-7/2	1185.012	1185.359	-292.978	0.398	592.870	0.352	15	0.140	K.SNGIQNVLALR.G
R3/RRR3-7/2	1690.479	1689.011	277.786	0.404	537.141	0.376	15	0.137	K.SALGILMNLGLIEESK.I
R3/RRR3-7/2	1602.956	1603.761	-1129.274	0.345	716.263	0.308	17	0.136	K.GFLTINSQPAVNGER.S
R3/RRR3-8/2	1324.253	1324.550	-224.450	0.307	546.877	0.246	16	0.134	K.AFPSLTYIAVNK.D
R3/RRR3-7/3	1856.584	1856.163	227.207	0.512	892.746	0.465	30	0.119	R.VKEDVRPIFWANRPK.S
R3/RRR3-7/3	1856.005	1856.163	-85.311	0.503	643.113	0.475	26	0.111	R.VKEDVRPIFWANRPK.S
R3/RRR3-7/3	1327.388	1327.553	-124.681	0.507	1422.247	0.210	24	0.100	-.KLQEEWAVPVK.-
R3/RRR3-7/3	1855.861	1856.163	-163.396	0.441	566.157	0.368	25	0.098	R.VKEDVRPIFWANRPK.S
R3/RRR3-7/3	1688.859	1689.011	-89.984	0.339	1028.127	0.306	24	0.098	K.SALGILMNLGLIEESK.I
R3/RRR3-7/3	1688.858	1689.011	-90.854	0.341	778.941	0.295	25	0.090	K.SALGILMNLGLIEESK.I
R3/RRR3-7/3	1705.031	1705.010	12.208	0.371	851.112	0.277	25	0.089	-.SALGILM*NLGLIEESK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1967.627	1968.196	-799.822	0.581	3860.975	0.526	29	0.785	K.EYVFVANSDNLGAIVDIK.I
R3/RRR3-8/2	1967.733	1968.196	-236.046	0.602	3826.705	0.536	28	0.777	K.EYVFVANSDNLGAIVDIK.I
R3/RRR3-9/2	1967.697	1968.196	-254.158	0.545	3254.143	0.524	27	0.588	K.EYVFVANSDNLGAIVDIK.I
R3/RRR3-8/2	1967.455	1968.196	-887.264	0.558	2488.037	0.530	24	0.392	K.EYVFVANSDNLGAIVDIK.I
R3/RRR3-9/2	1313.301	1313.528	-173.741	0.495	2409.917	0.435	21	0.346	K.VLQLETAAGAAIR.F
R3/RRR3-9/2	1313.124	1313.528	-309.056	0.412	2430.883	0.340	21	0.321	K.VLQLETAAGAAIR.F
R3/RRR3-8/2	1453.233	1452.636	-277.996	0.583	1760.966	0.515	22	0.258	K.VSGDVWFGSGVTLK.G
R3/RRR3-8/2	1452.215	1452.636	-291.006	0.521	1799.061	0.484	22	0.256	K.VSGDVWFGSGVTLK.G
R3/RRR3-8/2	1452.189	1452.636	-308.801	0.526	1815.500	0.452	22	0.250	K.VSGDVWFGSGVTLK.G
R3/RRR3-9/2	1359.286	1359.592	-225.691	0.466	1963.242	0.356	20	0.246	R.IVTEDFLPLPSK.G
R3/RRR3-8/2	1359.395	1359.592	-145.513	0.502	1926.396	0.378	20	0.246	R.IVTEDFLPLPSK.G
R3/RRR3-8/2	1359.330	1359.592	-193.798	0.518	1872.526	0.398	20	0.243	R.IVTEDFLPLPSK.G
R3/RRR3-9/2	1477.315	1476.704	-264.596	0.479	1803.750	0.381	19	0.230	K.IFNTNNLWVNLK.A
R3/RRR3-8/2	1475.707	1476.704	-1357.159	0.414	2058.970	0.235	18	0.229	K.IFNTNNLWVNLK.A
R3/RRR3-9/2	1312.715	1313.528	-1385.485	0.468	1627.225	0.428	20	0.220	K.VLQLETAAGAAIR.F
R3/RRR3-9/2	1359.235	1359.592	-263.442	0.457	1805.239	0.330	20	0.219	R.IVTEDFLPLPSK.G
R3/RRR3-2/2	1477.396	1476.704	-209.305	0.457	1786.217	0.341	17	0.218	K.IFNTNNLWVNLK.A
R3/RRR3-8/2	1475.528	1476.704	-1478.969	0.389	1832.662	0.194	19	0.193	K.IFNTNNLWVNLK.A
R3/RRR3-8/2	1477.169	1476.704	315.662	0.539	1484.007	0.363	18	0.188	K.IFNTNNLWVNLK.A
R3/RRR3-8/2	1359.250	1359.592	-252.359	0.377	1594.081	0.290	19	0.188	R.IVTEDFLPLPSK.G
R3/RRR3-9/2	1358.742	1359.592	-1365.946	0.362	1426.842	0.307	18	0.175	R.IVTEDFLPLPSK.G
R3/RRR3-2/2	1313.305	1313.528	-170.291	0.389	1270.343	0.318	20	0.165	K.VLQLETAAGAAIR.F
R3/RRR3-8/2	1758.526	1758.953	-243.728	0.485	474.912	0.632	18	0.162	R.TNPSNPSIELGPEFKK.V
R3/RRR3-8/2	1758.500	1758.953	-258.632	0.526	512.824	0.584	19	0.159	R.TNPSNPSIELGPEFKK.V
R3/RRR3-8/2	1630.381	1630.780	-245.387	0.480	599.562	0.557	19	0.159	R.TNPSNPSIELGPEFK.K
R3/RRR3-8/2	1631.152	1630.780	228.591	0.502	608.057	0.528	20	0.158	R.TNPSNPSIELGPEFK.K
R3/RRR3-8/2	1631.420	1630.780	-221.215	0.496	590.408	0.528	20	0.157	R.TNPSNPSIELGPEFK.K
R3/RRR3-8/2	1359.124	1359.592	-345.530	0.322	1229.251	0.275	18	0.156	R.IVTEDFLPLPSK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1476.106	1476.704	-1085.975	0.330	1351.721	0.222	17	0.156	K.IFNTNNLWVNLK.A
R3/RRR3-9/2	958.886	959.122	-246.959	0.428	697.565	0.428	15	0.154	K.LDTLLAQGK.E
R3/RRR3-9/2	1758.519	1758.953	-247.628	0.459	413.098	0.566	18	0.153	R.TNPSNPSIELGPEFKK.V
R3/RRR3-8/2	1758.401	1758.953	-885.521	0.457	459.866	0.548	18	0.152	R.TNPSNPSIELGPEFKK.V
R3/RRR3-9/2	839.847	840.006	-188.807	0.399	517.498	0.436	12	0.150	K.AIGINVPR.S
R3/RRR3-8/2	958.764	959.122	-374.693	0.410	636.131	0.405	15	0.150	K.LDTLLAQGK.E
R3/RRR3-8/2	790.962	790.933	37.288	0.446	727.497	0.372	11	0.150	K.VANFLAR.F
R3/RRR3-8/2	791.048	790.933	145.319	0.440	753.447	0.365	11	0.149	K.VANFLAR.F
R3/RRR3-7/2	1452.307	1452.636	-227.253	0.410	936.937	0.365	17	0.149	K.VSGDVWFGSGVTLK.G
R3/RRR3-8/2	790.843	790.933	-113.963	0.436	756.665	0.360	11	0.149	K.VANFLAR.F
R3/RRR3-9/2	958.476	959.122	-1722.216	0.429	559.643	0.396	15	0.149	K.LDTLLAQGK.E
R3/RRR3-9/2	790.799	790.933	-170.326	0.392	739.886	0.365	11	0.148	K.VANFLAR.F
R3/RRR3-9/2	790.957	790.933	30.632	0.428	595.868	0.374	11	0.148	K.VANFLAR.F
R3/RRR3-9/2	790.844	790.933	-112.569	0.387	748.331	0.358	11	0.148	K.VANFLAR.F
R3/RRR3-8/2	790.813	790.933	-152.518	0.455	581.005	0.368	11	0.148	K.VANFLAR.F
R3/RRR3-9/2	839.474	840.006	-1829.693	0.380	447.581	0.436	11	0.147	K.AIGINVPR.S
R3/RRR3-9/2	958.423	959.122	-1778.265	0.451	594.905	0.366	15	0.147	K.LDTLLAQGK.E
R3/RRR3-1/2	1313.033	1313.528	-378.081	0.350	789.167	0.418	14	0.147	-.VLQLETAAGAAIR.-
R3/RRR3-8/2	839.868	840.006	-164.602	0.393	441.609	0.406	11	0.146	K.AIGINVPR.S
R3/RRR3-8/2	839.379	840.006	-1943.675	0.344	537.557	0.380	12	0.144	K.AIGINVPR.S
R3/RRR3-8/2	839.943	840.006	-74.212	0.342	516.831	0.370	12	0.144	K.AIGINVPR.S
R3/RRR3-8/3	1812.525	1812.164	199.839	0.452	1632.685	0.302	30	0.140	R.LVEAEALKM*EIIPNPK.E
R3/RRR3-9/2	839.827	840.006	-213.158	0.263	588.581	0.347	13	0.140	K.AIGINVPR.S
R3/RRR3-8/2	1028.579	1029.215	-1596.090	0.363	915.680	0.253	13	0.139	-.RLVEAEALK.-
R3/RRR3-8/3	1313.429	1313.528	-76.087	0.412	1782.654	0.236	26	0.139	K.VLQLETAAGAAIR.F
R3/RRR3-8/2	1359.594	1359.592	1.116	0.356	570.457	0.360	13	0.137	-.IVTEDFLPLPSK.-
R3/RRR3-8/2	1028.520	1029.215	-1653.082	0.416	863.803	0.245	14	0.137	K.RLVEAEALK.M
R3/RRR3-9/2	1475.529	1476.704	-1478.387	0.299	1037.355	0.062	17	0.126	K.IFNTNNLWVNLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/3	1967.962	1968.196	-119.186	0.346	992.611	0.356	25	0.100	K.EYVFVANSDNLGAIVDIK.I
R3/RRR3-8/3	1313.159	1313.528	-281.973	0.276	1259.473	0.162	24	0.087	K.VLQLETAAGAAIR.F
R3/RRR3-8/3	1313.189	1313.528	-259.030	0.330	879.177	0.117	21	0.077	K.VLQLETAAGAAIR.F
R3/RRR3-15/2	1819.535	1820.040	-829.256	0.554	1992.756	0.584	24	0.314	K.SAQDIALADLPTTHPIR.L
R3/RRR3-15/2	1820.519	1820.040	264.198	0.565	1885.325	0.558	24	0.288	K.SAQDIALADLPTTHPIR.L
R3/RRR3-15/2	1820.335	1820.040	162.998	0.571	1858.813	0.556	23	0.282	K.SAQDIALADLPTTHPIR.L
R3/RRR3-15/2	1337.030	1337.504	-354.995	0.546	1573.468	0.552	19	0.244	R.KEAAENTLVAYK.S
R3/RRR3-15/2	1337.179	1337.504	-243.523	0.519	1588.833	0.539	19	0.242	R.KEAAENTLVAYK.S
R3/RRR3-15/2	1337.224	1337.504	-210.004	0.545	1473.987	0.563	19	0.234	R.KEAAENTLVAYK.S
R3/RRR3-15/2	1319.062	1319.400	-257.449	0.502	1610.913	0.457	19	0.224	K.TADVGELTVEER.N
R3/RRR3-15/2	1639.361	1639.832	-288.332	0.467	1393.309	0.545	24	0.218	K.LLDSHLVPSATAAESK.V
R3/RRR3-14/2	1419.098	1419.563	-328.426	0.491	1458.623	0.505	19	0.217	R.IISSIEQKEESR.G
R3/RRR3-16/2	1319.054	1319.400	-263.205	0.438	1703.920	0.374	18	0.216	K.TADVGELTVEER.N
R3/RRR3-16/2	1419.324	1419.563	-168.785	0.487	1452.461	0.497	19	0.215	R.IISSIEQKEESR.G
R3/RRR3-16/2	1319.236	1319.400	-124.513	0.474	1547.222	0.437	19	0.213	K.TADVGELTVEER.N
R3/RRR3-15/2	1638.842	1639.832	-1217.955	0.428	1432.441	0.472	23	0.206	K.LLDSHLVPSATAAESK.V
R3/RRR3-15/2	1419.214	1419.563	-246.787	0.517	1345.017	0.493	19	0.203	R.IISSIEQKEESR.G
R3/RRR3-15/2	1319.040	1319.400	-274.161	0.516	1404.499	0.456	18	0.201	K.TADVGELTVEER.N
R3/RRR3-14/2	1419.171	1419.563	-276.904	0.479	1364.811	0.465	19	0.199	R.IISSIEQKEESR.G
R3/RRR3-14/2	1320.196	1319.400	-155.305	0.526	1386.355	0.455	18	0.198	K.TADVGELTVEER.N
R3/RRR3-15/2	1319.108	1319.400	-222.169	0.530	1529.905	0.386	18	0.198	K.TADVGELTVEER.N
R3/RRR3-14/2	1418.669	1419.563	-1339.143	0.462	1341.002	0.461	19	0.196	R.IISSIEQKEESR.G
R3/RRR3-16/2	1419.186	1419.563	-266.117	0.489	1279.814	0.483	19	0.195	R.IISSIEQKEESR.G
R3/RRR3-15/2	1051.803	1052.163	-343.237	0.361	1227.483	0.525	15	0.195	R.GNEAYVASIK.E
R3/RRR3-16/2	1319.213	1319.400	-142.056	0.455	1364.204	0.440	18	0.194	K.TADVGELTVEER.N
R3/RRR3-15/2	1640.369	1639.832	-283.004	0.505	1226.439	0.516	21	0.193	K.LLDSHLVPSATAAESK.V
R3/RRR3-14/2	1419.197	1419.563	-258.350	0.471	1213.090	0.508	18	0.193	R.IISSIEQKEESR.G
R3/RRR3-15/2	1419.110	1419.563	-320.313	0.456	1249.228	0.479	19	0.192	R.IISSIEQKEESR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1419.231	1419.563	-234.361	0.485	1209.895	0.481	18	0.188	R.IISSIEQKEESR.G
R3/RRR3-15/2	1419.241	1419.563	-227.803	0.472	1186.816	0.490	18	0.188	R.IISSIEQKEESR.G
R3/RRR3-16/2	1051.996	1052.163	-158.587	0.386	1036.604	0.560	15	0.185	R.GNEAYVASIK.E
R3/RRR3-15/2	1190.057	1190.439	-321.881	0.468	1655.012	0.225	16	0.178	K.DSTLIMQLLR.D
R3/RRR3-15/2	1206.223	1206.438	-178.854	0.407	1580.006	0.249	16	0.178	K.DSTLIM*QLLR.D
R3/RRR3-15/2	1210.466	1209.331	112.516	0.433	975.539	0.475	17	0.170	K.EAAENTLVAYK.S
R3/RRR3-16/2	1052.008	1052.163	-147.529	0.457	863.167	0.520	14	0.169	R.GNEAYVASIK.E
R3/RRR3-15/2	1366.868	1367.527	-1217.572	0.407	1562.630	0.196	16	0.168	R.YEEM*VEFM*EK.V
R3/RRR3-14/2	1208.799	1209.331	-1271.122	0.335	1011.870	0.463	16	0.167	K.EAAENTLVAYK.S
R3/RRR3-16/2	1639.466	1639.832	-223.640	0.432	952.827	0.480	21	0.167	K.LLDSHLVPSATAAESK.V
R3/RRR3-15/2	1190.078	1190.439	-303.871	0.489	1530.752	0.212	15	0.165	-.DSTLIMQLLR.-
R3/RRR3-15/2	1210.062	1209.331	-222.966	0.397	923.366	0.453	16	0.163	K.EAAENTLVAYK.S
R3/RRR3-14/2	1051.809	1052.163	-337.065	0.363	897.978	0.468	14	0.161	R.GNEAYVASIK.E
R3/RRR3-16/3	1819.822	1820.040	-119.738	0.436	1395.715	0.446	31	0.152	K.SAQDIALADLPTTHPIR.L
R3/RRR3-15/2	1319.382	1319.400	-13.884	0.417	904.299	0.370	16	0.151	K.TADVGELTVEER.N
R3/RRR3-15/2	1640.345	1639.832	-297.862	0.423	670.065	0.477	18	0.151	K.LLDSHLVPSATAAESK.V
R3/RRR3-15/2	1190.088	1190.439	-295.226	0.428	1489.500	0.140	15	0.150	K.DSTLIMQLLR.D
R3/RRR3-15/2	1519.598	1518.786	-124.049	0.398	738.533	0.467	15	0.150	R.NLLSVAYKNVIGAR.R
R3/RRR3-16/2	1208.710	1209.331	-1344.553	0.300	804.698	0.397	15	0.147	K.EAAENTLVAYK.S
R3/RRR3-14/2	1419.310	1419.563	-178.966	0.421	498.689	0.389	16	0.145	R.IISSIEQKEESR.G
R3/RRR3-15/2	1205.953	1206.438	-403.573	0.404	714.618	0.290	14	0.140	K.DSTLIM*QLLR.D
R3/RRR3-14/2	1419.406	1419.563	-110.637	0.357	512.886	0.337	13	0.138	R.IISSIEQKEESR.G
R3/RRR3-16/2	1208.472	1209.331	-1542.585	0.249	665.283	0.345	14	0.137	K.EAAENTLVAYK.S
R3/RRR3-15/2	1519.761	1518.786	-16.242	0.383	394.753	0.328	15	0.135	R.NLLSVAYKNVIGAR.R
R3/RRR3-15/2	1206.205	1206.438	-193.981	0.419	1228.401	0.124	15	0.135	K.DSTLIM*QLLR.D
R3/RRR3-15/2	1206.401	1206.438	-31.161	0.395	813.595	0.201	14	0.133	K.DSTLIM*QLLR.D
R3/RRR3-14/2	1206.219	1206.438	-181.798	0.450	964.185	0.181	14	0.132	K.DSTLIM*QLLR.D
R3/RRR3-14/2	1205.935	1206.438	-1250.427	0.410	888.185	0.165	15	0.132	K.DSTLIM*QLLR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/3	1337.503	1337.504	-0.112	0.501	1376.618	0.381	28	0.130	R.KEAAENTLVAYK.S
R3/RRR3-16/3	1640.623	1639.832	-127.892	0.387	1217.166	0.427	31	0.130	K.LLDSHLVPSATAAESK.V
R3/RRR3-16/2	1205.954	1206.438	-402.354	0.330	772.278	0.114	15	0.130	K.DSTLIM*QLLR.D
R3/RRR3-14/2	1519.129	1518.786	226.588	0.306	291.445	0.323	12	0.127	-.NLLSVAYKNVIGAR.-
R3/RRR3-16/2	1190.180	1190.439	-218.049	0.341	888.307	0.063	14	0.124	-.DSTLIMQLLR.-
R3/RRR3-15/3	1337.129	1337.504	-280.718	0.473	1014.116	0.468	26	0.123	R.KEAAENTLVAYK.S
R3/RRR3-15/3	1640.674	1639.832	-96.545	0.386	1176.422	0.403	29	0.123	K.LLDSHLVPSATAAESK.V
R3/RRR3-15/3	1337.418	1337.504	-63.966	0.485	1107.400	0.388	25	0.115	R.KEAAENTLVAYK.S
R3/RRR3-15/3	1500.980	1500.638	228.503	0.349	629.622	0.542	21	0.113	R.GNEAYVASIKEYR.S
R3/RRR3-15/3	1845.676	1846.033	-194.048	0.398	538.230	0.535	27	0.113	-.M*SPAEASREENVYM*AK.L
R3/RRR3-15/3	1639.875	1639.832	26.414	0.378	1042.316	0.385	28	0.112	K.LLDSHLVPSATAAESK.V
R3/RRR3-15/3	1819.786	1820.040	-139.925	0.395	1175.292	0.329	30	0.109	K.SAQDIALADLPTTHPIR.L
R3/RRR3-15/3	1846.761	1846.033	-147.923	0.389	359.769	0.512	23	0.107	-.M*SPAEASREENVYM*AK.L
R3/RRR3-16/3	1819.558	1820.040	-265.504	0.365	1292.578	0.263	31	0.105	K.SAQDIALADLPTTHPIR.L
R3/RRR3-15/3	1500.949	1500.638	207.707	0.299	612.425	0.448	21	0.099	R.GNEAYVASIKEYR.S
R3/RRR3-15/3	1845.770	1846.033	-142.696	0.295	244.039	0.339	20	0.097	-.M*SPAEASREENVYM*AK.L
R3/RRR3-14/3	1639.927	1639.832	57.994	0.302	902.748	0.282	28	0.092	K.LLDSHLVPSATAAESK.V
R3/RRR3-19/2	1901.478	1902.048	-828.162	0.548	2196.248	0.550	28	0.800	K.FLDGIYVSDKGTITEDQ.-
R3/RRR3-19/2	1901.093	1902.048	-1031.264	0.494	2139.130	0.586	27	0.774	K.FLDGIYVSDKGTITEDQ.-
R3/RRR3-19/2	1901.403	1902.048	-867.796	0.506	1827.907	0.607	26	0.550	K.FLDGIYVSDKGTITEDQ.-
R3/RRR3-19/3	1911.503	1911.194	162.135	0.603	1245.010	0.473	30	0.144	K.HLNLDFQLLEVEGVRK.L
R3/RRR3-19/3	1910.691	1911.194	-789.220	0.540	736.229	0.496	26	0.117	K.HLNLDFQLLEVEGVRK.L
R3/RRR3-19/3	1911.191	1911.194	-1.680	0.431	1082.147	0.392	25	0.116	K.HLNLDFQLLEVEGVRK.L
R3/RRR3-19/3	1911.121	1911.194	-38.293	0.397	514.358	0.418	22	0.100	K.HLNLDFQLLEVEGVRK.L
R3/RRR3-22/2	1652.448	1652.849	-243.444	0.489	2400.118	0.607	23	1.000	K.MIEDYLVAHPTEYA.-
R3/RRR3-22/1	1219.544	1220.313	-1455.331	0.148	774.229	0.213	15	0.919	K.LNPAVDDGGSFK.T
R3/RRR3-23/1	1219.634	1220.313	-1381.439	0.184	880.189	0.246	16	0.919	K.LNPAVDDGGSFK.T
R3/RRR3-22/1	1219.585	1220.313	-1421.349	0.203	865.427	0.312	16	0.916	K.LNPAVDDGGSFK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/1	1219.575	1220.313	-1429.392	0.168	543.755	0.233	13	0.916	K.LNPAVDDGGSFK.T
R3/RRR3-22/1	1219.560	1220.313	-1442.462	0.130	628.647	0.231	14	0.916	K.LNPAVDDGGSFK.T
R3/RRR3-23/1	1219.592	1220.313	-1415.920	0.164	579.525	0.283	13	0.913	K.LNPAVDDGGSFK.T
R3/RRR3-23/2	1930.559	1931.131	-816.638	0.634	3741.836	0.657	30	0.814	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-23/2	1930.694	1931.131	-227.067	0.597	3650.540	0.641	30	0.775	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-22/2	1913.374	1914.037	-871.729	0.595	3652.708	0.623	27	0.761	K.M*NVEYELEDGGSLSPEK.E
R3/RRR3-22/2	1668.246	1668.849	-963.352	0.488	2089.425	0.606	22	0.740	K.M*IEDYLVAHPTEYA.-
R3/RRR3-23/2	1668.285	1668.849	-940.211	0.490	2056.759	0.621	21	0.720	K.M*IEDYLVAHPTEYA.-
R3/RRR3-23/2	1931.589	1931.131	237.977	0.650	3247.292	0.672	29	0.655	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-23/2	1912.602	1914.037	-1277.172	0.554	3266.664	0.585	27	0.618	K.M*NVEYELEDGGSLSPEK.E
R3/RRR3-23/2	1913.443	1914.037	-835.736	0.608	3205.550	0.618	27	0.614	K.M*NVEYELEDGGSLSPEK.E
R3/RRR3-23/2	1913.493	1914.037	-809.416	0.606	3094.500	0.631	26	0.587	K.M*NVEYELEDGGSLSPEK.E
R3/RRR3-22/2	1668.335	1668.849	-910.314	0.517	1867.233	0.627	20	0.582	K.M*IEDYLVAHPTEYA.-
R3/RRR3-22/2	1653.274	1652.849	257.895	0.528	1849.043	0.631	20	0.569	K.MIEDYLVAHPTEYA.-
R3/RRR3-22/3	1930.985	1931.131	-75.436	0.571	2864.655	0.669	39	0.545	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-22/2	1653.308	1652.849	278.033	0.530	1800.266	0.630	21	0.533	K.MIEDYLVAHPTEYA.-
R3/RRR3-22/2	1897.460	1898.038	-834.368	0.599	2862.957	0.586	26	0.503	K.MNVEYELEDGGSLSPEK.E
R3/RRR3-23/2	1668.344	1668.849	-904.732	0.521	1738.637	0.623	21	0.493	K.M*IEDYLVAHPTEYA.-
R3/RRR3-23/2	1667.760	1668.849	-1256.333	0.425	1726.628	0.534	20	0.482	K.M*IEDYLVAHPTEYA.-
R3/RRR3-23/2	1651.388	1652.849	-1495.036	0.328	1704.588	0.500	21	0.470	K.MIEDYLVAHPTEYA.-
R3/RRR3-23/3	1931.180	1931.131	25.758	0.570	2441.709	0.657	35	0.423	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-22/2	1897.564	1898.038	-250.324	0.568	2598.881	0.548	25	0.423	K.MNVEYELEDGGSLSPEK.E
R3/RRR3-23/3	1930.521	1931.131	-836.068	0.541	2321.027	0.677	37	0.400	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-1/2	1669.765	1668.849	-50.232	0.509	1572.019	0.565	20	0.386	K.M*IEDYLVAHPTEYA.-
R3/RRR3-23/2	1653.619	1652.849	-139.762	0.501	1508.921	0.637	18	0.369	K.MIEDYLVAHPTEYA.-
R3/RRR3-23/3	1951.327	1951.170	80.394	0.554	2387.932	0.531	34	0.350	R.DNAAHVIKSEVLDVPAGSK.V
R3/RRR3-23/2	1338.934	1339.455	-1139.712	0.501	2216.274	0.566	23	0.350	K.VEGDGGAGTVTTM*K.L
R3/RRR3-23/2	1652.251	1652.849	-970.126	0.420	1482.281	0.573	20	0.347	K.MIEDYLVAHPTEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/3	1931.197	1931.131	34.697	0.520	2191.375	0.627	36	0.347	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-23/2	1651.581	1652.849	-1377.732	0.265	1485.389	0.439	19	0.344	K.MIEDYLVAHPTEYA.-
R3/RRR3-22/3	1951.625	1951.170	233.959	0.532	2487.137	0.454	34	0.339	R.DNAAHVIKSEVLDVPAGSK.V
R3/RRR3-22/3	1930.387	1931.131	-906.148	0.478	2010.697	0.648	34	0.319	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-22/3	1950.399	1951.170	-910.755	0.553	2290.051	0.497	35	0.311	R.DNAAHVIKSEVLDVPAGSK.V
R3/RRR3-23/3	1931.131	1931.131	0.081	0.509	1860.687	0.658	35	0.291	K.SHVTETKIEAAGAGSCLAK.M
R3/RRR3-23/3	1950.809	1951.170	-185.444	0.574	2016.800	0.535	34	0.271	R.DNAAHVIKSEVLDVPAGSK.V
R3/RRR3-23/3	1951.113	1951.170	-29.256	0.547	2034.662	0.499	34	0.261	R.DNAAHVIKSEVLDVPAGSK.V
R3/RRR3-23/2	1339.003	1339.455	-338.468	0.462	1565.311	0.546	20	0.238	K.VEGDGGAGTVTTM*K.L
R3/RRR3-23/2	1339.044	1339.455	-308.192	0.475	1472.243	0.556	20	0.229	K.VEGDGGAGTVTTM*K.L
R3/RRR3-22/2	1338.598	1339.455	-1391.530	0.490	1384.057	0.600	20	0.228	K.VEGDGGAGTVTTM*K.L
R3/RRR3-22/2	1323.348	1323.456	-81.844	0.497	1379.120	0.587	22	0.227	K.VEGDGGAGTVTTMK.L
R3/RRR3-22/2	1338.778	1339.455	-1256.631	0.493	1330.380	0.560	20	0.214	K.VEGDGGAGTVTTM*K.L
R3/RRR3-23/2	1147.903	1148.285	-334.554	0.457	1427.914	0.462	19	0.205	K.IEAAGAGSCLAK.M
R3/RRR3-22/3	1950.187	1951.170	-1019.718	0.510	1713.407	0.448	32	0.193	R.DNAAHVIKSEVLDVPAGSK.V
R3/RRR3-22/2	1147.949	1148.285	-294.331	0.475	1242.137	0.477	18	0.190	K.IEAAGAGSCLAK.M
R3/RRR3-23/2	1287.201	1286.565	-283.368	0.516	1138.439	0.483	18	0.184	K.LILDGYFGM*LK.M
R3/RRR3-22/2	1148.053	1148.285	-203.121	0.445	1157.208	0.484	18	0.184	K.IEAAGAGSCLAK.M
R3/RRR3-22/2	1286.164	1286.565	-312.441	0.496	1092.815	0.486	18	0.182	K.LILDGYFGM*LK.M
R3/RRR3-22/2	1286.085	1286.565	-374.436	0.490	1089.281	0.480	18	0.180	K.LILDGYFGM*LK.M
R3/RRR3-23/2	1287.173	1286.565	-305.347	0.501	1076.814	0.481	18	0.180	K.LILDGYFGM*LK.M
R3/RRR3-23/2	1147.948	1148.285	-295.185	0.439	1229.587	0.422	18	0.179	K.IEAAGAGSCLAK.M
R3/RRR3-22/2	1286.159	1286.565	-316.631	0.466	1101.772	0.451	18	0.176	K.LILDGYFGM*LK.M
R3/RRR3-22/2	1101.970	1102.220	-227.726	0.391	1305.279	0.358	17	0.174	K.SEVLDVPAGSK.V
R3/RRR3-23/2	1147.918	1148.285	-321.111	0.465	1064.932	0.465	17	0.174	K.IEAAGAGSCLAK.M
R3/RRR3-23/2	1285.827	1286.565	-1355.849	0.378	1121.196	0.412	18	0.170	K.LILDGYFGM*LK.M
R3/RRR3-22/2	1270.364	1270.565	-159.084	0.474	930.727	0.469	18	0.169	K.LILDGYFGMLK.M
R3/RRR3-22/2	1147.528	1148.285	-1535.952	0.398	1197.198	0.373	18	0.169	K.IEAAGAGSCLAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1269.898	1270.565	-1316.598	0.431	956.054	0.434	18	0.165	K.LILDGYFGMLK.M
R3/RRR3-22/2	1101.398	1102.220	-1659.200	0.333	1193.895	0.293	16	0.156	K.SEVLDVPAGSK.V
R3/RRR3-23/2	1269.720	1270.565	-1457.761	0.387	920.391	0.372	18	0.155	K.LILDGYFGMLK.M
R3/RRR3-23/2	1269.585	1270.565	-1564.480	0.399	928.818	0.366	18	0.155	K.LILDGYFGMLK.M
R3/RRR3-23/2	1094.150	1094.279	-118.907	0.328	1125.481	0.305	16	0.154	K.VCAGFIDAIK.V
R3/RRR3-23/2	1286.129	1286.565	-340.152	0.354	898.831	0.386	17	0.154	K.LILDGYFGM*LK.M
R3/RRR3-23/2	1102.017	1102.220	-184.831	0.385	1134.631	0.290	16	0.153	K.SEVLDVPAGSK.V
R3/RRR3-23/2	1102.031	1102.220	-172.274	0.383	1092.502	0.298	16	0.152	K.SEVLDVPAGSK.V
R3/RRR3-22/2	1219.942	1220.313	-305.364	0.281	937.900	0.372	19	0.152	K.LNPAVDDGGSFK.T
R3/RRR3-22/2	1093.950	1094.279	-302.256	0.354	1190.112	0.249	16	0.151	K.VCAGFIDAIK.V
R3/RRR3-23/2	1101.559	1102.220	-1512.241	0.308	1174.504	0.258	16	0.151	K.SEVLDVPAGSK.V
R3/RRR3-21/2	1101.996	1102.220	-204.055	0.361	1073.292	0.295	15	0.150	K.SEVLDVPAGSK.V
R3/RRR3-22/2	1078.892	1079.252	-334.046	0.379	597.501	0.439	14	0.149	K.VFSDAPAM*PK.V
R3/RRR3-23/2	1093.538	1094.279	-1597.679	0.318	1026.931	0.301	16	0.149	K.VCAGFIDAIK.V
R3/RRR3-22/2	1101.943	1102.220	-252.176	0.408	1060.034	0.293	15	0.149	K.SEVLDVPAGSK.V
R3/RRR3-23/2	1093.364	1094.279	-1756.721	0.311	1071.554	0.280	16	0.148	K.VCAGFIDAIK.V
R3/RRR3-22/2	1269.890	1270.565	-1323.549	0.346	545.266	0.418	15	0.147	K.LILDGYFGMLK.M
R3/RRR3-22/2	1062.912	1063.252	-321.104	0.357	537.529	0.420	14	0.146	K.VFSDAPAMPK.V
R3/RRR3-21/2	1101.434	1102.220	-1626.799	0.243	1081.489	0.273	15	0.146	K.SEVLDVPAGSK.V
R3/RRR3-22/2	1219.964	1220.313	-287.595	0.324	609.226	0.412	16	0.145	K.LNPAVDDGGSFK.T
R3/RRR3-23/2	1285.455	1286.565	-1645.984	0.284	827.416	0.351	15	0.145	K.LILDGYFGM*LK.M
R3/RRR3-23/2	1078.948	1079.252	-282.283	0.307	701.380	0.380	15	0.145	K.VFSDAPAM*PK.V
R3/RRR3-23/2	1270.081	1270.565	-382.480	0.332	519.074	0.396	15	0.145	K.LILDGYFGMLK.M
R3/RRR3-24/2	1338.615	1339.455	-1378.707	0.287	563.818	0.471	15	0.143	K.VEGDGGAGTVTTM*K.L
R3/RRR3-22/2	1286.360	1286.565	-159.819	0.437	688.184	0.336	15	0.143	K.LILDGYFGM*LK.M
R3/RRR3-22/2	1078.959	1079.252	-271.613	0.334	744.712	0.328	15	0.143	K.VFSDAPAM*PK.V
R3/RRR3-25/2	1103.076	1102.220	-130.931	0.387	825.334	0.322	14	0.142	-.SEVLDVPAGSK.-
R3/RRR3-27/2	1339.420	1339.455	-26.471	0.329	540.387	0.431	14	0.141	K.VEGDGGAGTVTTM*K.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1221.145	1220.313	-138.225	0.320	489.171	0.336	15	0.139	K.LNPAVDDGGSFK.T
R3/RRR3-23/2	1220.236	1220.313	-63.475	0.283	398.650	0.380	13	0.139	K.LNPAVDDGGSFK.T
R3/RRR3-23/2	1220.068	1220.313	-201.669	0.261	435.608	0.367	14	0.138	K.LNPAVDDGGSFK.T
R3/RRR3-23/2	1219.957	1220.313	-293.116	0.273	441.535	0.345	14	0.138	K.LNPAVDDGGSFK.T
R3/RRR3-23/2	1078.625	1079.252	-1512.835	0.294	612.408	0.298	14	0.138	K.VFSDAPAM*PK.V
R3/RRR3-23/2	1063.309	1063.252	53.243	0.321	525.476	0.285	13	0.137	K.VFSDAPAMPK.V
R3/RRR3-22/2	1078.926	1079.252	-303.056	0.302	721.784	0.258	15	0.137	K.VFSDAPAM*PK.V
R3/RRR3-23/2	1219.903	1220.313	-337.089	0.274	376.013	0.356	13	0.136	-.LNPAVDDGGSFK.-
R3/RRR3-22/2	1219.964	1220.313	-287.294	0.272	600.087	0.230	16	0.134	K.LNPAVDDGGSFK.T
R3/RRR3-21/2	1219.777	1220.313	-1263.395	0.195	351.401	0.319	12	0.134	K.LNPAVDDGGSFK.T
R3/RRR3-26/2	1102.122	1102.220	-89.274	0.315	720.267	0.244	12	0.133	-.SEVLDVPAGSK.-
R3/RRR3-21/2	1219.867	1220.313	-367.210	0.190	549.242	0.211	15	0.132	K.LNPAVDDGGSFK.T
R3/RRR3-25/2	1101.311	1102.220	-1738.375	0.252	631.242	0.273	12	0.126	-.SEVLDVPAGSK.-
R3/RRR3-8/2	1985.230	1985.085	72.984	0.578	2844.407	0.649	27	0.529	R.GNPTVEVDVCCSDGTFAR.A
R3/RRR3-8/2	1984.466	1985.085	-818.578	0.567	2812.542	0.655	27	0.523	R.GNPTVEVDVCCSDGTFAR.A
R3/RRR3-8/2	1985.352	1985.085	134.896	0.580	2782.660	0.655	27	0.515	R.GNPTVEVDVCCSDGTFAR.A
R3/RRR3-8/2	1492.214	1492.656	-296.908	0.526	2411.190	0.543	24	0.379	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/2	1552.351	1552.802	-291.637	0.510	2356.831	0.497	23	0.358	K.IPLYQHIANLAGNK.Q
R3/RRR3-8/2	1492.350	1492.656	-205.485	0.543	2196.244	0.554	24	0.340	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/2	1872.351	1872.241	58.847	0.658	1930.674	0.631	26	0.312	K.LAM*QEFMILPTGAASFK.E
R3/RRR3-8/2	1552.492	1552.802	-200.364	0.569	2098.758	0.469	22	0.299	K.IPLYQHIANLAGNK.Q
R3/RRR3-8/2	1492.260	1492.656	-265.885	0.492	1994.464	0.525	23	0.295	R.IEEELGAAAVYAGAK.F
R3/RRR3-7/2	1493.180	1492.656	-319.429	0.539	1930.260	0.547	23	0.291	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/2	1902.543	1902.953	-216.334	0.567	1841.035	0.577	23	0.287	K.TYDLNFKEENNDGSQK.I
R3/RRR3-8/2	1901.724	1902.953	-1175.523	0.502	1870.094	0.560	22	0.287	K.TYDLNFKEENNDGSQK.I
R3/RRR3-2/2	1491.945	1492.656	-1149.945	0.377	2156.292	0.368	23	0.278	R.IEEELGAAAVYAGAK.F
R3/RRR3-3/2	1492.104	1492.656	-1043.150	0.377	2101.055	0.371	22	0.270	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/2	1872.575	1872.241	178.623	0.645	1634.669	0.584	25	0.253	K.LAM*QEFMILPTGAASFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1492.162	1492.656	-331.791	0.464	1796.418	0.477	22	0.251	R.IEEELGAAAVYAGAK.F
R3/RRR3-7/2	1581.641	1581.839	-125.298	0.490	1710.003	0.516	23	0.250	K.AVDNVNSVIAPALIGK.D
R3/RRR3-1/2	1492.093	1492.656	-1050.214	0.400	1861.232	0.415	21	0.245	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/2	1871.507	1872.241	-929.512	0.540	1485.269	0.564	24	0.230	K.LAM*QEFMILPTGAASFK.E
R3/RRR3-8/2	1888.446	1888.241	108.976	0.599	1553.431	0.527	25	0.229	K.LAM*QEFM*ILPTGAASFK.E
R3/RRR3-8/2	1871.467	1872.241	-950.795	0.535	1346.656	0.610	25	0.226	K.LAMQEFM*ILPTGAASFK.E
R3/RRR3-7/2	1574.390	1574.758	-234.595	0.524	1472.149	0.545	22	0.225	K.VNQIGSVTESIEAVK.M
R3/RRR3-2/2	1574.270	1574.758	-310.675	0.499	1433.597	0.546	22	0.221	K.VNQIGSVTESIEAVK.M
R3/RRR3-2/2	1582.218	1581.839	240.304	0.511	1414.948	0.551	22	0.221	K.AVDNVNSVIAPALIGK.D
R3/RRR3-8/2	1554.347	1552.802	-293.940	0.574	1519.047	0.490	21	0.220	K.IPLYQHIANLAGNK.Q
R3/RRR3-8/2	1574.462	1574.758	-188.703	0.512	1450.888	0.532	22	0.220	K.VNQIGSVTESIEAVK.M
R3/RRR3-2/2	1491.532	1492.656	-1427.884	0.370	1640.741	0.413	21	0.216	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/2	1887.594	1888.241	-874.959	0.561	1453.905	0.514	25	0.216	K.LAM*QEFM*ILPTGAASFK.E
R3/RRR3-8/2	1902.370	1902.953	-834.789	0.526	1359.107	0.557	21	0.215	K.TYDLNFKEENNDGSQK.I
R3/RRR3-8/2	1887.495	1888.241	-927.872	0.562	1368.462	0.530	25	0.210	K.LAM*QEFM*ILPTGAASFK.E
R3/RRR3-8/2	1574.359	1574.758	-254.119	0.490	1380.622	0.509	22	0.208	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/2	1574.293	1574.758	-296.205	0.509	1398.813	0.497	22	0.207	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/2	1871.475	1872.241	-946.669	0.562	1210.859	0.588	24	0.207	K.LAMQEFM*ILPTGAASFK.E
R3/RRR3-1/2	1574.681	1574.758	-49.343	0.546	1381.457	0.505	22	0.207	K.VNQIGSVTESIEAVK.M
R3/RRR3-7/2	1574.205	1574.758	-989.367	0.503	1302.634	0.538	22	0.206	K.VNQIGSVTESIEAVK.M
R3/RRR3-3/2	1575.047	1574.758	184.107	0.527	1299.279	0.538	21	0.205	K.VNQIGSVTESIEAVK.M
R3/RRR3-2/2	1574.350	1574.758	-260.187	0.509	1277.772	0.526	21	0.200	K.VNQIGSVTESIEAVK.M
R3/RRR3-1/2	1574.104	1574.758	-1053.678	0.464	1351.632	0.476	22	0.198	K.VNQIGSVTESIEAVK.M
R3/RRR3-2/2	1574.097	1574.758	-1058.662	0.471	1183.923	0.535	21	0.194	K.VNQIGSVTESIEAVK.M
R3/RRR3-1/2	1491.991	1492.656	-1119.219	0.369	1483.632	0.375	20	0.191	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/2	1191.035	1190.397	-304.963	0.542	1403.762	0.398	16	0.190	K.MGVEVYHNLK.S
R3/RRR3-3/2	1574.091	1574.758	-1062.477	0.480	1160.484	0.525	20	0.189	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/2	1855.744	1856.242	-269.029	0.527	1038.802	0.578	22	0.189	K.LAMQEFMILPTGAASFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1191.150	1190.397	-207.901	0.517	1467.202	0.344	16	0.185	K.MGVEVYHNLK.S
R3/RRR3-7/2	1574.258	1574.758	-318.455	0.475	1190.491	0.475	21	0.183	K.VNQIGSVTESIEAVK.M
R3/RRR3-10/2	1574.374	1574.758	-244.629	0.499	1118.091	0.515	19	0.183	K.VNQIGSVTESIEAVK.M
R3/RRR3-9/2	1574.433	1574.758	-207.137	0.494	1202.774	0.466	21	0.183	K.VNQIGSVTESIEAVK.M
R3/RRR3-5/2	1574.285	1574.758	-301.339	0.479	1113.676	0.505	20	0.182	K.VNQIGSVTESIEAVK.M
R3/RRR3-3/2	1574.498	1574.758	-165.448	0.500	1047.212	0.527	20	0.181	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/2	1189.992	1190.397	-341.447	0.513	1287.047	0.392	16	0.179	K.MGVEVYHNLK.S
R3/RRR3-7/2	1581.436	1581.839	-255.382	0.408	1404.116	0.352	20	0.179	K.AVDNVNSVIAPALIGK.D
R3/RRR3-4/2	1575.144	1574.758	245.736	0.486	1064.989	0.499	20	0.178	K.VNQIGSVTESIEAVK.M
R3/RRR3-7/2	1856.527	1856.242	153.885	0.510	1090.165	0.493	21	0.176	K.LAMQEFMILPTGAASFK.E
R3/RRR3-5/2	1574.151	1574.758	-1023.780	0.511	1038.702	0.490	19	0.173	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/2	1791.414	1791.983	-878.497	0.466	734.401	0.587	24	0.171	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/2	1855.702	1856.242	-832.558	0.499	1062.415	0.472	20	0.170	K.LAMQEFMILPTGAASFK.E
R3/RRR3-8/2	1581.246	1581.839	-1010.359	0.421	1022.953	0.485	19	0.170	K.AVDNVNSVIAPALIGK.D
R3/RRR3-10/2	1575.318	1574.758	-280.157	0.481	1060.583	0.457	19	0.170	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/3	1492.707	1492.656	34.268	0.491	1638.829	0.410	29	0.169	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/3	1492.787	1492.656	88.275	0.520	1543.223	0.450	29	0.168	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/3	1574.782	1574.758	15.066	0.500	1547.169	0.440	28	0.167	K.VNQIGSVTESIEAVK.M
R3/RRR3-9/2	1792.491	1791.983	-275.175	0.518	624.813	0.567	24	0.165	R.AAVPSGASTGVYEALELR.D
R3/RRR3-9/2	1573.910	1574.758	-1177.964	0.381	1026.724	0.438	19	0.165	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/2	1205.547	1206.397	-1539.006	0.503	997.587	0.411	16	0.164	K.M*GVEVYHNLK.S
R3/RRR3-8/2	1101.872	1102.252	-345.863	0.476	1099.789	0.369	16	0.163	R.AGWGVMTSHR.S
R3/RRR3-8/2	1791.229	1791.983	-982.006	0.452	608.686	0.554	23	0.161	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/2	1205.637	1206.397	-1463.537	0.517	1004.113	0.387	16	0.160	K.M*GVEVYHNLK.S
R3/RRR3-9/2	1792.234	1791.983	140.277	0.512	537.017	0.565	22	0.160	R.AAVPSGASTGVYEALELR.D
R3/RRR3-7/2	1791.412	1791.983	-879.796	0.457	588.704	0.562	21	0.159	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/2	1791.376	1791.983	-899.840	0.452	544.153	0.566	22	0.159	R.AAVPSGASTGVYEALELR.D
R3/RRR3-9/2	1791.592	1791.983	-219.002	0.435	686.475	0.513	23	0.158	R.AAVPSGASTGVYEALELR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1680.548	1680.975	-254.819	0.492	786.870	0.461	21	0.157	K.KIPLYQHIANLAGNK.Q
R3/RRR3-8/2	1855.509	1856.242	-936.571	0.480	817.722	0.451	20	0.155	K.LAMQEFMILPTGAASFK.E
R3/RRR3-3/2	1793.031	1791.983	26.589	0.519	502.274	0.534	21	0.155	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/2	1680.431	1680.975	-921.507	0.484	781.275	0.444	21	0.155	K.KIPLYQHIANLAGNK.Q
R3/RRR3-2/2	1492.251	1492.656	-271.958	0.354	1168.349	0.290	21	0.154	R.IEEELGAAAVYAGAK.F
R3/RRR3-1/2	1888.117	1888.241	-65.635	0.457	701.599	0.483	19	0.154	K.LAM*QEFM*ILPTGAASFK.E
R3/RRR3-2/2	1791.328	1791.983	-926.999	0.447	614.042	0.494	22	0.154	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/2	1206.038	1206.397	-297.809	0.520	935.751	0.357	16	0.153	K.M*GVEVYHNLK.S
R3/RRR3-8/2	1679.935	1680.975	-1218.044	0.523	786.496	0.423	21	0.152	K.KIPLYQHIANLAGNK.Q
R3/RRR3-7/2	1491.361	1492.656	-1543.395	0.328	879.543	0.380	20	0.150	R.IEEELGAAAVYAGAK.F
R3/RRR3-1/2	1791.745	1791.983	-133.292	0.461	255.580	0.514	19	0.150	R.AAVPSGASTGVYEALELR.D
R3/RRR3-7/2	1855.285	1856.242	-1057.848	0.414	736.566	0.420	18	0.147	K.LAMQEFMILPTGAASFK.E
R3/RRR3-9/2	1581.571	1581.839	-169.740	0.385	634.504	0.426	18	0.145	K.AVDNVNSVIAPALIGK.D
R3/RRR3-1/2	1581.270	1581.839	-995.013	0.317	658.452	0.404	20	0.144	K.AVDNVNSVIAPALIGK.D
R3/RRR3-3/2	1581.348	1581.839	-310.910	0.346	628.098	0.385	19	0.142	K.AVDNVNSVIAPALIGK.D
R3/RRR3-8/2	1117.413	1118.251	-1649.473	0.391	750.420	0.295	15	0.140	R.AGWGVM*TSHR.S
R3/RRR3-8/2	1872.957	1872.241	-152.450	0.434	710.790	0.350	18	0.140	K.LAMQEFM*ILPTGAASFK.E
R3/RRR3-2/2	1205.588	1206.397	-1505.033	0.363	671.781	0.291	14	0.139	K.M*GVEVYHNLK.S
R3/RRR3-8/2	1118.299	1118.251	42.713	0.354	671.217	0.276	15	0.138	R.AGWGVM*TSHR.S
R3/RRR3-26/2	1790.961	1791.983	-1132.416	0.308	309.929	0.399	17	0.137	-.AAVPSGASTGVYEALELR.-
R3/RRR3-8/2	919.044	919.094	-54.702	0.420	726.120	0.273	13	0.136	-.SCNALLLK.-
R3/RRR3-8/2	1871.582	1872.241	-889.177	0.367	612.088	0.334	16	0.136	K.LAMQEFM*ILPTGAASFK.E
R3/RRR3-8/2	1855.403	1856.242	-993.837	0.307	585.774	0.351	15	0.136	K.LAMQEFMILPTGAASFK.E
R3/RRR3-16/2	1887.725	1888.241	-805.239	0.267	174.977	0.366	12	0.136	-.LAM*QEFM*ILPTGAASFK.-
R3/RRR3-1/2	1790.802	1791.983	-1221.397	0.282	424.540	0.297	19	0.136	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/2	1117.307	1118.251	-1744.966	0.324	608.481	0.251	14	0.135	R.AGWGVM*TSHR.S
R3/RRR3-10/2	919.438	919.094	374.777	0.342	777.042	0.247	12	0.135	-.SCNALLLK.-
R3/RRR3-7/2	1854.699	1856.242	-1915.905	0.281	525.500	0.241	16	0.132	K.LAMQEFMILPTGAASFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1872.538	1872.241	158.619	0.240	620.773	0.091	15	0.126	K.LAMQEFM*ILPTGAASFK.E
R3/RRR3-8/3	1902.563	1902.953	-205.527	0.392	621.022	0.608	29	0.126	K.TYDLNFKEENNDGSQK.I
R3/RRR3-8/3	1902.950	1902.953	-1.558	0.397	540.497	0.620	28	0.124	K.TYDLNFKEENNDGSQK.I
R3/RRR3-8/3	1492.825	1492.656	113.862	0.467	1265.882	0.359	25	0.121	R.IEEELGAAAVYAGAK.F
R3/RRR3-8/3	1902.498	1902.953	-239.707	0.376	476.952	0.593	26	0.118	K.TYDLNFKEENNDGSQK.I
R3/RRR3-8/3	1792.123	1791.983	78.040	0.438	816.765	0.458	31	0.113	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/3	1792.579	1791.983	-225.889	0.454	741.119	0.473	30	0.112	R.AAVPSGASTGVYEALELR.D
R3/RRR3-9/2	919.639	919.094	-496.676	0.277	218.927	0.329	12	0.108	-.SCNALLLK.-
R3/RRR3-8/3	1792.592	1791.983	-218.921	0.446	671.408	0.455	28	0.107	R.AAVPSGASTGVYEALELR.D
R3/RRR3-8/3	1574.577	1574.758	-115.333	0.448	951.781	0.375	24	0.106	K.VNQIGSVTESIEAVK.M
R3/RRR3-8/3	1574.767	1574.758	5.853	0.327	842.963	0.406	21	0.105	K.VNQIGSVTESIEAVK.M
R3/RRR3-1/2	919.948	919.094	-159.258	0.355	276.130	0.304	10	0.104	-.SCNALLLK.-
R3/RRR3-8/3	1904.568	1902.953	-202.578	0.224	542.796	0.365	23	0.092	K.TYDLNFKEENNDGSQK.I
R3/RRR3-9/3	1554.127	1552.802	209.935	0.323	623.016	0.301	22	0.089	K.IPLYQHIANLAGNK.Q
R3/RRR3-1/3	1552.450	1552.802	-227.627	0.308	1055.082	0.235	27	0.088	K.IPLYQHIANLAGNK.Q
R3/RRR3-8/3	1855.781	1856.242	-249.106	0.352	1055.577	0.179	28	0.084	-.LAMQEFMILPTGAASFK.-
R3/RRR3-7/3	1574.380	1574.758	-241.098	0.259	724.571	0.157	23	0.082	-.VNQIGSVTESIEAVK.-
R3/RRR3-8/3	1855.308	1856.242	-1045.469	0.295	928.714	0.090	28	0.074	K.LAMQEFMILPTGAASFK.E
R3/RRR3-8/2	1745.296	1745.940	-944.433	0.545	2730.717	0.610	26	0.480	R.HMDGFGVNTYTFVTR.D
R3/RRR3-2/2	1983.662	1983.204	231.607	0.600	2746.503	0.586	26	0.471	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-8/2	1983.398	1983.204	97.867	0.636	2731.852	0.586	26	0.466	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-7/2	1983.662	1983.204	231.422	0.631	2712.239	0.588	26	0.462	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-8/2	1745.331	1745.940	-924.491	0.570	2613.306	0.624	26	0.457	R.HMDGFGVNTYTFVTR.D
R3/RRR3-7/2	1983.442	1983.204	120.335	0.617	2661.982	0.573	26	0.445	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-8/2	1983.108	1983.204	-48.318	0.596	2650.475	0.567	26	0.440	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-8/2	1745.659	1745.940	-161.360	0.540	2568.442	0.602	26	0.438	R.HMDGFGVNTYTFVTR.D
R3/RRR3-7/2	1746.340	1745.940	230.059	0.566	2549.089	0.604	26	0.434	R.HMDGFGVNTYTFVTR.D
R3/RRR3-2/2	1983.175	1983.204	-14.484	0.571	2612.399	0.558	26	0.429	R.AIWVNYLSQCDESLGVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1983.537	1983.204	168.167	0.644	2576.745	0.575	26	0.425	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-7/2	1745.223	1745.940	-986.425	0.500	2514.938	0.562	26	0.411	R.HMDGFGVNTYTFVTR.D
R3/RRR3-7/2	1982.492	1983.204	-866.021	0.560	2538.284	0.554	26	0.411	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-7/2	1746.285	1745.940	198.446	0.533	2431.967	0.598	26	0.406	R.HMDGFGVNTYTFVTR.D
R3/RRR3-7/3	1983.653	1983.204	227.095	0.529	2544.774	0.459	34	0.350	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-7/2	1539.873	1540.785	-1245.267	0.585	1854.517	0.546	20	0.279	R.GPILLEDYHLIEK.L
R3/RRR3-8/2	1541.345	1540.785	-286.332	0.601	1807.923	0.557	20	0.274	R.GPILLEDYHLIEK.L
R3/RRR3-7/2	1539.693	1540.785	-1362.625	0.547	1900.166	0.502	20	0.274	R.GPILLEDYHLIEK.L
R3/RRR3-7/2	1540.242	1540.785	-1004.586	0.576	1820.513	0.534	20	0.270	R.GPILLEDYHLIEK.L
R3/RRR3-4/2	1540.341	1540.785	-288.903	0.538	1804.477	0.501	20	0.260	R.GPILLEDYHLIEK.L
R3/RRR3-2/2	1540.157	1540.785	-1060.448	0.555	1830.796	0.489	20	0.260	R.GPILLEDYHLIEK.L
R3/RRR3-8/2	1540.148	1540.785	-1065.859	0.561	1700.193	0.536	20	0.254	R.GPILLEDYHLIEK.L
R3/RRR3-8/2	1528.169	1527.856	205.138	0.597	1611.582	0.585	20	0.250	R.LGPNYLMLPVNAPK.C
R3/RRR3-7/2	1528.780	1527.856	-50.104	0.575	1652.193	0.533	21	0.243	R.LGPNYLMLPVNAPK.C
R3/RRR3-7/2	1527.551	1527.856	-200.109	0.558	1564.276	0.535	21	0.233	R.LGPNYLMLPVNAPK.C
R3/RRR3-8/2	1529.318	1527.856	302.656	0.588	1459.013	0.539	19	0.220	R.LGPNYLMLPVNAPK.C
R3/RRR3-8/3	1983.649	1983.204	225.244	0.519	1821.965	0.466	31	0.213	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-2/2	1543.320	1543.855	-998.043	0.495	1390.252	0.519	19	0.209	R.LGPNYLM*LPVNAPK.C
R3/RRR3-1/2	1543.290	1543.855	-1017.102	0.511	1330.595	0.537	19	0.207	R.LGPNYLM*LPVNAPK.C
R3/RRR3-7/2	1544.120	1543.855	171.558	0.584	1287.867	0.553	20	0.206	R.LGPNYLM*LPVNAPK.C
R3/RRR3-6/2	1124.722	1125.303	-1409.795	0.534	1318.547	0.481	18	0.198	R.SPGAQTPVIVR.F
R3/RRR3-5/2	1529.011	1527.856	101.567	0.534	1237.801	0.537	18	0.197	R.LGPNYLMLPVNAPK.C
R3/RRR3-7/2	1544.374	1543.855	-312.549	0.560	1094.212	0.574	19	0.193	R.LGPNYLM*LPVNAPK.C
R3/RRR3-8/2	1542.853	1543.855	-1301.886	0.492	1301.708	0.471	19	0.191	R.LGPNYLM*LPVNAPK.C
R3/RRR3-8/2	969.454	970.107	-1710.103	0.516	1234.270	0.468	16	0.191	R.FAGELAHPK.V
R3/RRR3-3/2	1543.274	1543.855	-1027.902	0.498	1319.548	0.462	19	0.191	R.LGPNYLM*LPVNAPK.C
R3/RRR3-6/2	1124.473	1125.303	-1632.229	0.481	1234.522	0.468	18	0.188	R.SPGAQTPVIVR.F
R3/RRR3-8/2	1762.280	1761.939	194.172	0.598	872.087	0.613	23	0.188	R.HM*DGFGVNTYTFVTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1274.119	1273.287	-132.285	0.442	1494.444	0.338	15	0.187	R.DEEVDYYPSR.H
R3/RRR3-4/2	1124.527	1125.303	-1584.463	0.491	1132.895	0.495	18	0.186	R.SPGAQTPVIVR.F
R3/RRR3-8/2	1273.932	1273.287	-279.736	0.484	1352.565	0.396	15	0.185	R.DEEVDYYPSR.H
R3/RRR3-1/2	1125.040	1125.303	-234.483	0.478	1280.922	0.426	18	0.184	R.SPGAQTPVIVR.F
R3/RRR3-1/2	1544.539	1543.855	-205.262	0.545	1151.732	0.499	19	0.184	R.LGPNYLM*LPVNAPK.C
R3/RRR3-8/2	1125.117	1125.303	-165.692	0.500	1159.758	0.471	18	0.183	R.SPGAQTPVIVR.F
R3/RRR3-5/2	1124.664	1125.303	-1461.796	0.478	1170.581	0.468	17	0.183	R.SPGAQTPVIVR.F
R3/RRR3-3/2	1070.931	1071.168	-221.293	0.435	1149.593	0.470	15	0.183	R.VFAYADTQR.Y
R3/RRR3-6/2	1543.407	1543.855	-291.643	0.491	1107.528	0.515	18	0.183	R.LGPNYLM*LPVNAPK.C
R3/RRR3-6/2	1125.154	1125.303	-133.259	0.520	1078.523	0.503	17	0.182	R.SPGAQTPVIVR.F
R3/RRR3-8/2	1125.065	1125.303	-211.951	0.494	1111.139	0.486	17	0.182	R.SPGAQTPVIVR.F
R3/RRR3-1/2	1543.515	1543.855	-220.946	0.505	1120.338	0.500	18	0.181	R.LGPNYLM*LPVNAPK.C
R3/RRR3-8/2	1761.358	1761.939	-900.132	0.498	910.624	0.555	23	0.179	R.HM*DGFGVNTYTFVTR.D
R3/RRR3-8/3	1984.033	1983.204	-86.316	0.491	1532.142	0.479	29	0.178	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-3/2	970.026	970.107	-83.003	0.419	1208.368	0.420	14	0.178	R.FAGELAHPK.V
R3/RRR3-8/2	1544.423	1543.855	-280.670	0.556	1034.264	0.520	18	0.178	R.LGPNYLM*LPVNAPK.C
R3/RRR3-8/2	1125.402	1125.303	88.274	0.418	1169.488	0.442	17	0.178	R.SPGAQTPVIVR.F
R3/RRR3-8/2	1273.048	1273.287	-188.275	0.420	1495.470	0.275	15	0.177	-.DEEVDYYPSR.-
R3/RRR3-3/2	1124.959	1125.303	-307.094	0.504	1119.413	0.455	17	0.177	R.SPGAQTPVIVR.F
R3/RRR3-8/2	1104.643	1105.188	-1402.835	0.467	876.587	0.539	13	0.176	R.SHVQEYWR.V
R3/RRR3-1/2	1071.234	1071.168	62.335	0.467	952.106	0.505	15	0.176	R.VFAYADTQR.Y
R3/RRR3-9/2	1125.131	1125.303	-153.502	0.489	970.599	0.501	17	0.175	R.SPGAQTPVIVR.F
R3/RRR3-2/2	1543.454	1543.855	-261.173	0.487	1010.548	0.510	18	0.175	R.LGPNYLM*LPVNAPK.C
R3/RRR3-7/3	1982.897	1983.204	-155.151	0.486	1532.354	0.468	29	0.175	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-8/2	969.979	970.107	-131.604	0.458	1025.675	0.470	15	0.175	R.FAGELAHPK.V
R3/RRR3-8/2	969.579	970.107	-1580.067	0.506	1020.488	0.468	15	0.175	R.FAGELAHPK.V
R3/RRR3-2/2	1124.511	1125.303	-1598.531	0.480	933.464	0.510	17	0.174	R.SPGAQTPVIVR.F
R3/RRR3-3/2	1124.590	1125.303	-1527.869	0.512	994.601	0.480	17	0.173	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1125.163	1125.303	-124.770	0.476	1081.354	0.441	18	0.173	R.SPGAQTPVIVR.F
R3/RRR3-7/2	1543.281	1543.855	-1023.296	0.507	1067.684	0.476	18	0.173	R.LGPNYLM*LPVNAPK.C
R3/RRR3-8/2	1126.157	1125.303	-130.096	0.492	1126.370	0.428	17	0.173	R.SPGAQTPVIVR.F
R3/RRR3-8/2	1125.103	1125.303	-178.426	0.489	1021.543	0.464	17	0.172	R.SPGAQTPVIVR.F
R3/RRR3-2/2	1124.600	1125.303	-1519.255	0.432	1059.325	0.447	17	0.171	R.SPGAQTPVIVR.F
R3/RRR3-7/2	1125.954	1125.303	-311.172	0.435	1044.755	0.449	17	0.171	R.SPGAQTPVIVR.F
R3/RRR3-2/2	1125.423	1125.303	106.658	0.470	1009.535	0.458	17	0.171	R.SPGAQTPVIVR.F
R3/RRR3-1/2	1124.876	1125.303	-380.804	0.490	1073.224	0.420	18	0.169	R.SPGAQTPVIVR.F
R3/RRR3-2/2	1527.375	1527.856	-315.965	0.456	895.348	0.510	19	0.169	R.LGPNYLMLPVNAPK.C
R3/RRR3-7/2	970.023	970.107	-86.033	0.483	964.371	0.460	14	0.169	R.FAGELAHPK.V
R3/RRR3-4/2	1125.030	1125.303	-243.627	0.491	913.493	0.475	17	0.168	R.SPGAQTPVIVR.F
R3/RRR3-7/2	1126.147	1125.303	-139.447	0.478	1086.891	0.414	17	0.168	R.SPGAQTPVIVR.F
R3/RRR3-10/2	1125.183	1125.303	-107.140	0.492	1037.962	0.430	17	0.168	R.SPGAQTPVIVR.F
R3/RRR3-3/2	1542.768	1543.855	-1357.273	0.406	1185.201	0.390	17	0.167	R.LGPNYLM*LPVNAPK.C
R3/RRR3-9/2	1124.467	1125.303	-1637.900	0.417	1005.023	0.432	18	0.167	R.SPGAQTPVIVR.F
R3/RRR3-7/2	969.960	970.107	-151.804	0.412	897.695	0.476	14	0.167	R.FAGELAHPK.V
R3/RRR3-1/2	1071.987	1071.168	-168.879	0.507	855.913	0.471	14	0.166	R.VFAYADTQR.Y
R3/RRR3-7/2	1273.073	1273.287	-168.748	0.391	1472.979	0.225	15	0.165	R.DEEVDYYPSR.H
R3/RRR3-9/2	1540.372	1540.785	-268.549	0.452	982.354	0.443	18	0.165	R.GPILLEDYHLIEK.L
R3/RRR3-4/2	1072.128	1071.168	-37.185	0.416	975.591	0.420	15	0.164	R.VFAYADTQR.Y
R3/RRR3-2/2	1070.954	1071.168	-200.367	0.474	939.928	0.425	15	0.164	R.VFAYADTQR.Y
R3/RRR3-7/2	1070.945	1071.168	-208.600	0.501	916.288	0.431	15	0.164	R.VFAYADTQR.Y
R3/RRR3-4/2	1543.375	1543.855	-312.434	0.494	1093.640	0.404	18	0.163	R.LGPNYLM*LPVNAPK.C
R3/RRR3-8/2	1543.156	1543.855	-1104.307	0.486	1094.350	0.402	18	0.163	R.LGPNYLM*LPVNAPK.C
R3/RRR3-6/2	1070.882	1071.168	-267.951	0.412	1073.681	0.373	15	0.163	R.VFAYADTQR.Y
R3/RRR3-7/2	1526.600	1527.856	-1482.264	0.396	993.833	0.435	18	0.163	R.LGPNYLMLPVNAPK.C
R3/RRR3-10/2	1125.067	1125.303	-210.318	0.494	951.615	0.423	17	0.163	R.SPGAQTPVIVR.F
R3/RRR3-6/2	1071.195	1071.168	25.419	0.416	935.475	0.410	15	0.161	R.VFAYADTQR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1070.965	1071.168	-190.076	0.472	901.172	0.412	15	0.161	R.VFAYADTQR.Y
R3/RRR3-5/2	1124.422	1125.303	-1678.473	0.440	1011.681	0.388	17	0.161	R.SPGAQTPVIVR.F
R3/RRR3-8/2	1070.849	1071.168	-298.143	0.474	885.227	0.408	15	0.160	R.VFAYADTQR.Y
R3/RRR3-3/2	1071.022	1071.168	-136.793	0.436	885.374	0.418	14	0.159	R.VFAYADTQR.Y
R3/RRR3-8/2	1126.142	1125.303	-144.014	0.445	1043.170	0.366	17	0.159	R.SPGAQTPVIVR.F
R3/RRR3-7/2	1070.617	1071.168	-1452.336	0.443	930.567	0.388	15	0.159	R.VFAYADTQR.Y
R3/RRR3-3/2	1071.071	1071.168	-90.262	0.386	1044.578	0.355	15	0.159	R.VFAYADTQR.Y
R3/RRR3-2/2	1542.533	1543.855	-1510.035	0.357	972.477	0.413	17	0.158	R.LGPNYLM*LPVNAPK.C
R3/RRR3-6/2	1071.074	1071.168	-87.976	0.466	768.980	0.429	14	0.157	R.VFAYADTQR.Y
R3/RRR3-8/2	1104.295	1105.188	-1719.043	0.374	864.719	0.417	13	0.157	R.SHVQEYWR.V
R3/RRR3-2/2	1070.380	1071.168	-1675.024	0.368	838.092	0.424	14	0.157	R.VFAYADTQR.Y
R3/RRR3-7/2	1105.755	1105.188	-392.483	0.457	728.312	0.449	12	0.157	R.SHVQEYWR.V
R3/RRR3-8/2	989.164	989.110	55.377	0.396	783.027	0.440	12	0.156	R.FSTVIHER.G
R3/RRR3-16/2	1126.115	1125.303	-167.720	0.465	768.391	0.418	17	0.156	R.SPGAQTPVIVR.F
R3/RRR3-5/2	1124.806	1125.303	-443.418	0.469	853.499	0.390	17	0.155	R.SPGAQTPVIVR.F
R3/RRR3-7/2	1104.939	1105.188	-225.674	0.366	770.776	0.444	12	0.153	-.SHVQEYWR.-
R3/RRR3-2/2	1527.075	1527.856	-1169.753	0.428	719.662	0.429	18	0.152	R.LGPNYLMLPVNAPK.C
R3/RRR3-2/2	1070.539	1071.168	-1525.982	0.356	815.648	0.376	14	0.151	R.VFAYADTQR.Y
R3/RRR3-7/2	988.900	989.110	-212.906	0.467	643.197	0.421	11	0.150	R.FSTVIHER.G
R3/RRR3-7/2	988.562	989.110	-1570.286	0.424	632.330	0.425	11	0.150	R.FSTVIHER.G
R3/RRR3-1/2	970.032	970.107	-77.449	0.378	893.668	0.334	14	0.149	R.FAGELAHPK.V
R3/RRR3-8/2	1104.902	1105.188	-259.479	0.424	715.962	0.391	12	0.148	-.SHVQEYWR.-
R3/RRR3-3/2	969.850	970.107	-264.934	0.329	892.463	0.324	14	0.147	R.FAGELAHPK.V
R3/RRR3-2/2	1527.424	1527.856	-284.052	0.432	508.224	0.455	15	0.147	R.LGPNYLMLPVNAPK.C
R3/RRR3-2/2	989.033	989.110	-78.066	0.383	549.367	0.411	11	0.147	R.FSTVIHER.G
R3/RRR3-8/2	988.878	989.110	-234.702	0.357	606.743	0.411	11	0.147	R.FSTVIHER.G
R3/RRR3-24/2	970.105	970.107	-1.339	0.305	774.139	0.370	13	0.146	R.FAGELAHPK.V
R3/RRR3-1/2	970.018	970.107	-91.713	0.328	975.654	0.287	14	0.146	R.FAGELAHPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	988.376	989.110	-1759.865	0.371	629.504	0.387	11	0.146	R.FSTVIHER.G
R3/RRR3-6/2	969.778	970.107	-339.948	0.452	721.395	0.331	13	0.144	R.FAGELAHPK.V
R3/RRR3-7/2	1273.101	1273.287	-146.625	0.410	1168.622	0.204	14	0.143	-.DEEVDYYPSR.-
R3/RRR3-8/2	1984.041	1983.204	-82.298	0.331	803.318	0.379	17	0.143	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-8/2	988.123	989.110	-2017.178	0.313	652.412	0.336	11	0.141	R.FSTVIHER.G
R3/RRR3-5/2	1541.226	1540.785	287.051	0.396	718.562	0.336	15	0.140	R.GPILLEDYHLIEK.L
R3/RRR3-7/2	1273.105	1273.287	-142.970	0.398	967.351	0.230	13	0.137	-.DEEVDYYPSR.-
R3/RRR3-6/2	1105.075	1105.188	-101.999	0.359	648.544	0.289	11	0.137	-.SHVQEYWR.-
R3/RRR3-9/2	1528.747	1527.856	-71.569	0.282	523.970	0.276	16	0.137	R.LGPNYLMLPVNAPK.C
R3/RRR3-9/2	1528.835	1527.856	-13.904	0.198	536.421	0.334	16	0.136	R.LGPNYLMLPVNAPK.C
R3/RRR3-27/2	969.886	970.107	-228.442	0.283	540.587	0.246	11	0.135	R.FAGELAHPK.V
R3/RRR3-7/3	1952.353	1952.248	54.076	0.460	1117.532	0.463	29	0.132	R.DGIKFPDVIHAFKPNPR.S
R3/RRR3-8/3	1541.042	1540.785	167.305	0.398	841.364	0.509	22	0.126	R.GPILLEDYHLIEK.L
R3/RRR3-1/3	1541.317	1540.785	-304.258	0.395	850.232	0.492	23	0.123	R.GPILLEDYHLIEK.L
R3/RRR3-7/3	1541.070	1540.785	185.297	0.450	867.648	0.483	23	0.123	R.GPILLEDYHLIEK.L
R3/RRR3-8/3	1539.756	1540.785	-1321.627	0.369	842.997	0.482	21	0.122	R.GPILLEDYHLIEK.L
R3/RRR3-1/3	1540.803	1540.785	11.544	0.403	697.350	0.508	20	0.121	R.GPILLEDYHLIEK.L
R3/RRR3-7/3	1541.038	1540.785	164.922	0.469	660.888	0.513	21	0.120	R.GPILLEDYHLIEK.L
R3/RRR3-7/3	1126.235	1126.293	-51.608	0.533	1163.621	0.395	22	0.119	R.RFAGELAHPK.V
R3/RRR3-4/3	1541.624	1540.785	-104.654	0.386	780.325	0.461	22	0.116	R.GPILLEDYHLIEK.L
R3/RRR3-2/3	1541.023	1540.785	154.794	0.459	838.161	0.448	23	0.116	R.GPILLEDYHLIEK.L
R3/RRR3-6/3	1540.055	1540.785	-1126.512	0.406	762.277	0.448	22	0.114	R.GPILLEDYHLIEK.L
R3/RRR3-1/3	1540.872	1540.785	56.836	0.444	728.578	0.444	22	0.112	R.GPILLEDYHLIEK.L
R3/RRR3-3/3	1540.937	1540.785	98.905	0.361	620.948	0.455	21	0.111	R.GPILLEDYHLIEK.L
R3/RRR3-4/3	1540.449	1540.785	-218.908	0.394	734.514	0.434	21	0.111	R.GPILLEDYHLIEK.L
R3/RRR3-5/3	1539.430	1540.785	-1534.142	0.329	397.998	0.476	17	0.111	R.GPILLEDYHLIEK.L
R3/RRR3-2/3	1540.426	1540.785	-233.457	0.390	768.512	0.421	22	0.110	R.GPILLEDYHLIEK.L
R3/RRR3-7/3	1126.333	1126.293	35.468	0.504	968.659	0.377	20	0.108	R.RFAGELAHPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/3	1540.888	1540.785	67.204	0.400	660.799	0.411	20	0.107	R.GPILLEDYHLIEK.L
R3/RRR3-4/3	1540.488	1540.785	-193.152	0.365	705.991	0.400	21	0.107	R.GPILLEDYHLIEK.L
R3/RRR3-2/3	1540.353	1540.785	-281.279	0.400	770.177	0.373	23	0.104	R.GPILLEDYHLIEK.L
R3/RRR3-8/3	1761.499	1761.939	-250.699	0.427	1040.579	0.349	28	0.104	R.HM*DGFGVNTYTFVTR.D
R3/RRR3-8/3	1125.935	1126.293	-318.475	0.516	1075.435	0.328	21	0.104	R.RFAGELAHPK.V
R3/RRR3-3/3	1540.541	1540.785	-159.050	0.379	602.087	0.380	19	0.104	R.GPILLEDYHLIEK.L
R3/RRR3-3/3	1540.651	1540.785	-87.276	0.351	588.113	0.356	20	0.102	R.GPILLEDYHLIEK.L
R3/RRR3-5/3	1951.317	1952.248	-992.618	0.354	765.147	0.397	23	0.101	R.DGIKFPDVIHAFKPNPR.S
R3/RRR3-10/3	1541.048	1540.785	171.118	0.327	633.155	0.345	20	0.101	R.GPILLEDYHLIEK.L
R3/RRR3-5/3	1540.968	1540.785	119.402	0.324	712.787	0.331	20	0.100	R.GPILLEDYHLIEK.L
R3/RRR3-7/3	1127.017	1126.293	-245.545	0.513	1143.115	0.291	22	0.100	R.RFAGELAHPK.V
R3/RRR3-7/3	1540.859	1540.785	48.016	0.440	733.359	0.336	21	0.100	R.GPILLEDYHLIEK.L
R3/RRR3-9/3	1540.363	1540.785	-274.719	0.377	563.008	0.327	19	0.099	R.GPILLEDYHLIEK.L
R3/RRR3-10/3	1540.827	1540.785	27.158	0.278	791.510	0.311	20	0.099	R.GPILLEDYHLIEK.L
R3/RRR3-5/3	1540.765	1540.785	-13.129	0.306	630.960	0.321	18	0.099	R.GPILLEDYHLIEK.L
R3/RRR3-3/3	1126.508	1126.293	191.319	0.471	838.636	0.330	19	0.099	R.RFAGELAHPK.V
R3/RRR3-5/3	1950.808	1952.248	-1254.311	0.325	1055.926	0.280	26	0.097	R.DGIKFPDVIHAFKPNPR.S
R3/RRR3-9/3	1540.332	1540.785	-295.233	0.237	665.403	0.249	19	0.094	R.GPILLEDYHLIEK.L
R3/RRR3-3/3	1126.758	1126.293	413.601	0.456	888.944	0.284	19	0.090	-.RFAGELAHPK.-
R3/RRR3-7/3	1984.311	1983.204	54.007	0.319	892.513	0.251	24	0.089	R.AIWVNYLSQCDESLGVK.I
R3/RRR3-8/3	1951.623	1952.248	-834.838	0.328	705.667	0.222	23	0.084	-.DGIKFPDVIHAFKPNPR.-
R3/RRR3-3/3	1126.317	1126.293	21.608	0.431	905.546	0.218	20	0.084	-.RFAGELAHPK.-
R3/RRR3-8/3	1126.966	1126.293	-290.697	0.418	782.081	0.211	19	0.077	-.RFAGELAHPK.-
R3/RRR3-12/2	1919.613	1919.128	253.558	0.642	3773.809	0.626	30	0.806	K.VQQVDTTGAGDAFVGALLR.R
R3/RRR3-12/2	1919.569	1919.128	230.347	0.620	3500.265	0.639	29	0.719	K.VQQVDTTGAGDAFVGALLR.R
R3/RRR3-12/2	1918.642	1919.128	-254.147	0.609	3516.012	0.568	29	0.688	K.VQQVDTTGAGDAFVGALLR.R
R3/RRR3-12/2	1578.218	1578.622	-256.989	0.564	2428.658	0.598	27	0.408	R.DNGVDDAGVVFDAGAR.T
R3/RRR3-12/2	1578.212	1578.622	-260.869	0.571	2396.354	0.587	26	0.397	R.DNGVDDAGVVFDAGAR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1578.302	1578.622	-203.759	0.549	1834.481	0.588	24	0.290	R.DNGVDDAGVVFDAGAR.T
R3/RRR3-12/2	1225.028	1225.370	-280.109	0.489	1854.105	0.438	19	0.253	K.FANACGAITATK.K
R3/RRR3-12/2	991.595	992.197	-1620.615	0.448	1680.076	0.498	15	0.245	R.TALAFVTLR.A
R3/RRR3-12/2	991.959	992.197	-240.824	0.479	1677.312	0.485	15	0.242	R.TALAFVTLR.A
R3/RRR3-12/3	1918.950	1919.128	-93.200	0.491	1855.999	0.501	33	0.233	K.VQQVDTTGAGDAFVGALLR.R
R3/RRR3-12/2	1402.330	1401.632	-216.231	0.572	1502.693	0.531	20	0.230	K.ILSIWDQADIVK.V
R3/RRR3-12/2	1317.303	1317.550	-188.549	0.512	1623.395	0.467	19	0.229	K.LLLVTLGDQGCK.Y
R3/RRR3-12/2	1400.879	1401.632	-1255.639	0.483	1406.246	0.557	20	0.224	K.ILSIWDQADIVK.V
R3/RRR3-12/2	991.491	992.197	-1725.501	0.482	1531.755	0.481	15	0.223	R.TALAFVTLR.A
R3/RRR3-12/2	1224.418	1225.370	-1598.792	0.463	1580.655	0.445	19	0.219	K.FANACGAITATK.K
R3/RRR3-12/2	1225.977	1225.370	-321.638	0.507	1540.993	0.442	19	0.214	K.FANACGAITATK.K
R3/RRR3-12/2	1358.077	1358.480	-297.113	0.479	1417.632	0.437	20	0.200	R.IVQDPSSLQDQK.K
R3/RRR3-12/2	1358.176	1358.480	-224.433	0.509	1249.490	0.493	19	0.195	R.IVQDPSSLQDQK.K
R3/RRR3-12/3	1918.886	1919.128	-126.797	0.426	1704.207	0.438	31	0.190	K.VQQVDTTGAGDAFVGALLR.R
R3/RRR3-12/2	1401.254	1401.632	-270.658	0.518	1117.033	0.518	18	0.188	K.ILSIWDQADIVK.V
R3/RRR3-12/2	1317.146	1317.550	-307.648	0.497	1225.230	0.466	18	0.187	K.LLLVTLGDQGCK.Y
R3/RRR3-12/2	1317.172	1317.550	-288.028	0.489	1175.832	0.448	18	0.180	K.LLLVTLGDQGCK.Y
R3/RRR3-12/2	1358.248	1358.480	-171.146	0.494	1131.949	0.439	18	0.175	R.IVQDPSSLQDQK.K
R3/RRR3-12/2	1891.195	1892.141	-1031.805	0.417	1316.544	0.380	20	0.175	R.AAVFHYGSISLIAEPCR.S
R3/RRR3-12/2	1581.795	1581.879	-53.223	0.501	1070.669	0.462	23	0.173	K.KGAIPSLPTEVEVLK.L
R3/RRR3-1/2	1402.664	1401.632	22.816	0.401	279.775	0.372	14	0.142	K.ILSIWDQADIVK.V
R3/RRR3-3/2	1918.707	1919.128	-220.127	0.387	290.452	0.374	17	0.136	K.VQQVDTTGAGDAFVGALLR.R
R3/RRR3-12/2	1419.486	1419.565	-55.945	0.386	622.023	0.328	15	0.135	-.EAGALLSYDPNLR.-
R3/RRR3-12/3	1515.778	1514.666	74.093	0.506	1165.772	0.451	27	0.131	R.RIVQDPSSLQDQK.K
R3/RRR3-12/2	1318.695	1317.550	109.874	0.281	623.177	0.249	13	0.131	K.LLLVTLGDQGCK.Y
R3/RRR3-12/2	1418.471	1419.565	-1480.542	0.226	846.059	0.140	17	0.126	K.EAGALLSYDPNLR.E
R3/RRR3-12/3	1514.493	1514.666	-114.371	0.515	1069.963	0.445	26	0.124	R.RIVQDPSSLQDQK.K
R3/RRR3-12/3	1515.001	1514.666	222.065	0.485	890.791	0.470	24	0.119	R.RIVQDPSSLQDQK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1835.487	1836.033	-844.462	0.562	2515.239	0.587	29	0.422	R.VPYTAGIGLESVGVETDK.A
R3/RRR3-8/2	1835.445	1836.033	-867.895	0.591	2389.897	0.604	28	0.399	R.VPYTAGIGLESVGVETDK.A
R3/RRR3-8/2	1835.244	1836.033	-977.668	0.524	2328.144	0.543	28	0.366	R.VPYTAGIGLESVGVETDK.A
R3/RRR3-7/2	1948.445	1948.118	168.179	0.567	1987.038	0.640	27	0.329	K.LASPSEVSVDLSDGGSTVVK.G
R3/RRR3-7/2	1948.712	1948.118	-209.009	0.561	2015.309	0.604	28	0.323	K.LASPSEVSVDLSDGGSTVVK.G
R3/RRR3-8/2	1835.393	1836.033	-896.204	0.555	2093.798	0.517	27	0.312	R.VPYTAGIGLESVGVETDK.A
R3/RRR3-8/2	1947.490	1948.118	-838.709	0.518	1693.245	0.630	26	0.276	K.LASPSEVSVDLSDGGSTVVK.G
R3/RRR3-8/2	1947.548	1948.118	-808.760	0.526	1561.402	0.609	25	0.251	K.LASPSEVSVDLSDGGSTVVK.G
R3/RRR3-8/2	1947.523	1948.118	-821.532	0.524	1405.397	0.651	24	0.240	K.LASPSEVSVDLSDGGSTVVK.G
R3/RRR3-8/2	1131.041	1131.305	-233.889	0.425	1446.503	0.459	18	0.207	K.NIIIATGSDVK.S
R3/RRR3-8/2	1130.557	1131.305	-1550.670	0.396	1212.523	0.478	17	0.187	K.NIIIATGSDVK.S
R3/RRR3-8/2	1130.815	1131.305	-434.565	0.381	1299.127	0.432	18	0.187	K.NIIIATGSDVK.S
R3/RRR3-7/2	1694.358	1694.997	-970.513	0.436	1417.192	0.379	20	0.186	K.FSNLEVDLPAMMAQK.D
R3/RRR3-7/2	1130.771	1131.305	-1359.917	0.376	1256.809	0.414	17	0.180	K.NIIIATGSDVK.S
R3/RRR3-8/2	1451.005	1451.603	-1105.099	0.497	1165.713	0.450	19	0.178	R.TCHAHPTVSEALK.E
R3/RRR3-7/2	1030.937	1031.142	-198.881	0.518	846.805	0.457	17	0.164	K.AIDDAEGLVK.V
R3/RRR3-8/2	1030.614	1031.142	-1487.325	0.415	875.700	0.441	17	0.162	K.AIDDAEGLVK.V
R3/RRR3-8/2	1031.018	1031.142	-120.607	0.425	880.477	0.415	17	0.159	K.AIDDAEGLVK.V
R3/RRR3-8/2	1132.513	1133.234	-1524.640	0.396	730.208	0.482	18	0.157	K.VVGVDTSGDGVK.L
R3/RRR3-7/2	1030.481	1031.142	-1616.074	0.404	897.578	0.359	17	0.153	K.AIDDAEGLVK.V
R3/RRR3-8/2	1030.318	1031.142	-1775.686	0.382	707.108	0.425	16	0.152	K.AIDDAEGLVK.V
R3/RRR3-7/2	1031.048	1031.142	-91.272	0.493	789.777	0.380	16	0.151	K.AIDDAEGLVK.V
R3/RRR3-8/2	1132.978	1133.234	-227.113	0.403	539.780	0.472	16	0.149	K.VVGVDTSGDGVK.L
R3/RRR3-8/2	1186.733	1187.368	-1382.143	0.416	308.611	0.448	16	0.147	K.SLPGVTIDEKK.I
R3/RRR3-7/2	1132.878	1133.234	-315.323	0.394	476.756	0.446	15	0.145	K.VVGVDTSGDGVK.L
R3/RRR3-8/2	917.971	918.075	-113.185	0.383	892.488	0.304	13	0.145	-.FPLLANSR.-
R3/RRR3-8/2	1524.090	1524.729	-1079.098	0.367	732.209	0.432	15	0.145	-.ALLHSSHMYHEAK.-
R3/RRR3-7/2	1187.102	1187.368	-225.112	0.395	204.337	0.414	14	0.144	K.SLPGVTIDEKK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1575.422	1575.823	-254.880	0.360	1139.177	0.244	19	0.143	K.IVSSTGALCLSEIPK.K
R3/RRR3-7/2	1130.338	1131.305	-1745.294	0.325	712.465	0.353	14	0.142	K.NIIIATGSDVK.S
R3/RRR3-7/2	1132.441	1133.234	-1587.769	0.325	513.121	0.392	16	0.141	K.VVGVDTSGDGVK.L
R3/RRR3-7/2	1130.226	1131.305	-1845.022	0.303	700.060	0.248	15	0.135	K.NIIIATGSDVK.S
R3/RRR3-8/2	917.841	918.075	-255.802	0.383	783.465	0.309	12	0.134	-.FPLLANSR.-
R3/RRR3-7/2	917.977	918.075	-106.382	0.433	820.224	0.301	12	0.133	-.FPLLANSR.-
R3/RRR3-23/2	1131.120	1131.305	-163.406	0.265	590.283	0.213	12	0.129	-.NIIIATGSDVK.-
R3/RRR3-8/2	918.057	918.075	-19.819	0.338	676.765	0.273	11	0.129	-.FPLLANSR.-
R3/RRR3-7/2	918.125	918.075	54.461	0.453	656.388	0.295	11	0.128	-.FPLLANSR.-
R3/RRR3-7/2	917.360	918.075	-1875.148	0.375	892.160	0.187	12	0.124	-.FPLLANSR.-
R3/RRR3-7/3	1451.232	1451.603	-256.917	0.484	1166.521	0.381	25	0.118	R.TCHAHPTVSEALK.E
R3/RRR3-8/3	1452.742	1451.603	96.018	0.478	903.057	0.351	23	0.102	R.TCHAHPTVSEALK.E
R3/RRR3-7/3	1202.428	1202.431	-2.212	0.444	1308.363	0.242	22	0.101	R.VGKFPLLANSR.A
R3/RRR3-7/3	1451.229	1451.603	-258.436	0.419	795.589	0.340	21	0.097	-.TCHAHPTVSEALK.-
R3/RRR3-8/3	1451.324	1451.603	-193.376	0.419	1030.936	0.272	24	0.095	R.TCHAHPTVSEALK.E
R3/RRR3-7/3	1451.866	1451.603	181.756	0.423	884.753	0.302	22	0.094	-.TCHAHPTVSEALK.-
R3/RRR3-8/3	1202.224	1202.431	-172.237	0.431	849.572	0.277	20	0.092	R.VGKFPLLANSR.A
R3/RRR3-8/3	1202.027	1202.431	-337.123	0.426	1133.520	0.196	21	0.088	-.VGKFPLLANSR.-
R3/RRR3-8/3	1451.687	1451.603	57.544	0.418	676.666	0.235	21	0.087	-.TCHAHPTVSEALK.-
R3/RRR3-7/3	1202.531	1202.431	83.466	0.426	932.033	0.223	20	0.086	-.VGKFPLLANSR.-
R3/RRR3-15/2	1530.391	1530.747	-233.099	0.528	2421.984	0.566	22	0.395	K.KGGLYTLDVSSVYK.Y
R3/RRR3-15/2	1531.339	1530.747	-267.255	0.564	2413.835	0.550	22	0.387	K.KGGLYTLDVSSVYK.Y
R3/RRR3-15/2	1794.468	1795.025	-870.178	0.434	2219.233	0.592	25	0.359	K.LTVSTVSSSGVGLTSTAVK.K
R3/RRR3-15/2	1794.472	1795.025	-868.266	0.446	2172.082	0.589	25	0.349	K.LTVSTVSSSGVGLTSTAVK.K
R3/RRR3-15/2	1794.521	1795.025	-840.952	0.457	2122.321	0.599	25	0.342	K.LTVSTVSSSGVGLTSTAVK.K
R3/RRR3-15/2	1531.173	1530.747	279.101	0.533	2116.627	0.554	22	0.329	K.KGGLYTLDVSSVYK.Y
R3/RRR3-15/2	1297.092	1297.436	-265.868	0.431	1697.667	0.549	19	0.258	K.SVLTISGEFDTK.A
R3/RRR3-15/2	1298.066	1297.436	-285.948	0.534	1390.376	0.609	18	0.234	K.SVLTISGEFDTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1766.394	1766.977	-898.634	0.555	1383.484	0.560	22	0.220	R.RLSTNENTLTVGGLYK.V
R3/RRR3-15/2	1610.349	1610.790	-275.051	0.524	1225.063	0.557	21	0.203	R.LSTNENTLTVGGLYK.V
R3/RRR3-15/2	1347.265	1347.631	-272.598	0.528	1440.903	0.424	17	0.197	K.LAALLQHEVKPK.S
R3/RRR3-15/2	1610.310	1610.790	-299.084	0.480	1178.271	0.494	20	0.186	R.LSTNENTLTVGGLYK.V
R3/RRR3-15/2	1766.363	1766.977	-916.395	0.507	1102.519	0.519	21	0.183	R.RLSTNENTLTVGGLYK.V
R3/RRR3-15/2	1346.721	1347.631	-1422.686	0.469	1299.018	0.405	17	0.181	K.LAALLQHEVKPK.S
R3/RRR3-15/2	990.678	991.123	-450.185	0.451	857.060	0.576	16	0.178	K.GPGLFSDIGK.K
R3/RRR3-15/2	1132.927	1133.236	-273.269	0.480	1137.395	0.429	16	0.175	K.VSGVYHLDDK.Q
R3/RRR3-15/2	1765.973	1766.977	-1138.248	0.500	985.793	0.528	19	0.174	R.RLSTNENTLTVGGLYK.V
R3/RRR3-15/2	990.937	991.123	-187.634	0.440	816.662	0.557	16	0.173	K.GPGLFSDIGK.K
R3/RRR3-15/2	990.850	991.123	-275.630	0.432	770.468	0.585	15	0.172	K.GPGLFSDIGK.K
R3/RRR3-15/2	1610.381	1610.790	-254.973	0.480	926.855	0.522	19	0.171	R.LSTNENTLTVGGLYK.V
R3/RRR3-15/2	1347.379	1347.631	-187.793	0.450	1192.282	0.378	17	0.168	K.LAALLQHEVKPK.S
R3/RRR3-15/2	1388.971	1389.539	-1132.064	0.470	1187.479	0.353	18	0.164	K.VSGVYHLDDKQK.S
R3/RRR3-15/2	1147.222	1147.309	-75.733	0.448	892.730	0.490	14	0.164	K.GPGLFSDIGKR.A
R3/RRR3-15/3	1794.846	1795.025	-100.121	0.507	1206.004	0.566	32	0.163	K.LTVSTVSSSGVGLTSTAVK.K
R3/RRR3-15/2	1133.032	1133.236	-180.095	0.443	1035.337	0.374	16	0.159	K.VSGVYHLDDK.Q
R3/RRR3-15/3	1530.868	1530.747	79.001	0.483	1751.790	0.323	28	0.157	K.KGGLYTLDVSSVYK.Y
R3/RRR3-15/2	1297.034	1297.436	-311.097	0.361	854.160	0.447	15	0.155	K.SVLTISGEFDTK.A
R3/RRR3-15/2	1389.126	1389.539	-297.612	0.465	1004.608	0.351	17	0.153	K.VSGVYHLDDKQK.S
R3/RRR3-15/2	1146.981	1147.309	-286.467	0.435	812.094	0.416	14	0.151	K.GPGLFSDIGKR.A
R3/RRR3-15/2	1148.307	1147.309	-1.664	0.497	775.310	0.425	14	0.151	K.GPGLFSDIGKR.A
R3/RRR3-15/2	1389.298	1389.539	-173.578	0.481	899.580	0.343	17	0.147	K.VSGVYHLDDKQK.S
R3/RRR3-15/2	1118.077	1118.269	-171.882	0.327	1085.298	0.243	15	0.144	K.SSVVAELTRR.L
R3/RRR3-15/2	1117.559	1118.269	-1534.523	0.288	1125.472	0.122	15	0.133	K.SSVVAELTRR.L
R3/RRR3-15/2	1117.708	1118.269	-1400.458	0.296	957.133	0.126	15	0.129	K.SSVVAELTRR.L
R3/RRR3-15/3	1530.427	1530.747	-209.822	0.422	1456.611	0.283	26	0.120	K.KGGLYTLDVSSVYK.Y
R3/RRR3-15/3	1147.118	1147.309	-167.116	0.340	670.754	0.558	22	0.116	K.GPGLFSDIGKR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/3	1147.467	1147.309	138.155	0.400	683.322	0.495	21	0.112	K.GPGLFSDIGKR.A
R3/RRR3-15/3	1530.926	1530.747	117.266	0.471	1414.458	0.212	26	0.102	K.KGGLYTLDVSSVYK.Y
R3/RRR3-15/3	1147.519	1147.309	183.282	0.317	589.673	0.448	21	0.101	K.GPGLFSDIGKR.A
R3/RRR3-1/2	1806.485	1806.059	236.565	0.583	3223.191	0.664	29	0.653	R.HNEAALGTVNQLVAVLR.L
R3/RRR3-2/2	1938.234	1939.113	-972.590	0.551	2891.963	0.560	25	0.503	K.TGSEATQEAALDSLYLLR.Q
R3/RRR3-2/2	1887.648	1886.184	246.112	0.605	2772.228	0.573	26	0.477	R.LLAALALGDLFQNEGLAR.S
R3/RRR3-2/2	1885.541	1886.184	-874.252	0.547	2616.970	0.622	25	0.459	R.LLAALALGDLFQNEGLAR.S
R3/RRR3-2/2	1886.317	1886.184	70.645	0.598	2589.331	0.595	25	0.440	R.LLAALALGDLFQNEGLAR.S
R3/RRR3-1/2	1938.290	1939.113	-943.126	0.499	2682.963	0.508	23	0.431	K.TGSEATQEAALDSLYLLR.Q
R3/RRR3-2/2	1938.317	1939.113	-929.343	0.522	2148.895	0.541	22	0.328	K.TGSEATQEAALDSLYLLR.Q
R3/RRR3-2/2	1803.037	1802.086	-27.270	0.516	1628.414	0.624	24	0.268	R.QAIQPLVEILSTGM*ER.E
R3/RRR3-2/2	1856.861	1858.169	-1246.586	0.497	1710.503	0.561	23	0.262	K.VSLKNESLVDGLLTGALK.N
R3/RRR3-2/2	1568.092	1567.857	150.256	0.512	1225.700	0.539	22	0.200	K.ALANLALAWPNTIAK.E
R3/RRR3-2/2	1803.463	1802.086	209.807	0.512	1158.013	0.542	22	0.193	R.QAIQPLVEILSTGM*ER.E
R3/RRR3-2/3	1859.163	1858.169	-3.307	0.459	1631.568	0.457	28	0.185	K.VSLKNESLVDGLLTGALK.N
R3/RRR3-2/2	1568.006	1567.857	95.215	0.416	1131.273	0.512	20	0.184	K.ALANLALAWPNTIAK.E
R3/RRR3-2/2	1902.689	1903.210	-802.152	0.500	1098.430	0.515	21	0.182	K.IFSTENVVPVLWEQLK.V
R3/RRR3-2/2	1785.488	1786.087	-897.870	0.486	884.246	0.564	20	0.174	R.QAIQPLVEILSTGMER.E
R3/RRR3-2/2	1568.049	1567.857	122.854	0.447	854.512	0.577	19	0.174	K.ALANLALAWPNTIAK.E
R3/RRR3-2/2	1903.544	1903.210	175.877	0.543	871.353	0.547	21	0.172	K.IFSTENVVPVLWEQLK.V
R3/RRR3-2/2	1154.821	1155.372	-1347.075	0.386	1193.574	0.389	14	0.170	R.LIEALLNNVR.I
R3/RRR3-2/2	1903.418	1903.210	109.505	0.583	837.452	0.539	21	0.169	K.IFSTENVVPVLWEQLK.V
R3/RRR3-2/2	1902.404	1903.210	-952.357	0.520	830.936	0.542	20	0.168	K.IFSTENVVPVLWEQLK.V
R3/RRR3-2/2	960.045	960.112	-69.583	0.473	1153.033	0.361	13	0.165	K.APFLVQER.V
R3/RRR3-2/2	1231.211	1231.509	-242.605	0.408	755.576	0.492	18	0.161	K.VVQPLFSLLSK.A
R3/RRR3-2/2	1231.334	1231.509	-142.450	0.353	720.625	0.481	16	0.154	K.VVQPLFSLLSK.A
R3/RRR3-2/2	959.975	960.112	-142.924	0.418	1154.988	0.277	13	0.153	K.APFLVQER.V
R3/RRR3-1/2	1155.085	1155.372	-249.690	0.356	716.606	0.400	15	0.147	R.LIEALLNNVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	959.383	960.112	-1807.306	0.337	1149.003	0.220	13	0.145	K.APFLVQER.V
R3/RRR3-2/2	1231.291	1231.509	-177.756	0.362	589.523	0.400	16	0.144	K.VVQPLFSLLSK.A
R3/RRR3-2/2	982.152	982.119	33.458	0.464	576.586	0.414	11	0.143	K.LTLGNNPPR.L
R3/RRR3-2/2	1857.215	1858.169	-1055.430	0.366	565.230	0.454	18	0.141	K.VSLKNESLVDGLLTGALK.N
R3/RRR3-2/2	981.807	982.119	-318.324	0.316	811.362	0.321	12	0.140	K.LTLGNNPPR.L
R3/RRR3-2/2	1215.749	1216.414	-1374.131	0.335	550.445	0.461	11	0.138	K.ALNALLSNFPR.L
R3/RRR3-2/2	1154.527	1155.372	-1602.890	0.311	798.724	0.224	13	0.133	R.LIEALLNNVR.I
R3/RRR3-2/2	1994.298	1994.281	8.619	0.375	676.398	0.315	20	0.130	R.QIANSNGIPALINATIAPSK.E
R3/RRR3-2/3	1705.389	1705.983	-937.644	0.430	1223.898	0.346	24	0.117	R.SNAALHSIPVLSNLLR.S
R3/RRR3-2/3	1705.959	1705.983	-14.047	0.439	1007.956	0.403	27	0.113	R.SNAALHSIPVLSNLLR.S
R3/RRR3-2/3	1705.851	1705.983	-77.568	0.432	1035.521	0.384	24	0.112	R.SNAALHSIPVLSNLLR.S
R3/RRR3-1/3	1706.574	1705.983	-240.287	0.382	609.705	0.269	24	0.090	R.SNAALHSIPVLSNLLR.S
R3/RRR3-16/2	1419.023	1419.517	-348.978	0.488	2167.010	0.527	19	0.329	K.TVDVEELTVEER.N
R3/RRR3-15/2	1420.138	1419.517	-267.231	0.564	2081.835	0.555	19	0.321	K.TVDVEELTVEER.N
R3/RRR3-15/2	1419.118	1419.517	-281.832	0.515	1985.283	0.546	19	0.302	K.TVDVEELTVEER.N
R3/RRR3-16/2	1419.209	1419.517	-217.542	0.485	2038.922	0.484	19	0.293	K.TVDVEELTVEER.N
R3/RRR3-15/2	1419.108	1419.517	-289.081	0.482	2017.088	0.483	19	0.289	K.TVDVEELTVEER.N
R3/RRR3-16/2	1419.229	1419.517	-203.132	0.509	1737.436	0.531	18	0.259	K.TVDVEELTVEER.N
R3/RRR3-15/2	1774.388	1774.014	211.449	0.602	1607.118	0.592	23	0.253	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/2	1773.000	1774.014	-1139.330	0.530	1517.479	0.587	22	0.240	K.AAQDIALADLAPTHPIR.L
R3/RRR3-14/2	1773.466	1774.014	-875.444	0.541	1509.761	0.585	23	0.239	K.AAQDIALADLAPTHPIR.L
R3/RRR3-16/2	1774.311	1774.014	167.847	0.574	1476.672	0.591	22	0.235	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/2	1215.842	1216.343	-1238.714	0.419	1727.983	0.437	18	0.235	K.EAAESTM*VAYK.A
R3/RRR3-16/2	1774.340	1774.014	184.061	0.543	1484.450	0.581	22	0.234	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/2	1773.408	1774.014	-908.543	0.543	1466.453	0.590	22	0.234	K.AAQDIALADLAPTHPIR.L
R3/RRR3-14/2	1773.441	1774.014	-889.540	0.569	1475.054	0.577	22	0.232	K.AAQDIALADLAPTHPIR.L
R3/RRR3-14/2	1772.877	1774.014	-1208.815	0.499	1511.688	0.544	22	0.229	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/2	1383.948	1383.526	305.734	0.546	1732.336	0.388	16	0.223	R.YEEM*VEYM*EK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1773.657	1774.014	-202.164	0.530	1392.657	0.572	22	0.221	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/2	1382.985	1383.526	-1118.068	0.499	1717.788	0.381	16	0.221	R.YEEM*VEYM*EK.V
R3/RRR3-15/2	1383.035	1383.526	-356.515	0.497	1632.500	0.405	16	0.217	R.YEEM*VEYM*EK.V
R3/RRR3-15/2	1655.299	1655.831	-928.620	0.449	1513.948	0.445	23	0.209	K.LLDSHLVPSSTAAESK.V
R3/RRR3-15/2	1327.416	1328.517	-1587.820	0.493	1342.029	0.514	19	0.208	R.KEAAESTMVAYK.A
R3/RRR3-15/3	1774.154	1774.014	78.796	0.421	1439.206	0.588	29	0.199	K.AAQDIALADLAPTHPIR.L
R3/RRR3-14/3	1773.827	1774.014	-105.794	0.374	1593.534	0.514	31	0.197	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/2	1655.400	1655.831	-261.501	0.500	1239.826	0.491	23	0.192	K.LLDSHLVPSSTAAESK.V
R3/RRR3-15/2	1375.187	1375.510	-235.813	0.436	1361.631	0.417	19	0.190	R.IVSSIEQKEEGR.G
R3/RRR3-15/2	1216.096	1216.343	-204.271	0.417	1212.897	0.454	17	0.183	K.EAAESTM*VAYK.A
R3/RRR3-16/3	1774.036	1774.014	12.235	0.408	1505.412	0.505	31	0.182	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/2	1374.673	1375.510	-1340.764	0.455	1251.105	0.427	18	0.182	R.IVSSIEQKEEGR.G
R3/RRR3-15/2	1374.538	1375.510	-1439.234	0.485	1203.067	0.439	19	0.181	R.IVSSIEQKEEGR.G
R3/RRR3-16/2	1375.217	1375.510	-213.906	0.472	1052.397	0.493	18	0.178	R.IVSSIEQKEEGR.G
R3/RRR3-15/3	1773.594	1774.014	-237.420	0.434	1481.716	0.495	31	0.176	K.AAQDIALADLAPTHPIR.L
R3/RRR3-16/2	1655.260	1655.831	-951.793	0.454	1057.027	0.484	21	0.174	K.LLDSHLVPSSTAAESK.V
R3/RRR3-16/2	1375.171	1375.510	-247.657	0.479	1107.935	0.436	19	0.174	R.IVSSIEQKEEGR.G
R3/RRR3-15/2	1375.054	1375.510	-332.712	0.441	1165.729	0.410	18	0.172	R.IVSSIEQKEEGR.G
R3/RRR3-14/3	1774.204	1774.014	107.260	0.460	1467.141	0.482	30	0.171	K.AAQDIALADLAPTHPIR.L
R3/RRR3-16/2	1655.520	1655.831	-188.782	0.474	1011.091	0.476	21	0.170	K.LLDSHLVPSSTAAESK.V
R3/RRR3-15/2	1655.408	1655.831	-256.692	0.422	1033.818	0.423	21	0.163	K.LLDSHLVPSSTAAESK.V
R3/RRR3-14/3	1774.349	1774.014	189.434	0.405	1265.632	0.532	28	0.163	K.AAQDIALADLAPTHPIR.L
R3/RRR3-16/3	1656.002	1655.831	103.456	0.406	1373.332	0.503	31	0.163	K.LLDSHLVPSSTAAESK.V
R3/RRR3-16/2	1655.334	1655.831	-301.526	0.457	853.683	0.486	19	0.161	K.LLDSHLVPSSTAAESK.V
R3/RRR3-15/2	1215.684	1216.343	-1369.098	0.406	879.577	0.431	15	0.157	K.EAAESTM*VAYK.A
R3/RRR3-16/2	1375.116	1375.510	-287.823	0.413	772.383	0.393	16	0.149	R.IVSSIEQKEEGR.G
R3/RRR3-16/2	1376.797	1375.510	208.839	0.442	706.862	0.384	16	0.146	R.IVSSIEQKEEGR.G
R3/RRR3-15/2	1199.945	1200.344	-333.309	0.337	628.974	0.425	14	0.146	K.EAAESTMVAYK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1199.948	1200.344	-331.267	0.289	765.121	0.378	15	0.144	K.EAAESTMVAYK.A
R3/RRR3-15/2	975.213	975.121	94.210	0.376	924.719	0.308	14	0.144	R.GKIEAELSK.I
R3/RRR3-15/2	1140.019	1140.271	-221.951	0.489	680.663	0.371	13	0.144	R.GNEEHVTLIK.E
R3/RRR3-15/2	1140.029	1140.271	-213.357	0.461	746.282	0.330	14	0.142	R.GNEEHVTLIK.E
R3/RRR3-15/3	1656.037	1655.831	124.636	0.327	1505.872	0.364	32	0.142	K.LLDSHLVPSSTAAESK.V
R3/RRR3-16/3	1773.756	1774.014	-145.869	0.408	1099.097	0.508	28	0.141	K.AAQDIALADLAPTHPIR.L
R3/RRR3-16/2	1140.111	1140.271	-141.176	0.413	795.151	0.297	13	0.139	R.GNEEHVTLIK.E
R3/RRR3-16/2	1140.022	1140.271	-219.373	0.407	580.787	0.324	13	0.139	R.GNEEHVTLIK.E
R3/RRR3-15/2	1140.111	1140.271	-140.961	0.495	697.535	0.324	13	0.137	-.GNEEHVTLIK.-
R3/RRR3-16/3	1656.007	1655.831	106.339	0.377	1289.889	0.419	29	0.136	K.LLDSHLVPSSTAAESK.V
R3/RRR3-15/2	1199.967	1200.344	-314.937	0.208	543.814	0.260	13	0.132	K.EAAESTMVAYK.A
R3/RRR3-16/3	1774.075	1774.014	34.181	0.409	1133.481	0.402	27	0.123	K.AAQDIALADLAPTHPIR.L
R3/RRR3-15/3	975.018	975.121	-106.608	0.552	846.537	0.305	19	0.097	R.GKIEAELSK.I
R3/RRR3-15/3	975.227	975.121	108.099	0.551	1023.231	0.266	20	0.094	R.GKIEAELSK.I
R3/RRR3-15/3	974.939	975.121	-188.089	0.538	698.468	0.296	16	0.091	-.GKIEAELSK.-
R3/RRR3-16/3	1655.290	1655.831	-933.588	0.296	715.948	0.231	24	0.086	-.LLDSHLVPSSTAAESK.-
R3/RRR3-14/3	1655.726	1655.831	-63.796	0.220	789.694	0.101	22	0.078	K.LLDSHLVPSSTAAESK.V
R3/RRR3-8/2	1296.200	1296.501	-232.991	0.439	2063.707	0.532	21	0.312	K.VVAAGANPVQITR.G
R3/RRR3-7/2	1296.173	1296.501	-254.155	0.523	1805.797	0.565	21	0.280	K.VVAAGANPVQITR.G
R3/RRR3-7/2	1296.211	1296.501	-224.110	0.541	1664.331	0.616	20	0.272	K.VVAAGANPVQITR.G
R3/RRR3-8/2	1296.005	1296.501	-384.182	0.492	1600.286	0.579	20	0.253	K.VVAAGANPVQITR.G
R3/RRR3-7/2	1285.141	1285.472	-257.956	0.452	1628.359	0.437	17	0.222	R.DLINVLEEAIR.G
R3/RRR3-7/2	1285.127	1285.472	-269.392	0.442	1553.103	0.442	17	0.215	R.DLINVLEEAIR.G
R3/RRR3-7/2	1043.959	1044.187	-219.504	0.506	1354.144	0.470	17	0.202	K.IVNDGVTVAR.E
R3/RRR3-7/2	1284.595	1285.472	-1465.471	0.387	1497.025	0.408	17	0.201	R.DLINVLEEAIR.G
R3/RRR3-7/2	1543.430	1542.670	-155.530	0.589	1347.271	0.405	21	0.183	R.EVELEDPVENIGAK.L
R3/RRR3-7/2	1506.791	1506.638	102.171	0.416	1129.132	0.419	20	0.171	R.GYISPYFVTDSEK.M
R3/RRR3-7/2	1183.681	1183.423	218.913	0.352	1251.503	0.355	17	0.168	K.LADLVGVTLGPK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1174.978	1175.274	-253.173	0.449	979.995	0.465	17	0.168	K.NAGVNGSVVTEK.V
R3/RRR3-7/2	1542.255	1542.670	-269.650	0.483	1221.870	0.357	20	0.166	R.EVELEDPVENIGAK.L
R3/RRR3-7/2	1174.962	1175.274	-266.306	0.427	990.526	0.453	17	0.166	K.NAGVNGSVVTEK.V
R3/RRR3-7/2	1246.092	1246.383	-233.910	0.569	756.357	0.503	18	0.165	R.CCLEHAASVAK.T
R3/RRR3-7/2	1937.412	1938.040	-842.946	0.487	852.361	0.535	20	0.165	K.ESTTIVGDGSTQEEVTKR.V
R3/RRR3-7/2	1543.241	1542.670	-278.681	0.531	1203.754	0.361	20	0.164	R.EVELEDPVENIGAK.L
R3/RRR3-7/2	1043.535	1044.187	-1587.410	0.398	931.175	0.417	16	0.159	K.IVNDGVTVAR.E
R3/RRR3-7/2	1506.076	1506.638	-1040.139	0.338	1041.962	0.363	19	0.155	R.GYISPYFVTDSEK.M
R3/RRR3-7/2	1246.067	1246.383	-253.665	0.495	758.188	0.424	17	0.153	R.CCLEHAASVAK.T
R3/RRR3-7/2	960.162	960.067	99.194	0.431	895.670	0.336	14	0.148	K.GVVTLEEGR.S
R3/RRR3-7/2	1937.402	1938.040	-848.259	0.498	644.063	0.491	18	0.147	K.ESTTIVGDGSTQEEVTKR.V
R3/RRR3-7/2	1175.142	1175.274	-113.108	0.406	723.895	0.409	15	0.147	K.NAGVNGSVVTEK.V
R3/RRR3-7/2	959.265	960.067	-1883.790	0.438	873.975	0.319	14	0.146	K.GVVTLEEGR.S
R3/RRR3-7/2	959.720	960.067	-362.072	0.395	938.462	0.268	14	0.142	K.GVVTLEEGR.S
R3/RRR3-7/2	1183.780	1183.423	302.879	0.212	1022.343	0.241	16	0.138	K.LADLVGVTLGPK.G
R3/RRR3-7/2	1284.687	1285.472	-1393.602	0.307	623.244	0.300	15	0.137	R.DLINVLEEAIR.G
R3/RRR3-7/2	1284.330	1285.472	-1672.450	0.216	562.795	0.237	14	0.131	R.DLINVLEEAIR.G
R3/RRR3-7/3	1246.367	1246.383	-12.645	0.442	925.630	0.433	23	0.112	R.CCLEHAASVAK.T
R3/RRR3-7/3	1230.738	1230.396	278.727	0.494	1075.223	0.289	22	0.095	-.LRVEDALNATK.-
R3/RRR3-7/3	1087.895	1088.240	-317.907	0.404	1032.641	0.254	20	0.091	R.KGVVTLEEGR.S
R3/RRR3-7/3	1230.192	1230.396	-166.181	0.461	939.686	0.274	21	0.089	-.LRVEDALNATK.-
R3/RRR3-7/3	1229.843	1230.396	-1266.555	0.405	690.526	0.211	20	0.083	-.LRVEDALNATK.-
R3/RRR3-7/3	1088.189	1088.240	-47.112	0.361	715.185	0.174	17	0.072	-.KGVVTLEEGR.-
R3/RRR3-14/2	1564.850	1565.732	-1206.282	0.475	2143.656	0.505	23	0.318	R.LAIAGM*GTDENSLTR.I
R3/RRR3-13/2	1565.380	1565.732	-225.211	0.522	2018.871	0.568	23	0.314	R.LAIAGM*GTDENSLTR.I
R3/RRR3-13/2	1566.191	1565.732	294.298	0.544	1972.788	0.588	23	0.312	R.LAIAGM*GTDENSLTR.I
R3/RRR3-13/2	1565.144	1565.732	-1017.529	0.492	2005.730	0.568	23	0.312	R.LAIAGM*GTDENSLTR.I
R3/RRR3-13/2	1400.796	1401.503	-1222.325	0.463	1990.375	0.431	19	0.272	R.AYADTYGEELLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1564.662	1565.732	-1326.856	0.406	1871.208	0.500	23	0.270	R.LAIAGM*GTDENSLTR.I
R3/RRR3-13/2	1401.219	1401.503	-202.946	0.465	1540.644	0.510	18	0.228	R.AYADTYGEELLR.S
R3/RRR3-13/2	1030.843	1031.225	-371.595	0.433	1402.845	0.473	15	0.206	R.VLVEIACAR.G
R3/RRR3-13/2	1369.174	1369.416	-177.203	0.452	1427.240	0.454	19	0.204	R.SITDEISGDFER.A
R3/RRR3-13/2	1030.412	1031.225	-1764.711	0.434	1299.773	0.488	15	0.199	R.VLVEIACAR.G
R3/RRR3-13/2	958.497	959.127	-1706.148	0.530	1224.148	0.515	14	0.197	R.GPAQLFAVR.Q
R3/RRR3-13/2	1368.709	1369.416	-1251.338	0.331	1598.096	0.329	19	0.196	R.SITDEISGDFER.A
R3/RRR3-13/2	1369.220	1369.416	-143.932	0.379	1455.707	0.403	18	0.196	R.SITDEISGDFER.A
R3/RRR3-14/2	1031.028	1031.225	-191.738	0.425	1293.567	0.474	15	0.195	R.VLVEIACAR.G
R3/RRR3-13/2	958.917	959.127	-220.074	0.533	1217.304	0.503	14	0.194	R.GPAQLFAVR.Q
R3/RRR3-13/2	958.986	959.127	-146.902	0.570	1141.722	0.534	14	0.194	R.GPAQLFAVR.Q
R3/RRR3-14/2	959.142	959.127	15.623	0.541	1167.614	0.517	14	0.193	R.GPAQLFAVR.Q
R3/RRR3-13/2	1031.125	1031.225	-96.727	0.484	1228.139	0.479	15	0.191	R.VLVEIACAR.G
R3/RRR3-14/2	958.954	959.127	-181.252	0.551	1170.557	0.502	14	0.190	R.GPAQLFAVR.Q
R3/RRR3-14/2	958.677	959.127	-470.832	0.510	1145.259	0.497	14	0.187	R.GPAQLFAVR.Q
R3/RRR3-13/2	1034.114	1034.194	-77.623	0.402	1245.922	0.441	14	0.184	K.AQLIATFNR.Y
R3/RRR3-14/2	1030.610	1031.225	-1571.560	0.431	1216.460	0.380	15	0.173	R.VLVEIACAR.G
R3/RRR3-13/2	1350.066	1350.418	-261.603	0.488	1133.473	0.410	17	0.170	R.YNDEYGHPINK.D
R3/RRR3-13/2	1057.974	1058.171	-186.623	0.444	1200.227	0.362	16	0.168	R.DAVLANEVAR.K
R3/RRR3-13/2	1349.883	1350.418	-1140.174	0.476	1122.441	0.395	17	0.167	R.YNDEYGHPINK.D
R3/RRR3-14/2	1146.494	1145.419	65.719	0.425	691.813	0.516	17	0.163	K.LLVPLISAYR.Y
R3/RRR3-13/2	1384.124	1384.605	-348.312	0.284	1056.352	0.395	16	0.158	R.AVILWTLDPAER.D
R3/RRR3-13/2	1057.969	1058.171	-190.674	0.380	1154.623	0.321	16	0.158	R.DAVLANEVAR.K
R3/RRR3-13/2	1146.116	1145.419	-265.424	0.469	489.283	0.512	14	0.155	K.LLVPLISAYR.Y
R3/RRR3-13/2	1146.222	1145.419	-172.255	0.436	479.576	0.516	14	0.155	K.LLVPLISAYR.Y
R3/RRR3-13/2	1146.152	1145.419	-233.476	0.383	527.860	0.479	15	0.152	K.LLVPLISAYR.Y
R3/RRR3-14/2	1033.952	1034.194	-234.773	0.356	695.565	0.449	13	0.151	K.AQLIATFNR.Y
R3/RRR3-14/2	1384.407	1384.605	-143.768	0.298	936.604	0.356	14	0.147	R.AVILWTLDPAER.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1037.019	1037.105	-83.427	0.315	412.617	0.485	13	0.142	R.YEGPEVNTK.L
R3/RRR3-13/2	1384.135	1384.605	-340.879	0.289	739.720	0.391	13	0.142	R.AVILWTLDPAER.D
R3/RRR3-14/2	1033.607	1034.194	-1539.639	0.237	547.540	0.435	12	0.139	K.AQLIATFNR.Y
R3/RRR3-14/2	1033.505	1034.194	-1638.830	0.217	701.258	0.392	12	0.139	K.AQLIATFNR.Y
R3/RRR3-13/2	1384.453	1384.605	-110.512	0.274	1020.193	0.209	14	0.136	R.AVILWTLDPAER.D
R3/RRR3-13/2	1401.435	1401.503	-48.279	0.318	666.734	0.316	14	0.135	R.AYADTYGEELLR.S
R3/RRR3-14/2	1145.154	1145.419	-232.503	0.176	370.559	0.306	12	0.132	K.LLVPLISAYR.Y
R3/RRR3-14/2	1384.316	1384.605	-209.670	0.138	476.262	0.254	12	0.127	R.AVILWTLDPAER.D
R3/RRR3-2/2	1458.300	1458.725	-292.730	0.502	1904.592	0.450	19	0.263	K.VTSLLDQLIQLSK.T
R3/RRR3-2/2	1458.476	1458.725	-171.725	0.446	1488.383	0.413	18	0.200	K.VTSLLDQLIQLSK.T
R3/RRR3-2/2	1556.462	1555.758	-190.964	0.547	1281.662	0.505	22	0.200	K.LLDVLNTPSEAVQR.A
R3/RRR3-2/2	989.922	990.181	-262.531	0.470	1326.119	0.448	17	0.193	R.GAAFGLAGVVK.G
R3/RRR3-2/2	1696.440	1696.970	-904.584	0.491	1203.116	0.483	23	0.187	K.SAGLQAIDEIVPTLLR.A
R3/RRR3-2/2	1457.768	1458.725	-1346.479	0.453	1479.513	0.338	18	0.184	K.VTSLLDQLIQLSK.T
R3/RRR3-2/2	1696.751	1696.970	-129.426	0.517	1199.841	0.462	23	0.183	K.SAGLQAIDEIVPTLLR.A
R3/RRR3-2/2	1994.324	1994.298	13.162	0.512	1081.070	0.543	18	0.180	R.LANAQAVLCQVLMDGSFR.Q
R3/RRR3-2/2	1696.425	1696.970	-913.180	0.458	1248.720	0.398	23	0.175	K.SAGLQAIDEIVPTLLR.A
R3/RRR3-2/2	1554.945	1555.758	-1169.181	0.375	1173.187	0.418	20	0.172	K.LLDVLNTPSEAVQR.A
R3/RRR3-2/2	1280.137	1280.361	-175.373	0.400	1256.201	0.350	16	0.168	R.TALCDSTQEVR.E
R3/RRR3-2/2	1555.474	1555.758	-182.978	0.476	1088.660	0.417	20	0.167	K.LLDVLNTPSEAVQR.A
R3/RRR3-2/2	1137.119	1137.354	-207.443	0.355	842.083	0.459	14	0.155	K.VLVDPIPEVR.A
R3/RRR3-2/2	876.953	877.066	-128.811	0.389	758.861	0.430	13	0.152	K.YGIAAILR.Q
R3/RRR3-1/2	1555.524	1555.758	-151.173	0.466	781.777	0.424	18	0.151	K.LLDVLNTPSEAVQR.A
R3/RRR3-2/2	1449.033	1449.674	-1136.007	0.415	508.235	0.488	18	0.150	R.QSSVELLGDLLFK.V
R3/RRR3-2/2	1449.706	1449.634	49.946	0.365	1040.233	0.293	16	0.143	K.SNDLAQALVGVYAK.E
R3/RRR3-2/2	1070.080	1070.181	-95.037	0.364	742.080	0.372	13	0.141	R.ALADPNVDVR.G
R3/RRR3-2/2	1449.676	1449.674	1.469	0.319	506.956	0.362	17	0.138	R.QSSVELLGDLLFK.V
R3/RRR3-2/2	1450.163	1449.674	338.257	0.400	508.037	0.328	16	0.137	R.QSSVELLGDLLFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1340.512	1341.537	-1514.765	0.363	889.256	0.248	16	0.136	R.LDGIYALFSVSR.L
R3/RRR3-1/2	1342.528	1341.537	-6.713	0.263	586.655	0.257	15	0.130	R.LDGIYALFSVSR.L
R3/RRR3-2/3	1030.566	1030.248	309.105	0.472	1261.877	0.269	22	0.100	R.HTLPHLLAK.A
R3/RRR3-2/3	1376.711	1376.453	187.498	0.412	1111.296	0.284	22	0.097	-.TLHDGFSENDIK.-
R3/RRR3-2/3	1030.070	1030.248	-173.565	0.446	934.044	0.195	19	0.085	R.HTLPHLLAK.A
R3/RRR3-12/1	987.551	988.160	-1634.490	0.271	754.982	0.421	12	0.908	K.LLIVTDGEK.G
R3/RRR3-12/1	987.645	988.160	-1538.382	0.247	680.618	0.355	11	0.893	K.LLIVTDGEK.G
R3/RRR3-12/2	1953.502	1953.995	-253.184	0.553	1990.979	0.511	24	0.291	K.VSDDEVAFLTQGDANDEK.N
R3/RRR3-12/2	1953.455	1953.995	-790.457	0.501	1951.523	0.485	24	0.278	K.VSDDEVAFLTQGDANDEK.N
R3/RRR3-12/2	1331.087	1330.456	-278.211	0.512	1776.680	0.554	20	0.273	K.FSNACGAICTTK.K
R3/RRR3-12/2	1452.135	1452.588	-313.197	0.507	1816.939	0.517	20	0.267	K.SAGILCSYDPNVR.L
R3/RRR3-12/2	1329.993	1330.456	-349.324	0.500	1772.194	0.524	20	0.264	K.FSNACGAICTTK.K
R3/RRR3-12/2	1329.452	1330.456	-1511.803	0.427	1825.056	0.475	20	0.259	K.FSNACGAICTTK.K
R3/RRR3-12/2	1953.447	1953.995	-794.847	0.537	1762.427	0.519	23	0.257	K.VSDDEVAFLTQGDANDEK.N
R3/RRR3-12/2	1452.988	1452.588	276.339	0.528	1597.316	0.512	19	0.235	K.SAGILCSYDPNVR.L
R3/RRR3-12/2	1452.180	1452.588	-281.654	0.486	1577.111	0.497	19	0.229	K.SAGILCSYDPNVR.L
R3/RRR3-12/2	1907.396	1907.287	57.347	0.505	1195.021	0.588	26	0.205	K.KGAIPALPTVAVAQELISK.A
R3/RRR3-12/2	1458.255	1458.629	-257.224	0.474	1159.429	0.534	19	0.192	K.FSNACGAICTTKK.G
R3/RRR3-12/2	1906.489	1907.287	-945.821	0.513	840.838	0.624	22	0.179	K.KGAIPALPTVAVAQELISK.A
R3/RRR3-9/2	1779.343	1779.114	129.321	0.403	806.656	0.579	23	0.171	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	1778.427	1779.114	-951.486	0.448	824.136	0.515	24	0.166	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	1906.850	1907.287	-229.521	0.507	741.736	0.578	21	0.165	K.KGAIPALPTVAVAQELISK.A
R3/RRR3-11/2	1778.822	1779.114	-164.339	0.467	559.885	0.545	20	0.156	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	1255.067	1255.404	-269.308	0.424	563.446	0.472	16	0.153	R.LPLWPSEDAAR.A
R3/RRR3-12/2	1255.254	1255.404	-120.325	0.429	464.782	0.496	15	0.153	R.LPLWPSEDAAR.A
R3/RRR3-12/2	1255.197	1255.404	-165.591	0.411	560.832	0.479	15	0.152	R.LPLWPSEDAAR.A
R3/RRR3-12/2	1503.496	1503.599	-68.536	0.418	644.961	0.463	16	0.150	K.DDSIFHNEEKLR.E
R3/RRR3-9/2	1780.846	1779.114	-150.952	0.409	393.226	0.541	18	0.150	K.GAIPALPTVAVAQELISK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1778.445	1779.114	-940.942	0.316	547.854	0.517	20	0.149	K.GAIPALPTVAVAQELISK.A
R3/RRR3-13/2	1778.450	1779.114	-938.393	0.362	513.594	0.499	19	0.148	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	1778.112	1779.114	-1129.031	0.342	469.033	0.506	20	0.148	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	1233.882	1234.254	-301.914	0.417	942.677	0.310	15	0.146	K.DDSIFHNEEK.L
R3/RRR3-13/2	1778.659	1779.114	-256.251	0.364	390.146	0.498	18	0.146	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	987.880	988.160	-284.205	0.363	624.571	0.383	14	0.145	K.LLIVTDGEK.G
R3/RRR3-12/2	1503.080	1503.599	-1013.213	0.423	822.013	0.353	17	0.145	K.DDSIFHNEEKLR.E
R3/RRR3-12/2	987.478	988.160	-1708.584	0.414	475.962	0.376	13	0.144	K.LLIVTDGEK.G
R3/RRR3-12/2	1233.428	1234.254	-1484.472	0.394	960.575	0.265	15	0.142	K.DDSIFHNEEK.L
R3/RRR3-11/2	1255.203	1255.404	-160.420	0.295	307.531	0.448	12	0.142	R.LPLWPSEDAAR.A
R3/RRR3-9/2	1780.603	1779.114	275.622	0.363	294.318	0.442	16	0.141	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	1778.409	1779.114	-961.685	0.339	434.893	0.407	19	0.141	K.GAIPALPTVAVAQELISK.A
R3/RRR3-12/2	988.099	988.160	-61.969	0.384	571.648	0.358	13	0.141	-.LLIVTDGEK.-
R3/RRR3-12/2	1778.452	1779.114	-937.015	0.353	452.680	0.391	19	0.141	K.GAIPALPTVAVAQELISK.A
R3/RRR3-2/2	1777.696	1779.114	-1364.224	0.265	527.258	0.428	18	0.139	K.GAIPALPTVAVAQELISK.A
R3/RRR3-18/2	1256.581	1255.404	141.028	0.315	419.666	0.360	12	0.138	R.LPLWPSEDAAR.A
R3/RRR3-12/2	1233.979	1234.254	-223.308	0.379	801.350	0.275	14	0.138	K.DDSIFHNEEK.L
R3/RRR3-14/2	1255.775	1255.404	296.044	0.264	336.482	0.344	12	0.138	R.LPLWPSEDAAR.A
R3/RRR3-13/2	1778.136	1779.114	-1115.451	0.295	295.154	0.390	15	0.137	K.GAIPALPTVAVAQELISK.A
R3/RRR3-10/2	1453.395	1452.588	-133.322	0.313	632.616	0.356	13	0.136	K.SAGILCSYDPNVR.L
R3/RRR3-12/2	1255.357	1255.404	-37.804	0.298	384.914	0.319	11	0.136	R.LPLWPSEDAAR.A
R3/RRR3-12/2	987.922	988.160	-241.932	0.309	395.887	0.283	11	0.135	-.LLIVTDGEK.-
R3/RRR3-14/2	1254.364	1255.404	-1631.487	0.289	270.816	0.337	11	0.134	-.LPLWPSEDAAR.-
R3/RRR3-3/2	1778.698	1779.114	-234.287	0.255	215.683	0.368	13	0.129	-.GAIPALPTVAVAQELISK.-
R3/RRR3-10/2	1453.195	1452.588	-271.179	0.274	525.502	0.347	12	0.127	-.SAGILCSYDPNVR.-
R3/RRR3-12/3	1906.592	1907.287	-891.256	0.350	1098.157	0.380	28	0.113	K.KGAIPALPTVAVAQELISK.A
R3/RRR3-12/3	1907.318	1907.287	16.451	0.376	903.269	0.439	25	0.111	K.KGAIPALPTVAVAQELISK.A
R3/RRR3-22/1	1177.639	1178.320	-1431.845	0.285	488.863	0.518	14	0.929	K.LNPAAGVGSTYK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/1	1177.605	1178.320	-1460.790	0.267	672.602	0.529	16	0.923	K.LNPAAGVGSTYK.T
R3/RRR3-22/1	1177.559	1178.320	-1500.046	0.260	619.217	0.476	15	0.916	K.LNPAAGVGSTYK.T
R3/RRR3-23/1	1177.634	1178.320	-1436.218	0.239	622.501	0.446	15	0.908	K.LNPAAGVGSTYK.T
R3/RRR3-22/2	1639.114	1638.823	178.510	0.548	2300.510	0.605	22	0.905	K.M*IEDYLVAHPAEYA.-
R3/RRR3-23/2	1638.252	1638.823	-961.794	0.506	2274.207	0.587	21	0.888	K.M*IEDYLVAHPAEYA.-
R3/RRR3-22/2	1638.278	1638.823	-945.935	0.493	2199.466	0.593	21	0.828	K.M*IEDYLVAHPAEYA.-
R3/RRR3-22/2	1923.068	1924.095	-1057.298	0.605	3777.009	0.556	27	0.769	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-23/2	1639.294	1638.823	288.581	0.547	1954.567	0.618	20	0.638	K.M*IEDYLVAHPAEYA.-
R3/RRR3-22/2	1923.533	1924.095	-814.465	0.627	3249.424	0.618	26	0.627	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-21/2	1638.534	1638.823	-176.736	0.506	1936.225	0.557	20	0.617	K.M*IEDYLVAHPAEYA.-
R3/RRR3-22/2	1923.627	1924.095	-244.132	0.621	3210.707	0.609	26	0.611	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-23/2	1923.375	1924.095	-897.159	0.601	3109.278	0.615	26	0.585	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-21/2	1638.508	1638.823	-192.356	0.438	1832.185	0.522	20	0.546	K.M*IEDYLVAHPAEYA.-
R3/RRR3-22/2	1978.438	1979.086	-835.553	0.580	2853.170	0.677	28	0.543	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-23/2	1638.218	1638.823	-982.142	0.467	1822.871	0.545	20	0.541	K.M*IEDYLVAHPAEYA.-
R3/RRR3-22/2	1637.396	1638.823	-1486.620	0.328	1697.109	0.481	19	0.467	K.M*IEDYLVAHPAEYA.-
R3/RRR3-22/2	1978.342	1979.086	-884.176	0.601	2453.321	0.663	27	0.435	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1979.328	1979.086	122.873	0.606	2349.290	0.674	27	0.416	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1682.196	1682.764	-935.025	0.514	2444.222	0.482	23	0.370	K.VEYELEDGSSLSPEK.E
R3/RRR3-23/3	1978.560	1979.086	-773.658	0.517	2309.180	0.600	38	0.358	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1682.364	1682.764	-238.679	0.512	2251.146	0.476	23	0.329	K.VEYELEDGSSLSPEK.E
R3/RRR3-22/2	1682.331	1682.764	-258.188	0.484	2105.602	0.461	22	0.299	K.VEYELEDGSSLSPEK.E
R3/RRR3-20/2	1638.030	1638.823	-1097.813	0.299	1332.770	0.530	19	0.278	K.M*IEDYLVAHPAEYA.-
R3/RRR3-20/3	1978.628	1979.086	-231.907	0.506	1757.863	0.604	34	0.252	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-23/3	1978.747	1979.086	-171.843	0.493	1709.963	0.623	35	0.250	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/3	1924.828	1924.095	-139.222	0.487	2026.854	0.428	34	0.231	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-22/2	1207.971	1208.295	-268.557	0.464	1668.282	0.448	20	0.230	K.LEATGDGSCVAK.L
R3/RRR3-21/3	1978.470	1979.086	-819.271	0.521	1645.797	0.582	35	0.225	K.SHSTETKLEATGDGSCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1207.913	1208.295	-316.920	0.443	1589.657	0.467	20	0.225	K.LEATGDGSCVAK.L
R3/RRR3-22/2	1208.119	1208.295	-145.694	0.435	1589.774	0.452	20	0.221	K.LEATGDGSCVAK.L
R3/RRR3-22/3	1978.942	1979.086	-72.896	0.497	1668.757	0.548	36	0.216	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1270.001	1270.454	-357.824	0.449	1511.187	0.449	19	0.211	R.VAVCDAASHVLK.S
R3/RRR3-22/3	1924.843	1924.095	-131.302	0.477	1912.722	0.415	35	0.207	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-22/2	1207.468	1208.295	-1517.301	0.399	1587.452	0.382	20	0.206	K.LEATGDGSCVAK.L
R3/RRR3-23/3	1978.836	1979.086	-126.637	0.445	1435.370	0.597	34	0.201	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1270.021	1270.454	-342.201	0.456	1475.474	0.417	19	0.201	R.VAVCDAASHVLK.S
R3/RRR3-23/2	1207.997	1208.295	-247.368	0.439	1376.591	0.463	19	0.200	K.LEATGDGSCVAK.L
R3/RRR3-22/2	1270.164	1270.454	-228.899	0.471	1418.327	0.438	18	0.199	R.VAVCDAASHVLK.S
R3/RRR3-22/2	1547.135	1547.755	-1050.090	0.474	1387.518	0.438	22	0.198	K.EKDIVDGYYGM*LK.M
R3/RRR3-21/3	1979.015	1979.086	-35.773	0.488	1476.877	0.563	34	0.196	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-23/2	1207.262	1208.295	-1688.853	0.358	1406.465	0.426	19	0.195	K.LEATGDGSCVAK.L
R3/RRR3-21/2	1178.158	1178.320	-138.072	0.421	1058.772	0.579	20	0.193	K.LNPAAGVGSTYK.T
R3/RRR3-22/3	1980.027	1979.086	-29.757	0.496	1400.793	0.574	35	0.188	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1177.587	1178.320	-1476.160	0.408	952.567	0.605	20	0.188	K.LNPAAGVGSTYK.T
R3/RRR3-23/2	1270.107	1270.454	-273.638	0.436	1415.840	0.364	18	0.184	R.VAVCDAASHVLK.S
R3/RRR3-22/2	977.807	978.036	-234.667	0.463	1136.032	0.465	15	0.181	K.SDVLEAESK.V
R3/RRR3-22/2	1177.951	1178.320	-314.171	0.241	1471.250	0.335	18	0.181	K.LNPAAGVGSTYK.T
R3/RRR3-20/2	1082.768	1083.240	-437.676	0.375	1213.757	0.442	16	0.181	K.AFM*DASSLPK.A
R3/RRR3-22/2	977.976	978.036	-61.359	0.490	1172.854	0.443	15	0.181	K.SDVLEAESK.V
R3/RRR3-23/2	1177.954	1178.320	-311.676	0.435	928.891	0.553	20	0.180	K.LNPAAGVGSTYK.T
R3/RRR3-21/2	1178.099	1178.320	-187.860	0.393	889.128	0.579	20	0.179	K.LNPAAGVGSTYK.T
R3/RRR3-23/2	1177.958	1178.320	-308.037	0.423	916.434	0.522	20	0.175	K.LNPAAGVGSTYK.T
R3/RRR3-23/2	1177.941	1178.320	-322.489	0.422	826.260	0.560	19	0.174	K.LNPAAGVGSTYK.T
R3/RRR3-21/2	1083.272	1083.240	29.659	0.396	1201.380	0.395	15	0.173	K.AFM*DASSLPK.A
R3/RRR3-22/3	1978.396	1979.086	-856.805	0.489	1166.988	0.604	32	0.172	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1083.024	1083.240	-200.618	0.473	1205.856	0.386	15	0.171	K.AFM*DASSLPK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1269.909	1270.454	-1220.270	0.464	1329.822	0.322	18	0.169	R.VAVCDAASHVLK.S
R3/RRR3-22/3	1978.076	1979.086	-1018.865	0.435	1317.099	0.530	32	0.169	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1177.756	1178.320	-1331.758	0.373	780.629	0.544	19	0.168	K.LNPAAGVGSTYK.T
R3/RRR3-20/2	1177.983	1178.320	-286.411	0.414	711.105	0.554	18	0.167	K.LNPAAGVGSTYK.T
R3/RRR3-22/2	977.799	978.036	-243.059	0.395	1217.539	0.337	15	0.166	K.SDVLEAESK.V
R3/RRR3-19/2	1178.158	1178.320	-138.176	0.355	771.904	0.542	18	0.165	K.LNPAAGVGSTYK.T
R3/RRR3-21/2	1177.402	1178.320	-1633.518	0.353	686.120	0.577	18	0.165	K.LNPAAGVGSTYK.T
R3/RRR3-22/2	1177.497	1178.320	-1553.114	0.341	771.673	0.526	19	0.163	K.LNPAAGVGSTYK.T
R3/RRR3-23/2	1269.472	1270.454	-1565.680	0.395	1080.768	0.385	17	0.162	R.VAVCDAASHVLK.S
R3/RRR3-22/2	1546.624	1547.755	-1381.500	0.400	1176.551	0.336	20	0.162	K.EKDIVDGYYGM*LK.M
R3/RRR3-20/2	1178.072	1178.320	-211.352	0.364	585.948	0.567	17	0.160	K.LNPAAGVGSTYK.T
R3/RRR3-22/3	1978.635	1979.086	-228.750	0.461	1184.641	0.543	32	0.158	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-23/2	1269.353	1270.454	-1660.257	0.328	1183.384	0.298	18	0.157	R.VAVCDAASHVLK.S
R3/RRR3-22/2	1179.191	1178.320	-109.501	0.378	584.645	0.495	18	0.156	K.LNPAAGVGSTYK.T
R3/RRR3-22/2	1179.056	1178.320	-224.468	0.385	591.548	0.451	18	0.152	K.LNPAAGVGSTYK.T
R3/RRR3-19/2	1177.899	1178.320	-357.945	0.331	618.687	0.479	17	0.152	K.LNPAAGVGSTYK.T
R3/RRR3-22/2	1066.918	1067.241	-303.258	0.362	656.465	0.455	14	0.152	K.AFMDASSLPK.A
R3/RRR3-20/2	1083.907	1083.240	-307.991	0.408	525.194	0.481	13	0.152	K.AFM*DASSLPK.A
R3/RRR3-20/3	1979.048	1979.086	-19.254	0.514	1053.072	0.561	31	0.150	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-19/2	1083.343	1083.240	95.546	0.292	637.500	0.470	13	0.149	K.AFM*DASSLPK.A
R3/RRR3-20/2	1270.847	1270.454	309.971	0.347	1028.234	0.304	16	0.148	R.VAVCDAASHVLK.S
R3/RRR3-22/2	1547.290	1547.755	-300.865	0.474	791.891	0.377	18	0.148	K.EKDIVDGYYGM*LK.M
R3/RRR3-22/2	1531.403	1531.755	-230.306	0.459	770.744	0.379	18	0.147	K.EKDIVDGYYGMLK.M
R3/RRR3-19/2	1083.329	1083.240	81.759	0.329	428.447	0.486	11	0.146	K.AFM*DASSLPK.A
R3/RRR3-20/2	1084.115	1083.240	-116.052	0.363	600.315	0.397	13	0.145	K.AFM*DASSLPK.A
R3/RRR3-22/3	1978.664	1979.086	-213.711	0.414	1187.493	0.481	32	0.144	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1530.350	1531.755	-1576.479	0.366	917.442	0.278	19	0.142	K.EKDIVDGYYGMLK.M
R3/RRR3-22/2	1066.453	1067.241	-1681.422	0.259	701.352	0.360	14	0.142	K.AFMDASSLPK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1177.944	1178.320	-320.097	0.244	425.892	0.363	15	0.139	K.LNPAAGVGSTYK.T
R3/RRR3-18/2	1082.936	1083.240	-281.811	0.286	312.747	0.373	12	0.139	-.AFM*DASSLPK.-
R3/RRR3-22/2	1066.581	1067.241	-1560.917	0.236	547.740	0.378	13	0.139	K.AFMDASSLPK.A
R3/RRR3-22/3	1978.399	1979.086	-854.947	0.456	974.469	0.514	28	0.135	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1923.479	1924.095	-842.623	0.355	649.538	0.290	17	0.132	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-22/3	1923.337	1924.095	-916.981	0.425	1218.292	0.404	29	0.128	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-23/3	1924.115	1924.095	10.135	0.443	1287.656	0.371	29	0.126	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-23/3	1978.524	1979.086	-791.866	0.484	770.673	0.528	27	0.126	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-20/3	1978.080	1979.086	-1017.285	0.423	664.656	0.490	26	0.116	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-22/2	1623.522	1622.823	-186.017	0.406	875.740	0.557	17	0.106	K.MIEDYLVAHPAEYA.-
R3/RRR3-2/3	1978.950	1979.086	-68.720	0.326	390.845	0.409	22	0.104	K.SHSTETKLEATGDGSCVAK.L
R3/RRR3-23/3	1923.668	1924.095	-222.812	0.390	1003.724	0.321	28	0.101	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-22/2	1624.039	1622.823	133.545	0.461	849.306	0.510	17	0.092	K.MIEDYLVAHPAEYA.-
R3/RRR3-23/3	1923.391	1924.095	-888.788	0.358	642.926	0.260	25	0.090	K.LKVEYELEDGSSLSPEK.E
R3/RRR3-23/2	1623.955	1622.823	81.153	0.380	609.114	0.410	16	0.039	K.MIEDYLVAHPAEYA.-
R3/RRR3-8/2	1523.293	1522.682	-255.645	0.615	3698.101	0.605	25	0.772	R.IEEELGAAAVYAGTK.F
R3/RRR3-8/2	1523.197	1522.682	-318.841	0.604	2745.566	0.596	25	0.481	R.IEEELGAAAVYAGTK.F
R3/RRR3-8/2	1515.460	1514.829	-243.959	0.566	2485.332	0.563	23	0.407	K.LGANAILAVSLALCK.A
R3/RRR3-8/2	1523.232	1522.682	-296.006	0.608	2243.167	0.617	23	0.374	R.IEEELGAAAVYAGTK.F
R3/RRR3-8/2	1872.635	1872.241	210.882	0.607	2070.398	0.613	27	0.336	K.LAMQEFMILPTGASSFK.E
R3/RRR3-8/2	1514.047	1514.829	-1180.466	0.432	2240.936	0.501	22	0.336	K.LGANAILAVSLALCK.A
R3/RRR3-8/2	1515.468	1514.829	-238.626	0.568	2054.111	0.592	22	0.328	K.LGANAILAVSLALCK.A
R3/RRR3-8/2	1582.603	1581.839	-149.360	0.508	2004.273	0.532	24	0.302	K.AVDNVNSIIGPALIGK.D
R3/RRR3-8/2	1998.286	1999.112	-916.464	0.512	1713.052	0.627	24	0.281	R.GNPTVEVDICCSDGTFAR.A
R3/RRR3-8/2	1581.177	1581.839	-1053.998	0.355	1950.421	0.468	23	0.274	K.AVDNVNSIIGPALIGK.D
R3/RRR3-8/2	1582.742	1581.839	-61.159	0.550	1607.914	0.544	22	0.243	K.AVDNVNSIIGPALIGK.D
R3/RRR3-8/2	1872.553	1872.241	166.953	0.578	1452.168	0.577	25	0.232	K.LAMQEFMILPTGASSFK.E
R3/RRR3-8/2	1905.730	1904.240	257.853	0.485	1126.153	0.626	24	0.206	K.LAM*QEFM*ILPTGASSFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1871.653	1872.241	-851.105	0.487	1273.379	0.535	22	0.201	K.LAMQEFMILPTGASSFK.E
R3/RRR3-8/2	1905.622	1904.240	200.942	0.402	841.740	0.615	23	0.178	K.LAM*QEFM*ILPTGASSFK.E
R3/RRR3-8/2	1887.377	1888.241	-990.482	0.396	433.527	0.317	15	0.133	K.LAM*QEFMILPTGASSFK.E
R3/RRR3-7/2	1873.716	1872.241	253.953	0.293	619.305	0.248	19	0.132	K.LAMQEFMILPTGASSFK.E
R3/RRR3-2/2	1471.605	1471.724	-81.420	0.507	3229.636	0.533	25	0.591	K.LVSEAGVGVVASGVVK.G
R3/RRR3-2/2	1766.421	1767.020	-907.978	0.550	2355.590	0.614	26	0.395	K.VAIIGSGPAGLAAADQLNK.M
R3/RRR3-2/2	1766.485	1767.020	-871.557	0.509	2273.258	0.590	25	0.369	K.VAIIGSGPAGLAAADQLNK.M
R3/RRR3-2/2	1471.289	1471.724	-296.637	0.430	2108.664	0.440	23	0.294	K.LVSEAGVGVVASGVVK.G
R3/RRR3-2/2	1171.009	1170.341	-284.562	0.482	1866.922	0.447	18	0.258	R.VGLLVESAEPR.E
R3/RRR3-2/2	1170.283	1170.341	-49.236	0.530	1786.288	0.464	18	0.250	R.VGLLVESAEPR.E
R3/RRR3-2/2	1170.092	1170.341	-213.003	0.452	1699.660	0.458	17	0.237	R.VGLLVESAEPR.E
R3/RRR3-2/2	1538.606	1538.686	-52.489	0.478	1061.280	0.561	20	0.190	R.LLETNNFPEFTGR.V
R3/RRR3-2/2	1432.202	1432.607	-283.189	0.429	1182.514	0.452	18	0.180	R.VFIETPIQNTNR.A
R3/RRR3-2/2	1432.205	1432.607	-280.881	0.450	1165.103	0.433	18	0.176	R.VFIETPIQNTNR.A
R3/RRR3-2/3	1844.173	1844.926	-953.323	0.525	1308.363	0.572	36	0.175	K.GHADHVLISGHDGGTGASR.W
R3/RRR3-2/2	1432.240	1432.607	-256.938	0.478	973.788	0.452	18	0.167	R.VFIETPIQNTNR.A
R3/RRR3-2/2	1767.075	1767.020	31.484	0.468	951.376	0.495	21	0.165	K.VAIIGSGPAGLAAADQLNK.M
R3/RRR3-2/3	1843.341	1844.926	-1950.999	0.489	1290.929	0.510	36	0.157	K.GHADHVLISGHDGGTGASR.W
R3/RRR3-2/2	1322.003	1322.491	-370.171	0.407	1003.469	0.344	18	0.151	R.M*EPLADGSM*NPK.R
R3/RRR3-2/3	1844.867	1844.926	-32.401	0.544	1062.376	0.556	34	0.148	K.GHADHVLISGHDGGTGASR.W
R3/RRR3-2/2	949.205	949.126	84.215	0.390	754.111	0.365	13	0.147	K.VLDITYPK.K
R3/RRR3-2/2	1087.143	1087.252	-100.190	0.300	775.093	0.392	14	0.145	R.AILQTDGQLK.T
R3/RRR3-2/2	948.377	949.126	-1849.129	0.393	611.825	0.319	13	0.142	K.VLDITYPK.K
R3/RRR3-2/2	1126.496	1127.316	-1620.821	0.286	240.179	0.472	15	0.141	R.VAPGISGSLTPK.N
R3/RRR3-2/2	1375.962	1376.580	-1179.161	0.400	843.403	0.316	17	0.141	R.DILSNFDTLLPK.F
R3/RRR3-2/2	949.553	949.126	451.538	0.393	493.392	0.298	12	0.139	K.VLDITYPK.K
R3/RRR3-2/2	1126.991	1127.316	-289.484	0.255	264.923	0.444	15	0.138	R.VAPGISGSLTPK.N
R3/RRR3-2/2	1538.463	1538.686	-145.687	0.347	450.556	0.330	13	0.132	R.LLETNNFPEFTGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1126.977	1127.316	-301.873	0.300	214.141	0.479	13	0.132	-.VAPGISGSLTPK.-
R3/RRR3-2/2	1087.191	1087.252	-56.490	0.296	646.443	0.245	13	0.131	R.AILQTDGQLK.T
R3/RRR3-2/3	1680.522	1680.867	-206.073	0.478	836.659	0.499	28	0.119	K.M*AQGAKPGEGGELPGHK.V
R3/RRR3-2/3	1102.493	1102.266	205.926	0.461	1077.583	0.205	18	0.086	-.TDKIEIVQR.-
R3/RRR3-14/2	1688.314	1688.864	-921.121	0.520	2012.481	0.628	25	0.329	K.VDGLVSGIGTGGTITGAGR.Y
R3/RRR3-13/2	1688.723	1688.864	-83.785	0.536	1909.383	0.663	27	0.322	K.VDGLVSGIGTGGTITGAGR.Y
R3/RRR3-13/2	1688.470	1688.864	-234.407	0.522	1922.720	0.650	26	0.320	K.VDGLVSGIGTGGTITGAGR.Y
R3/RRR3-14/2	1689.358	1688.864	292.973	0.532	1853.007	0.647	26	0.307	K.VDGLVSGIGTGGTITGAGR.Y
R3/RRR3-13/2	1689.303	1688.864	260.657	0.530	1748.527	0.627	26	0.284	K.VDGLVSGIGTGGTITGAGR.Y
R3/RRR3-13/2	1356.512	1357.512	-1478.486	0.383	1972.652	0.487	19	0.282	R.IGYSMITDAEEK.G
R3/RRR3-14/2	1705.304	1706.040	-1020.766	0.463	1566.695	0.560	20	0.240	K.AFGAELILTDPLLGM*K.G
R3/RRR3-14/2	1706.831	1706.040	-122.470	0.565	1429.081	0.593	19	0.229	K.AFGAELILTDPLLGM*K.G
R3/RRR3-13/2	1372.510	1373.511	-1462.559	0.396	1678.679	0.420	18	0.224	R.IGYSM*ITDAEEK.G
R3/RRR3-14/2	1817.493	1818.064	-866.767	0.484	1508.609	0.500	21	0.219	K.DVTELIGNTPLVYLNR.V
R3/RRR3-13/2	1373.093	1373.511	-305.245	0.432	1564.681	0.452	18	0.217	R.IGYSM*ITDAEEK.G
R3/RRR3-14/2	1688.275	1688.864	-944.059	0.497	1274.586	0.606	23	0.214	K.VDGLVSGIGTGGTITGAGR.Y
R3/RRR3-14/3	1818.039	1818.064	-13.854	0.437	1798.513	0.481	31	0.213	K.DVTELIGNTPLVYLNR.V
R3/RRR3-14/2	1372.909	1373.511	-1170.692	0.431	1452.917	0.472	18	0.209	R.IGYSM*ITDAEEK.G
R3/RRR3-13/2	1372.614	1373.511	-1386.271	0.386	1491.574	0.444	18	0.207	R.IGYSM*ITDAEEK.G
R3/RRR3-14/2	1613.340	1613.841	-932.963	0.429	1113.475	0.601	26	0.198	K.EGLLVGISSGAAAAAAVR.L
R3/RRR3-14/2	1818.468	1818.064	222.820	0.520	1341.005	0.481	20	0.196	K.DVTELIGNTPLVYLNR.V
R3/RRR3-13/2	1818.661	1818.064	-222.340	0.533	1394.538	0.457	20	0.196	K.DVTELIGNTPLVYLNR.V
R3/RRR3-14/2	1817.276	1818.064	-986.661	0.453	1482.490	0.392	21	0.194	K.DVTELIGNTPLVYLNR.V
R3/RRR3-13/2	1356.429	1357.512	-1540.318	0.275	1418.653	0.320	18	0.176	R.IGYSMITDAEEK.G
R3/RRR3-14/2	1705.341	1706.040	-999.421	0.376	1138.831	0.464	18	0.174	K.AFGAELILTDPLLGM*K.G
R3/RRR3-13/2	1817.312	1818.064	-966.564	0.419	1330.356	0.354	19	0.172	K.DVTELIGNTPLVYLNR.V
R3/RRR3-14/2	1475.087	1474.642	302.329	0.498	742.052	0.510	16	0.162	K.IHYETTGPEIWK.S
R3/RRR3-14/2	1373.171	1373.511	-248.609	0.422	1012.976	0.405	17	0.161	R.IGYSM*ITDAEEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1474.383	1474.642	-176.101	0.473	762.901	0.494	16	0.160	K.IHYETTGPEIWK.S
R3/RRR3-14/2	1285.265	1285.513	-194.106	0.411	970.444	0.405	16	0.159	R.YLSSVLFQSIK.K
R3/RRR3-14/2	1474.260	1474.642	-259.913	0.491	727.943	0.494	16	0.159	K.IHYETTGPEIWK.S
R3/RRR3-13/2	1474.228	1474.642	-281.345	0.473	706.300	0.484	16	0.157	K.IHYETTGPEIWK.S
R3/RRR3-13/2	1817.362	1818.064	-939.185	0.417	1258.484	0.287	19	0.156	K.DVTELIGNTPLVYLNR.V
R3/RRR3-13/2	1473.702	1474.642	-1320.290	0.406	725.915	0.460	16	0.154	K.IHYETTGPEIWK.S
R3/RRR3-14/2	1396.931	1397.645	-1231.228	0.432	800.914	0.423	15	0.151	K.LFVVVFPSFGER.Y
R3/RRR3-14/2	1473.508	1474.642	-1452.247	0.366	733.934	0.434	16	0.151	K.IHYETTGPEIWK.S
R3/RRR3-14/2	1283.233	1283.425	-149.721	0.414	967.137	0.349	15	0.150	K.LESM*EPCSSVK.D
R3/RRR3-14/2	1396.818	1397.645	-1312.320	0.376	858.451	0.381	16	0.149	K.LFVVVFPSFGER.Y
R3/RRR3-14/2	1413.436	1413.686	-177.284	0.387	789.898	0.402	14	0.147	R.YLSSVLFQSIKK.E
R3/RRR3-14/3	1986.124	1986.176	-26.429	0.481	1186.953	0.502	31	0.145	K.THNSFILQQFENPANPK.I
R3/RRR3-13/2	1413.660	1413.686	-18.327	0.357	673.297	0.427	14	0.145	R.YLSSVLFQSIKK.E
R3/RRR3-13/2	1356.167	1357.512	-1733.997	0.251	940.105	0.263	17	0.140	R.IGYSMITDAEEK.G
R3/RRR3-13/2	1285.147	1285.513	-285.679	0.416	730.786	0.314	14	0.139	R.YLSSVLFQSIK.K
R3/RRR3-14/2	1397.224	1397.645	-302.810	0.371	784.332	0.270	15	0.135	K.LFVVVFPSFGER.Y
R3/RRR3-13/2	1414.750	1413.686	45.123	0.373	585.753	0.342	12	0.134	R.YLSSVLFQSIKK.E
R3/RRR3-14/2	1284.780	1285.513	-1353.285	0.356	790.968	0.248	15	0.134	-.YLSSVLFQSIK.-
R3/RRR3-13/2	1286.049	1285.513	-361.927	0.191	618.356	0.187	15	0.130	R.YLSSVLFQSIK.K
R3/RRR3-14/2	1285.452	1285.513	-47.873	0.270	601.559	0.162	13	0.128	-.YLSSVLFQSIK.-
R3/RRR3-14/3	1985.911	1986.176	-134.077	0.437	998.962	0.478	29	0.126	K.THNSFILQQFENPANPK.I
R3/RRR3-14/3	1613.233	1613.841	-999.252	0.397	1111.410	0.441	29	0.125	K.EGLLVGISSGAAAAAAVR.L
R3/RRR3-14/2	1283.307	1283.425	-91.991	0.265	758.443	0.081	15	0.124	K.LESM*EPCSSVK.D
R3/RRR3-13/3	1986.793	1986.176	-193.301	0.462	994.739	0.438	29	0.119	K.THNSFILQQFENPANPK.I
R3/RRR3-14/3	1613.684	1613.841	-97.097	0.236	501.809	0.360	26	0.087	-.EGLLVGISSGAAAAAAVR.-
R3/RRR3-11/2	1318.007	1318.495	-371.359	0.414	1611.311	0.375	20	0.208	K.CDVIASGIVNAAK.Q
R3/RRR3-11/2	1475.141	1474.642	339.170	0.525	1267.951	0.481	20	0.191	R.GAAAGSVEEVKNTLK.N
R3/RRR3-11/2	1474.165	1474.642	-324.214	0.484	1209.926	0.496	20	0.189	R.GAAAGSVEEVKNTLK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1182.680	1183.255	-1335.842	0.398	1312.338	0.392	17	0.182	K.LNFDDNAAFR.Q
R3/RRR3-11/2	1474.333	1474.642	-210.072	0.456	1291.255	0.418	20	0.181	R.GAAAGSVEEVKNTLK.N
R3/RRR3-11/2	1924.784	1926.046	-1179.108	0.495	1036.713	0.532	23	0.179	K.ESGM*TLITAEDLDDAAEK.A
R3/RRR3-11/3	1619.495	1619.824	-204.026	0.552	1710.432	0.424	31	0.177	R.LNIHEYQGAELM*GK.Y
R3/RRR3-11/2	1182.771	1183.255	-410.507	0.530	1159.952	0.356	17	0.165	K.LNFDDNAAFR.Q
R3/RRR3-11/2	1018.916	1019.284	-362.147	0.531	1172.985	0.340	16	0.164	K.M*LGQILVTK.Q
R3/RRR3-11/2	818.903	818.943	-49.281	0.428	763.875	0.490	11	0.162	K.YGINVPR.G
R3/RRR3-11/3	1619.653	1619.824	-106.150	0.501	1697.987	0.360	28	0.160	R.LNIHEYQGAELM*GK.Y
R3/RRR3-2/2	819.746	818.943	-241.007	0.374	826.180	0.457	11	0.159	K.YGINVPR.G
R3/RRR3-11/2	1003.073	1003.285	-211.485	0.445	949.487	0.382	15	0.158	K.MLGQILVTK.Q
R3/RRR3-11/2	1094.546	1095.277	-1586.251	0.470	846.679	0.451	14	0.157	K.SGLQGGVHIVK.A
R3/RRR3-11/2	818.848	818.943	-117.018	0.370	782.329	0.457	11	0.157	K.YGINVPR.G
R3/RRR3-11/2	1002.778	1003.285	-1507.122	0.416	903.722	0.377	15	0.155	K.MLGQILVTK.Q
R3/RRR3-10/2	817.941	817.995	-65.954	0.416	381.560	0.480	11	0.153	K.VPIDVFK.G
R3/RRR3-11/2	1095.116	1095.277	-147.871	0.407	886.212	0.393	15	0.152	K.SGLQGGVHIVK.A
R3/RRR3-11/2	1094.432	1095.277	-1690.681	0.379	794.711	0.436	14	0.152	K.SGLQGGVHIVK.A
R3/RRR3-11/2	1292.272	1292.616	-266.630	0.310	941.683	0.399	16	0.151	K.AILVNIFGGIM*K.C
R3/RRR3-11/2	817.624	817.995	-455.471	0.372	320.110	0.479	11	0.151	K.VPIDVFK.G
R3/RRR3-11/2	817.504	817.995	-602.611	0.356	364.989	0.497	11	0.147	-.VPIDVFK.-
R3/RRR3-11/2	1002.419	1003.285	-1866.267	0.364	887.223	0.319	14	0.146	K.MLGQILVTK.Q
R3/RRR3-10/2	1183.980	1183.255	-232.841	0.404	422.552	0.363	14	0.143	K.LNFDDNAAFR.Q
R3/RRR3-11/2	1245.204	1245.444	-193.665	0.341	558.500	0.437	17	0.142	R.NTAGPLIIACSK.G
R3/RRR3-10/2	1183.549	1183.255	248.731	0.351	460.452	0.341	15	0.141	K.LNFDDNAAFR.Q
R3/RRR3-11/3	1605.022	1603.825	123.219	0.529	1026.642	0.527	24	0.139	R.LNIHEYQGAELMGK.Y
R3/RRR3-11/3	1619.587	1619.824	-146.977	0.534	1323.078	0.423	27	0.138	R.LNIHEYQGAELM*GK.Y
R3/RRR3-10/2	1474.062	1474.642	-1075.188	0.331	448.166	0.383	17	0.134	-.GAAAGSVEEVKNTLK.-
R3/RRR3-11/2	817.466	817.995	-1875.731	0.221	270.886	0.357	10	0.114	-.VPIDVFK.-
R3/RRR3-11/3	1095.429	1095.277	138.906	0.415	797.247	0.430	20	0.109	K.SGLQGGVHIVK.A

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/3	1604.300	1603.825	297.088	0.440	1021.405	0.331	24	0.103	R.LNIHEYQGAELMGK.Y
R3/RRR3-10/3	1095.356	1095.277	72.687	0.416	458.677	0.364	18	0.101	K.SGLQGGVHIVK.A
R3/RRR3-10/3	1095.263	1095.277	-12.657	0.387	393.598	0.270	18	0.099	K.SGLQGGVHIVK.A
R3/RRR3-11/3	1095.685	1095.277	373.201	0.379	656.300	0.364	20	0.099	K.SGLQGGVHIVK.A
R3/RRR3-10/3	1095.653	1095.277	343.711	0.356	527.032	0.363	19	0.099	K.SGLQGGVHIVK.A
R3/RRR3-11/3	1095.506	1095.277	209.977	0.332	570.413	0.318	19	0.095	K.SGLQGGVHIVK.A
R3/RRR3-10/3	1603.953	1603.825	80.058	0.294	832.177	0.239	23	0.088	-.LNIHEYQGAELMGK.-
R3/RRR3-11/2	1831.245	1832.134	-1034.695	0.518	2083.190	0.605	22	0.339	R.MFVADGGELLMAQSYAK.N
R3/RRR3-11/2	1449.178	1449.629	-311.893	0.533	1899.813	0.539	22	0.287	R.VATVQCLSGTGSLR.V
R3/RRR3-11/2	1574.342	1574.798	-290.518	0.490	1813.650	0.546	23	0.274	R.VGALSIVCGSADVAVR.V
R3/RRR3-11/2	1449.215	1449.629	-286.286	0.517	1828.710	0.517	22	0.270	R.VATVQCLSGTGSLR.V
R3/RRR3-11/2	1573.832	1574.798	-1252.705	0.406	1791.505	0.508	23	0.260	R.VGALSIVCGSADVAVR.V
R3/RRR3-11/2	1532.315	1531.695	-248.627	0.539	1715.047	0.530	21	0.255	K.LIFGADSPAIQENR.V
R3/RRR3-11/2	1531.382	1531.695	-204.965	0.488	1779.239	0.466	22	0.249	K.LIFGADSPAIQENR.V
R3/RRR3-11/2	1450.170	1449.629	-317.589	0.553	1545.424	0.566	22	0.243	R.VATVQCLSGTGSLR.V
R3/RRR3-11/2	1531.220	1531.695	-311.254	0.465	1646.367	0.464	21	0.230	K.LIFGADSPAIQENR.V
R3/RRR3-11/2	1573.662	1574.798	-1361.688	0.341	1542.843	0.398	21	0.202	R.VGALSIVCGSADVAVR.V
R3/RRR3-11/2	1482.178	1481.674	-335.760	0.482	1269.143	0.496	20	0.196	K.EYLPITGLADFNK.L
R3/RRR3-11/2	1708.469	1708.979	-886.318	0.513	1359.473	0.443	24	0.195	R.VKEYLPITGLADFNK.L
R3/RRR3-11/3	1709.656	1708.979	-189.258	0.511	1810.468	0.394	30	0.186	R.VKEYLPITGLADFNK.L
R3/RRR3-11/2	1481.205	1481.674	-317.796	0.415	1149.230	0.462	20	0.179	K.EYLPITGLADFNK.L
R3/RRR3-11/2	1481.452	1481.674	-150.549	0.450	1007.557	0.476	19	0.171	K.EYLPITGLADFNK.L
R3/RRR3-11/2	949.043	949.089	-48.651	0.511	954.314	0.473	15	0.171	K.VNLGVGAYR.D
R3/RRR3-11/2	948.482	949.089	-1699.701	0.428	851.975	0.517	15	0.169	K.VNLGVGAYR.D
R3/RRR3-11/2	1454.267	1454.697	-296.741	0.475	735.182	0.519	21	0.165	R.TEEGKPLVLNVVR.R
R3/RRR3-11/2	1708.412	1708.979	-920.175	0.510	1107.471	0.391	22	0.164	R.VKEYLPITGLADFNK.L
R3/RRR3-11/2	849.050	848.969	94.798	0.559	1150.518	0.360	13	0.164	R.VGGEFLAR.H
R3/RRR3-11/2	1708.419	1708.979	-915.727	0.476	1097.888	0.389	22	0.164	R.VKEYLPITGLADFNK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1454.458	1454.697	-164.539	0.541	685.109	0.514	20	0.162	R.TEEGKPLVLNVVR.R
R3/RRR3-11/2	1455.307	1454.697	-268.598	0.550	683.706	0.511	20	0.162	R.TEEGKPLVLNVVR.R
R3/RRR3-11/3	1531.355	1531.695	-222.687	0.488	1698.960	0.356	28	0.160	K.LIFGADSPAIQENR.V
R3/RRR3-11/2	848.901	848.969	-80.857	0.545	1074.321	0.307	13	0.151	R.VGGEFLAR.H
R3/RRR3-11/2	1076.644	1077.302	-1544.053	0.420	744.297	0.388	17	0.150	K.VFTLAGLTVR.S
R3/RRR3-11/2	848.986	848.969	19.958	0.544	1042.947	0.285	13	0.147	R.VGGEFLAR.H
R3/RRR3-11/2	1077.167	1077.302	-125.442	0.527	826.752	0.338	16	0.146	K.VFTLAGLTVR.S
R3/RRR3-1/2	1531.300	1531.695	-258.706	0.352	742.201	0.325	17	0.139	K.LIFGADSPAIQENR.V
R3/RRR3-11/2	1076.675	1077.302	-1515.693	0.298	305.306	0.248	13	0.134	-.VFTLAGLTVR.-
R3/RRR3-11/3	1531.725	1531.695	19.686	0.490	1384.580	0.373	27	0.133	K.LIFGADSPAIQENR.V
R3/RRR3-1/2	1531.126	1531.695	-1028.079	0.310	612.893	0.217	16	0.130	K.LIFGADSPAIQENR.V
R3/RRR3-11/3	1531.841	1531.695	95.336	0.495	1312.910	0.359	27	0.124	K.LIFGADSPAIQENR.V
R3/RRR3-11/3	1500.750	1500.618	88.092	0.398	664.089	0.537	23	0.115	R.QEYHIYMTSDGR.I
R3/RRR3-11/3	1500.713	1500.618	63.496	0.339	754.065	0.510	23	0.112	R.QEYHIYMTSDGR.I
R3/RRR3-11/3	1573.998	1574.798	-1146.752	0.376	955.493	0.419	25	0.111	R.VGALSIVCGSADVAVR.V
R3/RRR3-11/3	1574.332	1574.798	-297.100	0.364	994.950	0.335	25	0.100	R.VGALSIVCGSADVAVR.V
R3/RRR3-11/3	1708.444	1708.979	-900.923	0.440	1033.304	0.284	27	0.096	R.VKEYLPITGLADFNK.L
R3/RRR3-11/3	1709.409	1708.979	252.427	0.421	649.250	0.319	25	0.094	R.VKEYLPITGLADFNK.L
R3/RRR3-6/2	1427.225	1427.588	-255.181	0.474	2287.083	0.586	21	0.373	K.STVHDVVLVGGSTR.I
R3/RRR3-6/2	1427.253	1427.588	-235.789	0.458	2237.946	0.570	21	0.357	K.STVHDVVLVGGSTR.I
R3/RRR3-6/2	1427.258	1427.588	-232.357	0.482	2005.647	0.596	20	0.321	K.STVHDVVLVGGSTR.I
R3/RRR3-6/2	1529.213	1528.753	301.556	0.549	1803.797	0.411	21	0.237	K.MKETAEAYLGSTVK.N
R3/RRR3-6/2	1248.068	1248.435	-294.721	0.493	1429.248	0.507	20	0.216	K.DAGVISGLNVM*R.I
R3/RRR3-6/2	1233.081	1232.436	-288.110	0.536	1426.738	0.482	20	0.210	K.DAGVISGLNVMR.I
R3/RRR3-6/2	1247.971	1248.435	-373.231	0.443	1438.033	0.473	19	0.209	K.DAGVISGLNVM*R.I
R3/RRR3-6/2	1247.602	1248.435	-1473.462	0.455	1339.607	0.486	19	0.201	K.DAGVISGLNVM*R.I
R3/RRR3-6/2	1544.364	1544.752	-252.421	0.524	1304.557	0.478	20	0.195	K.M*KETAEAYLGSTVK.N
R3/RRR3-6/2	1231.429	1232.436	-1634.033	0.339	1258.130	0.431	18	0.181	K.DAGVISGLNVMR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1231.908	1232.436	-1243.500	0.391	1134.081	0.478	17	0.179	K.DAGVISGLNVMR.I
R3/RRR3-6/2	1584.240	1583.788	285.749	0.570	1141.318	0.461	22	0.179	K.QFSAEEISSMVLNK.M
R3/RRR3-6/2	1583.270	1583.788	-962.050	0.491	900.384	0.401	20	0.154	-.QFSAEEISSMVLNK.-
R3/RRR3-6/2	1599.019	1599.788	-1109.345	0.489	831.182	0.398	20	0.152	K.QFSAEEISSM*VLNK.M
R3/RRR3-6/2	1583.200	1583.788	-1006.251	0.476	919.794	0.348	20	0.149	K.QFSAEEISSMVLNK.M
R3/RRR3-6/2	1600.476	1599.788	-195.231	0.543	598.700	0.427	18	0.147	K.QFSAEEISSM*VLNK.M
R3/RRR3-6/2	1600.092	1599.788	190.605	0.558	620.863	0.404	19	0.143	-.QFSAEEISSM*VLNK.-
R3/RRR3-2/2	1233.131	1232.436	-247.787	0.270	152.718	0.336	11	0.128	-.DAGVISGLNVMR.-
R3/RRR3-6/3	1544.243	1544.752	-980.134	0.397	1225.433	0.321	27	0.111	K.M*KETAEAYLGSTVK.N
R3/RRR3-6/3	1544.671	1544.752	-52.793	0.459	1061.404	0.351	27	0.107	K.M*KETAEAYLGSTVK.N
R3/RRR3-6/3	1528.104	1528.753	-1081.920	0.459	895.463	0.343	25	0.101	K.MKETAEAYLGSTVK.N
R3/RRR3-6/3	1545.048	1544.752	192.085	0.442	818.073	0.311	24	0.095	K.M*KETAEAYLGSTVK.N
R3/RRR3-6/3	1528.062	1528.753	-1110.075	0.389	1008.995	0.257	27	0.093	K.MKETAEAYLGSTVK.N
R3/RRR3-6/3	1528.341	1528.753	-269.991	0.458	1058.078	0.157	28	0.082	K.MKETAEAYLGSTVK.N
R3/RRR3-1/3	1270.376	1270.420	-35.199	0.518	1948.919	0.430	27	0.211	R.RPGSVSLNQSPK.T
R3/RRR3-2/2	1497.337	1497.637	-201.039	0.512	1100.547	0.561	20	0.194	R.QGNVGIVEYAYQR.T
R3/RRR3-2/3	1270.468	1270.420	37.515	0.559	1667.448	0.456	27	0.179	R.RPGSVSLNQSPK.T
R3/RRR3-3/2	1497.285	1497.637	-235.800	0.508	1004.652	0.516	19	0.178	R.QGNVGIVEYAYQR.T
R3/RRR3-3/2	1497.124	1497.637	-1013.482	0.487	995.147	0.512	19	0.177	R.QGNVGIVEYAYQR.T
R3/RRR3-2/2	991.977	992.114	-137.820	0.495	1237.702	0.404	16	0.176	K.GAGGSAVFVAR.N
R3/RRR3-2/2	1497.097	1497.637	-1031.901	0.460	959.316	0.513	19	0.174	R.QGNVGIVEYAYQR.T
R3/RRR3-2/2	1498.500	1497.637	-91.642	0.470	876.212	0.544	19	0.174	R.QGNVGIVEYAYQR.T
R3/RRR3-3/2	1497.180	1497.637	-306.391	0.412	879.059	0.509	18	0.167	R.QGNVGIVEYAYQR.T
R3/RRR3-3/3	1269.871	1270.420	-1223.498	0.505	1551.114	0.445	26	0.164	R.RPGSVSLNQSPK.T
R3/RRR3-3/2	1321.108	1321.501	-298.014	0.492	843.109	0.475	15	0.162	R.VIGNNIFCLDR.D
R3/RRR3-3/3	1270.471	1270.420	39.973	0.602	1488.956	0.462	26	0.160	R.RPGSVSLNQSPK.T
R3/RRR3-2/2	1321.065	1321.501	-330.925	0.387	741.083	0.506	14	0.158	R.VIGNNIFCLDR.D
R3/RRR3-2/2	1268.504	1268.527	-18.591	0.377	1036.612	0.383	15	0.158	R.LILGELQAPSVK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1191.081	1191.402	-269.590	0.428	718.436	0.449	16	0.156	K.TLDVPIYITR.V
R3/RRR3-3/2	1268.402	1268.527	-99.579	0.370	1020.740	0.361	16	0.155	R.LILGELQAPSVK.Y
R3/RRR3-1/2	1192.119	1191.402	-238.133	0.419	740.252	0.414	16	0.153	K.TLDVPIYITR.V
R3/RRR3-3/2	1268.276	1268.527	-199.023	0.364	861.223	0.395	15	0.151	R.LILGELQAPSVK.Y
R3/RRR3-3/2	991.521	992.114	-1611.289	0.422	687.867	0.417	16	0.150	K.GAGGSAVFVAR.N
R3/RRR3-2/2	1268.116	1268.527	-325.819	0.284	571.453	0.515	13	0.147	R.LILGELQAPSVK.Y
R3/RRR3-5/3	1270.397	1270.420	-18.574	0.565	1307.403	0.469	24	0.146	R.RPGSVSLNQSPK.T
R3/RRR3-3/2	1191.926	1191.402	-399.855	0.429	587.706	0.394	14	0.146	K.TLDVPIYITR.V
R3/RRR3-3/2	1191.210	1191.402	-161.227	0.395	637.966	0.376	15	0.146	K.TLDVPIYITR.V
R3/RRR3-1/2	992.018	992.114	-96.468	0.414	601.362	0.393	15	0.146	K.GAGGSAVFVAR.N
R3/RRR3-2/2	991.478	992.114	-1654.950	0.397	716.350	0.387	15	0.145	-.GAGGSAVFVAR.-
R3/RRR3-2/2	1191.224	1191.402	-149.611	0.411	722.987	0.342	16	0.145	K.TLDVPIYITR.V
R3/RRR3-3/2	991.358	992.114	-1776.184	0.421	655.881	0.367	16	0.145	K.GAGGSAVFVAR.N
R3/RRR3-3/2	771.375	771.928	-2019.794	0.317	1154.347	0.207	12	0.145	R.LGIEALR.Q
R3/RRR3-1/2	1831.262	1831.079	100.034	0.440	618.696	0.492	16	0.145	K.YVVWSSDM*ESVALLSK.H
R3/RRR3-3/2	991.378	992.114	-1755.770	0.423	438.595	0.422	14	0.143	-.GAGGSAVFVAR.-
R3/RRR3-3/3	1269.901	1270.420	-1199.751	0.492	1372.135	0.426	25	0.142	R.RPGSVSLNQSPK.T
R3/RRR3-3/3	1269.534	1270.420	-1490.148	0.485	1326.337	0.432	24	0.141	R.RPGSVSLNQSPK.T
R3/RRR3-3/2	1267.517	1268.527	-1591.278	0.247	640.228	0.398	14	0.140	R.LILGELQAPSVK.Y
R3/RRR3-2/2	1321.197	1321.501	-230.807	0.316	517.174	0.410	12	0.140	R.VIGNNIFCLDR.D
R3/RRR3-4/2	771.958	771.928	38.682	0.370	1160.693	0.153	12	0.139	R.LGIEALR.Q
R3/RRR3-2/3	1270.742	1270.420	253.718	0.576	1291.203	0.443	24	0.139	R.RPGSVSLNQSPK.T
R3/RRR3-3/2	1321.166	1321.501	-253.888	0.288	466.914	0.416	12	0.139	R.VIGNNIFCLDR.D
R3/RRR3-2/2	1120.250	1120.283	-30.013	0.382	803.940	0.284	12	0.138	-.VTIFDLQQR.-
R3/RRR3-5/3	1591.562	1591.750	-118.525	0.545	1523.894	0.341	24	0.138	-.AEDRVTIFDLQQR.-
R3/RRR3-2/2	1321.464	1321.501	-27.760	0.337	477.581	0.391	11	0.138	R.VIGNNIFCLDR.D
R3/RRR3-5/3	1270.701	1270.420	221.207	0.549	1237.996	0.453	24	0.137	R.RPGSVSLNQSPK.T
R3/RRR3-5/2	771.812	771.928	-151.038	0.370	861.745	0.191	11	0.136	R.LGIEALR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/3	1270.788	1270.420	290.272	0.559	1382.981	0.399	25	0.136	R.RPGSVSLNQSPK.T
R3/RRR3-3/2	771.868	771.928	-77.426	0.434	1043.563	0.170	11	0.135	R.LGIEALR.Q
R3/RRR3-1/2	771.976	771.928	61.679	0.414	715.307	0.215	10	0.135	R.LGIEALR.Q
R3/RRR3-2/2	771.838	771.928	-116.610	0.413	967.652	0.174	11	0.135	R.LGIEALR.Q
R3/RRR3-4/2	1120.144	1120.283	-125.001	0.278	827.252	0.225	13	0.134	R.VTIFDLQQR.L
R3/RRR3-4/2	1119.374	1120.283	-1711.199	0.311	771.036	0.211	13	0.133	R.VTIFDLQQR.L
R3/RRR3-5/2	1268.174	1268.527	-279.751	0.292	618.675	0.251	13	0.132	R.LILGELQAPSVK.Y
R3/RRR3-5/2	771.550	771.928	-491.954	0.403	845.723	0.167	11	0.132	-.LGIEALR.-
R3/RRR3-5/2	1268.132	1268.527	-312.877	0.223	675.204	0.223	14	0.131	R.LILGELQAPSVK.Y
R3/RRR3-2/2	772.285	771.928	463.865	0.440	982.246	0.134	11	0.130	R.LGIEALR.Q
R3/RRR3-3/2	772.191	771.928	341.673	0.417	997.109	0.107	11	0.129	R.LGIEALR.Q
R3/RRR3-1/2	771.962	771.928	44.075	0.378	1016.612	0.080	11	0.128	-.LGIEALR.-
R3/RRR3-3/3	1592.054	1591.750	191.361	0.547	1320.159	0.372	25	0.126	-.AEDRVTIFDLQQR.-
R3/RRR3-3/3	1270.575	1270.420	121.926	0.491	1345.746	0.361	24	0.126	R.RPGSVSLNQSPK.T
R3/RRR3-2/2	1267.646	1268.527	-1488.735	0.177	533.470	0.340	12	0.124	-.LILGELQAPSVK.-
R3/RRR3-6/3	1270.699	1270.420	220.195	0.443	1128.491	0.391	24	0.118	R.RPGSVSLNQSPK.T
R3/RRR3-3/3	1120.453	1120.287	148.917	0.360	958.814	0.275	21	0.090	K.KGAGGSAVFVAR.N
R3/RRR3-3/3	1271.430	1270.420	7.827	0.409	766.226	0.318	20	0.089	-.RPGSVSLNQSPK.-
R3/RRR3-3/3	1591.313	1591.750	-275.964	0.354	666.907	0.207	20	0.079	-.AEDRVTIFDLQQR.-
R3/RRR3-5/3	1269.908	1270.420	-1194.684	0.398	593.191	0.296	19	0.077	-.RPGSVSLNQSPK.-
R3/RRR3-7/2	1726.699	1726.956	-148.950	0.587	3064.420	0.468	26	0.508	R.LDQLQLLLNGASANGAK.K
R3/RRR3-7/2	1727.022	1726.956	38.665	0.601	3095.591	0.438	26	0.502	R.LDQLQLLLNGASANGAK.K
R3/RRR3-7/2	1726.575	1726.956	-221.363	0.553	2714.745	0.460	25	0.418	R.LDQLQLLLNGASANGAK.K
R3/RRR3-7/2	1133.627	1134.219	-1408.766	0.523	2416.645	0.481	20	0.365	K.GIDACIASGGGR.M
R3/RRR3-7/2	1133.443	1134.219	-1571.350	0.463	2429.066	0.445	20	0.356	K.GIDACIASGGGR.M
R3/RRR3-7/2	1133.798	1134.219	-372.300	0.516	2358.838	0.483	20	0.354	K.GIDACIASGGGR.M
R3/RRR3-7/2	1549.023	1548.635	251.303	0.504	1676.024	0.526	18	0.250	K.ALEYEDFDKFDR.V
R3/RRR3-7/2	1547.549	1548.635	-1351.831	0.376	1733.041	0.474	18	0.244	K.ALEYEDFDKFDR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1727.257	1726.956	174.901	0.537	1446.852	0.555	20	0.223	R.LDQLQLLLNGASANGAK.K
R3/RRR3-7/2	1548.291	1548.635	-222.259	0.432	1385.400	0.497	17	0.207	K.ALEYEDFDKFDR.V
R3/RRR3-7/2	975.035	975.121	-88.856	0.424	860.429	0.526	16	0.170	K.LVDTALASGK.I
R3/RRR3-7/2	974.482	975.121	-1687.206	0.392	723.674	0.538	15	0.163	K.LVDTALASGK.I
R3/RRR3-7/2	974.655	975.121	-479.946	0.357	802.242	0.494	16	0.160	K.LVDTALASGK.I
R3/RRR3-7/3	1563.945	1564.730	-1144.690	0.513	1339.634	0.496	28	0.157	K.RGWDAQVLGEAPHK.F
R3/RRR3-7/3	1726.184	1726.956	-1029.763	0.451	1095.510	0.267	27	0.094	R.LDQLQLLLNGASANGAK.K
R3/RRR3-7/3	1564.097	1564.730	-1047.004	0.372	1074.960	0.225	25	0.089	K.RGWDAQVLGEAPHK.F
R3/RRR3-7/2	1868.589	1869.112	-817.577	0.536	2165.191	0.568	24	0.345	K.WGAPNKIDFLSLSYTR.H
R3/RRR3-7/2	1215.245	1215.380	-111.794	0.434	1783.471	0.375	17	0.229	K.IDFLSLSYTR.H
R3/RRR3-7/2	1215.977	1215.380	-332.237	0.563	1446.065	0.480	17	0.213	K.IDFLSLSYTR.H
R3/RRR3-8/2	1321.380	1321.504	-94.104	0.542	1497.868	0.465	19	0.213	K.LGDLSQTQIFAK.I
R3/RRR3-7/2	1569.378	1569.808	-274.853	0.502	1312.012	0.553	18	0.211	-.M*HSTNLLLEEPIR.M
R3/RRR3-7/2	1320.590	1321.504	-1453.619	0.474	1435.351	0.482	19	0.210	K.LGDLSQTQIFAK.I
R3/RRR3-7/2	1322.182	1321.504	-244.711	0.551	1336.124	0.527	19	0.210	K.LGDLSQTQIFAK.I
R3/RRR3-8/2	1320.956	1321.504	-1175.802	0.536	1445.798	0.453	19	0.205	K.LGDLSQTQIFAK.I
R3/RRR3-7/3	1869.957	1869.112	-83.627	0.465	1845.382	0.405	29	0.198	K.WGAPNKIDFLSLSYTR.H
R3/RRR3-8/2	1321.032	1321.504	-358.367	0.471	1209.084	0.480	18	0.188	K.LGDLSQTQIFAK.I
R3/RRR3-7/2	1214.534	1215.380	-1524.098	0.356	1390.296	0.372	16	0.184	K.IDFLSLSYTR.H
R3/RRR3-1/2	1321.222	1321.504	-214.122	0.470	1125.558	0.496	17	0.183	K.LGDLSQTQIFAK.I
R3/RRR3-7/2	1321.227	1321.504	-210.507	0.495	1340.242	0.394	18	0.183	K.LGDLSQTQIFAK.I
R3/RRR3-2/2	1322.259	1321.504	-185.620	0.488	1040.098	0.516	17	0.180	K.LGDLSQTQIFAK.I
R3/RRR3-7/3	1869.309	1869.112	105.503	0.480	1549.188	0.472	27	0.178	K.WGAPNKIDFLSLSYTR.H
R3/RRR3-7/2	1377.197	1376.623	-309.791	0.511	834.487	0.553	20	0.174	R.GLYPVETISIVGK.I
R3/RRR3-7/2	1628.432	1629.007	-969.880	0.469	764.599	0.540	20	0.167	K.YRPTMPVLSVVIPR.L
R3/RRR3-7/3	1869.139	1869.112	14.036	0.466	1448.164	0.452	28	0.160	K.WGAPNKIDFLSLSYTR.H
R3/RRR3-7/2	1111.065	1110.234	-152.470	0.464	847.436	0.441	14	0.158	R.SVDTISSCLK.A
R3/RRR3-7/2	1628.507	1629.007	-923.974	0.407	709.086	0.416	19	0.149	K.YRPTMPVLSVVIPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/3	1304.555	1304.538	13.025	0.411	1517.993	0.384	25	0.146	K.CNMAGKPAVVTR.V
R3/RRR3-7/2	1111.184	1110.234	-44.692	0.349	882.286	0.303	14	0.142	R.SVDTISSCLK.A
R3/RRR3-7/2	1629.671	1629.007	-206.427	0.306	481.129	0.404	17	0.140	K.YRPTMPVLSVVIPR.L
R3/RRR3-7/2	1174.003	1174.330	-278.935	0.401	701.963	0.327	14	0.140	K.VFNQDLYFK.R
R3/RRR3-7/2	1117.111	1117.346	-211.597	0.297	941.687	0.252	15	0.138	-.GLFPMLADPR.-
R3/RRR3-7/2	1644.573	1645.006	-264.435	0.203	133.204	0.315	13	0.138	K.YRPTM*PVLSVVIPR.L
R3/RRR3-7/2	1109.723	1110.234	-1365.409	0.292	475.460	0.300	12	0.134	R.SVDTISSCLK.A
R3/RRR3-7/3	1320.695	1320.538	119.399	0.390	1378.632	0.373	24	0.132	K.CNM*AGKPAVVTR.V
R3/RRR3-7/3	1304.509	1304.538	-22.593	0.403	1401.649	0.350	24	0.129	K.CNMAGKPAVVTR.V
R3/RRR3-7/2	1375.591	1376.623	-1481.657	0.165	658.728	0.251	18	0.127	R.GLYPVETISIVGK.I
R3/RRR3-7/3	1304.730	1304.538	147.168	0.493	1220.431	0.361	23	0.117	-.CNMAGKPAVVTR.-
R3/RRR3-7/3	1998.708	1999.383	-840.622	0.385	886.772	0.466	24	0.115	R.MASILEPSKPSFFPAM*TK.I
R3/RRR3-7/3	1319.941	1320.538	-1213.249	0.343	1063.195	0.309	22	0.101	K.CNM*AGKPAVVTR.V
R3/RRR3-8/3	1304.931	1304.538	301.818	0.319	700.464	0.384	20	0.100	K.CNMAGKPAVVTR.V
R3/RRR3-7/3	1983.566	1983.384	91.926	0.360	651.491	0.438	25	0.099	-.MASILEPSKPSFFPAMTK.-
R3/RRR3-7/2	1645.631	1645.006	-228.924	0.170	64.019	0.416	12	0.095	-.YRPTM*PVLSVVIPR.-
R3/RRR3-8/3	1304.337	1304.538	-154.669	0.341	733.862	0.284	19	0.091	-.CNMAGKPAVVTR.-
R3/RRR3-7/2	1644.284	1645.006	-1050.650	0.150	56.440	0.431	10	0.088	-.YRPTM*PVLSVVIPR.-
R3/RRR3-7/2	1568.162	1567.722	280.872	0.580	2317.070	0.603	26	0.387	K.IAVFAGGVDTSATETK.G
R3/RRR3-7/3	1773.659	1773.968	-174.421	0.559	2563.683	0.521	33	0.383	K.GTVLIHSAEQLENYAK.T
R3/RRR3-7/2	1567.148	1567.722	-1007.808	0.501	1953.116	0.580	25	0.309	K.IAVFAGGVDTSATETK.G
R3/RRR3-7/2	1773.488	1773.968	-271.220	0.547	1833.627	0.594	23	0.293	K.GTVLIHSAEQLENYAK.T
R3/RRR3-7/2	1289.317	1289.457	-108.980	0.554	2052.736	0.444	18	0.286	K.TEEAKVEELIK.A
R3/RRR3-7/3	1773.903	1773.968	-36.700	0.531	2083.914	0.502	31	0.270	K.GTVLIHSAEQLENYAK.T
R3/RRR3-7/2	1228.809	1229.387	-1288.435	0.476	1809.734	0.497	17	0.264	K.FAESFEM*VPR.T
R3/RRR3-7/2	1227.212	1227.343	-106.513	0.528	1558.805	0.524	18	0.236	K.YSADAACTVLR.V
R3/RRR3-7/2	1228.263	1227.343	-65.353	0.549	1378.544	0.541	17	0.218	K.YSADAACTVLR.V
R3/RRR3-7/2	1309.227	1309.500	-208.790	0.477	1383.533	0.516	21	0.213	K.LLGGGLHNSSVVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1260.158	1260.341	-145.702	0.495	1355.996	0.506	18	0.208	K.NPANFNVDNVR.V
R3/RRR3-7/2	1260.152	1260.341	-150.560	0.487	1242.662	0.526	18	0.201	K.NPANFNVDNVR.V
R3/RRR3-7/2	1259.567	1260.341	-1412.743	0.460	1269.798	0.499	18	0.198	K.NPANFNVDNVR.V
R3/RRR3-7/2	1289.074	1289.457	-298.201	0.445	1334.712	0.364	16	0.177	K.TEEAKVEELIK.A
R3/RRR3-7/2	1309.163	1309.500	-258.180	0.404	1145.462	0.412	20	0.171	K.LLGGGLHNSSVVR.G
R3/RRR3-7/2	1425.163	1425.656	-346.959	0.438	856.236	0.504	21	0.166	R.IIPGAAATEIELAR.R
R3/RRR3-7/2	1183.117	1182.352	-198.757	0.428	978.004	0.422	18	0.162	K.HLSGLDEAVLK.N
R3/RRR3-7/2	1228.259	1229.387	-1737.584	0.341	1124.735	0.363	16	0.161	K.FAESFEM*VPR.T
R3/RRR3-7/2	1425.190	1425.656	-327.537	0.478	659.453	0.504	21	0.159	R.IIPGAAATEIELAR.R
R3/RRR3-7/2	1425.057	1425.656	-1125.393	0.424	685.456	0.507	21	0.159	R.IIPGAAATEIELAR.R
R3/RRR3-7/2	1321.204	1321.373	-128.127	0.366	1135.665	0.311	16	0.154	R.GSTDSILDDLER.A
R3/RRR3-7/2	1321.079	1321.373	-223.135	0.417	935.056	0.321	16	0.145	R.GSTDSILDDLER.A
R3/RRR3-7/2	1320.886	1321.373	-369.901	0.360	1190.714	0.197	18	0.143	R.GSTDSILDDLER.A
R3/RRR3-7/2	1288.064	1288.469	-315.830	0.218	848.912	0.255	14	0.131	K.TVEILEDLVEK.G
R3/RRR3-8/2	1932.719	1933.303	-822.280	0.520	2349.582	0.480	27	0.348	K.DPGAAMMLAELAM*EAGLPK.G
R3/RRR3-8/2	1444.283	1444.573	-201.134	0.503	2399.420	0.399	20	0.333	K.AESLDDAIQIVNR.N
R3/RRR3-8/2	1443.653	1444.573	-1333.693	0.392	2483.213	0.278	20	0.314	K.AESLDDAIQIVNR.N
R3/RRR3-8/2	1933.649	1933.303	179.440	0.567	2055.516	0.498	26	0.297	K.DPGAAMMLAELAM*EAGLPK.G
R3/RRR3-8/2	1444.192	1444.573	-264.476	0.501	2137.647	0.388	19	0.282	K.AESLDDAIQIVNR.N
R3/RRR3-8/3	1968.685	1968.071	-196.634	0.514	1707.451	0.550	32	0.225	R.ADEHVDVTNPATQEVVSR.I
R3/RRR3-8/2	1162.471	1163.305	-1582.247	0.464	1451.190	0.428	16	0.201	R.IPLTTADEFR.A
R3/RRR3-8/2	1203.655	1204.312	-1380.919	0.588	1168.056	0.556	18	0.201	K.LAENITTEQGK.T
R3/RRR3-8/2	1203.498	1204.312	-1511.929	0.552	1273.615	0.507	18	0.201	K.LAENITTEQGK.T
R3/RRR3-8/2	1290.212	1290.405	-150.659	0.498	1130.244	0.579	18	0.200	K.ASFAGDLNFYGK.A
R3/RRR3-9/2	1162.880	1163.305	-366.991	0.403	1455.777	0.411	16	0.198	R.IPLTTADEFR.A
R3/RRR3-8/2	1203.627	1204.312	-1404.755	0.535	1238.078	0.469	18	0.190	K.LAENITTEQGK.T
R3/RRR3-8/2	1162.507	1163.305	-1551.339	0.388	1387.812	0.393	16	0.188	R.IPLTTADEFR.A
R3/RRR3-8/2	1162.297	1163.305	-1732.593	0.404	1325.371	0.420	16	0.187	R.IPLTTADEFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1289.535	1290.405	-1454.444	0.355	1293.072	0.424	18	0.183	K.ASFAGDLNFYGK.A
R3/RRR3-9/2	1220.365	1220.400	-28.354	0.368	1323.508	0.356	17	0.175	R.LLIGGEFVESR.A
R3/RRR3-8/2	1588.155	1588.703	-977.593	0.454	1016.988	0.454	20	0.164	K.YGNGASIFTTSGVSAR.K
R3/RRR3-9/2	1162.373	1163.305	-1667.279	0.367	974.286	0.386	14	0.156	R.IPLTTADEFR.A
R3/RRR3-8/3	1967.744	1968.071	-166.924	0.444	1270.098	0.501	29	0.154	R.ADEHVDVTNPATQEVVSR.I
R3/RRR3-9/2	1219.758	1220.400	-1350.041	0.344	1151.648	0.288	17	0.154	R.LLIGGEFVESR.A
R3/RRR3-8/2	1139.112	1139.328	-190.313	0.332	1028.344	0.347	13	0.153	-.AGVQFFTQIK.-
R3/RRR3-8/2	1221.595	1220.400	160.101	0.409	776.486	0.399	18	0.152	R.LLIGGEFVESR.A
R3/RRR3-8/2	1139.163	1139.328	-145.378	0.390	969.062	0.360	13	0.152	-.AGVQFFTQIK.-
R3/RRR3-8/2	1139.186	1139.328	-125.491	0.421	1062.983	0.317	13	0.151	-.AGVQFFTQIK.-
R3/RRR3-8/3	1968.176	1968.071	53.236	0.450	1306.350	0.465	28	0.149	R.ADEHVDVTNPATQEVVSR.I
R3/RRR3-8/2	1094.002	1094.265	-241.163	0.369	835.962	0.349	14	0.145	R.VSLSM*PTSQK.-
R3/RRR3-8/2	1093.885	1094.265	-348.192	0.350	538.906	0.470	12	0.144	R.VSLSM*PTSQK.-
R3/RRR3-1/2	1290.118	1290.405	-223.745	0.385	401.330	0.417	12	0.137	-.ASFAGDLNFYGK.-
R3/RRR3-12/2	1102.172	1102.183	-10.621	0.387	863.115	0.249	15	0.136	-.LIQSGADNGAR.-
R3/RRR3-8/2	1948.609	1949.303	-871.627	0.381	627.125	0.397	15	0.135	K.DPGAAM*M*LAELAMEAGLPK.G
R3/RRR3-8/2	1220.499	1220.400	81.396	0.176	245.614	0.292	13	0.134	R.LLIGGEFVESR.A
R3/RRR3-6/2	1163.008	1163.305	-256.200	0.288	453.775	0.289	10	0.133	R.IPLTTADEFR.A
R3/RRR3-12/2	1102.147	1102.183	-32.728	0.337	741.945	0.175	14	0.128	-.LIQSGADNGAR.-
R3/RRR3-8/2	1931.995	1933.303	-1198.644	0.267	586.867	0.228	16	0.127	-.DPGAAM*MLAELAMEAGLPK.-
R3/RRR3-12/2	1101.180	1102.183	-1824.641	0.263	915.012	0.086	15	0.126	K.LIQSGADNGAR.V
R3/RRR3-8/3	1932.168	1933.303	-1108.752	0.322	1043.662	0.131	30	0.075	K.DPGAAMMLAELAM*EAGLPK.G
R3/RRR3-8/2	1708.719	1709.007	-169.147	0.598	2438.359	0.630	23	0.418	R.LVLEVAQHLGENMVR.T
R3/RRR3-8/2	1492.819	1493.647	-1227.762	0.425	2582.302	0.441	23	0.382	R.FTQANSEVSALLGR.I
R3/RRR3-9/2	1475.077	1474.791	193.987	0.495	2476.263	0.446	20	0.359	K.TVLIM*ELINNVAK.A
R3/RRR3-9/2	1493.298	1493.647	-234.215	0.522	2478.160	0.442	22	0.359	R.FTQANSEVSALLGR.I
R3/RRR3-8/2	1708.536	1709.007	-276.371	0.603	2183.419	0.608	22	0.356	R.LVLEVAQHLGENMVR.T
R3/RRR3-8/2	1475.204	1474.791	280.535	0.570	2329.423	0.516	20	0.351	K.TVLIM*ELINNVAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1458.592	1458.792	-137.548	0.527	2456.422	0.404	20	0.339	K.TVLIMELINNVAK.A
R3/RRR3-9/2	1459.301	1458.792	-337.500	0.556	2388.308	0.424	20	0.332	K.TVLIMELINNVAK.A
R3/RRR3-8/2	1457.925	1458.792	-1284.189	0.426	2367.209	0.420	20	0.330	K.TVLIMELINNVAK.A
R3/RRR3-9/2	1458.992	1458.792	137.743	0.525	2354.571	0.429	20	0.328	K.TVLIMELINNVAK.A
R3/RRR3-8/2	1865.481	1866.064	-851.033	0.536	2210.388	0.490	24	0.326	R.DAEGQDVLLFIDNIFR.F
R3/RRR3-8/2	1459.308	1458.792	-332.800	0.576	2388.754	0.411	20	0.326	K.TVLIMELINNVAK.A
R3/RRR3-8/2	1492.867	1493.647	-1195.902	0.443	2443.359	0.347	23	0.323	R.FTQANSEVSALLGR.I
R3/RRR3-8/2	1709.414	1709.007	238.754	0.616	1986.534	0.620	21	0.322	R.LVLEVAQHLGENMVR.T
R3/RRR3-8/2	1475.290	1474.791	339.028	0.570	2276.192	0.448	20	0.318	K.TVLIM*ELINNVAK.A
R3/RRR3-8/2	1458.131	1458.792	-1142.353	0.489	2199.393	0.439	20	0.304	K.TVLIMELINNVAK.A
R3/RRR3-8/2	1473.822	1474.791	-1340.311	0.417	2271.570	0.371	20	0.298	K.TVLIM*ELINNVAK.A
R3/RRR3-8/2	1492.809	1493.647	-1234.906	0.425	2164.358	0.424	22	0.296	R.FTQANSEVSALLGR.I
R3/RRR3-9/2	1493.242	1493.647	-272.105	0.499	2185.908	0.411	22	0.295	R.FTQANSEVSALLGR.I
R3/RRR3-8/2	1474.318	1474.791	-322.046	0.421	2284.190	0.330	20	0.288	K.TVLIM*ELINNVAK.A
R3/RRR3-8/2	1865.420	1866.064	-884.010	0.522	1860.859	0.546	23	0.282	R.DAEGQDVLLFIDNIFR.F
R3/RRR3-9/2	1474.707	1474.791	-57.279	0.465	2034.959	0.402	19	0.266	K.TVLIM*ELINNVAK.A
R3/RRR3-8/2	1392.141	1391.516	-270.319	0.559	1531.868	0.643	23	0.261	K.AHGGFSVFAGVGER.T
R3/RRR3-9/2	1474.288	1474.791	-1022.810	0.420	1977.919	0.348	19	0.245	K.TVLIM*ELINNVAK.A
R3/RRR3-8/2	1856.564	1857.040	-257.345	0.551	1438.503	0.611	23	0.239	R.M*LSPHVLGEDHYNTAR.G
R3/RRR3-8/2	1410.180	1410.644	-329.982	0.422	1619.262	0.494	23	0.233	R.VLNTGSPITVPVGR.A
R3/RRR3-8/2	1410.316	1410.644	-233.238	0.453	1453.282	0.521	22	0.220	R.VLNTGSPITVPVGR.A
R3/RRR3-8/2	1279.185	1279.446	-204.378	0.441	1435.165	0.518	20	0.218	R.TIAM*DGTEGLVR.G
R3/RRR3-8/2	1724.341	1725.007	-968.933	0.529	1207.331	0.633	22	0.218	R.LVLEVAQHLGENM*VR.T
R3/RRR3-9/2	1492.822	1493.647	-1226.202	0.432	1542.650	0.452	20	0.214	R.FTQANSEVSALLGR.I
R3/RRR3-8/2	1400.265	1400.608	-245.405	0.467	1356.853	0.522	19	0.210	R.VGLTGLTVAEHFR.D
R3/RRR3-8/2	1279.058	1279.446	-304.047	0.407	1349.672	0.515	19	0.207	R.TIAM*DGTEGLVR.G
R3/RRR3-8/2	1391.167	1391.516	-251.498	0.497	1228.101	0.554	24	0.206	K.AHGGFSVFAGVGER.T
R3/RRR3-8/2	1410.476	1410.644	-119.410	0.399	1302.772	0.535	22	0.205	R.VLNTGSPITVPVGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1724.484	1725.007	-885.570	0.537	1152.671	0.597	19	0.202	R.LVLEVAQHLGENM*VR.T
R3/RRR3-8/2	1856.410	1857.040	-880.757	0.573	1032.197	0.600	23	0.195	R.M*LSPHVLGEDHYNTAR.G
R3/RRR3-8/2	1391.954	1391.516	315.459	0.526	941.627	0.620	23	0.194	K.AHGGFSVFAGVGER.T
R3/RRR3-8/2	1411.190	1410.644	-322.805	0.410	1258.631	0.483	20	0.191	R.VLNTGSPITVPVGR.A
R3/RRR3-8/3	1866.077	1866.064	6.973	0.484	1785.790	0.423	34	0.191	R.DAEGQDVLLFIDNIFR.F
R3/RRR3-8/2	1400.108	1400.608	-358.065	0.451	1175.119	0.526	17	0.191	R.VGLTGLTVAEHFR.D
R3/RRR3-8/2	1724.491	1725.007	-881.236	0.472	1110.916	0.548	21	0.190	R.LVLEVAQHLGENM*VR.T
R3/RRR3-8/2	1856.478	1857.040	-843.990	0.564	1039.107	0.573	23	0.190	R.M*LSPHVLGEDHYNTAR.G
R3/RRR3-8/2	1401.218	1400.608	-279.053	0.501	1095.907	0.542	17	0.187	R.VGLTGLTVAEHFR.D
R3/RRR3-8/3	1840.247	1841.041	-977.745	0.493	1562.603	0.505	32	0.186	R.MLSPHVLGEDHYNTAR.G
R3/RRR3-2/2	1410.282	1410.644	-257.466	0.413	1151.505	0.483	20	0.182	R.VLNTGSPITVPVGR.A
R3/RRR3-8/2	1263.177	1263.447	-213.881	0.487	1312.061	0.393	18	0.180	R.TIAMDGTEGLVR.G
R3/RRR3-8/2	1279.075	1279.446	-291.025	0.408	1085.191	0.490	18	0.179	R.TIAM*DGTEGLVR.G
R3/RRR3-9/2	1279.067	1279.446	-297.057	0.401	1106.520	0.471	18	0.177	R.TIAM*DGTEGLVR.G
R3/RRR3-9/2	1279.267	1279.446	-140.527	0.381	1093.096	0.461	18	0.174	R.TIAM*DGTEGLVR.G
R3/RRR3-8/2	976.010	976.154	-148.667	0.437	1142.777	0.427	17	0.174	K.IGLFGGAGVGK.T
R3/RRR3-9/2	1279.276	1279.446	-133.348	0.409	1066.413	0.464	18	0.174	R.TIAM*DGTEGLVR.G
R3/RRR3-9/2	1410.255	1410.644	-277.005	0.394	1080.745	0.457	20	0.172	R.VLNTGSPITVPVGR.A
R3/RRR3-9/2	975.504	976.154	-1697.175	0.402	1015.372	0.432	16	0.165	K.IGLFGGAGVGK.T
R3/RRR3-9/2	976.125	976.154	-29.992	0.452	1006.059	0.430	16	0.165	K.IGLFGGAGVGK.T
R3/RRR3-8/2	975.649	976.154	-1547.209	0.441	1083.533	0.387	17	0.164	K.IGLFGGAGVGK.T
R3/RRR3-8/2	1174.142	1174.374	-198.399	0.514	894.326	0.456	15	0.163	K.VVDLLAPYQR.G
R3/RRR3-8/2	975.328	976.154	-1878.501	0.434	955.992	0.435	16	0.163	K.IGLFGGAGVGK.T
R3/RRR3-8/3	1840.811	1841.041	-125.490	0.525	1465.699	0.455	31	0.161	R.MLSPHVLGEDHYNTAR.G
R3/RRR3-9/2	975.261	976.154	-1946.798	0.402	895.437	0.431	15	0.158	K.IGLFGGAGVGK.T
R3/RRR3-12/2	976.050	976.154	-107.517	0.400	989.889	0.385	16	0.158	K.IGLFGGAGVGK.T
R3/RRR3-9/2	1410.132	1410.644	-1075.310	0.387	846.358	0.440	18	0.156	R.VLNTGSPITVPVGR.A
R3/RRR3-3/2	1411.622	1410.644	-15.839	0.321	870.666	0.446	18	0.156	R.VLNTGSPITVPVGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1174.106	1174.374	-229.168	0.462	968.108	0.342	16	0.152	K.VVDLLAPYQR.G
R3/RRR3-8/2	1411.375	1410.644	-191.076	0.351	1015.547	0.346	18	0.152	R.VLNTGSPITVPVGR.A
R3/RRR3-8/3	1856.940	1857.040	-53.958	0.518	1195.906	0.521	29	0.151	R.M*LSPHVLGEDHYNTAR.G
R3/RRR3-8/3	1709.990	1709.007	-9.968	0.445	1005.148	0.620	34	0.151	R.LVLEVAQHLGENMVR.T
R3/RRR3-8/2	1493.378	1493.647	-180.338	0.351	981.373	0.337	17	0.149	R.FTQANSEVSALLGR.I
R3/RRR3-8/3	1857.959	1857.040	-43.780	0.498	1354.190	0.445	29	0.148	R.M*LSPHVLGEDHYNTAR.G
R3/RRR3-7/2	1410.265	1410.644	-269.710	0.376	881.835	0.350	18	0.147	R.VLNTGSPITVPVGR.A
R3/RRR3-8/2	1174.254	1174.374	-102.871	0.443	738.612	0.373	14	0.146	K.VVDLLAPYQR.G
R3/RRR3-8/3	1725.599	1725.007	-236.921	0.476	1055.453	0.526	32	0.138	R.LVLEVAQHLGENM*VR.T
R3/RRR3-9/3	1400.610	1400.608	1.511	0.483	1130.869	0.489	28	0.135	R.VGLTGLTVAEHFR.D
R3/RRR3-8/2	975.890	976.154	-271.387	0.267	552.657	0.349	12	0.135	-.IGLFGGAGVGK.-
R3/RRR3-8/3	1400.699	1400.608	65.233	0.495	1086.953	0.496	27	0.135	R.VGLTGLTVAEHFR.D
R3/RRR3-16/2	1493.448	1493.647	-133.599	0.340	812.293	0.232	17	0.134	R.FTQANSEVSALLGR.I
R3/RRR3-15/2	1492.546	1493.647	-1411.821	0.312	723.768	0.213	18	0.133	R.FTQANSEVSALLGR.I
R3/RRR3-2/2	1411.253	1410.644	-278.023	0.281	626.358	0.243	15	0.132	R.VLNTGSPITVPVGR.A
R3/RRR3-8/2	1391.314	1391.516	-145.783	0.241	573.818	0.215	17	0.131	K.AHGGFSVFAGVGER.T
R3/RRR3-8/3	1709.001	1709.007	-3.276	0.454	937.769	0.534	34	0.130	R.LVLEVAQHLGENMVR.T
R3/RRR3-8/2	1391.970	1391.516	327.154	0.245	410.367	0.306	12	0.128	-.AHGGFSVFAGVGER.-
R3/RRR3-8/3	1840.826	1841.041	-117.208	0.514	1016.591	0.470	27	0.127	R.MLSPHVLGEDHYNTAR.G
R3/RRR3-8/3	1857.216	1857.040	94.974	0.504	917.963	0.497	26	0.126	R.M*LSPHVLGEDHYNTAR.G
R3/RRR3-8/3	1400.811	1400.608	145.465	0.511	1088.909	0.431	28	0.122	R.VGLTGLTVAEHFR.D
R3/RRR3-9/3	1401.608	1400.608	-0.107	0.473	808.546	0.475	25	0.117	R.VGLTGLTVAEHFR.D
R3/RRR3-8/3	1400.359	1400.608	-178.162	0.464	814.553	0.471	25	0.116	R.VGLTGLTVAEHFR.D
R3/RRR3-9/3	1400.677	1400.608	49.631	0.468	678.706	0.494	23	0.115	R.VGLTGLTVAEHFR.D
R3/RRR3-8/3	1495.104	1493.647	307.076	0.447	1069.545	0.370	25	0.109	-.FTQANSEVSALLGR.-
R3/RRR3-8/3	1708.869	1709.007	-80.978	0.382	385.852	0.461	25	0.106	R.LVLEVAQHLGENMVR.T
R3/RRR3-8/3	1724.509	1725.007	-289.218	0.405	770.484	0.384	26	0.102	R.LVLEVAQHLGENM*VR.T
R3/RRR3-8/3	1474.613	1474.791	-121.391	0.378	930.440	0.330	23	0.097	K.TVLIM*ELINNVAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/3	1474.532	1474.791	-176.698	0.412	596.584	0.264	22	0.081	-.TVLIM*ELINNVAK.-
R3/RRR3-5/3	1952.262	1951.170	47.336	0.587	3023.222	0.561	34	0.531	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1952.976	1951.170	-99.970	0.631	2063.711	0.559	23	0.314	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1241.085	1241.379	-237.813	0.543	1953.271	0.544	20	0.299	K.IDNPIGATNIGR.A
R3/RRR3-5/2	1240.993	1241.379	-311.826	0.535	1964.507	0.535	20	0.298	K.IDNPIGATNIGR.A
R3/RRR3-5/2	1859.501	1860.057	-839.548	0.562	1787.038	0.555	25	0.274	R.AYLPVQELLNGEEIDR.W
R3/RRR3-5/3	1951.416	1951.170	126.443	0.492	2316.240	0.367	29	0.266	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1240.986	1241.379	-317.452	0.517	1746.923	0.497	20	0.254	K.IDNPIGATNIGR.A
R3/RRR3-5/2	1859.398	1860.057	-895.170	0.568	1646.119	0.509	24	0.241	R.AYLPVQELLNGEEIDR.W
R3/RRR3-5/2	1860.363	1860.057	164.822	0.615	1450.429	0.586	23	0.234	R.AYLPVQELLNGEEIDR.W
R3/RRR3-5/2	1950.667	1951.170	-772.756	0.586	1544.644	0.537	21	0.230	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1949.880	1951.170	-1178.076	0.515	1642.371	0.461	21	0.225	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1949.925	1951.170	-1154.942	0.504	1508.370	0.522	22	0.224	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1406.515	1406.561	-32.697	0.487	1689.920	0.412	17	0.224	R.DYLTFFCLGNR.E
R3/RRR3-6/2	1952.942	1951.170	-117.463	0.447	1563.174	0.464	20	0.217	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1200.965	1201.378	-345.306	0.457	1652.797	0.329	17	0.203	-.M*ITNEPINPR.W
R3/RRR3-5/2	1288.196	1287.449	-196.991	0.480	1351.151	0.435	16	0.192	R.SIQDAYIHAIR.R
R3/RRR3-5/2	1881.003	1880.989	7.446	0.558	951.617	0.646	22	0.192	R.SIDGGAAFGFPDTPEEAAK.A
R3/RRR3-5/2	1288.117	1287.449	-259.262	0.452	1384.976	0.364	16	0.182	R.SIQDAYIHAIR.R
R3/RRR3-5/2	1372.282	1372.553	-197.947	0.461	1091.938	0.490	18	0.178	K.AGLVSGKDQIIDR.S
R3/RRR3-5/2	1880.360	1880.989	-868.847	0.491	854.921	0.611	22	0.178	R.SIDGGAAFGFPDTPEEAAK.A
R3/RRR3-5/2	1288.442	1287.449	-5.950	0.416	1146.762	0.435	17	0.175	R.SIQDAYIHAIR.R
R3/RRR3-5/2	1406.351	1406.561	-149.970	0.406	1002.637	0.475	14	0.168	R.DYLTFFCLGNR.E
R3/RRR3-5/2	1880.421	1880.989	-836.263	0.479	669.985	0.618	19	0.165	R.SIDGGAAFGFPDTPEEAAK.A
R3/RRR3-5/2	1201.018	1201.378	-300.945	0.450	1165.767	0.340	16	0.162	-.M*ITNEPINPR.W
R3/RRR3-5/2	1951.758	1951.170	-211.694	0.433	983.202	0.420	19	0.159	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1858.432	1858.086	186.668	0.485	587.904	0.566	17	0.156	K.VTLYQDAHVPDNFIPK.I
R3/RRR3-2/2	1950.743	1951.170	-219.587	0.452	975.893	0.375	17	0.150	R.LEGPIAWDVLYNFEQR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1463.671	1462.633	25.964	0.427	529.955	0.433	18	0.148	K.YPGVPYTFFSQR.Q
R3/RRR3-1/2	1951.476	1951.170	157.378	0.384	755.842	0.425	16	0.146	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/2	1462.135	1462.633	-341.200	0.361	521.722	0.439	18	0.146	K.YPGVPYTFFSQR.Q
R3/RRR3-5/2	1406.481	1406.561	-57.246	0.321	722.988	0.404	16	0.146	R.DYLTFFCLGNR.E
R3/RRR3-5/2	1200.400	1201.378	-1652.961	0.357	921.724	0.275	15	0.142	-.M*ITNEPINPR.-
R3/RRR3-5/2	1857.473	1858.086	-871.379	0.457	408.381	0.486	13	0.139	K.VTLYQDAHVPDNFIPK.I
R3/RRR3-5/2	1462.433	1462.633	-137.354	0.376	344.366	0.416	14	0.139	-.YPGVPYTFFSQR.-
R3/RRR3-5/3	1819.877	1820.000	-67.864	0.469	1031.886	0.526	29	0.138	K.IVVVDHELPNQGSQQR.R
R3/RRR3-5/2	1857.444	1858.086	-887.147	0.414	504.335	0.416	15	0.137	K.VTLYQDAHVPDNFIPK.I
R3/RRR3-1/2	1951.319	1951.170	76.198	0.394	606.157	0.380	14	0.137	R.LEGPIAWDVLYNFEQR.W
R3/RRR3-5/3	1819.366	1820.000	-900.607	0.404	985.171	0.472	29	0.122	K.IVVVDHELPNQGSQQR.R
R3/RRR3-5/3	1820.113	1820.000	62.410	0.455	790.329	0.496	27	0.118	K.IVVVDHELPNQGSQQR.R
R3/RRR3-15/3	1529.617	1529.764	-96.471	0.591	2606.851	0.591	34	0.422	K.VKIQLGEGSAAQVTK.N
R3/RRR3-15/2	1461.054	1460.637	286.337	0.546	2158.076	0.470	20	0.308	K.NM*LANEGIGSFYK.G
R3/RRR3-15/3	1529.314	1529.764	-294.998	0.550	2178.369	0.553	31	0.308	K.VKIQLGEGSAAQVTK.N
R3/RRR3-15/2	1529.374	1529.764	-255.750	0.508	1670.468	0.439	23	0.229	K.VKIQLGEGSAAQVTK.N
R3/RRR3-15/2	1328.300	1328.581	-212.336	0.517	1485.414	0.527	20	0.226	R.IIADEGVLALWK.G
R3/RRR3-15/2	1303.329	1302.459	-100.011	0.524	1483.980	0.499	22	0.221	K.IQLGEGSAAQVTK.N
R3/RRR3-15/2	1328.156	1328.581	-321.507	0.519	1506.654	0.471	20	0.216	R.IIADEGVLALWK.G
R3/RRR3-15/2	1302.122	1302.459	-259.388	0.507	1465.995	0.485	21	0.215	K.IQLGEGSAAQVTK.N
R3/RRR3-15/2	1328.354	1328.581	-171.956	0.537	1464.748	0.465	20	0.210	R.IIADEGVLALWK.G
R3/RRR3-15/2	1328.278	1328.581	-229.208	0.546	1340.048	0.520	19	0.209	R.IIADEGVLALWK.G
R3/RRR3-15/2	1301.635	1302.459	-1405.744	0.456	1399.183	0.479	21	0.206	K.IQLGEGSAAQVTK.N
R3/RRR3-15/2	1745.262	1744.890	213.715	0.584	967.033	0.662	23	0.201	K.QQQQQQTAAAATGVWK.T
R3/RRR3-15/2	1650.406	1650.944	-934.488	0.543	1361.665	0.485	21	0.201	K.AIEKNDGKPLPLVQK.A
R3/RRR3-15/2	1331.212	1331.524	-235.049	0.496	1401.635	0.448	20	0.201	R.MQADSTLPIAQR.R
R3/RRR3-15/2	1328.217	1328.581	-275.217	0.524	1342.248	0.480	19	0.200	R.IIADEGVLALWK.G
R3/RRR3-15/2	1745.373	1744.890	277.958	0.577	979.550	0.646	22	0.198	K.QQQQQQTAAAATGVWK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1302.183	1302.459	-212.928	0.511	1264.593	0.457	20	0.189	K.IQLGEGSAAQVTK.N
R3/RRR3-15/2	1347.079	1347.523	-330.725	0.494	1150.457	0.473	19	0.183	R.M*QADSTLPIAQR.R
R3/RRR3-15/2	1650.454	1650.944	-297.744	0.532	1146.135	0.479	20	0.180	K.AIEKNDGKPLPLVQK.A
R3/RRR3-14/2	1328.319	1328.581	-198.046	0.430	1326.480	0.380	18	0.180	R.IIADEGVLALWK.G
R3/RRR3-14/2	1327.956	1328.581	-1227.504	0.500	1071.157	0.496	17	0.179	R.IIADEGVLALWK.G
R3/RRR3-15/2	1331.940	1331.524	313.495	0.510	1156.220	0.445	19	0.178	R.MQADSTLPIAQR.R
R3/RRR3-15/2	1348.146	1347.523	-280.513	0.531	1032.636	0.488	18	0.176	R.M*QADSTLPIAQR.R
R3/RRR3-15/2	1746.143	1744.890	145.523	0.569	699.885	0.618	22	0.175	K.QQQQQQTAAAATGVWK.T
R3/RRR3-15/2	1330.535	1331.524	-1499.623	0.408	1131.331	0.424	18	0.172	R.MQADSTLPIAQR.R
R3/RRR3-15/2	1410.017	1409.607	291.707	0.546	1015.421	0.466	17	0.172	K.FYTGFPVYCVR.I
R3/RRR3-15/2	1410.195	1409.607	-292.905	0.545	967.304	0.491	16	0.172	K.FYTGFPVYCVR.I
R3/RRR3-15/2	1347.093	1347.523	-320.451	0.512	972.983	0.474	18	0.170	R.M*QADSTLPIAQR.R
R3/RRR3-14/2	1329.104	1328.581	-360.520	0.463	847.177	0.450	17	0.160	R.IIADEGVLALWK.G
R3/RRR3-15/2	1328.040	1328.581	-1164.090	0.381	957.312	0.387	17	0.156	R.IIADEGVLALWK.G
R3/RRR3-15/2	1461.478	1460.637	-109.336	0.493	651.606	0.450	18	0.152	K.NM*LANEGIGSFYK.G
R3/RRR3-15/2	1444.209	1444.638	-297.875	0.416	1465.905	0.127	20	0.148	K.NMLANEGIGSFYK.G
R3/RRR3-15/2	1208.681	1209.420	-1443.351	0.391	511.002	0.450	16	0.148	K.NDGKPLPLVQK.A
R3/RRR3-15/2	1208.560	1209.420	-1543.790	0.390	436.105	0.469	15	0.147	K.NDGKPLPLVQK.A
R3/RRR3-15/2	1460.120	1460.637	-1041.891	0.449	970.863	0.336	16	0.147	K.NM*LANEGIGSFYK.G
R3/RRR3-15/2	991.886	992.115	-232.386	0.375	981.549	0.288	13	0.146	K.NAFHALYR.I
R3/RRR3-15/2	1460.740	1460.637	70.483	0.490	919.555	0.335	17	0.145	K.NM*LANEGIGSFYK.G
R3/RRR3-15/2	1209.160	1209.420	-216.145	0.413	537.047	0.403	16	0.145	K.NDGKPLPLVQK.A
R3/RRR3-15/2	991.412	992.115	-1723.478	0.410	699.862	0.347	13	0.145	K.NAFHALYR.I
R3/RRR3-15/3	1744.527	1744.890	-208.740	0.485	1160.993	0.503	30	0.143	K.QQQQQQTAAAATGVWK.T
R3/RRR3-15/2	991.466	992.115	-1668.183	0.349	632.293	0.306	12	0.139	K.NAFHALYR.I
R3/RRR3-15/2	1409.223	1409.607	-273.211	0.319	664.256	0.325	14	0.137	K.FYTGFPVYCVR.I
R3/RRR3-15/3	1744.704	1744.890	-106.613	0.411	1205.535	0.385	29	0.121	K.QQQQQQTAAAATGVWK.T
R3/RRR3-15/3	1744.022	1744.890	-1074.235	0.308	538.969	0.383	25	0.095	K.QQQQQQTAAAATGVWK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1290.736	1291.478	-1353.300	0.430	2075.699	0.554	19	0.318	R.AIADGSLLDFLR.Q
R3/RRR3-4/2	1291.330	1291.478	-115.162	0.538	1942.728	0.570	19	0.301	R.AIADGSLLDFLR.Q
R3/RRR3-4/2	1291.341	1291.478	-106.628	0.522	1928.657	0.525	19	0.285	R.AIADGSLLDFLR.Q
R3/RRR3-5/2	1291.741	1291.478	204.297	0.479	1702.737	0.519	19	0.250	R.AIADGSLLDFLR.Q
R3/RRR3-4/2	1328.345	1328.497	-114.811	0.510	1523.904	0.494	20	0.223	K.LADLESAPAALTR.L
R3/RRR3-4/2	1078.058	1077.212	-143.396	0.493	1485.396	0.502	16	0.220	K.SPAEVFDALK.S
R3/RRR3-4/2	1328.212	1328.497	-215.116	0.472	1408.938	0.458	20	0.203	K.LADLESAPAALTR.L
R3/RRR3-4/2	1886.345	1886.995	-877.124	0.533	1278.497	0.515	23	0.200	K.DITPDDKQELDEALQR.E
R3/RRR3-3/2	1292.055	1291.478	-328.026	0.455	1294.238	0.503	16	0.197	R.AIADGSLLDFLR.Q
R3/RRR3-4/2	1329.201	1328.497	-223.246	0.520	1282.504	0.497	19	0.197	K.LADLESAPAALTR.L
R3/RRR3-1/2	1077.726	1077.212	-452.450	0.381	1214.630	0.520	15	0.193	K.SPAEVFDALK.S
R3/RRR3-3/2	1077.461	1077.212	231.290	0.407	1217.041	0.510	14	0.192	K.SPAEVFDALK.S
R3/RRR3-4/2	1852.374	1853.070	-918.129	0.522	1086.431	0.578	20	0.190	K.SQTVDLVLTAHPTQSVR.R
R3/RRR3-2/2	1292.257	1291.478	-171.928	0.318	1284.900	0.485	16	0.190	R.AIADGSLLDFLR.Q
R3/RRR3-4/2	1886.444	1886.995	-824.832	0.512	1282.659	0.473	21	0.190	K.DITPDDKQELDEALQR.E
R3/RRR3-4/2	1852.742	1853.070	-177.277	0.520	1040.699	0.574	19	0.185	K.SQTVDLVLTAHPTQSVR.R
R3/RRR3-1/2	1290.921	1291.478	-1209.892	0.337	1187.179	0.448	17	0.177	R.AIADGSLLDFLR.Q
R3/RRR3-3/2	1077.999	1077.212	-198.262	0.292	1004.878	0.508	14	0.170	K.SPAEVFDALK.S
R3/RRR3-1/2	1078.016	1077.212	-182.245	0.428	967.242	0.473	13	0.167	K.SPAEVFDALK.S
R3/RRR3-1/2	1077.611	1077.212	371.463	0.314	835.749	0.432	13	0.152	-.SPAEVFDALK.-
R3/RRR3-4/3	1886.526	1886.995	-249.330	0.514	1403.391	0.439	29	0.151	K.DITPDDKQELDEALQR.E
R3/RRR3-3/2	1329.042	1328.497	-343.310	0.340	1359.682	0.182	18	0.150	K.LADLESAPAALTR.L
R3/RRR3-2/2	1291.810	1291.478	257.931	0.344	515.246	0.480	13	0.146	R.AIADGSLLDFLR.Q
R3/RRR3-1/2	1292.019	1291.478	-356.275	0.337	576.128	0.430	15	0.146	R.AIADGSLLDFLR.Q
R3/RRR3-4/2	1125.343	1125.293	44.215	0.471	634.259	0.402	13	0.145	R.NCLVQLYSK.D
R3/RRR3-3/2	1291.758	1291.478	217.658	0.379	602.160	0.278	15	0.137	R.AIADGSLLDFLR.Q
R3/RRR3-3/2	1292.089	1291.478	-302.243	0.177	503.511	0.277	13	0.132	R.AIADGSLLDFLR.Q
R3/RRR3-4/3	1887.727	1886.995	-142.283	0.542	1254.068	0.407	28	0.130	K.DITPDDKQELDEALQR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1077.493	1077.212	261.282	0.182	355.908	0.320	10	0.129	-.SPAEVFDALK.-
R3/RRR3-4/3	1887.114	1886.995	63.244	0.464	1336.765	0.335	29	0.121	K.DITPDDKQELDEALQR.E
R3/RRR3-5/2	1077.109	1077.212	-96.235	0.374	354.271	0.360	10	0.120	-.SPAEVFDALK.-
R3/RRR3-4/3	1168.478	1168.373	89.881	0.442	1020.010	0.363	21	0.106	K.RPLFGPDLPR.T
R3/RRR3-4/3	1168.458	1168.373	73.064	0.458	1054.455	0.296	22	0.098	K.RPLFGPDLPR.T
R3/RRR3-4/3	1168.313	1168.373	-51.269	0.384	873.765	0.190	19	0.084	K.RPLFGPDLPR.T
R3/RRR3-6/2	1582.517	1582.844	-206.775	0.501	919.655	0.390	20	0.154	K.QFSAEEISSMVLIK.M
R3/RRR3-6/2	1582.646	1582.844	-125.451	0.513	990.640	0.358	21	0.153	K.QFSAEEISSMVLIK.M
R3/RRR3-6/2	1598.722	1598.843	-75.878	0.451	637.857	0.317	17	0.136	K.QFSAEEISSM*VLIK.M
R3/RRR3-6/3	1744.198	1743.940	148.415	0.540	2886.290	0.545	33	0.485	K.DNLGGDKLVTVEDIVR.Q
R3/RRR3-6/2	1316.038	1316.355	-241.853	0.527	1983.562	0.546	20	0.306	R.YDYENVDAGAAK.E
R3/RRR3-6/3	1986.137	1986.216	-40.052	0.509	2119.219	0.514	33	0.285	K.NKDNLGGDKLVTVEDIVR.Q
R3/RRR3-6/2	1725.240	1725.815	-915.924	0.576	1673.280	0.600	24	0.269	K.YNM*ENGGPAPESVTDK.I
R3/RRR3-6/2	1743.376	1743.940	-899.613	0.557	1752.046	0.532	23	0.262	K.DNLGGDKLVTVEDIVR.Q
R3/RRR3-6/2	1725.225	1725.815	-924.590	0.577	1445.969	0.605	23	0.239	K.YNM*ENGGPAPESVTDK.I
R3/RRR3-6/3	1986.183	1986.216	-16.750	0.529	1691.067	0.515	30	0.211	K.NKDNLGGDKLVTVEDIVR.Q
R3/RRR3-6/3	1985.592	1986.216	-820.186	0.516	1734.435	0.479	31	0.206	K.NKDNLGGDKLVTVEDIVR.Q
R3/RRR3-6/2	1031.952	1032.133	-175.668	0.431	1361.666	0.473	18	0.201	K.GATIVVSGDGR.Y
R3/RRR3-6/2	1031.230	1032.133	-1850.814	0.460	1165.514	0.476	17	0.184	K.GATIVVSGDGR.Y
R3/RRR3-6/2	1556.334	1555.755	-271.066	0.496	961.444	0.476	20	0.167	R.DSQDALAPLVDVALK.L
R3/RRR3-6/2	1306.146	1306.511	-280.717	0.441	637.453	0.569	19	0.165	R.SM*PTSAALDVVAK.N
R3/RRR3-6/2	888.063	888.044	21.217	0.485	1037.977	0.389	13	0.163	K.DAVQIITK.M
R3/RRR3-6/2	1555.424	1555.755	-213.447	0.358	1215.829	0.327	21	0.161	R.DSQDALAPLVDVALK.L
R3/RRR3-6/2	1305.973	1306.511	-1181.328	0.415	635.242	0.509	19	0.158	R.SM*PTSAALDVVAK.N
R3/RRR3-6/2	1555.263	1555.755	-317.070	0.258	1369.823	0.225	22	0.157	R.DSQDALAPLVDVALK.L
R3/RRR3-6/2	1306.048	1306.511	-355.922	0.397	681.291	0.496	19	0.157	R.SM*PTSAALDVVAK.N
R3/RRR3-6/2	1291.059	1290.512	-351.703	0.378	439.198	0.422	18	0.146	R.SMPTSAALDVVAK.N
R3/RRR3-6/2	1043.451	1044.227	-1707.223	0.359	653.308	0.348	15	0.143	K.LVTVEDIVR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1119.003	1119.254	-225.026	0.330	737.795	0.370	17	0.143	R.LSGTGSVGATIR.V
R3/RRR3-6/2	1043.710	1044.227	-1457.753	0.326	690.418	0.324	15	0.141	K.LVTVEDIVR.Q
R3/RRR3-6/2	887.941	888.044	-116.255	0.392	954.877	0.246	13	0.141	K.DAVQIITK.M
R3/RRR3-6/2	1290.133	1290.512	-294.160	0.376	465.165	0.301	18	0.139	R.SMPTSAALDVVAK.N
R3/RRR3-6/2	1043.475	1044.227	-1683.834	0.318	593.441	0.287	14	0.137	K.LVTVEDIVR.Q
R3/RRR3-6/2	1290.022	1290.512	-381.028	0.308	412.676	0.281	16	0.137	R.SMPTSAALDVVAK.N
R3/RRR3-12/2	1119.639	1119.254	345.053	0.309	336.010	0.297	14	0.108	-.LSGTGSVGATIR.-
R3/RRR3-6/3	1761.523	1761.960	-248.777	0.439	972.580	0.376	26	0.107	K.KATTPFDGQKPGTSGLR.K
R3/RRR3-6/3	1761.792	1761.960	-95.606	0.420	902.638	0.357	27	0.101	K.KATTPFDGQKPGTSGLR.K
R3/RRR3-6/3	1761.079	1761.960	-1071.687	0.321	869.006	0.198	24	0.082	K.KATTPFDGQKPGTSGLR.K
R3/RRR3-11/2	1685.438	1684.961	284.356	0.597	3004.788	0.594	26	0.554	R.ILVTGGAGFIGSHLVDK.L
R3/RRR3-11/2	1446.327	1445.753	-295.661	0.597	2041.407	0.552	23	0.311	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/2	1204.938	1204.404	-387.815	0.653	2106.411	0.517	19	0.309	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1461.116	1461.753	-1123.883	0.512	2017.678	0.520	23	0.299	K.TNVIGTLNM*LGLAK.R
R3/RRR3-11/2	1461.365	1461.753	-266.179	0.528	2050.645	0.501	23	0.299	K.TNVIGTLNM*LGLAK.R
R3/RRR3-11/2	1445.397	1445.753	-247.060	0.575	2056.634	0.500	23	0.298	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/2	1203.803	1204.404	-1333.659	0.527	2121.794	0.439	19	0.291	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1445.548	1445.753	-142.177	0.542	1994.500	0.496	23	0.288	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/2	1461.301	1461.753	-309.927	0.519	1954.670	0.504	23	0.284	K.TNVIGTLNM*LGLAK.R
R3/RRR3-11/2	1204.212	1204.404	-159.384	0.552	1977.777	0.484	19	0.281	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1205.570	1204.404	138.465	0.547	2030.042	0.438	19	0.276	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1633.403	1633.884	-295.250	0.458	1999.263	0.375	22	0.258	R.SFCYVADM*VNGLIK.L
R3/RRR3-11/3	1445.590	1445.753	-113.427	0.516	2311.255	0.347	30	0.249	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/3	1445.746	1445.753	-5.185	0.499	2253.402	0.358	31	0.241	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/2	1617.400	1617.885	-300.574	0.474	1780.893	0.416	21	0.236	R.SFCYVADMVNGLIK.L
R3/RRR3-11/2	1634.215	1633.884	203.119	0.557	1796.632	0.406	21	0.234	R.SFCYVADM*VNGLIK.L
R3/RRR3-13/2	1204.055	1204.404	-290.378	0.396	1739.664	0.367	18	0.219	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1633.970	1633.884	52.836	0.498	1631.961	0.392	20	0.211	R.SFCYVADM*VNGLIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1204.349	1204.404	-45.098	0.387	1474.912	0.424	17	0.201	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1156.395	1157.344	-1690.510	0.483	1291.699	0.494	16	0.199	K.AKEVLGWEPK.I
R3/RRR3-11/2	1157.245	1157.344	-85.339	0.491	1368.651	0.427	16	0.193	K.AKEVLGWEPK.I
R3/RRR3-10/2	1446.832	1445.753	54.869	0.482	1313.898	0.446	20	0.189	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/2	1512.289	1512.693	-268.273	0.470	937.336	0.574	21	0.183	R.GEPLTVQKPGTQTR.S
R3/RRR3-11/2	1512.705	1512.693	7.559	0.488	950.842	0.551	21	0.181	R.GEPLTVQKPGTQTR.S
R3/RRR3-11/2	1512.357	1512.693	-222.925	0.481	956.320	0.547	21	0.180	R.GEPLTVQKPGTQTR.S
R3/RRR3-11/2	1512.205	1512.693	-323.507	0.456	920.456	0.562	20	0.179	R.GEPLTVQKPGTQTR.S
R3/RRR3-10/2	1512.164	1512.693	-1014.008	0.429	1025.839	0.500	21	0.176	R.GEPLTVQKPGTQTR.S
R3/RRR3-10/2	1512.442	1512.693	-166.569	0.454	924.150	0.538	21	0.176	R.GEPLTVQKPGTQTR.S
R3/RRR3-3/2	1205.249	1204.404	-128.975	0.369	1188.533	0.379	16	0.168	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1157.042	1157.344	-261.225	0.505	1128.082	0.391	15	0.167	K.AKEVLGWEPK.I
R3/RRR3-2/2	1204.160	1204.404	-203.113	0.409	1113.769	0.350	15	0.159	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1513.359	1512.693	-221.564	0.438	639.005	0.512	18	0.157	R.GEPLTVQKPGTQTR.S
R3/RRR3-13/2	967.785	968.091	-316.357	0.438	856.325	0.376	13	0.154	R.IFNTYGPR.M
R3/RRR3-12/2	1204.294	1204.404	-91.562	0.436	833.763	0.394	16	0.153	R.VVSNFIAQAVR.G
R3/RRR3-11/2	967.905	968.091	-192.478	0.409	898.106	0.353	13	0.153	R.IFNTYGPR.M
R3/RRR3-4/2	1205.013	1204.404	-324.998	0.397	980.136	0.340	16	0.152	R.VVSNFIAQAVR.G
R3/RRR3-12/2	967.276	968.091	-1881.796	0.396	656.856	0.443	11	0.150	-.IFNTYGPR.-
R3/RRR3-10/2	968.203	968.091	116.517	0.409	658.722	0.407	11	0.150	R.IFNTYGPR.M
R3/RRR3-9/2	1204.045	1204.404	-298.617	0.325	910.618	0.337	18	0.149	R.VVSNFIAQAVR.G
R3/RRR3-10/2	967.735	968.091	-368.626	0.375	653.523	0.399	12	0.149	R.IFNTYGPR.M
R3/RRR3-11/2	1311.607	1310.458	113.641	0.383	649.214	0.442	16	0.149	R.DGLVLMEDDFR.E
R3/RRR3-12/2	967.953	968.091	-142.252	0.437	711.251	0.364	12	0.148	R.IFNTYGPR.M
R3/RRR3-2/2	1204.088	1204.404	-262.814	0.416	744.395	0.380	15	0.148	R.VVSNFIAQAVR.G
R3/RRR3-11/3	1564.467	1564.724	-164.678	0.463	1463.386	0.408	29	0.147	K.HEVIVADNFFTGSK.D
R3/RRR3-11/2	1311.570	1310.458	85.639	0.303	756.908	0.416	15	0.146	R.DGLVLMEDDFR.E
R3/RRR3-9/2	1204.360	1204.404	-36.152	0.316	285.040	0.421	13	0.145	R.VVSNFIAQAVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	967.861	968.091	-238.407	0.411	644.614	0.362	12	0.144	-.IFNTYGPR.-
R3/RRR3-11/2	968.081	968.091	-10.069	0.434	584.059	0.385	11	0.144	-.IFNTYGPR.-
R3/RRR3-11/2	967.883	968.091	-214.873	0.437	577.765	0.382	11	0.144	-.IFNTYGPR.-
R3/RRR3-10/2	1203.537	1204.404	-1555.217	0.255	576.710	0.410	16	0.143	R.VVSNFIAQAVR.G
R3/RRR3-13/2	1462.424	1461.753	-225.800	0.317	691.172	0.375	17	0.143	K.TNVIGTLNM*LGLAK.R
R3/RRR3-10/2	968.052	968.091	-40.297	0.420	601.896	0.390	11	0.142	-.IFNTYGPR.-
R3/RRR3-13/2	968.238	968.091	152.678	0.409	551.576	0.351	11	0.142	-.IFNTYGPR.-
R3/RRR3-10/2	1203.902	1204.404	-1250.765	0.261	433.441	0.382	15	0.142	R.VVSNFIAQAVR.G
R3/RRR3-11/2	1205.000	1204.404	-336.077	0.426	585.693	0.379	13	0.141	-.VVSNFIAQAVR.-
R3/RRR3-12/2	967.336	968.091	-1819.026	0.348	711.123	0.308	12	0.141	-.IFNTYGPR.-
R3/RRR3-11/3	1383.678	1382.570	78.468	0.555	931.405	0.568	25	0.138	R.VAETLMFDYHR.Q
R3/RRR3-11/2	967.469	968.091	-1681.086	0.409	669.021	0.308	12	0.138	-.IFNTYGPR.-
R3/RRR3-11/3	1382.210	1382.570	-261.154	0.480	922.923	0.569	25	0.136	R.VAETLMFDYHR.Q
R3/RRR3-11/2	1446.850	1445.753	66.970	0.358	568.856	0.294	15	0.135	K.TNVIGTLNMLGLAK.R
R3/RRR3-15/2	967.995	968.091	-98.988	0.238	681.323	0.071	12	0.130	R.IFNTYGPR.M
R3/RRR3-11/2	1445.354	1445.753	-277.055	0.268	585.795	0.157	15	0.129	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/3	1382.392	1382.570	-128.931	0.479	799.902	0.528	23	0.124	R.VAETLMFDYHR.Q
R3/RRR3-11/3	1444.983	1445.753	-1228.932	0.410	1524.619	0.273	28	0.122	K.TNVIGTLNMLGLAK.R
R3/RRR3-11/3	1398.572	1398.569	1.942	0.392	615.453	0.547	23	0.117	R.VAETLM*FDYHR.Q
R3/RRR3-11/3	1398.923	1398.569	253.611	0.433	568.773	0.517	22	0.114	R.VAETLM*FDYHR.Q
R3/RRR3-11/3	1398.853	1398.569	203.865	0.465	501.024	0.511	19	0.114	R.VAETLM*FDYHR.Q
R3/RRR3-10/2	1500.357	1499.734	-252.536	0.575	2256.671	0.666	22	0.386	R.VPTVDVSVVDLTVR.I
R3/RRR3-13/2	1499.409	1499.734	-217.583	0.506	2230.805	0.652	22	0.376	R.VPTVDVSVVDLTVR.I
R3/RRR3-1/2	1500.258	1499.734	-318.738	0.528	2204.448	0.656	22	0.372	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/2	1498.903	1499.734	-1225.720	0.469	2340.378	0.556	22	0.366	R.VPTVDVSVVDLTVR.I
R3/RRR3-1/2	1500.337	1499.734	-265.432	0.558	2133.384	0.644	22	0.354	R.VPTVDVSVVDLTVR.I
R3/RRR3-12/2	1499.245	1499.734	-327.202	0.519	2130.561	0.634	22	0.350	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/2	1499.308	1499.734	-285.214	0.520	2125.563	0.628	22	0.347	R.VPTVDVSVVDLTVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1499.366	1499.734	-246.496	0.509	2150.027	0.611	21	0.346	R.VPTVDVSVVDLTVR.I
R3/RRR3-10/2	1500.253	1499.734	-322.085	0.543	2018.999	0.676	22	0.343	R.VPTVDVSVVDLTVR.I
R3/RRR3-10/2	1499.437	1499.734	-198.961	0.520	2040.504	0.649	22	0.338	R.VPTVDVSVVDLTVR.I
R3/RRR3-2/2	1499.488	1499.734	-164.742	0.509	2024.806	0.626	21	0.328	R.VPTVDVSVVDLTVR.I
R3/RRR3-2/2	1499.414	1499.734	-213.989	0.517	2023.805	0.619	22	0.326	R.VPTVDVSVVDLTVR.I
R3/RRR3-1/2	1499.389	1499.734	-231.304	0.503	2013.704	0.623	21	0.325	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/2	1498.821	1499.734	-1280.191	0.519	2052.928	0.592	22	0.323	R.VPTVDVSVVDLTVR.I
R3/RRR3-12/2	1499.358	1499.734	-251.642	0.512	1961.089	0.624	20	0.315	R.VPTVDVSVVDLTVR.I
R3/RRR3-13/2	1499.741	1499.734	4.604	0.517	2017.272	0.587	20	0.314	R.VPTVDVSVVDLTVR.I
R3/RRR3-2/2	1500.375	1499.734	-240.455	0.566	1870.824	0.660	21	0.311	R.VPTVDVSVVDLTVR.I
R3/RRR3-16/2	1500.021	1499.734	191.602	0.557	1904.685	0.633	21	0.309	R.VPTVDVSVVDLTVR.I
R3/RRR3-25/2	1499.065	1499.734	-1116.632	0.499	2045.103	0.548	21	0.307	R.VPTVDVSVVDLTVR.I
R3/RRR3-7/2	1499.608	1499.734	-84.308	0.499	1918.467	0.618	21	0.307	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/2	1756.537	1757.017	-273.977	0.570	1790.129	0.646	21	0.298	K.TLLFGEKEVTVFGCR.N
R3/RRR3-12/2	1499.437	1499.734	-198.798	0.521	1813.441	0.624	21	0.291	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/2	1756.581	1757.017	-248.668	0.521	1846.943	0.589	22	0.291	K.TLLFGEKEVTVFGCR.N
R3/RRR3-16/2	1499.551	1499.734	-122.360	0.475	1769.060	0.574	21	0.271	R.VPTVDVSVVDLTVR.I
R3/RRR3-12/2	1762.458	1762.859	-228.179	0.492	1637.519	0.588	20	0.257	K.LVSWYDNEWGYSSR.V
R3/RRR3-12/3	1500.758	1499.734	15.564	0.471	2241.141	0.393	29	0.255	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/2	1756.580	1757.017	-249.784	0.507	1632.161	0.539	21	0.246	K.TLLFGEKEVTVFGCR.N
R3/RRR3-11/2	1762.325	1762.859	-873.197	0.544	1536.529	0.584	19	0.242	K.LVSWYDNEWGYSSR.V
R3/RRR3-14/2	1498.986	1499.734	-1170.028	0.453	1487.298	0.537	20	0.224	R.VPTVDVSVVDLTVR.I
R3/RRR3-12/2	1762.043	1762.859	-1033.779	0.516	1472.621	0.541	18	0.223	K.LVSWYDNEWGYSSR.V
R3/RRR3-11/2	1762.278	1762.859	-900.038	0.506	1458.127	0.523	19	0.218	K.LVSWYDNEWGYSSR.V
R3/RRR3-11/2	1763.305	1762.859	253.746	0.557	1345.670	0.584	18	0.218	K.LVSWYDNEWGYSSR.V
R3/RRR3-11/3	1756.866	1757.017	-86.397	0.508	1721.413	0.540	31	0.218	K.TLLFGEKEVTVFGCR.N
R3/RRR3-12/2	1756.252	1757.017	-1007.768	0.474	1354.755	0.566	18	0.215	K.TLLFGEKEVTVFGCR.N
R3/RRR3-12/2	1762.399	1762.859	-261.464	0.466	1357.014	0.543	18	0.211	K.LVSWYDNEWGYSSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1762.549	1762.859	-176.346	0.510	1306.663	0.535	18	0.204	K.LVSWYDNEWGYSSR.V
R3/RRR3-13/2	1162.036	1162.320	-245.140	0.416	1428.106	0.438	17	0.198	K.AGIALNDNFVK.-
R3/RRR3-11/2	1161.696	1162.320	-1402.656	0.453	1329.488	0.468	17	0.195	K.AGIALNDNFVK.-
R3/RRR3-11/2	1162.002	1162.320	-274.440	0.437	1452.784	0.387	17	0.191	K.AGIALNDNFVK.-
R3/RRR3-10/2	1162.126	1162.320	-167.685	0.435	1415.943	0.399	16	0.189	K.AGIALNDNFVK.-
R3/RRR3-11/3	1499.267	1499.734	-312.915	0.414	2091.706	0.263	29	0.186	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/2	1763.362	1762.859	-282.776	0.536	1122.757	0.528	17	0.185	K.LVSWYDNEWGYSSR.V
R3/RRR3-11/2	1762.025	1762.859	-1044.004	0.446	987.647	0.595	16	0.185	K.LVSWYDNEWGYSSR.V
R3/RRR3-11/2	1498.676	1499.734	-1377.697	0.395	1049.024	0.574	16	0.185	R.VPTVDVSVVDLTVR.I
R3/RRR3-17/2	1499.360	1499.734	-250.172	0.428	1004.394	0.559	18	0.182	R.VPTVDVSVVDLTVR.I
R3/RRR3-1/2	1161.875	1162.320	-384.590	0.346	1352.954	0.389	16	0.182	K.AGIALNDNFVK.-
R3/RRR3-12/2	1133.967	1134.226	-229.074	0.435	992.639	0.491	14	0.174	K.YDTVHGQWK.H
R3/RRR3-11/2	1133.992	1134.226	-206.719	0.406	1028.170	0.472	14	0.173	K.YDTVHGQWK.H
R3/RRR3-17/2	1498.652	1499.734	-1393.814	0.356	1108.372	0.457	19	0.173	R.VPTVDVSVVDLTVR.I
R3/RRR3-13/2	1162.028	1162.320	-252.729	0.357	1229.513	0.392	16	0.173	K.AGIALNDNFVK.-
R3/RRR3-11/2	1162.085	1162.320	-203.513	0.469	1133.524	0.429	16	0.172	K.AGIALNDNFVK.-
R3/RRR3-11/2	1763.419	1762.859	-249.995	0.499	924.724	0.544	15	0.172	K.LVSWYDNEWGYSSR.V
R3/RRR3-16/2	1499.101	1499.734	-1092.512	0.426	872.184	0.546	18	0.171	R.VPTVDVSVVDLTVR.I
R3/RRR3-13/2	1161.831	1162.320	-422.648	0.401	1337.267	0.319	17	0.170	K.AGIALNDNFVK.-
R3/RRR3-10/2	1435.389	1435.607	-152.651	0.434	982.284	0.458	21	0.167	R.AASFNIIPSSTGAAK.A
R3/RRR3-11/2	1133.937	1134.226	-255.642	0.440	867.011	0.488	13	0.166	K.YDTVHGQWK.H
R3/RRR3-18/2	1162.807	1162.320	420.058	0.335	1071.458	0.422	15	0.165	K.AGIALNDNFVK.-
R3/RRR3-11/2	1435.296	1435.607	-217.236	0.446	932.331	0.450	23	0.165	R.AASFNIIPSSTGAAK.A
R3/RRR3-13/2	1762.658	1762.859	-114.237	0.392	1009.079	0.446	17	0.164	K.LVSWYDNEWGYSSR.V
R3/RRR3-9/2	1162.058	1162.320	-226.276	0.394	1116.618	0.379	16	0.164	K.AGIALNDNFVK.-
R3/RRR3-12/2	1501.001	1499.734	178.099	0.449	561.122	0.579	18	0.163	R.VPTVDVSVVDLTVR.I
R3/RRR3-3/2	1162.169	1162.320	-130.595	0.407	1143.400	0.367	15	0.163	K.AGIALNDNFVK.-
R3/RRR3-12/2	1133.826	1134.226	-353.178	0.403	928.103	0.438	14	0.162	K.YDTVHGQWK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1162.226	1162.320	-81.392	0.454	1091.998	0.377	15	0.161	K.AGIALNDNFVK.-
R3/RRR3-12/2	1133.977	1134.226	-219.463	0.422	889.736	0.439	13	0.160	K.YDTVHGQWK.H
R3/RRR3-12/2	929.065	929.139	-79.942	0.423	972.022	0.384	15	0.159	K.KVVISAPSK.D
R3/RRR3-11/2	1435.260	1435.607	-242.492	0.443	859.863	0.441	21	0.159	R.AASFNIIPSSTGAAK.A
R3/RRR3-11/2	1133.919	1134.226	-270.871	0.418	841.523	0.443	13	0.159	K.YDTVHGQWK.H
R3/RRR3-12/2	1306.948	1306.513	334.010	0.294	1233.875	0.290	18	0.158	K.DAPMFVVGVNEK.E
R3/RRR3-15/2	1435.197	1435.607	-286.437	0.423	703.794	0.485	20	0.157	R.AASFNIIPSSTGAAK.A
R3/RRR3-11/2	1435.264	1435.607	-240.018	0.445	782.663	0.451	21	0.157	R.AASFNIIPSSTGAAK.A
R3/RRR3-11/2	929.053	929.139	-93.385	0.376	847.992	0.429	14	0.157	K.KVVISAPSK.D
R3/RRR3-9/2	1161.621	1162.320	-1467.675	0.341	1022.617	0.373	15	0.157	K.AGIALNDNFVK.-
R3/RRR3-11/2	1162.118	1162.320	-174.324	0.366	1066.921	0.348	15	0.156	K.AGIALNDNFVK.-
R3/RRR3-11/2	929.018	929.139	-130.686	0.378	881.779	0.398	15	0.156	K.KVVISAPSK.D
R3/RRR3-11/2	1323.058	1322.512	-344.794	0.404	762.065	0.442	18	0.156	K.DAPM*FVVGVNEK.E
R3/RRR3-10/2	833.825	833.958	-159.702	0.390	803.269	0.418	12	0.156	K.IGINGFGR.I
R3/RRR3-12/2	1307.000	1306.513	373.435	0.364	1014.953	0.352	17	0.154	K.DAPMFVVGVNEK.E
R3/RRR3-10/2	1435.152	1435.607	-318.097	0.423	705.764	0.452	20	0.154	R.AASFNIIPSSTGAAK.A
R3/RRR3-10/2	1161.620	1162.320	-1468.519	0.400	951.032	0.370	15	0.154	K.AGIALNDNFVK.-
R3/RRR3-12/2	928.674	929.139	-501.996	0.392	740.006	0.434	13	0.153	K.KVVISAPSK.D
R3/RRR3-12/2	928.565	929.139	-1699.963	0.385	743.366	0.432	13	0.153	K.KVVISAPSK.D
R3/RRR3-15/2	1435.312	1435.607	-206.144	0.463	503.657	0.475	19	0.152	R.AASFNIIPSSTGAAK.A
R3/RRR3-11/2	833.961	833.958	3.287	0.443	789.332	0.380	12	0.152	K.IGINGFGR.I
R3/RRR3-11/2	1162.898	1162.320	-364.037	0.433	896.911	0.369	15	0.152	K.AGIALNDNFVK.-
R3/RRR3-27/2	833.772	833.958	-223.296	0.403	807.663	0.373	12	0.151	K.IGINGFGR.I
R3/RRR3-2/2	833.974	833.958	18.849	0.391	901.263	0.339	12	0.150	K.IGINGFGR.I
R3/RRR3-3/2	1162.038	1162.320	-243.665	0.368	911.425	0.353	15	0.150	K.AGIALNDNFVK.-
R3/RRR3-1/2	1162.379	1162.320	50.917	0.396	912.576	0.354	14	0.149	K.AGIALNDNFVK.-
R3/RRR3-2/2	1435.257	1435.607	-244.967	0.388	446.492	0.457	18	0.148	R.AASFNIIPSSTGAAK.A
R3/RRR3-17/2	1161.998	1162.320	-278.023	0.344	688.065	0.439	12	0.148	K.AGIALNDNFVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	833.860	833.958	-117.848	0.415	636.688	0.380	11	0.148	K.IGINGFGR.I
R3/RRR3-11/2	1435.340	1435.607	-186.862	0.404	624.846	0.401	20	0.148	R.AASFNIIPSSTGAAK.A
R3/RRR3-10/2	833.794	833.958	-196.712	0.387	739.104	0.350	12	0.147	K.IGINGFGR.I
R3/RRR3-11/2	1323.113	1322.512	-302.953	0.399	673.582	0.412	17	0.147	-.DAPM*FVVGVNEK.-
R3/RRR3-11/2	833.859	833.958	-118.729	0.423	746.280	0.340	12	0.147	K.IGINGFGR.I
R3/RRR3-12/2	1162.205	1162.320	-99.935	0.419	1003.455	0.296	15	0.147	K.AGIALNDNFVK.-
R3/RRR3-12/2	1292.187	1292.463	-213.722	0.494	639.057	0.366	17	0.146	R.LEKPASYDQIK.A
R3/RRR3-11/2	928.906	929.139	-251.964	0.416	669.474	0.373	13	0.146	K.KVVISAPSK.D
R3/RRR3-10/2	1435.827	1435.607	153.268	0.446	593.523	0.407	18	0.146	R.AASFNIIPSSTGAAK.A
R3/RRR3-8/2	1435.224	1435.607	-267.494	0.319	351.074	0.465	17	0.146	R.AASFNIIPSSTGAAK.A
R3/RRR3-13/2	1435.256	1435.607	-245.564	0.390	526.884	0.399	19	0.146	R.AASFNIIPSSTGAAK.A
R3/RRR3-17/2	1435.448	1435.607	-110.936	0.354	495.931	0.419	18	0.145	R.AASFNIIPSSTGAAK.A
R3/RRR3-27/2	833.718	833.958	-289.102	0.350	691.050	0.342	11	0.144	K.IGINGFGR.I
R3/RRR3-10/2	833.522	833.958	-524.195	0.355	861.528	0.291	12	0.144	K.IGINGFGR.I
R3/RRR3-24/2	833.858	833.958	-120.051	0.314	725.741	0.343	11	0.144	K.IGINGFGR.I
R3/RRR3-11/2	833.881	833.958	-92.003	0.390	554.806	0.360	10	0.144	K.IGINGFGR.I
R3/RRR3-16/2	1435.032	1435.607	-1101.274	0.384	687.921	0.358	19	0.144	R.AASFNIIPSSTGAAK.A
R3/RRR3-15/2	1435.181	1435.607	-297.702	0.358	463.565	0.406	17	0.144	R.AASFNIIPSSTGAAK.A
R3/RRR3-11/2	1434.676	1435.607	-1350.316	0.317	744.230	0.349	19	0.143	R.AASFNIIPSSTGAAK.A
R3/RRR3-2/2	834.017	833.958	70.963	0.371	688.682	0.324	11	0.143	K.IGINGFGR.I
R3/RRR3-13/2	833.849	833.958	-130.918	0.376	696.766	0.321	11	0.143	K.IGINGFGR.I
R3/RRR3-8/2	1435.230	1435.607	-263.483	0.326	259.873	0.424	14	0.143	R.AASFNIIPSSTGAAK.A
R3/RRR3-12/2	1162.102	1162.320	-188.760	0.437	857.482	0.316	14	0.143	K.AGIALNDNFVK.-
R3/RRR3-12/2	1292.035	1292.463	-331.916	0.470	699.867	0.307	18	0.143	R.LEKPASYDQIK.A
R3/RRR3-12/2	834.009	833.958	61.422	0.294	502.093	0.326	11	0.142	K.IGINGFGR.I
R3/RRR3-3/2	1435.245	1435.607	-253.073	0.360	412.374	0.352	17	0.142	R.AASFNIIPSSTGAAK.A
R3/RRR3-12/2	1292.152	1292.463	-241.017	0.438	586.809	0.312	17	0.142	R.LEKPASYDQIK.A
R3/RRR3-12/2	834.325	833.958	441.772	0.354	565.492	0.301	11	0.141	K.IGINGFGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	833.908	833.958	-59.993	0.336	726.509	0.299	11	0.141	K.IGINGFGR.I
R3/RRR3-13/2	1435.274	1435.607	-232.680	0.359	454.917	0.408	17	0.141	-.AASFNIIPSSTGAAK.-
R3/RRR3-1/2	1764.614	1762.859	-139.366	0.316	213.785	0.369	13	0.141	K.LVSWYDNEWGYSSR.V
R3/RRR3-11/2	834.439	833.958	578.317	0.337	633.468	0.276	12	0.141	K.IGINGFGR.I
R3/RRR3-25/2	833.551	833.958	-489.365	0.363	607.067	0.302	10	0.140	K.IGINGFGR.I
R3/RRR3-1/2	1435.152	1435.607	-318.268	0.377	455.006	0.396	16	0.140	-.AASFNIIPSSTGAAK.-
R3/RRR3-15/2	1162.276	1162.320	-38.409	0.295	788.239	0.303	13	0.140	K.AGIALNDNFVK.-
R3/RRR3-27/2	833.127	833.958	-2204.641	0.334	636.855	0.257	12	0.140	K.IGINGFGR.I
R3/RRR3-9/2	833.903	833.958	-66.454	0.353	648.456	0.273	11	0.140	K.IGINGFGR.I
R3/RRR3-11/2	1292.108	1292.463	-275.138	0.476	610.340	0.286	17	0.139	R.LEKPASYDQIK.A
R3/RRR3-11/2	1162.057	1162.320	-227.014	0.319	726.829	0.303	13	0.139	K.AGIALNDNFVK.-
R3/RRR3-11/2	1305.786	1306.513	-1326.639	0.238	326.449	0.294	16	0.139	K.DAPMFVVGVNEK.E
R3/RRR3-13/2	1434.687	1435.607	-1342.454	0.384	366.504	0.380	15	0.139	-.AASFNIIPSSTGAAK.-
R3/RRR3-1/2	1434.854	1435.607	-1225.395	0.377	451.816	0.292	17	0.139	R.AASFNIIPSSTGAAK.A
R3/RRR3-11/2	834.760	833.958	-237.259	0.377	617.211	0.229	12	0.138	K.IGINGFGR.I
R3/RRR3-11/2	834.260	833.958	362.996	0.348	641.116	0.233	12	0.138	K.IGINGFGR.I
R3/RRR3-12/2	1161.593	1162.320	-1491.108	0.359	724.638	0.275	14	0.138	K.AGIALNDNFVK.-
R3/RRR3-11/2	1321.947	1322.512	-1188.003	0.275	471.662	0.340	15	0.138	K.DAPM*FVVGVNEK.E
R3/RRR3-11/2	1291.676	1292.463	-1387.103	0.428	549.868	0.272	16	0.138	R.LEKPASYDQIK.A
R3/RRR3-15/2	1162.072	1162.320	-214.262	0.310	716.163	0.271	14	0.138	K.AGIALNDNFVK.-
R3/RRR3-26/2	833.772	833.958	-223.590	0.286	625.944	0.272	10	0.138	K.IGINGFGR.I
R3/RRR3-4/2	833.954	833.958	-4.788	0.294	852.567	0.230	11	0.138	K.IGINGFGR.I
R3/RRR3-12/2	1322.288	1322.512	-170.547	0.372	643.310	0.276	16	0.137	K.DAPM*FVVGVNEK.E
R3/RRR3-11/2	1292.032	1292.463	-334.476	0.387	631.967	0.229	17	0.136	R.LEKPASYDQIK.A
R3/RRR3-11/2	1498.310	1499.734	-1622.938	0.218	408.603	0.333	13	0.136	R.VPTVDVSVVDLTVR.I
R3/RRR3-4/2	1435.375	1435.607	-162.462	0.390	486.611	0.312	16	0.135	-.AASFNIIPSSTGAAK.-
R3/RRR3-11/2	1435.235	1435.607	-259.899	0.356	361.221	0.357	15	0.135	-.AASFNIIPSSTGAAK.-
R3/RRR3-1/2	1161.855	1162.320	-402.090	0.253	768.783	0.238	13	0.135	K.AGIALNDNFVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1762.446	1762.859	-234.989	0.323	344.957	0.331	12	0.134	-.LVSWYDNEWGYSSR.-
R3/RRR3-12/2	1322.110	1322.512	-305.220	0.338	573.176	0.245	14	0.134	K.DAPM*FVVGVNEK.E
R3/RRR3-18/2	1434.689	1435.607	-1340.916	0.357	345.104	0.387	15	0.133	-.AASFNIIPSSTGAAK.-
R3/RRR3-4/2	1161.985	1162.320	-289.828	0.326	557.466	0.203	13	0.133	-.AGIALNDNFVK.-
R3/RRR3-12/2	1307.095	1306.513	-321.067	0.296	787.889	0.200	15	0.132	-.DAPMFVVGVNEK.-
R3/RRR3-11/3	1756.944	1757.017	-41.863	0.462	979.442	0.514	26	0.132	K.TLLFGEKEVTVFGCR.N
R3/RRR3-11/3	1499.725	1499.734	-6.182	0.445	1575.788	0.280	25	0.130	R.VPTVDVSVVDLTVR.I
R3/RRR3-3/2	1161.842	1162.320	-412.949	0.240	803.648	0.121	13	0.129	-.AGIALNDNFVK.-
R3/RRR3-12/2	1435.791	1435.607	128.713	0.328	306.425	0.344	13	0.129	-.AASFNIIPSSTGAAK.-
R3/RRR3-11/3	1756.516	1757.017	-857.238	0.502	993.685	0.483	26	0.127	K.TLLFGEKEVTVFGCR.N
R3/RRR3-12/3	1499.890	1499.734	103.775	0.443	1406.669	0.333	25	0.127	R.VPTVDVSVVDLTVR.I
R3/RRR3-10/3	1292.383	1292.463	-62.121	0.524	1014.255	0.465	24	0.124	R.LEKPASYDQIK.A
R3/RRR3-19/2	1434.586	1435.607	-1413.215	0.248	296.352	0.354	13	0.122	-.AASFNIIPSSTGAAK.-
R3/RRR3-16/2	1434.603	1435.607	-1401.079	0.267	297.176	0.339	15	0.120	-.AASFNIIPSSTGAAK.-
R3/RRR3-11/3	1292.681	1292.463	169.472	0.548	985.203	0.452	25	0.119	R.LEKPASYDQIK.A
R3/RRR3-10/3	1292.393	1292.463	-54.021	0.512	733.256	0.492	22	0.119	R.LEKPASYDQIK.A
R3/RRR3-13/3	1292.376	1292.463	-67.521	0.516	979.227	0.436	23	0.115	-.LEKPASYDQIK.-
R3/RRR3-19/3	1292.818	1292.463	275.713	0.489	445.376	0.489	18	0.115	R.LEKPASYDQIK.A
R3/RRR3-12/3	1292.466	1292.463	2.395	0.518	570.096	0.464	20	0.113	R.LEKPASYDQIK.A
R3/RRR3-11/3	1292.210	1292.463	-196.295	0.488	988.069	0.413	25	0.113	R.LEKPASYDQIK.A
R3/RRR3-2/3	1291.186	1292.463	-1768.789	0.467	666.845	0.457	21	0.113	R.LEKPASYDQIK.A
R3/RRR3-11/3	1292.214	1292.463	-192.741	0.477	894.951	0.413	23	0.111	R.LEKPASYDQIK.A
R3/RRR3-12/3	1292.823	1292.463	279.690	0.525	798.599	0.426	23	0.111	R.LEKPASYDQIK.A
R3/RRR3-13/3	1292.240	1292.463	-172.698	0.496	609.005	0.420	20	0.108	R.LEKPASYDQIK.A
R3/RRR3-24/3	1292.580	1292.463	90.629	0.470	674.454	0.440	20	0.108	-.LEKPASYDQIK.-
R3/RRR3-7/3	1292.548	1292.463	66.476	0.388	830.808	0.390	22	0.107	R.LEKPASYDQIK.A
R3/RRR3-1/3	1292.039	1292.463	-328.656	0.423	681.491	0.403	21	0.107	R.LEKPASYDQIK.A
R3/RRR3-16/3	1292.107	1292.463	-276.191	0.389	387.467	0.366	17	0.106	R.LEKPASYDQIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/3	1292.622	1292.463	123.304	0.417	499.849	0.395	18	0.106	R.LEKPASYDQIK.A
R3/RRR3-13/3	1292.409	1292.463	-42.083	0.509	711.045	0.417	21	0.105	-.LEKPASYDQIK.-
R3/RRR3-10/3	1292.586	1292.463	95.317	0.489	580.043	0.381	21	0.105	R.LEKPASYDQIK.A
R3/RRR3-6/3	1292.627	1292.463	127.282	0.441	465.243	0.364	18	0.105	R.LEKPASYDQIK.A
R3/RRR3-9/3	1292.000	1292.463	-359.512	0.374	469.124	0.359	18	0.104	R.LEKPASYDQIK.A
R3/RRR3-26/3	1293.137	1292.463	-253.011	0.325	464.467	0.365	17	0.104	R.LEKPASYDQIK.A
R3/RRR3-9/3	1293.721	1292.463	200.235	0.442	469.708	0.409	18	0.104	-.LEKPASYDQIK.-
R3/RRR3-17/3	1291.940	1292.463	-1182.508	0.401	568.752	0.354	19	0.103	R.LEKPASYDQIK.A
R3/RRR3-25/3	1292.719	1292.463	198.875	0.473	672.851	0.389	21	0.102	-.LEKPASYDQIK.-
R3/RRR3-11/3	1499.284	1499.734	-301.519	0.442	1179.550	0.273	24	0.101	R.VPTVDVSVVDLTVR.I
R3/RRR3-11/3	1293.522	1292.463	46.075	0.487	757.099	0.343	22	0.101	R.LEKPASYDQIK.A
R3/RRR3-12/3	1293.518	1292.463	42.810	0.453	1006.623	0.314	23	0.100	R.LEKPASYDQIK.A
R3/RRR3-6/3	1292.242	1292.463	-171.135	0.381	561.436	0.359	19	0.100	-.LEKPASYDQIK.-
R3/RRR3-19/3	1292.742	1292.463	216.630	0.388	358.859	0.333	17	0.100	-.LEKPASYDQIK.-
R3/RRR3-11/3	1292.609	1292.463	113.217	0.371	579.124	0.366	18	0.096	-.LEKPASYDQIK.-
R3/RRR3-26/3	1292.298	1292.463	-127.498	0.368	504.759	0.308	17	0.094	-.LEKPASYDQIK.-
R3/RRR3-12/3	1498.524	1499.734	-1479.732	0.333	1100.891	0.216	23	0.092	-.VPTVDVSVVDLTVR.-
R3/RRR3-12/3	1756.820	1757.017	-112.533	0.351	558.655	0.337	21	0.092	-.TLLFGEKEVTVFGCR.-
R3/RRR3-23/3	1292.689	1292.463	175.154	0.387	489.727	0.346	17	0.088	-.LEKPASYDQIK.-
R3/RRR3-6/2	1249.147	1249.443	-237.259	0.530	2002.480	0.484	17	0.289	R.LWALEIANYR.K
R3/RRR3-6/2	1717.495	1717.987	-287.405	0.507	1760.192	0.605	25	0.284	K.KVPVVVGNCTGFAVNR.T
R3/RRR3-6/2	1636.562	1635.906	-211.318	0.542	1828.283	0.577	22	0.283	R.ASDLDIASILGMGFPK.F
R3/RRR3-6/2	1635.534	1635.906	-228.370	0.462	1806.201	0.516	22	0.263	R.ASDLDIASILGMGFPK.F
R3/RRR3-6/2	1634.589	1635.906	-1422.315	0.313	1821.926	0.480	22	0.255	R.ASDLDIASILGMGFPK.F
R3/RRR3-6/2	1652.411	1651.906	-300.685	0.561	1593.055	0.599	22	0.254	R.ASDLDIASILGM*GFPK.F
R3/RRR3-6/2	1651.255	1651.906	-1002.925	0.489	1560.568	0.608	22	0.252	R.ASDLDIASILGM*GFPK.F
R3/RRR3-6/2	1249.331	1249.443	-89.633	0.474	1705.959	0.455	17	0.238	R.LWALEIANYR.K
R3/RRR3-6/2	1249.196	1249.443	-198.241	0.585	1592.339	0.488	17	0.231	R.LWALEIANYR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1652.340	1651.906	263.565	0.556	1401.817	0.574	21	0.223	R.ASDLDIASILGM*GFPK.F
R3/RRR3-6/2	1530.330	1530.739	-267.511	0.465	1493.590	0.439	20	0.207	R.GLVDALCSPDELIK.M
R3/RRR3-6/3	1456.610	1456.709	-68.608	0.530	1832.467	0.437	29	0.202	K.TSPQAILDLITVGK.M
R3/RRR3-6/2	1309.051	1309.540	-374.274	0.449	1152.928	0.562	19	0.197	K.VPGVTDVQLKPR.K
R3/RRR3-6/2	1628.359	1628.769	-252.534	0.517	1125.136	0.550	25	0.194	R.SLPLSAPNATQQASSR.S
R3/RRR3-6/2	1160.140	1160.353	-183.908	0.365	1258.892	0.504	16	0.194	K.ALVHAFFAQR.L
R3/RRR3-6/2	1628.307	1628.769	-284.574	0.484	994.854	0.564	24	0.185	R.SLPLSAPNATQQASSR.S
R3/RRR3-6/2	1628.279	1628.769	-301.874	0.498	906.305	0.590	23	0.182	R.SLPLSAPNATQQASSR.S
R3/RRR3-6/3	1456.363	1456.709	-238.483	0.524	1660.825	0.437	29	0.178	K.TSPQAILDLITVGK.M
R3/RRR3-6/2	1530.379	1530.739	-235.781	0.465	1256.138	0.407	19	0.177	R.GLVDALCSPDELIK.M
R3/RRR3-6/2	1159.342	1159.425	-71.667	0.473	1018.906	0.434	17	0.168	K.MIAANLEGLVK.R
R3/RRR3-6/2	1159.021	1159.425	-349.198	0.462	919.396	0.466	17	0.167	K.MIAANLEGLVK.R
R3/RRR3-6/2	1160.420	1159.425	-3.757	0.458	986.084	0.445	16	0.166	K.MIAANLEGLVK.R
R3/RRR3-6/2	1455.831	1456.709	-1294.278	0.363	895.032	0.496	20	0.165	K.TSPQAILDLITVGK.M
R3/RRR3-6/2	1159.137	1159.425	-248.394	0.473	1000.327	0.429	16	0.165	K.MIAANLEGLVK.R
R3/RRR3-6/2	1176.308	1175.424	-98.627	0.503	941.553	0.432	17	0.163	K.M*IAANLEGLVK.R
R3/RRR3-6/2	1090.958	1091.264	-281.298	0.541	868.684	0.438	15	0.162	R.VM*DENVVIR.A
R3/RRR3-6/2	887.047	887.059	-13.956	0.403	962.667	0.407	16	0.160	K.AIVLTGAGGK.F
R3/RRR3-6/2	1456.215	1456.709	-340.570	0.438	837.181	0.460	20	0.160	K.TSPQAILDLITVGK.M
R3/RRR3-6/2	1090.840	1091.264	-389.528	0.510	873.411	0.407	15	0.158	R.VM*DENVVIR.A
R3/RRR3-6/2	1176.327	1175.424	-82.700	0.355	882.714	0.431	16	0.157	K.M*IAANLEGLVK.R
R3/RRR3-6/2	1176.059	1175.424	-311.235	0.466	892.454	0.395	17	0.156	K.M*IAANLEGLVK.R
R3/RRR3-6/2	1090.876	1091.264	-356.518	0.454	845.260	0.378	15	0.153	R.VM*DENVVIR.A
R3/RRR3-6/2	1455.856	1456.709	-1277.268	0.371	670.752	0.449	20	0.151	K.TSPQAILDLITVGK.M
R3/RRR3-6/2	1717.540	1717.987	-261.307	0.409	763.334	0.458	17	0.149	K.KVPVVVGNCTGFAVNR.T
R3/RRR3-6/2	886.909	887.059	-169.539	0.349	778.328	0.386	14	0.147	K.AIVLTGAGGK.F
R3/RRR3-5/2	1455.607	1456.709	-1448.489	0.305	755.483	0.342	17	0.140	K.TSPQAILDLITVGK.M
R3/RRR3-1/2	1455.710	1456.709	-1377.737	0.218	433.555	0.442	14	0.135	K.TSPQAILDLITVGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	886.297	887.059	-1994.538	0.260	981.246	0.092	15	0.128	K.AIVLTGAGGK.F
R3/RRR3-6/3	1160.463	1160.353	95.091	0.490	620.859	0.480	18	0.112	K.ALVHAFFAQR.L
R3/RRR3-6/3	1159.839	1160.353	-1308.639	0.412	449.956	0.466	19	0.107	K.ALVHAFFAQR.L
R3/RRR3-6/3	1160.430	1160.353	66.606	0.442	778.614	0.372	20	0.101	K.ALVHAFFAQR.L
R3/RRR3-12/2	1747.556	1748.146	-912.384	0.554	2625.538	0.564	27	0.437	K.VAVLGAAGGIGQPLGLLIK.M
R3/RRR3-12/2	1748.455	1748.146	176.982	0.611	2349.004	0.587	27	0.382	K.VAVLGAAGGIGQPLGLLIK.M
R3/RRR3-12/2	1348.274	1348.616	-254.232	0.542	1824.432	0.443	20	0.250	K.KLFGVTTLDVVR.A
R3/RRR3-13/2	1748.772	1748.146	-214.632	0.554	1685.031	0.507	23	0.241	K.VAVLGAAGGIGQPLGLLIK.M
R3/RRR3-12/3	1982.868	1983.123	-128.973	0.550	2098.030	0.406	32	0.237	K.TRPSVTFTNEETEELTK.R
R3/RRR3-12/2	1485.252	1485.648	-267.250	0.485	1659.134	0.486	21	0.235	K.AGAGSATLSM*AYAAAR.F
R3/RRR3-12/2	1348.354	1348.616	-194.740	0.540	1738.793	0.424	20	0.234	K.KLFGVTTLDVVR.A
R3/RRR3-12/2	1278.131	1278.526	-309.950	0.387	1723.938	0.436	20	0.233	K.GVDVVVIPAGVPR.K
R3/RRR3-12/3	1747.544	1748.146	-919.615	0.524	1971.671	0.447	38	0.228	K.VAVLGAAGGIGQPLGLLIK.M
R3/RRR3-12/2	1349.282	1349.514	-172.374	0.482	1729.843	0.405	19	0.228	R.DDLFNINASIVK.S
R3/RRR3-12/2	1486.108	1485.648	310.439	0.506	1613.703	0.465	22	0.225	K.AGAGSATLSM*AYAAAR.F
R3/RRR3-12/3	1982.978	1983.123	-73.303	0.550	1899.725	0.463	32	0.224	K.TRPSVTFTNEETEELTK.R
R3/RRR3-13/2	1747.452	1748.146	-972.065	0.397	1692.751	0.404	23	0.220	K.VAVLGAAGGIGQPLGLLIK.M
R3/RRR3-12/2	1278.236	1278.526	-227.645	0.392	1520.040	0.484	19	0.218	K.GVDVVVIPAGVPR.K
R3/RRR3-12/2	1348.449	1348.616	-124.358	0.525	1616.396	0.420	20	0.218	K.KLFGVTTLDVVR.A
R3/RRR3-12/2	1349.465	1349.514	-36.892	0.520	1635.425	0.343	19	0.201	R.DDLFNINASIVK.S
R3/RRR3-12/2	1348.833	1349.514	-1250.533	0.436	1675.507	0.310	18	0.200	R.DDLFNINASIVK.S
R3/RRR3-12/2	1415.114	1415.578	-328.225	0.485	1460.250	0.347	21	0.186	K.RIQNAGTEVVEAK.A
R3/RRR3-12/2	1220.316	1220.443	-104.306	0.566	1276.790	0.425	19	0.185	K.LFGVTTLDVVR.A
R3/RRR3-13/2	1278.171	1278.526	-278.138	0.392	1336.713	0.408	18	0.184	K.GVDVVVIPAGVPR.K
R3/RRR3-12/2	1220.239	1220.443	-167.325	0.525	1282.260	0.390	19	0.179	K.LFGVTTLDVVR.A
R3/RRR3-13/2	1220.586	1220.443	117.803	0.479	1262.610	0.390	18	0.177	K.LFGVTTLDVVR.A
R3/RRR3-12/2	1258.643	1259.391	-1392.865	0.491	1022.402	0.472	19	0.174	R.IQNAGTEVVEAK.A
R3/RRR3-12/2	1259.058	1259.391	-265.732	0.495	1023.964	0.471	19	0.173	R.IQNAGTEVVEAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1485.322	1485.648	-220.499	0.469	1070.495	0.480	19	0.172	K.AGAGSATLSM*AYAAAR.F
R3/RRR3-12/3	1747.888	1748.146	-148.168	0.501	1584.473	0.430	34	0.169	K.VAVLGAAGGIGQPLGLLIK.M
R3/RRR3-12/2	1259.149	1259.391	-192.590	0.520	976.427	0.450	19	0.168	R.IQNAGTEVVEAK.A
R3/RRR3-12/2	1219.789	1220.443	-1360.346	0.499	1199.986	0.341	19	0.165	K.LFGVTTLDVVR.A
R3/RRR3-12/2	1277.645	1278.526	-1476.605	0.335	1187.740	0.326	18	0.160	K.GVDVVVIPAGVPR.K
R3/RRR3-12/2	1415.111	1415.578	-330.562	0.424	938.420	0.343	18	0.149	K.RIQNAGTEVVEAK.A
R3/RRR3-12/2	1415.150	1415.578	-302.781	0.446	961.694	0.328	18	0.147	K.RIQNAGTEVVEAK.A
R3/RRR3-13/2	1278.350	1278.526	-137.882	0.301	968.540	0.282	17	0.142	K.GVDVVVIPAGVPR.K
R3/RRR3-2/2	1221.111	1220.443	-272.886	0.399	701.612	0.360	13	0.142	K.LFGVTTLDVVR.A
R3/RRR3-13/2	1277.926	1278.526	-1255.153	0.258	1042.086	0.246	16	0.141	K.GVDVVVIPAGVPR.K
R3/RRR3-12/3	1747.501	1748.146	-944.020	0.368	1369.427	0.383	32	0.135	K.VAVLGAAGGIGQPLGLLIK.M
R3/RRR3-12/2	1127.860	1128.344	-430.058	0.372	752.122	0.259	13	0.132	K.ALESLKPELK.A
R3/RRR3-11/2	1220.937	1220.443	405.875	0.301	610.874	0.159	12	0.124	-.LFGVTTLDVVR.-
R3/RRR3-11/2	1221.075	1220.443	-301.972	0.336	611.097	0.109	12	0.110	-.LFGVTTLDVVR.-
R3/RRR3-12/3	1348.358	1348.616	-192.025	0.528	975.930	0.291	26	0.087	-.KLFGVTTLDVVR.-
R3/RRR3-12/3	1348.690	1348.616	55.175	0.500	917.685	0.268	25	0.077	-.KLFGVTTLDVVR.-
R3/RRR3-12/3	1348.630	1348.616	10.784	0.491	834.538	0.284	25	0.076	-.KLFGVTTLDVVR.-
R3/RRR3-5/2	1651.326	1650.813	-295.955	0.551	2025.777	0.487	20	0.291	K.GILQNDPFEVFDQK.G
R3/RRR3-5/2	1345.257	1344.495	-177.259	0.556	1674.509	0.615	20	0.275	K.VFANAETTISYK.I
R3/RRR3-5/2	1649.875	1650.813	-1178.196	0.451	1922.419	0.437	20	0.262	K.GILQNDPFEVFDQK.G
R3/RRR3-4/2	1263.285	1263.491	-163.562	0.570	1536.454	0.492	18	0.223	K.LSEVNPMLGFR.G
R3/RRR3-5/2	1824.375	1824.025	192.099	0.563	1354.875	0.577	22	0.220	R.LLSSGNVYTQEEILTR.I
R3/RRR3-5/2	1823.425	1824.025	-880.264	0.559	1371.105	0.563	23	0.220	R.LLSSGNVYTQEEILTR.I
R3/RRR3-5/2	1344.395	1344.495	-74.279	0.516	1380.516	0.545	19	0.219	K.VFANAETTISYK.I
R3/RRR3-5/2	1650.648	1650.813	-100.404	0.521	1521.110	0.465	19	0.214	K.GILQNDPFEVFDQK.G
R3/RRR3-5/2	1344.234	1344.495	-194.517	0.517	1189.137	0.520	18	0.194	K.VFANAETTISYK.I
R3/RRR3-5/2	1823.155	1824.025	-1028.944	0.533	1057.919	0.566	21	0.188	R.LLSSGNVYTQEEILTR.I
R3/RRR3-4/2	1280.428	1279.491	-48.818	0.461	1096.120	0.449	18	0.176	K.LSEVNPM*LGFR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1288.293	1287.361	-52.994	0.462	716.578	0.562	18	0.167	K.ANADTPADALTAR.N
R3/RRR3-4/2	1280.359	1279.491	-103.424	0.483	853.886	0.436	16	0.159	K.LSEVNPM*LGFR.G
R3/RRR3-5/2	1400.228	1399.570	-245.061	0.512	737.829	0.507	15	0.157	K.VGLNYVSCSPFR.V
R3/RRR3-5/2	1279.318	1279.491	-135.186	0.489	883.387	0.404	16	0.156	K.LSEVNPM*LGFR.G
R3/RRR3-5/2	1288.630	1287.361	209.066	0.446	684.477	0.456	18	0.153	K.ANADTPADALTAR.N
R3/RRR3-5/2	1514.749	1514.666	55.238	0.499	810.340	0.434	18	0.149	K.VKANADTPADALTAR.N
R3/RRR3-5/2	1263.152	1263.491	-269.717	0.352	744.143	0.423	13	0.148	K.LSEVNPMLGFR.G
R3/RRR3-5/2	1288.574	1287.361	165.557	0.463	574.847	0.436	17	0.147	K.ANADTPADALTAR.N
R3/RRR3-5/2	996.853	997.129	-277.287	0.419	602.882	0.386	12	0.147	R.LDFEGIFR.A
R3/RRR3-5/2	997.148	997.129	19.325	0.403	778.697	0.349	12	0.147	R.LDFEGIFR.A
R3/RRR3-5/2	996.541	997.129	-1598.135	0.370	713.146	0.353	12	0.145	R.LDFEGIFR.A
R3/RRR3-4/2	1279.077	1279.491	-324.551	0.419	595.160	0.378	14	0.144	K.LSEVNPM*LGFR.G
R3/RRR3-5/2	1263.109	1263.491	-303.749	0.390	668.738	0.367	13	0.142	K.LSEVNPMLGFR.G
R3/RRR3-5/2	1550.226	1550.805	-1021.494	0.371	518.408	0.444	16	0.139	R.LGISYPELTAMQAR.A
R3/RRR3-5/2	1279.099	1279.491	-307.124	0.299	527.920	0.332	13	0.138	K.LSEVNPM*LGFR.G
R3/RRR3-4/2	1288.148	1287.361	-166.013	0.381	594.245	0.356	16	0.136	-.ANADTPADALTAR.-
R3/RRR3-5/2	1072.641	1073.292	-1543.194	0.368	747.537	0.276	14	0.136	-.AMDGLPVTIR.-
R3/RRR3-5/2	1263.666	1263.491	138.397	0.287	680.796	0.282	13	0.136	K.LSEVNPMLGFR.G
R3/RRR3-6/2	996.930	997.129	-199.647	0.344	478.385	0.268	11	0.133	-.LDFEGIFR.-
R3/RRR3-6/2	996.922	997.129	-207.754	0.209	500.278	0.238	11	0.132	-.LDFEGIFR.-
R3/RRR3-4/2	1072.309	1073.292	-1854.929	0.227	632.768	0.276	12	0.130	R.AMDGLPVTIR.L
R3/RRR3-5/3	1501.800	1501.670	86.482	0.401	855.943	0.422	22	0.104	-.AALGLRNDTELTAR.-
R3/RRR3-3/2	1251.944	1252.528	-1268.879	0.431	1696.584	0.465	19	0.238	R.LILGELQAPAVK.Y
R3/RRR3-2/3	1298.637	1298.434	156.674	0.423	1688.189	0.389	25	0.167	R.RPGSVSLNQSPR.T
R3/RRR3-3/3	1298.596	1298.434	125.565	0.490	1631.265	0.388	25	0.159	R.RPGSVSLNQSPR.T
R3/RRR3-2/3	1298.362	1298.434	-55.753	0.459	1393.757	0.400	25	0.138	-.RPGSVSLNQSPR.-
R3/RRR3-2/3	1298.547	1298.434	87.525	0.463	1366.513	0.396	25	0.135	R.RPGSVSLNQSPR.T
R3/RRR3-3/2	1251.540	1252.528	-1592.906	0.259	648.795	0.311	13	0.133	R.LILGELQAPAVK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1252.238	1252.528	-231.980	0.271	520.216	0.330	12	0.132	-.LILGELQAPAVK.-
R3/RRR3-3/3	1298.522	1298.434	68.433	0.451	1057.367	0.334	23	0.105	R.RPGSVSLNQSPR.T
R3/RRR3-3/3	1298.511	1298.434	59.948	0.441	745.963	0.391	21	0.101	-.RPGSVSLNQSPR.-
R3/RRR3-5/3	1298.017	1298.434	-321.908	0.345	492.479	0.283	22	0.096	R.RPGSVSLNQSPR.T
R3/RRR3-4/2	1433.044	1433.508	-324.802	0.520	2173.984	0.427	20	0.301	R.WSNEVQEAVQSR.A
R3/RRR3-4/2	1245.206	1245.534	-263.771	0.445	1962.137	0.516	19	0.291	R.SIATLAITTLLK.T
R3/RRR3-4/2	1434.125	1433.508	-268.296	0.555	2081.725	0.434	19	0.286	R.WSNEVQEAVQSR.A
R3/RRR3-4/2	1401.669	1402.619	-1395.041	0.370	2237.956	0.323	19	0.284	R.IIDSTLLTQIER.Y
R3/RRR3-4/2	1432.885	1433.508	-1136.590	0.543	2022.027	0.435	20	0.278	R.WSNEVQEAVQSR.A
R3/RRR3-4/2	1402.109	1402.619	-1079.891	0.489	2051.270	0.389	19	0.270	R.IIDSTLLTQIER.Y
R3/RRR3-4/2	1245.379	1245.534	-124.524	0.416	1884.414	0.460	19	0.263	R.SIATLAITTLLK.T
R3/RRR3-4/2	1244.831	1245.534	-1371.830	0.401	1704.638	0.462	19	0.238	R.SIATLAITTLLK.T
R3/RRR3-4/2	1170.653	1171.408	-1504.462	0.538	1587.460	0.407	17	0.212	R.SPLAQCLLIR.Y
R3/RRR3-4/2	1170.429	1171.408	-1696.601	0.441	1464.073	0.411	16	0.199	R.SPLAQCLLIR.Y
R3/RRR3-4/2	1170.662	1171.408	-1496.187	0.507	1383.377	0.432	16	0.196	R.SPLAQCLLIR.Y
R3/RRR3-4/2	1160.906	1161.291	-332.283	0.439	1264.759	0.472	18	0.192	R.AITELNGVTSR.E
R3/RRR3-4/2	1160.397	1161.291	-1636.987	0.405	1174.583	0.488	19	0.187	R.AITELNGVTSR.E
R3/RRR3-4/2	1162.109	1161.291	-156.520	0.520	1104.895	0.425	18	0.172	R.AITELNGVTSR.E
R3/RRR3-4/2	1526.610	1526.758	-97.574	0.491	920.118	0.497	18	0.168	K.LLYLLNQGDTFTK.V
R3/RRR3-4/2	1203.326	1203.416	-74.644	0.489	957.400	0.451	16	0.165	K.FGALVDSLKPR.I
R3/RRR3-4/2	1367.413	1366.587	-127.021	0.425	759.226	0.511	21	0.164	K.LLSSIPEFAGFGK.L
R3/RRR3-4/2	1367.276	1366.587	-227.954	0.416	592.940	0.507	19	0.156	K.LLSSIPEFAGFGK.L
R3/RRR3-4/2	1015.091	1015.189	-96.748	0.438	794.743	0.405	15	0.154	R.VILENATVR.A
R3/RRR3-4/2	1015.101	1015.189	-86.736	0.429	685.351	0.420	15	0.152	R.VILENATVR.A
R3/RRR3-4/2	1161.939	1161.291	-304.064	0.381	762.304	0.402	16	0.150	R.AITELNGVTSR.E
R3/RRR3-4/2	1202.342	1203.416	-1729.673	0.389	939.633	0.353	15	0.149	-.FGALVDSLKPR.-
R3/RRR3-4/2	1015.059	1015.189	-128.594	0.414	686.257	0.376	15	0.148	R.VILENATVR.A
R3/RRR3-4/2	898.779	899.113	-372.660	0.452	657.311	0.348	13	0.144	K.IVVVEAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	899.086	899.113	-29.906	0.425	493.494	0.358	12	0.140	-.IVVVEAIR.-
R3/RRR3-4/2	1526.001	1526.758	-1155.092	0.335	501.837	0.365	17	0.138	K.LLYLLNQGDTFTK.V
R3/RRR3-4/2	1365.607	1366.587	-1454.206	0.252	382.499	0.387	15	0.136	K.LLSSIPEFAGFGK.L
R3/RRR3-3/2	1402.072	1402.619	-1106.117	0.378	1010.512	0.207	15	0.135	R.IIDSTLLTQIER.Y
R3/RRR3-13/2	1366.276	1366.587	-227.672	0.239	270.933	0.362	11	0.125	-.LLSSIPEFAGFGK.-
R3/RRR3-2/2	1170.662	1171.408	-1496.710	0.357	380.069	0.294	10	0.098	-.SPLAQCLLIR.-
R3/RRR3-4/3	1198.530	1198.313	181.661	0.384	938.030	0.303	20	0.095	R.VFHDPQLDAR.R
R3/RRR3-4/3	1198.417	1198.313	87.584	0.378	892.755	0.311	20	0.094	R.VFHDPQLDAR.R
R3/RRR3-4/3	1198.304	1198.313	-6.970	0.352	828.734	0.216	19	0.085	R.VFHDPQLDAR.R
R3/RRR3-7/2	1719.480	1719.960	-280.166	0.492	2509.756	0.556	24	0.410	R.ALDSGIVAQAALDVFTK.E
R3/RRR3-7/2	1182.692	1183.426	-1470.616	0.562	2503.832	0.536	22	0.402	R.LAVQLVAGGGGIK.S
R3/RRR3-7/2	1184.240	1183.426	-157.006	0.579	2486.915	0.488	22	0.380	R.LAVQLVAGGGGIK.S
R3/RRR3-7/2	1183.159	1183.426	-226.380	0.540	2266.956	0.544	22	0.356	R.LAVQLVAGGGGIK.S
R3/RRR3-7/3	1540.124	1540.767	-1069.721	0.505	2691.885	0.400	33	0.348	K.HAVM*AIGVDEEPKK.S
R3/RRR3-7/2	1718.940	1719.960	-1178.937	0.400	2171.501	0.532	22	0.330	R.ALDSGIVAQAALDVFTK.E
R3/RRR3-7/2	1719.479	1719.960	-280.807	0.463	1710.517	0.526	20	0.251	R.ALDSGIVAQAALDVFTK.E
R3/RRR3-7/3	1540.387	1540.767	-247.314	0.555	2041.690	0.468	32	0.242	K.HAVM*AIGVDEEPKK.S
R3/RRR3-7/3	1540.921	1540.767	100.673	0.470	2091.542	0.411	32	0.230	K.HAVM*AIGVDEEPKK.S
R3/RRR3-7/2	1650.667	1651.796	-1294.011	0.485	1589.726	0.462	24	0.223	K.FPSAISESGEITVEGK.V
R3/RRR3-7/2	1651.383	1651.796	-251.015	0.505	1108.543	0.550	21	0.189	K.FPSAISESGEITVEGK.V
R3/RRR3-7/2	1650.616	1651.796	-1324.536	0.475	1270.959	0.461	22	0.188	K.FPSAISESGEITVEGK.V
R3/RRR3-7/3	1719.402	1719.960	-909.174	0.463	1406.053	0.480	30	0.162	R.ALDSGIVAQAALDVFTK.E
R3/RRR3-7/2	1605.401	1605.899	-311.133	0.520	855.041	0.446	22	0.160	K.IGEIPAIEEFVFLK.-
R3/RRR3-7/2	919.480	920.131	-1800.783	0.375	694.714	0.490	14	0.156	K.TLAILGFGK.V
R3/RRR3-7/2	1605.581	1605.899	-198.314	0.459	648.036	0.415	20	0.148	K.IGEIPAIEEFVFLK.-
R3/RRR3-7/2	1606.789	1605.899	-68.397	0.361	610.988	0.407	19	0.144	K.IGEIPAIEEFVFLK.-
R3/RRR3-7/2	920.052	920.131	-85.383	0.413	665.988	0.325	14	0.142	K.TLAILGFGK.V
R3/RRR3-7/2	920.047	920.131	-90.839	0.416	643.634	0.318	14	0.141	K.TLAILGFGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1144.064	1144.260	-172.259	0.318	361.446	0.343	14	0.140	R.GGVIDEDALVR.A
R3/RRR3-7/3	1826.981	1827.014	-18.497	0.512	1247.674	0.447	31	0.138	K.GLGM*HVIAHDPYASADR.A
R3/RRR3-4/2	1145.190	1144.260	-61.541	0.338	740.423	0.274	13	0.135	-.GGVIDEDALVR.-
R3/RRR3-9/2	1144.053	1144.260	-181.250	0.346	357.415	0.272	14	0.132	-.GGVIDEDALVR.-
R3/RRR3-7/3	1720.628	1719.960	-193.601	0.421	883.345	0.552	26	0.132	R.ALDSGIVAQAALDVFTK.E
R3/RRR3-7/3	1827.033	1827.014	10.051	0.500	1187.311	0.438	30	0.131	K.GLGM*HVIAHDPYASADR.A
R3/RRR3-1/2	1144.474	1144.260	187.793	0.224	640.316	0.114	14	0.129	R.GGVIDEDALVR.A
R3/RRR3-1/2	1145.343	1144.260	72.199	0.292	677.755	0.173	13	0.128	-.GGVIDEDALVR.-
R3/RRR3-7/3	1668.538	1668.940	-241.418	0.450	962.947	0.448	28	0.118	R.KHAVM*AIGVDEEPKK.S
R3/RRR3-7/3	1826.344	1827.014	-917.431	0.461	1068.848	0.410	31	0.118	K.GLGM*HVIAHDPYASADR.A
R3/RRR3-2/2	1145.239	1144.260	-18.774	0.341	636.354	0.226	12	0.116	-.GGVIDEDALVR.-
R3/RRR3-7/3	1164.285	1164.379	-80.944	0.429	1492.495	0.238	22	0.112	R.NKYVGVSLVGK.T
R3/RRR3-7/3	1163.843	1164.379	-1323.862	0.397	1484.615	0.215	22	0.109	-.NKYVGVSLVGK.-
R3/RRR3-7/3	1668.664	1668.940	-165.678	0.478	585.188	0.438	26	0.106	R.KHAVM*AIGVDEEPKK.S
R3/RRR3-7/3	1720.020	1719.960	34.864	0.359	917.506	0.382	28	0.104	R.ALDSGIVAQAALDVFTK.E
R3/RRR3-7/3	1668.212	1668.940	-1038.669	0.377	777.878	0.395	25	0.102	R.KHAVM*AIGVDEEPKK.S
R3/RRR3-8/2	1973.548	1974.161	-819.570	0.618	2786.112	0.579	27	0.476	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-8/2	1974.703	1974.161	-232.237	0.633	2453.267	0.570	27	0.394	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-8/2	1624.274	1623.946	202.800	0.532	2101.286	0.625	21	0.347	R.LHFFMVGFAPLTSR.G
R3/RRR3-8/2	1972.738	1974.161	-1231.455	0.540	2206.972	0.544	26	0.338	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-8/2	1625.319	1623.946	230.316	0.555	2034.210	0.575	21	0.318	R.LHFFMVGFAPLTSR.G
R3/RRR3-9/2	1343.171	1343.427	-190.934	0.565	1767.326	0.552	20	0.271	R.INVYYNEASGGR.Y
R3/RRR3-8/2	1624.996	1623.946	31.147	0.537	1688.883	0.582	19	0.263	R.LHFFMVGFAPLTSR.G
R3/RRR3-8/2	1343.035	1343.427	-292.875	0.542	1771.429	0.500	20	0.258	R.INVYYNEASGGR.Y
R3/RRR3-9/2	1343.100	1343.427	-243.999	0.545	1701.711	0.526	20	0.255	R.INVYYNEASGGR.Y
R3/RRR3-12/2	1975.513	1974.161	179.076	0.543	1887.924	0.445	25	0.253	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-9/2	1402.669	1401.719	-35.598	0.401	1372.292	0.579	18	0.221	-.MM*LTFSVFPSPK.-
R3/RRR3-8/2	1232.022	1232.391	-300.019	0.484	1632.580	0.394	17	0.213	R.VSEQFTAM*FR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1216.083	1216.391	-254.281	0.505	1463.195	0.438	16	0.204	R.VSEQFTAMFR.R
R3/RRR3-9/2	1385.970	1385.720	181.131	0.485	1246.324	0.549	17	0.203	R.MMLTFSVFPSPK.V
R3/RRR3-8/2	1640.439	1639.945	302.253	0.488	1305.771	0.516	20	0.202	R.LHFFM*VGFAPLTSR.G
R3/RRR3-9/2	1231.942	1232.391	-365.632	0.438	1519.330	0.389	17	0.200	R.VSEQFTAM*FR.R
R3/RRR3-8/2	1232.006	1232.391	-313.339	0.512	1414.965	0.438	17	0.200	R.VSEQFTAM*FR.R
R3/RRR3-9/2	1231.948	1232.391	-360.860	0.508	1336.567	0.458	16	0.196	R.VSEQFTAM*FR.R
R3/RRR3-9/2	1733.370	1731.994	217.654	0.562	923.727	0.625	22	0.192	R.ALTVPELTQQMWDAK.N
R3/RRR3-9/2	1231.752	1232.391	-1334.643	0.478	1402.300	0.371	17	0.186	R.VSEQFTAM*FR.R
R3/RRR3-9/2	1733.566	1731.994	-247.520	0.553	926.470	0.589	22	0.186	R.ALTVPELTQQMWDAK.N
R3/RRR3-9/2	1698.103	1697.871	136.733	0.526	1029.668	0.546	20	0.185	K.NSSYFVEWIPNNVK.S
R3/RRR3-9/2	1385.054	1385.720	-1206.515	0.469	1129.088	0.504	16	0.184	R.MMLTFSVFPSPK.V
R3/RRR3-8/3	1974.399	1974.161	121.127	0.510	1652.689	0.443	31	0.183	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-9/2	1697.445	1697.871	-251.849	0.485	1044.127	0.524	20	0.182	K.NSSYFVEWIPNNVK.S
R3/RRR3-9/2	1385.209	1385.720	-1094.215	0.430	1152.105	0.485	15	0.181	R.MMLTFSVFPSPK.V
R3/RRR3-9/2	1140.167	1140.403	-207.103	0.576	1051.256	0.493	17	0.181	K.LAVNLIPFPR.L
R3/RRR3-9/3	1975.266	1974.161	53.541	0.479	1592.332	0.457	30	0.180	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-8/2	1139.684	1140.403	-1512.253	0.482	1071.371	0.479	17	0.180	K.LAVNLIPFPR.L
R3/RRR3-8/2	1141.160	1140.403	-213.146	0.533	1053.226	0.470	17	0.177	K.LAVNLIPFPR.L
R3/RRR3-9/2	1140.184	1140.403	-192.281	0.584	1074.882	0.465	17	0.177	K.LAVNLIPFPR.L
R3/RRR3-9/2	1733.468	1731.994	274.005	0.504	800.034	0.590	21	0.176	R.ALTVPELTQQMWDAK.N
R3/RRR3-8/2	1385.275	1385.720	-321.773	0.406	997.990	0.530	15	0.176	R.MMLTFSVFPSPK.V
R3/RRR3-7/2	1974.224	1974.161	32.397	0.510	937.633	0.551	22	0.176	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-2/2	1140.196	1140.403	-181.434	0.542	1046.348	0.464	17	0.176	K.LAVNLIPFPR.L
R3/RRR3-9/2	1747.237	1747.994	-1008.170	0.491	933.265	0.522	22	0.175	R.ALTVPELTQQM*WDAK.N
R3/RRR3-8/2	1698.330	1697.871	271.023	0.544	959.453	0.516	19	0.174	K.NSSYFVEWIPNNVK.S
R3/RRR3-8/2	1747.329	1747.994	-955.704	0.485	804.133	0.562	21	0.172	R.ALTVPELTQQM*WDAK.N
R3/RRR3-9/2	1401.186	1401.719	-1097.572	0.457	989.115	0.494	16	0.171	-.MM*LTFSVFPSPK.-
R3/RRR3-9/2	1215.543	1216.391	-1525.352	0.374	1205.592	0.384	15	0.171	R.VSEQFTAMFR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1140.036	1140.403	-322.364	0.525	1015.673	0.428	17	0.168	K.LAVNLIPFPR.L
R3/RRR3-8/2	1732.696	1731.994	-172.389	0.483	788.056	0.546	20	0.168	R.ALTVPELTQQMWDAK.N
R3/RRR3-8/2	1697.454	1697.871	-246.871	0.422	937.295	0.483	19	0.167	K.NSSYFVEWIPNNVK.S
R3/RRR3-8/2	1139.638	1140.403	-1553.140	0.434	925.179	0.455	17	0.167	K.LAVNLIPFPR.L
R3/RRR3-8/2	1747.564	1747.994	-246.766	0.466	778.209	0.513	21	0.164	R.ALTVPELTQQM*WDAK.N
R3/RRR3-10/2	1139.732	1140.403	-1470.079	0.421	676.008	0.537	14	0.163	K.LAVNLIPFPR.L
R3/RRR3-8/2	1697.324	1697.871	-914.283	0.461	861.440	0.481	18	0.162	K.NSSYFVEWIPNNVK.S
R3/RRR3-9/2	1139.723	1140.403	-1478.255	0.422	736.490	0.494	15	0.162	K.LAVNLIPFPR.L
R3/RRR3-13/2	1699.409	1697.871	-272.884	0.523	814.961	0.496	17	0.161	K.NSSYFVEWIPNNVK.S
R3/RRR3-1/2	1140.343	1140.403	-52.032	0.491	876.702	0.423	15	0.159	K.LAVNLIPFPR.L
R3/RRR3-15/2	1140.137	1140.403	-233.848	0.533	745.494	0.462	14	0.158	K.LAVNLIPFPR.L
R3/RRR3-9/2	1215.806	1216.391	-1307.703	0.389	1163.998	0.305	16	0.158	R.VSEQFTAMFR.R
R3/RRR3-15/2	1140.479	1140.403	67.246	0.488	769.238	0.431	15	0.157	K.LAVNLIPFPR.L
R3/RRR3-12/2	1140.175	1140.403	-200.444	0.406	808.561	0.415	15	0.155	K.LAVNLIPFPR.L
R3/RRR3-8/3	1973.839	1974.161	-163.555	0.471	1659.993	0.341	31	0.155	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-8/2	1640.987	1639.945	26.015	0.415	852.158	0.431	18	0.155	R.LHFFM*VGFAPLTSR.G
R3/RRR3-13/2	1141.516	1140.403	99.899	0.403	1059.277	0.317	16	0.154	K.LAVNLIPFPR.L
R3/RRR3-10/2	1972.772	1974.161	-1214.615	0.396	714.637	0.491	20	0.154	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-10/2	1972.722	1974.161	-1240.030	0.394	605.217	0.543	18	0.154	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-4/2	1140.251	1140.403	-133.642	0.405	682.941	0.436	14	0.153	K.LAVNLIPFPR.L
R3/RRR3-14/2	1140.354	1140.403	-42.798	0.322	770.244	0.379	14	0.148	K.LAVNLIPFPR.L
R3/RRR3-8/2	1147.199	1147.266	-58.765	0.422	750.538	0.366	15	0.147	R.FPGQLNSDLR.K
R3/RRR3-8/2	1698.758	1697.871	-67.145	0.446	772.233	0.396	16	0.146	K.NSSYFVEWIPNNVK.S
R3/RRR3-9/2	1147.091	1147.266	-153.019	0.381	693.737	0.373	15	0.146	R.FPGQLNSDLR.K
R3/RRR3-9/3	1823.858	1824.025	-91.715	0.426	1501.168	0.373	29	0.145	R.EILHIQGGQCGNQIGAK.F
R3/RRR3-3/2	1139.952	1140.403	-396.175	0.426	590.487	0.360	13	0.144	K.LAVNLIPFPR.L
R3/RRR3-9/2	1972.570	1974.161	-1825.814	0.321	430.278	0.472	17	0.142	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-9/3	1823.115	1824.025	-1050.599	0.391	1566.758	0.328	29	0.142	R.EILHIQGGQCGNQIGAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1972.240	1974.161	-1993.610	0.381	770.274	0.368	17	0.141	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-8/2	1215.578	1216.391	-1495.997	0.356	829.025	0.269	15	0.140	R.VSEQFTAMFR.R
R3/RRR3-8/2	1402.941	1401.719	158.414	0.335	277.446	0.280	13	0.140	R.M*MLTFSVFPSPK.V
R3/RRR3-9/2	1148.091	1147.266	-152.245	0.404	600.772	0.278	15	0.139	R.FPGQLNSDLR.K
R3/RRR3-9/2	1976.060	1974.161	-51.155	0.358	222.695	0.341	15	0.138	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-7/2	1697.396	1697.871	-280.782	0.414	682.813	0.328	16	0.138	K.NSSYFVEWIPNNVK.S
R3/RRR3-14/2	1140.380	1140.403	-19.821	0.365	472.001	0.363	13	0.138	-.LAVNLIPFPR.-
R3/RRR3-8/2	1146.881	1147.266	-336.347	0.337	988.694	0.199	17	0.138	R.FPGQLNSDLR.K
R3/RRR3-8/2	1216.126	1216.391	-219.035	0.369	693.403	0.221	16	0.137	R.VSEQFTAMFR.R
R3/RRR3-8/2	1730.776	1731.994	-1285.687	0.271	632.304	0.329	17	0.137	R.ALTVPELTQQMWDAK.N
R3/RRR3-8/2	1730.631	1731.994	-1369.417	0.261	435.240	0.389	15	0.136	R.ALTVPELTQQMWDAK.N
R3/RRR3-2/2	1139.611	1140.403	-1576.813	0.270	492.914	0.311	10	0.136	K.LAVNLIPFPR.L
R3/RRR3-14/2	1385.210	1385.720	-1092.976	0.284	461.846	0.362	12	0.136	R.MMLTFSVFPSPK.V
R3/RRR3-10/2	1139.641	1140.403	-1550.773	0.192	357.395	0.377	10	0.136	K.LAVNLIPFPR.L
R3/RRR3-8/2	1147.033	1147.266	-203.088	0.343	479.864	0.339	13	0.135	-.FPGQLNSDLR.-
R3/RRR3-8/2	1343.633	1343.427	154.125	0.224	301.458	0.348	13	0.134	R.INVYYNEASGGR.Y
R3/RRR3-3/2	1699.557	1697.871	-185.692	0.318	343.982	0.315	13	0.134	-.NSSYFVEWIPNNVK.-
R3/RRR3-1/2	1975.549	1974.161	197.418	0.418	293.199	0.378	14	0.131	-.GHYTEGAELIDSVLDVVR.-
R3/RRR3-4/2	1140.131	1140.403	-238.682	0.194	530.640	0.283	11	0.129	-.LAVNLIPFPR.-
R3/RRR3-8/3	1975.420	1974.161	131.725	0.483	1166.209	0.425	30	0.129	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-17/2	1640.803	1639.945	-86.583	0.312	234.354	0.332	11	0.127	-.LHFFM*VGFAPLTSR.-
R3/RRR3-9/3	1973.920	1974.161	-122.424	0.438	1184.760	0.371	26	0.120	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-9/3	1973.594	1974.161	-796.294	0.393	1246.438	0.269	28	0.106	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-10/3	1973.555	1974.161	-816.038	0.369	923.507	0.274	24	0.093	K.GHYTEGAELIDSVLDVVR.K
R3/RRR3-2/3	1973.640	1974.161	-772.640	0.347	797.252	0.286	23	0.093	-.GHYTEGAELIDSVLDVVR.-
R3/RRR3-2/3	1973.167	1974.161	-1013.334	0.300	782.866	0.221	25	0.088	-.GHYTEGAELIDSVLDVVR.-
R3/RRR3-7/3	1902.075	1902.181	-55.887	0.494	2876.337	0.535	41	0.478	K.AAVEEGIVPGGGVALLYASK.E
R3/RRR3-7/3	1901.765	1902.181	-219.391	0.480	2643.667	0.593	39	0.445	K.AAVEEGIVPGGGVALLYASK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1419.024	1418.685	239.726	0.521	2366.208	0.436	21	0.336	R.GISMAVDAVVTNLK.G
R3/RRR3-7/2	1418.259	1418.685	-300.995	0.480	2255.789	0.385	21	0.301	R.GISMAVDAVVTNLK.G
R3/RRR3-7/2	1434.349	1434.684	-234.159	0.501	2133.166	0.361	21	0.272	R.GISM*AVDAVVTNLK.G
R3/RRR3-7/2	1320.536	1321.461	-1462.208	0.430	1872.361	0.486	19	0.268	R.NVVIEQSYGSPK.V
R3/RRR3-7/2	1321.086	1321.461	-284.951	0.540	1671.585	0.557	18	0.257	R.NVVIEQSYGSPK.V
R3/RRR3-7/2	1321.167	1321.461	-223.028	0.475	1630.579	0.532	18	0.245	R.NVVIEQSYGSPK.V
R3/RRR3-7/2	1386.170	1386.576	-294.095	0.530	1326.554	0.568	19	0.218	R.GYISPYFVTNPK.T
R3/RRR3-7/2	1387.312	1386.576	-191.390	0.514	1333.616	0.551	19	0.215	R.GYISPYFVTNPK.T
R3/RRR3-7/2	1901.637	1902.181	-814.378	0.495	1268.454	0.579	27	0.210	K.AAVEEGIVPGGGVALLYASK.E
R3/RRR3-7/2	1386.188	1386.576	-280.754	0.486	1237.051	0.557	18	0.205	R.GYISPYFVTNPK.T
R3/RRR3-7/2	1146.538	1147.218	-1468.934	0.457	1370.235	0.487	18	0.204	K.IGGASEAEVGEK.K
R3/RRR3-7/2	1902.241	1902.181	31.950	0.482	1214.335	0.566	26	0.202	K.AAVEEGIVPGGGVALLYASK.E
R3/RRR3-7/2	1146.448	1147.218	-1548.079	0.446	1307.029	0.487	18	0.198	K.IGGASEAEVGEK.K
R3/RRR3-7/2	1434.209	1434.684	-332.356	0.371	1479.086	0.396	18	0.195	R.GISM*AVDAVVTNLK.G
R3/RRR3-7/2	1146.914	1147.218	-265.240	0.470	1267.716	0.474	18	0.192	K.IGGASEAEVGEK.K
R3/RRR3-7/2	1902.263	1902.181	43.599	0.464	1130.992	0.554	25	0.191	K.AAVEEGIVPGGGVALLYASK.E
R3/RRR3-7/2	1268.913	1268.447	368.888	0.425	1014.246	0.510	18	0.177	K.SVAAGM*NAM*DLR.R
R3/RRR3-7/2	1267.959	1268.447	-385.369	0.449	1358.774	0.332	19	0.174	K.SVAAGM*NAM*DLR.R
R3/RRR3-7/2	1586.295	1586.679	-242.791	0.521	1053.313	0.489	18	0.174	R.SAIELSTSDYDKEK.L
R3/RRR3-7/2	1030.582	1031.142	-1517.784	0.405	1294.513	0.353	16	0.173	R.GVEELADAVK.V
R3/RRR3-7/2	1267.905	1268.447	-1219.426	0.391	1220.976	0.370	18	0.170	K.SVAAGM*NAM*DLR.R
R3/RRR3-7/2	1030.539	1031.142	-1560.382	0.453	1176.814	0.381	16	0.170	R.GVEELADAVK.V
R3/RRR3-7/3	1861.449	1862.072	-874.590	0.510	1573.449	0.430	31	0.168	K.VTVSKDDTVILDGAGDKK.S
R3/RRR3-7/3	1862.936	1862.072	-72.999	0.521	1410.449	0.489	31	0.166	K.VTVSKDDTVILDGAGDKK.S
R3/RRR3-7/2	1434.103	1434.684	-1106.135	0.353	1281.933	0.334	16	0.165	R.GISM*AVDAVVTNLK.G
R3/RRR3-7/2	1030.890	1031.142	-244.972	0.450	1239.680	0.322	16	0.164	R.GVEELADAVK.V
R3/RRR3-7/2	1586.212	1586.679	-295.446	0.496	917.677	0.471	17	0.162	R.SAIELSTSDYDKEK.L
R3/RRR3-7/2	1586.173	1586.679	-952.725	0.451	939.695	0.431	17	0.157	R.SAIELSTSDYDKEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/3	1861.971	1862.072	-54.362	0.518	1324.766	0.441	30	0.144	K.VTVSKDDTVILDGAGDKK.S
R3/RRR3-7/2	844.298	844.034	313.508	0.251	987.445	0.191	15	0.135	K.LSGGVAVLK.I
R3/RRR3-7/2	844.037	844.034	3.901	0.302	685.703	0.148	13	0.129	K.LSGGVAVLK.I
R3/RRR3-7/2	844.045	844.034	12.604	0.229	717.522	0.079	13	0.126	K.LSGGVAVLK.I
R3/RRR3-7/3	1901.986	1902.181	-102.528	0.318	838.568	0.323	27	0.093	K.AAVEEGIVPGGGVALLYASK.E
R3/RRR3-5/2	1427.667	1426.728	-43.190	0.580	2065.306	0.539	18	0.314	R.LPLLDLNIYVPR.D
R3/RRR3-5/2	1426.294	1426.728	-305.222	0.497	1963.351	0.553	19	0.302	R.LPLLDLNIYVPR.D
R3/RRR3-5/2	1087.162	1087.252	-83.070	0.514	1485.941	0.488	18	0.219	K.VANASALAEIK.K
R3/RRR3-5/2	1426.590	1426.728	-96.948	0.478	1322.043	0.511	17	0.203	R.LPLLDLNIYVPR.D
R3/RRR3-5/2	1402.229	1402.576	-248.204	0.491	1329.669	0.443	18	0.192	R.VFFANDTYLPSK.M
R3/RRR3-4/2	1161.970	1161.353	-330.609	0.387	1005.322	0.513	15	0.176	K.MSDFLGYSLK.A
R3/RRR3-5/2	1401.893	1402.576	-1203.551	0.420	1190.026	0.411	17	0.173	R.VFFANDTYLPSK.M
R3/RRR3-5/2	1781.625	1782.079	-256.031	0.453	1123.361	0.442	21	0.172	K.LVRPVLGGSQELPYPR.R
R3/RRR3-5/2	1401.788	1402.576	-1278.843	0.419	1203.057	0.361	17	0.166	R.VFFANDTYLPSK.M
R3/RRR3-5/2	1180.168	1180.465	-252.475	0.391	1181.007	0.353	17	0.165	K.AIVEGVLPIIR.T
R3/RRR3-5/2	1025.256	1025.097	155.174	0.435	943.663	0.453	15	0.164	K.STAAGESVFR.V
R3/RRR3-5/2	1181.054	1180.465	-348.903	0.390	1100.779	0.363	15	0.159	K.AIVEGVLPIIR.T
R3/RRR3-5/2	1534.512	1534.609	-63.720	0.432	860.656	0.437	20	0.157	K.STLDPNVYGDHTSK.I
R3/RRR3-5/2	1781.685	1782.079	-222.006	0.450	879.328	0.450	19	0.156	K.LVRPVLGGSQELPYPR.R
R3/RRR3-5/2	1024.908	1025.097	-185.476	0.352	832.496	0.444	14	0.154	K.STAAGESVFR.V
R3/RRR3-4/2	1161.992	1161.353	-311.426	0.388	681.378	0.487	13	0.154	K.MSDFLGYSLK.A
R3/RRR3-5/2	1179.742	1180.465	-1464.745	0.359	848.345	0.390	16	0.150	K.AIVEGVLPIIR.T
R3/RRR3-5/2	1534.228	1534.609	-249.354	0.466	693.691	0.443	18	0.150	K.STLDPNVYGDHTSK.I
R3/RRR3-5/2	1177.318	1177.352	-29.055	0.369	914.158	0.337	16	0.149	K.M*SDFLGYSLK.A
R3/RRR3-5/2	1240.143	1240.474	-267.810	0.436	625.297	0.429	17	0.148	K.SLLPVAGDQVLK.L
R3/RRR3-5/2	1533.587	1534.609	-1322.783	0.381	666.141	0.419	18	0.146	K.STLDPNVYGDHTSK.I
R3/RRR3-5/2	1239.515	1240.474	-1585.345	0.370	552.849	0.363	15	0.138	K.SLLPVAGDQVLK.L
R3/RRR3-5/2	1177.162	1177.352	-161.672	0.203	561.399	0.285	13	0.132	K.M*SDFLGYSLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1781.864	1782.079	-121.224	0.475	1024.191	0.435	30	0.120	K.LVRPVLGGSQELPYPR.R
R3/RRR3-5/3	1782.034	1782.079	-25.471	0.536	1054.813	0.409	31	0.117	K.LVRPVLGGSQELPYPR.R
R3/RRR3-5/3	1471.617	1471.665	-32.193	0.474	1259.287	0.333	23	0.115	K.HNM*EGLTVQNALK.G
R3/RRR3-5/3	1781.520	1782.079	-877.954	0.446	996.556	0.356	30	0.105	K.LVRPVLGGSQELPYPR.R
R3/RRR3-6/2	1596.448	1596.852	-253.671	0.559	2551.643	0.617	24	0.439	R.TGAATNVIFGLALGYK.S
R3/RRR3-6/2	1596.326	1596.852	-958.553	0.528	2281.558	0.611	23	0.377	R.TGAATNVIFGLALGYK.S
R3/RRR3-6/2	1596.455	1596.852	-249.222	0.530	2164.045	0.597	25	0.350	R.TGAATNVIFGLALGYK.S
R3/RRR3-6/2	1490.175	1490.598	-284.497	0.440	2267.987	0.518	25	0.341	K.TDALDAAGNTTAAIGK.G
R3/RRR3-6/2	1490.153	1490.598	-299.866	0.464	2162.293	0.554	25	0.332	K.TDALDAAGNTTAAIGK.G
R3/RRR3-5/2	1489.665	1490.598	-1301.457	0.425	2262.405	0.457	24	0.321	K.TDALDAAGNTTAAIGK.G
R3/RRR3-1/2	1490.192	1490.598	-273.566	0.459	2022.638	0.522	24	0.298	K.TDALDAAGNTTAAIGK.G
R3/RRR3-3/2	1490.180	1490.598	-281.620	0.435	1977.028	0.536	24	0.294	K.TDALDAAGNTTAAIGK.G
R3/RRR3-7/2	1490.227	1490.598	-249.651	0.458	1994.881	0.520	24	0.293	K.TDALDAAGNTTAAIGK.G
R3/RRR3-5/2	1490.201	1490.598	-267.485	0.455	1976.418	0.520	24	0.290	K.TDALDAAGNTTAAIGK.G
R3/RRR3-2/2	1489.619	1490.598	-1332.401	0.403	2020.457	0.491	23	0.288	K.TDALDAAGNTTAAIGK.G
R3/RRR3-1/2	1490.058	1490.598	-1036.447	0.407	1982.041	0.510	24	0.287	K.TDALDAAGNTTAAIGK.G
R3/RRR3-3/2	1490.022	1490.598	-1061.124	0.409	2002.557	0.496	23	0.287	K.TDALDAAGNTTAAIGK.G
R3/RRR3-6/2	1490.142	1490.598	-306.934	0.444	2047.391	0.449	24	0.281	K.TDALDAAGNTTAAIGK.G
R3/RRR3-2/2	1490.006	1490.598	-1071.488	0.432	1975.853	0.473	23	0.276	K.TDALDAAGNTTAAIGK.G
R3/RRR3-1/2	1490.158	1490.598	-296.414	0.415	1933.278	0.497	23	0.276	K.TDALDAAGNTTAAIGK.G
R3/RRR3-5/2	1490.131	1490.598	-314.495	0.423	1987.424	0.452	23	0.272	K.TDALDAAGNTTAAIGK.G
R3/RRR3-2/2	1490.314	1490.598	-190.896	0.458	1899.955	0.485	23	0.268	K.TDALDAAGNTTAAIGK.G
R3/RRR3-7/2	1490.170	1490.598	-288.031	0.469	1746.170	0.537	23	0.258	K.TDALDAAGNTTAAIGK.G
R3/RRR3-3/2	1490.120	1490.598	-321.810	0.421	1899.578	0.449	23	0.258	K.TDALDAAGNTTAAIGK.G
R3/RRR3-2/2	1399.943	1400.563	-1160.624	0.476	1654.647	0.551	22	0.251	K.AADVGADLVGKVER.N
R3/RRR3-5/2	1400.011	1400.563	-1112.118	0.482	1796.866	0.467	22	0.249	K.AADVGADLVGKVER.N
R3/RRR3-6/2	1400.350	1400.563	-152.361	0.493	1662.763	0.490	22	0.237	K.AADVGADLVGKVER.N
R3/RRR3-5/2	1400.400	1400.563	-116.335	0.488	1675.275	0.481	22	0.237	K.AADVGADLVGKVER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1270.285	1270.457	-136.058	0.379	1734.680	0.441	20	0.236	K.AAVIGDTIGDPLK.D
R3/RRR3-1/2	1596.325	1596.852	-959.475	0.490	1474.483	0.579	21	0.233	R.TGAATNVIFGLALGYK.S
R3/RRR3-6/2	1400.094	1400.563	-335.682	0.485	1583.674	0.499	22	0.230	K.AADVGADLVGKVER.N
R3/RRR3-1/2	1401.413	1400.563	-107.165	0.470	1440.155	0.571	22	0.229	K.AADVGADLVGKVER.N
R3/RRR3-1/2	1400.185	1400.563	-270.690	0.469	1688.432	0.440	22	0.229	K.AADVGADLVGKVER.N
R3/RRR3-6/2	1271.292	1270.457	-130.268	0.476	1595.049	0.481	19	0.227	K.AAVIGDTIGDPLK.D
R3/RRR3-6/2	1400.366	1400.563	-141.168	0.489	1543.927	0.492	21	0.223	K.AADVGADLVGKVER.N
R3/RRR3-1/2	1400.260	1400.563	-216.726	0.500	1570.925	0.471	22	0.222	K.AADVGADLVGKVER.N
R3/RRR3-6/2	1015.969	1016.130	-158.969	0.513	1337.256	0.508	18	0.206	K.AADVGADLVGK.V
R3/RRR3-6/2	1269.841	1270.457	-1276.933	0.295	1638.359	0.355	18	0.204	K.AAVIGDTIGDPLK.D
R3/RRR3-7/2	1597.053	1596.852	126.219	0.479	1289.312	0.532	20	0.202	R.TGAATNVIFGLALGYK.S
R3/RRR3-4/2	1400.223	1400.563	-243.663	0.416	1399.929	0.452	20	0.198	K.AADVGADLVGKVER.N
R3/RRR3-2/2	1400.407	1400.563	-111.351	0.474	1392.692	0.449	21	0.198	K.AADVGADLVGKVER.N
R3/RRR3-3/2	1400.383	1400.563	-129.101	0.511	1383.087	0.453	21	0.197	K.AADVGADLVGKVER.N
R3/RRR3-6/2	1015.823	1016.130	-303.747	0.468	1213.385	0.518	17	0.195	K.AADVGADLVGK.V
R3/RRR3-2/2	1269.744	1270.457	-1353.303	0.299	1506.355	0.376	18	0.193	K.AAVIGDTIGDPLK.D
R3/RRR3-6/2	1269.718	1270.457	-1374.063	0.346	1459.728	0.387	18	0.192	K.AAVIGDTIGDPLK.D
R3/RRR3-6/2	1015.878	1016.130	-249.496	0.463	1235.352	0.470	17	0.188	K.AADVGADLVGK.V
R3/RRR3-1/2	1015.577	1016.130	-1534.000	0.385	1223.259	0.435	18	0.181	K.AADVGADLVGK.V
R3/RRR3-1/2	1015.850	1016.130	-276.982	0.431	1197.521	0.421	17	0.177	K.AADVGADLVGK.V
R3/RRR3-5/2	1015.755	1016.130	-370.907	0.394	1080.543	0.473	17	0.176	K.AADVGADLVGK.V
R3/RRR3-1/3	1332.367	1332.447	-59.981	0.584	1236.284	0.578	25	0.167	K.KYIEAGASEHAR.T
R3/RRR3-6/2	1231.186	1231.381	-159.274	0.448	975.252	0.447	15	0.166	K.FTIFNFGEQK.E
R3/RRR3-5/2	1015.308	1016.130	-1800.068	0.318	1170.512	0.373	17	0.166	K.AADVGADLVGK.V
R3/RRR3-1/3	1332.476	1332.447	21.481	0.553	1187.105	0.591	25	0.165	K.KYIEAGASEHAR.T
R3/RRR3-1/2	1015.302	1016.130	-1806.591	0.347	1133.974	0.347	17	0.161	K.AADVGADLVGK.V
R3/RRR3-6/2	1232.227	1231.381	-125.257	0.489	1025.873	0.386	15	0.160	K.FTIFNFGEQK.E
R3/RRR3-5/2	1015.498	1016.130	-1611.886	0.352	1082.914	0.355	17	0.159	K.AADVGADLVGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1015.380	1016.130	-1729.400	0.341	1022.022	0.378	17	0.158	K.AADVGADLVGK.V
R3/RRR3-5/3	1332.735	1332.447	216.330	0.567	1035.502	0.614	25	0.157	K.KYIEAGASEHAR.T
R3/RRR3-3/2	1015.494	1016.130	-1615.871	0.342	1075.253	0.340	17	0.157	K.AADVGADLVGK.V
R3/RRR3-7/2	1400.373	1400.563	-135.747	0.404	864.057	0.436	18	0.156	K.AADVGADLVGKVER.N
R3/RRR3-2/2	1596.522	1596.852	-207.109	0.435	958.867	0.420	18	0.156	-.TGAATNVIFGLALGYK.-
R3/RRR3-3/3	1331.893	1332.447	-1170.063	0.487	1154.195	0.569	25	0.156	K.KYIEAGASEHAR.T
R3/RRR3-2/2	1015.812	1016.130	-314.598	0.423	927.348	0.380	16	0.155	K.AADVGADLVGK.V
R3/RRR3-6/2	856.908	857.030	-142.540	0.461	487.037	0.414	12	0.150	K.VVDVLSPK.V
R3/RRR3-2/2	1015.388	1016.130	-1720.945	0.339	993.824	0.317	17	0.150	K.AADVGADLVGK.V
R3/RRR3-2/2	1269.849	1270.457	-1270.465	0.297	1178.512	0.245	17	0.148	K.AAVIGDTIGDPLK.D
R3/RRR3-2/2	856.907	857.030	-143.684	0.433	510.068	0.381	12	0.148	K.VVDVLSPK.V
R3/RRR3-1/2	856.877	857.030	-179.267	0.403	568.933	0.369	13	0.147	K.VVDVLSPK.V
R3/RRR3-5/2	1400.151	1400.563	-295.356	0.352	632.685	0.434	16	0.146	K.AADVGADLVGKVER.N
R3/RRR3-3/2	857.128	857.030	115.046	0.379	592.703	0.330	13	0.144	K.VVDVLSPK.V
R3/RRR3-6/2	857.089	857.030	69.053	0.382	491.420	0.324	12	0.143	K.VVDVLSPK.V
R3/RRR3-2/2	1258.746	1258.446	238.832	0.334	894.902	0.340	16	0.143	K.DTSGPSLNILIK.L
R3/RRR3-3/2	856.661	857.030	-432.001	0.352	401.632	0.308	11	0.142	K.VVDVLSPK.V
R3/RRR3-6/2	856.747	857.030	-330.921	0.352	519.230	0.313	12	0.142	K.VVDVLSPK.V
R3/RRR3-1/2	856.265	857.030	-2066.564	0.346	523.396	0.309	12	0.142	K.VVDVLSPK.V
R3/RRR3-1/2	856.333	857.030	-1987.764	0.310	452.153	0.340	11	0.141	K.VVDVLSPK.V
R3/RRR3-3/2	1015.827	1016.130	-299.889	0.304	846.396	0.276	16	0.141	K.AADVGADLVGK.V
R3/RRR3-3/2	1015.137	1016.130	-1969.347	0.304	838.954	0.258	16	0.139	K.AADVGADLVGK.V
R3/RRR3-7/2	1015.238	1016.130	-1869.899	0.252	627.854	0.312	15	0.138	K.AADVGADLVGK.V
R3/RRR3-5/3	1332.579	1332.447	99.209	0.527	1025.658	0.523	25	0.136	K.KYIEAGASEHAR.T
R3/RRR3-6/3	1332.593	1332.447	109.407	0.482	1040.403	0.513	24	0.135	K.KYIEAGASEHAR.T
R3/RRR3-6/2	1230.807	1231.381	-1282.513	0.235	681.084	0.210	13	0.130	K.FTIFNFGEQK.E
R3/RRR3-1/3	1776.009	1775.899	62.237	0.394	1066.105	0.322	28	0.102	-.ERTDALDAAGNTTAAIGK.-
R3/RRR3-1/3	1775.681	1775.899	-122.991	0.313	812.318	0.212	26	0.082	-.ERTDALDAAGNTTAAIGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1504.412	1504.744	-221.905	0.432	2077.144	0.488	22	0.302	K.ECILSGLLSVDGLK.V
R3/RRR3-9/2	1505.210	1504.744	310.269	0.492	1755.597	0.500	21	0.254	K.ECILSGLLSVDGLK.V
R3/RRR3-9/2	1505.274	1504.744	-313.202	0.497	1663.633	0.510	21	0.244	K.ECILSGLLSVDGLK.V
R3/RRR3-9/2	1172.024	1172.404	-324.583	0.412	1261.168	0.452	16	0.187	K.FM*M*ANGTLVR.T
R3/RRR3-9/2	1863.864	1864.003	-74.663	0.390	1304.449	0.393	19	0.177	R.NFFIYVQDYNEADPK.T
R3/RRR3-9/2	1291.947	1292.456	-1171.687	0.370	1255.663	0.380	17	0.174	K.VVCDPSYLPNK.V
R3/RRR3-9/2	1073.031	1073.180	-139.960	0.487	727.710	0.506	16	0.163	K.AVDGSYVFSK.G
R3/RRR3-9/2	1072.947	1073.180	-218.138	0.488	686.003	0.510	16	0.163	K.AVDGSYVFSK.G
R3/RRR3-9/2	1072.899	1073.180	-262.996	0.459	699.417	0.465	16	0.157	K.AVDGSYVFSK.G
R3/RRR3-9/2	922.717	923.048	-359.674	0.356	710.142	0.373	13	0.143	K.LYAESLAR.F
R3/RRR3-9/3	1626.779	1626.798	-11.871	0.459	1246.277	0.464	28	0.141	R.FRGEDKPPAHLGSSK.D
R3/RRR3-9/3	1626.347	1626.798	-277.924	0.456	1229.047	0.432	28	0.133	R.FRGEDKPPAHLGSSK.D
R3/RRR3-9/3	1469.637	1469.732	-64.986	0.479	1301.965	0.395	26	0.130	K.IHKVPATDM*EALK.S
R3/RRR3-9/3	1469.848	1469.732	79.213	0.514	1402.182	0.356	27	0.129	K.IHKVPATDM*EALK.S
R3/RRR3-9/3	1805.178	1805.970	-995.587	0.483	1309.950	0.380	28	0.128	R.DDRYLNEPAIDTVKR.M
R3/RRR3-9/2	1021.611	1022.243	-1602.961	0.315	850.680	0.136	14	0.127	K.SPLMGLFEK.R
R3/RRR3-9/2	1291.425	1292.456	-1577.557	0.219	907.204	0.088	14	0.124	K.VVCDPSYLPNK.V
R3/RRR3-9/3	1626.485	1626.798	-192.763	0.452	1057.188	0.442	26	0.123	R.FRGEDKPPAHLGSSK.D
R3/RRR3-9/3	1806.056	1805.970	47.948	0.498	1135.984	0.360	25	0.112	R.DDRYLNEPAIDTVKR.M
R3/RRR3-9/3	1469.866	1469.732	91.832	0.497	953.763	0.360	23	0.104	K.IHKVPATDM*EALK.S
R3/RRR3-9/3	1805.612	1805.970	-199.000	0.449	1040.160	0.255	23	0.091	R.DDRYLNEPAIDTVKR.M
R3/RRR3-8/2	1850.379	1851.159	-964.510	0.484	2153.613	0.498	25	0.316	K.AVGEEMGIGFLGIGFQPK.W
R3/RRR3-8/2	1531.200	1530.662	-303.102	0.522	2064.573	0.536	24	0.315	R.EVDAVISSGVTPAER.L
R3/RRR3-8/2	1866.824	1867.158	-179.480	0.527	1899.559	0.604	24	0.302	K.AVGEEM*GIGFLGIGFQPK.W
R3/RRR3-8/2	1850.513	1851.159	-891.925	0.474	2052.276	0.506	24	0.300	K.AVGEEMGIGFLGIGFQPK.W
R3/RRR3-8/2	1866.354	1867.158	-969.636	0.434	1719.602	0.504	23	0.247	K.AVGEEM*GIGFLGIGFQPK.W
R3/RRR3-8/2	1849.675	1851.159	-1346.880	0.364	1692.009	0.442	23	0.228	K.AVGEEMGIGFLGIGFQPK.W
R3/RRR3-8/2	1930.588	1931.267	-872.181	0.551	1217.080	0.655	27	0.223	R.AGLALQPIATAIFANSPFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1258.672	1259.431	-1401.588	0.439	1754.943	0.367	17	0.222	R.DLAEEILQLSK.N
R3/RRR3-8/2	1867.225	1868.058	-984.741	0.509	1333.845	0.572	23	0.218	R.SGM*LPFVFDDSFGFER.Y
R3/RRR3-8/2	1930.336	1931.267	-1003.019	0.490	1160.621	0.595	26	0.203	R.AGLALQPIATAIFANSPFK.E
R3/RRR3-8/2	1259.131	1259.431	-239.364	0.533	1589.735	0.367	17	0.201	R.DLAEEILQLSK.N
R3/RRR3-8/2	1258.545	1259.431	-1502.905	0.449	1549.193	0.377	17	0.201	R.DLAEEILQLSK.N
R3/RRR3-8/3	1930.938	1931.267	-170.866	0.478	1688.212	0.466	30	0.196	R.AGLALQPIATAIFANSPFK.E
R3/RRR3-8/2	1916.611	1915.200	215.051	0.576	962.622	0.638	20	0.195	R.YVDYALDVPMYFVYR.N
R3/RRR3-8/2	1272.212	1271.553	-269.239	0.447	1293.458	0.461	17	0.192	K.WALSDIPIMPK.G
R3/RRR3-8/2	1851.169	1852.059	-1024.088	0.462	1166.620	0.517	21	0.188	R.SGMLPFVFDDSFGFER.Y
R3/RRR3-8/2	1286.637	1287.553	-1493.514	0.371	1141.115	0.384	16	0.166	K.WALSDIPIM*PK.G
R3/RRR3-8/2	1530.173	1530.662	-320.508	0.321	1269.818	0.298	20	0.160	R.EVDAVISSGVTPAER.L
R3/RRR3-8/2	1271.179	1271.553	-295.079	0.459	1056.873	0.384	15	0.160	K.WALSDIPIMPK.G
R3/RRR3-8/2	1530.215	1530.662	-293.295	0.311	1263.125	0.279	20	0.157	R.EVDAVISSGVTPAER.L
R3/RRR3-8/2	1271.263	1271.553	-229.182	0.408	872.274	0.425	14	0.155	K.WALSDIPIMPK.G
R3/RRR3-8/2	1931.286	1931.199	44.976	0.412	737.865	0.480	18	0.154	R.YVDYALDVPM*YFVYR.N
R3/RRR3-8/2	1000.729	1001.119	-390.424	0.295	1097.397	0.289	14	0.148	R.DILNGLAER.F
R3/RRR3-8/2	994.234	994.166	68.333	0.519	578.141	0.413	13	0.148	-.LLNLYETK.-
R3/RRR3-8/2	994.139	994.166	-27.971	0.511	612.939	0.381	13	0.145	-.LLNLYETK.-
R3/RRR3-8/2	1931.998	1931.199	-104.347	0.402	383.509	0.490	13	0.141	R.YVDYALDVPM*YFVYR.N
R3/RRR3-8/2	1930.870	1931.199	-171.243	0.361	478.563	0.435	15	0.140	R.YVDYALDVPM*YFVYR.N
R3/RRR3-8/2	1423.908	1422.653	179.487	0.439	890.820	0.335	13	0.139	K.FGFEVDTLRPIK.Y
R3/RRR3-8/2	993.676	994.166	-494.478	0.432	593.062	0.286	13	0.138	-.LLNLYETK.-
R3/RRR3-8/3	1931.254	1931.267	-6.797	0.485	1172.872	0.410	30	0.125	R.AGLALQPIATAIFANSPFK.E
R3/RRR3-22/2	1339.117	1339.436	-239.422	0.445	1493.568	0.429	20	0.205	R.NIIHGSDGPETAK.A
R3/RRR3-23/2	1218.187	1218.386	-163.586	0.389	1520.918	0.374	16	0.197	K.AEIGLWFEPR.E
R3/RRR3-23/2	1218.020	1218.386	-301.423	0.502	1339.974	0.430	16	0.191	K.AEIGLWFEPR.E
R3/RRR3-23/2	1339.098	1339.436	-253.414	0.451	1291.005	0.397	19	0.179	R.NIIHGSDGPETAK.A
R3/RRR3-23/2	1218.050	1218.386	-276.186	0.435	1112.230	0.465	15	0.178	K.AEIGLWFEPR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1339.028	1339.436	-306.187	0.427	1250.766	0.393	19	0.175	R.NIIHGSDGPETAK.A
R3/RRR3-23/2	885.470	886.031	-1768.873	0.416	1169.582	0.383	14	0.169	R.GDLAVVVGR.N
R3/RRR3-23/2	1217.767	1218.386	-1333.145	0.460	1026.874	0.452	14	0.169	K.AEIGLWFEPR.E
R3/RRR3-22/2	1339.085	1339.436	-263.108	0.429	1077.514	0.426	18	0.168	R.NIIHGSDGPETAK.A
R3/RRR3-23/2	885.399	886.031	-1848.387	0.407	1075.199	0.403	14	0.166	R.GDLAVVVGR.N
R3/RRR3-22/2	885.942	886.031	-101.384	0.390	1136.556	0.375	14	0.165	R.GDLAVVVGR.N
R3/RRR3-23/2	885.543	886.031	-552.854	0.389	1063.859	0.392	14	0.163	R.GDLAVVVGR.N
R3/RRR3-22/2	988.014	988.163	-151.756	0.488	1064.761	0.391	13	0.163	R.GLISEILSR.F
R3/RRR3-22/2	1339.000	1339.436	-326.949	0.450	1057.226	0.397	18	0.162	R.NIIHGSDGPETAK.A
R3/RRR3-23/2	1339.012	1339.436	-318.077	0.447	963.988	0.433	17	0.161	R.NIIHGSDGPETAK.A
R3/RRR3-23/2	1299.153	1299.366	-163.947	0.408	1033.982	0.398	16	0.161	R.ELVSYTSNEEK.W
R3/RRR3-23/2	1300.045	1299.366	-247.465	0.458	960.331	0.430	15	0.160	R.ELVSYTSNEEK.W
R3/RRR3-23/2	1217.900	1218.386	-399.571	0.462	868.458	0.448	13	0.159	K.AEIGLWFEPR.E
R3/RRR3-23/2	987.830	988.163	-338.197	0.468	1030.008	0.365	13	0.157	R.GLISEILSR.F
R3/RRR3-22/2	988.111	988.163	-53.357	0.453	1024.674	0.348	13	0.155	R.GLISEILSR.F
R3/RRR3-22/2	988.082	988.163	-82.850	0.463	979.005	0.356	13	0.154	R.GLISEILSR.F
R3/RRR3-23/2	988.075	988.163	-90.161	0.424	1093.094	0.310	13	0.153	R.GLISEILSR.F
R3/RRR3-23/2	988.004	988.163	-161.547	0.476	994.588	0.345	13	0.153	R.GLISEILSR.F
R3/RRR3-23/2	987.975	988.163	-191.419	0.404	983.904	0.352	12	0.153	R.GLISEILSR.F
R3/RRR3-23/3	1811.878	1812.061	-101.309	0.468	1262.592	0.504	35	0.150	R.KLIGATDPQKSEPGTIR.G
R3/RRR3-23/2	1346.232	1345.572	-253.344	0.427	627.666	0.471	15	0.150	R.TFIAIKPDGVQR.G
R3/RRR3-23/2	942.622	943.079	-486.450	0.442	660.028	0.366	15	0.147	K.LIGATDPQK.S
R3/RRR3-23/2	1071.064	1071.252	-176.455	0.427	734.792	0.369	15	0.146	R.KLIGATDPQK.S
R3/RRR3-23/2	1217.974	1218.386	-339.332	0.362	795.926	0.368	13	0.146	K.AEIGLWFEPR.E
R3/RRR3-23/2	1345.275	1345.572	-221.579	0.377	565.166	0.436	14	0.143	R.TFIAIKPDGVQR.G
R3/RRR3-23/2	943.062	943.079	-18.060	0.441	458.141	0.331	13	0.141	K.LIGATDPQK.S
R3/RRR3-23/2	942.755	943.079	-344.692	0.482	651.424	0.296	15	0.141	K.LIGATDPQK.S
R3/RRR3-23/2	1071.028	1071.252	-210.184	0.397	587.094	0.365	14	0.140	-.KLIGATDPQK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1344.839	1345.572	-1292.211	0.368	547.652	0.385	14	0.139	R.TFIAIKPDGVQR.G
R3/RRR3-23/2	987.919	988.163	-248.067	0.281	822.630	0.250	13	0.137	R.GLISEILSR.F
R3/RRR3-23/2	1071.083	1071.252	-158.505	0.324	569.193	0.316	14	0.136	-.KLIGATDPQK.-
R3/RRR3-23/2	987.798	988.163	-370.683	0.301	765.353	0.248	12	0.134	-.GLISEILSR.-
R3/RRR3-23/3	1811.921	1812.061	-77.487	0.432	870.910	0.476	31	0.117	R.KLIGATDPQKSEPGTIR.G
R3/RRR3-7/2	1815.298	1815.103	107.537	0.630	2712.905	0.568	25	0.454	R.TLKEWIVSSLGPDAVAK.H
R3/RRR3-7/2	1814.562	1815.103	-851.973	0.572	2713.430	0.554	25	0.451	R.TLKEWIVSSLGPDAVAK.H
R3/RRR3-7/2	1814.036	1815.103	-1142.782	0.588	2472.424	0.569	24	0.400	R.TLKEWIVSSLGPDAVAK.H
R3/RRR3-7/2	1372.079	1372.530	-329.321	0.484	1215.011	0.513	19	0.195	K.TFTTAETM*LNAR.T
R3/RRR3-7/3	1703.560	1703.901	-200.590	0.526	1594.083	0.470	33	0.177	K.FAPHIQQLSM*ESNGK.G
R3/RRR3-7/2	1896.331	1896.130	106.557	0.560	951.391	0.532	24	0.176	R.YLAVEPSTPYNTTTLPK.-
R3/RRR3-7/2	1895.183	1896.130	-1030.151	0.473	798.610	0.586	22	0.172	R.YLAVEPSTPYNTTTLPK.-
R3/RRR3-7/2	1426.355	1426.562	-145.549	0.473	1022.109	0.492	15	0.172	K.NAFAFWDWVGGR.Y
R3/RRR3-7/2	1895.362	1896.130	-935.612	0.498	824.459	0.534	23	0.168	R.YLAVEPSTPYNTTTLPK.-
R3/RRR3-7/2	1316.236	1316.488	-191.399	0.460	950.385	0.386	19	0.157	R.FLANVDPVDVAR.S
R3/RRR3-7/3	1703.898	1703.901	-1.686	0.505	1253.068	0.525	31	0.155	K.FAPHIQQLSM*ESNGK.G
R3/RRR3-7/2	1472.511	1472.667	-106.813	0.366	956.680	0.403	18	0.153	K.EWIVSSLGPDAVAK.H
R3/RRR3-7/3	1844.043	1844.139	-52.500	0.470	1450.249	0.418	30	0.151	R.SIKDLDPETTLVVVVSK.T
R3/RRR3-7/2	950.185	950.031	163.052	0.430	498.336	0.487	15	0.150	R.SGSWVGATGK.A
R3/RRR3-7/2	1315.765	1316.488	-1312.762	0.372	902.051	0.362	17	0.148	-.FLANVDPVDVAR.-
R3/RRR3-7/2	1316.386	1316.488	-77.069	0.459	810.806	0.373	17	0.148	R.FLANVDPVDVAR.S
R3/RRR3-7/2	1425.995	1426.562	-1102.672	0.441	795.578	0.394	15	0.147	K.NAFAFWDWVGGR.Y
R3/RRR3-7/2	1233.962	1233.438	-387.027	0.431	529.703	0.412	17	0.146	R.AILPYSQALEK.F
R3/RRR3-7/3	1843.282	1844.139	-1010.742	0.455	1404.682	0.383	28	0.139	R.SIKDLDPETTLVVVVSK.T
R3/RRR3-7/2	1232.553	1233.438	-1534.002	0.267	392.808	0.267	15	0.134	R.AILPYSQALEK.F
R3/RRR3-7/2	1425.701	1426.562	-1309.264	0.316	641.412	0.295	14	0.134	K.NAFAFWDWVGGR.Y
R3/RRR3-7/3	1843.913	1844.139	-123.420	0.444	1228.932	0.428	28	0.133	R.SIKDLDPETTLVVVVSK.T
R3/RRR3-10/2	1814.798	1815.103	-168.503	0.408	1043.621	0.210	17	0.132	R.TLKEWIVSSLGPDAVAK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1814.482	1815.103	-896.006	0.361	1032.384	0.143	17	0.126	R.TLKEWIVSSLGPDAVAK.H
R3/RRR3-11/2	1815.266	1815.103	90.272	0.392	1040.050	0.152	17	0.126	R.TLKEWIVSSLGPDAVAK.H
R3/RRR3-11/2	1815.190	1815.103	48.119	0.383	852.739	0.167	16	0.124	-.TLKEWIVSSLGPDAVAK.-
R3/RRR3-10/2	1814.135	1815.103	-1088.120	0.321	1039.767	0.090	17	0.123	R.TLKEWIVSSLGPDAVAK.H
R3/RRR3-7/3	1703.586	1703.901	-185.602	0.500	1278.862	0.353	30	0.120	K.FAPHIQQLSM*ESNGK.G
R3/RRR3-6/2	1939.794	1940.214	-217.102	0.586	2909.896	0.582	27	0.518	K.GVNPDEAVAMGAAIQGGILR.G
R3/RRR3-6/2	1939.613	1940.214	-828.039	0.540	2679.804	0.559	28	0.451	K.GVNPDEAVAMGAAIQGGILR.G
R3/RRR3-6/2	1777.460	1777.956	-279.913	0.566	1982.960	0.566	26	0.308	R.IINEPTAAALSYGTNNK.E
R3/RRR3-6/2	1523.776	1522.728	31.448	0.523	2014.282	0.496	21	0.293	R.SKFESLVNSLIER.T
R3/RRR3-6/2	1777.573	1777.956	-216.183	0.528	1730.918	0.587	25	0.273	R.IINEPTAAALSYGTNNK.E
R3/RRR3-6/2	1522.158	1522.728	-1034.619	0.492	1669.062	0.525	20	0.249	R.SKFESLVNSLIER.T
R3/RRR3-6/2	1355.995	1355.433	-324.026	0.517	1490.014	0.541	19	0.231	R.NNADTTIYSVEK.S
R3/RRR3-6/2	1523.350	1522.728	-248.724	0.574	1592.076	0.497	19	0.230	R.SKFESLVNSLIER.T
R3/RRR3-6/2	1777.382	1777.956	-888.532	0.539	1382.053	0.562	23	0.219	R.IINEPTAAALSYGTNNK.E
R3/RRR3-6/2	1355.110	1355.433	-238.764	0.488	1422.765	0.442	18	0.201	R.NNADTTIYSVEK.S
R3/RRR3-6/2	1250.140	1249.438	-238.735	0.572	1210.760	0.510	17	0.194	K.VQEIVSEIFGK.S
R3/RRR3-6/2	1207.201	1206.285	-70.043	0.518	1395.589	0.391	17	0.186	R.SSGGLSEAEIQK.M
R3/RRR3-6/2	1206.987	1206.285	-247.575	0.505	1358.208	0.395	17	0.184	R.SSGGLSEAEIQK.M
R3/RRR3-6/2	1205.964	1206.285	-267.278	0.484	1327.420	0.367	17	0.176	R.SSGGLSEAEIQK.M
R3/RRR3-6/2	1355.077	1355.433	-263.437	0.467	1153.634	0.434	17	0.174	R.NNADTTIYSVEK.S
R3/RRR3-6/2	1554.218	1553.701	-311.374	0.508	647.734	0.562	19	0.162	R.QAVTNPQNTFFGTK.R
R3/RRR3-7/2	1814.368	1813.042	180.270	0.456	868.714	0.488	18	0.157	K.IPAEVATEIETAIADLR.S
R3/RRR3-7/2	1522.539	1522.728	-124.613	0.381	831.954	0.385	15	0.146	R.SKFESLVNSLIER.T
R3/RRR3-6/2	967.954	968.135	-188.168	0.423	718.526	0.331	13	0.143	K.HLNITLTR.S
R3/RRR3-7/2	994.045	994.276	-233.086	0.440	1419.710	0.093	14	0.141	K.M*VPYKIVK.A
R3/RRR3-6/2	968.044	968.135	-94.303	0.389	542.171	0.257	12	0.136	K.HLNITLTR.S
R3/RRR3-7/2	1207.228	1206.285	-47.425	0.262	723.186	0.260	16	0.134	R.SSGGLSEAEIQK.M
R3/RRR3-1/2	993.669	994.276	-1621.701	0.420	1059.131	0.073	13	0.126	-.M*VPYKIVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	994.319	994.276	43.665	0.390	864.469	0.056	12	0.121	-.M*VPYKIVK.-
R3/RRR3-2/2	995.087	994.276	-190.762	0.406	941.130	0.020	12	0.119	-.M*VPYKIVK.-
R3/RRR3-6/3	1522.759	1522.728	20.083	0.558	1157.990	0.349	24	0.112	R.SKFESLVNSLIER.T
R3/RRR3-6/3	1522.783	1522.728	36.124	0.536	1011.791	0.333	23	0.102	R.SKFESLVNSLIER.T
R3/RRR3-6/3	1522.667	1522.728	-40.222	0.530	1141.048	0.293	24	0.101	R.SKFESLVNSLIER.T
R3/RRR3-16/2	1435.491	1435.650	-111.103	0.571	2632.181	0.465	23	0.400	K.YIGLLATGLTADAR.S
R3/RRR3-16/2	1435.204	1435.650	-312.200	0.544	2449.657	0.504	23	0.376	K.YIGLLATGLTADAR.S
R3/RRR3-17/2	1435.165	1435.650	-339.081	0.519	2424.759	0.496	23	0.368	K.YIGLLATGLTADAR.S
R3/RRR3-17/2	1849.804	1850.063	-140.427	0.592	2408.559	0.491	24	0.363	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-17/2	1435.467	1435.650	-127.993	0.479	2397.061	0.408	23	0.334	K.YIGLLATGLTADAR.S
R3/RRR3-17/2	1849.363	1850.063	-921.875	0.569	2184.950	0.490	23	0.319	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-16/2	1434.384	1435.650	-1584.472	0.430	1514.680	0.448	20	0.210	K.YIGLLATGLTADAR.S
R3/RRR3-17/2	1073.205	1073.225	-18.780	0.595	1447.193	0.438	16	0.201	K.ATEIEVGVVR.K
R3/RRR3-16/2	946.938	947.071	-140.884	0.500	1053.826	0.482	17	0.179	K.SAGVTSIGVR.G
R3/RRR3-16/2	1158.018	1157.304	-247.154	0.461	778.143	0.586	15	0.175	R.HITIFSPEGR.L
R3/RRR3-17/2	947.940	947.071	-138.926	0.557	1044.308	0.461	17	0.175	K.SAGVTSIGVR.G
R3/RRR3-17/2	1072.909	1073.225	-295.517	0.523	1205.303	0.389	15	0.171	K.ATEIEVGVVR.K
R3/RRR3-17/2	1072.405	1073.225	-1701.888	0.456	1115.104	0.399	15	0.168	K.ATEIEVGVVR.K
R3/RRR3-16/2	946.578	947.071	-522.768	0.384	1098.962	0.398	17	0.167	K.SAGVTSIGVR.G
R3/RRR3-16/2	946.422	947.071	-1747.967	0.420	1005.880	0.434	16	0.167	K.SAGVTSIGVR.G
R3/RRR3-17/2	1157.247	1157.304	-49.579	0.438	730.646	0.534	16	0.167	R.HITIFSPEGR.L
R3/RRR3-16/2	1072.857	1073.225	-344.033	0.426	1214.136	0.331	15	0.164	K.ATEIEVGVVR.K
R3/RRR3-17/3	1851.300	1850.063	128.454	0.512	1472.970	0.462	33	0.164	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-16/2	1073.151	1073.225	-69.665	0.537	983.491	0.419	15	0.163	K.ATEIEVGVVR.K
R3/RRR3-17/2	1157.024	1157.304	-242.287	0.409	624.130	0.554	15	0.162	R.HITIFSPEGR.L
R3/RRR3-17/2	947.948	947.071	-130.401	0.470	949.014	0.414	16	0.162	K.SAGVTSIGVR.G
R3/RRR3-17/2	1157.204	1157.304	-86.929	0.430	573.655	0.556	14	0.161	R.HITIFSPEGR.L
R3/RRR3-16/2	1158.103	1157.304	-174.294	0.414	554.718	0.550	14	0.159	R.HITIFSPEGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1408.036	1408.647	-1147.605	0.401	801.240	0.482	16	0.159	K.WGYEMPVDVLAK.W
R3/RRR3-17/3	1850.168	1850.063	57.194	0.433	1434.688	0.451	31	0.158	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-16/2	1073.141	1073.225	-78.222	0.500	1004.076	0.376	15	0.158	K.ATEIEVGVVR.K
R3/RRR3-16/3	1849.512	1850.063	-840.780	0.417	1512.810	0.415	32	0.157	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-17/2	1713.657	1713.999	-199.882	0.471	879.100	0.447	19	0.157	K.LLDQTSVTHLFPITK.Y
R3/RRR3-16/2	1156.600	1157.304	-1477.221	0.390	518.606	0.486	14	0.152	R.HITIFSPEGR.L
R3/RRR3-17/2	1713.554	1713.999	-260.200	0.453	642.310	0.439	17	0.145	K.LLDQTSVTHLFPITK.Y
R3/RRR3-17/2	1407.846	1408.647	-1283.343	0.402	718.833	0.364	16	0.144	K.WGYEMPVDVLAK.W
R3/RRR3-17/2	1684.078	1683.995	49.902	0.429	831.252	0.371	16	0.142	R.FKWGYEMPVDVLAK.W
R3/RRR3-14/2	1436.803	1435.650	106.296	0.327	848.612	0.296	18	0.140	K.YIGLLATGLTADAR.S
R3/RRR3-17/2	1409.074	1408.647	303.807	0.264	457.132	0.367	14	0.136	K.WGYEMPVDVLAK.W
R3/RRR3-17/3	1850.185	1850.063	66.425	0.397	1136.040	0.466	30	0.134	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-16/3	1849.423	1850.063	-889.479	0.474	1067.964	0.486	31	0.133	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-17/2	1424.410	1424.646	-166.579	0.304	394.962	0.329	13	0.132	-.WGYEM*PVDVLAK.-
R3/RRR3-14/2	1435.452	1435.650	-138.571	0.299	606.140	0.105	15	0.125	-.YIGLLATGLTADAR.-
R3/RRR3-16/3	1849.569	1850.063	-267.485	0.423	1233.538	0.384	31	0.124	K.ATSAGLKEQEAINFLEK.K
R3/RRR3-17/3	1221.538	1221.380	130.379	0.519	1345.203	0.350	21	0.124	-.GKDSVCVVTQK.-
R3/RRR3-17/3	1714.213	1713.999	125.441	0.361	542.402	0.525	28	0.112	K.LLDQTSVTHLFPITK.Y
R3/RRR3-16/3	1713.888	1713.999	-64.953	0.366	380.565	0.508	25	0.110	K.LLDQTSVTHLFPITK.Y
R3/RRR3-16/3	1715.152	1713.999	89.680	0.397	331.862	0.418	25	0.106	K.LLDQTSVTHLFPITK.Y
R3/RRR3-16/3	1714.911	1713.999	-51.242	0.390	514.928	0.443	29	0.106	K.LLDQTSVTHLFPITK.Y
R3/RRR3-17/3	1714.573	1713.999	-249.199	0.410	418.369	0.416	26	0.105	K.LLDQTSVTHLFPITK.Y
R3/RRR3-17/3	1713.602	1713.999	-232.049	0.321	512.967	0.442	27	0.103	K.LLDQTSVTHLFPITK.Y
R3/RRR3-17/3	1221.253	1221.380	-104.037	0.472	1244.072	0.243	20	0.099	-.GKDSVCVVTQK.-
R3/RRR3-16/3	1221.303	1221.380	-62.528	0.466	1081.171	0.303	20	0.096	-.GKDSVCVVTQK.-
R3/RRR3-16/3	1221.248	1221.380	-108.097	0.466	933.223	0.316	19	0.084	-.GKDSVCVVTQK.-
R3/RRR3-17/3	1221.403	1221.380	19.425	0.432	778.700	0.284	18	0.073	-.GKDSVCVVTQK.-
R3/RRR3-16/3	1220.814	1221.380	-1286.403	0.495	648.525	0.359	18	0.056	-.GKDSVCVVTQK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1688.301	1687.833	277.637	0.540	2875.125	0.527	26	0.485	K.VVTAAAAGGGGELTVEER.N
R3/RRR3-15/2	1687.224	1687.833	-956.403	0.455	2863.763	0.479	25	0.464	K.VVTAAAAGGGGELTVEER.N
R3/RRR3-15/2	1954.598	1955.136	-789.063	0.573	2503.925	0.632	26	0.432	K.DAADATLAAYQAAQDIAM*K.E
R3/RRR3-15/2	1687.481	1687.833	-209.585	0.475	2569.155	0.545	25	0.418	K.VVTAAAAGGGGELTVEER.N
R3/RRR3-15/2	1773.463	1773.021	250.083	0.568	2566.307	0.512	25	0.406	R.ARVEAELSNICAGILR.L
R3/RRR3-15/2	1954.238	1955.136	-973.906	0.534	2339.558	0.562	25	0.371	K.DAADATLAAYQAAQDIAM*K.E
R3/RRR3-15/2	1955.507	1955.136	190.354	0.605	2163.712	0.620	25	0.354	K.DAADATLAAYQAAQDIAM*K.E
R3/RRR3-15/3	1939.547	1939.136	212.217	0.600	2270.416	0.607	38	0.352	K.DAADATLAAYQAAQDIAMK.E
R3/RRR3-15/2	1772.690	1773.021	-187.355	0.533	2186.056	0.537	23	0.336	R.ARVEAELSNICAGILR.L
R3/RRR3-15/3	1954.723	1955.136	-212.046	0.547	2084.149	0.628	38	0.321	K.DAADATLAAYQAAQDIAM*K.E
R3/RRR3-15/2	1938.435	1939.136	-880.588	0.496	1996.668	0.582	25	0.312	K.DAADATLAAYQAAQDIAMK.E
R3/RRR3-15/2	1546.336	1545.757	-272.660	0.627	2159.251	0.478	22	0.310	R.VEAELSNICAGILR.L
R3/RRR3-15/2	1545.308	1545.757	-291.461	0.527	2171.061	0.439	22	0.303	R.VEAELSNICAGILR.L
R3/RRR3-15/2	1773.389	1773.021	208.185	0.525	1995.430	0.511	22	0.293	R.ARVEAELSNICAGILR.L
R3/RRR3-15/2	1545.447	1545.757	-200.960	0.540	2032.739	0.437	22	0.279	R.VEAELSNICAGILR.L
R3/RRR3-15/2	1938.313	1939.136	-943.810	0.448	1613.422	0.618	23	0.259	K.DAADATLAAYQAAQDIAMK.E
R3/RRR3-15/3	1955.949	1955.136	-95.889	0.538	1627.064	0.630	38	0.236	K.DAADATLAAYQAAQDIAM*K.E
R3/RRR3-15/2	1938.103	1939.136	-1052.507	0.414	1539.216	0.528	22	0.227	K.DAADATLAAYQAAQDIAMK.E
R3/RRR3-15/3	1954.327	1955.136	-928.574	0.442	1539.565	0.513	33	0.189	K.DAADATLAAYQAAQDIAM*K.E
R3/RRR3-15/2	1025.820	1026.212	-382.485	0.384	308.142	0.579	15	0.153	R.LVPAAAAVDAK.V
R3/RRR3-15/2	1025.860	1026.212	-343.801	0.336	338.935	0.590	17	0.152	R.LVPAAAAVDAK.V
R3/RRR3-15/2	1025.957	1026.212	-248.775	0.334	400.555	0.465	17	0.146	R.LVPAAAAVDAK.V
R3/RRR3-15/2	1689.018	1687.833	109.923	0.336	503.170	0.343	14	0.130	-.VVTAAAAGGGGELTVEER.-
R3/RRR3-15/3	1772.160	1773.021	-1053.206	0.400	1167.405	0.358	26	0.114	R.ARVEAELSNICAGILR.L
R3/RRR3-15/3	1772.495	1773.021	-863.705	0.352	804.302	0.182	27	0.081	R.ARVEAELSNICAGILR.L
R3/RRR3-7/2	1172.910	1173.345	-371.786	0.382	1242.171	0.362	16	0.171	K.FTIFNFGAQK.E
R3/RRR3-2/2	1173.129	1173.345	-184.272	0.326	925.460	0.400	14	0.154	K.FTIFNFGAQK.E
R3/RRR3-6/2	1172.749	1173.345	-1365.111	0.413	802.892	0.401	14	0.151	K.FTIFNFGAQK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1172.445	1173.345	-1625.596	0.344	773.190	0.247	13	0.135	-.FTIFNFGAQK.-
R3/RRR3-5/2	1172.997	1173.345	-297.336	0.186	530.806	0.203	11	0.129	K.FTIFNFGAQK.E
R3/RRR3-12/2	1347.376	1347.648	-202.605	0.464	2786.827	0.326	20	0.385	K.MELVDAAFPLLK.G
R3/RRR3-12/2	1346.599	1347.648	-1526.012	0.385	2675.873	0.366	20	0.377	K.MELVDAAFPLLK.G
R3/RRR3-11/2	1348.185	1347.648	-344.702	0.502	2488.731	0.390	20	0.344	K.MELVDAAFPLLK.G
R3/RRR3-12/2	1347.224	1347.648	-315.684	0.500	2472.181	0.361	20	0.331	K.MELVDAAFPLLK.G
R3/RRR3-12/2	1352.015	1352.451	-323.259	0.549	2088.418	0.497	20	0.305	K.MDATAQELSEEK.T
R3/RRR3-12/2	1555.157	1555.668	-974.560	0.538	1874.987	0.604	24	0.300	K.SQASALEAHAAPNCK.V
R3/RRR3-11/2	1555.209	1555.668	-296.454	0.529	1831.720	0.622	24	0.299	K.SQASALEAHAAPNCK.V
R3/RRR3-12/3	1842.274	1843.115	-1002.123	0.468	2304.606	0.456	33	0.297	R.ALGQISEKLNVQVTDVK.N
R3/RRR3-11/2	1555.271	1555.668	-256.057	0.550	1859.402	0.602	24	0.297	K.SQASALEAHAAPNCK.V
R3/RRR3-12/3	1789.786	1789.922	-76.564	0.567	2163.809	0.538	38	0.295	R.KQSSALSAASSACDHIR.D
R3/RRR3-12/2	1555.199	1555.668	-302.754	0.520	1835.002	0.606	24	0.294	K.SQASALEAHAAPNCK.V
R3/RRR3-12/2	1352.060	1352.451	-289.380	0.541	2057.333	0.464	20	0.290	K.MDATAQELSEEK.T
R3/RRR3-11/3	1843.222	1843.115	58.473	0.522	2075.568	0.520	32	0.277	R.ALGQISEKLNVQVTDVK.N
R3/RRR3-12/2	1651.414	1650.987	259.298	0.559	1729.200	0.591	25	0.273	K.VLVVANPANTNALILK.E
R3/RRR3-11/2	1346.821	1347.648	-1360.763	0.440	2177.176	0.329	18	0.270	K.MELVDAAFPLLK.G
R3/RRR3-11/2	1555.252	1555.668	-268.814	0.525	1666.550	0.591	23	0.264	K.SQASALEAHAAPNCK.V
R3/RRR3-12/2	1555.210	1555.668	-295.588	0.538	1688.083	0.578	23	0.264	K.SQASALEAHAAPNCK.V
R3/RRR3-12/2	1650.455	1650.987	-930.900	0.488	1790.426	0.518	25	0.262	K.VLVVANPANTNALILK.E
R3/RRR3-12/3	1789.460	1789.922	-259.159	0.519	2012.989	0.505	36	0.255	R.KQSSALSAASSACDHIR.D
R3/RRR3-12/2	1351.572	1352.451	-1394.390	0.455	1866.178	0.431	19	0.252	K.MDATAQELSEEK.T
R3/RRR3-12/2	1650.521	1650.987	-283.192	0.542	1664.645	0.541	23	0.249	K.VLVVANPANTNALILK.E
R3/RRR3-12/2	1369.052	1368.450	-291.583	0.548	1502.030	0.552	20	0.235	K.M*DATAQELSEEK.T
R3/RRR3-11/2	1650.479	1650.987	-916.495	0.479	1556.919	0.520	24	0.231	K.VLVVANPANTNALILK.E
R3/RRR3-12/2	1367.966	1368.450	-354.825	0.532	1665.594	0.447	19	0.228	K.M*DATAQELSEEK.T
R3/RRR3-12/2	1368.051	1368.450	-292.692	0.504	1643.387	0.446	20	0.226	K.M*DATAQELSEEK.T
R3/RRR3-11/3	1844.399	1843.115	154.691	0.527	1736.075	0.496	32	0.209	R.ALGQISEKLNVQVTDVK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1649.920	1650.987	-1256.453	0.372	1577.856	0.401	24	0.207	K.VLVVANPANTNALILK.E
R3/RRR3-12/2	1362.404	1363.648	-1651.338	0.352	1720.696	0.304	19	0.204	K.M*ELVDAAFPLLK.G
R3/RRR3-12/3	1842.608	1843.115	-820.341	0.460	1633.070	0.509	29	0.201	R.ALGQISEKLNVQVTDVK.N
R3/RRR3-12/2	1016.364	1016.174	188.274	0.506	1545.423	0.379	15	0.200	K.LNVQVTDVK.N
R3/RRR3-12/2	1652.019	1650.987	19.298	0.548	1316.170	0.499	23	0.199	K.VLVVANPANTNALILK.E
R3/RRR3-12/2	1015.940	1016.174	-230.198	0.539	1536.137	0.379	15	0.198	K.LNVQVTDVK.N
R3/RRR3-11/2	1363.772	1363.648	91.649	0.502	1556.346	0.368	19	0.198	K.M*ELVDAAFPLLK.G
R3/RRR3-11/2	1650.503	1650.987	-294.471	0.466	1288.587	0.508	22	0.198	K.VLVVANPANTNALILK.E
R3/RRR3-11/2	1352.003	1352.451	-331.955	0.463	1427.425	0.422	19	0.197	K.MDATAQELSEEK.T
R3/RRR3-12/2	1015.751	1016.174	-417.557	0.499	1509.076	0.356	15	0.192	K.LNVQVTDVK.N
R3/RRR3-12/3	1651.934	1650.987	-31.998	0.503	1482.764	0.551	31	0.190	K.VLVVANPANTNALILK.E
R3/RRR3-13/2	1650.650	1650.987	-205.138	0.464	1210.773	0.478	22	0.186	K.VLVVANPANTNALILK.E
R3/RRR3-10/2	1015.482	1016.174	-1670.267	0.467	1356.042	0.389	15	0.185	K.LNVQVTDVK.N
R3/RRR3-11/2	1649.823	1650.987	-1315.897	0.444	1175.438	0.473	21	0.181	K.VLVVANPANTNALILK.E
R3/RRR3-11/2	1346.628	1347.648	-1504.522	0.339	1695.422	0.163	18	0.174	K.MELVDAAFPLLK.G
R3/RRR3-11/3	1651.963	1650.987	-14.543	0.429	1472.380	0.465	30	0.164	K.VLVVANPANTNALILK.E
R3/RRR3-12/3	1624.676	1624.796	-73.743	0.490	1466.959	0.455	27	0.161	R.KKM*DATAQELSEEK.T
R3/RRR3-10/2	1015.565	1016.174	-1588.753	0.419	1139.634	0.277	14	0.152	K.LNVQVTDVK.N
R3/RRR3-12/3	1661.804	1661.749	33.102	0.467	1169.079	0.531	29	0.150	K.QSSALSAASSACDHIR.D
R3/RRR3-11/2	1363.196	1363.648	-332.063	0.419	879.717	0.336	16	0.146	K.M*ELVDAAFPLLK.G
R3/RRR3-6/2	1651.291	1650.987	184.282	0.443	945.937	0.341	18	0.146	K.VLVVANPANTNALILK.E
R3/RRR3-1/2	1016.656	1016.174	476.169	0.312	254.012	0.237	11	0.144	K.LNVQVTDVK.N
R3/RRR3-16/2	1017.103	1016.174	-69.471	0.451	474.217	0.307	12	0.141	K.LNVQVTDVK.N
R3/RRR3-10/2	1015.630	1016.174	-1524.639	0.418	768.841	0.280	13	0.140	K.LNVQVTDVK.N
R3/RRR3-1/2	1016.881	1016.174	-288.501	0.310	413.679	0.220	13	0.140	K.LNVQVTDVK.N
R3/RRR3-10/2	1651.814	1650.987	-105.003	0.352	265.198	0.325	15	0.139	K.VLVVANPANTNALILK.E
R3/RRR3-11/2	1555.059	1555.668	-1038.397	0.329	439.795	0.374	15	0.137	K.SQASALEAHAAPNCK.V
R3/RRR3-12/3	1661.799	1661.749	29.786	0.475	983.631	0.512	26	0.132	K.QSSALSAASSACDHIR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1015.558	1016.174	-1595.274	0.352	888.009	0.143	14	0.132	K.LNVQVTDVK.N
R3/RRR3-12/3	1661.742	1661.749	-4.253	0.449	956.057	0.517	27	0.130	K.QSSALSAASSACDHIR.D
R3/RRR3-17/2	1016.033	1016.174	-139.075	0.323	693.733	0.126	12	0.128	-.LNVQVTDVK.-
R3/RRR3-12/2	1016.335	1016.174	159.849	0.432	762.924	0.222	12	0.120	-.LNVQVTDVK.-
R3/RRR3-12/3	1624.828	1624.796	19.853	0.492	917.433	0.425	24	0.113	R.KKM*DATAQELSEEK.T
R3/RRR3-11/3	1843.505	1843.115	212.281	0.377	924.867	0.423	24	0.113	R.ALGQISEKLNVQVTDVK.N
R3/RRR3-11/3	1624.680	1624.796	-71.708	0.420	853.740	0.426	22	0.110	R.KKM*DATAQELSEEK.T
R3/RRR3-11/3	1625.071	1624.796	169.818	0.449	803.780	0.414	23	0.107	R.KKM*DATAQELSEEK.T
R3/RRR3-19/2	1838.317	1837.967	190.909	0.577	1929.709	0.607	23	0.312	R.NNTEYKLDTFSSVYR.R
R3/RRR3-19/2	1292.333	1292.509	-136.579	0.486	1651.211	0.542	20	0.251	K.FSGKDVVLVATR.R
R3/RRR3-19/2	1292.149	1292.509	-279.488	0.509	1637.461	0.540	20	0.249	K.FSGKDVVLVATR.R
R3/RRR3-19/2	1836.723	1837.967	-1225.724	0.515	1461.715	0.563	21	0.230	R.NNTEYKLDTFSSVYR.R
R3/RRR3-19/2	1837.520	1837.967	-244.311	0.541	1332.061	0.587	20	0.219	R.NNTEYKLDTFSSVYR.R
R3/RRR3-19/2	1292.314	1292.509	-151.550	0.468	1427.618	0.504	19	0.214	K.FSGKDVVLVATR.R
R3/RRR3-19/2	1292.158	1292.509	-272.474	0.510	1323.987	0.558	18	0.214	K.FSGKDVVLVATR.R
R3/RRR3-19/2	1292.251	1292.509	-200.163	0.512	1356.299	0.478	18	0.201	K.FSGKDVVLVATR.R
R3/RRR3-19/2	1292.388	1292.509	-94.131	0.478	1368.224	0.441	18	0.195	K.FSGKDVVLVATR.R
R3/RRR3-19/2	1196.166	1196.469	-254.318	0.491	1353.682	0.421	16	0.191	R.KAVIIHVPYR.L
R3/RRR3-19/2	872.842	873.032	-218.491	0.389	1145.931	0.366	13	0.165	K.DVVLVATR.R
R3/RRR3-19/2	873.803	873.032	-263.369	0.455	1132.306	0.338	13	0.161	K.DVVLVATR.R
R3/RRR3-19/2	1067.713	1068.297	-1487.592	0.343	1084.446	0.360	15	0.159	K.AVIIHVPYR.L
R3/RRR3-19/2	1067.958	1068.297	-317.982	0.399	923.767	0.343	14	0.150	K.AVIIHVPYR.L
R3/RRR3-19/2	1087.957	1088.195	-219.518	0.387	436.211	0.409	14	0.146	K.LDTFSSVYR.R
R3/RRR3-19/2	1087.366	1088.195	-1686.804	0.350	420.127	0.391	13	0.143	K.LDTFSSVYR.R
R3/RRR3-19/2	1067.586	1068.297	-1606.582	0.384	638.142	0.352	12	0.141	K.AVIIHVPYR.L
R3/RRR3-19/2	873.156	873.032	141.820	0.414	994.250	0.239	12	0.141	K.DVVLVATR.R
R3/RRR3-19/2	1088.105	1088.195	-82.773	0.355	389.397	0.322	13	0.140	K.LDTFSSVYR.R
R3/RRR3-19/2	1029.212	1029.219	-6.734	0.398	714.748	0.261	13	0.136	-.DVVLVATRR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1028.549	1029.219	-1627.799	0.382	738.148	0.233	13	0.135	K.DVVLVATRR.I
R3/RRR3-19/2	1029.115	1029.219	-100.842	0.414	858.182	0.208	14	0.135	K.DVVLVATRR.I
R3/RRR3-19/3	1837.939	1837.967	-15.536	0.546	778.980	0.577	29	0.133	R.NNTEYKLDTFSSVYR.R
R3/RRR3-19/2	1029.192	1029.219	-26.126	0.367	617.525	0.182	12	0.130	-.DVVLVATRR.-
R3/RRR3-19/2	872.221	873.032	-2082.944	0.242	758.924	0.144	12	0.129	K.DVVLVATR.R
R3/RRR3-19/3	1837.752	1837.967	-117.171	0.480	605.144	0.522	27	0.116	R.NNTEYKLDTFSSVYR.R
R3/RRR3-19/3	1421.273	1420.682	-288.866	0.408	1175.429	0.312	24	0.107	K.KFSGKDVVLVATR.R
R3/RRR3-19/3	1421.305	1420.682	-265.988	0.405	1148.125	0.306	24	0.104	K.KFSGKDVVLVATR.R
R3/RRR3-19/3	1292.959	1292.509	349.214	0.402	1406.872	0.214	24	0.102	K.FSGKDVVLVATR.R
R3/RRR3-19/3	1836.848	1837.967	-1156.892	0.355	366.260	0.443	20	0.100	R.NNTEYKLDTFSSVYR.R
R3/RRR3-19/3	1196.744	1196.469	230.375	0.479	770.393	0.336	18	0.092	-.KAVIIHVPYR.-
R3/RRR3-19/3	1196.493	1196.469	19.369	0.368	1148.410	0.230	21	0.091	R.KAVIIHVPYR.L
R3/RRR3-19/3	1292.224	1292.509	-221.638	0.391	1039.689	0.212	21	0.088	-.FSGKDVVLVATR.-
R3/RRR3-19/3	1292.701	1292.509	148.822	0.371	1292.279	0.146	22	0.087	K.FSGKDVVLVATR.R
R3/RRR3-19/3	1292.735	1292.509	175.242	0.419	1241.772	0.144	21	0.086	-.FSGKDVVLVATR.-
R3/RRR3-19/3	1196.897	1196.469	358.470	0.460	921.720	0.235	21	0.084	-.KAVIIHVPYR.-
R3/RRR3-19/3	1420.045	1420.682	-1156.534	0.355	819.320	0.192	22	0.084	K.KFSGKDVVLVATR.R
R3/RRR3-19/3	1292.561	1292.509	40.142	0.426	1016.642	0.218	20	0.084	-.FSGKDVVLVATR.-
R3/RRR3-19/3	1421.459	1420.682	-157.559	0.343	797.914	0.182	22	0.083	-.KFSGKDVVLVATR.-
R3/RRR3-19/3	1292.624	1292.509	89.442	0.349	1184.477	0.100	21	0.081	-.FSGKDVVLVATR.-
R3/RRR3-19/3	1420.656	1420.682	-18.247	0.366	887.203	0.122	23	0.079	-.KFSGKDVVLVATR.-
R3/RRR3-13/2	1900.329	1900.935	-847.669	0.549	2324.906	0.621	25	0.391	K.SADLFDSEGQSSQSNSIK.Q
R3/RRR3-13/2	1790.795	1791.895	-1176.552	0.513	2403.201	0.520	25	0.378	K.YEDAADLFDKGANSFK.L
R3/RRR3-13/2	1650.393	1649.845	-275.054	0.579	2306.099	0.579	24	0.375	K.LLSDLAAAM*EEGDVAK.F
R3/RRR3-13/3	1491.618	1491.671	-35.273	0.578	2453.686	0.533	30	0.353	K.VAEIAAQLEQYQK.A
R3/RRR3-13/2	1900.440	1900.935	-261.671	0.557	1962.478	0.578	24	0.306	K.SADLFDSEGQSSQSNSIK.Q
R3/RRR3-13/2	1900.358	1900.935	-832.709	0.548	1952.168	0.577	24	0.304	K.SADLFDSEGQSSQSNSIK.Q
R3/RRR3-13/2	1648.672	1649.845	-1322.386	0.364	1921.290	0.495	23	0.277	K.LLSDLAAAM*EEGDVAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1490.698	1491.671	-1327.577	0.363	1930.007	0.356	19	0.243	K.VAEIAAQLEQYQK.A
R3/RRR3-13/2	1717.215	1717.815	-934.495	0.518	1433.608	0.414	19	0.194	K.DIGEIYHQEQDLEK.A
R3/RRR3-13/2	1135.092	1134.267	-154.636	0.524	1251.813	0.435	16	0.185	K.ANEIFEAIAR.Q
R3/RRR3-13/3	1491.615	1491.671	-37.243	0.528	1635.837	0.462	26	0.183	K.VAEIAAQLEQYQK.A
R3/RRR3-13/2	1400.112	1400.475	-260.210	0.441	1232.739	0.429	18	0.181	R.YQDIDPTFSGTR.E
R3/RRR3-13/2	1134.103	1134.267	-144.947	0.465	1389.296	0.318	17	0.176	K.ANEIFEAIAR.Q
R3/RRR3-13/2	1490.426	1491.671	-1510.847	0.344	1168.294	0.420	18	0.171	K.VAEIAAQLEQYQK.A
R3/RRR3-13/2	1400.402	1400.475	-52.249	0.436	1042.528	0.460	17	0.171	R.YQDIDPTFSGTR.E
R3/RRR3-13/2	1308.185	1308.444	-198.657	0.446	1070.394	0.427	17	0.168	R.GDVVAITNSM*ER.Y
R3/RRR3-13/2	1400.198	1400.475	-198.547	0.446	1058.613	0.422	17	0.166	R.YQDIDPTFSGTR.E
R3/RRR3-13/2	1134.307	1134.267	35.446	0.481	1148.333	0.344	15	0.161	K.ANEIFEAIAR.Q
R3/RRR3-13/2	1488.256	1488.745	-329.289	0.365	742.228	0.439	15	0.145	R.GILLNAGICQLCR.G
R3/RRR3-13/2	1307.955	1308.444	-375.426	0.353	810.698	0.362	15	0.144	R.GDVVAITNSM*ER.Y
R3/RRR3-13/2	1307.914	1308.444	-1173.293	0.314	746.231	0.349	15	0.140	R.GDVVAITNSM*ER.Y
R3/RRR3-13/2	1491.008	1491.671	-1118.314	0.272	849.387	0.280	17	0.137	K.VAEIAAQLEQYQK.A
R3/RRR3-13/3	1792.854	1791.895	-22.824	0.368	837.379	0.518	30	0.117	K.YEDAADLFDKGANSFK.L
R3/RRR3-13/3	1901.725	1900.935	-110.944	0.334	1124.740	0.354	29	0.109	K.SADLFDSEGQSSQSNSIK.Q
R3/RRR3-13/3	1901.374	1900.935	231.385	0.310	388.876	0.369	21	0.067	-.SADLFDSEGQSSQSNSIK.-
R3/RRR3-4/3	1974.267	1974.290	-11.766	0.585	2837.692	0.585	39	0.493	R.LFASNVLVSGLNGLGAEIAK.N
R3/RRR3-3/2	1570.945	1570.728	138.838	0.576	2548.128	0.489	24	0.389	R.YDAQISVFGSNLQK.K
R3/RRR3-4/2	1973.574	1974.290	-872.106	0.553	2360.524	0.555	28	0.375	R.LFASNVLVSGLNGLGAEIAK.N
R3/RRR3-4/2	1571.105	1570.728	240.523	0.581	2278.073	0.503	24	0.339	R.YDAQISVFGSNLQK.K
R3/RRR3-4/2	1570.121	1570.728	-1026.407	0.539	2270.062	0.457	24	0.324	R.YDAQISVFGSNLQK.K
R3/RRR3-4/2	1570.239	1570.728	-312.252	0.563	2166.575	0.514	24	0.323	R.YDAQISVFGSNLQK.K
R3/RRR3-4/2	1973.700	1974.290	-808.155	0.551	2087.226	0.555	27	0.321	R.LFASNVLVSGLNGLGAEIAK.N
R3/RRR3-4/2	1973.305	1974.290	-1009.099	0.559	1931.600	0.540	26	0.289	R.LFASNVLVSGLNGLGAEIAK.N
R3/RRR3-2/3	1973.844	1974.290	-226.607	0.465	1930.070	0.463	34	0.233	R.LFASNVLVSGLNGLGAEIAK.N
R3/RRR3-4/2	1292.064	1292.380	-245.013	0.493	1641.640	0.448	20	0.227	R.FPIAGSSDDVQR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1291.929	1292.380	-350.139	0.471	1697.932	0.390	20	0.220	R.FPIAGSSDDVQR.L
R3/RRR3-1/2	1571.103	1570.728	239.666	0.451	1646.856	0.398	24	0.216	R.YDAQISVFGSNLQK.K
R3/RRR3-3/2	1572.114	1570.728	246.210	0.564	1482.897	0.422	22	0.200	R.YDAQISVFGSNLQK.K
R3/RRR3-4/2	1292.006	1292.380	-289.848	0.469	1446.211	0.426	19	0.200	R.FPIAGSSDDVQR.L
R3/RRR3-3/2	1571.391	1570.728	-215.096	0.526	1406.415	0.431	22	0.196	R.YDAQISVFGSNLQK.K
R3/RRR3-3/2	1292.010	1292.380	-286.720	0.466	1520.488	0.342	19	0.190	R.FPIAGSSDDVQR.L
R3/RRR3-3/2	1291.610	1292.380	-1374.662	0.404	1301.486	0.403	18	0.181	R.FPIAGSSDDVQR.L
R3/RRR3-4/2	1248.041	1248.362	-257.678	0.433	1219.985	0.414	18	0.178	K.LTVTDDDVIEK.S
R3/RRR3-1/2	1571.144	1570.728	265.844	0.456	1222.642	0.408	23	0.177	R.YDAQISVFGSNLQK.K
R3/RRR3-3/2	1247.870	1248.362	-395.763	0.473	1204.697	0.397	18	0.175	K.LTVTDDDVIEK.S
R3/RRR3-4/3	1974.266	1974.290	-12.231	0.437	1442.186	0.480	33	0.168	R.LFASNVLVSGLNGLGAEIAK.N
R3/RRR3-3/2	1248.195	1248.362	-134.150	0.460	1151.039	0.374	18	0.167	K.LTVTDDDVIEK.S
R3/RRR3-4/2	1318.544	1319.447	-1447.517	0.444	877.844	0.435	15	0.159	R.LKFEDYFSNR.V
R3/RRR3-4/2	1247.871	1248.362	-394.586	0.414	963.331	0.385	17	0.157	K.LTVTDDDVIEK.S
R3/RRR3-2/2	1292.188	1292.380	-148.723	0.446	1048.364	0.340	19	0.156	R.FPIAGSSDDVQR.L
R3/RRR3-4/2	1247.467	1248.362	-1523.515	0.391	991.345	0.363	17	0.156	K.LTVTDDDVIEK.S
R3/RRR3-3/2	1474.418	1473.697	-189.881	0.463	654.788	0.478	18	0.153	R.AETFGIPIPDWVK.N
R3/RRR3-2/2	1570.446	1570.728	-179.830	0.377	859.174	0.358	20	0.149	R.YDAQISVFGSNLQK.K
R3/RRR3-3/2	1247.518	1248.362	-1482.330	0.334	813.508	0.377	16	0.148	K.LTVTDDDVIEK.S
R3/RRR3-4/2	1052.019	1052.160	-133.911	0.343	702.561	0.392	14	0.146	R.SEFEGLLEK.T
R3/RRR3-4/2	1318.212	1319.447	-1700.518	0.337	704.312	0.393	13	0.144	R.LKFEDYFSNR.V
R3/RRR3-3/2	1080.039	1080.223	-170.567	0.331	984.597	0.296	14	0.144	K.LHVEALQNR.A
R3/RRR3-4/2	1051.865	1052.160	-280.594	0.363	471.484	0.391	12	0.142	R.SEFEGLLEK.T
R3/RRR3-3/2	958.206	958.053	160.090	0.397	1043.876	0.244	12	0.141	R.DWNIGQPK.S
R3/RRR3-3/2	1318.975	1319.447	-358.926	0.478	599.985	0.339	14	0.141	R.LKFEDYFSNR.V
R3/RRR3-4/2	1281.148	1282.342	-1717.412	0.284	954.320	0.299	15	0.141	R.APEIDEDLHSR.Q
R3/RRR3-4/2	1051.523	1052.160	-1561.030	0.281	545.831	0.407	12	0.140	R.SEFEGLLEK.T
R3/RRR3-3/2	1291.154	1292.380	-1728.662	0.324	803.417	0.307	15	0.140	R.FPIAGSSDDVQR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1319.015	1319.447	-328.283	0.427	626.504	0.306	13	0.137	R.LKFEDYFSNR.V
R3/RRR3-2/2	1571.469	1570.728	-165.065	0.440	486.353	0.317	16	0.137	R.YDAQISVFGSNLQK.K
R3/RRR3-2/2	1473.666	1473.697	-21.237	0.394	394.114	0.279	15	0.133	R.AETFGIPIPDWVK.N
R3/RRR3-4/3	1282.488	1282.342	114.493	0.440	534.549	0.576	20	0.121	R.APEIDEDLHSR.Q
R3/RRR3-2/3	1282.603	1282.342	204.262	0.346	479.382	0.564	18	0.115	R.APEIDEDLHSR.Q
R3/RRR3-2/3	1282.483	1282.342	110.627	0.352	414.737	0.487	19	0.108	R.APEIDEDLHSR.Q
R3/RRR3-4/3	1281.347	1282.342	-1561.692	0.310	448.572	0.502	18	0.107	R.APEIDEDLHSR.Q
R3/RRR3-2/3	1282.521	1282.342	140.266	0.310	347.136	0.491	17	0.106	R.APEIDEDLHSR.Q
R3/RRR3-4/3	1281.665	1282.342	-1312.259	0.250	357.497	0.408	16	0.099	R.APEIDEDLHSR.Q
R3/RRR3-4/3	1318.987	1319.447	-349.604	0.429	935.705	0.306	19	0.091	-.LKFEDYFSNR.-
R3/RRR3-4/3	1319.846	1319.447	303.370	0.439	796.691	0.266	18	0.075	-.LKFEDYFSNR.-
R3/RRR3-4/3	1319.552	1319.447	79.776	0.481	878.112	0.250	20	0.075	-.LKFEDYFSNR.-
R3/RRR3-3/3	1319.634	1319.447	142.676	0.395	656.096	0.292	17	0.067	-.LKFEDYFSNR.-
R3/RRR3-11/1	1101.612	1102.220	-1464.533	0.107	697.097	0.398	13	0.877	R.TLSGPVTDPSK.L
R3/RRR3-11/1	1101.558	1102.220	-1513.175	0.146	554.605	0.323	11	0.870	-.TLSGPVTDPSK.-
R3/RRR3-11/2	1818.419	1818.927	-831.919	0.638	3500.413	0.724	28	0.765	R.HETADINTFSWGVANR.G
R3/RRR3-11/2	1818.335	1818.927	-878.553	0.626	3144.194	0.677	28	0.627	R.HETADINTFSWGVANR.G
R3/RRR3-11/2	1818.402	1818.927	-841.151	0.616	2496.220	0.718	26	0.468	R.HETADINTFSWGVANR.G
R3/RRR3-11/2	1811.440	1811.095	191.490	0.617	2301.273	0.572	25	0.368	K.IIAEYIWIGGSGM*DLR.S
R3/RRR3-11/2	1795.404	1795.095	172.422	0.563	2346.610	0.524	23	0.360	K.IIAEYIWIGGSGMDLR.S
R3/RRR3-11/2	1810.667	1811.095	-236.798	0.541	2240.153	0.504	25	0.334	K.IIAEYIWIGGSGM*DLR.S
R3/RRR3-11/3	1627.900	1627.700	123.443	0.525	2305.757	0.509	31	0.312	R.HKEHISAYGEGNER.R
R3/RRR3-11/2	1810.476	1811.095	-896.454	0.516	1906.747	0.494	23	0.273	K.IIAEYIWIGGSGM*DLR.S
R3/RRR3-11/3	1627.569	1627.700	-80.434	0.550	1950.787	0.517	29	0.248	R.HKEHISAYGEGNER.R
R3/RRR3-11/3	1628.722	1627.700	13.966	0.537	1844.401	0.539	29	0.238	R.HKEHISAYGEGNER.R
R3/RRR3-11/3	1810.992	1811.095	-56.657	0.537	1497.402	0.493	29	0.176	K.IIAEYIWIGGSGM*DLR.S
R3/RRR3-11/3	1817.912	1818.927	-1112.133	0.483	1470.510	0.424	28	0.155	R.HETADINTFSWGVANR.G
R3/RRR3-11/2	1439.782	1440.667	-1313.383	0.397	977.418	0.359	18	0.151	R.TLSGPVTDPSKLPK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1440.262	1440.667	-282.115	0.405	802.384	0.390	16	0.145	-.TLSGPVTDPSKLPK.-
R3/RRR3-11/3	1399.568	1399.555	9.090	0.502	1493.821	0.367	26	0.139	K.SM*RNDGGYEIIK.S
R3/RRR3-11/2	1439.730	1440.667	-1349.488	0.375	876.712	0.282	17	0.138	-.TLSGPVTDPSKLPK.-
R3/RRR3-11/2	1794.296	1795.095	-1005.985	0.376	853.428	0.249	16	0.132	K.IIAEYIWIGGSGMDLR.S
R3/RRR3-10/2	1818.410	1818.927	-837.041	0.303	571.730	0.176	17	0.128	R.HETADINTFSWGVANR.G
R3/RRR3-11/3	1783.651	1783.886	-131.983	0.464	852.534	0.462	29	0.115	R.HKEHISAYGEGNERR.L
R3/RRR3-11/3	1424.495	1424.543	-33.540	0.522	807.497	0.435	23	0.111	K.SFGRDIVDSHYK.A
R3/RRR3-11/3	1818.273	1818.927	-912.629	0.448	959.120	0.406	24	0.110	R.HETADINTFSWGVANR.G
R3/RRR3-11/3	1784.026	1783.886	78.463	0.395	875.645	0.416	27	0.107	R.HKEHISAYGEGNERR.L
R3/RRR3-11/3	1398.887	1399.555	-1196.158	0.493	854.655	0.358	20	0.101	K.SM*RNDGGYEIIK.S
R3/RRR3-11/3	1399.594	1399.555	27.854	0.480	868.310	0.348	22	0.101	K.SM*RNDGGYEIIK.S
R3/RRR3-11/3	1400.014	1399.555	328.512	0.418	1010.156	0.311	22	0.098	-.SM*RNDGGYEIIK.-
R3/RRR3-11/3	1810.888	1811.095	-114.569	0.384	1004.810	0.288	26	0.095	K.IIAEYIWIGGSGM*DLR.S
R3/RRR3-11/3	1362.567	1362.387	132.430	0.479	1259.948	0.218	25	0.094	-.EHISAYGEGNER.-
R3/RRR3-11/3	1810.785	1811.095	-171.677	0.382	816.517	0.317	25	0.094	K.IIAEYIWIGGSGM*DLR.S
R3/RRR3-11/3	1361.416	1362.387	-1451.766	0.416	1046.519	0.193	23	0.085	-.EHISAYGEGNER.-
R3/RRR3-11/3	1362.019	1362.387	-270.824	0.368	949.742	0.195	22	0.084	-.EHISAYGEGNER.-
R3/RRR3-5/3	1893.169	1893.091	41.376	0.510	2822.004	0.528	34	0.455	R.HAQLPDEAKELDKELR.Q
R3/RRR3-5/2	1610.584	1610.834	-155.355	0.555	1576.727	0.576	22	0.250	K.VPEPTVDETIQILR.G
R3/RRR3-5/2	1159.768	1160.260	-424.772	0.498	1646.054	0.494	18	0.239	K.AIDLIDEAGSR.V
R3/RRR3-5/2	1160.989	1160.260	-233.656	0.568	1591.258	0.512	18	0.237	K.AIDLIDEAGSR.V
R3/RRR3-5/2	1160.948	1160.260	-269.627	0.527	1480.287	0.522	18	0.226	K.AIDLIDEAGSR.V
R3/RRR3-5/2	1514.183	1513.695	323.434	0.530	1451.002	0.474	22	0.212	K.M*PTLEEYGTNLTK.L
R3/RRR3-5/3	1893.247	1893.091	82.990	0.447	1667.443	0.492	29	0.199	R.HAQLPDEAKELDKELR.Q
R3/RRR3-5/2	1158.545	1159.315	-1532.126	0.419	1276.324	0.448	15	0.187	R.VLELSLEEAR.Q
R3/RRR3-5/3	1960.967	1960.225	-131.974	0.493	1616.526	0.465	30	0.186	K.NPNRPIASFIFSGPTGVGK.S
R3/RRR3-5/2	1030.184	1030.160	23.460	0.471	1116.374	0.375	17	0.165	K.TAIAEGLAQR.I
R3/RRR3-5/2	1477.629	1477.689	-40.486	0.458	1014.925	0.408	17	0.158	R.GSGFVAVEIPFTPR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1477.232	1477.689	-310.031	0.346	1024.764	0.341	17	0.150	R.GSGFVAVEIPFTPR.A
R3/RRR3-5/2	1421.044	1421.446	-283.776	0.392	955.163	0.362	18	0.149	K.EGDSAIVDVDSEGK.V
R3/RRR3-5/2	1158.445	1159.315	-1618.501	0.293	817.640	0.181	13	0.129	R.VLELSLEEAR.Q
R3/RRR3-8/2	1611.022	1610.834	117.525	0.392	763.409	0.185	17	0.127	-.VPEPTVDETIQILR.-
R3/RRR3-5/2	1476.384	1477.689	-1565.769	0.198	653.282	0.115	16	0.125	R.GSGFVAVEIPFTPR.A
R3/RRR3-5/3	1959.820	1960.225	-207.269	0.385	1084.384	0.397	26	0.115	K.NPNRPIASFIFSGPTGVGK.S
R3/RRR3-5/3	1383.687	1383.575	81.122	0.420	926.832	0.336	25	0.098	K.LAEEGKLDPVVGR.Q
R3/RRR3-3/2	1601.452	1601.825	-233.535	0.527	2611.399	0.441	23	0.393	R.FNAILEELGIEQPK.G
R3/RRR3-3/2	1602.075	1601.825	156.469	0.558	2124.555	0.436	22	0.294	R.FNAILEELGIEQPK.G
R3/RRR3-3/2	1633.294	1633.698	-247.948	0.470	1352.485	0.564	23	0.218	K.IWGTSPDSIDAAEDR.K
R3/RRR3-3/2	1141.939	1142.331	-344.021	0.452	1291.516	0.545	17	0.208	K.VPIITTVDGAR.A
R3/RRR3-3/2	1142.113	1142.331	-190.992	0.469	1333.203	0.495	18	0.203	K.VPIITTVDGAR.A
R3/RRR3-3/2	1141.807	1142.331	-1338.731	0.397	1157.594	0.493	17	0.185	K.VPIITTVDGAR.A
R3/RRR3-2/2	1142.477	1142.331	128.750	0.462	1142.247	0.485	17	0.184	K.VPIITTVDGAR.A
R3/RRR3-2/2	1536.155	1534.865	189.486	0.536	977.015	0.507	19	0.173	K.VLQLEGIPVEPVLK.I
R3/RRR3-3/2	1534.545	1534.865	-209.330	0.477	981.724	0.468	19	0.168	K.VLQLEGIPVEPVLK.I
R3/RRR3-3/2	1534.345	1534.865	-993.844	0.326	1062.557	0.414	19	0.163	K.VLQLEGIPVEPVLK.I
R3/RRR3-2/2	1535.351	1534.865	317.496	0.484	729.680	0.525	17	0.161	K.VLQLEGIPVEPVLK.I
R3/RRR3-3/2	1777.476	1777.996	-858.108	0.460	692.962	0.469	19	0.151	K.LSVGYTLDQIPNDITK.K
R3/RRR3-3/2	1105.341	1105.309	29.064	0.251	984.491	0.346	13	0.145	R.LALEVAPTYK.R
R3/RRR3-3/2	1534.072	1534.865	-1172.000	0.295	788.560	0.398	17	0.145	K.VLQLEGIPVEPVLK.I
R3/RRR3-3/2	1777.430	1777.996	-884.100	0.428	605.124	0.461	17	0.145	K.LSVGYTLDQIPNDITK.K
R3/RRR3-3/2	1206.866	1206.419	371.346	0.486	1205.106	0.221	15	0.144	R.LRDYSVAIIR.E
R3/RRR3-3/2	1777.121	1777.996	-1058.422	0.402	729.743	0.374	19	0.142	K.LSVGYTLDQIPNDITK.K
R3/RRR3-3/2	1926.329	1926.093	122.894	0.461	446.910	0.496	15	0.138	R.STGEVM*GIDYEFSGAFAK.A
R3/RRR3-3/2	1421.469	1422.608	-1509.634	0.297	685.785	0.361	15	0.137	R.ELGFNIIATSGTAK.V
R3/RRR3-3/2	995.597	996.189	-1603.092	0.366	683.145	0.267	13	0.134	K.VLILGGGPNR.I
R3/RRR3-2/2	1422.497	1422.608	-78.205	0.333	485.308	0.330	14	0.133	R.ELGFNIIATSGTAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	995.992	996.189	-198.606	0.374	811.997	0.195	14	0.131	K.VLILGGGPNR.I
R3/RRR3-3/2	1423.623	1422.608	10.182	0.342	288.289	0.368	11	0.131	-.ELGFNIIATSGTAK.-
R3/RRR3-3/2	996.161	996.189	-27.852	0.410	662.868	0.217	13	0.130	-.VLILGGGPNR.-
R3/RRR3-6/2	1741.429	1740.944	279.432	0.600	2366.587	0.588	24	0.390	R.NIIHFNTLANQAVER.A
R3/RRR3-6/2	1741.316	1740.944	214.340	0.625	2249.991	0.577	24	0.361	R.NIIHFNTLANQAVER.A
R3/RRR3-6/2	1519.069	1519.635	-1034.063	0.489	2197.222	0.565	24	0.349	K.FEDPAEGEDVLVAK.F
R3/RRR3-7/2	1562.325	1562.774	-288.425	0.497	2329.645	0.450	22	0.335	R.TTLVANTSNM*PVAAR.E
R3/RRR3-6/2	1741.537	1740.944	-234.646	0.592	2106.935	0.572	24	0.333	R.NIIHFNTLANQAVER.A
R3/RRR3-6/2	1520.165	1519.635	-309.570	0.552	2063.964	0.576	24	0.328	K.FEDPAEGEDVLVAK.F
R3/RRR3-6/2	1562.278	1562.774	-318.763	0.495	2265.576	0.464	22	0.327	R.TTLVANTSNM*PVAAR.E
R3/RRR3-6/2	1562.224	1562.774	-994.978	0.433	2229.109	0.433	22	0.312	R.TTLVANTSNM*PVAAR.E
R3/RRR3-6/2	1796.414	1797.025	-899.156	0.506	1836.906	0.569	27	0.284	R.LAEMPADSGYPAYLAAR.L
R3/RRR3-6/2	1563.320	1562.774	-291.453	0.543	2027.334	0.462	22	0.283	R.TTLVANTSNM*PVAAR.E
R3/RRR3-6/2	1518.911	1519.635	-1138.236	0.395	1825.752	0.512	22	0.267	K.FEDPAEGEDVLVAK.F
R3/RRR3-6/2	1605.313	1605.769	-284.837	0.553	1754.688	0.539	22	0.263	K.DALAESDKITLETAK.L
R3/RRR3-6/2	1812.538	1813.024	-269.074	0.554	1625.258	0.597	25	0.259	R.LAEM*PADSGYPAYLAAR.L
R3/RRR3-6/2	1812.482	1813.024	-853.271	0.545	1538.024	0.614	25	0.252	R.LAEM*PADSGYPAYLAAR.L
R3/RRR3-6/2	1796.405	1797.025	-904.341	0.488	1618.360	0.547	26	0.246	R.LAEMPADSGYPAYLAAR.L
R3/RRR3-6/2	1473.428	1472.623	-132.756	0.523	1676.900	0.506	21	0.245	R.EDDLNEIVQLVGK.D
R3/RRR3-6/2	1813.448	1813.024	234.526	0.588	1430.370	0.598	24	0.233	R.LAEM*PADSGYPAYLAAR.L
R3/RRR3-6/2	1472.248	1472.623	-255.444	0.436	1591.120	0.471	20	0.225	R.EDDLNEIVQLVGK.D
R3/RRR3-6/2	1605.393	1605.769	-234.869	0.551	1411.835	0.530	21	0.216	K.DALAESDKITLETAK.L
R3/RRR3-7/2	1473.030	1472.623	277.649	0.441	1461.240	0.454	20	0.207	R.EDDLNEIVQLVGK.D
R3/RRR3-6/2	1473.145	1472.623	-324.937	0.502	1488.654	0.438	20	0.206	R.EDDLNEIVQLVGK.D
R3/RRR3-6/2	1796.411	1797.025	-901.066	0.499	1230.959	0.571	23	0.205	R.LAEMPADSGYPAYLAAR.L
R3/RRR3-7/2	1472.753	1472.623	88.654	0.456	1470.515	0.415	19	0.199	R.EDDLNEIVQLVGK.D
R3/RRR3-6/3	1741.835	1740.944	-63.067	0.563	1819.009	0.434	29	0.199	R.NIIHFNTLANQAVER.A
R3/RRR3-6/2	1605.220	1605.769	-967.658	0.506	1275.137	0.515	20	0.198	K.DALAESDKITLETAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1200.897	1201.310	-344.769	0.476	1334.528	0.407	17	0.187	K.LYDDLTTGFR.N
R3/RRR3-6/2	1200.616	1201.310	-1415.416	0.573	1298.788	0.421	17	0.186	K.LYDDLTTGFR.N
R3/RRR3-7/2	1200.827	1201.310	-403.417	0.472	1194.904	0.436	17	0.181	K.LYDDLTTGFR.N
R3/RRR3-6/2	1200.451	1201.310	-1553.198	0.467	1166.975	0.437	17	0.179	K.LYDDLTTGFR.N
R3/RRR3-7/3	1740.884	1740.944	-34.477	0.528	1628.071	0.445	28	0.178	R.NIIHFNTLANQAVER.A
R3/RRR3-6/2	1200.664	1201.310	-1374.978	0.495	1175.702	0.409	17	0.175	K.LYDDLTTGFR.N
R3/RRR3-6/3	1563.714	1562.774	-38.797	0.513	1354.694	0.452	28	0.149	R.TTLVANTSNM*PVAAR.E
R3/RRR3-3/2	1202.295	1201.310	-12.792	0.364	703.607	0.398	14	0.148	K.LYDDLTTGFR.N
R3/RRR3-6/2	918.093	918.052	44.565	0.361	631.469	0.401	11	0.148	R.M*GDLFYR.L
R3/RRR3-6/2	1578.472	1578.795	-205.133	0.475	484.984	0.462	18	0.146	K.HFPSVNWLISYSK.Y
R3/RRR3-6/2	918.207	918.052	169.635	0.389	597.702	0.371	11	0.146	R.M*GDLFYR.L
R3/RRR3-6/2	902.022	902.052	-34.017	0.417	861.601	0.292	11	0.144	R.MGDLFYR.L
R3/RRR3-6/2	901.356	902.052	-1887.523	0.391	893.565	0.239	11	0.139	R.MGDLFYR.L
R3/RRR3-6/2	901.836	902.052	-241.063	0.366	856.096	0.237	11	0.138	R.MGDLFYR.L
R3/RRR3-4/2	1202.374	1201.310	53.093	0.238	525.849	0.237	13	0.134	K.LYDDLTTGFR.N
R3/RRR3-6/3	1605.450	1605.769	-199.330	0.461	1204.129	0.445	29	0.133	K.DALAESDKITLETAK.L
R3/RRR3-7/2	1200.511	1201.310	-1503.249	0.212	509.629	0.247	12	0.133	K.LYDDLTTGFR.N
R3/RRR3-6/3	1562.929	1562.774	99.646	0.463	1150.332	0.446	29	0.129	R.TTLVANTSNM*PVAAR.E
R3/RRR3-6/3	1605.978	1605.769	130.541	0.483	959.450	0.492	27	0.127	K.DALAESDKITLETAK.L
R3/RRR3-6/3	1813.471	1813.024	247.310	0.406	1182.661	0.335	25	0.110	R.LAEM*PADSGYPAYLAAR.L
R3/RRR3-7/3	1606.736	1605.769	-20.553	0.482	620.540	0.463	23	0.109	K.DALAESDKITLETAK.L
R3/RRR3-6/3	1607.242	1605.769	294.945	0.471	913.915	0.384	26	0.106	K.DALAESDKITLETAK.L
R3/RRR3-7/3	1740.524	1740.944	-242.036	0.398	859.352	0.332	24	0.097	R.NIIHFNTLANQAVER.A
R3/RRR3-7/3	1740.151	1740.944	-1033.353	0.377	727.601	0.309	21	0.088	-.NIIHFNTLANQAVER.-
R3/RRR3-8/3	1814.190	1813.024	91.382	0.274	901.665	0.154	24	0.077	R.LAEM*PADSGYPAYLAAR.L
R3/RRR3-10/2	1870.285	1871.077	-961.250	0.503	3048.328	0.517	25	0.530	K.LAYIALDYEQELETAK.S
R3/RRR3-10/2	1870.570	1871.077	-808.137	0.571	2671.011	0.515	24	0.430	K.LAYIALDYEQELETAK.S
R3/RRR3-10/2	1870.231	1871.077	-989.820	0.531	2557.640	0.511	24	0.404	K.LAYIALDYEQELETAK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1748.437	1748.915	-274.483	0.475	2159.157	0.491	31	0.282	K.SYELPDGQVITIGAER.F
R3/RRR3-10/3	1750.232	1748.915	181.691	0.573	2274.989	0.396	33	0.262	K.SYELPDGQVITIGAER.F
R3/RRR3-10/2	1748.468	1748.915	-256.264	0.537	1727.047	0.540	26	0.258	K.SYELPDGQVITIGAER.F
R3/RRR3-15/2	1749.361	1748.915	255.768	0.581	1675.594	0.548	26	0.252	K.SYELPDGQVITIGAER.F
R3/RRR3-12/2	1748.426	1748.915	-280.780	0.521	1748.939	0.489	26	0.247	K.SYELPDGQVITIGAER.F
R3/RRR3-10/2	1749.423	1748.915	-282.370	0.562	1610.321	0.555	26	0.246	K.SYELPDGQVITIGAER.F
R3/RRR3-12/2	1748.434	1748.915	-276.227	0.514	1703.620	0.497	26	0.243	K.SYELPDGQVITIGAER.F
R3/RRR3-10/2	1748.346	1748.915	-900.348	0.539	1521.329	0.562	25	0.236	K.SYELPDGQVITIGAER.F
R3/RRR3-3/2	1748.342	1748.915	-902.310	0.511	1541.119	0.512	25	0.227	K.SYELPDGQVITIGAER.F
R3/RRR3-15/2	1748.162	1748.915	-1006.059	0.496	1427.753	0.516	24	0.214	K.SYELPDGQVITIGAER.F
R3/RRR3-11/2	1748.327	1748.915	-911.002	0.528	1412.001	0.491	24	0.207	K.SYELPDGQVITIGAER.F
R3/RRR3-15/2	1748.719	1748.915	-112.207	0.525	1281.958	0.536	24	0.204	K.SYELPDGQVITIGAER.F
R3/RRR3-11/2	1749.806	1748.915	-62.387	0.553	1203.940	0.575	23	0.204	K.SYELPDGQVITIGAER.F
R3/RRR3-2/2	1749.494	1748.915	-241.627	0.560	1223.811	0.561	23	0.203	K.SYELPDGQVITIGAER.F
R3/RRR3-24/2	1748.705	1748.915	-120.610	0.499	1255.780	0.544	23	0.202	K.SYELPDGQVITIGAER.F
R3/RRR3-2/2	1748.270	1748.915	-943.597	0.506	1287.738	0.511	24	0.199	K.SYELPDGQVITIGAER.F
R3/RRR3-12/2	1747.992	1748.915	-1103.447	0.466	1227.351	0.516	23	0.194	K.SYELPDGQVITIGAER.F
R3/RRR3-9/2	1748.663	1748.915	-144.558	0.512	1305.936	0.474	24	0.194	K.SYELPDGQVITIGAER.F
R3/RRR3-22/2	1748.315	1748.915	-917.731	0.447	1316.086	0.462	22	0.191	K.SYELPDGQVITIGAER.F
R3/RRR3-10/2	976.934	977.013	-80.787	0.522	1203.274	0.485	16	0.189	K.AGFAGDDAPR.A
R3/RRR3-14/2	1750.146	1748.915	132.458	0.471	1192.198	0.506	22	0.189	K.SYELPDGQVITIGAER.F
R3/RRR3-9/2	1748.382	1748.915	-879.250	0.514	1212.713	0.487	22	0.187	K.SYELPDGQVITIGAER.F
R3/RRR3-10/2	1968.586	1969.270	-858.145	0.517	975.109	0.584	21	0.183	R.VAPEEHPILLTEAPLNPK.A
R3/RRR3-9/2	976.817	977.013	-200.749	0.492	1194.684	0.448	16	0.182	K.AGFAGDDAPR.A
R3/RRR3-1/2	976.916	977.013	-99.212	0.474	1205.998	0.440	16	0.181	K.AGFAGDDAPR.A
R3/RRR3-14/2	976.882	977.013	-134.184	0.451	1237.624	0.424	16	0.181	K.AGFAGDDAPR.A
R3/RRR3-10/2	1132.965	1133.193	-201.612	0.465	920.430	0.554	16	0.180	R.GYSFTTTAER.E
R3/RRR3-11/2	1747.883	1748.915	-1166.210	0.417	1235.721	0.435	23	0.180	K.SYELPDGQVITIGAER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1747.971	1748.915	-1115.649	0.459	1115.477	0.493	21	0.180	K.SYELPDGQVITIGAER.F
R3/RRR3-9/2	1748.122	1748.915	-1029.054	0.503	1176.895	0.454	22	0.178	K.SYELPDGQVITIGAER.F
R3/RRR3-10/2	976.420	977.013	-1636.334	0.332	1453.605	0.303	16	0.177	K.AGFAGDDAPR.A
R3/RRR3-9/2	976.427	977.013	-1629.426	0.395	1275.884	0.384	16	0.177	K.AGFAGDDAPR.A
R3/RRR3-9/2	976.195	977.013	-1868.241	0.352	1244.999	0.391	16	0.175	K.AGFAGDDAPR.A
R3/RRR3-10/2	1516.307	1516.687	-251.494	0.444	1129.442	0.438	17	0.175	K.IWHHTFYNELR.V
R3/RRR3-12/2	1134.010	1133.193	-161.910	0.540	802.876	0.538	16	0.173	R.GYSFTTTAER.E
R3/RRR3-9/2	1132.883	1133.193	-274.469	0.464	859.121	0.508	16	0.170	R.GYSFTTTAER.E
R3/RRR3-10/2	1969.543	1969.270	138.963	0.489	877.470	0.549	20	0.169	R.VAPEEHPILLTEAPLNPK.A
R3/RRR3-10/2	976.770	977.013	-248.893	0.424	1186.888	0.371	16	0.169	K.AGFAGDDAPR.A
R3/RRR3-10/2	1165.042	1164.355	-269.039	0.444	963.672	0.463	17	0.168	K.EITALAPSSM*K.I
R3/RRR3-10/2	1516.249	1516.687	-289.940	0.423	1080.425	0.421	17	0.168	K.IWHHTFYNELR.V
R3/RRR3-10/2	1132.946	1133.193	-218.149	0.461	968.397	0.449	16	0.168	R.GYSFTTTAER.E
R3/RRR3-10/2	976.466	977.013	-1588.860	0.372	1190.984	0.348	16	0.165	K.AGFAGDDAPR.A
R3/RRR3-10/2	1968.610	1969.270	-845.820	0.480	728.563	0.578	19	0.164	R.VAPEEHPILLTEAPLNPK.A
R3/RRR3-1/2	977.170	977.013	161.181	0.413	1016.742	0.400	15	0.162	K.AGFAGDDAPR.A
R3/RRR3-10/2	976.345	977.013	-1713.583	0.325	1215.232	0.313	16	0.161	K.AGFAGDDAPR.A
R3/RRR3-10/2	1132.490	1133.193	-1507.913	0.308	838.296	0.479	16	0.159	R.GYSFTTTAER.E
R3/RRR3-10/2	1516.202	1516.687	-320.958	0.410	960.614	0.399	17	0.158	K.IWHHTFYNELR.V
R3/RRR3-9/2	1133.004	1133.193	-167.457	0.485	774.774	0.436	16	0.158	R.GYSFTTTAER.E
R3/RRR3-11/2	976.493	977.013	-1561.232	0.333	1027.881	0.352	15	0.155	K.AGFAGDDAPR.A
R3/RRR3-10/2	1148.047	1148.355	-269.137	0.311	774.417	0.472	16	0.155	K.EITALAPSSMK.I
R3/RRR3-10/2	1163.883	1164.355	-406.483	0.341	782.697	0.441	16	0.154	K.EITALAPSSM*K.I
R3/RRR3-12/2	1164.017	1164.355	-291.470	0.349	656.917	0.498	14	0.153	K.EITALAPSSM*K.I
R3/RRR3-10/2	1144.838	1145.381	-1352.191	0.346	339.816	0.566	17	0.152	R.HTGVMVGMGQK.D
R3/RRR3-11/2	976.820	977.013	-198.242	0.325	937.453	0.324	14	0.148	K.AGFAGDDAPR.A
R3/RRR3-10/2	1145.099	1145.381	-247.697	0.301	306.197	0.521	17	0.147	R.HTGVMVGMGQK.D
R3/RRR3-10/2	1144.863	1145.381	-1330.559	0.278	299.680	0.551	16	0.145	R.HTGVMVGMGQK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1164.300	1164.355	-47.220	0.375	717.055	0.369	15	0.145	K.EITALAPSSM*K.I
R3/RRR3-12/2	1163.941	1164.355	-356.497	0.360	699.697	0.373	15	0.145	K.EITALAPSSM*K.I
R3/RRR3-7/2	977.054	977.013	42.028	0.327	827.641	0.318	14	0.144	K.AGFAGDDAPR.A
R3/RRR3-16/2	1132.800	1133.193	-347.553	0.337	633.748	0.365	15	0.144	R.GYSFTTTAER.E
R3/RRR3-11/2	976.464	977.013	-1590.744	0.258	1090.178	0.201	16	0.141	K.AGFAGDDAPR.A
R3/RRR3-10/2	1163.898	1164.355	-393.960	0.300	591.809	0.364	14	0.140	K.EITALAPSSM*K.I
R3/RRR3-10/2	1147.384	1148.355	-1722.886	0.205	690.764	0.376	14	0.138	K.EITALAPSSMK.I
R3/RRR3-10/2	1160.820	1161.381	-1348.449	0.206	211.259	0.350	14	0.137	R.HTGVM*VGMGQK.D
R3/RRR3-12/2	976.666	977.013	-355.728	0.302	452.948	0.251	12	0.136	-.AGFAGDDAPR.-
R3/RRR3-10/3	1516.504	1516.687	-121.162	0.498	1332.016	0.391	25	0.129	K.IWHHTFYNELR.V
R3/RRR3-10/3	1516.858	1516.687	113.148	0.501	1173.817	0.399	24	0.121	K.IWHHTFYNELR.V
R3/RRR3-10/3	1516.709	1516.687	14.472	0.494	1220.122	0.367	24	0.117	K.IWHHTFYNELR.V
R3/RRR3-10/3	1976.271	1977.143	-950.372	0.398	1098.379	0.377	27	0.112	K.YPIEHGIVNNWDDM*EK.I
R3/RRR3-10/3	1145.333	1145.381	-42.116	0.460	1072.477	0.364	22	0.109	R.HTGVMVGMGQK.D
R3/RRR3-10/3	1162.409	1161.381	24.094	0.421	1101.292	0.243	21	0.092	-.HTGVM*VGMGQK.-
R3/RRR3-10/3	1977.693	1977.143	-228.328	0.380	948.065	0.100	25	0.074	K.YPIEHGIVNNWDDM*EK.I
R3/RRR3-4/2	1832.601	1831.958	-195.127	0.599	2021.934	0.560	24	0.311	K.TEDLWAALEEGSGEPVK.T
R3/RRR3-4/2	1831.359	1831.958	-875.715	0.530	1803.171	0.535	23	0.269	K.TEDLWAALEEGSGEPVK.T
R3/RRR3-4/2	1831.485	1831.958	-259.155	0.510	1785.663	0.516	23	0.261	K.TEDLWAALEEGSGEPVK.T
R3/RRR3-4/2	1211.949	1212.339	-323.037	0.501	1448.809	0.440	17	0.205	K.LNVNQTGFYR.V
R3/RRR3-4/2	1582.029	1582.787	-1114.493	0.478	1345.361	0.512	19	0.204	R.GVGAAGHEVAWTWLK.E
R3/RRR3-4/2	1516.321	1516.744	-279.510	0.433	1540.498	0.392	19	0.202	R.MLQSYLGAETFQK.S
R3/RRR3-4/2	1029.302	1029.172	126.253	0.510	1339.717	0.392	17	0.185	R.AEANLGNVLK.E
R3/RRR3-4/2	1212.044	1212.339	-244.219	0.538	1152.983	0.444	17	0.179	K.LNVNQTGFYR.V
R3/RRR3-4/2	1213.261	1212.339	-64.950	0.544	1284.889	0.333	16	0.168	K.LNVNQTGFYR.V
R3/RRR3-4/2	1168.461	1169.223	-1512.942	0.420	1206.952	0.331	15	0.163	R.VSYDEELASR.L
R3/RRR3-4/2	1516.043	1516.744	-1124.963	0.331	1215.715	0.322	17	0.160	R.MLQSYLGAETFQK.S
R3/RRR3-4/2	1168.226	1169.223	-1715.102	0.354	1057.088	0.336	14	0.153	R.VSYDEELASR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1106.000	1106.257	-233.096	0.458	890.433	0.365	14	0.152	R.NQDSIFLLR.G
R3/RRR3-1/2	1169.086	1169.223	-118.198	0.420	1022.329	0.302	16	0.150	R.VSYDEELASR.L
R3/RRR3-4/2	1105.701	1106.257	-1411.458	0.445	711.047	0.389	13	0.148	R.NQDSIFLLR.G
R3/RRR3-4/2	1833.486	1834.148	-908.822	0.477	464.540	0.497	19	0.146	R.FNEVLPVGEGTLVIAFK.G
R3/RRR3-4/2	1168.117	1168.285	-143.975	0.399	904.162	0.328	14	0.142	K.SGEGHLDALLR.G
R3/RRR3-4/2	1105.620	1106.257	-1485.093	0.383	633.225	0.337	13	0.141	R.NQDSIFLLR.G
R3/RRR3-4/2	1832.784	1834.148	-1293.759	0.341	426.749	0.378	18	0.135	R.FNEVLPVGEGTLVIAFK.G
R3/RRR3-4/3	1168.861	1168.285	-363.501	0.509	629.878	0.483	20	0.113	K.SGEGHLDALLR.G
R3/RRR3-4/3	1168.391	1168.285	91.145	0.499	761.167	0.450	21	0.112	K.SGEGHLDALLR.G
R3/RRR3-4/3	1354.025	1354.488	-342.953	0.439	977.457	0.348	23	0.102	K.IYKETDLSQEK.V
R3/RRR3-4/3	1168.338	1168.285	45.563	0.387	548.078	0.339	19	0.096	K.SGEGHLDALLR.G
R3/RRR3-4/3	1354.854	1354.488	271.177	0.434	1013.934	0.240	25	0.090	K.IYKETDLSQEK.V
R3/RRR3-5/3	1354.797	1354.488	229.165	0.357	668.699	0.293	21	0.078	-.IYKETDLSQEK.-
R3/RRR3-9/2	1121.975	1122.296	-286.740	0.462	1790.689	0.530	18	0.268	K.ALIAAEYSGVK.V
R3/RRR3-9/2	1575.366	1575.815	-285.744	0.500	1815.826	0.437	20	0.248	R.YFWTMVNQPNFK.K
R3/RRR3-9/2	1951.593	1952.155	-802.817	0.580	1361.272	0.639	26	0.235	K.VPVLETPDGPVSESNAIAR.Y
R3/RRR3-9/2	1575.166	1575.815	-1049.704	0.367	1820.457	0.371	20	0.232	R.YFWTMVNQPNFK.K
R3/RRR3-9/2	1121.926	1122.296	-331.169	0.432	1530.018	0.500	16	0.224	K.ALIAAEYSGVK.V
R3/RRR3-9/2	1575.745	1575.815	-44.259	0.493	1589.904	0.450	19	0.221	R.YFWTMVNQPNFK.K
R3/RRR3-9/2	1123.014	1122.296	-251.914	0.496	1387.510	0.521	16	0.213	K.ALIAAEYSGVK.V
R3/RRR3-9/2	1952.036	1952.155	-61.005	0.536	847.666	0.623	22	0.179	K.VPVLETPDGPVSESNAIAR.Y
R3/RRR3-9/2	1218.140	1218.490	-288.226	0.473	1332.110	0.371	17	0.179	K.MLVIGSEPPFK.V
R3/RRR3-9/2	1094.061	1094.286	-206.319	0.397	747.905	0.590	15	0.171	K.NPLDLLPPSK.M
R3/RRR3-9/2	1094.110	1094.286	-161.212	0.393	775.694	0.553	15	0.167	K.NPLDLLPPSK.M
R3/RRR3-9/2	1094.126	1094.286	-146.886	0.369	801.219	0.499	15	0.161	K.NPLDLLPPSK.M
R3/RRR3-9/2	1218.134	1218.490	-293.253	0.366	1037.488	0.335	15	0.153	-.MLVIGSEPPFK.-
R3/RRR3-17/2	776.916	776.906	12.196	0.468	968.097	0.254	11	0.142	K.VGGFLQR.M
R3/RRR3-9/2	1218.494	1218.490	3.154	0.413	965.705	0.283	14	0.142	-.MLVIGSEPPFK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	777.117	776.906	271.524	0.376	376.496	0.188	11	0.141	K.VGGFLQR.M
R3/RRR3-9/2	776.913	776.906	8.414	0.519	833.149	0.276	11	0.140	K.VGGFLQR.M
R3/RRR3-9/2	776.401	776.906	-1944.190	0.453	874.591	0.244	11	0.139	K.VGGFLQR.M
R3/RRR3-9/2	1094.104	1094.286	-166.584	0.263	462.073	0.386	12	0.137	K.NPLDLLPPSK.M
R3/RRR3-9/2	776.754	776.906	-197.129	0.485	843.480	0.213	11	0.133	-.VGGFLQR.-
R3/RRR3-9/2	1364.565	1363.460	77.199	0.318	814.687	0.247	14	0.132	K.NFTSEFPHVER.Y
R3/RRR3-9/2	1090.563	1091.309	-1605.404	0.396	914.446	0.116	13	0.128	-.MILDEWKR.-
R3/RRR3-9/2	1091.073	1091.309	-216.759	0.270	668.381	0.099	12	0.122	-.MILDEWKR.-
R3/RRR3-9/3	1907.665	1908.099	-228.275	0.390	834.390	0.446	25	0.109	K.AAEKPEEEEEAPKPKPK.N
R3/RRR3-9/3	1906.316	1908.099	-1990.273	0.315	554.319	0.325	20	0.087	K.AAEKPEEEEEAPKPKPK.N
R3/RRR3-10/2	1937.065	1937.204	-71.716	0.572	2678.622	0.571	24	0.451	R.TLMELLNQLDGFDELGK.V
R3/RRR3-10/2	1937.550	1937.204	179.299	0.604	2546.895	0.516	24	0.398	R.TLMELLNQLDGFDELGK.V
R3/RRR3-10/2	1936.818	1937.204	-199.925	0.561	2342.696	0.506	23	0.352	R.TLMELLNQLDGFDELGK.V
R3/RRR3-10/2	1952.340	1953.203	-957.363	0.472	2219.320	0.527	22	0.337	R.TLM*ELLNQLDGFDELGK.V
R3/RRR3-10/2	1722.359	1722.964	-934.831	0.510	1978.880	0.583	22	0.312	K.IVSSAIIDKYIGESAR.L
R3/RRR3-10/2	1260.045	1260.378	-264.746	0.561	1961.749	0.572	18	0.308	K.HGEIDYEAVVK.L
R3/RRR3-10/2	1260.057	1260.378	-254.929	0.585	1847.697	0.592	18	0.295	K.HGEIDYEAVVK.L
R3/RRR3-10/2	1953.824	1953.203	-194.754	0.475	1957.799	0.523	22	0.289	R.TLM*ELLNQLDGFDELGK.V
R3/RRR3-10/2	1162.881	1163.265	-331.087	0.481	2156.205	0.376	19	0.284	K.LAEGFNGADLR.N
R3/RRR3-10/2	1259.956	1260.378	-335.508	0.575	1600.277	0.601	17	0.260	K.HGEIDYEAVVK.L
R3/RRR3-10/2	1163.129	1163.265	-117.119	0.508	2034.660	0.352	19	0.257	K.LAEGFNGADLR.N
R3/RRR3-10/2	1722.342	1722.964	-944.651	0.529	1459.440	0.587	21	0.234	K.IVSSAIIDKYIGESAR.L
R3/RRR3-10/2	1722.452	1722.964	-880.260	0.533	1400.309	0.575	20	0.223	K.IVSSAIIDKYIGESAR.L
R3/RRR3-10/2	1158.708	1159.360	-1429.731	0.462	1178.817	0.468	18	0.183	K.GVLLYGPPGTGK.T
R3/RRR3-10/2	1158.484	1159.360	-1623.837	0.374	1054.174	0.492	17	0.175	K.GVLLYGPPGTGK.T
R3/RRR3-9/2	1159.190	1159.360	-146.668	0.469	895.285	0.530	16	0.172	K.GVLLYGPPGTGK.T
R3/RRR3-10/2	1308.899	1309.469	-1202.846	0.435	1351.398	0.330	17	0.172	R.NVCTEAGM*AAIR.A
R3/RRR3-10/2	1158.503	1159.360	-1607.747	0.367	879.523	0.522	16	0.167	K.GVLLYGPPGTGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1159.148	1159.360	-182.798	0.421	911.114	0.446	16	0.161	K.GVLLYGPPGTGK.T
R3/RRR3-9/2	1158.955	1159.360	-349.957	0.463	721.600	0.491	14	0.156	K.GVLLYGPPGTGK.T
R3/RRR3-10/3	1722.617	1722.964	-201.836	0.397	1263.647	0.498	32	0.148	K.IVSSAIIDKYIGESAR.L
R3/RRR3-10/2	1817.583	1818.127	-851.844	0.447	629.326	0.461	19	0.147	R.ESIELPLM*NPELFLR.V
R3/RRR3-10/2	1164.149	1163.265	-99.978	0.474	1038.017	0.280	16	0.145	K.LAEGFNGADLR.N
R3/RRR3-10/3	1652.991	1652.751	145.568	0.476	1271.396	0.440	25	0.139	R.RFSEGTSADREIQR.T
R3/RRR3-10/3	1652.507	1652.751	-147.792	0.471	1266.109	0.438	26	0.137	R.RFSEGTSADREIQR.T
R3/RRR3-8/2	1159.180	1159.360	-155.120	0.260	497.594	0.330	14	0.136	K.GVLLYGPPGTGK.T
R3/RRR3-10/3	1723.710	1722.964	-147.831	0.443	1009.989	0.505	29	0.131	K.IVSSAIIDKYIGESAR.L
R3/RRR3-10/3	1722.697	1722.964	-155.238	0.372	987.807	0.446	29	0.117	K.IVSSAIIDKYIGESAR.L
R3/RRR3-10/3	1652.362	1652.751	-236.055	0.437	916.703	0.408	22	0.109	R.RFSEGTSADREIQR.T
R3/RRR3-10/3	1408.744	1408.628	82.504	0.435	1312.677	0.256	28	0.101	R.KIEIPLPNEQAR.M
R3/RRR3-10/3	1408.747	1408.628	84.850	0.407	1134.836	0.265	25	0.096	R.KIEIPLPNEQAR.M
R3/RRR3-10/2	1826.366	1827.024	-910.824	0.502	2066.797	0.483	22	0.297	K.LAYVALDYEQELEAAK.S
R3/RRR3-10/2	1430.007	1430.504	-349.123	0.449	2007.999	0.469	20	0.286	K.GEYDESGPAIVHR.K
R3/RRR3-10/2	1827.346	1827.024	176.443	0.584	1918.905	0.516	21	0.279	K.LAYVALDYEQELEAAK.S
R3/RRR3-10/3	1934.754	1934.118	-188.786	0.545	2161.209	0.455	32	0.265	K.YPIEHGIVSNWDDMEK.I
R3/RRR3-10/2	1826.479	1827.024	-848.560	0.550	1846.723	0.494	21	0.263	K.LAYVALDYEQELEAAK.S
R3/RRR3-10/3	1934.235	1934.118	60.437	0.598	2009.428	0.509	33	0.255	K.YPIEHGIVSNWDDMEK.I
R3/RRR3-10/2	1429.651	1430.504	-1300.080	0.448	1595.244	0.505	18	0.233	K.GEYDESGPAIVHR.K
R3/RRR3-10/3	1933.192	1934.118	-999.296	0.460	1427.068	0.419	29	0.148	K.YPIEHGIVSNWDDMEK.I
R3/RRR3-10/3	1430.165	1430.504	-238.015	0.279	711.314	0.507	27	0.107	K.GEYDESGPAIVHR.K
R3/RRR3-10/3	1430.412	1430.504	-64.643	0.274	785.590	0.466	28	0.104	K.GEYDESGPAIVHR.K
R3/RRR3-10/3	1430.822	1430.504	222.893	0.208	740.142	0.477	28	0.099	K.GEYDESGPAIVHR.K
R3/RRR3-10/2	1439.290	1438.656	-254.658	0.601	2888.896	0.627	25	0.535	K.YVILGGGVAAGYAAR.E
R3/RRR3-10/2	1439.420	1438.656	-164.047	0.596	2831.764	0.624	25	0.518	K.YVILGGGVAAGYAAR.E
R3/RRR3-10/2	1731.848	1732.057	-121.359	0.490	2962.950	0.492	27	0.501	K.AVIVGGGYIGLELSAALK.I
R3/RRR3-10/2	1533.038	1533.665	-1063.934	0.511	2729.322	0.327	24	0.376	K.VLGAFLEGGSPDENK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1533.235	1533.665	-280.899	0.532	2617.937	0.360	24	0.363	K.VLGAFLEGGSPDENK.A
R3/RRR3-10/2	1533.342	1533.665	-211.091	0.510	2333.962	0.297	23	0.288	K.VLGAFLEGGSPDENK.A
R3/RRR3-10/2	1316.271	1315.581	-236.415	0.490	1653.237	0.489	18	0.238	K.GIELILSTEIVK.A
R3/RRR3-10/2	1985.449	1985.143	154.561	0.576	1547.884	0.513	23	0.226	K.LSDFGTQGADSNNILYLR.E
R3/RRR3-10/2	1587.308	1586.769	-291.539	0.525	1590.176	0.439	23	0.218	R.EVDDADKLVAAIQAK.K
R3/RRR3-10/2	1984.668	1985.143	-240.448	0.573	1307.007	0.521	21	0.199	K.LSDFGTQGADSNNILYLR.E
R3/RRR3-10/2	1984.535	1985.143	-813.120	0.553	1282.296	0.512	21	0.195	K.LSDFGTQGADSNNILYLR.E
R3/RRR3-10/2	1587.369	1586.769	-252.499	0.544	1376.312	0.435	22	0.193	R.EVDDADKLVAAIQAK.K
R3/RRR3-10/2	1917.487	1917.152	175.173	0.522	1090.617	0.540	21	0.182	K.VLGAFLEGGSPDENKAIAK.V
R3/RRR3-10/2	1315.307	1315.581	-208.942	0.446	1280.936	0.414	18	0.182	K.GIELILSTEIVK.A
R3/RRR3-10/2	1315.413	1315.581	-127.760	0.471	1163.858	0.413	17	0.172	K.GIELILSTEIVK.A
R3/RRR3-9/2	1137.014	1137.273	-227.706	0.376	714.467	0.459	16	0.155	K.GYLFPQNAAR.L
R3/RRR3-10/2	1585.696	1586.769	-1311.203	0.473	924.024	0.400	21	0.155	R.EVDDADKLVAAIQAK.K
R3/RRR3-10/2	1137.019	1137.273	-223.506	0.430	727.760	0.424	16	0.154	K.GYLFPQNAAR.L
R3/RRR3-10/2	1916.679	1917.152	-247.700	0.491	734.301	0.519	18	0.153	K.VLGAFLEGGSPDENKAIAK.V
R3/RRR3-9/2	1137.109	1137.273	-144.241	0.367	725.560	0.418	16	0.152	K.GYLFPQNAAR.L
R3/RRR3-9/2	1136.985	1137.273	-253.664	0.420	619.664	0.412	15	0.149	K.GYLFPQNAAR.L
R3/RRR3-10/2	1136.274	1137.273	-1764.408	0.345	806.997	0.371	16	0.149	K.GYLFPQNAAR.L
R3/RRR3-10/2	1430.768	1431.619	-1297.440	0.395	551.434	0.455	17	0.147	K.EAVAPYERPALSK.G
R3/RRR3-10/2	1431.229	1431.619	-273.116	0.418	661.294	0.386	19	0.145	K.EAVAPYERPALSK.G
R3/RRR3-10/2	1432.139	1431.619	-335.523	0.474	452.951	0.409	16	0.142	K.EAVAPYERPALSK.G
R3/RRR3-10/2	1136.420	1137.273	-1634.786	0.294	746.061	0.300	16	0.140	K.GYLFPQNAAR.L
R3/RRR3-5/2	1996.702	1997.232	-768.676	0.641	2518.050	0.607	24	0.425	K.KISEEEYISAIKEEISK.V
R3/RRR3-6/2	1996.726	1997.232	-756.894	0.630	2335.962	0.620	24	0.390	K.KISEEEYISAIKEEISK.V
R3/RRR3-5/2	1996.696	1997.232	-771.805	0.627	2288.748	0.597	24	0.372	K.KISEEEYISAIKEEISK.V
R3/RRR3-6/2	1996.605	1997.232	-817.526	0.630	1998.201	0.607	24	0.320	K.KISEEEYISAIKEEISK.V
R3/RRR3-6/2	1997.503	1997.232	135.976	0.624	1952.793	0.579	23	0.302	K.KISEEEYISAIKEEISK.V
R3/RRR3-5/3	1997.438	1997.232	103.118	0.585	1961.793	0.583	36	0.272	K.KISEEEYISAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1868.271	1869.059	-960.320	0.554	1907.749	0.489	23	0.271	K.ISEEEYISAIKEEISK.V
R3/RRR3-6/2	1868.549	1869.059	-811.042	0.576	1815.698	0.540	23	0.271	K.ISEEEYISAIKEEISK.V
R3/RRR3-5/2	1868.340	1869.059	-923.193	0.601	1641.940	0.517	22	0.239	K.ISEEEYISAIKEEISK.V
R3/RRR3-5/2	1868.717	1869.059	-183.624	0.580	1623.880	0.507	22	0.234	K.ISEEEYISAIKEEISK.V
R3/RRR3-6/2	1868.368	1869.059	-907.976	0.551	1594.373	0.514	22	0.233	K.ISEEEYISAIKEEISK.V
R3/RRR3-6/2	1868.519	1869.059	-826.781	0.584	1567.891	0.510	22	0.228	K.ISEEEYISAIKEEISK.V
R3/RRR3-6/3	1997.262	1997.232	15.036	0.591	1731.405	0.526	35	0.213	K.KISEEEYISAIKEEISK.V
R3/RRR3-1/3	1998.946	1997.232	-143.615	0.564	1606.643	0.569	33	0.212	K.KISEEEYISAIKEEISK.V
R3/RRR3-2/3	1997.114	1997.232	-59.450	0.544	1606.705	0.550	34	0.205	K.KISEEEYISAIKEEISK.V
R3/RRR3-4/3	1997.138	1997.232	-47.587	0.558	1739.511	0.491	35	0.203	K.KISEEEYISAIKEEISK.V
R3/RRR3-4/3	1997.015	1997.232	-109.114	0.590	1654.126	0.523	34	0.202	K.KISEEEYISAIKEEISK.V
R3/RRR3-1/3	1997.071	1997.232	-80.787	0.480	1474.693	0.514	32	0.180	K.KISEEEYISAIKEEISK.V
R3/RRR3-2/3	1996.861	1997.232	-186.563	0.584	1381.148	0.548	32	0.176	K.KISEEEYISAIKEEISK.V
R3/RRR3-5/3	1996.613	1997.232	-813.482	0.606	1517.059	0.492	34	0.174	K.KISEEEYISAIKEEISK.V
R3/RRR3-5/3	1997.390	1997.232	79.123	0.601	1367.351	0.538	32	0.172	K.KISEEEYISAIKEEISK.V
R3/RRR3-10/3	1997.413	1997.232	90.983	0.510	1408.606	0.411	31	0.145	K.KISEEEYISAIKEEISK.V
R3/RRR3-3/3	1997.188	1997.232	-22.298	0.414	1187.212	0.456	30	0.138	K.KISEEEYISAIKEEISK.V
R3/RRR3-6/3	1997.013	1997.232	-110.034	0.507	1175.977	0.467	31	0.138	K.KISEEEYISAIKEEISK.V
R3/RRR3-4/3	1996.608	1997.232	-815.876	0.503	1329.956	0.406	33	0.136	K.KISEEEYISAIKEEISK.V
R3/RRR3-5/2	1282.840	1282.422	327.116	0.249	925.147	0.209	15	0.131	K.ISEEEYISAIK.E
R3/RRR3-3/3	1996.518	1997.232	-861.354	0.441	1356.716	0.303	31	0.118	K.KISEEEYISAIKEEISK.V
R3/RRR3-5/3	1869.384	1869.059	174.008	0.430	571.854	0.515	27	0.115	K.ISEEEYISAIKEEISK.V
R3/RRR3-6/3	1869.270	1869.059	113.202	0.427	546.750	0.491	27	0.112	K.ISEEEYISAIKEEISK.V
R3/RRR3-6/3	1869.403	1869.059	184.223	0.399	458.375	0.464	25	0.107	K.ISEEEYISAIKEEISK.V
R3/RRR3-5/3	1869.489	1869.059	230.681	0.384	560.954	0.452	27	0.107	K.ISEEEYISAIKEEISK.V
R3/RRR3-5/3	1868.776	1869.059	-152.309	0.409	520.172	0.447	26	0.106	K.ISEEEYISAIKEEISK.V
R3/RRR3-6/3	1869.883	1869.059	-94.794	0.387	527.528	0.423	26	0.104	K.ISEEEYISAIKEEISK.V
R3/RRR3-1/3	1996.068	1997.232	-1087.429	0.408	545.735	0.376	22	0.101	K.KISEEEYISAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1996.199	1997.232	-1021.852	0.355	711.616	0.326	25	0.098	K.KISEEEYISAIKEEISK.V
R3/RRR3-2/3	1868.806	1869.059	-136.091	0.365	495.560	0.357	23	0.098	K.ISEEEYISAIKEEISK.V
R3/RRR3-9/2	1870.007	1870.114	-57.526	0.596	2746.414	0.629	25	0.491	R.AVCMISNNTAVAEVFSR.I
R3/RRR3-9/2	1885.261	1886.113	-985.547	0.540	2768.703	0.588	24	0.480	R.AVCM*ISNNTAVAEVFSR.I
R3/RRR3-9/2	1886.699	1886.113	-220.403	0.642	2721.463	0.591	24	0.466	R.AVCM*ISNNTAVAEVFSR.I
R3/RRR3-9/2	1794.679	1794.107	-239.569	0.599	2583.221	0.662	24	0.463	R.IHFMLSSYAPVISAEK.A
R3/RRR3-9/2	1793.546	1794.107	-873.220	0.546	2591.106	0.600	23	0.441	R.IHFMLSSYAPVISAEK.A
R3/RRR3-9/2	1869.542	1870.114	-843.291	0.588	2563.340	0.598	25	0.434	R.AVCMISNNTAVAEVFSR.I
R3/RRR3-9/2	1885.148	1886.113	-1045.943	0.560	2312.506	0.569	24	0.368	R.AVCM*ISNNTAVAEVFSR.I
R3/RRR3-9/2	1869.561	1870.114	-833.197	0.557	2281.648	0.577	24	0.365	R.AVCMISNNTAVAEVFSR.I
R3/RRR3-9/2	1811.489	1810.107	211.940	0.584	1844.786	0.627	22	0.299	R.IHFM*LSSYAPVISAEK.A
R3/RRR3-9/2	1533.279	1532.807	308.183	0.539	1879.573	0.549	20	0.285	R.LISQIISSLTTSLR.F
R3/RRR3-9/2	1533.251	1532.807	290.381	0.492	1895.672	0.514	20	0.279	R.LISQIISSLTTSLR.F
R3/RRR3-9/2	1810.463	1810.107	197.385	0.539	1739.894	0.605	23	0.278	R.IHFM*LSSYAPVISAEK.A
R3/RRR3-9/2	1809.161	1810.107	-1078.908	0.521	1678.070	0.608	23	0.269	R.IHFM*LSSYAPVISAEK.A
R3/RRR3-9/2	1793.299	1794.107	-1011.118	0.513	1761.989	0.567	20	0.269	R.IHFMLSSYAPVISAEK.A
R3/RRR3-2/2	1717.310	1716.956	206.856	0.529	1874.312	0.419	23	0.248	R.AIFVDLEPTVIDEVR.T
R3/RRR3-9/2	1532.453	1532.807	-231.906	0.419	1536.386	0.475	19	0.218	R.LISQIISSLTTSLR.F
R3/RRR3-9/2	1717.396	1716.956	256.964	0.548	1446.712	0.470	24	0.209	R.AIFVDLEPTVIDEVR.T
R3/RRR3-9/2	1001.526	1002.147	-1623.187	0.436	1201.256	0.577	16	0.205	K.DVNAAVATIK.T
R3/RRR3-8/2	1002.064	1002.147	-83.160	0.388	1430.504	0.440	16	0.201	K.DVNAAVATIK.T
R3/RRR3-9/2	1872.450	1873.093	-879.775	0.465	1138.286	0.555	26	0.194	K.CGINYQPPSVVPGGDLAK.V
R3/RRR3-9/2	1001.925	1002.147	-221.992	0.477	1030.136	0.564	15	0.189	K.DVNAAVATIK.T
R3/RRR3-9/2	1872.281	1873.093	-970.426	0.474	1065.633	0.553	25	0.187	K.CGINYQPPSVVPGGDLAK.V
R3/RRR3-9/2	1001.916	1002.147	-230.793	0.421	1086.053	0.526	16	0.186	K.DVNAAVATIK.T
R3/RRR3-9/2	1716.472	1716.956	-282.726	0.516	1234.603	0.426	23	0.180	R.AIFVDLEPTVIDEVR.T
R3/RRR3-7/2	1002.971	1002.147	-175.739	0.392	1137.577	0.400	15	0.169	K.DVNAAVATIK.T
R3/RRR3-9/2	1715.467	1716.956	-1455.393	0.397	1065.350	0.412	22	0.165	R.AIFVDLEPTVIDEVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1002.086	1002.147	-60.554	0.370	1081.059	0.384	15	0.163	K.DVNAAVATIK.T
R3/RRR3-9/2	1872.363	1873.093	-926.637	0.443	762.156	0.527	22	0.161	K.CGINYQPPSVVPGGDLAK.V
R3/RRR3-9/3	1716.899	1716.956	-33.283	0.529	1518.646	0.410	28	0.155	R.AIFVDLEPTVIDEVR.T
R3/RRR3-4/2	1716.479	1716.956	-278.873	0.430	842.969	0.382	19	0.148	R.AIFVDLEPTVIDEVR.T
R3/RRR3-1/2	1001.417	1002.147	-1733.035	0.326	664.384	0.366	15	0.144	K.DVNAAVATIK.T
R3/RRR3-9/3	1717.011	1716.956	31.966	0.474	1417.774	0.400	30	0.141	R.AIFVDLEPTVIDEVR.T
R3/RRR3-9/2	1267.518	1268.518	-1582.873	0.277	724.230	0.412	12	0.141	K.YMACCLMYR.G
R3/RRR3-1/2	1001.524	1002.147	-1624.902	0.269	640.322	0.365	14	0.141	K.DVNAAVATIK.T
R3/RRR3-9/2	1718.010	1716.956	31.243	0.391	723.686	0.363	16	0.140	R.AIFVDLEPTVIDEVR.T
R3/RRR3-9/2	1133.632	1133.271	319.625	0.306	908.214	0.223	13	0.136	K.EIVDLCLDR.V
R3/RRR3-9/2	1132.954	1133.271	-280.395	0.319	758.132	0.237	13	0.134	-.EIVDLCLDR.-
R3/RRR3-14/2	1810.732	1810.107	-207.604	0.288	588.396	0.284	17	0.133	R.IHFM*LSSYAPVISAEK.A
R3/RRR3-9/2	1132.198	1133.271	-1835.859	0.211	494.387	0.248	11	0.130	K.EIVDLCLDR.V
R3/RRR3-9/3	1382.747	1381.625	89.102	0.572	905.189	0.389	22	0.108	R.IDHKFDLMYAK.R
R3/RRR3-9/3	1382.695	1381.625	51.383	0.521	765.650	0.386	21	0.104	R.IDHKFDLMYAK.R
R3/RRR3-9/3	1794.880	1794.107	-127.030	0.406	943.008	0.352	28	0.102	R.IHFMLSSYAPVISAEK.A
R3/RRR3-9/3	1381.680	1381.625	40.300	0.420	669.090	0.299	20	0.093	R.IDHKFDLMYAK.R
R3/RRR3-9/3	1795.355	1794.107	138.355	0.391	737.636	0.303	26	0.092	R.IHFMLSSYAPVISAEK.A
R3/RRR3-9/3	1794.856	1794.107	-140.641	0.379	864.796	0.223	28	0.086	R.IHFMLSSYAPVISAEK.A
R3/RRR3-9/3	1794.653	1794.107	-254.043	0.373	781.479	0.186	26	0.083	R.IHFMLSSYAPVISAEK.A
R3/RRR3-20/2	1576.580	1576.776	-124.613	0.572	1886.520	0.501	22	0.273	K.SNGQILAINEIFEK.N
R3/RRR3-20/3	1274.002	1274.574	-1236.974	0.540	2606.632	0.198	25	0.236	R.VRFPCIQIIK.T
R3/RRR3-20/2	1576.214	1576.776	-993.622	0.513	1476.339	0.463	20	0.209	K.SNGQILAINEIFEK.N
R3/RRR3-20/2	1577.272	1576.776	315.733	0.578	1435.445	0.458	21	0.203	K.SNGQILAINEIFEK.N
R3/RRR3-20/3	1274.892	1274.574	250.587	0.550	2558.192	0.123	25	0.198	R.VRFPCIQIIK.T
R3/RRR3-19/2	1576.868	1576.776	58.885	0.507	1167.674	0.481	18	0.182	K.SNGQILAINEIFEK.N
R3/RRR3-20/2	1134.093	1134.272	-157.903	0.417	1223.380	0.386	15	0.174	R.FHQYQVVGR.G
R3/RRR3-20/2	1133.697	1134.272	-1393.775	0.387	1119.200	0.416	15	0.171	R.FHQYQVVGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/3	1274.191	1274.574	-301.454	0.557	2191.969	0.187	25	0.164	R.VRFPCIQIIK.T
R3/RRR3-20/2	1274.281	1274.574	-230.657	0.426	1160.629	0.321	15	0.158	R.VRFPCIQIIK.T
R3/RRR3-19/2	1134.155	1134.272	-103.486	0.378	862.474	0.405	14	0.155	R.FHQYQVVGR.G
R3/RRR3-19/2	1133.715	1134.272	-1377.229	0.362	795.147	0.404	13	0.151	R.FHQYQVVGR.G
R3/RRR3-20/2	1134.223	1134.272	-43.461	0.429	789.425	0.382	14	0.151	R.FHQYQVVGR.G
R3/RRR3-20/2	1192.945	1192.303	-301.601	0.355	377.261	0.551	15	0.150	R.GLPTPTDEHPK.I
R3/RRR3-20/2	1147.277	1147.352	-66.124	0.442	632.046	0.408	12	0.149	K.SKFWYFLR.K
R3/RRR3-20/2	1274.389	1274.574	-145.035	0.426	1181.056	0.250	15	0.149	R.VRFPCIQIIK.T
R3/RRR3-20/2	1191.866	1192.303	-368.030	0.329	395.655	0.555	15	0.149	R.GLPTPTDEHPK.I
R3/RRR3-19/2	1133.919	1134.272	-311.902	0.389	989.380	0.302	14	0.149	R.FHQYQVVGR.G
R3/RRR3-20/2	1191.796	1192.303	-1268.196	0.311	363.416	0.570	15	0.148	R.GLPTPTDEHPK.I
R3/RRR3-20/2	1263.582	1264.479	-1505.948	0.420	1271.968	0.183	16	0.146	R.M*KLWATNEVR.A
R3/RRR3-20/2	1264.064	1264.479	-329.694	0.425	1217.449	0.181	16	0.142	R.M*KLWATNEVR.A
R3/RRR3-19/2	1019.067	1019.256	-185.819	0.494	863.239	0.259	14	0.141	R.FPCIQIIK.T
R3/RRR3-20/2	1147.275	1147.352	-67.192	0.406	558.856	0.298	12	0.140	K.SKFWYFLR.K
R3/RRR3-20/2	1147.362	1147.352	8.579	0.411	434.459	0.329	10	0.139	K.SKFWYFLR.K
R3/RRR3-20/2	1018.531	1019.256	-1698.144	0.496	807.763	0.249	14	0.139	R.FPCIQIIK.T
R3/RRR3-20/2	1134.469	1134.272	174.124	0.265	915.159	0.236	14	0.138	R.FHQYQVVGR.G
R3/RRR3-20/2	1275.476	1274.574	-77.045	0.493	852.986	0.295	13	0.138	-.VRFPCIQIIK.-
R3/RRR3-20/2	1264.196	1264.479	-224.578	0.414	890.520	0.243	15	0.138	R.M*KLWATNEVR.A
R3/RRR3-20/2	1146.945	1147.352	-355.756	0.366	354.737	0.301	9	0.137	K.SKFWYFLR.K
R3/RRR3-20/2	1018.582	1019.256	-1647.815	0.451	789.854	0.210	14	0.136	R.FPCIQIIK.T
R3/RRR3-20/2	1019.043	1019.256	-209.733	0.463	795.167	0.191	14	0.134	R.FPCIQIIK.T
R3/RRR3-19/2	1018.507	1019.256	-1721.505	0.450	634.336	0.214	13	0.129	-.FPCIQIIK.-
R3/RRR3-20/3	1238.527	1238.460	54.596	0.440	750.216	0.536	19	0.121	K.SDIKFPLVYR.K
R3/RRR3-20/3	1238.621	1238.460	130.805	0.484	738.691	0.442	19	0.110	K.SDIKFPLVYR.K
R3/RRR3-20/3	1238.480	1238.460	16.043	0.405	734.374	0.309	19	0.094	K.SDIKFPLVYR.K
R3/RRR3-4/2	1343.229	1343.599	-276.607	0.390	1904.143	0.337	17	0.236	R.IIWSNLLQSLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1352.098	1352.561	-343.523	0.428	1451.968	0.434	19	0.201	K.YVVTLSSGGSILR.A
R3/RRR3-4/2	1697.724	1697.998	-161.444	0.466	1093.573	0.522	20	0.182	K.QLLIGTIGDQVLALDK.R
R3/RRR3-4/2	1280.549	1281.397	-1447.632	0.334	1203.604	0.440	17	0.178	K.FTSDVTNEVIR.E
R3/RRR3-4/2	1280.549	1281.397	-1447.154	0.404	953.842	0.460	16	0.165	K.FTSDVTNEVIR.E
R3/RRR3-4/2	1344.290	1343.599	-230.394	0.464	1218.259	0.310	16	0.159	R.IIWSNLLQSLR.S
R3/RRR3-4/2	1865.028	1863.193	-88.797	0.411	1176.742	0.364	18	0.159	K.GTLMLASADELAAIQAMR.L
R3/RRR3-4/2	1077.069	1077.259	-176.153	0.430	1117.072	0.302	14	0.154	K.LNLYQLNAK.T
R3/RRR3-4/2	1280.588	1281.397	-1416.514	0.329	789.666	0.452	15	0.152	K.FTSDVTNEVIR.E
R3/RRR3-4/2	1697.585	1697.998	-243.823	0.388	677.387	0.497	17	0.149	-.QLLIGTIGDQVLALDK.-
R3/RRR3-4/2	1077.108	1077.259	-139.999	0.367	966.477	0.300	14	0.146	K.LNLYQLNAK.T
R3/RRR3-1/2	1553.823	1553.785	24.300	0.379	766.327	0.404	18	0.144	K.VHISDLVQGLSGTVK.L
R3/RRR3-4/2	1580.152	1579.735	264.483	0.373	715.338	0.395	16	0.142	K.ELWSIVFPSDTER.I
R3/RRR3-4/2	1863.838	1863.193	-190.805	0.337	884.963	0.257	16	0.132	-.GTLMLASADELAAIQAMR.-
R3/RRR3-4/2	1351.958	1352.561	-1189.683	0.323	546.028	0.315	13	0.131	K.YVVTLSSGGSILR.A
R3/RRR3-4/2	1495.223	1495.772	-1039.468	0.289	950.476	0.064	15	0.120	R.VM*HENPSILIIGR.S
R3/RRR3-4/3	1410.031	1410.644	-1147.207	0.453	772.557	0.423	21	0.103	-.SSKPLLHVLSSNK.-
R3/RRR3-4/3	1409.385	1410.644	-1607.852	0.452	817.676	0.395	22	0.102	-.SSKPLLHVLSSNK.-
R3/RRR3-9/3	1638.631	1638.812	-110.937	0.531	1698.519	0.478	31	0.195	R.FRGEDKPPAHLGASR.D
R3/RRR3-9/3	1638.553	1638.812	-158.689	0.567	1473.403	0.556	31	0.189	R.FRGEDKPPAHLGASR.D
R3/RRR3-9/3	1638.539	1638.812	-166.873	0.511	1322.932	0.498	29	0.157	R.FRGEDKPPAHLGASR.D
R3/RRR3-9/2	1638.498	1638.812	-192.238	0.386	515.035	0.439	18	0.140	R.FRGEDKPPAHLGASR.D
R3/RRR3-23/1	1549.872	1548.681	123.474	0.468	995.221	0.550	18	0.999	R.AWSAADAVASWVGEK.K
R3/RRR3-24/1	1549.769	1548.681	57.277	0.468	793.765	0.591	17	0.996	R.AWSAADAVASWVGEK.K
R3/RRR3-23/1	1549.910	1548.681	148.196	0.427	514.548	0.611	16	0.986	R.AWSAADAVASWVGEK.K
R3/RRR3-24/1	1549.928	1548.681	160.123	0.419	736.791	0.572	16	0.983	R.AWSAADAVASWVGEK.K
R3/RRR3-23/1	1549.819	1548.681	89.192	0.435	580.367	0.523	15	0.966	R.AWSAADAVASWVGEK.K
R3/RRR3-23/1	1548.789	1548.681	69.962	0.403	531.338	0.530	15	0.964	R.AWSAADAVASWVGEK.K
R3/RRR3-24/1	1548.910	1548.681	148.213	0.378	431.654	0.519	15	0.958	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/1	1547.716	1548.681	-1273.637	0.225	198.329	0.465	13	0.945	R.AWSAADAVASWVGEK.K
R3/RRR3-20/2	1548.366	1548.681	-204.061	0.510	2595.919	0.530	24	0.409	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1549.170	1548.681	316.561	0.520	2481.913	0.574	23	0.399	R.AWSAADAVASWVGEK.K
R3/RRR3-15/2	1548.373	1548.681	-199.157	0.448	2600.351	0.496	24	0.398	R.AWSAADAVASWVGEK.K
R3/RRR3-22/2	1548.216	1548.681	-301.510	0.453	2259.773	0.547	23	0.345	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1548.200	1548.681	-311.399	0.524	2252.699	0.548	23	0.343	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1548.251	1548.681	-278.649	0.503	2211.207	0.544	24	0.335	R.AWSAADAVASWVGEK.K
R3/RRR3-18/2	1549.295	1548.681	-249.932	0.556	2180.286	0.564	23	0.334	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1548.262	1548.681	-271.293	0.477	2121.042	0.582	23	0.330	R.AWSAADAVASWVGEK.K
R3/RRR3-18/2	1548.185	1548.681	-321.445	0.439	2287.847	0.476	23	0.328	R.AWSAADAVASWVGEK.K
R3/RRR3-25/2	1548.031	1548.681	-1069.211	0.368	2339.178	0.434	23	0.325	R.AWSAADAVASWVGEK.K
R3/RRR3-9/2	1549.351	1548.681	-213.414	0.522	2179.930	0.518	23	0.320	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1548.138	1548.681	-999.699	0.455	2059.759	0.577	23	0.317	R.AWSAADAVASWVGEK.K
R3/RRR3-22/2	1549.192	1548.681	-316.494	0.528	2057.725	0.574	23	0.316	R.AWSAADAVASWVGEK.K
R3/RRR3-24/3	1384.748	1384.522	163.907	0.608	2156.137	0.586	28	0.308	R.RADGVGPVSWDPK.V
R3/RRR3-21/2	1548.336	1548.681	-223.518	0.503	2104.327	0.519	23	0.308	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1549.857	1548.681	113.789	0.550	2009.070	0.576	22	0.307	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1548.257	1548.681	-274.298	0.455	2126.852	0.499	23	0.306	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1548.152	1548.681	-990.595	0.433	2101.843	0.508	22	0.304	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1548.320	1548.681	-233.800	0.445	2093.039	0.511	23	0.304	R.AWSAADAVASWVGEK.K
R3/RRR3-16/2	1548.845	1548.681	106.195	0.474	2104.903	0.504	22	0.303	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1548.329	1548.681	-228.263	0.507	2029.922	0.544	23	0.302	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1549.166	1548.681	314.032	0.569	2056.936	0.532	23	0.302	R.AWSAADAVASWVGEK.K
R3/RRR3-15/2	1547.958	1548.681	-1116.086	0.343	2281.728	0.378	23	0.298	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1549.171	1548.681	317.509	0.538	2020.074	0.536	22	0.297	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1549.107	1548.681	275.632	0.534	2012.007	0.531	23	0.295	R.AWSAADAVASWVGEK.K
R3/RRR3-21/2	1548.128	1548.681	-1005.874	0.440	2079.063	0.487	23	0.294	R.AWSAADAVASWVGEK.K
R3/RRR3-1/2	1548.342	1548.681	-219.326	0.475	2061.528	0.498	23	0.294	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1549.274	1548.681	-263.529	0.576	1988.652	0.544	22	0.294	R.AWSAADAVASWVGEK.K
R3/RRR3-24/3	1384.342	1384.522	-130.695	0.537	2064.691	0.585	28	0.292	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1547.880	1548.681	-1167.082	0.347	2222.115	0.391	23	0.291	R.AWSAADAVASWVGEK.K
R3/RRR3-16/2	1548.058	1548.681	-1051.555	0.398	2097.837	0.464	23	0.291	R.AWSAADAVASWVGEK.K
R3/RRR3-15/2	1548.604	1548.681	-49.541	0.466	2076.742	0.468	23	0.288	R.AWSAADAVASWVGEK.K
R3/RRR3-23/3	1384.711	1384.522	136.988	0.479	2075.967	0.561	29	0.284	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1548.245	1548.681	-282.288	0.460	1999.055	0.489	22	0.281	R.AWSAADAVASWVGEK.K
R3/RRR3-17/2	1549.662	1548.681	-12.532	0.564	1869.706	0.560	22	0.280	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1549.155	1548.681	307.079	0.528	1882.147	0.548	22	0.279	R.AWSAADAVASWVGEK.K
R3/RRR3-20/2	1548.054	1548.681	-1054.326	0.415	1879.560	0.550	22	0.279	R.AWSAADAVASWVGEK.K
R3/RRR3-14/2	1547.682	1548.681	-1295.627	0.338	2082.363	0.427	23	0.278	R.AWSAADAVASWVGEK.K
R3/RRR3-2/2	1548.280	1548.681	-259.586	0.477	1912.698	0.516	22	0.275	R.AWSAADAVASWVGEK.K
R3/RRR3-19/2	1548.569	1548.681	-72.629	0.526	1847.064	0.549	22	0.274	R.AWSAADAVASWVGEK.K
R3/RRR3-22/2	1549.046	1548.681	236.597	0.538	1838.085	0.553	22	0.274	R.AWSAADAVASWVGEK.K
R3/RRR3-12/2	1548.227	1548.681	-294.232	0.399	1998.434	0.453	23	0.272	R.AWSAADAVASWVGEK.K
R3/RRR3-18/2	1548.390	1548.681	-188.559	0.479	1922.292	0.496	22	0.271	R.AWSAADAVASWVGEK.K
R3/RRR3-20/2	1548.234	1548.681	-289.328	0.466	1830.309	0.523	22	0.265	R.AWSAADAVASWVGEK.K
R3/RRR3-2/2	1549.338	1548.681	-221.951	0.557	1800.449	0.530	22	0.261	R.AWSAADAVASWVGEK.K
R3/RRR3-2/2	1548.282	1548.681	-258.162	0.459	1836.213	0.505	21	0.260	R.AWSAADAVASWVGEK.K
R3/RRR3-1/2	1548.403	1548.681	-180.097	0.462	1869.613	0.480	22	0.259	R.AWSAADAVASWVGEK.K
R3/RRR3-16/2	1548.355	1548.681	-211.100	0.462	1873.833	0.477	21	0.258	R.AWSAADAVASWVGEK.K
R3/RRR3-5/2	1549.858	1548.681	114.816	0.576	1755.068	0.543	21	0.257	R.AWSAADAVASWVGEK.K
R3/RRR3-23/3	1383.802	1384.522	-1246.547	0.512	1860.607	0.584	27	0.256	R.RADGVGPVSWDPK.V
R3/RRR3-21/2	1548.220	1548.681	-298.821	0.435	1808.205	0.498	22	0.255	R.AWSAADAVASWVGEK.K
R3/RRR3-25/2	1548.104	1548.681	-1021.866	0.411	1911.759	0.430	23	0.253	R.AWSAADAVASWVGEK.K
R3/RRR3-17/2	1548.059	1548.681	-1050.526	0.422	1835.728	0.472	22	0.253	R.AWSAADAVASWVGEK.K
R3/RRR3-2/2	1549.240	1548.681	-285.663	0.526	1742.763	0.497	22	0.245	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1548.014	1548.681	-1079.821	0.378	1857.727	0.430	22	0.245	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1547.706	1548.681	-1279.705	0.384	1769.384	0.471	22	0.243	R.AWSAADAVASWVGEK.K
R3/RRR3-24/3	1384.232	1384.522	-210.444	0.525	1763.601	0.581	27	0.238	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1384.891	1384.522	267.594	0.549	1790.801	0.571	27	0.238	R.RADGVGPVSWDPK.V
R3/RRR3-19/2	1548.052	1548.681	-1055.514	0.415	1830.190	0.410	21	0.236	R.AWSAADAVASWVGEK.K
R3/RRR3-6/2	1549.502	1548.681	-115.729	0.474	1616.531	0.521	22	0.236	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1547.927	1548.681	-1136.199	0.291	1931.085	0.322	22	0.230	R.AWSAADAVASWVGEK.K
R3/RRR3-24/3	1384.760	1384.522	172.527	0.559	1685.950	0.590	26	0.229	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1384.629	1384.522	77.441	0.529	1655.532	0.598	26	0.228	R.RADGVGPVSWDPK.V
R3/RRR3-13/2	1548.480	1548.681	-130.037	0.483	1657.532	0.469	21	0.227	R.AWSAADAVASWVGEK.K
R3/RRR3-6/2	1548.351	1548.681	-213.394	0.401	1787.568	0.392	21	0.226	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1677.446	1676.854	-243.685	0.556	1472.821	0.552	22	0.224	R.AWSAADAVASWVGEKK.N
R3/RRR3-19/2	1547.638	1548.681	-1323.906	0.342	1691.354	0.430	22	0.223	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1676.362	1676.854	-294.165	0.549	1398.920	0.575	20	0.220	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1677.358	1676.854	-296.545	0.574	1483.305	0.530	21	0.219	R.AWSAADAVASWVGEKK.N
R3/RRR3-20/2	1676.210	1676.854	-983.358	0.488	1554.598	0.487	21	0.219	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1549.258	1548.681	-273.489	0.478	1463.014	0.527	20	0.217	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1676.686	1676.854	-100.378	0.520	1493.659	0.504	22	0.216	R.AWSAADAVASWVGEKK.N
R3/RRR3-24/2	1228.139	1228.336	-160.766	0.421	1593.533	0.419	20	0.214	R.ADGVGPVSWDPK.V
R3/RRR3-23/2	1675.610	1676.854	-1342.848	0.479	1431.232	0.519	22	0.213	R.AWSAADAVASWVGEKK.N
R3/RRR3-3/2	1548.554	1548.681	-81.881	0.446	1520.953	0.473	20	0.212	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1676.263	1676.854	-951.554	0.528	1422.837	0.519	22	0.212	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1676.061	1676.854	-1072.859	0.456	1511.172	0.462	21	0.209	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1405.312	1405.579	-190.593	0.496	1524.164	0.428	18	0.208	K.VCGHYTQVVWR.K
R3/RRR3-24/3	1384.574	1384.522	37.651	0.524	1507.533	0.595	25	0.207	R.RADGVGPVSWDPK.V
R3/RRR3-17/3	1384.589	1384.522	48.660	0.515	1588.158	0.559	26	0.205	R.RADGVGPVSWDPK.V
R3/RRR3-22/3	1384.475	1384.522	-33.846	0.536	1552.920	0.577	27	0.204	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1384.635	1384.522	81.818	0.517	1597.111	0.546	26	0.202	R.RADGVGPVSWDPK.V
R3/RRR3-26/2	1547.486	1548.681	-1422.857	0.328	1633.840	0.359	21	0.202	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1676.235	1676.854	-968.735	0.541	1284.823	0.532	22	0.201	R.AWSAADAVASWVGEKK.N
R3/RRR3-22/2	1676.501	1676.854	-211.250	0.541	1263.223	0.528	23	0.199	R.AWSAADAVASWVGEKK.N
R3/RRR3-24/2	1229.136	1228.336	-162.727	0.455	1366.810	0.461	19	0.199	R.ADGVGPVSWDPK.V
R3/RRR3-23/3	1384.727	1384.522	148.657	0.574	1498.961	0.579	26	0.198	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1675.817	1676.854	-1219.283	0.524	1278.579	0.507	21	0.195	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1228.006	1228.336	-269.061	0.419	1453.602	0.398	18	0.194	R.ADGVGPVSWDPK.V
R3/RRR3-20/3	1384.678	1384.522	112.719	0.535	1544.323	0.542	26	0.194	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1142.853	1143.274	-369.351	0.505	1020.488	0.585	18	0.193	K.VASFAQSYAAK.R
R3/RRR3-27/2	1142.941	1143.274	-291.978	0.522	1084.468	0.554	18	0.192	K.VASFAQSYAAK.R
R3/RRR3-24/2	1404.627	1405.579	-1393.934	0.463	1384.303	0.417	17	0.192	K.VCGHYTQVVWR.K
R3/RRR3-24/2	1405.028	1405.579	-1107.886	0.488	1372.048	0.419	17	0.191	K.VCGHYTQVVWR.K
R3/RRR3-23/3	1548.888	1548.681	133.890	0.506	1627.186	0.489	29	0.190	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1406.263	1405.579	-225.813	0.533	1376.503	0.417	17	0.190	K.VCGHYTQVVWR.K
R3/RRR3-23/2	1406.174	1405.579	-289.128	0.513	1318.466	0.446	16	0.190	K.VCGHYTQVVWR.K
R3/RRR3-25/2	1142.997	1143.274	-243.332	0.528	957.778	0.589	18	0.190	K.VASFAQSYAAK.R
R3/RRR3-22/2	1143.043	1143.274	-202.298	0.502	1003.326	0.572	18	0.190	K.VASFAQSYAAK.R
R3/RRR3-24/2	1405.056	1405.579	-1087.822	0.487	1374.256	0.410	17	0.189	K.VCGHYTQVVWR.K
R3/RRR3-22/2	1143.079	1143.274	-171.443	0.524	1012.072	0.564	18	0.189	K.VASFAQSYAAK.R
R3/RRR3-24/2	1142.949	1143.274	-285.442	0.483	1038.815	0.555	18	0.189	K.VASFAQSYAAK.R
R3/RRR3-22/2	1676.236	1676.854	-968.150	0.507	1258.728	0.479	22	0.189	R.AWSAADAVASWVGEKK.N
R3/RRR3-28/2	1144.072	1143.274	-177.073	0.515	900.074	0.600	18	0.188	K.VASFAQSYAAK.R
R3/RRR3-24/2	1143.020	1143.274	-222.975	0.463	990.378	0.569	18	0.187	K.VASFAQSYAAK.R
R3/RRR3-17/2	1547.427	1548.681	-1461.127	0.325	1459.319	0.380	19	0.187	R.AWSAADAVASWVGEK.K
R3/RRR3-12/2	1142.998	1143.274	-242.261	0.485	1006.268	0.554	18	0.186	K.VASFAQSYAAK.R
R3/RRR3-23/2	1405.064	1405.579	-1081.715	0.484	1386.776	0.389	17	0.186	K.VCGHYTQVVWR.K
R3/RRR3-24/2	1142.954	1143.274	-280.942	0.455	1012.832	0.553	18	0.186	K.VASFAQSYAAK.R
R3/RRR3-18/3	1384.621	1384.522	71.738	0.504	1480.838	0.536	25	0.186	R.RADGVGPVSWDPK.V
R3/RRR3-1/2	1144.045	1143.274	-200.676	0.538	895.867	0.583	18	0.185	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/2	1142.891	1143.274	-335.700	0.451	1025.326	0.544	18	0.185	K.VASFAQSYAAK.R
R3/RRR3-3/2	1143.081	1143.274	-168.979	0.490	946.732	0.568	18	0.185	K.VASFAQSYAAK.R
R3/RRR3-23/2	1548.428	1548.681	-163.647	0.420	1385.337	0.406	19	0.185	R.AWSAADAVASWVGEK.K
R3/RRR3-22/2	1228.122	1228.336	-174.127	0.373	1286.347	0.436	18	0.185	R.ADGVGPVSWDPK.V
R3/RRR3-14/2	1142.956	1143.274	-279.013	0.500	989.001	0.549	18	0.185	K.VASFAQSYAAK.R
R3/RRR3-23/2	1405.998	1405.579	298.375	0.530	1251.564	0.449	16	0.185	K.VCGHYTQVVWR.K
R3/RRR3-3/2	1548.225	1548.681	-295.656	0.393	1384.510	0.402	19	0.184	R.AWSAADAVASWVGEK.K
R3/RRR3-24/3	1384.738	1384.522	156.349	0.546	1456.445	0.544	25	0.184	R.RADGVGPVSWDPK.V
R3/RRR3-7/2	1143.075	1143.274	-174.443	0.472	963.068	0.558	18	0.184	K.VASFAQSYAAK.R
R3/RRR3-26/2	1142.992	1143.274	-247.725	0.485	950.338	0.561	18	0.184	K.VASFAQSYAAK.R
R3/RRR3-24/2	1144.143	1143.274	-114.996	0.478	1198.380	0.457	18	0.183	K.VASFAQSYAAK.R
R3/RRR3-20/2	1143.153	1143.274	-106.099	0.509	943.889	0.555	18	0.183	K.VASFAQSYAAK.R
R3/RRR3-12/2	1142.925	1143.274	-306.016	0.451	932.223	0.569	18	0.183	K.VASFAQSYAAK.R
R3/RRR3-24/2	1405.172	1405.579	-290.815	0.504	1266.679	0.432	16	0.183	K.VCGHYTQVVWR.K
R3/RRR3-28/2	1142.883	1143.274	-343.416	0.517	875.021	0.578	18	0.183	K.VASFAQSYAAK.R
R3/RRR3-26/2	1142.907	1143.274	-321.983	0.459	963.382	0.549	18	0.182	K.VASFAQSYAAK.R
R3/RRR3-26/2	1142.907	1143.274	-322.411	0.449	980.499	0.541	18	0.182	K.VASFAQSYAAK.R
R3/RRR3-23/2	1585.027	1585.607	-999.607	0.419	1180.558	0.469	18	0.182	K.NYHYDTNTCDPGK.V
R3/RRR3-22/2	1143.005	1143.274	-236.261	0.472	948.836	0.549	18	0.182	K.VASFAQSYAAK.R
R3/RRR3-3/2	1143.801	1143.274	-414.538	0.492	836.042	0.587	18	0.182	K.VASFAQSYAAK.R
R3/RRR3-14/2	1676.505	1676.854	-208.913	0.462	1129.392	0.507	19	0.181	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1143.621	1143.274	304.093	0.430	1038.351	0.513	18	0.181	K.VASFAQSYAAK.R
R3/RRR3-7/2	1548.382	1548.681	-193.858	0.350	1412.455	0.356	20	0.179	R.AWSAADAVASWVGEK.K
R3/RRR3-2/2	1675.709	1676.854	-1283.513	0.481	1160.311	0.475	20	0.179	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1405.327	1405.579	-180.050	0.531	1252.740	0.415	16	0.178	K.VCGHYTQVVWR.K
R3/RRR3-13/2	1142.961	1143.274	-274.834	0.504	926.433	0.529	18	0.178	K.VASFAQSYAAK.R
R3/RRR3-3/2	1676.859	1676.854	3.168	0.519	1217.716	0.451	20	0.178	R.AWSAADAVASWVGEKK.N
R3/RRR3-18/2	1143.097	1143.274	-154.946	0.477	907.537	0.531	18	0.177	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1142.957	1143.274	-277.941	0.467	966.923	0.508	18	0.176	K.VASFAQSYAAK.R
R3/RRR3-24/2	1143.856	1143.274	-366.779	0.429	1073.789	0.475	17	0.176	K.VASFAQSYAAK.R
R3/RRR3-4/2	1142.902	1143.274	-326.484	0.453	868.930	0.552	17	0.176	K.VASFAQSYAAK.R
R3/RRR3-24/2	1143.033	1143.274	-211.726	0.474	806.726	0.569	17	0.176	K.VASFAQSYAAK.R
R3/RRR3-16/3	1384.542	1384.522	14.704	0.468	1404.239	0.532	25	0.176	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1547.626	1548.681	-1331.907	0.344	1381.441	0.346	21	0.176	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1675.459	1676.854	-1433.365	0.423	1411.764	0.346	19	0.176	R.AWSAADAVASWVGEKK.N
R3/RRR3-16/2	1144.150	1143.274	-108.360	0.491	748.824	0.575	17	0.175	K.VASFAQSYAAK.R
R3/RRR3-23/2	1549.526	1548.681	-100.240	0.437	957.604	0.534	19	0.175	R.AWSAADAVASWVGEK.K
R3/RRR3-2/2	1142.404	1143.274	-1641.442	0.441	871.055	0.530	18	0.174	K.VASFAQSYAAK.R
R3/RRR3-2/2	1676.345	1676.854	-902.719	0.517	1105.007	0.478	19	0.174	R.AWSAADAVASWVGEKK.N
R3/RRR3-22/3	1384.072	1384.522	-326.308	0.515	1267.922	0.582	25	0.174	R.RADGVGPVSWDPK.V
R3/RRR3-20/2	1676.391	1676.854	-276.996	0.510	1126.340	0.452	21	0.173	R.AWSAADAVASWVGEKK.N
R3/RRR3-2/2	1142.478	1143.274	-1576.929	0.376	830.394	0.557	18	0.173	K.VASFAQSYAAK.R
R3/RRR3-1/2	1142.441	1143.274	-1609.345	0.379	913.960	0.518	18	0.172	K.VASFAQSYAAK.R
R3/RRR3-24/2	1229.055	1228.336	-229.382	0.395	1024.486	0.485	16	0.172	R.ADGVGPVSWDPK.V
R3/RRR3-20/2	1142.474	1143.274	-1580.578	0.366	928.045	0.516	18	0.172	K.VASFAQSYAAK.R
R3/RRR3-25/2	1143.015	1143.274	-227.261	0.440	902.863	0.500	18	0.171	K.VASFAQSYAAK.R
R3/RRR3-3/2	1142.987	1143.274	-251.797	0.452	860.797	0.511	18	0.171	K.VASFAQSYAAK.R
R3/RRR3-24/2	1142.443	1143.274	-1607.842	0.339	1005.174	0.482	18	0.171	K.VASFAQSYAAK.R
R3/RRR3-9/2	1142.933	1143.274	-299.158	0.463	790.296	0.527	17	0.169	K.VASFAQSYAAK.R
R3/RRR3-15/2	1143.157	1143.274	-102.885	0.460	788.234	0.528	17	0.169	K.VASFAQSYAAK.R
R3/RRR3-23/2	1142.504	1143.274	-1553.637	0.410	878.692	0.499	18	0.169	K.VASFAQSYAAK.R
R3/RRR3-23/2	1585.113	1585.607	-312.257	0.395	1079.712	0.428	18	0.168	K.NYHYDTNTCDPGK.V
R3/RRR3-23/2	1585.717	1585.607	69.675	0.444	1004.283	0.460	17	0.167	K.NYHYDTNTCDPGK.V
R3/RRR3-17/2	1142.555	1143.274	-1508.667	0.436	734.923	0.521	18	0.167	K.VASFAQSYAAK.R
R3/RRR3-2/3	1383.537	1384.522	-1438.731	0.423	1364.878	0.511	25	0.167	R.RADGVGPVSWDPK.V
R3/RRR3-2/2	1142.426	1143.274	-1622.763	0.391	871.941	0.486	18	0.167	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-26/3	1384.485	1384.522	-26.948	0.537	1265.205	0.565	27	0.166	R.RADGVGPVSWDPK.V
R3/RRR3-29/2	1142.401	1143.274	-1644.770	0.373	835.948	0.507	17	0.166	K.VASFAQSYAAK.R
R3/RRR3-18/2	1142.481	1143.274	-1574.352	0.397	817.240	0.506	17	0.166	K.VASFAQSYAAK.R
R3/RRR3-24/3	1548.596	1548.681	-54.887	0.535	1418.798	0.492	29	0.165	R.AWSAADAVASWVGEK.K
R3/RRR3-24/3	1548.502	1548.681	-115.970	0.525	1503.575	0.456	29	0.165	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1675.540	1676.854	-1384.775	0.419	1104.302	0.414	19	0.165	R.AWSAADAVASWVGEKK.N
R3/RRR3-22/2	1228.823	1228.336	397.990	0.313	1200.411	0.352	18	0.164	R.ADGVGPVSWDPK.V
R3/RRR3-15/2	1142.938	1143.274	-294.979	0.421	852.273	0.473	17	0.164	K.VASFAQSYAAK.R
R3/RRR3-1/2	1547.633	1548.681	-1327.075	0.314	1395.058	0.267	20	0.164	R.AWSAADAVASWVGEK.K
R3/RRR3-1/2	1678.382	1676.854	-281.847	0.522	981.471	0.464	19	0.164	R.AWSAADAVASWVGEKK.N
R3/RRR3-10/2	1142.971	1143.274	-266.262	0.402	763.238	0.503	17	0.164	K.VASFAQSYAAK.R
R3/RRR3-12/2	1142.526	1143.274	-1534.747	0.381	838.722	0.477	18	0.164	K.VASFAQSYAAK.R
R3/RRR3-9/2	1548.060	1548.681	-1050.051	0.323	1162.892	0.373	19	0.163	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	1228.078	1228.336	-210.423	0.385	1044.866	0.403	17	0.163	R.ADGVGPVSWDPK.V
R3/RRR3-19/2	1143.047	1143.274	-198.762	0.375	784.014	0.493	17	0.162	K.VASFAQSYAAK.R
R3/RRR3-4/2	1142.570	1143.274	-1496.004	0.429	624.129	0.520	16	0.161	K.VASFAQSYAAK.R
R3/RRR3-21/3	1384.270	1384.522	-182.577	0.479	1177.800	0.559	23	0.161	R.RADGVGPVSWDPK.V
R3/RRR3-25/2	1142.216	1143.274	-1807.217	0.359	719.137	0.503	17	0.160	K.VASFAQSYAAK.R
R3/RRR3-23/2	1384.239	1384.522	-205.347	0.419	727.770	0.459	22	0.159	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1228.026	1228.336	-253.104	0.389	1124.505	0.346	17	0.159	R.ADGVGPVSWDPK.V
R3/RRR3-1/3	1384.600	1384.522	56.751	0.554	1186.369	0.558	25	0.159	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1384.943	1384.522	305.112	0.499	1344.553	0.490	24	0.159	R.RADGVGPVSWDPK.V
R3/RRR3-22/2	1229.165	1228.336	-139.514	0.406	925.499	0.419	16	0.158	R.ADGVGPVSWDPK.V
R3/RRR3-17/2	1142.310	1143.274	-1724.215	0.311	847.558	0.449	18	0.158	K.VASFAQSYAAK.R
R3/RRR3-24/2	1584.692	1585.607	-1211.670	0.403	974.305	0.407	16	0.157	K.NYHYDTNTCDPGK.V
R3/RRR3-9/2	1547.714	1548.681	-1274.557	0.262	1185.404	0.317	21	0.157	R.AWSAADAVASWVGEK.K
R3/RRR3-3/2	1547.782	1548.681	-1230.440	0.321	1051.209	0.387	17	0.157	R.AWSAADAVASWVGEK.K
R3/RRR3-18/2	1142.554	1143.274	-1509.419	0.416	558.683	0.489	16	0.157	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1548.354	1548.681	-211.812	0.348	1034.587	0.381	17	0.156	R.AWSAADAVASWVGEK.K
R3/RRR3-21/2	1384.236	1384.522	-207.559	0.438	592.483	0.457	20	0.155	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1548.981	1548.681	194.398	0.382	1052.161	0.371	17	0.155	R.AWSAADAVASWVGEK.K
R3/RRR3-28/2	1142.321	1143.274	-1714.660	0.339	668.816	0.463	17	0.155	K.VASFAQSYAAK.R
R3/RRR3-5/2	1548.269	1548.681	-266.546	0.332	1258.151	0.270	18	0.154	R.AWSAADAVASWVGEK.K
R3/RRR3-24/2	1383.777	1384.522	-1264.964	0.444	605.767	0.440	20	0.154	R.RADGVGPVSWDPK.V
R3/RRR3-21/2	1383.762	1384.522	-1275.772	0.428	535.202	0.453	19	0.153	R.RADGVGPVSWDPK.V
R3/RRR3-6/2	1143.369	1143.274	83.246	0.376	837.043	0.410	17	0.153	-.VASFAQSYAAK.-
R3/RRR3-1/3	1384.839	1384.522	229.410	0.531	1097.607	0.556	22	0.153	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1585.226	1585.607	-240.560	0.394	890.851	0.406	16	0.153	K.NYHYDTNTCDPGK.V
R3/RRR3-12/3	1384.872	1384.522	253.806	0.515	1015.350	0.583	22	0.152	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1228.253	1228.336	-67.148	0.295	1124.808	0.298	17	0.152	R.ADGVGPVSWDPK.V
R3/RRR3-20/3	1383.948	1384.522	-1140.518	0.505	994.474	0.590	23	0.152	R.RADGVGPVSWDPK.V
R3/RRR3-24/3	1548.296	1548.681	-249.193	0.411	1407.120	0.435	26	0.152	R.AWSAADAVASWVGEK.K
R3/RRR3-13/2	1142.430	1143.274	-1618.577	0.345	591.241	0.448	16	0.151	K.VASFAQSYAAK.R
R3/RRR3-14/2	1676.257	1676.854	-955.429	0.438	885.725	0.393	19	0.151	R.AWSAADAVASWVGEKK.N
R3/RRR3-21/3	1383.922	1384.522	-1159.383	0.453	1110.770	0.545	24	0.151	R.RADGVGPVSWDPK.V
R3/RRR3-22/2	1384.236	1384.522	-207.117	0.425	503.643	0.472	19	0.151	-.RADGVGPVSWDPK.-
R3/RRR3-21/3	1384.167	1384.522	-257.158	0.499	1063.685	0.557	22	0.151	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1142.761	1143.274	-1327.649	0.332	492.863	0.470	15	0.150	K.VASFAQSYAAK.R
R3/RRR3-24/2	1584.482	1585.607	-1345.203	0.423	871.586	0.391	16	0.150	K.NYHYDTNTCDPGK.V
R3/RRR3-20/3	1384.631	1384.522	78.900	0.531	1094.283	0.546	22	0.150	R.RADGVGPVSWDPK.V
R3/RRR3-21/2	1142.182	1143.274	-1836.856	0.318	581.569	0.447	16	0.150	K.VASFAQSYAAK.R
R3/RRR3-22/2	1384.377	1384.522	-105.300	0.419	454.665	0.415	18	0.149	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1228.190	1228.336	-118.890	0.322	983.319	0.335	15	0.149	R.ADGVGPVSWDPK.V
R3/RRR3-19/2	1384.392	1384.522	-94.155	0.412	470.373	0.404	18	0.148	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1383.768	1384.522	-1271.254	0.443	506.148	0.437	19	0.148	-.RADGVGPVSWDPK.-
R3/RRR3-20/2	1384.296	1384.522	-163.769	0.380	407.438	0.418	17	0.148	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1383.894	1384.522	-1180.011	0.433	402.738	0.401	17	0.148	R.RADGVGPVSWDPK.V
R3/RRR3-18/2	1676.402	1676.854	-270.129	0.483	413.895	0.468	17	0.148	R.AWSAADAVASWVGEKK.N
R3/RRR3-24/2	1383.766	1384.522	-1272.848	0.372	416.707	0.397	18	0.148	R.RADGVGPVSWDPK.V
R3/RRR3-1/2	1384.251	1384.522	-196.412	0.386	445.455	0.414	17	0.148	R.RADGVGPVSWDPK.V
R3/RRR3-20/2	1384.168	1384.522	-256.485	0.382	421.378	0.412	17	0.148	R.RADGVGPVSWDPK.V
R3/RRR3-25/2	1676.520	1676.854	-199.563	0.440	626.220	0.443	17	0.147	R.AWSAADAVASWVGEKK.N
R3/RRR3-24/3	1383.949	1384.522	-1140.252	0.464	1215.317	0.492	25	0.147	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1677.036	1676.854	109.029	0.459	539.192	0.462	16	0.147	R.AWSAADAVASWVGEKK.N
R3/RRR3-19/2	1384.189	1384.522	-241.532	0.399	458.980	0.374	18	0.147	R.RADGVGPVSWDPK.V
R3/RRR3-18/2	1384.370	1384.522	-110.076	0.437	467.605	0.364	18	0.146	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1675.585	1676.854	-1358.287	0.409	754.410	0.407	16	0.146	R.AWSAADAVASWVGEKK.N
R3/RRR3-1/2	1384.132	1384.522	-282.586	0.393	404.509	0.362	17	0.146	R.RADGVGPVSWDPK.V
R3/RRR3-22/2	1384.123	1384.522	-289.311	0.428	547.959	0.395	19	0.145	-.RADGVGPVSWDPK.-
R3/RRR3-23/2	1384.216	1384.522	-221.980	0.365	596.060	0.346	20	0.145	R.RADGVGPVSWDPK.V
R3/RRR3-21/2	1384.212	1384.522	-224.634	0.397	341.929	0.355	16	0.145	R.RADGVGPVSWDPK.V
R3/RRR3-18/3	1384.477	1384.522	-32.652	0.528	964.436	0.569	23	0.145	R.RADGVGPVSWDPK.V
R3/RRR3-26/2	1676.217	1676.854	-979.191	0.449	862.953	0.346	19	0.145	R.AWSAADAVASWVGEKK.N
R3/RRR3-17/2	1384.320	1384.522	-146.696	0.415	586.045	0.324	20	0.145	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1384.247	1384.522	-199.509	0.393	356.952	0.336	16	0.144	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1675.317	1676.854	-2117.320	0.335	976.088	0.305	18	0.144	R.AWSAADAVASWVGEKK.N
R3/RRR3-24/2	1384.154	1384.522	-266.837	0.374	572.883	0.372	20	0.144	-.RADGVGPVSWDPK.-
R3/RRR3-20/2	1383.267	1384.522	-1634.881	0.347	608.033	0.331	20	0.144	R.RADGVGPVSWDPK.V
R3/RRR3-23/2	1384.061	1384.522	-333.820	0.344	438.262	0.336	18	0.144	R.RADGVGPVSWDPK.V
R3/RRR3-21/2	1547.169	1548.681	-2276.787	0.350	708.039	0.375	17	0.144	R.AWSAADAVASWVGEK.K
R3/RRR3-21/2	1677.567	1676.854	-171.631	0.508	680.190	0.377	20	0.144	R.AWSAADAVASWVGEKK.N
R3/RRR3-24/2	1547.909	1548.681	-1147.998	0.323	990.251	0.290	17	0.143	R.AWSAADAVASWVGEK.K
R3/RRR3-20/2	1676.040	1676.854	-1085.218	0.437	759.646	0.341	20	0.143	R.AWSAADAVASWVGEKK.N
R3/RRR3-23/2	1384.100	1384.522	-305.592	0.373	401.309	0.378	17	0.143	-.RADGVGPVSWDPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/3	1384.254	1384.522	-194.520	0.476	1105.398	0.509	24	0.142	R.RADGVGPVSWDPK.V
R3/RRR3-6/2	1144.084	1143.274	-166.477	0.358	680.402	0.335	16	0.142	-.VASFAQSYAAK.-
R3/RRR3-18/2	1383.667	1384.522	-1344.880	0.349	420.494	0.291	17	0.142	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	1383.611	1384.522	-1385.020	0.303	639.785	0.296	21	0.142	R.RADGVGPVSWDPK.V
R3/RRR3-24/2	789.802	789.897	-120.236	0.333	501.587	0.399	10	0.142	R.VVCAANR.G
R3/RRR3-1/2	1385.049	1384.522	-342.157	0.394	353.942	0.349	16	0.141	-.RADGVGPVSWDPK.-
R3/RRR3-23/2	1384.156	1384.522	-265.067	0.351	566.817	0.328	19	0.141	-.RADGVGPVSWDPK.-
R3/RRR3-11/2	1143.094	1143.274	-157.517	0.274	510.123	0.302	15	0.141	K.VASFAQSYAAK.R
R3/RRR3-16/2	1676.150	1676.854	-1019.771	0.396	517.108	0.371	15	0.139	R.AWSAADAVASWVGEKK.N
R3/RRR3-17/2	1677.419	1676.854	-259.674	0.478	896.311	0.307	21	0.138	-.AWSAADAVASWVGEKK.-
R3/RRR3-13/2	1548.130	1548.681	-1005.003	0.276	802.548	0.291	17	0.138	R.AWSAADAVASWVGEK.K
R3/RRR3-23/2	789.273	789.897	-2063.110	0.254	697.686	0.350	11	0.138	R.VVCAANR.G
R3/RRR3-24/2	1677.603	1676.854	-149.806	0.337	297.124	0.397	14	0.138	-.AWSAADAVASWVGEKK.-
R3/RRR3-16/2	1384.147	1384.522	-271.792	0.354	335.446	0.344	16	0.138	-.RADGVGPVSWDPK.-
R3/RRR3-5/2	1548.408	1548.681	-176.696	0.302	768.422	0.287	16	0.137	R.AWSAADAVASWVGEK.K
R3/RRR3-21/2	1227.982	1228.336	-288.908	0.237	868.325	0.267	14	0.137	R.ADGVGPVSWDPK.V
R3/RRR3-23/2	1384.167	1384.522	-257.458	0.302	431.977	0.306	18	0.136	-.RADGVGPVSWDPK.-
R3/RRR3-23/2	1227.701	1228.336	-1335.622	0.234	957.338	0.208	15	0.136	R.ADGVGPVSWDPK.V
R3/RRR3-23/2	1383.763	1384.522	-1275.063	0.264	390.139	0.269	17	0.135	-.RADGVGPVSWDPK.-
R3/RRR3-12/3	1384.819	1384.522	215.223	0.527	810.548	0.575	20	0.135	-.RADGVGPVSWDPK.-
R3/RRR3-19/3	1384.521	1384.522	-0.417	0.463	949.671	0.520	23	0.134	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1405.696	1405.579	82.813	0.588	1557.199	0.347	26	0.133	K.VCGHYTQVVWR.K
R3/RRR3-8/2	1228.229	1228.336	-87.186	0.318	573.149	0.200	14	0.133	R.ADGVGPVSWDPK.V
R3/RRR3-3/2	1384.229	1384.522	-212.337	0.335	262.710	0.288	14	0.132	-.RADGVGPVSWDPK.-
R3/RRR3-17/2	1676.693	1676.854	-96.215	0.470	635.611	0.312	18	0.132	-.AWSAADAVASWVGEKK.-
R3/RRR3-16/3	1384.377	1384.522	-105.221	0.480	1000.565	0.484	23	0.130	R.RADGVGPVSWDPK.V
R3/RRR3-13/3	1384.268	1384.522	-183.904	0.442	774.918	0.544	21	0.130	R.RADGVGPVSWDPK.V
R3/RRR3-4/2	1548.318	1548.681	-235.382	0.343	753.192	0.195	16	0.130	-.AWSAADAVASWVGEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1547.983	1548.681	-1100.170	0.232	662.283	0.148	14	0.129	-.AWSAADAVASWVGEK.-
R3/RRR3-1/2	1676.264	1676.854	-951.115	0.401	606.497	0.210	16	0.126	-.AWSAADAVASWVGEKK.-
R3/RRR3-19/3	1384.209	1384.522	-226.767	0.433	492.452	0.575	21	0.125	R.RADGVGPVSWDPK.V
R3/RRR3-16/3	1384.557	1384.522	25.714	0.473	890.340	0.481	22	0.124	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1384.314	1384.522	-150.465	0.445	1342.368	0.341	25	0.124	R.RADGVGPVSWDPK.V
R3/RRR3-24/3	1406.545	1405.579	-24.741	0.569	1376.593	0.343	24	0.120	K.VCGHYTQVVWR.K
R3/RRR3-13/3	1383.940	1384.522	-1146.629	0.466	713.735	0.497	21	0.120	R.RADGVGPVSWDPK.V
R3/RRR3-12/3	1384.323	1384.522	-144.495	0.468	819.394	0.462	21	0.118	R.RADGVGPVSWDPK.V
R3/RRR3-13/3	1383.999	1384.522	-1103.984	0.457	974.471	0.420	23	0.118	R.RADGVGPVSWDPK.V
R3/RRR3-15/3	1384.575	1384.522	38.712	0.366	784.927	0.452	22	0.116	R.RADGVGPVSWDPK.V
R3/RRR3-26/3	1384.330	1384.522	-139.320	0.463	517.457	0.496	19	0.116	R.RADGVGPVSWDPK.V
R3/RRR3-24/3	1384.364	1384.522	-114.508	0.484	832.513	0.426	23	0.113	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1405.148	1405.579	-307.821	0.557	1030.332	0.396	23	0.112	K.VCGHYTQVVWR.K
R3/RRR3-23/3	1405.106	1405.579	-338.023	0.469	1145.611	0.355	23	0.112	K.VCGHYTQVVWR.K
R3/RRR3-24/3	1405.871	1405.579	207.820	0.567	1314.949	0.317	24	0.111	K.VCGHYTQVVWR.K
R3/RRR3-23/3	1405.267	1405.579	-222.846	0.524	1096.640	0.364	23	0.110	K.VCGHYTQVVWR.K
R3/RRR3-19/3	1384.653	1384.522	94.683	0.434	564.716	0.453	19	0.109	-.RADGVGPVSWDPK.-
R3/RRR3-23/3	1405.581	1405.579	1.418	0.531	1228.161	0.319	24	0.108	K.VCGHYTQVVWR.K
R3/RRR3-24/3	1405.053	1405.579	-1089.532	0.531	968.891	0.372	22	0.107	K.VCGHYTQVVWR.K
R3/RRR3-14/3	1384.921	1384.522	289.204	0.321	334.843	0.287	22	0.107	R.RADGVGPVSWDPK.V
R3/RRR3-15/3	1384.240	1384.522	-204.074	0.368	488.450	0.426	19	0.106	-.RADGVGPVSWDPK.-
R3/RRR3-23/3	1585.739	1585.607	83.989	0.339	593.471	0.445	24	0.105	K.NYHYDTNTCDPGK.V
R3/RRR3-23/3	1585.863	1585.607	161.805	0.350	626.700	0.436	25	0.105	K.NYHYDTNTCDPGK.V
R3/RRR3-26/3	1383.401	1384.522	-1537.511	0.355	364.242	0.391	19	0.105	-.RADGVGPVSWDPK.-
R3/RRR3-27/3	1384.851	1384.522	238.426	0.313	414.667	0.320	20	0.104	R.RADGVGPVSWDPK.V
R3/RRR3-24/3	1405.748	1405.579	119.914	0.571	1105.667	0.328	23	0.104	K.VCGHYTQVVWR.K
R3/RRR3-5/3	1384.965	1384.522	320.622	0.343	623.772	0.358	19	0.103	R.RADGVGPVSWDPK.V
R3/RRR3-23/3	1585.798	1585.607	120.814	0.297	779.875	0.410	26	0.103	K.NYHYDTNTCDPGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/3	1405.246	1405.579	-237.748	0.510	862.717	0.350	21	0.102	K.VCGHYTQVVWR.K
R3/RRR3-1/3	1404.886	1405.579	-1208.753	0.463	510.355	0.385	18	0.102	-.VCGHYTQVVWR.-
R3/RRR3-24/3	1406.525	1405.579	-38.843	0.493	950.206	0.331	22	0.101	K.VCGHYTQVVWR.K
R3/RRR3-23/3	1405.872	1405.579	208.603	0.550	851.157	0.366	20	0.101	-.VCGHYTQVVWR.-
R3/RRR3-17/3	1406.404	1405.579	-125.293	0.511	677.838	0.347	19	0.100	K.VCGHYTQVVWR.K
R3/RRR3-26/3	1405.983	1405.579	287.745	0.509	743.624	0.340	19	0.099	K.VCGHYTQVVWR.K
R3/RRR3-24/3	1585.657	1585.607	31.989	0.352	434.165	0.324	22	0.099	K.NYHYDTNTCDPGK.V
R3/RRR3-24/3	1585.143	1585.607	-293.336	0.240	836.076	0.366	26	0.098	K.NYHYDTNTCDPGK.V
R3/RRR3-24/3	1585.567	1585.607	-25.229	0.313	558.791	0.348	24	0.097	K.NYHYDTNTCDPGK.V
R3/RRR3-2/3	1548.725	1548.681	28.482	0.365	764.813	0.345	26	0.097	R.AWSAADAVASWVGEK.K
R3/RRR3-26/3	1585.159	1585.607	-283.369	0.258	462.790	0.341	22	0.097	K.NYHYDTNTCDPGK.V
R3/RRR3-23/3	1384.256	1384.522	-192.795	0.358	909.109	0.267	21	0.096	R.RADGVGPVSWDPK.V
R3/RRR3-22/3	1405.172	1405.579	-290.563	0.475	560.225	0.309	18	0.096	-.VCGHYTQVVWR.-
R3/RRR3-19/3	1406.509	1405.579	-50.334	0.462	511.845	0.277	18	0.095	-.VCGHYTQVVWR.-
R3/RRR3-26/3	1405.423	1405.579	-111.616	0.453	614.880	0.262	18	0.095	K.VCGHYTQVVWR.K
R3/RRR3-24/3	1585.779	1585.607	109.118	0.348	768.687	0.310	26	0.094	K.NYHYDTNTCDPGK.V
R3/RRR3-1/3	1404.621	1405.579	-1398.831	0.421	501.282	0.301	18	0.094	-.VCGHYTQVVWR.-
R3/RRR3-22/3	1405.737	1405.579	112.468	0.507	878.789	0.301	21	0.094	-.VCGHYTQVVWR.-
R3/RRR3-24/3	1405.400	1405.579	-127.953	0.525	747.189	0.275	21	0.093	K.VCGHYTQVVWR.K
R3/RRR3-24/3	1383.818	1384.522	-1235.385	0.326	529.409	0.309	19	0.093	-.RADGVGPVSWDPK.-
R3/RRR3-23/3	1405.797	1405.579	155.444	0.391	452.957	0.329	17	0.090	-.VCGHYTQVVWR.-
R3/RRR3-24/3	1406.873	1405.579	209.064	0.475	897.340	0.229	22	0.089	K.VCGHYTQVVWR.K
R3/RRR3-24/3	1404.420	1405.579	-1542.354	0.460	842.576	0.242	20	0.087	-.VCGHYTQVVWR.-
R3/RRR3-2/3	1406.077	1405.579	355.254	0.393	570.485	0.293	18	0.086	-.VCGHYTQVVWR.-
R3/RRR3-4/3	1405.314	1405.579	-189.383	0.374	419.315	0.350	17	0.085	-.VCGHYTQVVWR.-
R3/RRR3-25/3	1384.016	1384.522	-1091.497	0.401	457.653	0.432	18	0.084	-.RADGVGPVSWDPK.-
R3/RRR3-23/3	1405.810	1405.579	164.718	0.420	620.991	0.267	19	0.082	-.VCGHYTQVVWR.-
R3/RRR3-21/3	1405.790	1405.579	149.958	0.421	573.387	0.256	19	0.082	-.VCGHYTQVVWR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1969.715	1969.163	-227.915	0.592	2568.707	0.545	24	0.417	R.TMLELLNQLDGFSSDER.I
R3/RRR3-9/2	1968.360	1969.163	-918.330	0.538	2059.850	0.542	23	0.313	R.TMLELLNQLDGFSSDER.I
R3/RRR3-9/2	1646.158	1645.948	127.958	0.500	1700.073	0.519	22	0.249	K.LAGPQLVQMFIGDGAK.L
R3/RRR3-9/2	1661.297	1661.947	-996.417	0.475	1600.634	0.513	22	0.234	K.LAGPQLVQM*FIGDGAK.L
R3/RRR3-9/2	1646.495	1645.948	-275.556	0.509	1473.302	0.502	21	0.215	K.LAGPQLVQMFIGDGAK.L
R3/RRR3-9/3	1645.565	1645.948	-233.533	0.468	1777.099	0.467	29	0.207	K.LAGPQLVQMFIGDGAK.L
R3/RRR3-9/2	1195.902	1196.249	-291.027	0.514	1300.618	0.508	17	0.203	R.STDDFNGAQLK.A
R3/RRR3-9/2	1670.413	1669.986	256.569	0.506	1257.408	0.478	24	0.193	R.QTIFLPVIGLVDPEK.L
R3/RRR3-9/3	1440.323	1440.586	-182.995	0.499	1747.771	0.446	26	0.190	R.KIEFPHPSEEAR.A
R3/RRR3-9/2	1661.088	1661.947	-1122.805	0.459	1052.507	0.514	19	0.177	K.LAGPQLVQM*FIGDGAK.L
R3/RRR3-9/2	1968.665	1969.163	-253.660	0.451	1265.395	0.411	20	0.176	R.TMLELLNQLDGFSSDER.I
R3/RRR3-9/2	1195.858	1196.249	-327.896	0.500	1046.486	0.450	17	0.171	R.STDDFNGAQLK.A
R3/RRR3-9/2	1661.143	1661.947	-1089.379	0.423	1120.231	0.444	19	0.171	K.LAGPQLVQM*FIGDGAK.L
R3/RRR3-9/2	1669.388	1669.986	-959.727	0.416	1155.120	0.409	22	0.171	R.QTIFLPVIGLVDPEK.L
R3/RRR3-9/3	1680.536	1680.761	-133.998	0.479	1664.067	0.395	27	0.168	K.RFDSEVSGDREVQR.T
R3/RRR3-9/2	1669.339	1669.986	-989.680	0.427	1031.125	0.411	22	0.163	R.QTIFLPVIGLVDPEK.L
R3/RRR3-9/2	1195.318	1196.249	-1620.302	0.361	933.173	0.457	16	0.162	R.STDDFNGAQLK.A
R3/RRR3-9/2	1889.174	1888.021	81.361	0.493	746.503	0.516	20	0.158	K.DSYLILDTLPSEYDSR.V
R3/RRR3-9/3	1441.029	1440.586	308.530	0.480	1531.210	0.424	25	0.158	R.KIEFPHPSEEAR.A
R3/RRR3-9/3	1680.733	1680.761	-16.516	0.509	1536.743	0.384	26	0.150	K.RFDSEVSGDREVQR.T
R3/RRR3-9/2	1850.437	1850.215	120.184	0.396	1059.850	0.337	17	0.148	K.QIQELVEAIVLPMTHK.D
R3/RRR3-8/2	1644.672	1645.948	-1387.688	0.352	797.604	0.383	17	0.144	K.LAGPQLVQMFIGDGAK.L
R3/RRR3-2/2	1645.913	1645.948	-21.097	0.364	665.497	0.440	15	0.144	K.LAGPQLVQMFIGDGAK.L
R3/RRR3-9/3	1680.842	1680.761	48.169	0.474	1426.907	0.330	26	0.127	K.RFDSEVSGDREVQR.T
R3/RRR3-9/3	1440.111	1440.586	-330.572	0.453	1201.553	0.362	23	0.116	R.KIEFPHPSEEAR.A
R3/RRR3-7/3	1680.841	1680.761	47.951	0.286	782.474	0.163	23	0.082	K.RFDSEVSGDREVQR.T
R3/RRR3-22/2	1556.168	1556.726	-1004.533	0.494	1571.959	0.499	19	0.231	R.LEFLDVDKCECK.S
R3/RRR3-22/3	1841.463	1842.027	-852.201	0.576	1793.410	0.534	27	0.230	K.ERLEFLDVDKCECK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1556.353	1556.726	-240.381	0.499	1580.278	0.437	19	0.217	R.LEFLDVDKCECK.S
R3/RRR3-22/2	1440.310	1441.695	-1660.409	0.378	1624.740	0.396	19	0.212	K.LLPGVEVKDEITK.A
R3/RRR3-22/3	1841.321	1842.027	-929.566	0.513	1750.777	0.488	27	0.208	K.ERLEFLDVDKCECK.S
R3/RRR3-22/2	1070.983	1071.209	-212.251	0.415	1354.226	0.498	16	0.205	K.AIETATSHIK.V
R3/RRR3-21/2	1017.961	1018.146	-182.232	0.448	1479.362	0.416	18	0.202	K.STLVEGGGIGK.A
R3/RRR3-23/2	1017.928	1018.146	-215.555	0.453	1364.729	0.444	18	0.196	K.STLVEGGGIGK.A
R3/RRR3-22/2	1556.133	1556.726	-1027.058	0.525	1273.501	0.477	18	0.193	R.LEFLDVDKCECK.S
R3/RRR3-22/2	1017.937	1018.146	-206.532	0.431	1376.913	0.371	18	0.183	K.STLVEGGGIGK.A
R3/RRR3-22/2	1356.191	1356.575	-284.060	0.494	1113.612	0.445	17	0.173	R.AAVM*DWHTLAPK.I
R3/RRR3-22/2	1070.969	1071.209	-225.401	0.386	1313.275	0.325	16	0.170	K.AIETATSHIK.V
R3/RRR3-23/2	1017.849	1018.146	-292.677	0.419	1113.827	0.412	17	0.170	K.STLVEGGGIGK.A
R3/RRR3-22/2	1441.194	1441.695	-1044.828	0.380	753.330	0.553	20	0.166	K.LLPGVEVKDEITK.A
R3/RRR3-22/2	1094.186	1094.286	-91.265	0.476	968.425	0.448	15	0.166	K.AKESLTGIFK.T
R3/RRR3-22/2	1440.279	1441.695	-1682.463	0.391	1183.555	0.367	17	0.165	K.LLPGVEVKDEITK.A
R3/RRR3-22/2	1093.945	1094.286	-312.331	0.501	896.123	0.453	15	0.163	K.AKESLTGIFK.T
R3/RRR3-21/2	1441.318	1441.695	-262.370	0.463	782.146	0.478	20	0.162	K.LLPGVEVKDEITK.A
R3/RRR3-22/2	1441.330	1441.695	-253.873	0.389	768.400	0.498	20	0.161	K.LLPGVEVKDEITK.A
R3/RRR3-21/2	1441.327	1441.695	-255.658	0.463	791.864	0.464	20	0.160	K.LLPGVEVKDEITK.A
R3/RRR3-22/2	1441.362	1441.695	-231.442	0.442	794.993	0.464	20	0.160	K.LLPGVEVKDEITK.A
R3/RRR3-22/2	1093.563	1094.286	-1580.512	0.481	870.184	0.426	16	0.159	K.AKESLTGIFK.T
R3/RRR3-21/2	1017.445	1018.146	-1676.792	0.330	926.484	0.380	16	0.153	K.STLVEGGGIGK.A
R3/RRR3-22/2	1356.287	1356.575	-212.904	0.405	986.517	0.359	16	0.152	R.AAVM*DWHTLAPK.I
R3/RRR3-22/2	1017.421	1018.146	-1700.900	0.339	887.570	0.384	16	0.152	K.STLVEGGGIGK.A
R3/RRR3-22/2	1705.157	1705.939	-1047.956	0.430	354.624	0.474	19	0.148	R.QFNFTSAM*PFSHM*K.E
R3/RRR3-22/2	1705.572	1705.939	-215.556	0.407	295.286	0.493	18	0.147	R.QFNFTSAM*PFSHM*K.E
R3/RRR3-22/2	1356.241	1356.575	-246.855	0.408	1084.516	0.277	17	0.147	R.AAVM*DWHTLAPK.I
R3/RRR3-21/2	1017.580	1018.146	-1543.856	0.392	652.581	0.387	15	0.146	K.STLVEGGGIGK.A
R3/RRR3-23/2	1017.289	1018.146	-1830.863	0.359	717.349	0.366	15	0.145	K.STLVEGGGIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1706.176	1705.939	139.378	0.429	192.205	0.402	16	0.143	R.QFNFTSAM*PFSHM*K.E
R3/RRR3-22/2	1070.964	1071.209	-229.746	0.357	978.423	0.258	14	0.141	K.AIETATSHIK.V
R3/RRR3-22/3	1841.778	1842.027	-135.861	0.483	1253.860	0.425	24	0.134	K.ERLEFLDVDKCECK.S
R3/RRR3-22/3	1355.928	1356.575	-1218.701	0.282	585.833	0.555	21	0.112	R.AAVM*DWHTLAPK.I
R3/RRR3-22/3	1356.884	1356.575	228.151	0.393	653.758	0.521	22	0.111	-.AAVM*DWHTLAPK.-
R3/RRR3-22/3	1356.111	1356.575	-343.494	0.304	368.704	0.468	16	0.102	R.AAVM*DWHTLAPK.I
R3/RRR3-22/3	1340.393	1340.576	-136.533	0.301	628.250	0.332	21	0.093	R.AAVMDWHTLAPK.I
R3/RRR3-7/2	1241.192	1240.477	-230.296	0.585	2405.982	0.459	18	0.350	R.ALNILADILQR.S
R3/RRR3-8/2	1240.081	1240.477	-320.250	0.568	2352.628	0.452	18	0.338	R.ALNILADILQR.S
R3/RRR3-7/2	1239.907	1240.477	-1270.237	0.515	2190.639	0.404	18	0.295	R.ALNILADILQR.S
R3/RRR3-8/2	1240.289	1240.477	-152.379	0.555	2113.053	0.419	18	0.285	R.ALNILADILQR.S
R3/RRR3-8/2	1240.181	1240.477	-239.468	0.575	2043.387	0.449	18	0.282	R.ALNILADILQR.S
R3/RRR3-8/2	1189.117	1189.344	-191.473	0.521	1729.196	0.458	19	0.242	R.IDAVDATTVKR.V
R3/RRR3-7/2	1240.268	1240.477	-169.756	0.525	1780.877	0.420	17	0.236	R.ALNILADILQR.S
R3/RRR3-8/2	1251.017	1251.372	-285.252	0.510	1434.287	0.523	16	0.220	K.YIETHYTAPR.M
R3/RRR3-8/2	1251.125	1251.372	-198.131	0.462	1454.727	0.474	16	0.211	K.YIETHYTAPR.M
R3/RRR3-8/2	1188.986	1189.344	-301.884	0.504	1364.348	0.475	18	0.203	R.IDAVDATTVKR.V
R3/RRR3-8/2	1251.084	1251.372	-231.020	0.368	1301.873	0.475	16	0.194	K.YIETHYTAPR.M
R3/RRR3-8/2	1189.111	1189.344	-196.829	0.454	1371.375	0.415	18	0.191	R.IDAVDATTVKR.V
R3/RRR3-8/2	1211.747	1212.469	-1424.845	0.441	1252.034	0.429	16	0.183	R.RIPIPELFAR.I
R3/RRR3-7/2	1213.306	1212.469	-134.879	0.472	1233.201	0.431	16	0.182	R.RIPIPELFAR.I
R3/RRR3-8/2	1211.866	1212.469	-1326.907	0.454	1215.849	0.429	16	0.181	R.RIPIPELFAR.I
R3/RRR3-8/2	1056.423	1057.209	-1695.647	0.431	856.675	0.513	15	0.169	K.HMGSELVQR.V
R3/RRR3-8/2	1211.711	1212.469	-1455.100	0.467	995.520	0.444	15	0.167	R.RIPIPELFAR.I
R3/RRR3-7/2	1211.712	1212.469	-1454.392	0.439	968.606	0.434	14	0.163	R.RIPIPELFAR.I
R3/RRR3-8/2	1056.715	1057.209	-469.557	0.354	942.965	0.432	15	0.160	K.HMGSELVQR.V
R3/RRR3-8/2	1159.128	1159.295	-144.986	0.387	732.885	0.498	14	0.155	K.HDDIVEMATK.L
R3/RRR3-8/2	1055.927	1056.282	-338.070	0.386	573.620	0.487	15	0.154	R.IPIPELFAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	961.011	961.205	-202.077	0.410	946.294	0.338	17	0.150	R.MVITAAGAVK.H
R3/RRR3-7/2	1211.827	1212.469	-1359.281	0.457	650.229	0.426	12	0.146	-.RIPIPELFAR.-
R3/RRR3-8/2	1055.960	1056.282	-306.174	0.260	582.362	0.457	15	0.144	R.IPIPELFAR.I
R3/RRR3-8/2	960.392	961.052	-1733.633	0.337	776.665	0.264	13	0.138	R.VTEEDVIR.A
R3/RRR3-8/2	960.534	961.052	-1584.366	0.342	749.935	0.258	13	0.138	R.VTEEDVIR.A
R3/RRR3-8/2	1055.662	1056.282	-1539.600	0.245	593.141	0.301	15	0.136	R.IPIPELFAR.I
R3/RRR3-7/2	1056.152	1056.282	-124.229	0.247	463.730	0.328	14	0.135	-.IPIPELFAR.-
R3/RRR3-8/2	960.748	961.052	-317.400	0.392	737.370	0.210	13	0.134	R.VTEEDVIR.A
R3/RRR3-4/2	1189.106	1189.344	-200.948	0.318	622.006	0.240	13	0.132	R.IDAVDATTVKR.V
R3/RRR3-8/3	1212.270	1212.469	-164.952	0.409	838.790	0.371	20	0.100	R.RIPIPELFAR.I
R3/RRR3-8/3	1212.370	1212.469	-82.076	0.375	906.701	0.347	20	0.098	R.RIPIPELFAR.I
R3/RRR3-15/3	1719.337	1719.920	-923.522	0.545	2917.337	0.515	33	0.471	R.ILDVVYNASNNELVR.T
R3/RRR3-15/2	1606.114	1606.584	-293.767	0.539	2693.332	0.529	24	0.442	K.DAAEGQEGEAATEEAK.K
R3/RRR3-15/2	1606.168	1606.584	-259.987	0.549	2622.328	0.558	24	0.436	K.DAAEGQEGEAATEEAK.K
R3/RRR3-15/2	1606.052	1606.584	-956.865	0.536	2678.210	0.523	24	0.436	K.DAAEGQEGEAATEEAK.K
R3/RRR3-15/2	1719.679	1719.920	-140.516	0.555	2102.577	0.504	23	0.310	R.ILDVVYNASNNELVR.T
R3/RRR3-15/2	1657.116	1656.735	230.847	0.582	1937.032	0.587	23	0.307	R.LDTGNYSWGSEAVTR.K
R3/RRR3-15/3	1735.720	1734.757	-21.424	0.590	2247.223	0.499	32	0.302	K.KDAAEGQEGEAATEEAK.K
R3/RRR3-15/2	1720.252	1719.920	193.549	0.577	1946.428	0.535	23	0.296	-.ILDVVYNASNNELVR.-
R3/RRR3-15/2	1720.450	1719.920	-274.030	0.586	2014.243	0.494	23	0.295	-.ILDVVYNASNNELVR.-
R3/RRR3-15/2	1656.184	1656.735	-939.212	0.554	1839.079	0.574	23	0.287	R.LDTGNYSWGSEAVTR.K
R3/RRR3-15/2	1735.140	1734.757	221.383	0.559	1833.093	0.510	25	0.268	K.DAAEGQEGEAATEEAKK.S
R3/RRR3-15/3	1734.793	1734.757	20.628	0.583	2020.016	0.521	33	0.264	K.KDAAEGQEGEAATEEAK.K
R3/RRR3-15/3	1734.702	1734.757	-31.989	0.617	2003.098	0.493	32	0.251	K.KDAAEGQEGEAATEEAK.K
R3/RRR3-15/2	1656.341	1656.735	-238.067	0.501	1723.949	0.504	22	0.250	R.LDTGNYSWGSEAVTR.K
R3/RRR3-15/2	1247.043	1246.437	-316.990	0.501	1576.730	0.546	18	0.242	K.SAIVQVDAAPFK.Q
R3/RRR3-15/2	1245.448	1246.437	-1601.878	0.363	1704.282	0.451	18	0.234	K.SAIVQVDAAPFK.Q
R3/RRR3-15/2	1247.079	1246.437	-288.411	0.510	1558.262	0.521	18	0.233	K.SAIVQVDAAPFK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/3	1862.772	1862.930	-85.362	0.569	1672.579	0.580	36	0.226	K.KDAAEGQEGEAATEEAKK.S
R3/RRR3-15/2	1734.251	1734.757	-871.094	0.523	1610.266	0.446	23	0.220	K.DAAEGQEGEAATEEAKK.S
R3/RRR3-15/2	1577.058	1576.650	259.723	0.565	1352.498	0.555	19	0.215	R.TLDSHIEEQFGSGR.L
R3/RRR3-15/2	1576.023	1576.650	-1034.916	0.528	1178.188	0.548	19	0.196	R.TLDSHIEEQFGSGR.L
R3/RRR3-15/2	1575.727	1576.650	-1223.692	0.522	1200.117	0.510	19	0.191	R.TLDSHIEEQFGSGR.L
R3/RRR3-15/3	1862.917	1862.930	-7.277	0.570	1440.238	0.573	37	0.190	K.KDAAEGQEGEAATEEAKK.S
R3/RRR3-15/3	1719.006	1719.920	-1116.648	0.489	1473.199	0.482	27	0.171	-.ILDVVYNASNNELVR.-
R3/RRR3-15/3	1863.851	1862.930	-42.385	0.587	1174.993	0.595	35	0.167	K.KDAAEGQEGEAATEEAKK.S
R3/RRR3-15/3	1577.550	1576.650	-63.116	0.434	847.525	0.514	23	0.121	R.TLDSHIEEQFGSGR.L
R3/RRR3-6/2	1690.150	1689.801	207.138	0.524	1632.538	0.602	20	0.262	K.YSNSQAVVYVGCGER.G
R3/RRR3-7/2	1256.174	1256.434	-206.984	0.507	1112.554	0.549	19	0.194	K.LAADTPLLTGQR.V
R3/RRR3-6/2	1256.237	1256.434	-156.682	0.481	1184.224	0.489	20	0.189	K.LAADTPLLTGQR.V
R3/RRR3-6/2	1256.977	1256.434	-364.454	0.513	1101.531	0.502	19	0.185	K.LAADTPLLTGQR.V
R3/RRR3-7/2	1255.427	1256.434	-1603.482	0.377	1020.033	0.481	19	0.173	K.LAADTPLLTGQR.V
R3/RRR3-6/2	1257.299	1256.434	-107.860	0.534	987.470	0.479	18	0.172	K.LAADTPLLTGQR.V
R3/RRR3-7/2	1255.535	1256.434	-1516.943	0.410	971.843	0.485	18	0.171	K.LAADTPLLTGQR.V
R3/RRR3-7/2	1171.992	1171.284	-249.744	0.461	912.664	0.414	15	0.157	K.LYDDLTAGFR.N
R3/RRR3-7/2	1707.504	1705.937	-254.453	0.613	2627.748	0.592	23	0.451	K.WPYEAAALAFEAIPR.T
R3/RRR3-7/2	1495.937	1496.569	-1094.331	0.538	1654.224	0.611	23	0.272	K.HANGENAWVGIDGR.S
R3/RRR3-7/2	1705.182	1705.937	-1032.206	0.417	1773.030	0.372	20	0.225	K.WPYEAAALAFEAIPR.T
R3/RRR3-7/2	1158.284	1158.327	-37.061	0.445	1548.444	0.480	18	0.224	K.ALEDALAVLDK.I
R3/RRR3-7/2	1157.649	1158.327	-1453.566	0.379	1436.727	0.414	16	0.195	K.ALEDALAVLDK.I
R3/RRR3-7/2	1363.425	1363.618	-141.311	0.455	989.549	0.399	15	0.157	R.IILLDCPVEYK.K
R3/RRR3-7/2	959.981	960.107	-131.253	0.472	932.286	0.358	15	0.154	R.IDDIVSGIK.K
R3/RRR3-7/2	1058.009	1058.127	-112.207	0.409	704.019	0.441	16	0.153	K.VPGGQLEDSR.V
R3/RRR3-7/2	1120.897	1121.250	-316.266	0.347	975.870	0.346	14	0.149	R.NLQDAM*SVAR.N
R3/RRR3-7/2	1598.581	1598.866	-179.039	0.299	472.111	0.589	22	0.148	K.LLPGGGATELTVSAALK.Q
R3/RRR3-7/2	959.220	960.107	-1973.101	0.369	806.033	0.361	14	0.147	R.IDDIVSGIK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1058.150	1058.127	21.683	0.415	574.209	0.400	15	0.146	K.VPGGQLEDSR.V
R3/RRR3-7/2	1057.992	1058.127	-128.179	0.403	694.145	0.355	15	0.144	K.VPGGQLEDSR.V
R3/RRR3-7/2	959.927	960.107	-188.147	0.433	719.435	0.329	13	0.142	R.IDDIVSGIK.K
R3/RRR3-7/2	1316.432	1317.431	-1523.222	0.334	830.948	0.297	16	0.137	R.GASKDVLNEVER.N
R3/RRR3-7/2	1599.151	1598.866	178.806	0.356	201.990	0.353	17	0.135	-.LLPGGGATELTVSAALK.-
R3/RRR3-7/2	1637.436	1637.688	-154.228	0.545	2343.577	0.554	26	0.373	K.TNDSAGDGTTTASVLAR.E
R3/RRR3-7/2	1915.609	1915.178	225.709	0.558	2365.155	0.510	25	0.360	K.DLGLLVESTTVEQLGIAR.K
R3/RRR3-7/2	1637.077	1637.688	-986.821	0.487	2173.194	0.502	25	0.323	K.TNDSAGDGTTTASVLAR.E
R3/RRR3-7/2	1636.640	1637.688	-1255.203	0.433	2103.434	0.479	25	0.304	K.TNDSAGDGTTTASVLAR.E
R3/RRR3-7/2	1915.075	1915.178	-53.871	0.542	1966.402	0.552	24	0.299	K.DLGLLVESTTVEQLGIAR.K
R3/RRR3-7/2	1914.644	1915.178	-803.346	0.523	1709.145	0.542	25	0.257	K.DLGLLVESTTVEQLGIAR.K
R3/RRR3-7/2	1480.114	1480.646	-1038.613	0.456	1387.298	0.516	20	0.212	R.GYISPQFVTNPEK.S
R3/RRR3-7/2	1291.032	1291.347	-244.545	0.514	1432.501	0.476	19	0.209	K.VGAATETELEDR.K
R3/RRR3-7/2	1479.748	1480.646	-1286.514	0.348	1595.746	0.395	21	0.209	R.GYISPQFVTNPEK.S
R3/RRR3-7/2	1481.183	1480.646	-313.833	0.519	1385.562	0.500	20	0.209	R.GYISPQFVTNPEK.S
R3/RRR3-7/3	1788.904	1789.066	-90.804	0.363	1884.338	0.331	30	0.183	K.ALLQDIAIVTGAEFQAK.D
R3/RRR3-7/2	1064.407	1065.161	-1653.251	0.334	1277.568	0.354	14	0.171	K.SLVEFENAR.I
R3/RRR3-7/2	1290.965	1291.347	-296.531	0.504	1115.887	0.402	18	0.167	K.VGAATETELEDR.K
R3/RRR3-7/2	1473.048	1473.478	-292.792	0.384	1032.048	0.427	19	0.165	R.ELSQTDSAYDSEK.L
R3/RRR3-7/2	898.910	899.113	-226.457	0.447	845.620	0.464	14	0.163	R.GILNVAAIK.A
R3/RRR3-7/2	898.625	899.113	-544.669	0.473	908.023	0.433	14	0.162	R.GILNVAAIK.A
R3/RRR3-7/2	898.597	899.113	-1691.663	0.418	932.558	0.417	14	0.160	R.GILNVAAIK.A
R3/RRR3-7/2	899.173	899.113	67.319	0.444	832.851	0.444	14	0.159	R.GILNVAAIK.A
R3/RRR3-7/2	1473.050	1473.478	-291.129	0.394	961.320	0.415	19	0.159	R.ELSQTDSAYDSEK.L
R3/RRR3-7/2	1064.893	1065.161	-252.556	0.346	1079.562	0.361	14	0.159	K.SLVEFENAR.I
R3/RRR3-7/2	1065.038	1065.161	-116.524	0.433	1096.227	0.330	14	0.157	K.SLVEFENAR.I
R3/RRR3-7/2	1290.498	1291.347	-1437.041	0.361	991.228	0.353	18	0.153	K.VGAATETELEDR.K
R3/RRR3-7/2	1472.486	1473.478	-1357.051	0.283	714.145	0.374	17	0.141	R.ELSQTDSAYDSEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	857.540	858.018	-558.914	0.444	1018.317	0.197	13	0.137	R.LGADIIQK.A
R3/RRR3-7/2	857.976	858.018	-48.892	0.549	1016.724	0.194	13	0.133	R.LGADIIQK.A
R3/RRR3-7/2	857.905	858.018	-132.242	0.571	1057.816	0.170	13	0.129	R.LGADIIQK.A
R3/RRR3-7/3	1788.486	1789.066	-886.070	0.289	572.125	0.298	24	0.089	K.ALLQDIAIVTGAEFQAK.D
R3/RRR3-7/3	1788.916	1789.066	-84.027	0.314	1122.915	0.185	26	0.086	K.ALLQDIAIVTGAEFQAK.D
R3/RRR3-7/2	1471.542	1471.678	-92.323	0.441	2822.692	0.458	21	0.450	K.ESIVDVEGVVSLPK.E
R3/RRR3-7/2	1531.217	1531.652	-284.867	0.540	2316.571	0.543	25	0.365	R.VWTEVGGLDEAAAGR.S
R3/RRR3-7/2	1470.991	1471.678	-1150.096	0.332	2665.696	0.294	20	0.358	K.ESIVDVEGVVSLPK.E
R3/RRR3-7/2	1531.123	1531.652	-1001.693	0.540	2331.362	0.489	25	0.350	R.VWTEVGGLDEAAAGR.S
R3/RRR3-7/2	1531.195	1531.652	-299.104	0.555	2203.245	0.496	25	0.327	R.VWTEVGGLDEAAAGR.S
R3/RRR3-7/2	1519.183	1519.593	-270.683	0.550	2129.521	0.465	21	0.305	R.SEAEIEKAEQAGEK.L
R3/RRR3-7/2	1451.044	1450.768	190.306	0.348	1625.520	0.305	17	0.194	R.VVMLFCALNNIR.K
R3/RRR3-7/2	1306.714	1307.477	-1353.619	0.366	1210.105	0.451	20	0.179	K.LIAGSSEGGAAVFK.L
R3/RRR3-7/2	1098.515	1098.281	213.594	0.487	1045.204	0.452	14	0.168	R.GAAQAIRPVSK.K
R3/RRR3-7/2	1098.112	1098.281	-153.934	0.469	1025.561	0.451	14	0.167	R.GAAQAIRPVSK.K
R3/RRR3-7/2	1451.158	1450.768	269.263	0.447	1413.355	0.260	17	0.165	R.VVMLFCALNNIR.K
R3/RRR3-8/2	1018.020	1018.151	-129.363	0.424	785.363	0.421	13	0.153	R.TPANQAIFR.I
R3/RRR3-7/2	1049.543	1050.235	-1616.470	0.386	736.516	0.425	12	0.150	R.VFEVGPVFR.A
R3/RRR3-7/2	1098.249	1098.281	-29.611	0.460	776.244	0.424	13	0.149	R.GAAQAIRPVSK.K
R3/RRR3-8/2	1018.169	1018.151	17.724	0.412	636.845	0.423	13	0.149	R.TPANQAIFR.I
R3/RRR3-7/2	1341.483	1341.556	-53.937	0.424	781.563	0.404	14	0.148	K.LTYEEGIQM*LK.E
R3/RRR3-7/2	1050.038	1050.235	-188.150	0.402	1013.605	0.281	14	0.147	R.VFEVGPVFR.A
R3/RRR3-7/2	1017.406	1018.151	-1720.722	0.363	616.512	0.399	13	0.145	R.TPANQAIFR.I
R3/RRR3-7/2	1341.274	1341.556	-210.680	0.379	650.952	0.382	13	0.140	K.LTYEEGIQM*LK.E
R3/RRR3-7/2	1049.931	1050.235	-290.440	0.384	707.998	0.292	13	0.139	R.VFEVGPVFR.A
R3/RRR3-8/2	1050.082	1050.235	-146.051	0.350	581.188	0.276	11	0.134	-.VFEVGPVFR.-
R3/RRR3-8/2	1049.874	1050.235	-344.451	0.350	553.245	0.277	11	0.132	-.VFEVGPVFR.-
R3/RRR3-7/3	1519.644	1519.593	33.821	0.432	661.734	0.478	28	0.110	R.SEAEIEKAEQAGEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/3	1518.966	1519.593	-1074.202	0.300	575.228	0.376	27	0.094	R.SEAEIEKAEQAGEK.L
R3/RRR3-5/2	1863.413	1864.066	-890.087	0.595	3132.053	0.556	25	0.566	R.MKEGQSEIYYITGESK.K
R3/RRR3-5/2	1880.206	1880.066	74.858	0.570	1488.263	0.612	26	0.247	R.M*KEGQSEIYYITGESK.K
R3/RRR3-5/2	1879.745	1880.066	-171.138	0.602	1342.938	0.599	26	0.227	R.M*KEGQSEIYYITGESK.K
R3/RRR3-5/2	1879.463	1880.066	-855.179	0.564	1015.417	0.605	23	0.194	R.M*KEGQSEIYYITGESK.K
R3/RRR3-5/2	1604.554	1604.696	-88.943	0.445	782.193	0.498	16	0.155	K.EGQSEIYYITGESK.K
R3/RRR3-5/3	1879.596	1880.066	-250.433	0.503	1109.119	0.532	24	0.147	R.M*KEGQSEIYYITGESK.K
R3/RRR3-5/3	1879.725	1880.066	-181.829	0.513	1154.659	0.510	24	0.146	R.M*KEGQSEIYYITGESK.K
R3/RRR3-5/3	1879.711	1880.066	-189.353	0.484	1227.152	0.461	25	0.140	R.M*KEGQSEIYYITGESK.K
R3/RRR3-12/3	1940.173	1940.190	-9.164	0.587	4146.915	0.614	38	1.000	K.VLIAVADNVGSNQLQEIR.K
R3/RRR3-12/3	1940.067	1940.190	-63.691	0.588	4042.784	0.614	39	0.950	K.VLIAVADNVGSNQLQEIR.K
R3/RRR3-12/2	1743.410	1743.942	-880.915	0.532	2427.233	0.627	32	0.418	K.FAVAAPVAADSGAAAPSAAK.E
R3/RRR3-12/3	1939.505	1940.190	-871.460	0.488	2562.294	0.564	34	0.410	K.VLIAVADNVGSNQLQEIR.K
R3/RRR3-12/2	1743.349	1743.942	-916.412	0.511	2318.857	0.611	31	0.388	K.FAVAAPVAADSGAAAPSAAK.E
R3/RRR3-12/2	1743.453	1743.942	-281.230	0.520	2145.147	0.614	31	0.354	K.FAVAAPVAADSGAAAPSAAK.E
R3/RRR3-12/2	1939.612	1940.190	-816.298	0.543	2221.558	0.537	26	0.341	K.VLIAVADNVGSNQLQEIR.K
R3/RRR3-13/2	1939.339	1940.190	-957.515	0.477	2172.938	0.472	27	0.313	K.VLIAVADNVGSNQLQEIR.K
R3/RRR3-12/2	1939.712	1940.190	-247.157	0.559	2092.415	0.509	25	0.307	K.VLIAVADNVGSNQLQEIR.K
R3/RRR3-12/2	1939.617	1940.190	-813.518	0.566	1910.691	0.548	24	0.288	K.VLIAVADNVGSNQLQEIR.K
R3/RRR3-12/2	1411.358	1411.619	-185.526	0.469	1455.892	0.464	16	0.208	K.KLCQLLDEYTK.V
R3/RRR3-12/2	1767.544	1768.131	-900.682	0.483	1323.848	0.488	19	0.196	K.INKGTVEIITPVELIK.K
R3/RRR3-12/2	1768.329	1768.131	112.540	0.513	1188.667	0.470	20	0.180	K.INKGTVEIITPVELIK.K
R3/RRR3-12/2	1061.949	1062.199	-236.308	0.459	920.653	0.465	18	0.168	K.VGSSESALLAK.L
R3/RRR3-12/2	1284.027	1283.446	-327.407	0.562	1213.305	0.360	16	0.166	K.LCQLLDEYTK.V
R3/RRR3-12/3	1743.859	1743.942	-47.688	0.409	1715.534	0.355	35	0.166	K.FAVAAPVAADSGAAAPSAAK.E
R3/RRR3-13/2	1412.403	1412.697	-208.794	0.415	999.331	0.404	16	0.158	K.GTVEIITPVELIK.K
R3/RRR3-12/2	1413.474	1412.697	-157.963	0.495	1010.282	0.393	17	0.157	K.GTVEIITPVELIK.K
R3/RRR3-12/2	1061.939	1062.199	-245.765	0.407	865.483	0.374	18	0.153	K.VGSSESALLAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1061.579	1062.199	-1530.326	0.373	696.849	0.354	18	0.146	K.VGSSESALLAK.L
R3/RRR3-15/2	1061.549	1062.199	-1559.320	0.401	602.332	0.378	16	0.146	K.VGSSESALLAK.L
R3/RRR3-15/2	1062.060	1062.199	-131.261	0.376	738.291	0.306	17	0.142	K.VGSSESALLAK.L
R3/RRR3-13/2	1063.109	1062.199	-85.065	0.406	722.998	0.305	16	0.141	K.VGSSESALLAK.L
R3/RRR3-15/2	1062.007	1062.199	-181.879	0.371	653.098	0.309	16	0.141	K.VGSSESALLAK.L
R3/RRR3-12/2	1541.450	1540.870	-272.730	0.463	676.495	0.413	14	0.140	K.GTVEIITPVELIKK.G
R3/RRR3-13/2	1412.120	1412.697	-1119.662	0.370	649.721	0.372	14	0.139	K.GTVEIITPVELIK.K
R3/RRR3-12/2	1061.364	1062.199	-1734.243	0.303	708.267	0.255	17	0.137	K.VGSSESALLAK.L
R3/RRR3-15/2	1412.238	1412.697	-325.946	0.279	587.882	0.229	14	0.130	K.GTVEIITPVELIK.K
R3/RRR3-16/2	1412.298	1412.697	-282.846	0.382	507.411	0.283	12	0.128	-.GTVEIITPVELIK.-
R3/RRR3-13/2	1541.547	1540.870	-209.967	0.304	576.594	0.195	14	0.126	K.GTVEIITPVELIKK.G
R3/RRR3-12/3	1744.087	1743.942	83.524	0.340	1116.970	0.369	34	0.111	K.FAVAAPVAADSGAAAPSAAK.E
R3/RRR3-12/3	1768.223	1768.131	52.021	0.478	1231.862	0.275	28	0.103	-.INKGTVEIITPVELIK.-
R3/RRR3-12/3	1768.313	1768.131	103.220	0.377	848.093	0.230	24	0.085	K.INKGTVEIITPVELIK.K
R3/RRR3-12/3	1769.322	1768.131	108.524	0.323	954.043	0.162	24	0.080	K.INKGTVEIITPVELIK.K
R3/RRR3-17/3	1806.316	1807.001	-935.514	0.561	3234.249	0.531	39	0.578	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-17/2	1806.296	1807.001	-946.566	0.579	3020.695	0.638	27	0.573	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-17/2	1806.412	1807.001	-882.251	0.563	2593.169	0.673	27	0.474	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-17/2	1806.469	1807.001	-850.503	0.598	2487.317	0.664	26	0.444	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-17/3	1806.924	1807.001	-42.873	0.582	2533.509	0.535	36	0.381	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-17/2	1498.300	1498.663	-243.321	0.536	1766.593	0.536	19	0.266	K.AFFEDYKEAHLK.L
R3/RRR3-17/3	1807.297	1807.001	164.031	0.556	2084.019	0.482	32	0.264	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-17/2	1506.283	1506.644	-240.162	0.492	1626.720	0.479	22	0.232	R.LAWHSAGTFDVSSK.T
R3/RRR3-17/2	1497.693	1498.663	-1319.414	0.474	1573.302	0.466	19	0.223	K.AFFEDYKEAHLK.L
R3/RRR3-17/2	1506.199	1506.644	-296.590	0.472	1336.939	0.491	20	0.201	R.LAWHSAGTFDVSSK.T
R3/RRR3-17/2	1499.133	1498.663	314.467	0.547	1151.643	0.526	17	0.191	K.AFFEDYKEAHLK.L
R3/RRR3-17/2	1506.170	1506.644	-315.861	0.492	1169.743	0.507	19	0.188	R.LAWHSAGTFDVSSK.T
R3/RRR3-17/2	1556.421	1556.831	-264.285	0.488	982.105	0.549	21	0.182	K.ALLSDPAFRPLVEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1008.945	1009.096	-150.428	0.453	1205.737	0.413	15	0.178	R.SGFEGPWTK.N
R3/RRR3-16/2	1100.029	1100.247	-199.189	0.509	1006.017	0.411	16	0.164	K.EGLLQLPSDK.A
R3/RRR3-17/2	1556.376	1556.831	-293.243	0.506	754.984	0.510	19	0.162	K.ALLSDPAFRPLVEK.Y
R3/RRR3-16/2	1099.987	1100.247	-236.930	0.430	900.922	0.418	15	0.159	K.EGLLQLPSDK.A
R3/RRR3-17/2	1556.376	1556.831	-293.007	0.454	690.965	0.504	19	0.158	K.ALLSDPAFRPLVEK.Y
R3/RRR3-17/2	1008.862	1009.096	-233.209	0.450	944.949	0.381	14	0.157	R.SGFEGPWTK.N
R3/RRR3-17/2	1008.963	1009.096	-132.830	0.441	901.251	0.394	14	0.157	R.SGFEGPWTK.N
R3/RRR3-17/2	1008.873	1009.096	-222.162	0.457	1000.616	0.343	14	0.154	R.SGFEGPWTK.N
R3/RRR3-17/2	1008.830	1009.096	-264.892	0.460	980.880	0.331	14	0.152	R.SGFEGPWTK.N
R3/RRR3-16/2	896.025	896.046	-24.133	0.352	633.279	0.474	12	0.151	K.TGGPFGTMK.T
R3/RRR3-16/2	1099.992	1100.247	-233.033	0.434	845.575	0.373	15	0.151	K.EGLLQLPSDK.A
R3/RRR3-16/2	896.386	896.046	380.317	0.285	687.812	0.480	12	0.150	K.TGGPFGTMK.T
R3/RRR3-17/2	1100.013	1100.247	-213.216	0.426	925.580	0.326	15	0.148	K.EGLLQLPSDK.A
R3/RRR3-17/2	911.842	912.046	-223.934	0.366	498.851	0.484	12	0.147	-.TGGPFGTM*K.-
R3/RRR3-17/2	1008.826	1009.096	-268.898	0.425	944.757	0.301	14	0.147	R.SGFEGPWTK.N
R3/RRR3-17/2	1100.018	1100.247	-208.763	0.333	755.748	0.355	14	0.143	-.EGLLQLPSDK.-
R3/RRR3-17/2	1099.503	1100.247	-1590.791	0.344	781.642	0.327	14	0.143	K.EGLLQLPSDK.A
R3/RRR3-17/2	911.878	912.046	-184.182	0.309	454.197	0.437	12	0.141	-.TGGPFGTM*K.-
R3/RRR3-17/2	911.473	912.046	-1730.381	0.266	483.406	0.356	12	0.138	K.TGGPFGTM*K.T
R3/RRR3-17/2	896.409	896.046	405.439	0.312	616.735	0.310	12	0.138	K.TGGPFGTMK.T
R3/RRR3-17/3	1807.443	1807.001	245.205	0.426	1339.875	0.332	28	0.123	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-16/3	1310.724	1310.441	215.993	0.523	875.111	0.472	26	0.119	R.LPDATKGSDHLR.Q
R3/RRR3-16/3	1310.428	1310.441	-10.578	0.415	744.928	0.412	25	0.105	R.LPDATKGSDHLR.Q
R3/RRR3-16/3	1310.276	1310.441	-126.776	0.427	638.727	0.346	23	0.095	-.LPDATKGSDHLR.-
R3/RRR3-15/3	1310.660	1310.441	167.381	0.421	710.593	0.303	24	0.095	R.LPDATKGSDHLR.Q
R3/RRR3-16/3	1311.168	1310.441	-209.518	0.359	978.985	0.297	27	0.094	R.LPDATKGSDHLR.Q
R3/RRR3-2/3	1808.440	1807.001	243.411	0.330	797.407	0.246	28	0.088	K.TPAELSHAANAGLDIAVR.M
R3/RRR3-8/3	1705.456	1705.914	-269.268	0.481	2516.701	0.354	32	0.295	R.DNGMHALIIYDDLSK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1726.534	1725.963	-249.166	0.527	1684.004	0.564	22	0.261	K.QIVVIYAAVNGFCDR.M
R3/RRR3-8/2	1704.877	1705.914	-1198.285	0.521	1562.300	0.529	21	0.233	R.DNGMHALIIYDDLSK.Q
R3/RRR3-8/2	1313.193	1312.580	-295.987	0.492	1651.949	0.348	19	0.204	K.AILSTINPELLK.S
R3/RRR3-8/2	1705.464	1705.914	-264.736	0.548	1266.702	0.530	18	0.198	R.DNGMHALIIYDDLSK.Q
R3/RRR3-8/2	1705.357	1705.914	-915.505	0.521	1202.610	0.510	18	0.188	R.DNGMHALIIYDDLSK.Q
R3/RRR3-8/2	1312.167	1312.580	-316.000	0.427	1485.041	0.320	18	0.182	K.AILSTINPELLK.S
R3/RRR3-8/2	1721.236	1721.913	-977.290	0.497	1088.902	0.517	19	0.182	R.DNGM*HALIIYDDLSK.Q
R3/RRR3-8/3	1440.483	1439.689	-143.026	0.488	1788.348	0.383	29	0.178	R.GIRPAINVGLSVSR.V
R3/RRR3-2/2	1313.012	1312.580	329.950	0.431	1568.959	0.256	18	0.177	K.AILSTINPELLK.S
R3/RRR3-8/2	1721.290	1721.913	-945.678	0.458	891.293	0.484	19	0.164	R.DNGM*HALIIYDDLSK.Q
R3/RRR3-8/2	1313.191	1312.580	-297.666	0.452	1175.220	0.355	16	0.162	K.AILSTINPELLK.S
R3/RRR3-8/2	1438.755	1439.689	-1347.764	0.462	733.897	0.477	18	0.155	R.GIRPAINVGLSVSR.V
R3/RRR3-8/2	1439.375	1439.689	-218.322	0.511	619.559	0.517	17	0.155	R.GIRPAINVGLSVSR.V
R3/RRR3-8/2	1721.326	1721.913	-924.888	0.474	725.111	0.475	17	0.153	R.DNGM*HALIIYDDLSK.Q
R3/RRR3-8/2	1538.219	1538.688	-305.937	0.431	503.110	0.510	17	0.153	R.EAFPGDVFYLHSR.L
R3/RRR3-8/2	1076.901	1077.298	-370.141	0.477	985.891	0.334	14	0.152	R.KIELDAFLK.Q
R3/RRR3-7/2	1313.225	1312.580	-271.180	0.424	1045.439	0.326	16	0.151	K.AILSTINPELLK.S
R3/RRR3-1/2	1313.051	1312.580	359.872	0.359	1126.362	0.283	16	0.150	-.AILSTINPELLK.-
R3/RRR3-2/2	1312.131	1312.580	-343.629	0.393	1256.358	0.216	17	0.150	-.AILSTINPELLK.-
R3/RRR3-8/2	1439.423	1439.689	-185.396	0.428	571.399	0.473	17	0.148	R.GIRPAINVGLSVSR.V
R3/RRR3-8/2	1705.299	1705.914	-949.424	0.427	1016.396	0.313	19	0.147	R.DNGMHALIIYDDLSK.Q
R3/RRR3-8/2	1538.347	1538.688	-222.343	0.311	601.937	0.445	19	0.147	R.EAFPGDVFYLHSR.L
R3/RRR3-8/2	1078.126	1077.298	-160.763	0.530	866.681	0.337	14	0.147	R.KIELDAFLK.Q
R3/RRR3-8/2	1538.198	1538.688	-319.553	0.310	557.293	0.447	18	0.146	R.EAFPGDVFYLHSR.L
R3/RRR3-8/2	1538.347	1538.688	-222.183	0.369	532.056	0.414	18	0.145	R.EAFPGDVFYLHSR.L
R3/RRR3-8/2	1539.190	1538.688	-324.597	0.318	412.621	0.426	17	0.143	R.EAFPGDVFYLHSR.L
R3/RRR3-8/2	1077.178	1077.298	-112.370	0.505	782.717	0.325	13	0.142	R.KIELDAFLK.Q
R3/RRR3-8/2	1301.216	1301.514	-230.211	0.176	1217.541	0.138	17	0.138	K.TAIAIDTILNQK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1538.541	1538.688	-95.544	0.299	386.679	0.370	13	0.136	R.EAFPGDVFYLHSR.L
R3/RRR3-7/2	1312.282	1312.580	-228.083	0.354	903.029	0.216	16	0.136	-.AILSTINPELLK.-
R3/RRR3-7/2	1312.107	1312.580	-361.738	0.252	1005.099	0.175	15	0.134	K.AILSTINPELLK.S
R3/RRR3-9/2	1302.397	1301.514	-90.588	0.185	856.595	0.215	14	0.130	K.TAIAIDTILNQK.Q
R3/RRR3-8/3	1439.668	1439.689	-14.476	0.476	1558.762	0.292	27	0.130	R.GIRPAINVGLSVSR.V
R3/RRR3-1/2	1300.985	1301.514	-1179.170	0.330	756.631	0.080	14	0.123	-.TAIAIDTILNQK.-
R3/RRR3-3/2	1301.506	1301.514	-6.737	0.372	1110.991	0.045	17	0.123	K.TAIAIDTILNQK.Q
R3/RRR3-8/3	1077.461	1077.298	150.995	0.489	1569.892	0.290	23	0.122	R.KIELDAFLK.Q
R3/RRR3-8/3	1077.354	1077.298	51.456	0.478	1508.069	0.312	23	0.121	R.KIELDAFLK.Q
R3/RRR3-8/3	1242.936	1243.415	-386.865	0.422	498.251	0.442	18	0.106	K.SVHEPM*QTGLK.A
R3/RRR3-8/3	1243.581	1243.415	133.768	0.450	672.070	0.398	20	0.104	K.SVHEPM*QTGLK.A
R3/RRR3-8/3	1354.995	1355.589	-1179.797	0.393	874.040	0.382	22	0.103	R.KSVHEPMQTGLK.A
R3/RRR3-8/3	1721.804	1721.913	-63.433	0.415	1313.282	0.247	29	0.103	R.DNGM*HALIIYDDLSK.Q
R3/RRR3-8/3	1227.929	1227.416	-397.665	0.439	966.557	0.353	23	0.099	-.SVHEPMQTGLK.-
R3/RRR3-8/3	1077.376	1077.298	71.741	0.492	1022.328	0.307	20	0.099	R.KIELDAFLK.Q
R3/RRR3-8/3	1243.359	1243.415	-45.674	0.400	748.559	0.343	21	0.098	K.SVHEPM*QTGLK.A
R3/RRR3-8/3	1721.361	1721.913	-904.642	0.412	1205.198	0.244	26	0.097	R.DNGM*HALIIYDDLSK.Q
R3/RRR3-8/3	1371.347	1371.588	-176.139	0.393	581.212	0.263	22	0.092	R.KSVHEPM*QTGLK.A
R3/RRR3-8/3	1354.978	1355.589	-1192.282	0.343	1074.455	0.243	25	0.090	R.KSVHEPMQTGLK.A
R3/RRR3-8/3	1705.340	1705.914	-925.286	0.408	1036.463	0.211	25	0.087	R.DNGMHALIIYDDLSK.Q
R3/RRR3-7/3	1439.484	1439.689	-142.317	0.408	1011.936	0.216	22	0.086	R.GIRPAINVGLSVSR.V
R3/RRR3-8/3	1244.081	1243.415	-269.789	0.370	437.621	0.360	18	0.082	-.SVHEPM*QTGLK.-
R3/RRR3-8/3	1227.567	1227.416	123.505	0.408	629.040	0.288	21	0.079	-.SVHEPMQTGLK.-
R3/RRR3-8/3	1226.237	1227.416	-1781.947	0.370	392.808	0.353	18	0.075	-.SVHEPMQTGLK.-
R3/RRR3-22/2	1838.498	1838.095	219.926	0.543	2206.380	0.597	26	0.831	K.ITLIGTSGISGSYVELRA.-
R3/RRR3-22/2	1837.199	1838.095	-1034.940	0.471	2004.881	0.645	26	0.692	K.ITLIGTSGISGSYVELRA.-
R3/RRR3-22/2	1837.684	1838.095	-224.502	0.507	1929.208	0.651	24	0.637	K.ITLIGTSGISGSYVELRA.-
R3/RRR3-22/2	1766.506	1767.017	-857.615	0.487	2451.501	0.570	27	0.403	K.ITLIGTSGISGSYVELR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1748.352	1748.918	-898.734	0.543	2323.895	0.545	25	0.366	K.ATDDKAGQEALLNVFR.A
R3/RRR3-22/2	1721.402	1721.929	-890.257	0.513	2432.987	0.477	25	0.366	R.AAEACEQFGGVLVTLR.M
R3/RRR3-22/2	1748.337	1748.918	-907.145	0.546	2269.454	0.524	25	0.348	K.ATDDKAGQEALLNVFR.A
R3/RRR3-22/2	1721.460	1721.929	-273.372	0.524	2305.651	0.486	25	0.343	R.AAEACEQFGGVLVTLR.M
R3/RRR3-22/2	1767.355	1767.017	192.201	0.545	2023.214	0.563	25	0.314	K.ITLIGTSGISGSYVELR.-
R3/RRR3-22/2	1722.193	1721.929	153.234	0.590	2087.289	0.488	24	0.301	R.AAEACEQFGGVLVTLR.M
R3/RRR3-22/2	1747.622	1748.918	-1318.202	0.535	1905.951	0.559	22	0.292	K.ATDDKAGQEALLNVFR.A
R3/RRR3-22/2	1766.313	1767.017	-967.438	0.452	1252.703	0.552	23	0.203	K.ITLIGTSGISGSYVELR.-
R3/RRR3-22/2	1218.018	1218.387	-303.534	0.475	1375.690	0.476	16	0.202	K.AGQEALLNVFR.A
R3/RRR3-22/3	1748.683	1748.918	-134.762	0.416	1899.226	0.358	30	0.191	K.ATDDKAGQEALLNVFR.A
R3/RRR3-22/2	1217.933	1218.387	-373.724	0.514	1379.103	0.409	16	0.189	K.AGQEALLNVFR.A
R3/RRR3-22/2	1218.130	1218.387	-212.041	0.401	1288.486	0.407	16	0.181	K.AGQEALLNVFR.A
R3/RRR3-22/2	1617.362	1617.740	-234.493	0.496	1192.851	0.414	20	0.175	K.YLESFGPEENYLR.K
R3/RRR3-22/2	1616.964	1617.740	-1101.469	0.459	1079.016	0.372	19	0.160	K.YLESFGPEENYLR.K
R3/RRR3-22/2	1617.176	1617.740	-969.892	0.504	948.845	0.386	18	0.154	K.YLESFGPEENYLR.K
R3/RRR3-22/2	1067.210	1067.128	77.255	0.416	910.737	0.386	15	0.153	R.CSGVGSEWGK.I
R3/RRR3-22/2	1654.462	1654.845	-232.269	0.405	394.567	0.539	18	0.146	K.HLPAISDPEIESAFK.D
R3/RRR3-22/2	1067.023	1067.128	-98.866	0.353	927.490	0.313	15	0.145	R.CSGVGSEWGK.I
R3/RRR3-22/3	1748.537	1748.918	-218.590	0.396	1157.246	0.322	25	0.107	K.ATDDKAGQEALLNVFR.A
R3/RRR3-22/3	1748.433	1748.918	-278.686	0.351	904.065	0.204	22	0.083	-.ATDDKAGQEALLNVFR.-
R3/RRR3-7/2	1272.111	1272.473	-285.238	0.359	1068.554	0.429	16	0.167	R.DLITILEDAIR.G
R3/RRR3-9/2	1703.105	1701.940	97.152	0.334	1010.963	0.415	20	0.157	K.AAVEEGIVVGGGCTLLR.L
R3/RRR3-8/2	1272.258	1272.473	-169.722	0.491	913.303	0.418	14	0.155	R.DLITILEDAIR.G
R3/RRR3-9/2	1702.925	1701.940	-8.528	0.392	909.315	0.364	20	0.146	K.AAVEEGIVVGGGCTLLR.L
R3/RRR3-7/2	1271.831	1272.473	-1294.573	0.217	457.342	0.279	12	0.130	-.DLITILEDAIR.-
R3/RRR3-16/1	1131.750	1132.377	-1441.867	0.304	775.817	0.494	14	0.956	K.SGLLLVTGPFK.I
R3/RRR3-16/2	1311.094	1311.466	-284.695	0.517	1831.365	0.577	20	0.287	R.VNQSYVIATSTK.V
R3/RRR3-17/2	1740.407	1740.890	-277.993	0.595	1827.753	0.545	23	0.277	K.KTEGELFETEKEATK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1740.301	1740.890	-915.555	0.575	1766.404	0.562	23	0.273	K.KTEGELFETEKEATK.N
R3/RRR3-16/2	1311.279	1311.466	-142.729	0.501	1729.096	0.584	19	0.273	R.VNQSYVIATSTK.V
R3/RRR3-16/2	1311.163	1311.466	-231.826	0.509	1808.961	0.522	19	0.268	R.VNQSYVIATSTK.V
R3/RRR3-19/2	1311.070	1311.466	-302.817	0.461	1718.819	0.557	20	0.264	R.VNQSYVIATSTK.V
R3/RRR3-19/2	1311.006	1311.466	-351.862	0.432	1678.130	0.567	19	0.259	R.VNQSYVIATSTK.V
R3/RRR3-16/2	1131.493	1132.377	-1670.039	0.421	1701.732	0.452	17	0.235	K.SGLLLVTGPFK.I
R3/RRR3-16/3	1211.405	1211.350	45.358	0.536	1996.784	0.385	27	0.207	K.AEKPDAAAAAAPK.F
R3/RRR3-17/2	1612.548	1612.717	-104.902	0.539	1265.912	0.534	20	0.203	K.TEGELFETEKEATK.N
R3/RRR3-16/3	1211.578	1211.350	189.204	0.518	1859.860	0.415	27	0.197	K.AEKPDAAAAAAPK.F
R3/RRR3-16/2	1059.904	1060.183	-263.795	0.486	1172.554	0.512	16	0.192	K.VDISGVNVEK.F
R3/RRR3-16/2	1059.994	1060.183	-179.222	0.483	1173.515	0.504	16	0.191	K.VDISGVNVEK.F
R3/RRR3-19/2	1060.018	1060.183	-156.810	0.453	1136.119	0.498	16	0.186	K.VDISGVNVEK.F
R3/RRR3-16/2	1131.468	1132.377	-1692.259	0.415	1258.715	0.441	15	0.183	K.SGLLLVTGPFK.I
R3/RRR3-16/2	1059.374	1060.183	-1712.652	0.363	1095.222	0.499	15	0.179	K.VDISGVNVEK.F
R3/RRR3-17/2	1613.026	1612.717	192.145	0.553	1107.610	0.479	19	0.177	K.TEGELFETEKEATK.N
R3/RRR3-16/3	1211.520	1211.350	140.856	0.528	1708.842	0.406	26	0.175	K.AEKPDAAAAAAPK.F
R3/RRR3-16/2	1131.425	1132.377	-1730.306	0.362	987.968	0.477	15	0.168	K.SGLLLVTGPFK.I
R3/RRR3-15/3	1210.832	1211.350	-1256.965	0.474	1555.997	0.446	27	0.167	K.AEKPDAAAAAAPK.F
R3/RRR3-16/2	1498.510	1498.793	-189.198	0.434	1043.024	0.431	21	0.166	R.SSITPGTVLILLAGR.F
R3/RRR3-16/3	1498.194	1498.793	-1070.423	0.381	1970.422	0.231	31	0.160	R.SSITPGTVLILLAGR.F
R3/RRR3-16/2	1211.020	1211.350	-273.340	0.436	652.224	0.537	19	0.160	K.AEKPDAAAAAAPK.F
R3/RRR3-16/2	1498.463	1498.793	-220.907	0.412	999.648	0.408	21	0.160	R.SSITPGTVLILLAGR.F
R3/RRR3-16/2	1498.370	1498.793	-283.186	0.420	934.625	0.428	20	0.158	R.SSITPGTVLILLAGR.F
R3/RRR3-19/2	1132.169	1132.377	-184.234	0.463	898.047	0.422	15	0.157	K.SGLLLVTGPFK.I
R3/RRR3-16/2	1210.772	1211.350	-1306.870	0.400	663.325	0.460	20	0.152	K.AEKPDAAAAAAPK.F
R3/RRR3-17/2	1208.086	1208.348	-217.452	0.418	460.694	0.485	15	0.151	K.FYPADDVKPR.Q
R3/RRR3-17/2	1208.066	1208.348	-233.469	0.363	408.940	0.525	14	0.150	K.FYPADDVKPR.Q
R3/RRR3-17/2	1207.952	1208.348	-328.768	0.380	473.205	0.459	15	0.148	K.FYPADDVKPR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1132.173	1132.377	-180.989	0.403	741.657	0.402	14	0.148	K.SGLLLVTGPFK.I
R3/RRR3-16/3	1498.642	1498.793	-101.079	0.396	1585.613	0.316	27	0.140	R.SSITPGTVLILLAGR.F
R3/RRR3-15/3	1211.487	1211.350	113.573	0.491	1179.135	0.412	22	0.126	K.AEKPDAAAAAAPK.F
R3/RRR3-16/3	1740.823	1740.890	-38.241	0.498	948.234	0.456	28	0.121	K.KTEGELFETEKEATK.N
R3/RRR3-16/3	1740.639	1740.890	-144.494	0.532	942.322	0.452	27	0.120	K.KTEGELFETEKEATK.N
R3/RRR3-17/3	1740.092	1740.890	-1036.203	0.476	986.992	0.413	28	0.115	K.KTEGELFETEKEATK.N
R3/RRR3-17/3	1740.403	1740.890	-280.323	0.543	898.586	0.432	27	0.114	K.KTEGELFETEKEATK.N
R3/RRR3-19/3	1741.851	1740.890	-22.122	0.501	838.062	0.433	26	0.113	K.KTEGELFETEKEATK.N
R3/RRR3-17/3	1740.793	1740.890	-55.966	0.484	790.416	0.439	26	0.112	K.KTEGELFETEKEATK.N
R3/RRR3-19/3	1740.434	1740.890	-262.379	0.499	693.960	0.445	25	0.110	K.KTEGELFETEKEATK.N
R3/RRR3-16/3	1740.562	1740.890	-188.922	0.468	978.587	0.378	28	0.109	K.KTEGELFETEKEATK.N
R3/RRR3-15/3	1740.146	1740.890	-1004.931	0.445	890.323	0.396	27	0.109	K.KTEGELFETEKEATK.N
R3/RRR3-19/3	1742.318	1740.890	246.675	0.469	738.958	0.390	26	0.104	K.KTEGELFETEKEATK.N
R3/RRR3-27/3	1210.876	1211.350	-392.800	0.465	926.845	0.346	23	0.102	K.AEKPDAAAAAAPK.F
R3/RRR3-21/3	1740.313	1740.890	-908.486	0.407	737.610	0.370	24	0.102	K.KTEGELFETEKEATK.N
R3/RRR3-16/3	1497.563	1498.793	-1493.599	0.341	1259.023	0.236	27	0.098	R.SSITPGTVLILLAGR.F
R3/RRR3-6/2	1581.211	1581.658	-283.526	0.503	2464.180	0.559	22	0.405	K.AVTTSATADGIEECR.K
R3/RRR3-6/2	1787.333	1787.948	-906.191	0.557	2480.846	0.548	25	0.404	K.CGVNTAEDWLNPAAIR.E
R3/RRR3-6/2	1662.338	1662.822	-292.080	0.475	1318.394	0.548	21	0.210	K.TDEFVIHSPTLTSSK.W
R3/RRR3-6/2	1369.844	1369.635	152.606	0.475	1032.904	0.521	18	0.181	R.LFPLLASAYAFR.F
R3/RRR3-6/2	1663.259	1662.822	263.340	0.519	1021.233	0.509	20	0.176	K.TDEFVIHSPTLTSSK.W
R3/RRR3-6/2	1187.979	1188.313	-281.837	0.477	1241.447	0.313	16	0.163	R.LTEEEANLLR.L
R3/RRR3-6/2	1128.993	1129.249	-227.372	0.436	622.623	0.551	17	0.162	R.QGALANEQLGK.L
R3/RRR3-6/2	1369.384	1369.635	-184.150	0.409	770.327	0.512	17	0.161	R.LFPLLASAYAFR.F
R3/RRR3-6/2	1187.988	1188.313	-274.002	0.540	1006.863	0.388	16	0.160	R.LTEEEANLLR.L
R3/RRR3-6/2	1369.180	1369.635	-333.424	0.278	1045.885	0.410	17	0.159	R.LFPLLASAYAFR.F
R3/RRR3-6/2	1128.917	1129.249	-294.521	0.406	505.700	0.573	16	0.158	R.QGALANEQLGK.L
R3/RRR3-6/2	1662.188	1662.822	-985.908	0.462	931.236	0.426	20	0.158	K.TDEFVIHSPTLTSSK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1128.239	1129.249	-1786.523	0.382	612.944	0.526	17	0.157	R.QGALANEQLGK.L
R3/RRR3-6/2	1864.163	1865.036	-1007.820	0.499	784.842	0.497	19	0.156	K.QFGPQTGGPETQVLNYK.T
R3/RRR3-6/2	1003.993	1004.164	-170.865	0.445	631.734	0.431	14	0.151	R.LVASDPVFR.K
R3/RRR3-6/2	1865.581	1865.036	-244.640	0.529	526.742	0.516	18	0.148	K.QFGPQTGGPETQVLNYK.T
R3/RRR3-6/2	1188.048	1188.313	-223.490	0.505	904.666	0.326	16	0.147	R.LTEEEANLLR.L
R3/RRR3-6/2	1004.071	1004.164	-93.176	0.402	524.061	0.362	14	0.144	R.LVASDPVFR.K
R3/RRR3-6/3	1893.053	1893.087	-18.479	0.449	1349.854	0.414	29	0.141	R.SLEDHSPLPGVTLGDIGGK.F
R3/RRR3-6/2	1003.505	1004.164	-1658.847	0.312	425.296	0.352	12	0.139	R.LVASDPVFR.K
R3/RRR3-6/3	1894.211	1893.087	65.657	0.215	801.701	0.139	25	0.075	R.SLEDHSPLPGVTLGDIGGK.F
R3/RRR3-15/2	1264.239	1264.456	-172.251	0.489	2123.247	0.571	19	0.329	R.LQAALSTGLFSR.I
R3/RRR3-16/2	1608.858	1609.806	-1214.170	0.465	2105.436	0.446	23	0.290	K.LDISGHTVSAVGPDIK.H
R3/RRR3-23/2	1265.046	1264.456	-325.157	0.471	1782.666	0.581	20	0.276	R.LQAALSTGLFSR.I
R3/RRR3-13/2	1312.518	1312.497	15.988	0.473	1764.858	0.562	20	0.267	R.VLVGVVASPEADR.D
R3/RRR3-16/2	1263.674	1264.456	-1414.547	0.521	1701.541	0.581	19	0.264	R.LQAALSTGLFSR.I
R3/RRR3-25/2	1263.806	1264.456	-1309.673	0.472	1647.588	0.576	19	0.255	R.LQAALSTGLFSR.I
R3/RRR3-15/2	1263.526	1264.456	-1532.253	0.478	1642.461	0.570	19	0.253	R.LQAALSTGLFSR.I
R3/RRR3-25/2	1265.458	1264.456	1.586	0.453	1695.163	0.540	19	0.252	R.LQAALSTGLFSR.I
R3/RRR3-24/2	1263.734	1264.456	-1366.327	0.411	1624.363	0.556	19	0.246	R.LQAALSTGLFSR.I
R3/RRR3-16/2	1264.294	1264.456	-128.471	0.553	1593.382	0.562	19	0.245	R.LQAALSTGLFSR.I
R3/RRR3-14/2	1264.186	1264.456	-213.807	0.508	1614.442	0.543	19	0.243	R.LQAALSTGLFSR.I
R3/RRR3-24/2	1264.146	1264.456	-245.679	0.453	1503.939	0.607	18	0.243	R.LQAALSTGLFSR.I
R3/RRR3-16/2	1264.097	1264.456	-285.012	0.514	1625.579	0.533	19	0.242	R.LQAALSTGLFSR.I
R3/RRR3-15/2	1609.408	1609.806	-247.748	0.509	1640.611	0.532	21	0.242	K.LDISGHTVSAVGPDIK.H
R3/RRR3-16/2	1609.337	1609.806	-292.037	0.459	1614.729	0.534	21	0.239	K.LDISGHTVSAVGPDIK.H
R3/RRR3-1/2	1264.099	1264.456	-283.171	0.394	1642.633	0.517	19	0.239	R.LQAALSTGLFSR.I
R3/RRR3-25/2	1264.144	1264.456	-247.616	0.518	1547.282	0.552	19	0.237	R.LQAALSTGLFSR.I
R3/RRR3-15/2	1608.846	1609.806	-1221.865	0.421	1733.840	0.455	21	0.236	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/2	1264.166	1264.456	-230.082	0.424	1584.022	0.533	18	0.235	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1312.263	1312.497	-178.917	0.516	1543.873	0.551	20	0.235	R.VLVGVVASPEADR.D
R3/RRR3-19/2	1313.324	1312.497	-132.159	0.495	1473.330	0.575	19	0.231	R.VLVGVVASPEADR.D
R3/RRR3-16/2	1312.070	1312.497	-326.381	0.484	1462.655	0.573	20	0.230	R.VLVGVVASPEADR.D
R3/RRR3-23/2	1264.161	1264.456	-233.763	0.443	1451.081	0.578	18	0.229	R.LQAALSTGLFSR.I
R3/RRR3-20/2	1313.107	1312.497	-297.778	0.473	1494.771	0.548	19	0.228	R.VLVGVVASPEADR.D
R3/RRR3-15/2	1313.160	1312.497	-257.301	0.540	1438.656	0.569	19	0.226	R.VLVGVVASPEADR.D
R3/RRR3-22/2	1312.157	1312.497	-259.737	0.457	1521.617	0.509	19	0.222	R.VLVGVVASPEADR.D
R3/RRR3-26/2	1312.152	1312.497	-263.750	0.474	1458.877	0.538	19	0.221	R.VLVGVVASPEADR.D
R3/RRR3-26/2	1264.157	1264.456	-236.960	0.420	1381.487	0.575	18	0.220	R.LQAALSTGLFSR.I
R3/RRR3-23/2	1264.576	1264.456	95.212	0.494	1456.336	0.530	18	0.220	R.LQAALSTGLFSR.I
R3/RRR3-16/2	1311.708	1312.497	-1368.347	0.416	1538.858	0.490	20	0.220	R.VLVGVVASPEADR.D
R3/RRR3-16/2	1609.455	1609.806	-218.301	0.466	1441.589	0.536	22	0.219	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/2	1264.086	1264.456	-293.344	0.504	1423.959	0.536	19	0.219	R.LQAALSTGLFSR.I
R3/RRR3-1/2	1264.289	1264.456	-132.346	0.472	1648.918	0.424	19	0.219	R.LQAALSTGLFSR.I
R3/RRR3-24/2	1263.523	1264.456	-1534.485	0.418	1577.901	0.463	18	0.219	R.LQAALSTGLFSR.I
R3/RRR3-12/2	1313.147	1312.497	-267.839	0.524	1383.023	0.562	19	0.218	R.VLVGVVASPEADR.D
R3/RRR3-15/2	1312.071	1312.497	-326.008	0.471	1463.759	0.519	19	0.217	R.VLVGVVASPEADR.D
R3/RRR3-16/2	1312.069	1312.497	-327.501	0.486	1340.070	0.577	19	0.217	R.VLVGVVASPEADR.D
R3/RRR3-24/2	1312.323	1312.497	-133.193	0.415	1436.443	0.528	20	0.216	R.VLVGVVASPEADR.D
R3/RRR3-13/2	1312.201	1312.497	-226.138	0.496	1386.724	0.545	20	0.216	R.VLVGVVASPEADR.D
R3/RRR3-20/2	1312.422	1312.497	-57.804	0.458	1464.611	0.511	19	0.216	R.VLVGVVASPEADR.D
R3/RRR3-27/2	1312.184	1312.497	-239.017	0.432	1457.110	0.513	19	0.215	R.VLVGVVASPEADR.D
R3/RRR3-26/2	1264.045	1264.456	-325.802	0.465	1304.839	0.574	18	0.213	R.LQAALSTGLFSR.I
R3/RRR3-23/2	1312.063	1312.497	-331.795	0.482	1345.083	0.553	19	0.212	R.VLVGVVASPEADR.D
R3/RRR3-24/2	1609.403	1609.806	-251.249	0.418	1526.843	0.460	22	0.212	K.LDISGHTVSAVGPDIK.H
R3/RRR3-20/2	1313.017	1312.497	-366.896	0.492	1290.154	0.569	19	0.210	R.VLVGVVASPEADR.D
R3/RRR3-25/2	1312.088	1312.497	-313.126	0.467	1266.991	0.580	19	0.210	R.VLVGVVASPEADR.D
R3/RRR3-14/2	1311.413	1312.497	-1593.844	0.351	1355.919	0.551	19	0.210	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1312.110	1312.497	-295.765	0.394	1277.848	0.580	19	0.209	R.VLVGVVASPEADR.D
R3/RRR3-23/2	1313.261	1312.497	-180.272	0.490	1258.512	0.572	19	0.208	R.VLVGVVASPEADR.D
R3/RRR3-14/2	1312.015	1312.497	-368.389	0.404	1347.569	0.535	19	0.208	R.VLVGVVASPEADR.D
R3/RRR3-24/2	1312.177	1312.497	-244.804	0.438	1300.182	0.554	19	0.207	R.VLVGVVASPEADR.D
R3/RRR3-26/2	1311.777	1312.497	-1315.073	0.378	1450.520	0.480	19	0.207	R.VLVGVVASPEADR.D
R3/RRR3-25/2	1311.572	1312.497	-1471.921	0.382	1487.853	0.460	19	0.207	R.VLVGVVASPEADR.D
R3/RRR3-25/2	1312.364	1312.497	-102.028	0.445	1430.476	0.483	19	0.206	R.VLVGVVASPEADR.D
R3/RRR3-2/2	1264.401	1264.456	-43.731	0.436	1451.343	0.463	19	0.206	R.LQAALSTGLFSR.I
R3/RRR3-15/2	1312.040	1312.497	-349.625	0.460	1352.291	0.515	19	0.205	R.VLVGVVASPEADR.D
R3/RRR3-26/2	1311.934	1312.497	-1194.713	0.431	1388.704	0.498	19	0.205	R.VLVGVVASPEADR.D
R3/RRR3-15/2	1048.878	1049.270	-374.672	0.514	1554.022	0.402	17	0.205	R.LGVM*LTATAR.C
R3/RRR3-15/2	1610.181	1609.806	233.850	0.469	1376.752	0.497	22	0.204	K.LDISGHTVSAVGPDIK.H
R3/RRR3-2/2	1312.349	1312.497	-113.505	0.475	1276.851	0.542	19	0.204	R.VLVGVVASPEADR.D
R3/RRR3-15/2	1109.977	1110.271	-265.462	0.459	1296.888	0.515	15	0.203	K.WMAAYPQSR.V
R3/RRR3-23/2	1312.108	1312.497	-297.818	0.462	1234.312	0.561	19	0.203	R.VLVGVVASPEADR.D
R3/RRR3-22/2	1313.193	1312.497	-232.494	0.478	1268.841	0.537	19	0.202	R.VLVGVVASPEADR.D
R3/RRR3-24/2	1312.244	1312.497	-193.568	0.463	1306.996	0.513	19	0.201	R.VLVGVVASPEADR.D
R3/RRR3-27/2	1312.283	1312.497	-164.079	0.477	1246.881	0.536	19	0.200	R.VLVGVVASPEADR.D
R3/RRR3-22/2	1312.201	1312.497	-226.325	0.478	1315.864	0.501	19	0.199	R.VLVGVVASPEADR.D
R3/RRR3-25/2	1610.330	1609.806	-296.039	0.475	1375.060	0.470	21	0.198	K.LDISGHTVSAVGPDIK.H
R3/RRR3-19/2	1312.326	1312.497	-131.046	0.399	1213.192	0.546	19	0.197	R.VLVGVVASPEADR.D
R3/RRR3-17/2	1264.518	1264.456	49.128	0.468	1191.243	0.547	17	0.197	R.LQAALSTGLFSR.I
R3/RRR3-14/2	1265.190	1264.456	-211.025	0.459	1320.506	0.473	18	0.195	R.LQAALSTGLFSR.I
R3/RRR3-26/2	1049.149	1049.270	-115.733	0.457	1449.859	0.405	16	0.195	R.LGVM*LTATAR.C
R3/RRR3-24/2	1049.096	1049.270	-166.506	0.478	1397.246	0.425	16	0.194	R.LGVM*LTATAR.C
R3/RRR3-1/2	1312.289	1312.497	-158.760	0.464	1182.344	0.539	18	0.194	R.VLVGVVASPEADR.D
R3/RRR3-14/2	1049.085	1049.270	-176.895	0.447	1477.128	0.378	16	0.192	R.LGVM*LTATAR.C
R3/RRR3-17/2	1312.152	1312.497	-263.843	0.399	1301.688	0.474	19	0.192	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1312.271	1312.497	-173.131	0.431	1216.436	0.514	18	0.192	R.VLVGVVASPEADR.D
R3/RRR3-16/2	1049.090	1049.270	-171.992	0.491	1402.694	0.397	16	0.189	R.LGVM*LTATAR.C
R3/RRR3-18/2	1312.277	1312.497	-168.372	0.441	1188.812	0.505	18	0.188	R.VLVGVVASPEADR.D
R3/RRR3-15/2	1311.677	1312.497	-1392.089	0.365	1255.583	0.476	19	0.188	R.VLVGVVASPEADR.D
R3/RRR3-24/2	1048.843	1049.270	-408.655	0.403	1371.186	0.392	16	0.185	R.LGVM*LTATAR.C
R3/RRR3-26/2	1049.152	1049.270	-112.815	0.444	1326.435	0.409	16	0.185	R.LGVM*LTATAR.C
R3/RRR3-25/2	1610.445	1609.806	-224.401	0.479	1147.112	0.501	20	0.183	K.LDISGHTVSAVGPDIK.H
R3/RRR3-15/2	1109.782	1110.271	-441.918	0.454	1249.396	0.421	15	0.182	K.WMAAYPQSR.V
R3/RRR3-25/2	1049.029	1049.270	-230.476	0.435	1310.664	0.397	16	0.182	R.LGVM*LTATAR.C
R3/RRR3-27/2	1312.249	1312.497	-189.368	0.460	1007.832	0.550	17	0.181	R.VLVGVVASPEADR.D
R3/RRR3-14/2	1312.161	1312.497	-257.310	0.419	992.003	0.527	17	0.176	R.VLVGVVASPEADR.D
R3/RRR3-16/2	1049.072	1049.270	-189.619	0.456	1334.275	0.355	16	0.176	R.LGVM*LTATAR.C
R3/RRR3-24/2	1048.949	1049.270	-306.714	0.492	1313.055	0.352	16	0.173	R.LGVM*LTATAR.C
R3/RRR3-25/2	1033.142	1033.271	-124.625	0.504	1111.893	0.426	15	0.171	R.LGVMLTATAR.C
R3/RRR3-16/2	1049.045	1049.270	-215.300	0.485	1186.360	0.394	15	0.171	R.LGVM*LTATAR.C
R3/RRR3-25/2	1110.042	1110.271	-206.547	0.414	1124.716	0.405	15	0.170	K.WMAAYPQSR.V
R3/RRR3-15/2	1032.556	1033.271	-1665.712	0.445	1082.490	0.415	16	0.169	R.LGVMLTATAR.C
R3/RRR3-16/2	1110.023	1110.271	-223.427	0.342	1128.861	0.405	15	0.169	K.WMAAYPQSR.V
R3/RRR3-15/2	1110.039	1110.271	-209.415	0.448	1000.646	0.433	15	0.168	K.WMAAYPQSR.V
R3/RRR3-16/2	1126.079	1126.270	-170.344	0.496	962.589	0.441	15	0.168	K.WM*AAYPQSR.V
R3/RRR3-25/2	1610.184	1609.806	235.978	0.443	1055.595	0.440	21	0.167	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/2	1125.854	1126.270	-370.696	0.413	935.652	0.459	15	0.167	K.WM*AAYPQSR.V
R3/RRR3-1/2	1263.977	1264.456	-380.259	0.413	976.618	0.477	16	0.167	-.LQAALSTGLFSR.-
R3/RRR3-1/2	1312.053	1312.497	-339.917	0.331	1074.056	0.440	16	0.166	R.VLVGVVASPEADR.D
R3/RRR3-13/2	1311.826	1312.497	-1277.597	0.366	1126.561	0.403	17	0.166	R.VLVGVVASPEADR.D
R3/RRR3-12/2	1263.647	1264.456	-1435.505	0.395	1027.166	0.439	16	0.166	R.LQAALSTGLFSR.I
R3/RRR3-14/2	1263.530	1264.456	-1528.371	0.419	1012.978	0.436	17	0.166	R.LQAALSTGLFSR.I
R3/RRR3-2/2	1311.539	1312.497	-1497.164	0.292	1058.836	0.440	16	0.164	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1109.907	1110.271	-328.798	0.297	1001.374	0.441	14	0.163	K.WMAAYPQSR.V
R3/RRR3-25/2	1109.939	1110.271	-299.667	0.417	826.544	0.469	14	0.163	K.WMAAYPQSR.V
R3/RRR3-15/2	1125.986	1126.270	-253.434	0.443	843.999	0.465	13	0.163	K.WM*AAYPQSR.V
R3/RRR3-25/2	1109.832	1110.271	-396.226	0.386	1070.104	0.371	15	0.162	K.WMAAYPQSR.V
R3/RRR3-25/2	1125.451	1126.270	-1621.466	0.401	686.112	0.517	13	0.162	K.WM*AAYPQSR.V
R3/RRR3-25/2	1125.556	1126.270	-1527.111	0.413	777.071	0.466	14	0.161	K.WM*AAYPQSR.V
R3/RRR3-14/2	1048.911	1049.270	-343.377	0.438	1104.823	0.352	15	0.160	R.LGVM*LTATAR.C
R3/RRR3-18/2	1312.288	1312.497	-159.880	0.365	947.755	0.430	16	0.159	R.VLVGVVASPEADR.D
R3/RRR3-25/2	1126.936	1126.270	-297.004	0.439	742.545	0.443	15	0.159	K.WM*AAYPQSR.V
R3/RRR3-15/2	1032.697	1033.271	-1528.429	0.442	969.843	0.382	15	0.158	R.LGVMLTATAR.C
R3/RRR3-23/2	1610.420	1609.806	-239.990	0.449	933.540	0.424	20	0.158	K.LDISGHTVSAVGPDIK.H
R3/RRR3-2/2	1111.226	1110.271	-40.724	0.328	984.516	0.378	13	0.156	K.WMAAYPQSR.V
R3/RRR3-22/2	1133.908	1133.194	-253.057	0.501	736.737	0.415	16	0.155	R.NTDQLEGSLR.E
R3/RRR3-15/2	1125.966	1126.270	-270.510	0.420	790.574	0.412	14	0.155	K.WM*AAYPQSR.V
R3/RRR3-13/2	1134.070	1133.194	-110.187	0.479	629.923	0.439	15	0.155	R.NTDQLEGSLR.E
R3/RRR3-25/2	1033.088	1033.271	-177.134	0.458	965.599	0.360	15	0.154	R.LGVMLTATAR.C
R3/RRR3-16/2	1032.557	1033.271	-1664.762	0.351	839.776	0.400	15	0.154	R.LGVMLTATAR.C
R3/RRR3-20/2	1132.885	1133.194	-273.604	0.436	793.991	0.384	16	0.153	R.NTDQLEGSLR.E
R3/RRR3-1/2	1133.026	1133.194	-149.299	0.466	640.083	0.419	15	0.153	R.NTDQLEGSLR.E
R3/RRR3-26/2	1132.935	1133.194	-229.715	0.488	717.741	0.394	16	0.153	R.NTDQLEGSLR.E
R3/RRR3-16/2	1125.947	1126.270	-287.587	0.367	708.223	0.431	13	0.153	K.WM*AAYPQSR.V
R3/RRR3-16/2	1032.907	1033.271	-353.428	0.390	874.429	0.382	14	0.153	R.LGVMLTATAR.C
R3/RRR3-24/2	1608.673	1609.806	-1329.540	0.401	957.954	0.367	21	0.152	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/2	921.393	922.014	-1764.621	0.382	777.252	0.377	12	0.152	R.CVFPDQR.L
R3/RRR3-21/2	1133.042	1133.194	-135.033	0.446	757.848	0.370	16	0.151	R.NTDQLEGSLR.E
R3/RRR3-21/2	1311.978	1312.497	-1161.637	0.316	648.593	0.442	19	0.151	R.VLVGVVASPEADR.D
R3/RRR3-18/2	1132.451	1133.194	-1543.535	0.402	779.887	0.361	16	0.150	R.NTDQLEGSLR.E
R3/RRR3-12/2	1133.781	1133.194	-365.719	0.412	646.930	0.393	15	0.150	R.NTDQLEGSLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-26/2	921.879	922.014	-147.104	0.429	756.851	0.349	12	0.150	R.CVFPDQR.L
R3/RRR3-19/2	1132.983	1133.194	-187.344	0.479	730.518	0.362	16	0.150	R.NTDQLEGSLR.E
R3/RRR3-17/2	1311.819	1312.497	-1283.298	0.316	1111.564	0.289	16	0.149	R.VLVGVVASPEADR.D
R3/RRR3-23/3	1609.825	1609.806	11.924	0.418	1229.206	0.495	29	0.149	K.LDISGHTVSAVGPDIK.H
R3/RRR3-3/2	1312.272	1312.497	-172.104	0.367	812.653	0.409	14	0.149	R.VLVGVVASPEADR.D
R3/RRR3-24/2	1132.602	1133.194	-1409.824	0.398	733.807	0.353	16	0.149	R.NTDQLEGSLR.E
R3/RRR3-1/2	1133.169	1133.194	-22.756	0.414	732.364	0.352	16	0.149	R.NTDQLEGSLR.E
R3/RRR3-15/2	1132.584	1133.194	-1425.737	0.434	751.821	0.339	16	0.148	R.NTDQLEGSLR.E
R3/RRR3-3/2	1134.054	1133.194	-124.440	0.422	725.345	0.342	16	0.148	R.NTDQLEGSLR.E
R3/RRR3-19/2	1133.001	1133.194	-171.131	0.454	699.459	0.341	16	0.147	R.NTDQLEGSLR.E
R3/RRR3-20/2	1133.049	1133.194	-128.332	0.420	760.058	0.328	16	0.147	R.NTDQLEGSLR.E
R3/RRR3-25/2	1033.075	1033.271	-190.410	0.479	735.445	0.445	13	0.147	-.LGVMLTATAR.-
R3/RRR3-2/2	1311.483	1312.497	-1540.453	0.297	661.797	0.432	15	0.146	R.VLVGVVASPEADR.D
R3/RRR3-27/2	1132.890	1133.194	-269.496	0.517	682.489	0.350	15	0.146	R.NTDQLEGSLR.E
R3/RRR3-15/2	1133.069	1133.194	-110.501	0.418	685.278	0.340	15	0.146	R.NTDQLEGSLR.E
R3/RRR3-21/2	1132.950	1133.194	-215.987	0.499	732.324	0.329	16	0.146	R.NTDQLEGSLR.E
R3/RRR3-2/2	1132.347	1133.194	-1636.234	0.351	760.991	0.327	16	0.146	R.NTDQLEGSLR.E
R3/RRR3-20/2	1132.777	1133.194	-369.177	0.398	649.441	0.343	15	0.146	R.NTDQLEGSLR.E
R3/RRR3-22/2	1132.391	1133.194	-1596.921	0.319	574.553	0.365	15	0.145	R.NTDQLEGSLR.E
R3/RRR3-23/2	1048.841	1049.270	-410.173	0.339	723.539	0.367	13	0.145	R.LGVM*LTATAR.C
R3/RRR3-1/2	1132.397	1133.194	-1591.723	0.390	666.714	0.335	15	0.145	R.NTDQLEGSLR.E
R3/RRR3-27/2	1132.597	1133.194	-1414.370	0.459	714.838	0.331	15	0.145	R.NTDQLEGSLR.E
R3/RRR3-25/2	1132.900	1133.194	-260.631	0.427	762.641	0.305	16	0.145	R.NTDQLEGSLR.E
R3/RRR3-15/2	1264.019	1264.456	-346.635	0.331	448.670	0.416	14	0.145	R.LQAALSTGLFSR.I
R3/RRR3-15/2	1263.435	1264.456	-1604.560	0.310	428.115	0.429	14	0.145	R.LQAALSTGLFSR.I
R3/RRR3-25/2	1126.458	1126.270	167.309	0.273	401.454	0.383	14	0.145	K.WM*AAYPQSR.V
R3/RRR3-15/2	1125.395	1126.270	-1670.938	0.344	654.792	0.346	13	0.144	K.WM*AAYPQSR.V
R3/RRR3-26/2	1133.097	1133.194	-85.861	0.474	733.755	0.309	16	0.144	R.NTDQLEGSLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-27/2	1132.445	1133.194	-1549.166	0.454	791.226	0.299	16	0.144	R.NTDQLEGSLR.E
R3/RRR3-15/2	1133.030	1133.194	-145.624	0.413	688.937	0.295	16	0.143	R.NTDQLEGSLR.E
R3/RRR3-26/2	1048.370	1049.270	-1818.231	0.307	695.963	0.330	14	0.143	R.LGVM*LTATAR.C
R3/RRR3-16/2	921.274	922.014	-1894.559	0.385	583.460	0.312	10	0.142	R.CVFPDQR.L
R3/RRR3-16/2	921.772	922.014	-262.681	0.354	523.121	0.311	10	0.142	R.CVFPDQR.L
R3/RRR3-2/2	1133.090	1133.194	-92.669	0.421	639.693	0.292	15	0.142	R.NTDQLEGSLR.E
R3/RRR3-22/2	1132.952	1133.194	-214.798	0.369	759.280	0.275	16	0.142	R.NTDQLEGSLR.E
R3/RRR3-25/2	921.848	922.014	-180.047	0.327	711.557	0.286	12	0.142	R.CVFPDQR.L
R3/RRR3-26/2	1132.484	1133.194	-1515.057	0.352	681.619	0.279	16	0.142	R.NTDQLEGSLR.E
R3/RRR3-15/2	1264.063	1264.456	-311.365	0.279	298.992	0.323	13	0.142	R.LQAALSTGLFSR.I
R3/RRR3-25/2	1133.150	1133.194	-39.180	0.442	633.277	0.288	15	0.142	R.NTDQLEGSLR.E
R3/RRR3-17/2	1132.921	1133.194	-241.606	0.343	574.390	0.278	15	0.141	R.NTDQLEGSLR.E
R3/RRR3-23/2	1132.995	1133.194	-176.103	0.492	723.699	0.295	15	0.141	R.NTDQLEGSLR.E
R3/RRR3-24/2	1132.714	1133.194	-425.189	0.357	778.707	0.264	16	0.141	R.NTDQLEGSLR.E
R3/RRR3-21/2	1132.944	1133.194	-221.716	0.456	532.066	0.289	14	0.141	R.NTDQLEGSLR.E
R3/RRR3-16/2	921.836	922.014	-193.331	0.435	548.828	0.286	10	0.141	R.CVFPDQR.L
R3/RRR3-21/2	1126.095	1126.270	-155.555	0.301	378.120	0.285	11	0.141	K.WM*AAYPQSR.V
R3/RRR3-25/2	921.237	922.014	-1934.373	0.344	630.280	0.276	11	0.141	R.CVFPDQR.L
R3/RRR3-1/2	1049.083	1049.270	-178.879	0.315	726.477	0.289	14	0.140	R.LGVM*LTATAR.C
R3/RRR3-15/2	921.334	922.014	-1828.787	0.270	559.599	0.322	10	0.140	R.CVFPDQR.L
R3/RRR3-24/2	1132.650	1133.194	-1367.390	0.392	770.865	0.244	16	0.140	R.NTDQLEGSLR.E
R3/RRR3-24/2	921.843	922.014	-185.759	0.264	503.543	0.289	10	0.139	R.CVFPDQR.L
R3/RRR3-15/2	922.013	922.014	-1.276	0.292	651.077	0.264	11	0.139	R.CVFPDQR.L
R3/RRR3-25/2	1126.069	1126.270	-179.262	0.365	587.112	0.217	14	0.138	K.WM*AAYPQSR.V
R3/RRR3-15/2	921.896	922.014	-128.508	0.354	678.103	0.232	11	0.138	R.CVFPDQR.L
R3/RRR3-1/2	1610.284	1609.806	297.703	0.407	442.093	0.398	14	0.138	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/2	1312.332	1312.497	-126.101	0.341	546.340	0.284	15	0.138	R.VLVGVVASPEADR.D
R3/RRR3-3/2	1311.958	1312.497	-1176.773	0.260	726.810	0.298	15	0.138	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1311.930	1312.497	-1198.357	0.289	651.328	0.258	17	0.137	R.VLVGVVASPEADR.D
R3/RRR3-1/2	1610.236	1609.806	268.210	0.361	533.009	0.343	16	0.137	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/3	1910.586	1911.131	-811.179	0.460	932.511	0.544	25	0.137	R.REELEKWM*AAYPQSR.V
R3/RRR3-23/2	1132.389	1133.194	-1598.546	0.368	766.370	0.215	15	0.137	R.NTDQLEGSLR.E
R3/RRR3-24/2	921.547	922.014	-507.605	0.248	420.510	0.301	9	0.137	-.CVFPDQR.-
R3/RRR3-24/2	921.856	922.014	-171.280	0.318	335.330	0.349	8	0.137	-.CVFPDQR.-
R3/RRR3-15/2	1032.413	1033.271	-1804.814	0.318	613.905	0.202	14	0.136	R.LGVMLTATAR.C
R3/RRR3-24/3	1609.617	1609.806	-117.348	0.484	922.169	0.541	28	0.135	K.LDISGHTVSAVGPDIK.H
R3/RRR3-19/2	1132.520	1133.194	-1482.792	0.360	769.073	0.174	16	0.135	R.NTDQLEGSLR.E
R3/RRR3-2/2	1132.289	1133.194	-1687.247	0.284	808.707	0.169	16	0.135	R.NTDQLEGSLR.E
R3/RRR3-16/3	1610.590	1609.806	-134.077	0.478	998.850	0.510	28	0.134	K.LDISGHTVSAVGPDIK.H
R3/RRR3-1/2	921.692	922.014	-350.510	0.372	478.234	0.243	9	0.134	-.CVFPDQR.-
R3/RRR3-15/3	1911.099	1911.131	-16.670	0.445	837.799	0.546	24	0.131	R.REELEKWM*AAYPQSR.V
R3/RRR3-1/2	1048.774	1049.270	-474.641	0.323	655.285	0.248	13	0.131	-.LGVM*LTATAR.-
R3/RRR3-23/2	1132.457	1133.194	-1538.229	0.298	696.769	0.093	14	0.131	R.NTDQLEGSLR.E
R3/RRR3-16/3	1910.476	1911.131	-868.711	0.426	759.221	0.566	23	0.130	R.REELEKWM*AAYPQSR.V
R3/RRR3-15/3	1910.818	1911.131	-164.302	0.529	748.745	0.562	23	0.130	R.REELEKWM*AAYPQSR.V
R3/RRR3-24/3	1609.600	1609.806	-128.303	0.481	915.551	0.496	29	0.126	K.LDISGHTVSAVGPDIK.H
R3/RRR3-16/3	1609.912	1609.806	66.338	0.451	863.680	0.506	27	0.126	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/3	1910.469	1911.131	-872.848	0.469	707.276	0.549	23	0.125	R.REELEKWM*AAYPQSR.V
R3/RRR3-25/3	1911.860	1911.131	-142.439	0.449	925.769	0.485	25	0.125	R.REELEKWM*AAYPQSR.V
R3/RRR3-16/3	1910.178	1911.131	-1025.756	0.477	734.470	0.534	22	0.124	R.REELEKWM*AAYPQSR.V
R3/RRR3-24/3	1610.043	1609.806	147.892	0.455	810.726	0.492	27	0.121	K.LDISGHTVSAVGPDIK.H
R3/RRR3-16/3	1910.726	1911.131	-212.561	0.341	803.043	0.494	23	0.120	R.REELEKWM*AAYPQSR.V
R3/RRR3-15/3	1610.686	1609.806	-74.322	0.471	693.242	0.515	26	0.120	K.LDISGHTVSAVGPDIK.H
R3/RRR3-14/3	1610.418	1609.806	-241.177	0.457	832.064	0.476	27	0.119	K.LDISGHTVSAVGPDIK.H
R3/RRR3-25/3	1910.512	1911.131	-850.238	0.371	1085.927	0.399	27	0.118	R.REELEKWM*AAYPQSR.V
R3/RRR3-25/3	1910.392	1911.131	-913.164	0.401	757.366	0.492	24	0.118	R.REELEKWM*AAYPQSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/3	1910.678	1911.131	-237.750	0.449	996.377	0.411	25	0.116	R.REELEKWM*AAYPQSR.V
R3/RRR3-16/3	1609.927	1609.806	75.806	0.488	680.854	0.481	26	0.115	K.LDISGHTVSAVGPDIK.H
R3/RRR3-22/3	1610.035	1609.806	142.873	0.412	957.656	0.401	29	0.112	K.LDISGHTVSAVGPDIK.H
R3/RRR3-18/3	1610.029	1609.806	139.224	0.378	671.777	0.389	25	0.103	K.LDISGHTVSAVGPDIK.H
R3/RRR3-26/3	1610.662	1609.806	-89.602	0.305	488.253	0.317	21	0.087	-.LDISGHTVSAVGPDIK.-
R3/RRR3-16/2	1281.142	1281.503	-283.100	0.488	1622.409	0.520	18	0.242	K.NM*GLLLAEFEK.I
R3/RRR3-16/2	1282.117	1281.503	-302.366	0.510	1444.960	0.549	17	0.226	K.NM*GLLLAEFEK.I
R3/RRR3-16/2	1370.193	1370.490	-217.460	0.430	1352.946	0.480	21	0.201	K.ITIDPDDPAAVSR.Y
R3/RRR3-16/2	1370.110	1370.490	-278.240	0.447	1217.799	0.505	21	0.194	K.ITIDPDDPAAVSR.Y
R3/RRR3-17/2	1280.320	1281.503	-1710.362	0.417	1235.720	0.487	16	0.190	K.NM*GLLLAEFEK.I
R3/RRR3-16/2	1251.126	1251.414	-231.110	0.487	1275.715	0.423	16	0.184	R.TYLNTLQEIR.I
R3/RRR3-17/2	1369.765	1370.490	-1263.513	0.428	1157.113	0.479	21	0.184	K.ITIDPDDPAAVSR.Y
R3/RRR3-17/2	1370.941	1370.490	329.404	0.465	1055.032	0.523	20	0.183	K.ITIDPDDPAAVSR.Y
R3/RRR3-16/2	1251.041	1251.414	-298.654	0.496	1208.629	0.427	16	0.180	R.TYLNTLQEIR.I
R3/RRR3-17/2	1071.964	1072.194	-215.483	0.474	997.857	0.518	15	0.179	R.TPVNGDDLLK.G
R3/RRR3-16/2	1251.100	1251.414	-251.764	0.525	1178.161	0.434	16	0.178	R.TYLNTLQEIR.I
R3/RRR3-16/2	1281.235	1281.503	-210.262	0.441	1067.190	0.487	16	0.177	K.NM*GLLLAEFEK.I
R3/RRR3-17/2	1316.330	1316.479	-113.440	0.485	1182.325	0.423	18	0.177	K.IEEELELEIAK.S
R3/RRR3-16/2	1071.623	1072.194	-1470.396	0.385	993.211	0.508	15	0.174	R.TPVNGDDLLK.G
R3/RRR3-16/2	1071.859	1072.194	-313.283	0.420	1037.363	0.466	15	0.172	R.TPVNGDDLLK.G
R3/RRR3-17/2	1072.064	1072.194	-121.357	0.461	975.329	0.484	15	0.172	R.TPVNGDDLLK.G
R3/RRR3-16/2	1072.108	1072.194	-80.239	0.449	1008.246	0.446	15	0.168	R.TPVNGDDLLK.G
R3/RRR3-17/2	1369.577	1370.490	-1401.089	0.378	1027.846	0.437	20	0.166	K.ITIDPDDPAAVSR.Y
R3/RRR3-17/2	1071.578	1072.194	-1512.963	0.365	968.572	0.433	15	0.162	R.TPVNGDDLLK.G
R3/RRR3-17/2	1280.941	1281.503	-1223.014	0.356	949.629	0.445	16	0.162	K.NM*GLLLAEFEK.I
R3/RRR3-17/2	1281.118	1281.503	-301.454	0.438	849.001	0.445	15	0.158	K.NM*GLLLAEFEK.I
R3/RRR3-17/2	1261.916	1262.352	-346.727	0.278	185.519	0.513	16	0.145	R.QKADLLSDSER.I
R3/RRR3-16/2	1263.022	1262.352	-261.698	0.281	115.342	0.492	14	0.145	R.QKADLLSDSER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1262.959	1262.352	-312.316	0.255	162.417	0.491	16	0.144	R.QKADLLSDSER.I
R3/RRR3-17/2	1262.131	1262.352	-175.352	0.197	158.592	0.302	13	0.139	R.QKADLLSDSER.I
R3/RRR3-16/3	1234.616	1234.513	84.124	0.562	1441.093	0.384	24	0.139	K.KFETALGVLKK.E
R3/RRR3-17/2	1261.480	1262.352	-1488.344	0.178	141.760	0.409	14	0.134	-.QKADLLSDSER.-
R3/RRR3-16/3	1230.605	1230.435	139.169	0.470	954.198	0.390	20	0.109	R.IKYTIDTFTK.G
R3/RRR3-17/3	1230.613	1230.435	145.287	0.461	930.245	0.391	19	0.108	R.IKYTIDTFTK.G
R3/RRR3-17/3	1230.376	1230.435	-47.688	0.401	1038.142	0.327	21	0.101	R.IKYTIDTFTK.G
R3/RRR3-17/3	1230.082	1230.435	-287.480	0.416	1052.517	0.320	21	0.101	R.IKYTIDTFTK.G
R3/RRR3-16/3	1234.238	1234.513	-222.825	0.452	1042.710	0.320	23	0.101	K.KFETALGVLKK.E
R3/RRR3-16/3	1230.382	1230.435	-42.463	0.392	636.561	0.334	18	0.097	R.IKYTIDTFTK.G
R3/RRR3-16/3	1230.281	1230.435	-125.167	0.359	721.929	0.266	18	0.091	R.IKYTIDTFTK.G
R3/RRR3-14/2	1505.168	1505.610	-294.190	0.493	1691.842	0.608	21	0.273	K.YYSDIAGPEYAQK.Y
R3/RRR3-14/2	1708.095	1708.932	-1079.117	0.522	1647.014	0.594	25	0.263	R.GWVPTLLGYSAQGACK.F
R3/RRR3-14/2	1708.362	1708.932	-922.137	0.510	1582.191	0.564	25	0.247	R.GWVPTLLGYSAQGACK.F
R3/RRR3-14/2	1505.092	1505.610	-1011.126	0.500	1510.945	0.584	20	0.242	K.YYSDIAGPEYAQK.Y
R3/RRR3-13/2	1506.226	1505.610	-255.209	0.581	1425.768	0.610	20	0.238	K.YYSDIAGPEYAQK.Y
R3/RRR3-14/2	1709.373	1708.932	258.457	0.557	1426.760	0.601	24	0.236	R.GWVPTLLGYSAQGACK.F
R3/RRR3-14/2	1505.184	1505.610	-283.693	0.518	1325.990	0.577	19	0.218	K.YYSDIAGPEYAQK.Y
R3/RRR3-13/2	1506.123	1505.610	-324.244	0.563	1316.008	0.560	20	0.214	K.YYSDIAGPEYAQK.Y
R3/RRR3-14/2	1575.470	1575.786	-201.561	0.483	1298.433	0.448	18	0.188	K.FASFETIVEQIYK.H
R3/RRR3-13/2	1504.522	1505.610	-1392.038	0.342	1187.734	0.497	19	0.185	K.YYSDIAGPEYAQK.Y
R3/RRR3-14/2	1062.637	1063.277	-1548.160	0.430	1177.006	0.451	15	0.182	K.LGLWGLFTR.G
R3/RRR3-14/2	1213.032	1213.407	-310.233	0.546	1098.991	0.451	13	0.174	K.FGFYEFFKK.C
R3/RRR3-14/2	1212.800	1213.407	-1329.419	0.467	983.573	0.476	13	0.170	K.FGFYEFFKK.C
R3/RRR3-14/2	1062.963	1063.277	-295.863	0.478	896.914	0.448	14	0.164	K.LGLWGLFTR.G
R3/RRR3-14/2	1213.318	1213.407	-74.332	0.411	1053.828	0.398	13	0.163	K.FGFYEFFKK.C
R3/RRR3-13/2	937.802	938.060	-275.751	0.452	741.363	0.486	15	0.162	K.SEGALGLYK.G
R3/RRR3-13/2	937.831	938.060	-244.932	0.431	600.919	0.515	14	0.159	K.SEGALGLYK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1085.096	1085.234	-127.572	0.365	857.264	0.449	12	0.158	K.FGFYEFFK.K
R3/RRR3-14/2	1062.940	1063.277	-317.640	0.437	857.513	0.410	14	0.157	K.LGLWGLFTR.G
R3/RRR3-14/2	1062.532	1063.277	-1646.604	0.414	863.522	0.404	14	0.156	K.LGLWGLFTR.G
R3/RRR3-13/2	937.420	938.060	-1754.108	0.436	682.404	0.456	14	0.155	K.SEGALGLYK.G
R3/RRR3-14/2	1575.000	1575.786	-1137.502	0.299	1109.799	0.343	17	0.155	K.FASFETIVEQIYK.H
R3/RRR3-14/2	937.856	938.060	-218.032	0.469	604.554	0.465	14	0.155	K.SEGALGLYK.G
R3/RRR3-14/2	747.398	747.908	-2025.942	0.430	700.857	0.473	11	0.152	-.HAVPVPK.-
R3/RRR3-14/2	1063.105	1063.277	-162.228	0.406	697.005	0.419	13	0.152	K.LGLWGLFTR.G
R3/RRR3-14/2	1574.431	1575.786	-1500.534	0.260	1134.304	0.303	18	0.151	K.FASFETIVEQIYK.H
R3/RRR3-13/2	1063.130	1063.277	-138.845	0.440	590.500	0.444	12	0.151	K.LGLWGLFTR.G
R3/RRR3-14/2	747.422	747.908	-652.808	0.450	768.430	0.403	11	0.151	-.HAVPVPK.-
R3/RRR3-14/2	1062.283	1063.277	-1882.001	0.340	727.388	0.416	13	0.150	K.LGLWGLFTR.G
R3/RRR3-14/2	1084.942	1085.234	-270.121	0.348	849.429	0.379	12	0.150	K.FGFYEFFK.K
R3/RRR3-14/2	1062.547	1063.277	-1633.100	0.340	627.144	0.438	12	0.148	K.LGLWGLFTR.G
R3/RRR3-14/2	1063.003	1063.277	-258.419	0.380	687.702	0.379	13	0.147	K.LGLWGLFTR.G
R3/RRR3-14/2	1085.014	1085.234	-203.525	0.277	870.965	0.360	12	0.146	K.FGFYEFFK.K
R3/RRR3-13/2	1062.231	1063.277	-1931.888	0.346	486.743	0.388	13	0.145	K.LGLWGLFTR.G
R3/RRR3-14/2	1709.007	1708.932	43.515	0.401	220.552	0.429	15	0.137	-.GWVPTLLGYSAQGACK.-
R3/RRR3-14/2	1084.565	1085.234	-1544.065	0.300	691.596	0.250	11	0.135	K.FGFYEFFK.K
R3/RRR3-14/3	1213.282	1213.407	-103.509	0.460	601.523	0.462	19	0.109	K.FGFYEFFKK.C
R3/RRR3-14/3	1213.030	1213.407	-312.314	0.455	658.249	0.428	19	0.106	K.FGFYEFFKK.C
R3/RRR3-14/3	1212.900	1213.407	-1246.494	0.444	578.340	0.433	18	0.106	K.FGFYEFFKK.C
R3/RRR3-14/3	1709.352	1708.932	245.989	0.380	711.731	0.460	22	0.106	R.GWVPTLLGYSAQGACK.F
R3/RRR3-14/3	1213.398	1213.407	-8.145	0.306	354.389	0.333	15	0.086	-.FGFYEFFKK.-
R3/RRR3-14/3	1708.807	1708.932	-73.672	0.340	449.106	0.458	20	0.081	-.GWVPTLLGYSAQGACK.-
R3/RRR3-6/2	1259.342	1259.434	-73.171	0.554	2239.367	0.589	20	0.365	R.VNLVQVLGSDSK.V
R3/RRR3-6/2	1258.695	1259.434	-1385.804	0.493	2152.317	0.598	20	0.351	R.VNLVQVLGSDSK.V
R3/RRR3-6/2	1544.305	1544.596	-188.820	0.564	1971.065	0.549	23	0.305	K.CSVDSGVYDDVATR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1258.742	1259.434	-1348.499	0.508	1968.363	0.543	20	0.301	R.VNLVQVLGSDSK.V
R3/RRR3-6/2	1087.997	1088.240	-224.236	0.512	1234.091	0.562	17	0.207	K.GPITTSASVVR.G
R3/RRR3-6/2	1207.402	1207.446	-36.162	0.403	1192.209	0.601	18	0.205	K.FFLGIGLPGSAK.D
R3/RRR3-6/2	1246.225	1246.520	-237.815	0.474	1259.465	0.484	18	0.195	K.IVLDFLGLVEK.F
R3/RRR3-6/3	1454.431	1453.667	-162.826	0.417	1984.143	0.330	28	0.192	K.APKPPAQAVDPFSK.F
R3/RRR3-6/2	1246.090	1246.520	-346.316	0.481	1119.795	0.517	18	0.189	K.IVLDFLGLVEK.F
R3/RRR3-6/2	1247.215	1246.520	-245.480	0.590	1088.447	0.525	18	0.189	K.IVLDFLGLVEK.F
R3/RRR3-6/2	1400.187	1400.520	-238.161	0.436	1191.048	0.460	18	0.181	K.DTSVSLSANHLQK.L
R3/RRR3-6/2	1400.094	1400.520	-304.812	0.452	1192.348	0.440	18	0.178	K.DTSVSLSANHLQK.L
R3/RRR3-6/2	1400.232	1400.520	-206.150	0.446	1155.703	0.457	18	0.178	K.DTSVSLSANHLQK.L
R3/RRR3-6/2	1087.633	1088.240	-1481.510	0.380	974.621	0.475	16	0.167	K.GPITTSASVVR.G
R3/RRR3-6/2	1191.169	1191.402	-195.460	0.347	1053.256	0.436	16	0.166	R.LSFQLSTPLGK.T
R3/RRR3-6/2	1299.481	1299.626	-112.085	0.481	957.948	0.444	19	0.165	R.VFVPLVLSLPSK.V
R3/RRR3-6/2	1190.952	1191.402	-378.284	0.433	840.742	0.462	14	0.157	R.LSFQLSTPLGK.T
R3/RRR3-6/3	1453.995	1453.667	225.698	0.467	1579.952	0.379	26	0.154	K.APKPPAQAVDPFSK.F
R3/RRR3-6/2	1299.314	1299.626	-241.102	0.372	774.040	0.405	17	0.149	R.VFVPLVLSLPSK.V
R3/RRR3-6/2	1087.542	1088.240	-1565.845	0.297	713.900	0.443	14	0.146	K.GPITTSASVVR.G
R3/RRR3-6/2	1299.420	1299.626	-159.485	0.344	859.933	0.354	17	0.146	R.VFVPLVLSLPSK.V
R3/RRR3-6/3	1453.622	1453.667	-31.478	0.425	1268.561	0.285	25	0.107	K.APKPPAQAVDPFSK.F
R3/RRR3-14/2	1939.605	1940.234	-841.992	0.576	4093.527	0.500	28	0.857	R.SSVQAALQQEIALAAGLLR.I
R3/RRR3-14/2	1940.364	1940.234	67.604	0.609	4007.210	0.535	29	0.843	R.SSVQAALQQEIALAAGLLR.I
R3/RRR3-14/2	1939.487	1940.234	-903.278	0.574	3474.924	0.472	28	0.630	R.SSVQAALQQEIALAAGLLR.I
R3/RRR3-14/3	1866.255	1866.072	98.361	0.585	2426.610	0.470	37	0.327	R.GLRDAADLVALSGGHTVGR.T
R3/RRR3-14/3	1866.074	1866.072	1.527	0.552	2405.485	0.448	36	0.315	R.GLRDAADLVALSGGHTVGR.T
R3/RRR3-14/3	1865.289	1866.072	-958.777	0.536	2284.540	0.421	35	0.279	R.GLRDAADLVALSGGHTVGR.T
R3/RRR3-14/2	1859.407	1859.999	-858.899	0.481	1583.240	0.497	21	0.226	R.GGSNSEQGM*GPNLTLQPR.A
R3/RRR3-14/2	1277.750	1277.451	234.322	0.569	1484.388	0.510	18	0.222	R.VQDLIDLFASR.G
R3/RRR3-14/3	1860.624	1859.999	-202.377	0.475	1712.056	0.541	33	0.221	R.GGSNSEQGM*GPNLTLQPR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1277.160	1277.451	-228.891	0.523	1388.976	0.516	17	0.212	R.VQDLIDLFASR.G
R3/RRR3-14/2	1539.165	1539.676	-984.527	0.491	1280.549	0.550	22	0.206	R.DAADLVALSGGHTVGR.T
R3/RRR3-15/2	1744.475	1744.970	-284.364	0.516	1299.316	0.537	25	0.205	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-16/2	1277.037	1277.451	-325.172	0.527	1330.004	0.509	17	0.205	R.VQDLIDLFASR.G
R3/RRR3-14/2	1539.170	1539.676	-980.864	0.486	1329.404	0.512	22	0.203	R.DAADLVALSGGHTVGR.T
R3/RRR3-15/2	1277.092	1277.451	-282.208	0.539	1371.224	0.471	17	0.201	R.VQDLIDLFASR.G
R3/RRR3-15/2	1277.011	1277.451	-346.176	0.569	1321.235	0.492	17	0.200	R.VQDLIDLFASR.G
R3/RRR3-14/2	1539.211	1539.676	-302.638	0.482	1262.258	0.527	22	0.200	R.DAADLVALSGGHTVGR.T
R3/RRR3-13/2	1276.920	1277.451	-1203.119	0.489	1329.440	0.478	17	0.199	R.VQDLIDLFASR.G
R3/RRR3-14/2	1859.378	1859.999	-874.847	0.478	1385.728	0.470	20	0.197	R.GGSNSEQGM*GPNLTLQPR.A
R3/RRR3-14/2	1276.675	1277.451	-1395.730	0.438	1427.795	0.409	17	0.194	R.VQDLIDLFASR.G
R3/RRR3-15/2	1539.401	1539.676	-178.923	0.466	1212.024	0.516	22	0.193	R.DAADLVALSGGHTVGR.T
R3/RRR3-14/3	1940.186	1940.234	-24.783	0.450	1762.786	0.425	33	0.193	R.SSVQAALQQEIALAAGLLR.I
R3/RRR3-14/2	1860.104	1859.999	56.157	0.533	1399.229	0.441	20	0.191	R.GGSNSEQGM*GPNLTLQPR.A
R3/RRR3-15/2	1056.494	1057.226	-1644.427	0.441	1288.859	0.425	14	0.185	R.ALQLVEDIR.A
R3/RRR3-15/2	1539.251	1539.676	-276.381	0.479	1231.518	0.468	21	0.185	R.DAADLVALSGGHTVGR.T
R3/RRR3-15/2	1744.641	1744.970	-189.104	0.496	1031.220	0.542	23	0.181	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-15/2	1745.573	1744.970	-227.861	0.521	946.375	0.544	22	0.175	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-14/2	1744.492	1744.970	-274.675	0.470	913.599	0.538	22	0.172	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-14/2	1031.887	1031.188	-293.145	0.444	1011.774	0.465	14	0.171	K.AAFFTQFAK.S
R3/RRR3-14/2	1744.380	1744.970	-914.046	0.423	929.446	0.492	22	0.166	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-14/2	1744.325	1744.970	-945.590	0.437	796.493	0.510	21	0.160	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-14/3	1859.351	1859.999	-888.992	0.445	1274.629	0.523	30	0.160	R.GGSNSEQGM*GPNLTLQPR.A
R3/RRR3-14/2	1057.077	1057.226	-140.683	0.461	1033.069	0.351	13	0.156	R.ALQLVEDIR.A
R3/RRR3-14/3	1539.874	1539.676	129.346	0.412	1319.025	0.476	31	0.150	R.DAADLVALSGGHTVGR.T
R3/RRR3-14/2	1057.031	1057.226	-184.589	0.476	1027.748	0.311	13	0.148	-.ALQLVEDIR.-
R3/RRR3-14/2	1030.356	1031.188	-1783.939	0.294	824.365	0.351	14	0.144	K.AAFFTQFAK.S
R3/RRR3-13/2	1276.884	1277.451	-1231.343	0.334	600.982	0.403	14	0.144	R.VQDLIDLFASR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/3	1540.816	1539.676	91.324	0.453	1325.883	0.437	30	0.143	R.DAADLVALSGGHTVGR.T
R3/RRR3-14/2	1030.388	1031.188	-1752.513	0.270	858.569	0.308	14	0.141	K.AAFFTQFAK.S
R3/RRR3-14/3	1745.471	1744.970	-286.419	0.442	1328.187	0.418	28	0.140	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-15/2	1056.431	1057.226	-1703.631	0.378	763.316	0.288	12	0.138	-.ALQLVEDIR.-
R3/RRR3-14/3	1539.785	1539.676	71.149	0.454	1274.060	0.439	32	0.138	R.DAADLVALSGGHTVGR.T
R3/RRR3-14/2	1057.044	1057.226	-172.656	0.328	531.972	0.280	12	0.137	R.ALQLVEDIR.A
R3/RRR3-13/2	1744.503	1744.970	-268.006	0.329	499.184	0.320	17	0.134	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-14/2	1057.904	1057.226	-304.917	0.404	704.219	0.263	12	0.133	-.ALQLVEDIR.-
R3/RRR3-15/3	1540.351	1539.676	-211.610	0.421	993.676	0.461	29	0.122	R.DAADLVALSGGHTVGR.T
R3/RRR3-1/2	1057.974	1057.226	-239.048	0.274	642.518	0.124	12	0.112	-.ALQLVEDIR.-
R3/RRR3-14/3	1745.741	1744.970	-131.202	0.415	943.550	0.396	26	0.108	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-14/3	1277.711	1277.451	204.038	0.415	1340.941	0.256	21	0.106	-.VQDLIDLFASR.-
R3/RRR3-14/3	1745.214	1744.970	140.191	0.379	805.500	0.397	24	0.102	R.DAVVVSGGPSYAVPLGQK.D
R3/RRR3-15/3	1859.704	1859.999	-159.584	0.322	970.979	0.268	25	0.091	R.GGSNSEQGM*GPNLTLQPR.A
R3/RRR3-15/3	1539.783	1539.676	70.195	0.303	783.014	0.258	25	0.088	R.DAADLVALSGGHTVGR.T
R3/RRR3-17/2	1375.098	1375.547	-327.449	0.494	1997.546	0.481	19	0.285	K.VIACVGETLEQR.E
R3/RRR3-17/2	1375.156	1375.547	-285.143	0.481	1875.244	0.488	19	0.268	K.VIACVGETLEQR.E
R3/RRR3-17/2	1341.048	1340.501	-339.050	0.543	1558.127	0.571	22	0.247	R.IIYGGSVTGANCK.E
R3/RRR3-17/2	1375.153	1375.547	-287.192	0.502	1795.984	0.452	19	0.247	K.VIACVGETLEQR.E
R3/RRR3-17/2	1340.109	1340.501	-293.057	0.464	1619.044	0.499	22	0.237	R.IIYGGSVTGANCK.E
R3/RRR3-17/2	1340.057	1340.501	-332.448	0.498	1514.289	0.535	21	0.232	R.IIYGGSVTGANCK.E
R3/RRR3-17/2	1395.367	1395.497	-92.888	0.467	1382.321	0.551	19	0.218	R.SLLGESNEFVGDK.V
R3/RRR3-17/2	1424.017	1424.560	-1086.922	0.453	1443.032	0.461	20	0.205	R.ESGSTMDVVAAQTK.A
R3/RRR3-17/2	1636.217	1636.748	-938.551	0.466	1331.978	0.495	22	0.201	K.VATPDQAQEVHDGLR.K
R3/RRR3-17/2	1396.048	1395.497	-322.535	0.490	1197.352	0.544	19	0.198	R.SLLGESNEFVGDK.V
R3/RRR3-17/2	1423.747	1424.560	-1277.351	0.409	1327.819	0.474	19	0.195	R.ESGSTMDVVAAQTK.A
R3/RRR3-17/3	1605.695	1604.746	-31.699	0.554	1636.486	0.497	32	0.192	K.WLAANVSAEVAESTR.I
R3/RRR3-17/2	1637.124	1636.748	230.151	0.505	1117.905	0.530	21	0.188	K.VATPDQAQEVHDGLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1394.610	1395.497	-1356.713	0.348	1149.177	0.509	19	0.184	R.SLLGESNEFVGDK.V
R3/RRR3-17/2	1375.428	1375.547	-86.579	0.400	1302.810	0.386	18	0.179	K.VIACVGETLEQR.E
R3/RRR3-17/2	1423.520	1424.560	-1437.188	0.357	1337.345	0.370	19	0.177	R.ESGSTMDVVAAQTK.A
R3/RRR3-17/2	1375.539	1375.547	-5.573	0.406	1471.789	0.248	19	0.171	-.VIACVGETLEQR.-
R3/RRR3-17/2	1440.164	1440.559	-275.302	0.418	1120.983	0.404	19	0.167	R.ESGSTM*DVVAAQTK.A
R3/RRR3-17/2	1375.403	1375.547	-105.185	0.377	1303.369	0.299	18	0.166	-.VIACVGETLEQR.-
R3/RRR3-17/2	1440.083	1440.559	-331.601	0.384	1033.903	0.440	18	0.165	R.ESGSTM*DVVAAQTK.A
R3/RRR3-17/2	1764.366	1764.921	-884.123	0.433	881.604	0.495	18	0.161	K.VATPDQAQEVHDGLRK.W
R3/RRR3-17/2	1440.036	1440.559	-1060.771	0.362	1007.254	0.400	18	0.158	R.ESGSTM*DVVAAQTK.A
R3/RRR3-17/2	1764.462	1764.921	-261.019	0.428	926.596	0.448	18	0.158	K.VATPDQAQEVHDGLRK.W
R3/RRR3-17/2	1440.154	1440.559	-282.105	0.421	877.493	0.437	17	0.156	R.ESGSTM*DVVAAQTK.A
R3/RRR3-17/2	1636.210	1636.748	-942.821	0.435	704.518	0.495	18	0.154	K.VATPDQAQEVHDGLR.K
R3/RRR3-17/2	1764.580	1764.921	-194.114	0.466	825.853	0.453	19	0.154	K.VATPDQAQEVHDGLRK.W
R3/RRR3-17/2	1441.255	1440.559	-211.550	0.377	908.857	0.400	17	0.153	R.ESGSTM*DVVAAQTK.A
R3/RRR3-17/2	1440.019	1440.559	-1072.517	0.350	830.243	0.398	17	0.149	R.ESGSTM*DVVAAQTK.A
R3/RRR3-17/2	1439.469	1440.559	-1456.192	0.295	998.480	0.257	18	0.141	R.ESGSTM*DVVAAQTK.A
R3/RRR3-17/3	1604.810	1604.746	40.190	0.459	1125.910	0.487	28	0.136	K.WLAANVSAEVAESTR.I
R3/RRR3-17/3	1478.738	1478.624	77.232	0.498	1159.234	0.365	26	0.114	K.CNGTTDQVDKIVK.I
R3/RRR3-17/3	1375.062	1375.547	-353.734	0.458	1168.688	0.344	27	0.109	K.VIACVGETLEQR.E
R3/RRR3-17/3	1479.883	1478.624	175.543	0.454	1025.648	0.362	25	0.107	K.CNGTTDQVDKIVK.I
R3/RRR3-17/3	1375.584	1375.547	26.905	0.484	1047.849	0.340	25	0.105	K.VIACVGETLEQR.E
R3/RRR3-17/3	1479.102	1478.624	324.304	0.476	812.909	0.293	23	0.093	K.CNGTTDQVDKIVK.I
R3/RRR3-17/3	1604.669	1604.746	-48.277	0.210	673.779	0.267	22	0.085	K.WLAANVSAEVAESTR.I
R3/RRR3-17/3	1375.043	1375.547	-1096.794	0.366	859.683	0.205	24	0.085	K.VIACVGETLEQR.E
R3/RRR3-17/3	1478.795	1478.624	116.350	0.316	839.339	0.199	20	0.083	K.CNGTTDQVDKIVK.I
R3/RRR3-13/2	1700.371	1699.843	-278.130	0.613	1941.278	0.597	24	0.308	K.GNAYAQVAIGTEDVYK.S
R3/RRR3-14/2	1699.624	1699.843	-129.135	0.566	1849.942	0.635	24	0.305	K.GNAYAQVAIGTEDVYK.S
R3/RRR3-13/2	1699.166	1699.843	-989.456	0.493	1890.919	0.606	24	0.303	K.GNAYAQVAIGTEDVYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1699.352	1699.843	-289.681	0.511	1889.037	0.602	24	0.301	K.GNAYAQVAIGTEDVYK.S
R3/RRR3-13/2	1699.362	1699.843	-283.339	0.532	1851.897	0.534	24	0.276	K.GNAYAQVAIGTEDVYK.S
R3/RRR3-14/2	1699.324	1699.843	-896.564	0.538	1687.502	0.550	23	0.256	K.GNAYAQVAIGTEDVYK.S
R3/RRR3-13/2	1046.877	1047.184	-294.913	0.483	1772.192	0.487	16	0.253	K.SAEAVELVTK.E
R3/RRR3-14/2	1046.899	1047.184	-273.504	0.464	1724.149	0.492	16	0.248	K.SAEAVELVTK.E
R3/RRR3-13/2	1047.029	1047.184	-148.815	0.481	1626.238	0.502	16	0.238	K.SAEAVELVTK.E
R3/RRR3-13/2	1046.963	1047.184	-212.209	0.457	1531.020	0.510	15	0.227	K.SAEAVELVTK.E
R3/RRR3-14/2	1046.856	1047.184	-314.333	0.455	1489.601	0.514	15	0.223	K.SAEAVELVTK.E
R3/RRR3-14/2	1047.066	1047.184	-113.145	0.499	1516.703	0.495	15	0.222	K.SAEAVELVTK.E
R3/RRR3-13/2	1233.014	1233.438	-345.421	0.400	1401.631	0.522	18	0.214	K.VVLVDNADFLK.E
R3/RRR3-13/2	1233.387	1233.438	-41.555	0.378	1343.546	0.439	18	0.192	K.VVLVDNADFLK.E
R3/RRR3-14/2	1184.142	1184.366	-189.900	0.493	1391.175	0.398	15	0.188	K.SPEVVLEWPK.K
R3/RRR3-14/2	1184.134	1184.366	-196.725	0.451	1223.103	0.441	15	0.183	-.SPEVVLEWPK.-
R3/RRR3-13/2	1184.188	1184.366	-150.603	0.503	1229.091	0.341	15	0.165	K.SPEVVLEWPK.K
R3/RRR3-13/2	1604.445	1603.841	-247.523	0.531	1132.941	0.446	21	0.164	K.VVLVDNADFLKELQ.-
R3/RRR3-14/2	1248.515	1249.396	-1511.154	0.402	1260.822	0.290	18	0.161	K.IASFLDPDGWK.V
R3/RRR3-14/2	1233.085	1233.438	-287.513	0.348	1102.708	0.372	16	0.161	K.VVLVDNADFLK.E
R3/RRR3-13/2	1248.580	1249.396	-1458.907	0.409	993.883	0.394	17	0.160	K.IASFLDPDGWK.V
R3/RRR3-14/2	1515.218	1514.766	299.439	0.487	488.347	0.556	17	0.158	R.GPTPEPLCQVM*LR.V
R3/RRR3-14/2	1184.149	1184.366	-184.108	0.357	1060.646	0.372	13	0.158	K.SPEVVLEWPK.K
R3/RRR3-13/2	1249.986	1249.396	-328.977	0.483	960.589	0.337	17	0.151	K.IASFLDPDGWK.V
R3/RRR3-13/2	1184.476	1184.366	93.381	0.407	853.876	0.371	14	0.150	K.SPEVVLEWPK.K
R3/RRR3-13/2	1514.390	1514.766	-249.037	0.389	382.720	0.530	15	0.149	R.GPTPEPLCQVM*LR.V
R3/RRR3-14/2	1497.715	1498.767	-1374.167	0.376	471.998	0.450	17	0.146	R.GPTPEPLCQVMLR.V
R3/RRR3-14/2	1249.018	1249.396	-304.137	0.451	977.632	0.286	18	0.146	K.IASFLDPDGWK.V
R3/RRR3-14/2	1498.273	1498.767	-330.111	0.324	551.108	0.445	17	0.145	R.GPTPEPLCQVMLR.V
R3/RRR3-14/2	1514.282	1514.766	-320.773	0.303	569.021	0.420	18	0.143	R.GPTPEPLCQVM*LR.V
R3/RRR3-14/2	1602.600	1603.841	-1402.497	0.329	1076.131	0.284	20	0.140	K.VVLVDNADFLKELQ.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1604.458	1603.841	-239.737	0.492	1058.753	0.406	21	0.137	K.VVLVDNADFLKELQ.-
R3/RRR3-14/2	1233.310	1233.438	-104.100	0.240	324.788	0.288	13	0.134	-.VVLVDNADFLK.-
R3/RRR3-13/2	1603.449	1603.841	-245.462	0.417	991.962	0.323	20	0.112	K.VVLVDNADFLKELQ.-
R3/RRR3-13/3	1028.598	1028.236	353.441	0.493	747.857	0.449	17	0.111	K.RLLHAVYR.V
R3/RRR3-14/3	1027.759	1028.236	-465.585	0.484	591.420	0.441	15	0.108	K.RLLHAVYR.V
R3/RRR3-14/3	1028.359	1028.236	120.195	0.505	622.692	0.423	15	0.107	K.RLLHAVYR.V
R3/RRR3-13/3	1028.580	1028.236	336.306	0.465	563.563	0.408	15	0.105	K.RLLHAVYR.V
R3/RRR3-25/3	1775.242	1775.858	-912.508	0.580	3047.672	0.456	36	0.467	K.FEANRDVDNPDVIDR.L
R3/RRR3-25/2	1414.067	1414.542	-336.781	0.467	1692.750	0.527	18	0.451	K.GIEIIYNYGKED.-
R3/RRR3-25/2	1414.224	1414.542	-225.061	0.471	1562.117	0.570	18	0.383	K.GIEIIYNYGKED.-
R3/RRR3-25/2	1415.189	1414.542	-249.651	0.541	1516.183	0.594	18	0.355	K.GIEIIYNYGKED.-
R3/RRR3-25/3	1775.772	1775.858	-48.520	0.553	2493.832	0.471	34	0.335	K.FEANRDVDNPDVIDR.L
R3/RRR3-25/3	1622.856	1622.763	57.473	0.489	1873.498	0.533	27	0.240	R.HLFYQDASDLREK.F
R3/RRR3-25/2	1193.944	1194.276	-279.403	0.536	1149.074	0.468	17	0.184	R.LIDDAEAQYR.N
R3/RRR3-25/3	1621.963	1622.763	-1113.105	0.444	1573.772	0.486	28	0.178	R.HLFYQDASDLREK.F
R3/RRR3-25/3	1423.753	1424.632	-1323.749	0.532	1634.964	0.434	25	0.173	R.ALKDTLNWAVHR.H
R3/RRR3-25/2	1365.776	1365.476	220.296	0.404	1206.119	0.396	16	0.172	R.HLFYQDASDLR.E
R3/RRR3-25/2	1193.442	1194.276	-1541.186	0.423	1092.546	0.424	17	0.171	R.LIDDAEAQYR.N
R3/RRR3-25/2	1193.259	1194.276	-1695.743	0.336	1182.199	0.380	17	0.168	R.LIDDAEAQYR.N
R3/RRR3-25/2	1157.960	1158.201	-208.256	0.451	1076.679	0.402	16	0.166	R.DVDNPDVIDR.L
R3/RRR3-25/2	1365.288	1365.476	-137.621	0.278	1266.792	0.282	16	0.158	R.HLFYQDASDLR.E
R3/RRR3-25/2	1157.924	1158.201	-239.561	0.435	914.203	0.402	15	0.156	R.DVDNPDVIDR.L
R3/RRR3-25/2	1365.079	1365.476	-291.374	0.406	1040.616	0.365	15	0.156	R.HLFYQDASDLR.E
R3/RRR3-25/2	1157.375	1158.201	-1582.020	0.370	937.484	0.370	15	0.153	R.DVDNPDVIDR.L
R3/RRR3-25/3	1425.863	1424.632	162.530	0.546	1439.063	0.396	26	0.141	R.ALKDTLNWAVHR.H
R3/RRR3-24/2	1365.093	1365.476	-280.787	0.332	584.337	0.357	13	0.138	R.HLFYQDASDLR.E
R3/RRR3-25/3	1622.472	1622.763	-180.222	0.427	1408.976	0.383	27	0.135	R.HLFYQDASDLREK.F
R3/RRR3-25/3	1424.440	1424.632	-135.483	0.531	1485.306	0.344	25	0.133	R.ALKDTLNWAVHR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/3	1775.162	1775.858	-957.864	0.441	1075.420	0.345	24	0.107	K.FEANRDVDNPDVIDR.L
R3/RRR3-14/2	1073.606	1074.255	-1539.983	0.492	1676.586	0.588	17	0.442	R.TFLLSLVGSH.-
R3/RRR3-14/2	1073.569	1074.255	-1574.706	0.420	1490.622	0.511	16	0.335	R.TFLLSLVGSH.-
R3/RRR3-14/2	1116.065	1115.393	-294.731	0.527	2034.805	0.434	17	0.280	K.LLLAYVGIPR.Y
R3/RRR3-14/2	1373.442	1372.661	-159.798	0.501	1758.055	0.449	18	0.242	K.AM*LLWILDPAGR.D
R3/RRR3-14/2	1189.932	1190.286	-297.940	0.394	1724.081	0.369	17	0.219	R.EALSGDTIDLR.A
R3/RRR3-14/2	1608.291	1608.692	-249.595	0.529	1123.275	0.542	22	0.192	K.SLAEAIHSETSGSYR.T
R3/RRR3-14/2	1608.255	1608.692	-272.516	0.530	940.302	0.577	21	0.183	K.SLAEAIHSETSGSYR.T
R3/RRR3-14/2	1189.490	1190.286	-1514.089	0.366	1385.013	0.363	17	0.182	R.EALSGDTIDLR.A
R3/RRR3-14/2	1608.228	1608.692	-288.812	0.519	880.667	0.568	20	0.176	K.SLAEAIHSETSGSYR.T
R3/RRR3-14/2	1114.723	1115.393	-1502.841	0.498	1127.346	0.413	15	0.170	K.LLLAYVGIPR.Y
R3/RRR3-14/2	1190.120	1190.286	-139.565	0.458	1324.605	0.283	17	0.163	R.EALSGDTIDLR.A
R3/RRR3-14/2	1371.349	1372.661	-1691.136	0.403	1050.481	0.417	15	0.162	K.AM*LLWILDPAGR.D
R3/RRR3-14/2	1020.392	1021.152	-1730.385	0.345	1052.015	0.358	13	0.157	R.ALIQQEYR.T
R3/RRR3-14/2	1436.132	1436.554	-294.265	0.442	1103.159	0.355	16	0.157	K.FGTYLEHDIGQR.T
R3/RRR3-14/2	1020.674	1021.152	-469.403	0.361	951.815	0.325	13	0.149	R.ALIQQEYR.T
R3/RRR3-14/2	1114.537	1115.393	-1670.620	0.311	633.151	0.284	12	0.134	K.LLLAYVGIPR.Y
R3/RRR3-14/3	1436.657	1436.554	72.037	0.387	868.474	0.482	21	0.117	K.FGTYLEHDIGQR.T
R3/RRR3-14/3	1772.303	1771.906	224.885	0.455	307.435	0.576	24	0.110	-.YEGPEVDPTIVTHDAK.-
R3/RRR3-14/3	1772.865	1771.906	-23.013	0.408	288.497	0.513	23	0.108	R.YEGPEVDPTIVTHDAK.D
R3/RRR3-14/3	1771.761	1771.906	-81.869	0.374	287.806	0.534	22	0.108	R.YEGPEVDPTIVTHDAK.D
R3/RRR3-14/3	1436.669	1436.554	80.090	0.322	757.000	0.423	21	0.103	K.FGTYLEHDIGQR.T
R3/RRR3-14/3	1436.019	1436.554	-1072.220	0.286	720.057	0.356	20	0.094	K.FGTYLEHDIGQR.T
R3/RRR3-14/2	1073.410	1074.255	-1723.335	0.305	854.407	0.430	12	0.093	R.TFLLSLVGSH.-
R3/RRR3-15/2	1406.797	1407.463	-1187.345	0.383	1860.341	0.353	19	0.232	K.TVDSEELTVEER.N
R3/RRR3-14/2	1406.667	1407.463	-1280.240	0.409	1870.367	0.335	19	0.229	K.TVDSEELTVEER.N
R3/RRR3-15/2	1406.801	1407.463	-1184.557	0.393	1888.865	0.310	19	0.226	K.TVDSEELTVEER.N
R3/RRR3-14/2	1813.493	1814.078	-876.848	0.536	1453.219	0.490	23	0.211	K.AAQDIALAELPPTHPIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1407.112	1407.463	-250.040	0.469	1588.142	0.408	18	0.210	K.TVDSEELTVEER.N
R3/RRR3-14/2	1407.068	1407.463	-281.635	0.473	1635.970	0.379	18	0.209	K.TVDSEELTVEER.N
R3/RRR3-14/2	1228.899	1229.342	-362.045	0.462	1392.845	0.441	18	0.198	K.DAAENTM*VAYK.A
R3/RRR3-14/2	1407.115	1407.463	-247.865	0.465	1490.404	0.396	18	0.198	K.TVDSEELTVEER.N
R3/RRR3-14/2	1813.399	1814.078	-928.815	0.528	1137.396	0.499	21	0.181	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/2	1682.387	1681.869	-287.216	0.484	863.010	0.584	21	0.177	K.LLDSHLVPSSTAPESK.V
R3/RRR3-14/2	1229.910	1229.342	-352.788	0.517	956.105	0.514	16	0.175	K.DAAENTM*VAYK.A
R3/RRR3-14/2	1813.495	1814.078	-875.835	0.546	1028.495	0.494	22	0.173	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/2	1813.357	1814.078	-952.266	0.509	926.232	0.525	21	0.171	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/2	1680.893	1681.869	-1178.744	0.425	889.795	0.525	21	0.168	K.LLDSHLVPSSTAPESK.V
R3/RRR3-15/2	1228.961	1229.342	-310.919	0.468	979.790	0.427	16	0.163	K.DAAENTM*VAYK.A
R3/RRR3-14/2	1681.493	1681.869	-224.166	0.438	671.322	0.523	19	0.156	K.LLDSHLVPSSTAPESK.V
R3/RRR3-14/2	1813.390	1814.078	-933.748	0.513	839.570	0.451	21	0.156	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/2	1228.988	1229.342	-289.194	0.450	741.520	0.443	15	0.153	K.DAAENTM*VAYK.A
R3/RRR3-14/3	1814.352	1814.078	151.516	0.412	1370.618	0.452	33	0.151	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/3	1813.634	1814.078	-245.477	0.337	1550.286	0.362	32	0.149	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/3	1813.682	1814.078	-219.143	0.357	1467.877	0.368	32	0.142	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/3	1990.615	1991.106	-247.671	0.416	930.222	0.543	31	0.133	R.IISSIEQKEESRGNEDR.V
R3/RRR3-14/2	1812.937	1814.078	-1184.874	0.293	627.370	0.250	19	0.132	K.AAQDIALAELPPTHPIR.L
R3/RRR3-15/3	1814.740	1814.078	-186.968	0.418	992.419	0.496	30	0.131	K.AAQDIALAELPPTHPIR.L
R3/RRR3-15/3	1815.062	1814.078	-8.953	0.403	1146.308	0.436	30	0.130	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/3	1813.964	1814.078	-63.293	0.386	1021.909	0.479	29	0.130	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/3	1814.296	1814.078	120.242	0.393	1122.366	0.408	31	0.122	K.AAQDIALAELPPTHPIR.L
R3/RRR3-15/3	1813.845	1814.078	-128.908	0.342	995.248	0.451	30	0.122	K.AAQDIALAELPPTHPIR.L
R3/RRR3-15/3	1990.813	1991.106	-147.923	0.394	849.972	0.474	29	0.117	R.IISSIEQKEESRGNEDR.V
R3/RRR3-14/3	1991.310	1991.106	102.513	0.414	606.429	0.511	28	0.114	R.IISSIEQKEESRGNEDR.V
R3/RRR3-14/3	1813.548	1814.078	-846.449	0.313	1089.257	0.364	30	0.113	K.AAQDIALAELPPTHPIR.L
R3/RRR3-15/3	1990.696	1991.106	-206.884	0.423	581.507	0.428	27	0.104	R.IISSIEQKEESRGNEDR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/3	1991.694	1991.106	-207.548	0.408	505.878	0.397	24	0.100	R.IISSIEQKEESRGNEDR.V
R3/RRR3-15/3	1814.582	1814.078	-274.127	0.243	793.143	0.244	25	0.090	K.AAQDIALAELPPTHPIR.L
R3/RRR3-14/3	1815.571	1814.078	272.262	0.322	680.654	0.204	23	0.087	-.AAQDIALAELPPTHPIR.-
R3/RRR3-9/2	1711.401	1711.936	-900.110	0.537	2608.992	0.559	24	0.439	K.KLEEVYGTFEAPSLK.K
R3/RRR3-9/2	1886.321	1886.970	-877.222	0.541	1698.885	0.533	24	0.254	K.TM*ISDSDYAEFDNFSK.W
R3/RRR3-9/2	1349.359	1349.557	-147.230	0.504	1503.396	0.533	19	0.228	R.KGPLIVYGTEGSK.I
R3/RRR3-9/2	1350.244	1349.557	-232.643	0.500	1359.672	0.565	18	0.218	R.KGPLIVYGTEGSK.I
R3/RRR3-9/2	1349.244	1349.557	-232.815	0.460	1368.227	0.553	18	0.216	R.KGPLIVYGTEGSK.I
R3/RRR3-9/2	1886.619	1886.970	-186.965	0.531	1350.499	0.547	23	0.214	K.TM*ISDSDYAEFDNFSK.W
R3/RRR3-10/2	1349.184	1349.557	-277.837	0.455	1203.384	0.539	18	0.197	R.KGPLIVYGTEGSK.I
R3/RRR3-10/2	1349.006	1349.557	-1153.349	0.461	1248.282	0.513	18	0.196	R.KGPLIVYGTEGSK.I
R3/RRR3-9/2	1446.480	1446.680	-138.107	0.523	1141.264	0.521	22	0.191	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/2	1447.330	1446.680	-241.908	0.581	1119.932	0.532	21	0.190	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/2	1349.143	1349.557	-308.428	0.457	1075.578	0.488	17	0.176	R.KGPLIVYGTEGSK.I
R3/RRR3-10/2	1796.608	1797.132	-850.810	0.299	1276.997	0.410	22	0.176	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-13/2	1446.087	1446.680	-1104.539	0.515	853.868	0.538	20	0.172	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/2	1447.117	1446.680	303.096	0.528	975.419	0.491	20	0.172	R.LNLLDLAPGGHLGR.F
R3/RRR3-13/2	1797.833	1797.132	-166.960	0.448	952.249	0.527	20	0.170	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-2/3	1446.456	1446.680	-154.709	0.382	1484.331	0.469	27	0.169	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/2	1446.166	1446.680	-1049.786	0.499	833.312	0.526	19	0.168	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/2	1446.359	1446.680	-222.601	0.485	812.433	0.523	19	0.167	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/2	1283.954	1283.416	-361.183	0.498	489.341	0.581	17	0.164	R.NLPGVDVANVER.L
R3/RRR3-10/2	1446.180	1446.680	-346.573	0.437	962.631	0.432	20	0.162	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/3	1445.927	1446.680	-1216.021	0.489	1595.849	0.405	27	0.162	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/2	1797.308	1797.132	97.850	0.436	986.571	0.429	20	0.158	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-1/2	1798.247	1797.132	64.232	0.426	902.326	0.452	20	0.157	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-10/2	1796.638	1797.132	-275.835	0.339	974.372	0.400	21	0.154	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-3/2	1447.107	1446.680	295.991	0.405	552.352	0.552	15	0.154	R.LNLLDLAPGGHLGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1283.197	1283.416	-171.329	0.384	415.533	0.506	18	0.154	R.NLPGVDVANVER.L
R3/RRR3-10/2	1282.912	1283.416	-1175.644	0.395	442.391	0.490	18	0.154	R.NLPGVDVANVER.L
R3/RRR3-9/2	1283.093	1283.416	-252.834	0.385	496.231	0.475	19	0.153	R.NLPGVDVANVER.L
R3/RRR3-13/2	1283.059	1283.416	-278.987	0.344	438.772	0.507	18	0.152	R.NLPGVDVANVER.L
R3/RRR3-12/2	1797.611	1797.132	266.816	0.375	830.863	0.434	20	0.151	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-9/2	1282.921	1283.416	-387.050	0.303	400.381	0.502	18	0.149	R.NLPGVDVANVER.L
R3/RRR3-9/2	1038.923	1039.169	-237.656	0.363	416.480	0.466	13	0.148	K.LNPYFGTAR.K
R3/RRR3-9/2	1797.405	1797.132	151.999	0.385	962.522	0.350	21	0.148	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-1/3	1446.411	1446.680	-186.457	0.405	1512.681	0.373	27	0.147	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/3	1446.691	1446.680	8.064	0.449	1456.674	0.403	28	0.147	R.LNLLDLAPGGHLGR.F
R3/RRR3-2/2	1284.269	1283.416	-114.842	0.338	356.548	0.420	17	0.147	R.NLPGVDVANVER.L
R3/RRR3-13/3	1446.956	1446.680	191.596	0.463	1514.169	0.377	28	0.146	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/2	1282.915	1283.416	-1173.255	0.313	347.299	0.411	17	0.145	R.NLPGVDVANVER.L
R3/RRR3-7/3	1446.809	1446.680	90.065	0.448	1513.876	0.367	27	0.145	R.LNLLDLAPGGHLGR.F
R3/RRR3-8/2	1797.640	1797.132	-274.591	0.345	892.008	0.359	19	0.145	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-2/2	1283.309	1283.416	-83.348	0.293	269.757	0.438	15	0.144	R.NLPGVDVANVER.L
R3/RRR3-8/3	1446.860	1446.680	125.222	0.456	1355.333	0.429	27	0.144	R.LNLLDLAPGGHLGR.F
R3/RRR3-15/2	1284.465	1283.416	38.261	0.283	329.691	0.323	16	0.142	R.NLPGVDVANVER.L
R3/RRR3-9/3	1446.904	1446.680	155.428	0.359	1426.084	0.369	26	0.140	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/2	1038.438	1039.169	-1671.958	0.252	416.386	0.386	13	0.139	K.LNPYFGTAR.K
R3/RRR3-9/2	1796.744	1797.132	-216.874	0.320	723.238	0.348	18	0.138	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-9/2	1038.976	1039.169	-186.618	0.274	476.575	0.310	13	0.138	K.LNPYFGTAR.K
R3/RRR3-10/2	1038.843	1039.169	-314.518	0.213	518.152	0.377	14	0.137	K.LNPYFGTAR.K
R3/RRR3-13/3	1446.813	1446.680	92.603	0.447	1400.051	0.375	27	0.136	R.LNLLDLAPGGHLGR.F
R3/RRR3-8/2	1039.881	1039.169	-278.176	0.228	439.345	0.286	13	0.135	K.LNPYFGTAR.K
R3/RRR3-13/2	1282.709	1283.416	-1334.661	0.240	242.870	0.320	14	0.135	-.NLPGVDVANVER.-
R3/RRR3-10/2	1796.361	1797.132	-988.811	0.243	834.961	0.279	18	0.135	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-14/3	1446.519	1446.680	-111.154	0.443	1285.108	0.402	26	0.133	R.LNLLDLAPGGHLGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1796.521	1797.132	-899.853	0.277	876.913	0.234	19	0.133	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-2/2	1283.232	1283.416	-144.131	0.299	219.883	0.291	13	0.132	-.NLPGVDVANVER.-
R3/RRR3-3/2	1796.698	1797.132	-242.639	0.255	621.064	0.267	17	0.131	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-9/3	1796.962	1797.132	-95.336	0.344	1405.633	0.340	33	0.130	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-15/2	1871.362	1870.971	209.652	0.302	535.087	0.248	15	0.128	K.TMISDSDYAEFDNFSK.W
R3/RRR3-2/3	1446.450	1446.680	-159.408	0.325	1297.607	0.364	26	0.128	R.LNLLDLAPGGHLGR.F
R3/RRR3-13/3	1446.713	1446.680	23.297	0.374	1160.514	0.411	25	0.127	R.LNLLDLAPGGHLGR.F
R3/RRR3-12/3	1446.733	1446.680	37.134	0.394	1241.644	0.380	25	0.127	R.LNLLDLAPGGHLGR.F
R3/RRR3-8/3	1446.338	1446.680	-236.877	0.314	1232.700	0.376	25	0.126	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/3	1446.558	1446.680	-84.108	0.368	1327.885	0.339	26	0.125	R.LNLLDLAPGGHLGR.F
R3/RRR3-10/3	1446.430	1446.680	-173.377	0.412	1285.958	0.363	27	0.125	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/3	1446.673	1446.680	-4.885	0.439	1193.666	0.358	24	0.119	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/3	1841.210	1840.109	55.012	0.468	1051.698	0.398	27	0.114	-.KLEEVYGTFEAPSLKK.-
R3/RRR3-14/3	1446.946	1446.680	184.743	0.441	1167.297	0.340	25	0.113	R.LNLLDLAPGGHLGR.F
R3/RRR3-6/3	1446.508	1446.680	-118.646	0.415	1255.970	0.305	26	0.112	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/3	1840.182	1840.109	39.507	0.495	1036.320	0.387	27	0.112	K.KLEEVYGTFEAPSLKK.K
R3/RRR3-1/3	1446.685	1446.680	3.621	0.418	1056.719	0.357	25	0.111	R.LNLLDLAPGGHLGR.F
R3/RRR3-12/3	1446.242	1446.680	-303.561	0.419	1121.404	0.333	24	0.110	R.LNLLDLAPGGHLGR.F
R3/RRR3-7/3	1446.526	1446.680	-106.456	0.447	931.252	0.374	23	0.109	R.LNLLDLAPGGHLGR.F
R3/RRR3-14/3	1446.363	1446.680	-219.350	0.427	1134.357	0.321	25	0.109	R.LNLLDLAPGGHLGR.F
R3/RRR3-1/3	1446.484	1446.680	-135.915	0.330	794.647	0.381	22	0.107	R.LNLLDLAPGGHLGR.F
R3/RRR3-7/3	1446.727	1446.680	32.818	0.372	889.765	0.359	23	0.106	R.LNLLDLAPGGHLGR.F
R3/RRR3-8/3	1446.831	1446.680	105.296	0.400	886.612	0.323	23	0.101	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/3	1841.824	1840.109	-155.136	0.430	905.959	0.350	25	0.100	K.KLEEVYGTFEAPSLKK.K
R3/RRR3-3/3	1446.330	1446.680	-242.720	0.319	1072.694	0.269	26	0.099	R.LNLLDLAPGGHLGR.F
R3/RRR3-9/3	1796.377	1797.132	-980.154	0.267	852.861	0.264	29	0.088	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-13/3	1796.848	1797.132	-158.814	0.336	794.067	0.175	27	0.081	R.VAVASALAATSVPSLVLAR.G
R3/RRR3-13/3	1796.032	1797.132	-1172.685	0.213	828.358	0.098	28	0.077	R.VAVASALAATSVPSLVLAR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1718.645	1718.030	-225.020	0.591	3014.334	0.610	27	0.561	K.AVVVGGGYIGLELSAALK.T
R3/RRR3-9/2	1916.587	1916.121	243.737	0.607	2665.642	0.622	24	0.467	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-9/2	1995.549	1995.225	163.166	0.612	2685.353	0.569	26	0.450	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-10/2	1915.626	1916.121	-259.469	0.542	2584.961	0.594	24	0.438	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-10/2	1915.534	1916.121	-830.969	0.566	2538.649	0.606	24	0.431	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-10/2	1916.694	1916.121	-223.552	0.600	2528.765	0.612	24	0.430	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-9/2	1915.431	1916.121	-884.963	0.536	2528.404	0.594	24	0.425	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-9/2	1915.426	1916.121	-887.458	0.546	2541.405	0.529	24	0.403	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-9/2	1995.324	1995.225	50.156	0.596	2298.077	0.573	25	0.365	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-9/2	1994.628	1995.225	-802.806	0.592	2244.508	0.541	24	0.343	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-10/2	1994.665	1995.225	-784.008	0.595	2185.984	0.568	24	0.341	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-10/2	1994.808	1995.225	-209.642	0.594	2124.636	0.571	23	0.329	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-10/2	1994.715	1995.225	-759.130	0.584	1963.566	0.555	23	0.296	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-9/3	1996.174	1995.225	-25.406	0.513	1357.885	0.578	30	0.185	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-10/3	1995.723	1995.225	250.323	0.473	1402.992	0.557	31	0.184	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-9/3	1620.687	1620.807	-74.452	0.316	1866.072	0.296	28	0.170	R.DIDDADKLVAAM*QAK.K
R3/RRR3-10/3	1915.826	1916.121	-154.416	0.513	1215.995	0.527	28	0.155	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-10/2	1447.168	1447.618	-311.649	0.411	574.658	0.473	18	0.151	K.ESVAPYERPALSK.G
R3/RRR3-9/2	1446.507	1447.618	-1463.442	0.423	592.723	0.456	18	0.150	K.ESVAPYERPALSK.G
R3/RRR3-10/2	1447.312	1447.618	-211.879	0.427	477.899	0.449	18	0.148	K.ESVAPYERPALSK.G
R3/RRR3-10/2	1447.149	1447.618	-324.851	0.407	479.948	0.444	17	0.146	K.ESVAPYERPALSK.G
R3/RRR3-10/2	1719.374	1718.030	200.413	0.387	553.713	0.381	15	0.132	K.AVVVGGGYIGLELSAALK.T
R3/RRR3-9/3	1915.042	1916.121	-1088.780	0.427	1149.634	0.443	27	0.129	R.LFTSGLAAFYEGYYANK.G
R3/RRR3-10/3	1620.966	1620.807	98.343	0.350	1609.120	0.241	29	0.125	R.DIDDADKLVAAM*QAK.K
R3/RRR3-9/3	1621.000	1620.807	119.527	0.384	1358.056	0.330	25	0.124	R.DIDDADKLVAAM*QAK.K
R3/RRR3-9/3	1995.918	1995.225	-154.323	0.440	896.368	0.492	27	0.123	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-10/3	1620.490	1620.807	-196.407	0.364	1348.374	0.327	26	0.122	R.DIDDADKLVAAM*QAK.K
R3/RRR3-9/3	1474.806	1474.597	142.193	0.438	851.195	0.425	26	0.110	R.LPGFHTCVGSGGER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/3	1474.306	1474.597	-198.210	0.439	572.957	0.407	22	0.102	R.LPGFHTCVGSGGER.L
R3/RRR3-10/3	1620.272	1620.807	-950.350	0.321	1256.458	0.243	27	0.100	R.DIDDADKLVAAM*QAK.K
R3/RRR3-10/3	1474.679	1474.597	55.900	0.456	630.891	0.375	23	0.100	R.LPGFHTCVGSGGER.L
R3/RRR3-10/3	1473.478	1474.597	-1442.148	0.400	683.801	0.368	22	0.099	R.LPGFHTCVGSGGER.L
R3/RRR3-10/3	1474.502	1474.597	-64.662	0.421	826.695	0.327	26	0.097	R.LPGFHTCVGSGGER.L
R3/RRR3-10/3	1994.832	1995.225	-197.647	0.242	672.263	0.196	24	0.083	K.LTDFGVQGAEANNILYLR.D
R3/RRR3-15/2	1237.088	1237.387	-242.343	0.544	1548.052	0.579	18	0.245	K.TLASDGLAGLYR.G
R3/RRR3-15/2	1237.272	1237.387	-93.179	0.521	1592.989	0.514	19	0.236	K.TLASDGLAGLYR.G
R3/RRR3-16/2	1237.240	1237.387	-119.405	0.419	1858.503	0.343	19	0.229	K.TLASDGLAGLYR.G
R3/RRR3-15/2	1236.627	1237.387	-1427.564	0.453	1586.936	0.446	19	0.219	K.TLASDGLAGLYR.G
R3/RRR3-15/2	1237.079	1237.387	-249.668	0.489	1289.527	0.555	18	0.210	K.TLASDGLAGLYR.G
R3/RRR3-15/2	1360.721	1361.590	-1377.595	0.498	1462.475	0.452	17	0.207	K.LLVQNQEEM*LK.A
R3/RRR3-15/2	1362.054	1361.590	341.841	0.592	1461.046	0.444	18	0.205	K.LLVQNQEEM*LK.A
R3/RRR3-16/2	1237.076	1237.387	-252.044	0.386	1610.449	0.366	19	0.205	K.TLASDGLAGLYR.G
R3/RRR3-15/2	1362.123	1361.590	-343.921	0.580	1311.873	0.472	17	0.196	K.LLVQNQEEM*LK.A
R3/RRR3-15/2	1046.146	1046.115	30.007	0.378	1069.603	0.499	14	0.178	K.YSSSLDAFR.Q
R3/RRR3-15/2	1236.275	1237.387	-1713.493	0.414	822.082	0.470	16	0.159	K.TLASDGLAGLYR.G
R3/RRR3-15/2	1475.405	1475.675	-183.033	0.453	614.554	0.464	17	0.152	R.YFPTQALNFAFR.D
R3/RRR3-15/2	1475.130	1475.675	-1050.007	0.398	572.781	0.473	17	0.150	R.YFPTQALNFAFR.D
R3/RRR3-15/2	1474.671	1475.675	-1362.596	0.303	543.186	0.386	17	0.140	R.YFPTQALNFAFR.D
R3/RRR3-15/2	1046.031	1046.115	-80.718	0.262	771.427	0.315	13	0.138	K.YSSSLDAFR.Q
R3/RRR3-15/2	1045.423	1046.115	-1623.426	0.223	742.101	0.331	13	0.137	K.YSSSLDAFR.Q
R3/RRR3-15/2	1381.162	1380.552	-283.123	0.372	826.755	0.246	14	0.132	-.TTAEEGVM*ALWR.-
R3/RRR3-17/2	1609.176	1608.861	196.257	0.541	2392.479	0.437	20	0.345	K.ALLTELQALEEHLK.A
R3/RRR3-18/3	1828.835	1828.957	-66.996	0.514	1681.530	0.476	34	0.193	K.AAVGHPDTLGDCPFSQR.V
R3/RRR3-18/3	1828.828	1828.957	-70.812	0.558	1516.526	0.498	32	0.179	K.AAVGHPDTLGDCPFSQR.V
R3/RRR3-17/3	1828.571	1828.957	-211.634	0.482	1589.686	0.433	34	0.169	K.AAVGHPDTLGDCPFSQR.V
R3/RRR3-18/2	1616.591	1616.885	-182.043	0.502	1244.868	0.350	18	0.166	K.LIDVQNKPDWFLK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/3	1829.209	1828.957	138.037	0.441	1334.957	0.506	30	0.162	K.AAVGHPDTLGDCPFSQR.V
R3/RRR3-18/2	990.846	990.095	-251.350	0.349	795.189	0.489	14	0.159	K.VPVFNGGDGK.W
R3/RRR3-18/2	990.182	990.095	88.397	0.308	654.673	0.545	13	0.155	K.VPVFNGGDGK.W
R3/RRR3-18/2	1122.116	1122.301	-165.372	0.399	372.024	0.545	14	0.153	K.EHLIAGWAPK.V
R3/RRR3-17/2	989.820	990.095	-277.834	0.338	651.097	0.484	14	0.152	K.VPVFNGGDGK.W
R3/RRR3-18/3	1829.035	1828.957	42.861	0.532	1265.230	0.494	30	0.151	K.AAVGHPDTLGDCPFSQR.V
R3/RRR3-18/3	1498.858	1498.753	70.518	0.578	1551.845	0.385	24	0.150	K.LYHLQVALEHFK.G
R3/RRR3-18/2	1122.089	1122.301	-189.926	0.382	286.820	0.534	13	0.149	K.EHLIAGWAPK.V
R3/RRR3-18/2	1616.120	1616.885	-1094.999	0.460	1003.602	0.321	16	0.146	K.LIDVQNKPDWFLK.I
R3/RRR3-18/3	1121.479	1122.301	-1629.503	0.448	1647.418	0.336	22	0.145	K.EHLIAGWAPK.V
R3/RRR3-17/2	989.990	990.095	-106.003	0.305	518.256	0.440	13	0.144	K.VPVFNGGDGK.W
R3/RRR3-18/2	1617.336	1616.885	279.751	0.544	967.538	0.329	16	0.143	-.LIDVQNKPDWFLK.-
R3/RRR3-18/2	1121.461	1122.301	-1645.566	0.286	257.392	0.510	12	0.141	K.EHLIAGWAPK.V
R3/RRR3-17/2	1773.463	1772.977	275.351	0.516	761.421	0.348	22	0.141	K.WIPDSDVITQVIEEK.Y
R3/RRR3-18/2	990.714	990.095	-385.843	0.275	473.276	0.442	11	0.140	K.VPVFNGGDGK.W
R3/RRR3-17/2	989.739	990.095	-360.369	0.253	411.575	0.390	11	0.137	K.VPVFNGGDGK.W
R3/RRR3-18/3	1392.803	1392.630	124.368	0.481	1114.864	0.464	23	0.130	K.AAKEHLIAGWAPK.V
R3/RRR3-18/3	1498.679	1498.753	-49.689	0.498	1374.084	0.365	28	0.126	K.LYHLQVALEHFK.G
R3/RRR3-18/3	1122.127	1122.301	-155.507	0.453	1295.757	0.386	21	0.126	K.EHLIAGWAPK.V
R3/RRR3-18/3	1498.222	1498.753	-1024.761	0.447	1332.257	0.355	27	0.121	K.LYHLQVALEHFK.G
R3/RRR3-18/3	1122.456	1122.301	138.561	0.486	1328.775	0.316	20	0.115	K.EHLIAGWAPK.V
R3/RRR3-17/3	1121.976	1122.301	-290.162	0.528	1071.357	0.393	19	0.115	K.EHLIAGWAPK.V
R3/RRR3-17/3	1828.714	1828.957	-133.183	0.462	911.604	0.416	27	0.112	K.AAVGHPDTLGDCPFSQR.V
R3/RRR3-17/3	1122.152	1122.301	-132.755	0.524	984.781	0.384	19	0.110	K.EHLIAGWAPK.V
R3/RRR3-11/2	1238.982	1239.397	-335.654	0.496	1702.270	0.491	17	0.247	K.CYLSLAEQVR.E
R3/RRR3-11/2	1594.268	1593.752	-304.704	0.496	1576.369	0.562	21	0.246	K.YVFTIDDDCFVAK.D
R3/RRR3-11/2	1593.289	1593.752	-291.213	0.467	1624.954	0.493	21	0.236	K.YVFTIDDDCFVAK.D
R3/RRR3-11/2	1239.030	1239.397	-296.905	0.509	1668.561	0.458	17	0.234	K.CYLSLAEQVR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1501.730	1502.609	-1254.964	0.483	1179.880	0.575	19	0.204	R.VPEGFDYELYNR.N
R3/RRR3-11/2	1239.145	1239.397	-203.406	0.479	1436.807	0.441	16	0.203	K.CYLSLAEQVR.E
R3/RRR3-10/2	1503.195	1502.609	-276.250	0.489	1115.552	0.577	19	0.199	R.VPEGFDYELYNR.N
R3/RRR3-11/2	1502.190	1502.609	-279.695	0.499	1114.054	0.553	19	0.194	R.VPEGFDYELYNR.N
R3/RRR3-11/2	1592.498	1593.752	-1419.236	0.297	1462.586	0.378	20	0.190	K.YVFTIDDDCFVAK.D
R3/RRR3-11/2	1123.258	1123.348	-80.291	0.556	843.122	0.576	16	0.181	R.YVDAVMTVPK.G
R3/RRR3-11/2	1501.683	1502.609	-1286.720	0.414	1133.858	0.466	19	0.179	R.VPEGFDYELYNR.N
R3/RRR3-11/2	1138.963	1139.347	-338.473	0.549	946.114	0.489	16	0.173	R.YVDAVM*TVPK.G
R3/RRR3-11/2	1138.538	1139.347	-1593.788	0.431	802.914	0.525	16	0.169	R.YVDAVM*TVPK.G
R3/RRR3-11/2	1122.307	1123.348	-1824.003	0.405	891.419	0.492	16	0.168	R.YVDAVMTVPK.G
R3/RRR3-2/2	1138.847	1139.347	-440.319	0.329	970.157	0.474	16	0.167	R.YVDAVM*TVPK.G
R3/RRR3-11/2	1138.408	1139.347	-1708.188	0.439	862.669	0.480	16	0.166	R.YVDAVM*TVPK.G
R3/RRR3-10/2	1138.985	1139.347	-318.472	0.416	918.057	0.443	16	0.164	R.YVDAVM*TVPK.G
R3/RRR3-11/2	1122.370	1123.348	-1767.065	0.384	856.754	0.471	16	0.163	R.YVDAVMTVPK.G
R3/RRR3-11/2	1242.122	1241.456	-269.749	0.412	922.004	0.404	16	0.156	K.VICDHLSLGVK.T
R3/RRR3-10/2	1138.375	1139.347	-1737.062	0.335	645.678	0.431	14	0.149	R.YVDAVM*TVPK.G
R3/RRR3-10/2	1122.956	1123.348	-349.946	0.349	969.715	0.316	14	0.148	R.YVDAVMTVPK.G
R3/RRR3-11/2	1201.718	1202.386	-1392.009	0.399	603.155	0.406	15	0.146	K.TGLPYIWHSK.A
R3/RRR3-11/2	1240.442	1241.456	-1628.083	0.332	648.047	0.420	16	0.145	K.VICDHLSLGVK.T
R3/RRR3-11/2	1201.478	1202.386	-1592.530	0.324	635.766	0.421	15	0.145	K.TGLPYIWHSK.A
R3/RRR3-10/2	1503.312	1502.609	-198.123	0.366	411.942	0.384	16	0.143	R.VPEGFDYELYNR.N
R3/RRR3-11/2	1119.010	1118.311	-269.228	0.401	684.284	0.335	15	0.143	K.ASNPFVNLKK.E
R3/RRR3-11/2	1119.003	1118.311	-275.685	0.353	660.205	0.315	15	0.140	K.ASNPFVNLKK.E
R3/RRR3-2/2	1138.339	1139.347	-1769.385	0.274	486.710	0.371	12	0.140	R.YVDAVM*TVPK.G
R3/RRR3-11/2	1118.213	1118.311	-87.771	0.365	592.696	0.284	14	0.137	K.ASNPFVNLKK.E
R3/RRR3-20/2	1503.345	1502.609	-176.047	0.304	588.161	0.301	15	0.136	R.VPEGFDYELYNR.N
R3/RRR3-3/2	1138.889	1139.347	-403.644	0.206	618.055	0.250	14	0.134	R.YVDAVM*TVPK.G
R3/RRR3-10/2	1117.337	1118.311	-1772.067	0.263	389.287	0.306	11	0.127	-.ASNPFVNLKK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/3	1665.881	1665.829	30.816	0.481	617.999	0.487	30	0.111	K.DPSGKDINALEQHIK.N
R3/RRR3-16/2	1950.419	1951.208	-920.501	0.564	2136.012	0.577	29	0.338	K.TAFIPFITAGDPDLATTAK.A
R3/RRR3-16/2	1950.593	1951.208	-830.722	0.548	2028.068	0.549	28	0.310	K.TAFIPFITAGDPDLATTAK.A
R3/RRR3-16/2	1950.620	1951.208	-816.650	0.547	1989.349	0.559	28	0.306	K.TAFIPFITAGDPDLATTAK.A
R3/RRR3-16/3	1922.715	1922.086	-193.630	0.539	1562.434	0.613	35	0.222	R.AEAAAVGEDERVISGTFAK.L
R3/RRR3-16/3	1921.503	1922.086	-826.292	0.481	1388.640	0.553	33	0.181	R.AEAAAVGEDERVISGTFAK.L
R3/RRR3-16/2	1095.372	1096.325	-1788.565	0.272	1146.959	0.373	15	0.161	R.GIANFM*TVVK.E
R3/RRR3-16/2	1095.928	1096.325	-363.234	0.418	998.218	0.406	14	0.160	R.GIANFM*TVVK.E
R3/RRR3-17/2	1950.498	1951.208	-879.599	0.412	931.624	0.437	21	0.156	K.TAFIPFITAGDPDLATTAK.A
R3/RRR3-16/3	1921.521	1922.086	-816.535	0.405	1247.367	0.520	32	0.156	R.AEAAAVGEDERVISGTFAK.L
R3/RRR3-16/2	1913.036	1913.162	-66.088	0.368	1077.207	0.350	20	0.154	K.NNLELVLLTTPTTPTER.M
R3/RRR3-16/2	1329.154	1329.438	-214.318	0.384	682.944	0.439	18	0.148	R.QLGEAASPEEGLK.R
R3/RRR3-16/2	1330.229	1329.438	-157.724	0.421	723.281	0.401	19	0.148	R.QLGEAASPEEGLK.R
R3/RRR3-16/2	1827.549	1828.059	-828.768	0.362	1029.087	0.347	19	0.147	K.ASEGFIYLVSTVGVTGAR.A
R3/RRR3-16/3	1921.565	1922.086	-793.865	0.480	1032.107	0.556	30	0.145	R.AEAAAVGEDERVISGTFAK.L
R3/RRR3-16/2	1044.118	1044.227	-104.201	0.391	791.425	0.322	15	0.144	K.VQSLLQDIK.Q
R3/RRR3-16/2	1043.959	1044.227	-257.269	0.431	834.151	0.316	14	0.144	K.VQSLLQDIK.Q
R3/RRR3-16/2	1043.622	1044.227	-1542.462	0.370	680.080	0.369	13	0.144	K.VQSLLQDIK.Q
R3/RRR3-16/2	1913.237	1913.162	39.446	0.394	772.222	0.389	19	0.144	K.NNLELVLLTTPTTPTER.M
R3/RRR3-16/2	1512.918	1512.735	121.342	0.455	564.673	0.414	16	0.138	K.AVAVGFGISTPEHVK.Q
R3/RRR3-16/2	1913.227	1913.162	34.070	0.401	719.130	0.356	17	0.137	K.NNLELVLLTTPTTPTER.M
R3/RRR3-12/2	1740.510	1739.942	-248.924	0.629	2083.946	0.519	23	0.311	R.LYEALDKCEEILSR.Q
R3/RRR3-12/2	1497.159	1497.546	-258.963	0.538	1904.903	0.591	22	0.303	R.SALDEVTDTGAFDR.S
R3/RRR3-12/2	1496.684	1497.546	-1248.070	0.367	2019.476	0.503	22	0.295	R.SALDEVTDTGAFDR.S
R3/RRR3-12/2	1740.378	1739.942	251.601	0.608	1949.713	0.531	23	0.293	R.LYEALDKCEEILSR.Q
R3/RRR3-12/2	1739.469	1739.942	-272.653	0.589	1853.566	0.518	22	0.273	R.LYEALDKCEEILSR.Q
R3/RRR3-12/2	1539.355	1539.666	-202.710	0.530	1903.177	0.462	21	0.267	R.YICGNQLTEADVR.L
R3/RRR3-12/2	1497.148	1497.546	-266.898	0.503	1683.098	0.531	21	0.252	R.SALDEVTDTGAFDR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1540.136	1539.666	306.175	0.575	1734.698	0.498	21	0.251	R.YICGNQLTEADVR.L
R3/RRR3-12/3	1888.976	1888.159	-96.947	0.483	1865.858	0.505	33	0.232	K.GLDHAIGFTSVKPIFER.T
R3/RRR3-12/2	1360.717	1361.484	-1301.787	0.460	1677.049	0.448	19	0.232	K.TVVNNESSEIIR.M
R3/RRR3-12/2	1361.086	1361.484	-293.038	0.437	1634.717	0.461	19	0.229	K.TVVNNESSEIIR.M
R3/RRR3-12/2	1361.031	1361.484	-333.172	0.459	1578.137	0.482	19	0.227	K.TVVNNESSEIIR.M
R3/RRR3-12/2	1539.129	1539.666	-1001.573	0.543	1479.735	0.497	20	0.218	R.YICGNQLTEADVR.L
R3/RRR3-12/2	1255.213	1255.403	-151.445	0.530	1603.188	0.376	16	0.207	R.FDEVYAVHFK.C
R3/RRR3-12/3	1887.809	1888.159	-185.795	0.521	1694.049	0.467	32	0.194	K.GLDHAIGFTSVKPIFER.T
R3/RRR3-10/2	1498.957	1497.546	274.889	0.340	1294.181	0.410	18	0.179	R.SALDEVTDTGAFDR.S
R3/RRR3-12/3	1888.842	1888.159	-168.127	0.532	1519.286	0.484	32	0.176	K.GLDHAIGFTSVKPIFER.T
R3/RRR3-12/3	1255.748	1255.403	275.857	0.475	1513.903	0.465	22	0.164	R.FDEVYAVHFK.C
R3/RRR3-12/2	1335.828	1336.432	-1204.598	0.449	1032.971	0.338	17	0.154	K.KQEPYDEAVTR.L
R3/RRR3-12/2	1326.073	1326.501	-323.607	0.480	1099.629	0.308	17	0.153	R.M*LNTEFNEIAK.N
R3/RRR3-12/3	1255.491	1255.403	70.389	0.436	1472.037	0.435	22	0.151	R.FDEVYAVHFK.C
R3/RRR3-12/3	1336.834	1336.432	301.209	0.553	1562.586	0.391	25	0.150	K.KQEPYDEAVTR.L
R3/RRR3-12/2	1336.057	1336.432	-282.125	0.426	996.149	0.316	17	0.150	K.KQEPYDEAVTR.L
R3/RRR3-12/3	1255.391	1255.403	-9.189	0.457	1475.843	0.433	24	0.148	R.FDEVYAVHFK.C
R3/RRR3-11/3	1336.525	1336.432	69.602	0.510	1601.017	0.352	24	0.145	K.KQEPYDEAVTR.L
R3/RRR3-12/2	1335.608	1336.432	-1369.895	0.423	968.826	0.287	17	0.145	K.KQEPYDEAVTR.L
R3/RRR3-12/2	1326.281	1326.501	-166.619	0.483	782.264	0.323	17	0.143	R.M*LNTEFNEIAK.N
R3/RRR3-12/2	1325.442	1326.501	-1558.434	0.411	760.799	0.264	16	0.137	R.M*LNTEFNEIAK.N
R3/RRR3-12/3	1336.388	1336.432	-33.323	0.542	1337.369	0.380	24	0.128	K.KQEPYDEAVTR.L
R3/RRR3-11/3	1336.524	1336.432	68.503	0.448	780.485	0.309	19	0.092	-.KQEPYDEAVTR.-
R3/RRR3-15/2	1401.008	1401.636	-1165.072	0.466	1513.725	0.523	20	0.229	R.TIKDEGVIALWR.G
R3/RRR3-15/2	1401.128	1401.636	-1079.161	0.435	1395.993	0.493	19	0.208	R.TIKDEGVIALWR.G
R3/RRR3-15/2	1401.496	1401.636	-100.082	0.478	1124.466	0.476	18	0.180	R.TIKDEGVIALWR.G
R3/RRR3-15/3	1401.279	1401.636	-255.503	0.509	1745.429	0.348	26	0.162	R.TIKDEGVIALWR.G
R3/RRR3-15/2	895.813	895.976	-183.367	0.267	736.232	0.363	12	0.140	K.GIADCFGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	895.375	895.976	-1793.471	0.225	674.225	0.431	12	0.140	K.GIADCFGR.T
R3/RRR3-15/3	1401.511	1401.636	-89.302	0.455	1375.397	0.247	25	0.105	R.TIKDEGVIALWR.G
R3/RRR3-10/2	1525.794	1524.699	62.141	0.573	2864.020	0.616	23	0.526	K.AWAGLLNAFCTSGR.L
R3/RRR3-10/2	1688.974	1688.818	92.238	0.531	1843.632	0.463	20	0.259	K.FLQSLEFFEENER.K
R3/RRR3-10/2	1255.031	1255.316	-227.659	0.507	1641.114	0.534	17	0.248	K.SIESSDLNFSR.Y
R3/RRR3-10/2	1254.781	1255.316	-1227.078	0.477	1545.255	0.527	17	0.233	K.SIESSDLNFSR.Y
R3/RRR3-10/2	1254.939	1255.316	-301.336	0.434	1220.583	0.419	16	0.177	K.SIESSDLNFSR.Y
R3/RRR3-10/3	1406.492	1406.526	-24.350	0.568	1692.323	0.427	27	0.175	K.RTSEALSEHFTK.E
R3/RRR3-10/2	1557.278	1557.749	-303.975	0.436	1066.942	0.430	17	0.166	K.M*EDNLLEFFPSAK.R
R3/RRR3-10/2	1639.369	1639.960	-973.118	0.402	640.541	0.479	20	0.151	K.LSGLPPETVFQPLLK.D
R3/RRR3-10/2	1374.353	1374.650	-217.070	0.476	696.537	0.430	18	0.151	R.EAILPSVLYIQK.T
R3/RRR3-10/2	1639.406	1639.960	-950.692	0.376	738.064	0.382	21	0.145	K.LSGLPPETVFQPLLK.D
R3/RRR3-10/2	1559.027	1557.749	178.407	0.465	761.761	0.406	14	0.144	K.M*EDNLLEFFPSAK.R
R3/RRR3-10/2	1639.292	1639.960	-1020.218	0.341	596.464	0.396	21	0.142	K.LSGLPPETVFQPLLK.D
R3/RRR3-10/2	975.099	975.123	-24.373	0.480	794.316	0.369	13	0.142	-.FPDIEVVR.-
R3/RRR3-10/2	1374.164	1374.650	-354.935	0.373	681.109	0.342	17	0.140	R.EAILPSVLYIQK.T
R3/RRR3-10/3	1406.562	1406.526	25.921	0.536	1274.994	0.432	24	0.136	K.RTSEALSEHFTK.E
R3/RRR3-9/3	1406.049	1406.526	-340.452	0.444	1522.294	0.332	24	0.135	K.RTSEALSEHFTK.E
R3/RRR3-10/3	1406.427	1406.526	-70.708	0.521	1226.607	0.419	24	0.129	K.RTSEALSEHFTK.E
R3/RRR3-10/2	974.912	975.123	-217.531	0.458	610.411	0.285	12	0.125	-.FPDIEVVR.-
R3/RRR3-3/2	1648.279	1648.802	-926.632	0.517	2869.821	0.485	25	0.471	K.YLAAEQGGGQTIVANR.V
R3/RRR3-3/2	1648.489	1648.802	-190.702	0.518	2647.669	0.462	24	0.408	K.YLAAEQGGGQTIVANR.V
R3/RRR3-3/2	1624.188	1623.746	272.615	0.615	1977.428	0.578	22	0.307	R.LAGESNTELLDFASR.F
R3/RRR3-8/2	1268.078	1268.403	-256.889	0.493	1966.550	0.524	18	0.293	R.FAQAQLDVYGR.A
R3/RRR3-2/2	1623.430	1623.746	-195.078	0.547	1967.829	0.535	21	0.293	R.LAGESNTELLDFASR.F
R3/RRR3-8/2	1268.167	1268.403	-186.876	0.520	1965.258	0.485	18	0.282	R.FAQAQLDVYGR.A
R3/RRR3-3/2	1624.758	1623.746	7.640	0.612	1758.973	0.602	22	0.279	R.LAGESNTELLDFASR.F
R3/RRR3-2/2	1624.018	1623.746	168.001	0.562	1832.187	0.561	21	0.278	R.LAGESNTELLDFASR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1623.348	1623.746	-245.696	0.557	1829.344	0.556	21	0.277	R.LAGESNTELLDFASR.F
R3/RRR3-3/2	1268.121	1268.403	-223.185	0.466	1830.953	0.505	18	0.267	R.FAQAQLDVYGR.A
R3/RRR3-8/2	1267.650	1268.403	-1387.123	0.405	1885.501	0.428	18	0.254	R.FAQAQLDVYGR.A
R3/RRR3-3/2	1268.177	1268.403	-178.475	0.485	1782.151	0.479	17	0.252	R.FAQAQLDVYGR.A
R3/RRR3-3/2	1263.129	1263.340	-167.944	0.424	1302.987	0.562	15	0.211	K.YYQDAYNAVR.K
R3/RRR3-2/2	1262.884	1263.340	-361.876	0.378	1415.858	0.427	16	0.197	K.YYQDAYNAVR.K
R3/RRR3-2/2	1263.142	1263.340	-157.668	0.471	1290.983	0.481	15	0.195	K.YYQDAYNAVR.K
R3/RRR3-3/2	1262.993	1263.340	-275.567	0.422	1136.938	0.552	15	0.194	K.YYQDAYNAVR.K
R3/RRR3-3/2	1263.961	1263.340	-300.929	0.476	1258.667	0.486	15	0.194	K.YYQDAYNAVR.K
R3/RRR3-3/2	1267.509	1268.403	-1499.039	0.415	1361.691	0.424	16	0.190	R.FAQAQLDVYGR.A
R3/RRR3-1/2	1623.156	1623.746	-982.461	0.419	1097.048	0.415	19	0.166	R.LAGESNTELLDFASR.F
R3/RRR3-3/2	1179.125	1178.323	-168.694	0.400	1059.482	0.342	17	0.156	K.FISSNGLNAVR.I
R3/RRR3-2/2	1624.632	1623.746	-70.510	0.481	795.369	0.460	17	0.154	R.LAGESNTELLDFASR.F
R3/RRR3-3/2	1447.018	1447.618	-1108.735	0.489	708.797	0.472	14	0.150	K.NLNVEQNIEFVK.N
R3/RRR3-3/2	1107.992	1108.229	-214.885	0.446	836.601	0.344	14	0.147	R.INETTFNLR.V
R3/RRR3-2/2	1179.202	1178.323	-102.544	0.389	896.858	0.290	17	0.144	K.FISSNGLNAVR.I
R3/RRR3-3/2	1277.841	1278.436	-1252.267	0.323	982.075	0.272	15	0.140	K.DLLDGTQLQFK.S
R3/RRR3-3/2	1107.946	1108.229	-256.998	0.365	641.556	0.278	13	0.136	R.INETTFNLR.V
R3/RRR3-3/2	1179.223	1178.323	-85.306	0.414	838.062	0.222	16	0.135	K.FISSNGLNAVR.I
R3/RRR3-1/2	1623.835	1623.746	54.845	0.193	152.308	0.350	12	0.133	-.LAGESNTELLDFASR.-
R3/RRR3-3/2	1595.703	1596.767	-1297.533	0.268	772.993	0.273	16	0.131	R.VVASDWESFTLWR.V
R3/RRR3-3/2	1179.085	1178.323	-202.448	0.324	587.575	0.205	14	0.130	-.FISSNGLNAVR.-
R3/RRR3-2/2	1179.447	1178.323	105.510	0.357	578.399	0.174	14	0.121	-.FISSNGLNAVR.-
R3/RRR3-7/2	1408.913	1407.722	135.687	0.600	2673.533	0.545	20	0.445	K.MLIAMVETELEK.R
R3/RRR3-7/2	1414.231	1414.577	-244.713	0.490	2257.980	0.499	18	0.339	K.SVTDYITDIVCK.R
R3/RRR3-7/2	1415.328	1414.577	-175.923	0.550	1942.342	0.601	18	0.313	K.SVTDYITDIVCK.R
R3/RRR3-7/2	1652.235	1652.828	-966.726	0.396	1653.672	0.437	21	0.226	K.YVELTADYVYPYR.N
R3/RRR3-7/2	1243.143	1243.435	-235.154	0.434	1415.450	0.265	16	0.168	K.TIQEQLLLER.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1352.215	1352.520	-225.875	0.470	1271.138	0.325	17	0.166	K.FASLRDEWSLK.N
R3/RRR3-7/2	1234.964	1235.368	-328.319	0.463	1144.899	0.349	16	0.162	R.DKIETPEQFK.Q
R3/RRR3-7/2	1352.251	1352.520	-199.430	0.481	1252.542	0.312	15	0.160	K.FASLRDEWSLK.N
R3/RRR3-7/2	1651.645	1652.828	-1325.268	0.282	1124.205	0.378	18	0.160	K.YVELTADYVYPYR.N
R3/RRR3-7/2	1353.212	1352.520	-228.242	0.469	1267.764	0.283	16	0.158	K.FASLRDEWSLK.N
R3/RRR3-7/2	1235.107	1235.368	-212.100	0.433	1025.403	0.334	15	0.153	R.DKIETPEQFK.Q
R3/RRR3-7/2	1570.222	1570.763	-984.470	0.379	809.316	0.460	15	0.151	K.SVTDYITDIVCKR.A
R3/RRR3-7/2	1459.077	1459.576	-343.090	0.266	528.059	0.523	19	0.145	K.EVPTSFGFDTACK.I
R3/RRR3-7/2	1244.677	1243.435	195.299	0.421	685.573	0.358	13	0.142	K.TIQEQLLLER.D
R3/RRR3-7/2	1235.147	1235.368	-179.381	0.387	794.320	0.297	14	0.140	R.DKIETPEQFK.Q
R3/RRR3-7/2	1458.974	1459.576	-1101.244	0.282	370.655	0.454	18	0.139	K.EVPTSFGFDTACK.I
R3/RRR3-7/2	1244.432	1243.435	-2.225	0.399	897.487	0.260	14	0.139	K.TIQEQLLLER.D
R3/RRR3-7/2	1408.072	1407.722	249.503	0.294	777.472	0.245	14	0.131	K.MLIAMVETELEK.R
R3/RRR3-22/1	955.496	956.120	-1704.251	0.319	711.467	0.286	10	0.888	K.ALVAYYQK.Y
R3/RRR3-22/1	955.444	956.120	-1759.705	0.272	740.282	0.323	10	0.884	-.ALVAYYQK.-
R3/RRR3-22/2	884.944	885.043	-112.014	0.429	1067.228	0.486	13	0.179	R.TLLVADPR.R
R3/RRR3-22/2	1086.402	1087.297	-1748.820	0.395	1011.185	0.486	16	0.174	K.AFEPILLAGR.S
R3/RRR3-22/2	951.980	952.090	-115.251	0.492	976.717	0.467	13	0.172	K.TSQIYAIR.Q
R3/RRR3-23/2	1087.238	1087.297	-54.123	0.513	847.006	0.474	16	0.166	K.AFEPILLAGR.S
R3/RRR3-22/2	951.904	952.090	-195.521	0.462	939.155	0.440	13	0.166	K.TSQIYAIR.Q
R3/RRR3-22/2	1086.830	1087.297	-431.086	0.402	799.516	0.503	15	0.164	K.AFEPILLAGR.S
R3/RRR3-22/2	1086.894	1087.297	-371.695	0.370	823.053	0.502	15	0.164	K.AFEPILLAGR.S
R3/RRR3-23/2	1087.082	1087.297	-198.182	0.370	944.883	0.417	16	0.160	K.AFEPILLAGR.S
R3/RRR3-23/2	952.067	952.090	-23.548	0.406	1063.133	0.360	13	0.160	K.TSQIYAIR.Q
R3/RRR3-22/2	955.987	956.120	-139.102	0.407	894.801	0.426	13	0.160	K.ALVAYYQK.Y
R3/RRR3-21/2	951.559	952.090	-1613.787	0.414	832.618	0.439	13	0.160	K.TSQIYAIR.Q
R3/RRR3-22/2	951.496	952.090	-1679.389	0.392	949.660	0.383	13	0.158	K.TSQIYAIR.Q
R3/RRR3-23/2	951.389	952.090	-1792.441	0.422	766.902	0.432	13	0.157	K.TSQIYAIR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	884.866	885.043	-200.717	0.333	842.779	0.448	11	0.156	R.TLLVADPR.R
R3/RRR3-23/2	955.739	956.120	-399.579	0.393	783.933	0.435	13	0.156	K.ALVAYYQK.Y
R3/RRR3-22/2	1087.131	1087.297	-152.448	0.297	783.751	0.488	14	0.156	K.AFEPILLAGR.S
R3/RRR3-23/2	885.077	885.043	38.926	0.354	911.533	0.398	11	0.155	R.TLLVADPR.R
R3/RRR3-23/2	955.996	956.120	-129.623	0.434	759.604	0.405	13	0.153	K.ALVAYYQK.Y
R3/RRR3-22/2	884.508	885.043	-1741.174	0.365	883.453	0.393	11	0.153	R.TLLVADPR.R
R3/RRR3-23/2	1309.147	1309.490	-262.485	0.403	800.924	0.435	16	0.153	K.TAVAVSYCKPGR.G
R3/RRR3-22/2	955.934	956.120	-195.337	0.421	761.333	0.392	13	0.152	K.ALVAYYQK.Y
R3/RRR3-23/2	951.867	952.090	-234.117	0.364	957.281	0.336	13	0.152	K.TSQIYAIR.Q
R3/RRR3-21/2	951.861	952.090	-241.193	0.353	844.340	0.377	13	0.152	K.TSQIYAIR.Q
R3/RRR3-20/2	884.962	885.043	-91.397	0.323	839.747	0.399	12	0.152	R.TLLVADPR.R
R3/RRR3-23/2	1309.212	1309.490	-213.281	0.374	758.865	0.438	16	0.151	K.TAVAVSYCKPGR.G
R3/RRR3-21/2	1087.163	1087.297	-123.726	0.338	539.842	0.483	13	0.149	K.AFEPILLAGR.S
R3/RRR3-22/2	955.966	956.120	-161.903	0.345	833.566	0.327	13	0.146	K.ALVAYYQK.Y
R3/RRR3-22/2	884.964	885.043	-89.875	0.300	626.218	0.405	10	0.143	R.TLLVADPR.R
R3/RRR3-22/2	1086.840	1087.297	-421.393	0.358	638.135	0.364	13	0.143	K.AFEPILLAGR.S
R3/RRR3-21/2	951.984	952.090	-110.878	0.389	717.151	0.295	13	0.143	K.TSQIYAIR.Q
R3/RRR3-22/2	1308.431	1309.490	-1578.107	0.359	619.301	0.398	15	0.142	K.TAVAVSYCKPGR.G
R3/RRR3-22/2	1040.432	1041.229	-1733.242	0.404	658.267	0.363	12	0.141	R.TLLVADPRR.C
R3/RRR3-21/2	1087.105	1087.297	-176.892	0.304	633.343	0.359	13	0.141	K.AFEPILLAGR.S
R3/RRR3-22/2	1327.811	1328.628	-1372.315	0.261	757.906	0.328	15	0.135	R.LKAFEPILLAGR.S
R3/RRR3-19/2	885.091	885.043	54.142	0.271	613.296	0.233	11	0.134	R.TLLVADPR.R
R3/RRR3-22/2	1040.488	1041.229	-1678.430	0.392	596.121	0.263	12	0.134	R.TLLVADPRR.C
R3/RRR3-10/2	1906.477	1907.088	-847.429	0.572	2069.957	0.546	24	0.315	K.LSYIALDYDQEM*ETAK.T
R3/RRR3-10/2	1906.433	1907.088	-870.955	0.591	2070.140	0.530	24	0.309	K.LSYIALDYDQEM*ETAK.T
R3/RRR3-10/2	1907.236	1907.088	77.841	0.642	1951.056	0.579	23	0.302	K.LSYIALDYDQEM*ETAK.T
R3/RRR3-10/2	1890.541	1891.089	-821.036	0.581	1847.680	0.554	23	0.280	K.LSYIALDYDQEMETAK.T
R3/RRR3-10/2	1890.404	1891.089	-893.635	0.558	1561.173	0.557	22	0.239	K.LSYIALDYDQEMETAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1890.378	1891.089	-907.702	0.547	1482.091	0.519	22	0.221	K.LSYIALDYDQEMETAK.T
R3/RRR3-10/2	1730.498	1730.933	-252.487	0.529	1972.350	0.474	23	0.280	R.FFYASSACIYPEFK.Q
R3/RRR3-10/2	1282.963	1283.370	-317.753	0.527	1720.931	0.586	21	0.272	K.TQGVDIAGYGSSK.V
R3/RRR3-10/2	1283.131	1283.370	-186.891	0.520	1714.071	0.580	21	0.269	K.TQGVDIAGYGSSK.V
R3/RRR3-10/2	1730.211	1730.933	-998.664	0.472	1979.418	0.422	22	0.266	R.FFYASSACIYPEFK.Q
R3/RRR3-10/2	1730.333	1730.933	-927.693	0.504	1823.102	0.494	22	0.262	R.FFYASSACIYPEFK.Q
R3/RRR3-10/2	1283.173	1283.370	-153.489	0.502	1687.459	0.561	21	0.261	K.TQGVDIAGYGSSK.V
R3/RRR3-9/2	1282.957	1283.370	-322.240	0.453	1754.756	0.507	21	0.256	K.TQGVDIAGYGSSK.V
R3/RRR3-9/2	1556.561	1557.779	-1429.113	0.428	1649.377	0.416	22	0.218	R.ISITGAGGFIGSHIAR.R
R3/RRR3-9/2	1557.210	1557.779	-1010.701	0.456	1553.335	0.451	21	0.214	R.ISITGAGGFIGSHIAR.R
R3/RRR3-10/2	1558.211	1557.779	277.951	0.512	1494.616	0.480	21	0.213	R.ISITGAGGFIGSHIAR.R
R3/RRR3-9/2	1557.448	1557.779	-213.327	0.451	1534.858	0.434	21	0.208	R.ISITGAGGFIGSHIAR.R
R3/RRR3-10/2	1456.206	1455.685	-329.810	0.574	1247.087	0.561	21	0.207	K.VVSTQAPVQLGSLR.A
R3/RRR3-10/2	1455.427	1455.685	-177.385	0.524	1321.489	0.514	20	0.204	K.VVSTQAPVQLGSLR.A
R3/RRR3-9/3	1455.903	1455.685	150.346	0.486	1782.569	0.439	28	0.196	K.VVSTQAPVQLGSLR.A
R3/RRR3-10/2	1556.664	1557.779	-1362.635	0.430	1370.382	0.425	20	0.189	R.ISITGAGGFIGSHIAR.R
R3/RRR3-9/2	1455.186	1455.685	-343.503	0.535	1264.959	0.449	21	0.186	K.VVSTQAPVQLGSLR.A
R3/RRR3-9/2	1456.395	1455.685	-199.629	0.574	1204.606	0.470	20	0.184	K.VVSTQAPVQLGSLR.A
R3/RRR3-10/2	1455.193	1455.685	-338.874	0.498	1182.231	0.462	21	0.182	K.VVSTQAPVQLGSLR.A
R3/RRR3-9/2	1455.340	1455.685	-237.716	0.512	1077.833	0.502	20	0.181	K.VVSTQAPVQLGSLR.A
R3/RRR3-10/2	1406.218	1406.524	-218.855	0.434	1233.066	0.412	17	0.176	K.SEGHYIIASDWK.K
R3/RRR3-9/2	1283.071	1283.370	-233.371	0.354	1032.677	0.448	18	0.167	K.TQGVDIAGYGSSK.V
R3/RRR3-10/2	1906.453	1906.983	-804.871	0.427	721.162	0.515	22	0.158	K.ESDAWPAEPQDAYGLEK.L
R3/RRR3-9/2	1467.461	1467.654	-132.044	0.423	787.499	0.440	16	0.154	R.FHNIYGPFGTWK.G
R3/RRR3-10/2	1907.336	1906.983	185.349	0.516	522.522	0.538	20	0.154	K.ESDAWPAEPQDAYGLEK.L
R3/RRR3-10/2	1468.471	1467.654	-125.533	0.487	840.103	0.415	16	0.154	R.FHNIYGPFGTWK.G
R3/RRR3-10/2	1468.374	1467.654	-191.664	0.476	733.095	0.424	15	0.150	R.FHNIYGPFGTWK.G
R3/RRR3-10/2	1467.451	1467.654	-139.137	0.417	805.707	0.386	16	0.149	R.FHNIYGPFGTWK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1906.341	1906.983	-863.814	0.446	464.001	0.497	19	0.147	K.ESDAWPAEPQDAYGLEK.L
R3/RRR3-11/2	1732.054	1730.933	69.939	0.311	250.167	0.490	18	0.145	R.FFYASSACIYPEFK.Q
R3/RRR3-9/2	1467.238	1467.654	-284.605	0.351	715.852	0.371	16	0.144	R.FHNIYGPFGTWK.G
R3/RRR3-10/3	1467.538	1467.654	-79.777	0.441	1376.039	0.427	25	0.142	R.FHNIYGPFGTWK.G
R3/RRR3-11/2	1468.361	1467.654	-200.254	0.343	586.005	0.360	15	0.141	R.FHNIYGPFGTWK.G
R3/RRR3-9/2	1467.458	1467.654	-133.880	0.375	497.693	0.369	13	0.137	-.FHNIYGPFGTWK.-
R3/RRR3-10/2	1731.601	1730.933	-192.791	0.277	425.342	0.293	12	0.131	R.FFYASSACIYPEFK.Q
R3/RRR3-9/2	1283.136	1283.370	-182.310	0.258	652.417	0.156	16	0.129	K.TQGVDIAGYGSSK.V
R3/RRR3-9/3	1467.691	1467.654	25.091	0.454	1103.405	0.445	23	0.126	R.FHNIYGPFGTWK.G
R3/RRR3-10/3	1467.793	1467.654	94.783	0.409	1055.361	0.436	24	0.120	R.FHNIYGPFGTWK.G
R3/RRR3-10/3	1407.590	1406.524	46.821	0.514	981.632	0.416	21	0.114	K.SEGHYIIASDWK.K
R3/RRR3-10/3	1673.777	1672.854	-46.174	0.376	1057.081	0.398	25	0.111	R.SFTFIDECVEGVLR.Y
R3/RRR3-10/3	1467.813	1467.654	108.170	0.416	1106.625	0.349	23	0.109	R.FHNIYGPFGTWK.G
R3/RRR3-11/3	1557.958	1557.779	115.467	0.363	541.563	0.511	22	0.108	R.ISITGAGGFIGSHIAR.R
R3/RRR3-10/3	1557.348	1557.779	-277.541	0.336	867.899	0.420	27	0.107	R.ISITGAGGFIGSHIAR.R
R3/RRR3-9/3	1455.724	1455.685	26.727	0.423	990.171	0.356	22	0.104	K.VVSTQAPVQLGSLR.A
R3/RRR3-10/3	1406.620	1406.524	68.049	0.460	754.580	0.349	19	0.097	K.SEGHYIIASDWK.K
R3/RRR3-9/3	1558.872	1557.779	59.989	0.298	351.993	0.408	19	0.095	R.ISITGAGGFIGSHIAR.R
R3/RRR3-9/3	1467.685	1467.654	21.087	0.378	1024.370	0.266	22	0.094	R.FHNIYGPFGTWK.G
R3/RRR3-10/3	1405.565	1406.524	-1398.240	0.385	919.542	0.295	20	0.094	K.SEGHYIIASDWK.K
R3/RRR3-9/3	1455.444	1455.685	-165.699	0.367	1288.286	0.184	24	0.092	K.VVSTQAPVQLGSLR.A
R3/RRR3-13/2	1766.320	1767.022	-966.395	0.533	1783.939	0.509	22	0.259	R.VLDTHVEGGNLFIVPR.F
R3/RRR3-13/2	1205.252	1205.299	-39.274	0.524	1637.967	0.469	18	0.231	R.AWDLAESDAVK.L
R3/RRR3-12/2	1766.535	1767.022	-276.099	0.533	1456.547	0.546	21	0.224	R.VLDTHVEGGNLFIVPR.F
R3/RRR3-13/2	1204.469	1205.299	-1523.722	0.408	1588.054	0.428	17	0.215	R.AWDLAESDAVK.L
R3/RRR3-12/2	1204.296	1205.299	-1668.409	0.381	1594.322	0.404	17	0.211	R.AWDLAESDAVK.L
R3/RRR3-12/2	1205.936	1205.299	-301.398	0.533	1520.469	0.439	17	0.209	R.AWDLAESDAVK.L
R3/RRR3-12/2	1734.521	1734.932	-237.572	0.475	1164.923	0.618	24	0.207	K.LSLNAGGLALPSFSDSGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1734.508	1734.932	-244.986	0.457	1276.932	0.558	23	0.206	K.LSLNAGGLALPSFSDSGK.V
R3/RRR3-13/2	1204.787	1205.299	-1258.892	0.457	1482.686	0.420	17	0.202	R.AWDLAESDAVK.L
R3/RRR3-12/2	1186.108	1186.383	-232.423	0.468	1161.155	0.506	20	0.190	K.LVSSQPASGIVK.I
R3/RRR3-13/2	1734.140	1734.932	-1036.151	0.489	1108.213	0.551	24	0.190	K.LSLNAGGLALPSFSDSGK.V
R3/RRR3-13/2	1734.287	1734.932	-951.205	0.441	1094.828	0.559	23	0.189	K.LSLNAGGLALPSFSDSGK.V
R3/RRR3-13/2	1186.019	1186.383	-308.214	0.456	1138.630	0.509	20	0.189	K.LVSSQPASGIVK.I
R3/RRR3-12/2	1204.479	1205.299	-1515.476	0.360	1435.583	0.376	17	0.188	R.AWDLAESDAVK.L
R3/RRR3-12/2	1186.124	1186.383	-218.898	0.470	1055.850	0.498	19	0.180	K.LVSSQPASGIVK.I
R3/RRR3-12/2	1734.527	1734.932	-233.901	0.455	1005.901	0.541	23	0.179	K.LSLNAGGLALPSFSDSGK.V
R3/RRR3-13/2	1185.539	1186.383	-1560.652	0.416	1044.668	0.505	19	0.179	K.LVSSQPASGIVK.I
R3/RRR3-13/2	1735.267	1734.932	193.709	0.454	937.305	0.571	22	0.178	K.LSLNAGGLALPSFSDSGK.V
R3/RRR3-13/2	1399.373	1398.740	-263.147	0.472	896.121	0.493	18	0.167	R.VVVLNTANLPMVK.E
R3/RRR3-12/2	1186.012	1186.383	-313.894	0.447	887.124	0.484	18	0.166	K.LVSSQPASGIVK.I
R3/RRR3-13/2	1414.263	1414.739	-337.826	0.354	989.106	0.456	17	0.164	R.VVVLNTANLPM*VK.E
R3/RRR3-12/2	1028.877	1029.172	-287.696	0.374	920.871	0.417	17	0.160	K.EVGLGADLVR.I
R3/RRR3-12/2	1905.085	1905.153	-36.245	0.463	777.318	0.505	21	0.159	R.EGM*ALNCLEAPLDVDIK.N
R3/RRR3-13/2	1186.118	1186.383	-224.267	0.468	883.499	0.422	18	0.158	K.LVSSQPASGIVK.I
R3/RRR3-13/2	1888.414	1889.154	-924.077	0.408	971.478	0.408	19	0.154	R.EGMALNCLEAPLDVDIK.N
R3/RRR3-12/2	1029.046	1029.172	-123.575	0.431	669.868	0.440	15	0.153	K.EVGLGADLVR.I
R3/RRR3-13/2	1028.617	1029.172	-1516.160	0.351	757.126	0.431	15	0.152	K.EVGLGADLVR.I
R3/RRR3-12/2	1414.107	1414.739	-1157.450	0.288	955.899	0.385	16	0.151	R.VVVLNTANLPM*VK.E
R3/RRR3-13/2	1029.045	1029.172	-124.289	0.419	648.495	0.417	14	0.149	K.EVGLGADLVR.I
R3/RRR3-13/2	877.874	878.051	-201.549	0.447	589.617	0.411	12	0.149	K.VAYVLQGK.G
R3/RRR3-13/2	877.988	878.051	-71.135	0.413	592.905	0.398	12	0.147	K.VAYVLQGK.G
R3/RRR3-13/2	1029.042	1029.172	-126.787	0.397	550.620	0.414	14	0.147	K.EVGLGADLVR.I
R3/RRR3-13/2	1413.848	1414.739	-1341.423	0.276	946.547	0.321	16	0.144	R.VVVLNTANLPM*VK.E
R3/RRR3-12/2	1028.913	1029.172	-253.058	0.386	576.667	0.385	13	0.144	K.EVGLGADLVR.I
R3/RRR3-13/2	877.902	878.051	-169.884	0.328	389.829	0.321	10	0.139	K.VAYVLQGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	878.110	878.051	67.749	0.401	411.988	0.219	11	0.135	-.VAYVLQGK.-
R3/RRR3-13/2	1398.158	1398.740	-1134.609	0.273	493.995	0.329	14	0.135	R.VVVLNTANLPMVK.E
R3/RRR3-12/2	1414.268	1414.739	-334.362	0.263	638.736	0.325	13	0.134	R.VVVLNTANLPM*VK.E
R3/RRR3-8/2	1836.535	1836.033	-271.976	0.583	2891.998	0.531	27	0.496	R.VPYTSGLGLDALGVETDK.G
R3/RRR3-8/2	1104.465	1105.224	-1597.391	0.387	899.211	0.577	19	0.178	K.VVGVDTSGSGVK.L
R3/RRR3-8/2	1104.990	1105.224	-212.034	0.450	746.545	0.550	18	0.167	K.VVGVDTSGSGVK.L
R3/RRR3-8/2	1104.748	1105.224	-431.963	0.436	709.250	0.539	18	0.164	K.VVGVDTSGSGVK.L
R3/RRR3-10/2	1638.390	1638.910	-930.506	0.507	1792.585	0.626	25	0.293	R.TPMGGFLGALSSLSATK.L
R3/RRR3-10/2	1198.040	1198.397	-299.194	0.506	1857.724	0.537	18	0.281	K.AQELGLQVIAR.I
R3/RRR3-10/2	1198.266	1198.397	-109.802	0.485	1864.138	0.513	18	0.275	K.AQELGLQVIAR.I
R3/RRR3-10/2	1655.273	1654.910	220.282	0.435	1776.342	0.564	24	0.272	R.TPM*GGFLGALSSLSATK.L
R3/RRR3-10/2	1540.051	1539.543	-320.201	0.512	1872.969	0.470	19	0.263	R.EDQDAYAIQSNER.G
R3/RRR3-10/2	1539.113	1539.543	-279.985	0.541	1683.253	0.488	20	0.241	R.EDQDAYAIQSNER.G
R3/RRR3-10/2	1198.169	1198.397	-191.253	0.449	1560.296	0.459	17	0.220	K.AQELGLQVIAR.I
R3/RRR3-10/2	1097.016	1097.419	-368.712	0.504	1604.058	0.400	17	0.213	R.ILVTLLGVLR.E
R3/RRR3-10/2	1638.686	1638.910	-137.150	0.492	1273.510	0.591	22	0.213	R.TPMGGFLGALSSLSATK.L
R3/RRR3-10/2	1942.362	1942.207	80.268	0.520	1301.049	0.574	23	0.212	R.NSGAFAWEIVPIEVPVGR.G
R3/RRR3-10/2	1088.959	1089.185	-208.072	0.502	1308.249	0.536	18	0.210	K.ALANAGLESSR.V
R3/RRR3-10/2	1941.822	1942.207	-198.464	0.473	1172.573	0.614	22	0.206	R.NSGAFAWEIVPIEVPVGR.G
R3/RRR3-10/2	1089.086	1089.185	-90.455	0.483	1159.410	0.543	17	0.196	K.ALANAGLESSR.V
R3/RRR3-10/2	1088.432	1089.185	-1615.297	0.432	1162.931	0.509	17	0.189	K.ALANAGLESSR.V
R3/RRR3-10/3	1941.366	1942.207	-950.910	0.300	1842.338	0.363	33	0.184	R.NSGAFAWEIVPIEVPVGR.G
R3/RRR3-10/2	974.960	975.118	-163.144	0.369	1502.075	0.291	14	0.183	-.DVCVVGVAR.-
R3/RRR3-10/2	1538.563	1539.543	-1290.653	0.337	1344.193	0.396	19	0.183	R.EDQDAYAIQSNER.G
R3/RRR3-10/2	1655.760	1654.910	-90.947	0.479	849.223	0.564	19	0.170	R.TPM*GGFLGALSSLSATK.L
R3/RRR3-10/2	1638.596	1638.910	-192.226	0.450	822.298	0.530	20	0.164	R.TPMGGFLGALSSLSATK.L
R3/RRR3-10/2	974.347	975.118	-1823.342	0.368	1348.082	0.238	14	0.159	R.DVCVVGVAR.T
R3/RRR3-10/2	1941.014	1942.207	-1133.120	0.474	874.224	0.469	21	0.158	R.NSGAFAWEIVPIEVPVGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	974.938	975.118	-185.376	0.398	1256.231	0.250	14	0.155	R.DVCVVGVAR.T
R3/RRR3-9/2	1942.070	1942.207	-70.774	0.457	720.235	0.493	18	0.152	R.NSGAFAWEIVPIEVPVGR.G
R3/RRR3-10/3	1959.398	1960.180	-912.071	0.463	1002.555	0.500	31	0.131	K.INVHGGAVSLGHPLGCSGAR.I
R3/RRR3-10/3	1959.265	1960.180	-980.655	0.495	946.923	0.496	32	0.126	K.INVHGGAVSLGHPLGCSGAR.I
R3/RRR3-10/3	1958.686	1960.180	-1277.146	0.406	1042.987	0.386	32	0.112	K.INVHGGAVSLGHPLGCSGAR.I
R3/RRR3-19/2	1632.384	1632.831	-274.413	0.543	2968.270	0.457	23	0.475	K.TIAECLADELINAAK.G
R3/RRR3-20/2	1632.168	1632.831	-1022.196	0.509	2997.177	0.435	23	0.475	K.TIAECLADELINAAK.G
R3/RRR3-19/2	1632.211	1632.831	-995.389	0.457	2778.260	0.426	22	0.419	K.TIAECLADELINAAK.G
R3/RRR3-18/2	1632.404	1632.831	-262.259	0.500	2625.513	0.491	22	0.407	K.TIAECLADELINAAK.G
R3/RRR3-20/2	1632.286	1632.831	-949.438	0.512	2647.638	0.446	22	0.395	K.TIAECLADELINAAK.G
R3/RRR3-19/2	1632.517	1632.831	-193.167	0.539	2621.475	0.461	22	0.394	K.TIAECLADELINAAK.G
R3/RRR3-20/2	1632.409	1632.831	-259.558	0.527	2408.689	0.430	21	0.339	K.TIAECLADELINAAK.G
R3/RRR3-20/2	1420.217	1420.639	-297.907	0.516	2138.177	0.543	21	0.326	R.VNQAIYLLTTGAR.E
R3/RRR3-19/2	1419.869	1420.639	-1250.400	0.416	2109.980	0.534	21	0.318	R.VNQAIYLLTTGAR.E
R3/RRR3-19/2	1420.255	1420.639	-271.434	0.522	2068.037	0.529	20	0.309	R.VNQAIYLLTTGAR.E
R3/RRR3-20/2	1420.364	1420.639	-193.918	0.501	1962.594	0.515	20	0.287	R.VNQAIYLLTTGAR.E
R3/RRR3-20/3	1633.927	1632.831	58.882	0.612	2421.606	0.380	33	0.278	K.TIAECLADELINAAK.G
R3/RRR3-18/2	1632.252	1632.831	-970.085	0.440	2060.584	0.368	19	0.261	K.TIAECLADELINAAK.G
R3/RRR3-19/2	1420.460	1420.639	-126.070	0.468	1732.634	0.526	20	0.256	R.VNQAIYLLTTGAR.E
R3/RRR3-19/3	1631.610	1632.831	-1365.150	0.506	2254.596	0.387	33	0.252	K.TIAECLADELINAAK.G
R3/RRR3-18/2	1419.872	1420.639	-1247.896	0.518	1622.606	0.488	19	0.231	R.VNQAIYLLTTGAR.E
R3/RRR3-19/2	1421.745	1420.639	74.525	0.437	1437.852	0.579	19	0.229	R.VNQAIYLLTTGAR.E
R3/RRR3-19/2	1421.005	1420.639	258.692	0.390	1350.776	0.506	18	0.203	R.VNQAIYLLTTGAR.E
R3/RRR3-19/2	1422.013	1420.639	263.674	0.473	1034.126	0.624	17	0.196	R.VNQAIYLLTTGAR.E
R3/RRR3-19/2	1225.132	1224.354	-181.447	0.430	651.169	0.575	18	0.168	K.HATYLPHTAGR.Y
R3/RRR3-19/2	1576.350	1576.825	-302.187	0.602	553.001	0.603	19	0.168	R.RVNQAIYLLTTGAR.E
R3/RRR3-20/2	1577.358	1576.825	-297.259	0.593	512.884	0.612	18	0.166	R.RVNQAIYLLTTGAR.E
R3/RRR3-19/2	1577.267	1576.825	280.803	0.580	611.614	0.567	20	0.166	R.RVNQAIYLLTTGAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1224.117	1224.354	-193.400	0.322	751.943	0.543	19	0.163	K.HATYLPHTAGR.Y
R3/RRR3-20/2	1575.818	1576.825	-1277.621	0.573	491.160	0.574	19	0.162	R.RVNQAIYLLTTGAR.E
R3/RRR3-20/2	1223.951	1224.354	-329.572	0.392	735.250	0.496	18	0.161	K.HATYLPHTAGR.Y
R3/RRR3-20/2	1224.027	1224.354	-267.635	0.407	591.958	0.554	16	0.161	K.HATYLPHTAGR.Y
R3/RRR3-19/2	1223.522	1224.354	-1501.595	0.334	676.406	0.543	17	0.160	K.HATYLPHTAGR.Y
R3/RRR3-18/2	1420.300	1420.639	-239.443	0.405	783.656	0.502	14	0.158	R.VNQAIYLLTTGAR.E
R3/RRR3-19/2	1223.888	1224.354	-381.510	0.350	547.343	0.546	16	0.156	K.HATYLPHTAGR.Y
R3/RRR3-19/2	1577.423	1576.825	-255.799	0.541	376.199	0.549	17	0.155	R.RVNQAIYLLTTGAR.E
R3/RRR3-20/2	1224.084	1224.354	-220.912	0.391	473.167	0.537	15	0.155	K.HATYLPHTAGR.Y
R3/RRR3-18/2	1420.680	1420.639	29.077	0.390	742.858	0.479	15	0.154	R.VNQAIYLLTTGAR.E
R3/RRR3-20/2	1575.563	1576.825	-1440.475	0.507	438.252	0.502	18	0.152	R.RVNQAIYLLTTGAR.E
R3/RRR3-19/2	1155.117	1155.333	-187.040	0.536	550.375	0.382	16	0.146	R.RQAVDISPLR.R
R3/RRR3-19/2	972.876	973.102	-233.088	0.361	560.219	0.414	11	0.145	K.AQCPLVER.L
R3/RRR3-19/2	972.801	973.102	-310.132	0.326	476.716	0.394	11	0.141	K.AQCPLVER.L
R3/RRR3-19/2	1223.912	1224.354	-361.495	0.262	264.714	0.460	12	0.140	K.HATYLPHTAGR.Y
R3/RRR3-19/2	1154.965	1155.333	-318.939	0.556	401.483	0.379	14	0.140	-.RQAVDISPLR.-
R3/RRR3-19/2	1155.088	1155.333	-212.060	0.529	405.770	0.327	14	0.140	R.RQAVDISPLR.R
R3/RRR3-2/2	1632.509	1632.831	-198.043	0.365	691.219	0.265	15	0.132	-.TIAECLADELINAAK.-
R3/RRR3-20/2	972.326	973.102	-1832.547	0.267	437.020	0.298	10	0.125	-.AQCPLVER.-
R3/RRR3-19/3	1224.366	1224.354	10.528	0.533	636.341	0.548	21	0.125	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1224.116	1224.354	-194.412	0.528	631.361	0.522	22	0.121	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.784	1224.354	352.407	0.562	515.672	0.531	20	0.121	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.488	1224.354	110.417	0.550	618.575	0.517	22	0.120	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.333	1224.354	-16.472	0.538	609.995	0.508	22	0.119	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.644	1224.354	237.874	0.542	756.820	0.475	23	0.116	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.549	1224.354	160.054	0.557	523.524	0.494	20	0.116	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.598	1224.354	200.390	0.557	532.321	0.493	20	0.116	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1224.569	1224.354	176.549	0.499	552.451	0.489	21	0.116	K.HATYLPHTAGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/3	1224.545	1224.354	157.055	0.501	452.697	0.483	19	0.115	K.HATYLPHTAGR.Y
R3/RRR3-17/3	1224.276	1224.354	-63.727	0.482	523.308	0.483	20	0.115	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1223.654	1224.354	-1392.831	0.523	589.962	0.478	21	0.115	K.HATYLPHTAGR.Y
R3/RRR3-18/3	1224.041	1224.354	-255.940	0.523	491.338	0.480	19	0.114	K.HATYLPHTAGR.Y
R3/RRR3-18/2	1632.391	1632.831	-270.137	0.343	679.594	0.094	14	0.114	-.TIAECLADELINAAK.-
R3/RRR3-19/3	1224.567	1224.354	175.049	0.511	554.773	0.475	20	0.114	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1223.845	1224.354	-1236.097	0.478	423.739	0.477	18	0.114	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.410	1224.354	46.526	0.452	452.393	0.478	18	0.114	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1224.465	1224.354	91.221	0.496	570.489	0.469	21	0.114	K.HATYLPHTAGR.Y
R3/RRR3-18/3	1224.295	1224.354	-48.275	0.540	512.967	0.467	20	0.113	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.553	1224.354	163.053	0.507	379.760	0.458	18	0.113	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.903	1224.354	-368.560	0.533	477.381	0.466	19	0.113	K.HATYLPHTAGR.Y
R3/RRR3-17/3	1225.404	1224.354	41.343	0.456	440.993	0.460	19	0.113	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1224.300	1224.354	-43.474	0.505	558.206	0.463	19	0.113	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1224.441	1224.354	71.724	0.484	626.336	0.447	21	0.111	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1225.098	1224.354	-209.597	0.469	267.787	0.496	15	0.111	-.HATYLPHTAGR.-
R3/RRR3-19/3	1224.510	1224.354	128.563	0.500	364.956	0.438	17	0.111	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.156	1224.354	-161.550	0.489	538.978	0.444	20	0.111	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1631.627	1632.831	-1355.118	0.385	1245.987	0.306	25	0.111	K.TIAECLADELINAAK.G
R3/RRR3-19/3	1224.346	1224.354	-6.422	0.436	452.874	0.431	19	0.110	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1223.875	1224.354	-391.929	0.490	495.052	0.430	19	0.110	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1224.352	1224.354	-0.872	0.439	545.149	0.433	20	0.110	K.HATYLPHTAGR.Y
R3/RRR3-19/3	1224.616	1224.354	214.634	0.437	527.440	0.427	21	0.109	K.HATYLPHTAGR.Y
R3/RRR3-20/3	1224.698	1224.354	282.251	0.373	356.576	0.387	17	0.108	K.HATYLPHTAGR.Y
R3/RRR3-13/3	1224.419	1224.354	54.026	0.358	342.409	0.362	16	0.107	K.HATYLPHTAGR.Y
R3/RRR3-18/3	1223.988	1224.354	-299.614	0.429	510.321	0.375	19	0.105	K.HATYLPHTAGR.Y
R3/RRR3-3/3	1224.786	1224.354	354.206	0.342	355.283	0.306	16	0.105	K.HATYLPHTAGR.Y
R3/RRR3-22/3	1223.861	1224.354	-403.488	0.442	477.756	0.414	17	0.105	-.HATYLPHTAGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/3	1224.277	1224.354	-62.527	0.418	443.381	0.336	19	0.104	K.HATYLPHTAGR.Y
R3/RRR3-21/3	1224.380	1224.354	22.078	0.388	399.812	0.385	18	0.104	-.HATYLPHTAGR.-
R3/RRR3-19/3	1101.776	1101.275	-454.754	0.466	1064.913	0.331	20	0.103	R.KAQCPLVER.L
R3/RRR3-23/3	1224.675	1224.354	263.361	0.401	359.197	0.329	17	0.103	-.HATYLPHTAGR.-
R3/RRR3-24/3	1223.995	1224.354	-293.761	0.365	391.892	0.337	17	0.102	-.HATYLPHTAGR.-
R3/RRR3-19/3	1101.953	1101.275	-293.518	0.436	701.182	0.295	19	0.094	R.KAQCPLVER.L
R3/RRR3-19/3	1631.572	1632.831	-1388.933	0.409	1059.511	0.244	24	0.092	K.TIAECLADELINAAK.G
R3/RRR3-20/3	1631.730	1632.831	-1291.778	0.383	1073.591	0.229	25	0.091	K.TIAECLADELINAAK.G
R3/RRR3-19/3	1101.128	1101.275	-134.400	0.439	856.588	0.246	18	0.090	R.KAQCPLVER.L
R3/RRR3-19/3	1101.059	1101.275	-196.457	0.382	638.639	0.266	18	0.089	-.KAQCPLVER.-
R3/RRR3-3/2	1496.388	1496.516	-86.372	0.478	2079.320	0.539	21	0.318	R.GYYEEATTDSFGR.F
R3/RRR3-2/2	1664.265	1664.798	-923.764	0.506	1845.764	0.486	24	0.262	K.FTPSAVAIDLNSGESR.E
R3/RRR3-3/2	1664.315	1664.798	-291.512	0.525	1743.116	0.478	24	0.246	K.FTPSAVAIDLNSGESR.E
R3/RRR3-3/2	1664.345	1664.798	-273.042	0.522	1668.387	0.512	24	0.244	K.FTPSAVAIDLNSGESR.E
R3/RRR3-3/2	1155.091	1155.288	-170.826	0.442	1851.911	0.400	19	0.244	K.FQVTGFSVGGR.V
R3/RRR3-3/2	1664.418	1664.798	-228.894	0.500	1645.820	0.514	24	0.242	K.FTPSAVAIDLNSGESR.E
R3/RRR3-3/2	1496.174	1496.516	-229.919	0.383	1668.172	0.473	20	0.235	R.GYYEEATTDSFGR.F
R3/RRR3-3/2	1965.682	1965.190	251.041	0.560	1483.978	0.496	25	0.215	K.TGLYLEGSVSPAISDVDIK.I
R3/RRR3-3/2	1173.110	1172.272	-138.457	0.505	1542.602	0.422	16	0.210	R.AVTDNLGYYR.L
R3/RRR3-3/2	1495.884	1496.516	-1094.370	0.342	1494.380	0.450	20	0.208	R.GYYEEATTDSFGR.F
R3/RRR3-2/2	1664.395	1664.798	-243.021	0.463	1316.984	0.485	22	0.197	K.FTPSAVAIDLNSGESR.E
R3/RRR3-3/2	1155.030	1155.288	-224.155	0.428	1356.082	0.370	19	0.182	K.FQVTGFSVGGR.V
R3/RRR3-3/2	1171.981	1172.272	-249.329	0.459	1264.593	0.387	16	0.177	R.AVTDNLGYYR.L
R3/RRR3-3/2	1154.999	1155.288	-250.768	0.448	1344.915	0.338	18	0.175	K.FQVTGFSVGGR.V
R3/RRR3-2/2	1155.029	1155.288	-225.109	0.284	1305.596	0.290	16	0.162	K.FQVTGFSVGGR.V
R3/RRR3-3/2	1171.445	1172.272	-1564.168	0.366	1011.520	0.308	16	0.149	R.AVTDNLGYYR.L
R3/RRR3-3/2	1162.192	1162.364	-147.975	0.319	598.031	0.461	16	0.144	R.GLIPGSIYSVR.V
R3/RRR3-3/2	906.845	907.006	-177.693	0.319	759.678	0.269	13	0.135	K.EGVFVEAR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1794.172	1795.057	-1053.739	0.395	871.084	0.547	28	0.128	K.AM*VTLTHGPENVKPQR.K
R3/RRR3-3/3	1794.364	1795.057	-946.157	0.428	668.121	0.588	26	0.125	K.AM*VTLTHGPENVKPQR.K
R3/RRR3-3/3	1317.648	1317.389	196.785	0.418	1231.232	0.175	22	0.087	R.ASHPNYEIETR.G
R3/RRR3-2/3	1318.555	1317.389	126.125	0.436	850.178	0.225	19	0.083	-.ASHPNYEIETR.-
R3/RRR3-3/3	1317.317	1317.389	-54.671	0.409	754.810	0.173	19	0.077	-.ASHPNYEIETR.-
R3/RRR3-8/2	1663.362	1663.805	-267.021	0.568	3049.454	0.498	25	0.520	K.ATDSESTEVILDAALK.S
R3/RRR3-8/2	1664.537	1663.805	-161.426	0.580	2979.463	0.531	25	0.515	K.ATDSESTEVILDAALK.S
R3/RRR3-8/2	1663.324	1663.805	-290.508	0.572	2709.500	0.522	23	0.442	K.ATDSESTEVILDAALK.S
R3/RRR3-8/2	1761.493	1761.914	-239.842	0.553	1663.149	0.459	22	0.229	K.VENQEGVVNFDEILR.E
R3/RRR3-8/2	1761.439	1761.914	-270.503	0.533	1424.164	0.452	21	0.200	K.VENQEGVVNFDEILR.E
R3/RRR3-8/2	1760.734	1761.914	-1241.838	0.452	1566.788	0.348	21	0.194	K.VENQEGVVNFDEILR.E
R3/RRR3-8/2	1155.887	1155.369	-418.466	0.468	990.137	0.611	19	0.193	R.GLVPLLAEGSAK.A
R3/RRR3-8/2	956.010	956.208	-207.552	0.512	1237.270	0.424	15	0.182	K.AALIVVLTR.G
R3/RRR3-8/2	955.991	956.208	-227.023	0.462	1332.987	0.374	15	0.181	K.AALIVVLTR.G
R3/RRR3-8/2	1186.629	1187.285	-1399.701	0.448	1206.886	0.385	17	0.172	K.ILAGLENDDAR.V
R3/RRR3-8/2	956.071	956.208	-143.252	0.509	1156.077	0.393	14	0.170	K.AALIVVLTR.G
R3/RRR3-8/2	1187.070	1187.285	-181.283	0.437	1101.661	0.395	17	0.166	K.ILAGLENDDAR.V
R3/RRR3-8/2	1813.946	1814.097	-83.198	0.543	629.313	0.579	22	0.165	R.SAPLPMSPLESLASSAVR.T
R3/RRR3-8/2	1813.464	1814.097	-903.261	0.495	566.477	0.579	20	0.160	R.SAPLPMSPLESLASSAVR.T
R3/RRR3-8/2	1814.568	1814.097	260.544	0.467	625.626	0.541	22	0.159	R.SAPLPMSPLESLASSAVR.T
R3/RRR3-8/2	1187.120	1187.285	-139.402	0.442	960.663	0.368	16	0.154	K.ILAGLENDDAR.V
R3/RRR3-8/2	1829.398	1830.096	-930.839	0.366	510.174	0.551	22	0.154	R.SAPLPM*SPLESLASSAVR.T
R3/RRR3-8/2	1205.098	1204.376	-231.136	0.424	973.861	0.351	17	0.152	R.GDLGM*EIPVEK.I
R3/RRR3-8/2	1154.891	1155.369	-415.434	0.299	747.689	0.475	19	0.152	R.GLVPLLAEGSAK.A
R3/RRR3-2/2	1761.119	1761.914	-1022.433	0.453	1031.946	0.350	18	0.151	K.VENQEGVVNFDEILR.E
R3/RRR3-7/2	1187.082	1187.285	-171.380	0.378	980.850	0.323	16	0.149	K.ILAGLENDDAR.V
R3/RRR3-2/2	1812.993	1814.097	-1163.834	0.356	512.545	0.518	19	0.148	R.SAPLPMSPLESLASSAVR.T
R3/RRR3-7/2	1813.919	1814.097	-98.386	0.402	465.123	0.509	19	0.148	R.SAPLPMSPLESLASSAVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1762.164	1761.914	142.324	0.451	729.139	0.440	16	0.148	K.VENQEGVVNFDEILR.E
R3/RRR3-8/2	1829.434	1830.096	-911.480	0.369	475.563	0.490	21	0.148	R.SAPLPM*SPLESLASSAVR.T
R3/RRR3-8/2	1155.011	1155.369	-311.400	0.266	576.288	0.438	16	0.141	R.GLVPLLAEGSAK.A
R3/RRR3-8/2	1828.414	1830.096	-2019.895	0.275	361.711	0.391	20	0.139	R.SAPLPM*SPLESLASSAVR.T
R3/RRR3-11/2	1761.431	1761.914	-274.745	0.265	308.367	0.316	15	0.136	K.VENQEGVVNFDEILR.E
R3/RRR3-2/2	1812.961	1814.097	-1181.751	0.265	253.410	0.347	13	0.134	R.SAPLPMSPLESLASSAVR.T
R3/RRR3-8/2	1055.980	1056.175	-185.189	0.194	1054.196	0.137	15	0.129	R.ETDAFM*VAR.G
R3/RRR3-8/2	1203.192	1204.376	-1820.277	0.264	655.169	0.199	14	0.129	-.GDLGM*EIPVEK.-
R3/RRR3-7/2	1814.737	1814.097	-198.667	0.374	256.455	0.354	14	0.129	-.SAPLPMSPLESLASSAVR.-
R3/RRR3-4/2	1760.911	1761.914	-1140.894	0.314	617.745	0.171	14	0.126	K.VENQEGVVNFDEILR.E
R3/RRR3-10/3	1935.892	1935.129	-122.710	0.402	1314.598	0.502	32	0.157	K.LASLADLYVNDAFGTAHR.A
R3/RRR3-10/2	999.400	1000.219	-1825.658	0.347	728.953	0.399	14	0.145	K.FSLAPLVPR.L
R3/RRR3-10/2	1851.344	1853.153	-2063.483	0.365	648.123	0.453	19	0.143	K.LVSELPNGSVLLLENVR.F
R3/RRR3-10/2	1432.040	1432.562	-1066.127	0.444	844.694	0.366	16	0.142	K.SVGDLTAADLEGKR.V
R3/RRR3-10/2	1540.393	1540.826	-282.217	0.375	590.110	0.400	18	0.138	K.GVSLLLPSDVIIADK.F
R3/RRR3-10/2	1447.942	1448.777	-1270.973	0.258	837.509	0.268	17	0.133	K.FLKPSVAGFLLQK.E
R3/RRR3-10/3	1935.224	1935.129	49.240	0.358	811.565	0.468	28	0.111	K.LASLADLYVNDAFGTAHR.A
R3/RRR3-8/2	1258.104	1257.423	-254.839	0.545	2232.712	0.383	17	0.299	-.GWNLNLAELAR.-
R3/RRR3-8/2	1257.203	1257.423	-175.455	0.507	1969.938	0.405	17	0.260	K.GWNLNLAELAR.I
R3/RRR3-9/2	1124.042	1124.318	-247.000	0.532	1653.644	0.548	17	0.254	R.LPANLIQAQR.D
R3/RRR3-8/2	1123.440	1124.318	-1676.888	0.548	1607.848	0.507	17	0.238	R.LPANLIQAQR.D
R3/RRR3-8/2	1123.720	1124.318	-1426.524	0.522	1484.702	0.537	17	0.230	R.LPANLIQAQR.D
R3/RRR3-9/2	1124.072	1124.318	-220.199	0.522	1397.543	0.551	17	0.223	R.LPANLIQAQR.D
R3/RRR3-8/2	1123.743	1124.318	-1406.229	0.536	1392.763	0.545	17	0.221	R.LPANLIQAQR.D
R3/RRR3-8/2	1965.270	1965.112	80.391	0.504	927.149	0.564	19	0.172	R.VGGLSNSEIADVFAEWNR.G
R3/RRR3-9/2	1123.448	1124.318	-1670.119	0.398	888.572	0.515	16	0.170	R.LPANLIQAQR.D
R3/RRR3-8/2	1209.745	1209.292	375.219	0.379	908.180	0.434	16	0.160	R.DLFGAHTYER.I
R3/RRR3-9/2	1057.244	1056.284	-37.824	0.396	948.356	0.384	13	0.154	R.TVVLLVQAGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1210.062	1209.292	-191.296	0.386	727.869	0.411	15	0.150	R.DLFGAHTYER.I
R3/RRR3-8/2	1209.683	1209.292	324.126	0.369	693.377	0.375	15	0.146	R.DLFGAHTYER.I
R3/RRR3-8/2	1055.410	1056.284	-1780.568	0.378	847.863	0.338	13	0.144	-.TVVLLVQAGR.-
R3/RRR3-8/2	1055.576	1056.284	-1623.239	0.360	843.930	0.329	13	0.143	R.TVVLLVQAGR.A
R3/RRR3-9/2	1256.398	1257.423	-1616.567	0.453	747.096	0.323	16	0.142	K.GWNLNLAELAR.I
R3/RRR3-8/2	1132.330	1132.341	-9.797	0.361	699.717	0.333	13	0.137	R.GFVLSLSRPR.T
R3/RRR3-8/2	1256.560	1257.423	-1486.961	0.317	811.881	0.243	15	0.135	K.GWNLNLAELAR.I
R3/RRR3-9/2	1209.891	1209.292	-333.200	0.274	712.479	0.244	15	0.134	R.DLFGAHTYER.I
R3/RRR3-8/2	1055.577	1056.284	-1621.845	0.336	624.033	0.272	12	0.133	-.TVVLLVQAGR.-
R3/RRR3-8/3	1573.472	1574.722	-1433.993	0.438	733.964	0.464	21	0.110	R.IDRPGSFHTEWTK.L
R3/RRR3-8/3	1574.445	1574.722	-176.193	0.438	1021.390	0.377	23	0.109	R.IDRPGSFHTEWTK.L
R3/RRR3-8/3	1575.150	1574.722	272.893	0.411	597.109	0.365	20	0.097	R.IDRPGSFHTEWTK.L
R3/RRR3-11/2	1560.692	1559.788	-61.788	0.544	1817.091	0.500	21	0.260	K.ATAELLFGADNPVLK.Q
R3/RRR3-11/2	1560.756	1559.788	-20.993	0.540	1715.531	0.507	20	0.247	K.ATAELLFGADNPVLK.Q
R3/RRR3-11/2	1560.611	1559.788	-113.728	0.503	1741.402	0.481	20	0.244	K.ATAELLFGADNPVLK.Q
R3/RRR3-10/2	1560.894	1559.788	68.038	0.527	1558.083	0.482	19	0.220	K.ATAELLFGADNPVLK.Q
R3/RRR3-10/2	1854.755	1854.988	-125.860	0.429	1220.851	0.521	21	0.218	K.CEYLADAIIDSFHNVS.-
R3/RRR3-10/2	1560.276	1559.788	313.758	0.422	1596.411	0.431	20	0.215	K.ATAELLFGADNPVLK.Q
R3/RRR3-10/2	1561.141	1559.788	226.373	0.542	1458.490	0.501	19	0.212	K.ATAELLFGADNPVLK.Q
R3/RRR3-11/2	1390.076	1390.568	-354.836	0.458	1273.481	0.527	22	0.203	R.VATLQSLSGTGSLR.L
R3/RRR3-10/2	1389.824	1390.568	-1258.843	0.419	1396.701	0.465	21	0.202	R.VATLQSLSGTGSLR.L
R3/RRR3-10/2	1390.206	1390.568	-261.096	0.454	1274.221	0.514	22	0.200	R.VATLQSLSGTGSLR.L
R3/RRR3-10/2	1389.801	1390.568	-1275.073	0.419	1296.729	0.504	22	0.200	R.VATLQSLSGTGSLR.L
R3/RRR3-10/2	973.053	973.192	-142.702	0.485	1310.829	0.389	17	0.182	R.ISLAGLSLAK.C
R3/RRR3-11/2	1532.504	1532.763	-169.182	0.430	1180.571	0.451	21	0.181	R.TEELQPYVLNVVK.K
R3/RRR3-11/2	973.003	973.192	-194.930	0.452	1284.092	0.395	17	0.181	R.ISLAGLSLAK.C
R3/RRR3-10/2	962.754	963.116	-376.892	0.461	1251.809	0.391	15	0.177	K.LNLGVGAYR.T
R3/RRR3-10/2	973.169	973.192	-24.044	0.516	1166.823	0.419	16	0.175	R.ISLAGLSLAK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	973.076	973.192	-119.673	0.485	1157.484	0.408	16	0.173	R.ISLAGLSLAK.C
R3/RRR3-11/2	1389.769	1390.568	-1298.273	0.424	964.562	0.497	21	0.172	R.VATLQSLSGTGSLR.L
R3/RRR3-10/2	1533.038	1532.763	179.808	0.515	1105.361	0.412	21	0.170	R.TEELQPYVLNVVK.K
R3/RRR3-10/2	889.860	890.065	-230.411	0.504	880.586	0.446	13	0.163	R.LAAAFIQR.Y
R3/RRR3-10/2	962.456	963.116	-1729.405	0.424	932.174	0.433	14	0.161	K.LNLGVGAYR.T
R3/RRR3-11/2	1389.717	1390.568	-1335.676	0.359	952.107	0.411	20	0.158	R.VATLQSLSGTGSLR.L
R3/RRR3-10/2	889.534	890.065	-1725.416	0.480	920.275	0.387	13	0.157	R.LAAAFIQR.Y
R3/RRR3-10/2	889.333	890.065	-1953.242	0.447	946.239	0.374	13	0.156	R.LAAAFIQR.Y
R3/RRR3-10/2	1531.937	1532.763	-1195.292	0.407	860.350	0.393	19	0.153	R.TEELQPYVLNVVK.K
R3/RRR3-11/2	1531.988	1532.763	-1161.926	0.404	940.132	0.355	20	0.152	R.TEELQPYVLNVVK.K
R3/RRR3-10/2	1532.769	1532.763	4.025	0.421	896.948	0.339	18	0.147	R.TEELQPYVLNVVK.K
R3/RRR3-10/3	1894.398	1894.117	148.540	0.437	1277.062	0.432	28	0.137	K.GENKEYLPIEGLAAFNK.A
R3/RRR3-10/2	1533.931	1532.763	109.862	0.215	287.262	0.313	15	0.136	R.TEELQPYVLNVVK.K
R3/RRR3-10/2	1854.434	1854.988	-840.389	0.362	640.988	0.457	19	0.048	K.CEYLADAIIDSFHNVS.-
R3/RRR3-10/2	1853.984	1854.988	-1084.214	0.349	558.784	0.431	18	0.034	K.CEYLADAIIDSFHNVS.-
R3/RRR3-14/2	1797.506	1798.032	-851.884	0.626	2675.086	0.592	26	0.460	K.KVLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1798.457	1798.032	236.736	0.608	2515.571	0.598	25	0.425	K.KVLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1798.393	1798.032	201.342	0.621	2433.658	0.598	26	0.407	K.KVLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1670.306	1669.860	267.800	0.579	2424.064	0.605	24	0.400	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1738.570	1738.962	-226.314	0.588	2286.387	0.616	21	0.381	K.SPFQEYTDLLAKPTK.A
R3/RRR3-14/2	1669.547	1669.860	-187.636	0.538	2355.696	0.566	24	0.372	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1739.286	1738.962	187.066	0.604	2212.328	0.607	21	0.362	K.SPFQEYTDLLAKPTK.A
R3/RRR3-14/2	1669.616	1669.860	-146.489	0.528	2249.094	0.540	23	0.342	K.VLQFAGIEDVFTSSR.G
R3/RRR3-12/2	1669.745	1669.860	-68.898	0.433	2061.501	0.533	21	0.305	K.VLQFAGIEDVFTSSR.G
R3/RRR3-15/2	1670.377	1669.860	-290.088	0.550	1987.189	0.540	22	0.294	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1739.495	1738.962	-269.200	0.579	1865.873	0.585	21	0.293	K.SPFQEYTDLLAKPTK.A
R3/RRR3-15/2	1671.319	1669.860	275.843	0.509	1321.960	0.560	19	0.210	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1388.103	1388.569	-336.656	0.427	1214.066	0.442	17	0.205	K.ALM*IDAPVENVEA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/3	1798.223	1798.032	106.542	0.488	1828.722	0.415	33	0.195	K.KVLQFAGIEDVFTSSR.G
R3/RRR3-6/2	1670.943	1669.860	49.782	0.485	1238.505	0.511	19	0.192	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1670.128	1669.860	161.383	0.445	1228.772	0.513	19	0.192	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1669.871	1669.860	6.847	0.419	1268.785	0.477	18	0.188	K.VLQFAGIEDVFTSSR.G
R3/RRR3-10/2	1671.110	1669.860	150.152	0.491	1128.907	0.532	18	0.186	K.VLQFAGIEDVFTSSR.G
R3/RRR3-2/2	1669.801	1669.860	-34.947	0.422	1154.680	0.512	18	0.184	K.VLQFAGIEDVFTSSR.G
R3/RRR3-15/2	1671.215	1669.860	213.001	0.474	1040.625	0.518	18	0.177	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1403.529	1403.565	-25.787	0.499	922.489	0.538	15	0.176	K.TYGFLTPDFWR.E
R3/RRR3-14/2	1404.045	1403.565	342.479	0.560	859.869	0.498	15	0.166	K.TYGFLTPDFWR.E
R3/RRR3-14/2	1403.139	1403.565	-304.849	0.495	1009.128	0.439	15	0.165	K.TYGFLTPDFWR.E
R3/RRR3-10/2	1669.860	1669.860	0.395	0.430	968.097	0.437	19	0.161	K.VLQFAGIEDVFTSSR.G
R3/RRR3-7/2	1669.872	1669.860	7.287	0.385	886.520	0.443	17	0.156	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1403.089	1403.565	-340.725	0.472	736.411	0.469	14	0.156	K.TYGFLTPDFWR.E
R3/RRR3-14/2	1670.309	1669.860	269.559	0.403	889.334	0.419	18	0.155	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1402.641	1403.565	-1376.005	0.400	764.647	0.449	14	0.154	K.TYGFLTPDFWR.E
R3/RRR3-12/2	1670.817	1669.860	-25.326	0.422	638.113	0.500	15	0.152	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1404.061	1403.565	354.334	0.429	616.149	0.469	13	0.151	K.TYGFLTPDFWR.E
R3/RRR3-11/2	1404.294	1403.565	-193.609	0.345	794.796	0.415	14	0.150	K.TYGFLTPDFWR.E
R3/RRR3-15/2	1404.237	1403.565	-234.858	0.297	562.771	0.482	15	0.148	K.TYGFLTPDFWR.E
R3/RRR3-14/2	1402.644	1403.565	-1373.907	0.364	694.953	0.407	14	0.147	K.TYGFLTPDFWR.E
R3/RRR3-14/2	1671.024	1669.860	98.577	0.386	497.580	0.477	14	0.146	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1137.024	1137.307	-250.318	0.390	671.273	0.363	14	0.142	K.IGQPHTVPCK.V
R3/RRR3-14/3	1797.752	1798.032	-156.487	0.448	1385.683	0.403	30	0.140	K.KVLQFAGIEDVFTSSR.G
R3/RRR3-16/2	1671.230	1669.860	222.523	0.445	648.791	0.372	15	0.140	K.VLQFAGIEDVFTSSR.G
R3/RRR3-18/2	1669.839	1669.860	-12.510	0.296	507.197	0.405	14	0.140	K.VLQFAGIEDVFTSSR.G
R3/RRR3-18/2	1670.655	1669.860	-123.020	0.324	377.844	0.382	13	0.139	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	770.095	769.955	181.866	0.294	683.114	0.321	10	0.138	K.LSVVPVR.R
R3/RRR3-7/2	1670.827	1669.860	-19.830	0.281	394.735	0.323	14	0.137	K.VLQFAGIEDVFTSSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1670.558	1669.860	-181.220	0.242	443.051	0.353	15	0.137	K.VLQFAGIEDVFTSSR.G
R3/RRR3-20/2	1669.988	1669.860	76.937	0.316	602.077	0.281	16	0.135	K.VLQFAGIEDVFTSSR.G
R3/RRR3-5/2	1671.041	1669.860	108.980	0.293	518.281	0.262	16	0.135	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	769.387	769.955	-2044.108	0.202	627.858	0.371	10	0.135	K.LSVVPVR.R
R3/RRR3-14/2	1136.965	1137.307	-302.128	0.340	575.072	0.301	13	0.135	K.IGQPHTVPCK.V
R3/RRR3-11/2	1670.350	1669.860	294.328	0.234	684.665	0.254	15	0.133	K.VLQFAGIEDVFTSSR.G
R3/RRR3-14/2	1799.396	1798.032	202.863	0.385	448.589	0.369	13	0.133	K.KVLQFAGIEDVFTSSR.G
R3/RRR3-14/2	770.234	769.955	363.047	0.236	636.326	0.255	10	0.133	K.LSVVPVR.R
R3/RRR3-20/2	1670.109	1669.860	149.949	0.286	359.038	0.340	13	0.132	-.VLQFAGIEDVFTSSR.-
R3/RRR3-15/2	1403.233	1403.565	-237.382	0.255	600.463	0.207	13	0.132	K.TYGFLTPDFWR.E
R3/RRR3-14/3	1739.195	1738.962	134.621	0.465	1143.601	0.415	28	0.124	K.SPFQEYTDLLAKPTK.A
R3/RRR3-14/3	1738.792	1738.962	-97.927	0.472	847.473	0.432	25	0.112	K.SPFQEYTDLLAKPTK.A
R3/RRR3-14/3	1738.998	1738.962	21.001	0.451	575.294	0.490	22	0.112	K.SPFQEYTDLLAKPTK.A
R3/RRR3-15/3	1737.776	1738.962	-1261.704	0.353	762.215	0.364	23	0.100	K.SPFQEYTDLLAKPTK.A
R3/RRR3-13/3	1739.029	1738.962	38.743	0.318	595.565	0.392	20	0.099	K.SPFQEYTDLLAKPTK.A
R3/RRR3-15/3	1738.080	1738.962	-1085.656	0.389	563.057	0.319	20	0.094	K.SPFQEYTDLLAKPTK.A
R3/RRR3-13/3	1738.384	1738.962	-910.092	0.356	501.610	0.313	20	0.076	-.SPFQEYTDLLAKPTK.-
R3/RRR3-14/2	1372.024	1372.570	-1129.895	0.245	677.078	0.237	15	0.043	K.ALMIDAPVENVEA.-
R3/RRR3-16/2	1491.122	1491.759	-1100.903	0.543	2521.324	0.433	22	0.369	K.KYHAFLASEAIIK.Q
R3/RRR3-16/2	1616.326	1616.797	-292.062	0.518	2239.227	0.541	23	0.349	K.FPTLVTHQESLESK.V
R3/RRR3-16/2	1617.406	1616.797	-241.981	0.582	2040.929	0.525	22	0.306	K.FPTLVTHQESLESK.V
R3/RRR3-16/2	1491.379	1491.759	-255.616	0.512	2067.998	0.409	21	0.278	K.KYHAFLASEAIIK.Q
R3/RRR3-16/2	1491.277	1491.759	-324.352	0.517	1865.058	0.468	20	0.262	K.KYHAFLASEAIIK.Q
R3/RRR3-16/2	1617.348	1616.797	-278.024	0.542	1739.243	0.494	22	0.251	K.FPTLVTHQESLESK.V
R3/RRR3-16/2	1363.337	1363.586	-182.991	0.499	1797.663	0.399	20	0.236	K.YHAFLASEAIIK.Q
R3/RRR3-16/2	1146.901	1147.261	-315.097	0.473	1546.668	0.486	18	0.225	K.EAISQVVGESK.E
R3/RRR3-16/2	1363.238	1363.586	-255.752	0.464	1762.019	0.369	20	0.224	K.YHAFLASEAIIK.Q
R3/RRR3-16/2	1363.180	1363.586	-298.606	0.443	1701.663	0.358	19	0.214	K.YHAFLASEAIIK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1147.100	1147.261	-141.063	0.434	1526.307	0.433	18	0.211	K.EAISQVVGESK.E
R3/RRR3-16/2	1404.017	1404.548	-1094.208	0.435	659.547	0.495	18	0.153	K.EAISQVVGESKEK.G
R3/RRR3-16/3	1491.822	1491.759	42.331	0.546	1549.987	0.392	27	0.151	K.KYHAFLASEAIIK.Q
R3/RRR3-16/3	1873.836	1873.099	-140.986	0.509	998.139	0.578	31	0.147	K.AGKFPTLVTHQESLESK.V
R3/RRR3-16/3	1873.240	1873.099	75.183	0.497	996.208	0.566	29	0.145	K.AGKFPTLVTHQESLESK.V
R3/RRR3-16/3	1873.217	1873.099	63.223	0.479	913.971	0.580	30	0.141	K.AGKFPTLVTHQESLESK.V
R3/RRR3-16/3	1491.525	1491.759	-156.888	0.506	1267.598	0.396	25	0.128	-.KYHAFLASEAIIK.-
R3/RRR3-16/3	1873.365	1873.099	142.136	0.494	745.786	0.554	27	0.126	K.AGKFPTLVTHQESLESK.V
R3/RRR3-16/3	1491.392	1491.759	-246.797	0.504	1416.965	0.303	26	0.119	-.KYHAFLASEAIIK.-
R3/RRR3-16/3	1491.298	1491.759	-310.235	0.456	1336.495	0.324	26	0.118	K.KYHAFLASEAIIK.Q
R3/RRR3-16/3	1616.986	1616.797	117.726	0.468	800.223	0.485	23	0.118	K.FPTLVTHQESLESK.V
R3/RRR3-16/3	1491.320	1491.759	-295.330	0.460	1290.599	0.306	25	0.112	K.KYHAFLASEAIIK.Q
R3/RRR3-16/3	1732.459	1732.888	-248.149	0.415	899.078	0.420	28	0.110	K.VCM*LGDAQHVEEAEK.M
R3/RRR3-17/3	1616.468	1616.797	-204.107	0.382	1139.203	0.326	24	0.108	K.FPTLVTHQESLESK.V
R3/RRR3-16/3	1616.700	1616.797	-59.694	0.380	1123.768	0.322	23	0.107	K.FPTLVTHQESLESK.V
R3/RRR3-16/3	1732.917	1732.888	16.655	0.387	641.521	0.356	25	0.096	K.VCM*LGDAQHVEEAEK.M
R3/RRR3-16/3	1732.392	1732.888	-286.959	0.344	820.246	0.304	28	0.092	K.VCM*LGDAQHVEEAEK.M
R3/RRR3-16/3	1616.399	1616.797	-246.950	0.304	837.779	0.275	21	0.091	K.FPTLVTHQESLESK.V
R3/RRR3-16/3	1491.854	1491.759	64.243	0.366	947.920	0.152	22	0.082	-.KYHAFLASEAIIK.-
R3/RRR3-18/3	1616.377	1616.797	-260.134	0.283	701.023	0.119	20	0.080	-.FPTLVTHQESLESK.-
R3/RRR3-18/3	1616.481	1616.797	-195.698	0.301	704.105	0.173	20	0.077	-.FPTLVTHQESLESK.-
R3/RRR3-8/2	1500.426	1499.803	-251.789	0.566	1563.708	0.528	21	0.234	R.LGPNYLMLPANAPK.C
R3/RRR3-8/2	1500.377	1499.803	-284.521	0.504	1449.117	0.488	20	0.211	R.LGPNYLMLPANAPK.C
R3/RRR3-8/2	1968.899	1970.240	-1192.752	0.504	1397.341	0.488	22	0.204	R.EGNFDLVGNNMPVFFIR.D
R3/RRR3-8/2	1969.163	1970.240	-1058.165	0.535	1275.917	0.521	21	0.198	R.EGNFDLVGNNMPVFFIR.D
R3/RRR3-8/2	1681.192	1680.796	235.916	0.496	1259.189	0.469	20	0.188	K.DLTDSIAAGNYPEWK.L
R3/RRR3-8/2	1970.341	1970.240	51.290	0.560	1102.280	0.543	20	0.185	R.EGNFDLVGNNMPVFFIR.D
R3/RRR3-8/2	1151.643	1151.384	225.747	0.487	985.131	0.544	17	0.181	R.APGVQTPIIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1499.442	1499.803	-241.258	0.482	1115.585	0.493	18	0.180	R.LGPNYLMLPANAPK.C
R3/RRR3-8/2	1680.097	1680.796	-1014.606	0.434	1341.537	0.378	20	0.179	K.DLTDSIAAGNYPEWK.L
R3/RRR3-9/2	1515.640	1515.802	-107.308	0.399	1238.165	0.392	18	0.172	R.LGPNYLM*LPANAPK.C
R3/RRR3-8/2	1515.106	1515.802	-1122.811	0.456	885.041	0.525	16	0.167	R.LGPNYLM*LPANAPK.C
R3/RRR3-8/2	1515.166	1515.802	-1083.090	0.469	1044.313	0.408	19	0.163	R.LGPNYLM*LPANAPK.C
R3/RRR3-8/2	1680.302	1680.796	-294.714	0.462	1082.052	0.398	19	0.162	K.DLTDSIAAGNYPEWK.L
R3/RRR3-8/2	1257.014	1256.303	-230.222	0.453	985.300	0.375	14	0.155	R.DEEVNYFPSR.F
R3/RRR3-8/2	1622.112	1621.861	154.989	0.458	676.228	0.451	17	0.148	K.TWPEDIIPLQPVGR.M
R3/RRR3-8/2	1257.251	1256.303	-41.350	0.354	968.885	0.307	14	0.145	R.DEEVNYFPSR.F
R3/RRR3-8/2	1622.217	1621.861	220.189	0.341	640.817	0.411	16	0.141	K.TWPEDIIPLQPVGR.M
R3/RRR3-9/2	1515.438	1515.802	-240.711	0.430	747.308	0.324	15	0.137	R.LGPNYLM*LPANAPK.C
R3/RRR3-8/3	1144.363	1144.351	10.301	0.435	1012.477	0.379	21	0.108	R.HAEKVPIPPR.V
R3/RRR3-8/3	1144.852	1144.351	-437.483	0.434	1196.243	0.304	22	0.104	R.HAEKVPIPPR.V
R3/RRR3-8/3	1143.859	1144.351	-432.030	0.330	558.879	0.355	17	0.095	-.HAEKVPIPPR.-
R3/RRR3-8/3	1144.851	1144.351	437.650	0.444	863.822	0.290	19	0.094	R.HAEKVPIPPR.V
R3/RRR3-8/3	1143.613	1144.351	-1524.360	0.316	660.174	0.286	18	0.092	R.HAEKVPIPPR.V
R3/RRR3-8/3	1144.250	1144.351	-88.567	0.422	717.266	0.268	19	0.090	-.HAEKVPIPPR.-
R3/RRR3-18/2	1699.460	1699.882	-249.281	0.491	3022.777	0.589	25	0.556	K.AITEIFAEAGFSDVTK.N
R3/RRR3-18/2	1699.348	1699.882	-905.918	0.427	2869.676	0.559	25	0.501	K.AITEIFAEAGFSDVTK.N
R3/RRR3-18/3	1701.077	1699.882	114.750	0.565	2922.343	0.535	34	0.488	K.AITEIFAEAGFSDVTK.N
R3/RRR3-18/2	1189.938	1190.334	-333.437	0.616	2148.985	0.464	19	0.306	K.NFLAVLADNGR.L
R3/RRR3-18/2	1189.999	1190.334	-281.770	0.586	1722.422	0.496	17	0.248	K.NFLAVLADNGR.L
R3/RRR3-18/2	1190.662	1190.334	276.140	0.527	1735.638	0.416	17	0.230	K.NFLAVLADNGR.L
R3/RRR3-18/2	1066.863	1067.262	-374.886	0.397	577.938	0.462	12	0.149	K.SPLFSQFIK.D
R3/RRR3-18/2	1491.144	1491.737	-1071.635	0.419	868.961	0.338	20	0.147	R.FVDLTM*AHKGEVK.V
R3/RRR3-18/2	1185.849	1186.430	-1337.431	0.421	245.222	0.415	12	0.146	R.AKQM*EM*FLR.Q
R3/RRR3-18/2	1491.366	1491.737	-249.932	0.448	645.690	0.382	19	0.145	R.FVDLTM*AHKGEVK.V
R3/RRR3-18/2	1388.301	1387.604	-219.122	0.344	350.650	0.420	19	0.145	K.ELKETLQDILGK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1491.315	1491.737	-283.848	0.472	704.094	0.353	20	0.144	R.FVDLTM*AHKGEVK.V
R3/RRR3-18/2	1067.155	1067.262	-100.575	0.415	580.068	0.396	12	0.144	K.SPLFSQFIK.D
R3/RRR3-18/2	1195.355	1195.435	-67.255	0.418	705.770	0.358	14	0.143	K.KSPLFSQFIK.D
R3/RRR3-18/2	1387.222	1387.604	-276.308	0.331	180.546	0.291	15	0.142	K.ELKETLQDILGK.N
R3/RRR3-18/2	1185.730	1186.430	-1438.139	0.385	400.943	0.324	14	0.142	R.AKQM*EM*FLR.Q
R3/RRR3-18/2	1387.534	1387.604	-50.351	0.322	387.371	0.357	19	0.141	K.ELKETLQDILGK.N
R3/RRR3-18/2	1067.175	1067.262	-82.216	0.444	611.466	0.337	12	0.140	K.SPLFSQFIK.D
R3/RRR3-18/2	1195.151	1195.435	-238.553	0.389	747.854	0.235	14	0.134	K.KSPLFSQFIK.D
R3/RRR3-18/2	1194.309	1195.435	-1785.287	0.276	509.512	0.226	14	0.133	K.KSPLFSQFIK.D
R3/RRR3-18/2	1186.168	1186.430	-221.674	0.370	189.174	0.325	10	0.128	-.AKQM*EM*FLR.-
R3/RRR3-6/2	1879.366	1880.002	-873.215	0.520	2515.178	0.462	24	0.377	K.SWEDLTSDKDAIETIR.A
R3/RRR3-7/2	1879.798	1880.002	-109.137	0.531	2361.028	0.477	23	0.350	K.SWEDLTSDKDAIETIR.A
R3/RRR3-6/2	1880.181	1880.002	95.426	0.528	2368.452	0.468	24	0.349	K.SWEDLTSDKDAIETIR.A
R3/RRR3-6/2	1162.758	1163.348	-1371.575	0.492	1531.004	0.385	17	0.202	R.IDLAALEVYR.D
R3/RRR3-6/2	1628.046	1628.720	-1031.327	0.509	1107.729	0.544	21	0.192	R.FFTSNFNEETYTK.K
R3/RRR3-6/2	1752.185	1752.050	77.171	0.471	1300.359	0.458	24	0.189	K.DTFGHIGGPILGGLVGLK.K
R3/RRR3-7/2	1454.629	1455.770	-1475.893	0.380	906.694	0.628	18	0.184	K.VPVPIGLLYLNTR.R
R3/RRR3-7/2	1455.556	1455.770	-146.919	0.439	721.190	0.652	17	0.178	K.VPVPIGLLYLNTR.R
R3/RRR3-7/2	1022.462	1022.181	275.165	0.470	973.915	0.475	15	0.172	R.ANWYGLLGK.K
R3/RRR3-2/2	1455.975	1455.770	141.224	0.411	783.409	0.587	17	0.172	K.VPVPIGLLYLNTR.R
R3/RRR3-6/2	1522.423	1521.700	-182.688	0.489	980.754	0.473	19	0.170	R.SDRIDLAALEVYR.D
R3/RRR3-6/2	1022.062	1022.181	-116.812	0.432	869.319	0.501	14	0.168	R.ANWYGLLGK.K
R3/RRR3-6/2	1455.454	1455.770	-217.256	0.440	689.300	0.583	17	0.168	K.VPVPIGLLYLNTR.R
R3/RRR3-6/2	1021.895	1022.181	-281.215	0.436	989.287	0.358	15	0.156	R.ANWYGLLGK.K
R3/RRR3-6/2	1521.627	1521.700	-48.247	0.455	881.170	0.411	18	0.154	R.SDRIDLAALEVYR.D
R3/RRR3-6/2	1521.292	1521.700	-268.778	0.437	844.139	0.426	17	0.154	R.SDRIDLAALEVYR.D
R3/RRR3-7/2	1454.616	1455.770	-1484.744	0.341	558.645	0.539	15	0.152	K.VPVPIGLLYLNTR.R
R3/RRR3-5/2	1454.714	1455.770	-1417.059	0.326	650.485	0.421	15	0.145	K.VPVPIGLLYLNTR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1021.523	1022.181	-1628.869	0.337	767.634	0.323	13	0.142	R.ANWYGLLGK.K
R3/RRR3-5/2	1455.315	1455.770	-313.438	0.303	524.742	0.389	15	0.141	K.VPVPIGLLYLNTR.R
R3/RRR3-2/2	1455.518	1455.770	-173.673	0.309	364.128	0.411	13	0.140	K.VPVPIGLLYLNTR.R
R3/RRR3-6/3	1880.149	1880.002	78.033	0.470	1237.860	0.464	32	0.140	K.SWEDLTSDKDAIETIR.A
R3/RRR3-6/3	1455.079	1454.695	264.279	0.538	1364.643	0.415	25	0.139	K.VHTIDWTVELLK.T
R3/RRR3-1/2	1456.426	1455.770	-236.614	0.281	465.449	0.339	14	0.137	K.VPVPIGLLYLNTR.R
R3/RRR3-6/3	1521.080	1521.700	-1068.524	0.435	1558.119	0.306	24	0.134	R.SDRIDLAALEVYR.D
R3/RRR3-1/2	1455.157	1455.770	-1111.453	0.321	570.998	0.263	14	0.134	K.VPVPIGLLYLNTR.R
R3/RRR3-6/2	1454.622	1455.770	-1480.613	0.212	422.364	0.297	13	0.133	K.VPVPIGLLYLNTR.R
R3/RRR3-6/3	1521.704	1521.700	2.477	0.507	1228.753	0.398	24	0.125	-.SDRIDLAALEVYR.-
R3/RRR3-6/3	1879.568	1880.002	-231.688	0.408	1180.785	0.340	31	0.110	K.SWEDLTSDKDAIETIR.A
R3/RRR3-6/3	1454.523	1454.695	-118.834	0.490	637.980	0.356	20	0.095	-.VHTIDWTVELLK.-
R3/RRR3-6/3	1454.312	1454.695	-264.076	0.443	642.705	0.307	19	0.093	K.VHTIDWTVELLK.T
R3/RRR3-7/3	1454.454	1454.695	-166.443	0.332	560.770	0.308	19	0.091	-.VHTIDWTVELLK.-
R3/RRR3-8/2	1243.841	1244.405	-1261.495	0.490	1934.587	0.484	20	0.277	R.AFATGGYAAMQR.V
R3/RRR3-8/2	1260.073	1260.404	-263.519	0.500	1782.640	0.539	19	0.269	R.AFATGGYAAM*QR.V
R3/RRR3-8/2	1259.277	1260.404	-1694.488	0.388	1735.849	0.507	19	0.252	R.AFATGGYAAM*QR.V
R3/RRR3-8/2	1259.957	1260.404	-355.957	0.481	1630.688	0.490	19	0.235	R.AFATGGYAAM*QR.V
R3/RRR3-8/2	1420.284	1420.639	-250.308	0.504	1682.834	0.453	21	0.234	R.AYAQSVATLNLLR.A
R3/RRR3-8/2	1243.716	1244.405	-1362.133	0.452	1562.808	0.480	20	0.225	R.AFATGGYAAMQR.V
R3/RRR3-8/2	1420.283	1420.639	-250.997	0.442	1432.267	0.438	19	0.200	R.AYAQSVATLNLLR.A
R3/RRR3-8/2	1420.244	1420.639	-279.108	0.497	1288.252	0.474	19	0.193	R.AYAQSVATLNLLR.A
R3/RRR3-8/2	1529.321	1529.669	-228.298	0.513	1283.840	0.467	21	0.192	R.AFVLQGGDCAESFK.E
R3/RRR3-8/2	1324.963	1325.320	-270.071	0.439	1067.665	0.427	18	0.168	R.GDNINGDTFDEK.S
R3/RRR3-8/2	1450.966	1451.696	-1195.755	0.466	947.263	0.433	18	0.161	K.LIEILNPSNKPGR.I
R3/RRR3-8/2	1404.016	1404.596	-1129.090	0.445	836.300	0.448	16	0.157	K.TRPFDSILAEVR.A
R3/RRR3-8/2	1404.448	1404.596	-106.061	0.465	881.136	0.411	16	0.154	K.TRPFDSILAEVR.A
R3/RRR3-8/2	1324.748	1325.320	-1190.181	0.416	764.351	0.414	16	0.149	R.GDNINGDTFDEK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1635.218	1634.857	221.733	0.427	469.835	0.451	19	0.147	K.TIETFPPVVFAGEAR.H
R3/RRR3-8/2	1451.243	1451.696	-313.474	0.443	676.034	0.417	16	0.146	K.LIEILNPSNKPGR.I
R3/RRR3-8/2	1450.720	1451.696	-1366.102	0.491	669.665	0.425	16	0.145	-.LIEILNPSNKPGR.-
R3/RRR3-8/2	1635.353	1634.857	304.070	0.479	335.088	0.430	17	0.143	K.TIETFPPVVFAGEAR.H
R3/RRR3-8/2	1636.459	1634.857	-243.877	0.370	471.772	0.405	17	0.141	K.TIETFPPVVFAGEAR.H
R3/RRR3-8/2	1404.145	1404.596	-322.419	0.439	727.359	0.348	15	0.141	K.TRPFDSILAEVR.A
R3/RRR3-8/2	1635.362	1634.857	-303.337	0.308	313.988	0.351	16	0.137	K.TIETFPPVVFAGEAR.H
R3/RRR3-8/2	1635.260	1634.857	247.409	0.385	224.693	0.234	13	0.135	K.TIETFPPVVFAGEAR.H
R3/RRR3-8/3	976.033	976.244	-216.825	0.388	902.150	0.370	16	0.102	R.VKLPHLIR.A
R3/RRR3-8/3	976.098	976.244	-149.546	0.437	873.753	0.357	16	0.101	R.VKLPHLIR.A
R3/RRR3-8/3	976.224	976.244	-20.095	0.399	842.616	0.278	16	0.091	R.VKLPHLIR.A
R3/RRR3-8/3	1404.739	1404.596	102.001	0.412	1049.686	0.148	21	0.076	-.TRPFDSILAEVR.-
R3/RRR3-8/3	1404.703	1404.596	76.378	0.373	962.569	0.097	21	0.066	-.TRPFDSILAEVR.-
R3/RRR3-8/3	1404.694	1404.596	69.711	0.417	878.164	0.149	20	0.058	-.TRPFDSILAEVR.-
R3/RRR3-25/2	1457.151	1456.668	332.266	0.484	1604.731	0.594	21	0.410	R.SGTLIDAIGIYVHP.-
R3/RRR3-22/2	1456.320	1456.668	-239.406	0.407	1593.697	0.535	21	0.401	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1457.418	1456.668	-172.186	0.519	1571.645	0.603	21	0.390	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1456.294	1456.668	-257.738	0.453	1563.813	0.475	21	0.369	R.SGTLIDAIGIYVHP.-
R3/RRR3-24/2	1457.607	1456.668	-42.302	0.502	1509.719	0.612	20	0.361	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1457.426	1456.668	-166.305	0.487	1485.751	0.612	20	0.349	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1536.096	1536.798	-1111.314	0.570	2147.394	0.551	23	0.333	K.KLLGVTIYSSDAIR.S
R3/RRR3-24/2	1457.445	1456.668	-153.617	0.522	1443.385	0.632	20	0.328	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1536.339	1536.798	-299.458	0.529	2068.583	0.575	23	0.327	K.KLLGVTIYSSDAIR.S
R3/RRR3-25/2	1536.437	1536.798	-235.768	0.523	1958.906	0.534	23	0.295	K.KLLGVTIYSSDAIR.S
R3/RRR3-24/2	1535.956	1536.798	-1202.687	0.544	1916.013	0.550	23	0.293	K.KLLGVTIYSSDAIR.S
R3/RRR3-24/2	1536.148	1536.798	-1077.482	0.536	1939.011	0.524	23	0.289	K.KLLGVTIYSSDAIR.S
R3/RRR3-24/2	1456.262	1456.668	-279.856	0.383	1383.741	0.442	20	0.280	R.SGTLIDAIGIYVHP.-
R3/RRR3-24/2	1456.163	1456.668	-1036.862	0.345	1317.831	0.473	18	0.261	R.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1837.298	1838.014	-936.792	0.520	1710.922	0.565	26	0.259	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1838.353	1838.014	185.444	0.516	1655.753	0.581	26	0.256	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1409.120	1408.625	352.454	0.579	1608.911	0.555	21	0.247	K.LLGVTIYSSDAIR.S
R3/RRR3-25/2	1839.064	1838.014	27.721	0.571	1645.379	0.555	26	0.247	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-23/2	1456.361	1456.668	-211.824	0.426	1296.463	0.460	19	0.241	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1408.438	1408.625	-133.144	0.557	1551.243	0.541	21	0.237	K.LLGVTIYSSDAIR.S
R3/RRR3-25/2	1456.893	1456.668	155.086	0.458	1254.649	0.538	19	0.232	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1407.714	1408.625	-1361.828	0.443	1608.461	0.476	21	0.228	K.LLGVTIYSSDAIR.S
R3/RRR3-25/2	1838.126	1838.014	61.440	0.507	1468.813	0.567	25	0.228	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1837.781	1838.014	-126.822	0.507	1475.308	0.561	26	0.228	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-24/2	1407.672	1408.625	-1391.440	0.427	1642.695	0.456	21	0.228	K.LLGVTIYSSDAIR.S
R3/RRR3-25/2	1839.134	1838.014	65.800	0.547	1455.885	0.562	25	0.225	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1837.545	1838.014	-255.968	0.549	1409.979	0.578	25	0.223	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-24/2	1408.066	1408.625	-1110.278	0.491	1584.103	0.451	21	0.220	K.LLGVTIYSSDAIR.S
R3/RRR3-24/2	1456.033	1456.668	-1126.088	0.371	1223.973	0.491	19	0.219	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1837.311	1838.014	-929.454	0.468	1374.369	0.573	25	0.219	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1839.468	1838.014	248.032	0.503	1455.927	0.531	25	0.218	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-19/2	1409.432	1408.625	-137.394	0.476	1490.734	0.486	21	0.217	K.LLGVTIYSSDAIR.S
R3/RRR3-25/2	1837.729	1838.014	-155.274	0.485	1353.471	0.552	24	0.211	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-23/2	1408.146	1408.625	-340.892	0.483	1357.676	0.529	20	0.211	K.LLGVTIYSSDAIR.S
R3/RRR3-25/2	1837.661	1838.014	-192.324	0.506	1257.050	0.593	24	0.210	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1736.288	1735.876	237.597	0.502	1280.567	0.536	25	0.204	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-24/2	1992.562	1993.210	-829.815	0.505	1062.599	0.643	23	0.202	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-25/2	1837.443	1838.014	-857.156	0.519	1150.119	0.606	23	0.202	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-24/2	1736.474	1735.876	-232.228	0.510	1289.775	0.521	25	0.202	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/2	1992.515	1993.210	-853.677	0.471	1047.696	0.659	21	0.201	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-25/2	1838.515	1838.014	-271.883	0.487	1322.007	0.508	24	0.199	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-24/2	1736.299	1735.876	244.294	0.490	1181.023	0.553	24	0.197	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1838.696	1838.014	-172.972	0.554	1162.125	0.578	23	0.197	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1735.697	1735.876	-103.596	0.493	1161.643	0.552	24	0.195	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/2	1837.080	1838.014	-1055.535	0.466	1271.633	0.507	24	0.194	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1838.513	1838.014	272.534	0.505	1112.041	0.561	23	0.190	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1735.402	1735.876	-274.068	0.455	1062.137	0.568	23	0.189	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/2	1837.407	1838.014	-877.097	0.499	1120.715	0.551	23	0.189	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1992.455	1993.210	-883.936	0.488	961.119	0.613	22	0.187	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-25/2	1736.291	1735.876	239.359	0.483	1216.136	0.480	24	0.187	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/2	1993.601	1993.210	196.613	0.530	923.728	0.619	22	0.186	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-23/2	1735.357	1735.876	-878.018	0.497	945.245	0.595	22	0.185	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-24/2	1992.361	1993.210	-931.173	0.460	873.240	0.638	22	0.185	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-25/2	1992.606	1993.210	-807.369	0.502	958.971	0.594	21	0.183	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-24/2	1736.205	1735.876	189.584	0.496	1125.675	0.501	23	0.182	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-23/2	1735.389	1735.876	-281.549	0.471	1011.472	0.551	23	0.182	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-22/2	1457.041	1456.668	256.747	0.403	1125.367	0.513	18	0.182	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/2	1993.480	1993.210	135.390	0.483	866.002	0.630	20	0.182	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-25/2	1735.369	1735.876	-871.098	0.479	1027.510	0.537	23	0.182	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/2	1992.214	1993.210	-1005.114	0.452	935.881	0.591	22	0.181	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-25/2	1992.722	1993.210	-245.805	0.477	870.660	0.618	21	0.181	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-24/2	1735.405	1735.876	-272.304	0.469	969.684	0.563	22	0.181	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/2	1992.301	1993.210	-961.376	0.470	907.148	0.595	21	0.180	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-25/2	1837.388	1838.014	-887.568	0.533	1042.899	0.538	22	0.179	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-25/2	1735.398	1735.876	-276.467	0.486	904.641	0.561	22	0.176	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-24/2	1407.594	1408.625	-1447.012	0.427	1071.822	0.463	18	0.173	K.LLGVTIYSSDAIR.S
R3/RRR3-25/2	1992.368	1993.210	-927.606	0.474	818.856	0.587	20	0.172	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-24/2	1735.159	1735.876	-992.852	0.377	986.277	0.497	23	0.171	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-23/2	1993.246	1993.210	17.776	0.454	776.555	0.559	19	0.165	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-19/2	1457.005	1456.668	231.964	0.431	1087.446	0.469	17	0.162	R.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1736.313	1735.876	252.119	0.423	951.376	0.420	22	0.159	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-2/2	1735.093	1735.876	-1031.136	0.436	691.851	0.523	19	0.158	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-13/2	1993.083	1993.210	-63.925	0.419	692.544	0.534	18	0.157	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-23/2	1407.957	1408.625	-1188.454	0.327	917.440	0.412	17	0.155	K.LLGVTIYSSDAIR.S
R3/RRR3-2/2	1992.888	1993.210	-162.415	0.395	549.980	0.542	17	0.151	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-24/2	1838.849	1838.014	-89.595	0.392	847.609	0.393	19	0.147	K.IGPWGGNGGSAQDISVPPK.K
R3/RRR3-19/2	1456.152	1456.668	-1044.605	0.417	1027.223	0.492	17	0.145	R.SGTLIDAIGIYVHP.-
R3/RRR3-20/2	1735.391	1735.876	-280.561	0.412	434.854	0.459	15	0.142	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/2	1992.304	1993.210	-959.899	0.335	607.693	0.428	17	0.142	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-24/3	1967.980	1966.187	-105.249	0.414	958.870	0.532	33	0.138	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-23/2	1408.151	1408.625	-337.239	0.274	472.081	0.385	13	0.137	K.LLGVTIYSSDAIR.S
R3/RRR3-17/2	1994.058	1993.210	-76.666	0.283	234.015	0.389	13	0.137	K.EFSIPLQDSGHVVGFFGR.S
R3/RRR3-20/2	1457.433	1456.668	-162.103	0.423	976.898	0.565	17	0.136	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/3	1967.581	1966.187	201.197	0.442	1190.679	0.441	38	0.134	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1966.876	1966.187	-158.407	0.463	1145.299	0.454	39	0.133	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1967.657	1966.187	239.831	0.433	931.599	0.455	35	0.122	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1966.508	1966.187	164.075	0.469	885.017	0.469	36	0.121	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1967.440	1966.187	129.428	0.448	908.453	0.458	35	0.121	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-21/2	1455.883	1456.668	-1229.982	0.401	970.401	0.409	16	0.120	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/3	1966.066	1966.187	-61.386	0.462	830.588	0.467	35	0.119	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1966.239	1966.187	26.606	0.442	779.654	0.467	35	0.117	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1967.177	1966.187	-4.713	0.337	784.695	0.444	32	0.114	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1967.656	1966.187	239.364	0.394	838.237	0.422	34	0.113	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1967.486	1966.187	152.481	0.445	794.349	0.433	35	0.113	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-24/3	1735.841	1735.876	-20.224	0.411	745.717	0.470	26	0.112	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/3	1967.018	1966.187	-86.129	0.439	720.994	0.443	33	0.112	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1966.563	1966.187	192.180	0.391	663.259	0.449	31	0.112	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1966.966	1966.187	-112.555	0.325	1103.314	0.317	29	0.110	K.IGPWGGNGGSAQDISVPPKK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/3	1966.031	1966.187	-79.135	0.420	657.963	0.410	33	0.107	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-24/3	1966.873	1966.187	-160.088	0.444	628.484	0.415	31	0.107	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1967.995	1966.187	-97.783	0.373	549.488	0.420	27	0.107	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1966.315	1966.187	65.647	0.403	776.680	0.388	34	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1967.391	1966.187	104.226	0.319	748.678	0.388	32	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-24/3	1734.863	1735.876	-1164.207	0.322	756.448	0.430	23	0.106	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-25/3	1965.609	1966.187	-805.073	0.396	691.384	0.390	32	0.105	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-24/3	1966.144	1966.187	-21.778	0.390	473.569	0.379	28	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-25/3	1965.808	1966.187	-193.309	0.346	449.655	0.370	26	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-24/3	1735.689	1735.876	-108.472	0.354	500.829	0.436	22	0.101	K.IVTSANNTYEAGVPNGK.E
R3/RRR3-23/2	1456.081	1456.668	-1093.089	0.381	864.906	0.510	16	0.100	R.SGTLIDAIGIYVHP.-
R3/RRR3-24/3	1966.106	1966.187	-40.834	0.349	667.806	0.306	29	0.097	K.IGPWGGNGGSAQDISVPPKK.L
R3/RRR3-21/2	1456.479	1456.668	-130.518	0.374	868.368	0.463	17	0.097	R.SGTLIDAIGIYVHP.-
R3/RRR3-25/3	1736.686	1735.876	-109.714	0.386	574.479	0.373	21	0.095	-.IVTSANNTYEAGVPNGK.-
R3/RRR3-25/3	1737.324	1735.876	258.308	0.436	394.692	0.341	20	0.093	-.IVTSANNTYEAGVPNGK.-
R3/RRR3-24/3	1967.073	1966.187	-57.744	0.403	371.636	0.426	24	0.092	-.IGPWGGNGGSAQDISVPPKK.-
R3/RRR3-18/2	1457.007	1456.668	233.644	0.329	787.391	0.469	17	0.079	R.SGTLIDAIGIYVHP.-
R3/RRR3-2/2	1456.490	1456.668	-122.615	0.327	726.186	0.466	15	0.066	R.SGTLIDAIGIYVHP.-
R3/RRR3-2/2	1456.043	1456.668	-1119.775	0.403	721.948	0.356	14	0.055	R.SGTLIDAIGIYVHP.-
R3/RRR3-23/2	1455.797	1456.668	-1288.841	0.367	712.220	0.365	14	0.055	R.SGTLIDAIGIYVHP.-
R3/RRR3-21/2	1456.170	1456.668	-343.271	0.311	598.419	0.525	15	0.046	R.SGTLIDAIGIYVHP.-
R3/RRR3-24/2	1455.586	1456.668	-1434.631	0.310	658.147	0.321	14	0.044	R.SGTLIDAIGIYVHP.-
R3/RRR3-2/2	1456.229	1456.668	-302.311	0.353	548.479	0.474	14	0.038	-.SGTLIDAIGIYVHP.-
R3/RRR3-7/2	1615.416	1615.850	-269.716	0.562	1903.462	0.545	23	0.290	R.TQNVVACQAVANIVK.S
R3/RRR3-7/2	1614.662	1615.850	-1359.490	0.417	1972.258	0.484	22	0.283	R.TQNVVACQAVANIVK.S
R3/RRR3-7/2	1558.137	1557.689	287.943	0.525	1970.954	0.458	21	0.277	K.DSYLLNGYALNTGR.A
R3/RRR3-7/2	1885.762	1886.221	-244.229	0.517	1486.203	0.545	24	0.229	R.EQLAIAEFAESLLIIPK.V
R3/RRR3-7/2	1561.690	1560.863	-110.984	0.382	1619.747	0.283	19	0.188	K.IIQFATEAAITILR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	973.781	974.137	-366.274	0.516	1062.760	0.505	16	0.183	K.AGANVVLTTK.G
R3/RRR3-13/2	974.072	974.137	-66.507	0.468	1149.236	0.466	16	0.182	K.AGANVVLTTK.G
R3/RRR3-13/2	974.007	974.137	-133.386	0.471	1008.844	0.518	15	0.179	K.AGANVVLTTK.G
R3/RRR3-7/2	973.326	974.137	-1865.885	0.436	1133.688	0.441	16	0.176	K.AGANVVLTTK.G
R3/RRR3-7/2	974.006	974.137	-134.517	0.460	933.838	0.512	15	0.174	K.AGANVVLTTK.G
R3/RRR3-13/2	975.059	974.137	-80.001	0.401	988.688	0.453	16	0.168	K.AGANVVLTTK.G
R3/RRR3-7/2	1472.614	1472.736	-82.958	0.352	1275.261	0.340	18	0.167	K.M*QLGVQVLVTDPR.E
R3/RRR3-7/2	1101.599	1101.275	295.132	0.392	787.106	0.404	16	0.151	R.IADDDVILVK.G
R3/RRR3-7/2	1562.238	1560.863	240.791	0.395	932.068	0.280	17	0.138	K.IIQFATEAAITILR.I
R3/RRR3-7/2	973.950	973.106	-160.170	0.393	715.597	0.294	15	0.134	-.SSLGPVGLDK.-
R3/RRR3-13/2	1101.128	1101.275	-134.499	0.214	569.338	0.259	13	0.129	-.IADDDVILVK.-
R3/RRR3-7/2	973.243	973.106	141.891	0.305	592.768	0.148	14	0.114	-.SSLGPVGLDK.-
R3/RRR3-2/2	1826.500	1827.071	-862.426	0.533	2529.710	0.570	24	0.417	K.FAALQQSIQSYLDTIK.G
R3/RRR3-2/2	1069.986	1070.266	-262.110	0.526	1434.940	0.459	16	0.208	R.YAFLTSLVR.F
R3/RRR3-2/2	1174.265	1173.345	-67.837	0.474	1478.945	0.443	18	0.208	K.ITLGDALSLNR.A
R3/RRR3-1/2	1599.416	1600.799	-1494.164	0.295	1858.500	0.181	20	0.195	K.VSGGIDLDTVNIIQR.D
R3/RRR3-1/2	1599.961	1600.799	-1151.820	0.337	1841.810	0.136	20	0.183	K.VSGGIDLDTVNIIQR.D
R3/RRR3-2/2	1071.317	1070.266	47.930	0.447	918.063	0.503	13	0.169	R.YAFLTSLVR.F
R3/RRR3-3/2	1599.716	1600.799	-1305.604	0.302	1479.072	0.233	18	0.166	K.VSGGIDLDTVNIIQR.D
R3/RRR3-2/2	1291.986	1292.335	-271.089	0.418	1175.005	0.355	18	0.164	R.SLDSSDSPLSQR.A
R3/RRR3-2/2	1292.062	1292.335	-212.227	0.413	1188.880	0.325	18	0.160	R.SLDSSDSPLSQR.A
R3/RRR3-2/2	1825.766	1827.071	-1266.208	0.403	947.449	0.385	18	0.151	K.FAALQQSIQSYLDTIK.G
R3/RRR3-3/2	1601.567	1600.799	-145.298	0.403	1076.917	0.312	19	0.150	K.VSGGIDLDTVNIIQR.D
R3/RRR3-2/2	1667.251	1666.943	184.941	0.415	993.332	0.353	18	0.149	R.VLEGTQAELVLQPLR.L
R3/RRR3-1/2	1826.611	1827.071	-252.339	0.415	652.549	0.433	19	0.147	K.FAALQQSIQSYLDTIK.G
R3/RRR3-1/2	1826.471	1827.071	-878.595	0.401	152.983	0.536	15	0.146	K.FAALQQSIQSYLDTIK.G
R3/RRR3-2/3	1942.357	1941.991	189.123	0.419	1085.101	0.527	29	0.143	K.DASDLQPSTGEAASADIHR.V
R3/RRR3-1/2	1581.845	1581.575	171.319	0.402	373.820	0.559	14	0.143	K.QGSVAEACENDSSAR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1827.938	1827.071	-72.648	0.408	452.733	0.448	14	0.140	K.FAALQQSIQSYLDTIK.G
R3/RRR3-1/2	1825.936	1827.071	-1172.281	0.314	243.623	0.345	15	0.138	K.FAALQQSIQSYLDTIK.G
R3/RRR3-2/2	1667.535	1666.943	-245.941	0.393	788.573	0.315	16	0.135	R.VLEGTQAELVLQPLR.L
R3/RRR3-2/2	1305.445	1305.540	-72.275	0.359	724.904	0.273	14	0.130	-.GSSLQCLVSILK.-
R3/RRR3-2/3	1941.770	1941.991	-114.047	0.351	776.207	0.466	25	0.110	K.DASDLQPSTGEAASADIHR.V
R3/RRR3-14/3	1941.739	1941.991	-129.939	0.259	599.068	0.316	23	0.088	K.DASDLQPSTGEAASADIHR.V
R3/RRR3-7/2	1577.197	1577.721	-968.704	0.576	2115.353	0.514	27	0.317	K.FAGAISDGGDIVLEGR.V
R3/RRR3-7/2	1578.399	1577.721	-204.057	0.585	1978.616	0.514	26	0.292	K.FAGAISDGGDIVLEGR.V
R3/RRR3-7/2	1577.055	1577.721	-1059.005	0.500	1751.787	0.492	25	0.252	K.FAGAISDGGDIVLEGR.V
R3/RRR3-7/2	1029.175	1029.215	-39.212	0.502	1954.162	0.372	17	0.250	K.LSEAGLAVLR.G
R3/RRR3-7/2	1029.057	1029.215	-154.865	0.467	2032.224	0.317	17	0.248	K.LSEAGLAVLR.G
R3/RRR3-7/2	1028.967	1029.215	-242.574	0.483	1841.104	0.366	17	0.234	K.LSEAGLAVLR.G
R3/RRR3-7/2	1548.354	1548.722	-238.697	0.469	1425.118	0.423	21	0.196	R.AIGAELVSFDEAIGR.A
R3/RRR3-7/2	1548.455	1548.722	-172.816	0.444	1334.047	0.394	21	0.182	R.AIGAELVSFDEAIGR.A
R3/RRR3-7/2	1133.267	1132.337	-62.080	0.418	962.086	0.357	15	0.152	-.VAQFDALIVR.-
R3/RRR3-7/3	1922.954	1921.101	-76.387	0.489	1436.150	0.421	30	0.150	R.VSHESPAAEAPLESIQVR.L
R3/RRR3-7/2	1548.423	1548.722	-193.774	0.341	923.543	0.344	19	0.146	R.AIGAELVSFDEAIGR.A
R3/RRR3-2/2	1029.736	1029.215	-466.996	0.216	759.505	0.083	15	0.127	K.LSEAGLAVLR.G
R3/RRR3-6/2	1132.146	1132.337	-169.314	0.204	365.559	0.282	11	0.114	-.VAQFDALIVR.-
R3/RRR3-7/3	1151.743	1151.381	315.651	0.490	1554.963	0.229	23	0.114	R.TKYVGVSLVGK.T
R3/RRR3-7/3	1729.514	1730.022	-874.267	0.369	1035.137	0.331	28	0.101	R.ADFISLHMPLTPATSK.V
R3/RRR3-6/3	1746.926	1746.021	-54.558	0.237	648.642	0.232	22	0.082	-.ADFISLHM*PLTPATSK.-
R3/RRR3-7/3	1151.197	1151.381	-160.089	0.367	951.104	0.169	19	0.081	R.TKYVGVSLVGK.T
R3/RRR3-7/2	1265.215	1264.453	-188.279	0.531	1349.122	0.564	20	0.220	R.ILAFSQDVVSGK.I
R3/RRR3-7/2	1816.375	1816.951	-870.536	0.482	1324.694	0.601	21	0.220	K.QGVAVTQENSLLDNTAR.I
R3/RRR3-7/2	1218.203	1218.336	-109.211	0.449	1517.418	0.479	18	0.219	R.ALIAEGSCGSPR.S
R3/RRR3-7/2	1217.919	1218.336	-342.967	0.449	1614.162	0.419	19	0.218	R.ALIAEGSCGSPR.S
R3/RRR3-8/2	1264.417	1264.453	-27.850	0.489	1342.683	0.545	20	0.215	R.ILAFSQDVVSGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1264.147	1264.453	-242.289	0.457	1278.806	0.562	20	0.211	R.ILAFSQDVVSGK.I
R3/RRR3-7/2	1816.307	1816.951	-907.711	0.493	1207.052	0.611	21	0.209	K.QGVAVTQENSLLDNTAR.I
R3/RRR3-7/2	1264.164	1264.453	-228.532	0.494	1168.440	0.545	19	0.198	R.ILAFSQDVVSGK.I
R3/RRR3-8/2	1264.230	1264.453	-176.417	0.489	1134.715	0.543	18	0.193	R.ILAFSQDVVSGK.I
R3/RRR3-7/2	1193.134	1193.334	-168.253	0.473	1114.563	0.524	17	0.188	R.VNQGLTVYGNK.G
R3/RRR3-7/2	1816.493	1816.951	-253.003	0.485	935.191	0.617	19	0.184	K.QGVAVTQENSLLDNTAR.I
R3/RRR3-7/2	1267.064	1266.429	-288.403	0.462	445.390	0.432	14	0.150	R.YVEWLYQHK.Q
R3/RRR3-8/2	1264.006	1264.453	-354.678	0.343	798.467	0.404	16	0.149	R.ILAFSQDVVSGK.I
R3/RRR3-7/2	1188.236	1187.330	-79.404	0.402	739.875	0.379	16	0.147	R.DPGLAPNSFLR.T
R3/RRR3-7/2	1266.132	1266.429	-235.140	0.391	616.090	0.369	14	0.144	R.YVEWLYQHK.Q
R3/RRR3-7/2	1146.087	1146.298	-185.027	0.385	688.196	0.358	13	0.143	R.M*GFTEEFLR.R
R3/RRR3-7/2	1186.922	1187.330	-344.806	0.387	616.220	0.368	15	0.142	R.DPGLAPNSFLR.T
R3/RRR3-7/2	1146.060	1146.298	-208.107	0.379	667.564	0.328	13	0.141	R.M*GFTEEFLR.R
R3/RRR3-7/2	1162.542	1162.364	153.595	0.398	477.127	0.462	12	0.139	-.AVGALVALYER.-
R3/RRR3-7/2	1146.121	1146.298	-155.110	0.346	894.050	0.248	14	0.139	-.M*GFTEEFLR.-
R3/RRR3-7/2	1266.138	1266.429	-230.110	0.283	415.690	0.325	13	0.138	R.YVEWLYQHK.Q
R3/RRR3-7/2	1187.447	1187.330	99.231	0.413	603.127	0.301	15	0.137	R.DPGLAPNSFLR.T
R3/RRR3-14/2	1146.068	1146.276	-182.534	0.471	1368.707	0.440	19	0.195	R.LSGVTADGQGIK.V
R3/RRR3-15/2	1145.473	1146.276	-1578.577	0.422	1273.987	0.458	19	0.190	R.LSGVTADGQGIK.V
R3/RRR3-14/2	1146.002	1146.276	-239.916	0.503	1199.509	0.459	20	0.185	R.LSGVTADGQGIK.V
R3/RRR3-14/2	1151.087	1151.338	-218.009	0.571	1166.967	0.452	15	0.182	K.KLDEYLLTR.S
R3/RRR3-14/2	1107.980	1108.293	-283.580	0.397	1261.700	0.412	15	0.180	K.M*EGLLWGASK.L
R3/RRR3-14/2	1108.100	1108.293	-174.824	0.414	1240.679	0.419	15	0.180	K.M*EGLLWGASK.L
R3/RRR3-15/2	1145.775	1146.276	-1313.898	0.427	1261.302	0.407	18	0.179	R.LSGVTADGQGIK.V
R3/RRR3-14/2	1151.176	1151.338	-140.670	0.558	1126.726	0.448	15	0.178	K.KLDEYLLTR.S
R3/RRR3-14/2	1108.150	1108.293	-129.517	0.475	1138.399	0.428	15	0.174	K.M*EGLLWGASK.L
R3/RRR3-14/2	1145.588	1146.276	-1478.169	0.417	1079.143	0.450	19	0.173	R.LSGVTADGQGIK.V
R3/RRR3-14/2	1150.826	1151.338	-1317.387	0.521	1069.652	0.416	15	0.169	K.KLDEYLLTR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1272.312	1272.480	-132.377	0.371	1064.875	0.431	16	0.168	R.WFTHIDALLR.L
R3/RRR3-14/2	1746.216	1745.866	200.697	0.451	641.867	0.559	24	0.163	K.VESTAVPSASTPDVADAK.A
R3/RRR3-15/2	1108.322	1108.293	26.045	0.397	1070.688	0.380	14	0.161	K.M*EGLLWGASK.L
R3/RRR3-15/2	1745.347	1745.866	-873.203	0.442	516.137	0.586	22	0.160	K.VESTAVPSASTPDVADAK.A
R3/RRR3-15/2	1746.356	1745.866	281.307	0.462	523.635	0.568	22	0.159	K.VESTAVPSASTPDVADAK.A
R3/RRR3-15/2	1151.109	1151.338	-199.285	0.462	969.380	0.367	15	0.157	K.KLDEYLLTR.S
R3/RRR3-14/2	1271.709	1272.480	-1396.559	0.449	844.125	0.415	16	0.156	R.WFTHIDALLR.L
R3/RRR3-14/2	1022.829	1023.165	-328.899	0.495	1069.951	0.325	13	0.155	K.LDEYLLTR.S
R3/RRR3-15/2	1745.435	1745.866	-247.731	0.436	399.137	0.588	19	0.154	K.VESTAVPSASTPDVADAK.A
R3/RRR3-14/2	1745.179	1745.866	-969.542	0.441	513.538	0.519	21	0.152	K.VESTAVPSASTPDVADAK.A
R3/RRR3-15/2	1145.500	1146.276	-1555.239	0.379	924.995	0.363	17	0.151	R.LSGVTADGQGIK.V
R3/RRR3-14/2	1022.359	1023.165	-1771.066	0.396	964.444	0.330	13	0.151	K.LDEYLLTR.S
R3/RRR3-14/2	1022.368	1023.165	-1762.308	0.448	1033.852	0.300	13	0.150	K.LDEYLLTR.S
R3/RRR3-14/2	1272.137	1272.480	-270.122	0.358	631.065	0.452	14	0.149	R.WFTHIDALLR.L
R3/RRR3-15/2	1151.077	1151.338	-226.626	0.406	1041.464	0.276	15	0.148	K.KLDEYLLTR.S
R3/RRR3-15/2	1151.399	1151.338	53.423	0.445	725.128	0.358	13	0.146	K.KLDEYLLTR.S
R3/RRR3-14/2	1744.945	1745.866	-1104.251	0.371	431.864	0.474	20	0.145	K.VESTAVPSASTPDVADAK.A
R3/RRR3-14/2	1091.820	1092.294	-435.395	0.357	670.099	0.323	14	0.141	K.MEGLLWGASK.L
R3/RRR3-15/2	1107.236	1108.293	-1863.495	0.249	510.168	0.310	14	0.137	K.M*EGLLWGASK.L
R3/RRR3-14/2	1744.695	1745.866	-1248.553	0.278	348.340	0.397	17	0.137	K.VESTAVPSASTPDVADAK.A
R3/RRR3-14/2	946.823	946.168	-365.323	0.260	270.271	0.446	13	0.136	K.LVPVGYGIK.K
R3/RRR3-13/2	1744.659	1745.866	-1269.140	0.237	247.949	0.352	15	0.135	K.VESTAVPSASTPDVADAK.A
R3/RRR3-15/2	1107.342	1108.293	-1766.790	0.221	585.513	0.255	13	0.134	K.M*EGLLWGASK.L
R3/RRR3-14/2	1091.500	1092.294	-1648.222	0.268	508.971	0.268	12	0.132	-.MEGLLWGASK.-
R3/RRR3-14/2	1091.241	1092.294	-1886.363	0.261	493.030	0.238	12	0.110	-.MEGLLWGASK.-
R3/RRR3-14/3	1272.614	1272.480	105.856	0.376	1009.289	0.259	20	0.091	R.WFTHIDALLR.L
R3/RRR3-14/3	1272.337	1272.480	-112.441	0.326	862.458	0.230	18	0.085	R.WFTHIDALLR.L
R3/RRR3-15/2	1238.895	1239.449	-1258.724	0.507	1944.449	0.475	18	0.277	R.VNALENVVKPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1240.138	1239.449	-251.817	0.491	1735.023	0.452	18	0.241	R.VNALENVVKPR.L
R3/RRR3-15/2	1240.123	1239.449	-263.766	0.494	1530.273	0.422	16	0.207	R.VNALENVVKPR.L
R3/RRR3-15/2	937.911	938.109	-211.949	0.472	685.370	0.462	14	0.160	R.HVVLQSVR.S
R3/RRR3-15/2	1010.871	1011.111	-238.256	0.437	701.745	0.454	16	0.155	R.ASSFSLAEAK.Y
R3/RRR3-15/2	938.088	938.109	-22.268	0.416	555.670	0.464	13	0.155	R.HVVLQSVR.S
R3/RRR3-15/2	1081.030	1081.244	-198.159	0.480	921.206	0.372	14	0.154	R.LENTISYIK.G
R3/RRR3-15/2	937.991	938.109	-126.303	0.408	560.642	0.449	13	0.153	R.HVVLQSVR.S
R3/RRR3-14/2	937.965	938.109	-154.632	0.377	622.601	0.446	13	0.153	R.HVVLQSVR.S
R3/RRR3-15/2	1080.912	1081.244	-307.941	0.491	921.613	0.361	14	0.152	R.LENTISYIK.G
R3/RRR3-15/2	1010.901	1011.111	-208.212	0.443	463.270	0.493	14	0.152	R.ASSFSLAEAK.Y
R3/RRR3-14/2	937.901	938.109	-222.656	0.362	505.333	0.423	12	0.148	R.HVVLQSVR.S
R3/RRR3-15/2	1080.616	1081.244	-1511.412	0.407	841.358	0.348	14	0.148	R.LENTISYIK.G
R3/RRR3-14/2	938.296	938.109	199.959	0.336	336.541	0.421	10	0.145	R.HVVLQSVR.S
R3/RRR3-16/2	938.036	938.109	-78.786	0.398	427.070	0.365	11	0.145	R.HVVLQSVR.S
R3/RRR3-16/2	937.980	938.109	-138.705	0.365	449.047	0.362	11	0.144	R.HVVLQSVR.S
R3/RRR3-15/2	1010.784	1011.111	-324.279	0.328	432.569	0.342	13	0.136	-.ASSFSLAEAK.-
R3/RRR3-15/3	1395.905	1395.636	193.165	0.528	1459.498	0.312	27	0.122	R.RVNALENVVKPR.L
R3/RRR3-15/3	1395.563	1395.636	-52.615	0.544	1263.505	0.368	25	0.121	R.RVNALENVVKPR.L
R3/RRR3-15/3	1654.885	1655.747	-1128.360	0.420	595.450	0.545	23	0.116	K.GELDELEREDFFR.L
R3/RRR3-15/3	1395.209	1395.636	-306.547	0.528	1104.821	0.378	24	0.114	R.RVNALENVVKPR.L
R3/RRR3-16/3	1395.308	1395.636	-235.712	0.557	1038.904	0.373	23	0.110	R.RVNALENVVKPR.L
R3/RRR3-15/3	1408.202	1407.600	-283.330	0.472	1039.989	0.366	25	0.108	R.SHQENVAGVKLPK.F
R3/RRR3-15/3	1655.196	1655.747	-939.522	0.382	704.263	0.466	24	0.107	K.GELDELEREDFFR.L
R3/RRR3-15/3	1408.774	1407.600	123.393	0.515	1082.317	0.330	24	0.105	R.SHQENVAGVKLPK.F
R3/RRR3-14/3	1408.457	1407.600	-101.901	0.417	674.997	0.328	21	0.094	R.SHQENVAGVKLPK.F
R3/RRR3-19/1	1057.640	1058.254	-1530.051	0.327	1033.459	0.436	15	0.944	K.VIILGDSGVGK.T
R3/RRR3-19/1	1057.592	1058.254	-1575.966	0.282	962.758	0.420	15	0.925	K.VIILGDSGVGK.T
R3/RRR3-19/2	1678.316	1678.870	-928.359	0.534	1962.329	0.429	21	0.265	R.LFTLQIWDTAGQER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1678.361	1678.870	-901.415	0.459	1655.180	0.409	21	0.219	R.LFTLQIWDTAGQER.F
R3/RRR3-19/2	1036.893	1037.191	-288.070	0.369	1203.934	0.437	17	0.180	K.ATIGADFLTK.E
R3/RRR3-19/2	1057.979	1058.254	-260.572	0.412	1137.403	0.432	18	0.175	K.VIILGDSGVGK.T
R3/RRR3-19/2	1615.166	1613.746	260.721	0.574	1148.340	0.452	19	0.174	K.EGFNVEAAFECIAR.N
R3/RRR3-19/2	1188.006	1188.359	-298.629	0.506	1064.655	0.406	17	0.167	R.FQSLGVAFYR.G
R3/RRR3-19/2	1188.107	1188.359	-212.865	0.538	1069.662	0.398	17	0.166	R.FQSLGVAFYR.G
R3/RRR3-19/2	1036.435	1037.191	-1699.169	0.329	824.689	0.496	15	0.160	K.ATIGADFLTK.E
R3/RRR3-19/2	1058.058	1058.254	-185.798	0.336	1149.682	0.333	18	0.160	K.VIILGDSGVGK.T
R3/RRR3-19/2	1058.000	1058.254	-239.967	0.353	806.756	0.470	15	0.157	K.VIILGDSGVGK.T
R3/RRR3-18/2	1037.385	1037.191	186.878	0.355	842.139	0.426	15	0.155	K.ATIGADFLTK.E
R3/RRR3-19/2	1226.897	1227.348	-368.100	0.418	376.512	0.536	15	0.152	K.GNIPYFETSAK.D
R3/RRR3-19/2	1214.022	1214.374	-290.913	0.420	1023.928	0.336	15	0.152	K.TSLM*NQYVNK.K
R3/RRR3-19/2	1227.916	1227.348	-352.838	0.470	408.877	0.476	16	0.151	K.GNIPYFETSAK.D
R3/RRR3-19/2	1187.429	1188.359	-1630.757	0.335	896.429	0.355	16	0.149	R.FQSLGVAFYR.G
R3/RRR3-18/2	1058.086	1058.254	-158.369	0.342	855.387	0.362	15	0.147	K.VIILGDSGVGK.T
R3/RRR3-19/2	1678.458	1678.870	-246.237	0.404	837.433	0.369	17	0.145	R.LFTLQIWDTAGQER.F
R3/RRR3-19/2	1057.245	1058.254	-1905.446	0.326	702.429	0.371	15	0.143	-.VIILGDSGVGK.-
R3/RRR3-18/2	1227.077	1227.348	-221.171	0.266	311.043	0.424	14	0.138	K.GNIPYFETSAK.D
R3/RRR3-18/2	1058.176	1058.254	-73.312	0.243	601.883	0.366	13	0.137	K.VIILGDSGVGK.T
R3/RRR3-19/2	1036.327	1037.191	-1804.141	0.236	441.055	0.301	11	0.128	-.ATIGADFLTK.-
R3/RRR3-14/2	1618.334	1617.743	-253.720	0.572	2653.110	0.547	24	0.439	R.ELTAEVQQSGVTGAAR.V
R3/RRR3-14/2	1618.341	1617.743	-249.180	0.564	2757.040	0.480	24	0.437	R.ELTAEVQQSGVTGAAR.V
R3/RRR3-14/2	1617.291	1617.743	-280.229	0.503	2003.877	0.521	22	0.298	R.ELTAEVQQSGVTGAAR.V
R3/RRR3-14/2	1363.142	1363.455	-230.262	0.482	1627.548	0.480	20	0.233	K.VFGESSPEAQPSK.S
R3/RRR3-14/2	1363.078	1363.455	-277.520	0.480	1487.884	0.443	20	0.208	K.VFGESSPEAQPSK.S
R3/RRR3-14/2	1637.364	1637.818	-278.065	0.503	1099.807	0.589	21	0.197	K.GYTGAQYLPAIPTER.I
R3/RRR3-14/2	1362.528	1363.455	-1418.222	0.403	1358.134	0.436	19	0.192	K.VFGESSPEAQPSK.S
R3/RRR3-14/2	1637.404	1637.818	-253.233	0.429	1266.659	0.479	22	0.192	K.GYTGAQYLPAIPTER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1318.155	1318.416	-198.087	0.503	1162.888	0.486	16	0.185	R.KVDDTVQELDR.H
R3/RRR3-14/2	1630.282	1630.785	-924.695	0.515	1177.156	0.457	23	0.182	R.YEPAAEHLAVSTWR.S
R3/RRR3-14/2	1637.541	1637.818	-169.172	0.421	1203.127	0.456	22	0.182	K.GYTGAQYLPAIPTER.I
R3/RRR3-14/2	1631.367	1630.785	-257.322	0.558	972.921	0.543	22	0.182	R.YEPAAEHLAVSTWR.S
R3/RRR3-14/2	1299.228	1299.495	-206.062	0.468	1195.356	0.414	19	0.174	K.ACAVALGVPDVAR.E
R3/RRR3-14/2	1317.938	1318.416	-363.203	0.466	1061.826	0.413	16	0.166	R.KVDDTVQELDR.H
R3/RRR3-14/2	1317.804	1318.416	-1226.276	0.451	935.756	0.397	15	0.155	R.KVDDTVQELDR.H
R3/RRR3-14/2	918.006	918.075	-75.437	0.334	911.674	0.327	14	0.145	K.GIVGPVYGR.F
R3/RRR3-14/2	1298.669	1299.495	-1410.464	0.329	779.746	0.315	16	0.138	-.ACAVALGVPDVAR.-
R3/RRR3-5/2	1761.887	1762.000	-64.183	0.532	2875.011	0.563	24	0.506	R.FLVLNAAELAVDGSSVR.F
R3/RRR3-5/2	1754.646	1754.916	-154.323	0.516	2312.848	0.465	24	0.340	R.ETALLYDELLSSASNK.Q
R3/RRR3-5/2	1213.079	1213.324	-202.932	0.502	1413.824	0.404	17	0.194	K.LNVDQTGFYR.V
R3/RRR3-5/2	1157.069	1156.269	-173.497	0.473	1362.227	0.435	17	0.194	K.AAEVSEFFAGK.T
R3/RRR3-5/2	1213.328	1213.324	3.268	0.520	1278.442	0.324	16	0.166	K.LNVDQTGFYR.V
R3/RRR3-5/2	1468.383	1467.648	-180.990	0.440	689.456	0.493	20	0.158	K.TWPSSSLISDFVK.S
R3/RRR3-5/2	1212.456	1213.324	-1545.494	0.385	1019.811	0.351	15	0.155	K.LNVDQTGFYR.V
R3/RRR3-5/3	1761.952	1762.000	-27.637	0.452	1520.338	0.386	30	0.150	R.FLVLNAAELAVDGSSVR.F
R3/RRR3-5/2	1467.325	1467.648	-220.421	0.327	619.762	0.416	18	0.144	K.TWPSSSLISDFVK.S
R3/RRR3-5/2	850.830	850.982	-178.887	0.395	835.678	0.268	13	0.140	R.AGYDALLK.I
R3/RRR3-5/2	1466.998	1467.648	-1127.603	0.288	422.893	0.379	16	0.137	K.TWPSSSLISDFVK.S
R3/RRR3-5/2	850.977	850.982	-5.627	0.388	848.902	0.178	13	0.132	R.AGYDALLK.I
R3/RRR3-5/3	1451.314	1451.603	-200.084	0.462	1823.786	0.163	27	0.124	R.VKYDDELAAGLEK.A
R3/RRR3-5/3	1451.306	1451.603	-205.780	0.507	1396.571	0.209	25	0.101	-.VKYDDELAAGLEK.-
R3/RRR3-5/2	1931.551	1930.111	228.347	0.570	862.769	0.575	20	0.098	R.SEPNLAQTVHELLQHNV.-
R3/RRR3-5/2	1931.224	1930.111	58.795	0.516	819.431	0.490	19	0.082	R.SEPNLAQTVHELLQHNV.-
R3/RRR3-5/2	1931.577	1930.111	242.036	0.511	597.173	0.517	17	0.042	R.SEPNLAQTVHELLQHNV.-
R3/RRR3-18/2	1225.677	1226.449	-1450.607	0.451	1505.528	0.530	17	0.230	K.LLANILYSYR.G
R3/RRR3-18/2	1332.923	1333.429	-1132.636	0.500	1441.360	0.521	19	0.220	K.LSGDDVGELHYK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1226.152	1226.449	-242.906	0.580	1567.552	0.451	17	0.219	K.LLANILYSYR.G
R3/RRR3-18/2	1226.283	1226.449	-136.248	0.481	1409.181	0.527	17	0.219	K.LLANILYSYR.G
R3/RRR3-18/2	1384.003	1384.476	-342.592	0.525	1429.085	0.520	20	0.218	K.GPGLYYVDSEGAR.L
R3/RRR3-18/2	1334.160	1333.429	-202.043	0.503	1251.756	0.519	18	0.199	K.LSGDDVGELHYK.Y
R3/RRR3-18/2	1225.939	1226.449	-1235.673	0.468	1325.315	0.477	16	0.199	K.LLANILYSYR.G
R3/RRR3-18/2	1333.005	1333.429	-318.500	0.480	1231.217	0.502	18	0.194	K.LSGDDVGELHYK.Y
R3/RRR3-18/2	1373.012	1373.518	-1100.061	0.477	1053.047	0.504	20	0.180	R.ASM*GGYISSQTVR.K
R3/RRR3-18/2	1494.201	1494.695	-331.399	0.518	991.298	0.516	21	0.179	R.YVM*PVEEAAELAR.R
R3/RRR3-18/2	1372.940	1373.518	-1152.555	0.463	1020.448	0.513	20	0.179	R.ASM*GGYISSQTVR.K
R3/RRR3-18/2	1494.244	1494.695	-302.956	0.518	863.414	0.537	20	0.174	R.YVM*PVEEAAELAR.R
R3/RRR3-18/2	1495.483	1494.695	-141.911	0.488	827.036	0.519	20	0.169	R.YVM*PVEEAAELAR.R
R3/RRR3-18/2	1478.203	1478.696	-334.344	0.425	943.065	0.473	20	0.167	R.YVMPVEEAAELAR.R
R3/RRR3-18/2	1373.151	1373.518	-268.222	0.483	861.042	0.499	18	0.166	R.ASM*GGYISSQTVR.K
R3/RRR3-18/2	1125.490	1126.293	-1606.604	0.544	508.274	0.413	14	0.149	R.RAIYQATFR.D
R3/RRR3-18/2	1358.419	1357.518	-73.422	0.432	389.688	0.446	17	0.147	R.ASMGGYISSQTVR.K
R3/RRR3-18/2	969.691	970.107	-430.130	0.314	722.753	0.413	12	0.144	R.AIYQATFR.D
R3/RRR3-18/2	1125.880	1126.293	-368.068	0.529	448.944	0.379	13	0.144	R.RAIYQATFR.D
R3/RRR3-18/2	1125.691	1126.293	-1427.289	0.467	510.972	0.368	13	0.143	R.RAIYQATFR.D
R3/RRR3-18/2	1358.310	1357.518	-153.471	0.301	254.635	0.321	16	0.140	R.ASMGGYISSQTVR.K
R3/RRR3-16/2	1820.324	1820.945	-893.131	0.555	2330.747	0.574	28	0.377	K.NPGEQSHAANAGLDIAVR.L
R3/RRR3-16/2	1820.422	1820.945	-838.873	0.548	2064.643	0.619	26	0.339	K.NPGEQSHAANAGLDIAVR.L
R3/RRR3-16/2	1821.252	1820.945	169.235	0.573	1994.878	0.566	28	0.311	K.NPGEQSHAANAGLDIAVR.L
R3/RRR3-16/3	1821.003	1820.945	32.326	0.568	2041.523	0.550	33	0.282	K.NPGEQSHAANAGLDIAVR.L
R3/RRR3-16/3	1821.880	1820.945	-35.565	0.552	1974.778	0.520	34	0.257	K.NPGEQSHAANAGLDIAVR.L
R3/RRR3-16/2	1534.160	1534.657	-325.182	0.475	1432.632	0.537	20	0.221	R.LAWHSAGTFDVSSR.T
R3/RRR3-16/2	1535.280	1534.657	-246.552	0.563	1390.755	0.543	21	0.218	R.LAWHSAGTFDVSSR.T
R3/RRR3-16/2	1534.009	1534.657	-1077.867	0.485	1406.871	0.520	21	0.215	R.LAWHSAGTFDVSSR.T
R3/RRR3-16/2	1310.217	1310.398	-138.453	0.487	1539.961	0.424	20	0.211	R.LPDATQGSDHLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1309.556	1310.398	-1411.079	0.462	1501.983	0.438	18	0.208	R.LPDATQGSDHLR.Q
R3/RRR3-16/2	1311.093	1310.398	-233.520	0.508	1328.621	0.468	19	0.197	R.LPDATQGSDHLR.Q
R3/RRR3-16/2	1601.384	1600.751	-229.799	0.483	705.128	0.569	23	0.169	K.SYPTVSDEYLAAVGK.A
R3/RRR3-16/3	1821.077	1820.945	72.866	0.539	1387.813	0.507	29	0.168	K.NPGEQSHAANAGLDIAVR.L
R3/RRR3-16/2	1601.259	1600.751	-308.268	0.448	565.638	0.547	22	0.160	K.SYPTVSDEYLAAVGK.A
R3/RRR3-16/2	1600.333	1600.751	-261.777	0.387	610.015	0.542	22	0.158	K.SYPTVSDEYLAAVGK.A
R3/RRR3-16/2	1558.463	1558.870	-261.975	0.473	862.264	0.378	20	0.151	K.ALMADPAFRPLVEK.Y
R3/RRR3-16/2	1558.484	1558.870	-248.223	0.449	791.336	0.394	19	0.150	K.ALMADPAFRPLVEK.Y
R3/RRR3-16/2	1574.301	1574.870	-999.516	0.448	638.555	0.429	19	0.149	K.ALM*ADPAFRPLVEK.Y
R3/RRR3-16/2	1575.243	1574.870	237.617	0.464	693.959	0.386	20	0.147	K.ALM*ADPAFRPLVEK.Y
R3/RRR3-16/2	1560.429	1558.870	-283.772	0.467	714.201	0.383	19	0.146	K.ALMADPAFRPLVEK.Y
R3/RRR3-16/2	1574.466	1574.870	-257.310	0.429	642.912	0.381	19	0.145	K.ALM*ADPAFRPLVEK.Y
R3/RRR3-16/3	1534.860	1534.657	132.441	0.503	1427.705	0.405	27	0.144	R.LAWHSAGTFDVSSR.T
R3/RRR3-17/2	1559.479	1558.870	-251.284	0.354	786.730	0.207	18	0.132	-.ALMADPAFRPLVEK.-
R3/RRR3-16/3	1535.656	1534.657	-0.895	0.506	1089.750	0.443	25	0.125	R.LAWHSAGTFDVSSR.T
R3/RRR3-16/2	1600.451	1600.751	-188.010	0.406	126.126	0.467	12	0.111	-.SYPTVSDEYLAAVGK.-
R3/RRR3-16/3	1310.241	1310.398	-120.566	0.479	793.423	0.424	25	0.109	R.LPDATQGSDHLR.Q
R3/RRR3-16/3	1310.456	1310.398	44.125	0.452	735.203	0.446	24	0.106	-.LPDATQGSDHLR.-
R3/RRR3-15/3	1310.282	1310.398	-88.885	0.411	860.763	0.403	25	0.106	R.LPDATQGSDHLR.Q
R3/RRR3-18/3	1310.024	1310.398	-286.853	0.394	379.613	0.446	19	0.106	R.LPDATQGSDHLR.Q
R3/RRR3-16/3	1310.667	1310.398	205.960	0.482	669.525	0.427	24	0.103	-.LPDATQGSDHLR.-
R3/RRR3-16/3	1534.811	1534.657	100.616	0.427	761.467	0.403	21	0.103	R.LAWHSAGTFDVSSR.T
R3/RRR3-18/3	1310.270	1310.398	-98.137	0.307	439.541	0.412	19	0.101	R.LPDATQGSDHLR.Q
R3/RRR3-9/2	1847.727	1848.048	-174.379	0.553	1821.096	0.591	23	0.288	R.ELDHLANFLQAAVDYK.K
R3/RRR3-9/2	1847.564	1848.048	-262.930	0.554	1786.387	0.575	23	0.278	R.ELDHLANFLQAAVDYK.K
R3/RRR3-9/2	1848.047	1848.048	-0.570	0.574	1491.294	0.546	22	0.229	R.ELDHLANFLQAAVDYK.K
R3/RRR3-9/2	1931.572	1932.162	-825.591	0.547	1616.281	0.435	22	0.217	K.TLTETNKNLDEIVELAK.K
R3/RRR3-9/2	1071.056	1070.223	-155.994	0.463	1366.858	0.461	16	0.200	K.VYAYGAAQVK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/3	1932.908	1932.162	-131.546	0.460	1645.965	0.424	33	0.174	K.TLTETNKNLDEIVELAK.K
R3/RRR3-9/2	1070.044	1070.223	-167.584	0.417	908.719	0.451	16	0.163	K.VYAYGAAQVK.K
R3/RRR3-9/2	1069.692	1070.223	-1435.852	0.335	1013.779	0.358	16	0.155	K.VYAYGAAQVK.K
R3/RRR3-9/2	1105.887	1105.182	-268.326	0.415	647.940	0.482	16	0.150	R.GTGGDPFGAPTK.S
R3/RRR3-9/2	1640.088	1639.782	186.884	0.390	793.660	0.359	17	0.141	K.CGDWEGEFFPGIPK.I
R3/RRR3-9/3	1847.777	1848.048	-147.215	0.408	1348.591	0.386	26	0.134	R.ELDHLANFLQAAVDYK.K
R3/RRR3-9/3	1975.558	1976.221	-844.463	0.494	1166.998	0.443	27	0.130	R.ELDHLANFLQAAVDYKK.K
R3/RRR3-9/3	1848.809	1848.048	-129.980	0.418	1126.166	0.398	26	0.118	R.ELDHLANFLQAAVDYK.K
R3/RRR3-9/3	1932.241	1932.162	41.237	0.379	1428.868	0.262	29	0.115	K.TLTETNKNLDEIVELAK.K
R3/RRR3-9/3	1931.827	1932.162	-173.608	0.339	1197.300	0.325	28	0.110	K.TLTETNKNLDEIVELAK.K
R3/RRR3-9/3	1290.911	1291.458	-1202.467	0.469	971.382	0.292	26	0.096	R.YMHGAATSPEVK.V
R3/RRR3-10/2	1856.473	1857.050	-852.327	0.576	2406.463	0.506	24	0.366	K.LAYVALDYEQELETAK.N
R3/RRR3-10/2	1856.426	1857.050	-877.608	0.556	2356.751	0.485	24	0.350	K.LAYVALDYEQELETAK.N
R3/RRR3-10/2	1857.337	1857.050	155.005	0.611	2148.291	0.519	23	0.319	K.LAYVALDYEQELETAK.N
R3/RRR3-10/2	1764.380	1764.915	-872.180	0.542	1166.044	0.562	22	0.197	K.SYELPDGQVITIGSER.F
R3/RRR3-10/2	1118.953	1119.166	-190.787	0.435	488.079	0.548	14	0.157	R.GYSFTTSAER.E
R3/RRR3-10/2	1118.302	1119.166	-1672.002	0.303	469.196	0.452	14	0.143	R.GYSFTTSAER.E
R3/RRR3-10/2	1118.487	1119.166	-1505.775	0.293	475.078	0.456	14	0.143	R.GYSFTTSAER.E
R3/RRR3-9/2	1857.940	1857.050	-59.745	0.393	543.911	0.397	19	0.142	K.LAYVALDYEQELETAK.N
R3/RRR3-10/3	1856.773	1857.050	-149.535	0.398	1220.815	0.457	24	0.138	K.LAYVALDYEQELETAK.N
R3/RRR3-9/2	1858.106	1857.050	30.073	0.370	395.667	0.366	17	0.138	K.LAYVALDYEQELETAK.N
R3/RRR3-10/3	1856.928	1857.050	-66.246	0.317	1167.622	0.354	23	0.113	K.LAYVALDYEQELETAK.N
R3/RRR3-16/2	1667.695	1668.820	-1278.449	0.378	2283.720	0.243	22	0.271	R.NDFDTCVDLLSQLK.V
R3/RRR3-16/2	1191.586	1192.390	-1518.001	0.474	1540.693	0.470	17	0.221	K.LVEVTQLFSR.F
R3/RRR3-16/2	1192.087	1192.390	-254.881	0.523	1496.126	0.488	17	0.220	K.LVEVTQLFSR.F
R3/RRR3-16/2	1192.169	1192.390	-185.643	0.582	1480.881	0.476	17	0.215	K.LVEVTQLFSR.F
R3/RRR3-15/2	1833.250	1833.078	93.861	0.576	1256.080	0.571	24	0.210	K.EIPSLQVINQTLSYAR.E
R3/RRR3-16/2	1832.535	1833.078	-844.553	0.505	1236.355	0.576	24	0.209	K.EIPSLQVINQTLSYAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1191.901	1192.390	-411.266	0.435	1364.027	0.474	16	0.202	K.LVEVTQLFSR.F
R3/RRR3-16/2	1832.478	1833.078	-875.848	0.512	1092.202	0.538	23	0.188	K.EIPSLQVINQTLSYAR.E
R3/RRR3-16/2	1831.828	1833.078	-1232.141	0.432	1105.708	0.536	23	0.187	K.EIPSLQVINQTLSYAR.E
R3/RRR3-15/2	1832.565	1833.078	-828.103	0.486	971.146	0.521	21	0.174	K.EIPSLQVINQTLSYAR.E
R3/RRR3-16/2	1373.394	1373.579	-134.847	0.462	1071.308	0.454	17	0.172	R.DIYEHAVVLSVK.I
R3/RRR3-16/2	1373.201	1373.579	-275.741	0.413	952.029	0.476	17	0.167	R.DIYEHAVVLSVK.I
R3/RRR3-16/2	1373.771	1373.579	140.495	0.413	840.268	0.447	17	0.158	R.DIYEHAVVLSVK.I
R3/RRR3-16/2	1123.002	1123.155	-136.240	0.533	834.440	0.365	15	0.151	K.IEDQDAFER.D
R3/RRR3-16/2	1122.719	1123.155	-388.842	0.495	820.028	0.329	15	0.146	K.IEDQDAFER.D
R3/RRR3-15/2	1192.199	1192.390	-160.374	0.405	885.481	0.307	14	0.144	K.LVEVTQLFSR.F
R3/RRR3-16/2	1122.967	1123.155	-167.863	0.503	815.310	0.302	15	0.143	K.IEDQDAFER.D
R3/RRR3-15/2	1373.022	1373.579	-1137.635	0.275	472.660	0.332	13	0.133	-.DIYEHAVVLSVK.-
R3/RRR3-15/2	1276.815	1276.401	325.783	0.354	715.979	0.275	13	0.131	-.GYDYMSIAEAR.-
R3/RRR3-16/3	1365.980	1365.466	-356.713	0.446	1123.122	0.433	22	0.125	K.TVRDELAGCSEK.G
R3/RRR3-16/3	1365.884	1365.466	307.263	0.444	706.064	0.389	20	0.101	K.TVRDELAGCSEK.G
R3/RRR3-15/3	1364.763	1365.466	-1251.512	0.330	600.435	0.321	20	0.092	K.TVRDELAGCSEK.G
R3/RRR3-6/3	1435.346	1435.574	-158.892	0.573	3896.187	0.533	36	0.819	R.RVHVAGPAGSAAADR.E
R3/RRR3-6/2	1586.341	1586.683	-216.002	0.423	1854.824	0.439	24	0.254	R.VDVSPETLEPTGGER.R
R3/RRR3-6/2	1352.393	1352.479	-63.700	0.485	1604.411	0.540	17	0.244	R.VAEDGWWSVFR.V
R3/RRR3-6/2	1352.360	1352.479	-88.237	0.486	1607.211	0.530	17	0.242	R.VAEDGWWSVFR.V
R3/RRR3-6/2	1586.354	1586.683	-207.510	0.426	1768.209	0.430	24	0.239	R.VDVSPETLEPTGGER.R
R3/RRR3-6/2	1162.993	1163.348	-306.105	0.525	1482.026	0.465	17	0.214	R.VLETEVAVFR.A
R3/RRR3-6/2	1162.598	1163.348	-1509.829	0.428	1459.950	0.468	17	0.211	R.VLETEVAVFR.A
R3/RRR3-6/2	1586.162	1586.683	-961.840	0.442	1451.632	0.460	22	0.207	R.VDVSPETLEPTGGER.R
R3/RRR3-6/2	1351.638	1352.479	-1365.697	0.337	1333.202	0.412	16	0.184	R.VAEDGWWSVFR.V
R3/RRR3-5/2	1353.396	1352.479	-61.391	0.386	1049.160	0.495	14	0.174	R.VAEDGWWSVFR.V
R3/RRR3-5/2	1353.642	1352.479	120.786	0.377	882.185	0.434	14	0.156	R.VAEDGWWSVFR.V
R3/RRR3-6/2	856.391	857.033	-1922.792	0.320	566.835	0.482	11	0.146	K.TPGVTILR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1719.956	1720.875	-1118.665	0.437	1323.119	0.428	31	0.139	R.RVHVAGPAGSAAADRER.I
R3/RRR3-6/2	856.377	857.033	-1939.695	0.265	670.120	0.365	12	0.139	K.TPGVTILR.S
R3/RRR3-6/3	1279.918	1279.387	-367.593	0.421	1071.613	0.426	28	0.119	R.VHVAGPAGSAAADR.E
R3/RRR3-6/3	1279.156	1279.387	-181.691	0.342	747.784	0.361	23	0.096	R.VHVAGPAGSAAADR.E
R3/RRR3-6/3	1279.376	1279.387	-8.969	0.376	625.514	0.292	23	0.091	R.VHVAGPAGSAAADR.E
R3/RRR3-4/2	1845.468	1846.109	-891.510	0.533	2785.798	0.495	25	0.456	R.IVCQQVNVSSLEEVIK.H
R3/RRR3-4/2	1476.204	1476.703	-338.612	0.500	2308.779	0.537	20	0.358	R.VLQQASQIFQSVK.I
R3/RRR3-4/3	1661.515	1661.754	-144.448	0.589	2373.563	0.486	31	0.315	K.YGASHLELENEKDR.N
R3/RRR3-4/3	1662.766	1661.754	6.832	0.580	2159.567	0.526	30	0.289	K.YGASHLELENEKDR.N
R3/RRR3-4/2	1475.813	1476.703	-1284.221	0.355	2182.327	0.381	20	0.287	R.VLQQASQIFQSVK.I
R3/RRR3-4/2	1477.151	1476.703	304.393	0.522	1755.167	0.514	18	0.255	R.VLQQASQIFQSVK.I
R3/RRR3-4/2	1563.820	1564.767	-1248.355	0.324	1811.519	0.410	20	0.238	K.IATELSLWQEAFR.S
R3/RRR3-4/2	1564.070	1564.767	-1087.680	0.341	1525.285	0.407	18	0.202	K.IATELSLWQEAFR.S
R3/RRR3-4/2	1564.181	1564.767	-1016.999	0.346	1437.838	0.371	19	0.187	K.IATELSLWQEAFR.S
R3/RRR3-4/3	1662.143	1661.754	234.486	0.599	1506.957	0.528	27	0.186	K.YGASHLELENEKDR.N
R3/RRR3-1/2	1476.054	1476.703	-1120.105	0.342	1278.277	0.388	16	0.174	R.VLQQASQIFQSVK.I
R3/RRR3-1/2	1566.172	1564.767	259.496	0.487	915.492	0.515	14	0.166	K.IATELSLWQEAFR.S
R3/RRR3-3/3	1969.831	1970.007	-89.953	0.441	1237.039	0.540	33	0.161	R.GGDGGSSAGGQRPAVAPEQDR.W
R3/RRR3-1/2	1476.053	1476.703	-1121.101	0.272	951.275	0.377	15	0.149	R.VLQQASQIFQSVK.I
R3/RRR3-3/2	1476.197	1476.703	-1023.205	0.391	958.954	0.322	16	0.146	R.VLQQASQIFQSVK.I
R3/RRR3-2/2	1476.202	1476.703	-1019.801	0.337	749.310	0.375	14	0.142	R.VLQQASQIFQSVK.I
R3/RRR3-4/3	1970.017	1970.007	4.679	0.464	994.273	0.548	31	0.141	R.GGDGGSSAGGQRPAVAPEQDR.W
R3/RRR3-1/2	1475.421	1476.703	-1550.941	0.272	556.148	0.269	14	0.133	R.VLQQASQIFQSVK.I
R3/RRR3-4/3	1969.736	1970.007	-137.975	0.450	1032.041	0.489	31	0.132	R.GGDGGSSAGGQRPAVAPEQDR.W
R3/RRR3-4/2	1403.146	1402.539	-280.939	0.366	799.965	0.233	14	0.130	R.SDREHVTPWFK.F
R3/RRR3-4/2	1036.281	1037.191	-1848.764	0.142	687.219	0.294	13	0.125	R.ASLFSELAAK.G
R3/RRR3-4/3	1266.648	1266.433	169.572	0.412	978.531	0.471	23	0.121	K.VNHLSGAVHFGK.M
R3/RRR3-4/3	1266.477	1266.433	34.298	0.420	1106.575	0.422	23	0.120	K.VNHLSGAVHFGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/3	1968.740	1970.007	-1155.354	0.385	820.975	0.475	27	0.116	R.GGDGGSSAGGQRPAVAPEQDR.W
R3/RRR3-2/3	1968.604	1970.007	-1224.283	0.406	783.676	0.482	30	0.115	R.GGDGGSSAGGQRPAVAPEQDR.W
R3/RRR3-11/3	1644.407	1643.995	251.311	0.506	2085.290	0.531	36	0.269	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/3	1645.126	1643.995	79.803	0.523	1759.130	0.560	33	0.228	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/3	1644.097	1643.995	62.576	0.474	1571.803	0.500	32	0.184	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/3	1644.949	1643.995	-27.817	0.503	1326.045	0.549	31	0.169	K.TLLLGEKPVTVFGIR.N
R3/RRR3-10/3	1644.007	1643.995	7.841	0.479	1419.099	0.502	32	0.166	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/2	1643.611	1643.995	-234.101	0.485	817.083	0.499	20	0.163	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/2	1643.693	1643.995	-184.107	0.515	726.935	0.534	19	0.163	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/2	1643.872	1643.995	-74.526	0.450	758.963	0.516	20	0.163	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/2	1643.747	1643.995	-151.402	0.455	570.721	0.502	17	0.152	K.TLLLGEKPVTVFGIR.N
R3/RRR3-10/2	1643.392	1643.995	-977.963	0.431	588.361	0.463	18	0.149	K.TLLLGEKPVTVFGIR.N
R3/RRR3-15/2	1644.176	1643.995	110.389	0.363	670.666	0.449	17	0.148	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/2	1643.547	1643.995	-272.996	0.377	446.536	0.412	15	0.140	K.TLLLGEKPVTVFGIR.N
R3/RRR3-9/2	1643.385	1643.995	-982.363	0.308	484.225	0.424	15	0.140	K.TLLLGEKPVTVFGIR.N
R3/RRR3-12/3	1643.386	1643.995	-981.663	0.447	1134.723	0.493	29	0.140	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/3	1644.069	1643.995	45.151	0.499	1081.598	0.512	30	0.139	K.TLLLGEKPVTVFGIR.N
R3/RRR3-7/2	1643.188	1643.995	-1102.966	0.334	499.811	0.386	15	0.138	K.TLLLGEKPVTVFGIR.N
R3/RRR3-13/3	1644.358	1643.995	221.833	0.418	1026.165	0.520	27	0.138	K.TLLLGEKPVTVFGIR.N
R3/RRR3-13/3	1644.177	1643.995	111.274	0.467	1052.999	0.506	27	0.137	K.TLLLGEKPVTVFGIR.N
R3/RRR3-11/3	1644.323	1643.995	200.393	0.440	961.647	0.476	28	0.125	K.TLLLGEKPVTVFGIR.N
R3/RRR3-13/3	1643.761	1643.995	-142.656	0.415	834.207	0.432	25	0.113	K.TLLLGEKPVTVFGIR.N
R3/RRR3-9/3	1643.732	1643.995	-160.424	0.371	935.486	0.403	27	0.112	K.TLLLGEKPVTVFGIR.N
R3/RRR3-10/3	1643.006	1643.995	-1213.944	0.327	671.982	0.362	24	0.101	K.TLLLGEKPVTVFGIR.N
R3/RRR3-10/3	1643.394	1643.995	-976.852	0.267	536.180	0.304	20	0.091	-.TLLLGEKPVTVFGIR.-
R3/RRR3-14/2	1651.463	1651.891	-259.677	0.569	2362.278	0.490	24	0.356	R.HLAAQFQEIPLDLR.M
R3/RRR3-14/2	1652.491	1651.891	-242.400	0.628	2252.917	0.551	24	0.354	R.HLAAQFQEIPLDLR.M
R3/RRR3-14/2	1651.410	1651.891	-292.159	0.573	2052.412	0.515	23	0.306	R.HLAAQFQEIPLDLR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1297.125	1296.411	-221.309	0.510	1721.530	0.503	19	0.251	K.AYISSNLSLGDR.H
R3/RRR3-14/2	1296.275	1296.411	-105.750	0.438	1715.671	0.463	19	0.240	K.AYISSNLSLGDR.H
R3/RRR3-14/2	1269.525	1269.511	11.129	0.499	1342.653	0.419	16	0.189	K.LYVLIDEIYK.Y
R3/RRR3-14/2	1833.426	1834.153	-944.580	0.488	1019.858	0.591	21	0.187	R.VIGTLLGSVLPDGTVHVR.N
R3/RRR3-14/2	1182.156	1182.372	-183.054	0.484	1410.068	0.362	18	0.186	-.FISDAVASM*PK.-
R3/RRR3-14/2	1269.246	1269.511	-209.579	0.477	1454.805	0.352	15	0.186	K.LYVLIDEIYK.Y
R3/RRR3-14/2	1181.899	1182.372	-400.950	0.473	1239.858	0.384	18	0.175	R.FISDAVASM*PK.L
R3/RRR3-14/2	1834.417	1834.153	144.394	0.483	897.779	0.548	20	0.170	R.VIGTLLGSVLPDGTVHVR.N
R3/RRR3-14/2	1051.900	1052.120	-209.001	0.479	864.938	0.494	15	0.169	K.YVDDVVEGR.V
R3/RRR3-14/2	1181.528	1182.372	-1564.998	0.354	1290.995	0.313	18	0.166	R.FISDAVASM*PK.L
R3/RRR3-14/2	1295.570	1296.411	-1425.650	0.319	1197.062	0.368	17	0.166	K.AYISSNLSLGDR.H
R3/RRR3-14/2	1833.380	1834.153	-969.981	0.420	827.530	0.529	20	0.162	R.VIGTLLGSVLPDGTVHVR.N
R3/RRR3-14/2	1268.381	1269.511	-1684.021	0.360	1097.061	0.370	15	0.161	K.LYVLIDEIYK.Y
R3/RRR3-14/2	1051.513	1052.120	-1532.867	0.347	879.591	0.445	15	0.159	K.YVDDVVEGR.V
R3/RRR3-14/2	1051.433	1052.120	-1608.557	0.404	917.347	0.403	15	0.158	K.YVDDVVEGR.V
R3/RRR3-14/2	1494.294	1494.676	-256.346	0.313	831.143	0.405	16	0.145	K.LSPAAFDKLFNDR.I
R3/RRR3-14/3	1833.816	1834.153	-184.155	0.458	780.754	0.516	32	0.120	R.VIGTLLGSVLPDGTVHVR.N
R3/RRR3-14/3	1834.759	1834.153	-215.324	0.415	749.822	0.508	29	0.117	R.VIGTLLGSVLPDGTVHVR.N
R3/RRR3-14/3	1833.567	1834.153	-867.322	0.400	662.011	0.509	30	0.113	R.VIGTLLGSVLPDGTVHVR.N
R3/RRR3-15/2	1056.874	1057.139	-251.808	0.467	1297.397	0.524	17	0.206	R.APIGEEVEGR.R
R3/RRR3-15/3	1915.236	1915.200	18.822	0.467	1540.391	0.527	31	0.192	K.M*SQYFASLKPGDVVEVK.G
R3/RRR3-15/2	1056.455	1057.139	-1599.173	0.446	1236.777	0.475	17	0.191	R.APIGEEVEGR.R
R3/RRR3-15/2	1056.914	1057.139	-213.918	0.460	1075.088	0.541	17	0.189	R.APIGEEVEGR.R
R3/RRR3-15/2	1460.327	1460.702	-257.446	0.405	1017.373	0.395	17	0.158	K.VALNPDKWLEFK.L
R3/RRR3-15/2	1318.172	1318.538	-278.893	0.457	716.711	0.455	15	0.152	K.LGLDVASCLITR.A
R3/RRR3-15/2	1318.251	1318.538	-218.599	0.332	953.278	0.370	15	0.150	K.LGLDVASCLITR.A
R3/RRR3-15/2	1046.033	1046.200	-160.311	0.363	761.122	0.389	15	0.147	R.SQGELTGILK.E
R3/RRR3-15/2	1259.427	1260.384	-1558.530	0.363	654.452	0.392	16	0.145	K.ATVSHNSQLFR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1260.053	1260.384	-263.967	0.376	537.942	0.403	15	0.143	K.ATVSHNSQLFR.F
R3/RRR3-15/2	1259.497	1260.384	-1502.644	0.373	597.948	0.358	15	0.141	K.ATVSHNSQLFR.F
R3/RRR3-15/2	1045.511	1046.200	-1619.776	0.295	633.325	0.364	14	0.139	R.SQGELTGILK.E
R3/RRR3-15/2	1318.218	1318.538	-243.403	0.291	737.273	0.331	14	0.137	K.LGLDVASCLITR.A
R3/RRR3-15/2	1318.316	1317.474	-120.421	0.435	857.918	0.248	17	0.134	K.DRSQGELTGILK.E
R3/RRR3-15/3	1460.496	1460.702	-141.108	0.455	585.634	0.575	25	0.121	K.VALNPDKWLEFK.L
R3/RRR3-15/3	1260.172	1260.384	-168.640	0.379	738.681	0.500	22	0.113	K.ATVSHNSQLFR.F
R3/RRR3-15/3	1460.429	1460.702	-187.392	0.380	345.344	0.504	20	0.108	K.VALNPDKWLEFK.L
R3/RRR3-15/3	1460.499	1460.702	-139.221	0.391	514.168	0.484	23	0.107	K.VALNPDKWLEFK.L
R3/RRR3-15/3	1260.520	1260.384	107.941	0.376	582.867	0.448	20	0.104	K.ATVSHNSQLFR.F
R3/RRR3-15/3	1260.431	1260.384	37.134	0.352	474.440	0.365	19	0.097	K.ATVSHNSQLFR.F
R3/RRR3-15/3	1915.074	1915.200	-66.048	0.394	780.947	0.357	23	0.096	K.M*SQYFASLKPGDVVEVK.G
R3/RRR3-15/3	1914.802	1915.200	-208.200	0.385	767.220	0.303	26	0.091	K.M*SQYFASLKPGDVVEVK.G
R3/RRR3-10/3	1491.328	1491.714	-259.820	0.576	3477.241	0.419	31	0.577	K.KVSPEVIAEYTVR.T
R3/RRR3-10/3	1492.077	1491.714	244.350	0.565	3206.277	0.423	30	0.497	K.KVSPEVIAEYTVR.T
R3/RRR3-11/3	1492.659	1491.714	-36.807	0.608	3215.431	0.418	30	0.494	K.KVSPEVIAEYTVR.T
R3/RRR3-11/3	1491.517	1491.714	-132.714	0.577	3029.436	0.420	29	0.445	K.KVSPEVIAEYTVR.T
R3/RRR3-10/3	1492.772	1491.714	39.105	0.617	2802.657	0.446	29	0.395	K.KVSPEVIAEYTVR.T
R3/RRR3-11/3	1491.908	1491.714	130.263	0.568	2673.690	0.402	28	0.346	K.KVSPEVIAEYTVR.T
R3/RRR3-11/2	1569.259	1569.698	-280.926	0.529	2111.224	0.504	25	0.313	K.GDAVLGEGASESLHVK.D
R3/RRR3-11/2	1569.324	1569.698	-239.175	0.496	2123.687	0.445	25	0.297	K.GDAVLGEGASESLHVK.D
R3/RRR3-11/2	1492.343	1491.714	-249.133	0.527	1712.518	0.557	21	0.264	K.KVSPEVIAEYTVR.T
R3/RRR3-11/2	1492.613	1491.714	-67.805	0.600	1548.544	0.582	20	0.247	K.KVSPEVIAEYTVR.T
R3/RRR3-11/2	1491.256	1491.714	-308.265	0.528	1718.785	0.478	21	0.244	K.KVSPEVIAEYTVR.T
R3/RRR3-11/2	1569.294	1569.698	-258.450	0.512	1674.040	0.485	23	0.238	K.GDAVLGEGASESLHVK.D
R3/RRR3-11/3	1312.541	1312.501	31.136	0.533	1596.018	0.420	23	0.163	K.KPWSLSFSFGR.A
R3/RRR3-11/2	1312.240	1312.501	-198.887	0.341	704.739	0.527	17	0.159	K.KPWSLSFSFGR.A
R3/RRR3-11/2	1312.111	1312.501	-297.631	0.337	1005.713	0.389	17	0.158	K.KPWSLSFSFGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1363.253	1363.541	-212.011	0.424	772.374	0.435	18	0.155	K.VSPEVIAEYTVR.T
R3/RRR3-10/2	1364.172	1363.541	-271.104	0.480	702.488	0.456	17	0.155	K.VSPEVIAEYTVR.T
R3/RRR3-11/2	1312.369	1312.501	-100.535	0.355	870.913	0.413	16	0.154	K.KPWSLSFSFGR.A
R3/RRR3-11/2	1363.236	1363.541	-224.228	0.434	750.483	0.418	18	0.153	K.VSPEVIAEYTVR.T
R3/RRR3-10/2	1363.226	1363.541	-231.415	0.445	864.634	0.383	18	0.153	K.VSPEVIAEYTVR.T
R3/RRR3-11/2	1313.251	1312.501	-190.809	0.408	641.673	0.438	17	0.151	K.KPWSLSFSFGR.A
R3/RRR3-10/2	1363.038	1363.541	-1106.355	0.380	669.137	0.430	17	0.150	K.VSPEVIAEYTVR.T
R3/RRR3-13/2	1364.498	1363.541	-31.909	0.357	906.903	0.348	18	0.150	K.VSPEVIAEYTVR.T
R3/RRR3-11/2	1363.303	1363.541	-175.002	0.378	678.277	0.409	17	0.148	K.VSPEVIAEYTVR.T
R3/RRR3-11/2	1155.032	1155.240	-180.905	0.446	433.837	0.484	16	0.148	K.ANSEATLGTYK.G
R3/RRR3-11/2	1444.920	1443.578	237.209	0.323	561.690	0.475	20	0.145	R.CKANSEATLGTYK.G
R3/RRR3-11/3	1312.301	1312.501	-152.751	0.507	1413.863	0.407	23	0.141	K.KPWSLSFSFGR.A
R3/RRR3-12/2	1363.293	1363.541	-182.188	0.238	392.049	0.291	15	0.136	K.VSPEVIAEYTVR.T
R3/RRR3-11/3	1312.497	1312.501	-2.446	0.507	1348.171	0.380	23	0.129	K.KPWSLSFSFGR.A
R3/RRR3-10/3	1312.434	1312.501	-50.723	0.422	1130.774	0.360	22	0.112	K.KPWSLSFSFGR.A
R3/RRR3-10/3	1312.101	1312.501	-305.342	0.356	850.192	0.338	22	0.097	K.KPWSLSFSFGR.A
R3/RRR3-10/3	1312.063	1312.501	-334.185	0.387	1150.775	0.251	22	0.095	K.KPWSLSFSFGR.A
R3/RRR3-12/2	1457.138	1456.618	-330.439	0.550	2291.657	0.479	20	0.336	R.YWLCAATQDSIK.I
R3/RRR3-13/2	1456.218	1456.618	-275.997	0.472	2224.681	0.464	20	0.320	R.YWLCAATQDSIK.I
R3/RRR3-12/2	1249.116	1249.398	-226.090	0.526	2025.141	0.535	19	0.307	R.LWDLSTGVTTR.R
R3/RRR3-12/2	1249.026	1249.398	-298.842	0.507	2095.456	0.475	19	0.301	R.LWDLSTGVTTR.R
R3/RRR3-12/2	1603.278	1603.887	-1007.014	0.528	1872.382	0.602	22	0.300	K.HIVQDLKPEIPVSK.N
R3/RRR3-13/2	1457.097	1456.618	329.253	0.540	2266.846	0.372	20	0.297	R.YWLCAATQDSIK.I
R3/RRR3-12/2	1603.409	1603.887	-299.226	0.550	1912.718	0.571	22	0.297	K.HIVQDLKPEIPVSK.N
R3/RRR3-13/2	1603.562	1603.887	-203.451	0.516	1835.434	0.601	22	0.293	K.HIVQDLKPEIPVSK.N
R3/RRR3-12/2	1603.469	1603.887	-261.647	0.529	1751.093	0.590	21	0.276	K.HIVQDLKPEIPVSK.N
R3/RRR3-13/2	1603.405	1603.887	-301.899	0.501	1658.409	0.588	21	0.262	K.HIVQDLKPEIPVSK.N
R3/RRR3-12/2	1456.025	1456.618	-1097.925	0.441	1833.893	0.437	18	0.249	R.YWLCAATQDSIK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1603.397	1603.887	-306.711	0.538	1540.175	0.586	20	0.245	K.HIVQDLKPEIPVSK.N
R3/RRR3-12/2	1248.566	1249.398	-1471.770	0.498	1627.991	0.495	19	0.237	R.LWDLSTGVTTR.R
R3/RRR3-13/2	1249.243	1249.398	-124.139	0.468	1606.308	0.495	19	0.234	R.LWDLSTGVTTR.R
R3/RRR3-13/2	1940.340	1940.104	121.809	0.521	1456.214	0.575	26	0.233	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-12/2	1322.333	1322.449	-87.833	0.460	1502.020	0.527	19	0.228	K.DVLSVAFSVDNR.Q
R3/RRR3-12/2	1940.627	1940.104	-246.473	0.517	1411.554	0.568	25	0.225	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-13/2	1249.086	1249.398	-250.601	0.452	1510.964	0.508	18	0.225	R.LWDLSTGVTTR.R
R3/RRR3-13/2	1939.480	1940.104	-839.837	0.446	1424.951	0.534	25	0.219	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-12/2	1940.486	1940.104	197.010	0.501	1290.007	0.587	24	0.215	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-13/2	1940.484	1940.104	196.127	0.533	1101.486	0.547	23	0.189	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-12/2	1939.507	1940.104	-826.064	0.470	1150.588	0.494	23	0.183	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-12/2	1574.475	1573.775	-191.112	0.506	961.394	0.534	18	0.176	K.DGVTLLWDLAEGKR.L
R3/RRR3-12/2	1321.469	1322.449	-1502.591	0.259	1386.866	0.343	16	0.175	K.DVLSVAFSVDNR.Q
R3/RRR3-13/2	1573.490	1573.775	-181.427	0.484	1016.826	0.500	18	0.174	K.DGVTLLWDLAEGKR.L
R3/RRR3-13/2	1573.636	1573.775	-88.589	0.463	977.525	0.498	18	0.171	K.DGVTLLWDLAEGKR.L
R3/RRR3-12/2	1573.458	1573.775	-201.974	0.479	976.758	0.475	18	0.168	K.DGVTLLWDLAEGKR.L
R3/RRR3-12/3	1941.508	1940.104	208.376	0.467	1635.310	0.400	32	0.167	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-12/3	1941.618	1940.104	-251.178	0.379	1625.858	0.398	32	0.165	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-13/2	1573.316	1573.775	-292.575	0.473	1094.730	0.392	19	0.163	K.DGVTLLWDLAEGKR.L
R3/RRR3-12/2	1573.550	1573.775	-143.450	0.488	876.081	0.466	17	0.160	K.DGVTLLWDLAEGKR.L
R3/RRR3-13/2	1122.099	1121.262	-145.843	0.513	679.940	0.437	13	0.153	K.LWNTLGECK.Y
R3/RRR3-13/2	1122.228	1121.262	-30.179	0.460	699.009	0.409	13	0.150	K.LWNTLGECK.Y
R3/RRR3-12/3	1940.860	1940.104	-126.528	0.431	1496.141	0.383	30	0.148	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-13/2	1122.211	1121.262	-45.017	0.388	299.392	0.368	11	0.139	-.LWNTLGECK.-
R3/RRR3-12/2	1121.115	1121.262	-131.118	0.303	650.586	0.301	13	0.138	K.LWNTLGECK.Y
R3/RRR3-10/2	1574.217	1573.775	281.891	0.381	646.211	0.344	14	0.137	K.DGVTLLWDLAEGKR.L
R3/RRR3-12/2	1456.161	1456.618	-315.358	0.295	663.858	0.277	13	0.133	R.YWLCAATQDSIK.I
R3/RRR3-13/2	1456.693	1456.618	51.388	0.248	673.134	0.178	13	0.128	R.YWLCAATQDSIK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/3	1941.130	1940.104	13.137	0.457	1169.493	0.421	27	0.127	R.FSPNTFQPTIVSGSWDR.T
R3/RRR3-12/3	1604.149	1603.887	163.700	0.381	717.844	0.453	21	0.108	K.HIVQDLKPEIPVSK.N
R3/RRR3-12/3	1603.863	1603.887	-15.361	0.364	585.944	0.425	21	0.102	K.HIVQDLKPEIPVSK.N
R3/RRR3-12/3	1603.349	1603.887	-962.572	0.366	718.431	0.401	22	0.101	K.HIVQDLKPEIPVSK.N
R3/RRR3-12/3	1573.852	1573.775	48.760	0.375	1001.220	0.332	29	0.101	K.DGVTLLWDLAEGKR.L
R3/RRR3-12/3	1574.013	1573.775	151.783	0.315	983.935	0.322	28	0.098	K.DGVTLLWDLAEGKR.L
R3/RRR3-13/3	1573.853	1573.775	49.693	0.349	615.339	0.324	24	0.095	K.DGVTLLWDLAEGKR.L
R3/RRR3-13/3	1573.612	1573.775	-103.888	0.358	531.318	0.333	22	0.093	-.DGVTLLWDLAEGKR.-
R3/RRR3-12/3	1604.727	1603.887	-100.539	0.277	635.194	0.338	21	0.092	K.HIVQDLKPEIPVSK.N
R3/RRR3-12/3	1573.873	1573.775	62.529	0.330	858.324	0.265	28	0.090	K.DGVTLLWDLAEGKR.L
R3/RRR3-12/2	1328.153	1328.495	-258.729	0.386	1013.417	0.530	16	0.178	R.YLSSALFEELR.A
R3/RRR3-12/2	1215.632	1216.373	-1436.205	0.480	1148.973	0.441	16	0.176	K.IRDSASQLIGR.T
R3/RRR3-12/2	946.853	947.028	-185.249	0.357	1376.261	0.319	15	0.174	R.DSASQLIGR.T
R3/RRR3-12/2	1297.312	1297.569	-198.721	0.449	904.042	0.534	18	0.174	K.LIVTVLPSLGER.Y
R3/RRR3-12/2	1327.997	1328.495	-376.033	0.383	1076.763	0.445	16	0.170	R.YLSSALFEELR.A
R3/RRR3-12/2	947.121	947.028	98.556	0.445	1217.306	0.355	15	0.169	R.DSASQLIGR.T
R3/RRR3-12/2	1296.709	1297.569	-1438.372	0.361	1027.060	0.427	19	0.164	K.LIVTVLPSLGER.Y
R3/RRR3-12/2	1216.050	1216.373	-266.370	0.441	1147.483	0.340	17	0.161	K.IRDSASQLIGR.T
R3/RRR3-12/3	1491.315	1491.649	-224.611	0.484	1437.359	0.468	27	0.159	K.DRPAISM*LEDAEK.K
R3/RRR3-12/2	1216.027	1216.373	-285.304	0.477	1014.895	0.386	16	0.159	K.IRDSASQLIGR.T
R3/RRR3-12/2	1327.711	1328.495	-1347.889	0.289	687.656	0.419	14	0.143	R.YLSSALFEELR.A
R3/RRR3-12/2	981.820	982.179	-366.418	0.373	888.133	0.300	13	0.142	R.TPM*VYLNK.V
R3/RRR3-13/2	1297.022	1297.569	-1196.461	0.345	575.650	0.394	14	0.140	K.LIVTVLPSLGER.Y
R3/RRR3-12/3	1491.529	1491.649	-80.761	0.451	904.358	0.407	27	0.109	K.DRPAISM*LEDAEK.K
R3/RRR3-12/3	1618.297	1619.822	-2185.246	0.468	977.717	0.378	28	0.107	K.DRPAISM*LEDAEKK.G
R3/RRR3-12/3	1619.248	1619.822	-975.323	0.431	744.958	0.389	26	0.101	K.DRPAISM*LEDAEKK.G
R3/RRR3-12/3	1490.561	1491.649	-1405.382	0.349	556.546	0.333	25	0.095	K.DRPAISM*LEDAEK.K
R3/RRR3-10/2	1283.468	1283.502	-26.483	0.428	1115.402	0.538	19	0.189	K.NVGPSGVTIAIVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1283.169	1283.502	-260.643	0.374	1155.379	0.521	19	0.188	K.NVGPSGVTIAIVR.K
R3/RRR3-11/2	1239.207	1239.405	-159.824	0.517	1105.226	0.518	19	0.187	K.KFSAASVAWSGK.D
R3/RRR3-10/2	1111.099	1111.232	-119.738	0.427	1128.233	0.479	17	0.181	K.FSAASVAWSGK.D
R3/RRR3-11/2	1282.577	1283.502	-1505.675	0.391	1030.009	0.534	18	0.180	K.NVGPSGVTIAIVR.K
R3/RRR3-10/2	1283.131	1283.502	-290.422	0.409	1030.955	0.506	18	0.176	K.NVGPSGVTIAIVR.K
R3/RRR3-11/2	1067.674	1068.250	-1480.766	0.436	1134.795	0.434	16	0.175	R.FGLIYAGAQK.N
R3/RRR3-10/2	1068.103	1068.250	-138.084	0.457	1160.292	0.413	16	0.174	R.FGLIYAGAQK.N
R3/RRR3-11/2	1480.045	1480.711	-1129.378	0.401	1169.316	0.421	20	0.173	R.ASIYNAM*PLAGVEK.L
R3/RRR3-10/2	1068.085	1068.250	-155.511	0.463	1176.134	0.393	16	0.172	R.FGLIYAGAQK.N
R3/RRR3-10/2	1481.222	1480.711	-331.647	0.509	1034.656	0.472	18	0.170	R.ASIYNAM*PLAGVEK.L
R3/RRR3-10/2	1111.077	1111.232	-140.017	0.429	1030.206	0.450	17	0.169	K.FSAASVAWSGK.D
R3/RRR3-10/2	1068.214	1068.250	-34.341	0.458	1129.492	0.385	16	0.167	R.FGLIYAGAQK.N
R3/RRR3-10/2	1948.134	1949.109	-1017.109	0.487	694.890	0.589	21	0.167	K.YTSLPPFDAIEQNPEAR.F
R3/RRR3-10/2	1282.669	1283.502	-1433.212	0.387	948.792	0.486	17	0.167	K.NVGPSGVTIAIVR.K
R3/RRR3-10/2	1222.038	1221.494	-374.473	0.446	1027.900	0.399	17	0.163	R.SLMNVPFTLAK.G
R3/RRR3-11/2	1282.583	1283.502	-1500.990	0.347	785.853	0.510	16	0.158	K.NVGPSGVTIAIVR.K
R3/RRR3-10/2	1949.200	1949.109	46.381	0.497	589.199	0.549	21	0.158	K.YTSLPPFDAIEQNPEAR.F
R3/RRR3-10/2	1479.557	1480.711	-1460.594	0.341	1056.628	0.324	20	0.152	R.ASIYNAM*PLAGVEK.L
R3/RRR3-10/2	1237.068	1237.494	-345.447	0.422	682.143	0.390	16	0.147	R.SLM*NVPFTLAK.G
R3/RRR3-10/2	1236.563	1237.494	-1565.930	0.356	759.598	0.373	17	0.147	R.SLM*NVPFTLAK.G
R3/RRR3-10/2	1222.540	1221.494	37.094	0.379	684.797	0.394	15	0.146	R.SLMNVPFTLAK.G
R3/RRR3-11/2	1948.413	1949.109	-873.502	0.449	507.485	0.477	19	0.146	K.YTSLPPFDAIEQNPEAR.F
R3/RRR3-11/2	1067.609	1068.250	-1541.523	0.346	834.089	0.284	14	0.140	R.FGLIYAGAQK.N
R3/RRR3-10/2	1237.014	1237.494	-389.111	0.395	679.285	0.287	16	0.137	-.SLM*NVPFTLAK.-
R3/RRR3-11/2	1067.658	1068.250	-1495.351	0.303	893.149	0.230	15	0.137	R.FGLIYAGAQK.N
R3/RRR3-3/3	1728.941	1727.984	-24.660	0.470	2127.386	0.438	31	0.249	R.REVDEVKELIEIVR.E
R3/RRR3-3/3	1822.525	1822.938	-227.360	0.564	1729.009	0.505	33	0.211	K.SSLAGEHAAAGNFDTAM*R.L
R3/RRR3-3/3	1823.386	1822.938	246.443	0.560	1526.122	0.534	33	0.192	K.SSLAGEHAAAGNFDTAM*R.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1706.679	1705.958	-164.471	0.450	1089.990	0.570	18	0.189	R.GPPALVFTFPQMEDR.L
R3/RRR3-3/2	1705.882	1705.958	-44.902	0.504	1017.511	0.558	18	0.182	R.GPPALVFTFPQMEDR.L
R3/RRR3-2/3	1822.861	1822.938	-42.138	0.518	1396.263	0.487	33	0.163	K.SSLAGEHAAAGNFDTAM*R.L
R3/RRR3-3/2	1190.009	1190.248	-201.104	0.454	1138.636	0.349	18	0.163	K.GWSESASPNVR.G
R3/RRR3-3/2	1163.851	1164.255	-348.485	0.461	1041.623	0.335	15	0.152	K.NFATAEHFAR.M
R3/RRR3-2/2	1190.189	1190.248	-49.544	0.491	961.996	0.339	17	0.151	K.GWSESASPNVR.G
R3/RRR3-3/2	1571.892	1571.797	60.084	0.469	655.251	0.425	19	0.149	R.EVDEVKELIEIVR.E
R3/RRR3-3/3	1822.746	1822.938	-105.517	0.511	1338.964	0.441	31	0.146	K.SSLAGEHAAAGNFDTAM*R.L
R3/RRR3-2/3	1822.798	1822.938	-76.899	0.522	1163.489	0.507	31	0.145	K.SSLAGEHAAAGNFDTAM*R.L
R3/RRR3-3/2	1189.961	1190.248	-241.857	0.447	825.187	0.299	16	0.142	K.GWSESASPNVR.G
R3/RRR3-2/2	1394.421	1393.697	-198.404	0.299	450.450	0.477	16	0.142	R.ALATAPIIPVAVEK.G
R3/RRR3-2/2	1190.033	1190.248	-180.729	0.428	875.852	0.269	16	0.140	K.GWSESASPNVR.G
R3/RRR3-3/2	1572.437	1571.797	-230.136	0.369	383.850	0.380	17	0.140	R.EVDEVKELIEIVR.E
R3/RRR3-3/2	1393.299	1393.697	-286.263	0.295	332.177	0.438	15	0.139	R.ALATAPIIPVAVEK.G
R3/RRR3-3/2	1720.966	1721.958	-1160.657	0.366	470.497	0.424	14	0.137	R.GPPALVFTFPQM*EDR.L
R3/RRR3-3/2	1393.458	1393.697	-171.567	0.274	314.624	0.428	14	0.136	R.ALATAPIIPVAVEK.G
R3/RRR3-2/2	1393.193	1393.697	-1082.760	0.239	317.573	0.402	14	0.134	R.ALATAPIIPVAVEK.G
R3/RRR3-2/2	1190.024	1190.248	-188.138	0.372	708.921	0.220	16	0.133	-.GWSESASPNVR.-
R3/RRR3-3/2	1190.006	1190.248	-203.780	0.410	742.648	0.219	15	0.132	-.GWSESASPNVR.-
R3/RRR3-3/3	1727.497	1727.984	-282.772	0.343	1253.442	0.216	23	0.095	R.REVDEVKELIEIVR.E
R3/RRR3-6/2	1665.049	1665.740	-1018.702	0.486	2593.049	0.513	25	0.415	K.AEEAAAAAGDGLSEFQK.K
R3/RRR3-6/2	1665.100	1665.740	-987.861	0.480	2454.768	0.502	25	0.380	K.AEEAAAAAGDGLSEFQK.K
R3/RRR3-6/2	1851.389	1852.034	-891.040	0.505	1411.493	0.533	24	0.217	K.ANFLSADDFEPSLIPSK.T
R3/RRR3-6/2	1335.291	1334.632	-256.246	0.486	1111.871	0.593	22	0.202	K.KPAAPVKPVAEVK.K
R3/RRR3-6/2	1334.567	1334.632	-49.413	0.470	999.213	0.533	21	0.182	K.KPAAPVKPVAEVK.K
R3/RRR3-6/2	1851.522	1852.034	-819.228	0.482	1175.731	0.471	22	0.180	K.ANFLSADDFEPSLIPSK.T
R3/RRR3-6/2	1468.163	1468.641	-326.540	0.448	1103.229	0.428	18	0.171	K.WHAPLIDNPNYK.G
R3/RRR3-6/2	1335.213	1334.632	-314.764	0.500	788.473	0.539	20	0.170	K.KPAAPVKPVAEVK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1468.228	1468.641	-281.578	0.457	925.458	0.417	17	0.158	K.WHAPLIDNPNYK.G
R3/RRR3-6/2	1468.167	1468.641	-323.787	0.426	995.390	0.353	17	0.153	K.WHAPLIDNPNYK.G
R3/RRR3-6/2	1026.362	1026.253	105.978	0.490	667.802	0.394	13	0.150	K.KIFDVLYK.L
R3/RRR3-6/2	1027.231	1026.253	-21.527	0.511	640.602	0.408	12	0.149	K.KIFDVLYK.L
R3/RRR3-6/2	1143.278	1144.343	-1812.071	0.322	968.601	0.337	16	0.148	K.IIDVIEKGEK.Q
R3/RRR3-6/2	1306.308	1306.531	-171.390	0.359	633.810	0.404	15	0.143	K.LADIPFLEPYK.T
R3/RRR3-6/2	1850.674	1852.034	-1278.672	0.321	862.143	0.342	19	0.141	K.ANFLSADDFEPSLIPSK.T
R3/RRR3-6/2	1027.093	1026.253	-156.114	0.446	663.449	0.333	12	0.141	-.KIFDVLYK.-
R3/RRR3-6/2	1306.191	1306.531	-261.017	0.251	354.767	0.335	12	0.132	K.LADIPFLEPYK.T
R3/RRR3-6/3	1468.867	1468.641	154.521	0.532	1589.573	0.281	27	0.126	K.WHAPLIDNPNYK.G
R3/RRR3-6/3	1467.782	1468.641	-1269.818	0.507	1414.252	0.205	25	0.099	K.WHAPLIDNPNYK.G
R3/RRR3-6/3	1468.093	1468.641	-1057.134	0.448	938.550	0.245	21	0.089	K.WHAPLIDNPNYK.G
R3/RRR3-13/2	1317.189	1317.560	-282.633	0.419	1269.542	0.514	18	0.198	R.GLVVVHPYFTGK.E
R3/RRR3-13/2	1156.120	1156.316	-170.251	0.477	1231.914	0.506	17	0.195	R.AGAIGVSVYYR.L
R3/RRR3-13/2	1738.579	1738.839	-150.186	0.485	1234.534	0.499	22	0.192	R.GDGADPWLLDHADLSR.L
R3/RRR3-13/2	1317.328	1317.560	-176.649	0.420	1054.450	0.562	16	0.186	R.GLVVVHPYFTGK.E
R3/RRR3-13/2	1317.304	1317.560	-195.334	0.429	1055.546	0.519	16	0.180	R.GLVVVHPYFTGK.E
R3/RRR3-13/2	1737.727	1738.839	-1218.682	0.494	1076.020	0.457	20	0.170	R.GDGADPWLLDHADLSR.L
R3/RRR3-13/2	1390.228	1389.495	-193.102	0.446	1019.854	0.461	18	0.166	K.EAVGAEAAFGPDVR.E
R3/RRR3-13/2	1501.236	1500.591	-237.218	0.509	671.786	0.538	18	0.161	K.ANGYGGEVELFESK.G
R3/RRR3-13/2	1500.106	1500.591	-324.239	0.462	906.037	0.455	18	0.160	K.ANGYGGEVELFESK.G
R3/RRR3-13/2	1330.304	1330.466	-122.557	0.464	827.205	0.435	20	0.155	R.CGGGGALPDGVTLR.G
R3/RRR3-13/2	1135.160	1134.224	-56.584	0.406	725.182	0.448	15	0.154	R.VNPFVDDATR.A
R3/RRR3-13/2	1133.989	1134.224	-207.368	0.370	976.692	0.357	16	0.154	R.VNPFVDDATR.A
R3/RRR3-13/2	1330.275	1330.466	-144.004	0.486	795.407	0.431	20	0.153	R.CGGGGALPDGVTLR.G
R3/RRR3-13/2	1500.146	1500.591	-297.868	0.430	733.197	0.454	18	0.152	K.ANGYGGEVELFESK.G
R3/RRR3-13/2	1737.839	1738.839	-1154.280	0.375	985.147	0.324	20	0.147	R.GDGADPWLLDHADLSR.L
R3/RRR3-13/2	1133.816	1134.224	-360.524	0.314	538.836	0.338	12	0.136	R.VNPFVDDATR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1852.525	1851.071	245.886	0.577	1697.133	0.582	21	0.265	K.EIAWM*EEVIAAESSLR.A
R3/RRR3-3/2	1354.033	1354.405	-274.943	0.459	811.878	0.453	20	0.160	R.QAIEEFSSDATR.F
R3/RRR3-4/2	1927.000	1925.153	-79.715	0.490	822.653	0.476	19	0.156	R.SFITTDMNPFYDAFVR.W
R3/RRR3-3/2	1924.464	1925.153	-880.555	0.494	813.812	0.469	18	0.154	R.SFITTDMNPFYDAFVR.W
R3/RRR3-4/2	1451.419	1452.640	-1534.579	0.328	876.839	0.422	17	0.151	K.AGWPIAGTPDPTLR.I
R3/RRR3-3/2	1353.986	1354.405	-309.948	0.406	717.582	0.410	19	0.150	R.QAIEEFSSDATR.F
R3/RRR3-3/2	1353.528	1354.405	-1390.475	0.378	675.170	0.396	20	0.148	R.QAIEEFSSDATR.F
R3/RRR3-2/2	1451.457	1452.640	-1508.390	0.331	921.651	0.360	16	0.146	K.AGWPIAGTPDPTLR.I
R3/RRR3-3/2	1452.387	1452.640	-174.722	0.361	705.367	0.418	17	0.145	K.AGWPIAGTPDPTLR.I
R3/RRR3-3/2	1196.494	1196.380	95.718	0.346	977.128	0.277	14	0.144	K.LGFYDLQLAR.D
R3/RRR3-3/2	1464.599	1463.571	19.176	0.385	539.149	0.452	17	0.143	R.SFAPDEEINEALK.N
R3/RRR3-3/2	1618.336	1618.813	-295.482	0.424	773.969	0.350	19	0.142	R.ASGEGVQPQEYVLIK.M
R3/RRR3-4/2	1619.234	1617.765	290.471	0.470	614.129	0.409	17	0.142	K.GFTDGTM*IVGEFNGR.K
R3/RRR3-3/2	1195.608	1196.380	-1486.064	0.344	901.214	0.279	14	0.141	K.LGFYDLQLAR.D
R3/RRR3-3/2	1618.700	1617.765	-40.505	0.446	696.448	0.383	16	0.141	K.GFTDGTM*IVGEFNGR.K
R3/RRR3-3/2	1619.402	1618.813	-254.612	0.470	712.857	0.339	18	0.138	R.ASGEGVQPQEYVLIK.M
R3/RRR3-2/2	1618.892	1618.813	49.340	0.446	596.386	0.324	16	0.134	R.ASGEGVQPQEYVLIK.M
R3/RRR3-2/2	1618.243	1618.813	-972.809	0.408	496.414	0.304	16	0.133	R.ASGEGVQPQEYVLIK.M
R3/RRR3-3/2	1850.349	1851.071	-933.427	0.311	214.006	0.304	14	0.133	K.EIAWM*EEVIAAESSLR.A
R3/RRR3-3/2	1619.375	1617.765	-241.754	0.377	681.863	0.260	16	0.131	K.GFTDGTM*IVGEFNGR.K
R3/RRR3-3/2	1196.073	1196.380	-257.000	0.307	484.361	0.226	12	0.130	-.LGFYDLQLAR.-
R3/RRR3-4/2	1196.045	1196.380	-280.857	0.281	799.726	0.125	14	0.128	K.LGFYDLQLAR.D
R3/RRR3-2/2	1619.259	1617.765	305.967	0.199	570.930	0.193	15	0.127	K.GFTDGTM*IVGEFNGR.K
R3/RRR3-2/2	1195.851	1196.380	-1282.325	0.301	419.852	0.352	10	0.123	-.LGFYDLQLAR.-
R3/RRR3-12/2	1424.263	1424.628	-256.399	0.522	1604.278	0.541	21	0.245	R.IHNAILQTISEGK.F
R3/RRR3-12/2	1801.499	1802.018	-845.646	0.490	1501.228	0.592	26	0.242	R.ATLFPGDGIGPEIAESVK.Q
R3/RRR3-12/2	1424.055	1424.628	-1107.871	0.521	1653.454	0.489	21	0.239	R.IHNAILQTISEGK.F
R3/RRR3-12/2	1802.345	1802.018	182.084	0.530	1455.326	0.551	26	0.227	R.ATLFPGDGIGPEIAESVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1423.436	1424.628	-1544.276	0.433	1443.620	0.411	19	0.196	R.IHNAILQTISEGK.F
R3/RRR3-12/2	1801.832	1802.018	-103.735	0.437	1288.267	0.491	25	0.195	R.ATLFPGDGIGPEIAESVK.Q
R3/RRR3-12/2	1242.929	1243.314	-310.454	0.492	1171.593	0.467	17	0.185	R.HLQFNNQADR.I
R3/RRR3-12/2	1243.057	1243.314	-207.395	0.494	1185.282	0.440	17	0.181	R.HLQFNNQADR.I
R3/RRR3-12/2	1466.205	1465.637	-295.244	0.533	1260.136	0.369	19	0.172	K.TRYDDVNLVTIR.E
R3/RRR3-12/2	1465.403	1465.637	-159.885	0.490	1247.692	0.345	19	0.168	K.TRYDDVNLVTIR.E
R3/RRR3-12/2	1464.642	1465.637	-1365.991	0.430	1169.841	0.340	18	0.162	K.TRYDDVNLVTIR.E
R3/RRR3-12/2	887.922	888.067	-164.023	0.422	842.662	0.449	13	0.158	K.GPM*ATPIGK.G
R3/RRR3-12/2	1242.943	1243.314	-298.728	0.427	936.557	0.386	16	0.156	R.HLQFNNQADR.I
R3/RRR3-12/2	1848.492	1847.921	-232.462	0.500	553.192	0.545	20	0.156	R.ENTEGEYSGLEHQVVR.G
R3/RRR3-12/2	888.945	888.067	-137.527	0.437	736.275	0.467	13	0.155	-.GPM*ATPIGK.-
R3/RRR3-12/2	1848.396	1847.921	258.028	0.500	434.428	0.482	18	0.145	R.ENTEGEYSGLEHQVVR.G
R3/RRR3-12/2	888.889	888.067	-200.759	0.381	529.670	0.463	11	0.142	-.GPM*ATPIGK.-
R3/RRR3-12/2	945.044	945.142	-103.465	0.339	881.393	0.158	12	0.130	R.SLNLTLRK.E
R3/RRR3-12/2	945.010	945.142	-140.005	0.357	813.878	0.168	12	0.130	R.SLNLTLRK.E
R3/RRR3-10/2	1650.218	1650.767	-941.198	0.535	2936.581	0.534	26	0.506	K.SVIGETGSDVTTDQLK.E
R3/RRR3-10/2	1650.162	1650.767	-975.509	0.543	2768.449	0.553	25	0.471	K.SVIGETGSDVTTDQLK.E
R3/RRR3-10/2	1650.247	1650.767	-923.449	0.527	2696.643	0.577	25	0.462	K.SVIGETGSDVTTDQLK.E
R3/RRR3-10/2	1553.450	1553.781	-213.324	0.539	1660.447	0.489	21	0.239	K.YLTEDPLFQLVSK.L
R3/RRR3-10/2	1554.368	1553.781	-265.973	0.608	1458.477	0.577	21	0.235	K.YLTEDPLFQLVSK.L
R3/RRR3-10/2	1553.374	1553.781	-262.754	0.537	1539.633	0.516	21	0.231	K.YLTEDPLFQLVSK.L
R3/RRR3-10/2	1344.628	1345.529	-1417.889	0.363	1332.864	0.442	18	0.190	R.SIGIGSQLIWDR.A
R3/RRR3-10/2	1344.429	1345.529	-1566.907	0.344	1348.179	0.428	18	0.189	R.SIGIGSQLIWDR.A
R3/RRR3-10/2	1139.335	1139.328	5.737	0.435	1383.635	0.335	17	0.178	R.LPAVASYVYR.R
R3/RRR3-10/2	1345.282	1345.529	-183.990	0.489	1083.841	0.484	17	0.178	R.SIGIGSQLIWDR.A
R3/RRR3-9/2	1139.069	1139.328	-228.048	0.388	1071.165	0.457	15	0.172	R.LPAVASYVYR.R
R3/RRR3-10/2	1572.166	1571.882	181.329	0.387	536.648	0.561	19	0.157	K.LYEVVPPILTELGK.V
R3/RRR3-10/2	1572.639	1571.882	-154.977	0.386	552.531	0.553	19	0.157	K.LYEVVPPILTELGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1571.704	1571.882	-113.704	0.388	536.147	0.471	19	0.150	K.LYEVVPPILTELGK.V
R3/RRR3-10/2	1094.086	1094.332	-225.786	0.429	476.888	0.464	14	0.149	R.ALGLPLERPK.S
R3/RRR3-9/2	1139.400	1139.328	63.334	0.375	700.090	0.424	13	0.149	R.LPAVASYVYR.R
R3/RRR3-10/2	1094.205	1094.332	-116.216	0.405	654.362	0.404	16	0.149	R.ALGLPLERPK.S
R3/RRR3-9/2	1572.525	1571.882	-227.710	0.419	480.498	0.460	18	0.148	K.LYEVVPPILTELGK.V
R3/RRR3-10/2	1584.306	1584.713	-258.011	0.467	681.875	0.407	20	0.147	K.SQLQELIPEQQDR.L
R3/RRR3-10/2	1093.842	1094.332	-449.813	0.365	442.875	0.455	13	0.145	R.ALGLPLERPK.S
R3/RRR3-10/2	1572.375	1571.882	314.536	0.387	528.785	0.419	18	0.145	K.LYEVVPPILTELGK.V
R3/RRR3-9/2	1138.919	1139.328	-360.414	0.379	653.232	0.349	13	0.141	R.LPAVASYVYR.R
R3/RRR3-10/2	1139.036	1139.328	-257.400	0.307	859.093	0.287	14	0.140	R.LPAVASYVYR.R
R3/RRR3-9/2	1571.286	1571.882	-1018.946	0.236	374.956	0.444	14	0.136	K.LYEVVPPILTELGK.V
R3/RRR3-26/2	1837.411	1837.921	-824.053	0.407	1426.496	0.578	23	0.325	K.TSFWDAEPAPVEATAASS.-
R3/RRR3-26/2	1837.007	1837.921	-1044.646	0.282	1399.912	0.501	23	0.311	K.TSFWDAEPAPVEATAASS.-
R3/RRR3-26/2	1837.119	1837.921	-983.601	0.371	1388.277	0.550	23	0.304	K.TSFWDAEPAPVEATAASS.-
R3/RRR3-26/2	1384.059	1384.537	-346.273	0.543	1778.214	0.434	20	0.241	K.M*QGVESFDVDIK.E
R3/RRR3-26/2	1384.006	1384.537	-1109.742	0.496	1676.280	0.427	19	0.226	K.M*QGVESFDVDIK.E
R3/RRR3-26/2	1383.959	1384.537	-1143.928	0.512	1585.980	0.415	19	0.213	K.M*QGVESFDVDIK.E
R3/RRR3-26/2	1429.278	1429.601	-226.631	0.460	1070.062	0.554	22	0.190	K.GNVTPDAVLQTVSK.T
R3/RRR3-26/2	1369.943	1370.542	-1170.751	0.376	1365.782	0.355	18	0.178	R.VGM*SCEGCVGAVK.R
R3/RRR3-26/2	1429.097	1429.601	-1055.471	0.484	931.611	0.526	21	0.175	K.GNVTPDAVLQTVSK.T
R3/RRR3-26/2	1429.100	1429.601	-1053.670	0.493	799.087	0.559	20	0.172	K.GNVTPDAVLQTVSK.T
R3/RRR3-27/2	1429.159	1429.601	-310.093	0.448	897.875	0.505	21	0.170	K.GNVTPDAVLQTVSK.T
R3/RRR3-27/2	1428.642	1429.601	-1375.559	0.285	1071.126	0.467	22	0.170	K.GNVTPDAVLQTVSK.T
R3/RRR3-26/2	1369.873	1370.542	-1222.204	0.389	1137.150	0.372	18	0.163	R.VGM*SCEGCVGAVK.R
R3/RRR3-27/2	1428.532	1429.601	-1452.802	0.292	842.506	0.427	20	0.152	K.GNVTPDAVLQTVSK.T
R3/RRR3-26/3	1769.820	1769.955	-76.162	0.490	1428.860	0.425	28	0.150	K.M*QGVESFDVDIKEQK.V
R3/RRR3-26/2	1370.083	1370.542	-336.237	0.388	963.523	0.338	16	0.147	R.VGM*SCEGCVGAVK.R
R3/RRR3-26/3	1769.595	1769.955	-203.514	0.466	1459.753	0.374	28	0.141	K.M*QGVESFDVDIKEQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1428.484	1429.601	-1486.192	0.180	911.903	0.263	18	0.136	K.GNVTPDAVLQTVSK.T
R3/RRR3-27/3	1769.822	1769.955	-75.020	0.505	1208.640	0.414	29	0.128	K.M*QGVESFDVDIKEQK.V
R3/RRR3-27/3	1769.439	1769.955	-859.225	0.459	1133.854	0.427	27	0.126	K.M*QGVESFDVDIKEQK.V
R3/RRR3-26/3	1526.572	1526.729	-102.963	0.381	1198.553	0.403	27	0.123	R.VGM*SCEGCVGAVKR.V
R3/RRR3-26/3	1769.604	1769.955	-198.428	0.483	1038.705	0.441	28	0.122	K.M*QGVESFDVDIKEQK.V
R3/RRR3-27/3	1769.756	1769.955	-112.278	0.487	1163.842	0.383	29	0.119	K.M*QGVESFDVDIKEQK.V
R3/RRR3-26/3	1526.541	1526.729	-123.056	0.446	1096.699	0.387	26	0.115	R.VGM*SCEGCVGAVKR.V
R3/RRR3-26/3	1525.711	1526.729	-1326.294	0.416	939.365	0.433	26	0.114	R.VGM*SCEGCVGAVKR.V
R3/RRR3-25/3	1769.908	1769.955	-26.662	0.394	1241.802	0.303	28	0.110	K.M*QGVESFDVDIKEQK.V
R3/RRR3-25/3	1770.079	1769.955	70.766	0.394	997.883	0.375	27	0.109	K.M*QGVESFDVDIKEQK.V
R3/RRR3-10/3	1770.189	1769.891	168.680	0.600	2657.860	0.534	32	0.407	R.HYAHVDCPGHADYVK.N
R3/RRR3-10/3	1770.663	1769.891	-129.182	0.589	2679.979	0.497	33	0.392	R.HYAHVDCPGHADYVK.N
R3/RRR3-9/3	1770.021	1769.891	73.757	0.562	2464.293	0.515	31	0.353	R.HYAHVDCPGHADYVK.N
R3/RRR3-10/3	1769.901	1769.891	5.381	0.572	2503.385	0.487	32	0.347	R.HYAHVDCPGHADYVK.N
R3/RRR3-10/2	1693.053	1692.898	91.943	0.568	2208.043	0.546	24	0.346	K.ILDHGEAGDNVGLLLR.G
R3/RRR3-10/2	1634.335	1633.848	299.016	0.479	1173.450	0.449	21	0.179	K.LMDAVDEYIPDPVR.Q
R3/RRR3-10/2	1561.250	1561.676	-273.741	0.447	1140.072	0.419	20	0.168	R.GSALSALQGTNDEIGK.N
R3/RRR3-10/2	1755.584	1756.016	-246.635	0.510	900.745	0.503	20	0.168	K.SFLM*PIEDVFSIQGR.G
R3/RRR3-10/2	1157.145	1157.344	-172.322	0.429	1113.910	0.377	16	0.165	K.FPGDEIPIIR.G
R3/RRR3-10/2	1757.153	1756.016	78.219	0.538	699.309	0.540	18	0.161	K.SFLM*PIEDVFSIQGR.G
R3/RRR3-10/2	1755.060	1756.016	-1117.478	0.443	832.488	0.482	19	0.160	K.SFLM*PIEDVFSIQGR.G
R3/RRR3-10/2	1156.525	1157.344	-1577.678	0.379	971.121	0.385	16	0.157	K.FPGDEIPIIR.G
R3/RRR3-10/2	1561.147	1561.676	-982.271	0.453	961.923	0.425	19	0.157	R.GSALSALQGTNDEIGK.N
R3/RRR3-10/2	1156.576	1157.344	-1533.041	0.369	957.941	0.297	16	0.146	K.FPGDEIPIIR.G
R3/RRR3-10/2	1633.813	1633.848	-21.029	0.424	866.188	0.352	18	0.145	-.LMDAVDEYIPDPVR.-
R3/RRR3-10/2	1739.430	1740.016	-915.028	0.350	524.024	0.360	16	0.136	K.SFLMPIEDVFSIQGR.G
R3/RRR3-10/3	1796.972	1797.011	-21.750	0.507	423.275	0.557	26	0.116	R.TKPHVNVGTIGHVDHGK.T
R3/RRR3-10/3	1796.918	1797.011	-52.208	0.418	705.507	0.479	32	0.111	R.TKPHVNVGTIGHVDHGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1797.058	1797.011	26.182	0.412	470.177	0.505	27	0.109	R.TKPHVNVGTIGHVDHGK.T
R3/RRR3-28/3	1769.473	1769.891	-236.969	0.343	710.905	0.349	22	0.096	R.HYAHVDCPGHADYVK.N
R3/RRR3-8/2	1493.734	1494.716	-1331.190	0.408	2946.423	0.478	22	0.487	K.VADFFDAAVNLALK.V
R3/RRR3-8/2	1494.250	1494.716	-312.973	0.455	2778.927	0.503	22	0.453	K.VADFFDAAVNLALK.V
R3/RRR3-8/2	1493.552	1494.716	-1453.498	0.420	2592.271	0.476	22	0.400	K.VADFFDAAVNLALK.V
R3/RRR3-9/2	1092.124	1092.273	-137.402	0.521	1956.752	0.571	19	0.306	K.LIVAGASAYAR.L
R3/RRR3-8/2	1208.232	1208.392	-132.912	0.528	2020.845	0.462	18	0.285	K.VLENVHIAANK.N
R3/RRR3-8/2	1092.016	1092.273	-236.641	0.483	1822.538	0.539	19	0.275	K.LIVAGASAYAR.L
R3/RRR3-8/2	1091.934	1092.273	-311.785	0.589	1808.709	0.541	19	0.274	K.LIVAGASAYAR.L
R3/RRR3-8/2	1208.099	1208.392	-243.395	0.568	1777.494	0.509	18	0.261	K.VLENVHIAANK.N
R3/RRR3-9/2	1091.896	1092.273	-346.220	0.503	1673.696	0.537	19	0.253	K.LIVAGASAYAR.L
R3/RRR3-8/2	1091.500	1092.273	-1629.152	0.468	1712.491	0.505	19	0.250	K.LIVAGASAYAR.L
R3/RRR3-8/2	1208.107	1208.392	-236.603	0.547	1473.439	0.509	17	0.221	K.VLENVHIAANK.N
R3/RRR3-9/2	1091.537	1092.273	-1595.784	0.430	1467.733	0.497	17	0.216	K.LIVAGASAYAR.L
R3/RRR3-8/2	1043.053	1042.123	-67.684	0.315	749.126	0.473	13	0.153	R.GFVEEDFAK.V
R3/RRR3-8/2	1586.360	1586.796	-275.227	0.369	803.277	0.453	22	0.152	K.NTVPGDVSAM*VPGGIR.M
R3/RRR3-8/2	1000.072	1000.046	25.758	0.362	740.324	0.416	13	0.148	K.YSEGYPGAR.Y
R3/RRR3-8/2	999.980	1000.046	-66.192	0.321	744.758	0.383	13	0.144	K.YSEGYPGAR.Y
R3/RRR3-8/2	1043.083	1042.123	-39.042	0.335	449.540	0.438	12	0.141	-.GFVEEDFAK.-
R3/RRR3-8/2	1043.024	1042.123	-95.389	0.297	613.385	0.338	12	0.137	-.GFVEEDFAK.-
R3/RRR3-9/2	1493.733	1494.716	-1331.929	0.269	687.530	0.325	17	0.136	K.VADFFDAAVNLALK.V
R3/RRR3-9/3	1260.463	1260.381	65.254	0.496	1430.134	0.357	22	0.130	K.LRHDVEEYAK.Q
R3/RRR3-9/3	1260.793	1260.381	327.582	0.476	1113.521	0.351	21	0.109	K.LRHDVEEYAK.Q
R3/RRR3-9/3	1260.133	1260.381	-197.648	0.434	1161.382	0.323	20	0.107	K.LRHDVEEYAK.Q
R3/RRR3-8/3	1260.086	1260.381	-234.530	0.456	977.378	0.361	19	0.105	K.LRHDVEEYAK.Q
R3/RRR3-10/2	1545.242	1545.760	-985.409	0.526	2141.854	0.559	20	0.336	K.TYVVQDGDIIFFK.F
R3/RRR3-10/2	1545.146	1545.760	-1047.832	0.507	2126.327	0.525	20	0.322	K.TYVVQDGDIIFFK.F
R3/RRR3-10/2	1849.851	1850.063	-114.478	0.459	2257.263	0.440	25	0.321	K.SEVSAYLEINDIAGLVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1545.415	1545.760	-223.623	0.515	2001.092	0.540	20	0.304	K.TYVVQDGDIIFFK.F
R3/RRR3-10/2	1514.440	1514.625	-121.965	0.525	1542.087	0.599	22	0.251	K.APQAAGTIHTDFER.G
R3/RRR3-10/2	1849.487	1850.063	-854.487	0.470	1798.781	0.452	24	0.248	K.SEVSAYLEINDIAGLVR.G
R3/RRR3-10/2	1514.105	1514.625	-1006.401	0.497	1374.054	0.577	21	0.224	K.APQAAGTIHTDFER.G
R3/RRR3-10/2	1067.122	1067.307	-173.664	0.479	952.857	0.483	17	0.171	K.IGIVGLPNVGK.S
R3/RRR3-10/2	1067.941	1067.307	-343.209	0.492	957.377	0.448	17	0.166	K.IGIVGLPNVGK.S
R3/RRR3-10/3	1539.419	1538.681	-170.658	0.542	1316.847	0.545	31	0.166	K.FDDLKELGSESAVK.A
R3/RRR3-10/2	1067.446	1067.307	130.689	0.456	830.849	0.487	16	0.163	K.IGIVGLPNVGK.S
R3/RRR3-10/2	1057.302	1057.224	73.463	0.266	517.172	0.509	12	0.141	K.STFFNIVTK.L
R3/RRR3-10/3	1947.756	1948.206	-231.623	0.561	1042.769	0.515	30	0.137	R.LKDIEFVQNKIDDLEK.S
R3/RRR3-10/3	1514.966	1514.625	226.151	0.419	866.582	0.542	24	0.128	K.APQAAGTIHTDFER.G
R3/RRR3-10/3	1538.704	1538.681	15.021	0.460	1055.763	0.470	28	0.127	K.FDDLKELGSESAVK.A
R3/RRR3-10/3	1948.901	1948.206	-157.167	0.582	861.073	0.497	31	0.124	R.LKDIEFVQNKIDDLEK.S
R3/RRR3-10/3	1538.694	1538.681	8.696	0.443	1152.586	0.391	29	0.118	K.FDDLKELGSESAVK.A
R3/RRR3-10/3	1514.529	1514.625	-63.478	0.404	575.383	0.488	21	0.108	K.APQAAGTIHTDFER.G
R3/RRR3-10/3	1513.928	1514.625	-1123.794	0.289	525.957	0.317	20	0.090	K.APQAAGTIHTDFER.G
R3/RRR3-8/2	1726.631	1726.953	-186.609	0.587	2503.055	0.593	26	0.420	R.LNLEAAGVEVDNIGAIK.V
R3/RRR3-8/2	1858.541	1859.065	-822.195	0.516	2542.312	0.492	24	0.395	K.ELAITSDEALSLEELPK.R
R3/RRR3-8/2	1726.696	1726.953	-148.879	0.570	2366.807	0.568	27	0.382	R.LNLEAAGVEVDNIGAIK.V
R3/RRR3-8/2	1858.398	1859.065	-899.275	0.466	2006.999	0.490	23	0.290	K.ELAITSDEALSLEELPK.R
R3/RRR3-8/2	1727.798	1726.953	-89.543	0.597	1646.053	0.599	22	0.260	R.LNLEAAGVEVDNIGAIK.V
R3/RRR3-8/2	1630.176	1629.799	231.958	0.467	1092.592	0.568	22	0.193	R.TSVPNIWAVGDVTNR.M
R3/RRR3-8/2	1629.483	1629.799	-194.429	0.495	848.823	0.536	20	0.169	R.TSVPNIWAVGDVTNR.M
R3/RRR3-9/2	1629.305	1629.799	-304.089	0.464	862.377	0.524	20	0.168	R.TSVPNIWAVGDVTNR.M
R3/RRR3-8/2	1045.794	1046.160	-350.477	0.332	1087.481	0.378	17	0.161	R.TVVASNLEGR.G
R3/RRR3-8/2	1041.566	1042.213	-1585.945	0.397	782.822	0.441	14	0.155	K.ILVYGSSFR.G
R3/RRR3-8/2	1466.267	1466.623	-243.376	0.384	611.091	0.489	17	0.151	K.TVFGGQPTKPDYR.D
R3/RRR3-8/2	1041.439	1042.213	-1708.288	0.396	756.821	0.402	14	0.150	K.ILVYGSSFR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1466.177	1466.623	-304.853	0.384	640.892	0.372	18	0.143	K.TVFGGQPTKPDYR.D
R3/RRR3-8/2	1466.360	1466.623	-179.987	0.324	433.204	0.365	15	0.137	K.TVFGGQPTKPDYR.D
R3/RRR3-8/2	1045.959	1046.160	-192.630	0.209	615.909	0.281	15	0.131	R.TVVASNLEGR.G
R3/RRR3-7/2	1727.405	1726.953	262.917	0.359	290.202	0.363	15	0.131	-.LNLEAAGVEVDNIGAIK.-
R3/RRR3-9/3	1296.506	1296.455	39.453	0.460	1129.895	0.230	24	0.091	-.LHPGTNLSELSK.-
R3/RRR3-9/3	1296.244	1296.455	-163.428	0.416	608.606	0.246	19	0.065	-.LHPGTNLSELSK.-
R3/RRR3-24/3	1892.114	1892.096	9.077	0.448	2914.049	0.445	34	0.441	R.FAIYDFDFLTAEDVPK.S
R3/RRR3-24/2	1891.298	1892.096	-953.742	0.540	2566.103	0.578	26	0.430	R.FAIYDFDFLTAEDVPK.S
R3/RRR3-24/2	1891.398	1892.096	-900.739	0.556	2206.193	0.615	23	0.364	R.FAIYDFDFLTAEDVPK.S
R3/RRR3-23/2	1891.396	1892.096	-901.517	0.550	2172.136	0.626	23	0.360	R.FAIYDFDFLTAEDVPK.S
R3/RRR3-24/2	1891.536	1892.096	-827.336	0.569	2154.195	0.628	23	0.357	R.FAIYDFDFLTAEDVPK.S
R3/RRR3-24/2	1468.012	1467.693	218.048	0.583	1738.845	0.514	20	0.253	R.IFYILWSPDNAK.V
R3/RRR3-23/2	1468.448	1467.693	-167.308	0.548	1771.731	0.493	19	0.252	R.IFYILWSPDNAK.V
R3/RRR3-23/2	1965.404	1965.999	-814.245	0.523	1530.046	0.612	25	0.250	R.TTSYEDFTSSLPEGDCR.F
R3/RRR3-24/2	1964.785	1965.999	-1130.503	0.474	1311.919	0.589	24	0.217	R.TTSYEDFTSSLPEGDCR.F
R3/RRR3-23/2	1466.991	1467.693	-1163.080	0.413	1742.840	0.342	19	0.213	R.IFYILWSPDNAK.V
R3/RRR3-23/2	1965.440	1965.999	-795.978	0.506	1164.445	0.598	24	0.205	R.TTSYEDFTSSLPEGDCR.F
R3/RRR3-24/2	1965.482	1965.999	-774.282	0.498	1209.474	0.572	24	0.204	R.TTSYEDFTSSLPEGDCR.F
R3/RRR3-23/2	1965.193	1965.999	-921.991	0.523	1105.562	0.608	24	0.202	R.TTSYEDFTSSLPEGDCR.F
R3/RRR3-24/2	1468.305	1467.693	-264.969	0.565	1392.730	0.459	18	0.198	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1467.052	1467.693	-1121.637	0.384	1551.461	0.371	19	0.198	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1467.238	1467.693	-310.891	0.420	1589.761	0.348	19	0.198	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1965.431	1965.999	-800.280	0.506	1034.580	0.608	23	0.195	R.TTSYEDFTSSLPEGDCR.F
R3/RRR3-24/2	1467.108	1467.693	-1083.121	0.357	1468.158	0.377	18	0.191	R.IFYILWSPDNAK.V
R3/RRR3-23/2	1891.845	1892.096	-133.165	0.516	966.078	0.604	22	0.189	R.FAIYDFDFLTAEDVPK.S
R3/RRR3-24/2	1467.253	1467.693	-300.373	0.408	1374.557	0.411	18	0.189	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1467.704	1467.693	7.540	0.509	1245.747	0.445	18	0.184	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1070.910	1071.190	-262.227	0.455	1103.213	0.421	15	0.172	K.MLYASSNER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1466.766	1467.693	-1317.100	0.380	1187.220	0.374	17	0.167	R.IFYILWSPDNAK.V
R3/RRR3-23/2	1466.928	1467.693	-1206.615	0.351	1377.145	0.274	17	0.165	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1467.177	1467.693	-1035.754	0.350	1122.256	0.347	16	0.158	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1158.114	1158.330	-187.296	0.475	863.887	0.375	17	0.153	K.EIIVDKIGDR.T
R3/RRR3-24/2	1158.072	1158.330	-223.672	0.457	802.054	0.366	17	0.150	K.EIIVDKIGDR.T
R3/RRR3-24/2	1070.867	1071.190	-302.026	0.360	856.832	0.351	15	0.148	K.MLYASSNER.F
R3/RRR3-24/2	1158.026	1158.330	-262.906	0.475	584.476	0.380	15	0.145	K.EIIVDKIGDR.T
R3/RRR3-23/2	1466.797	1467.693	-1296.121	0.335	887.857	0.312	14	0.142	R.IFYILWSPDNAK.V
R3/RRR3-24/2	1070.812	1071.190	-354.066	0.346	586.688	0.308	13	0.138	K.MLYASSNER.F
R3/RRR3-23/2	1468.427	1467.693	-181.568	0.387	719.298	0.296	14	0.138	R.IFYILWSPDNAK.V
R3/RRR3-24/3	1343.684	1343.554	96.795	0.525	1246.164	0.450	25	0.137	K.GKEIIVDKIGDR.T
R3/RRR3-24/2	1467.143	1467.693	-1059.312	0.223	741.154	0.188	14	0.131	R.IFYILWSPDNAK.V
R3/RRR3-24/3	1344.025	1343.554	351.204	0.485	1015.597	0.372	23	0.108	K.GKEIIVDKIGDR.T
R3/RRR3-12/2	1990.635	1991.298	-837.876	0.538	1867.266	0.590	28	0.294	R.AFSGLGGLGVDEPAMVSALAK.W
R3/RRR3-12/2	1579.135	1578.665	297.993	0.556	1685.119	0.580	21	0.267	R.HIEEDLGHEETLR.E
R3/RRR3-12/2	1579.222	1578.665	-281.868	0.553	1551.538	0.606	21	0.255	R.HIEEDLGHEETLR.E
R3/RRR3-12/2	1990.311	1991.298	-1001.092	0.519	1580.525	0.601	26	0.252	R.AFSGLGGLGVDEPAMVSALAK.W
R3/RRR3-12/2	1578.253	1578.665	-262.103	0.491	1362.674	0.582	20	0.224	R.HIEEDLGHEETLR.E
R3/RRR3-12/2	1172.396	1173.338	-1661.798	0.378	1717.800	0.385	19	0.223	R.EAALCLATPAR.Y
R3/RRR3-12/2	959.797	960.067	-282.316	0.495	1621.729	0.362	15	0.206	R.TAEELLGAR.K
R3/RRR3-12/2	959.316	960.067	-1830.597	0.412	1626.591	0.297	15	0.194	R.TAEELLGAR.K
R3/RRR3-12/2	959.728	960.067	-354.415	0.437	1654.841	0.252	15	0.187	R.TAEELLGAR.K
R3/RRR3-12/3	1578.727	1578.665	39.186	0.482	1435.440	0.548	26	0.182	R.HIEEDLGHEETLR.E
R3/RRR3-12/2	1172.821	1173.338	-1297.065	0.368	1281.684	0.315	18	0.166	R.EAALCLATPAR.Y
R3/RRR3-12/2	1187.089	1186.385	-250.281	0.427	538.670	0.570	15	0.161	R.SKPHLVETFK.H
R3/RRR3-12/2	1186.173	1186.385	-179.253	0.411	473.853	0.562	14	0.156	R.SKPHLVETFK.H
R3/RRR3-12/2	1186.096	1186.385	-244.090	0.428	561.096	0.506	15	0.155	R.SKPHLVETFK.H
R3/RRR3-12/2	1173.086	1173.338	-215.277	0.474	935.997	0.368	16	0.152	R.EAALCLATPAR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1058.954	1059.155	-190.497	0.487	696.524	0.385	15	0.150	K.LVENDDVVR.I
R3/RRR3-12/2	1058.911	1059.155	-231.667	0.504	711.645	0.370	15	0.149	K.LVENDDVVR.I
R3/RRR3-12/2	1058.515	1059.155	-1554.420	0.425	706.009	0.342	15	0.145	K.LVENDDVVR.I
R3/RRR3-12/3	1579.711	1578.665	29.125	0.486	1145.049	0.493	25	0.140	R.HIEEDLGHEETLR.E
R3/RRR3-13/3	1578.041	1578.665	-1032.476	0.455	1155.945	0.484	25	0.138	R.HIEEDLGHEETLR.E
R3/RRR3-12/3	1578.592	1578.665	-46.902	0.470	1032.743	0.508	24	0.135	R.HIEEDLGHEETLR.E
R3/RRR3-13/3	1578.587	1578.665	-50.044	0.438	929.635	0.529	23	0.132	R.HIEEDLGHEETLR.E
R3/RRR3-14/3	1578.611	1578.665	-34.686	0.434	1061.278	0.479	24	0.131	R.HIEEDLGHEETLR.E
R3/RRR3-12/3	1812.764	1812.096	-183.795	0.392	926.825	0.378	24	0.104	R.DKPYCGLLVGLVSAYR.Y
R3/RRR3-13/3	1578.774	1578.665	69.198	0.334	632.979	0.418	20	0.103	R.HIEEDLGHEETLR.E
R3/RRR3-12/3	1812.018	1812.096	-42.752	0.313	639.796	0.315	20	0.082	-.DKPYCGLLVGLVSAYR.-
R3/RRR3-17/2	1549.588	1549.750	-105.135	0.523	2876.306	0.412	24	0.446	K.KEDIDGFLVGGASLK.G
R3/RRR3-17/2	1752.249	1751.956	168.004	0.577	2206.920	0.557	25	0.345	R.IIYGGSVNAANCAELAK.K
R3/RRR3-17/2	1751.328	1751.956	-932.372	0.528	2162.423	0.500	25	0.320	R.IIYGGSVNAANCAELAK.K
R3/RRR3-17/2	1449.843	1450.619	-1228.688	0.569	1920.098	0.586	22	0.304	K.GPDFATIINSVTSK.K
R3/RRR3-17/2	1449.721	1450.619	-1312.654	0.550	1925.568	0.533	22	0.289	K.GPDFATIINSVTSK.K
R3/RRR3-17/2	1451.142	1450.619	-329.611	0.576	1793.582	0.564	22	0.277	K.GPDFATIINSVTSK.K
R3/RRR3-17/2	1750.859	1751.956	-1201.220	0.502	1932.948	0.470	24	0.272	R.IIYGGSVNAANCAELAK.K
R3/RRR3-17/2	1229.655	1230.353	-1385.077	0.420	1384.180	0.436	20	0.196	K.TNVSPEVASGIR.I
R3/RRR3-17/2	1229.502	1230.353	-1510.126	0.401	1265.940	0.404	20	0.180	K.TNVSPEVASGIR.I
R3/RRR3-17/2	1230.020	1230.353	-271.208	0.454	1203.951	0.428	19	0.179	K.TNVSPEVASGIR.I
R3/RRR3-17/2	1606.393	1606.765	-232.436	0.493	872.905	0.518	21	0.167	K.VATPEQAQEVHAAVR.D
R3/RRR3-17/3	1578.362	1578.792	-272.915	0.366	544.695	0.545	22	0.113	K.GPDFATIINSVTSKK.V
R3/RRR3-17/3	1578.549	1578.792	-153.979	0.361	504.407	0.502	22	0.107	K.GPDFATIINSVTSKK.V
R3/RRR3-17/3	1578.893	1578.792	64.152	0.357	629.432	0.456	24	0.104	K.GPDFATIINSVTSKK.V
R3/RRR3-7/2	1474.387	1474.730	-232.818	0.546	2702.157	0.610	23	0.477	R.LGANSLLDIVVFGR.A
R3/RRR3-7/2	1296.024	1295.427	-311.434	0.495	1820.544	0.562	20	0.281	R.ATNTILATGGYGR.A
R3/RRR3-7/2	1473.614	1474.730	-1440.262	0.395	1797.148	0.529	20	0.266	R.LGANSLLDIVVFGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1473.783	1474.730	-1325.202	0.367	1684.827	0.468	20	0.235	R.LGANSLLDIVVFGR.A
R3/RRR3-7/2	1294.993	1295.427	-335.696	0.432	1465.583	0.526	20	0.222	R.ATNTILATGGYGR.A
R3/RRR3-7/2	1294.884	1295.427	-1194.937	0.425	1260.067	0.575	18	0.208	R.ATNTILATGGYGR.A
R3/RRR3-7/2	1166.021	1166.336	-270.766	0.485	1553.232	0.398	17	0.207	R.VM*QNNAAVFR.T
R3/RRR3-7/2	1127.089	1127.231	-126.404	0.481	1266.878	0.449	17	0.188	R.AFGGQSLDFGK.G
R3/RRR3-7/2	1128.061	1127.231	-151.041	0.513	1114.546	0.498	18	0.185	R.AFGGQSLDFGK.G
R3/RRR3-7/2	1166.108	1166.336	-196.199	0.458	1273.111	0.404	17	0.181	R.VM*QNNAAVFR.T
R3/RRR3-7/2	1127.149	1127.231	-72.954	0.462	1006.476	0.490	17	0.175	R.AFGGQSLDFGK.G
R3/RRR3-7/2	1115.485	1116.338	-1665.906	0.416	1219.959	0.373	15	0.171	K.TIAWLDKLR.N
R3/RRR3-7/2	1166.101	1166.336	-202.290	0.490	1063.406	0.408	16	0.166	R.VM*QNNAAVFR.T
R3/RRR3-7/2	1608.276	1608.819	-962.279	0.404	920.673	0.459	19	0.160	K.AVIELENYGLPFSR.T
R3/RRR3-7/3	1790.842	1790.992	-83.732	0.432	744.854	0.585	27	0.126	R.AAIGLSEHGFNTACITK.L
R3/RRR3-16/2	1247.497	1248.325	-1469.792	0.478	1214.908	0.381	18	0.172	R.EAISQITNESR.E
R3/RRR3-16/2	1248.084	1248.325	-193.610	0.500	1068.491	0.384	17	0.162	R.EAISQITNESR.E
R3/RRR3-16/2	1247.675	1248.325	-1326.703	0.483	975.848	0.366	17	0.155	R.EAISQITNESR.E
R3/RRR3-9/2	1986.630	1987.203	-794.144	0.481	1645.762	0.582	26	0.258	K.EALAAPGLSYTDVPNAQIR.K
R3/RRR3-9/2	1514.205	1514.706	-994.368	0.526	1561.883	0.502	21	0.229	R.KLAEDNNVPLSSVK.G
R3/RRR3-9/2	1514.108	1514.706	-1058.395	0.542	1484.479	0.532	21	0.227	R.KLAEDNNVPLSSVK.G
R3/RRR3-9/2	1986.416	1987.203	-902.032	0.455	1408.786	0.514	25	0.211	K.EALAAPGLSYTDVPNAQIR.K
R3/RRR3-9/2	1232.688	1233.438	-1424.279	0.430	1313.414	0.464	19	0.194	R.VIDGAIGAEFLK.A
R3/RRR3-9/2	1233.223	1233.438	-175.194	0.520	1254.362	0.489	18	0.194	R.VIDGAIGAEFLK.A
R3/RRR3-9/2	1234.074	1233.438	-296.212	0.530	1250.585	0.451	18	0.186	R.VIDGAIGAEFLK.A
R3/RRR3-9/2	1144.075	1143.402	-286.017	0.501	1218.349	0.378	16	0.172	K.KISINDLVIK.A
R3/RRR3-9/2	1144.333	1143.402	-60.089	0.526	1123.956	0.402	16	0.169	K.KISINDLVIK.A
R3/RRR3-9/2	1015.075	1015.229	-151.510	0.449	870.141	0.285	15	0.143	K.ISINDLVIK.A
R3/RRR3-13/2	1232.840	1233.438	-1300.758	0.329	602.340	0.411	13	0.141	R.VIDGAIGAEFLK.A
R3/RRR3-9/2	1142.696	1143.402	-1497.339	0.314	917.176	0.243	15	0.139	K.KISINDLVIK.A
R3/RRR3-9/2	1015.152	1015.229	-75.876	0.447	721.358	0.264	14	0.137	K.ISINDLVIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1014.594	1015.229	-1615.615	0.399	766.622	0.261	14	0.137	-.ISINDLVIK.-
R3/RRR3-2/2	1143.174	1143.402	-199.704	0.204	647.901	0.091	14	0.128	K.KISINDLVIK.A
R3/RRR3-9/2	1038.188	1038.133	53.116	0.171	975.748	0.135	14	0.126	K.ADIEDYLAK.G
R3/RRR3-9/3	1585.279	1585.744	-294.508	0.439	1162.955	0.396	27	0.120	K.LRGELNPLQESSGGK.K
R3/RRR3-6/2	1222.004	1221.346	-281.103	0.478	1275.024	0.518	16	0.202	R.HFEVDLSAFR.N
R3/RRR3-7/2	1514.122	1514.615	-326.332	0.428	1303.690	0.491	19	0.197	K.EIAQGYCDSFAPR.D
R3/RRR3-6/2	1221.809	1221.346	380.233	0.429	1208.370	0.518	16	0.195	R.HFEVDLSAFR.N
R3/RRR3-7/2	1514.048	1514.615	-1037.654	0.429	1348.524	0.439	18	0.191	K.EIAQGYCDSFAPR.D
R3/RRR3-7/3	1447.633	1448.611	-1370.632	0.533	1705.964	0.465	27	0.189	R.ARHFEVDLSAFR.N
R3/RRR3-7/2	1221.234	1221.346	-92.197	0.434	1212.682	0.457	17	0.185	R.HFEVDLSAFR.N
R3/RRR3-7/2	1514.128	1514.615	-322.206	0.399	1158.814	0.469	17	0.179	K.EIAQGYCDSFAPR.D
R3/RRR3-7/2	1210.884	1211.348	-384.495	0.411	1198.730	0.428	16	0.178	K.GEFVEYIPTR.E
R3/RRR3-7/2	1115.167	1115.264	-87.022	0.380	1240.743	0.400	15	0.176	K.VGDALEFVHK.E
R3/RRR3-7/2	1221.051	1221.346	-242.618	0.449	1045.162	0.429	16	0.169	R.HFEVDLSAFR.N
R3/RRR3-7/2	1374.174	1373.604	-313.709	0.473	586.219	0.514	18	0.158	K.VEPLVNM*GQITR.A
R3/RRR3-7/2	1220.694	1221.346	-1357.431	0.325	982.519	0.369	16	0.155	R.HFEVDLSAFR.N
R3/RRR3-7/2	1372.978	1373.604	-1187.728	0.386	697.093	0.461	19	0.154	K.VEPLVNM*GQITR.A
R3/RRR3-1/2	1116.227	1115.264	-32.973	0.351	933.899	0.262	15	0.141	K.VGDALEFVHK.E
R3/RRR3-7/2	1338.887	1339.521	-1223.792	0.452	854.932	0.296	15	0.138	K.KGEFVEYIPTR.E
R3/RRR3-1/2	1115.405	1115.264	126.935	0.348	794.195	0.266	15	0.138	K.VGDALEFVHK.E
R3/RRR3-7/2	1372.440	1373.604	-1581.881	0.265	434.830	0.313	16	0.135	K.VEPLVNM*GQITR.A
R3/RRR3-7/3	1448.866	1448.611	176.639	0.550	995.802	0.444	22	0.120	R.ARHFEVDLSAFR.N
R3/RRR3-7/3	1448.109	1448.611	-1040.440	0.521	977.430	0.427	21	0.116	R.ARHFEVDLSAFR.N
R3/RRR3-22/3	1994.191	1993.113	39.557	0.527	1900.170	0.605	36	0.276	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-23/3	1993.793	1993.113	-160.506	0.513	1901.656	0.602	37	0.274	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-21/3	1992.352	1993.113	-886.169	0.533	1991.738	0.542	35	0.269	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-23/3	1992.971	1993.113	-71.246	0.519	1799.938	0.591	35	0.254	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-22/3	1993.198	1993.113	42.832	0.526	1724.738	0.606	34	0.247	K.SHSTETKLEATGDASCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1222.034	1222.321	-235.509	0.479	1625.021	0.480	20	0.232	K.LEATGDASCVAK.L
R3/RRR3-21/2	1222.087	1222.321	-192.319	0.473	1579.415	0.502	20	0.231	K.LEATGDASCVAK.L
R3/RRR3-23/3	1992.356	1993.113	-884.232	0.470	1712.673	0.566	35	0.231	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-23/2	1221.927	1222.321	-323.605	0.454	1610.634	0.464	20	0.226	K.LEATGDASCVAK.L
R3/RRR3-22/2	1221.520	1222.321	-1478.797	0.442	1554.898	0.477	20	0.222	K.LEATGDASCVAK.L
R3/RRR3-23/2	1221.478	1222.321	-1513.329	0.425	1548.512	0.477	20	0.222	K.LEATGDASCVAK.L
R3/RRR3-22/2	1221.935	1222.321	-316.790	0.459	1553.834	0.470	20	0.221	K.LEATGDASCVAK.L
R3/RRR3-22/2	1221.499	1222.321	-1495.963	0.425	1580.605	0.445	20	0.218	K.LEATGDASCVAK.L
R3/RRR3-21/2	1222.071	1222.321	-205.246	0.420	1523.154	0.442	20	0.211	K.LEATGDASCVAK.L
R3/RRR3-22/3	1993.385	1993.113	137.171	0.522	1544.743	0.572	34	0.207	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-22/3	1992.919	1993.113	-97.328	0.517	1491.552	0.543	34	0.191	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-23/2	1221.381	1222.321	-1593.044	0.389	1322.452	0.439	19	0.190	K.LEATGDASCVAK.L
R3/RRR3-22/3	1992.819	1993.113	-147.928	0.513	1413.634	0.543	33	0.182	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-21/3	1992.606	1993.113	-758.588	0.501	1449.976	0.512	33	0.178	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-23/2	1221.989	1222.329	-279.604	0.493	733.185	0.585	18	0.174	K.LNPSADAGSVYK.T
R3/RRR3-21/3	1992.873	1993.113	-120.369	0.486	1512.045	0.457	33	0.170	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-23/2	1221.659	1222.329	-1371.191	0.355	962.885	0.456	20	0.165	K.LNPSADAGSVYK.T
R3/RRR3-23/3	1993.048	1993.113	-32.726	0.485	1247.081	0.541	30	0.164	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-22/2	1221.947	1222.329	-313.981	0.398	837.717	0.441	19	0.158	K.LNPSADAGSVYK.T
R3/RRR3-22/2	1222.070	1222.329	-212.960	0.375	622.049	0.519	17	0.156	K.LNPSADAGSVYK.T
R3/RRR3-23/2	1160.601	1161.201	-1382.881	0.336	1181.209	0.289	17	0.155	K.DGASLSPEQEK.M
R3/RRR3-22/2	1221.908	1222.329	-345.955	0.378	778.448	0.429	19	0.154	K.LNPSADAGSVYK.T
R3/RRR3-22/3	1993.224	1993.113	55.915	0.473	1204.841	0.520	32	0.154	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-23/2	1222.001	1222.329	-269.682	0.332	932.846	0.375	20	0.154	K.LNPSADAGSVYK.T
R3/RRR3-23/2	995.004	995.151	-148.475	0.352	691.445	0.389	13	0.148	K.LTVEYELK.D
R3/RRR3-21/2	1168.137	1168.361	-193.130	0.435	826.571	0.355	14	0.148	K.VCLDVHSLPK.V
R3/RRR3-22/2	995.273	995.151	123.189	0.359	545.754	0.378	12	0.144	K.LTVEYELK.D
R3/RRR3-22/2	1168.114	1168.361	-212.630	0.489	690.518	0.345	14	0.143	K.VCLDVHSLPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	994.973	995.151	-179.120	0.346	685.476	0.327	13	0.143	K.LTVEYELK.D
R3/RRR3-22/2	1168.069	1168.361	-251.107	0.440	654.048	0.333	14	0.142	K.VCLDVHSLPK.V
R3/RRR3-23/2	994.412	995.151	-1753.737	0.313	644.671	0.324	13	0.141	K.LTVEYELK.D
R3/RRR3-21/2	1169.185	1168.361	-151.174	0.450	700.631	0.326	14	0.140	-.VCLDVHSLPK.-
R3/RRR3-23/2	1168.339	1168.361	-19.241	0.452	724.450	0.282	14	0.138	K.VCLDVHSLPK.V
R3/RRR3-23/3	1992.133	1993.113	-996.618	0.457	1103.868	0.482	29	0.138	K.SHSTETKLEATGDASCVAK.L
R3/RRR3-22/2	995.296	995.151	145.821	0.272	418.895	0.297	11	0.138	K.LTVEYELK.D
R3/RRR3-23/2	1160.550	1161.201	-1427.357	0.357	873.092	0.232	16	0.136	-.DGASLSPEQEK.-
R3/RRR3-22/2	1167.623	1168.361	-1493.265	0.381	803.554	0.200	14	0.133	K.VCLDVHSLPK.V
R3/RRR3-23/2	1168.328	1168.361	-28.778	0.453	689.637	0.220	14	0.133	K.VCLDVHSLPK.V
R3/RRR3-23/2	1160.393	1161.201	-1562.605	0.328	623.766	0.244	14	0.132	-.DGASLSPEQEK.-
R3/RRR3-23/2	1168.301	1168.361	-51.520	0.327	553.080	0.198	13	0.128	-.VCLDVHSLPK.-
R3/RRR3-6/3	1994.291	1993.113	89.744	0.366	268.365	0.446	20	0.104	-.SHSTETKLEATGDASCVAK.-
R3/RRR3-17/2	1628.454	1628.852	-245.076	0.520	2719.950	0.550	25	0.458	R.GELLVGIIGTLDTGNR.Y
R3/RRR3-17/2	1628.101	1628.852	-1078.819	0.467	2355.015	0.572	25	0.382	R.GELLVGIIGTLDTGNR.Y
R3/RRR3-17/2	1627.795	1628.852	-1267.664	0.390	1822.283	0.487	24	0.260	R.GELLVGIIGTLDTGNR.Y
R3/RRR3-17/2	1698.411	1698.866	-268.936	0.509	1315.589	0.625	22	0.226	R.VDFAPGGTNPPHVHPR.A
R3/RRR3-17/2	1699.300	1698.866	256.026	0.504	1254.951	0.570	23	0.209	R.VDFAPGGTNPPHVHPR.A
R3/RRR3-16/2	1698.310	1698.866	-919.088	0.435	1161.865	0.590	20	0.200	R.VDFAPGGTNPPHVHPR.A
R3/RRR3-17/2	1698.347	1698.866	-897.007	0.494	1173.881	0.573	21	0.200	R.VDFAPGGTNPPHVHPR.A
R3/RRR3-16/2	1698.327	1698.866	-908.769	0.488	1189.500	0.550	22	0.197	R.VDFAPGGTNPPHVHPR.A
R3/RRR3-17/2	1278.147	1278.508	-282.933	0.514	1347.946	0.416	16	0.187	R.GLMHFQFNVGK.T
R3/RRR3-17/2	957.201	958.137	-2029.066	0.434	1387.349	0.367	15	0.184	R.ATEVGIVLR.G
R3/RRR3-20/2	957.586	958.137	-1624.853	0.417	1505.360	0.295	15	0.181	R.ATEVGIVLR.G
R3/RRR3-17/2	1278.114	1278.508	-309.092	0.487	1256.858	0.421	16	0.181	R.GLMHFQFNVGK.T
R3/RRR3-16/2	1697.829	1698.866	-1203.476	0.400	1026.358	0.532	20	0.178	R.VDFAPGGTNPPHVHPR.A
R3/RRR3-17/2	1277.814	1278.508	-1329.138	0.452	1375.009	0.328	16	0.174	R.GLMHFQFNVGK.T
R3/RRR3-20/2	957.802	958.137	-351.421	0.394	1320.942	0.342	14	0.173	R.ATEVGIVLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	989.398	990.138	-1763.987	0.436	820.972	0.427	14	0.158	R.AGETFVIPR.G
R3/RRR3-17/2	989.927	990.138	-213.799	0.424	896.096	0.400	14	0.158	R.AGETFVIPR.G
R3/RRR3-15/2	989.828	990.138	-313.642	0.426	879.359	0.392	14	0.156	R.AGETFVIPR.G
R3/RRR3-17/2	1295.101	1294.507	-314.486	0.501	666.606	0.455	16	0.155	R.GLM*HFQFNVGK.T
R3/RRR3-18/2	989.870	990.138	-271.327	0.470	839.448	0.383	14	0.154	R.AGETFVIPR.G
R3/RRR3-15/2	990.149	990.138	11.177	0.517	769.987	0.382	14	0.152	R.AGETFVIPR.G
R3/RRR3-18/2	989.760	990.138	-382.937	0.469	778.310	0.375	14	0.152	R.AGETFVIPR.G
R3/RRR3-16/2	989.883	990.138	-257.965	0.469	821.212	0.361	14	0.151	R.AGETFVIPR.G
R3/RRR3-16/2	989.854	990.138	-287.535	0.468	884.686	0.345	14	0.151	R.AGETFVIPR.G
R3/RRR3-17/2	989.940	990.138	-200.438	0.496	798.669	0.364	14	0.151	R.AGETFVIPR.G
R3/RRR3-17/2	989.927	990.138	-213.304	0.409	811.269	0.355	14	0.150	R.AGETFVIPR.G
R3/RRR3-17/2	989.889	990.138	-251.779	0.443	770.773	0.359	14	0.150	R.AGETFVIPR.G
R3/RRR3-19/2	989.739	990.138	-404.594	0.421	892.553	0.329	14	0.149	R.AGETFVIPR.G
R3/RRR3-19/2	989.841	990.138	-301.145	0.440	907.242	0.312	14	0.148	R.AGETFVIPR.G
R3/RRR3-17/2	1293.573	1294.507	-1499.779	0.431	722.466	0.370	16	0.147	R.GLM*HFQFNVGK.T
R3/RRR3-20/2	991.049	990.138	-90.261	0.483	804.729	0.331	14	0.147	R.AGETFVIPR.G
R3/RRR3-18/2	989.984	990.138	-155.412	0.415	778.944	0.330	14	0.147	R.AGETFVIPR.G
R3/RRR3-20/2	957.587	958.137	-1623.701	0.246	1094.588	0.266	14	0.147	R.ATEVGIVLR.G
R3/RRR3-16/2	989.730	990.138	-413.381	0.439	892.821	0.302	14	0.146	R.AGETFVIPR.G
R3/RRR3-16/2	1294.036	1294.507	-365.175	0.478	655.575	0.374	15	0.145	R.GLM*HFQFNVGK.T
R3/RRR3-17/2	1293.594	1294.507	-1483.381	0.419	682.832	0.346	16	0.144	R.GLM*HFQFNVGK.T
R3/RRR3-14/2	990.026	990.138	-112.986	0.443	773.946	0.293	14	0.143	R.AGETFVIPR.G
R3/RRR3-19/2	989.867	990.138	-274.172	0.439	792.249	0.287	14	0.143	R.AGETFVIPR.G
R3/RRR3-12/2	989.588	990.138	-1571.257	0.326	746.110	0.306	13	0.143	R.AGETFVIPR.G
R3/RRR3-16/2	989.905	990.138	-236.067	0.347	895.953	0.265	13	0.142	R.AGETFVIPR.G
R3/RRR3-17/2	1412.878	1413.688	-1284.751	0.451	1025.425	0.292	16	0.142	K.ALRVDTGVVELLK.S
R3/RRR3-16/2	1293.493	1294.507	-1561.492	0.395	637.745	0.337	15	0.142	R.GLM*HFQFNVGK.T
R3/RRR3-13/2	990.003	990.138	-136.610	0.355	605.806	0.293	13	0.142	R.AGETFVIPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/2	989.746	990.138	-397.045	0.409	794.303	0.268	14	0.142	R.AGETFVIPR.G
R3/RRR3-25/2	989.943	990.138	-196.975	0.277	806.693	0.283	14	0.141	R.AGETFVIPR.G
R3/RRR3-25/2	990.045	990.138	-94.434	0.384	793.044	0.258	14	0.141	R.AGETFVIPR.G
R3/RRR3-14/2	989.920	990.138	-220.974	0.363	739.042	0.259	14	0.140	R.AGETFVIPR.G
R3/RRR3-5/2	990.021	990.138	-118.552	0.347	677.183	0.268	13	0.140	R.AGETFVIPR.G
R3/RRR3-14/2	990.000	990.138	-139.208	0.381	735.037	0.241	14	0.139	R.AGETFVIPR.G
R3/RRR3-1/2	989.906	990.138	-235.324	0.261	865.373	0.242	14	0.139	R.AGETFVIPR.G
R3/RRR3-17/2	989.979	990.138	-161.225	0.409	759.152	0.236	14	0.139	R.AGETFVIPR.G
R3/RRR3-25/2	989.417	990.138	-1744.401	0.342	638.524	0.227	13	0.138	R.AGETFVIPR.G
R3/RRR3-16/2	990.128	990.138	-9.844	0.342	747.138	0.214	14	0.137	R.AGETFVIPR.G
R3/RRR3-20/2	989.831	990.138	-311.167	0.323	783.885	0.209	13	0.136	R.AGETFVIPR.G
R3/RRR3-17/2	957.239	958.137	-1989.335	0.282	706.355	0.249	13	0.135	R.ATEVGIVLR.G
R3/RRR3-17/2	989.694	990.138	-449.767	0.385	674.356	0.196	13	0.135	R.AGETFVIPR.G
R3/RRR3-3/2	989.942	990.138	-198.830	0.276	660.639	0.184	13	0.135	R.AGETFVIPR.G
R3/RRR3-1/2	958.450	958.137	327.650	0.223	651.623	0.112	12	0.125	-.ATEVGIVLR.-
R3/RRR3-17/3	1414.261	1413.688	-302.461	0.526	1040.986	0.442	26	0.117	-.ALRVDTGVVELLK.-
R3/RRR3-17/3	1413.629	1413.688	-41.809	0.539	985.726	0.337	26	0.100	-.ALRVDTGVVELLK.-
R3/RRR3-17/3	1413.731	1413.688	30.942	0.536	953.610	0.334	25	0.092	-.ALRVDTGVVELLK.-
R3/RRR3-15/2	1695.752	1695.895	-84.809	0.499	1088.889	0.516	23	0.184	K.LLESHLVPSSTAPESK.V
R3/RRR3-14/2	1695.365	1695.895	-905.663	0.461	954.979	0.484	22	0.168	K.LLESHLVPSSTAPESK.V
R3/RRR3-15/2	1696.295	1695.895	236.486	0.504	770.271	0.554	20	0.167	K.LLESHLVPSSTAPESK.V
R3/RRR3-14/2	1695.486	1695.895	-242.247	0.467	850.540	0.507	21	0.165	K.LLESHLVPSSTAPESK.V
R3/RRR3-14/2	1696.455	1695.895	-260.441	0.477	625.251	0.526	18	0.155	K.LLESHLVPSSTAPESK.V
R3/RRR3-6/2	1390.403	1390.615	-152.747	0.528	2334.717	0.605	22	0.391	K.LPFAAAQIGQAFR.N
R3/RRR3-6/2	1116.194	1116.290	-85.955	0.488	1590.755	0.513	17	0.236	R.VGIDEVASVVK.Q
R3/RRR3-6/2	1768.512	1766.974	-261.598	0.350	1650.504	0.381	21	0.211	K.HVLAVLDDLSADELGAK.I
R3/RRR3-6/2	977.045	977.144	-101.079	0.493	1046.232	0.518	13	0.183	K.ANVLAFWR.Q
R3/RRR3-6/2	1115.575	1116.290	-1541.862	0.372	1340.661	0.365	17	0.178	R.VGIDEVASVVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1389.941	1390.615	-1207.911	0.416	1100.286	0.471	17	0.175	K.LPFAAAQIGQAFR.N
R3/RRR3-6/2	1606.293	1606.847	-970.213	0.405	948.388	0.462	19	0.161	R.VFTPSVIEPSFGIGR.I
R3/RRR3-6/2	1541.373	1541.690	-206.417	0.423	1043.948	0.412	16	0.159	K.GTVNNETLGYFIGR.V
R3/RRR3-6/2	1229.017	1229.325	-251.904	0.465	714.497	0.487	19	0.159	R.QAAVDAQAEAVR.A
R3/RRR3-6/2	1229.163	1229.325	-132.641	0.455	556.482	0.485	18	0.153	R.QAAVDAQAEAVR.A
R3/RRR3-1/2	1390.540	1390.615	-53.852	0.418	771.487	0.421	15	0.148	K.LPFAAAQIGQAFR.N
R3/RRR3-6/2	1116.048	1116.290	-217.832	0.387	633.397	0.353	16	0.142	R.VGIDEVASVVK.Q
R3/RRR3-6/2	1541.189	1541.690	-976.719	0.328	941.181	0.297	16	0.140	K.GTVNNETLGYFIGR.V
R3/RRR3-17/2	1294.167	1294.482	-244.332	0.493	1499.768	0.474	17	0.215	K.SDLLLASNPVHK.S
R3/RRR3-17/2	1458.762	1458.775	-8.696	0.461	1282.677	0.498	18	0.196	K.VRPAWLAILFGSK.T
R3/RRR3-17/2	1293.683	1294.482	-1394.700	0.486	1261.438	0.469	18	0.190	K.SDLLLASNPVHK.S
R3/RRR3-17/2	1293.641	1294.482	-1427.113	0.515	1272.880	0.463	17	0.189	K.SDLLLASNPVHK.S
R3/RRR3-17/2	1362.332	1362.601	-198.134	0.503	1049.443	0.515	18	0.182	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1362.213	1362.601	-286.055	0.490	1000.460	0.523	18	0.180	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1362.330	1362.601	-199.842	0.454	1035.157	0.462	18	0.172	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1458.618	1458.775	-108.082	0.488	1028.571	0.475	17	0.171	K.VRPAWLAILFGSK.T
R3/RRR3-17/2	1362.046	1362.601	-1145.274	0.475	833.447	0.517	17	0.168	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1362.200	1362.601	-295.226	0.503	862.440	0.493	17	0.166	K.LLGVWSSPYAIR.V
R3/RRR3-19/2	1363.334	1362.601	-196.282	0.526	1031.868	0.418	19	0.166	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1458.594	1458.775	-124.620	0.466	983.662	0.408	16	0.157	K.VRPAWLAILFGSK.T
R3/RRR3-17/2	1657.284	1656.771	-294.744	0.533	654.078	0.476	21	0.156	K.SLPYEYVEENLGDK.S
R3/RRR3-17/2	1362.079	1362.601	-1121.156	0.412	761.413	0.400	16	0.150	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1363.310	1362.601	-214.427	0.480	708.405	0.397	16	0.148	K.LLGVWSSPYAIR.V
R3/RRR3-16/2	1362.078	1362.601	-1121.876	0.445	551.393	0.450	14	0.148	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1115.157	1115.219	-55.952	0.438	813.324	0.341	14	0.146	R.FWAAYVDDK.V
R3/RRR3-17/2	1655.711	1656.771	-1247.769	0.342	583.732	0.382	20	0.142	K.SLPYEYVEENLGDK.S
R3/RRR3-19/2	1362.114	1362.601	-358.705	0.399	549.025	0.353	14	0.140	K.LLGVWSSPYAIR.V
R3/RRR3-17/2	1656.075	1656.771	-1027.327	0.424	382.890	0.378	17	0.140	K.SLPYEYVEENLGDK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	941.218	941.196	23.596	0.425	978.480	0.153	13	0.132	R.VRVVLNLK.S
R3/RRR3-17/2	1114.253	1115.219	-1769.829	0.276	814.821	0.152	14	0.129	R.FWAAYVDDK.V
R3/RRR3-17/2	941.127	941.196	-74.104	0.484	857.486	0.193	12	0.129	-.VRVVLNLK.-
R3/RRR3-17/2	942.117	941.196	-83.903	0.444	827.060	0.156	12	0.125	-.VRVVLNLK.-
R3/RRR3-17/3	1458.318	1458.775	-314.145	0.483	1134.097	0.407	23	0.122	K.VRPAWLAILFGSK.T
R3/RRR3-17/3	1459.050	1458.775	189.001	0.463	1305.053	0.339	23	0.120	K.VRPAWLAILFGSK.T
R3/RRR3-17/3	1458.737	1458.775	-26.499	0.434	1066.313	0.311	21	0.102	K.VRPAWLAILFGSK.T
R3/RRR3-17/3	1457.893	1458.775	-1294.598	0.351	303.217	0.255	22	0.099	-.VRPAWLAILFGSK.-
R3/RRR3-17/3	1458.597	1458.775	-122.321	0.440	445.186	0.300	23	0.092	-.VRPAWLAILFGSK.-
R3/RRR3-15/2	1564.980	1565.532	-994.730	0.492	2641.708	0.586	23	0.454	K.DAEGQDAEATTEEAK.K
R3/RRR3-15/2	1565.178	1565.532	-226.823	0.532	2305.995	0.536	22	0.360	K.DAEGQDAEATTEEAK.K
R3/RRR3-15/2	1560.097	1560.650	-998.471	0.469	1640.916	0.574	22	0.257	R.TLDAHIEEQFGSGR.L
R3/RRR3-15/2	1560.262	1560.650	-249.510	0.505	1158.120	0.571	19	0.199	R.TLDAHIEEQFGSGR.L
R3/RRR3-15/2	1560.135	1560.650	-973.883	0.487	1148.825	0.575	19	0.198	R.TLDAHIEEQFGSGR.L
R3/RRR3-15/3	1560.645	1560.650	-2.959	0.421	1554.667	0.464	30	0.170	R.TLDAHIEEQFGSGR.L
R3/RRR3-15/3	1821.939	1821.878	33.653	0.563	1118.416	0.561	31	0.154	K.KDAEGQDAEATTEEAKK.S
R3/RRR3-15/3	1561.882	1560.650	149.042	0.426	726.416	0.499	25	0.115	R.TLDAHIEEQFGSGR.L
R3/RRR3-15/3	1559.366	1560.650	-1469.186	0.301	692.785	0.431	23	0.101	R.TLDAHIEEQFGSGR.L
R3/RRR3-21/2	1566.608	1566.739	-84.376	0.564	1844.722	0.541	21	0.278	K.VYFDVEIDGKPAGR.V
R3/RRR3-21/2	1565.834	1566.739	-1220.242	0.507	1639.989	0.571	20	0.255	K.VYFDVEIDGKPAGR.V
R3/RRR3-21/3	1639.624	1639.905	-171.506	0.500	2067.619	0.438	32	0.243	K.IKHTGPGLLSM*ANAGR.D
R3/RRR3-21/2	1925.644	1925.198	232.545	0.594	1276.989	0.633	26	0.225	R.IIPSFMIQGGDFTLGDGR.G
R3/RRR3-21/2	1566.414	1566.739	-208.588	0.507	1328.769	0.548	19	0.211	K.VYFDVEIDGKPAGR.V
R3/RRR3-21/2	1924.178	1925.198	-1052.870	0.544	1213.859	0.578	27	0.207	R.IIPSFMIQGGDFTLGDGR.G
R3/RRR3-21/2	1940.443	1941.197	-906.572	0.511	668.937	0.613	26	0.173	R.IIPSFM*IQGGDFTLGDGR.G
R3/RRR3-21/2	1940.183	1941.197	-1041.235	0.469	756.092	0.586	26	0.173	R.IIPSFM*IQGGDFTLGDGR.G
R3/RRR3-21/2	1940.485	1941.197	-884.847	0.498	742.890	0.573	25	0.170	R.IIPSFM*IQGGDFTLGDGR.G
R3/RRR3-21/2	1013.717	1014.115	-393.695	0.411	902.583	0.336	14	0.148	K.ADLTEVTHK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	866.804	867.091	-332.012	0.349	692.282	0.358	12	0.144	R.VVM*GLFGK.T
R3/RRR3-21/2	1013.996	1014.115	-117.077	0.432	855.063	0.297	14	0.142	K.ADLTEVTHK.V
R3/RRR3-21/2	851.080	851.092	-14.186	0.305	379.476	0.387	11	0.142	R.VVMGLFGK.T
R3/RRR3-21/2	866.530	867.091	-1807.098	0.330	597.726	0.312	13	0.141	R.VVM*GLFGK.T
R3/RRR3-21/2	866.912	867.091	-206.838	0.338	666.341	0.286	13	0.140	R.VVM*GLFGK.T
R3/RRR3-21/2	851.018	851.092	-86.842	0.159	447.870	0.415	11	0.133	R.VVMGLFGK.T
R3/RRR3-21/3	1229.084	1229.365	-229.787	0.510	1040.953	0.346	20	0.106	K.SKADLTEVTHK.V
R3/RRR3-21/3	1229.598	1229.365	189.867	0.512	1127.413	0.321	21	0.104	-.SKADLTEVTHK.-
R3/RRR3-21/3	1229.645	1229.365	228.244	0.495	1039.130	0.300	20	0.092	-.SKADLTEVTHK.-
R3/RRR3-4/2	1579.162	1579.672	-959.088	0.537	1928.967	0.498	24	0.281	K.VM*ANADTPEDATTAR.Q
R3/RRR3-4/2	970.997	971.048	-52.784	0.421	1042.905	0.353	13	0.157	R.SDFEGIFR.A
R3/RRR3-4/2	970.426	971.048	-1676.468	0.351	1055.332	0.228	13	0.142	R.SDFEGIFR.A
R3/RRR3-5/2	974.085	974.180	-97.867	0.341	763.261	0.268	15	0.138	R.SINKITGLK.G
R3/RRR3-6/2	1578.130	1579.672	-2250.855	0.278	472.748	0.373	17	0.134	K.VM*ANADTPEDATTAR.Q
R3/RRR3-5/2	973.834	974.180	-356.385	0.283	754.642	0.229	15	0.133	R.SINKITGLK.G
R3/RRR3-1/2	1371.964	1372.501	-1123.787	0.339	735.384	0.253	13	0.129	-.AGLDYVSCSPFR.-
R3/RRR3-4/3	1975.656	1976.215	-791.435	0.408	1180.550	0.337	26	0.112	K.VGICGEHGGEPLSVAFFAK.A
R3/RRR3-4/3	1975.976	1976.215	-121.150	0.319	1228.790	0.267	26	0.103	K.VGICGEHGGEPLSVAFFAK.A
R3/RRR3-4/3	1976.116	1976.215	-50.045	0.370	754.436	0.264	23	0.084	-.VGICGEHGGEPLSVAFFAK.-
R3/RRR3-6/2	1248.176	1247.334	-127.188	0.501	1499.977	0.437	17	0.207	K.DIVDAGLAESEK.Q
R3/RRR3-6/2	1382.389	1381.644	-185.163	0.441	974.473	0.579	16	0.183	K.VTIFYTAPTLVR.S
R3/RRR3-6/2	1382.088	1381.644	322.229	0.441	935.043	0.562	16	0.178	K.VTIFYTAPTLVR.S
R3/RRR3-6/2	1062.043	1062.246	-191.788	0.459	1049.214	0.468	13	0.173	-.GPVQISWFK.-
R3/RRR3-6/2	1583.594	1582.785	-120.969	0.473	714.196	0.626	18	0.172	R.VLGSVGEPINPSAWR.W
R3/RRR3-6/2	1247.219	1247.334	-92.337	0.418	1137.507	0.418	16	0.169	K.DIVDAGLAESEK.Q
R3/RRR3-6/2	1062.015	1062.246	-218.078	0.427	883.918	0.501	12	0.166	K.GPVQISWFK.G
R3/RRR3-5/2	1708.755	1708.894	-81.871	0.458	1121.650	0.412	17	0.166	R.DVWWQDVVTSFPTK.C
R3/RRR3-6/2	1225.897	1226.315	-341.733	0.412	980.700	0.451	15	0.164	K.TNICYNAVDR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1061.876	1062.246	-349.436	0.468	832.837	0.487	13	0.164	K.GPVQISWFK.G
R3/RRR3-6/2	1381.154	1381.644	-355.887	0.359	961.946	0.445	16	0.161	K.VTIFYTAPTLVR.S
R3/RRR3-5/2	1582.364	1582.785	-267.148	0.441	655.182	0.460	18	0.149	R.VLGSVGEPINPSAWR.W
R3/RRR3-6/2	1709.242	1708.894	203.893	0.423	778.869	0.415	15	0.147	R.DVWWQDVVTSFPTK.C
R3/RRR3-5/2	1211.416	1211.310	87.868	0.489	494.873	0.463	15	0.147	R.VDDVINVSGHR.I
R3/RRR3-5/2	1708.596	1708.894	-174.820	0.388	871.251	0.379	15	0.146	R.DVWWQDVVTSFPTK.C
R3/RRR3-5/2	1582.101	1582.785	-1068.010	0.361	652.163	0.450	17	0.145	R.VLGSVGEPINPSAWR.W
R3/RRR3-6/2	1709.006	1708.894	65.294	0.340	633.904	0.423	15	0.142	R.DVWWQDVVTSFPTK.C
R3/RRR3-6/2	1708.960	1708.894	38.787	0.218	449.043	0.333	13	0.131	R.DVWWQDVVTSFPTK.C
R3/RRR3-6/3	1211.561	1211.310	208.306	0.484	746.502	0.453	21	0.111	R.VDDVINVSGHR.I
R3/RRR3-6/3	1211.136	1211.310	-143.877	0.462	892.105	0.407	22	0.108	R.VDDVINVSGHR.I
R3/RRR3-5/3	1211.465	1211.310	128.280	0.429	606.722	0.413	19	0.103	R.VDDVINVSGHR.I
R3/RRR3-14/2	1970.511	1970.261	127.027	0.645	3375.858	0.614	29	0.666	K.SAELIGQAIANNPAFLALR.Q
R3/RRR3-14/2	1969.496	1970.261	-898.902	0.569	3333.145	0.555	29	0.628	K.SAELIGQAIANNPAFLALR.Q
R3/RRR3-14/2	1970.159	1970.261	-52.054	0.624	3225.195	0.591	28	0.609	K.SAELIGQAIANNPAFLALR.Q
R3/RRR3-14/2	1661.706	1662.872	-1307.297	0.376	1817.292	0.377	23	0.233	K.AVVAQYNASQLITQR.E
R3/RRR3-14/2	1663.646	1662.872	-136.417	0.563	1631.464	0.406	22	0.213	K.AVVAQYNASQLITQR.E
R3/RRR3-14/2	1374.257	1374.485	-166.480	0.492	1209.782	0.508	20	0.194	R.ARPNLVESTSGSR.D
R3/RRR3-14/2	1374.384	1374.485	-74.262	0.502	1162.061	0.501	20	0.188	R.ARPNLVESTSGSR.D
R3/RRR3-14/2	1662.374	1662.872	-300.396	0.477	1349.939	0.407	21	0.185	K.AVVAQYNASQLITQR.E
R3/RRR3-14/2	1374.280	1374.485	-149.728	0.524	1182.774	0.447	20	0.180	R.ARPNLVESTSGSR.D
R3/RRR3-14/2	1205.709	1206.459	-1455.946	0.333	544.551	0.599	18	0.157	R.VPVPPAGAGTLVK.L
R3/RRR3-14/2	1079.942	1080.133	-177.498	0.409	629.006	0.378	15	0.147	R.TLGENFNER.V
R3/RRR3-14/2	1079.795	1080.133	-313.589	0.460	621.690	0.354	15	0.145	R.TLGENFNER.V
R3/RRR3-14/2	1250.274	1250.512	-190.921	0.317	287.797	0.406	15	0.142	R.VLPSIIHETLK.A
R3/RRR3-14/2	1250.247	1250.512	-212.665	0.290	303.813	0.459	15	0.142	R.VLPSIIHETLK.A
R3/RRR3-14/2	1251.346	1250.512	-133.127	0.296	222.752	0.403	14	0.141	R.VLPSIIHETLK.A
R3/RRR3-14/2	1206.029	1206.459	-357.718	0.301	320.876	0.514	13	0.141	R.VPVPPAGAGTLVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1206.193	1206.459	-221.143	0.276	333.222	0.519	14	0.140	R.VPVPPAGAGTLVK.L
R3/RRR3-14/2	1207.345	1206.459	-95.286	0.278	296.468	0.484	14	0.139	R.VPVPPAGAGTLVK.L
R3/RRR3-14/3	1970.332	1970.261	35.779	0.394	1033.514	0.517	28	0.136	K.SAELIGQAIANNPAFLALR.Q
R3/RRR3-14/2	1079.232	1080.133	-1766.792	0.356	558.903	0.234	14	0.136	R.TLGENFNER.V
R3/RRR3-14/3	1969.357	1970.261	-969.909	0.346	953.329	0.377	26	0.105	K.SAELIGQAIANNPAFLALR.Q
R3/RRR3-14/3	1969.410	1970.261	-942.653	0.402	853.185	0.359	26	0.099	K.SAELIGQAIANNPAFLALR.Q
R3/RRR3-21/2	1344.197	1344.496	-223.397	0.481	2342.317	0.458	22	0.339	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/2	1344.158	1344.496	-252.096	0.451	2149.772	0.473	22	0.309	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/3	1639.888	1639.792	58.556	0.538	2443.646	0.426	32	0.308	K.HSGNISLDDVIEIAR.I
R3/RRR3-21/3	1254.573	1254.544	23.010	0.488	2304.657	0.453	29	0.289	K.VSVVPSAAALVIK.A
R3/RRR3-21/3	1344.518	1344.496	16.462	0.484	2246.574	0.391	33	0.253	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/2	1344.192	1344.496	-226.768	0.467	1563.869	0.504	20	0.227	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/2	1639.326	1639.792	-284.902	0.568	1145.183	0.606	23	0.207	K.HSGNISLDDVIEIAR.I
R3/RRR3-21/2	1639.342	1639.792	-275.414	0.585	1113.701	0.586	22	0.199	K.HSGNISLDDVIEIAR.I
R3/RRR3-21/2	1639.272	1639.792	-929.931	0.580	1075.288	0.597	22	0.198	K.HSGNISLDDVIEIAR.I
R3/RRR3-21/3	1344.371	1344.496	-92.961	0.439	1997.038	0.335	33	0.192	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/3	1254.502	1254.544	-33.644	0.477	1788.804	0.401	27	0.184	K.VSVVPSAAALVIK.A
R3/RRR3-21/2	1731.932	1731.793	80.123	0.264	1196.695	0.225	22	0.182	K.DLQEEISDGEVEIPSA.-
R3/RRR3-20/2	1255.027	1254.544	386.071	0.525	793.045	0.549	21	0.174	K.VSVVPSAAALVIK.A
R3/RRR3-21/2	1254.342	1254.544	-161.312	0.436	901.248	0.496	22	0.170	K.VSVVPSAAALVIK.A
R3/RRR3-21/2	1254.252	1254.544	-233.853	0.443	876.028	0.490	22	0.168	K.VSVVPSAAALVIK.A
R3/RRR3-20/2	1254.129	1254.544	-331.600	0.441	919.392	0.469	22	0.168	K.VSVVPSAAALVIK.A
R3/RRR3-20/2	1639.019	1639.792	-1085.004	0.506	857.468	0.505	21	0.167	K.HSGNISLDDVIEIAR.I
R3/RRR3-21/2	1253.814	1254.544	-1384.267	0.429	783.825	0.527	20	0.167	K.VSVVPSAAALVIK.A
R3/RRR3-21/3	1639.834	1639.792	25.855	0.469	1596.614	0.390	26	0.160	K.HSGNISLDDVIEIAR.I
R3/RRR3-22/2	1638.630	1639.792	-1323.092	0.374	677.012	0.528	19	0.157	K.HSGNISLDDVIEIAR.I
R3/RRR3-21/2	1639.258	1639.792	-938.304	0.404	679.627	0.469	20	0.153	K.HSGNISLDDVIEIAR.I
R3/RRR3-21/2	881.971	882.082	-127.245	0.401	370.180	0.507	13	0.153	K.IGPLGLSPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	882.016	882.082	-75.600	0.406	382.522	0.500	13	0.153	K.IGPLGLSPK.K
R3/RRR3-21/2	881.535	882.082	-1760.656	0.377	391.202	0.512	13	0.152	K.IGPLGLSPK.K
R3/RRR3-20/2	881.379	882.082	-1938.919	0.378	323.246	0.493	12	0.150	K.IGPLGLSPK.K
R3/RRR3-20/2	1639.528	1639.792	-161.425	0.432	646.516	0.421	20	0.148	K.HSGNISLDDVIEIAR.I
R3/RRR3-20/2	881.756	882.082	-371.384	0.359	330.746	0.448	12	0.147	K.IGPLGLSPK.K
R3/RRR3-20/2	1343.706	1344.496	-1335.853	0.300	1080.179	0.270	19	0.145	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/2	881.580	882.082	-1709.040	0.294	326.392	0.451	12	0.144	K.IGPLGLSPK.K
R3/RRR3-22/2	1254.300	1254.544	-195.384	0.336	373.565	0.423	15	0.142	K.VSVVPSAAALVIK.A
R3/RRR3-21/2	881.492	882.082	-1809.077	0.261	319.081	0.397	11	0.140	K.IGPLGLSPK.K
R3/RRR3-20/2	1254.282	1254.544	-209.346	0.246	512.206	0.414	16	0.139	K.VSVVPSAAALVIK.A
R3/RRR3-21/2	1695.360	1695.880	-899.382	0.344	778.031	0.346	16	0.137	K.EILGTCVSVGCTVDGK.D
R3/RRR3-21/3	1638.748	1639.792	-1250.757	0.458	1510.080	0.318	25	0.133	K.HSGNISLDDVIEIAR.I
R3/RRR3-20/2	1343.602	1344.496	-1413.595	0.266	790.289	0.229	18	0.132	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/2	1696.258	1695.880	223.354	0.313	621.476	0.173	16	0.124	K.EILGTCVSVGCTVDGK.D
R3/RRR3-21/3	1344.363	1344.496	-99.518	0.351	819.304	0.340	25	0.096	R.VTGGEVGAASSLAPK.I
R3/RRR3-21/3	1639.374	1639.792	-255.663	0.382	699.899	0.266	21	0.079	-.HSGNISLDDVIEIAR.-
R3/RRR3-17/2	1406.126	1406.551	-303.043	0.553	3236.380	0.511	25	0.575	K.AM*AQVSQAGSGGLGR.V
R3/RRR3-17/2	1406.123	1406.551	-305.482	0.551	3094.026	0.522	25	0.540	K.AM*AQVSQAGSGGLGR.V
R3/RRR3-18/2	1406.088	1406.551	-330.306	0.546	2912.132	0.508	25	0.485	K.AM*AQVSQAGSGGLGR.V
R3/RRR3-18/2	1531.373	1531.776	-264.291	0.530	2425.790	0.584	24	0.400	K.AVASINSVLTDLVTK.G
R3/RRR3-17/2	1406.159	1406.551	-279.527	0.568	2431.988	0.537	25	0.384	K.AM*AQVSQAGSGGLGR.V
R3/RRR3-18/2	1406.143	1406.551	-290.849	0.553	2404.993	0.539	25	0.379	K.AM*AQVSQAGSGGLGR.V
R3/RRR3-17/2	1532.417	1531.776	-235.108	0.591	2179.074	0.662	23	0.375	K.AVASINSVLTDLVTK.G
R3/RRR3-18/2	1530.708	1531.776	-1355.026	0.416	2356.223	0.520	24	0.363	K.AVASINSVLTDLVTK.G
R3/RRR3-18/2	1406.025	1406.551	-1088.613	0.564	2342.384	0.523	25	0.360	K.AM*AQVSQAGSGGLGR.V
R3/RRR3-17/2	1532.297	1531.776	-313.752	0.580	2045.673	0.604	23	0.330	K.AVASINSVLTDLVTK.G
R3/RRR3-18/2	1531.367	1531.776	-268.449	0.523	2037.797	0.587	23	0.323	K.AVASINSVLTDLVTK.G
R3/RRR3-17/2	1530.811	1531.776	-1287.991	0.409	2063.065	0.519	22	0.306	K.AVASINSVLTDLVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1880.437	1880.077	192.037	0.588	1518.124	0.639	25	0.256	R.DLSPLTCAQCLSTAVSR.F
R3/RRR3-17/2	1879.270	1880.077	-964.667	0.534	1313.535	0.629	25	0.228	R.DLSPLTCAQCLSTAVSR.F
R3/RRR3-17/2	1490.071	1490.547	-320.260	0.498	1647.917	0.422	18	0.222	R.FDQYCGAQQGCR.I
R3/RRR3-17/2	1879.486	1880.077	-848.926	0.568	1269.902	0.624	24	0.222	R.DLSPLTCAQCLSTAVSR.F
R3/RRR3-17/2	1240.957	1241.333	-303.942	0.427	1205.570	0.555	21	0.200	K.GSTGVGFATSTAGK.G
R3/RRR3-17/2	1241.102	1241.333	-186.413	0.456	904.637	0.573	19	0.178	K.GSTGVGFATSTAGK.G
R3/RRR3-17/2	1240.480	1241.333	-1498.341	0.328	1038.727	0.507	19	0.173	K.GSTGVGFATSTAGK.G
R3/RRR3-17/2	1392.964	1393.567	-1154.485	0.418	1216.126	0.384	16	0.170	K.GNNVIYGLVQCR.G
R3/RRR3-17/2	1392.635	1393.567	-1391.519	0.337	623.385	0.370	14	0.138	K.GNNVIYGLVQCR.G
R3/RRR3-19/2	1609.500	1610.741	-1396.561	0.374	1551.753	0.462	20	0.217	K.DGTNVEEAFQCIVK.N
R3/RRR3-19/2	1610.358	1610.741	-238.326	0.511	1502.250	0.472	20	0.214	K.DGTNVEEAFQCIVK.N
R3/RRR3-19/2	1609.793	1610.741	-1213.312	0.430	1343.829	0.509	19	0.204	K.DGTNVEEAFQCIVK.N
R3/RRR3-14/2	1594.314	1594.754	-277.049	0.554	3033.214	0.613	27	0.567	R.VADHAGVALAGLTADGR.V
R3/RRR3-14/2	1594.259	1594.754	-311.848	0.543	2832.665	0.596	26	0.504	R.VADHAGVALAGLTADGR.V
R3/RRR3-14/2	1595.458	1594.754	-186.450	0.585	2807.933	0.580	26	0.490	R.VADHAGVALAGLTADGR.V
R3/RRR3-14/2	1711.341	1711.770	-251.665	0.522	2029.623	0.583	23	0.322	R.NQYDTDVTTWSPAGR.L
R3/RRR3-14/2	1712.291	1711.770	-280.842	0.595	2003.298	0.589	23	0.319	R.NQYDTDVTTWSPAGR.L
R3/RRR3-14/2	1711.188	1711.770	-927.554	0.547	1976.443	0.557	23	0.305	R.NQYDTDVTTWSPAGR.L
R3/RRR3-14/2	1444.024	1444.678	-1148.263	0.522	2147.870	0.436	19	0.297	R.LFQVEYAM*EAVK.Q
R3/RRR3-14/2	1443.534	1444.678	-1489.109	0.435	1909.995	0.378	19	0.245	R.LFQVEYAM*EAVK.Q
R3/RRR3-14/2	1378.096	1378.551	-330.912	0.456	1830.989	0.362	20	0.231	K.LTSSNCTVAIVGR.K
R3/RRR3-14/2	1444.212	1444.678	-323.145	0.503	1792.424	0.375	19	0.228	R.LFQVEYAM*EAVK.Q
R3/RRR3-14/2	1874.400	1874.043	191.088	0.548	1248.290	0.504	20	0.193	R.RFEGYNDYTPEQLIK.D
R3/RRR3-14/2	1378.077	1378.551	-345.043	0.442	1336.573	0.420	18	0.187	K.LTSSNCTVAIVGR.K
R3/RRR3-14/2	1378.052	1378.551	-362.996	0.417	1358.368	0.380	18	0.181	K.LTSSNCTVAIVGR.K
R3/RRR3-14/2	1428.218	1428.678	-323.328	0.403	1144.399	0.304	17	0.154	R.LFQVEYAMEAVK.Q
R3/RRR3-14/2	1873.316	1874.043	-924.597	0.488	809.463	0.456	17	0.153	R.RFEGYNDYTPEQLIK.D
R3/RRR3-14/2	1873.242	1874.043	-963.980	0.531	813.348	0.450	17	0.152	R.RFEGYNDYTPEQLIK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1444.184	1444.678	-342.820	0.405	645.074	0.330	15	0.139	R.LFQVEYAM*EAVK.Q
R3/RRR3-14/3	1503.657	1503.680	-15.448	0.410	778.863	0.474	26	0.113	K.DALSAIKETLQGEK.L
R3/RRR3-14/3	1503.586	1503.680	-62.474	0.454	592.466	0.473	23	0.109	K.DALSAIKETLQGEK.L
R3/RRR3-14/3	1503.751	1503.680	47.084	0.361	422.440	0.475	21	0.104	K.DALSAIKETLQGEK.L
R3/RRR3-15/2	1199.029	1198.305	-230.531	0.586	1477.193	0.459	17	0.211	R.TCYAQASQIR.Q
R3/RRR3-14/2	1776.999	1777.978	-1116.981	0.463	1329.226	0.546	20	0.210	K.NVLTNFWGM*SFTTDK.L
R3/RRR3-15/2	1197.983	1198.305	-269.161	0.560	1466.793	0.451	17	0.208	R.TCYAQASQIR.Q
R3/RRR3-14/2	1197.473	1198.305	-1533.850	0.513	1420.983	0.445	17	0.203	R.TCYAQASQIR.Q
R3/RRR3-15/2	1197.398	1198.305	-1596.934	0.490	1499.582	0.374	17	0.196	R.TCYAQASQIR.Q
R3/RRR3-14/2	1197.951	1198.305	-296.252	0.559	1258.494	0.469	16	0.191	R.TCYAQASQIR.Q
R3/RRR3-14/2	1580.324	1579.824	317.215	0.458	1097.952	0.529	21	0.187	K.ATSSIFPLQNVFVR.K
R3/RRR3-14/2	1579.286	1579.824	-977.036	0.447	856.616	0.560	19	0.174	K.ATSSIFPLQNVFVR.K
R3/RRR3-14/3	1354.405	1354.491	-63.480	0.474	1839.484	0.324	23	0.168	K.RTCYAQASQIR.Q
R3/RRR3-14/2	1580.383	1579.824	-280.111	0.448	795.555	0.537	19	0.168	K.ATSSIFPLQNVFVR.K
R3/RRR3-15/2	1579.435	1579.824	-247.295	0.424	897.632	0.428	20	0.159	K.ATSSIFPLQNVFVR.K
R3/RRR3-19/2	1579.487	1579.824	-214.226	0.407	892.772	0.422	19	0.157	K.ATSSIFPLQNVFVR.K
R3/RRR3-15/2	986.046	986.182	-139.021	0.400	734.984	0.454	13	0.157	R.LFCIGFTK.R
R3/RRR3-14/2	889.984	890.021	-41.768	0.399	676.793	0.470	12	0.156	K.APSVFNVR.N
R3/RRR3-14/2	889.819	890.021	-228.082	0.419	646.904	0.446	12	0.153	K.APSVFNVR.N
R3/RRR3-14/2	889.823	890.021	-223.541	0.369	668.210	0.456	12	0.153	K.APSVFNVR.N
R3/RRR3-19/2	1580.279	1579.824	288.790	0.421	814.584	0.407	19	0.153	K.ATSSIFPLQNVFVR.K
R3/RRR3-18/2	1580.187	1579.824	230.153	0.461	721.420	0.438	18	0.152	K.ATSSIFPLQNVFVR.K
R3/RRR3-15/2	1578.754	1579.824	-1315.573	0.282	835.137	0.404	19	0.150	K.ATSSIFPLQNVFVR.K
R3/RRR3-19/2	1579.428	1579.824	-251.908	0.394	733.929	0.408	18	0.149	K.ATSSIFPLQNVFVR.K
R3/RRR3-18/2	1579.878	1579.824	33.974	0.444	798.955	0.380	19	0.149	K.ATSSIFPLQNVFVR.K
R3/RRR3-16/2	1579.672	1579.824	-96.854	0.399	585.364	0.453	16	0.148	K.ATSSIFPLQNVFVR.K
R3/RRR3-13/2	1579.226	1579.824	-1014.908	0.374	599.721	0.430	16	0.146	K.ATSSIFPLQNVFVR.K
R3/RRR3-16/2	1579.319	1579.824	-955.851	0.333	749.089	0.377	18	0.146	K.ATSSIFPLQNVFVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	889.788	890.021	-262.766	0.302	662.334	0.387	12	0.144	K.APSVFNVR.N
R3/RRR3-14/2	986.005	986.182	-180.377	0.374	593.423	0.376	13	0.144	-.LFCIGFTK.-
R3/RRR3-14/2	1578.720	1579.824	-1337.161	0.292	822.161	0.333	19	0.144	K.ATSSIFPLQNVFVR.K
R3/RRR3-16/2	1579.512	1579.824	-198.409	0.355	674.983	0.372	17	0.144	K.ATSSIFPLQNVFVR.K
R3/RRR3-14/2	985.355	986.182	-1860.565	0.327	622.141	0.336	13	0.142	R.LFCIGFTK.R
R3/RRR3-14/2	985.786	986.182	-403.359	0.354	580.883	0.334	13	0.140	-.LFCIGFTK.-
R3/RRR3-18/2	1579.141	1579.824	-1069.158	0.299	618.567	0.315	17	0.138	K.ATSSIFPLQNVFVR.K
R3/RRR3-15/2	986.045	986.182	-140.015	0.368	688.956	0.277	13	0.138	-.LFCIGFTK.-
R3/RRR3-26/2	890.129	890.021	121.510	0.266	361.839	0.351	9	0.137	K.APSVFNVR.N
R3/RRR3-17/2	1579.363	1579.824	-293.006	0.266	435.810	0.328	14	0.136	K.ATSSIFPLQNVFVR.K
R3/RRR3-2/2	1579.178	1579.824	-1045.641	0.286	562.328	0.235	15	0.133	K.ATSSIFPLQNVFVR.K
R3/RRR3-15/2	889.353	890.021	-1881.195	0.247	267.823	0.369	8	0.105	-.APSVFNVR.-
R3/RRR3-4/2	1700.278	1698.943	198.199	0.554	1832.189	0.585	21	0.291	R.LIWSTQFENFLATK.W
R3/RRR3-4/2	1374.272	1374.524	-184.029	0.491	1311.917	0.333	17	0.170	R.DWLSAYWTGFK.S
R3/RRR3-4/2	1778.274	1779.023	-986.268	0.491	702.386	0.421	18	0.148	R.VEQLCPFPYDLIQR.E
R3/RRR3-4/2	983.564	984.178	-1646.171	0.469	861.400	0.345	13	0.147	R.LNVLGNVVR.K
R3/RRR3-4/2	1779.328	1779.023	171.984	0.536	690.346	0.412	18	0.146	R.VEQLCPFPYDLIQR.E
R3/RRR3-4/2	1215.483	1216.278	-1481.610	0.450	826.973	0.345	15	0.146	K.VYYELDEER.K
R3/RRR3-4/2	1778.482	1779.023	-868.844	0.470	720.888	0.366	18	0.143	R.VEQLCPFPYDLIQR.E
R3/RRR3-4/2	983.646	984.178	-1562.389	0.385	830.688	0.316	13	0.143	R.LNVLGNVVR.K
R3/RRR3-1/2	1780.362	1779.023	191.415	0.463	483.993	0.416	15	0.141	R.VEQLCPFPYDLIQR.E
R3/RRR3-4/2	984.025	984.178	-156.291	0.449	803.149	0.294	13	0.140	R.LNVLGNVVR.K
R3/RRR3-4/2	1779.792	1779.023	-130.129	0.443	576.376	0.334	16	0.137	R.VEQLCPFPYDLIQR.E
R3/RRR3-4/3	1708.999	1708.964	20.640	0.409	822.760	0.537	28	0.125	R.AADLGVENIVIGM*PHR.G
R3/RRR3-4/3	1709.159	1708.964	114.445	0.417	815.212	0.498	28	0.118	R.AADLGVENIVIGM*PHR.G
R3/RRR3-4/3	1013.287	1013.323	-35.230	0.489	1238.217	0.359	19	0.118	R.KPLIVM*APK.N
R3/RRR3-4/3	1709.020	1708.964	32.675	0.323	711.765	0.396	25	0.097	-.AADLGVENIVIGM*PHR.-
R3/RRR3-4/2	1202.090	1202.388	-248.584	0.516	1449.788	0.553	19	0.230	R.HALSAISAIYR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1201.538	1202.388	-1544.048	0.463	1355.593	0.569	18	0.221	R.HALSAISAIYR.L
R3/RRR3-4/2	1201.274	1202.388	-1764.744	0.368	1597.283	0.442	19	0.220	R.HALSAISAIYR.L
R3/RRR3-4/2	1221.096	1221.388	-239.400	0.581	1547.785	0.428	17	0.209	R.AVAYLLTNAER.V
R3/RRR3-4/2	1221.059	1221.388	-269.890	0.512	1556.589	0.344	17	0.193	R.AVAYLLTNAER.V
R3/RRR3-4/2	1162.341	1163.257	-1653.421	0.331	1462.189	0.272	17	0.173	R.LLCNTGDDVR.K
R3/RRR3-4/2	1220.524	1221.388	-1531.666	0.400	1435.356	0.274	17	0.171	R.AVAYLLTNAER.V
R3/RRR3-4/2	1162.998	1163.257	-222.935	0.440	1243.638	0.321	16	0.164	R.LLCNTGDDVR.K
R3/RRR3-4/3	1819.885	1819.009	-68.267	0.541	1300.452	0.528	29	0.163	K.LVDRPQNYTLAPESSK.Q
R3/RRR3-4/2	1169.265	1169.354	-76.399	0.467	759.690	0.378	14	0.149	R.LIDTFYQIR.A
R3/RRR3-4/2	1168.659	1169.354	-1454.959	0.421	779.091	0.350	14	0.146	R.LIDTFYQIR.A
R3/RRR3-4/2	1398.251	1398.509	-185.076	0.464	653.442	0.419	15	0.145	R.NNLQHPNEYIR.G
R3/RRR3-8/2	1221.355	1221.388	-27.027	0.295	1030.519	0.276	15	0.144	R.AVAYLLTNAER.V
R3/RRR3-4/2	1169.206	1169.354	-127.505	0.404	720.888	0.345	14	0.144	R.LIDTFYQIR.A
R3/RRR3-4/2	1290.934	1291.430	-385.501	0.405	796.906	0.301	14	0.138	R.LLCNTGDDVRK.V
R3/RRR3-4/3	1818.866	1819.009	-78.470	0.510	1234.035	0.452	29	0.138	K.LVDRPQNYTLAPESSK.Q
R3/RRR3-4/2	1291.058	1291.430	-288.828	0.389	803.544	0.298	14	0.138	R.LLCNTGDDVRK.V
R3/RRR3-4/2	1290.966	1291.430	-360.643	0.419	687.368	0.344	13	0.138	-.LLCNTGDDVRK.-
R3/RRR3-4/3	1819.582	1819.009	-235.322	0.525	913.251	0.503	26	0.127	K.LVDRPQNYTLAPESSK.Q
R3/RRR3-1/3	1819.370	1819.009	199.451	0.426	621.004	0.369	21	0.093	-.LVDRPQNYTLAPESSK.-
R3/RRR3-2/3	1818.929	1819.009	-43.835	0.356	500.878	0.340	20	0.076	-.LVDRPQNYTLAPESSK.-
R3/RRR3-18/2	1874.529	1875.067	-823.020	0.538	1824.245	0.540	25	0.274	K.LAEEIEKGASSVEGVEVK.L
R3/RRR3-18/2	1242.071	1241.401	-266.237	0.537	1770.526	0.531	18	0.264	K.AFM*DATGGLWR.T
R3/RRR3-18/2	1242.071	1241.401	-266.336	0.548	1725.806	0.535	18	0.259	K.AFM*DATGGLWR.T
R3/RRR3-18/2	1242.155	1241.401	-198.602	0.550	1669.623	0.563	18	0.258	K.AFM*DATGGLWR.T
R3/RRR3-18/2	1875.582	1875.067	-259.459	0.560	1677.086	0.548	25	0.254	K.LAEEIEKGASSVEGVEVK.L
R3/RRR3-18/2	1225.034	1225.402	-301.297	0.400	1834.301	0.386	18	0.236	K.AFMDATGGLWR.T
R3/RRR3-18/2	1699.822	1699.889	-39.444	0.514	1485.136	0.569	19	0.232	R.VATELELQQAFHQGK.Y
R3/RRR3-18/2	1031.945	1031.277	-322.672	0.447	1482.368	0.472	15	0.214	R.FGMMAAQFK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1240.937	1241.401	-375.012	0.482	1339.996	0.490	18	0.203	K.AFM*DATGGLWR.T
R3/RRR3-18/2	1744.459	1744.966	-866.769	0.533	1057.489	0.617	24	0.202	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1699.317	1699.889	-927.693	0.481	1205.261	0.578	18	0.202	R.VATELELQQAFHQGK.Y
R3/RRR3-18/2	1473.141	1473.486	-234.677	0.408	1142.497	0.596	22	0.199	K.GGSPYGSGTFAGDGSR.V
R3/RRR3-18/2	1744.526	1744.966	-253.404	0.561	974.575	0.595	23	0.191	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1030.978	1031.277	-291.029	0.347	1419.769	0.390	15	0.190	R.FGMMAAQFK.A
R3/RRR3-18/2	1473.103	1473.486	-260.698	0.410	1046.078	0.548	23	0.184	K.GGSPYGSGTFAGDGSR.V
R3/RRR3-18/2	1744.379	1744.966	-912.783	0.514	909.074	0.576	23	0.183	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1472.995	1473.486	-334.695	0.448	1000.945	0.561	22	0.183	K.GGSPYGSGTFAGDGSR.V
R3/RRR3-18/2	1698.654	1699.889	-1319.803	0.443	1083.435	0.522	18	0.180	R.VATELELQQAFHQGK.Y
R3/RRR3-18/2	1225.218	1225.402	-150.656	0.386	1218.031	0.435	16	0.179	K.AFMDATGGLWR.T
R3/RRR3-18/2	1746.408	1744.966	253.957	0.485	1024.093	0.467	23	0.172	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1030.929	1031.277	-338.073	0.301	1425.746	0.273	15	0.170	R.FGMMAAQFK.A
R3/RRR3-18/2	1063.006	1063.276	-254.837	0.473	1058.417	0.428	14	0.170	R.FGM*M*AAQFK.A
R3/RRR3-18/2	1225.032	1225.402	-302.596	0.425	1273.728	0.335	17	0.168	K.AFMDATGGLWR.T
R3/RRR3-18/2	1062.887	1063.276	-366.717	0.467	953.197	0.431	14	0.164	R.FGM*M*AAQFK.A
R3/RRR3-18/2	1744.966	1744.966	-0.464	0.448	838.844	0.491	19	0.162	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1745.197	1744.966	132.553	0.443	775.546	0.434	21	0.154	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1746.486	1744.966	-275.623	0.459	677.210	0.438	20	0.151	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1062.277	1063.276	-1886.726	0.370	963.122	0.312	14	0.149	R.FGM*M*AAQFK.A
R3/RRR3-16/2	1745.416	1744.966	258.240	0.321	281.058	0.365	12	0.136	K.LWQVPETLSDDVLTK.M
R3/RRR3-18/2	1046.896	1047.276	-364.590	0.333	684.141	0.143	13	0.131	R.FGMM*AAQFK.A
R3/RRR3-18/2	1242.309	1241.401	-74.102	0.221	649.216	0.186	14	0.131	K.AFM*DATGGLWR.T
R3/RRR3-18/3	1744.760	1744.966	-118.609	0.402	918.580	0.354	25	0.099	K.LWQVPETLSDDVLTK.M
R3/RRR3-3/2	1218.035	1218.296	-214.470	0.432	1771.339	0.301	19	0.211	R.EGETAAEILER.I
R3/RRR3-3/2	1243.243	1243.349	-85.247	0.457	1078.311	0.460	18	0.174	K.VELSNPDAELR.L
R3/RRR3-2/2	1566.406	1565.711	-195.379	0.430	1010.734	0.380	15	0.154	K.IENINDQYWTLR.A
R3/RRR3-3/2	1218.040	1218.296	-210.549	0.405	1091.809	0.311	16	0.153	R.EGETAAEILER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1158.998	1159.360	-313.181	0.412	1080.768	0.291	15	0.149	K.AEAHLYTIIK.V
R3/RRR3-3/2	1247.309	1247.339	-23.913	0.413	375.361	0.455	13	0.145	K.LHTYDDVVER.V
R3/RRR3-3/2	1306.073	1306.445	-285.414	0.346	794.749	0.321	17	0.141	K.NSTISDVITDLK.T
R3/RRR3-3/2	1246.375	1247.339	-1580.352	0.248	168.384	0.286	11	0.133	-.LHTYDDVVER.-
R3/RRR3-3/2	1217.187	1218.296	-1737.548	0.249	891.916	0.210	15	0.133	R.EGETAAEILER.I
R3/RRR3-3/2	1305.972	1306.445	-363.156	0.251	567.847	0.315	15	0.132	K.NSTISDVITDLK.T
R3/RRR3-3/3	1737.715	1736.908	-111.445	0.473	1211.050	0.434	26	0.132	R.YPDVPSFLEYVHNR.Q
R3/RRR3-3/3	1737.913	1736.908	2.908	0.460	868.146	0.508	24	0.123	R.YPDVPSFLEYVHNR.Q
R3/RRR3-8/2	1671.413	1671.791	-226.910	0.589	1868.619	0.450	20	0.257	R.NYLHYNLYDQAEK.L
R3/RRR3-8/2	1645.179	1644.762	254.029	0.477	1660.594	0.424	23	0.223	R.LDSDNPVADAESIVAK.A
R3/RRR3-8/2	963.015	963.112	-101.598	0.529	1451.666	0.398	13	0.196	R.IGDLELFR.A
R3/RRR3-8/2	963.021	963.112	-94.859	0.522	1308.494	0.367	13	0.177	R.IGDLELFR.A
R3/RRR3-8/2	962.998	963.112	-118.764	0.520	1328.905	0.357	13	0.177	R.IGDLELFR.A
R3/RRR3-8/2	1182.158	1182.305	-124.762	0.475	925.556	0.511	15	0.172	R.TIQLEYTDAK.E
R3/RRR3-8/2	1643.571	1644.762	-1337.291	0.352	1235.153	0.309	20	0.158	R.LDSDNPVADAESIVAK.A
R3/RRR3-8/2	1001.834	1002.062	-228.795	0.469	752.398	0.402	15	0.153	K.FASTFSADR.T
R3/RRR3-8/2	1182.254	1182.305	-43.145	0.312	820.446	0.404	14	0.148	R.TIQLEYTDAK.E
R3/RRR3-8/2	1001.183	1002.062	-1882.819	0.267	560.850	0.365	14	0.139	K.FASTFSADR.T
R3/RRR3-8/2	1001.892	1002.062	-170.368	0.330	622.822	0.264	14	0.136	K.FASTFSADR.T
R3/RRR3-8/3	1424.678	1424.497	128.031	0.492	771.306	0.450	21	0.112	R.FEAHSNQQFCR.Y
R3/RRR3-8/3	1424.532	1424.497	24.648	0.482	654.819	0.404	19	0.103	R.FEAHSNQQFCR.Y
R3/RRR3-8/3	1424.995	1424.497	350.838	0.473	434.432	0.404	19	0.100	-.FEAHSNQQFCR.-
R3/RRR3-15/2	1410.098	1410.578	-341.727	0.513	2092.855	0.468	20	0.298	R.SVQM*EGLTWGASK.L
R3/RRR3-15/2	1394.204	1394.579	-269.568	0.432	1967.550	0.503	20	0.287	R.SVQMEGLTWGASK.L
R3/RRR3-15/2	1511.286	1511.659	-247.631	0.516	1550.315	0.572	22	0.245	K.TYVSGNAISKDDIK.V
R3/RRR3-15/2	1511.181	1511.659	-317.001	0.507	1560.693	0.528	21	0.235	K.TYVSGNAISKDDIK.V
R3/RRR3-15/2	1411.061	1410.578	343.549	0.547	1585.676	0.487	20	0.228	R.SVQM*EGLTWGASK.L
R3/RRR3-15/2	1879.563	1880.095	-817.819	0.566	1205.997	0.692	30	0.228	K.AVGVNLPGGGAASSAAAAAPAAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1879.434	1880.095	-886.343	0.532	1156.344	0.676	30	0.219	K.AVGVNLPGGGAASSAAAAAPAAK.D
R3/RRR3-15/2	1879.516	1880.095	-842.659	0.523	1126.726	0.655	29	0.210	K.AVGVNLPGGGAASSAAAAAPAAK.D
R3/RRR3-15/3	1880.108	1880.095	6.726	0.488	1484.591	0.606	39	0.210	K.AVGVNLPGGGAASSAAAAAPAAK.D
R3/RRR3-15/2	1410.225	1410.578	-251.402	0.494	1685.875	0.353	20	0.209	R.SVQM*EGLTWGASK.L
R3/RRR3-15/2	1879.459	1880.095	-873.303	0.519	1056.994	0.668	29	0.206	K.AVGVNLPGGGAASSAAAAAPAAK.D
R3/RRR3-15/2	1511.213	1511.659	-296.092	0.502	1184.393	0.544	20	0.197	K.TYVSGNAISKDDIK.V
R3/RRR3-16/2	1879.606	1880.095	-260.793	0.512	903.503	0.641	26	0.186	K.AVGVNLPGGGAASSAAAAAPAAK.D
R3/RRR3-15/2	1829.304	1830.079	-973.413	0.383	620.523	0.409	21	0.142	K.VFAAVPSKPGAEFPNAAR.W
R3/RRR3-15/2	1996.935	1995.197	-131.675	0.401	550.937	0.456	18	0.140	K.SSVLLDVKPWDDETDM*K.K
R3/RRR3-15/2	1829.495	1830.079	-868.844	0.425	586.053	0.383	21	0.140	K.VFAAVPSKPGAEFPNAAR.W
R3/RRR3-15/2	1829.237	1830.079	-1010.329	0.386	551.283	0.368	20	0.137	K.VFAAVPSKPGAEFPNAAR.W
R3/RRR3-15/3	1879.856	1880.095	-127.801	0.249	650.831	0.220	28	0.080	K.AVGVNLPGGGAASSAAAAAPAAK.D
R3/RRR3-10/2	1571.422	1571.806	-244.855	0.512	1959.398	0.514	23	0.288	R.ISITGAGGFIASHIAR.R
R3/RRR3-10/2	1572.328	1571.806	-304.907	0.530	1493.269	0.560	20	0.231	R.ISITGAGGFIASHIAR.R
R3/RRR3-1/2	1572.693	1571.806	-72.060	0.225	793.670	0.264	16	0.131	R.ISITGAGGFIASHIAR.R
R3/RRR3-9/2	1784.364	1784.047	178.292	0.602	1874.709	0.496	23	0.268	R.LINSDEVQSVVKPINK.E
R3/RRR3-9/2	1784.288	1784.047	135.344	0.566	1824.976	0.480	23	0.257	R.LINSDEVQSVVKPINK.E
R3/RRR3-9/2	1784.441	1784.047	221.579	0.561	1534.980	0.492	21	0.220	R.LINSDEVQSVVKPINK.E
R3/RRR3-10/2	1794.608	1795.160	-866.972	0.351	1227.045	0.406	21	0.171	R.IAVASALAATAVPSLVLAR.G
R3/RRR3-10/2	1794.509	1795.160	-922.558	0.392	1249.796	0.389	22	0.171	R.IAVASALAATAVPSLVLAR.G
R3/RRR3-8/2	1539.877	1538.901	-15.695	0.553	3082.772	0.580	26	0.572	R.M*AAFIGAMAIADLVK.T
R3/RRR3-8/2	1313.052	1313.356	-232.239	0.520	1497.611	0.531	18	0.229	R.GASEHVLDEAER.S
R3/RRR3-8/2	1312.978	1313.356	-288.296	0.479	1387.895	0.521	17	0.212	R.GASEHVLDEAER.S
R3/RRR3-7/3	1930.292	1930.103	98.396	0.465	1837.287	0.445	33	0.208	R.SLHDALCVLSQTVNDTR.V
R3/RRR3-8/2	1319.191	1319.487	-224.847	0.381	1270.998	0.376	19	0.174	R.SVTVTNDGATILK.S
R3/RRR3-8/2	1320.136	1319.487	-266.607	0.436	1064.662	0.410	18	0.164	R.SVTVTNDGATILK.S
R3/RRR3-8/2	1319.103	1319.487	-291.877	0.380	1187.848	0.337	19	0.162	R.SVTVTNDGATILK.S
R3/RRR3-8/2	1004.130	1004.081	48.699	0.236	814.409	0.403	13	0.144	K.SHAIDAFSR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1004.104	1004.081	22.362	0.236	505.911	0.318	11	0.132	K.SHAIDAFSR.A
R3/RRR3-8/3	1488.619	1488.625	-4.048	0.489	953.346	0.473	23	0.122	R.VLKDDAVEEKGER.A
R3/RRR3-7/3	1929.607	1930.103	-257.532	0.354	907.012	0.208	26	0.082	R.SLHDALCVLSQTVNDTR.V
R3/RRR3-24/2	1369.260	1369.592	-243.003	0.541	2209.706	0.509	19	0.330	R.LVVIVDVVDQNR.A
R3/RRR3-23/2	1370.111	1369.592	-351.785	0.578	2137.014	0.538	19	0.326	R.LVVIVDVVDQNR.A
R3/RRR3-24/2	1369.434	1369.592	-116.015	0.590	2139.339	0.525	19	0.321	R.LVVIVDVVDQNR.A
R3/RRR3-23/2	1369.376	1369.592	-158.132	0.534	2023.865	0.533	19	0.305	R.LVVIVDVVDQNR.A
R3/RRR3-24/2	1368.655	1369.592	-1419.298	0.430	1855.085	0.421	18	0.247	R.LVVIVDVVDQNR.A
R3/RRR3-24/2	1356.209	1355.524	-232.703	0.499	1206.458	0.577	17	0.205	R.VALVNYGKDYGR.L
R3/RRR3-23/2	1355.027	1355.524	-367.719	0.453	1115.212	0.585	17	0.197	R.VALVNYGKDYGR.L
R3/RRR3-24/2	1354.732	1355.524	-1326.246	0.446	1211.771	0.494	18	0.190	R.VALVNYGKDYGR.L
R3/RRR3-23/2	1355.087	1355.524	-323.249	0.462	1264.684	0.460	18	0.189	R.VALVNYGKDYGR.L
R3/RRR3-23/2	1354.896	1355.524	-1205.176	0.416	1114.681	0.530	17	0.187	R.VALVNYGKDYGR.L
R3/RRR3-24/2	1356.433	1355.524	-66.940	0.430	1025.849	0.513	16	0.177	R.VALVNYGKDYGR.L
R3/RRR3-24/3	1369.519	1369.592	-53.124	0.462	1514.452	0.398	25	0.149	R.LVVIVDVVDQNR.A
R3/RRR3-23/2	863.439	864.024	-1840.663	0.325	574.834	0.461	12	0.149	R.VALVNYGK.D
R3/RRR3-23/2	863.907	864.024	-135.575	0.340	525.575	0.429	12	0.147	R.VALVNYGK.D
R3/RRR3-23/3	1370.385	1369.592	-151.235	0.431	1396.859	0.432	24	0.146	R.LVVIVDVVDQNR.A
R3/RRR3-24/2	863.402	864.024	-1884.278	0.301	554.937	0.441	12	0.146	R.VALVNYGK.D
R3/RRR3-24/2	863.912	864.024	-130.472	0.332	570.636	0.391	13	0.145	R.VALVNYGK.D
R3/RRR3-24/2	1260.046	1259.517	-375.226	0.464	770.021	0.314	17	0.142	R.LSLTDIKIDIK.R
R3/RRR3-24/2	1260.232	1259.517	-227.205	0.459	810.372	0.344	15	0.141	-.LSLTDIKIDIK.-
R3/RRR3-23/2	1102.553	1103.275	-1566.533	0.337	801.894	0.304	15	0.141	R.ALVDAPDM*VR.C
R3/RRR3-23/2	1368.785	1369.592	-1323.990	0.316	661.172	0.382	14	0.141	R.LVVIVDVVDQNR.A
R3/RRR3-23/2	1102.879	1103.275	-359.999	0.375	602.867	0.350	13	0.140	R.ALVDAPDM*VR.C
R3/RRR3-24/2	1259.141	1259.517	-299.553	0.424	870.614	0.271	17	0.140	R.LSLTDIKIDIK.R
R3/RRR3-24/2	1086.949	1087.275	-301.275	0.323	563.735	0.386	12	0.139	-.ALVDAPDMVR.-
R3/RRR3-23/2	863.382	864.024	-1907.010	0.270	489.867	0.356	11	0.139	R.VALVNYGK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1102.201	1103.275	-1886.843	0.324	796.884	0.253	14	0.136	R.ALVDAPDM*VR.C
R3/RRR3-13/2	1809.388	1810.238	-1025.405	0.513	1928.172	0.543	25	0.291	K.VAILGASGGIGQPLALLMK.M
R3/RRR3-13/2	1185.772	1186.427	-1399.370	0.486	1539.412	0.534	19	0.236	R.LLGVTTLDVVR.A
R3/RRR3-13/2	1457.252	1457.635	-263.639	0.494	1482.625	0.532	22	0.225	K.AGAGSATLSM*AYAAAK.F
R3/RRR3-13/2	1348.291	1347.502	-156.700	0.566	1530.128	0.491	18	0.222	R.DDLFNINAGIVR.T
R3/RRR3-13/2	1457.035	1457.635	-1101.386	0.484	1359.510	0.573	21	0.219	K.AGAGSATLSM*AYAAAK.F
R3/RRR3-13/2	1347.278	1347.502	-166.815	0.508	1779.303	0.338	19	0.217	R.DDLFNINAGIVR.T
R3/RRR3-13/2	1348.210	1347.502	-216.829	0.497	1473.915	0.442	18	0.206	R.DDLFNINAGIVR.T
R3/RRR3-13/2	1187.317	1186.427	-92.871	0.557	1356.067	0.480	19	0.204	R.LLGVTTLDVVR.A
R3/RRR3-13/2	1457.290	1457.635	-237.419	0.478	1298.719	0.532	21	0.203	K.AGAGSATLSM*AYAAAK.F
R3/RRR3-13/2	1443.072	1441.635	303.267	0.525	1020.792	0.657	21	0.202	K.AGAGSATLSMAYAAAK.F
R3/RRR3-13/2	1186.218	1186.427	-176.665	0.478	1415.403	0.428	19	0.199	R.LLGVTTLDVVR.A
R3/RRR3-13/3	1824.951	1826.237	-1256.399	0.363	1358.715	0.486	29	0.159	K.VAILGASGGIGQPLALLM*K.M
R3/RRR3-13/2	1245.026	1245.365	-272.463	0.459	810.516	0.437	19	0.158	R.IQNGGTEVVEAK.A
R3/RRR3-13/2	1244.495	1245.365	-1506.690	0.444	794.703	0.443	19	0.158	R.IQNGGTEVVEAK.A
R3/RRR3-13/3	1825.859	1826.237	-207.741	0.412	1350.141	0.475	30	0.155	K.VAILGASGGIGQPLALLM*K.M
R3/RRR3-13/2	1245.419	1245.365	44.278	0.481	554.310	0.479	18	0.155	R.IQNGGTEVVEAK.A
R3/RRR3-12/2	1245.234	1245.365	-104.775	0.476	749.036	0.423	18	0.154	R.IQNGGTEVVEAK.A
R3/RRR3-13/2	1245.038	1245.365	-263.315	0.465	704.375	0.425	18	0.153	R.IQNGGTEVVEAK.A
R3/RRR3-13/2	1826.379	1826.237	77.739	0.402	873.155	0.448	18	0.151	K.VAILGASGGIGQPLALLM*K.M
R3/RRR3-13/2	1502.304	1502.697	-262.314	0.325	953.896	0.378	16	0.149	R.ANTFVAEVLGLDPR.D
R3/RRR3-13/2	1245.398	1245.365	26.779	0.385	359.826	0.395	15	0.144	R.IQNGGTEVVEAK.A
R3/RRR3-13/2	1245.951	1245.365	-332.892	0.468	486.768	0.349	17	0.143	R.IQNGGTEVVEAK.A
R3/RRR3-13/2	1501.983	1502.697	-1144.543	0.263	961.979	0.318	16	0.142	R.ANTFVAEVLGLDPR.D
R3/RRR3-13/3	1502.264	1502.697	-289.144	0.421	1118.862	0.408	26	0.119	R.ANTFVAEVLGLDPR.D
R3/RRR3-13/3	1502.604	1502.697	-62.230	0.400	871.500	0.299	23	0.092	R.ANTFVAEVLGLDPR.D
R3/RRR3-10/2	1694.258	1694.909	-977.436	0.536	2343.654	0.503	22	0.356	R.IVTFNSDWQLLTEK.E
R3/RRR3-10/2	1694.444	1694.909	-275.201	0.545	2263.105	0.506	22	0.341	R.IVTFNSDWQLLTEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1928.575	1929.246	-869.155	0.508	1880.365	0.604	27	0.302	K.TAPINIGLAAFELIDEIK.A
R3/RRR3-10/2	1695.317	1694.909	241.244	0.605	1951.984	0.537	20	0.292	R.IVTFNSDWQLLTEK.E
R3/RRR3-10/2	1742.668	1742.950	-162.620	0.491	1906.029	0.455	24	0.265	R.DEDPAAVAATIPSFLPK.L
R3/RRR3-10/2	1928.617	1929.246	-847.298	0.501	1547.575	0.593	25	0.247	K.TAPINIGLAAFELIDEIK.A
R3/RRR3-10/2	1928.669	1929.246	-819.850	0.507	1516.982	0.585	25	0.242	K.TAPINIGLAAFELIDEIK.A
R3/RRR3-10/3	1929.339	1929.246	48.406	0.441	1607.798	0.358	32	0.153	K.TAPINIGLAAFELIDEIK.A
R3/RRR3-10/2	1455.386	1455.683	-204.815	0.364	680.372	0.475	20	0.153	R.LTAPPEQILPGYR.S
R3/RRR3-10/2	1607.196	1607.786	-992.598	0.396	966.480	0.349	20	0.151	R.DLPDSTFTISELIR.N
R3/RRR3-10/2	1607.223	1607.786	-975.822	0.364	1022.832	0.320	21	0.150	R.DLPDSTFTISELIR.N
R3/RRR3-10/2	1607.209	1607.786	-984.210	0.373	939.047	0.356	20	0.150	R.DLPDSTFTISELIR.N
R3/RRR3-10/2	1455.304	1455.683	-261.026	0.356	550.551	0.477	17	0.147	R.LTAPPEQILPGYR.S
R3/RRR3-10/2	1455.175	1455.683	-1039.585	0.331	458.802	0.461	17	0.144	R.LTAPPEQILPGYR.S
R3/RRR3-10/2	1116.945	1117.231	-257.010	0.342	542.070	0.424	15	0.143	-.SCPGVENVVR.-
R3/RRR3-10/2	1116.890	1117.231	-306.353	0.290	469.478	0.359	15	0.139	K.SCPGVENVVR.Y
R3/RRR3-10/2	1116.544	1117.231	-1516.291	0.263	343.099	0.384	13	0.137	K.SCPGVENVVR.Y
R3/RRR3-10/3	1928.455	1929.246	-931.277	0.428	781.398	0.458	28	0.111	K.TAPINIGLAAFELIDEIK.A
R3/RRR3-10/3	1929.103	1929.246	-74.303	0.401	957.887	0.364	27	0.104	K.TAPINIGLAAFELIDEIK.A
R3/RRR3-9/2	1136.980	1136.323	-302.447	0.469	1260.307	0.504	15	0.196	K.ALIAAEYTGVK.V
R3/RRR3-9/2	1135.954	1136.323	-326.002	0.342	1159.598	0.394	15	0.167	K.ALIAAEYTGVK.V
R3/RRR3-9/2	1336.068	1336.434	-274.974	0.491	926.366	0.470	16	0.166	K.SFTSEFPHVER.Y
R3/RRR3-9/2	1336.124	1336.434	-232.627	0.483	847.278	0.474	15	0.161	K.SFTSEFPHVER.Y
R3/RRR3-9/2	1136.029	1136.323	-259.159	0.324	1153.312	0.348	15	0.160	K.ALIAAEYTGVK.V
R3/RRR3-9/2	1335.287	1336.434	-1613.120	0.370	892.410	0.378	16	0.151	K.SFTSEFPHVER.Y
R3/RRR3-8/2	1531.365	1531.821	-298.991	0.487	2425.099	0.539	25	0.386	K.ALGVDILTGFGAIVGK.Q
R3/RRR3-8/2	1530.989	1531.821	-1200.511	0.352	2126.353	0.503	23	0.314	K.ALGVDILTGFGAIVGK.Q
R3/RRR3-8/2	1413.212	1413.605	-279.024	0.512	2048.056	0.452	20	0.286	K.GLGLENINVVTQR.G
R3/RRR3-8/2	1413.354	1413.605	-177.814	0.534	2014.813	0.468	20	0.285	K.GLGLENINVVTQR.G
R3/RRR3-8/2	1530.821	1531.821	-1310.697	0.407	1860.032	0.497	23	0.268	K.ALGVDILTGFGAIVGK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1457.366	1456.754	-267.126	0.443	1380.089	0.463	22	0.201	R.NIIIATGSVPFVPK.G
R3/RRR3-8/3	1426.210	1426.640	-302.631	0.496	1891.161	0.358	25	0.187	K.DGKPVQIELIDAK.T
R3/RRR3-8/2	1378.823	1379.500	-1220.225	0.427	1037.437	0.504	17	0.175	K.SLGLQVSSPGYDR.Q
R3/RRR3-8/2	1379.228	1379.500	-198.104	0.454	810.170	0.514	17	0.163	K.SLGLQVSSPGYDR.Q
R3/RRR3-8/2	1413.130	1413.605	-336.657	0.419	832.566	0.461	16	0.156	K.GLGLENINVVTQR.G
R3/RRR3-8/2	1426.230	1426.640	-288.753	0.382	717.478	0.461	17	0.151	K.DGKPVQIELIDAK.T
R3/RRR3-8/3	1426.821	1426.640	127.281	0.527	1618.417	0.346	24	0.149	K.DGKPVQIELIDAK.T
R3/RRR3-8/2	1457.369	1456.754	-264.941	0.436	940.810	0.331	18	0.146	R.NIIIATGSVPFVPK.G
R3/RRR3-8/2	1456.318	1456.754	-300.443	0.369	1077.451	0.236	18	0.141	R.NIIIATGSVPFVPK.G
R3/RRR3-8/2	1378.466	1379.500	-1480.520	0.328	519.267	0.421	14	0.139	K.SLGLQVSSPGYDR.Q
R3/RRR3-8/2	1426.107	1426.640	-1078.031	0.355	695.002	0.327	18	0.139	K.DGKPVQIELIDAK.T
R3/RRR3-8/3	1426.806	1426.640	116.470	0.481	1500.258	0.342	23	0.137	K.DGKPVQIELIDAK.T
R3/RRR3-8/2	1466.509	1467.566	-1406.831	0.204	921.268	0.397	20	0.112	K.VNSGVSHSVNEPVAA.-
R3/RRR3-8/2	1467.055	1467.566	-1033.086	0.337	826.403	0.453	19	0.086	K.VNSGVSHSVNEPVAA.-
R3/RRR3-24/3	1721.218	1721.810	-927.598	0.587	2879.618	0.518	32	0.452	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1721.029	1721.810	-1038.148	0.572	2647.919	0.540	31	0.404	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1721.367	1721.810	-258.315	0.596	2544.895	0.529	31	0.371	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1721.527	1721.810	-164.625	0.607	2303.236	0.490	29	0.302	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1721.368	1721.810	-257.248	0.576	2019.081	0.551	28	0.273	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1637.797	1637.818	-12.912	0.507	2008.677	0.445	33	0.226	R.FDVGVKEIESWTAR.L
R3/RRR3-24/3	1637.977	1637.818	97.867	0.547	2043.174	0.430	33	0.226	R.FDVGVKEIESWTAR.L
R3/RRR3-24/3	1722.351	1721.810	-267.053	0.492	1754.677	0.513	26	0.218	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1722.640	1721.810	-98.988	0.493	1870.772	0.464	28	0.217	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1721.272	1721.810	-895.880	0.553	1843.809	0.478	28	0.216	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/2	1637.353	1637.818	-284.498	0.501	1023.143	0.492	21	0.176	R.FDVGVKEIESWTAR.L
R3/RRR3-24/2	1638.312	1637.818	302.400	0.544	883.166	0.544	21	0.176	R.FDVGVKEIESWTAR.L
R3/RRR3-24/2	1638.325	1637.818	-301.517	0.584	840.128	0.550	21	0.174	R.FDVGVKEIESWTAR.L
R3/RRR3-24/3	1722.944	1721.810	77.869	0.534	1434.235	0.506	25	0.172	K.HGYIGEFEFVDDHR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/3	1637.285	1637.818	-939.144	0.446	1473.740	0.465	27	0.164	R.FDVGVKEIESWTAR.L
R3/RRR3-24/2	958.493	959.122	-1704.174	0.364	964.238	0.367	15	0.156	R.VSVLNDALK.T
R3/RRR3-24/2	958.901	959.122	-231.506	0.369	1012.702	0.325	15	0.153	R.VSVLNDALK.T
R3/RRR3-23/2	958.996	959.122	-131.516	0.378	788.706	0.390	14	0.152	R.VSVLNDALK.T
R3/RRR3-24/2	959.004	959.122	-123.216	0.430	909.414	0.327	15	0.150	R.VSVLNDALK.T
R3/RRR3-24/2	991.813	992.067	-257.710	0.278	858.950	0.392	13	0.149	K.EIESWTAR.L
R3/RRR3-24/2	900.021	900.058	-40.690	0.442	598.626	0.378	12	0.144	-.IVVELNGR.-
R3/RRR3-23/2	958.893	959.122	-239.424	0.341	749.028	0.317	14	0.143	R.VSVLNDALK.T
R3/RRR3-24/2	991.926	992.067	-143.011	0.251	719.210	0.361	12	0.140	K.EIESWTAR.L
R3/RRR3-23/2	958.214	959.122	-1997.277	0.286	568.487	0.338	12	0.140	R.VSVLNDALK.T
R3/RRR3-24/2	959.492	959.122	386.886	0.286	857.101	0.235	15	0.138	R.VSVLNDALK.T
R3/RRR3-26/2	958.946	959.122	-184.509	0.292	629.704	0.281	13	0.138	R.VSVLNDALK.T
R3/RRR3-24/2	959.346	959.122	234.688	0.329	877.046	0.194	15	0.136	R.VSVLNDALK.T
R3/RRR3-24/2	900.566	900.058	-547.778	0.321	529.454	0.202	12	0.135	K.IVVELNGR.L
R3/RRR3-24/2	958.856	959.122	-277.740	0.302	540.894	0.297	12	0.134	-.VSVLNDALK.-
R3/RRR3-24/2	959.354	959.122	242.599	0.328	541.619	0.218	12	0.132	-.VSVLNDALK.-
R3/RRR3-24/2	991.404	992.067	-1682.366	0.202	487.047	0.286	10	0.131	K.EIESWTAR.L
R3/RRR3-24/2	899.338	900.058	-1918.375	0.343	660.201	0.161	12	0.129	-.IVVELNGR.-
R3/RRR3-24/2	899.604	900.058	-505.628	0.310	528.673	0.239	11	0.128	-.IVVELNGR.-
R3/RRR3-24/2	899.693	900.058	-406.371	0.349	470.073	0.236	11	0.124	-.IVVELNGR.-
R3/RRR3-24/3	1637.462	1637.818	-217.603	0.406	905.213	0.386	24	0.103	-.FDVGVKEIESWTAR.-
R3/RRR3-24/3	1722.122	1721.810	181.600	0.360	519.867	0.297	23	0.097	K.HGYIGEFEFVDDHR.S
R3/RRR3-24/3	1636.576	1637.818	-1373.726	0.366	581.726	0.293	22	0.091	-.FDVGVKEIESWTAR.-
R3/RRR3-11/2	1307.360	1307.650	-222.480	0.446	1202.557	0.502	17	0.190	R.VVLLIDVPIIGR.I
R3/RRR3-10/2	1307.484	1307.650	-127.692	0.415	1140.673	0.478	17	0.180	R.VVLLIDVPIIGR.I
R3/RRR3-11/2	1307.228	1307.650	-323.469	0.435	1123.338	0.480	17	0.180	R.VVLLIDVPIIGR.I
R3/RRR3-11/2	1307.354	1307.650	-227.070	0.440	974.109	0.465	16	0.167	R.VVLLIDVPIIGR.I
R3/RRR3-11/2	1523.554	1524.699	-1412.178	0.368	1120.212	0.376	17	0.160	R.FSFEETTATLHLK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1936.893	1937.228	-173.811	0.489	562.715	0.594	18	0.156	K.STYNDIKPGSIIPYLVR.V
R3/RRR3-11/2	1084.695	1085.319	-1501.664	0.394	863.199	0.425	14	0.153	R.ADLVVDVLIK.N
R3/RRR3-11/2	1786.722	1787.003	-158.131	0.428	773.209	0.434	19	0.149	-.SGEIPIPYKPDVDVEK.-
R3/RRR3-10/2	1307.413	1307.650	-181.453	0.355	364.065	0.332	14	0.137	-.VVLLIDVPIIGR.-
R3/RRR3-11/2	1787.480	1787.003	267.301	0.441	628.463	0.358	17	0.131	-.SGEIPIPYKPDVDVEK.-
R3/RRR3-11/3	1937.882	1937.228	-179.415	0.436	1106.500	0.423	27	0.123	K.STYNDIKPGSIIPYLVR.V
R3/RRR3-11/3	1977.113	1977.314	-101.765	0.478	751.604	0.539	26	0.122	K.GKIDVDTPFGNM*KLPISK.E
R3/RRR3-10/2	1307.426	1307.650	-171.806	0.341	216.202	0.324	11	0.111	-.VVLLIDVPIIGR.-
R3/RRR3-11/3	1936.286	1937.228	-1006.077	0.371	1067.420	0.349	25	0.107	K.STYNDIKPGSIIPYLVR.V
R3/RRR3-11/3	1936.462	1937.228	-915.034	0.368	842.440	0.364	24	0.099	K.STYNDIKPGSIIPYLVR.V
R3/RRR3-11/3	1978.313	1977.314	-0.453	0.252	425.233	0.354	19	0.083	-.GKIDVDTPFGNM*KLPISK.-
R3/RRR3-7/2	1372.421	1372.553	-96.047	0.404	1433.190	0.458	21	0.203	R.NVNSALAASGIGGIK.V
R3/RRR3-7/2	1755.584	1755.949	-208.569	0.507	956.885	0.576	20	0.182	R.DISLNYATFQPGTTVK.D
R3/RRR3-7/2	1074.661	1075.201	-1437.187	0.432	1113.529	0.464	14	0.178	R.HFGLFNPDK.T
R3/RRR3-14/2	1755.576	1755.949	-213.242	0.443	994.709	0.535	20	0.177	R.DISLNYATFQPGTTVK.D
R3/RRR3-7/2	1755.372	1755.949	-901.487	0.471	1007.763	0.497	20	0.172	R.DISLNYATFQPGTTVK.D
R3/RRR3-14/2	1755.353	1755.949	-911.889	0.462	934.543	0.532	19	0.172	R.DISLNYATFQPGTTVK.D
R3/RRR3-7/2	1756.405	1755.949	260.389	0.521	882.471	0.549	19	0.171	R.DISLNYATFQPGTTVK.D
R3/RRR3-7/2	1799.495	1797.989	-275.669	0.551	870.600	0.520	20	0.167	R.EISLNYATFQPGTTVR.D
R3/RRR3-7/2	1799.297	1797.989	171.369	0.535	854.931	0.522	20	0.166	R.EISLNYATFQPGTTVR.D
R3/RRR3-14/2	1755.653	1755.949	-169.368	0.487	895.842	0.509	19	0.166	R.DISLNYATFQPGTTVK.D
R3/RRR3-7/2	1799.436	1797.989	249.195	0.524	896.039	0.504	20	0.166	R.EISLNYATFQPGTTVR.D
R3/RRR3-7/2	1075.090	1075.201	-103.933	0.348	1025.776	0.407	14	0.162	R.HFGLFNPDK.T
R3/RRR3-9/2	1371.944	1372.553	-1176.368	0.398	990.104	0.417	21	0.160	R.NVNSALAASGIGGIK.V
R3/RRR3-7/2	1075.117	1075.201	-78.306	0.333	1019.008	0.368	13	0.156	R.HFGLFNPDK.T
R3/RRR3-14/2	1074.961	1075.201	-223.766	0.317	785.492	0.434	13	0.152	R.HFGLFNPDK.T
R3/RRR3-7/2	1611.391	1611.845	-282.591	0.380	1168.606	0.272	21	0.151	R.SEVVQM*YVSLGINR.M
R3/RRR3-7/2	1371.717	1372.553	-1341.867	0.344	982.257	0.348	18	0.148	R.NVNSALAASGIGGIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1074.435	1075.201	-1648.875	0.293	642.584	0.316	13	0.139	R.HFGLFNPDK.T
R3/RRR3-14/2	1074.378	1075.201	-1702.182	0.294	569.195	0.240	12	0.135	R.HFGLFNPDK.T
R3/RRR3-3/2	1076.227	1075.201	24.390	0.187	618.922	0.213	13	0.131	R.HFGLFNPDK.T
R3/RRR3-14/3	1231.593	1231.388	167.290	0.426	925.010	0.399	22	0.106	R.RHFGLFNPDK.T
R3/RRR3-14/3	1231.388	1231.388	0.575	0.404	891.893	0.285	20	0.093	R.RHFGLFNPDK.T
R3/RRR3-7/3	1231.425	1231.388	30.403	0.424	742.856	0.340	20	0.091	-.RHFGLFNPDK.-
R3/RRR3-6/2	1695.473	1694.874	-236.977	0.583	3040.546	0.629	28	0.582	R.AHDAVSAGSIALNAIQR.R
R3/RRR3-6/2	1729.303	1728.924	220.077	0.519	1738.169	0.535	25	0.262	K.SALAATVGIDSDFAYVK.I
R3/RRR3-6/2	1697.606	1697.871	-156.912	0.493	1255.958	0.512	21	0.195	R.DGTGVHDSIVNQLLTK.I
R3/RRR3-6/2	980.783	981.088	-311.541	0.477	1273.220	0.441	15	0.188	K.SAVSYALNR.Q
R3/RRR3-6/2	1130.881	1131.349	-415.810	0.403	1242.713	0.370	16	0.171	R.LLEYVAIGPR.F
R3/RRR3-6/2	1172.921	1173.386	-398.088	0.376	1151.665	0.318	17	0.155	K.GILLYGPPGTGK.T
R3/RRR3-6/3	1694.709	1694.874	-97.693	0.457	1488.383	0.393	29	0.149	R.AHDAVSAGSIALNAIQR.R
R3/RRR3-6/3	1694.417	1694.874	-270.589	0.413	1240.524	0.417	27	0.131	R.AHDAVSAGSIALNAIQR.R
R3/RRR3-2/2	1594.240	1593.932	193.487	0.538	1635.695	0.568	22	0.254	R.IVLNPISSLADLPLK.N
R3/RRR3-2/2	1594.457	1593.932	-298.832	0.557	1530.245	0.613	22	0.251	R.IVLNPISSLADLPLK.N
R3/RRR3-2/2	1594.265	1593.932	209.305	0.533	1565.066	0.559	22	0.242	R.IVLNPISSLADLPLK.N
R3/RRR3-3/2	1593.245	1593.932	-1062.461	0.426	1514.839	0.548	22	0.232	R.IVLNPISSLADLPLK.N
R3/RRR3-2/2	1274.730	1275.479	-1375.576	0.439	1319.273	0.396	16	0.182	K.VIFVDADQIVR.A
R3/RRR3-2/2	1549.565	1548.726	-103.793	0.448	1278.037	0.387	18	0.173	K.LGLEFGSNAVITNGR.V
R3/RRR3-2/3	1887.129	1887.038	48.548	0.530	1304.883	0.539	31	0.167	K.GVALEDPKTEDLSQEVR.G
R3/RRR3-3/2	1592.716	1593.932	-1395.441	0.324	1015.701	0.464	19	0.165	R.IVLNPISSLADLPLK.N
R3/RRR3-2/2	976.424	977.182	-1805.607	0.340	1152.834	0.373	14	0.164	R.GLQFILGTK.R
R3/RRR3-2/2	1275.169	1275.479	-243.459	0.413	999.935	0.381	16	0.157	K.VIFVDADQIVR.A
R3/RRR3-3/2	1275.795	1275.479	248.980	0.343	1070.506	0.319	15	0.152	K.VIFVDADQIVR.A
R3/RRR3-2/2	1273.491	1274.484	-1569.776	0.414	731.672	0.376	13	0.142	K.VLDFLHELCK.F
R3/RRR3-3/2	1276.076	1275.479	-316.590	0.302	698.843	0.320	13	0.137	-.VIFVDADQIVR.-
R3/RRR3-2/3	1886.947	1887.038	-48.192	0.499	899.219	0.542	26	0.133	K.GVALEDPKTEDLSQEVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1886.671	1887.038	-195.188	0.493	879.246	0.517	27	0.127	K.GVALEDPKTEDLSQEVR.G
R3/RRR3-2/2	1303.126	1302.499	-287.469	0.270	795.881	0.180	14	0.126	K.TEEDISILIIR.L
R3/RRR3-2/3	1886.447	1887.038	-845.963	0.443	777.267	0.416	24	0.105	K.GVALEDPKTEDLSQEVR.G
R3/RRR3-8/2	1854.335	1854.950	-873.184	0.559	1796.457	0.639	24	0.300	K.HLTSTYSSDETKEDIK.L
R3/RRR3-8/2	1660.535	1659.861	-197.429	0.545	1738.849	0.539	23	0.262	K.ELQGVVFDDVPEALK.H
R3/RRR3-8/2	1660.258	1659.861	239.333	0.523	1654.896	0.565	23	0.257	K.ELQGVVFDDVPEALK.H
R3/RRR3-8/2	1341.112	1340.509	-296.855	0.476	1723.425	0.506	19	0.252	R.LLFGNTAYGDLR.Q
R3/RRR3-8/2	1341.193	1340.509	-236.495	0.518	1528.446	0.496	18	0.223	R.LLFGNTAYGDLR.Q
R3/RRR3-8/2	1341.142	1340.509	-274.664	0.452	1464.178	0.514	18	0.220	R.LLFGNTAYGDLR.Q
R3/RRR3-8/2	1660.282	1659.861	254.299	0.519	1444.769	0.500	21	0.213	K.ELQGVVFDDVPEALK.H
R3/RRR3-8/2	1032.068	1032.132	-61.761	0.326	1143.743	0.353	15	0.160	K.VYIYSSGSR.E
R3/RRR3-8/2	989.829	990.130	-305.045	0.316	1051.492	0.183	13	0.138	R.ELVAELCR.H
R3/RRR3-8/3	1855.056	1854.950	57.638	0.532	1012.554	0.520	32	0.136	K.HLTSTYSSDETKEDIK.L
R3/RRR3-16/2	1341.413	1340.509	-71.523	0.222	436.971	0.292	14	0.132	R.LLFGNTAYGDLR.Q
R3/RRR3-8/2	989.933	990.130	-199.388	0.320	719.465	0.193	11	0.131	-.ELVAELCR.-
R3/RRR3-8/2	989.754	990.130	-380.651	0.305	793.964	0.189	12	0.131	-.ELVAELCR.-
R3/RRR3-8/3	1854.514	1854.950	-235.676	0.500	928.208	0.506	33	0.128	K.HLTSTYSSDETKEDIK.L
R3/RRR3-16/3	1854.955	1854.950	3.088	0.529	892.603	0.508	31	0.127	K.HLTSTYSSDETKEDIK.L
R3/RRR3-10/2	1660.517	1659.861	-208.049	0.351	354.276	0.353	12	0.127	-.ELQGVVFDDVPEALK.-
R3/RRR3-7/3	1854.748	1854.950	-108.902	0.569	924.825	0.499	33	0.127	K.HLTSTYSSDETKEDIK.L
R3/RRR3-7/3	1854.384	1854.950	-846.989	0.515	864.552	0.506	32	0.125	K.HLTSTYSSDETKEDIK.L
R3/RRR3-16/3	1855.072	1854.950	65.953	0.459	850.489	0.497	31	0.123	K.HLTSTYSSDETKEDIK.L
R3/RRR3-7/3	1854.551	1854.950	-215.667	0.554	837.791	0.470	32	0.118	K.HLTSTYSSDETKEDIK.L
R3/RRR3-8/3	1854.463	1854.950	-263.412	0.547	720.443	0.459	29	0.113	K.HLTSTYSSDETKEDIK.L
R3/RRR3-8/3	1982.465	1983.123	-838.556	0.409	1069.630	0.388	32	0.113	R.KHLTSTYSSDETKEDIK.L
R3/RRR3-16/3	1854.414	1854.950	-830.832	0.510	730.482	0.452	31	0.113	K.HLTSTYSSDETKEDIK.L
R3/RRR3-2/3	1854.470	1854.950	-259.251	0.471	538.133	0.407	26	0.105	K.HLTSTYSSDETKEDIK.L
R3/RRR3-2/3	1854.780	1854.950	-91.869	0.483	622.794	0.402	28	0.105	K.HLTSTYSSDETKEDIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/3	1854.749	1854.950	-108.605	0.488	907.665	0.362	32	0.104	K.HLTSTYSSDETKEDIK.L
R3/RRR3-3/3	1854.730	1854.950	-119.003	0.471	544.794	0.360	26	0.101	K.HLTSTYSSDETKEDIK.L
R3/RRR3-3/3	1854.408	1854.950	-833.608	0.399	436.573	0.368	23	0.097	-.HLTSTYSSDETKEDIK.-
R3/RRR3-8/3	1982.524	1983.123	-808.888	0.381	985.699	0.302	32	0.096	R.KHLTSTYSSDETKEDIK.L
R3/RRR3-8/3	1983.282	1983.123	80.426	0.382	767.087	0.356	28	0.096	-.KHLTSTYSSDETKEDIK.-
R3/RRR3-23/2	1558.945	1559.526	-1017.194	0.380	1948.366	0.437	21	0.609	R.YFNIAENEGEEED.-
R3/RRR3-23/2	1558.692	1559.526	-1180.588	0.370	1562.336	0.421	19	0.369	R.YFNIAENEGEEED.-
R3/RRR3-23/2	1558.977	1559.526	-996.675	0.385	1370.529	0.358	18	0.263	R.YFNIAENEGEEED.-
R3/RRR3-24/2	1559.213	1559.526	-201.778	0.371	1349.935	0.370	17	0.258	R.YFNIAENEGEEED.-
R3/RRR3-24/2	1559.168	1559.526	-230.367	0.355	1311.690	0.276	18	0.227	R.YFNIAENEGEEED.-
R3/RRR3-23/2	1111.979	1112.215	-212.684	0.438	1215.791	0.493	18	0.192	K.VTVTSDGAFSK.R
R3/RRR3-24/2	1558.918	1559.526	-1034.884	0.356	1180.696	0.391	17	0.190	R.YFNIAENEGEEED.-
R3/RRR3-23/2	1111.825	1112.215	-351.577	0.406	1199.425	0.469	17	0.185	K.VTVTSDGAFSK.R
R3/RRR3-24/2	1267.966	1268.401	-344.687	0.464	1024.165	0.486	17	0.173	K.VTVTSDGAFSKR.Y
R3/RRR3-23/2	1267.900	1268.401	-1187.826	0.408	1108.588	0.432	17	0.170	K.VTVTSDGAFSKR.Y
R3/RRR3-24/2	1112.060	1112.215	-139.783	0.323	901.160	0.454	16	0.159	K.VTVTSDGAFSK.R
R3/RRR3-24/2	1111.471	1112.215	-1573.442	0.298	1098.605	0.342	17	0.156	K.VTVTSDGAFSK.R
R3/RRR3-23/2	1111.361	1112.215	-1673.631	0.310	900.560	0.354	16	0.148	K.VTVTSDGAFSK.R
R3/RRR3-24/2	1189.920	1190.289	-311.320	0.444	781.492	0.399	16	0.148	K.AGNLGDSVTVTR.D
R3/RRR3-24/2	1050.033	1050.252	-208.768	0.318	958.950	0.288	14	0.145	K.IM*EIASLEK.F
R3/RRR3-23/2	1049.772	1050.252	-458.412	0.409	930.080	0.254	14	0.141	K.IM*EIASLEK.F
R3/RRR3-23/2	1050.037	1050.252	-205.269	0.465	808.761	0.286	14	0.141	K.IM*EIASLEK.F
R3/RRR3-23/2	1049.813	1050.252	-419.090	0.429	993.443	0.239	14	0.141	K.IM*EIASLEK.F
R3/RRR3-24/2	1049.754	1050.252	-475.915	0.416	647.867	0.255	13	0.136	K.IM*EIASLEK.F
R3/RRR3-24/2	1190.193	1190.289	-80.817	0.271	626.937	0.255	15	0.131	K.AGNLGDSVTVTR.D
R3/RRR3-6/2	1805.477	1804.102	208.351	0.617	2846.891	0.584	24	0.496	K.SAIGIGTLLMDGLGDTIR.V
R3/RRR3-6/2	1644.463	1644.958	-301.807	0.470	2214.323	0.261	23	0.258	R.GIAMEGATDALIQLIK.D
R3/RRR3-6/2	1519.715	1520.712	-1318.423	0.359	1936.933	0.332	20	0.240	R.TLFDLQEVSAQIR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1522.025	1520.712	206.207	0.492	1751.838	0.428	18	0.235	R.TLFDLQEVSAQIR.E
R3/RRR3-6/2	1643.980	1644.958	-1207.148	0.373	2070.406	0.186	23	0.222	R.GIAMEGATDALIQLIK.D
R3/RRR3-6/2	1819.472	1820.101	-898.361	0.451	1266.220	0.561	22	0.204	K.SAIGIGTLLM*DGLGDTIR.V
R3/RRR3-6/2	1819.555	1820.101	-852.227	0.439	1089.635	0.528	19	0.180	K.SAIGIGTLLM*DGLGDTIR.V
R3/RRR3-6/2	1820.159	1820.101	31.876	0.481	914.367	0.536	19	0.169	K.SAIGIGTLLM*DGLGDTIR.V
R3/RRR3-6/2	1644.187	1644.958	-1080.328	0.351	1530.960	0.176	20	0.160	R.GIAMEGATDALIQLIK.D
R3/RRR3-6/2	862.075	862.008	77.672	0.447	678.801	0.418	11	0.151	K.APELLYR.S
R3/RRR3-6/2	1215.356	1216.409	-1694.227	0.331	1275.711	0.221	17	0.151	K.DLATVDSILLR.E
R3/RRR3-5/2	1803.254	1804.102	-1028.078	0.341	648.205	0.429	15	0.140	K.SAIGIGTLLMDGLGDTIR.V
R3/RRR3-6/2	1348.627	1349.584	-1455.265	0.371	703.316	0.382	14	0.139	K.ASNPVIMVQAYR.L
R3/RRR3-6/2	861.243	862.008	-2054.975	0.276	586.832	0.346	11	0.136	-.APELLYR.-
R3/RRR3-7/2	1556.500	1556.829	-212.277	0.435	1402.601	0.443	21	0.196	K.LGLLSVTSGANPVSLK.K
R3/RRR3-7/2	1496.253	1496.689	-292.097	0.408	1091.961	0.325	19	0.153	R.GYISPQFVTNLEK.S
R3/RRR3-7/2	1553.594	1554.856	-1460.292	0.349	784.425	0.306	18	0.139	K.EILPILEKTTQLR.A
R3/RRR3-7/2	1554.242	1554.856	-1042.015	0.342	895.794	0.197	19	0.133	K.EILPILEKTTQLR.A
R3/RRR3-7/2	1202.458	1202.419	32.114	0.518	1763.366	0.490	20	0.254	R.LLAVEGCAALGK.L
R3/RRR3-7/2	1201.506	1202.419	-1597.283	0.393	1734.041	0.342	19	0.215	R.LLAVEGCAALGK.L
R3/RRR3-7/2	1202.105	1202.419	-262.534	0.483	1436.012	0.494	18	0.213	R.LLAVEGCAALGK.L
R3/RRR3-7/2	1121.802	1122.258	-407.933	0.469	1228.891	0.549	17	0.204	R.LAAGEWFTAR.V
R3/RRR3-7/2	1121.620	1122.258	-1465.109	0.416	1344.851	0.484	17	0.202	R.LAAGEWFTAR.V
R3/RRR3-7/2	1284.141	1284.442	-235.656	0.480	1395.741	0.453	18	0.201	K.FAATVEQNYLK.T
R3/RRR3-7/3	1766.058	1766.115	-32.218	0.519	1551.837	0.527	31	0.192	K.VLQALIPILDQSVVEK.N
R3/RRR3-7/2	1284.246	1284.442	-153.551	0.465	1347.864	0.420	18	0.190	K.FAATVEQNYLK.T
R3/RRR3-7/2	1122.065	1122.258	-172.253	0.442	1230.865	0.465	17	0.189	R.LAAGEWFTAR.V
R3/RRR3-7/2	1284.199	1284.442	-190.168	0.505	1303.334	0.417	18	0.186	K.FAATVEQNYLK.T
R3/RRR3-7/2	1766.602	1766.115	276.767	0.533	1020.290	0.551	24	0.186	K.VLQALIPILDQSVVEK.N
R3/RRR3-7/3	1765.472	1766.115	-933.648	0.448	1367.249	0.491	29	0.160	K.VLQALIPILDQSVVEK.N
R3/RRR3-7/2	1765.432	1766.115	-955.992	0.427	812.090	0.465	22	0.158	K.VLQALIPILDQSVVEK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1765.388	1766.115	-981.053	0.437	742.347	0.479	21	0.156	K.VLQALIPILDQSVVEK.N
R3/RRR3-7/2	1190.271	1190.335	-54.375	0.461	935.211	0.356	14	0.152	K.INNPHYLYR.M
R3/RRR3-7/2	1533.307	1533.749	-289.350	0.375	1063.221	0.312	16	0.149	-.ESDIVDWFVPVVK.-
R3/RRR3-7/2	1190.061	1190.335	-231.549	0.423	924.928	0.311	14	0.146	K.INNPHYLYR.M
R3/RRR3-6/2	1284.217	1284.442	-175.959	0.374	1060.672	0.259	16	0.145	K.FAATVEQNYLK.T
R3/RRR3-6/2	1285.607	1284.442	128.797	0.278	384.881	0.470	15	0.143	K.FAATVEQNYLK.T
R3/RRR3-7/3	1765.552	1766.115	-887.940	0.445	1279.649	0.448	27	0.142	K.VLQALIPILDQSVVEK.N
R3/RRR3-6/2	1203.300	1202.419	-99.065	0.333	496.230	0.333	14	0.136	R.LLAVEGCAALGK.L
R3/RRR3-7/2	1765.889	1766.115	-128.449	0.324	271.109	0.355	13	0.130	-.VLQALIPILDQSVVEK.-
R3/RRR3-5/2	1323.915	1324.468	-1176.503	0.470	1877.976	0.560	20	0.291	K.ILVAGSHADDLGR.Q
R3/RRR3-5/2	1058.903	1059.198	-279.422	0.552	1723.146	0.447	17	0.236	R.IGEATALEVR.A
R3/RRR3-5/2	1058.956	1059.198	-229.576	0.547	1677.619	0.435	17	0.228	R.IGEATALEVR.A
R3/RRR3-6/2	1058.887	1059.198	-294.574	0.527	1655.979	0.439	17	0.226	R.IGEATALEVR.A
R3/RRR3-6/2	1059.097	1059.198	-95.907	0.552	1644.218	0.435	17	0.223	R.IGEATALEVR.A
R3/RRR3-5/2	1058.413	1059.198	-1691.765	0.454	1437.504	0.461	17	0.207	R.IGEATALEVR.A
R3/RRR3-5/2	1781.358	1782.063	-960.024	0.431	1038.453	0.490	21	0.174	R.ATGIPYVFAPCVAVCR.D
R3/RRR3-5/3	1453.859	1454.659	-1241.472	0.409	1327.360	0.541	30	0.164	K.ATIFPHNVGLGATR.D
R3/RRR3-5/2	1781.345	1782.063	-967.523	0.421	1000.079	0.439	20	0.163	R.ATGIPYVFAPCVAVCR.D
R3/RRR3-5/2	1781.293	1782.063	-996.969	0.436	980.853	0.425	20	0.160	R.ATGIPYVFAPCVAVCR.D
R3/RRR3-5/2	1188.239	1188.398	-133.809	0.450	867.309	0.411	16	0.156	K.SSYSPVLPLPK.K
R3/RRR3-5/2	1187.628	1188.398	-1494.813	0.334	828.850	0.426	16	0.154	K.SSYSPVLPLPK.K
R3/RRR3-5/2	1188.057	1188.398	-287.486	0.375	822.607	0.396	16	0.152	K.SSYSPVLPLPK.K
R3/RRR3-5/3	1453.665	1454.659	-1375.557	0.368	1262.720	0.514	29	0.151	K.ATIFPHNVGLGATR.D
R3/RRR3-6/2	1188.204	1188.398	-163.696	0.411	703.836	0.418	15	0.150	K.SSYSPVLPLPK.K
R3/RRR3-6/3	1454.507	1454.659	-104.609	0.443	1160.902	0.533	28	0.148	K.ATIFPHNVGLGATR.D
R3/RRR3-6/2	1188.060	1188.398	-285.218	0.403	759.255	0.366	16	0.147	K.SSYSPVLPLPK.K
R3/RRR3-5/2	1454.194	1454.659	-320.247	0.315	727.606	0.455	19	0.147	K.ATIFPHNVGLGATR.D
R3/RRR3-6/2	1187.407	1188.398	-1681.519	0.297	781.162	0.379	15	0.146	K.SSYSPVLPLPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1783.348	1782.063	160.269	0.325	702.344	0.370	16	0.139	R.ATGIPYVFAPCVAVCR.D
R3/RRR3-6/3	1454.835	1454.659	121.632	0.462	1036.220	0.528	28	0.138	K.ATIFPHNVGLGATR.D
R3/RRR3-2/2	1783.666	1782.063	-223.270	0.312	273.780	0.405	14	0.137	R.ATGIPYVFAPCVAVCR.D
R3/RRR3-4/2	1060.147	1059.198	-48.576	0.332	811.516	0.239	14	0.137	R.IGEATALEVR.A
R3/RRR3-3/2	1781.338	1782.063	-971.444	0.310	455.596	0.302	15	0.133	R.ATGIPYVFAPCVAVCR.D
R3/RRR3-2/2	1059.059	1059.198	-131.633	0.290	684.258	0.187	14	0.132	-.IGEATALEVR.-
R3/RRR3-3/2	1188.107	1188.398	-245.532	0.305	526.963	0.303	12	0.132	-.SSYSPVLPLPK.-
R3/RRR3-4/2	1059.877	1059.198	-304.696	0.322	805.073	0.211	14	0.129	-.IGEATALEVR.-
R3/RRR3-6/3	1454.508	1454.659	-103.978	0.385	1041.355	0.478	27	0.127	K.ATIFPHNVGLGATR.D
R3/RRR3-5/3	1453.764	1454.659	-1307.371	0.397	740.845	0.493	24	0.115	K.ATIFPHNVGLGATR.D
R3/RRR3-5/3	1594.111	1593.835	174.035	0.367	1245.779	0.261	22	0.101	K.M*HANHHLITDFLK.N
R3/RRR3-5/3	1595.310	1593.835	299.003	0.435	955.272	0.336	22	0.099	-.M*HANHHLITDFLK.-
R3/RRR3-16/2	1937.432	1937.097	173.496	0.657	3114.075	0.616	24	0.592	K.IEDLSSQLQTQAAEQFK.A
R3/RRR3-16/2	1479.443	1479.682	-161.776	0.432	2280.442	0.483	21	0.341	K.DIELVM*TQATVSR.S
R3/RRR3-16/2	1520.415	1520.840	-280.449	0.541	2189.659	0.462	21	0.314	K.NILFVISKPDVFK.S
R3/RRR3-16/2	1520.395	1520.840	-293.498	0.542	2166.856	0.454	21	0.307	K.NILFVISKPDVFK.S
R3/RRR3-16/2	1520.405	1520.840	-287.215	0.511	1931.110	0.400	20	0.253	K.NILFVISKPDVFK.S
R3/RRR3-16/2	1528.115	1528.645	-1004.306	0.505	1512.719	0.569	21	0.238	K.SPNSDTYVIFGEAK.I
R3/RRR3-16/2	1528.385	1528.645	-170.520	0.542	1414.038	0.584	20	0.229	K.SPNSDTYVIFGEAK.I
R3/RRR3-16/2	1528.337	1528.645	-202.009	0.513	1439.840	0.553	20	0.225	K.SPNSDTYVIFGEAK.I
R3/RRR3-16/3	1937.131	1937.097	17.652	0.506	1589.729	0.513	32	0.193	K.IEDLSSQLQTQAAEQFK.A
R3/RRR3-19/2	1528.214	1528.645	-282.943	0.479	1136.102	0.523	19	0.188	K.SPNSDTYVIFGEAK.I
R3/RRR3-19/2	1528.049	1528.645	-1047.216	0.479	1083.085	0.452	18	0.171	K.SPNSDTYVIFGEAK.I
R3/RRR3-16/2	1044.291	1044.184	103.337	0.438	743.970	0.424	14	0.149	K.APDLSNVISK.A
R3/RRR3-19/2	1527.318	1528.645	-1527.982	0.315	1055.160	0.302	19	0.149	K.SPNSDTYVIFGEAK.I
R3/RRR3-16/3	1936.947	1937.097	-77.922	0.427	1307.593	0.450	28	0.145	K.IEDLSSQLQTQAAEQFK.A
R3/RRR3-16/3	1528.403	1528.645	-158.470	0.389	1102.542	0.169	21	0.080	-.SPNSDTYVIFGEAK.-
R3/RRR3-4/2	1548.543	1548.762	-142.129	0.439	2667.261	0.483	22	0.422	R.EVVEIATNALDVFK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1548.659	1548.762	-67.091	0.495	2251.098	0.497	21	0.337	R.EVVEIATNALDVFK.S
R3/RRR3-4/2	1935.659	1936.194	-795.384	0.514	1548.355	0.531	22	0.232	R.IVLEADGYQPYLISPEK.G
R3/RRR3-4/2	1937.506	1936.194	161.609	0.579	1514.820	0.513	22	0.222	R.IVLEADGYQPYLISPEK.G
R3/RRR3-4/2	1781.715	1782.035	-179.878	0.478	1329.727	0.541	25	0.210	R.VLLDIVNASANATPGLGR.Y
R3/RRR3-4/2	1646.412	1645.881	-285.758	0.534	1384.171	0.477	22	0.202	R.GYVEAVLNSLAANVPK.A
R3/RRR3-4/2	1140.170	1140.358	-164.901	0.450	1307.811	0.437	17	0.189	R.LPNLLSGLQGK.S
R3/RRR3-4/2	1781.607	1782.035	-240.914	0.416	1167.290	0.515	23	0.187	R.VLLDIVNASANATPGLGR.Y
R3/RRR3-4/2	1937.589	1936.194	204.318	0.474	1301.453	0.396	20	0.176	R.IVLEADGYQPYLISPEK.G
R3/RRR3-4/2	1644.823	1645.881	-1254.913	0.359	1453.620	0.297	20	0.174	R.GYVEAVLNSLAANVPK.A
R3/RRR3-4/2	1644.818	1645.881	-1258.341	0.375	1105.040	0.318	19	0.151	R.GYVEAVLNSLAANVPK.A
R3/RRR3-2/2	1783.793	1782.035	-135.877	0.281	194.412	0.374	13	0.129	-.VLLDIVNASANATPGLGR.-
R3/RRR3-4/3	1143.407	1143.280	111.233	0.511	988.805	0.345	19	0.104	R.HFDINNVKR.I
R3/RRR3-4/3	1143.530	1143.280	218.504	0.522	1159.173	0.298	19	0.101	-.HFDINNVKR.-
R3/RRR3-24/2	1805.515	1806.035	-844.307	0.522	1729.682	0.508	25	0.253	R.VCCLSIIDPGDSDIIK.T
R3/RRR3-24/2	1318.592	1318.521	54.449	0.551	1817.887	0.420	17	0.241	K.SEIEYYAMLAK.T
R3/RRR3-24/2	1333.352	1334.520	-1630.806	0.403	1825.477	0.325	17	0.222	K.SEIEYYAM*LAK.T
R3/RRR3-24/2	1333.648	1334.520	-1407.723	0.457	1829.514	0.325	17	0.221	K.SEIEYYAM*LAK.T
R3/RRR3-24/2	1806.401	1806.035	203.500	0.462	1412.362	0.494	23	0.209	R.VCCLSIIDPGDSDIIK.T
R3/RRR3-24/2	1396.370	1396.654	-203.914	0.423	1122.876	0.454	16	0.174	K.LVIISNNCPPLR.K
R3/RRR3-24/2	1805.309	1806.035	-959.020	0.455	1064.687	0.450	21	0.169	R.VCCLSIIDPGDSDIIK.T
R3/RRR3-24/2	1462.092	1462.693	-1097.859	0.507	881.897	0.437	19	0.159	R.KSEIEYYAM*LAK.T
R3/RRR3-24/2	1396.386	1396.654	-192.426	0.370	993.526	0.371	16	0.154	K.LVIISNNCPPLR.K
R3/RRR3-24/2	1319.731	1318.521	159.700	0.436	375.292	0.334	15	0.142	K.SEIEYYAMLAK.T
R3/RRR3-24/2	1396.304	1396.654	-251.450	0.290	364.358	0.359	11	0.128	-.LVIISNNCPPLR.-
R3/RRR3-24/3	1634.328	1634.880	-952.692	0.407	832.897	0.490	24	0.118	K.STDNINNKLQLVM*K.S
R3/RRR3-24/3	1634.291	1634.880	-975.526	0.419	787.379	0.483	26	0.115	K.STDNINNKLQLVM*K.S
R3/RRR3-24/3	1634.220	1634.880	-1018.834	0.470	772.306	0.449	26	0.111	K.STDNINNKLQLVM*K.S
R3/RRR3-6/2	1805.204	1805.925	-956.295	0.532	1809.395	0.621	22	0.295	R.SLGYAYVNYSSPADAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1315.357	1315.415	-44.364	0.417	907.472	0.510	15	0.168	R.FDDKEWYVGR.A
R3/RRR3-6/2	1198.233	1198.418	-154.253	0.348	962.252	0.350	17	0.151	K.FGTITSAVVM*R.E
R3/RRR3-6/3	1816.119	1815.173	-29.577	0.394	1211.379	0.454	27	0.138	R.ALEMLNFTPINGKPIR.I
R3/RRR3-6/2	1033.741	1034.212	-457.318	0.342	864.218	0.267	12	0.136	-.VAEAM*EVLR.-
R3/RRR3-6/2	1183.587	1182.418	142.898	0.271	574.632	0.375	13	0.135	K.FGTITSAVVMR.E
R3/RRR3-6/3	1549.651	1549.863	-137.569	0.429	1293.096	0.358	25	0.124	-.M*VGSKPLYVALAQR.-
R3/RRR3-6/3	1831.763	1831.172	-224.225	0.404	854.829	0.470	24	0.117	R.ALEM*LNFTPINGKPIR.I
R3/RRR3-6/3	1816.297	1815.173	68.710	0.309	952.630	0.405	24	0.111	R.ALEMLNFTPINGKPIR.I
R3/RRR3-6/3	1533.586	1533.864	-181.726	0.414	1102.211	0.350	26	0.109	K.MVGSKPLYVALAQR.K
R3/RRR3-6/3	1830.795	1831.172	-206.856	0.289	1185.150	0.236	24	0.097	R.ALEM*LNFTPINGKPIR.I
R3/RRR3-6/3	1533.935	1533.864	46.636	0.444	745.461	0.295	22	0.092	K.MVGSKPLYVALAQR.K
R3/RRR3-6/3	1533.158	1533.864	-1116.048	0.362	1019.249	0.246	24	0.091	K.MVGSKPLYVALAQR.K
R3/RRR3-6/3	1830.567	1831.172	-879.405	0.275	856.740	0.229	23	0.086	R.ALEM*LNFTPINGKPIR.I
R3/RRR3-18/2	1664.076	1663.767	186.103	0.599	2715.299	0.608	26	0.476	K.DLASAGADVGSATDWVK.N
R3/RRR3-17/2	1662.366	1663.767	-1448.632	0.373	3122.231	0.309	27	0.465	K.DLASAGADVGSATDWVK.N
R3/RRR3-18/2	1663.320	1663.767	-269.751	0.547	2456.648	0.643	25	0.428	K.DLASAGADVGSATDWVK.N
R3/RRR3-18/2	1664.267	1663.767	301.215	0.588	2378.687	0.625	25	0.403	K.DLASAGADVGSATDWVK.N
R3/RRR3-17/2	1247.720	1248.478	-1413.601	0.493	2096.068	0.476	18	0.298	K.LLNANSITM*VR.I
R3/RRR3-18/2	1247.604	1248.478	-1506.766	0.514	1963.252	0.489	19	0.281	K.LLNANSITM*VR.I
R3/RRR3-18/2	1248.060	1248.478	-336.258	0.533	1757.730	0.508	18	0.255	K.LLNANSITM*VR.I
R3/RRR3-18/2	1248.378	1248.478	-80.781	0.520	1666.358	0.504	19	0.242	K.LLNANSITM*VR.I
R3/RRR3-18/2	1535.265	1534.736	-307.483	0.554	1505.956	0.579	22	0.241	R.IYDTDPTVLNALAK.T
R3/RRR3-17/2	1247.624	1248.478	-1490.353	0.478	1564.733	0.476	18	0.223	K.LLNANSITM*VR.I
R3/RRR3-16/2	1248.117	1248.478	-290.137	0.435	1532.144	0.481	18	0.220	K.LLNANSITM*VR.I
R3/RRR3-17/2	1662.449	1663.767	-1398.405	0.331	1647.565	0.423	23	0.219	K.DLASAGADVGSATDWVK.N
R3/RRR3-16/2	1247.411	1248.478	-1661.884	0.420	1415.030	0.482	17	0.207	K.LLNANSITM*VR.I
R3/RRR3-17/2	1248.265	1248.478	-171.027	0.509	1404.405	0.483	17	0.206	K.LLNANSITM*VR.I
R3/RRR3-17/2	1232.165	1232.479	-255.235	0.490	1350.569	0.503	18	0.206	K.LLNANSITMVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1232.010	1232.479	-381.280	0.496	1363.762	0.493	18	0.205	K.LLNANSITMVR.I
R3/RRR3-18/2	1533.715	1534.736	-1321.236	0.389	1415.344	0.465	23	0.204	R.IYDTDPTVLNALAK.T
R3/RRR3-18/2	1534.218	1534.736	-992.410	0.526	1271.075	0.516	22	0.201	R.IYDTDPTVLNALAK.T
R3/RRR3-16/2	1248.222	1248.478	-205.658	0.438	1260.648	0.486	17	0.193	K.LLNANSITM*VR.I
R3/RRR3-17/2	1233.205	1232.479	-223.051	0.520	1249.165	0.452	17	0.186	K.LLNANSITMVR.I
R3/RRR3-17/2	1232.085	1232.479	-320.639	0.469	1133.526	0.471	17	0.181	K.LLNANSITMVR.I
R3/RRR3-18/2	1232.987	1232.479	-399.845	0.485	1008.058	0.479	16	0.173	K.LLNANSITMVR.I
R3/RRR3-17/2	1398.205	1397.556	-251.283	0.523	1177.785	0.409	19	0.172	R.DASNLIDPPEVVK.L
R3/RRR3-18/2	1231.353	1232.479	-1731.379	0.389	1025.020	0.446	17	0.169	K.LLNANSITMVR.I
R3/RRR3-17/2	1397.243	1397.556	-224.291	0.420	1075.983	0.352	18	0.157	R.DASNLIDPPEVVK.L
R3/RRR3-18/2	963.851	964.229	-393.481	0.437	678.423	0.359	12	0.145	K.VM*VM*LPNK.D
R3/RRR3-18/2	963.339	964.229	-1967.775	0.336	632.028	0.369	12	0.143	K.VM*VM*LPNK.D
R3/RRR3-18/2	963.961	964.229	-278.235	0.450	589.866	0.371	12	0.143	-.VM*VM*LPNK.-
R3/RRR3-17/2	1396.700	1397.556	-1332.944	0.355	866.548	0.284	16	0.139	-.DASNLIDPPEVVK.-
R3/RRR3-17/2	964.112	964.229	-121.226	0.472	611.093	0.325	12	0.135	-.VM*VM*LPNK.-
R3/RRR3-3/2	1535.286	1534.736	-294.001	0.284	362.872	0.332	14	0.134	R.IYDTDPTVLNALAK.T
R3/RRR3-18/2	1396.420	1397.556	-1533.995	0.331	612.360	0.228	14	0.130	-.DASNLIDPPEVVK.-
R3/RRR3-18/2	1397.030	1397.556	-1095.298	0.230	622.982	0.129	14	0.127	R.DASNLIDPPEVVK.L
R3/RRR3-16/2	1398.219	1397.556	-241.298	0.411	595.064	0.188	13	0.117	-.DASNLIDPPEVVK.-
R3/RRR3-23/2	1737.364	1737.720	-205.400	0.583	2185.400	0.564	25	0.343	K.DATDDFEDVGHSTTAR.A
R3/RRR3-22/2	1737.391	1737.720	-189.752	0.582	2155.422	0.576	23	0.339	K.DATDDFEDVGHSTTAR.A
R3/RRR3-22/2	1737.284	1737.720	-251.289	0.540	1809.256	0.566	22	0.277	K.DATDDFEDVGHSTTAR.A
R3/RRR3-23/2	1737.047	1737.720	-965.976	0.554	1758.098	0.583	23	0.275	K.DATDDFEDVGHSTTAR.A
R3/RRR3-23/2	1737.219	1737.720	-866.646	0.546	1736.589	0.559	23	0.265	K.DATDDFEDVGHSTTAR.A
R3/RRR3-22/2	1737.197	1737.720	-879.203	0.543	1620.382	0.532	22	0.241	K.DATDDFEDVGHSTTAR.A
R3/RRR3-23/2	1901.570	1902.051	-254.046	0.560	1407.618	0.624	26	0.238	K.FLEDHPGGDDVLLSSTAK.D
R3/RRR3-23/2	1901.443	1902.051	-848.138	0.593	1268.348	0.608	26	0.219	K.FLEDHPGGDDVLLSSTAK.D
R3/RRR3-23/2	1901.537	1902.051	-798.839	0.567	1187.224	0.613	25	0.210	K.FLEDHPGGDDVLLSSTAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1177.022	1177.325	-258.039	0.514	1448.469	0.338	15	0.182	K.DDCWLIIGGK.V
R3/RRR3-23/2	1017.937	1018.186	-245.743	0.410	393.469	0.468	15	0.152	K.VLTLEEVSK.H
R3/RRR3-22/2	1177.214	1177.325	-94.604	0.396	575.600	0.448	14	0.147	K.DDCWLIIGGK.V
R3/RRR3-23/2	1017.992	1018.186	-191.487	0.345	290.446	0.460	13	0.147	K.VLTLEEVSK.H
R3/RRR3-23/3	1659.020	1657.845	105.592	0.517	1035.481	0.545	24	0.142	K.HNTKDDCWLIIGGK.V
R3/RRR3-23/2	1017.325	1018.186	-1835.373	0.245	307.362	0.319	13	0.138	K.VLTLEEVSK.H
R3/RRR3-22/3	1737.770	1737.720	29.189	0.315	1005.050	0.496	28	0.129	K.DATDDFEDVGHSTTAR.A
R3/RRR3-22/2	1017.715	1018.186	-464.151	0.230	169.286	0.336	11	0.122	-.VLTLEEVSK.-
R3/RRR3-23/3	1737.830	1737.720	63.534	0.356	738.789	0.516	26	0.119	K.DATDDFEDVGHSTTAR.A
R3/RRR3-23/3	1657.446	1657.845	-241.647	0.423	790.768	0.512	22	0.118	K.HNTKDDCWLIIGGK.V
R3/RRR3-23/3	1902.058	1902.051	3.430	0.469	1074.367	0.410	31	0.118	K.FLEDHPGGDDVLLSSTAK.D
R3/RRR3-22/3	1738.598	1737.720	-70.473	0.356	975.976	0.433	28	0.117	K.DATDDFEDVGHSTTAR.A
R3/RRR3-21/3	1737.573	1737.720	-84.537	0.334	675.202	0.449	25	0.108	K.DATDDFEDVGHSTTAR.A
R3/RRR3-23/3	1901.989	1902.051	-32.973	0.421	1009.189	0.354	29	0.105	K.FLEDHPGGDDVLLSSTAK.D
R3/RRR3-23/3	1737.975	1737.720	147.326	0.308	464.931	0.440	21	0.103	K.DATDDFEDVGHSTTAR.A
R3/RRR3-21/3	1737.484	1737.720	-136.335	0.324	564.948	0.423	23	0.103	K.DATDDFEDVGHSTTAR.A
R3/RRR3-22/3	1736.988	1737.720	-999.815	0.278	668.156	0.385	24	0.100	K.DATDDFEDVGHSTTAR.A
R3/RRR3-23/3	1737.661	1737.720	-34.013	0.297	652.559	0.364	24	0.098	K.DATDDFEDVGHSTTAR.A
R3/RRR3-23/3	1901.804	1902.051	-130.414	0.380	707.649	0.319	26	0.092	K.FLEDHPGGDDVLLSSTAK.D
R3/RRR3-16/2	1868.462	1868.124	181.079	0.600	2847.858	0.642	30	0.527	R.LQAQSALAEAAAASGVALPK.G
R3/RRR3-16/2	1867.556	1868.124	-842.417	0.538	2528.319	0.633	29	0.443	R.LQAQSALAEAAAASGVALPK.G
R3/RRR3-16/2	1867.878	1868.124	-132.448	0.539	2447.687	0.619	29	0.419	R.LQAQSALAEAAAASGVALPK.G
R3/RRR3-16/3	1868.060	1868.124	-34.358	0.498	2633.889	0.480	38	0.387	R.LQAQSALAEAAAASGVALPK.G
R3/RRR3-16/3	1868.056	1868.124	-36.816	0.486	2360.889	0.446	37	0.308	R.LQAQSALAEAAAASGVALPK.G
R3/RRR3-15/3	1869.538	1868.124	221.834	0.428	1967.054	0.463	35	0.239	R.LQAQSALAEAAAASGVALPK.G
R3/RRR3-16/2	1480.077	1480.565	-330.943	0.467	798.101	0.482	20	0.160	K.QYLAGGQDTSNLGR.G
R3/RRR3-16/2	1480.198	1480.565	-248.861	0.459	761.260	0.463	20	0.156	K.QYLAGGQDTSNLGR.G
R3/RRR3-16/2	1102.013	1102.222	-190.164	0.348	827.926	0.464	14	0.156	R.YSGSVDAFKK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1066.929	1067.174	-230.271	0.247	1001.990	0.382	14	0.153	K.SVIQVDDYK.K
R3/RRR3-16/2	1480.106	1480.565	-310.918	0.453	544.309	0.441	17	0.145	K.QYLAGGQDTSNLGR.G
R3/RRR3-16/2	1102.061	1102.222	-146.161	0.372	543.870	0.444	13	0.145	R.YSGSVDAFKK.I
R3/RRR3-16/2	1066.749	1067.174	-399.603	0.255	844.108	0.352	13	0.143	K.SVIQVDDYK.K
R3/RRR3-16/2	1064.055	1064.220	-155.639	0.261	241.843	0.495	11	0.138	R.SHPGQPLTVK.Q
R3/RRR3-16/2	1063.497	1064.220	-1624.733	0.259	214.125	0.375	11	0.137	R.SHPGQPLTVK.Q
R3/RRR3-16/2	1063.225	1064.220	-1881.485	0.179	382.159	0.505	14	0.134	R.SHPGQPLTVK.Q
R3/RRR3-16/2	1066.382	1067.174	-1685.782	0.113	826.786	0.129	13	0.124	K.SVIQVDDYK.K
R3/RRR3-7/2	1047.188	1047.188	0.163	0.472	1482.141	0.341	16	0.187	K.SSVLESIVGR.D
R3/RRR3-7/2	927.000	927.039	-42.081	0.411	852.040	0.420	13	0.155	R.FTDFAAVR.K
R3/RRR3-7/2	1100.677	1100.400	252.552	0.230	734.070	0.362	13	0.138	-.IPSIIAMINK.-
R3/RRR3-7/3	1506.962	1506.729	155.571	0.468	1154.131	0.477	27	0.136	R.GPAEASVDAVHLVLK.E
R3/RRR3-7/2	1100.924	1100.400	-433.908	0.274	455.362	0.369	11	0.134	-.IPSIIAMINK.-
R3/RRR3-7/2	1100.814	1100.400	377.091	0.177	593.527	0.099	12	0.126	-.IPSIIAMINK.-
R3/RRR3-7/3	1319.737	1319.540	150.226	0.472	1094.901	0.390	21	0.115	R.LQHPWVGIVNR.S
R3/RRR3-7/3	1320.032	1319.540	374.190	0.519	1013.453	0.389	21	0.111	R.LQHPWVGIVNR.S
R3/RRR3-7/3	1640.653	1640.785	-80.576	0.403	822.521	0.361	23	0.100	R.VFKEHLDGGRPGGDR.I
R3/RRR3-7/3	1505.914	1506.729	-1208.680	0.379	683.167	0.379	23	0.096	R.GPAEASVDAVHLVLK.E
R3/RRR3-7/3	1319.796	1319.540	194.888	0.506	1011.724	0.279	21	0.095	R.LQHPWVGIVNR.S
R3/RRR3-7/3	1639.954	1640.785	-1120.006	0.319	965.041	0.242	23	0.089	R.VFKEHLDGGRPGGDR.I
R3/RRR3-7/3	1640.647	1640.785	-83.934	0.338	723.891	0.274	23	0.087	-.VFKEHLDGGRPGGDR.-
R3/RRR3-6/3	1319.992	1319.540	344.149	0.340	916.220	0.254	19	0.085	-.LQHPWVGIVNR.-
R3/RRR3-6/3	1640.386	1640.785	-243.824	0.335	640.444	0.268	21	0.084	-.VFKEHLDGGRPGGDR.-
R3/RRR3-13/2	1840.336	1840.028	167.813	0.636	3760.312	0.629	29	0.802	R.AFIAGVADDNGYGWAIAK.A
R3/RRR3-13/2	1839.995	1840.028	-17.940	0.583	3788.447	0.589	29	0.792	R.AFIAGVADDNGYGWAIAK.A
R3/RRR3-13/2	1839.839	1840.028	-102.856	0.593	3678.475	0.586	28	0.751	R.AFIAGVADDNGYGWAIAK.A
R3/RRR3-13/2	1840.650	1840.028	-205.714	0.615	3538.898	0.600	29	0.711	R.AFIAGVADDNGYGWAIAK.A
R3/RRR3-13/2	1840.104	1840.028	41.213	0.570	3140.582	0.565	29	0.572	R.AFIAGVADDNGYGWAIAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1674.067	1674.858	-1073.313	0.477	1102.404	0.499	21	0.180	R.AM*SSESGPQGLPIDLR.G
R3/RRR3-13/2	1674.434	1674.858	-253.974	0.482	1011.007	0.453	21	0.166	R.AM*SSESGPQGLPIDLR.G
R3/RRR3-13/2	1674.278	1674.858	-946.666	0.451	933.495	0.404	21	0.155	R.AM*SSESGPQGLPIDLR.G
R3/RRR3-13/2	1112.979	1113.205	-203.472	0.427	817.490	0.348	16	0.147	R.YAGSSNWTVK.E
R3/RRR3-13/2	1112.977	1113.205	-204.902	0.472	735.996	0.345	16	0.145	R.YAGSSNWTVK.E
R3/RRR3-13/2	1113.015	1113.205	-170.794	0.418	508.321	0.403	14	0.145	R.YAGSSNWTVK.E
R3/RRR3-13/2	1346.142	1346.619	-355.392	0.404	714.457	0.365	16	0.144	R.KLPDGSLM*EIVK.V
R3/RRR3-13/2	1330.252	1330.619	-276.637	0.381	628.906	0.384	16	0.143	R.KLPDGSLMEIVK.V
R3/RRR3-13/2	1346.277	1346.619	-254.772	0.374	696.428	0.282	16	0.136	R.KLPDGSLM*EIVK.V
R3/RRR3-13/2	1346.287	1346.619	-247.131	0.341	592.879	0.291	15	0.135	R.KLPDGSLM*EIVK.V
R3/RRR3-13/2	1197.142	1196.359	-181.292	0.177	311.236	0.445	17	0.133	R.AIPGYGGGMSSAK.A
R3/RRR3-13/2	1211.432	1212.358	-1594.781	0.150	233.506	0.604	19	0.132	R.AIPGYGGGM*SSAK.A
R3/RRR3-13/2	1195.831	1196.359	-1281.220	0.075	213.187	0.390	13	0.121	-.AIPGYGGGMSSAK.-
R3/RRR3-13/2	1211.493	1212.358	-1544.170	0.057	149.458	0.567	16	0.119	R.AIPGYGGGM*SSAK.A
R3/RRR3-13/3	1331.611	1330.619	-5.813	0.429	1090.100	0.282	23	0.097	R.KLPDGSLMEIVK.V
R3/RRR3-13/3	1441.471	1441.661	-132.693	0.440	1997.534	0.304	29	0.184	K.IRVNTISAGPLGSR.A
R3/RRR3-13/2	1557.239	1556.808	277.574	0.534	1150.089	0.480	20	0.183	K.MIEYSYVNAPLQK.E
R3/RRR3-13/3	1442.518	1441.661	-99.537	0.471	1562.093	0.406	27	0.159	K.IRVNTISAGPLGSR.A
R3/RRR3-13/2	1172.045	1172.317	-232.914	0.453	481.770	0.490	16	0.151	R.VNTISAGPLGSR.A
R3/RRR3-13/2	1556.142	1556.808	-1073.709	0.361	1059.291	0.309	19	0.150	K.MIEYSYVNAPLQK.E
R3/RRR3-13/2	1171.653	1172.317	-1424.071	0.456	621.088	0.431	17	0.149	R.VNTISAGPLGSR.A
R3/RRR3-13/2	1171.457	1172.317	-1591.953	0.416	502.871	0.461	16	0.148	R.VNTISAGPLGSR.A
R3/RRR3-13/3	1440.300	1441.661	-1644.747	0.315	1039.331	0.199	23	0.085	K.IRVNTISAGPLGSR.A
R3/RRR3-17/2	1790.608	1791.081	-264.934	0.600	2554.225	0.606	23	0.438	K.KLQQVLNVYDEILSK.N
R3/RRR3-17/2	1791.302	1791.081	123.673	0.597	2270.866	0.544	22	0.353	K.KLQQVLNVYDEILSK.N
R3/RRR3-17/2	1662.473	1662.908	-262.524	0.588	2288.785	0.520	22	0.350	K.LQQVLNVYDEILSK.N
R3/RRR3-17/2	1790.793	1791.081	-161.600	0.579	1953.205	0.599	21	0.312	K.KLQQVLNVYDEILSK.N
R3/RRR3-17/2	1662.419	1662.908	-295.233	0.580	2149.366	0.480	22	0.311	K.LQQVLNVYDEILSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1663.280	1662.908	224.102	0.621	2008.223	0.498	22	0.291	K.LQQVLNVYDEILSK.N
R3/RRR3-17/2	1344.036	1343.460	-316.433	0.500	1875.092	0.531	18	0.282	R.YVCTQFPEGNK.T
R3/RRR3-17/2	1344.129	1343.460	-247.091	0.537	1446.481	0.538	17	0.225	R.YVCTQFPEGNK.T
R3/RRR3-17/2	1343.064	1343.460	-295.694	0.458	1428.744	0.475	17	0.208	R.YVCTQFPEGNK.T
R3/RRR3-17/2	1275.163	1275.439	-216.960	0.441	1208.922	0.413	16	0.176	K.LRDPNGQVTFK.H
R3/RRR3-17/2	1275.253	1275.439	-146.377	0.406	1189.541	0.403	17	0.173	K.LRDPNGQVTFK.H
R3/RRR3-17/2	1275.033	1275.439	-318.961	0.435	991.421	0.437	16	0.165	K.LRDPNGQVTFK.H
R3/RRR3-17/2	1096.959	1097.203	-223.744	0.329	973.010	0.409	17	0.159	K.TLYGTGSLER.A
R3/RRR3-17/2	1096.828	1097.203	-343.770	0.330	870.704	0.423	16	0.156	K.TLYGTGSLER.A
R3/RRR3-17/2	1096.983	1097.203	-201.416	0.289	839.650	0.449	16	0.155	K.TLYGTGSLER.A
R3/RRR3-17/2	1096.376	1097.203	-1671.490	0.287	789.771	0.424	16	0.150	K.TLYGTGSLER.A
R3/RRR3-17/2	1096.455	1097.203	-1599.457	0.283	769.538	0.370	16	0.145	K.TLYGTGSLER.A
R3/RRR3-17/2	1096.463	1097.203	-1592.523	0.257	724.872	0.371	14	0.142	K.TLYGTGSLER.A
R3/RRR3-17/3	1275.138	1275.439	-236.226	0.400	1106.031	0.437	26	0.118	K.LRDPNGQVTFK.H
R3/RRR3-17/3	1275.537	1275.439	77.441	0.383	735.605	0.420	23	0.103	K.LRDPNGQVTFK.H
R3/RRR3-17/3	1275.341	1275.439	-77.064	0.383	666.842	0.361	23	0.097	K.LRDPNGQVTFK.H
R3/RRR3-22/2	1877.241	1878.179	-1035.679	0.457	1463.144	0.524	22	0.220	K.GVDDILLVSVNDPFVM*K.A
R3/RRR3-23/2	1162.198	1161.379	-156.192	0.318	1770.764	0.161	16	0.183	R.RFALLADNLK.V
R3/RRR3-22/2	1004.617	1005.192	-1572.612	0.464	1367.463	0.351	16	0.180	R.FALLADNLK.V
R3/RRR3-22/2	1876.911	1878.179	-1212.316	0.361	1293.173	0.422	20	0.180	K.GVDDILLVSVNDPFVM*K.A
R3/RRR3-22/2	1005.065	1005.192	-127.254	0.484	1374.310	0.315	16	0.175	-.FALLADNLK.-
R3/RRR3-22/2	1185.674	1186.339	-1408.574	0.507	946.176	0.502	18	0.175	K.FLADGLGTYTK.A
R3/RRR3-22/2	1004.966	1005.192	-226.316	0.510	1322.331	0.334	16	0.174	-.FALLADNLK.-
R3/RRR3-23/2	1187.058	1186.339	-237.498	0.345	968.591	0.467	18	0.166	K.FLADGLGTYTK.A
R3/RRR3-22/2	1161.216	1161.379	-140.508	0.431	1508.617	0.187	16	0.161	R.RFALLADNLK.V
R3/RRR3-22/2	1188.111	1188.353	-204.414	0.404	918.047	0.452	16	0.161	K.ALGLELDLSEK.G
R3/RRR3-22/2	1185.634	1186.339	-1442.079	0.475	993.230	0.384	18	0.160	K.FLADGLGTYTK.A
R3/RRR3-22/2	1188.016	1188.353	-284.611	0.443	813.156	0.389	15	0.148	K.ALGLELDLSEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1185.970	1186.339	-311.840	0.379	819.974	0.296	17	0.142	K.FLADGLGTYTK.A
R3/RRR3-24/2	1185.671	1186.339	-1410.539	0.273	704.759	0.280	14	0.135	K.FLADGLGTYTK.A
R3/RRR3-21/2	1186.978	1186.339	-304.664	0.288	658.787	0.217	14	0.132	K.FLADGLGTYTK.A
R3/RRR3-12/2	1319.957	1319.488	356.319	0.547	2197.300	0.426	19	0.303	R.DDLFNINAGIVK.G
R3/RRR3-12/2	1319.465	1319.488	-17.502	0.520	1853.334	0.390	18	0.239	R.DDLFNINAGIVK.G
R3/RRR3-12/2	1318.554	1319.488	-1470.999	0.437	1772.141	0.339	18	0.218	R.DDLFNINAGIVK.G
R3/RRR3-12/2	1390.120	1390.482	-260.671	0.452	1442.047	0.410	20	0.196	K.RTQDGGTEVVEAK.A
R3/RRR3-12/2	1233.382	1234.295	-1555.604	0.499	881.941	0.531	18	0.174	R.TQDGGTEVVEAK.A
R3/RRR3-12/2	1389.918	1390.482	-1128.474	0.414	1154.953	0.366	18	0.163	K.RTQDGGTEVVEAK.A
R3/RRR3-12/2	1233.520	1234.295	-1443.368	0.472	889.055	0.433	18	0.160	R.TQDGGTEVVEAK.A
R3/RRR3-12/2	1234.114	1234.295	-147.387	0.483	795.269	0.411	17	0.153	R.TQDGGTEVVEAK.A
R3/RRR3-12/2	1234.407	1234.295	90.695	0.520	718.632	0.415	16	0.150	R.TQDGGTEVVEAK.A
R3/RRR3-12/2	1234.003	1234.295	-237.789	0.446	822.369	0.338	17	0.146	R.TQDGGTEVVEAK.A
R3/RRR3-11/2	1235.102	1234.295	-156.786	0.321	653.837	0.373	16	0.143	R.TQDGGTEVVEAK.A
R3/RRR3-11/2	1234.666	1234.295	301.205	0.361	462.533	0.393	15	0.143	R.TQDGGTEVVEAK.A
R3/RRR3-13/2	1234.786	1234.295	398.844	0.360	506.116	0.388	14	0.139	-.TQDGGTEVVEAK.-
R3/RRR3-12/3	1390.832	1390.482	252.850	0.359	801.955	0.415	26	0.104	K.RTQDGGTEVVEAK.A
R3/RRR3-12/3	1390.658	1390.482	127.290	0.353	472.421	0.327	22	0.095	K.RTQDGGTEVVEAK.A
R3/RRR3-12/3	1390.297	1390.482	-133.438	0.312	739.171	0.302	25	0.090	K.RTQDGGTEVVEAK.A
R3/RRR3-3/2	1425.323	1424.586	-184.997	0.311	930.584	0.463	17	0.156	K.AGWPVAGSPDPTLR.I
R3/RRR3-3/2	1249.276	1249.441	-132.956	0.435	984.886	0.371	16	0.152	R.AALNLAYQGLSK.V
R3/RRR3-15/2	1610.219	1609.850	229.738	0.474	801.190	0.477	19	0.160	K.STSSIFPLQNVFIR.K
R3/RRR3-14/2	1915.448	1915.005	231.865	0.470	1064.437	0.498	22	0.156	K.LDRPAETDEAVAGEVAAAE.-
R3/RRR3-14/2	1610.477	1609.850	-232.835	0.476	736.587	0.467	18	0.155	K.STSSIFPLQNVFIR.K
R3/RRR3-14/2	1610.133	1609.850	175.913	0.449	669.150	0.468	18	0.153	K.STSSIFPLQNVFIR.K
R3/RRR3-15/2	1609.858	1609.850	4.745	0.447	697.310	0.456	18	0.152	K.STSSIFPLQNVFIR.K
R3/RRR3-15/2	1609.342	1609.850	-939.998	0.377	745.164	0.381	18	0.145	K.STSSIFPLQNVFIR.K
R3/RRR3-14/2	1609.401	1609.850	-280.234	0.385	547.786	0.409	16	0.142	K.STSSIFPLQNVFIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1914.243	1915.005	-923.185	0.389	635.204	0.454	17	0.047	K.LDRPAETDEAVAGEVAAAE.-
R3/RRR3-14/2	1914.621	1915.005	-201.092	0.437	609.224	0.500	18	0.044	K.LDRPAETDEAVAGEVAAAE.-
R3/RRR3-15/2	1914.716	1915.005	-151.461	0.405	619.441	0.442	17	0.043	K.LDRPAETDEAVAGEVAAAE.-
R3/RRR3-15/2	1817.041	1818.019	-1091.770	0.525	2830.165	0.655	27	0.528	K.ALAVGADVSLDTATGNLTK.Y
R3/RRR3-15/2	1817.855	1818.019	-90.226	0.567	2626.346	0.653	27	0.473	K.ALAVGADVSLDTATGNLTK.Y
R3/RRR3-15/2	1816.689	1818.019	-1286.418	0.409	2543.994	0.587	27	0.429	K.ALAVGADVSLDTATGNLTK.Y
R3/RRR3-15/2	1590.457	1590.845	-244.927	0.615	1732.513	0.550	22	0.262	K.KADLIFGEIQSQIK.N
R3/RRR3-16/2	1590.290	1590.845	-981.286	0.577	1605.907	0.519	22	0.238	K.KADLIFGEIQSQIK.N
R3/RRR3-15/2	1590.404	1590.845	-278.115	0.600	1619.412	0.498	22	0.234	K.KADLIFGEIQSQIK.N
R3/RRR3-15/2	1462.317	1462.673	-243.783	0.405	1729.882	0.403	19	0.226	K.ADLIFGEIQSQIK.N
R3/RRR3-16/2	1591.300	1590.845	286.713	0.626	1477.075	0.506	21	0.217	K.KADLIFGEIQSQIK.N
R3/RRR3-15/2	1462.532	1462.673	-96.491	0.501	1519.147	0.472	19	0.216	K.ADLIFGEIQSQIK.N
R3/RRR3-15/2	1462.474	1462.673	-136.010	0.528	1582.087	0.440	19	0.216	K.ADLIFGEIQSQIK.N
R3/RRR3-16/2	1590.310	1590.845	-968.570	0.568	1435.189	0.495	21	0.211	K.KADLIFGEIQSQIK.N
R3/RRR3-15/2	1589.744	1590.845	-1326.117	0.576	1443.787	0.490	21	0.211	K.KADLIFGEIQSQIK.N
R3/RRR3-16/2	1462.052	1462.673	-1111.822	0.386	1547.723	0.309	18	0.186	K.ADLIFGEIQSQIK.N
R3/RRR3-16/2	1462.580	1462.673	-63.840	0.382	1546.787	0.273	18	0.179	K.ADLIFGEIQSQIK.N
R3/RRR3-15/2	1232.529	1233.399	-1521.118	0.407	741.096	0.388	17	0.149	K.SILSFAVPDQR.S
R3/RRR3-16/2	1233.295	1233.399	-83.949	0.492	695.493	0.388	17	0.149	K.SILSFAVPDQR.S
R3/RRR3-15/2	1233.109	1233.399	-235.281	0.429	679.059	0.332	17	0.143	K.SILSFAVPDQR.S
R3/RRR3-15/2	1435.932	1436.643	-1195.314	0.441	780.472	0.364	14	0.142	K.ASALLQHEWRPK.S
R3/RRR3-16/2	1233.008	1233.399	-318.016	0.434	574.778	0.343	16	0.142	K.SILSFAVPDQR.S
R3/RRR3-15/2	1436.254	1436.643	-272.161	0.452	687.756	0.341	14	0.137	-.ASALLQHEWRPK.-
R3/RRR3-15/2	1436.145	1436.643	-347.887	0.466	565.413	0.341	12	0.130	-.ASALLQHEWRPK.-
R3/RRR3-16/3	1590.328	1590.845	-956.980	0.386	1402.934	0.170	23	0.099	-.KADLIFGEIQSQIK.-
R3/RRR3-16/3	1590.734	1590.845	-70.020	0.477	1297.666	0.229	24	0.098	K.KADLIFGEIQSQIK.N
R3/RRR3-16/3	1590.911	1590.845	41.272	0.398	1102.008	0.163	22	0.082	K.KADLIFGEIQSQIK.N
R3/RRR3-15/3	1590.177	1590.845	-1052.353	0.389	1021.364	0.129	22	0.078	-.KADLIFGEIQSQIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1643.303	1643.608	-186.162	0.535	1208.631	0.563	23	0.202	R.SAFDSASNGPSSGSESR.S
R3/RRR3-4/2	1644.096	1643.608	297.836	0.553	1091.309	0.569	22	0.191	R.SAFDSASNGPSSGSESR.S
R3/RRR3-4/3	1116.079	1116.255	-158.160	0.537	1733.805	0.312	23	0.144	R.HFDLSNVKR.I
R3/RRR3-4/3	1116.597	1116.255	307.713	0.547	1533.671	0.301	21	0.126	R.HFDLSNVKR.I
R3/RRR3-19/2	1275.220	1275.434	-168.464	0.443	1372.341	0.464	17	0.200	R.GFGFVTFDEKK.A
R3/RRR3-19/2	1437.754	1438.614	-1297.778	0.480	1199.975	0.492	20	0.188	R.AITVDKAQPQGPGR.D
R3/RRR3-19/2	1275.306	1275.434	-100.480	0.437	1243.920	0.442	16	0.183	R.GFGFVTFDEKK.A
R3/RRR3-19/2	879.932	879.980	-54.768	0.500	1387.767	0.290	14	0.170	K.FGNLTEAK.V
R3/RRR3-18/2	879.975	879.980	-6.207	0.477	1264.141	0.258	14	0.157	K.FGNLTEAK.V
R3/RRR3-19/2	879.910	879.980	-80.233	0.507	1198.968	0.272	14	0.155	K.FGNLTEAK.V
R3/RRR3-19/2	879.865	879.980	-131.029	0.486	1087.385	0.282	14	0.151	K.FGNLTEAK.V
R3/RRR3-18/2	879.867	879.980	-129.637	0.478	1043.453	0.263	14	0.147	K.FGNLTEAK.V
R3/RRR3-19/2	1071.182	1071.211	-27.159	0.336	527.477	0.454	13	0.145	K.VVFDKYSGR.S
R3/RRR3-19/2	1147.798	1147.261	-404.454	0.387	795.005	0.358	14	0.145	R.GFGFVTFDEK.K
R3/RRR3-19/2	1071.245	1071.211	31.590	0.328	495.664	0.408	12	0.140	K.VVFDKYSGR.S
R3/RRR3-19/2	1147.228	1147.261	-29.094	0.324	672.892	0.353	14	0.139	-.GFGFVTFDEK.-
R3/RRR3-18/2	879.762	879.980	-249.060	0.473	875.279	0.215	14	0.137	K.FGNLTEAK.V
R3/RRR3-19/3	1438.986	1438.614	258.981	0.313	808.185	0.389	25	0.102	R.AITVDKAQPQGPGR.D
R3/RRR3-18/3	1438.581	1438.614	-23.339	0.336	429.021	0.352	20	0.097	R.AITVDKAQPQGPGR.D
R3/RRR3-19/3	1439.549	1438.614	-45.437	0.336	878.593	0.302	26	0.094	R.AITVDKAQPQGPGR.D
R3/RRR3-19/3	1439.365	1438.614	-173.675	0.331	675.002	0.316	23	0.093	R.AITVDKAQPQGPGR.D
R3/RRR3-18/3	1437.720	1438.614	-1321.876	0.256	531.301	0.310	22	0.092	R.AITVDKAQPQGPGR.D
R3/RRR3-18/2	1702.285	1701.922	213.804	0.608	1753.942	0.577	23	0.273	K.DM*GAFNCGAFVAGIVR.G
R3/RRR3-18/2	1701.788	1701.922	-78.521	0.537	1403.029	0.576	25	0.228	K.DM*GAFNCGAFVAGIVR.G
R3/RRR3-18/2	991.386	992.111	-1744.332	0.476	1283.722	0.321	13	0.168	K.FAEEVLQR.E
R3/RRR3-18/2	1122.084	1122.213	-115.620	0.367	1358.484	0.289	17	0.167	R.LEDAGYAVGAR.V
R3/RRR3-18/2	991.610	992.111	-1517.613	0.467	1257.588	0.293	13	0.161	K.FAEEVLQR.E
R3/RRR3-18/2	991.796	992.111	-318.513	0.506	1255.143	0.272	13	0.157	K.FAEEVLQR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1278.137	1278.399	-206.205	0.509	705.334	0.427	16	0.148	-.RLEDAGYAVGAR.-
R3/RRR3-18/2	1277.675	1278.399	-1353.527	0.494	709.378	0.423	16	0.148	-.RLEDAGYAVGAR.-
R3/RRR3-18/2	1278.195	1278.399	-160.792	0.502	674.459	0.389	16	0.143	-.RLEDAGYAVGAR.-
R3/RRR3-18/2	1040.013	1040.235	-214.451	0.345	735.199	0.289	12	0.136	R.VLELLCHR.E
R3/RRR3-5/2	1710.342	1710.825	-283.667	0.482	1601.751	0.517	22	0.237	R.SIQSFDPLASSSWER.V
R3/RRR3-5/2	1712.332	1710.825	-288.951	0.541	1349.888	0.621	21	0.230	R.SIQSFDPLASSSWER.V
R3/RRR3-5/2	1751.564	1752.004	-252.037	0.478	1217.461	0.526	21	0.194	K.EFQNGFLPAVLSLSTK.F
R3/RRR3-5/2	1859.652	1860.061	-220.533	0.570	953.159	0.638	23	0.194	R.GVVPASGFSFSSQQFWK.V
R3/RRR3-4/2	1294.638	1295.510	-1449.846	0.414	1015.139	0.422	15	0.162	K.TPLENLEPILR.E
R3/RRR3-5/2	1860.988	1860.061	-39.054	0.493	870.477	0.464	22	0.159	R.GVVPASGFSFSSQQFWK.V
R3/RRR3-5/2	1751.980	1752.004	-13.391	0.407	500.630	0.548	14	0.146	K.EFQNGFLPAVLSLSTK.F
R3/RRR3-5/2	1100.313	1101.283	-1796.369	0.463	816.551	0.255	13	0.135	K.STLLNHLFR.T
R3/RRR3-4/2	1295.448	1295.510	-47.787	0.342	676.205	0.273	14	0.133	K.TPLENLEPILR.E
R3/RRR3-5/2	1100.593	1101.283	-1540.379	0.314	548.334	0.219	13	0.132	-.STLLNHLFR.-
R3/RRR3-5/3	1566.801	1566.704	61.639	0.482	1290.321	0.377	31	0.124	K.RLADEGQRPAAPER.Q
R3/RRR3-5/3	1566.812	1566.704	69.140	0.437	1021.507	0.388	27	0.111	K.RLADEGQRPAAPER.Q
R3/RRR3-5/3	1565.980	1566.704	-1104.579	0.342	751.302	0.267	25	0.089	K.RLADEGQRPAAPER.Q
R3/RRR3-10/2	1318.028	1318.416	-294.901	0.486	2105.226	0.477	20	0.300	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1461.080	1460.527	-307.341	0.558	1950.011	0.541	20	0.295	K.AISTSNAYDDQFK.Q
R3/RRR3-10/2	1318.808	1318.416	298.327	0.517	1865.079	0.546	21	0.281	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1461.047	1460.527	-329.806	0.539	1733.711	0.589	20	0.275	K.AISTSNAYDDQFK.Q
R3/RRR3-10/2	1319.117	1318.416	-227.087	0.543	1698.672	0.526	20	0.251	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1460.088	1460.527	-301.764	0.494	1485.521	0.572	20	0.236	K.AISTSNAYDDQFK.Q
R3/RRR3-12/2	1318.226	1318.416	-144.392	0.532	1592.893	0.491	20	0.229	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1286.041	1286.493	-352.695	0.444	1443.555	0.556	20	0.228	K.IPATAECVPSIK.E
R3/RRR3-10/2	1318.456	1318.416	31.145	0.499	1526.157	0.507	20	0.225	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1318.085	1318.416	-251.416	0.488	1438.672	0.533	20	0.221	R.LANDTQGTVEAAK.W
R3/RRR3-9/2	1317.986	1318.416	-326.960	0.452	1577.397	0.451	21	0.219	R.LANDTQGTVEAAK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1318.130	1318.416	-217.597	0.511	1442.047	0.491	21	0.213	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1318.157	1318.416	-196.786	0.492	1439.447	0.490	20	0.211	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1286.100	1286.493	-306.506	0.451	1261.948	0.510	19	0.199	K.IPATAECVPSIK.E
R3/RRR3-12/2	1318.157	1318.416	-196.879	0.477	1340.716	0.471	19	0.197	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1286.128	1286.493	-284.890	0.458	1069.185	0.566	19	0.192	K.IPATAECVPSIK.E
R3/RRR3-9/2	1317.475	1318.416	-1477.129	0.353	1237.994	0.400	20	0.175	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1178.069	1178.320	-213.223	0.429	804.443	0.428	16	0.154	R.GVTSNPSIFQK.A
R3/RRR3-10/2	1178.139	1178.320	-153.663	0.444	675.216	0.449	15	0.151	R.GVTSNPSIFQK.A
R3/RRR3-1/2	1317.744	1318.416	-1272.604	0.370	749.177	0.422	15	0.149	R.LANDTQGTVEAAK.W
R3/RRR3-10/2	1202.536	1203.416	-1567.508	0.333	877.508	0.343	15	0.146	K.VVDRPNVYIK.I
R3/RRR3-10/2	1177.507	1178.320	-1544.158	0.385	693.697	0.350	15	0.142	R.GVTSNPSIFQK.A
R3/RRR3-10/2	1203.033	1203.416	-318.816	0.332	760.432	0.270	14	0.136	K.VVDRPNVYIK.I
R3/RRR3-10/2	1203.183	1203.416	-194.323	0.355	729.018	0.259	14	0.135	K.VVDRPNVYIK.I
R3/RRR3-9/2	1460.044	1460.527	-331.878	0.240	681.302	0.250	15	0.131	K.AISTSNAYDDQFK.Q
R3/RRR3-5/2	1485.856	1486.653	-1212.833	0.384	1321.240	0.416	21	0.185	K.GLVDSDTLPLNVSR.E
R3/RRR3-4/2	1486.237	1486.653	-280.308	0.410	1268.756	0.416	20	0.180	K.GLVDSDTLPLNVSR.E
R3/RRR3-5/2	1164.121	1164.245	-107.027	0.492	1115.595	0.433	18	0.174	K.ALDTESVDSVK.I
R3/RRR3-5/2	1101.484	1102.223	-1583.930	0.397	1212.342	0.383	17	0.172	K.LGIIEDATNR.N
R3/RRR3-5/2	1164.075	1164.245	-146.684	0.487	1108.711	0.401	18	0.169	K.ALDTESVDSVK.I
R3/RRR3-4/2	1578.511	1578.702	-121.126	0.457	1138.615	0.409	17	0.167	K.ETTTEWELLNDVK.A
R3/RRR3-5/2	1485.954	1486.653	-1146.507	0.411	1022.291	0.442	20	0.166	K.GLVDSDTLPLNVSR.E
R3/RRR3-4/2	1163.928	1164.245	-273.460	0.465	936.415	0.455	17	0.166	K.ALDTESVDSVK.I
R3/RRR3-5/2	1101.884	1102.223	-308.858	0.479	1161.888	0.356	17	0.165	K.LGIIEDATNR.N
R3/RRR3-4/2	1167.052	1167.294	-207.368	0.407	974.264	0.383	17	0.158	K.LASLDEYISR.M
R3/RRR3-5/2	1164.198	1164.245	-40.133	0.419	781.258	0.434	16	0.154	K.ALDTESVDSVK.I
R3/RRR3-4/2	1166.396	1167.294	-1631.717	0.337	758.413	0.406	16	0.149	K.LASLDEYISR.M
R3/RRR3-5/2	1166.406	1167.294	-1623.095	0.303	335.611	0.285	11	0.135	K.LASLDEYISR.M
R3/RRR3-4/2	1101.251	1102.223	-1796.729	0.334	764.398	0.238	14	0.134	K.LGIIEDATNR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/3	1864.410	1864.989	-849.362	0.500	802.704	0.569	30	0.133	R.DKVAQDSESESLKQTAK.L
R3/RRR3-4/2	1485.912	1486.653	-1174.719	0.264	639.557	0.221	16	0.130	K.GLVDSDTLPLNVSR.E
R3/RRR3-5/3	1864.424	1864.989	-841.968	0.522	617.466	0.547	27	0.121	R.DKVAQDSESESLKQTAK.L
R3/RRR3-4/3	1864.913	1864.989	-41.277	0.459	825.744	0.494	29	0.120	R.DKVAQDSESESLKQTAK.L
R3/RRR3-5/3	1864.588	1864.989	-216.017	0.509	724.354	0.510	29	0.119	R.DKVAQDSESESLKQTAK.L
R3/RRR3-5/3	1864.579	1864.989	-220.450	0.500	685.881	0.506	27	0.117	R.DKVAQDSESESLKQTAK.L
R3/RRR3-4/3	1864.778	1864.989	-113.569	0.454	425.476	0.492	24	0.109	R.DKVAQDSESESLKQTAK.L
R3/RRR3-17/2	1389.343	1389.582	-171.987	0.467	1220.832	0.513	20	0.195	K.LLGSTNPSPFVTR.V
R3/RRR3-16/2	1390.068	1389.582	350.943	0.512	1101.773	0.525	21	0.189	K.LLGSTNPSPFVTR.V
R3/RRR3-17/2	1447.865	1446.630	162.902	0.351	1131.127	0.476	19	0.178	R.GLPYDLVAVDLDR.K
R3/RRR3-17/2	1389.244	1389.582	-244.003	0.414	912.695	0.532	18	0.172	K.LLGSTNPSPFVTR.V
R3/RRR3-16/2	1446.089	1446.630	-1068.808	0.463	930.664	0.508	19	0.172	R.GLPYDLVAVDLDR.K
R3/RRR3-17/2	1390.289	1389.582	-210.971	0.513	979.952	0.469	19	0.169	K.LLGSTNPSPFVTR.V
R3/RRR3-17/2	1388.652	1389.582	-1394.100	0.368	902.466	0.509	18	0.167	K.LLGSTNPSPFVTR.V
R3/RRR3-16/2	1388.446	1389.582	-1542.540	0.353	920.406	0.485	18	0.165	K.LLGSTNPSPFVTR.V
R3/RRR3-16/2	1389.319	1389.582	-189.703	0.423	864.120	0.476	19	0.163	K.LLGSTNPSPFVTR.V
R3/RRR3-16/3	1492.280	1491.760	-323.118	0.583	1484.941	0.425	28	0.154	R.KTDLLLAANPVHAK.V
R3/RRR3-16/2	1446.665	1446.630	24.238	0.438	659.064	0.482	15	0.152	R.GLPYDLVAVDLDR.K
R3/RRR3-17/2	884.958	885.086	-145.009	0.417	837.184	0.362	13	0.150	R.VELALALR.G
R3/RRR3-16/2	885.029	885.086	-64.344	0.401	793.503	0.341	13	0.146	R.VELALALR.G
R3/RRR3-16/2	884.874	885.086	-240.495	0.384	765.186	0.334	13	0.145	R.VELALALR.G
R3/RRR3-16/2	833.983	834.044	-73.788	0.418	599.402	0.373	11	0.143	K.VPVLIHR.G
R3/RRR3-17/2	1446.931	1446.630	208.617	0.315	656.834	0.362	16	0.140	R.GLPYDLVAVDLDR.K
R3/RRR3-17/3	1491.696	1491.760	-43.233	0.542	1263.567	0.439	28	0.137	R.KTDLLLAANPVHAK.V
R3/RRR3-16/2	1445.842	1446.630	-1240.386	0.192	441.700	0.357	14	0.132	R.GLPYDLVAVDLDR.K
R3/RRR3-17/3	1491.892	1491.760	88.369	0.575	1168.787	0.441	25	0.131	R.KTDLLLAANPVHAK.V
R3/RRR3-3/2	1471.427	1471.596	-115.629	0.484	2467.143	0.522	20	0.388	K.TALSNFEAALDYR.N
R3/RRR3-3/2	1471.902	1471.596	207.906	0.495	2369.982	0.476	20	0.352	K.TALSNFEAALDYR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1470.798	1471.596	-1226.582	0.336	2170.843	0.416	19	0.297	K.TALSNFEAALDYR.N
R3/RRR3-3/2	1470.620	1471.596	-1347.783	0.335	1702.453	0.369	18	0.215	K.TALSNFEAALDYR.N
R3/RRR3-3/2	1808.106	1806.998	60.022	0.538	1390.479	0.509	20	0.209	K.NTLVEIVQSQDQYIR.D
R3/RRR3-3/2	1263.616	1264.370	-1392.229	0.351	1591.924	0.273	18	0.185	R.ADQSLFEAGVAR.E
R3/RRR3-3/2	1265.177	1264.370	-152.478	0.446	1326.120	0.373	18	0.178	R.ADQSLFEAGVAR.E
R3/RRR3-3/2	1384.325	1384.562	-171.372	0.407	1306.123	0.376	17	0.178	K.YIDNLTNIYVR.F
R3/RRR3-3/2	862.436	862.993	-1810.151	0.254	1059.764	0.330	13	0.150	R.GPEYGVLK.R
R3/RRR3-3/2	1384.009	1384.562	-1125.685	0.302	795.690	0.322	15	0.140	K.YIDNLTNIYVR.F
R3/RRR3-3/2	1174.285	1174.417	-112.670	0.417	929.697	0.254	15	0.139	R.LYLINSPVVR.A
R3/RRR3-1/2	1384.830	1384.562	194.189	0.327	700.265	0.280	13	0.134	K.YIDNLTNIYVR.F
R3/RRR3-2/2	1173.676	1174.417	-1487.754	0.421	706.182	0.298	13	0.134	-.LYLINSPVVR.-
R3/RRR3-2/2	862.588	862.993	-470.479	0.189	466.594	0.259	11	0.117	-.GPEYGVLK.-
R3/RRR3-14/2	1533.627	1533.580	30.847	0.522	2746.521	0.583	25	0.474	R.AAGGASGGEELTVEER.N
R3/RRR3-15/2	1533.071	1533.580	-987.242	0.502	2517.738	0.534	23	0.401	R.AAGGASGGEELTVEER.N
R3/RRR3-15/2	1533.160	1533.580	-274.923	0.486	2245.863	0.555	23	0.351	R.AAGGASGGEELTVEER.N
R3/RRR3-14/2	1533.122	1533.580	-299.288	0.517	2228.921	0.550	23	0.346	R.AAGGASGGEELTVEER.N
R3/RRR3-16/2	1533.036	1533.580	-1010.186	0.469	1953.909	0.567	22	0.301	R.AAGGASGGEELTVEER.N
R3/RRR3-15/2	1533.108	1533.580	-308.954	0.491	1813.657	0.540	21	0.270	R.AAGGASGGEELTVEER.N
R3/RRR3-15/2	1390.104	1389.537	-312.464	0.484	1217.779	0.558	19	0.204	R.IISSIEQKEEGR.G
R3/RRR3-14/2	1389.312	1389.537	-162.032	0.476	1299.904	0.512	19	0.203	R.IISSIEQKEEGR.G
R3/RRR3-15/2	1389.002	1389.537	-1108.063	0.509	1167.712	0.536	18	0.195	R.IISSIEQKEEGR.G
R3/RRR3-14/2	1389.161	1389.537	-271.340	0.490	1050.090	0.481	17	0.175	R.IISSIEQKEEGR.G
R3/RRR3-14/2	1389.143	1389.537	-284.299	0.484	1061.300	0.471	17	0.174	R.IISSIEQKEEGR.G
R3/RRR3-17/2	1518.025	1518.782	-1161.241	0.384	2489.803	0.429	21	0.364	K.ASILLLQDAAAYLR.K
R3/RRR3-17/2	1518.132	1518.782	-1090.753	0.456	2237.760	0.477	20	0.328	K.ASILLLQDAAAYLR.K
R3/RRR3-17/2	1146.958	1147.288	-288.031	0.427	1592.537	0.420	18	0.215	K.ALAAEM*GPNTR.V
R3/RRR3-17/2	1146.947	1147.288	-297.855	0.457	1328.893	0.436	17	0.191	K.ALAAEM*GPNTR.V
R3/RRR3-17/2	1146.834	1147.288	-396.745	0.414	1364.629	0.413	17	0.189	K.ALAAEM*GPNTR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1807.700	1808.026	-180.611	0.553	975.765	0.518	18	0.171	R.FLTTNETIKNELIDR.S
R3/RRR3-17/2	1102.040	1102.180	-127.610	0.504	1204.116	0.356	17	0.167	K.NVDEAVEGLR.A
R3/RRR3-17/2	1663.911	1663.895	9.447	0.459	511.945	0.439	16	0.139	R.VNCIAPGFVPTNFAR.F
R3/RRR3-13/2	1902.429	1902.181	131.122	0.601	3016.729	0.622	26	0.563	K.NPINYTQIAVLADDILK.N
R3/RRR3-13/2	1902.508	1902.181	172.690	0.606	2987.322	0.586	26	0.538	K.NPINYTQIAVLADDILK.N
R3/RRR3-13/2	1902.554	1902.181	196.690	0.618	2872.104	0.592	26	0.509	K.NPINYTQIAVLADDILK.N
R3/RRR3-13/2	1612.230	1612.674	-275.945	0.557	2843.240	0.583	25	0.498	K.VGDLDSYEIEGGETK.S
R3/RRR3-14/2	1612.271	1612.674	-250.422	0.558	2804.206	0.588	25	0.490	K.VGDLDSYEIEGGETK.S
R3/RRR3-14/2	1612.285	1612.674	-241.611	0.571	2799.620	0.572	25	0.482	K.VGDLDSYEIEGGETK.S
R3/RRR3-13/2	1612.027	1612.674	-1024.866	0.583	2753.422	0.567	25	0.468	K.VGDLDSYEIEGGETK.S
R3/RRR3-14/2	1612.215	1612.674	-285.592	0.569	2668.221	0.557	25	0.444	K.VGDLDSYEIEGGETK.S
R3/RRR3-14/2	1901.371	1902.181	-954.613	0.577	2552.136	0.600	25	0.434	K.NPINYTQIAVLADDILK.N
R3/RRR3-13/2	1612.307	1612.674	-228.242	0.556	2596.328	0.558	24	0.427	K.VGDLDSYEIEGGETK.S
R3/RRR3-12/2	1612.366	1612.674	-191.633	0.473	2113.452	0.478	23	0.303	K.VGDLDSYEIEGGETK.S
R3/RRR3-13/2	1192.941	1193.326	-324.181	0.453	1158.671	0.491	19	0.186	K.GLCGGINSTSVK.V
R3/RRR3-14/2	1193.193	1193.326	-111.910	0.473	1194.853	0.453	19	0.183	K.GLCGGINSTSVK.V
R3/RRR3-13/2	1193.901	1193.326	-357.147	0.549	1021.053	0.508	19	0.180	K.GLCGGINSTSVK.V
R3/RRR3-13/2	1754.410	1753.910	-285.832	0.565	1016.568	0.511	20	0.175	R.DSKDNIEM*TVSELQK.N
R3/RRR3-13/2	1192.568	1193.326	-1478.457	0.416	1000.463	0.481	18	0.172	K.GLCGGINSTSVK.V
R3/RRR3-14/2	1193.089	1193.326	-199.353	0.465	1082.102	0.429	18	0.170	K.GLCGGINSTSVK.V
R3/RRR3-14/2	1193.157	1193.326	-142.083	0.493	982.993	0.458	19	0.170	K.GLCGGINSTSVK.V
R3/RRR3-13/2	1753.122	1753.910	-1022.985	0.518	958.795	0.467	19	0.164	R.DSKDNIEM*TVSELQK.N
R3/RRR3-14/2	880.921	881.011	-102.935	0.334	642.529	0.359	11	0.143	R.LTLTYNR.T
R3/RRR3-14/2	881.029	881.011	19.788	0.298	619.585	0.358	11	0.141	R.LTLTYNR.T
R3/RRR3-14/2	880.496	881.011	-1726.720	0.152	389.531	0.325	9	0.130	R.LTLTYNR.T
R3/RRR3-13/3	1900.972	1902.181	-1165.529	0.373	1088.286	0.343	27	0.106	K.NPINYTQIAVLADDILK.N
R3/RRR3-14/3	1901.637	1902.181	-814.257	0.361	576.818	0.403	22	0.094	-.NPINYTQIAVLADDILK.-
R3/RRR3-18/1	1071.664	1072.280	-1512.313	0.236	958.175	0.339	15	0.906	K.LLLIGDSGVGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/1	1071.684	1072.280	-1493.663	0.239	928.280	0.290	15	0.899	K.LLLIGDSGVGK.S
R3/RRR3-19/1	1071.382	1072.280	-1777.268	0.192	482.794	0.301	11	0.889	K.LLLIGDSGVGK.S
R3/RRR3-18/2	1639.355	1638.849	-302.150	0.603	2240.729	0.552	22	0.348	K.TNLNVEQVFFSIAR.D
R3/RRR3-17/2	1639.381	1638.849	-286.162	0.590	2166.050	0.545	22	0.332	K.TNLNVEQVFFSIAR.D
R3/RRR3-18/2	1638.133	1638.849	-1050.388	0.546	2053.902	0.537	22	0.310	K.TNLNVEQVFFSIAR.D
R3/RRR3-17/2	1637.615	1638.849	-1367.874	0.382	2162.618	0.445	22	0.303	K.TNLNVEQVFFSIAR.D
R3/RRR3-18/2	1637.650	1638.849	-1346.836	0.432	2102.761	0.471	22	0.300	K.TNLNVEQVFFSIAR.D
R3/RRR3-17/2	1638.350	1638.849	-305.623	0.525	1865.684	0.562	21	0.286	K.TNLNVEQVFFSIAR.D
R3/RRR3-18/2	1165.060	1165.278	-187.125	0.478	1552.353	0.463	17	0.219	K.GQALADEYGIK.F
R3/RRR3-18/2	1164.976	1165.278	-260.076	0.448	1490.782	0.417	17	0.203	K.GQALADEYGIK.F
R3/RRR3-18/2	1164.737	1165.278	-1326.987	0.276	1199.926	0.302	16	0.156	K.GQALADEYGIK.F
R3/RRR3-6/2	1639.336	1638.849	298.178	0.435	941.581	0.389	18	0.154	K.TNLNVEQVFFSIAR.D
R3/RRR3-18/2	1000.944	1001.114	-170.284	0.445	772.400	0.387	13	0.152	R.ADYDYLIK.L
R3/RRR3-18/2	1001.096	1001.114	-18.359	0.450	681.258	0.357	13	0.147	R.ADYDYLIK.L
R3/RRR3-18/2	1000.812	1001.114	-302.920	0.426	545.883	0.371	12	0.146	R.ADYDYLIK.L
R3/RRR3-19/2	1001.603	1001.114	489.804	0.425	588.784	0.338	12	0.143	R.ADYDYLIK.L
R3/RRR3-17/2	1001.091	1001.114	-23.496	0.421	608.978	0.314	12	0.142	R.ADYDYLIK.L
R3/RRR3-18/2	1228.316	1228.379	-51.196	0.400	745.339	0.269	13	0.133	-.ARADYDYLIK.-
R3/RRR3-19/2	1165.005	1165.278	-235.162	0.259	670.690	0.204	13	0.130	-.GQALADEYGIK.-
R3/RRR3-15/2	1686.358	1686.932	-935.839	0.412	2942.252	0.342	26	0.434	R.LISEATAAAGTGLIELR.R
R3/RRR3-15/2	1236.011	1236.469	-371.982	0.537	2186.807	0.541	21	0.339	R.M*LLGLNAAGFGR.-
R3/RRR3-15/2	1236.230	1236.469	-193.644	0.566	1932.016	0.552	20	0.297	R.M*LLGLNAAGFGR.-
R3/RRR3-15/2	1235.647	1236.469	-1478.695	0.463	1521.496	0.487	20	0.222	R.M*LLGLNAAGFGR.-
R3/RRR3-15/2	1417.078	1417.509	-304.788	0.493	1024.153	0.586	21	0.192	R.SPNVAYVPAGDNGR.M
R3/RRR3-15/2	1220.010	1220.470	-378.206	0.435	1078.861	0.543	16	0.186	R.MLLGLNAAGFGR.-
R3/RRR3-15/2	1417.966	1417.509	323.402	0.545	913.443	0.589	20	0.184	R.SPNVAYVPAGDNGR.M
R3/RRR3-15/2	1418.064	1417.509	-314.592	0.513	894.462	0.596	19	0.183	R.SPNVAYVPAGDNGR.M
R3/RRR3-15/2	1418.134	1417.509	-265.364	0.488	1057.082	0.512	21	0.182	R.SPNVAYVPAGDNGR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1417.043	1417.509	-329.507	0.509	1002.144	0.529	20	0.180	R.SPNVAYVPAGDNGR.M
R3/RRR3-15/2	1417.048	1417.509	-326.136	0.458	1010.671	0.503	20	0.176	R.SPNVAYVPAGDNGR.M
R3/RRR3-15/2	1685.543	1686.932	-1421.594	0.344	1351.097	0.342	20	0.172	R.LISEATAAAGTGLIELR.R
R3/RRR3-15/2	1220.247	1219.437	-155.823	0.546	1582.531	0.236	16	0.172	K.DLQM*VNLTLR.L
R3/RRR3-15/2	1218.628	1219.437	-1488.473	0.398	1376.363	0.250	16	0.163	K.DLQM*VNLTLR.L
R3/RRR3-15/2	1219.176	1219.437	-214.206	0.428	1506.780	0.195	16	0.163	K.DLQM*VNLTLR.L
R3/RRR3-15/3	1687.711	1686.932	-130.852	0.450	1273.593	0.479	33	0.146	R.LISEATAAAGTGLIELR.R
R3/RRR3-15/2	1169.094	1169.396	-259.160	0.314	169.181	0.571	13	0.137	-.VLPSIGNEVLK.-
R3/RRR3-15/2	1169.302	1169.396	-80.795	0.227	261.845	0.444	15	0.136	K.VLPSIGNEVLK.A
R3/RRR3-15/2	1685.382	1686.932	-2112.376	0.310	848.032	0.284	18	0.135	R.LISEATAAAGTGLIELR.R
R3/RRR3-15/3	1686.166	1686.932	-1050.136	0.332	791.431	0.271	28	0.087	R.LISEATAAAGTGLIELR.R
R3/RRR3-14/2	1439.054	1439.641	-1106.194	0.553	2203.129	0.550	19	0.344	R.SQIQAYVFDVIR.A
R3/RRR3-14/2	1439.409	1439.641	-161.411	0.536	2065.484	0.551	19	0.319	R.SQIQAYVFDVIR.A
R3/RRR3-14/2	1329.388	1329.398	-8.161	0.413	1384.084	0.498	19	0.285	R.DGLLQGQATTTSH.-
R3/RRR3-14/2	1438.997	1439.641	-1145.887	0.477	1837.780	0.482	18	0.262	R.SQIQAYVFDVIR.A
R3/RRR3-14/2	1329.157	1329.398	-182.354	0.398	1281.182	0.438	18	0.233	R.DGLLQGQATTTSH.-
R3/RRR3-14/2	949.309	950.117	-1909.672	0.332	650.771	0.398	14	0.145	K.YLSGLGIAR.Q
R3/RRR3-14/2	949.846	950.117	-286.240	0.443	651.216	0.360	14	0.145	K.YLSGLGIAR.Q
R3/RRR3-14/2	949.952	950.117	-173.818	0.378	750.761	0.333	15	0.144	K.YLSGLGIAR.Q
R3/RRR3-14/2	1329.188	1329.398	-158.952	0.387	1043.342	0.432	17	0.144	R.DGLLQGQATTTSH.-
R3/RRR3-14/2	1193.136	1193.288	-128.129	0.327	725.929	0.315	15	0.137	K.LNLDDAFEQK.N
R3/RRR3-14/3	1734.967	1734.888	45.396	0.361	665.478	0.480	26	0.105	K.LNLDDAFEQKNDIAK.A
R3/RRR3-6/2	1884.614	1885.107	-262.179	0.564	2716.631	0.604	27	0.475	K.IYQEYGITAENVIATAK.S
R3/RRR3-6/2	1884.607	1885.107	-265.883	0.580	2625.450	0.603	27	0.452	K.IYQEYGITAENVIATAK.S
R3/RRR3-6/2	1885.489	1885.107	203.341	0.606	2501.300	0.631	26	0.433	K.IYQEYGITAENVIATAK.S
R3/RRR3-6/2	1885.555	1885.107	238.138	0.601	2468.253	0.613	26	0.419	K.IYQEYGITAENVIATAK.S
R3/RRR3-6/3	1885.217	1885.107	58.307	0.534	2707.850	0.496	34	0.410	K.IYQEYGITAENVIATAK.S
R3/RRR3-6/3	1886.299	1885.107	102.249	0.557	2394.609	0.605	34	0.382	K.IYQEYGITAENVIATAK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1885.021	1885.107	-45.643	0.560	2491.551	0.502	33	0.358	K.IYQEYGITAENVIATAK.S
R3/RRR3-6/2	1403.310	1403.608	-212.939	0.504	2337.000	0.495	24	0.353	K.AIGIDKFGASAPAGK.I
R3/RRR3-4/2	1885.278	1885.107	91.141	0.544	2162.083	0.555	25	0.335	K.IYQEYGITAENVIATAK.S
R3/RRR3-6/2	1403.110	1403.608	-356.601	0.511	2066.797	0.519	23	0.309	K.AIGIDKFGASAPAGK.I
R3/RRR3-6/2	1376.136	1376.540	-294.282	0.465	1827.000	0.409	19	0.241	R.VSLEAGSTLGWQK.Y
R3/RRR3-6/2	1376.215	1376.540	-236.882	0.477	1883.227	0.371	20	0.239	R.VSLEAGSTLGWQK.Y
R3/RRR3-6/2	1376.201	1376.540	-246.671	0.455	1577.775	0.372	19	0.202	R.VSLEAGSTLGWQK.Y
R3/RRR3-6/2	1403.387	1403.608	-158.051	0.489	1232.961	0.470	21	0.187	K.AIGIDKFGASAPAGK.I
R3/RRR3-2/2	1376.021	1376.540	-1106.949	0.369	1237.822	0.385	18	0.172	R.VSLEAGSTLGWQK.Y
R3/RRR3-5/2	1442.215	1442.640	-295.146	0.410	743.612	0.536	21	0.165	K.LAQLPGTSIEGVEK.G
R3/RRR3-2/2	1443.228	1442.640	-285.777	0.454	711.996	0.496	21	0.161	K.LAQLPGTSIEGVEK.G
R3/RRR3-6/2	1442.296	1442.640	-238.847	0.453	742.208	0.464	21	0.158	K.LAQLPGTSIEGVEK.G
R3/RRR3-2/2	1442.384	1442.640	-178.055	0.464	636.548	0.489	20	0.157	K.LAQLPGTSIEGVEK.G
R3/RRR3-2/2	1442.270	1442.640	-256.934	0.452	578.763	0.502	19	0.156	K.LAQLPGTSIEGVEK.G
R3/RRR3-1/2	1442.255	1442.640	-267.803	0.436	621.708	0.481	20	0.155	K.LAQLPGTSIEGVEK.G
R3/RRR3-6/2	1171.422	1172.314	-1620.013	0.383	477.555	0.477	15	0.148	K.ESVLPEAVTAR.V
R3/RRR3-6/2	1172.072	1172.314	-206.689	0.404	509.723	0.442	16	0.148	K.ESVLPEAVTAR.V
R3/RRR3-4/2	1442.185	1442.640	-316.207	0.393	444.521	0.444	17	0.146	K.LAQLPGTSIEGVEK.G
R3/RRR3-6/2	1172.101	1172.314	-181.509	0.396	478.757	0.426	16	0.146	K.ESVLPEAVTAR.V
R3/RRR3-3/2	1441.838	1442.640	-1253.512	0.362	295.210	0.479	14	0.144	K.LAQLPGTSIEGVEK.G
R3/RRR3-4/2	1442.578	1442.640	-42.913	0.412	407.238	0.399	17	0.144	K.LAQLPGTSIEGVEK.G
R3/RRR3-1/2	1441.567	1442.640	-1442.383	0.322	352.289	0.426	15	0.142	K.LAQLPGTSIEGVEK.G
R3/RRR3-17/2	1558.450	1557.814	-233.851	0.573	1386.459	0.571	22	0.225	K.KLPSILVDETSVQK.I
R3/RRR3-17/2	1073.062	1073.225	-152.279	0.439	1017.939	0.518	17	0.180	K.AANGVVIATEK.K
R3/RRR3-17/2	1561.228	1560.863	235.065	0.553	1065.861	0.485	21	0.179	R.LYKETIPVTQLVR.E
R3/RRR3-17/2	1073.000	1073.225	-210.711	0.436	975.106	0.537	16	0.178	K.AANGVVIATEK.K
R3/RRR3-17/2	1073.893	1073.225	-310.638	0.337	1183.109	0.449	17	0.178	K.AANGVVIATEK.K
R3/RRR3-17/2	1560.499	1560.863	-233.544	0.504	984.928	0.486	20	0.173	R.LYKETIPVTQLVR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1560.402	1560.863	-296.017	0.466	1025.895	0.454	20	0.170	R.LYKETIPVTQLVR.E
R3/RRR3-17/2	1073.038	1073.225	-174.418	0.439	932.831	0.474	16	0.167	K.AANGVVIATEK.K
R3/RRR3-17/2	1073.444	1073.225	204.211	0.314	1162.422	0.380	17	0.166	K.AANGVVIATEK.K
R3/RRR3-17/2	1156.015	1156.357	-296.938	0.296	459.012	0.513	13	0.141	K.ETIPVTQLVR.E
R3/RRR3-17/2	1718.270	1718.926	-966.342	0.477	898.684	0.472	20	0.100	K.VLSPAEIKDFLEEVE.-
R3/RRR3-17/3	1560.580	1560.863	-181.564	0.446	647.586	0.295	23	0.093	R.LYKETIPVTQLVR.E
R3/RRR3-17/3	1559.711	1560.863	-1383.335	0.321	1112.490	0.158	25	0.081	R.LYKETIPVTQLVR.E
R3/RRR3-17/2	1718.451	1718.926	-277.056	0.486	767.166	0.449	19	0.067	K.VLSPAEIKDFLEEVE.-
R3/RRR3-17/2	1718.691	1718.926	-136.821	0.447	745.623	0.453	19	0.064	K.VLSPAEIKDFLEEVE.-
R3/RRR3-23/2	1965.502	1965.195	156.255	0.594	2020.004	0.606	29	0.324	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-23/2	1964.731	1965.195	-236.843	0.540	2061.938	0.556	29	0.316	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-23/2	1965.277	1965.195	41.703	0.595	1897.732	0.621	28	0.307	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-22/2	1964.658	1965.195	-784.641	0.529	1879.388	0.594	28	0.296	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-22/2	1965.466	1965.195	138.005	0.592	1863.286	0.598	28	0.294	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-23/2	1964.508	1965.195	-861.359	0.553	1620.633	0.576	27	0.252	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-25/2	1964.406	1965.195	-913.447	0.503	1480.846	0.583	25	0.235	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-22/2	1963.882	1965.195	-1181.459	0.443	1444.938	0.579	25	0.229	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-23/2	1964.342	1965.195	-946.450	0.535	1325.322	0.572	24	0.214	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-23/2	1963.755	1965.195	-1246.628	0.395	1426.946	0.485	25	0.207	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-21/2	1965.214	1965.195	9.432	0.554	1227.586	0.576	24	0.205	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-21/2	1964.489	1965.195	-871.028	0.511	1231.006	0.578	23	0.205	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-22/2	1536.351	1536.713	-236.498	0.546	1063.079	0.519	21	0.185	K.HSTVYFNLAEVQK.A
R3/RRR3-22/2	1536.324	1536.713	-254.433	0.550	849.248	0.560	20	0.177	K.HSTVYFNLAEVQK.A
R3/RRR3-22/2	905.978	906.064	-95.426	0.406	1277.623	0.373	13	0.176	K.GLNFVTVR.G
R3/RRR3-23/2	1536.283	1536.713	-281.059	0.558	839.101	0.550	19	0.174	K.HSTVYFNLAEVQK.A
R3/RRR3-22/2	906.021	906.064	-47.448	0.396	1228.794	0.350	13	0.169	K.GLNFVTVR.G
R3/RRR3-22/2	905.493	906.064	-1740.507	0.426	1113.667	0.402	12	0.168	K.GLNFVTVR.G
R3/RRR3-22/3	1298.826	1298.479	267.886	0.507	1569.217	0.449	27	0.166	R.GAGHEVPLHRPK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/3	1298.945	1298.479	359.905	0.508	1369.898	0.486	26	0.155	R.GAGHEVPLHRPK.Q
R3/RRR3-24/2	1964.550	1965.195	-839.839	0.431	750.125	0.433	19	0.148	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-23/2	1091.611	1092.316	-1566.625	0.338	671.915	0.430	13	0.145	K.ALHVSPIINK.S
R3/RRR3-21/2	905.948	906.064	-128.810	0.367	856.925	0.319	12	0.145	-.GLNFVTVR.-
R3/RRR3-25/2	906.097	906.064	36.064	0.337	760.029	0.350	11	0.144	K.GLNFVTVR.G
R3/RRR3-21/3	1298.735	1298.479	197.907	0.464	1461.416	0.397	25	0.144	R.GAGHEVPLHRPK.Q
R3/RRR3-23/3	1298.702	1298.479	172.457	0.527	1328.740	0.444	25	0.142	R.GAGHEVPLHRPK.Q
R3/RRR3-23/2	905.444	906.064	-1794.419	0.305	437.868	0.275	12	0.140	K.GLNFVTVR.G
R3/RRR3-23/2	1091.496	1092.316	-1672.457	0.349	593.878	0.383	13	0.139	-.ALHVSPIINK.-
R3/RRR3-21/2	905.972	906.064	-101.913	0.263	644.661	0.261	11	0.134	-.GLNFVTVR.-
R3/RRR3-23/3	1298.561	1298.479	63.858	0.502	1377.536	0.357	24	0.128	R.GAGHEVPLHRPK.Q
R3/RRR3-25/3	1298.712	1298.479	180.092	0.514	1234.932	0.395	23	0.125	-.GAGHEVPLHRPK.-
R3/RRR3-23/3	1965.596	1965.195	204.452	0.417	1155.083	0.390	28	0.119	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-22/3	1298.273	1298.479	-158.787	0.523	1026.825	0.420	24	0.115	-.GAGHEVPLHRPK.-
R3/RRR3-23/3	1298.706	1298.479	175.285	0.521	937.135	0.418	23	0.114	R.GAGHEVPLHRPK.Q
R3/RRR3-21/3	1298.715	1298.479	182.072	0.471	850.968	0.435	22	0.113	R.GAGHEVPLHRPK.Q
R3/RRR3-25/3	1297.976	1298.479	-1161.067	0.501	889.909	0.454	22	0.111	-.GAGHEVPLHRPK.-
R3/RRR3-24/3	1298.091	1298.479	-299.583	0.438	894.999	0.377	21	0.105	-.GAGHEVPLHRPK.-
R3/RRR3-25/3	1298.710	1298.479	178.678	0.449	913.315	0.362	21	0.104	-.GAGHEVPLHRPK.-
R3/RRR3-24/3	1298.483	1298.479	3.468	0.454	806.678	0.344	22	0.100	R.GAGHEVPLHRPK.Q
R3/RRR3-23/3	1964.517	1965.195	-856.813	0.253	1024.411	0.200	25	0.083	R.IWVFSGDTDAVLPVTSTR.Y
R3/RRR3-16/2	1161.179	1160.303	-106.982	0.507	1424.714	0.549	19	0.224	K.AVDNSGTVVGIK.C
R3/RRR3-16/2	1350.086	1350.435	-259.084	0.386	1166.839	0.491	18	0.194	K.VAAQAALEEM*DAD.-
R3/RRR3-16/2	1159.632	1160.303	-1444.851	0.419	1184.409	0.524	19	0.193	K.AVDNSGTVVGIK.C
R3/RRR3-16/2	1085.294	1085.234	55.436	0.522	1120.318	0.441	14	0.175	R.VFQVEYATK.A
R3/RRR3-17/2	1085.030	1085.234	-188.966	0.481	1129.918	0.432	14	0.175	R.VFQVEYATK.A
R3/RRR3-16/2	1086.153	1085.234	-75.256	0.519	1091.251	0.438	14	0.173	R.VFQVEYATK.A
R3/RRR3-16/2	1084.035	1084.248	-197.158	0.399	858.505	0.542	16	0.172	K.VPADLLEQAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1083.632	1084.248	-1495.907	0.482	873.739	0.500	16	0.170	K.VPADLLEQAK.V
R3/RRR3-17/2	1084.200	1084.248	-44.111	0.467	762.889	0.517	16	0.167	K.VPADLLEQAK.V
R3/RRR3-16/2	1159.600	1160.303	-1472.660	0.385	912.773	0.488	17	0.166	K.AVDNSGTVVGIK.C
R3/RRR3-17/2	1159.767	1160.303	-1328.557	0.399	925.075	0.467	17	0.164	K.AVDNSGTVVGIK.C
R3/RRR3-17/2	1084.989	1084.248	-239.415	0.468	766.787	0.497	16	0.164	K.VPADLLEQAK.V
R3/RRR3-17/2	1085.081	1085.234	-142.130	0.442	974.113	0.388	14	0.159	R.VFQVEYATK.A
R3/RRR3-17/2	1084.494	1085.234	-1609.760	0.326	1072.749	0.362	14	0.159	R.VFQVEYATK.A
R3/RRR3-16/2	1085.377	1085.234	132.139	0.407	986.250	0.378	14	0.158	R.VFQVEYATK.A
R3/RRR3-17/2	1159.465	1160.303	-1589.834	0.355	832.093	0.456	17	0.157	K.AVDNSGTVVGIK.C
R3/RRR3-17/2	1085.121	1084.248	-117.640	0.434	734.206	0.446	16	0.156	K.VPADLLEQAK.V
R3/RRR3-17/2	1159.989	1160.303	-271.327	0.352	757.375	0.458	14	0.151	K.AVDNSGTVVGIK.C
R3/RRR3-17/2	991.209	992.150	-1964.885	0.361	366.458	0.458	12	0.134	-.VYGEPISVK.-
R3/RRR3-13/2	1308.075	1308.457	-293.401	0.481	2371.857	0.452	20	0.341	K.VSCADITTLATR.D
R3/RRR3-18/2	1308.087	1308.457	-283.570	0.445	2155.780	0.443	20	0.299	K.VSCADITTLATR.D
R3/RRR3-11/2	1308.293	1308.457	-126.116	0.451	2110.785	0.460	19	0.296	K.VSCADITTLATR.D
R3/RRR3-12/2	1307.636	1308.457	-1396.671	0.395	2152.305	0.377	20	0.280	K.VSCADITTLATR.D
R3/RRR3-14/2	1308.208	1308.457	-191.076	0.449	1979.551	0.471	19	0.278	K.VSCADITTLATR.D
R3/RRR3-12/2	1308.126	1308.457	-254.032	0.463	2069.290	0.409	20	0.275	K.VSCADITTLATR.D
R3/RRR3-13/2	1308.091	1308.457	-281.136	0.467	1990.193	0.403	19	0.261	K.VSCADITTLATR.D
R3/RRR3-18/2	1307.934	1308.457	-1168.131	0.441	1882.436	0.427	19	0.252	K.VSCADITTLATR.D
R3/RRR3-18/2	1308.119	1308.457	-259.228	0.453	1802.694	0.446	19	0.245	K.VSCADITTLATR.D
R3/RRR3-14/2	1308.072	1308.457	-295.180	0.417	1841.033	0.423	19	0.245	K.VSCADITTLATR.D
R3/RRR3-13/2	1307.506	1308.457	-1496.538	0.342	1914.885	0.375	19	0.243	K.VSCADITTLATR.D
R3/RRR3-18/2	1734.439	1734.933	-285.585	0.502	1569.832	0.556	25	0.239	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/2	1734.327	1734.933	-929.157	0.497	1409.980	0.574	24	0.223	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-14/2	984.438	985.163	-1757.515	0.486	1461.368	0.461	17	0.209	R.DIGIAAGLVR.I
R3/RRR3-13/2	1734.420	1734.933	-875.316	0.492	1343.091	0.533	23	0.207	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/2	1735.339	1734.933	234.340	0.564	1264.036	0.567	23	0.206	R.DAIVASGGPYFDVPLGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1735.445	1734.933	-282.175	0.539	1305.658	0.545	23	0.205	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-11/2	1308.214	1308.457	-186.115	0.343	1656.860	0.349	19	0.205	K.VSCADITTLATR.D
R3/RRR3-13/2	1734.792	1734.933	-81.842	0.515	1309.750	0.538	23	0.205	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-15/2	1734.440	1734.933	-285.374	0.517	1303.898	0.537	23	0.204	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-15/2	984.805	985.163	-363.790	0.351	1749.601	0.288	17	0.203	R.DIGIAAGLVR.I
R3/RRR3-14/2	1734.381	1734.933	-897.784	0.499	1290.430	0.538	23	0.203	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-13/2	1735.339	1734.933	234.411	0.546	1292.871	0.530	23	0.201	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-10/2	1735.591	1734.933	-197.921	0.554	1263.437	0.543	23	0.201	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-13/2	984.555	985.163	-1638.047	0.413	1384.609	0.462	17	0.200	R.DIGIAAGLVR.I
R3/RRR3-14/2	984.425	985.163	-1770.473	0.470	1397.641	0.435	17	0.197	R.DIGIAAGLVR.I
R3/RRR3-18/2	984.548	985.163	-1645.147	0.460	1369.518	0.448	17	0.197	R.DIGIAAGLVR.I
R3/RRR3-12/3	1736.352	1734.933	242.093	0.517	1593.609	0.519	32	0.196	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-11/2	984.976	985.163	-190.075	0.500	1345.864	0.442	17	0.194	R.DIGIAAGLVR.I
R3/RRR3-18/2	1734.301	1734.933	-943.714	0.449	1116.120	0.561	22	0.191	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-15/2	1734.085	1734.933	-1068.945	0.415	1324.882	0.459	23	0.191	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-10/2	1735.358	1734.933	245.414	0.517	1133.726	0.547	22	0.190	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/2	984.531	985.163	-1662.337	0.483	1198.964	0.480	16	0.188	R.DIGIAAGLVR.I
R3/RRR3-12/2	985.004	985.163	-161.604	0.464	1252.902	0.456	16	0.188	R.DIGIAAGLVR.I
R3/RRR3-12/2	1734.105	1734.933	-1057.212	0.457	1150.611	0.512	22	0.185	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-14/2	1734.335	1734.933	-924.352	0.495	1135.047	0.519	22	0.185	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-14/2	984.831	985.163	-338.171	0.515	1282.063	0.426	16	0.185	R.DIGIAAGLVR.I
R3/RRR3-18/2	984.435	985.163	-1759.758	0.454	1335.350	0.392	16	0.183	R.DIGIAAGLVR.I
R3/RRR3-12/2	984.984	985.163	-182.242	0.515	1253.852	0.429	16	0.183	R.DIGIAAGLVR.I
R3/RRR3-13/2	984.513	985.163	-1681.023	0.469	1229.928	0.427	16	0.181	R.DIGIAAGLVR.I
R3/RRR3-15/2	984.952	985.163	-214.443	0.466	1226.046	0.424	16	0.180	R.DIGIAAGLVR.I
R3/RRR3-18/2	985.011	985.163	-154.394	0.505	1175.822	0.445	16	0.180	R.DIGIAAGLVR.I
R3/RRR3-11/2	1735.761	1734.933	-99.713	0.529	997.339	0.528	21	0.176	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-9/2	1736.213	1734.933	161.658	0.495	970.464	0.540	20	0.175	R.DAIVASGGPYFDVPLGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	984.882	985.163	-285.443	0.391	1324.010	0.326	16	0.171	R.DIGIAAGLVR.I
R3/RRR3-14/2	1733.826	1734.933	-1219.094	0.326	1313.470	0.341	23	0.170	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/2	1572.389	1571.714	-207.796	0.565	728.589	0.542	21	0.169	K.DVPVNSVTQELDVR.T
R3/RRR3-3/2	1734.244	1734.933	-976.926	0.406	980.062	0.469	20	0.165	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-1/2	1734.178	1734.933	-1014.947	0.372	1199.041	0.362	22	0.164	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-15/2	1733.797	1734.933	-1235.921	0.300	1184.416	0.375	21	0.164	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/2	1571.306	1571.714	-260.925	0.462	729.417	0.482	22	0.161	K.DVPVNSVTQELDVR.T
R3/RRR3-2/2	1734.048	1734.933	-1090.715	0.340	920.820	0.474	20	0.161	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/2	1572.238	1571.714	-303.912	0.542	660.519	0.500	21	0.161	K.DVPVNSVTQELDVR.T
R3/RRR3-13/2	1571.269	1571.714	-284.541	0.450	773.143	0.458	22	0.160	K.DVPVNSVTQELDVR.T
R3/RRR3-4/2	1736.391	1734.933	264.589	0.497	866.064	0.473	20	0.160	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-11/2	1572.313	1571.714	-255.774	0.501	683.108	0.465	22	0.159	K.DVPVNSVTQELDVR.T
R3/RRR3-2/2	985.003	985.163	-162.848	0.428	1099.297	0.327	16	0.157	R.DIGIAAGLVR.I
R3/RRR3-13/2	1571.221	1571.714	-314.706	0.399	811.256	0.431	22	0.157	K.DVPVNSVTQELDVR.T
R3/RRR3-12/2	1571.267	1571.714	-285.788	0.432	791.486	0.429	22	0.157	K.DVPVNSVTQELDVR.T
R3/RRR3-15/2	1571.161	1571.714	-991.440	0.387	799.153	0.431	22	0.156	K.DVPVNSVTQELDVR.T
R3/RRR3-11/2	1571.082	1571.714	-1041.989	0.393	793.322	0.430	22	0.156	K.DVPVNSVTQELDVR.T
R3/RRR3-15/2	1571.236	1571.714	-305.119	0.419	755.183	0.433	22	0.156	K.DVPVNSVTQELDVR.T
R3/RRR3-14/2	1571.235	1571.714	-305.820	0.428	742.585	0.431	22	0.155	K.DVPVNSVTQELDVR.T
R3/RRR3-3/2	1734.325	1734.933	-930.146	0.385	804.115	0.455	19	0.154	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/2	1571.506	1571.714	-133.274	0.414	245.389	0.544	18	0.151	-.DVPVNSVTQELDVR.-
R3/RRR3-13/2	1570.761	1571.714	-1247.594	0.335	683.182	0.389	22	0.148	K.DVPVNSVTQELDVR.T
R3/RRR3-15/2	1570.766	1571.714	-1243.926	0.334	494.394	0.452	19	0.148	K.DVPVNSVTQELDVR.T
R3/RRR3-11/2	1571.157	1571.714	-993.936	0.344	759.168	0.361	22	0.147	K.DVPVNSVTQELDVR.T
R3/RRR3-1/2	1571.387	1571.714	-209.175	0.439	683.421	0.374	20	0.145	-.DVPVNSVTQELDVR.-
R3/RRR3-10/2	1571.238	1571.714	-303.794	0.351	420.419	0.338	18	0.142	K.DVPVNSVTQELDVR.T
R3/RRR3-17/2	1733.766	1734.933	-1253.527	0.289	935.833	0.288	19	0.141	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-9/2	1733.723	1734.933	-1278.629	0.292	576.316	0.389	18	0.141	R.DAIVASGGPYFDVPLGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1736.092	1734.933	91.568	0.374	624.318	0.361	16	0.138	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-4/2	985.238	985.163	77.159	0.237	311.375	0.273	14	0.136	-.DIGIAAGLVR.-
R3/RRR3-1/2	1733.732	1734.933	-1273.396	0.301	519.982	0.282	14	0.133	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-2/2	1308.180	1308.457	-212.139	0.228	782.306	0.207	15	0.133	K.VSCADITTLATR.D
R3/RRR3-15/2	1307.728	1308.457	-1326.448	0.266	645.821	0.199	14	0.132	K.VSCADITTLATR.D
R3/RRR3-3/2	1733.594	1734.933	-1353.658	0.255	929.341	0.152	18	0.130	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-12/3	982.059	982.121	-63.237	0.513	1163.895	0.281	18	0.099	R.WHVAEALR.R
R3/RRR3-12/3	982.306	982.121	189.646	0.523	985.500	0.236	17	0.087	-.WHVAEALR.-
R3/RRR3-13/3	982.341	982.121	225.068	0.433	960.499	0.180	17	0.084	R.WHVAEALR.R
R3/RRR3-12/3	982.383	982.121	268.056	0.511	963.487	0.219	17	0.083	-.WHVAEALR.-
R3/RRR3-13/3	982.286	982.121	169.364	0.471	1106.708	0.182	18	0.083	-.WHVAEALR.-
R3/RRR3-12/3	1735.240	1734.933	177.510	0.204	600.015	0.280	22	0.083	R.DAIVASGGPYFDVPLGR.R
R3/RRR3-13/3	982.203	982.121	84.489	0.441	1008.337	0.155	17	0.080	-.WHVAEALR.-
R3/RRR3-16/2	1030.923	1031.145	-216.223	0.497	1664.938	0.609	20	0.270	K.VAAATAAAGEAK.G
R3/RRR3-17/2	1031.079	1031.145	-64.077	0.505	1542.976	0.572	21	0.245	K.VAAATAAAGEAK.G
R3/RRR3-16/2	1030.783	1031.145	-352.493	0.439	1525.384	0.572	20	0.241	K.VAAATAAAGEAK.G
R3/RRR3-17/2	1030.980	1031.145	-161.108	0.398	1474.588	0.546	21	0.227	K.VAAATAAAGEAK.G
R3/RRR3-16/2	1140.565	1141.303	-1528.476	0.456	1308.427	0.527	18	0.206	R.VPSPVTAGSAVR.L
R3/RRR3-16/2	1140.604	1141.303	-1493.967	0.491	1086.027	0.616	18	0.202	R.VPSPVTAGSAVR.L
R3/RRR3-17/2	1211.005	1211.308	-251.607	0.431	1575.837	0.353	19	0.200	R.VSFGENFSPAR.A
R3/RRR3-16/2	1030.388	1031.145	-1710.568	0.396	1265.179	0.477	20	0.192	K.VAAATAAAGEAK.G
R3/RRR3-16/2	1140.649	1141.303	-1454.299	0.461	1040.125	0.568	17	0.188	R.VPSPVTAGSAVR.L
R3/RRR3-16/2	1211.027	1211.308	-232.696	0.464	1354.604	0.391	18	0.185	R.VSFGENFSPAR.A
R3/RRR3-16/3	1643.379	1643.829	-274.262	0.457	1392.147	0.518	29	0.170	R.SPAAEALGPTHVLHSR.Y
R3/RRR3-16/2	1211.899	1211.308	-338.710	0.469	1078.998	0.406	18	0.167	R.VSFGENFSPAR.A
R3/RRR3-16/2	1210.505	1211.308	-1494.176	0.431	1384.093	0.272	18	0.167	R.VSFGENFSPAR.A
R3/RRR3-16/2	1454.216	1454.694	-329.756	0.374	1141.891	0.385	19	0.166	K.VKEGVEVPQLVEK.V
R3/RRR3-16/3	1644.739	1643.829	-54.768	0.466	1305.747	0.533	30	0.164	R.SPAAEALGPTHVLHSR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1454.200	1454.694	-340.200	0.379	1023.423	0.384	17	0.157	K.VKEGVEVPQLVEK.V
R3/RRR3-17/2	1030.880	1031.145	-258.157	0.393	699.272	0.488	17	0.156	K.VAAATAAAGEAK.G
R3/RRR3-16/2	1453.568	1454.694	-1467.031	0.396	705.080	0.376	15	0.141	K.VKEGVEVPQLVEK.V
R3/RRR3-16/3	1644.137	1643.829	187.980	0.423	540.905	0.520	24	0.112	R.SPAAEALGPTHVLHSR.Y
R3/RRR3-12/2	1204.195	1204.404	-173.723	0.536	1990.323	0.443	19	0.274	R.VVSNFVAQALR.K
R3/RRR3-12/2	1204.102	1204.404	-250.812	0.547	1944.658	0.427	19	0.263	R.VVSNFVAQALR.K
R3/RRR3-12/2	1204.090	1204.404	-261.084	0.517	1730.569	0.445	18	0.237	R.VVSNFVAQALR.K
R3/RRR3-13/2	1204.452	1204.404	40.599	0.544	1689.070	0.423	18	0.226	R.VVSNFVAQALR.K
R3/RRR3-12/2	1430.561	1431.727	-1518.526	0.438	1563.251	0.466	21	0.220	K.TNVVGTLNMLGLAK.R
R3/RRR3-12/2	1431.712	1431.727	-10.229	0.472	1131.555	0.522	18	0.186	K.TNVVGTLNMLGLAK.R
R3/RRR3-12/2	1171.093	1171.370	-237.494	0.403	1518.123	0.283	15	0.179	R.AKELLGWEPK.I
R3/RRR3-13/2	1227.822	1228.337	-1237.367	0.440	1074.419	0.426	17	0.169	K.VVQDTIDPNAR.I
R3/RRR3-13/2	1228.163	1228.337	-141.821	0.479	980.600	0.426	15	0.162	K.VVQDTIDPNAR.I
R3/RRR3-13/2	1227.529	1228.337	-1477.144	0.318	999.879	0.396	17	0.157	K.VVQDTIDPNAR.I
R3/RRR3-13/2	1431.318	1431.727	-286.529	0.389	1088.590	0.353	17	0.156	K.TNVVGTLNMLGLAK.R
R3/RRR3-13/2	1430.888	1431.727	-1289.117	0.384	928.986	0.399	17	0.153	K.TNVVGTLNMLGLAK.R
R3/RRR3-13/2	1203.532	1204.404	-1560.006	0.384	653.016	0.411	15	0.147	R.VVSNFVAQALR.K
R3/RRR3-13/2	1431.289	1431.727	-306.723	0.370	693.048	0.369	15	0.140	K.TNVVGTLNMLGLAK.R
R3/RRR3-13/3	1170.978	1171.370	-336.285	0.432	967.692	0.286	20	0.094	R.AKELLGWEPK.I
R3/RRR3-10/2	1503.041	1502.729	208.486	0.438	2467.341	0.244	21	0.302	K.CDVIVINTPLTEK.T
R3/RRR3-10/2	1847.589	1848.090	-814.875	0.583	1887.971	0.591	24	0.301	R.YFKGEDFPVQNYIVK.E
R3/RRR3-10/2	1847.583	1848.090	-818.258	0.545	1801.727	0.547	23	0.274	R.YFKGEDFPVQNYIVK.E
R3/RRR3-10/2	1847.432	1848.090	-900.106	0.506	1707.454	0.586	23	0.270	R.YFKGEDFPVQNYIVK.E
R3/RRR3-10/2	1084.135	1084.297	-150.724	0.533	1313.428	0.487	17	0.201	K.KGVIIVNNAR.G
R3/RRR3-10/2	1084.279	1084.297	-17.120	0.539	1369.167	0.450	17	0.199	K.KGVIIVNNAR.G
R3/RRR3-10/2	1340.148	1340.481	-249.647	0.480	1356.849	0.401	18	0.187	K.YEEDLDAM*LPK.C
R3/RRR3-10/2	1084.107	1084.297	-176.139	0.480	1206.398	0.387	16	0.173	K.KGVIIVNNAR.G
R3/RRR3-10/3	1847.559	1848.090	-831.198	0.489	937.531	0.540	27	0.134	R.YFKGEDFPVQNYIVK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1848.608	1848.090	-261.762	0.513	1037.363	0.490	28	0.131	R.YFKGEDFPVQNYIVK.E
R3/RRR3-10/3	1848.243	1848.090	83.123	0.499	968.366	0.446	28	0.119	R.YFKGEDFPVQNYIVK.E
R3/RRR3-10/3	1084.879	1085.276	-366.896	0.474	1566.394	0.185	21	0.103	R.LKIDPELEK.E
R3/RRR3-10/3	1085.240	1085.276	-32.968	0.475	1632.288	0.145	22	0.098	R.LKIDPELEK.E
R3/RRR3-10/3	1084.670	1085.276	-1484.779	0.438	1388.042	0.144	20	0.087	R.LKIDPELEK.E
R3/RRR3-12/2	1644.813	1645.838	-1235.046	0.588	3139.911	0.539	25	0.563	K.IKDEEGNPAFALVNK.A
R3/RRR3-12/2	1645.250	1645.838	-968.226	0.603	3042.331	0.503	25	0.519	K.IKDEEGNPAFALVNK.A
R3/RRR3-12/2	1645.550	1645.838	-175.715	0.623	2874.137	0.520	24	0.481	K.IKDEEGNPAFALVNK.A
R3/RRR3-12/2	1845.474	1845.993	-825.429	0.554	1520.290	0.658	29	0.263	K.ILPWGDEAYAGGSANAPR.G
R3/RRR3-12/2	1845.471	1845.993	-826.890	0.571	1422.982	0.682	28	0.255	K.ILPWGDEAYAGGSANAPR.G
R3/RRR3-12/2	1722.564	1722.922	-208.586	0.570	1652.564	0.476	22	0.232	K.IRDEEGYPAFALVNK.V
R3/RRR3-12/2	1846.232	1845.993	130.272	0.589	1291.151	0.653	27	0.232	K.ILPWGDEAYAGGSANAPR.G
R3/RRR3-12/2	1722.343	1722.922	-920.054	0.564	1590.678	0.492	21	0.228	K.IRDEEGYPAFALVNK.V
R3/RRR3-12/2	1080.907	1081.161	-235.448	0.458	1590.377	0.454	17	0.223	K.ADEGFSVTVR.G
R3/RRR3-13/2	1723.182	1722.922	150.943	0.560	1508.772	0.509	21	0.222	K.IRDEEGYPAFALVNK.V
R3/RRR3-12/2	1080.878	1081.161	-262.754	0.488	1578.904	0.448	17	0.220	K.ADEGFSVTVR.G
R3/RRR3-13/2	1081.101	1081.161	-56.015	0.423	1639.815	0.406	17	0.218	K.ADEGFSVTVR.G
R3/RRR3-12/2	1722.491	1722.922	-251.102	0.559	1366.682	0.500	20	0.203	K.IRDEEGYPAFALVNK.V
R3/RRR3-12/2	1080.910	1081.161	-232.842	0.477	1489.084	0.413	17	0.203	K.ADEGFSVTVR.G
R3/RRR3-13/2	1081.190	1081.161	26.656	0.466	1351.967	0.430	16	0.192	K.ADEGFSVTVR.G
R3/RRR3-13/2	1082.048	1081.161	-104.962	0.486	1113.210	0.345	16	0.160	K.ADEGFSVTVR.G
R3/RRR3-13/2	1845.579	1845.993	-224.736	0.444	902.160	0.360	23	0.148	K.ILPWGDEAYAGGSANAPR.G
R3/RRR3-12/2	1228.469	1229.362	-1545.281	0.379	774.193	0.374	17	0.146	R.GGSVCLAPTNPR.D
R3/RRR3-12/2	1229.025	1229.362	-275.114	0.398	682.820	0.360	17	0.143	R.GGSVCLAPTNPR.D
R3/RRR3-13/2	1845.350	1845.993	-892.961	0.401	709.245	0.308	21	0.136	K.ILPWGDEAYAGGSANAPR.G
R3/RRR3-12/2	1228.618	1229.362	-1423.716	0.320	589.400	0.286	15	0.134	R.GGSVCLAPTNPR.D
R3/RRR3-12/3	1646.635	1645.838	-123.521	0.442	1175.712	0.383	29	0.119	K.IKDEEGNPAFALVNK.A
R3/RRR3-12/3	1846.981	1845.993	-6.080	0.450	874.395	0.441	29	0.113	K.ILPWGDEAYAGGSANAPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/3	1845.319	1845.993	-909.869	0.375	909.675	0.382	28	0.104	-.ILPWGDEAYAGGSANAPR.-
R3/RRR3-12/3	1846.038	1845.993	24.592	0.384	574.260	0.399	24	0.095	-.ILPWGDEAYAGGSANAPR.-
R3/RRR3-12/3	1645.312	1645.838	-930.544	0.386	710.112	0.334	24	0.095	K.IKDEEGNPAFALVNK.A
R3/RRR3-13/3	1646.402	1645.838	-265.875	0.342	645.025	0.351	23	0.091	-.IKDEEGNPAFALVNK.-
R3/RRR3-13/3	1645.188	1645.838	-1005.853	0.338	565.750	0.319	21	0.082	-.IKDEEGNPAFALVNK.-
R3/RRR3-16/3	1888.980	1888.964	8.444	0.562	1754.370	0.577	30	0.241	R.TIGHTVTSPDDTAEQCR.S
R3/RRR3-16/3	1888.362	1888.964	-851.233	0.487	1703.283	0.511	31	0.210	R.TIGHTVTSPDDTAEQCR.S
R3/RRR3-16/3	1888.802	1888.964	-85.969	0.571	1535.589	0.563	31	0.202	R.TIGHTVTSPDDTAEQCR.S
R3/RRR3-16/2	1401.925	1402.405	-342.929	0.513	1552.927	0.381	17	0.199	K.GGNDYEIFESDR.T
R3/RRR3-16/2	1401.900	1402.405	-1076.821	0.507	1443.622	0.369	17	0.186	K.GGNDYEIFESDR.T
R3/RRR3-16/2	1402.316	1402.405	-63.441	0.514	1430.399	0.337	17	0.178	K.GGNDYEIFESDR.T
R3/RRR3-16/2	1147.089	1147.331	-211.723	0.513	1036.449	0.474	17	0.174	R.SGM*LNVSPIGR.N
R3/RRR3-16/3	1484.504	1483.822	-214.873	0.508	1833.965	0.335	26	0.168	R.KVVTPEM*LQFM*K.Q
R3/RRR3-16/2	1146.859	1147.331	-412.150	0.456	971.164	0.422	16	0.161	R.SGM*LNVSPIGR.N
R3/RRR3-16/2	1159.990	1160.303	-270.271	0.486	793.532	0.470	16	0.160	K.NGELIGTQSLK.S
R3/RRR3-16/2	1159.514	1160.303	-1547.212	0.400	749.994	0.392	15	0.147	K.NGELIGTQSLK.S
R3/RRR3-16/2	1159.433	1160.303	-1617.228	0.389	734.480	0.379	15	0.145	K.NGELIGTQSLK.S
R3/RRR3-16/3	1483.506	1483.822	-213.243	0.475	1413.502	0.328	25	0.124	R.KVVTPEM*LQFM*K.Q
R3/RRR3-16/3	1483.789	1483.822	-21.848	0.464	1328.896	0.311	24	0.115	R.KVVTPEM*LQFM*K.Q
R3/RRR3-16/3	1483.634	1483.822	-126.945	0.398	866.865	0.303	21	0.094	R.KVVTPEM*LQFM*K.Q
R3/RRR3-24/2	1056.014	1056.151	-130.390	0.464	1070.319	0.518	18	0.185	K.ASGASYSSVVK.T
R3/RRR3-25/2	1056.024	1056.151	-121.345	0.476	1060.385	0.518	18	0.184	K.ASGASYSSVVK.T
R3/RRR3-25/2	1404.071	1404.596	-1089.456	0.436	1214.886	0.423	20	0.179	R.STYQVAALPLNAR.I
R3/RRR3-24/2	1405.133	1404.596	-330.993	0.508	1145.325	0.448	20	0.178	R.STYQVAALPLNAR.I
R3/RRR3-24/2	1404.122	1404.596	-338.643	0.448	1093.436	0.454	19	0.174	R.STYQVAALPLNAR.I
R3/RRR3-25/2	1287.103	1287.489	-300.750	0.418	833.652	0.521	17	0.166	K.APAALGPYSQAIK.A
R3/RRR3-25/2	1404.291	1404.596	-218.022	0.444	925.364	0.466	18	0.165	R.STYQVAALPLNAR.I
R3/RRR3-25/2	1055.959	1056.151	-182.805	0.435	873.445	0.472	17	0.165	K.ASGASYSSVVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1404.098	1404.596	-356.263	0.384	1005.639	0.418	19	0.162	R.STYQVAALPLNAR.I
R3/RRR3-25/2	1287.281	1287.489	-162.700	0.424	825.173	0.465	19	0.160	K.APAALGPYSQAIK.A
R3/RRR3-24/2	1287.224	1287.489	-207.127	0.426	726.215	0.521	16	0.160	K.APAALGPYSQAIK.A
R3/RRR3-24/2	1286.930	1287.489	-1215.452	0.451	616.859	0.563	15	0.160	K.APAALGPYSQAIK.A
R3/RRR3-24/2	1055.833	1056.151	-302.036	0.437	613.616	0.500	14	0.155	K.ASGASYSSVVK.T
R3/RRR3-24/2	1404.142	1404.596	-324.861	0.438	887.143	0.403	18	0.154	R.STYQVAALPLNAR.I
R3/RRR3-25/2	1056.155	1056.151	3.755	0.374	798.400	0.424	16	0.153	K.ASGASYSSVVK.T
R3/RRR3-25/2	1540.059	1540.807	-1138.560	0.445	877.148	0.395	18	0.151	K.TTIM*LADLQDFKK.V
R3/RRR3-24/2	1056.093	1056.151	-55.371	0.354	741.764	0.408	15	0.149	K.ASGASYSSVVK.T
R3/RRR3-24/2	1287.097	1287.489	-306.079	0.363	535.641	0.505	14	0.148	K.APAALGPYSQAIK.A
R3/RRR3-25/2	1964.950	1964.232	-143.964	0.466	695.985	0.460	22	0.147	K.ANNM*VFVSGVLGLNPETGK.F
R3/RRR3-25/2	1287.243	1287.489	-192.286	0.434	505.501	0.454	15	0.146	K.APAALGPYSQAIK.A
R3/RRR3-25/3	1964.987	1964.232	-125.213	0.424	1396.763	0.415	30	0.146	K.ANNM*VFVSGVLGLNPETGK.F
R3/RRR3-25/3	1963.672	1964.232	-797.190	0.398	732.894	0.414	26	0.100	-.ANNM*VFVSGVLGLNPETGK.-
R3/RRR3-4/2	1821.162	1821.066	52.667	0.581	2055.413	0.595	23	0.327	R.QAVALLQDNYPEFIAK.K
R3/RRR3-4/2	1821.457	1821.066	215.396	0.590	2018.505	0.596	23	0.321	R.QAVALLQDNYPEFIAK.K
R3/RRR3-4/2	1820.549	1821.066	-835.519	0.533	2037.051	0.580	23	0.320	R.QAVALLQDNYPEFIAK.K
R3/RRR3-4/2	1096.138	1096.303	-151.084	0.365	1144.343	0.378	15	0.164	K.SKFIFASPAK.S
R3/RRR3-4/2	1721.582	1722.024	-257.493	0.497	712.314	0.442	21	0.154	K.VFINVPWWYLAANK.M
R3/RRR3-9/2	1821.284	1821.066	119.889	0.508	453.570	0.536	18	0.153	R.QAVALLQDNYPEFIAK.K
R3/RRR3-4/3	1821.693	1821.066	-205.376	0.499	1175.002	0.513	26	0.148	R.QAVALLQDNYPEFIAK.K
R3/RRR3-9/2	1821.356	1821.066	159.680	0.443	367.098	0.500	17	0.147	R.QAVALLQDNYPEFIAK.K
R3/RRR3-4/2	1142.944	1143.362	-367.478	0.416	932.546	0.308	14	0.146	K.M*M*SPFLTQR.T
R3/RRR3-4/2	1143.016	1143.362	-303.506	0.454	871.169	0.312	14	0.145	K.M*M*SPFLTQR.T
R3/RRR3-4/2	1721.706	1722.024	-185.507	0.476	667.458	0.355	20	0.142	K.VFINVPWWYLAANK.M
R3/RRR3-4/3	1821.161	1821.066	52.256	0.450	1247.032	0.463	28	0.142	R.QAVALLQDNYPEFIAK.K
R3/RRR3-4/2	1142.429	1143.362	-1697.328	0.396	870.219	0.276	14	0.141	K.M*M*SPFLTQR.T
R3/RRR3-16/2	1820.715	1821.066	-193.442	0.368	439.769	0.347	14	0.134	R.QAVALLQDNYPEFIAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1721.931	1722.024	-54.083	0.334	418.914	0.310	14	0.133	K.VFINVPWWYLAANK.M
R3/RRR3-4/3	1821.415	1821.066	192.001	0.425	789.301	0.467	24	0.112	R.QAVALLQDNYPEFIAK.K
R3/RRR3-4/3	1256.382	1256.497	-91.723	0.463	1226.513	0.288	22	0.105	R.KVPANEEPIMK.G
R3/RRR3-4/3	1256.969	1256.497	376.746	0.461	1042.701	0.321	21	0.102	-.KVPANEEPIMK.-
R3/RRR3-4/3	1272.056	1272.496	-347.025	0.426	1002.738	0.277	22	0.094	-.KVPANEEPIM*K.-
R3/RRR3-9/3	1272.909	1272.496	325.262	0.407	886.052	0.300	21	0.093	-.KVPANEEPIM*K.-
R3/RRR3-9/3	1272.466	1272.496	-23.759	0.391	907.373	0.262	21	0.093	R.KVPANEEPIM*K.G
R3/RRR3-4/3	1272.233	1272.496	-207.384	0.464	932.303	0.280	22	0.093	-.KVPANEEPIM*K.-
R3/RRR3-10/3	1272.206	1272.496	-229.331	0.432	828.710	0.293	20	0.091	-.KVPANEEPIM*K.-
R3/RRR3-9/3	1272.640	1272.496	113.195	0.418	828.304	0.254	21	0.088	-.KVPANEEPIM*K.-
R3/RRR3-4/3	1272.560	1272.496	50.423	0.478	991.205	0.252	22	0.087	-.KVPANEEPIM*K.-
R3/RRR3-10/3	1271.672	1272.496	-1438.703	0.421	862.737	0.316	20	0.086	-.KVPANEEPIM*K.-
R3/RRR3-10/3	1272.248	1272.496	-195.978	0.423	731.481	0.305	20	0.084	-.KVPANEEPIM*K.-
R3/RRR3-7/3	1271.543	1272.496	-1540.820	0.372	637.236	0.212	18	0.079	-.KVPANEEPIM*K.-
R3/RRR3-3/3	1272.913	1272.496	328.291	0.397	569.543	0.284	18	0.071	-.KVPANEEPIM*K.-
R3/RRR3-10/2	1664.273	1663.850	254.646	0.518	3138.430	0.461	26	0.530	K.AFGASEVIAVDVLDEK.L
R3/RRR3-10/2	1664.494	1663.850	-214.834	0.534	2694.011	0.476	24	0.422	K.AFGASEVIAVDVLDEK.L
R3/RRR3-10/2	1855.624	1856.027	-218.175	0.543	2347.774	0.641	27	0.406	R.TLGATHTVNAAKEDAVEK.I
R3/RRR3-10/2	1855.600	1856.027	-231.176	0.541	2085.638	0.628	26	0.347	R.TLGATHTVNAAKEDAVEK.I
R3/RRR3-10/2	1663.288	1663.850	-941.826	0.396	2461.672	0.289	24	0.313	K.AFGASEVIAVDVLDEK.L
R3/RRR3-10/2	1049.563	1050.190	-1554.495	0.345	847.544	0.487	14	0.160	K.LAESGAFNLK.N
R3/RRR3-10/2	1050.018	1050.190	-164.600	0.385	828.793	0.445	14	0.156	K.LAESGAFNLK.N
R3/RRR3-10/2	1049.449	1050.190	-1663.982	0.353	1015.891	0.328	15	0.151	K.LAESGAFNLK.N
R3/RRR3-10/3	1961.970	1962.324	-181.425	0.392	1744.214	0.277	29	0.150	K.AVMIGLAATNVMGEVDITR.L
R3/RRR3-10/3	1855.404	1856.027	-877.670	0.486	723.200	0.575	32	0.129	R.TLGATHTVNAAKEDAVEK.I
R3/RRR3-10/3	1856.879	1856.027	-80.095	0.481	746.202	0.557	31	0.127	R.TLGATHTVNAAKEDAVEK.I
R3/RRR3-10/3	1855.465	1856.027	-844.681	0.468	702.286	0.538	31	0.121	R.TLGATHTVNAAKEDAVEK.I
R3/RRR3-10/3	1990.121	1991.238	-1066.715	0.407	846.852	0.461	27	0.114	R.GAVFWEPGRPLTLEDFR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1990.921	1991.238	-159.569	0.384	563.605	0.463	23	0.104	R.GAVFWEPGRPLTLEDFR.M
R3/RRR3-11/3	1855.922	1856.027	-56.650	0.424	387.999	0.454	24	0.104	R.TLGATHTVNAAKEDAVEK.I
R3/RRR3-10/3	1990.419	1991.238	-916.433	0.374	494.572	0.375	21	0.094	R.GAVFWEPGRPLTLEDFR.M
R3/RRR3-8/2	1536.065	1536.756	-1104.561	0.424	981.231	0.484	20	0.168	K.AALAPYFELTNAVR.V
R3/RRR3-15/3	1928.743	1929.100	-185.958	0.574	2443.921	0.526	31	0.358	K.YAHKDEEYDSM*LGVVR.E
R3/RRR3-15/3	1929.006	1929.100	-48.739	0.568	2434.719	0.502	31	0.345	K.YAHKDEEYDSM*LGVVR.E
R3/RRR3-15/2	1354.231	1354.536	-226.081	0.522	1906.796	0.520	22	0.284	R.IPSGEVWVGNPAK.F
R3/RRR3-15/2	1354.208	1354.536	-242.721	0.508	1686.236	0.533	20	0.254	R.IPSGEVWVGNPAK.F
R3/RRR3-15/2	1355.352	1354.536	-136.191	0.526	1737.819	0.474	21	0.246	R.IPSGEVWVGNPAK.F
R3/RRR3-15/2	1002.039	1002.150	-110.715	0.525	967.979	0.406	17	0.162	R.LGSTIQGGLR.V
R3/RRR3-15/2	1002.045	1002.150	-104.850	0.522	773.759	0.447	16	0.158	R.LGSTIQGGLR.V
R3/RRR3-15/2	1816.546	1816.131	229.458	0.374	391.739	0.440	19	0.144	R.EIPPELILPDNILPNK.A
R3/RRR3-15/2	1815.550	1816.131	-873.089	0.337	368.678	0.480	18	0.144	R.EIPPELILPDNILPNK.A
R3/RRR3-15/2	1815.409	1816.131	-951.121	0.329	283.247	0.446	19	0.143	R.EIPPELILPDNILPNK.A
R3/RRR3-15/2	1815.844	1816.131	-158.629	0.343	252.631	0.453	17	0.143	R.EIPPELILPDNILPNK.A
R3/RRR3-15/2	1817.335	1816.131	112.604	0.442	242.238	0.481	18	0.140	-.EIPPELILPDNILPNK.-
R3/RRR3-15/2	1815.073	1816.131	-1137.205	0.259	327.535	0.385	17	0.137	R.EIPPELILPDNILPNK.A
R3/RRR3-15/3	1102.738	1102.290	407.899	0.401	1553.071	0.280	24	0.124	K.HSM*VGAGSLVK.Q
R3/RRR3-15/3	1101.905	1102.290	-350.809	0.339	1507.146	0.208	24	0.105	K.HSM*VGAGSLVK.Q
R3/RRR3-8/2	1593.975	1594.702	-1086.169	0.535	2476.976	0.557	24	0.405	R.IEEELGDAAVYAGEK.F
R3/RRR3-8/2	1595.252	1594.702	-282.719	0.624	2407.330	0.563	24	0.390	R.IEEELGDAAVYAGEK.F
R3/RRR3-8/2	1792.090	1791.983	59.807	0.541	835.457	0.540	24	0.169	R.GAVPSGASTGIYEALELR.D
R3/RRR3-8/2	1790.767	1791.983	-1241.523	0.355	591.303	0.466	22	0.145	R.GAVPSGASTGIYEALELR.D
R3/RRR3-10/2	1799.844	1800.002	-88.135	0.583	2702.460	0.484	24	0.427	R.LDSYLEFQSANSALLK.G
R3/RRR3-10/2	1799.340	1800.002	-926.477	0.536	2232.675	0.497	22	0.332	R.LDSYLEFQSANSALLK.G
R3/RRR3-10/2	1453.218	1452.593	-259.126	0.550	2227.848	0.457	21	0.320	K.NIDSFISDWGIGK.V
R3/RRR3-10/2	1453.188	1452.593	-279.521	0.538	2103.446	0.503	21	0.312	K.NIDSFISDWGIGK.V
R3/RRR3-10/2	1414.970	1415.578	-1139.212	0.511	1974.752	0.476	21	0.281	R.GNIASAINTIQANK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1415.253	1415.578	-230.262	0.493	1689.109	0.459	21	0.235	R.GNIASAINTIQANK.V
R3/RRR3-10/2	1688.634	1689.883	-1335.827	0.303	1584.627	0.357	20	0.198	R.SQDEALQIAELICAK.L
R3/RRR3-10/2	1414.206	1415.578	-1682.055	0.356	1300.673	0.267	19	0.158	R.GNIASAINTIQANK.V
R3/RRR3-10/2	877.027	877.023	5.080	0.374	1060.029	0.219	13	0.140	R.DLFLAAAR.I
R3/RRR3-4/2	1760.433	1760.968	-874.414	0.570	3461.359	0.585	25	0.678	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-4/2	1761.210	1760.968	137.882	0.592	3171.046	0.614	24	0.601	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-6/2	1760.370	1760.968	-909.986	0.542	2377.238	0.570	23	0.383	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-4/2	1760.815	1760.968	-86.682	0.547	2316.963	0.596	22	0.379	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-4/3	1931.187	1931.146	21.637	0.506	1883.930	0.526	33	0.243	K.VRPAYSFGVDPVWHGSR.S
R3/RRR3-2/2	1760.608	1760.968	-204.914	0.414	1200.435	0.537	19	0.193	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-4/3	1931.083	1931.146	-32.286	0.472	1661.810	0.474	33	0.191	K.VRPAYSFGVDPVWHGSR.S
R3/RRR3-4/2	1745.395	1744.835	-252.787	0.482	972.123	0.599	22	0.186	R.QEPVDETVTDPLSGEK.V
R3/RRR3-4/2	1176.253	1176.262	-7.662	0.466	1250.119	0.389	16	0.176	K.AGEFFYSAQR.S
R3/RRR3-4/2	971.073	971.176	-105.987	0.453	960.163	0.471	17	0.171	K.LGSLSGLVPK.E
R3/RRR3-4/2	1175.916	1176.262	-295.452	0.419	1126.748	0.364	15	0.163	K.AGEFFYSAQR.S
R3/RRR3-4/2	971.012	971.176	-168.788	0.440	697.406	0.456	16	0.156	K.LGSLSGLVPK.E
R3/RRR3-4/2	970.986	971.176	-196.281	0.428	736.242	0.406	16	0.152	K.LGSLSGLVPK.E
R3/RRR3-4/3	1760.487	1760.968	-273.717	0.480	1339.580	0.451	27	0.148	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-2/2	971.048	971.176	-132.216	0.358	541.008	0.452	14	0.147	K.LGSLSGLVPK.E
R3/RRR3-1/2	1760.643	1760.968	-184.882	0.353	419.486	0.445	17	0.142	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-21/2	1177.094	1176.262	-143.397	0.276	681.291	0.364	13	0.139	K.AGEFFYSAQR.S
R3/RRR3-4/3	1930.313	1931.146	-952.264	0.455	941.258	0.439	26	0.116	K.VRPAYSFGVDPVWHGSR.S
R3/RRR3-4/3	1760.321	1760.968	-937.944	0.434	760.449	0.483	23	0.112	K.FTSAFQEIVDAYGIAK.Y
R3/RRR3-14/2	1293.195	1293.491	-229.556	0.584	1298.580	0.512	18	0.204	R.KLTDDEIAFIK.E
R3/RRR3-14/2	1293.189	1293.491	-234.196	0.548	1293.773	0.504	18	0.202	R.KLTDDEIAFIK.E
R3/RRR3-14/2	1098.014	1098.304	-265.615	0.403	1080.641	0.491	18	0.179	K.HGM*VAAGALVR.Q
R3/RRR3-14/2	1097.505	1098.304	-1644.272	0.342	1099.532	0.446	18	0.171	K.HGM*VAAGALVR.Q
R3/RRR3-14/2	1384.829	1385.543	-1241.723	0.478	1042.371	0.381	20	0.160	R.IPCGEVWGGNPAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1385.133	1385.543	-297.232	0.475	975.835	0.369	21	0.156	R.IPCGEVWGGNPAK.F
R3/RRR3-14/3	1800.448	1800.846	-221.634	0.429	1217.976	0.538	31	0.154	K.SAHQDEEHDSM*IGATR.E
R3/RRR3-14/3	1098.398	1098.304	85.590	0.465	1939.319	0.230	24	0.152	K.HGM*VAAGALVR.Q
R3/RRR3-14/2	1384.299	1385.543	-1626.056	0.418	685.730	0.353	19	0.143	R.IPCGEVWGGNPAK.F
R3/RRR3-14/3	1098.357	1098.304	47.804	0.517	1722.476	0.251	23	0.133	K.HGM*VAAGALVR.Q
R3/RRR3-14/2	1900.657	1900.082	-224.150	0.340	628.282	0.364	16	0.132	K.AHAAENAKPVEKTEFEK.L
R3/RRR3-14/3	1899.848	1900.082	-123.105	0.473	794.131	0.556	28	0.127	K.AHAAENAKPVEKTEFEK.L
R3/RRR3-14/3	1800.254	1800.846	-886.633	0.401	906.714	0.516	28	0.125	K.SAHQDEEHDSM*IGATR.E
R3/RRR3-14/3	1899.707	1900.082	-197.554	0.451	813.158	0.477	29	0.115	K.AHAAENAKPVEKTEFEK.L
R3/RRR3-14/3	1293.450	1293.491	-31.826	0.500	1389.908	0.278	24	0.111	R.KLTDDEIAFIK.E
R3/RRR3-14/3	1097.962	1098.304	-312.894	0.454	1470.266	0.211	21	0.105	K.HGM*VAAGALVR.Q
R3/RRR3-14/3	1293.396	1293.491	-73.148	0.388	828.471	0.163	20	0.075	-.KLTDDEIAFIK.-
R3/RRR3-18/2	1677.437	1675.904	-279.159	0.572	962.002	0.635	22	0.194	K.ALADEIGIPFLETSAK.D
R3/RRR3-18/3	1922.218	1922.177	21.026	0.453	1412.033	0.528	34	0.176	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/2	1130.919	1131.348	-380.829	0.492	1110.968	0.402	16	0.168	K.AFM*TM*AGEIK.N
R3/RRR3-18/2	1130.829	1131.348	-1347.399	0.405	1013.289	0.397	15	0.160	K.AFM*TM*AGEIK.N
R3/RRR3-18/2	1675.278	1675.904	-973.820	0.433	770.954	0.470	20	0.154	K.ALADEIGIPFLETSAK.D
R3/RRR3-18/3	1979.630	1980.127	-251.767	0.409	978.357	0.548	23	0.138	K.QWLNEIDRYASENVNK.L
R3/RRR3-18/3	1905.612	1906.178	-824.032	0.309	1162.399	0.388	32	0.122	R.M*ASQPATNASKPATVQMR.G
R3/RRR3-18/3	1923.754	1922.177	-220.681	0.431	1003.841	0.424	32	0.119	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1921.939	1922.177	-124.504	0.376	1007.619	0.424	34	0.118	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1921.578	1922.177	-834.873	0.353	995.122	0.420	32	0.117	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1922.235	1922.177	30.294	0.432	848.767	0.435	30	0.114	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1906.127	1906.178	-26.677	0.322	990.752	0.359	30	0.108	R.M*ASQPATNASKPATVQMR.G
R3/RRR3-19/3	1921.446	1922.177	-903.653	0.302	829.500	0.398	31	0.107	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1923.006	1922.177	-89.417	0.360	835.636	0.382	31	0.106	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1906.401	1906.178	117.349	0.350	895.951	0.349	30	0.103	R.M*ASQPATNASKPATVQMR.G
R3/RRR3-18/3	1979.998	1980.127	-65.468	0.370	787.991	0.402	24	0.102	K.QWLNEIDRYASENVNK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/3	1921.998	1922.177	-93.636	0.337	769.911	0.358	30	0.101	R.M*ASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1905.941	1906.178	-124.580	0.285	374.810	0.375	21	0.101	R.MASQPATNASKPATVQM*R.G
R3/RRR3-18/3	1979.965	1980.127	-82.072	0.376	496.615	0.403	20	0.092	-.QWLNEIDRYASENVNK.-
R3/RRR3-18/3	1906.806	1906.178	-195.348	0.326	188.883	0.390	18	0.090	-.MASQPATNASKPATVQM*R.-
R3/RRR3-7/2	1134.118	1133.320	-178.951	0.538	1826.237	0.557	20	0.280	K.ALVSAGLSSSIK.V
R3/RRR3-7/2	1132.466	1133.320	-1642.549	0.427	1916.032	0.509	20	0.280	K.ALVSAGLSSSIK.V
R3/RRR3-14/2	1133.137	1133.320	-162.034	0.410	1847.302	0.467	19	0.258	K.ALVSAGLSSSIK.V
R3/RRR3-14/2	1132.989	1133.320	-293.463	0.420	1659.435	0.466	19	0.233	K.ALVSAGLSSSIK.V
R3/RRR3-7/2	1133.058	1133.320	-232.176	0.470	1489.521	0.510	19	0.222	K.ALVSAGLSSSIK.V
R3/RRR3-14/2	1563.454	1562.751	-190.345	0.556	1572.108	0.446	21	0.217	R.DNVEAYWPSVIIR.Y
R3/RRR3-7/2	1783.422	1783.963	-866.300	0.507	1402.897	0.521	23	0.214	R.DISLNYATFQPGTTVR.D
R3/RRR3-7/2	1564.190	1562.751	281.506	0.604	1466.907	0.483	20	0.212	R.DNVEAYWPSVIIR.Y
R3/RRR3-7/2	1783.345	1783.963	-909.590	0.546	1287.143	0.562	22	0.210	R.DISLNYATFQPGTTVR.D
R3/RRR3-14/2	1132.489	1133.320	-1622.407	0.357	1399.732	0.451	18	0.198	K.ALVSAGLSSSIK.V
R3/RRR3-7/2	1561.942	1562.751	-1161.592	0.391	1529.072	0.294	20	0.182	R.DNVEAYWPSVIIR.Y
R3/RRR3-7/2	1562.655	1562.751	-61.319	0.484	1350.667	0.382	20	0.182	R.DNVEAYWPSVIIR.Y
R3/RRR3-7/2	1567.469	1567.767	-190.638	0.408	848.823	0.512	19	0.167	R.IYYPDKEALDALR.G
R3/RRR3-14/2	1783.258	1783.963	-958.657	0.404	1043.001	0.438	19	0.164	R.DISLNYATFQPGTTVR.D
R3/RRR3-14/2	1562.516	1562.751	-150.653	0.460	1043.773	0.381	19	0.160	R.DNVEAYWPSVIIR.Y
R3/RRR3-7/2	1567.300	1567.767	-299.089	0.402	818.569	0.461	18	0.158	R.IYYPDKEALDALR.G
R3/RRR3-14/2	915.838	916.097	-283.433	0.402	767.470	0.402	13	0.153	R.SEVVQLLK.S
R3/RRR3-14/2	915.950	916.097	-161.624	0.441	734.660	0.398	13	0.153	R.SEVVQLLK.S
R3/RRR3-7/2	1567.354	1567.767	-264.316	0.393	722.646	0.455	17	0.153	R.IYYPDKEALDALR.G
R3/RRR3-7/2	915.969	916.097	-139.832	0.480	730.136	0.388	13	0.152	R.SEVVQLLK.S
R3/RRR3-7/2	915.579	916.097	-1663.163	0.407	704.159	0.373	13	0.149	R.SEVVQLLK.S
R3/RRR3-7/2	915.562	916.097	-1682.049	0.365	765.386	0.364	13	0.148	R.SEVVQLLK.S
R3/RRR3-14/2	915.923	916.097	-191.037	0.398	719.057	0.345	13	0.145	-.SEVVQLLK.-
R3/RRR3-14/2	1566.440	1567.767	-1490.212	0.291	550.805	0.422	16	0.142	R.IYYPDKEALDALR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1566.571	1567.767	-1406.148	0.344	610.562	0.313	16	0.137	R.IYYPDKEALDALR.G
R3/RRR3-9/2	1567.003	1567.767	-1129.243	0.323	657.038	0.247	15	0.132	R.IYYPDKEALDALR.G
R3/RRR3-15/2	915.841	916.097	-280.892	0.246	646.587	0.264	11	0.130	-.SEVVQLLK.-
R3/RRR3-14/3	1567.678	1567.767	-56.992	0.470	673.966	0.467	26	0.112	R.IYYPDKEALDALR.G
R3/RRR3-7/3	1567.856	1567.767	56.521	0.444	552.806	0.435	24	0.107	R.IYYPDKEALDALR.G
R3/RRR3-14/3	1566.884	1567.767	-1205.602	0.397	360.209	0.430	20	0.107	R.IYYPDKEALDALR.G
R3/RRR3-14/3	1567.324	1567.767	-283.625	0.336	409.161	0.452	19	0.106	R.IYYPDKEALDALR.G
R3/RRR3-7/3	1567.227	1567.767	-985.500	0.395	358.942	0.404	20	0.105	R.IYYPDKEALDALR.G
R3/RRR3-7/3	1567.375	1567.767	-250.925	0.342	758.011	0.425	28	0.105	R.IYYPDKEALDALR.G
R3/RRR3-14/3	1567.654	1567.767	-72.574	0.371	496.978	0.406	23	0.104	R.IYYPDKEALDALR.G
R3/RRR3-14/3	1566.905	1567.767	-1192.342	0.280	426.864	0.406	23	0.101	R.IYYPDKEALDALR.G
R3/RRR3-14/3	1566.678	1567.767	-1337.288	0.317	500.626	0.385	23	0.101	R.IYYPDKEALDALR.G
R3/RRR3-11/2	1442.159	1442.643	-336.333	0.450	1621.298	0.585	19	0.254	R.VPTANVSVVDLTAR.I
R3/RRR3-11/2	1441.699	1442.643	-1352.145	0.450	1531.257	0.589	19	0.243	R.VPTANVSVVDLTAR.I
R3/RRR3-11/2	1442.128	1442.643	-1053.915	0.476	1514.525	0.582	19	0.240	R.VPTANVSVVDLTAR.I
R3/RRR3-11/2	1677.012	1675.781	137.942	0.475	1351.710	0.582	17	0.220	K.LVSWYDNEWGYSR.R
R3/RRR3-12/2	1441.661	1442.643	-1379.018	0.376	1281.790	0.560	18	0.205	R.VPTANVSVVDLTAR.I
R3/RRR3-11/2	1178.239	1178.320	-68.543	0.418	1334.018	0.415	17	0.187	K.AGISLNDNFVK.L
R3/RRR3-11/2	1387.287	1386.536	-180.361	0.475	1067.692	0.426	21	0.167	R.GAAQNIIPSSTGAAK.A
R3/RRR3-11/2	1178.181	1178.320	-117.909	0.329	1221.118	0.324	17	0.162	K.AGISLNDNFVK.L
R3/RRR3-11/2	1386.231	1386.536	-220.774	0.412	809.981	0.363	20	0.146	R.GAAQNIIPSSTGAAK.A
R3/RRR3-11/2	1386.113	1386.536	-306.297	0.403	769.027	0.368	20	0.146	R.GAAQNIIPSSTGAAK.A
R3/RRR3-12/2	819.835	819.931	-118.147	0.390	895.837	0.302	13	0.145	K.VGINGFGR.I
R3/RRR3-12/2	1386.105	1386.536	-312.305	0.450	727.854	0.367	20	0.144	R.GAAQNIIPSSTGAAK.A
R3/RRR3-12/2	820.133	819.931	247.056	0.435	824.336	0.316	13	0.144	K.VGINGFGR.I
R3/RRR3-12/2	1386.011	1386.536	-1104.006	0.329	710.372	0.361	20	0.143	R.GAAQNIIPSSTGAAK.A
R3/RRR3-12/2	1386.127	1386.536	-296.224	0.308	502.515	0.320	16	0.135	R.GAAQNIIPSSTGAAK.A
R3/RRR3-13/2	1443.905	1442.643	181.834	0.311	620.215	0.224	15	0.130	-.VPTANVSVVDLTAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1788.660	1786.919	-144.954	0.509	1516.986	0.585	23	0.241	R.AVFASGSPFDPVEYDGK.I
R3/RRR3-6/2	1786.295	1786.919	-911.515	0.529	1369.416	0.505	23	0.206	R.AVFASGSPFDPVEYDGK.I
R3/RRR3-7/2	981.039	980.100	-61.791	0.559	1467.085	0.441	15	0.205	K.AYELGLASR.L
R3/RRR3-6/2	1786.373	1786.919	-868.022	0.497	1313.418	0.513	23	0.202	R.AVFASGSPFDPVEYDGK.I
R3/RRR3-7/2	979.955	980.100	-147.944	0.515	1480.757	0.415	15	0.202	K.AYELGLASR.L
R3/RRR3-7/2	1165.583	1166.355	-1524.765	0.516	1312.249	0.491	19	0.200	K.ISAHIAANVAAK.A
R3/RRR3-7/2	1166.111	1166.355	-210.370	0.472	1253.117	0.510	19	0.198	K.ISAHIAANVAAK.A
R3/RRR3-7/2	979.841	980.100	-264.419	0.544	1433.367	0.421	15	0.198	K.AYELGLASR.L
R3/RRR3-3/2	979.904	980.100	-200.055	0.470	1391.672	0.409	15	0.192	K.AYELGLASR.L
R3/RRR3-6/2	980.001	980.100	-101.461	0.517	1443.293	0.385	15	0.192	K.AYELGLASR.L
R3/RRR3-7/2	1166.136	1166.355	-188.422	0.470	1193.269	0.468	18	0.184	K.ISAHIAANVAAK.A
R3/RRR3-7/2	1316.165	1315.584	-319.226	0.467	654.595	0.654	20	0.176	K.TIKPTVLIGTSGK.G
R3/RRR3-6/2	979.593	980.100	-1542.480	0.471	1254.556	0.371	14	0.173	K.AYELGLASR.L
R3/RRR3-1/2	979.664	980.100	-445.935	0.410	1108.783	0.387	14	0.166	K.AYELGLASR.L
R3/RRR3-6/2	1315.230	1315.584	-269.929	0.335	570.153	0.362	18	0.139	K.TIKPTVLIGTSGK.G
R3/RRR3-7/3	1294.373	1294.528	-120.152	0.452	1252.429	0.385	25	0.125	R.KISAHIAANVAAK.A
R3/RRR3-7/3	1294.487	1294.528	-31.753	0.438	922.919	0.376	23	0.105	R.KISAHIAANVAAK.A
R3/RRR3-7/3	1294.687	1294.528	123.296	0.405	1038.319	0.337	23	0.104	R.KISAHIAANVAAK.A
R3/RRR3-6/3	1294.400	1294.528	-99.292	0.436	932.790	0.348	22	0.102	R.KISAHIAANVAAK.A
R3/RRR3-10/2	1980.210	1981.107	-960.753	0.512	2044.909	0.604	24	0.329	R.ELGLEAVESGDADLVSYGR.L
R3/RRR3-10/2	1980.543	1981.107	-792.072	0.527	1982.844	0.598	24	0.316	R.ELGLEAVESGDADLVSYGR.L
R3/RRR3-10/2	875.867	875.072	-234.022	0.419	1435.617	0.326	13	0.181	K.LGMAVVER.L
R3/RRR3-10/2	875.850	875.072	-253.458	0.431	1364.701	0.267	13	0.167	-.LGMAVVER.-
R3/RRR3-10/2	1733.486	1733.948	-267.449	0.438	755.586	0.548	24	0.166	R.AIGGVPGPALAEYYAQR.T
R3/RRR3-10/2	1303.076	1303.489	-317.359	0.448	1024.911	0.370	17	0.158	R.LFISNPDLVER.F
R3/RRR3-10/2	1577.491	1577.807	-200.992	0.380	1022.336	0.324	15	0.146	K.GGIFFCQLWHVGR.A
R3/RRR3-10/2	1732.802	1733.948	-1242.354	0.286	547.768	0.458	20	0.141	R.AIGGVPGPALAEYYAQR.T
R3/RRR3-10/2	1303.319	1303.489	-130.731	0.384	531.323	0.331	13	0.135	R.LFISNPDLVER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1732.532	1733.948	-1398.726	0.276	295.849	0.353	16	0.133	R.AIGGVPGPALAEYYAQR.T
R3/RRR3-9/2	1585.737	1585.824	-55.253	0.552	2571.021	0.353	21	0.351	R.FELTFYALNPELK.V
R3/RRR3-9/2	1585.740	1585.824	-53.323	0.525	2487.455	0.358	21	0.337	R.FELTFYALNPELK.V
R3/RRR3-9/2	1042.067	1042.170	-98.532	0.524	1286.629	0.440	15	0.189	K.YAELVYAGR.W
R3/RRR3-9/2	1041.372	1042.170	-1731.795	0.398	1123.555	0.419	14	0.171	K.YAELVYAGR.W
R3/RRR3-9/2	960.034	960.110	-79.659	0.458	1098.539	0.415	17	0.170	K.ASGASQLVVK.D
R3/RRR3-9/2	1133.098	1133.369	-239.623	0.400	439.381	0.480	14	0.148	K.KHNVPIPVTK.K
R3/RRR3-9/2	1132.576	1133.369	-1587.580	0.363	408.635	0.477	13	0.145	K.KHNVPIPVTK.K
R3/RRR3-9/2	819.605	819.971	-448.320	0.342	725.820	0.304	11	0.140	R.LYGLPTR.V
R3/RRR3-9/2	819.462	819.971	-1846.584	0.179	745.805	0.225	11	0.130	R.LYGLPTR.V
R3/RRR3-9/2	819.205	819.971	-2162.221	0.182	614.716	0.242	10	0.130	R.LYGLPTR.V
R3/RRR3-9/2	1295.200	1295.420	-170.497	0.476	2159.951	0.395	20	0.290	K.ADIEDYLASVAK.G
R3/RRR3-9/2	1294.662	1295.420	-1361.964	0.374	1768.665	0.340	18	0.218	K.ADIEDYLASVAK.G
R3/RRR3-9/2	1986.155	1987.203	-1034.071	0.486	1285.108	0.517	24	0.198	K.ETAAAPGLGYVDLPNTQIR.K
R3/RRR3-9/2	1294.695	1295.420	-1336.964	0.338	1640.811	0.269	17	0.189	K.ADIEDYLASVAK.G
R3/RRR3-9/3	1649.698	1649.910	-128.895	0.393	1273.420	0.516	25	0.155	R.ILKADIEDYLASVAK.G
R3/RRR3-9/2	1436.153	1436.595	-308.839	0.467	2132.699	0.559	21	0.333	R.FTQAGSEVSALLGR.I
R3/RRR3-9/2	1503.525	1503.768	-161.694	0.559	2248.677	0.406	20	0.304	K.TVFIQELINNIAK.A
R3/RRR3-9/2	1503.345	1503.768	-282.330	0.498	2222.440	0.386	20	0.295	K.TVFIQELINNIAK.A
R3/RRR3-9/2	1503.278	1503.768	-326.975	0.464	2241.953	0.327	20	0.282	K.TVFIQELINNIAK.A
R3/RRR3-9/2	1436.296	1436.595	-208.646	0.495	1627.960	0.552	20	0.249	R.FTQAGSEVSALLGR.I
R3/RRR3-9/2	1406.232	1406.609	-269.178	0.472	1590.012	0.509	18	0.233	R.VALTGLTVAEEFR.S
R3/RRR3-9/2	1406.424	1406.609	-131.681	0.465	1624.875	0.473	18	0.229	R.VALTGLTVAEEFR.S
R3/RRR3-9/2	1774.377	1774.992	-912.876	0.457	1037.610	0.558	19	0.181	R.GISELGIYPAVDPLDSK.S
R3/RRR3-9/2	1436.064	1436.595	-1069.704	0.337	964.495	0.438	16	0.157	R.FTQAGSEVSALLGR.I
R3/RRR3-9/2	1505.208	1503.768	293.025	0.343	289.845	0.328	13	0.137	K.TVFIQELINNIAK.A
R3/RRR3-8/2	1446.323	1446.630	-212.617	0.502	1810.642	0.448	20	0.249	R.DAVTDLSLHYLAK.A
R3/RRR3-8/2	1446.387	1446.630	-168.759	0.514	1661.134	0.460	19	0.231	R.DAVTDLSLHYLAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1331.062	1331.414	-265.798	0.464	1330.295	0.444	18	0.192	R.GSNQLVIDEAER.S
R3/RRR3-8/2	1330.831	1331.414	-1193.297	0.440	1307.086	0.439	17	0.188	R.GSNQLVIDEAER.S
R3/RRR3-8/2	1289.203	1289.417	-166.542	0.464	1260.184	0.431	19	0.184	K.LGGTVDDTELIR.G
R3/RRR3-8/2	1445.851	1446.630	-1233.942	0.416	1276.088	0.427	18	0.183	R.DAVTDLSLHYLAK.A
R3/RRR3-8/2	1330.947	1331.414	-352.202	0.456	1210.230	0.400	17	0.173	R.GSNQLVIDEAER.S
R3/RRR3-8/2	1289.055	1289.417	-281.963	0.485	927.627	0.366	19	0.153	K.LGGTVDDTELIR.G
R3/RRR3-8/2	930.877	931.069	-207.040	0.408	1083.227	0.233	13	0.143	K.IDDIVTVR.-
R3/RRR3-8/2	1204.029	1203.407	-315.400	0.482	801.553	0.368	13	0.141	K.ASGCNVLLIQK.S
R3/RRR3-12/2	1509.505	1508.692	-123.986	0.476	1585.488	0.448	20	0.221	K.YVISIDDNCLPAK.D
R3/RRR3-12/2	1425.179	1425.558	-266.630	0.441	1309.062	0.511	18	0.201	K.LSSTSVTVEDCVK.E
R3/RRR3-12/2	1935.521	1935.169	182.017	0.509	929.034	0.583	21	0.180	K.TPATPFFFNTLYDPFR.K
R3/RRR3-12/2	1389.193	1389.578	-278.031	0.444	1150.542	0.473	16	0.180	K.ALESLKEWEGVK.V
R3/RRR3-12/2	1389.210	1389.578	-265.689	0.457	1093.553	0.400	16	0.164	K.ALESLKEWEGVK.V
R3/RRR3-12/2	1059.085	1059.243	-149.665	0.434	443.472	0.562	15	0.158	K.LGPQNAIFAK.A
R3/RRR3-12/2	1059.256	1059.243	12.413	0.461	545.355	0.509	16	0.158	K.LGPQNAIFAK.A
R3/RRR3-12/2	1389.081	1389.578	-359.321	0.436	954.281	0.404	15	0.155	K.ALESLKEWEGVK.V
R3/RRR3-12/2	1058.979	1059.243	-250.729	0.419	445.819	0.502	15	0.153	K.LGPQNAIFAK.A
R3/RRR3-12/2	1424.960	1425.558	-1124.352	0.376	806.214	0.438	17	0.152	K.LSSTSVTVEDCVK.E
R3/RRR3-12/2	1424.905	1425.558	-1163.578	0.352	816.969	0.385	17	0.147	K.LSSTSVTVEDCVK.E
R3/RRR3-8/2	1361.936	1362.428	-362.887	0.413	1528.225	0.244	21	0.172	K.SGVDSGATLVAGGDR.A
R3/RRR3-8/2	945.063	945.055	7.694	0.454	1151.863	0.401	15	0.172	R.LDAANTLAR.A
R3/RRR3-8/2	945.052	945.055	-3.447	0.481	942.055	0.404	14	0.159	R.LDAANTLAR.A
R3/RRR3-8/2	945.157	945.055	107.958	0.324	737.772	0.267	13	0.136	R.LDAANTLAR.A
R3/RRR3-7/2	1370.468	1369.629	-117.714	0.406	694.243	0.344	14	0.133	K.VGPALACGNAVVLK.T
R3/RRR3-4/2	1080.313	1080.261	48.325	0.306	848.775	0.432	13	0.150	R.LSAAWQLYK.S
R3/RRR3-4/2	1131.010	1131.261	-222.637	0.260	774.486	0.234	14	0.130	K.SQEELINVAK.E
R3/RRR3-15/2	1206.095	1206.330	-195.783	0.510	1162.179	0.487	18	0.184	K.GGAFVEAPVSGSK.K
R3/RRR3-15/2	1240.126	1240.390	-212.920	0.351	1344.610	0.367	19	0.179	K.SFFLGEIGNGAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1206.066	1206.330	-219.542	0.492	1047.596	0.439	17	0.166	K.GGAFVEAPVSGSK.K
R3/RRR3-15/2	1828.025	1827.067	-23.014	0.479	854.939	0.506	18	0.159	R.SLGLGDLDFSAVYEVLK.G
R3/RRR3-15/2	1697.989	1698.961	-1164.789	0.296	829.632	0.375	17	0.141	K.VLYDDM*VPAFDVLGK.K
R3/RRR3-15/2	1241.350	1240.390	-32.214	0.346	753.801	0.280	15	0.135	K.SFFLGEIGNGAK.M
R3/RRR3-15/2	1240.196	1240.390	-156.735	0.290	675.019	0.284	15	0.134	K.SFFLGEIGNGAK.M
R3/RRR3-15/3	1964.931	1965.305	-190.756	0.431	982.031	0.407	27	0.111	K.LKGPSM*LQGSYNPAFPLK.H
R3/RRR3-15/3	1964.704	1965.305	-817.480	0.421	771.404	0.369	24	0.096	K.LKGPSM*LQGSYNPAFPLK.H
R3/RRR3-7/2	1463.853	1462.626	155.185	0.571	1530.049	0.579	20	0.244	K.SPIVVFDDVDVEK.A
R3/RRR3-7/2	1463.047	1462.626	288.666	0.543	1472.806	0.534	20	0.226	K.SPIVVFDDVDVEK.A
R3/RRR3-7/2	1462.269	1462.626	-244.879	0.519	1452.144	0.539	20	0.225	K.SPIVVFDDVDVEK.A
R3/RRR3-7/2	1495.409	1494.628	-147.179	0.441	1420.182	0.456	20	0.202	R.ELGEGGIDNYLSVK.Q
R3/RRR3-7/2	1494.257	1494.628	-249.306	0.420	1457.460	0.434	20	0.201	R.ELGEGGIDNYLSVK.Q
R3/RRR3-7/2	1305.901	1306.446	-1187.013	0.415	1240.359	0.525	19	0.198	R.LGPVVSEGQYEK.I
R3/RRR3-7/2	1494.240	1494.628	-260.534	0.412	1509.700	0.389	20	0.198	R.ELGEGGIDNYLSVK.Q
R3/RRR3-7/2	1385.275	1385.595	-231.356	0.496	1271.673	0.506	19	0.196	K.SQGATILTGGVRPK.H
R3/RRR3-7/2	1306.144	1306.446	-232.342	0.480	1088.887	0.556	18	0.191	R.LGPVVSEGQYEK.I
R3/RRR3-7/2	1306.038	1306.446	-313.170	0.473	1067.865	0.466	18	0.175	R.LGPVVSEGQYEK.I
R3/RRR3-7/2	1162.172	1162.226	-46.208	0.430	1139.032	0.288	17	0.153	K.VSDPLEEGCR.L
R3/RRR3-3/2	1462.793	1462.626	114.284	0.285	855.492	0.305	16	0.139	K.SPIVVFDDVDVEK.A
R3/RRR3-8/2	1399.109	1399.660	-1111.785	0.464	1710.289	0.519	19	0.253	K.VLWLIENVDAVK.N
R3/RRR3-8/2	1400.138	1399.660	342.735	0.573	1601.119	0.543	19	0.245	K.VLWLIENVDAVK.N
R3/RRR3-8/2	1400.273	1399.660	-277.056	0.570	1577.363	0.521	19	0.236	K.VLWLIENVDAVK.N
R3/RRR3-8/2	1463.332	1463.613	-192.157	0.397	1846.040	0.213	20	0.199	R.DSLGIISTASEIEK.L
R3/RRR3-8/2	1462.939	1463.613	-1147.219	0.392	1676.856	0.207	19	0.179	R.DSLGIISTASEIEK.L
R3/RRR3-8/2	1022.269	1022.137	129.458	0.458	1353.501	0.298	15	0.169	K.SAEGEFLLR.V
R3/RRR3-8/2	1021.846	1022.137	-285.542	0.448	1290.106	0.312	15	0.167	K.SAEGEFLLR.V
R3/RRR3-8/2	1113.871	1114.237	-330.047	0.552	914.906	0.417	17	0.161	R.RLESELPGGR.T
R3/RRR3-8/2	1113.532	1114.237	-1536.445	0.559	1113.535	0.353	16	0.160	R.RLESELPGGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1021.962	1022.137	-171.575	0.455	1187.908	0.297	14	0.157	K.SAEGEFLLR.V
R3/RRR3-8/3	1578.952	1578.662	184.109	0.499	1068.173	0.579	31	0.149	K.VFGQHVTDCSNASR.T
R3/RRR3-8/2	1113.916	1114.237	-289.364	0.547	903.973	0.357	15	0.149	R.RLESELPGGR.T
R3/RRR3-8/3	1578.854	1578.662	122.004	0.555	1036.988	0.577	31	0.148	K.VFGQHVTDCSNASR.T
R3/RRR3-8/3	1578.871	1578.662	132.937	0.523	804.909	0.543	28	0.128	K.VFGQHVTDCSNASR.T
R3/RRR3-7/2	1144.322	1144.303	16.733	0.483	2385.653	0.310	18	0.303	R.AEVSDIAIAVR.E
R3/RRR3-7/2	1265.169	1264.496	-259.125	0.570	1863.998	0.508	19	0.273	R.AISSLLSAQFVK.E
R3/RRR3-8/2	1145.299	1144.303	-3.486	0.463	1979.385	0.406	17	0.263	R.AEVSDIAIAVR.E
R3/RRR3-7/2	1264.392	1264.496	-82.271	0.419	1655.272	0.477	18	0.235	R.AISSLLSAQFVK.E
R3/RRR3-7/2	1395.123	1395.540	-299.931	0.464	1567.176	0.371	20	0.201	K.EGDYVTLVQSGVK.S
R3/RRR3-7/2	1395.332	1395.540	-149.312	0.444	1490.541	0.347	19	0.188	K.EGDYVTLVQSGVK.S
R3/RRR3-7/2	1395.311	1395.540	-164.231	0.452	1315.174	0.360	19	0.175	K.EGDYVTLVQSGVK.S
R3/RRR3-7/2	1166.360	1165.324	30.693	0.442	926.629	0.430	16	0.158	K.SANADIHVIPK.I
R3/RRR3-7/2	1264.228	1264.496	-212.735	0.345	946.805	0.351	15	0.148	R.AISSLLSAQFVK.E
R3/RRR3-7/2	1779.087	1778.984	58.042	0.365	630.099	0.364	15	0.132	K.FGVENGVDFYAVSFVK.D
R3/RRR3-7/2	1143.655	1144.303	-1445.230	0.289	998.251	0.150	16	0.132	R.AEVSDIAIAVR.E
R3/RRR3-8/2	1821.040	1821.131	-50.332	0.536	1311.144	0.611	24	0.223	K.TAEQTPLSGLVMAQFVK.E
R3/RRR3-8/2	1354.706	1354.620	63.391	0.427	1542.070	0.480	21	0.221	K.IGPALATGNTVVLK.T
R3/RRR3-8/2	1521.637	1522.642	-1321.182	0.384	1581.811	0.364	21	0.202	R.ELGEAALANYTQNK.S
R3/RRR3-8/2	1820.390	1821.131	-959.482	0.490	1093.273	0.556	22	0.189	K.TAEQTPLSGLVMAQFVK.E
R3/RRR3-8/2	1663.867	1663.898	-18.883	0.452	1039.170	0.562	22	0.185	K.EAGFPAGVLNVISGFGK.I
R3/RRR3-8/2	1557.290	1556.789	-321.610	0.454	838.636	0.570	18	0.173	K.GYFIQPTIFTNVR.N
R3/RRR3-8/2	1663.617	1663.898	-169.685	0.440	837.377	0.533	20	0.165	K.EAGFPAGVLNVISGFGK.I
R3/RRR3-8/2	1663.251	1663.898	-993.597	0.327	922.475	0.481	20	0.161	K.EAGFPAGVLNVISGFGK.I
R3/RRR3-8/2	1556.323	1556.789	-300.254	0.369	891.701	0.460	18	0.159	K.GYFIQPTIFTNVR.N
R3/RRR3-8/2	1664.260	1663.898	217.864	0.387	768.330	0.497	19	0.156	K.EAGFPAGVLNVISGFGK.I
R3/RRR3-8/2	1664.417	1663.898	-289.729	0.384	700.037	0.492	18	0.151	K.EAGFPAGVLNVISGFGK.I
R3/RRR3-8/2	1354.320	1354.620	-222.631	0.394	788.491	0.436	17	0.151	K.IGPALATGNTVVLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1353.502	1354.620	-1569.610	0.278	640.205	0.368	15	0.136	K.IGPALATGNTVVLK.T
R3/RRR3-18/2	1202.059	1202.383	-269.776	0.496	1754.507	0.397	18	0.230	K.INIKDDVSAVK.K
R3/RRR3-18/2	1202.024	1202.383	-299.730	0.498	1663.904	0.356	18	0.209	K.INIKDDVSAVK.K
R3/RRR3-18/2	1201.667	1202.383	-1432.519	0.462	1590.090	0.367	18	0.204	K.INIKDDVSAVK.K
R3/RRR3-18/2	1196.890	1197.323	-362.700	0.530	1174.524	0.498	18	0.190	R.HLVAVQTDEGK.A
R3/RRR3-18/2	1196.614	1197.323	-1432.735	0.488	1081.479	0.460	18	0.176	R.HLVAVQTDEGK.A
R3/RRR3-18/2	1197.177	1197.323	-122.583	0.496	1083.685	0.449	18	0.175	R.HLVAVQTDEGK.A
R3/RRR3-18/3	1771.921	1771.955	-19.328	0.433	775.465	0.496	29	0.115	R.HLVAVQTDEGKAFAER.E
R3/RRR3-18/3	1331.831	1330.556	207.192	0.469	901.660	0.397	21	0.107	K.INIKDDVSAVKK.G
R3/RRR3-18/3	1330.646	1330.556	67.885	0.417	771.930	0.251	22	0.086	-.INIKDDVSAVKK.-
R3/RRR3-9/2	1479.980	1479.662	215.623	0.530	1945.241	0.580	22	0.308	K.IYDPGYLNTAPVR.S
R3/RRR3-9/2	1118.082	1118.311	-205.171	0.506	1880.368	0.475	18	0.267	K.APTIAAAAYLR.L
R3/RRR3-9/2	1480.622	1479.662	-26.760	0.536	1715.122	0.543	21	0.261	K.IYDPGYLNTAPVR.S
R3/RRR3-9/2	1598.185	1598.730	-969.466	0.401	2011.437	0.371	22	0.259	R.SSICYIDGDEGILR.Y
R3/RRR3-9/2	1117.939	1118.311	-333.336	0.484	1697.072	0.501	18	0.248	K.APTIAAAAYLR.L
R3/RRR3-9/2	1598.005	1598.730	-1082.664	0.446	1848.408	0.413	21	0.246	R.SSICYIDGDEGILR.Y
R3/RRR3-9/2	1118.037	1118.311	-245.260	0.524	1734.757	0.466	18	0.244	K.APTIAAAAYLR.L
R3/RRR3-9/2	1479.148	1479.662	-1026.295	0.452	1431.606	0.501	20	0.214	K.IYDPGYLNTAPVR.S
R3/RRR3-9/2	1598.329	1598.730	-251.610	0.466	1567.250	0.426	20	0.212	R.SSICYIDGDEGILR.Y
R3/RRR3-9/2	914.971	915.029	-64.313	0.490	1090.448	0.472	15	0.178	R.GGALAVVDGR.T
R3/RRR3-9/2	914.842	915.029	-205.650	0.439	1112.977	0.289	15	0.151	R.GGALAVVDGR.T
R3/RRR3-9/2	914.460	915.029	-1721.633	0.351	843.787	0.357	16	0.148	R.GGALAVVDGR.T
R3/RRR3-9/3	1763.923	1764.088	-93.646	0.361	1134.667	0.389	23	0.115	K.IM*RPQQVYTGVWLR.H
R3/RRR3-4/2	1868.756	1870.006	-1207.727	0.302	776.954	0.342	21	0.140	K.TYEPSEEPFDISLVSR.E
R3/RRR3-3/2	1871.604	1870.006	-215.658	0.337	299.654	0.307	14	0.131	K.TYEPSEEPFDISLVSR.E
R3/RRR3-4/3	1187.585	1187.416	142.818	0.461	675.405	0.472	20	0.111	K.FGALVDALKPR.I
R3/RRR3-4/3	1187.412	1187.416	-3.168	0.401	606.795	0.412	19	0.102	K.FGALVDALKPR.I
R3/RRR3-4/3	1187.672	1187.416	216.414	0.388	609.532	0.403	20	0.101	K.FGALVDALKPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1680.170	1679.898	162.823	0.478	1035.671	0.424	19	0.163	K.TPFQEYTDLLARPK.G
R3/RRR3-14/2	1678.759	1679.898	-1277.900	0.441	719.995	0.464	17	0.151	K.TPFQEYTDLLARPK.G
R3/RRR3-14/3	1678.585	1679.898	-1381.651	0.375	684.775	0.526	25	0.114	K.TPFQEYTDLLARPK.G
R3/RRR3-14/3	1679.145	1679.898	-1047.053	0.383	532.981	0.490	25	0.106	K.TPFQEYTDLLARPK.G
R3/RRR3-6/2	1506.703	1505.742	-26.053	0.574	2107.207	0.540	21	0.319	K.IAGIQGGFFELQPK.E
R3/RRR3-6/2	1505.541	1505.742	-133.909	0.544	2041.964	0.548	21	0.311	K.IAGIQGGFFELQPK.E
R3/RRR3-2/2	1506.569	1505.742	-115.532	0.578	2084.360	0.516	21	0.307	K.IAGIQGGFFELQPK.E
R3/RRR3-2/2	1505.594	1505.742	-98.855	0.518	1933.634	0.543	21	0.292	K.IAGIQGGFFELQPK.E
R3/RRR3-6/2	1505.431	1505.742	-207.278	0.542	1887.083	0.541	21	0.283	K.IAGIQGGFFELQPK.E
R3/RRR3-2/2	1504.710	1505.742	-1354.597	0.340	1718.086	0.388	20	0.221	K.IAGIQGGFFELQPK.E
R3/RRR3-6/2	1335.216	1335.534	-238.746	0.546	1397.793	0.473	20	0.205	R.INTLLQGYSGIR.F
R3/RRR3-6/2	1334.736	1335.534	-1351.160	0.440	1296.735	0.486	19	0.197	R.INTLLQGYSGIR.F
R3/RRR3-2/2	1335.144	1335.534	-293.138	0.474	1349.448	0.448	20	0.196	R.INTLLQGYSGIR.F
R3/RRR3-6/2	1334.620	1335.534	-1438.430	0.423	1157.724	0.427	19	0.175	R.INTLLQGYSGIR.F
R3/RRR3-6/2	1482.346	1481.759	-279.226	0.494	819.411	0.543	17	0.168	K.LLNANVTPCLPLR.G
R3/RRR3-2/2	1335.117	1335.534	-313.594	0.439	902.047	0.469	18	0.165	R.INTLLQGYSGIR.F
R3/RRR3-6/2	1482.195	1481.759	294.766	0.483	763.630	0.538	17	0.165	K.LLNANVTPCLPLR.G
R3/RRR3-6/2	1481.324	1481.759	-294.462	0.424	781.172	0.503	16	0.159	K.LLNANVTPCLPLR.G
R3/RRR3-7/2	1506.603	1505.742	-92.612	0.438	907.623	0.367	16	0.147	K.IAGIQGGFFELQPK.E
R3/RRR3-9/2	1336.392	1335.534	-106.423	0.399	713.755	0.394	15	0.146	R.INTLLQGYSGIR.F
R3/RRR3-10/3	1776.544	1776.995	-254.515	0.543	1603.603	0.527	27	0.201	R.RVHVTQEDFEM*AVAK.V
R3/RRR3-10/2	1428.179	1428.571	-275.586	0.421	876.354	0.445	17	0.157	R.AVAHHTDCTFIR.V
R3/RRR3-10/2	946.957	947.068	-117.931	0.444	698.574	0.369	13	0.143	R.VSGSELVQK.Y
R3/RRR3-10/3	1479.921	1480.738	-1231.150	0.392	1241.526	0.325	25	0.112	-.IDILDQALLRPGR.-
R3/RRR3-10/3	1480.900	1480.738	110.314	0.371	866.619	0.343	22	0.097	-.IDILDQALLRPGR.-
R3/RRR3-10/3	1479.986	1480.738	-1186.919	0.337	609.226	0.372	20	0.094	-.IDILDQALLRPGR.-
R3/RRR3-7/2	1502.493	1502.732	-159.279	0.468	1780.615	0.473	21	0.252	R.GCVLVASSPEILTR.V
R3/RRR3-7/2	1407.963	1408.535	-1120.098	0.290	1259.469	0.263	18	0.209	R.AIDLAESAFVDKE.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1167.495	1168.368	-1608.892	0.365	1162.439	0.622	20	0.205	R.AALPVGTVSGAPK.V
R3/RRR3-7/2	1167.905	1168.368	-397.910	0.382	1198.691	0.567	20	0.200	R.AALPVGTVSGAPK.V
R3/RRR3-7/2	1168.002	1168.368	-314.226	0.360	1102.905	0.496	20	0.179	R.AALPVGTVSGAPK.V
R3/RRR3-7/2	1319.964	1320.347	-291.222	0.476	618.551	0.600	17	0.167	R.HATTEDAFQDGK.S
R3/RRR3-7/2	1320.104	1320.347	-184.161	0.473	609.578	0.586	17	0.165	R.HATTEDAFQDGK.S
R3/RRR3-7/2	1610.442	1609.874	-268.877	0.380	805.966	0.401	19	0.147	R.IVNPSPYMAYVQAR.G
R3/RRR3-14/3	1897.854	1897.081	-119.847	0.569	1839.508	0.484	33	0.219	K.DPNRPFPSGQNETPLVK.W
R3/RRR3-14/3	1897.149	1897.081	35.901	0.547	1942.012	0.430	33	0.217	K.DPNRPFPSGQNETPLVK.W
R3/RRR3-18/2	1328.042	1328.628	-1197.924	0.424	610.252	0.564	16	0.158	R.IRIEGLLAAFPK.L
R3/RRR3-20/2	1417.335	1417.547	-150.363	0.433	589.973	0.385	17	0.146	K.QSNILEDLDTLR.L
R3/RRR3-18/2	1417.299	1417.547	-175.851	0.402	713.772	0.344	18	0.145	K.QSNILEDLDTLR.L
R3/RRR3-18/2	1417.033	1417.547	-1071.974	0.399	617.089	0.369	17	0.144	K.QSNILEDLDTLR.L
R3/RRR3-18/2	1417.285	1417.547	-185.269	0.366	584.137	0.361	17	0.143	K.QSNILEDLDTLR.L
R3/RRR3-17/2	1417.168	1417.547	-268.483	0.414	331.422	0.379	13	0.141	K.QSNILEDLDTLR.L
R3/RRR3-18/2	1822.757	1822.984	-125.315	0.348	231.981	0.528	18	0.140	K.LVPEYSPSLDEEGVCK.T
R3/RRR3-18/2	981.149	981.045	107.180	0.323	588.687	0.436	13	0.140	-.GGYSSISGPR.-
R3/RRR3-20/2	1416.936	1417.547	-1140.137	0.301	314.309	0.300	14	0.139	K.QSNILEDLDTLR.L
R3/RRR3-20/2	1417.263	1417.547	-201.340	0.343	665.263	0.307	16	0.139	K.QSNILEDLDTLR.L
R3/RRR3-14/3	1896.081	1897.081	-1057.954	0.490	986.515	0.412	26	0.114	K.DPNRPFPSGQNETPLVK.W
R3/RRR3-16/3	1896.726	1897.081	-187.665	0.393	647.065	0.324	26	0.094	K.DPNRPFPSGQNETPLVK.W
R3/RRR3-13/3	1958.875	1959.187	-159.991	0.479	3264.833	0.522	38	0.595	R.DADVVISTLGALQIADQTK.L
R3/RRR3-13/3	1959.223	1959.187	18.234	0.511	2753.872	0.546	37	0.450	R.DADVVISTLGALQIADQTK.L
R3/RRR3-13/2	1205.932	1205.432	-415.822	0.501	2225.357	0.576	21	0.356	R.ILVVGGTGYIGR.H
R3/RRR3-12/2	1205.000	1205.432	-359.040	0.424	2047.745	0.541	21	0.311	R.ILVVGGTGYIGR.H
R3/RRR3-12/2	1959.688	1959.187	-255.384	0.514	1710.389	0.578	25	0.265	R.DADVVISTLGALQIADQTK.L
R3/RRR3-13/2	1205.322	1205.432	-90.773	0.511	1560.970	0.558	20	0.243	R.ILVVGGTGYIGR.H
R3/RRR3-13/2	1205.150	1205.432	-234.034	0.481	1568.810	0.532	20	0.238	R.ILVVGGTGYIGR.H
R3/RRR3-13/2	1958.548	1959.187	-839.663	0.438	1509.297	0.514	24	0.222	R.DADVVISTLGALQIADQTK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1958.696	1959.187	-251.763	0.460	1464.456	0.521	24	0.218	R.DADVVISTLGALQIADQTK.L
R3/RRR3-13/2	1957.952	1959.187	-1145.079	0.342	1490.722	0.441	24	0.203	R.DADVVISTLGALQIADQTK.L
R3/RRR3-12/2	1205.310	1205.432	-101.338	0.423	1420.659	0.442	19	0.200	R.ILVVGGTGYIGR.H
R3/RRR3-12/3	1958.948	1959.187	-122.766	0.373	1527.298	0.492	29	0.184	R.DADVVISTLGALQIADQTK.L
R3/RRR3-12/2	1958.353	1959.187	-939.716	0.325	1205.186	0.425	22	0.173	R.DADVVISTLGALQIADQTK.L
R3/RRR3-13/2	963.047	963.116	-71.909	0.485	757.918	0.347	12	0.146	K.AQLLQSFR.D
R3/RRR3-13/2	962.995	963.116	-125.312	0.412	822.756	0.310	13	0.145	K.AQLLQSFR.D
R3/RRR3-13/2	963.042	963.116	-77.122	0.422	827.439	0.296	13	0.144	K.AQLLQSFR.D
R3/RRR3-12/2	963.072	963.116	-45.463	0.401	730.059	0.319	12	0.143	K.AQLLQSFR.D
R3/RRR3-12/2	962.832	963.116	-295.731	0.410	725.403	0.315	12	0.142	K.AQLLQSFR.D
R3/RRR3-12/2	1205.028	1205.432	-335.662	0.310	454.541	0.363	13	0.131	-.ILVVGGTGYIGR.-
R3/RRR3-12/2	1960.779	1959.187	-208.972	0.249	429.944	0.290	16	0.130	R.DADVVISTLGALQIADQTK.L
R3/RRR3-12/3	1065.306	1065.251	51.751	0.530	1201.627	0.347	21	0.113	R.LGHPTTALVR.D
R3/RRR3-13/3	1065.498	1065.251	232.294	0.502	1148.949	0.360	22	0.112	R.LGHPTTALVR.D
R3/RRR3-12/3	1065.743	1065.251	463.502	0.497	1080.598	0.375	21	0.111	R.LGHPTTALVR.D
R3/RRR3-12/3	1065.162	1065.251	-84.195	0.510	905.148	0.386	20	0.107	R.LGHPTTALVR.D
R3/RRR3-13/3	1065.546	1065.251	277.355	0.523	1043.614	0.353	21	0.106	R.LGHPTTALVR.D
R3/RRR3-13/3	1064.847	1065.251	-380.610	0.497	893.638	0.346	20	0.101	R.LGHPTTALVR.D
R3/RRR3-12/3	1959.608	1959.187	215.324	0.259	927.920	0.334	26	0.099	R.DADVVISTLGALQIADQTK.L
R3/RRR3-12/3	1957.947	1959.187	-1147.528	0.231	671.508	0.284	25	0.088	R.DADVVISTLGALQIADQTK.L
R3/RRR3-5/2	1611.083	1610.835	154.150	0.477	2669.746	0.545	22	0.445	R.NGILEAYSGILQGFK.S
R3/RRR3-5/2	1513.632	1513.764	-87.491	0.518	1637.147	0.573	21	0.256	K.GLLLQTLSSPVASAR.S
R3/RRR3-5/2	1337.095	1337.452	-268.170	0.541	1769.834	0.492	19	0.255	R.VVCEATQSTDVK.I
R3/RRR3-5/2	1366.312	1366.502	-139.489	0.562	1729.009	0.457	18	0.239	R.TAAYETLNEVVR.C
R3/RRR3-5/2	1336.962	1337.452	-367.467	0.495	1723.330	0.400	19	0.226	R.VVCEATQSTDVK.I
R3/RRR3-5/2	1513.306	1513.764	-303.854	0.462	1468.073	0.522	21	0.221	K.GLLLQTLSSPVASAR.S
R3/RRR3-5/2	1366.184	1366.502	-233.065	0.510	1464.106	0.451	17	0.206	R.TAAYETLNEVVR.C
R3/RRR3-5/2	1336.409	1337.452	-1533.067	0.378	1462.029	0.358	19	0.188	R.VVCEATQSTDVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1020.865	1021.109	-239.941	0.405	904.153	0.313	15	0.146	K.DTTAWTLGR.I
R3/RRR3-5/2	1610.425	1610.835	-255.651	0.331	739.815	0.439	15	0.144	R.NGILEAYSGILQGFK.S
R3/RRR3-5/2	1020.367	1021.109	-1711.768	0.352	765.829	0.318	13	0.140	K.DTTAWTLGR.I
R3/RRR3-6/2	1678.122	1678.891	-1057.386	0.529	2429.499	0.512	23	0.375	K.NQVAM*NPINTVFDAK.R
R3/RRR3-6/2	1678.393	1678.891	-298.039	0.552	2139.804	0.526	22	0.322	K.NQVAM*NPINTVFDAK.R
R3/RRR3-6/2	1678.297	1678.891	-952.881	0.541	1962.364	0.525	22	0.291	K.NQVAM*NPINTVFDAK.R
R3/RRR3-6/2	1662.365	1662.892	-921.284	0.575	1904.578	0.540	23	0.286	K.NQVAMNPINTVFDAK.R
R3/RRR3-6/2	1663.486	1662.892	-244.699	0.577	1836.908	0.537	22	0.274	K.NQVAMNPINTVFDAK.R
R3/RRR3-6/2	1228.994	1229.325	-270.040	0.525	1623.163	0.407	18	0.215	R.VEIIANDQGNR.I
R3/RRR3-6/2	1229.042	1229.325	-231.278	0.494	1406.121	0.357	17	0.182	R.VEIIANDQGNR.I
R3/RRR3-6/2	1834.321	1835.078	-960.445	0.536	612.094	0.537	19	0.156	K.NQVAM*NPINTVFDAKR.L
R3/RRR3-6/2	1834.482	1835.078	-872.529	0.528	915.108	0.422	21	0.156	K.NQVAM*NPINTVFDAKR.L
R3/RRR3-6/2	1834.246	1835.078	-1001.870	0.511	694.443	0.474	19	0.152	K.NQVAM*NPINTVFDAKR.L
R3/RRR3-6/2	1228.866	1229.325	-374.584	0.425	746.108	0.373	15	0.146	R.VEIIANDQGNR.I
R3/RRR3-6/2	1474.265	1474.554	-196.628	0.281	524.729	0.497	19	0.145	R.TTPSYVGFTDTER.L
R3/RRR3-6/2	1475.064	1474.554	-333.064	0.302	363.709	0.490	16	0.142	R.TTPSYVGFTDTER.L
R3/RRR3-6/2	1474.194	1474.554	-244.808	0.247	488.114	0.457	18	0.139	R.TTPSYVGFTDTER.L
R3/RRR3-6/2	1228.588	1229.325	-1418.569	0.368	668.844	0.249	16	0.136	R.VEIIANDQGNR.I
R3/RRR3-6/2	1229.180	1229.325	-118.097	0.448	766.530	0.239	15	0.131	-.VEIIANDQGNR.-
R3/RRR3-8/2	1422.279	1422.565	-201.663	0.507	1740.138	0.509	23	0.256	R.YGTAGLLSPNTEAK.I
R3/RRR3-8/2	1422.219	1422.565	-244.027	0.469	1630.785	0.478	23	0.233	R.YGTAGLLSPNTEAK.I
R3/RRR3-8/2	1422.050	1422.565	-1068.967	0.436	1650.494	0.456	23	0.230	R.YGTAGLLSPNTEAK.I
R3/RRR3-8/2	1367.481	1367.536	-40.703	0.465	1139.120	0.597	23	0.203	R.HSGVVALIDAATGR.R
R3/RRR3-8/2	989.918	990.178	-262.841	0.407	908.923	0.430	14	0.158	K.VAFVTDIPK.N
R3/RRR3-8/2	1784.329	1784.989	-932.899	0.303	1025.953	0.412	20	0.156	R.IVATIEEISATTPDPAR.R
R3/RRR3-8/3	1563.768	1562.799	-19.787	0.428	693.141	0.528	30	0.118	R.AVAGAASALAAHPVSLR.K
R3/RRR3-8/3	1562.842	1562.799	27.833	0.401	807.465	0.456	30	0.111	R.AVAGAASALAAHPVSLR.K
R3/RRR3-8/3	1562.983	1562.799	118.425	0.379	766.039	0.458	29	0.109	R.AVAGAASALAAHPVSLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1483.052	1483.562	-1021.365	0.395	1282.654	0.473	20	0.190	R.SGDLVSYTAEEGVR.I
R3/RRR3-8/2	1723.586	1724.038	-263.160	0.483	833.915	0.484	19	0.158	R.IAWEEPFGPVLPVIR.I
R3/RRR3-8/2	1334.154	1334.460	-230.034	0.356	553.238	0.443	14	0.140	K.LLVSDSFPGNER.N
R3/RRR3-8/2	1646.551	1644.998	-272.498	0.401	974.475	0.288	18	0.139	K.VVLIMESVADIVVEK.V
R3/RRR3-8/3	1244.448	1243.395	42.530	0.534	1082.025	0.361	22	0.110	R.GPDHFPFQGLK.D
R3/RRR3-8/3	1243.153	1243.395	-195.522	0.346	1010.111	0.336	21	0.101	R.GPDHFPFQGLK.D
R3/RRR3-8/3	1243.292	1243.395	-82.940	0.406	1014.286	0.298	21	0.091	-.GPDHFPFQGLK.-
R3/RRR3-13/2	1488.149	1488.629	-323.142	0.538	1787.926	0.590	24	0.284	R.TKGEAGTGNVVEAVR.H
R3/RRR3-13/2	1488.262	1488.629	-246.937	0.530	1703.179	0.559	23	0.263	R.TKGEAGTGNVVEAVR.H
R3/RRR3-13/2	1488.216	1488.629	-277.878	0.534	1701.674	0.532	23	0.255	R.TKGEAGTGNVVEAVR.H
R3/RRR3-13/2	1450.032	1450.509	-330.012	0.504	1380.402	0.474	18	0.203	R.NM*DDDEVFSYAK.R
R3/RRR3-13/2	1450.184	1450.509	-224.864	0.514	1367.731	0.435	18	0.193	R.NM*DDDEVFSYAK.R
R3/RRR3-13/2	1449.955	1450.509	-1075.311	0.436	1011.137	0.412	18	0.163	R.NM*DDDEVFSYAK.R
R3/RRR3-13/2	1366.194	1366.608	-303.952	0.457	611.299	0.518	17	0.157	R.IAAPYDLVM*QTK.Q
R3/RRR3-13/2	1258.902	1259.351	-358.353	0.441	958.644	0.385	19	0.154	K.GEAGTGNVVEAVR.H
R3/RRR3-13/2	1365.996	1366.608	-1183.910	0.372	490.418	0.416	15	0.142	R.IAAPYDLVM*QTK.Q
R3/RRR3-13/2	1365.483	1366.608	-1560.769	0.291	563.864	0.258	15	0.132	R.IAAPYDLVM*QTK.Q
R3/RRR3-13/3	1488.834	1488.629	138.674	0.483	998.018	0.338	28	0.102	-.TKGEAGTGNVVEAVR.-
R3/RRR3-14/3	1489.337	1488.629	-196.209	0.505	778.205	0.363	25	0.101	R.TKGEAGTGNVVEAVR.H
R3/RRR3-13/3	1488.179	1488.629	-302.823	0.486	934.303	0.295	27	0.094	-.TKGEAGTGNVVEAVR.-
R3/RRR3-14/3	1487.807	1488.629	-1227.751	0.457	684.782	0.374	23	0.090	-.TKGEAGTGNVVEAVR.-
R3/RRR3-13/3	1488.752	1488.629	83.415	0.510	814.220	0.318	26	0.089	-.TKGEAGTGNVVEAVR.-
R3/RRR3-14/3	1487.810	1488.629	-1225.897	0.453	821.787	0.252	23	0.079	-.TKGEAGTGNVVEAVR.-
R3/RRR3-7/2	1392.412	1392.496	-60.814	0.494	1819.864	0.402	19	0.239	K.IDEAAQLFEEAR.A
R3/RRR3-7/2	1393.304	1392.496	-138.105	0.499	1883.930	0.353	19	0.235	K.IDEAAQLFEEAR.A
R3/RRR3-7/2	1392.393	1392.496	-74.445	0.508	1308.948	0.471	17	0.194	K.IDEAAQLFEEAR.A
R3/RRR3-7/2	1121.044	1121.271	-203.865	0.363	876.020	0.546	14	0.168	R.HADAIPVLER.A
R3/RRR3-7/3	1508.697	1508.741	-29.558	0.514	901.007	0.455	27	0.117	R.VEDAIEILEHVLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/3	1557.993	1557.688	196.684	0.449	746.422	0.473	24	0.113	K.LGTANPDVEDEKLR.L
R3/RRR3-7/3	1500.101	1499.522	-281.236	0.440	1227.745	0.314	23	0.109	R.EHSAPASLEEASDR.R
R3/RRR3-7/3	1557.253	1557.688	-280.153	0.400	531.723	0.471	22	0.106	K.LGTANPDVEDEKLR.L
R3/RRR3-7/3	1508.559	1508.741	-120.989	0.455	536.110	0.399	25	0.102	R.VEDAIEILEHVLK.V
R3/RRR3-7/3	1558.560	1557.688	-81.874	0.385	626.174	0.404	25	0.101	K.LGTANPDVEDEKLR.L
R3/RRR3-3/2	1616.991	1616.883	67.116	0.520	2257.446	0.577	22	0.359	K.SQPDLAILAVNTFVK.D
R3/RRR3-4/2	1617.584	1616.883	-185.489	0.557	2088.175	0.619	21	0.339	K.SQPDLAILAVNTFVK.D
R3/RRR3-4/2	1616.594	1616.883	-179.089	0.489	2049.298	0.545	21	0.310	K.SQPDLAILAVNTFVK.D
R3/RRR3-3/2	1616.416	1616.883	-290.001	0.492	1879.989	0.593	20	0.295	K.SQPDLAILAVNTFVK.D
R3/RRR3-5/2	1616.687	1616.883	-121.446	0.475	1927.703	0.514	21	0.281	K.SQPDLAILAVNTFVK.D
R3/RRR3-4/2	1616.155	1616.883	-1072.475	0.436	1815.931	0.523	21	0.266	K.SQPDLAILAVNTFVK.D
R3/RRR3-2/2	1616.185	1616.883	-1053.971	0.365	1915.349	0.452	20	0.262	K.SQPDLAILAVNTFVK.D
R3/RRR3-3/2	1615.929	1616.883	-1213.100	0.393	1815.467	0.473	20	0.252	K.SQPDLAILAVNTFVK.D
R3/RRR3-2/2	1616.139	1616.883	-1082.410	0.440	1651.855	0.513	20	0.240	K.SQPDLAILAVNTFVK.D
R3/RRR3-5/2	1615.861	1616.883	-1255.280	0.314	1312.246	0.417	19	0.181	K.SQPDLAILAVNTFVK.D
R3/RRR3-3/2	981.951	982.114	-166.533	0.376	738.941	0.381	13	0.147	R.TSFLEAWK.S
R3/RRR3-3/2	941.393	942.138	-1858.620	0.448	803.286	0.252	13	0.137	R.NINLIVQK.R
R3/RRR3-3/2	942.093	942.138	-47.386	0.425	636.249	0.265	13	0.137	R.NINLIVQK.R
R3/RRR3-3/2	981.926	982.114	-191.725	0.371	577.181	0.370	12	0.136	-.TSFLEAWK.-
R3/RRR3-3/3	1511.935	1510.757	118.253	0.484	1082.996	0.279	26	0.097	R.LQHANCAVVLSAVK.I
R3/RRR3-5/3	1178.203	1178.409	-176.008	0.463	1135.188	0.271	22	0.097	K.RPTILAHEIK.V
R3/RRR3-3/3	1178.364	1178.409	-38.675	0.462	989.232	0.255	21	0.092	K.RPTILAHEIK.V
R3/RRR3-3/3	1177.811	1178.409	-1361.022	0.454	695.637	0.271	20	0.090	-.RPTILAHEIK.-
R3/RRR3-4/3	1178.792	1178.409	325.909	0.489	904.138	0.232	21	0.089	K.RPTILAHEIK.V
R3/RRR3-3/3	1178.353	1178.409	-47.559	0.437	582.736	0.251	19	0.088	-.RPTILAHEIK.-
R3/RRR3-4/3	1510.559	1510.757	-131.568	0.401	649.003	0.252	22	0.086	-.LQHANCAVVLSAVK.-
R3/RRR3-17/3	1672.079	1672.857	-1066.599	0.584	2702.498	0.491	32	0.392	R.AKDVALVYNECYAR.L
R3/RRR3-17/2	1446.083	1446.534	-312.391	0.449	1811.035	0.462	18	0.252	R.AACYDCGTSVWR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1445.668	1446.534	-1294.399	0.398	1778.072	0.419	18	0.237	R.AACYDCGTSVWR.D
R3/RRR3-17/3	1672.875	1672.857	10.926	0.616	1991.051	0.448	30	0.226	R.AKDVALVYNECYAR.L
R3/RRR3-17/2	1446.075	1446.534	-317.981	0.447	1550.093	0.453	18	0.216	R.AACYDCGTSVWR.D
R3/RRR3-16/2	1474.757	1473.606	102.647	0.536	1301.602	0.514	19	0.204	K.DVALVYNECYAR.L
R3/RRR3-16/2	1474.096	1473.606	333.845	0.523	1286.086	0.500	19	0.200	K.DVALVYNECYAR.L
R3/RRR3-16/3	1672.143	1672.857	-1028.227	0.541	1717.192	0.478	29	0.197	R.AKDVALVYNECYAR.L
R3/RRR3-16/2	1446.134	1446.534	-277.244	0.451	1362.888	0.456	17	0.196	R.AACYDCGTSVWR.D
R3/RRR3-17/2	1473.150	1473.606	-310.474	0.451	1244.864	0.478	18	0.190	K.DVALVYNECYAR.L
R3/RRR3-17/2	1472.321	1473.606	-1556.702	0.403	1406.036	0.359	19	0.183	K.DVALVYNECYAR.L
R3/RRR3-17/2	1266.635	1267.367	-1371.802	0.501	1285.569	0.377	18	0.177	R.LSDKDDFLADK.V
R3/RRR3-17/2	1267.093	1267.367	-216.505	0.499	1274.646	0.370	18	0.175	R.LSDKDDFLADK.V
R3/RRR3-17/2	1472.451	1473.606	-1467.758	0.379	1281.846	0.368	19	0.174	K.DVALVYNECYAR.L
R3/RRR3-16/2	1267.204	1267.367	-128.853	0.465	1243.070	0.378	18	0.174	R.LSDKDDFLADK.V
R3/RRR3-17/2	1266.977	1267.367	-308.910	0.533	1193.146	0.387	18	0.171	R.LSDKDDFLADK.V
R3/RRR3-16/3	1673.447	1672.857	-245.592	0.590	1580.322	0.446	28	0.170	R.AKDVALVYNECYAR.L
R3/RRR3-17/3	1673.252	1672.857	237.027	0.577	1493.811	0.403	26	0.150	R.AKDVALVYNECYAR.L
R3/RRR3-19/2	1474.803	1473.606	134.357	0.433	370.051	0.481	15	0.149	K.DVALVYNECYAR.L
R3/RRR3-17/3	1268.436	1267.367	54.467	0.514	1293.572	0.401	26	0.128	R.LSDKDDFLADK.V
R3/RRR3-16/3	1268.539	1267.367	135.827	0.514	953.623	0.336	24	0.102	R.LSDKDDFLADK.V
R3/RRR3-16/3	1268.607	1267.367	189.529	0.490	906.538	0.346	24	0.101	R.LSDKDDFLADK.V
R3/RRR3-19/2	1465.297	1464.562	-181.538	0.596	1579.638	0.523	22	0.237	K.FDSDGNLIDAQIR.E
R3/RRR3-19/2	1464.173	1464.562	-266.971	0.534	1552.048	0.421	22	0.210	K.FDSDGNLIDAQIR.E
R3/RRR3-19/2	1630.378	1630.999	-997.034	0.489	1290.975	0.505	22	0.201	R.IKQVLLSLQAFTLR.L
R3/RRR3-20/2	1464.142	1464.562	-288.050	0.551	1445.942	0.422	21	0.198	K.FDSDGNLIDAQIR.E
R3/RRR3-19/2	1465.075	1464.562	-333.496	0.596	1263.564	0.487	20	0.193	K.FDSDGNLIDAQIR.E
R3/RRR3-19/2	1630.075	1630.999	-1183.644	0.430	1105.459	0.559	21	0.192	R.IKQVLLSLQAFTLR.L
R3/RRR3-20/2	1464.237	1464.562	-222.642	0.564	1325.410	0.409	21	0.184	K.FDSDGNLIDAQIR.E
R3/RRR3-20/2	1464.437	1464.562	-86.082	0.552	1248.401	0.386	20	0.173	K.FDSDGNLIDAQIR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1631.664	1630.999	-206.100	0.465	737.504	0.483	19	0.157	R.IKQVLLSLQAFTLR.L
R3/RRR3-20/2	932.576	933.003	-459.590	0.385	884.992	0.373	13	0.154	K.NALDWASR.G
R3/RRR3-20/2	932.449	933.003	-1671.479	0.349	889.448	0.354	13	0.151	K.NALDWASR.G
R3/RRR3-19/2	1631.821	1630.999	-109.440	0.395	1045.140	0.328	18	0.151	R.IKQVLLSLQAFTLR.L
R3/RRR3-19/2	932.793	933.003	-226.500	0.385	864.072	0.340	13	0.150	K.NALDWASR.G
R3/RRR3-18/2	932.908	933.003	-102.186	0.370	895.418	0.329	13	0.149	K.NALDWASR.G
R3/RRR3-18/2	932.927	933.003	-82.236	0.406	873.390	0.326	13	0.149	K.NALDWASR.G
R3/RRR3-19/2	1389.070	1389.668	-1153.843	0.450	920.337	0.335	18	0.148	K.QVLLSLQAFTLR.L
R3/RRR3-19/2	1388.717	1389.668	-1409.198	0.366	828.126	0.315	19	0.144	K.QVLLSLQAFTLR.L
R3/RRR3-20/2	932.898	933.003	-112.687	0.393	866.177	0.256	13	0.141	K.NALDWASR.G
R3/RRR3-19/2	932.459	933.003	-1660.957	0.364	909.493	0.233	13	0.140	K.NALDWASR.G
R3/RRR3-19/3	1630.550	1630.999	-276.420	0.462	1249.629	0.456	26	0.140	R.IKQVLLSLQAFTLR.L
R3/RRR3-19/2	932.763	933.003	-258.404	0.371	803.137	0.217	13	0.137	K.NALDWASR.G
R3/RRR3-18/2	932.536	933.003	-502.543	0.351	854.603	0.192	13	0.136	K.NALDWASR.G
R3/RRR3-19/2	1389.097	1389.668	-1134.606	0.381	582.644	0.261	16	0.135	K.QVLLSLQAFTLR.L
R3/RRR3-19/2	932.369	933.003	-1758.030	0.358	599.636	0.225	11	0.134	-.NALDWASR.-
R3/RRR3-20/2	1389.225	1389.668	-319.624	0.352	630.758	0.173	16	0.130	K.QVLLSLQAFTLR.L
R3/RRR3-19/3	1630.486	1630.999	-930.895	0.295	695.910	0.358	24	0.094	R.IKQVLLSLQAFTLR.L
R3/RRR3-19/3	1630.686	1630.999	-192.604	0.305	585.756	0.375	19	0.094	R.IKQVLLSLQAFTLR.L
R3/RRR3-3/2	1843.617	1843.924	-166.732	0.574	2148.817	0.593	23	0.346	R.LPQDLSDEIEEDPTGGK.I
R3/RRR3-3/2	1843.307	1843.924	-879.803	0.532	2234.041	0.498	23	0.332	R.LPQDLSDEIEEDPTGGK.I
R3/RRR3-3/2	985.068	985.206	-140.029	0.507	1147.248	0.336	17	0.161	R.LLAGVGSVLR.L
R3/RRR3-3/2	1357.471	1356.509	-28.015	0.510	841.716	0.464	17	0.160	R.FLAVGSYDNTIR.I
R3/RRR3-3/2	1357.643	1356.509	99.597	0.469	939.487	0.423	17	0.159	R.FLAVGSYDNTIR.I
R3/RRR3-3/2	985.163	985.206	-43.574	0.506	1131.070	0.289	17	0.153	R.LLAGVGSVLR.L
R3/RRR3-3/2	984.790	985.206	-423.038	0.448	1000.049	0.304	16	0.149	R.LLAGVGSVLR.L
R3/RRR3-3/2	1356.180	1356.509	-243.000	0.364	680.438	0.336	15	0.139	R.FLAVGSYDNTIR.I
R3/RRR3-3/2	1461.237	1461.645	-279.825	0.344	683.907	0.305	15	0.135	R.LGETFNETAIPLR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1462.030	1461.645	264.162	0.416	635.700	0.275	15	0.132	R.LGETFNETAIPLR.Y
R3/RRR3-2/2	1461.367	1461.645	-190.320	0.275	881.322	0.192	16	0.131	R.LGETFNETAIPLR.Y
R3/RRR3-3/3	1852.922	1852.035	-61.301	0.363	1118.774	0.451	27	0.127	K.YLAVIESDKGALSAEER.E
R3/RRR3-2/3	1852.745	1852.035	-157.063	0.332	515.761	0.310	25	0.090	K.YLAVIESDKGALSAEER.E
R3/RRR3-25/3	1365.260	1365.565	-223.996	0.540	2323.868	0.395	28	0.265	R.HHVIGQYVVGQK.G
R3/RRR3-25/3	1365.607	1365.565	30.509	0.497	2329.640	0.347	27	0.250	R.HHVIGQYVVGQK.G
R3/RRR3-25/3	1364.815	1365.565	-1285.957	0.462	2346.984	0.272	28	0.224	R.HHVIGQYVVGQK.G
R3/RRR3-25/2	1270.126	1270.374	-195.552	0.418	714.356	0.590	19	0.171	K.VPPNSASLEEAR.H
R3/RRR3-25/2	1270.051	1270.374	-255.141	0.411	759.584	0.559	19	0.169	K.VPPNSASLEEAR.H
R3/RRR3-25/2	1269.993	1270.374	-301.235	0.368	702.408	0.567	19	0.165	K.VPPNSASLEEAR.H
R3/RRR3-25/2	1270.049	1270.374	-256.298	0.393	576.274	0.595	17	0.163	K.VPPNSASLEEAR.H
R3/RRR3-25/2	1270.079	1270.374	-233.349	0.404	535.184	0.580	17	0.161	K.VPPNSASLEEAR.H
R3/RRR3-25/2	1445.189	1445.581	-271.626	0.482	730.423	0.509	18	0.159	K.GM*EELGNITEHAK.Q
R3/RRR3-25/2	1269.949	1270.374	-335.471	0.361	549.785	0.513	17	0.153	K.VPPNSASLEEAR.H
R3/RRR3-25/3	1650.830	1649.881	-31.129	0.424	995.368	0.291	24	0.094	K.QRHHVIGQYVVGQK.G
R3/RRR3-4/3	1911.054	1910.163	-57.323	0.511	2415.469	0.365	35	0.278	K.KAPEPEPTFQILTNPAR.V
R3/RRR3-3/2	1179.429	1178.403	22.360	0.398	1260.823	0.474	17	0.190	K.LPTAILSTYAK.A
R3/RRR3-2/2	1178.429	1178.403	22.379	0.434	1290.246	0.451	17	0.190	K.LPTAILSTYAK.A
R3/RRR3-4/2	1177.527	1178.403	-1597.784	0.369	1092.729	0.429	17	0.170	K.LPTAILSTYAK.A
R3/RRR3-2/2	1178.442	1178.403	33.184	0.378	932.748	0.456	15	0.163	K.LPTAILSTYAK.A
R3/RRR3-4/2	1178.229	1178.403	-147.728	0.386	1088.450	0.380	16	0.162	K.LPTAILSTYAK.A
R3/RRR3-3/2	1177.328	1178.403	-1767.983	0.287	1045.653	0.375	16	0.157	K.LPTAILSTYAK.A
R3/RRR3-1/2	1178.696	1178.403	249.236	0.372	747.392	0.439	14	0.151	K.LPTAILSTYAK.A
R3/RRR3-3/2	1178.141	1178.403	-222.875	0.289	844.692	0.354	14	0.145	K.LPTAILSTYAK.A
R3/RRR3-3/3	1615.017	1614.827	117.642	0.425	706.599	0.615	28	0.133	R.IVSLLSESYNPHVR.Y
R3/RRR3-4/3	1614.472	1614.827	-220.626	0.456	756.039	0.542	28	0.124	R.IVSLLSESYNPHVR.Y
R3/RRR3-4/3	1614.839	1614.827	7.452	0.426	599.853	0.573	27	0.123	R.IVSLLSESYNPHVR.Y
R3/RRR3-2/3	1911.220	1910.163	30.127	0.396	1355.840	0.281	28	0.117	-.KAPEPEPTFQILTNPAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1229.750	1229.413	275.018	0.429	433.100	0.540	20	0.115	K.FSATAGLGVIHR.G
R3/RRR3-4/3	1910.427	1910.163	138.609	0.422	1429.218	0.248	28	0.112	K.KAPEPEPTFQILTNPAR.V
R3/RRR3-4/3	1229.261	1229.413	-124.225	0.395	551.773	0.501	22	0.111	K.FSATAGLGVIHR.G
R3/RRR3-4/3	1614.737	1614.827	-55.786	0.399	507.568	0.482	24	0.110	R.IVSLLSESYNPHVR.Y
R3/RRR3-3/3	1229.473	1229.413	49.073	0.420	406.780	0.480	20	0.109	K.FSATAGLGVIHR.G
R3/RRR3-4/3	1229.516	1229.413	84.174	0.430	433.844	0.473	20	0.109	K.FSATAGLGVIHR.G
R3/RRR3-3/3	1229.080	1229.413	-271.875	0.398	387.073	0.486	19	0.109	K.FSATAGLGVIHR.G
R3/RRR3-3/3	1909.861	1910.163	-158.488	0.410	1345.941	0.244	27	0.109	-.KAPEPEPTFQILTNPAR.-
R3/RRR3-4/3	1229.115	1229.413	-243.179	0.411	375.846	0.478	19	0.109	K.FSATAGLGVIHR.G
R3/RRR3-2/3	1615.979	1614.827	94.236	0.397	503.775	0.468	24	0.109	R.IVSLLSESYNPHVR.Y
R3/RRR3-3/3	1615.269	1614.827	274.302	0.375	424.960	0.457	22	0.107	R.IVSLLSESYNPHVR.Y
R3/RRR3-2/3	1614.501	1614.827	-202.763	0.365	411.478	0.434	22	0.105	R.IVSLLSESYNPHVR.Y
R3/RRR3-4/3	1329.381	1330.516	-1610.488	0.409	937.414	0.324	20	0.098	K.RLDKLEEAISR.S
R3/RRR3-4/3	1330.273	1330.516	-183.361	0.363	749.325	0.311	18	0.087	-.RLDKLEEAISR.-
R3/RRR3-2/3	1614.816	1614.827	-7.220	0.231	719.752	0.179	22	0.086	-.IVSLLSESYNPHVR.-
R3/RRR3-2/3	1910.907	1910.163	-134.406	0.398	1116.052	0.164	26	0.086	-.KAPEPEPTFQILTNPAR.-
R3/RRR3-3/3	1910.192	1910.163	15.177	0.328	890.258	0.192	23	0.084	K.KAPEPEPTFQILTNPAR.V
R3/RRR3-2/3	1910.328	1910.163	86.894	0.326	845.544	0.182	25	0.083	K.KAPEPEPTFQILTNPAR.V
R3/RRR3-4/3	1330.592	1330.516	57.536	0.394	737.041	0.229	18	0.083	-.RLDKLEEAISR.-
R3/RRR3-4/2	1193.335	1193.334	0.758	0.548	1765.959	0.400	18	0.231	R.AVAYLLSNADR.V
R3/RRR3-4/2	1192.465	1193.334	-1572.636	0.429	1416.817	0.287	17	0.171	R.AVAYLLSNADR.V
R3/RRR3-4/2	1192.859	1193.334	-399.953	0.304	559.657	0.229	13	0.131	R.AVAYLLSNADR.V
R3/RRR3-5/2	1241.215	1241.459	-196.852	0.450	1574.200	0.472	20	0.225	K.SPGLDDILVALK.T
R3/RRR3-5/2	1240.962	1241.459	-401.321	0.397	1502.279	0.369	19	0.195	K.SPGLDDILVALK.T
R3/RRR3-5/2	1590.266	1589.774	310.151	0.435	339.343	0.525	19	0.152	K.VIPIFNENDAISTR.K
R3/RRR3-5/2	1589.257	1589.774	-957.964	0.355	303.100	0.512	17	0.145	K.VIPIFNENDAISTR.K
R3/RRR3-5/2	1589.170	1589.774	-1012.563	0.350	310.702	0.500	17	0.144	K.VIPIFNENDAISTR.K
R3/RRR3-5/2	1618.224	1618.808	-981.673	0.361	1066.945	0.249	19	0.142	R.EQLTETVESLLDLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1618.074	1618.808	-1074.760	0.342	1003.127	0.174	18	0.131	R.EQLTETVESLLDLK.V
R3/RRR3-5/3	1531.571	1531.658	-57.296	0.432	1029.988	0.482	27	0.126	R.RVDSAAVFHNASTR.F
R3/RRR3-5/3	1885.272	1884.120	80.516	0.366	1042.827	0.366	25	0.105	K.ILLDVADALEANEDLIR.S
R3/RRR3-25/2	1799.410	1798.924	270.564	0.599	2433.004	0.594	24	0.401	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/2	1799.535	1798.924	-217.286	0.624	2403.535	0.577	24	0.387	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/2	1798.213	1798.924	-954.702	0.557	2280.029	0.588	22	0.366	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/2	1798.607	1798.924	-176.963	0.599	2329.944	0.548	23	0.362	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/2	1799.480	1798.924	-247.639	0.635	2242.913	0.590	23	0.358	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/2	1799.690	1798.924	-130.731	0.595	2064.986	0.575	23	0.321	K.CANGGLDLDWDTVFSK.I
R3/RRR3-24/2	1798.356	1798.924	-874.493	0.497	1687.855	0.537	23	0.252	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/3	1842.733	1842.041	-167.617	0.571	1625.084	0.608	31	0.230	R.SKYGWTAFCGPVGPTGR.D
R3/RRR3-25/2	1626.200	1626.790	-980.472	0.462	1588.712	0.495	21	0.229	K.YGWTAFCGPVGPTGR.D
R3/RRR3-25/2	1626.211	1626.790	-973.614	0.447	1385.400	0.528	20	0.212	K.YGWTAFCGPVGPTGR.D
R3/RRR3-25/2	1626.161	1626.790	-1004.890	0.462	1414.786	0.472	19	0.202	K.YGWTAFCGPVGPTGR.D
R3/RRR3-25/2	1626.358	1626.790	-266.396	0.437	1303.805	0.520	19	0.201	K.YGWTAFCGPVGPTGR.D
R3/RRR3-25/2	1627.116	1626.790	201.091	0.524	1210.957	0.562	18	0.199	K.YGWTAFCGPVGPTGR.D
R3/RRR3-25/2	1626.268	1626.790	-938.496	0.469	1189.359	0.501	19	0.187	K.YGWTAFCGPVGPTGR.D
R3/RRR3-24/2	1799.898	1798.924	-14.735	0.528	1133.497	0.503	19	0.181	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/2	1136.952	1137.185	-205.320	0.521	934.472	0.437	17	0.166	K.IDTDGQGFQR.G
R3/RRR3-24/2	1136.862	1137.185	-284.170	0.478	891.523	0.392	17	0.158	K.IDTDGQGFQR.G
R3/RRR3-25/2	1136.940	1137.185	-215.768	0.492	767.818	0.432	16	0.158	K.IDTDGQGFQR.G
R3/RRR3-25/2	1138.003	1137.185	-159.943	0.528	669.252	0.430	16	0.155	K.IDTDGQGFQR.G
R3/RRR3-25/2	1798.024	1798.924	-1059.941	0.454	773.342	0.457	18	0.153	K.CANGGLDLDWDTVFSK.I
R3/RRR3-25/2	1137.714	1137.185	-415.034	0.491	691.840	0.391	16	0.152	K.IDTDGQGFQR.G
R3/RRR3-26/2	1137.359	1137.185	153.981	0.360	702.200	0.399	16	0.151	K.IDTDGQGFQR.G
R3/RRR3-26/2	1136.977	1137.185	-183.132	0.439	768.666	0.360	16	0.150	K.IDTDGQGFQR.G
R3/RRR3-24/2	1136.233	1137.185	-1722.661	0.414	707.891	0.365	16	0.149	K.IDTDGQGFQR.G
R3/RRR3-24/2	1136.320	1137.185	-1645.813	0.405	662.933	0.362	16	0.148	K.IDTDGQGFQR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1136.902	1137.185	-248.944	0.498	589.573	0.370	15	0.147	K.IDTDGQGFQR.G
R3/RRR3-27/2	1137.092	1137.185	-81.253	0.435	473.778	0.372	14	0.146	K.IDTDGQGFQR.G
R3/RRR3-25/2	1137.016	1137.185	-148.667	0.459	586.399	0.351	15	0.146	K.IDTDGQGFQR.G
R3/RRR3-25/2	1138.019	1137.185	-145.954	0.360	545.201	0.337	17	0.146	K.IDTDGQGFQR.G
R3/RRR3-25/2	1136.415	1137.185	-1561.854	0.436	633.269	0.366	15	0.145	-.IDTDGQGFQR.-
R3/RRR3-25/2	1627.952	1626.790	99.681	0.318	674.544	0.425	16	0.144	K.YGWTAFCGPVGPTGR.D
R3/RRR3-26/2	1137.277	1137.185	81.108	0.257	591.424	0.345	16	0.141	K.IDTDGQGFQR.G
R3/RRR3-25/2	1137.043	1137.185	-125.190	0.265	512.988	0.254	16	0.139	K.IDTDGQGFQR.G
R3/RRR3-23/2	1136.298	1137.185	-1664.916	0.257	477.679	0.228	16	0.139	K.IDTDGQGFQR.G
R3/RRR3-25/2	1137.427	1137.185	213.607	0.244	545.995	0.264	16	0.138	K.IDTDGQGFQR.G
R3/RRR3-25/3	1841.870	1842.041	-92.879	0.414	1003.003	0.417	26	0.115	R.SKYGWTAFCGPVGPTGR.D
R3/RRR3-25/3	1841.118	1842.041	-1047.375	0.413	661.950	0.512	24	0.113	R.SKYGWTAFCGPVGPTGR.D
R3/RRR3-6/1	1063.651	1064.257	-1514.268	0.287	881.181	0.208	12	0.891	R.FEILEAITK.L
R3/RRR3-6/1	1063.596	1064.257	-1566.379	0.256	880.544	0.141	12	0.890	R.FEILEAITK.L
R3/RRR3-6/1	1063.505	1064.257	-1651.820	0.310	702.297	0.302	11	0.883	-.FEILEAITK.-
R3/RRR3-6/2	1063.527	1064.257	-1630.904	0.415	827.300	0.343	14	0.145	-.FEILEAITK.-
R3/RRR3-6/2	1064.069	1064.257	-177.154	0.468	815.241	0.337	14	0.143	-.FEILEAITK.-
R3/RRR3-19/2	1064.091	1064.257	-155.749	0.429	859.810	0.318	14	0.143	-.FEILEAITK.-
R3/RRR3-2/2	1064.108	1064.257	-139.868	0.384	829.500	0.325	14	0.143	-.FEILEAITK.-
R3/RRR3-2/2	1064.200	1064.257	-53.108	0.394	711.815	0.381	13	0.141	-.FEILEAITK.-
R3/RRR3-6/2	1063.697	1064.257	-1470.648	0.454	831.454	0.312	14	0.141	-.FEILEAITK.-
R3/RRR3-2/2	1064.121	1064.257	-127.440	0.369	830.433	0.346	13	0.140	-.FEILEAITK.-
R3/RRR3-8/2	1064.857	1064.257	-376.282	0.271	532.895	0.309	14	0.139	R.FEILEAITK.L
R3/RRR3-19/2	1064.087	1064.257	-160.237	0.372	829.918	0.231	14	0.135	-.FEILEAITK.-
R3/RRR3-19/2	1064.134	1064.257	-115.818	0.353	548.827	0.240	12	0.126	-.FEILEAITK.-
R3/RRR3-4/2	1688.397	1687.920	283.858	0.552	2187.063	0.580	24	0.350	R.AVSDEIKNVIIASATR.K
R3/RRR3-4/2	1687.737	1687.920	-108.644	0.503	2118.429	0.514	22	0.315	R.AVSDEIKNVIIASATR.K
R3/RRR3-4/2	1686.736	1687.920	-1298.568	0.501	1534.125	0.591	21	0.244	R.AVSDEIKNVIIASATR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1487.354	1486.653	-201.072	0.455	1267.727	0.392	21	0.176	R.LASSLSSPATPADLR.A
R3/RRR3-4/2	1157.930	1158.397	-404.515	0.345	1266.951	0.380	16	0.173	R.AAVAAM*PELLR.S
R3/RRR3-4/2	1236.248	1236.402	-125.245	0.499	1082.107	0.426	17	0.169	K.LNNVITHPEAK.H
R3/RRR3-4/2	1486.172	1486.653	-324.643	0.397	1139.468	0.329	20	0.156	R.LASSLSSPATPADLR.A
R3/RRR3-4/2	1486.299	1486.653	-238.366	0.399	1095.961	0.344	19	0.156	-.LASSLSSPATPADLR.-
R3/RRR3-4/2	998.054	998.245	-190.957	0.368	924.572	0.366	14	0.152	K.LLVLLQNGK.Q
R3/RRR3-4/2	998.323	998.245	78.784	0.412	846.716	0.330	14	0.145	K.LLVLLQNGK.Q
R3/RRR3-2/2	1486.377	1486.653	-186.212	0.302	517.017	0.238	14	0.128	-.LASSLSSPATPADLR.-
R3/RRR3-3/3	1236.589	1236.402	151.020	0.442	1079.972	0.455	21	0.126	K.LNNVITHPEAK.H
R3/RRR3-3/3	1236.297	1236.402	-85.737	0.398	1091.738	0.356	21	0.109	K.LNNVITHPEAK.H
R3/RRR3-3/3	1236.494	1236.402	74.094	0.399	837.574	0.353	19	0.099	K.LNNVITHPEAK.H
R3/RRR3-1/3	1235.943	1236.402	-373.144	0.329	780.418	0.217	19	0.086	K.LNNVITHPEAK.H
R3/RRR3-3/2	1784.469	1784.947	-268.728	0.488	1670.282	0.468	21	0.232	K.ATAAQQYDSSPFLSGLK.S
R3/RRR3-3/2	1403.059	1403.480	-301.550	0.494	1519.025	0.446	18	0.210	K.AGASQDQILNETR.L
R3/RRR3-3/2	1784.786	1784.947	-90.868	0.483	1346.297	0.488	19	0.197	K.ATAAQQYDSSPFLSGLK.S
R3/RRR3-3/2	1571.457	1571.671	-136.862	0.487	1232.781	0.513	21	0.196	K.ILFNTESSTTTSNR.I
R3/RRR3-3/2	1403.149	1403.480	-236.960	0.466	1207.222	0.393	17	0.170	K.AGASQDQILNETR.L
R3/RRR3-3/2	1403.060	1403.480	-300.765	0.510	1056.474	0.410	17	0.162	K.AGASQDQILNETR.L
R3/RRR3-3/2	998.065	998.205	-140.168	0.394	945.680	0.205	12	0.134	R.NLQLQLIR.D
R3/RRR3-3/3	1078.898	1078.197	-278.257	0.413	1097.277	0.368	17	0.108	R.LCHIYDTR.G
R3/RRR3-3/3	1079.259	1078.197	57.577	0.487	884.050	0.374	16	0.104	R.LCHIYDTR.G
R3/RRR3-20/2	1429.412	1429.604	-134.788	0.477	1342.164	0.513	18	0.207	R.DNFFFAGIDKVR.F
R3/RRR3-20/2	1175.283	1174.286	-2.876	0.534	1390.141	0.460	16	0.202	R.DNFFFAGIDK.V
R3/RRR3-20/2	1174.997	1174.286	-247.542	0.514	1323.791	0.461	15	0.195	R.DNFFFAGIDK.V
R3/RRR3-20/2	1174.920	1174.286	-312.793	0.528	1329.208	0.446	15	0.192	R.DNFFFAGIDK.V
R3/RRR3-20/2	1428.943	1429.604	-1166.459	0.440	1140.581	0.532	17	0.190	R.DNFFFAGIDKVR.F
R3/RRR3-20/2	1429.382	1429.604	-155.691	0.504	1175.783	0.484	17	0.185	R.DNFFFAGIDKVR.F
R3/RRR3-20/2	893.800	894.007	-232.477	0.416	1012.663	0.398	13	0.159	-.GGEYAVGIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/3	1619.162	1617.984	110.195	0.457	1494.053	0.433	26	0.159	R.FRKPVIAGDTLIMR.M
R3/RRR3-20/3	1618.066	1617.984	50.719	0.430	1595.432	0.351	26	0.149	R.FRKPVIAGDTLIMR.M
R3/RRR3-20/3	1633.835	1633.983	-90.813	0.437	942.891	0.383	24	0.108	R.FRKPVIAGDTLIM*R.M
R3/RRR3-20/3	1633.085	1633.983	-1166.223	0.481	733.317	0.382	22	0.101	R.FRKPVIAGDTLIM*R.M
R3/RRR3-20/3	1633.720	1633.983	-161.528	0.426	633.081	0.330	22	0.095	R.FRKPVIAGDTLIM*R.M
R3/RRR3-8/3	1170.619	1170.303	271.443	0.489	1498.012	0.469	21	0.168	K.FGAAVVSPEHR.Y
R3/RRR3-8/2	1331.944	1332.441	-374.275	0.454	1086.553	0.358	14	0.160	R.YYEFLDYYR.A
R3/RRR3-8/2	1333.381	1332.441	-45.234	0.427	940.634	0.352	13	0.150	R.YYEFLDYYR.A
R3/RRR3-8/2	1481.505	1481.590	-57.322	0.444	927.510	0.361	18	0.150	K.SSPFESLTTENLR.F
R3/RRR3-8/3	1170.533	1170.303	197.251	0.478	1183.834	0.512	19	0.148	K.FGAAVVSPEHR.Y
R3/RRR3-8/2	1481.221	1481.590	-249.350	0.414	890.792	0.348	18	0.147	K.SSPFESLTTENLR.F
R3/RRR3-8/2	1481.148	1481.590	-299.292	0.414	883.914	0.332	18	0.145	K.SSPFESLTTENLR.F
R3/RRR3-8/3	1170.732	1170.303	368.207	0.490	1227.868	0.460	20	0.139	K.FGAAVVSPEHR.Y
R3/RRR3-8/3	1298.141	1298.475	-258.685	0.520	1035.470	0.419	21	0.118	K.KFGAAVVSPEHR.Y
R3/RRR3-8/3	1299.030	1298.475	-344.089	0.523	1416.742	0.278	24	0.114	K.KFGAAVVSPEHR.Y
R3/RRR3-8/3	1297.350	1298.475	-1643.219	0.435	675.075	0.318	18	0.093	K.KFGAAVVSPEHR.Y
R3/RRR3-17/3	1298.641	1298.475	127.776	0.413	731.199	0.228	19	0.087	K.KFGAAVVSPEHR.Y
R3/RRR3-22/2	1887.420	1888.025	-852.428	0.572	1846.716	0.614	28	0.300	K.FLEDHPGGDDVLLSSTGK.D
R3/RRR3-22/2	1887.578	1888.025	-237.508	0.594	1756.267	0.574	28	0.274	K.FLEDHPGGDDVLLSSTGK.D
R3/RRR3-22/2	1887.385	1888.025	-871.127	0.574	1522.361	0.625	26	0.253	K.FLEDHPGGDDVLLSSTGK.D
R3/RRR3-22/3	1887.618	1888.025	-216.040	0.487	1751.232	0.428	36	0.188	K.FLEDHPGGDDVLLSSTGK.D
R3/RRR3-22/3	1643.961	1643.819	86.823	0.528	1215.952	0.551	26	0.160	K.HNSKDDCWLIIGGK.V
R3/RRR3-22/3	1645.119	1643.819	182.732	0.563	1110.803	0.579	25	0.157	K.HNSKDDCWLIIGGK.V
R3/RRR3-22/3	1889.338	1888.025	166.435	0.513	1537.576	0.408	34	0.157	K.FLEDHPGGDDVLLSSTGK.D
R3/RRR3-22/3	1643.560	1643.819	-157.982	0.550	1090.757	0.511	24	0.140	K.HNSKDDCWLIIGGK.V
R3/RRR3-20/3	1889.016	1888.025	-4.746	0.355	1094.630	0.306	30	0.102	K.FLEDHPGGDDVLLSSTGK.D
R3/RRR3-21/3	1888.393	1888.025	195.629	0.397	761.365	0.286	26	0.090	K.FLEDHPGGDDVLLSSTGK.D
R3/RRR3-18/2	1551.445	1551.685	-154.727	0.557	2610.108	0.540	21	0.426	K.LQIWDTAGQESFR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1551.184	1551.685	-970.505	0.485	2502.612	0.537	21	0.402	K.LQIWDTAGQESFR.S
R3/RRR3-18/2	1552.285	1551.685	-258.443	0.537	2501.314	0.516	21	0.393	K.LQIWDTAGQESFR.S
R3/RRR3-19/2	1550.769	1551.685	-1239.123	0.304	1547.121	0.359	19	0.195	K.LQIWDTAGQESFR.S
R3/RRR3-18/2	1358.924	1358.435	360.878	0.483	1073.057	0.462	16	0.172	R.AVSYEEGEQFAK.E
R3/RRR3-18/2	1320.322	1320.519	-150.098	0.392	1165.603	0.415	16	0.170	R.GAAGALLVYDITR.R
R3/RRR3-18/2	1689.430	1689.809	-224.998	0.471	975.728	0.455	21	0.166	R.ETFNHLASWLEDAR.Q
R3/RRR3-18/2	1357.579	1358.435	-1371.445	0.296	1039.984	0.465	16	0.166	R.AVSYEEGEQFAK.E
R3/RRR3-18/2	1358.103	1358.435	-245.000	0.417	926.346	0.442	15	0.159	R.AVSYEEGEQFAK.E
R3/RRR3-18/2	1689.231	1689.809	-937.001	0.467	772.345	0.469	19	0.156	R.ETFNHLASWLEDAR.Q
R3/RRR3-18/2	1320.087	1320.519	-328.851	0.366	679.186	0.353	15	0.139	R.GAAGALLVYDITR.R
R3/RRR3-18/2	1320.194	1320.519	-247.583	0.233	363.178	0.337	12	0.131	R.GAAGALLVYDITR.R
R3/RRR3-12/2	1707.938	1708.940	-1175.850	0.549	3078.840	0.610	27	0.581	R.HVVIVDDLVQSGGTLR.E
R3/RRR3-12/2	1708.546	1708.940	-231.294	0.595	3013.794	0.603	27	0.558	R.HVVIVDDLVQSGGTLR.E
R3/RRR3-12/2	1609.401	1608.731	-206.136	0.598	2725.583	0.552	25	0.463	R.VEEEGDVATAFTLAR.I
R3/RRR3-12/2	1319.104	1319.533	-326.497	0.415	1491.793	0.400	18	0.199	K.VSAYVTHAVFPK.Q
R3/RRR3-12/2	1319.205	1319.533	-249.439	0.438	1322.552	0.400	17	0.182	K.VSAYVTHAVFPK.Q
R3/RRR3-12/3	1768.624	1768.954	-187.551	0.347	553.601	0.589	25	0.118	K.VAASSDAIHLQSINWR.S
R3/RRR3-12/3	1769.167	1768.954	120.299	0.364	532.431	0.499	25	0.107	K.VAASSDAIHLQSINWR.S
R3/RRR3-12/2	1318.430	1319.533	-1599.849	0.322	706.943	0.111	13	0.107	-.VSAYVTHAVFPK.-
R3/RRR3-12/3	1768.952	1768.954	-1.157	0.381	455.330	0.430	24	0.101	K.VAASSDAIHLQSINWR.S
R3/RRR3-21/2	1420.966	1421.619	-1166.458	0.497	1469.726	0.537	18	0.226	K.CHFVAIDIFNGK.K
R3/RRR3-21/2	1421.361	1421.619	-181.809	0.474	1182.082	0.580	17	0.203	K.CHFVAIDIFNGK.K
R3/RRR3-21/2	1421.420	1421.619	-140.111	0.420	1135.512	0.550	17	0.192	K.CHFVAIDIFNGK.K
R3/RRR3-21/2	1299.969	1300.483	-1168.130	0.433	1349.991	0.365	20	0.180	R.LPTDDSLLGQIK.T
R3/RRR3-21/2	1421.922	1421.619	213.750	0.464	1006.656	0.477	17	0.171	K.CHFVAIDIFNGK.K
R3/RRR3-21/2	1299.712	1300.483	-1366.657	0.421	1308.176	0.313	19	0.168	R.LPTDDSLLGQIK.T
R3/RRR3-21/2	1300.045	1300.483	-338.442	0.463	832.066	0.370	18	0.149	R.LPTDDSLLGQIK.T
R3/RRR3-21/2	1134.848	1135.255	-359.657	0.285	264.167	0.459	15	0.147	K.TYPQQAGTIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1136.065	1135.255	-167.868	0.368	319.391	0.322	14	0.145	K.TYPQQAGTIR.K
R3/RRR3-22/2	1134.812	1135.255	-391.496	0.286	245.582	0.277	14	0.145	K.TYPQQAGTIR.K
R3/RRR3-20/2	1134.854	1135.255	-354.476	0.276	237.721	0.317	14	0.145	K.TYPQQAGTIR.K
R3/RRR3-21/2	1134.842	1135.255	-365.053	0.359	209.671	0.449	13	0.142	-.TYPQQAGTIR.-
R3/RRR3-21/2	1134.542	1135.255	-1514.467	0.198	225.198	0.213	14	0.141	-.TYPQQAGTIR.-
R3/RRR3-22/2	1134.900	1135.255	-313.574	0.339	218.611	0.335	13	0.140	-.TYPQQAGTIR.-
R3/RRR3-21/2	1135.402	1135.255	129.876	0.217	374.702	0.383	15	0.140	K.TYPQQAGTIR.K
R3/RRR3-21/2	1134.950	1135.255	-269.114	0.190	228.811	0.366	14	0.137	-.TYPQQAGTIR.-
R3/RRR3-21/2	1135.979	1135.255	-243.434	0.171	354.475	0.432	15	0.137	K.TYPQQAGTIR.K
R3/RRR3-21/2	1134.987	1135.255	-236.959	0.150	285.120	0.350	15	0.136	K.TYPQQAGTIR.K
R3/RRR3-20/2	1134.218	1135.255	-1800.961	0.213	199.484	0.366	12	0.130	-.TYPQQAGTIR.-
R3/RRR3-22/2	1134.503	1135.255	-1548.730	0.092	179.148	0.340	12	0.128	-.TYPQQAGTIR.-
R3/RRR3-22/3	1800.200	1800.004	109.724	0.412	1075.768	0.380	27	0.111	K.DDLRLPTDDSLLGQIK.T
R3/RRR3-4/3	1649.159	1649.744	-963.563	0.576	1779.784	0.647	30	0.266	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1570.709	1571.718	-1282.322	0.342	1789.597	0.453	19	0.245	R.GLEGLTVQQAIDGNR.L
R3/RRR3-4/3	1650.013	1649.744	163.491	0.554	1593.070	0.663	30	0.241	R.YGDQTSTITAAHVER.G
R3/RRR3-5/3	1649.849	1649.744	63.768	0.547	1492.386	0.659	29	0.225	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1649.277	1649.744	-283.851	0.477	1421.697	0.546	19	0.219	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1649.151	1649.744	-968.385	0.472	1503.728	0.488	19	0.216	R.YGDQTSTITAAHVER.G
R3/RRR3-4/3	1649.765	1649.744	12.897	0.554	1456.209	0.622	27	0.210	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1570.843	1571.718	-1196.943	0.341	1490.648	0.462	18	0.208	R.GLEGLTVQQAIDGNR.L
R3/RRR3-8/3	1649.494	1649.744	-152.107	0.506	1469.507	0.606	28	0.206	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1648.547	1649.744	-1336.597	0.465	1249.684	0.509	19	0.194	R.YGDQTSTITAAHVER.G
R3/RRR3-5/3	1649.910	1649.744	100.832	0.514	1227.391	0.648	27	0.189	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1384.118	1383.685	313.796	0.513	1182.624	0.461	18	0.181	R.EILAGVNPMVIAR.L
R3/RRR3-5/3	1649.817	1649.744	44.400	0.544	1227.538	0.608	27	0.177	R.YGDQTSTITAAHVER.G
R3/RRR3-1/3	1649.539	1649.744	-124.157	0.511	1070.641	0.651	24	0.174	R.YGDQTSTITAAHVER.G
R3/RRR3-1/3	1649.385	1649.744	-217.812	0.507	1138.521	0.627	26	0.174	R.YGDQTSTITAAHVER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/3	1649.199	1649.744	-939.486	0.522	1222.874	0.577	26	0.170	R.YGDQTSTITAAHVER.G
R3/RRR3-7/3	1650.782	1649.744	23.199	0.488	1139.902	0.600	26	0.167	R.YGDQTSTITAAHVER.G
R3/RRR3-6/3	1650.001	1649.744	156.702	0.495	1017.537	0.639	26	0.165	R.YGDQTSTITAAHVER.G
R3/RRR3-1/3	1649.249	1649.744	-300.679	0.490	1231.732	0.557	27	0.165	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1400.380	1399.685	-218.503	0.486	897.793	0.479	17	0.164	R.EILAGVNPM*VIAR.L
R3/RRR3-7/3	1650.785	1649.744	25.090	0.469	1012.819	0.602	24	0.157	R.YGDQTSTITAAHVER.G
R3/RRR3-7/3	1650.611	1649.744	-80.609	0.489	916.650	0.635	23	0.157	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1384.384	1383.685	-218.238	0.443	1090.032	0.356	17	0.157	R.EILAGVNPMVIAR.L
R3/RRR3-6/3	1649.426	1649.744	-192.977	0.458	1077.469	0.571	25	0.155	R.YGDQTSTITAAHVER.G
R3/RRR3-3/3	1649.471	1649.744	-165.915	0.513	1038.493	0.581	25	0.154	R.YGDQTSTITAAHVER.G
R3/RRR3-3/3	1649.681	1649.744	-37.979	0.515	793.331	0.645	23	0.150	R.YGDQTSTITAAHVER.G
R3/RRR3-5/2	1399.329	1399.685	-254.715	0.307	532.505	0.213	15	0.131	R.EILAGVNPM*VIAR.L
R3/RRR3-5/2	859.862	859.992	-152.089	0.189	801.863	0.184	11	0.128	R.LTEFPPR.S
R3/RRR3-5/2	860.093	859.992	117.568	0.094	534.041	0.269	10	0.123	R.LTEFPPR.S
R3/RRR3-6/3	1648.769	1649.744	-1201.161	0.421	757.592	0.471	23	0.117	R.YGDQTSTITAAHVER.G
R3/RRR3-5/3	1650.805	1649.744	36.993	0.453	496.397	0.465	24	0.111	R.YGDQTSTITAAHVER.G
R3/RRR3-5/3	1571.314	1571.718	-257.425	0.286	956.969	0.244	21	0.085	-.GLEGLTVQQAIDGNR.-
R3/RRR3-15/3	1757.031	1756.896	77.159	0.597	2925.594	0.528	34	0.478	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-15/3	1756.704	1756.896	-109.335	0.617	2496.764	0.531	33	0.365	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-15/3	1756.464	1756.896	-246.741	0.594	2044.100	0.562	31	0.284	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-15/2	1610.867	1609.716	94.050	0.567	1771.965	0.535	22	0.265	R.ISQEVSGDALGEEFK.G
R3/RRR3-15/2	1610.499	1609.716	-135.141	0.537	1582.471	0.549	21	0.242	R.ISQEVSGDALGEEFK.G
R3/RRR3-14/3	1756.455	1756.896	-251.447	0.532	1737.449	0.500	30	0.210	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-14/3	1757.102	1756.896	117.711	0.535	1664.439	0.518	29	0.206	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-12/3	1756.536	1756.896	-205.327	0.514	1719.021	0.448	31	0.190	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-15/2	1373.213	1373.537	-237.222	0.505	1250.435	0.331	18	0.166	K.KLEIDDDQKLR.A
R3/RRR3-15/2	1374.132	1373.537	-295.870	0.541	1081.814	0.365	18	0.161	K.KLEIDDDQKLR.A
R3/RRR3-14/2	1373.069	1373.537	-342.378	0.483	1137.820	0.307	18	0.156	K.KLEIDDDQKLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/3	1756.882	1756.896	-7.507	0.499	1512.662	0.398	29	0.152	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-15/2	1372.510	1373.537	-1481.592	0.471	1055.237	0.294	17	0.149	K.KLEIDDDQKLR.A
R3/RRR3-15/2	1350.966	1351.484	-1126.663	0.358	1071.346	0.264	17	0.144	K.FNIANPTTGCQK.K
R3/RRR3-15/3	1372.819	1373.537	-1255.181	0.462	1268.736	0.414	24	0.130	K.KLEIDDDQKLR.A
R3/RRR3-12/3	1756.399	1756.896	-283.765	0.490	1133.259	0.423	28	0.125	K.KGDNDLPGLTDTEKPR.M
R3/RRR3-15/3	1373.029	1373.537	-1102.104	0.447	1182.003	0.399	23	0.122	K.KLEIDDDQKLR.A
R3/RRR3-14/3	1373.782	1373.537	178.584	0.507	1208.514	0.369	24	0.116	K.KLEIDDDQKLR.A
R3/RRR3-13/3	1373.175	1373.537	-264.566	0.444	1042.122	0.402	23	0.114	K.KLEIDDDQKLR.A
R3/RRR3-14/3	1373.486	1373.537	-37.861	0.457	891.123	0.398	22	0.109	K.KLEIDDDQKLR.A
R3/RRR3-13/3	1373.881	1373.537	251.024	0.447	865.566	0.372	21	0.105	K.KLEIDDDQKLR.A
R3/RRR3-14/3	1373.352	1373.537	-135.619	0.423	724.268	0.374	19	0.103	K.KLEIDDDQKLR.A
R3/RRR3-1/3	1373.038	1373.537	-364.911	0.397	729.275	0.371	19	0.102	K.KLEIDDDQKLR.A
R3/RRR3-20/3	1373.742	1373.537	149.445	0.420	846.359	0.334	20	0.100	K.KLEIDDDQKLR.A
R3/RRR3-20/3	1373.722	1373.537	134.875	0.412	732.091	0.346	19	0.100	K.KLEIDDDQKLR.A
R3/RRR3-15/3	1373.740	1373.537	147.841	0.455	703.750	0.323	19	0.095	-.KLEIDDDQKLR.-
R3/RRR3-25/3	1373.310	1373.537	-166.248	0.364	826.211	0.287	22	0.094	K.KLEIDDDQKLR.A
R3/RRR3-2/3	1373.000	1373.537	-1123.261	0.337	784.209	0.249	21	0.091	K.KLEIDDDQKLR.A
R3/RRR3-3/3	1585.754	1584.799	-28.932	0.490	1542.492	0.415	31	0.159	R.LAGDKLVDGEGALAVR.A
R3/RRR3-3/2	1530.716	1530.745	-19.166	0.436	708.714	0.424	16	0.145	R.IQDVQSVLICAQR.L
R3/RRR3-3/3	1585.078	1584.799	176.522	0.367	584.039	0.367	21	0.089	-.LAGDKLVDGEGALAVR.-
R3/RRR3-20/2	1376.054	1376.528	-345.550	0.460	1582.320	0.417	18	0.210	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1375.436	1376.528	-1525.441	0.427	1561.716	0.404	18	0.205	K.CCDSIVQLPQR.I
R3/RRR3-21/2	1376.972	1376.528	323.249	0.492	1462.368	0.437	18	0.202	K.CCDSIVQLPQR.I
R3/RRR3-18/2	1377.154	1376.528	-272.727	0.501	1555.297	0.381	18	0.199	K.CCDSIVQLPQR.I
R3/RRR3-18/2	1377.231	1376.528	-216.260	0.487	1456.001	0.428	17	0.199	K.CCDSIVQLPQR.I
R3/RRR3-22/2	1375.987	1376.528	-1123.171	0.497	1406.763	0.450	17	0.198	K.CCDSIVQLPQR.I
R3/RRR3-22/2	1375.552	1376.528	-1441.200	0.430	1417.892	0.407	17	0.191	K.CCDSIVQLPQR.I
R3/RRR3-1/2	1376.331	1376.528	-143.545	0.455	1411.717	0.408	17	0.191	K.CCDSIVQLPQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1376.107	1376.528	-306.923	0.502	1394.600	0.414	17	0.190	K.CCDSIVQLPQR.I
R3/RRR3-21/2	1375.804	1376.528	-1257.076	0.435	1380.515	0.403	17	0.187	K.CCDSIVQLPQR.I
R3/RRR3-18/2	1376.511	1376.528	-12.240	0.397	1565.309	0.288	18	0.183	K.CCDSIVQLPQR.I
R3/RRR3-23/2	1376.070	1376.528	-333.801	0.433	1429.642	0.354	17	0.182	K.CCDSIVQLPQR.I
R3/RRR3-16/2	1376.147	1376.528	-277.820	0.392	1461.296	0.283	17	0.173	K.CCDSIVQLPQR.I
R3/RRR3-1/2	1376.098	1376.528	-313.776	0.466	1077.325	0.434	15	0.169	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1375.504	1376.528	-1475.964	0.359	1343.853	0.307	17	0.168	K.CCDSIVQLPQR.I
R3/RRR3-22/2	1375.560	1376.528	-1435.227	0.358	1428.047	0.264	17	0.167	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1377.122	1376.528	-296.027	0.402	1434.665	0.255	17	0.166	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1377.281	1376.528	-180.338	0.394	1388.952	0.260	17	0.164	K.CCDSIVQLPQR.I
R3/RRR3-1/2	1376.216	1376.528	-227.274	0.408	1232.030	0.328	16	0.163	K.CCDSIVQLPQR.I
R3/RRR3-2/2	1376.226	1376.528	-219.888	0.430	1011.934	0.407	15	0.161	K.CCDSIVQLPQR.I
R3/RRR3-21/2	1376.141	1376.528	-282.003	0.441	1109.501	0.359	15	0.159	K.CCDSIVQLPQR.I
R3/RRR3-16/2	1376.353	1376.528	-127.708	0.451	1020.737	0.386	15	0.159	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1278.478	1277.359	93.889	0.415	799.957	0.453	16	0.158	K.ECVEAPGDFPR.G
R3/RRR3-19/2	1755.167	1754.855	178.189	0.509	801.186	0.452	22	0.158	R.CDDELEPGKCTAACK.S
R3/RRR3-2/2	1376.058	1376.528	-342.702	0.397	1135.902	0.328	16	0.158	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1375.665	1376.528	-1358.487	0.439	1011.016	0.380	15	0.157	K.CCDSIVQLPQR.I
R3/RRR3-18/2	1375.476	1376.528	-1496.824	0.403	992.903	0.376	15	0.156	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1278.120	1277.359	-186.857	0.343	788.658	0.457	16	0.156	K.ECVEAPGDFPR.G
R3/RRR3-18/2	1754.461	1754.855	-225.102	0.503	774.239	0.433	22	0.155	R.CDDELEPGKCTAACK.S
R3/RRR3-26/2	1376.140	1376.528	-282.893	0.377	1036.663	0.339	15	0.153	K.CCDSIVQLPQR.I
R3/RRR3-18/2	1754.089	1754.855	-1009.988	0.502	680.954	0.453	20	0.152	R.CDDELEPGKCTAACK.S
R3/RRR3-18/2	1376.790	1376.528	190.521	0.394	1325.607	0.210	17	0.152	K.CCDSIVQLPQR.I
R3/RRR3-3/2	1377.237	1376.528	-211.992	0.418	695.747	0.417	15	0.151	K.CCDSIVQLPQR.I
R3/RRR3-18/2	1376.958	1376.528	313.204	0.432	1201.380	0.261	16	0.151	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1753.598	1754.855	-1291.088	0.495	667.549	0.441	20	0.151	R.CDDELEPGKCTAACK.S
R3/RRR3-18/2	1754.182	1754.855	-956.959	0.501	692.673	0.434	20	0.151	R.CDDELEPGKCTAACK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1062.907	1063.091	-174.123	0.429	910.762	0.336	14	0.150	R.CDDELEPGK.C
R3/RRR3-23/2	1062.630	1063.091	-435.257	0.385	906.983	0.330	14	0.149	R.CDDELEPGK.C
R3/RRR3-23/2	1375.967	1376.528	-1138.047	0.383	1090.707	0.275	16	0.149	K.CCDSIVQLPQR.I
R3/RRR3-23/2	1062.096	1063.091	-1884.409	0.322	911.742	0.325	14	0.148	R.CDDELEPGK.C
R3/RRR3-19/2	1754.156	1754.855	-971.491	0.484	643.479	0.408	20	0.147	R.CDDELEPGKCTAACK.S
R3/RRR3-3/2	1376.542	1376.528	10.263	0.403	902.517	0.312	16	0.146	K.CCDSIVQLPQR.I
R3/RRR3-22/2	1062.785	1063.091	-288.885	0.399	924.277	0.295	14	0.146	R.CDDELEPGK.C
R3/RRR3-19/2	1063.845	1063.091	-231.629	0.414	966.066	0.273	14	0.145	R.CDDELEPGK.C
R3/RRR3-20/2	1375.450	1376.528	-1515.456	0.328	957.728	0.264	15	0.142	K.CCDSIVQLPQR.I
R3/RRR3-22/2	1062.742	1063.091	-329.911	0.406	903.419	0.257	14	0.142	R.CDDELEPGK.C
R3/RRR3-23/2	1063.264	1063.091	163.560	0.328	902.577	0.258	14	0.142	R.CDDELEPGK.C
R3/RRR3-12/2	1376.257	1376.528	-197.820	0.354	889.887	0.269	15	0.141	K.CCDSIVQLPQR.I
R3/RRR3-23/2	1062.908	1063.091	-172.279	0.362	887.591	0.247	14	0.141	R.CDDELEPGK.C
R3/RRR3-1/2	1276.872	1277.359	-381.788	0.260	796.565	0.310	15	0.140	K.ECVEAPGDFPR.G
R3/RRR3-3/2	1376.308	1376.528	-160.271	0.364	958.699	0.237	15	0.140	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1062.562	1063.091	-1443.412	0.352	901.890	0.233	14	0.139	R.CDDELEPGK.C
R3/RRR3-19/2	1376.372	1376.528	-113.473	0.319	1155.895	0.165	16	0.139	K.CCDSIVQLPQR.I
R3/RRR3-19/2	1276.882	1277.359	-374.210	0.277	470.690	0.321	13	0.138	K.ECVEAPGDFPR.G
R3/RRR3-18/2	1062.289	1063.091	-1701.383	0.295	957.058	0.192	14	0.137	R.CDDELEPGK.C
R3/RRR3-18/2	1063.247	1063.091	147.326	0.285	825.874	0.230	13	0.137	R.CDDELEPGK.C
R3/RRR3-18/2	1062.778	1063.091	-295.569	0.348	1007.887	0.177	14	0.137	R.CDDELEPGK.C
R3/RRR3-1/2	1277.007	1277.359	-276.474	0.245	830.328	0.242	15	0.136	K.ECVEAPGDFPR.G
R3/RRR3-19/2	1062.803	1063.091	-272.292	0.373	975.427	0.175	14	0.135	R.CDDELEPGK.C
R3/RRR3-16/2	1277.054	1277.359	-238.881	0.270	630.754	0.261	14	0.135	K.ECVEAPGDFPR.G
R3/RRR3-2/2	1276.872	1277.359	-381.980	0.224	550.771	0.272	13	0.134	K.ECVEAPGDFPR.G
R3/RRR3-27/2	1276.922	1277.359	-342.940	0.197	663.905	0.203	15	0.132	K.ECVEAPGDFPR.G
R3/RRR3-27/2	1276.936	1277.359	-331.814	0.209	679.963	0.173	15	0.131	K.ECVEAPGDFPR.G
R3/RRR3-19/2	1276.821	1277.359	-1207.718	0.152	646.949	0.187	14	0.129	K.ECVEAPGDFPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1276.869	1277.359	-384.474	0.127	585.029	0.194	14	0.129	K.ECVEAPGDFPR.G
R3/RRR3-18/3	1754.548	1754.855	-175.693	0.440	796.268	0.480	27	0.118	R.CDDELEPGKCTAACK.S
R3/RRR3-18/3	1755.834	1754.855	-12.114	0.440	615.022	0.470	24	0.112	R.CDDELEPGKCTAACK.S
R3/RRR3-19/3	1755.114	1754.855	147.806	0.423	834.421	0.419	27	0.110	R.CDDELEPGKCTAACK.S
R3/RRR3-19/3	1754.871	1754.855	8.741	0.444	599.083	0.431	25	0.107	R.CDDELEPGKCTAACK.S
R3/RRR3-23/3	1756.064	1754.855	119.140	0.375	616.005	0.393	24	0.103	R.CDDELEPGKCTAACK.S
R3/RRR3-21/3	1754.264	1754.855	-909.741	0.365	675.828	0.379	24	0.102	R.CDDELEPGKCTAACK.S
R3/RRR3-21/3	1754.614	1754.855	-137.900	0.354	745.538	0.362	27	0.101	R.CDDELEPGKCTAACK.S
R3/RRR3-19/3	1754.746	1754.855	-62.429	0.390	859.994	0.328	27	0.099	R.CDDELEPGKCTAACK.S
R3/RRR3-23/3	1754.036	1754.855	-1040.321	0.365	565.362	0.290	24	0.096	R.CDDELEPGKCTAACK.S
R3/RRR3-23/3	1754.281	1754.855	-899.996	0.337	503.577	0.317	21	0.093	-.CDDELEPGKCTAACK.-
R3/RRR3-20/3	1754.017	1754.855	-1051.221	0.254	573.248	0.303	23	0.092	-.CDDELEPGKCTAACK.-
R3/RRR3-3/3	1754.095	1754.855	-1006.258	0.291	565.525	0.273	21	0.090	-.CDDELEPGKCTAACK.-
R3/RRR3-18/2	1610.310	1610.752	-275.438	0.509	2176.893	0.504	22	0.325	R.FALENQAVNEATFR.C
R3/RRR3-18/2	1610.205	1610.752	-963.446	0.488	1902.985	0.526	21	0.284	R.FALENQAVNEATFR.C
R3/RRR3-18/3	1357.662	1357.497	122.357	0.491	2189.621	0.350	29	0.222	K.KFHGVAENPTEK.I
R3/RRR3-18/3	1357.378	1357.497	-87.605	0.506	1883.585	0.406	26	0.197	K.KFHGVAENPTEK.I
R3/RRR3-18/2	1211.102	1211.393	-240.971	0.355	677.198	0.552	17	0.160	R.VPIVPSDGAISR.T
R3/RRR3-17/2	1609.458	1610.752	-1429.841	0.309	1213.403	0.322	19	0.160	R.FALENQAVNEATFR.C
R3/RRR3-18/2	1211.156	1211.393	-195.874	0.370	637.856	0.539	18	0.159	R.VPIVPSDGAISR.T
R3/RRR3-17/2	1211.132	1211.393	-215.996	0.325	691.442	0.497	18	0.155	R.VPIVPSDGAISR.T
R3/RRR3-17/2	1210.646	1211.393	-1447.177	0.310	581.557	0.512	18	0.151	R.VPIVPSDGAISR.T
R3/RRR3-18/2	1210.605	1211.393	-1481.106	0.283	599.723	0.509	16	0.149	R.VPIVPSDGAISR.T
R3/RRR3-17/2	1211.222	1211.393	-141.379	0.292	359.054	0.440	14	0.141	R.VPIVPSDGAISR.T
R3/RRR3-18/3	1229.106	1229.324	-177.983	0.419	1271.725	0.200	23	0.092	K.FHGVAENPTEK.I
R3/RRR3-18/3	1229.344	1229.324	16.411	0.390	971.700	0.176	21	0.082	-.FHGVAENPTEK.-
R3/RRR3-18/3	1229.553	1229.324	186.836	0.372	951.497	0.171	21	0.082	K.FHGVAENPTEK.I
R3/RRR3-21/2	1909.091	1910.072	-1040.925	0.547	2319.405	0.515	24	0.356	R.YALYDFDFVTGENVQK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1909.020	1910.072	-1077.777	0.529	1092.150	0.499	22	0.180	R.YALYDFDFVTGENVQK.S
R3/RRR3-21/2	1413.373	1412.617	-172.961	0.406	1235.465	0.403	17	0.175	K.IFFIAWSPSTSR.I
R3/RRR3-21/2	1412.544	1412.617	-52.146	0.355	1102.137	0.302	16	0.151	K.IFFIAWSPSTSR.I
R3/RRR3-21/2	1412.669	1412.617	36.869	0.325	784.358	0.337	14	0.139	K.IFFIAWSPSTSR.I
R3/RRR3-21/2	1170.046	1169.394	-298.609	0.336	931.926	0.262	14	0.139	R.YVIFKIEEK.Q
R3/RRR3-21/3	1602.145	1602.712	-980.751	0.427	1451.949	0.349	31	0.133	R.SHSNASSGM*GVAPDIR.D
R3/RRR3-18/2	1775.613	1775.896	-159.534	0.566	2875.285	0.456	25	0.458	R.TEDDIALANSVDVGSLR.H
R3/RRR3-18/2	1775.494	1775.896	-227.125	0.547	2680.203	0.427	24	0.400	R.TEDDIALANSVDVGSLR.H
R3/RRR3-18/2	1189.140	1188.359	-185.498	0.406	1937.868	0.541	17	0.294	R.AFAYFVLSGGR.F
R3/RRR3-18/2	1712.714	1712.926	-124.073	0.589	1814.485	0.565	25	0.277	R.NQDTGLAELPATVAALK.N
R3/RRR3-18/2	1712.330	1712.926	-934.729	0.560	1761.633	0.525	25	0.259	R.NQDTGLAELPATVAALK.N
R3/RRR3-19/2	1713.566	1712.926	-210.611	0.609	1744.429	0.540	24	0.259	R.NQDTGLAELPATVAALK.N
R3/RRR3-19/2	1713.125	1712.926	116.738	0.585	1746.527	0.534	23	0.257	R.NQDTGLAELPATVAALK.N
R3/RRR3-18/2	1711.672	1712.926	-1320.780	0.431	1719.987	0.496	24	0.246	R.NQDTGLAELPATVAALK.N
R3/RRR3-19/2	1712.454	1712.926	-276.311	0.555	1540.359	0.533	23	0.230	R.NQDTGLAELPATVAALK.N
R3/RRR3-18/2	1188.137	1188.359	-187.509	0.410	1768.341	0.385	17	0.229	R.AFAYFVLSGGR.F
R3/RRR3-19/2	1712.197	1712.926	-1012.603	0.546	1448.841	0.500	23	0.212	R.NQDTGLAELPATVAALK.N
R3/RRR3-18/2	1325.071	1324.380	-234.290	0.491	963.503	0.532	15	0.179	K.VVYDEYNHER.H
R3/RRR3-18/2	1324.074	1324.380	-231.693	0.440	722.572	0.517	14	0.161	K.VVYDEYNHER.H
R3/RRR3-18/2	1323.938	1324.380	-335.108	0.390	756.222	0.502	15	0.160	K.VVYDEYNHER.H
R3/RRR3-13/2	1563.675	1564.680	-1285.976	0.458	2450.891	0.496	22	0.377	K.SADWSHFLTGSLDK.S
R3/RRR3-13/2	1564.358	1564.680	-206.749	0.511	2220.354	0.504	22	0.333	K.SADWSHFLTGSLDK.S
R3/RRR3-13/2	1564.288	1564.680	-251.842	0.502	2237.157	0.473	22	0.326	K.SADWSHFLTGSLDK.S
R3/RRR3-13/2	1261.010	1261.407	-315.615	0.460	1778.158	0.520	20	0.264	R.TIITAGEDATIR.I
R3/RRR3-13/2	1260.726	1261.407	-1337.345	0.421	1558.927	0.518	19	0.232	R.TIITAGEDATIR.I
R3/RRR3-13/2	1261.008	1261.279	-215.900	0.443	1439.511	0.467	20	0.209	R.SFSSGGEDGYVR.L
R3/RRR3-13/2	1261.007	1261.279	-216.482	0.465	1241.522	0.499	19	0.195	R.SFSSGGEDGYVR.L
R3/RRR3-13/2	1260.427	1261.407	-1575.555	0.354	1355.111	0.450	19	0.194	R.TIITAGEDATIR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1261.892	1261.279	-308.311	0.503	1238.387	0.482	19	0.192	R.SFSSGGEDGYVR.L
R3/RRR3-13/2	1085.443	1086.264	-1682.574	0.377	1041.097	0.399	15	0.161	K.ILQEEIGGVK.G
R3/RRR3-13/2	1086.113	1086.264	-139.515	0.454	1077.708	0.319	16	0.154	K.ILQEEIGGVK.G
R3/RRR3-1/2	1323.111	1322.449	-256.384	0.570	1962.878	0.540	18	0.296	K.GVADFLQEVTSR.K
R3/RRR3-2/2	1322.126	1322.449	-244.999	0.459	1952.135	0.414	18	0.260	K.GVADFLQEVTSR.K
R3/RRR3-1/2	1561.244	1559.704	-295.544	0.555	1587.415	0.570	19	0.249	R.ENILEFFESAGFR.C
R3/RRR3-3/2	1322.134	1322.449	-239.163	0.428	1922.174	0.350	18	0.240	K.GVADFLQEVTSR.K
R3/RRR3-3/2	1322.740	1322.449	220.891	0.437	1293.963	0.436	18	0.187	K.GVADFLQEVTSR.K
R3/RRR3-2/2	1097.607	1097.243	332.012	0.369	1145.509	0.471	15	0.179	K.YGLSSLESLK.A
R3/RRR3-2/2	1450.312	1450.622	-214.227	0.376	1359.034	0.352	18	0.176	R.KGVADFLQEVTSR.K
R3/RRR3-2/2	1699.284	1699.887	-946.373	0.413	837.215	0.444	21	0.154	R.DALVGLPGVSGLSTEQR.K
R3/RRR3-1/2	1322.147	1322.449	-229.437	0.361	1030.425	0.315	17	0.150	K.GVADFLQEVTSR.K
R3/RRR3-2/2	1097.312	1097.243	62.751	0.289	652.139	0.489	13	0.148	K.YGLSSLESLK.A
R3/RRR3-1/2	1097.101	1097.243	-129.971	0.294	431.761	0.463	12	0.141	K.YGLSSLESLK.A
R3/RRR3-2/2	1698.394	1699.887	-1472.113	0.347	373.383	0.453	15	0.137	R.DALVGLPGVSGLSTEQR.K
R3/RRR3-1/2	1699.326	1699.887	-921.708	0.316	401.208	0.297	15	0.130	R.DALVGLPGVSGLSTEQR.K
R3/RRR3-14/2	1897.421	1898.214	-947.888	0.521	1692.567	0.582	29	0.265	K.VM*VGLPTTGGVTPVPGAAEK.A
R3/RRR3-14/2	1897.445	1898.214	-934.777	0.529	1651.820	0.598	28	0.263	K.VM*VGLPTTGGVTPVPGAAEK.A
R3/RRR3-14/2	1882.467	1882.214	134.789	0.559	1666.920	0.561	28	0.255	K.VMVGLPTTGGVTPVPGAAEK.A
R3/RRR3-14/2	1595.238	1594.853	241.984	0.544	1798.597	0.472	18	0.249	K.FASFETIVEM*IYK.H
R3/RRR3-14/2	1897.730	1898.214	-255.656	0.546	1429.692	0.569	27	0.226	K.VM*VGLPTTGGVTPVPGAAEK.A
R3/RRR3-14/2	1881.903	1882.214	-165.943	0.545	1379.663	0.578	26	0.221	K.VMVGLPTTGGVTPVPGAAEK.A
R3/RRR3-14/2	1881.531	1882.214	-897.264	0.508	1244.030	0.566	25	0.204	K.VMVGLPTTGGVTPVPGAAEK.A
R3/RRR3-14/2	1580.271	1578.853	265.315	0.466	1161.623	0.450	18	0.177	K.FASFETIVEMIYK.H
R3/RRR3-14/2	1594.250	1594.853	-1008.458	0.502	1092.576	0.436	18	0.170	K.FASFETIVEM*IYK.H
R3/RRR3-14/2	1594.392	1594.853	-289.979	0.486	998.357	0.448	18	0.166	K.FASFETIVEM*IYK.H
R3/RRR3-14/2	1594.520	1594.853	-209.330	0.492	940.877	0.449	19	0.164	K.FASFETIVEM*IYK.H
R3/RRR3-2/2	1580.367	1578.853	-308.702	0.412	903.101	0.488	16	0.164	K.FASFETIVEMIYK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1594.351	1594.853	-945.039	0.461	864.095	0.445	19	0.160	K.FASFETIVEM*IYK.H
R3/RRR3-13/2	1594.291	1594.853	-982.397	0.363	399.064	0.398	17	0.145	K.FASFETIVEM*IYK.H
R3/RRR3-14/2	1594.240	1594.853	-1014.762	0.250	166.447	0.239	13	0.143	K.FASFETIVEM*IYK.H
R3/RRR3-9/2	1594.378	1594.853	-298.889	0.301	365.359	0.328	11	0.131	-.FASFETIVEM*IYK.-
R3/RRR3-22/3	1982.073	1982.204	-66.479	0.472	2319.032	0.372	30	0.272	K.YGAKPDAETLDM*LNTVAR.Q
R3/RRR3-22/3	1981.821	1982.204	-194.001	0.495	2114.452	0.466	30	0.268	K.YGAKPDAETLDM*LNTVAR.Q
R3/RRR3-22/2	1381.402	1381.475	-53.322	0.553	1659.727	0.506	22	0.244	R.WVGAAVDFSEGSR.A
R3/RRR3-22/2	1381.159	1381.475	-229.297	0.520	1426.337	0.479	21	0.209	R.WVGAAVDFSEGSR.A
R3/RRR3-22/2	1381.235	1381.475	-174.414	0.552	1333.952	0.506	20	0.205	R.WVGAAVDFSEGSR.A
R3/RRR3-22/3	1981.346	1982.204	-940.805	0.463	1751.965	0.411	30	0.188	K.YGAKPDAETLDM*LNTVAR.Q
R3/RRR3-22/3	1966.091	1966.205	-58.427	0.379	1665.670	0.415	30	0.179	K.YGAKPDAETLDMLNTVAR.Q
R3/RRR3-22/2	958.988	959.084	-100.365	0.475	856.034	0.363	14	0.153	R.WAADNLLR.A
R3/RRR3-22/2	958.814	959.084	-281.966	0.435	694.797	0.336	13	0.145	R.WAADNLLR.A
R3/RRR3-21/2	1381.237	1381.475	-172.464	0.310	737.059	0.404	14	0.143	R.WVGAAVDFSEGSR.A
R3/RRR3-21/2	959.120	959.084	38.155	0.394	609.561	0.297	12	0.140	R.WAADNLLR.A
R3/RRR3-22/2	958.993	959.084	-95.002	0.447	599.544	0.283	12	0.139	R.WAADNLLR.A
R3/RRR3-22/3	1330.017	1329.616	302.983	0.491	1417.257	0.346	27	0.127	R.AGDHLILLHVLK.D
R3/RRR3-22/3	1965.721	1966.205	-246.790	0.323	794.910	0.322	23	0.094	-.YGAKPDAETLDMLNTVAR.-
R3/RRR3-22/3	1330.287	1329.616	-247.832	0.437	521.528	0.277	20	0.080	-.AGDHLILLHVLK.-
R3/RRR3-16/2	1474.334	1474.639	-207.498	0.439	755.719	0.377	16	0.143	R.EAYLIFQDFAEK.Y
R3/RRR3-15/2	1137.798	1138.169	-327.518	0.329	609.846	0.336	13	0.139	R.AVSAEDNFER.A
R3/RRR3-16/2	1138.054	1138.169	-101.517	0.376	776.396	0.265	15	0.138	R.AVSAEDNFER.A
R3/RRR3-15/2	1137.469	1138.169	-1499.376	0.291	601.366	0.294	13	0.135	R.AVSAEDNFER.A
R3/RRR3-16/2	1137.862	1138.169	-271.223	0.398	689.999	0.247	14	0.135	R.AVSAEDNFER.A
R3/RRR3-16/3	1145.574	1145.336	208.602	0.436	776.937	0.447	19	0.111	K.LSHPDHVLVK.R
R3/RRR3-16/3	1145.514	1145.336	155.706	0.439	829.791	0.423	20	0.109	K.LSHPDHVLVK.R
R3/RRR3-15/3	1145.099	1145.336	-207.987	0.454	798.747	0.395	19	0.105	K.LSHPDHVLVK.R
R3/RRR3-15/3	1145.379	1145.336	37.230	0.439	834.185	0.388	19	0.102	-.LSHPDHVLVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/3	1300.391	1301.522	-1644.273	0.363	935.112	0.340	21	0.097	K.LSHPDHVLVKR.A
R3/RRR3-16/3	1145.174	1145.336	-141.740	0.426	736.219	0.419	18	0.094	-.LSHPDHVLVK.-
R3/RRR3-15/3	1145.332	1145.336	-3.658	0.444	538.409	0.394	17	0.093	-.LSHPDHVLVK.-
R3/RRR3-17/2	1007.403	1008.107	-1696.546	0.504	2093.744	0.356	16	0.266	R.FGELDVAEK.V
R3/RRR3-17/2	1007.978	1008.107	-128.283	0.475	1914.328	0.391	16	0.249	R.FGELDVAEK.V
R3/RRR3-16/2	1007.441	1008.107	-1658.198	0.423	1941.278	0.335	16	0.239	R.FGELDVAEK.V
R3/RRR3-17/2	1008.067	1008.107	-39.487	0.487	1882.076	0.300	16	0.222	R.FGELDVAEK.V
R3/RRR3-16/2	1007.925	1008.107	-181.131	0.478	1850.050	0.286	16	0.215	R.FGELDVAEK.V
R3/RRR3-16/2	1007.583	1008.107	-1516.399	0.471	1619.092	0.314	15	0.195	R.FGELDVAEK.V
R3/RRR3-17/3	1844.575	1845.091	-824.245	0.451	1587.755	0.408	28	0.164	K.VFDEEKAPLLAAWAQR.F
R3/RRR3-17/2	1388.273	1388.590	-229.180	0.343	449.692	0.510	17	0.147	K.VLPDVDGVVEFAK.M
R3/RRR3-16/2	1456.383	1456.709	-224.683	0.401	826.475	0.358	18	0.145	K.QLLAAVETLEGALK.D
R3/RRR3-16/2	1388.194	1388.590	-286.258	0.311	331.546	0.393	16	0.139	K.VLPDVDGVVEFAK.M
R3/RRR3-17/3	1844.914	1845.091	-95.878	0.411	1641.280	0.282	30	0.137	K.VFDEEKAPLLAAWAQR.F
R3/RRR3-16/2	1456.212	1456.709	-342.756	0.294	607.620	0.402	14	0.137	-.QLLAAVETLEGALK.-
R3/RRR3-17/2	1455.422	1456.709	-1576.290	0.314	612.802	0.340	16	0.136	K.QLLAAVETLEGALK.D
R3/RRR3-17/2	1388.217	1388.590	-269.937	0.224	373.643	0.403	16	0.134	K.VLPDVDGVVEFAK.M
R3/RRR3-17/2	1845.456	1845.091	198.331	0.325	763.288	0.281	18	0.131	K.VFDEEKAPLLAAWAQR.F
R3/RRR3-16/2	1008.234	1008.107	127.009	0.225	948.350	0.049	12	0.125	R.FGELDVAEK.V
R3/RRR3-17/3	1844.842	1845.091	-135.403	0.338	1070.118	0.166	24	0.082	K.VFDEEKAPLLAAWAQR.F
R3/RRR3-17/2	1396.815	1397.561	-1253.243	0.447	1745.650	0.427	20	0.235	K.LYGSTLSWNVTR.C
R3/RRR3-17/2	1397.192	1397.561	-264.522	0.519	1705.870	0.452	19	0.235	K.LYGSTLSWNVTR.C
R3/RRR3-16/2	1398.259	1397.561	-216.248	0.494	1532.396	0.496	18	0.224	K.LYGSTLSWNVTR.C
R3/RRR3-17/2	1397.226	1397.561	-240.418	0.493	1622.459	0.444	19	0.223	K.LYGSTLSWNVTR.C
R3/RRR3-17/2	1106.966	1107.285	-288.748	0.468	1336.695	0.375	15	0.181	K.KVLEVYEAR.L
R3/RRR3-17/2	1106.718	1107.285	-1419.564	0.437	1289.764	0.389	15	0.180	K.KVLEVYEAR.L
R3/RRR3-17/2	1677.467	1677.908	-263.973	0.476	1580.895	0.267	20	0.179	K.AWWTDLMARPSSQK.V
R3/RRR3-17/2	1107.110	1107.285	-157.992	0.443	1138.058	0.395	15	0.170	K.KVLEVYEAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	978.895	979.112	-221.649	0.500	914.307	0.466	13	0.169	K.VLEVYEAR.L
R3/RRR3-17/2	978.862	979.112	-255.803	0.488	908.307	0.448	13	0.165	K.VLEVYEAR.L
R3/RRR3-16/2	978.786	979.112	-334.005	0.436	824.847	0.403	13	0.156	K.VLEVYEAR.L
R3/RRR3-16/2	978.827	979.112	-292.087	0.507	743.267	0.386	13	0.152	K.VLEVYEAR.L
R3/RRR3-16/2	978.879	979.112	-238.788	0.436	741.307	0.385	13	0.151	K.VLEVYEAR.L
R3/RRR3-17/2	978.882	979.112	-235.661	0.484	742.034	0.378	13	0.151	K.VLEVYEAR.L
R3/RRR3-16/2	979.054	979.112	-58.665	0.385	826.348	0.349	13	0.149	K.VLEVYEAR.L
R3/RRR3-17/2	1693.463	1693.908	-263.576	0.421	738.368	0.391	20	0.148	K.AWWTDLM*ARPSSQK.V
R3/RRR3-17/2	1397.081	1397.561	-344.644	0.403	904.631	0.334	16	0.146	K.LYGSTLSWNVTR.C
R3/RRR3-17/2	1693.253	1693.908	-980.475	0.448	422.692	0.418	18	0.145	K.AWWTDLM*ARPSSQK.V
R3/RRR3-17/2	1693.235	1693.908	-991.187	0.434	444.236	0.370	18	0.142	K.AWWTDLM*ARPSSQK.V
R3/RRR3-19/2	1396.445	1397.561	-1519.413	0.231	176.893	0.334	14	0.140	K.LYGSTLSWNVTR.C
R3/RRR3-17/2	978.197	979.112	-1963.485	0.307	530.103	0.325	11	0.138	-.VLEVYEAR.-
R3/RRR3-16/2	1678.806	1677.908	-61.306	0.397	589.579	0.171	13	0.123	K.AWWTDLMARPSSQK.V
R3/RRR3-24/2	1653.414	1653.905	-297.581	0.503	1538.432	0.568	23	0.240	R.TLLGATNPLASAPGTIR.G
R3/RRR3-23/2	1390.908	1391.468	-1125.383	0.475	1583.241	0.411	19	0.211	K.AGEVVNWSSENAK.W
R3/RRR3-24/2	1655.372	1653.905	283.234	0.508	1192.537	0.502	20	0.186	R.TLLGATNPLASAPGTIR.G
R3/RRR3-24/2	1654.586	1653.905	-193.181	0.448	1126.100	0.506	20	0.181	R.TLLGATNPLASAPGTIR.G
R3/RRR3-23/2	949.921	950.031	-116.081	0.433	1037.410	0.365	14	0.159	R.GDFAIDVGR.N
R3/RRR3-24/2	912.025	912.112	-95.800	0.373	917.249	0.410	13	0.157	R.GLVGPIISR.F
R3/RRR3-23/2	1390.556	1391.468	-1379.247	0.374	1196.734	0.277	18	0.153	K.AGEVVNWSSENAK.W
R3/RRR3-23/2	949.887	950.031	-151.660	0.420	1049.643	0.310	14	0.152	R.GDFAIDVGR.N
R3/RRR3-23/2	911.518	912.112	-1753.785	0.342	757.535	0.425	12	0.150	R.GLVGPIISR.F
R3/RRR3-24/2	912.219	912.112	117.493	0.319	905.267	0.344	13	0.148	R.GLVGPIISR.F
R3/RRR3-23/2	911.541	912.112	-1727.816	0.276	845.256	0.367	13	0.146	R.GLVGPIISR.F
R3/RRR3-23/2	1390.332	1391.468	-1540.712	0.335	993.471	0.294	18	0.145	K.AGEVVNWSSENAK.W
R3/RRR3-24/2	949.547	950.031	-510.302	0.363	1153.337	0.182	15	0.142	R.GDFAIDVGR.N
R3/RRR3-23/2	912.086	912.112	-27.735	0.347	608.322	0.347	12	0.141	R.GLVGPIISR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	949.895	950.031	-143.023	0.334	742.932	0.246	13	0.134	-.GDFAIDVGR.-
R3/RRR3-24/2	949.821	950.031	-220.893	0.327	548.284	0.343	12	0.131	-.GDFAIDVGR.-
R3/RRR3-23/2	1654.542	1653.905	-219.752	0.241	517.128	0.336	15	0.130	R.TLLGATNPLASAPGTIR.G
R3/RRR3-14/2	1895.295	1894.969	172.443	0.622	2445.996	0.571	28	0.399	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-14/2	1895.361	1894.969	207.320	0.607	2196.773	0.580	27	0.351	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-14/2	1895.376	1894.969	215.393	0.601	2117.793	0.574	26	0.333	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-14/2	1608.268	1608.814	-964.225	0.560	2260.912	0.475	23	0.331	K.FKDLVEEISESLAK.T
R3/RRR3-14/2	1608.221	1608.814	-993.717	0.556	2208.470	0.474	23	0.321	K.FKDLVEEISESLAK.T
R3/RRR3-14/2	1607.751	1608.814	-1287.200	0.519	2076.038	0.456	23	0.293	K.FKDLVEEISESLAK.T
R3/RRR3-14/2	1316.211	1315.495	-216.240	0.528	1488.160	0.547	19	0.232	K.ICANHLVASTTK.M
R3/RRR3-14/2	1316.158	1315.495	-256.808	0.523	1419.459	0.551	19	0.224	K.ICANHLVASTTK.M
R3/RRR3-14/2	1315.123	1315.495	-283.357	0.522	1438.112	0.507	19	0.217	K.ICANHLVASTTK.M
R3/RRR3-14/3	1895.031	1894.969	32.807	0.504	1608.713	0.352	31	0.151	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-14/3	1894.743	1894.969	-119.753	0.490	1342.989	0.412	31	0.140	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-14/3	1894.904	1894.969	-34.163	0.521	1220.479	0.420	29	0.131	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-14/3	1765.565	1765.898	-188.743	0.474	1143.572	0.428	31	0.126	K.KSEEVATKEESTEAVK.E
R3/RRR3-14/3	1765.996	1765.898	55.691	0.505	986.941	0.463	30	0.123	K.KSEEVATKEESTEAVK.E
R3/RRR3-14/3	1608.740	1608.814	-46.138	0.549	1362.696	0.334	28	0.122	K.FKDLVEEISESLAK.T
R3/RRR3-14/3	1609.148	1608.814	208.159	0.508	1247.233	0.330	28	0.113	K.FKDLVEEISESLAK.T
R3/RRR3-14/3	1608.567	1608.814	-154.036	0.465	917.023	0.394	25	0.106	-.FKDLVEEISESLAK.-
R3/RRR3-14/3	1764.985	1765.898	-1087.143	0.383	802.535	0.375	27	0.100	K.KSEEVATKEESTEAVK.E
R3/RRR3-16/3	1894.757	1894.969	-112.483	0.335	923.068	0.219	26	0.086	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-16/3	1894.444	1894.969	-807.428	0.282	765.372	0.185	25	0.083	K.TEGKETEEDSSAAGLLEK.L
R3/RRR3-17/2	1688.473	1687.870	-235.712	0.527	1375.048	0.564	24	0.221	R.DAVTPLSETEAVDLVK.D
R3/RRR3-17/2	1687.375	1687.870	-294.131	0.472	1330.650	0.541	24	0.211	R.DAVTPLSETEAVDLVK.D
R3/RRR3-17/2	1688.005	1687.870	80.250	0.502	1337.916	0.529	24	0.210	R.DAVTPLSETEAVDLVK.D
R3/RRR3-17/2	1051.058	1051.264	-197.054	0.477	1142.334	0.412	16	0.172	K.SPSPLLLPAR.D
R3/RRR3-17/2	1051.121	1051.264	-137.170	0.467	1103.749	0.428	16	0.172	K.SPSPLLLPAR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1050.550	1051.264	-1636.715	0.429	1014.545	0.447	15	0.168	K.SPSPLLLPAR.D
R3/RRR3-18/2	1051.367	1051.264	97.867	0.392	1061.896	0.429	15	0.168	K.SPSPLLLPAR.D
R3/RRR3-17/2	995.532	996.056	-1535.925	0.367	749.435	0.465	13	0.154	K.DVFASATER.D
R3/RRR3-17/2	1624.580	1624.726	-90.333	0.384	645.317	0.485	16	0.148	K.GCVFTYDAVGSYER.T
R3/RRR3-17/2	995.782	996.056	-276.232	0.267	932.338	0.348	15	0.147	K.DVFASATER.D
R3/RRR3-17/2	995.574	996.056	-485.849	0.247	801.668	0.315	14	0.139	K.DVFASATER.D
R3/RRR3-17/2	1623.476	1624.726	-1390.044	0.195	474.905	0.306	14	0.127	K.GCVFTYDAVGSYER.T
R3/RRR3-9/2	1886.556	1887.141	-843.019	0.509	1951.695	0.499	23	0.284	R.AVCMISNSTSVVEVFSR.I
R3/RRR3-9/2	1600.966	1599.804	101.132	0.555	1237.226	0.583	18	0.209	R.TIQFVDWCPTGFK.C
R3/RRR3-9/2	1599.320	1599.804	-304.125	0.508	1283.033	0.554	18	0.208	R.TIQFVDWCPTGFK.C
R3/RRR3-9/2	1598.942	1599.804	-1168.175	0.399	994.386	0.519	16	0.173	R.TIQFVDWCPTGFK.C
R3/RRR3-5/2	1601.084	1599.804	175.378	0.381	661.662	0.332	14	0.137	R.TIQFVDWCPTGFK.C
R3/RRR3-7/2	1601.337	1599.804	-292.808	0.351	766.405	0.284	14	0.135	R.TIQFVDWCPTGFK.C
R3/RRR3-3/3	1908.935	1909.022	-46.054	0.501	2546.112	0.499	35	0.368	K.TQEKDADAM*QVDNAVEK.K
R3/RRR3-3/3	1908.338	1909.022	-885.201	0.494	2389.790	0.436	35	0.304	K.TQEKDADAM*QVDNAVEK.K
R3/RRR3-4/3	1908.374	1909.022	-866.611	0.420	1993.484	0.485	30	0.252	K.TQEKDADAM*QVDNAVEK.K
R3/RRR3-4/3	1908.684	1909.022	-178.075	0.480	1584.194	0.459	30	0.178	K.TQEKDADAM*QVDNAVEK.K
R3/RRR3-3/3	1907.960	1909.022	-1084.436	0.469	1443.795	0.408	29	0.149	K.TQEKDADAM*QVDNAVEK.K
R3/RRR3-2/2	1423.223	1422.501	-195.827	0.431	929.116	0.306	18	0.142	K.DADAM*QVDNAVEK.K
R3/RRR3-11/2	1168.767	1169.442	-1437.749	0.435	1601.098	0.495	18	0.233	R.ALVDVLAALKR.A
R3/RRR3-11/2	1151.121	1150.310	-164.608	0.520	1254.371	0.546	18	0.206	K.SPLTTVYAAAR.A
R3/RRR3-11/2	1013.300	1013.256	43.364	0.546	1240.195	0.509	17	0.199	R.ALVDVLAALK.R
R3/RRR3-12/2	1012.721	1013.256	-1520.495	0.473	1175.957	0.492	16	0.189	R.ALVDVLAALK.R
R3/RRR3-11/2	1013.043	1013.256	-211.277	0.519	1099.871	0.514	16	0.187	R.ALVDVLAALK.R
R3/RRR3-11/2	1013.080	1013.256	-173.804	0.542	1106.457	0.507	16	0.186	R.ALVDVLAALK.R
R3/RRR3-12/2	1012.532	1013.256	-1708.146	0.479	1145.704	0.478	16	0.184	R.ALVDVLAALK.R
R3/RRR3-11/2	1168.409	1169.442	-1745.011	0.431	1072.186	0.490	17	0.178	R.ALVDVLAALKR.A
R3/RRR3-16/2	1150.422	1150.310	97.636	0.443	969.877	0.450	16	0.166	K.SPLTTVYAAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1151.287	1150.310	-19.633	0.425	849.384	0.398	16	0.154	K.SPLTTVYAAAR.A
R3/RRR3-12/2	1150.292	1150.310	-15.392	0.288	582.373	0.320	14	0.137	K.SPLTTVYAAAR.A
R3/RRR3-12/3	1523.791	1523.718	48.192	0.382	1458.633	0.365	27	0.136	R.EVVGDRDFFIVAR.T
R3/RRR3-9/2	1151.436	1150.310	110.310	0.284	429.432	0.348	12	0.135	-.SPLTTVYAAAR.-
R3/RRR3-12/2	1150.540	1150.310	200.850	0.213	464.915	0.275	12	0.132	K.SPLTTVYAAAR.A
R3/RRR3-1/2	1149.482	1150.310	-1595.014	0.273	257.028	0.309	11	0.131	-.SPLTTVYAAAR.-
R3/RRR3-11/3	1523.800	1523.718	54.218	0.398	1080.413	0.394	23	0.115	R.EVVGDRDFFIVAR.T
R3/RRR3-11/3	1523.891	1523.718	113.871	0.360	877.110	0.357	22	0.100	R.EVVGDRDFFIVAR.T
R3/RRR3-11/3	1523.129	1523.718	-1045.825	0.350	823.305	0.366	20	0.099	-.EVVGDRDFFIVAR.-
R3/RRR3-15/2	1634.235	1634.812	-968.159	0.565	2456.482	0.437	22	0.357	K.VLNFAIDDSILEER.I
R3/RRR3-15/2	1635.432	1634.812	-233.100	0.602	2463.577	0.417	22	0.349	K.VLNFAIDDSILEER.I
R3/RRR3-15/2	1595.220	1595.779	-980.325	0.512	1900.450	0.595	23	0.303	K.VPGVDDVTGEPLIQR.K
R3/RRR3-15/2	1595.257	1595.779	-956.816	0.513	1909.146	0.571	23	0.298	K.VPGVDDVTGEPLIQR.K
R3/RRR3-15/2	1595.289	1595.779	-308.117	0.488	1828.398	0.602	23	0.293	K.VPGVDDVTGEPLIQR.K
R3/RRR3-15/2	1022.019	1022.181	-158.986	0.480	1180.430	0.495	14	0.189	K.GFILDGFPR.T
R3/RRR3-15/2	1022.073	1022.181	-106.269	0.502	1257.091	0.435	14	0.185	K.GFILDGFPR.T
R3/RRR3-15/2	1022.036	1022.181	-143.050	0.443	1163.193	0.452	14	0.180	K.GFILDGFPR.T
R3/RRR3-15/2	1344.192	1343.463	-202.357	0.308	188.891	0.484	12	0.138	-.QTEPVIDYYSK.-
R3/RRR3-15/2	1343.357	1343.463	-79.258	0.260	152.874	0.438	11	0.135	-.QTEPVIDYYSK.-
R3/RRR3-15/2	1021.988	1022.181	-190.259	0.230	350.849	0.350	11	0.134	-.GFILDGFPR.-
R3/RRR3-15/2	1342.992	1343.463	-352.325	0.252	125.359	0.274	11	0.127	-.QTEPVIDYYSK.-
R3/RRR3-17/2	1582.345	1582.850	-954.024	0.570	4206.607	0.658	31	1.000	R.SPPVAGGAVAAGGAGALMK.G
R3/RRR3-17/2	1599.257	1598.849	255.575	0.641	3750.122	0.683	30	0.835	R.SPPVAGGAVAAGGAGALM*K.G
R3/RRR3-17/3	1295.656	1295.473	141.631	0.465	1725.475	0.440	25	0.186	R.DRGPLPASQVVR.D
R3/RRR3-16/2	1024.102	1024.199	-95.119	0.432	577.033	0.591	15	0.166	R.GPLPASQVVR.D
R3/RRR3-17/2	1023.878	1024.199	-313.854	0.463	549.425	0.574	15	0.164	R.GPLPASQVVR.D
R3/RRR3-16/2	1023.871	1024.199	-321.270	0.474	472.344	0.598	14	0.164	R.GPLPASQVVR.D
R3/RRR3-17/2	1024.038	1024.199	-157.537	0.406	635.295	0.534	16	0.161	R.GPLPASQVVR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/3	1295.791	1295.473	245.648	0.451	1386.128	0.480	24	0.157	R.DRGPLPASQVVR.D
R3/RRR3-16/2	1024.054	1024.199	-141.633	0.432	356.995	0.563	13	0.156	R.GPLPASQVVR.D
R3/RRR3-17/2	1023.588	1024.199	-1578.393	0.356	526.496	0.527	14	0.153	R.GPLPASQVVR.D
R3/RRR3-17/3	1295.057	1295.473	-322.454	0.410	1422.613	0.423	24	0.147	R.DRGPLPASQVVR.D
R3/RRR3-17/3	1598.656	1598.849	-121.108	0.418	938.728	0.508	31	0.125	R.SPPVAGGAVAAGGAGALM*K.G
R3/RRR3-17/3	1295.596	1295.473	95.426	0.381	1244.388	0.301	24	0.108	R.DRGPLPASQVVR.D
R3/RRR3-16/3	1295.008	1295.473	-360.474	0.369	718.630	0.363	24	0.099	R.DRGPLPASQVVR.D
R3/RRR3-16/3	1295.349	1295.473	-95.817	0.334	499.286	0.321	21	0.097	R.DRGPLPASQVVR.D
R3/RRR3-25/2	955.049	955.154	-110.232	0.420	879.462	0.482	13	0.166	R.YSM*VITPK.N
R3/RRR3-25/2	954.982	955.154	-179.728	0.393	964.737	0.424	13	0.162	R.YSM*VITPK.N
R3/RRR3-25/2	1247.982	1248.457	-381.404	0.307	510.597	0.509	14	0.144	K.TIHFWAPTFK.W
R3/RRR3-25/2	1617.996	1618.637	-1017.301	0.311	944.295	0.445	20	0.118	K.DYFSDEKDAAASLEG.-
R3/RRR3-25/3	1843.631	1844.103	-256.891	0.389	791.620	0.478	25	0.114	K.WGISIANVADFAKPPEK.I
R3/RRR3-25/3	1844.695	1844.103	-222.030	0.470	592.921	0.439	24	0.104	K.WGISIANVADFAKPPEK.I
R3/RRR3-25/3	1843.867	1844.103	-128.270	0.366	469.715	0.359	20	0.092	-.WGISIANVADFAKPPEK.-
R3/RRR3-25/3	1844.108	1844.103	2.907	0.301	716.385	0.288	23	0.088	-.WGISIANVADFAKPPEK.-
R3/RRR3-25/2	1618.348	1618.637	-179.046	0.447	794.464	0.482	18	0.077	K.DYFSDEKDAAASLEG.-
R3/RRR3-25/2	1617.382	1618.637	-1398.006	0.216	619.449	0.412	17	0.045	K.DYFSDEKDAAASLEG.-
R3/RRR3-19/2	1503.146	1502.650	330.977	0.579	1507.445	0.562	20	0.237	R.EIENGILWEVDGK.W
R3/RRR3-19/2	1502.369	1502.650	-187.979	0.478	1360.554	0.541	20	0.215	R.EIENGILWEVDGK.W
R3/RRR3-19/2	1769.479	1769.934	-258.065	0.520	1319.284	0.548	23	0.211	K.DGATDPTFLYFSHGLK.E
R3/RRR3-19/2	1769.570	1769.934	-206.574	0.524	1284.602	0.518	22	0.200	K.DGATDPTFLYFSHGLK.E
R3/RRR3-19/2	1502.294	1502.650	-238.110	0.518	1135.370	0.534	18	0.190	R.EIENGILWEVDGK.W
R3/RRR3-19/2	1501.755	1502.650	-1265.705	0.392	1187.759	0.500	19	0.188	R.EIENGILWEVDGK.W
R3/RRR3-19/2	1769.455	1769.934	-271.907	0.506	1139.212	0.504	22	0.185	K.DGATDPTFLYFSHGLK.E
R3/RRR3-19/2	1769.628	1769.934	-173.634	0.499	1084.511	0.492	21	0.177	K.DGATDPTFLYFSHGLK.E
R3/RRR3-19/2	1064.043	1064.217	-163.696	0.495	1180.263	0.356	15	0.166	K.VVDIVDTFR.L
R3/RRR3-18/2	1771.327	1769.934	222.390	0.458	624.488	0.457	18	0.147	K.DGATDPTFLYFSHGLK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1063.604	1064.217	-1520.736	0.375	830.128	0.279	14	0.141	K.VVDIVDTFR.L
R3/RRR3-19/2	1365.167	1365.514	-254.853	0.469	781.376	0.316	15	0.140	K.LDAEKQEEFKK.N
R3/RRR3-19/2	1063.571	1064.217	-1552.211	0.372	794.549	0.255	14	0.137	-.VVDIVDTFR.-
R3/RRR3-19/2	1064.092	1064.217	-117.779	0.347	646.290	0.242	12	0.133	-.VVDIVDTFR.-
R3/RRR3-19/2	1364.609	1365.514	-1399.730	0.407	697.441	0.217	15	0.131	K.LDAEKQEEFKK.N
R3/RRR3-19/2	1365.056	1365.514	-336.674	0.432	560.117	0.223	14	0.128	-.LDAEKQEEFKK.-
R3/RRR3-17/2	1389.136	1389.573	-315.943	0.525	1876.473	0.464	19	0.261	K.VIACIGETLEQR.E
R3/RRR3-17/2	1390.158	1389.573	-299.857	0.545	1554.973	0.507	19	0.229	K.VIACIGETLEQR.E
R3/RRR3-17/2	1453.052	1452.613	302.672	0.499	1529.865	0.504	20	0.224	R.EAGTTM*EVVAAQTK.A
R3/RRR3-17/2	1603.281	1602.773	-307.650	0.546	1326.321	0.596	23	0.223	K.WLATNVSPAVAESTR.I
R3/RRR3-16/2	1451.611	1452.613	-1383.427	0.458	1553.026	0.483	20	0.222	R.EAGTTM*EVVAAQTK.A
R3/RRR3-17/2	1389.071	1389.573	-1085.091	0.525	1569.909	0.467	19	0.222	K.VIACIGETLEQR.E
R3/RRR3-17/2	1451.969	1452.613	-1136.015	0.467	1429.897	0.490	19	0.209	R.EAGTTM*EVVAAQTK.A
R3/RRR3-17/2	1452.104	1452.613	-1042.487	0.464	1435.760	0.486	19	0.209	R.EAGTTM*EVVAAQTK.A
R3/RRR3-17/2	1602.263	1602.773	-945.450	0.532	1156.896	0.593	22	0.205	K.WLATNVSPAVAESTR.I
R3/RRR3-16/2	1452.074	1452.613	-1063.082	0.467	1429.781	0.446	19	0.200	R.EAGTTM*EVVAAQTK.A
R3/RRR3-16/2	1452.162	1452.613	-311.533	0.481	1378.731	0.462	19	0.198	R.EAGTTM*EVVAAQTK.A
R3/RRR3-17/2	1452.246	1452.613	-253.848	0.491	1319.921	0.477	19	0.195	R.EAGTTM*EVVAAQTK.A
R3/RRR3-16/2	1602.221	1602.773	-971.992	0.527	1080.793	0.546	21	0.188	K.WLATNVSPAVAESTR.I
R3/RRR3-17/2	1049.994	1050.233	-228.854	0.464	1308.853	0.421	16	0.187	K.VAYALSQGIK.V
R3/RRR3-17/2	1050.046	1050.233	-178.587	0.456	1281.362	0.426	16	0.185	K.VAYALSQGIK.V
R3/RRR3-17/2	1603.340	1602.773	-271.290	0.530	1022.720	0.560	20	0.185	K.WLATNVSPAVAESTR.I
R3/RRR3-17/2	1049.570	1050.233	-1589.832	0.426	1341.826	0.381	16	0.182	K.VAYALSQGIK.V
R3/RRR3-16/2	1389.204	1389.573	-266.572	0.455	1086.764	0.474	17	0.176	K.VIACIGETLEQR.E
R3/RRR3-17/2	1388.908	1389.573	-1202.815	0.398	1176.945	0.404	18	0.172	K.VIACIGETLEQR.E
R3/RRR3-17/2	1388.388	1389.573	-1578.761	0.282	1307.160	0.303	18	0.164	K.VIACIGETLEQR.E
R3/RRR3-17/2	1388.522	1389.573	-1482.143	0.316	1103.016	0.359	17	0.159	K.VIACIGETLEQR.E
R3/RRR3-15/3	1770.678	1770.922	-138.620	0.577	2414.132	0.545	35	0.351	K.KGENDLPGLTDTEKPR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/3	1771.887	1770.922	-19.778	0.624	2255.225	0.585	34	0.333	K.KGENDLPGLTDTEKPR.M
R3/RRR3-14/3	1771.205	1770.922	160.150	0.627	2081.063	0.557	33	0.286	K.KGENDLPGLTDTEKPR.M
R3/RRR3-15/3	1770.542	1770.922	-215.389	0.603	2085.281	0.539	31	0.283	K.KGENDLPGLTDTEKPR.M
R3/RRR3-14/3	1770.782	1770.922	-79.287	0.589	1838.557	0.549	31	0.241	K.KGENDLPGLTDTEKPR.M
R3/RRR3-15/3	1770.295	1770.922	-921.940	0.593	1629.318	0.575	30	0.218	K.KGENDLPGLTDTEKPR.M
R3/RRR3-17/3	1789.077	1788.082	-3.129	0.568	2549.574	0.476	33	0.356	R.NKFDPLWNSLVIGGVK.K
R3/RRR3-17/3	1787.943	1788.082	-78.184	0.587	1937.016	0.462	30	0.228	R.NKFDPLWNSLVIGGVK.K
R3/RRR3-17/2	1642.375	1641.889	296.881	0.490	1368.816	0.530	25	0.214	R.TQYPYVTGSSIIALK.Y
R3/RRR3-17/2	1789.323	1788.082	135.031	0.565	1242.501	0.525	23	0.198	R.NKFDPLWNSLVIGGVK.K
R3/RRR3-17/2	1641.469	1641.889	-256.858	0.440	1210.410	0.527	24	0.197	R.TQYPYVTGSSIIALK.Y
R3/RRR3-17/2	1788.615	1788.082	-262.286	0.554	1220.882	0.517	23	0.195	R.NKFDPLWNSLVIGGVK.K
R3/RRR3-17/2	1050.239	1050.313	-70.718	0.448	1400.963	0.386	14	0.190	K.CLLVLLYR.D
R3/RRR3-17/2	1787.489	1788.082	-894.262	0.487	1044.778	0.520	22	0.180	R.NKFDPLWNSLVIGGVK.K
R3/RRR3-17/2	1050.129	1050.313	-175.192	0.493	1167.049	0.370	13	0.168	K.CLLVLLYR.D
R3/RRR3-17/2	1640.695	1641.889	-1341.725	0.314	1051.625	0.441	22	0.165	R.TQYPYVTGSSIIALK.Y
R3/RRR3-17/2	1654.538	1654.885	-209.910	0.478	941.126	0.405	20	0.155	K.ITTEGATIYPPYSLK.T
R3/RRR3-17/2	1049.493	1050.313	-1739.160	0.341	783.205	0.395	10	0.146	K.CLLVLLYR.D
R3/RRR3-17/2	1654.535	1654.885	-212.131	0.455	806.118	0.369	19	0.145	K.ITTEGATIYPPYSLK.T
R3/RRR3-17/2	1654.348	1654.885	-931.818	0.431	574.206	0.354	16	0.136	K.ITTEGATIYPPYSLK.T
R3/RRR3-17/3	1787.007	1788.082	-1164.973	0.326	842.777	0.256	23	0.087	R.NKFDPLWNSLVIGGVK.K
R3/RRR3-19/2	1214.928	1214.437	405.968	0.517	2143.419	0.369	18	0.277	R.GSDVIIVLVGNK.T
R3/RRR3-19/2	1215.451	1214.437	12.127	0.507	2025.288	0.412	18	0.271	R.GSDVIIVLVGNK.T
R3/RRR3-19/2	1465.058	1465.633	-1078.285	0.384	1868.889	0.491	20	0.268	R.DSSVAVIVFDVASR.Q
R3/RRR3-19/2	1466.273	1465.633	-246.632	0.473	1631.494	0.485	20	0.233	R.DSSVAVIVFDVASR.Q
R3/RRR3-19/2	1464.614	1465.633	-1382.569	0.367	1415.039	0.427	18	0.194	R.DSSVAVIVFDVASR.Q
R3/RRR3-18/2	1317.144	1317.432	-219.619	0.476	921.063	0.383	16	0.155	R.LQLWDTAGQER.F
R3/RRR3-17/2	1317.218	1317.432	-163.278	0.399	848.548	0.411	15	0.154	R.LQLWDTAGQER.F
R3/RRR3-17/2	1317.149	1317.432	-216.086	0.415	921.250	0.352	16	0.151	R.LQLWDTAGQER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1461.655	1460.722	-45.955	0.411	611.472	0.499	21	0.151	K.IAAALPGMETLSSAK.Q
R3/RRR3-18/2	1316.966	1317.432	-355.569	0.419	866.542	0.377	15	0.150	-.LQLWDTAGQER.-
R3/RRR3-18/2	1317.172	1317.432	-198.328	0.468	867.183	0.355	15	0.147	-.LQLWDTAGQER.-
R3/RRR3-20/2	1317.207	1317.432	-171.459	0.372	746.326	0.340	15	0.144	R.LQLWDTAGQER.F
R3/RRR3-17/2	1316.560	1317.432	-1426.542	0.320	835.641	0.314	15	0.143	R.LQLWDTAGQER.F
R3/RRR3-20/2	1213.650	1214.437	-1476.281	0.310	731.764	0.365	15	0.141	R.GSDVIIVLVGNK.T
R3/RRR3-19/2	1317.079	1317.432	-268.992	0.356	829.196	0.260	15	0.139	R.LQLWDTAGQER.F
R3/RRR3-20/2	1317.204	1317.432	-174.249	0.386	866.079	0.256	15	0.138	-.LQLWDTAGQER.-
R3/RRR3-20/2	1317.111	1317.432	-244.909	0.358	835.539	0.250	15	0.137	-.LQLWDTAGQER.-
R3/RRR3-20/2	1317.017	1317.432	-316.417	0.300	545.389	0.269	13	0.136	R.LQLWDTAGQER.F
R3/RRR3-20/2	1317.171	1317.432	-198.979	0.297	514.522	0.261	12	0.135	R.LQLWDTAGQER.F
R3/RRR3-20/2	1316.869	1317.432	-1190.514	0.351	717.063	0.233	14	0.135	R.LQLWDTAGQER.F
R3/RRR3-19/2	1316.857	1317.432	-1199.544	0.378	782.901	0.212	15	0.132	-.LQLWDTAGQER.-
R3/RRR3-19/2	1316.686	1317.432	-1330.256	0.338	813.681	0.162	15	0.130	-.LQLWDTAGQER.-
R3/RRR3-19/2	1316.204	1317.432	-1698.461	0.289	401.364	0.285	12	0.129	-.LQLWDTAGQER.-
R3/RRR3-15/2	1618.210	1618.813	-993.030	0.556	2419.519	0.408	22	0.338	K.VLNFAIDDAILEER.I
R3/RRR3-15/2	1619.984	1618.813	105.991	0.566	2309.669	0.462	21	0.334	K.VLNFAIDDAILEER.I
R3/RRR3-15/2	1619.000	1618.813	116.265	0.582	2331.870	0.440	22	0.331	K.VLNFAIDDAILEER.I
R3/RRR3-15/2	1610.902	1611.778	-1168.471	0.506	1412.600	0.491	21	0.208	K.TPGLDDVTGEPLIQR.K
R3/RRR3-15/2	1611.345	1611.778	-269.562	0.493	1353.480	0.498	21	0.203	K.TPGLDDVTGEPLIQR.K
R3/RRR3-15/2	1611.363	1611.778	-258.769	0.510	1306.473	0.492	21	0.197	K.TPGLDDVTGEPLIQR.K
R3/RRR3-14/2	1612.262	1611.778	300.983	0.476	1280.087	0.471	20	0.190	K.TPGLDDVTGEPLIQR.K
R3/RRR3-15/2	1096.412	1097.326	-1751.727	0.344	509.555	0.457	12	0.141	-.VILVGPPGCGK.-
R3/RRR3-15/2	1096.997	1097.326	-300.859	0.371	647.237	0.312	13	0.136	R.VILVGPPGCGK.G
R3/RRR3-15/2	1096.575	1097.326	-1601.738	0.224	577.253	0.193	13	0.128	R.VILVGPPGCGK.G
R3/RRR3-2/2	1612.160	1611.778	237.132	0.260	513.930	0.208	14	0.128	-.TPGLDDVTGEPLIQR.-
R3/RRR3-13/2	1751.395	1752.092	-971.694	0.566	1809.751	0.532	26	0.268	K.AVVAGASGGIGQPLSLLLK.L
R3/RRR3-13/2	1751.681	1752.092	-235.315	0.552	1819.014	0.483	25	0.255	K.AVVAGASGGIGQPLSLLLK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1751.630	1752.092	-264.469	0.534	1541.081	0.488	24	0.219	K.AVVAGASGGIGQPLSLLLK.L
R3/RRR3-13/2	1211.827	1211.433	326.381	0.423	1279.109	0.336	16	0.166	K.GLIEIAAEVAPK.A
R3/RRR3-13/2	1233.289	1234.470	-1773.038	0.409	968.095	0.367	17	0.155	R.LFGVTTLDIVR.A
R3/RRR3-13/2	1234.275	1234.470	-158.478	0.374	1032.269	0.244	15	0.141	R.LFGVTTLDIVR.A
R3/RRR3-13/2	1234.189	1234.470	-228.131	0.302	689.920	0.268	13	0.133	R.LFGVTTLDIVR.A
R3/RRR3-25/2	1079.902	1080.176	-254.488	0.514	1693.984	0.564	19	0.263	R.LAGSSAAAFER.C
R3/RRR3-25/2	1079.518	1080.176	-1540.509	0.440	1644.179	0.560	19	0.254	R.LAGSSAAAFER.C
R3/RRR3-24/2	1079.992	1080.176	-170.688	0.547	1609.846	0.569	19	0.253	R.LAGSSAAAFER.C
R3/RRR3-25/2	1081.009	1080.176	-155.124	0.524	1558.042	0.570	19	0.247	R.LAGSSAAAFER.C
R3/RRR3-24/2	1079.783	1080.176	-365.298	0.445	1437.432	0.561	18	0.227	R.LAGSSAAAFER.C
R3/RRR3-24/2	1079.721	1080.176	-422.925	0.502	1394.752	0.553	18	0.222	R.LAGSSAAAFER.C
R3/RRR3-25/2	1734.404	1734.963	-901.867	0.506	1167.779	0.430	19	0.172	R.VGGPCGYGVCYLYLR.R
R3/RRR3-25/2	1734.281	1734.963	-972.882	0.485	1092.089	0.440	19	0.169	R.VGGPCGYGVCYLYLR.R
R3/RRR3-25/2	1734.275	1734.963	-976.132	0.498	1004.874	0.445	18	0.163	R.VGGPCGYGVCYLYLR.R
R3/RRR3-25/2	1200.326	1199.374	-40.251	0.483	747.424	0.374	13	0.146	R.TCWYTVQIK.T
R3/RRR3-25/2	1472.505	1473.569	-1406.008	0.232	813.270	0.441	15	0.142	R.TSDAVSLAFGDAYR.N
R3/RRR3-24/2	1735.521	1734.963	-255.495	0.449	725.025	0.357	15	0.138	R.VGGPCGYGVCYLYLR.R
R3/RRR3-25/2	1198.368	1199.374	-1678.807	0.308	701.408	0.293	12	0.135	R.TCWYTVQIK.T
R3/RRR3-24/2	1733.757	1734.963	-1276.627	0.359	607.444	0.203	14	0.126	-.VGGPCGYGVCYLYLR.-
R3/RRR3-16/2	1669.299	1669.904	-964.399	0.573	1346.962	0.569	22	0.220	R.RVEPYVAYGYPNLK.S
R3/RRR3-16/2	1669.335	1669.904	-942.815	0.548	1319.259	0.535	22	0.210	R.RVEPYVAYGYPNLK.S
R3/RRR3-16/2	1514.103	1513.718	254.996	0.463	1177.864	0.510	21	0.192	R.VEPYVAYGYPNLK.S
R3/RRR3-16/2	1670.314	1669.904	245.882	0.575	1190.450	0.508	21	0.191	R.RVEPYVAYGYPNLK.S
R3/RRR3-16/2	1514.245	1513.718	-313.449	0.484	1197.630	0.465	21	0.185	R.VEPYVAYGYPNLK.S
R3/RRR3-17/2	1669.213	1669.904	-1016.527	0.520	931.905	0.505	19	0.170	R.RVEPYVAYGYPNLK.S
R3/RRR3-16/2	1513.120	1513.718	-1059.248	0.362	1058.705	0.431	21	0.167	R.VEPYVAYGYPNLK.S
R3/RRR3-17/2	1669.382	1669.904	-914.625	0.531	791.494	0.518	18	0.164	R.RVEPYVAYGYPNLK.S
R3/RRR3-17/2	1668.818	1669.904	-1254.258	0.499	895.991	0.470	19	0.163	R.RVEPYVAYGYPNLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1267.039	1266.429	-308.508	0.463	958.492	0.414	15	0.161	K.EANNFLWPFK.L
R3/RRR3-16/2	1266.144	1266.429	-225.661	0.333	965.538	0.369	15	0.154	K.EANNFLWPFK.L
R3/RRR3-16/2	1012.896	1013.213	-313.812	0.305	729.814	0.394	16	0.146	K.AAVVPESVLK.K
R3/RRR3-17/2	1266.314	1266.429	-90.945	0.300	753.730	0.316	14	0.141	K.EANNFLWPFK.L
R3/RRR3-16/2	1267.114	1266.429	-248.968	0.348	716.636	0.304	13	0.139	K.EANNFLWPFK.L
R3/RRR3-17/2	1265.986	1266.429	-350.448	0.220	545.878	0.424	12	0.138	K.EANNFLWPFK.L
R3/RRR3-16/2	1012.637	1013.213	-1560.580	0.244	506.816	0.387	14	0.136	-.AAVVPESVLK.-
R3/RRR3-16/2	1012.549	1013.213	-1648.262	0.233	483.229	0.320	13	0.134	K.AAVVPESVLK.K
R3/RRR3-17/2	1012.485	1013.213	-1711.853	0.241	374.548	0.323	12	0.129	-.AAVVPESVLK.-
R3/RRR3-17/2	1266.086	1266.429	-271.122	0.161	564.184	0.172	11	0.129	-.EANNFLWPFK.-
R3/RRR3-16/2	1266.370	1266.429	-46.564	0.129	613.538	0.123	12	0.127	K.EANNFLWPFK.L
R3/RRR3-17/3	1670.382	1669.904	286.544	0.477	905.309	0.394	23	0.106	R.RVEPYVAYGYPNLK.S
R3/RRR3-26/2	1350.029	1350.542	-1124.180	0.367	1559.466	0.551	19	0.237	K.ETVASAPVVVYSK.S
R3/RRR3-26/2	1350.000	1350.542	-1146.061	0.365	1575.328	0.499	19	0.228	K.ETVASAPVVVYSK.S
R3/RRR3-26/2	1351.111	1350.542	-319.760	0.483	1224.337	0.606	18	0.212	K.ETVASAPVVVYSK.S
R3/RRR3-26/2	1542.085	1541.814	175.815	0.453	908.844	0.534	22	0.173	K.LVPLLTEAGAIASSAK.T
R3/RRR3-26/2	1542.175	1541.814	234.476	0.441	930.903	0.452	21	0.162	K.LVPLLTEAGAIASSAK.T
R3/RRR3-26/2	1281.892	1282.513	-1268.367	0.381	832.357	0.390	16	0.148	K.KLFEQLGATFK.A
R3/RRR3-25/2	1541.633	1541.814	-117.908	0.355	804.606	0.390	19	0.146	K.LVPLLTEAGAIASSAK.T
R3/RRR3-26/2	1541.385	1541.814	-279.493	0.338	684.350	0.389	19	0.142	K.LVPLLTEAGAIASSAK.T
R3/RRR3-25/2	1540.859	1541.814	-1272.837	0.244	847.945	0.230	21	0.134	K.LVPLLTEAGAIASSAK.T
R3/RRR3-26/3	1742.324	1742.862	-885.442	0.463	1059.560	0.277	25	0.094	K.HIGGCDDTLVLNNEGK.L
R3/RRR3-16/2	1750.372	1750.953	-905.740	0.512	2190.684	0.538	20	0.340	K.DLVVDMTNFYNQYK.S
R3/RRR3-16/2	1791.286	1791.093	107.944	0.561	1881.109	0.487	21	0.266	K.VDLSDCGPM*VLDVLLK.I
R3/RRR3-16/2	1790.400	1791.093	-948.756	0.499	1913.776	0.443	22	0.261	K.VDLSDCGPM*VLDVLLK.I
R3/RRR3-16/2	1790.455	1791.093	-917.544	0.529	1765.568	0.460	21	0.242	K.VDLSDCGPM*VLDVLLK.I
R3/RRR3-16/2	1448.305	1448.606	-208.268	0.408	906.792	0.338	16	0.146	K.IKNEQDPSLTFR.R
R3/RRR3-16/2	1508.167	1508.660	-327.539	0.362	564.615	0.437	17	0.144	R.WDPDSPSTKPHLK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1508.242	1508.660	-277.842	0.328	559.284	0.365	17	0.138	R.WDPDSPSTKPHLK.D
R3/RRR3-16/2	1448.377	1448.606	-158.637	0.420	595.394	0.260	14	0.128	-.IKNEQDPSLTFR.-
R3/RRR3-16/3	1447.932	1448.606	-1159.754	0.424	932.123	0.382	22	0.104	K.IKNEQDPSLTFR.R
R3/RRR3-6/2	1375.922	1375.492	313.351	0.535	1611.362	0.464	17	0.226	K.NSLENYAYNMR.N
R3/RRR3-6/2	1374.835	1375.492	-1209.249	0.476	1588.955	0.465	17	0.224	K.NSLENYAYNMR.N
R3/RRR3-6/2	1374.935	1375.492	-1136.052	0.471	1571.801	0.438	17	0.216	K.NSLENYAYNMR.N
R3/RRR3-6/2	1392.286	1391.492	-148.280	0.562	1311.181	0.508	17	0.203	K.NSLENYAYNM*R.N
R3/RRR3-6/2	1391.109	1391.492	-276.026	0.508	1357.375	0.473	16	0.199	K.NSLENYAYNM*R.N
R3/RRR3-6/2	1390.875	1391.492	-1166.040	0.496	1328.660	0.421	17	0.188	K.NSLENYAYNM*R.N
R3/RRR3-11/2	1578.206	1577.807	254.026	0.579	2838.304	0.597	25	0.506	R.IAVLGASGYTGAEIVR.L
R3/RRR3-11/2	1577.394	1577.807	-262.246	0.508	2934.077	0.517	25	0.499	R.IAVLGASGYTGAEIVR.L
R3/RRR3-11/2	1577.325	1577.807	-306.114	0.531	2593.976	0.545	24	0.425	R.IAVLGASGYTGAEIVR.L
R3/RRR3-11/2	1992.653	1993.205	-781.298	0.525	1736.242	0.551	21	0.260	K.EANLYTEIAEGIHAYGIK.G
R3/RRR3-11/2	1298.271	1298.597	-251.764	0.443	1643.509	0.518	18	0.243	R.AIIISVIDNLVK.G
R3/RRR3-11/2	1298.318	1298.597	-215.542	0.516	1509.299	0.539	18	0.232	R.AIIISVIDNLVK.G
R3/RRR3-11/2	1992.854	1993.205	-176.917	0.499	1370.820	0.551	19	0.211	K.EANLYTEIAEGIHAYGIK.G
R3/RRR3-11/2	1036.096	1036.163	-64.948	0.442	953.378	0.471	15	0.170	K.IVDLSADFR.L
R3/RRR3-11/2	1994.642	1993.205	219.651	0.430	663.539	0.505	19	0.151	K.EANLYTEIAEGIHAYGIK.G
R3/RRR3-11/2	1035.735	1036.163	-414.524	0.361	647.649	0.405	12	0.145	K.IVDLSADFR.L
R3/RRR3-11/2	1035.981	1036.163	-176.757	0.295	638.166	0.345	10	0.136	K.IVDLSADFR.L
R3/RRR3-16/2	1142.008	1142.332	-284.712	0.453	1136.852	0.559	16	0.196	R.HAGIIDIQFK.R
R3/RRR3-16/2	1141.609	1142.332	-1514.208	0.378	980.635	0.559	15	0.179	R.HAGIIDIQFK.R
R3/RRR3-16/2	1032.193	1032.211	-17.628	0.304	503.049	0.505	14	0.148	R.VPCNFPGLK.V
R3/RRR3-15/2	1100.901	1101.182	-256.307	0.379	914.511	0.301	15	0.144	K.GCGSCYQIR.C
R3/RRR3-16/2	1032.026	1032.211	-180.282	0.207	288.103	0.435	14	0.136	R.VPCNFPGLK.V
R3/RRR3-16/2	1031.913	1032.211	-289.460	0.291	202.791	0.406	11	0.130	-.VPCNFPGLK.-
R3/RRR3-16/3	1298.380	1298.519	-107.145	0.483	720.594	0.433	22	0.108	R.HAGIIDIQFKR.V
R3/RRR3-16/3	1298.668	1298.519	115.612	0.477	868.890	0.394	23	0.106	R.HAGIIDIQFKR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/3	1298.580	1298.519	47.593	0.442	549.455	0.373	19	0.096	-.HAGIIDIQFKR.-
R3/RRR3-12/2	1492.311	1492.742	-289.258	0.503	2179.666	0.458	21	0.311	K.LQFLSLLDNTVTK.Q
R3/RRR3-12/2	1491.713	1492.742	-1363.854	0.420	2264.977	0.382	21	0.305	K.LQFLSLLDNTVTK.Q
R3/RRR3-12/2	1493.717	1492.742	-16.362	0.583	2024.160	0.483	21	0.291	K.LQFLSLLDNTVTK.Q
R3/RRR3-12/2	1595.676	1595.862	-117.214	0.519	1936.837	0.512	21	0.286	R.LTNLAEIDPLASLPK.L
R3/RRR3-12/2	1114.129	1114.280	-136.116	0.442	813.760	0.337	16	0.146	R.LGTLLVNNNR.I
R3/RRR3-12/2	1114.115	1114.280	-148.536	0.475	829.512	0.318	16	0.144	R.LGTLLVNNNR.I
R3/RRR3-12/2	1501.227	1501.667	-293.902	0.357	818.108	0.256	18	0.132	K.AAIVNSQTLEEVAR.L
R3/RRR3-18/2	1274.905	1275.352	-351.934	0.494	1478.752	0.489	18	0.217	K.AQIWDTAGQER.F
R3/RRR3-17/2	1276.108	1275.352	-192.141	0.530	1374.310	0.474	17	0.202	K.AQIWDTAGQER.F
R3/RRR3-17/2	1275.356	1275.352	2.629	0.462	1354.362	0.476	17	0.200	K.AQIWDTAGQER.F
R3/RRR3-18/2	1274.935	1275.352	-328.013	0.514	1308.457	0.480	17	0.197	K.AQIWDTAGQER.F
R3/RRR3-19/2	1274.602	1275.352	-1377.636	0.345	1502.339	0.381	17	0.195	K.AQIWDTAGQER.F
R3/RRR3-18/2	1080.830	1081.204	-347.046	0.413	1289.336	0.480	16	0.195	K.STIGVEFATR.S
R3/RRR3-18/2	1275.054	1275.352	-234.551	0.537	1293.266	0.472	17	0.194	K.AQIWDTAGQER.F
R3/RRR3-17/2	1081.111	1081.204	-85.913	0.513	1163.424	0.492	16	0.188	K.STIGVEFATR.S
R3/RRR3-17/2	1274.391	1275.352	-1543.881	0.387	1358.062	0.400	17	0.186	K.AQIWDTAGQER.F
R3/RRR3-18/2	1081.076	1081.204	-118.760	0.453	1102.278	0.503	16	0.184	K.STIGVEFATR.S
R3/RRR3-19/2	1274.843	1275.352	-1187.311	0.423	1319.589	0.380	17	0.179	K.AQIWDTAGQER.F
R3/RRR3-17/2	1081.006	1081.204	-183.780	0.454	1125.990	0.440	16	0.176	K.STIGVEFATR.S
R3/RRR3-18/2	1080.452	1081.204	-1626.207	0.380	1017.072	0.479	15	0.172	K.STIGVEFATR.S
R3/RRR3-17/2	1080.319	1081.204	-1750.054	0.394	1141.302	0.376	16	0.166	K.STIGVEFATR.S
R3/RRR3-16/2	1045.015	1044.227	-203.114	0.390	975.078	0.424	16	0.160	K.VVLIGDSGVGK.S
R3/RRR3-20/2	1082.030	1081.204	-161.201	0.308	978.592	0.412	15	0.158	K.STIGVEFATR.S
R3/RRR3-18/2	1276.454	1275.352	79.650	0.355	825.959	0.267	16	0.140	K.AQIWDTAGQER.F
R3/RRR3-18/2	1306.435	1306.533	-75.032	0.326	719.960	0.379	15	0.138	R.GAVGALLVYDISK.H
R3/RRR3-21/2	1276.430	1275.352	60.755	0.272	482.892	0.273	12	0.131	-.AQIWDTAGQER.-
R3/RRR3-19/2	1043.425	1044.227	-1732.024	0.083	471.706	0.164	11	0.108	-.VVLIGDSGVGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1431.362	1431.702	-237.764	0.473	1328.370	0.568	19	0.265	K.LGSQIDILAPIKY.-
R3/RRR3-18/2	1431.252	1431.702	-315.371	0.498	1338.943	0.546	19	0.264	K.LGSQIDILAPIKY.-
R3/RRR3-18/3	1538.625	1538.759	-87.179	0.524	1735.796	0.444	29	0.185	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/3	1538.605	1538.759	-100.191	0.441	1679.375	0.395	29	0.165	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/2	1539.188	1538.759	279.291	0.515	504.185	0.543	19	0.159	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/2	1411.227	1411.594	-261.024	0.405	929.045	0.388	17	0.153	R.CEEMCISGGLVR.Q
R3/RRR3-18/3	1538.702	1538.759	-36.926	0.533	1346.945	0.473	27	0.151	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/2	1538.148	1538.759	-1050.476	0.427	508.814	0.468	18	0.149	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/2	1538.111	1538.759	-1074.541	0.443	543.273	0.444	19	0.149	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/3	1538.554	1538.759	-133.856	0.514	1238.282	0.480	26	0.144	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/2	886.433	887.016	-1791.122	0.339	797.041	0.329	12	0.142	R.GEAALANLK.A
R3/RRR3-18/2	1427.145	1427.594	-315.699	0.421	797.130	0.335	16	0.141	-.CEEM*CISGGLVR.-
R3/RRR3-18/3	1522.672	1522.760	-57.912	0.462	1388.945	0.411	27	0.141	R.MNTKPSHGPIHFR.A
R3/RRR3-18/3	1538.364	1538.759	-257.315	0.502	1268.297	0.445	26	0.139	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/2	886.440	887.016	-1783.650	0.385	690.057	0.277	12	0.136	R.GEAALANLK.A
R3/RRR3-18/2	886.877	887.016	-157.051	0.321	586.742	0.287	11	0.134	R.GEAALANLK.A
R3/RRR3-18/3	1538.295	1538.759	-302.456	0.462	1296.400	0.404	27	0.131	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/3	1539.523	1538.759	-153.734	0.338	1295.454	0.333	25	0.120	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/3	1521.498	1522.760	-1490.663	0.445	1040.949	0.392	23	0.115	R.MNTKPSHGPIHFR.A
R3/RRR3-18/3	1538.788	1538.759	19.052	0.439	1075.681	0.370	24	0.113	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/3	1538.387	1538.759	-242.508	0.460	667.508	0.444	22	0.110	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/3	1538.419	1538.759	-221.731	0.438	696.315	0.435	23	0.110	R.M*NTKPSHGPIHFR.A
R3/RRR3-17/3	1538.302	1538.759	-298.156	0.398	917.638	0.388	23	0.110	R.M*NTKPSHGPIHFR.A
R3/RRR3-17/3	1538.738	1538.759	-13.412	0.442	788.381	0.316	22	0.097	R.M*NTKPSHGPIHFR.A
R3/RRR3-18/3	1538.619	1538.759	-91.238	0.389	492.787	0.358	21	0.096	-.M*NTKPSHGPIHFR.-
R3/RRR3-18/2	1430.430	1431.702	-1592.532	0.280	867.802	0.395	15	0.095	K.LGSQIDILAPIKY.-
R3/RRR3-16/3	1538.015	1538.759	-1137.228	0.287	708.071	0.290	21	0.094	-.M*NTKPSHGPIHFR.-
R3/RRR3-5/2	1594.390	1594.813	-266.208	0.501	1676.524	0.516	22	0.245	K.ASNTLSIIDSGVGMTK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1594.394	1594.813	-263.443	0.434	1675.674	0.512	23	0.245	K.ASNTLSIIDSGVGMTK.S
R3/RRR3-5/3	1950.723	1951.255	-787.522	0.537	1774.906	0.568	31	0.241	K.SKLDAQPELFIHIVPDK.A
R3/RRR3-5/2	1610.348	1610.812	-289.017	0.478	1477.381	0.593	22	0.237	K.ASNTLSIIDSGVGM*TK.S
R3/RRR3-5/2	1610.355	1610.812	-284.834	0.449	1303.188	0.616	21	0.221	K.ASNTLSIIDSGVGM*TK.S
R3/RRR3-5/2	1594.472	1594.813	-214.132	0.465	1410.770	0.538	21	0.217	K.ASNTLSIIDSGVGMTK.S
R3/RRR3-5/3	1951.053	1951.255	-103.589	0.549	1609.310	0.533	30	0.203	K.SKLDAQPELFIHIVPDK.A
R3/RRR3-5/2	1736.556	1736.004	-258.868	0.558	1246.765	0.532	22	0.201	K.LDAQPELFIHIVPDK.A
R3/RRR3-5/3	1950.674	1951.255	-813.057	0.498	1533.871	0.514	29	0.188	K.SKLDAQPELFIHIVPDK.A
R3/RRR3-5/2	1735.627	1736.004	-218.303	0.494	999.944	0.522	20	0.177	K.LDAQPELFIHIVPDK.A
R3/RRR3-5/2	1735.390	1736.004	-932.962	0.498	876.283	0.551	19	0.173	K.LDAQPELFIHIVPDK.A
R3/RRR3-2/2	1735.082	1736.004	-1111.446	0.408	547.080	0.354	16	0.137	K.LDAQPELFIHIVPDK.A
R3/RRR3-2/2	1735.609	1736.004	-228.535	0.370	568.234	0.343	15	0.135	K.LDAQPELFIHIVPDK.A
R3/RRR3-5/3	1735.995	1736.004	-5.623	0.393	815.872	0.455	29	0.111	K.LDAQPELFIHIVPDK.A
R3/RRR3-5/3	1736.138	1736.004	76.995	0.404	653.658	0.480	27	0.110	K.LDAQPELFIHIVPDK.A
R3/RRR3-5/3	1735.859	1736.004	-83.810	0.321	638.176	0.325	25	0.092	K.LDAQPELFIHIVPDK.A
R3/RRR3-16/2	1295.183	1295.430	-191.675	0.521	1366.238	0.686	23	0.250	R.HSGLAVAGLAADGR.Q
R3/RRR3-16/2	1294.925	1295.430	-1165.967	0.460	1334.353	0.652	24	0.236	R.HSGLAVAGLAADGR.Q
R3/RRR3-16/2	1041.144	1041.182	-36.057	0.367	1008.548	0.324	15	0.150	R.VFQVEYAGK.A
R3/RRR3-16/2	1114.036	1114.231	-175.143	0.413	775.628	0.351	16	0.146	K.VPDDLVEQAK.A
R3/RRR3-15/2	1115.212	1114.231	-17.304	0.333	506.508	0.465	14	0.145	K.VPDDLVEQAK.A
R3/RRR3-13/2	1700.382	1700.782	-235.933	0.545	2141.218	0.536	26	0.327	R.ASGYDVESSASSDAILK.A
R3/RRR3-13/2	1700.457	1700.782	-191.714	0.547	1913.909	0.534	24	0.286	R.ASGYDVESSASSDAILK.A
R3/RRR3-13/2	1699.598	1700.782	-1289.029	0.421	1785.870	0.514	23	0.261	R.ASGYDVESSASSDAILK.A
R3/RRR3-13/2	1429.176	1428.615	-308.033	0.416	1418.450	0.614	17	0.232	K.AFSAAVSSLGIYNK.D
R3/RRR3-13/2	1624.584	1624.819	-144.746	0.520	1285.524	0.489	22	0.196	K.VYQGQLVGPSTFEAK.L
R3/RRR3-13/2	1623.844	1624.819	-1220.005	0.471	1283.358	0.444	23	0.188	K.VYQGQLVGPSTFEAK.L
R3/RRR3-13/2	1624.322	1624.819	-306.755	0.514	1102.236	0.523	22	0.186	K.VYQGQLVGPSTFEAK.L
R3/RRR3-13/2	1017.881	1018.105	-220.196	0.421	543.607	0.480	14	0.153	R.FDGTVPEPR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1017.935	1018.105	-167.502	0.415	622.862	0.436	15	0.152	R.FDGTVPEPR.K
R3/RRR3-13/2	1017.822	1018.105	-279.153	0.401	579.775	0.431	14	0.149	R.FDGTVPEPR.K
R3/RRR3-14/2	1066.433	1066.106	307.389	0.409	562.970	0.450	13	0.148	R.SLGENFNER.V
R3/RRR3-14/2	1066.293	1066.106	175.956	0.369	774.287	0.333	15	0.144	R.SLGENFNER.V
R3/RRR3-17/2	1405.062	1405.487	-303.473	0.465	1479.267	0.522	18	0.225	R.FYCWDTAGQEK.F
R3/RRR3-17/2	1404.433	1405.487	-1466.746	0.402	1612.488	0.423	18	0.218	R.FYCWDTAGQEK.F
R3/RRR3-17/2	1405.008	1405.487	-342.002	0.471	1510.609	0.445	18	0.212	R.FYCWDTAGQEK.F
R3/RRR3-17/3	1762.348	1762.988	-933.635	0.535	1554.696	0.568	29	0.203	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1762.395	1762.988	-906.856	0.563	1219.237	0.515	19	0.193	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1762.238	1762.988	-996.146	0.522	1156.369	0.505	18	0.185	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1516.194	1516.752	-1030.532	0.517	1109.634	0.448	21	0.176	R.VCENIPIVLCGNK.V
R3/RRR3-17/2	1516.187	1516.752	-1035.383	0.500	1127.177	0.440	21	0.176	R.VCENIPIVLCGNK.V
R3/RRR3-17/3	1763.393	1762.988	230.188	0.492	1404.988	0.540	29	0.175	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1762.451	1762.988	-874.802	0.564	919.676	0.539	18	0.174	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1517.399	1516.752	-233.481	0.563	1135.075	0.430	21	0.174	R.VCENIPIVLCGNK.V
R3/RRR3-17/3	1762.796	1762.988	-109.374	0.451	1264.539	0.551	25	0.165	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1762.078	1762.988	-1087.470	0.463	822.811	0.503	16	0.161	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1762.146	1762.988	-1048.379	0.486	769.018	0.452	16	0.152	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/3	1763.144	1762.988	88.350	0.497	1008.970	0.561	26	0.144	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1214.809	1215.337	-1261.204	0.365	757.039	0.324	14	0.141	K.NLQYYEVSAK.S
R3/RRR3-16/2	1763.036	1762.988	26.903	0.388	384.366	0.384	15	0.140	K.SNYNFEKPFLYLAR.K
R3/RRR3-19/2	1762.865	1762.988	-70.051	0.311	306.855	0.338	13	0.136	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1214.366	1215.337	-1628.158	0.266	837.098	0.195	14	0.132	K.NLQYYEVSAK.S
R3/RRR3-17/3	1761.902	1762.988	-1187.584	0.408	793.624	0.564	22	0.130	K.SNYNFEKPFLYLAR.K
R3/RRR3-17/2	1214.244	1215.337	-1729.156	0.246	600.790	0.191	13	0.130	-.NLQYYEVSAK.-
R3/RRR3-19/3	1762.218	1762.988	-1007.595	0.383	890.392	0.504	24	0.124	K.SNYNFEKPFLYLAR.K
R3/RRR3-9/2	1930.431	1931.043	-837.305	0.606	2401.485	0.625	25	0.408	R.YYGGNDVIDEIENLCR.D
R3/RRR3-8/2	1932.371	1931.043	170.148	0.631	2336.308	0.617	25	0.390	R.YYGGNDVIDEIENLCR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1816.465	1816.986	-840.229	0.554	2366.964	0.541	23	0.372	K.VSAATGYIDYEKLEEK.A
R3/RRR3-9/2	1931.462	1931.043	217.898	0.619	2176.955	0.600	24	0.351	R.YYGGNDVIDEIENLCR.D
R3/RRR3-9/2	1930.403	1931.043	-851.841	0.580	2146.005	0.576	24	0.338	R.YYGGNDVIDEIENLCR.D
R3/RRR3-8/2	1930.585	1931.043	-237.861	0.596	2063.027	0.594	24	0.329	R.YYGGNDVIDEIENLCR.D
R3/RRR3-9/2	1817.591	1816.986	-218.159	0.579	2060.346	0.532	22	0.308	K.VSAATGYIDYEKLEEK.A
R3/RRR3-8/2	1619.428	1619.839	-254.759	0.471	2027.532	0.470	22	0.287	K.ISATSIYFESLPYK.V
R3/RRR3-8/2	1930.545	1931.043	-258.732	0.575	1828.437	0.583	23	0.285	R.YYGGNDVIDEIENLCR.D
R3/RRR3-9/2	1619.398	1619.839	-273.136	0.451	2028.969	0.437	22	0.278	K.ISATSIYFESLPYK.V
R3/RRR3-9/2	1816.387	1816.986	-883.135	0.538	1876.022	0.518	21	0.274	K.VSAATGYIDYEKLEEK.A
R3/RRR3-9/2	1207.092	1207.398	-253.842	0.480	1739.220	0.527	19	0.260	K.LIICGGSAYPR.D
R3/RRR3-9/2	1207.030	1207.398	-305.791	0.532	1634.250	0.494	19	0.238	K.LIICGGSAYPR.D
R3/RRR3-8/2	1620.255	1619.839	257.484	0.487	1697.110	0.461	21	0.235	K.ISATSIYFESLPYK.V
R3/RRR3-8/2	1206.339	1207.398	-1711.560	0.352	1743.169	0.418	19	0.232	K.LIICGGSAYPR.D
R3/RRR3-8/2	1207.157	1207.398	-200.073	0.448	1573.834	0.480	18	0.226	K.LIICGGSAYPR.D
R3/RRR3-8/2	1207.049	1207.398	-289.658	0.465	1524.128	0.500	18	0.225	K.LIICGGSAYPR.D
R3/RRR3-8/2	1816.435	1816.986	-856.689	0.526	1449.300	0.502	20	0.212	K.VSAATGYIDYEKLEEK.A
R3/RRR3-9/2	1619.136	1619.839	-1054.848	0.378	1550.354	0.424	20	0.209	K.ISATSIYFESLPYK.V
R3/RRR3-9/2	1206.438	1207.398	-1628.911	0.422	1411.794	0.484	18	0.208	K.LIICGGSAYPR.D
R3/RRR3-9/3	1931.274	1931.043	119.838	0.455	1940.694	0.378	29	0.204	R.YYGGNDVIDEIENLCR.D
R3/RRR3-9/2	1619.283	1619.839	-963.564	0.384	1472.587	0.401	20	0.196	K.ISATSIYFESLPYK.V
R3/RRR3-8/2	1619.352	1619.839	-301.421	0.399	1422.935	0.407	19	0.192	K.ISATSIYFESLPYK.V
R3/RRR3-17/3	1472.382	1471.598	-146.912	0.518	1648.546	0.440	34	0.178	K.KPVASDEGGAGAAGGVK.E
R3/RRR3-17/2	1058.046	1058.254	-196.678	0.384	968.846	0.418	17	0.161	K.IVLIGDSGVGK.S
R3/RRR3-18/3	1471.947	1471.598	237.752	0.512	1526.691	0.411	34	0.155	K.KPVASDEGGAGAAGGVK.E
R3/RRR3-18/2	1057.713	1058.254	-1460.562	0.389	839.212	0.436	15	0.155	K.IVLIGDSGVGK.S
R3/RRR3-17/3	1471.546	1471.598	-35.629	0.498	1452.683	0.429	33	0.153	K.KPVASDEGGAGAAGGVK.E
R3/RRR3-17/2	1057.955	1058.254	-283.145	0.329	1053.952	0.297	18	0.150	K.IVLIGDSGVGK.S
R3/RRR3-18/3	1471.272	1471.598	-222.502	0.486	1476.731	0.397	32	0.148	K.KPVASDEGGAGAAGGVK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/3	1471.701	1471.598	70.322	0.389	565.458	0.308	23	0.092	K.KPVASDEGGAGAAGGVK.E
R3/RRR3-11/2	1440.349	1439.619	-188.483	0.520	2010.764	0.606	21	0.324	R.GGDLVSAFAELM*GR.Q
R3/RRR3-11/2	1440.011	1439.619	272.732	0.462	1970.858	0.471	20	0.277	R.GGDLVSAFAELM*GR.Q
R3/RRR3-11/2	1422.658	1423.620	-1383.583	0.378	1816.185	0.520	19	0.265	R.GGDLVSAFAELMGR.Q
R3/RRR3-11/2	1423.903	1423.620	199.694	0.505	1676.761	0.577	20	0.261	R.GGDLVSAFAELMGR.Q
R3/RRR3-11/2	1422.792	1423.620	-1288.879	0.402	1732.388	0.513	20	0.252	R.GGDLVSAFAELMGR.Q
R3/RRR3-11/2	1439.261	1439.619	-249.960	0.426	1684.004	0.427	20	0.225	R.GGDLVSAFAELM*GR.Q
R3/RRR3-11/2	1004.884	1005.152	-268.247	0.444	1303.844	0.415	16	0.186	K.RGDYVPGLK.V
R3/RRR3-11/3	1595.150	1595.678	-960.881	0.475	1633.002	0.472	29	0.184	R.YHGHSMSDPGSTYR.T
R3/RRR3-11/2	1270.137	1270.376	-188.610	0.411	1320.655	0.403	18	0.183	K.GFGVESFGADRK.E
R3/RRR3-11/2	1004.402	1005.152	-1748.119	0.432	934.300	0.345	14	0.151	K.RGDYVPGLK.V
R3/RRR3-11/2	1005.013	1005.152	-139.078	0.396	855.953	0.372	14	0.151	K.RGDYVPGLK.V
R3/RRR3-11/3	1611.525	1611.677	-94.899	0.452	1082.893	0.451	27	0.125	R.YHGHSM*SDPGSTYR.T
R3/RRR3-11/3	1611.673	1611.677	-2.589	0.407	889.596	0.397	25	0.106	R.YHGHSM*SDPGSTYR.T
R3/RRR3-14/2	1581.186	1580.723	293.580	0.593	1931.230	0.566	23	0.300	R.QSDVEAFFAAELPR.Y
R3/RRR3-14/2	1580.502	1580.723	-139.875	0.506	1902.456	0.520	23	0.283	R.QSDVEAFFAAELPR.Y
R3/RRR3-14/2	1580.224	1580.723	-316.788	0.447	1649.752	0.499	21	0.239	R.QSDVEAFFAAELPR.Y
R3/RRR3-14/2	885.786	886.074	-326.223	0.443	1020.882	0.401	14	0.162	R.GLVGSAILR.H
R3/RRR3-14/2	886.067	886.074	-8.168	0.364	1073.996	0.358	14	0.158	R.GLVGSAILR.H
R3/RRR3-14/2	1209.164	1209.375	-175.642	0.270	843.881	0.443	13	0.148	K.WYVENVISAK.-
R3/RRR3-13/2	1056.283	1056.155	121.638	0.367	704.312	0.425	14	0.148	R.THAELDLTR.Q
R3/RRR3-12/2	1359.068	1359.509	-325.635	0.473	1965.474	0.468	20	0.619	R.IGEVISGEGVHYV.-
R3/RRR3-12/2	1199.567	1200.327	-1471.362	0.431	1525.139	0.329	17	0.189	K.SGLSLNDQLPR.N
R3/RRR3-12/2	1199.948	1200.327	-317.085	0.486	1416.356	0.291	17	0.171	K.SGLSLNDQLPR.N
R3/RRR3-12/2	1199.875	1200.327	-377.512	0.413	1362.895	0.287	16	0.167	K.SGLSLNDQLPR.N
R3/RRR3-12/2	1533.621	1533.797	-115.171	0.389	577.939	0.408	15	0.140	K.IFTAAWEVPPVFR.W
R3/RRR3-12/2	1533.828	1533.797	20.227	0.273	360.684	0.335	15	0.130	-.IFTAAWEVPPVFR.-
R3/RRR3-12/3	1626.982	1626.798	113.654	0.396	727.518	0.489	23	0.109	-.GIAHITGGGFTDNIPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/3	1626.436	1626.798	-223.144	0.362	939.684	0.321	23	0.096	K.GIAHITGGGFTDNIPR.V
R3/RRR3-15/3	1621.941	1621.816	76.981	0.458	2260.920	0.375	30	0.252	R.KNESVFGELQTQLK.N
R3/RRR3-15/2	1264.174	1263.420	-195.020	0.533	1535.942	0.596	19	0.250	K.SLITISGEVDTK.A
R3/RRR3-15/2	1262.958	1263.420	-366.993	0.408	1551.504	0.416	18	0.209	K.SLITISGEVDTK.A
R3/RRR3-15/2	1623.341	1621.816	-293.440	0.640	1334.299	0.491	21	0.199	R.KNESVFGELQTQLK.N
R3/RRR3-15/3	1621.859	1621.816	26.141	0.471	1938.944	0.360	29	0.193	R.KNESVFGELQTQLK.N
R3/RRR3-15/3	1837.603	1837.934	-180.278	0.520	1532.020	0.537	33	0.192	K.HHSNTAVGAELSHSFSR.N
R3/RRR3-15/2	1263.346	1263.420	-58.692	0.385	1209.388	0.413	17	0.175	K.SLITISGEVDTK.A
R3/RRR3-15/3	1837.630	1837.934	-165.884	0.549	1362.227	0.490	33	0.159	K.HHSNTAVGAELSHSFSR.N
R3/RRR3-16/2	1227.542	1227.435	86.814	0.421	777.715	0.418	16	0.152	K.SILSLVVPDQR.S
R3/RRR3-15/2	1226.592	1227.435	-1507.320	0.333	932.802	0.363	16	0.150	K.SILSLVVPDQR.S
R3/RRR3-15/2	1226.775	1227.435	-1357.889	0.348	803.325	0.379	15	0.146	K.SILSLVVPDQR.S
R3/RRR3-15/3	1838.128	1837.934	105.928	0.524	1134.890	0.498	32	0.140	K.HHSNTAVGAELSHSFSR.N
R3/RRR3-15/3	1621.761	1621.816	-34.330	0.369	1024.122	0.341	22	0.103	R.KNESVFGELQTQLK.N
R3/RRR3-16/2	1413.176	1412.610	-308.142	0.523	1319.089	0.562	21	0.215	K.VVEVVESSPPEIK.A
R3/RRR3-16/2	1412.159	1412.610	-320.415	0.494	1163.101	0.561	20	0.199	K.VVEVVESSPPEIK.A
R3/RRR3-16/2	1413.166	1412.610	-315.595	0.503	1137.926	0.571	20	0.199	K.VVEVVESSPPEIK.A
R3/RRR3-21/2	1660.519	1659.948	-258.925	0.501	1132.344	0.554	23	0.194	K.SGTTPLSPAIVFILDK.V
R3/RRR3-21/2	1412.179	1412.610	-306.626	0.446	1051.769	0.543	18	0.185	K.VVEVVESSPPEIK.A
R3/RRR3-15/2	1412.162	1412.610	-318.247	0.452	1153.982	0.489	19	0.184	K.VVEVVESSPPEIK.A
R3/RRR3-21/2	1659.302	1659.948	-994.633	0.457	1045.518	0.543	22	0.184	K.SGTTPLSPAIVFILDK.V
R3/RRR3-15/2	1412.128	1412.610	-342.445	0.451	1112.587	0.493	19	0.182	K.VVEVVESSPPEIK.A
R3/RRR3-16/2	1659.413	1659.948	-927.941	0.413	1018.152	0.534	23	0.180	K.SGTTPLSPAIVFILDK.V
R3/RRR3-16/2	1660.267	1659.948	192.946	0.493	919.545	0.568	21	0.179	K.SGTTPLSPAIVFILDK.V
R3/RRR3-15/2	1412.834	1412.610	158.882	0.475	1050.963	0.493	19	0.178	K.VVEVVESSPPEIK.A
R3/RRR3-15/2	1659.454	1659.948	-298.564	0.463	910.963	0.551	21	0.175	K.SGTTPLSPAIVFILDK.V
R3/RRR3-16/2	1782.342	1782.844	-845.049	0.341	830.922	0.576	27	0.171	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-21/2	1412.215	1412.610	-280.782	0.411	1017.172	0.463	18	0.169	K.VVEVVESSPPEIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1782.514	1782.844	-185.430	0.374	816.052	0.530	28	0.167	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-15/2	1659.615	1659.948	-200.932	0.411	857.152	0.509	21	0.165	K.SGTTPLSPAIVFILDK.V
R3/RRR3-16/2	1659.488	1659.948	-277.752	0.406	1027.702	0.432	22	0.165	K.SGTTPLSPAIVFILDK.V
R3/RRR3-20/2	1659.211	1659.948	-1049.736	0.420	934.012	0.474	21	0.165	K.SGTTPLSPAIVFILDK.V
R3/RRR3-21/2	1659.211	1659.948	-1049.810	0.423	805.180	0.520	20	0.164	K.SGTTPLSPAIVFILDK.V
R3/RRR3-20/2	1411.796	1412.610	-1288.944	0.336	1090.531	0.390	18	0.162	K.VVEVVESSPPEIK.A
R3/RRR3-20/3	1784.565	1782.844	-156.854	0.508	1207.237	0.551	27	0.160	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-21/2	1411.744	1412.610	-1325.677	0.338	879.861	0.458	18	0.159	K.VVEVVESSPPEIK.A
R3/RRR3-20/2	1659.281	1659.948	-1007.706	0.399	780.276	0.484	20	0.158	K.SGTTPLSPAIVFILDK.V
R3/RRR3-21/2	1782.173	1782.844	-940.348	0.306	695.250	0.531	25	0.157	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-16/2	1782.157	1782.844	-949.288	0.314	630.242	0.556	24	0.157	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-16/2	1782.302	1782.844	-867.600	0.265	737.760	0.516	26	0.155	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-15/2	1782.221	1782.844	-912.981	0.264	768.611	0.500	26	0.155	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-20/2	1782.222	1782.844	-912.774	0.293	588.421	0.538	24	0.153	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-15/2	1782.305	1782.844	-865.950	0.263	730.832	0.483	25	0.151	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-21/2	1782.387	1782.844	-256.746	0.281	706.363	0.462	25	0.150	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-19/2	1661.604	1659.948	-207.691	0.426	568.066	0.488	17	0.149	K.SGTTPLSPAIVFILDK.V
R3/RRR3-21/3	1784.155	1782.844	175.320	0.511	1105.542	0.548	30	0.149	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-20/2	1412.104	1412.610	-1069.819	0.354	851.981	0.386	16	0.149	K.VVEVVESSPPEIK.A
R3/RRR3-15/2	1782.143	1782.844	-957.265	0.236	721.727	0.462	25	0.148	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-16/2	820.881	820.956	-91.149	0.239	449.056	0.481	11	0.137	-.AAAAEFLK.-
R3/RRR3-15/2	1658.620	1659.948	-1407.686	0.196	631.975	0.355	18	0.135	K.SGTTPLSPAIVFILDK.V
R3/RRR3-12/2	1660.428	1659.948	290.335	0.283	595.151	0.226	16	0.131	K.SGTTPLSPAIVFILDK.V
R3/RRR3-21/2	820.945	820.956	-13.290	0.238	421.429	0.340	10	0.124	-.AAAAEFLK.-
R3/RRR3-16/3	1782.708	1782.844	-76.490	0.480	932.075	0.487	28	0.124	K.AEPEPEPEAPAAETTSR.E
R3/RRR3-17/2	1289.229	1289.467	-185.247	0.460	1441.261	0.504	19	0.216	R.VVGGWASPFVNR.V
R3/RRR3-17/2	1288.633	1289.467	-1427.148	0.378	1283.192	0.564	18	0.207	R.VVGGWASPFVNR.V
R3/RRR3-17/2	1288.784	1289.467	-1309.940	0.411	1170.958	0.564	17	0.197	R.VVGGWASPFVNR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1158.879	1158.327	-387.486	0.522	1123.325	0.555	17	0.196	K.IAGVELLDEAK.V
R3/RRR3-17/2	1157.990	1158.327	-291.990	0.486	1260.589	0.489	17	0.195	K.IAGVELLDEAK.V
R3/RRR3-17/2	1112.629	1113.251	-1462.423	0.418	1346.893	0.431	17	0.192	K.VPNLAAWADR.F
R3/RRR3-17/2	1158.079	1158.327	-214.578	0.510	1293.936	0.450	17	0.190	K.IAGVELLDEAK.V
R3/RRR3-17/2	1112.555	1113.251	-1528.769	0.458	999.467	0.495	16	0.176	K.VPNLAAWADR.F
R3/RRR3-17/2	1112.601	1113.251	-1487.880	0.311	656.980	0.351	13	0.139	K.VPNLAAWADR.F
R3/RRR3-17/3	1699.009	1698.966	25.639	0.446	894.010	0.366	31	0.102	K.LKGVEHEMLQETVGK.K
R3/RRR3-17/3	1714.547	1714.965	-244.878	0.280	750.805	0.322	27	0.090	K.LKGVEHEM*LQETVGK.K
R3/RRR3-13/2	1850.531	1851.124	-862.989	0.523	1442.889	0.624	25	0.242	R.VM*QGHAGANLVPLVASNR.I
R3/RRR3-13/2	1850.529	1851.124	-864.313	0.531	1214.655	0.620	25	0.214	R.VM*QGHAGANLVPLVASNR.I
R3/RRR3-13/2	1292.943	1293.408	-360.565	0.369	1046.921	0.382	16	0.160	K.FYFNPGDTGFK.A
R3/RRR3-13/2	1293.067	1293.408	-264.518	0.434	931.774	0.409	16	0.158	K.FYFNPGDTGFK.A
R3/RRR3-13/2	1293.303	1293.408	-81.568	0.437	821.350	0.449	15	0.158	K.FYFNPGDTGFK.A
R3/RRR3-18/2	1293.230	1293.408	-137.810	0.395	743.318	0.374	15	0.146	K.FYFNPGDTGFK.A
R3/RRR3-13/2	1328.020	1328.412	-295.817	0.371	518.137	0.436	16	0.145	K.SHIPDGPGYQEK.F
R3/RRR3-13/2	1328.227	1328.412	-139.894	0.365	407.118	0.416	14	0.141	K.SHIPDGPGYQEK.F
R3/RRR3-18/2	1293.188	1293.408	-170.194	0.344	650.591	0.315	14	0.139	K.FYFNPGDTGFK.A
R3/RRR3-13/2	1328.233	1328.412	-135.561	0.306	386.784	0.364	14	0.137	K.SHIPDGPGYQEK.F
R3/RRR3-18/2	1293.048	1293.408	-279.483	0.321	606.156	0.244	13	0.133	K.FYFNPGDTGFK.A
R3/RRR3-24/2	1293.236	1293.408	-132.886	0.187	645.443	0.263	14	0.132	K.FYFNPGDTGFK.A
R3/RRR3-13/3	1456.494	1456.585	-62.687	0.459	777.872	0.502	21	0.118	R.KSHIPDGPGYQEK.F
R3/RRR3-13/3	1456.725	1456.585	96.428	0.446	696.758	0.519	21	0.117	R.KSHIPDGPGYQEK.F
R3/RRR3-13/3	1456.832	1456.585	170.295	0.442	686.496	0.470	21	0.110	R.KSHIPDGPGYQEK.F
R3/RRR3-13/3	1835.781	1835.124	-187.560	0.368	966.339	0.348	27	0.102	R.VMQGHAGANLVPLVASNR.I
R3/RRR3-13/3	1835.669	1835.124	-248.500	0.346	511.166	0.343	22	0.091	R.VMQGHAGANLVPLVASNR.I
R3/RRR3-13/3	1851.098	1851.124	-13.725	0.350	726.206	0.287	25	0.088	R.VM*QGHAGANLVPLVASNR.I
R3/RRR3-11/2	1651.547	1651.932	-234.088	0.549	2341.817	0.617	25	0.395	R.VPQVGSIAINDGVILR.N
R3/RRR3-11/2	1651.588	1651.932	-208.728	0.540	2382.561	0.580	25	0.391	R.VPQVGSIAINDGVILR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1651.208	1651.932	-1047.187	0.520	2248.978	0.609	24	0.373	R.VPQVGSIAINDGVILR.N
R3/RRR3-11/2	1107.106	1107.281	-158.877	0.512	1265.487	0.557	16	0.210	K.YGAVEDILVK.M
R3/RRR3-11/2	1107.249	1107.281	-29.260	0.520	1272.348	0.499	16	0.199	K.YGAVEDILVK.M
R3/RRR3-11/2	1108.071	1107.281	-190.893	0.518	1269.809	0.475	16	0.194	K.YGAVEDILVK.M
R3/RRR3-11/2	1922.807	1922.258	-235.194	0.546	1004.605	0.612	23	0.192	K.LIANIEAQPSIAVQNVLK.S
R3/RRR3-11/2	1922.228	1922.258	-15.899	0.572	989.858	0.564	23	0.182	K.LIANIEAQPSIAVQNVLK.S
R3/RRR3-11/2	1921.490	1922.258	-923.017	0.538	931.432	0.539	23	0.174	K.LIANIEAQPSIAVQNVLK.S
R3/RRR3-11/2	1922.761	1922.258	-259.206	0.548	802.216	0.547	21	0.166	K.LIANIEAQPSIAVQNVLK.S
R3/RRR3-11/3	1921.945	1922.258	-163.480	0.413	990.733	0.410	25	0.110	K.LIANIEAQPSIAVQNVLK.S
R3/RRR3-11/3	1652.006	1651.932	45.082	0.393	872.900	0.354	23	0.096	R.VPQVGSIAINDGVILR.N
R3/RRR3-6/3	1682.105	1680.816	172.090	0.216	1028.509	0.067	27	0.069	-.MAAANGSACGGGGVDKEK.E
R3/RRR3-18/2	1951.558	1951.227	169.919	0.566	1559.009	0.604	25	0.252	R.VCPSVTMGLEPGEAFTVR.N
R3/RRR3-18/2	1966.271	1967.226	-997.426	0.484	1242.950	0.609	25	0.214	R.VCPSVTM*GLEPGEAFTVR.N
R3/RRR3-18/2	1967.972	1967.226	-129.479	0.567	1103.930	0.611	24	0.201	R.VCPSVTM*GLEPGEAFTVR.N
R3/RRR3-18/2	1966.592	1967.226	-833.711	0.513	1057.428	0.598	23	0.193	R.VCPSVTM*GLEPGEAFTVR.N
R3/RRR3-18/2	1778.326	1777.874	254.976	0.538	1203.159	0.467	20	0.182	K.DGAPDSFHFVEDWVR.T
R3/RRR3-18/2	1777.901	1777.874	15.453	0.517	1267.066	0.434	20	0.181	K.DGAPDSFHFVEDWVR.T
R3/RRR3-18/2	1244.942	1245.365	-340.538	0.436	1039.474	0.394	16	0.161	K.EAVNQSLENLK.T
R3/RRR3-18/2	1245.017	1245.365	-280.136	0.433	979.651	0.407	16	0.160	K.EAVNQSLENLK.T
R3/RRR3-18/2	1244.822	1245.365	-1242.698	0.412	970.497	0.405	16	0.159	K.EAVNQSLENLK.T
R3/RRR3-18/2	1777.428	1777.874	-251.331	0.513	907.162	0.452	18	0.158	K.DGAPDSFHFVEDWVR.T
R3/RRR3-18/3	1078.489	1078.199	269.770	0.471	1058.102	0.295	18	0.098	K.FKTEFYDK.K
R3/RRR3-7/2	1346.483	1346.600	-86.894	0.547	2774.253	0.456	20	0.434	R.KFDLGALVDLVR.K
R3/RRR3-7/2	1347.155	1346.600	-330.969	0.569	2448.100	0.408	20	0.344	R.KFDLGALVDLVR.K
R3/RRR3-7/2	1346.063	1346.600	-1145.593	0.538	2447.839	0.383	20	0.337	R.KFDLGALVDLVR.K
R3/RRR3-7/2	1200.538	1201.312	-1481.798	0.430	1037.506	0.533	19	0.183	K.IVDPDTGASLGR.N
R3/RRR3-7/2	1108.058	1108.183	-112.995	0.292	1391.217	0.341	16	0.177	K.GYLNDPEATK.N
R3/RRR3-7/2	1200.939	1201.312	-311.726	0.394	969.477	0.482	19	0.169	K.IVDPDTGASLGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1200.452	1201.312	-1554.115	0.405	795.466	0.524	18	0.165	K.IVDPDTGASLGR.N
R3/RRR3-7/2	1107.863	1108.183	-290.172	0.394	1111.424	0.357	15	0.161	K.GYLNDPEATK.N
R3/RRR3-7/2	1958.312	1959.363	-1050.837	0.384	611.629	0.459	18	0.141	K.HNITIAPFVPPIVVEIAK.S
R3/RRR3-7/2	1107.800	1108.183	-346.776	0.291	792.159	0.282	14	0.137	K.GYLNDPEATK.N
R3/RRR3-7/3	1346.471	1346.600	-95.748	0.430	1582.434	0.205	25	0.114	-.KFDLGALVDLVR.-
R3/RRR3-7/3	1346.652	1346.600	38.802	0.482	1136.442	0.284	23	0.095	-.KFDLGALVDLVR.-
R3/RRR3-16/2	1908.522	1909.040	-797.776	0.541	2074.105	0.636	24	0.347	R.ASGSCDFAGAASIVNQQPK.I
R3/RRR3-16/2	927.988	928.023	-38.474	0.443	577.697	0.415	11	0.150	K.VYEVDFR.G
R3/RRR3-16/2	928.215	928.023	206.615	0.452	564.226	0.402	11	0.146	-.VYEVDFR.-
R3/RRR3-16/2	927.210	928.023	-1961.526	0.396	600.429	0.372	11	0.145	K.VYEVDFR.G
R3/RRR3-16/2	1285.329	1285.432	-80.360	0.317	653.488	0.361	14	0.139	R.NFGLFYPNGQK.V
R3/RRR3-16/2	1285.990	1285.432	-345.092	0.377	605.627	0.347	13	0.138	R.NFGLFYPNGQK.V
R3/RRR3-16/3	1963.076	1963.098	-11.396	0.498	1033.114	0.505	25	0.134	K.VAHATYAFNDFYQTTGR.A
R3/RRR3-16/3	1962.319	1963.098	-909.154	0.504	1046.859	0.489	25	0.132	K.VAHATYAFNDFYQTTGR.A
R3/RRR3-16/2	1286.155	1285.432	-216.057	0.378	704.897	0.193	14	0.129	R.NFGLFYPNGQK.V
R3/RRR3-20/3	1961.974	1963.098	-1085.763	0.390	803.409	0.347	22	0.095	K.VAHATYAFNDFYQTTGR.A
R3/RRR3-12/2	1557.365	1557.767	-259.329	0.416	1778.553	0.609	21	0.285	R.VPTPNVSVVDLTCR.I
R3/RRR3-12/2	1290.142	1290.402	-202.578	0.439	1922.535	0.391	20	0.253	K.VVDDSTLEINGK.K
R3/RRR3-12/2	1508.408	1508.854	-296.967	0.469	1593.469	0.509	20	0.234	R.VLDLIAHMALVNAK.-
R3/RRR3-12/2	1508.898	1508.854	28.919	0.557	1576.729	0.512	20	0.232	R.VLDLIAHMALVNAK.-
R3/RRR3-12/2	1557.381	1557.767	-249.028	0.426	1329.782	0.625	19	0.225	R.VPTPNVSVVDLTCR.I
R3/RRR3-12/2	1557.362	1557.767	-261.059	0.415	1145.529	0.592	18	0.198	R.VPTPNVSVVDLTCR.I
R3/RRR3-12/2	1508.880	1508.854	17.315	0.381	835.862	0.417	17	0.150	R.VLDLIAHMALVNAK.-
R3/RRR3-12/3	1508.389	1508.854	-309.277	0.359	671.718	0.482	25	0.105	R.VLDLIAHMALVNAK.-
R3/RRR3-13/2	1992.787	1993.197	-206.414	0.540	2456.545	0.588	26	0.413	K.ANDILGYDLLDLCTNGPK.E
R3/RRR3-13/2	1995.641	1995.261	190.951	0.634	1564.454	0.640	27	0.262	R.VQIANFLCPGNYAVSGGVK.G
R3/RRR3-13/2	1994.654	1995.261	-808.074	0.569	1120.605	0.614	24	0.202	R.VQIANFLCPGNYAVSGGVK.G
R3/RRR3-13/2	1994.373	1995.261	-949.572	0.571	1105.183	0.609	24	0.200	R.VQIANFLCPGNYAVSGGVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1204.113	1204.352	-199.359	0.516	1341.852	0.455	18	0.197	R.LESALAETEIK.T
R3/RRR3-13/2	1203.511	1204.352	-1534.803	0.371	1407.255	0.364	18	0.184	R.LESALAETEIK.T
R3/RRR3-13/2	1203.706	1204.352	-1371.910	0.415	1372.417	0.376	18	0.184	R.LESALAETEIK.T
R3/RRR3-13/2	1489.784	1489.655	86.613	0.386	657.553	0.483	20	0.153	R.QVTSPVQWESTVK.T
R3/RRR3-13/2	1488.426	1489.655	-1502.018	0.233	326.680	0.409	17	0.135	R.QVTSPVQWESTVK.T
R3/RRR3-13/3	1994.808	1995.261	-227.755	0.372	927.008	0.303	27	0.091	R.VQIANFLCPGNYAVSGGVK.G
R3/RRR3-12/2	1569.151	1569.657	-962.592	0.508	2107.781	0.454	25	0.299	K.NFGDEALIGEGSFGR.V
R3/RRR3-12/2	1569.443	1569.657	-136.882	0.522	1871.835	0.542	25	0.285	K.NFGDEALIGEGSFGR.V
R3/RRR3-12/2	996.049	996.189	-141.067	0.421	495.106	0.459	14	0.151	K.ALQPLLNAR.A
R3/RRR3-12/2	995.919	996.189	-271.400	0.386	422.575	0.459	13	0.148	K.ALQPLLNAR.A
R3/RRR3-6/2	1182.050	1181.372	-273.100	0.400	841.468	0.332	14	0.144	R.VYFGVLRNGR.S
R3/RRR3-6/2	1181.928	1181.372	-376.615	0.394	937.597	0.287	15	0.144	R.VYFGVLRNGR.S
R3/RRR3-12/2	1367.948	1367.538	300.678	0.368	483.670	0.418	16	0.142	K.GAQPGPVLSWAQR.V
R3/RRR3-11/2	1367.365	1367.538	-127.115	0.313	543.457	0.435	16	0.142	K.GAQPGPVLSWAQR.V
R3/RRR3-12/2	995.851	996.189	-340.145	0.289	581.653	0.363	14	0.140	K.ALQPLLNAR.A
R3/RRR3-6/2	1181.862	1181.372	416.497	0.364	787.774	0.269	14	0.137	R.VYFGVLRNGR.S
R3/RRR3-11/2	1367.533	1367.538	-3.904	0.273	472.062	0.375	16	0.136	K.GAQPGPVLSWAQR.V
R3/RRR3-9/2	1978.249	1978.192	28.556	0.596	4014.314	0.574	30	0.857	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-9/2	1978.721	1978.192	-239.129	0.627	3833.408	0.573	29	0.788	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-2/2	1979.718	1978.192	-240.245	0.597	3311.076	0.569	29	0.616	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-9/2	1977.759	1978.192	-219.559	0.588	3243.021	0.577	28	0.600	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-2/2	1978.451	1978.192	131.035	0.525	2623.628	0.556	25	0.428	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-5/2	1979.621	1978.192	217.174	0.549	2480.115	0.554	25	0.394	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-8/2	1978.461	1978.192	136.356	0.506	2394.202	0.545	25	0.374	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-8/2	1978.537	1978.192	174.718	0.479	2031.663	0.476	24	0.284	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-9/3	1977.354	1978.192	-932.364	0.403	2086.096	0.469	34	0.265	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-9/3	1978.282	1978.192	45.290	0.344	1931.912	0.405	32	0.217	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-1/2	1978.979	1978.192	-108.370	0.326	1147.263	0.463	20	0.172	R.SNFGALLDTVELQLASGGGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1978.898	1978.192	-149.023	0.410	1238.843	0.371	20	0.165	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-5/2	1979.677	1978.192	245.370	0.398	781.311	0.540	20	0.160	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-9/2	1124.028	1123.326	-265.412	0.415	474.086	0.426	15	0.146	K.SFPVLFDVAK.V
R3/RRR3-9/2	1123.897	1123.326	-382.225	0.233	395.320	0.342	14	0.134	K.SFPVLFDVAK.V
R3/RRR3-1/2	1978.259	1978.192	33.693	0.282	606.389	0.325	16	0.132	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-9/3	1601.805	1601.736	43.552	0.420	950.370	0.376	25	0.106	R.VCAYLDPSEPNHAK.I
R3/RRR3-9/3	1601.715	1601.736	-12.859	0.376	866.474	0.291	25	0.092	R.VCAYLDPSEPNHAK.I
R3/RRR3-9/3	1977.858	1978.192	-169.475	0.267	921.485	0.190	25	0.081	R.SNFGALLDTVELQLASGGGK.S
R3/RRR3-9/3	1601.607	1601.736	-80.629	0.374	511.081	0.303	21	0.080	-.VCAYLDPSEPNHAK.-
R3/RRR3-17/2	1316.947	1317.559	-1227.353	0.371	1102.318	0.476	18	0.174	K.VTVVFVLGGPGSGK.G
R3/RRR3-17/2	1858.839	1859.111	-146.595	0.553	795.480	0.545	21	0.166	K.VFVESSLPVIEYYNAK.D
R3/RRR3-17/2	1075.011	1075.155	-133.780	0.509	995.785	0.381	15	0.160	R.VDDNIETIR.K
R3/RRR3-17/2	1075.009	1075.155	-136.058	0.543	920.220	0.384	15	0.156	R.VDDNIETIR.K
R3/RRR3-17/2	1074.267	1075.155	-1762.307	0.402	773.720	0.289	14	0.140	R.VDDNIETIR.K
R3/RRR3-17/3	1799.565	1800.088	-848.841	0.430	1195.217	0.453	31	0.134	K.KIDAAKPIPEVFEDVK.A
R3/RRR3-17/3	1800.022	1800.088	-36.950	0.427	1159.723	0.458	31	0.132	K.KIDAAKPIPEVFEDVK.A
R3/RRR3-17/2	1316.747	1317.559	-1380.127	0.211	696.251	0.212	16	0.127	K.VTVVFVLGGPGSGK.G
R3/RRR3-17/3	1800.118	1800.088	16.819	0.401	610.104	0.390	25	0.099	K.KIDAAKPIPEVFEDVK.A
R3/RRR3-9/2	1489.161	1489.696	-1034.276	0.434	2210.346	0.480	22	0.325	K.IASLQSEITSLQAK.G
R3/RRR3-9/2	1489.570	1489.696	-85.123	0.516	2060.960	0.530	22	0.313	K.IASLQSEITSLQAK.G
R3/RRR3-9/2	1148.173	1148.249	-66.606	0.458	1381.614	0.456	17	0.200	K.ISGLESGISER.S
R3/RRR3-9/3	1187.825	1187.328	419.858	0.457	2236.936	0.179	27	0.172	R.AKEEAEAVALR.A
R3/RRR3-9/3	1187.612	1187.328	239.776	0.426	2252.864	0.155	26	0.169	R.AKEEAEAVALR.A
R3/RRR3-9/3	1187.298	1187.328	-25.906	0.408	1968.534	0.165	24	0.139	R.AKEEAEAVALR.A
R3/RRR3-9/3	1392.821	1391.510	224.096	0.373	928.472	0.365	24	0.100	R.DKISGLESGISER.S
R3/RRR3-5/2	1624.345	1623.811	-287.503	0.402	941.238	0.447	18	0.158	K.ANGTLTIQDSGIGM*TK.A
R3/RRR3-5/2	1624.235	1623.811	261.553	0.361	816.275	0.480	17	0.154	K.ANGTLTIQDSGIGM*TK.A
R3/RRR3-5/2	1561.278	1561.719	-283.852	0.450	813.449	0.400	21	0.152	R.EIISNSSDALDKIR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1624.494	1623.811	-195.978	0.401	832.936	0.438	17	0.151	K.ANGTLTIQDSGIGM*TK.A
R3/RRR3-5/2	1292.022	1292.375	-274.114	0.410	862.056	0.387	16	0.150	R.EIISNSSDALDK.I
R3/RRR3-5/2	1291.748	1292.375	-1263.334	0.347	885.748	0.357	17	0.148	R.EIISNSSDALDK.I
R3/RRR3-5/2	1292.052	1292.375	-250.701	0.384	792.489	0.342	16	0.143	R.EIISNSSDALDK.I
R3/RRR3-5/2	1561.270	1561.719	-288.951	0.442	789.914	0.312	20	0.141	R.EIISNSSDALDKIR.Y
R3/RRR3-5/2	1561.314	1561.719	-260.634	0.467	688.710	0.300	20	0.138	R.EIISNSSDALDKIR.Y
R3/RRR3-5/2	1609.360	1607.812	-281.306	0.327	539.765	0.276	15	0.130	K.ANGTLTIQDSGIGMTK.A
R3/RRR3-8/2	1345.109	1345.506	-296.001	0.488	1581.903	0.520	23	0.237	K.FDM*GGSAAVFGAAK.A
R3/RRR3-8/2	1318.873	1319.360	-370.837	0.478	1387.023	0.416	18	0.192	K.TIEVNNTDAEGR.L
R3/RRR3-8/3	1851.592	1852.072	-260.183	0.502	1583.073	0.499	30	0.190	R.LTLADALVYACNQGVDK.I
R3/RRR3-8/2	1272.983	1272.388	-319.379	0.471	1006.386	0.519	18	0.179	K.GLTFDSGGYNIK.T
R3/RRR3-8/2	1272.122	1272.388	-210.452	0.383	1006.757	0.365	18	0.155	K.GLTFDSGGYNIK.T
R3/RRR3-8/2	1271.654	1272.388	-1367.831	0.257	977.598	0.319	18	0.145	K.GLTFDSGGYNIK.T
R3/RRR3-8/2	1344.799	1345.506	-1273.250	0.364	541.673	0.351	17	0.136	K.FDM*GGSAAVFGAAK.A
R3/RRR3-25/3	1934.126	1934.877	-907.941	0.491	1587.876	0.485	34	0.188	R.GGGGYGGGGGYGNQGGYGDGNR.G
R3/RRR3-25/2	1794.000	1794.946	-1087.502	0.508	1065.116	0.466	20	0.170	K.LFVGGLSWNTNDDSLR.E
R3/RRR3-25/2	1431.565	1432.519	-1368.816	0.272	609.639	0.411	14	0.134	R.GFGFVSFANGDDAK.S
R3/RRR3-25/3	1542.608	1542.675	-43.332	0.408	601.794	0.592	26	0.122	K.SAM*DAM*DGKELEGR.S
R3/RRR3-25/3	1542.657	1542.675	-11.901	0.394	455.189	0.604	24	0.119	K.SAM*DAM*DGKELEGR.S
R3/RRR3-25/3	1542.633	1542.675	-27.616	0.411	327.774	0.564	20	0.112	K.SAM*DAM*DGKELEGR.S
R3/RRR3-9/2	1469.023	1469.712	-1153.137	0.359	1976.978	0.362	21	0.252	K.SGLVALNLDLAQVR.Q
R3/RRR3-9/2	1433.282	1432.653	-259.655	0.516	1579.739	0.408	20	0.210	K.WGNIQFPLPFGR.V
R3/RRR3-9/2	1433.178	1432.653	-332.204	0.523	1437.011	0.452	19	0.204	K.WGNIQFPLPFGR.V
R3/RRR3-9/2	1433.253	1432.653	-280.077	0.506	1509.628	0.378	20	0.197	K.WGNIQFPLPFGR.V
R3/RRR3-9/2	1432.367	1432.653	-200.585	0.506	1391.569	0.413	19	0.192	K.WGNIQFPLPFGR.V
R3/RRR3-9/2	1431.902	1432.653	-1226.725	0.496	1118.459	0.461	18	0.178	K.WGNIQFPLPFGR.V
R3/RRR3-9/2	1432.430	1432.653	-156.385	0.509	1237.449	0.399	18	0.175	K.WGNIQFPLPFGR.V
R3/RRR3-9/2	1469.067	1469.712	-1122.765	0.387	1219.231	0.364	20	0.168	K.SGLVALNLDLAQVR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1469.372	1469.712	-231.613	0.442	1115.199	0.371	19	0.161	K.SGLVALNLDLAQVR.Q
R3/RRR3-9/2	1729.486	1730.897	-1397.721	0.411	1140.819	0.288	19	0.149	R.VLSPSESFIHELDEK.T
R3/RRR3-9/2	1067.023	1067.131	-101.276	0.370	612.085	0.371	13	0.141	R.GELDDTAAFK.N
R3/RRR3-9/2	1066.613	1067.131	-1427.829	0.311	615.292	0.384	13	0.140	R.GELDDTAAFK.N
R3/RRR3-9/2	1066.779	1067.131	-330.729	0.273	654.731	0.280	13	0.134	R.GELDDTAAFK.N
R3/RRR3-14/2	1633.473	1633.912	-269.808	0.495	1469.464	0.506	22	0.217	K.VGPALLSGPVFATFEK.V
R3/RRR3-14/2	1400.372	1400.644	-194.938	0.429	1489.299	0.488	20	0.217	K.VVEIYEAAPAPLK.V
R3/RRR3-14/2	1401.213	1400.644	-309.025	0.447	1313.485	0.474	18	0.196	-.VVEIYEAAPAPLK.-
R3/RRR3-14/2	1556.085	1555.625	296.113	0.490	963.774	0.605	23	0.189	K.EAPAAEEAPAAAAEEK.K
R3/RRR3-14/2	1400.399	1400.644	-175.525	0.390	1287.973	0.435	18	0.185	K.VVEIYEAAPAPLK.V
R3/RRR3-14/2	1555.205	1555.625	-271.262	0.430	927.743	0.523	23	0.172	K.EAPAAEEAPAAAAEEK.K
R3/RRR3-14/2	1632.591	1633.912	-1425.930	0.328	1276.181	0.358	21	0.170	K.VGPALLSGPVFATFEK.V
R3/RRR3-14/3	1475.837	1475.583	172.499	0.438	1565.359	0.408	27	0.161	K.KEEAAAAAVATGEEK.K
R3/RRR3-14/2	1554.509	1555.625	-1365.469	0.332	819.845	0.456	23	0.154	K.EAPAAEEAPAAAAEEK.K
R3/RRR3-14/2	1633.458	1633.912	-278.655	0.346	498.083	0.479	16	0.142	K.VGPALLSGPVFATFEK.V
R3/RRR3-20/2	1401.097	1400.644	324.237	0.356	563.996	0.294	14	0.132	-.VVEIYEAAPAPLK.-
R3/RRR3-14/2	1632.915	1633.912	-1226.799	0.262	457.267	0.333	14	0.131	K.VGPALLSGPVFATFEK.V
R3/RRR3-14/3	1475.507	1475.583	-52.129	0.454	1220.789	0.394	25	0.125	K.KEEAAAAAVATGEEK.K
R3/RRR3-14/3	1474.439	1475.583	-1458.730	0.325	970.873	0.369	24	0.104	K.KEEAAAAAVATGEEK.K
R3/RRR3-12/2	1221.099	1221.345	-201.699	0.443	1293.870	0.448	19	0.190	K.VFGSPTSAEVAR.V
R3/RRR3-12/2	1222.149	1221.345	-160.752	0.498	1084.519	0.463	19	0.176	K.VFGSPTSAEVAR.V
R3/RRR3-12/2	1221.099	1221.345	-201.699	0.452	1166.137	0.392	19	0.170	K.VFGSPTSAEVAR.V
R3/RRR3-12/2	1441.256	1441.572	-220.076	0.460	688.298	0.569	18	0.165	R.QGNPDLIGTGALER.A
R3/RRR3-12/2	1441.166	1441.572	-282.193	0.413	730.652	0.522	20	0.161	R.QGNPDLIGTGALER.A
R3/RRR3-12/2	1442.354	1441.572	-151.744	0.393	716.424	0.494	19	0.156	R.QGNPDLIGTGALER.A
R3/RRR3-12/2	1063.069	1063.151	-77.351	0.426	848.828	0.384	13	0.151	-.WWNNISSR.-
R3/RRR3-12/2	1440.664	1441.572	-1328.556	0.429	557.989	0.476	18	0.150	R.QGNPDLIGTGALER.A
R3/RRR3-12/2	1049.902	1050.190	-275.404	0.461	785.464	0.339	13	0.147	K.LLDIYEQR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1050.019	1050.190	-162.850	0.416	827.527	0.285	13	0.142	K.LLDIYEQR.L
R3/RRR3-12/2	1049.904	1050.190	-273.305	0.372	802.865	0.291	13	0.142	K.LLDIYEQR.L
R3/RRR3-12/2	1062.662	1063.151	-461.053	0.185	609.565	0.059	12	0.124	-.WWNNISSR.-
R3/RRR3-13/2	1217.396	1217.442	-37.776	0.454	1908.476	0.429	18	0.259	R.EALFVLAQLGR.K
R3/RRR3-13/2	1291.085	1290.493	-317.082	0.502	1286.272	0.410	16	0.181	R.YQILAGVIEQR.M
R3/RRR3-13/2	1290.213	1290.493	-218.035	0.481	1258.639	0.398	16	0.177	R.YQILAGVIEQR.M
R3/RRR3-13/2	1217.281	1217.442	-132.729	0.435	1099.291	0.436	16	0.171	R.EALFVLAQLGR.K
R3/RRR3-13/2	1289.461	1290.493	-1581.099	0.364	1267.000	0.359	15	0.170	R.YQILAGVIEQR.M
R3/RRR3-13/2	1217.083	1217.442	-295.720	0.446	1053.303	0.400	15	0.162	R.EALFVLAQLGR.K
R3/RRR3-13/2	1225.172	1224.412	-196.831	0.339	855.139	0.446	15	0.153	R.FAEMEGSALLR.W
R3/RRR3-13/2	1119.253	1119.335	-73.359	0.391	676.630	0.385	16	0.147	R.LLADDLFLAK.L
R3/RRR3-13/2	1118.975	1119.335	-322.742	0.488	614.686	0.374	16	0.146	R.LLADDLFLAK.L
R3/RRR3-13/2	1118.588	1119.335	-1566.386	0.338	676.491	0.274	16	0.137	R.LLADDLFLAK.L
R3/RRR3-10/2	1223.845	1224.262	-342.106	0.483	1537.127	0.348	17	0.193	R.GDSVDQFSNVR.H
R3/RRR3-10/2	1223.974	1224.262	-236.237	0.488	1490.064	0.356	17	0.190	R.GDSVDQFSNVR.H
R3/RRR3-10/2	1223.950	1224.262	-256.048	0.454	1492.882	0.316	17	0.183	R.GDSVDQFSNVR.H
R3/RRR3-10/2	1273.184	1273.503	-250.570	0.453	1041.501	0.394	16	0.161	K.FKDEIVPVPTK.I
R3/RRR3-10/2	1273.163	1273.503	-267.596	0.438	998.701	0.380	16	0.157	K.FKDEIVPVPTK.I
R3/RRR3-10/2	972.036	972.209	-178.687	0.365	487.439	0.437	14	0.147	K.GLPILGVFR.S
R3/RRR3-10/2	972.007	972.209	-207.789	0.346	478.222	0.438	14	0.146	K.GLPILGVFR.S
R3/RRR3-10/2	971.944	972.209	-273.685	0.349	380.209	0.435	13	0.145	K.GLPILGVFR.S
R3/RRR3-10/3	1957.011	1957.218	-105.839	0.335	707.383	0.490	28	0.110	K.VVISVDDGIRPGTTASGLAK.L
R3/RRR3-10/3	1957.177	1957.218	-20.908	0.350	632.662	0.460	28	0.104	K.VVISVDDGIRPGTTASGLAK.L
R3/RRR3-10/3	1957.268	1957.218	25.821	0.338	534.808	0.470	25	0.102	K.VVISVDDGIRPGTTASGLAK.L
R3/RRR3-6/2	1949.927	1950.184	-132.086	0.590	759.840	0.663	19	0.182	K.VSFGNYTYPIAWDFLR.A
R3/RRR3-6/2	1859.448	1858.166	151.997	0.450	1040.001	0.510	23	0.177	K.QIVVSCGTLSSPLVLQR.S
R3/RRR3-6/2	1949.674	1950.184	-777.044	0.555	788.744	0.622	19	0.177	K.VSFGNYTYPIAWDFLR.A
R3/RRR3-6/2	1949.753	1950.184	-221.519	0.516	624.210	0.600	18	0.163	K.VSFGNYTYPIAWDFLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1858.049	1858.166	-63.234	0.399	416.773	0.443	18	0.140	K.QIVVSCGTLSSPLVLQR.S
R3/RRR3-6/3	1113.491	1113.248	218.626	0.479	1167.942	0.254	22	0.096	R.DLHGFEGPIK.V
R3/RRR3-6/3	1156.836	1157.345	-1308.544	0.473	1093.073	0.238	22	0.092	K.IDKVIIENGR.A
R3/RRR3-6/3	1113.650	1113.248	361.904	0.432	1050.861	0.244	21	0.091	R.DLHGFEGPIK.V
R3/RRR3-6/2	1771.954	1771.950	1.823	0.524	2872.637	0.544	25	0.495	R.LYLDQYGGSGDVWIGK.V
R3/RRR3-6/2	1772.303	1771.950	199.747	0.569	2258.727	0.507	24	0.341	R.LYLDQYGGSGDVWIGK.V
R3/RRR3-6/2	1847.371	1848.002	-885.688	0.465	1319.140	0.351	20	0.169	K.ESSQESIEGDTAILLVR.A
R3/RRR3-5/2	1618.238	1617.778	284.967	0.452	694.604	0.423	19	0.150	K.DLDLDIPYDEPALK.A
R3/RRR3-5/2	1618.066	1617.778	178.456	0.438	612.951	0.423	18	0.147	K.DLDLDIPYDEPALK.A
R3/RRR3-5/2	1618.599	1617.778	-111.167	0.448	543.084	0.444	17	0.147	K.DLDLDIPYDEPALK.A
R3/RRR3-6/2	1033.176	1033.120	54.796	0.333	1044.612	0.290	14	0.145	K.FPGDDGVLGR.A
R3/RRR3-6/2	1618.122	1617.778	212.953	0.470	574.284	0.411	17	0.145	K.DLDLDIPYDEPALK.A
R3/RRR3-6/2	1617.290	1617.778	-302.714	0.353	426.198	0.387	15	0.137	-.DLDLDIPYDEPALK.-
R3/RRR3-6/2	1616.974	1617.778	-1119.408	0.276	605.891	0.335	17	0.137	K.DLDLDIPYDEPALK.A
R3/RRR3-2/2	1617.603	1617.778	-108.359	0.354	440.321	0.342	15	0.136	-.DLDLDIPYDEPALK.-
R3/RRR3-14/2	1454.277	1454.561	-196.131	0.565	1641.861	0.579	21	0.260	R.DLVGVAYTEEETK.A
R3/RRR3-14/2	1454.067	1454.561	-340.567	0.506	1657.635	0.564	21	0.258	R.DLVGVAYTEEETK.A
R3/RRR3-14/2	1454.060	1454.561	-1034.993	0.564	1603.376	0.552	21	0.248	R.DLVGVAYTEEETK.A
R3/RRR3-14/2	1978.461	1979.247	-905.489	0.461	955.134	0.580	22	0.179	R.EGLHYNPYFPGGAIAM*PK.M
R3/RRR3-14/2	1665.332	1664.883	270.512	0.464	846.596	0.516	24	0.169	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1665.608	1664.883	-165.513	0.515	660.887	0.529	22	0.162	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1664.713	1664.883	-102.424	0.455	725.107	0.492	23	0.160	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1664.449	1664.883	-261.697	0.453	665.690	0.510	22	0.159	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1664.817	1664.883	-39.538	0.403	672.346	0.508	21	0.157	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1665.609	1664.883	-164.925	0.466	823.148	0.443	22	0.157	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1666.250	1664.883	220.837	0.478	745.232	0.473	21	0.157	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1666.341	1664.883	275.638	0.499	525.869	0.490	19	0.151	R.FANGGAYPPDLSLITK.A
R3/RRR3-15/2	1665.794	1664.883	-53.627	0.376	358.933	0.496	19	0.149	R.FANGGAYPPDLSLITK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1889.393	1890.049	-879.144	0.470	786.410	0.426	18	0.148	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-15/2	1665.457	1664.883	-256.466	0.356	445.283	0.432	19	0.144	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1889.524	1890.049	-809.037	0.457	516.895	0.450	17	0.143	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-14/3	1889.402	1890.049	-874.028	0.452	1528.442	0.354	31	0.142	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-14/2	1665.608	1664.883	-165.366	0.336	414.841	0.425	17	0.142	R.FANGGAYPPDLSLITK.A
R3/RRR3-14/2	1890.354	1890.049	162.013	0.470	423.647	0.463	16	0.142	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-15/2	1666.171	1664.883	173.303	0.245	259.579	0.359	18	0.137	-.FANGGAYPPDLSLITK.-
R3/RRR3-14/3	1889.225	1890.049	-968.016	0.494	1056.669	0.393	28	0.115	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-14/3	1890.817	1890.049	-122.948	0.396	1166.315	0.345	26	0.114	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-14/3	1979.112	1979.247	-68.420	0.412	972.885	0.355	26	0.101	R.EGLHYNPYFPGGAIAM*PK.M
R3/RRR3-20/3	1890.331	1890.049	149.766	0.421	959.745	0.328	25	0.101	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-14/3	1889.392	1890.049	-879.281	0.414	907.594	0.339	26	0.101	K.LSDRFPQPYPNEQAAR.F
R3/RRR3-14/3	1891.019	1890.049	-15.715	0.418	641.042	0.310	22	0.085	-.LSDRFPQPYPNEQAAR.-
R3/RRR3-20/3	1889.931	1890.049	-62.530	0.342	740.521	0.159	22	0.082	-.LSDRFPQPYPNEQAAR.-
R3/RRR3-7/2	1608.299	1607.833	290.991	0.523	2549.474	0.452	23	0.380	R.SPPIEEVINTGVVPR.F
R3/RRR3-8/2	1607.493	1607.833	-212.169	0.512	2433.776	0.505	23	0.375	R.SPPIEEVINTGVVPR.F
R3/RRR3-8/2	1607.365	1607.833	-292.167	0.501	2183.742	0.515	22	0.328	R.SPPIEEVINTGVVPR.F
R3/RRR3-8/2	1344.279	1344.624	-257.265	0.478	1799.118	0.589	21	0.284	K.VVVESGAVPIFVK.L
R3/RRR3-7/2	1607.254	1607.833	-985.249	0.416	2051.557	0.434	21	0.281	R.SPPIEEVINTGVVPR.F
R3/RRR3-8/2	1601.512	1601.903	-245.300	0.518	1784.802	0.499	22	0.258	R.IVTVCLEGLENILK.V
R3/RRR3-7/2	1344.540	1344.624	-62.433	0.449	1585.946	0.514	19	0.234	K.VVVESGAVPIFVK.L
R3/RRR3-8/2	1344.311	1344.624	-233.578	0.394	1500.964	0.542	18	0.227	K.VVVESGAVPIFVK.L
R3/RRR3-8/2	1601.631	1601.903	-170.672	0.511	1535.066	0.422	21	0.207	R.IVTVCLEGLENILK.V
R3/RRR3-8/2	1601.557	1601.903	-216.549	0.478	1535.261	0.404	19	0.202	R.IVTVCLEGLENILK.V
R3/RRR3-7/2	1344.177	1344.624	-333.341	0.436	1040.725	0.566	16	0.185	K.VVVESGAVPIFVK.L
R3/RRR3-7/2	1601.413	1601.903	-306.862	0.482	1293.448	0.434	19	0.185	R.IVTVCLEGLENILK.V
R3/RRR3-7/2	1601.410	1601.903	-308.774	0.520	1208.490	0.460	19	0.182	R.IVTVCLEGLENILK.V
R3/RRR3-2/2	1343.773	1344.624	-1381.891	0.352	1200.154	0.405	17	0.171	K.VVVESGAVPIFVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1344.035	1344.624	-1185.764	0.296	1230.618	0.355	17	0.165	K.VVVESGAVPIFVK.L
R3/RRR3-8/2	1959.689	1960.416	-884.033	0.411	1101.306	0.403	20	0.162	R.LVELLMHPSASVLIPALR.T
R3/RRR3-8/2	1960.376	1960.416	-20.773	0.334	898.720	0.320	19	0.140	R.LVELLMHPSASVLIPALR.T
R3/RRR3-8/2	1961.367	1960.416	-25.382	0.322	528.373	0.262	17	0.129	R.LVELLMHPSASVLIPALR.T
R3/RRR3-7/2	1966.710	1966.330	193.963	0.513	1550.205	0.556	25	0.239	R.YFELSGLPM*LVLIGPDGK.T
R3/RRR3-7/2	1966.860	1966.330	-239.310	0.531	1117.538	0.560	22	0.191	R.YFELSGLPM*LVLIGPDGK.T
R3/RRR3-7/2	1966.286	1966.330	-22.439	0.535	1100.839	0.543	22	0.186	R.YFELSGLPM*LVLIGPDGK.T
R3/RRR3-7/3	1422.594	1422.761	-118.006	0.437	1573.059	0.460	28	0.171	K.VM*GIPHLVILDAK.S
R3/RRR3-7/2	927.436	928.108	-1808.438	0.348	657.152	0.574	14	0.163	K.VPVSELVGK.T
R3/RRR3-7/2	928.046	928.108	-66.573	0.395	661.128	0.523	14	0.161	K.VPVSELVGK.T
R3/RRR3-7/2	928.107	928.108	-0.476	0.428	613.662	0.491	14	0.157	K.VPVSELVGK.T
R3/RRR3-6/2	928.536	928.108	461.956	0.396	566.643	0.442	13	0.150	K.VPVSELVGK.T
R3/RRR3-7/2	1761.764	1763.050	-1301.713	0.378	517.163	0.460	18	0.144	-.MPWLAVPFSDSEALAK.L
R3/RRR3-7/2	1761.883	1763.050	-1233.731	0.378	465.489	0.463	18	0.144	-.MPWLAVPFSDSEALAK.L
R3/RRR3-2/2	928.295	928.108	201.717	0.269	544.398	0.356	12	0.137	-.VPVSELVGK.-
R3/RRR3-7/2	1761.407	1763.050	-2074.657	0.277	457.296	0.406	17	0.136	-.MPWLAVPFSDSEALAK.L
R3/RRR3-2/2	928.399	928.108	314.847	0.219	388.883	0.406	11	0.135	-.VPVSELVGK.-
R3/RRR3-7/2	1777.787	1779.049	-1276.262	0.300	510.107	0.266	16	0.131	-.M*PWLAVPFSDSEALAK.L
R3/RRR3-7/3	1422.035	1422.761	-1217.414	0.379	1080.622	0.348	24	0.106	K.VM*GIPHLVILDAK.S
R3/RRR3-10/2	1274.913	1275.434	-1196.369	0.428	1364.851	0.467	19	0.200	K.EIVGSIQSQVSK.I
R3/RRR3-10/2	1916.507	1915.092	217.682	0.510	1031.426	0.574	20	0.186	K.DWLSSYESLDTFVVPR.S
R3/RRR3-11/2	1275.046	1275.434	-305.131	0.405	1315.681	0.398	18	0.182	K.EIVGSIQSQVSK.I
R3/RRR3-10/2	1775.422	1776.068	-930.132	0.376	661.820	0.461	22	0.148	R.YGLPPSFLSAVLAPSQK.G
R3/RRR3-10/2	1948.565	1949.189	-835.859	0.463	431.438	0.478	17	0.143	R.SILEELCGNVHSIYWK.S
R3/RRR3-10/2	1948.697	1949.189	-253.243	0.474	479.344	0.453	18	0.143	R.SILEELCGNVHSIYWK.S
R3/RRR3-10/2	1776.502	1776.068	244.693	0.405	422.805	0.412	19	0.139	R.YGLPPSFLSAVLAPSQK.G
R3/RRR3-10/2	1274.400	1275.434	-1600.745	0.279	690.797	0.307	14	0.134	K.EIVGSIQSQVSK.I
R3/RRR3-7/2	1554.034	1554.729	-1093.759	0.358	2109.464	0.494	20	0.309	R.LAIGDLATQYFADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1403.115	1403.521	-290.020	0.457	1889.884	0.437	18	0.259	K.TFSYAGFEQQPK.T
R3/RRR3-7/2	1553.615	1554.729	-1364.206	0.257	1636.409	0.342	19	0.201	R.LAIGDLATQYFADR.D
R3/RRR3-8/2	1323.127	1322.363	-179.021	0.464	1450.760	0.209	16	0.157	R.GGADQFIEEAER.S
R3/RRR3-7/2	1198.187	1197.365	-148.843	0.404	787.428	0.423	15	0.149	R.DSFLVNGVAFK.K
R3/RRR3-12/2	1361.147	1360.541	-290.237	0.539	1238.420	0.525	16	0.199	K.FVAYTSAWTWK.K
R3/RRR3-12/2	1292.418	1291.481	-49.036	0.430	1051.704	0.424	16	0.165	R.GVNVIYALTGQR.R
R3/RRR3-14/2	1360.398	1360.541	-105.086	0.464	1017.428	0.414	16	0.163	K.FVAYTSAWTWK.K
R3/RRR3-21/2	1291.907	1291.481	330.222	0.426	1028.548	0.416	16	0.163	R.GVNVIYALTGQR.R
R3/RRR3-14/2	1360.188	1360.541	-259.927	0.324	1039.074	0.414	15	0.161	K.FVAYTSAWTWK.K
R3/RRR3-13/2	1291.361	1291.481	-93.543	0.336	1058.062	0.401	16	0.161	R.GVNVIYALTGQR.R
R3/RRR3-21/2	1292.438	1291.481	-33.404	0.410	985.872	0.411	16	0.159	R.GVNVIYALTGQR.R
R3/RRR3-13/2	1592.021	1590.846	110.237	0.465	774.757	0.438	19	0.156	K.EVFWLPVDSAWLK.I
R3/RRR3-13/2	1592.174	1590.846	206.504	0.425	784.698	0.422	19	0.154	K.EVFWLPVDSAWLK.I
R3/RRR3-13/2	1591.496	1590.846	-220.533	0.459	679.246	0.410	18	0.149	K.EVFWLPVDSAWLK.I
R3/RRR3-14/2	1591.502	1590.846	-216.686	0.418	687.089	0.420	16	0.147	K.EVFWLPVDSAWLK.I
R3/RRR3-13/2	1291.471	1291.481	-8.021	0.331	927.378	0.345	15	0.147	R.GVNVIYALTGQR.R
R3/RRR3-21/2	1291.217	1291.481	-205.254	0.309	838.132	0.382	15	0.147	R.GVNVIYALTGQR.R
R3/RRR3-21/2	1360.282	1360.541	-190.872	0.337	429.302	0.482	12	0.144	K.FVAYTSAWTWK.K
R3/RRR3-14/2	1591.753	1590.846	-58.506	0.361	352.670	0.438	14	0.142	K.EVFWLPVDSAWLK.I
R3/RRR3-14/2	1591.955	1590.846	68.556	0.398	433.098	0.417	14	0.139	-.EVFWLPVDSAWLK.-
R3/RRR3-21/2	1359.314	1360.541	-1642.974	0.214	597.198	0.338	14	0.134	K.FVAYTSAWTWK.K
R3/RRR3-13/3	1715.951	1714.967	-9.064	0.456	1247.104	0.292	27	0.106	K.FRNEELYSVGKPM*K.E
R3/RRR3-13/2	1441.537	1442.646	-1467.809	0.380	960.786	0.465	15	0.161	R.WVLSAADPWVAAR.G
R3/RRR3-13/2	1443.156	1442.646	-340.937	0.403	820.678	0.466	15	0.154	-.WVLSAADPWVAAR.-
R3/RRR3-13/2	1666.869	1666.887	-10.916	0.391	461.214	0.517	17	0.144	R.LAAACPALCVSVDYR.L
R3/RRR3-13/3	1115.561	1115.267	264.097	0.447	1164.405	0.379	21	0.117	R.AHAYAAAVAAAK.G
R3/RRR3-13/3	1132.896	1133.196	-265.183	0.399	776.656	0.339	18	0.093	-.DVHLGDYSAR.-
R3/RRR3-13/3	1133.435	1133.196	211.322	0.294	952.142	0.266	18	0.088	R.DVHLGDYSAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1346.027	1346.496	-348.942	0.525	1108.438	0.535	20	0.190	R.DM*TALSGAHTIGR.A
R3/RRR3-15/2	1093.497	1093.218	256.002	0.469	1093.539	0.491	15	0.181	R.NINASFASLR.Q
R3/RRR3-14/2	1346.010	1346.496	-362.137	0.519	999.936	0.526	19	0.180	R.DM*TALSGAHTIGR.A
R3/RRR3-14/2	991.941	992.150	-211.575	0.463	1296.552	0.331	14	0.170	-.GFEVIDAIK.-
R3/RRR3-15/2	1093.220	1093.218	1.276	0.469	1003.422	0.447	16	0.169	R.NINASFASLR.Q
R3/RRR3-14/2	1346.091	1346.496	-301.082	0.477	961.496	0.464	19	0.168	R.DM*TALSGAHTIGR.A
R3/RRR3-15/2	1345.990	1346.496	-1121.781	0.476	838.961	0.506	19	0.167	R.DM*TALSGAHTIGR.A
R3/RRR3-15/2	992.017	992.150	-135.161	0.437	1371.225	0.267	14	0.166	-.GFEVIDAIK.-
R3/RRR3-14/2	991.830	992.150	-324.427	0.442	1261.879	0.308	14	0.164	-.GFEVIDAIK.-
R3/RRR3-14/2	1549.084	1549.732	-1067.017	0.472	802.295	0.468	23	0.161	K.M*GNLLPSSGTATEVR.L
R3/RRR3-15/2	1549.400	1549.732	-215.260	0.536	740.386	0.488	22	0.161	K.M*GNLLPSSGTATEVR.L
R3/RRR3-14/2	991.816	992.150	-338.258	0.447	1253.339	0.293	14	0.161	-.GFEVIDAIK.-
R3/RRR3-14/2	1549.247	1549.732	-313.752	0.482	803.189	0.460	23	0.161	K.M*GNLLPSSGTATEVR.L
R3/RRR3-15/2	1548.992	1549.732	-1126.758	0.436	716.922	0.445	22	0.154	K.M*GNLLPSSGTATEVR.L
R3/RRR3-15/2	1549.314	1549.732	-270.827	0.485	672.220	0.459	21	0.154	K.M*GNLLPSSGTATEVR.L
R3/RRR3-14/2	1533.215	1533.733	-992.660	0.479	432.686	0.524	19	0.154	K.MGNLLPSSGTATEVR.L
R3/RRR3-15/2	1346.729	1346.496	173.813	0.465	556.545	0.481	17	0.152	R.DM*TALSGAHTIGR.A
R3/RRR3-14/2	1533.197	1533.733	-1004.890	0.410	474.044	0.506	19	0.152	K.MGNLLPSSGTATEVR.L
R3/RRR3-14/2	1549.252	1549.732	-311.143	0.482	692.516	0.418	22	0.151	K.M*GNLLPSSGTATEVR.L
R3/RRR3-15/2	1093.686	1093.218	429.478	0.309	882.477	0.360	15	0.147	R.NINASFASLR.Q
R3/RRR3-14/2	1532.651	1533.733	-1362.096	0.366	543.290	0.371	21	0.143	K.MGNLLPSSGTATEVR.L
R3/RRR3-15/2	1346.929	1346.496	322.864	0.250	476.964	0.262	18	0.135	R.DM*TALSGAHTIGR.A
R3/RRR3-8/2	1980.611	1981.204	-806.757	0.528	2000.420	0.643	25	0.333	K.QIGVIGWGSQGPAQAQNLR.D
R3/RRR3-8/2	1980.756	1981.204	-227.262	0.559	1959.544	0.618	25	0.318	K.QIGVIGWGSQGPAQAQNLR.D
R3/RRR3-8/2	1980.582	1981.204	-821.729	0.533	1467.385	0.645	24	0.248	K.QIGVIGWGSQGPAQAQNLR.D
R3/RRR3-7/3	1982.877	1981.204	-165.711	0.401	1825.182	0.473	32	0.220	K.QIGVIGWGSQGPAQAQNLR.D
R3/RRR3-8/2	1360.398	1359.512	-84.115	0.417	785.604	0.389	16	0.148	K.VSLAGHDEYIVR.G
R3/RRR3-7/2	1699.460	1698.920	-271.291	0.505	737.634	0.448	17	0.147	K.GMLEVYNSLTEEGKK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1360.214	1359.512	-219.956	0.440	718.494	0.402	15	0.146	K.VSLAGHDEYIVR.G
R3/RRR3-8/2	1359.113	1359.512	-294.815	0.354	614.441	0.326	14	0.136	K.VSLAGHDEYIVR.G
R3/RRR3-8/3	1616.892	1616.800	56.852	0.387	906.257	0.441	25	0.110	K.EKVSLAGHDEYIVR.G
R3/RRR3-8/3	1981.300	1981.204	48.620	0.333	737.810	0.322	25	0.090	K.QIGVIGWGSQGPAQAQNLR.D
R3/RRR3-13/2	1419.156	1419.606	-318.146	0.453	1862.429	0.537	19	0.276	R.AFQLYSSGIFTGK.C
R3/RRR3-13/2	1419.377	1419.606	-162.050	0.471	1681.514	0.510	18	0.243	R.AFQLYSSGIFTGK.C
R3/RRR3-18/2	1419.546	1419.606	-42.315	0.499	1583.185	0.467	19	0.221	R.AFQLYSSGIFTGK.C
R3/RRR3-24/2	1539.263	1539.719	-296.821	0.564	1135.849	0.654	22	0.213	K.AVANQPVSVAIEAGGR.A
R3/RRR3-24/2	1539.448	1539.719	-176.214	0.552	1232.290	0.577	23	0.207	K.AVANQPVSVAIEAGGR.A
R3/RRR3-15/2	1539.283	1539.719	-283.931	0.524	1209.086	0.561	23	0.201	K.AVANQPVSVAIEAGGR.A
R3/RRR3-11/2	1540.214	1539.719	322.694	0.559	1114.537	0.585	22	0.197	K.AVANQPVSVAIEAGGR.A
R3/RRR3-13/2	1335.119	1334.536	-313.777	0.527	1335.491	0.469	18	0.197	K.CGIAVEPSYPLK.K
R3/RRR3-12/2	1539.313	1539.719	-264.041	0.550	1097.992	0.584	22	0.196	K.AVANQPVSVAIEAGGR.A
R3/RRR3-15/2	1539.173	1539.719	-1007.272	0.518	1125.461	0.558	24	0.195	K.AVANQPVSVAIEAGGR.A
R3/RRR3-18/2	1539.778	1539.719	38.437	0.534	1102.004	0.569	22	0.193	K.AVANQPVSVAIEAGGR.A
R3/RRR3-17/2	1539.621	1539.719	-63.349	0.551	1124.964	0.550	23	0.192	K.AVANQPVSVAIEAGGR.A
R3/RRR3-16/2	1539.159	1539.719	-1016.031	0.497	1072.192	0.563	23	0.190	K.AVANQPVSVAIEAGGR.A
R3/RRR3-13/2	1540.236	1539.719	-314.599	0.498	984.212	0.575	21	0.184	K.AVANQPVSVAIEAGGR.A
R3/RRR3-14/2	1539.113	1539.719	-1046.052	0.484	1031.918	0.546	22	0.184	K.AVANQPVSVAIEAGGR.A
R3/RRR3-18/2	1418.973	1419.606	-1154.118	0.416	1133.971	0.502	17	0.183	R.AFQLYSSGIFTGK.C
R3/RRR3-24/2	1539.246	1539.719	-308.278	0.507	954.461	0.562	22	0.181	K.AVANQPVSVAIEAGGR.A
R3/RRR3-12/2	1539.295	1539.719	-275.816	0.517	1033.668	0.519	23	0.180	K.AVANQPVSVAIEAGGR.A
R3/RRR3-11/2	1539.214	1539.719	-980.677	0.475	941.290	0.557	22	0.179	K.AVANQPVSVAIEAGGR.A
R3/RRR3-12/2	1539.215	1539.719	-979.563	0.495	1007.235	0.528	22	0.179	K.AVANQPVSVAIEAGGR.A
R3/RRR3-18/2	1419.037	1419.606	-1109.200	0.431	1078.792	0.489	17	0.177	R.AFQLYSSGIFTGK.C
R3/RRR3-18/2	1539.415	1539.719	-197.851	0.461	929.997	0.527	22	0.174	K.AVANQPVSVAIEAGGR.A
R3/RRR3-17/2	1540.345	1539.719	-243.436	0.494	984.926	0.505	21	0.173	K.AVANQPVSVAIEAGGR.A
R3/RRR3-11/2	1539.152	1539.719	-1020.889	0.516	810.434	0.563	21	0.172	K.AVANQPVSVAIEAGGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1539.128	1539.719	-1036.257	0.503	904.870	0.502	22	0.169	K.AVANQPVSVAIEAGGR.A
R3/RRR3-14/2	1538.718	1539.719	-1304.129	0.400	880.786	0.499	21	0.165	K.AVANQPVSVAIEAGGR.A
R3/RRR3-1/2	1539.365	1539.719	-230.149	0.462	821.201	0.502	21	0.164	K.AVANQPVSVAIEAGGR.A
R3/RRR3-13/2	1334.038	1334.536	-374.422	0.432	1151.233	0.346	17	0.160	K.CGIAVEPSYPLK.K
R3/RRR3-11/2	1418.777	1419.606	-1292.957	0.355	951.833	0.381	16	0.153	R.AFQLYSSGIFTGK.C
R3/RRR3-13/2	1418.911	1419.606	-1198.608	0.352	824.078	0.437	15	0.153	R.AFQLYSSGIFTGK.C
R3/RRR3-12/2	1419.438	1419.606	-119.087	0.404	582.059	0.490	16	0.153	R.AFQLYSSGIFTGK.C
R3/RRR3-24/2	1419.124	1419.606	-340.757	0.366	602.706	0.497	16	0.153	R.AFQLYSSGIFTGK.C
R3/RRR3-14/2	1538.576	1539.719	-1396.559	0.347	747.819	0.431	18	0.149	K.AVANQPVSVAIEAGGR.A
R3/RRR3-11/2	1419.305	1419.606	-213.128	0.279	768.584	0.424	14	0.146	R.AFQLYSSGIFTGK.C
R3/RRR3-13/2	1334.250	1334.536	-215.060	0.427	1017.775	0.293	16	0.145	K.CGIAVEPSYPLK.K
R3/RRR3-24/2	1419.250	1419.606	-252.043	0.321	536.786	0.416	16	0.144	R.AFQLYSSGIFTGK.C
R3/RRR3-13/2	1041.453	1041.099	341.802	0.382	889.047	0.214	14	0.136	K.SWGESGYVR.M
R3/RRR3-12/2	1419.177	1419.606	-303.216	0.303	594.285	0.286	15	0.136	R.AFQLYSSGIFTGK.C
R3/RRR3-19/2	1419.236	1419.606	-261.621	0.285	585.288	0.307	14	0.136	R.AFQLYSSGIFTGK.C
R3/RRR3-11/2	1418.914	1419.606	-1195.844	0.297	512.855	0.276	14	0.135	R.AFQLYSSGIFTGK.C
R3/RRR3-24/2	1419.328	1419.606	-196.648	0.200	419.116	0.383	12	0.134	R.AFQLYSSGIFTGK.C
R3/RRR3-13/2	1040.965	1041.099	-128.981	0.402	804.943	0.202	14	0.134	K.SWGESGYVR.M
R3/RRR3-11/2	1040.586	1041.099	-1458.247	0.298	808.441	0.198	14	0.133	K.SWGESGYVR.M
R3/RRR3-11/2	1040.802	1041.099	-285.341	0.205	690.115	0.116	13	0.128	K.SWGESGYVR.M
R3/RRR3-12/2	1335.536	1334.536	-0.331	0.376	684.767	0.174	14	0.117	-.CGIAVEPSYPLK.-
R3/RRR3-11/3	1504.642	1504.756	-75.735	0.586	3107.737	0.445	31	0.475	K.KVSPQLIAEYTVR.A
R3/RRR3-10/3	1504.433	1504.756	-215.400	0.539	2585.170	0.401	28	0.326	K.KVSPQLIAEYTVR.A
R3/RRR3-10/2	1503.888	1504.756	-1245.673	0.543	2020.051	0.503	22	0.295	K.KVSPQLIAEYTVR.A
R3/RRR3-10/2	1504.392	1504.756	-242.417	0.553	1755.998	0.552	21	0.268	K.KVSPQLIAEYTVR.A
R3/RRR3-11/2	1504.325	1504.756	-287.192	0.517	1803.439	0.515	21	0.265	K.KVSPQLIAEYTVR.A
R3/RRR3-11/2	1504.348	1504.756	-271.887	0.505	1551.203	0.537	20	0.235	K.KVSPQLIAEYTVR.A
R3/RRR3-10/2	1504.302	1504.756	-302.661	0.509	1575.796	0.506	20	0.231	K.KVSPQLIAEYTVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1505.301	1504.756	-302.867	0.542	1623.522	0.466	21	0.228	K.KVSPQLIAEYTVR.A
R3/RRR3-11/3	1296.519	1296.501	13.531	0.543	1692.465	0.453	25	0.182	K.KPWALSFSFGR.A
R3/RRR3-10/3	1503.956	1504.756	-1200.362	0.502	1846.619	0.363	25	0.182	K.KVSPQLIAEYTVR.A
R3/RRR3-1/2	1504.349	1504.756	-271.480	0.417	990.779	0.463	16	0.166	K.KVSPQLIAEYTVR.A
R3/RRR3-11/3	1296.448	1296.501	-41.008	0.558	1572.575	0.441	24	0.165	K.KPWALSFSFGR.A
R3/RRR3-11/2	1376.106	1376.583	-347.673	0.460	690.518	0.532	18	0.164	K.VSPQLIAEYTVR.A
R3/RRR3-10/2	1376.174	1376.583	-298.011	0.431	727.522	0.519	19	0.164	K.VSPQLIAEYTVR.A
R3/RRR3-10/2	1376.157	1376.583	-310.470	0.462	695.434	0.515	18	0.163	K.VSPQLIAEYTVR.A
R3/RRR3-10/2	1296.236	1296.501	-205.215	0.427	591.229	0.543	17	0.161	K.KPWALSFSFGR.A
R3/RRR3-11/2	1376.345	1376.583	-173.700	0.444	626.173	0.526	17	0.160	K.VSPQLIAEYTVR.A
R3/RRR3-10/3	1296.678	1296.501	136.610	0.558	1419.843	0.461	24	0.154	K.KPWALSFSFGR.A
R3/RRR3-11/2	1295.456	1296.501	-1583.327	0.387	661.174	0.439	17	0.152	K.KPWALSFSFGR.A
R3/RRR3-10/2	1296.334	1296.501	-129.546	0.410	651.607	0.429	17	0.151	K.KPWALSFSFGR.A
R3/RRR3-10/2	1295.602	1296.501	-1470.125	0.322	702.365	0.425	18	0.149	K.KPWALSFSFGR.A
R3/RRR3-10/2	1376.293	1376.583	-211.248	0.328	574.928	0.459	16	0.148	K.VSPQLIAEYTVR.A
R3/RRR3-11/2	1296.305	1296.501	-151.650	0.340	611.527	0.428	16	0.147	K.KPWALSFSFGR.A
R3/RRR3-10/3	1296.829	1296.501	253.146	0.542	1415.893	0.422	24	0.144	K.KPWALSFSFGR.A
R3/RRR3-9/2	1377.439	1376.583	-105.030	0.332	356.660	0.437	14	0.143	K.VSPQLIAEYTVR.A
R3/RRR3-11/2	1375.629	1376.583	-1424.564	0.281	584.531	0.409	17	0.143	K.VSPQLIAEYTVR.A
R3/RRR3-2/2	1376.637	1376.583	39.524	0.299	329.610	0.355	13	0.139	K.VSPQLIAEYTVR.A
R3/RRR3-11/3	1296.553	1296.501	40.160	0.540	1308.544	0.405	24	0.131	K.KPWALSFSFGR.A
R3/RRR3-12/3	1504.565	1504.756	-127.128	0.449	1422.056	0.338	25	0.128	K.KVSPQLIAEYTVR.A
R3/RRR3-10/3	1296.113	1296.501	-300.465	0.485	1236.428	0.371	23	0.120	K.KPWALSFSFGR.A
R3/RRR3-3/3	1504.598	1504.756	-105.276	0.413	1465.291	0.280	26	0.119	K.KVSPQLIAEYTVR.A
R3/RRR3-3/3	1505.039	1504.756	188.717	0.431	1158.785	0.317	25	0.107	K.KVSPQLIAEYTVR.A
R3/RRR3-3/3	1504.505	1504.756	-166.928	0.354	772.453	0.218	22	0.087	K.KVSPQLIAEYTVR.A
R3/RRR3-9/2	1295.115	1295.475	-278.942	0.375	908.209	0.456	17	0.160	K.AVAHHTTAAFIR.V
R3/RRR3-9/2	1066.959	1066.269	-291.657	0.346	793.541	0.459	14	0.156	R.LVFQVCTAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	992.982	993.138	-158.272	0.414	558.548	0.485	15	0.155	R.VVGSEFVQK.Y
R3/RRR3-9/2	993.113	993.138	-25.349	0.444	523.188	0.447	14	0.151	R.VVGSEFVQK.Y
R3/RRR3-9/2	993.202	993.138	64.397	0.402	545.324	0.458	14	0.151	R.VVGSEFVQK.Y
R3/RRR3-9/2	1066.341	1066.269	67.214	0.357	572.713	0.465	13	0.149	R.LVFQVCTAK.M
R3/RRR3-9/2	1295.130	1295.475	-267.122	0.345	730.809	0.427	16	0.148	K.AVAHHTTAAFIR.V
R3/RRR3-9/2	1295.080	1295.475	-305.988	0.340	621.000	0.416	16	0.144	K.AVAHHTTAAFIR.V
R3/RRR3-9/2	1066.957	1066.269	-293.723	0.334	528.495	0.340	12	0.138	R.LVFQVCTAK.M
R3/RRR3-6/2	1642.343	1642.792	-274.687	0.529	2115.157	0.554	25	0.329	K.LAGLSAGGGEEPQQLSK.N
R3/RRR3-6/2	1642.578	1642.792	-131.085	0.528	1697.769	0.590	23	0.268	K.LAGLSAGGGEEPQQLSK.N
R3/RRR3-6/2	1326.137	1325.403	-201.142	0.515	1157.455	0.484	16	0.184	R.TSELEDNEFIK.F
R3/RRR3-6/2	1375.321	1375.550	-166.885	0.467	1146.102	0.455	19	0.179	K.LLFYDLYGGGEK.V
R3/RRR3-6/2	1325.122	1325.403	-212.660	0.460	1240.981	0.376	16	0.172	R.TSELEDNEFIK.F
R3/RRR3-6/2	1374.641	1375.550	-1392.899	0.348	1046.035	0.451	17	0.167	K.LLFYDLYGGGEK.V
R3/RRR3-6/2	1374.339	1375.550	-1613.965	0.363	1085.938	0.365	16	0.158	K.LLFYDLYGGGEK.V
R3/RRR3-6/2	1497.352	1497.717	-244.702	0.455	820.547	0.459	16	0.154	K.FLANITVADYIEK.Y
R3/RRR3-8/2	1952.238	1952.120	60.859	0.604	1713.595	0.578	24	0.268	K.GLHSSLNHLANEFDQIR.S
R3/RRR3-8/2	1426.184	1426.561	-265.154	0.503	1333.380	0.489	19	0.200	R.SSGGFWTWLTGAR.S
R3/RRR3-8/2	1106.027	1106.318	-264.750	0.371	1319.545	0.437	15	0.188	K.SAILMNLESK.A
R3/RRR3-8/2	1427.091	1426.561	-329.760	0.534	1055.622	0.498	18	0.177	R.SSGGFWTWLTGAR.S
R3/RRR3-8/2	1218.293	1219.370	-1710.545	0.470	858.132	0.482	14	0.162	R.NPAFLDWEVK.E
R3/RRR3-8/2	1425.332	1426.561	-1567.905	0.400	853.950	0.411	17	0.152	R.SSGGFWTWLTGAR.S
R3/RRR3-8/2	1121.317	1122.318	-1790.157	0.258	645.371	0.121	12	0.111	-.SAILM*NLESK.-
R3/RRR3-8/2	1969.964	1970.255	-148.021	0.467	1116.579	0.508	26	0.184	K.ALQLPEYPNAAELEAVLK.T
R3/RRR3-8/2	1970.566	1970.255	158.463	0.506	872.888	0.557	23	0.173	K.ALQLPEYPNAAELEAVLK.T
R3/RRR3-8/2	1969.505	1970.255	-891.190	0.413	636.865	0.472	20	0.148	K.ALQLPEYPNAAELEAVLK.T
R3/RRR3-3/2	1497.244	1497.725	-322.324	0.515	2309.942	0.431	21	0.325	R.SALLQGQALQALQR.F
R3/RRR3-3/2	1497.083	1497.725	-1100.282	0.425	2167.463	0.400	20	0.291	R.SALLQGQALQALQR.F
R3/RRR3-1/2	1497.190	1497.725	-1028.239	0.413	1828.499	0.396	19	0.237	R.SALLQGQALQALQR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1057.166	1057.229	-59.253	0.417	918.201	0.337	15	0.148	K.SIQNVGLAVR.Y
R3/RRR3-3/2	1149.208	1148.377	-147.516	0.405	905.144	0.341	15	0.148	K.ATFEVVQLLK.N
R3/RRR3-3/2	1148.034	1148.377	-299.428	0.384	919.281	0.317	15	0.146	K.ATFEVVQLLK.N
R3/RRR3-3/2	1057.007	1057.229	-210.308	0.405	752.176	0.327	14	0.141	K.SIQNVGLAVR.Y
R3/RRR3-2/2	1497.868	1497.725	95.587	0.377	291.131	0.326	17	0.140	R.SALLQGQALQALQR.F
R3/RRR3-3/3	1102.670	1102.271	362.759	0.482	326.853	0.470	15	0.113	R.VLRPNFEAR.T
R3/RRR3-2/3	1102.299	1102.271	24.745	0.463	282.690	0.471	14	0.112	R.VLRPNFEAR.T
R3/RRR3-3/3	1102.086	1102.271	-168.306	0.429	348.127	0.483	15	0.112	R.VLRPNFEAR.T
R3/RRR3-2/3	1101.985	1102.271	-260.900	0.428	282.905	0.543	14	0.111	-.VLRPNFEAR.-
R3/RRR3-3/3	1102.148	1102.271	-112.224	0.478	343.021	0.473	15	0.107	-.VLRPNFEAR.-
R3/RRR3-2/3	1102.561	1102.271	263.602	0.458	278.090	0.549	14	0.104	-.VLRPNFEAR.-
R3/RRR3-1/3	1101.881	1102.271	-355.429	0.338	275.989	0.339	14	0.101	-.VLRPNFEAR.-
R3/RRR3-3/3	1101.661	1102.271	-1465.825	0.456	325.579	0.424	15	0.100	-.VLRPNFEAR.-
R3/RRR3-8/2	1356.120	1355.560	-325.892	0.553	1426.189	0.525	17	0.219	R.TFLDQLVEVYK.Q
R3/RRR3-8/2	1355.323	1355.560	-175.581	0.508	1495.440	0.473	18	0.216	R.TFLDQLVEVYK.Q
R3/RRR3-8/2	1355.177	1355.560	-284.107	0.500	1354.858	0.525	17	0.211	R.TFLDQLVEVYK.Q
R3/RRR3-8/2	889.113	889.077	41.021	0.497	1093.989	0.383	12	0.166	K.RPDIIFK.W
R3/RRR3-8/2	1150.479	1150.349	112.636	0.336	700.821	0.485	16	0.153	R.IPLVSFTGSTK.V
R3/RRR3-8/2	1151.227	1150.349	-106.312	0.383	704.534	0.416	15	0.148	R.IPLVSFTGSTK.V
R3/RRR3-8/3	1609.924	1609.854	44.017	0.497	1647.670	0.323	28	0.146	R.KEHQFLAELGLAPR.N
R3/RRR3-8/2	888.479	889.077	-1803.326	0.420	732.937	0.345	11	0.145	K.RPDIIFK.W
R3/RRR3-8/2	1151.112	1150.349	-207.049	0.361	468.028	0.387	13	0.140	R.IPLVSFTGSTK.V
R3/RRR3-7/2	1150.424	1150.349	64.962	0.207	347.553	0.326	12	0.133	R.IPLVSFTGSTK.V
R3/RRR3-8/3	1609.902	1609.854	30.100	0.305	885.571	0.303	23	0.091	R.KEHQFLAELGLAPR.N
R3/RRR3-7/2	1504.049	1503.597	301.717	0.455	1554.580	0.528	22	0.233	R.ASQPTDTTTSPLAGR.L
R3/RRR3-7/2	1089.248	1089.313	-59.643	0.377	1821.707	0.276	19	0.211	R.LFVVIGAGGAGK.A
R3/RRR3-7/2	1503.252	1503.597	-230.058	0.450	1330.732	0.490	21	0.199	R.ASQPTDTTTSPLAGR.L
R3/RRR3-7/2	1502.633	1503.597	-1310.840	0.330	1462.729	0.385	21	0.191	R.ASQPTDTTTSPLAGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1333.170	1332.525	-267.123	0.449	849.529	0.576	20	0.177	K.IATTATEIVDVAK.M
R3/RRR3-7/2	1072.753	1072.240	-455.803	0.427	1344.440	0.326	17	0.173	K.DIGAVNTIIR.K
R3/RRR3-7/2	1332.292	1332.525	-175.400	0.405	850.597	0.508	19	0.165	K.IATTATEIVDVAK.M
R3/RRR3-7/2	1073.116	1072.240	-116.560	0.417	1270.697	0.308	17	0.165	K.DIGAVNTIIR.K
R3/RRR3-7/2	1089.319	1089.313	5.776	0.320	983.689	0.370	17	0.153	R.LFVVIGAGGAGK.A
R3/RRR3-7/2	1072.801	1072.240	-411.044	0.372	1023.091	0.246	15	0.142	-.DIGAVNTIIR.-
R3/RRR3-7/2	1332.151	1332.525	-281.941	0.358	353.420	0.438	15	0.141	K.IATTATEIVDVAK.M
R3/RRR3-7/2	1089.125	1089.313	-172.629	0.312	1067.494	0.149	16	0.134	-.LFVVIGAGGAGK.-
R3/RRR3-8/2	1536.418	1536.926	-984.295	0.354	1462.856	0.532	20	0.220	R.VAPLQVIVIPVPYK.D
R3/RRR3-8/2	1675.207	1675.821	-966.187	0.516	1189.808	0.583	20	0.202	R.GVQGATSHCLGQNFAK.M
R3/RRR3-8/2	1536.750	1536.926	-114.697	0.384	1309.121	0.481	19	0.194	R.VAPLQVIVIPVPYK.D
R3/RRR3-8/2	1394.304	1394.558	-183.141	0.482	858.036	0.409	16	0.155	R.WEFSNPTPFIR.S
R3/RRR3-8/2	1395.283	1395.625	-245.316	0.338	996.614	0.395	16	0.154	R.IYEEFLAVPVSK.G
R3/RRR3-8/2	1395.262	1394.558	-212.763	0.491	893.729	0.357	16	0.149	R.WEFSNPTPFIR.S
R3/RRR3-8/2	1395.506	1394.558	-37.517	0.516	746.080	0.389	15	0.147	R.WEFSNPTPFIR.S
R3/RRR3-8/2	1536.499	1536.926	-278.230	0.302	830.073	0.407	16	0.146	R.VAPLQVIVIPVPYK.D
R3/RRR3-7/2	1394.301	1394.558	-185.162	0.325	424.672	0.309	12	0.135	R.WEFSNPTPFIR.S
R3/RRR3-10/2	1085.483	1086.224	-1608.518	0.414	1642.711	0.506	18	0.240	K.EAAIQAINAGK.N
R3/RRR3-10/2	1086.038	1086.224	-171.429	0.472	1498.160	0.428	18	0.207	K.EAAIQAINAGK.N
R3/RRR3-10/2	1085.450	1086.224	-1639.023	0.396	1575.071	0.364	18	0.202	K.EAAIQAINAGK.N
R3/RRR3-10/2	1671.917	1670.798	71.283	0.453	1033.524	0.356	17	0.151	K.ENDVLLFADEVYDK.L
R3/RRR3-10/2	1925.595	1926.245	-859.818	0.443	709.168	0.463	17	0.147	K.AITLRPPDFSVPLEELK.A
R3/RRR3-10/2	1926.036	1926.245	-109.251	0.436	621.425	0.459	17	0.143	K.AITLRPPDFSVPLEELK.A
R3/RRR3-10/3	1432.309	1432.554	-171.624	0.431	452.365	0.541	20	0.114	R.FTFCKDDETLR.A
R3/RRR3-10/3	1432.463	1432.554	-63.525	0.332	475.277	0.507	20	0.106	R.FTFCKDDETLR.A
R3/RRR3-10/3	1432.410	1432.554	-100.453	0.321	433.076	0.448	19	0.101	R.FTFCKDDETLR.A
R3/RRR3-6/2	1790.620	1789.966	-193.684	0.579	2330.180	0.494	23	0.346	R.ASSGDLDNTNIISQILK.L
R3/RRR3-6/2	1788.884	1789.966	-1167.200	0.543	2141.331	0.510	23	0.317	R.ASSGDLDNTNIISQILK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1789.654	1789.966	-174.701	0.563	1701.077	0.543	22	0.254	R.ASSGDLDNTNIISQILK.L
R3/RRR3-6/2	1124.133	1124.226	-82.407	0.530	1358.486	0.465	16	0.200	K.FSENVLDATK.K
R3/RRR3-6/2	1116.549	1117.232	-1511.239	0.379	932.478	0.346	16	0.149	R.LEGELADLEK.G
R3/RRR3-2/2	1791.725	1789.966	-134.934	0.446	701.207	0.410	17	0.142	R.ASSGDLDNTNIISQILK.L
R3/RRR3-6/3	1299.847	1299.455	302.245	0.279	844.545	0.368	27	0.091	R.AAVEDVQPDKVK.F
R3/RRR3-8/2	1159.973	1160.296	-279.670	0.431	1369.750	0.323	16	0.174	R.VDEIVTCAPR.R
R3/RRR3-4/2	1746.499	1746.858	-206.078	0.568	1283.453	0.418	19	0.177	R.FGHNEIDEPSFTQPK.M
R3/RRR3-4/3	1487.658	1487.646	8.624	0.457	669.235	0.479	23	0.108	-.NHQSALEIYQKR.-
R3/RRR3-4/3	1487.012	1487.646	-1102.103	0.456	443.590	0.445	21	0.106	R.NHQSALEIYQKR.L
R3/RRR3-4/3	1487.056	1487.646	-1072.306	0.442	673.647	0.425	23	0.105	R.NHQSALEIYQKR.L
R3/RRR3-4/2	1520.219	1520.624	-267.518	0.509	2560.954	0.507	24	0.402	R.VEQGSLTGETASVNK.T
R3/RRR3-4/2	1520.111	1520.624	-998.398	0.476	2244.253	0.538	23	0.347	R.VEQGSLTGETASVNK.T
R3/RRR3-4/2	1519.638	1520.624	-1310.673	0.395	2215.659	0.490	23	0.326	R.VEQGSLTGETASVNK.T
R3/RRR3-2/2	1978.938	1978.232	-149.392	0.528	1929.453	0.511	26	0.282	R.SGYIQLLDGSVVLLDEGAK.A
R3/RRR3-2/2	1520.226	1520.624	-262.846	0.499	1733.614	0.511	22	0.253	R.VEQGSLTGETASVNK.T
R3/RRR3-4/2	1978.677	1978.232	225.569	0.477	1651.239	0.489	23	0.234	R.SGYIQLLDGSVVLLDEGAK.A
R3/RRR3-3/2	1520.012	1520.624	-1063.466	0.434	1040.611	0.337	21	0.153	R.VEQGSLTGETASVNK.T
R3/RRR3-4/2	1001.017	1001.119	-102.633	0.443	1095.438	0.236	13	0.143	K.GAVENLLER.S
R3/RRR3-2/2	1978.986	1978.232	-124.826	0.416	602.406	0.428	21	0.143	R.SGYIQLLDGSVVLLDEGAK.A
R3/RRR3-4/2	1001.821	1001.119	-298.093	0.460	1119.162	0.224	13	0.141	K.GAVENLLER.S
R3/RRR3-4/2	1000.729	1001.119	-391.158	0.381	1065.732	0.218	13	0.140	K.GAVENLLER.S
R3/RRR3-4/2	887.126	887.102	26.415	0.250	732.895	0.222	11	0.126	-.ALILSTLR.-
R3/RRR3-5/2	1123.035	1123.284	-222.473	0.479	1735.717	0.448	17	0.240	K.LSEGYLTLAR.D
R3/RRR3-5/2	1349.111	1348.486	-279.485	0.524	1490.997	0.558	17	0.232	R.NLAGEIAQEFQK.R
R3/RRR3-5/2	1122.561	1123.284	-1539.575	0.448	1606.498	0.431	17	0.220	K.LSEGYLTLAR.D
R3/RRR3-5/2	1348.123	1348.486	-270.245	0.502	1549.458	0.441	17	0.213	R.NLAGEIAQEFQK.R
R3/RRR3-5/2	1370.091	1370.748	-1213.168	0.358	1330.540	0.535	21	0.207	R.LLPVALGLLYLGK.Q
R3/RRR3-5/2	1348.130	1348.486	-265.067	0.462	1610.684	0.376	17	0.206	R.NLAGEIAQEFQK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1123.078	1123.284	-183.763	0.393	1466.536	0.349	17	0.188	K.LSEGYLTLAR.D
R3/RRR3-5/2	1533.004	1532.809	127.339	0.463	1222.583	0.467	20	0.183	R.IGAILGLGIAYAGSQK.E
R3/RRR3-5/2	1370.376	1370.748	-271.753	0.333	932.543	0.485	19	0.164	R.LLPVALGLLYLGK.Q
R3/RRR3-1/2	1348.155	1348.486	-246.444	0.300	465.799	0.323	13	0.134	R.NLAGEIAQEFQK.R
R3/RRR3-5/2	1370.164	1370.748	-1159.488	0.124	319.161	0.362	10	0.122	-.LLPVALGLLYLGK.-
R3/RRR3-9/2	1167.873	1168.368	-425.389	0.417	1542.721	0.319	16	0.189	K.AEEIVLQPIR.E
R3/RRR3-9/2	1167.410	1168.368	-1682.004	0.426	1333.360	0.361	15	0.177	K.AEEIVLQPIR.E
R3/RRR3-9/2	1185.632	1186.340	-1445.077	0.338	1209.127	0.388	16	0.168	R.EISGAVQLPGSK.S
R3/RRR3-9/2	1297.273	1296.541	-207.033	0.509	701.587	0.487	17	0.158	R.ERPIGDLVVGLK.Q
R3/RRR3-9/2	1706.214	1706.922	-1003.739	0.432	546.768	0.529	20	0.153	K.TFPNYFDVLSTFVR.-
R3/RRR3-9/2	1296.361	1296.541	-139.083	0.391	747.677	0.454	16	0.153	R.ERPIGDLVVGLK.Q
R3/RRR3-9/2	1167.524	1168.368	-1584.523	0.270	870.158	0.253	13	0.136	K.AEEIVLQPIR.E
R3/RRR3-9/2	1296.862	1296.541	248.712	0.249	547.807	0.218	15	0.130	R.ERPIGDLVVGLK.Q
R3/RRR3-7/2	1369.325	1369.635	-227.255	0.440	630.643	0.535	19	0.161	K.QQQILLATQVVK.M
R3/RRR3-7/2	1369.198	1369.635	-319.917	0.413	637.042	0.509	19	0.158	K.QQQILLATQVVK.M
R3/RRR3-6/2	1108.653	1109.214	-1413.001	0.453	777.429	0.424	17	0.155	R.IAEGYELASR.I
R3/RRR3-7/2	1058.257	1057.226	29.548	0.461	908.252	0.349	14	0.147	K.AVLAVADLER.K
R3/RRR3-7/2	1368.701	1369.635	-1417.014	0.252	323.403	0.408	15	0.137	K.QQQILLATQVVK.M
R3/RRR3-7/2	977.928	978.081	-156.764	0.402	1017.166	0.179	14	0.136	R.FQELSPEK.L
R3/RRR3-7/2	978.035	978.081	-46.708	0.452	1031.627	0.155	14	0.133	R.FQELSPEK.L
R3/RRR3-6/2	1109.113	1109.214	-91.692	0.204	365.669	0.293	14	0.132	R.IAEGYELASR.I
R3/RRR3-3/2	1924.057	1922.169	-58.455	0.428	715.447	0.557	17	0.157	K.AISVGGQETNIITDYVLK.I
R3/RRR3-2/2	1921.542	1922.169	-849.015	0.402	556.573	0.469	16	0.140	K.AISVGGQETNIITDYVLK.I
R3/RRR3-2/2	1247.438	1247.447	-7.521	0.406	752.697	0.362	15	0.140	R.VTTGEM*IVGPAR.A
R3/RRR3-8/2	1754.344	1754.918	-899.991	0.525	3665.898	0.546	25	0.732	K.IPFSSFDILTDDEVR.Q
R3/RRR3-9/2	1754.155	1754.918	-1007.996	0.525	2555.409	0.559	24	0.422	K.IPFSSFDILTDDEVR.Q
R3/RRR3-9/2	1755.433	1754.918	-277.009	0.527	1577.317	0.552	19	0.240	K.IPFSSFDILTDDEVR.Q
R3/RRR3-8/2	1016.670	1016.091	-414.530	0.358	805.788	0.395	18	0.151	K.AELEAAAGGAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1016.850	1016.091	-237.337	0.355	700.914	0.379	17	0.146	K.AELEAAAGGAR.A
R3/RRR3-9/2	1016.162	1016.091	70.834	0.359	885.934	0.319	17	0.146	K.AELEAAAGGAR.A
R3/RRR3-8/2	1636.779	1635.950	-104.845	0.389	294.395	0.475	16	0.139	R.LESLVNSSPVMAFIK.G
R3/RRR3-9/2	1016.547	1016.091	450.325	0.325	620.588	0.279	15	0.136	K.AELEAAAGGAR.A
R3/RRR3-8/2	1198.271	1197.453	-152.001	0.487	1504.128	0.272	16	0.175	K.ELVQNLLVLR.F
R3/RRR3-7/2	1196.647	1197.453	-1513.321	0.421	1313.565	0.339	16	0.173	K.ELVQNLLVLR.F
R3/RRR3-7/2	1197.338	1197.453	-95.775	0.488	1421.940	0.292	16	0.172	K.ELVQNLLVLR.F
R3/RRR3-7/2	1199.192	1199.296	-86.949	0.452	948.995	0.503	17	0.171	R.GPPEADELSKR.M
R3/RRR3-7/2	1511.324	1511.661	-223.564	0.447	1185.273	0.389	17	0.169	R.YQDVKIPEAYER.L
R3/RRR3-8/2	1197.423	1197.453	-24.398	0.364	793.802	0.307	13	0.140	K.ELVQNLLVLR.F
R3/RRR3-14/2	1198.405	1197.453	-39.907	0.312	709.826	0.269	13	0.136	K.ELVQNLLVLR.F
R3/RRR3-7/3	1702.378	1701.950	252.642	0.449	1300.323	0.363	26	0.124	R.VNNERWEGVPFILK.A
R3/RRR3-7/3	1701.924	1701.950	-15.015	0.464	880.760	0.418	23	0.110	R.VNNERWEGVPFILK.A
R3/RRR3-7/3	1701.776	1701.950	-102.431	0.407	871.096	0.424	23	0.109	R.VNNERWEGVPFILK.A
R3/RRR3-24/3	1775.784	1774.911	-71.480	0.531	2222.331	0.470	30	0.283	R.HGTHAEFTTCLWTGR.V
R3/RRR3-24/2	1116.133	1116.296	-147.061	0.458	1250.516	0.457	17	0.189	R.KVTIQNLSGR.D
R3/RRR3-24/2	1115.597	1116.296	-1528.004	0.436	1217.352	0.472	17	0.189	R.KVTIQNLSGR.D
R3/RRR3-23/3	1775.638	1774.911	-154.437	0.443	1823.618	0.372	29	0.183	R.HGTHAEFTTCLWTGR.V
R3/RRR3-23/2	1116.007	1116.296	-259.639	0.430	1117.331	0.483	16	0.182	R.KVTIQNLSGR.D
R3/RRR3-24/2	987.934	988.123	-192.542	0.437	1117.979	0.457	14	0.177	K.VTIQNLSGR.D
R3/RRR3-24/2	987.671	988.123	-459.862	0.438	1047.028	0.475	14	0.175	K.VTIQNLSGR.D
R3/RRR3-24/2	1115.629	1116.296	-1499.426	0.480	1012.941	0.478	15	0.173	R.KVTIQNLSGR.D
R3/RRR3-24/2	988.080	988.123	-43.693	0.436	1056.287	0.447	14	0.172	K.VTIQNLSGR.D
R3/RRR3-23/2	988.007	988.123	-118.174	0.447	1164.927	0.341	14	0.162	K.VTIQNLSGR.D
R3/RRR3-23/2	987.990	988.123	-135.154	0.401	851.927	0.463	13	0.161	K.VTIQNLSGR.D
R3/RRR3-24/2	1117.030	1116.296	-239.563	0.337	708.270	0.350	14	0.143	R.KVTIQNLSGR.D
R3/RRR3-25/3	1116.501	1116.296	183.439	0.441	1173.225	0.331	20	0.109	R.KVTIQNLSGR.D
R3/RRR3-24/3	1775.102	1774.911	108.033	0.292	405.387	0.486	26	0.103	R.HGTHAEFTTCLWTGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/3	1116.289	1116.296	-6.221	0.387	1155.143	0.290	20	0.101	-.KVTIQNLSGR.-
R3/RRR3-24/3	1116.556	1116.296	233.103	0.377	978.705	0.285	20	0.095	R.KVTIQNLSGR.D
R3/RRR3-25/3	1115.781	1116.296	-1362.068	0.344	666.824	0.273	18	0.092	R.KVTIQNLSGR.D
R3/RRR3-24/3	1116.642	1116.296	310.880	0.405	1094.276	0.239	21	0.092	R.KVTIQNLSGR.D
R3/RRR3-23/3	1116.277	1116.296	-17.080	0.391	763.190	0.220	18	0.088	R.KVTIQNLSGR.D
R3/RRR3-24/3	1774.521	1774.911	-220.633	0.260	926.070	0.152	23	0.080	R.HGTHAEFTTCLWTGR.V
R3/RRR3-24/3	1115.651	1116.296	-1478.940	0.244	875.719	0.067	18	0.079	-.KVTIQNLSGR.-
R3/RRR3-6/2	1888.634	1889.099	-246.840	0.500	1520.052	0.503	20	0.220	R.APDQTLELTGQAIDFLR.G
R3/RRR3-6/2	1434.204	1434.662	-320.356	0.426	1475.128	0.513	19	0.219	R.NVLGGLSLEGFLSK.W
R3/RRR3-6/2	1434.445	1434.662	-151.983	0.427	1274.863	0.507	19	0.196	R.NVLGGLSLEGFLSK.W
R3/RRR3-6/2	1888.594	1889.099	-799.063	0.500	1083.134	0.494	19	0.174	R.APDQTLELTGQAIDFLR.G
R3/RRR3-6/2	1332.235	1332.533	-224.667	0.401	973.666	0.443	16	0.164	K.GRLETTWTVLR.K
R3/RRR3-6/2	1433.970	1434.662	-1183.801	0.411	985.233	0.444	17	0.162	R.NVLGGLSLEGFLSK.W
R3/RRR3-6/2	1888.576	1889.099	-808.535	0.444	785.163	0.528	17	0.159	R.APDQTLELTGQAIDFLR.G
R3/RRR3-6/2	1331.605	1332.533	-1452.168	0.417	1034.429	0.293	16	0.148	K.GRLETTWTVLR.K
R3/RRR3-6/2	1105.672	1106.300	-1477.051	0.274	719.941	0.404	13	0.140	K.TALLQSFLGR.Q
R3/RRR3-6/2	1331.496	1332.533	-1534.494	0.372	533.349	0.375	12	0.138	K.GRLETTWTVLR.K
R3/RRR3-5/2	1908.455	1909.090	-859.649	0.375	720.239	0.464	17	0.147	K.IEGPAAWDVLYNFEQR.W
R3/RRR3-5/2	1908.557	1909.090	-805.588	0.406	571.211	0.421	16	0.139	K.IEGPAAWDVLYNFEQR.W
R3/RRR3-8/2	1316.391	1315.498	-81.533	0.418	1250.139	0.123	17	0.133	K.QGGDKDLLLDLK.A
R3/RRR3-26/1	467.773	467.454	683.804	-2.532	22.127	0.000	2	0.830	R.GYGGGG.G
R3/RRR3-24/1	467.420	467.454	-74.653	-2.317	2.965	0.000	2	0.687	R.GYGGGG.G
R3/RRR3-24/1	467.840	467.454	826.991	-1.959	25.112	0.000	2	0.493	-.GYGGGG.-
R3/RRR3-27/1	467.839	467.454	823.460	-1.958	20.109	0.000	2	0.490	-.GYGGGG.-
R3/RRR3-26/1	467.499	467.454	94.938	-1.931	2.704	0.000	2	0.486	R.GYGGGG.G
R3/RRR3-17/1	467.062	467.454	-843.049	-1.873	15.433	0.000	2	0.465	R.GYGGGG.G
R3/RRR3-26/1	467.794	467.454	727.745	-1.999	25.570	0.523	2	0.441	-.GYGGGG.-
R3/RRR3-22/2	1925.249	1924.960	150.745	0.596	2367.185	0.658	27	0.411	R.SLNDGDVVEFSVGSGNDGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1924.551	1924.960	-213.033	0.560	2127.656	0.639	25	0.354	R.SLNDGDVVEFSVGSGNDGR.T
R3/RRR3-22/2	1924.740	1924.960	-114.540	0.568	2055.488	0.646	25	0.342	R.SLNDGDVVEFSVGSGNDGR.T
R3/RRR3-21/2	1924.465	1924.960	-257.831	0.570	1986.974	0.662	24	0.334	R.SLNDGDVVEFSVGSGNDGR.T
R3/RRR3-21/2	1925.403	1924.960	230.666	0.580	1946.995	0.680	24	0.332	R.SLNDGDVVEFSVGSGNDGR.T
R3/RRR3-22/2	1925.378	1924.960	217.887	0.593	1891.912	0.672	24	0.320	R.SLNDGDVVEFSVGSGNDGR.T
R3/RRR3-20/1	467.702	467.454	531.289	-1.493	25.281	0.000	2	0.319	R.GYGGGG.G
R3/RRR3-26/1	467.819	467.454	781.620	-1.506	43.882	0.000	3	0.313	R.GYGGGG.G
R3/RRR3-27/1	467.914	467.454	985.951	-1.390	10.000	0.000	1	0.305	R.GYGGGG.G
R3/RRR3-21/1	467.526	467.454	153.332	-1.449	1.733	0.000	2	0.297	R.GYGGGG.G
R3/RRR3-6/2	1233.185	1232.369	-149.583	0.513	1729.012	0.425	18	0.232	R.NELSGALTGLTR.V
R3/RRR3-6/2	1231.683	1232.369	-1372.955	0.411	1577.402	0.409	18	0.210	R.NELSGALTGLTR.V
R3/RRR3-6/2	1231.992	1232.369	-307.347	0.354	906.771	0.415	18	0.156	R.NELSGALTGLTR.V
R3/RRR3-6/2	1247.115	1247.468	-284.181	0.369	563.735	0.384	15	0.142	K.IDIGVFDALKR.K
R3/RRR3-6/2	1247.102	1247.468	-294.492	0.329	429.192	0.324	15	0.138	K.IDIGVFDALKR.K
R3/RRR3-6/2	1247.511	1247.468	33.996	0.337	836.215	0.230	19	0.137	K.IDIGVFDALKR.K
R3/RRR3-6/3	1985.711	1986.133	-213.137	0.452	898.331	0.419	27	0.110	R.DTFWHSSAHILGESLER.A
R3/RRR3-6/3	1986.147	1986.133	6.798	0.418	966.843	0.352	26	0.103	R.DTFWHSSAHILGESLER.A
R3/RRR3-6/3	1986.172	1986.133	19.559	0.413	603.849	0.387	24	0.097	R.DTFWHSSAHILGESLER.A
R3/RRR3-6/3	1262.412	1262.440	-22.474	0.490	1017.503	0.250	20	0.088	-.IRQFEEIQAK.-
R3/RRR3-6/3	1263.618	1262.440	141.153	0.504	951.355	0.240	19	0.088	-.IRQFEEIQAK.-
R3/RRR3-7/2	1116.319	1116.338	-16.848	0.357	986.759	0.368	13	0.152	R.AERPLVVFGK.G
R3/RRR3-7/2	1492.327	1492.662	-225.097	0.359	395.143	0.506	18	0.142	K.GVVPDTHPLSATAAR.S
R3/RRR3-7/3	1121.598	1121.315	253.179	0.482	1083.066	0.489	24	0.131	R.KPHVGIVGDAK.R
R3/RRR3-7/2	1115.846	1116.338	-442.260	0.293	572.920	0.246	11	0.129	-.AERPLVVFGK.-
R3/RRR3-7/3	1121.219	1121.315	-85.636	0.489	1051.353	0.451	23	0.123	R.KPHVGIVGDAK.R
R3/RRR3-7/3	1121.194	1121.315	-107.752	0.471	1033.807	0.459	23	0.123	R.KPHVGIVGDAK.R
R3/RRR3-7/3	1972.274	1971.246	14.047	0.444	1191.437	0.297	27	0.103	R.KPAVINVIIDPYAGAESGR.M
R3/RRR3-6/2	1345.109	1345.483	-278.770	0.548	1079.350	0.476	17	0.178	R.LDIDPESITWR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1345.086	1345.483	-295.523	0.484	911.098	0.451	16	0.163	R.LDIDPESITWR.R
R3/RRR3-6/2	1114.040	1114.322	-254.163	0.392	820.983	0.394	17	0.149	K.GAPSGFVLPIR.D
R3/RRR3-6/2	1344.521	1345.483	-1463.352	0.291	787.025	0.359	14	0.142	R.LDIDPESITWR.R
R3/RRR3-6/2	1486.020	1486.587	-1057.116	0.285	597.960	0.389	17	0.139	K.FASDTEAEM*DVVR.N
R3/RRR3-6/2	1485.935	1486.587	-1114.607	0.338	410.617	0.386	16	0.139	K.FASDTEAEM*DVVR.N
R3/RRR3-7/2	1784.011	1783.010	0.644	0.387	782.557	0.385	16	0.138	K.STTTVGLCQALGAFLDK.K
R3/RRR3-7/2	1485.999	1486.587	-1071.715	0.276	210.946	0.312	14	0.137	K.FASDTEAEM*DVVR.N
R3/RRR3-6/2	1209.160	1209.374	-177.060	0.450	959.453	0.478	17	0.167	R.GEVVVGGYSITK.G
R3/RRR3-6/2	1081.014	1081.241	-210.734	0.401	875.391	0.442	15	0.157	R.ACNFASGLIK.L
R3/RRR3-6/2	865.092	864.969	143.425	0.260	771.025	0.308	13	0.136	R.AAIFADTR.T
R3/RRR3-6/3	1075.122	1075.283	-149.438	0.502	1069.190	0.308	20	0.100	R.LEKFEIPAK.I
R3/RRR3-6/3	1075.335	1075.283	48.536	0.481	1058.674	0.309	20	0.100	R.LEKFEIPAK.I
R3/RRR3-6/3	1075.654	1075.283	346.117	0.492	749.440	0.275	18	0.090	-.LEKFEIPAK.-
R3/RRR3-4/2	1163.256	1163.351	-82.267	0.411	1382.255	0.413	16	0.193	-.VNLVQSLFSR.-
R3/RRR3-4/2	1118.088	1118.351	-235.613	0.520	1299.619	0.451	18	0.192	K.LGFGVVDAVIK.A
R3/RRR3-4/2	1163.116	1163.351	-202.912	0.440	1334.206	0.354	17	0.178	K.VNLVQSLFSR.V
R3/RRR3-4/2	1118.047	1118.351	-272.088	0.451	1113.018	0.448	17	0.175	K.LGFGVVDAVIK.A
R3/RRR3-4/2	1163.113	1163.351	-205.860	0.540	1274.117	0.359	17	0.173	K.VNLVQSLFSR.V
R3/RRR3-4/2	1212.151	1212.421	-222.985	0.438	659.908	0.518	16	0.157	K.TLSGNPPTIIAK.G
R3/RRR3-4/2	1212.302	1212.421	-98.532	0.412	657.612	0.478	16	0.153	K.TLSGNPPTIIAK.G
R3/RRR3-4/2	1212.370	1212.421	-41.972	0.384	691.888	0.436	16	0.149	K.TLSGNPPTIIAK.G
R3/RRR3-4/2	1118.283	1118.351	-60.394	0.429	928.107	0.306	16	0.145	K.LGFGVVDAVIK.A
R3/RRR3-4/3	1699.587	1698.861	-161.383	0.454	864.733	0.491	29	0.120	K.GAGVDGIITDFPATAHR.Y
R3/RRR3-4/3	1698.727	1698.861	-79.263	0.374	775.249	0.419	26	0.103	K.GAGVDGIITDFPATAHR.Y
R3/RRR3-23/2	1831.335	1832.006	-914.904	0.495	2791.511	0.516	29	0.456	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-23/2	1832.354	1832.006	190.661	0.541	2324.366	0.532	28	0.356	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-23/2	1831.158	1832.006	-1012.145	0.405	2286.504	0.470	28	0.331	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-22/2	1831.683	1832.006	-176.508	0.496	2130.711	0.551	27	0.326	K.GGTDSVIGVTLLGADGSGVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1831.782	1832.006	-122.358	0.460	1601.815	0.486	28	0.227	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-23/2	978.784	979.072	-294.602	0.449	1032.033	0.531	14	0.184	R.GNLDIFSGR.G
R3/RRR3-22/2	979.109	979.072	38.501	0.473	1062.967	0.506	14	0.182	R.GNLDIFSGR.G
R3/RRR3-24/2	978.956	979.072	-118.829	0.485	1045.604	0.500	14	0.180	R.GNLDIFSGR.G
R3/RRR3-23/2	978.544	979.072	-1566.155	0.452	1065.018	0.487	14	0.179	R.GNLDIFSGR.G
R3/RRR3-27/2	978.954	979.072	-120.580	0.456	1028.444	0.499	14	0.178	R.GNLDIFSGR.G
R3/RRR3-24/2	978.476	979.072	-1635.961	0.404	1032.192	0.502	14	0.178	R.GNLDIFSGR.G
R3/RRR3-27/2	978.794	979.072	-285.092	0.429	1022.590	0.498	14	0.177	R.GNLDIFSGR.G
R3/RRR3-23/2	978.874	979.072	-203.142	0.455	1086.323	0.459	14	0.176	R.GNLDIFSGR.G
R3/RRR3-22/2	978.703	979.072	-377.568	0.455	1023.521	0.471	14	0.174	R.GNLDIFSGR.G
R3/RRR3-25/2	978.656	979.072	-426.128	0.433	969.401	0.491	14	0.173	R.GNLDIFSGR.G
R3/RRR3-23/2	1833.067	1832.006	33.489	0.427	879.942	0.511	22	0.164	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-27/2	978.328	979.072	-1788.140	0.390	888.435	0.464	13	0.163	R.GNLDIFSGR.G
R3/RRR3-22/2	1831.712	1832.006	-160.597	0.429	759.373	0.485	24	0.156	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-23/2	1073.839	1074.248	-382.599	0.369	655.273	0.406	13	0.147	K.CVYTIYVR.T
R3/RRR3-24/2	1831.782	1832.006	-122.358	0.415	494.264	0.462	23	0.147	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-24/2	1831.611	1832.006	-215.888	0.374	394.472	0.480	23	0.146	K.GGTDSVIGVTLLGADGSGVR.I
R3/RRR3-23/2	1073.782	1074.248	-435.070	0.258	836.855	0.266	13	0.136	K.CVYTIYVR.T
R3/RRR3-24/2	1831.508	1832.006	-272.321	0.227	102.947	0.374	15	0.117	-.GGTDSVIGVTLLGADGSGVR.-
R3/RRR3-4/2	1177.446	1177.332	97.058	0.433	1331.448	0.390	15	0.182	K.SFEVTELPVR.S
R3/RRR3-4/2	1322.018	1322.449	-327.352	0.454	1257.712	0.404	18	0.179	R.LENTLNYGLER.V
R3/RRR3-1/2	1361.137	1361.397	-191.472	0.373	1116.175	0.376	19	0.161	K.TIGADNEIADGER.L
R3/RRR3-4/2	1322.087	1322.449	-274.548	0.446	995.048	0.365	17	0.155	R.LENTLNYGLER.V
R3/RRR3-4/2	1298.167	1298.341	-134.928	0.258	818.901	0.383	16	0.143	K.DTNTFASASLDR.T
R3/RRR3-4/2	1298.178	1298.341	-125.967	0.221	748.406	0.316	15	0.134	K.DTNTFASASLDR.T
R3/RRR3-18/2	1759.584	1759.979	-225.421	0.605	2484.755	0.585	25	0.414	K.IAELKEALESVTAEQK.Y
R3/RRR3-18/2	1759.569	1759.979	-234.121	0.587	2580.374	0.524	25	0.413	K.IAELKEALESVTAEQK.Y
R3/RRR3-18/2	1758.753	1759.979	-1269.412	0.537	2237.023	0.559	23	0.352	K.IAELKEALESVTAEQK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1204.882	1205.297	-345.560	0.425	1153.467	0.415	17	0.172	K.EALESVTAEQK.Y
R3/RRR3-18/2	1179.903	1180.292	-331.084	0.414	792.865	0.420	14	0.153	K.DEHLDPINVK.I
R3/RRR3-18/2	1179.966	1180.292	-277.525	0.415	795.758	0.417	14	0.152	K.DEHLDPINVK.I
R3/RRR3-18/2	1180.107	1180.292	-157.660	0.433	848.900	0.365	15	0.150	K.DEHLDPINVK.I
R3/RRR3-18/2	1180.404	1180.292	95.156	0.441	803.389	0.361	14	0.147	K.DEHLDPINVK.I
R3/RRR3-18/3	1759.685	1759.979	-167.526	0.496	720.726	0.531	28	0.121	K.IAELKEALESVTAEQK.Y
R3/RRR3-18/3	1180.611	1180.292	271.013	0.485	1015.168	0.367	21	0.107	K.DEHLDPINVK.I
R3/RRR3-18/3	1180.170	1180.292	-103.923	0.419	1056.866	0.314	21	0.100	K.DEHLDPINVK.I
R3/RRR3-18/3	1759.519	1759.979	-262.421	0.444	605.780	0.386	25	0.098	K.IAELKEALESVTAEQK.Y
R3/RRR3-18/3	1180.304	1180.292	9.676	0.422	1031.050	0.304	22	0.097	K.DEHLDPINVK.I
R3/RRR3-26/3	1673.048	1671.814	140.386	0.431	2125.408	0.387	32	0.232	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-27/3	1827.497	1828.001	-825.152	0.507	1981.488	0.415	30	0.221	R.RVTSGEQQVVSGM*NYR.L
R3/RRR3-27/2	1671.256	1671.814	-935.428	0.501	1233.497	0.489	21	0.190	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-26/2	1671.072	1671.814	-1045.433	0.467	1221.038	0.488	20	0.188	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-27/2	1672.441	1671.814	-223.766	0.554	1130.541	0.516	20	0.185	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-27/2	1671.246	1671.814	-941.147	0.491	1152.865	0.475	21	0.181	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-26/2	1671.271	1671.814	-926.408	0.507	1057.793	0.485	20	0.175	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-27/2	1042.494	1043.116	-1560.456	0.414	773.218	0.578	16	0.173	R.HASLSSDGLR.F
R3/RRR3-27/2	1042.927	1043.116	-181.567	0.406	795.214	0.543	16	0.169	R.HASLSSDGLR.F
R3/RRR3-27/2	1042.561	1043.116	-1495.765	0.433	657.782	0.575	15	0.167	R.HASLSSDGLR.F
R3/RRR3-27/3	1672.259	1671.814	266.568	0.503	1660.412	0.378	32	0.160	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-26/2	1042.951	1043.116	-159.024	0.374	643.258	0.506	15	0.157	R.HASLSSDGLR.F
R3/RRR3-26/2	1042.349	1043.116	-1700.218	0.329	468.031	0.492	14	0.148	R.HASLSSDGLR.F
R3/RRR3-26/2	1043.034	1043.116	-78.720	0.381	480.111	0.465	13	0.148	R.HASLSSDGLR.F
R3/RRR3-27/3	1827.579	1828.001	-231.583	0.426	1472.077	0.278	27	0.121	R.RVTSGEQQVVSGM*NYR.L
R3/RRR3-27/3	1671.456	1671.814	-214.786	0.385	1004.610	0.362	27	0.106	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-27/3	1671.013	1671.814	-1080.941	0.345	1055.368	0.268	26	0.095	R.VTSGEQQVVSGM*NYR.L
R3/RRR3-20/2	1737.338	1735.790	-260.866	0.628	2565.466	0.620	23	0.447	R.WSEYDFDQVFADGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/2	1735.154	1735.790	-946.002	0.551	2313.737	0.597	22	0.383	R.WSEYDFDQVFADGR.D
R3/RRR3-20/2	1734.533	1735.790	-1304.996	0.462	2339.290	0.518	22	0.361	R.WSEYDFDQVFADGR.D
R3/RRR3-20/2	1517.889	1517.668	145.869	0.532	1303.209	0.412	20	0.183	K.VSDTEVIGYHQLR.V
R3/RRR3-20/2	924.496	925.150	-1794.986	0.369	647.613	0.406	14	0.147	K.AVLGNPLLK.T
R3/RRR3-20/2	924.939	925.150	-229.482	0.410	533.348	0.338	13	0.141	K.AVLGNPLLK.T
R3/RRR3-20/2	924.431	925.150	-1865.838	0.302	423.565	0.338	11	0.137	K.AVLGNPLLK.T
R3/RRR3-20/3	1517.699	1517.668	20.110	0.439	686.094	0.486	24	0.112	K.VSDTEVIGYHQLR.V
R3/RRR3-20/3	1517.923	1517.668	168.079	0.445	676.774	0.448	25	0.108	K.VSDTEVIGYHQLR.V
R3/RRR3-20/3	1517.522	1517.668	-96.917	0.397	756.770	0.439	25	0.107	K.VSDTEVIGYHQLR.V
R3/RRR3-24/2	1259.499	1259.439	47.574	0.268	1019.281	0.106	15	0.126	R.FPGQLNADLRK.L
R3/RRR3-5/2	1721.006	1721.978	-1149.349	0.412	844.963	0.493	19	0.160	R.SPESLASPPLPYPPLR.C
R3/RRR3-5/2	1722.294	1721.978	184.078	0.469	586.562	0.508	18	0.152	R.SPESLASPPLPYPPLR.C
R3/RRR3-5/2	1721.353	1721.978	-946.402	0.414	745.009	0.432	20	0.150	R.SPESLASPPLPYPPLR.C
R3/RRR3-5/2	1931.177	1930.292	-59.683	0.462	560.422	0.506	18	0.145	R.IIALLGGPCTEGPGM*IVSK.D
R3/RRR3-5/2	1700.178	1699.843	198.138	0.379	738.306	0.349	16	0.136	-.NTSLTVFFDVSPSER.-
R3/RRR3-1/2	1722.644	1721.978	-194.291	0.321	234.662	0.329	12	0.132	-.SPESLASPPLPYPPLR.-
R3/RRR3-5/2	1929.020	1930.292	-1181.280	0.333	596.214	0.309	18	0.130	R.IIALLGGPCTEGPGM*IVSK.D
R3/RRR3-5/3	1385.691	1385.507	133.047	0.407	1187.434	0.339	22	0.110	K.DLDKDAAPHFQK.A
R3/RRR3-12/2	1510.535	1510.781	-163.038	0.479	3045.510	0.535	24	0.537	K.M*VGYALQAAEILSK.E
R3/RRR3-11/2	1510.132	1510.781	-1095.302	0.381	2341.573	0.436	22	0.335	K.M*VGYALQAAEILSK.E
R3/RRR3-11/2	1201.980	1201.355	-312.474	0.435	1246.540	0.390	18	0.176	K.EGISAEVINLR.S
R3/RRR3-11/2	1703.752	1704.929	-1281.417	0.413	958.082	0.416	22	0.158	R.IAGADVPM*PYAANLER.M
R3/RRR3-11/2	1703.979	1704.929	-1147.815	0.443	771.867	0.461	20	0.154	R.IAGADVPM*PYAANLER.M
R3/RRR3-11/2	1704.234	1704.929	-997.564	0.453	786.040	0.433	20	0.151	R.IAGADVPM*PYAANLER.M
R3/RRR3-12/2	1494.151	1494.781	-1094.164	0.338	629.173	0.230	14	0.128	K.MVGYALQAAEILSK.E
R3/RRR3-22/2	1072.031	1072.240	-196.054	0.461	1806.266	0.535	19	0.271	R.VLVVDGGGSLR.C
R3/RRR3-21/2	1072.172	1072.240	-64.133	0.491	1839.538	0.500	19	0.267	R.VLVVDGGGSLR.C
R3/RRR3-22/2	1071.526	1072.240	-1604.560	0.422	1700.811	0.554	19	0.260	R.VLVVDGGGSLR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1071.305	1072.240	-1811.637	0.437	1602.928	0.513	19	0.237	R.VLVVDGGGSLR.C
R3/RRR3-21/2	1072.004	1072.240	-221.186	0.383	1546.944	0.525	19	0.231	R.VLVVDGGGSLR.C
R3/RRR3-21/2	1071.477	1072.240	-1650.799	0.424	1222.676	0.475	17	0.188	R.VLVVDGGGSLR.C
R3/RRR3-22/2	1278.135	1278.484	-274.027	0.441	671.644	0.513	17	0.160	R.ALQPVFQVYGR.R
R3/RRR3-22/2	1107.179	1107.242	-56.797	0.540	872.212	0.419	15	0.159	K.VYEDNVLVR.E
R3/RRR3-22/2	1278.284	1278.484	-157.332	0.432	654.671	0.456	17	0.153	R.ALQPVFQVYGR.R
R3/RRR3-22/2	1278.035	1278.484	-352.701	0.250	556.309	0.384	14	0.137	R.ALQPVFQVYGR.R
R3/RRR3-22/2	1106.268	1107.242	-1789.466	0.342	631.738	0.309	13	0.135	-.VYEDNVLVR.-
R3/RRR3-22/2	1106.253	1107.242	-1802.771	0.321	731.870	0.267	13	0.134	-.VYEDNVLVR.-
R3/RRR3-22/2	1603.355	1603.798	-277.091	0.532	2631.970	0.503	23	0.418	R.GDPIEFELGTGQVIK.G
R3/RRR3-22/2	1603.145	1603.798	-1033.980	0.532	2430.376	0.486	22	0.367	R.GDPIEFELGTGQVIK.G
R3/RRR3-22/2	1603.209	1603.798	-993.998	0.501	2308.413	0.481	22	0.342	R.GDPIEFELGTGQVIK.G
R3/RRR3-22/2	1245.978	1246.392	-333.769	0.528	1834.052	0.350	18	0.226	K.SGDVTELQIGVK.H
R3/RRR3-22/2	1489.933	1490.553	-1091.017	0.402	1330.427	0.528	21	0.207	K.LTDGTVFDSSYER.G
R3/RRR3-22/2	1246.082	1246.392	-250.026	0.521	1575.435	0.365	19	0.200	K.SGDVTELQIGVK.H
R3/RRR3-22/2	1490.164	1490.553	-261.740	0.423	1253.026	0.527	20	0.200	K.LTDGTVFDSSYER.G
R3/RRR3-22/2	1490.209	1490.553	-231.825	0.444	1200.107	0.495	20	0.190	K.LTDGTVFDSSYER.G
R3/RRR3-22/2	1245.985	1246.392	-327.871	0.522	1520.714	0.319	18	0.183	K.SGDVTELQIGVK.H
R3/RRR3-10/2	1870.413	1871.037	-870.653	0.578	2787.443	0.531	24	0.465	K.LAYVALDYEQELDTAR.S
R3/RRR3-10/2	1871.430	1871.037	210.756	0.614	2590.065	0.573	24	0.433	K.LAYVALDYEQELDTAR.S
R3/RRR3-10/2	1870.342	1871.037	-909.047	0.560	2498.528	0.525	24	0.395	K.LAYVALDYEQELDTAR.S
R3/RRR3-10/3	1871.917	1871.037	-64.342	0.427	1487.760	0.413	29	0.153	K.LAYVALDYEQELDTAR.S
R3/RRR3-4/2	1338.403	1338.575	-128.493	0.463	1576.126	0.399	19	0.209	R.YITLLQTSGTLK.W
R3/RRR3-4/2	1526.345	1525.642	-195.614	0.479	1292.600	0.465	20	0.191	R.SSPESSVLTDVFTR.L
R3/RRR3-4/2	1392.096	1392.625	-1102.082	0.347	1122.278	0.276	15	0.146	R.SVEQLGYITLLR.Q
R3/RRR3-4/2	1525.410	1525.642	-152.793	0.350	815.469	0.369	17	0.143	R.SSPESSVLTDVFTR.L
R3/RRR3-4/3	1592.727	1592.777	-31.419	0.386	710.980	0.470	22	0.106	K.FGTGNWDTLEVKPK.E
R3/RRR3-23/2	1495.274	1495.659	-258.307	0.508	1975.019	0.582	23	0.311	K.ITLISDFGEISGSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1496.295	1495.659	-244.384	0.582	1849.839	0.642	22	0.308	K.ITLISDFGEISGSR.G
R3/RRR3-22/2	1495.369	1495.659	-194.508	0.525	1911.491	0.575	22	0.298	K.ITLISDFGEISGSR.G
R3/RRR3-22/2	1495.321	1495.659	-227.021	0.505	1869.156	0.582	22	0.293	K.ITLISDFGEISGSR.G
R3/RRR3-23/2	1494.791	1495.659	-1253.500	0.373	1891.873	0.526	22	0.279	K.ITLISDFGEISGSR.G
R3/RRR3-23/2	1495.035	1495.659	-1089.586	0.443	1814.278	0.560	22	0.277	K.ITLISDFGEISGSR.G
R3/RRR3-23/2	1536.440	1535.837	-259.112	0.431	1336.272	0.413	21	0.248	K.IM*LTHVLHGQGSII.-
R3/RRR3-22/2	1535.416	1535.837	-274.595	0.369	1289.321	0.331	20	0.223	K.IM*LTHVLHGQGSII.-
R3/RRR3-22/3	1495.520	1495.659	-93.553	0.399	1715.736	0.399	27	0.178	-.ITLISDFGEISGSR.-
R3/RRR3-23/2	1623.992	1623.832	98.793	0.432	808.727	0.541	18	0.164	R.KITLISDFGEISGSR.G
R3/RRR3-23/2	1624.485	1623.832	-214.397	0.420	588.493	0.462	17	0.145	R.KITLISDFGEISGSR.G
R3/RRR3-23/2	1495.712	1495.659	35.558	0.263	862.305	0.369	15	0.144	K.ITLISDFGEISGSR.G
R3/RRR3-23/2	1535.102	1535.837	-1133.005	0.362	966.709	0.298	20	0.106	K.IM*LTHVLHGQGSII.-
R3/RRR3-22/3	1623.320	1623.832	-934.325	0.333	920.160	0.383	25	0.101	R.KITLISDFGEISGSR.G
R3/RRR3-23/2	1521.350	1519.837	-321.401	0.385	898.692	0.424	18	0.100	K.IMLTHVLHGQGSII.-
R3/RRR3-22/2	1534.623	1535.837	-1446.426	0.321	963.774	0.198	20	0.097	K.IM*LTHVLHGQGSII.-
R3/RRR3-23/2	1535.417	1535.837	-274.036	0.372	835.218	0.390	19	0.080	K.IM*LTHVLHGQGSII.-
R3/RRR3-6/3	1660.935	1660.893	25.526	0.535	2896.660	0.353	37	0.378	R.IINEPTAAAIAYGIDK.K
R3/RRR3-6/2	1661.375	1660.893	291.496	0.550	1829.035	0.601	26	0.294	R.IINEPTAAAIAYGIDK.K
R3/RRR3-6/2	1661.316	1660.893	255.468	0.596	1740.171	0.606	25	0.280	R.IINEPTAAAIAYGIDK.K
R3/RRR3-6/2	1660.381	1660.893	-913.020	0.498	1744.064	0.546	26	0.265	R.IINEPTAAAIAYGIDK.K
R3/RRR3-6/2	1661.650	1660.893	-146.160	0.448	1748.567	0.488	22	0.249	R.IINEPTAAAIAYGIDK.K
R3/RRR3-6/2	1788.512	1789.066	-871.160	0.516	1476.821	0.585	25	0.237	R.IINEPTAAAIAYGIDKK.A
R3/RRR3-6/2	1789.504	1789.066	245.720	0.573	1395.936	0.553	25	0.220	R.IINEPTAAAIAYGIDKK.A
R3/RRR3-6/2	1788.629	1789.066	-244.760	0.543	1290.009	0.580	24	0.214	R.IINEPTAAAIAYGIDKK.A
R3/RRR3-6/3	1660.748	1660.893	-87.047	0.402	1821.445	0.256	29	0.152	R.IINEPTAAAIAYGIDK.K
R3/RRR3-6/3	1660.816	1660.893	-46.129	0.330	1587.172	0.304	27	0.139	R.IINEPTAAAIAYGIDK.K
R3/RRR3-9/2	1330.275	1329.534	-195.454	0.323	1036.236	0.170	15	0.131	R.VKRALSTQAQAR.L
R3/RRR3-24/2	1745.226	1744.825	230.581	0.570	1516.265	0.612	24	0.245	R.ASTAGGSGGFSGGGGSNM*LR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1744.258	1744.825	-901.451	0.515	1338.614	0.586	23	0.217	R.ASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-24/2	1744.268	1744.825	-895.761	0.481	1325.812	0.547	24	0.208	R.ASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-24/3	1901.161	1901.012	78.795	0.540	1745.317	0.474	36	0.205	R.RASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-24/3	1900.771	1901.012	-126.799	0.510	2061.989	0.314	38	0.200	R.RASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-24/2	1169.148	1169.268	-102.797	0.450	644.467	0.424	16	0.152	R.FYTDEAPGLR.L
R3/RRR3-25/2	1169.875	1169.268	-336.748	0.377	411.916	0.392	14	0.144	R.FYTDEAPGLR.L
R3/RRR3-24/2	1168.896	1169.268	-319.433	0.305	534.163	0.409	15	0.144	R.FYTDEAPGLR.L
R3/RRR3-25/2	1170.073	1169.268	-166.965	0.422	536.392	0.348	15	0.143	R.FYTDEAPGLR.L
R3/RRR3-25/2	1168.874	1169.268	-338.293	0.361	395.180	0.396	13	0.143	R.FYTDEAPGLR.L
R3/RRR3-24/3	1900.083	1901.012	-1018.144	0.436	1740.759	0.232	35	0.137	R.RASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-24/3	1744.382	1744.825	-254.638	0.501	899.879	0.488	33	0.122	R.ASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-24/3	1745.169	1744.825	197.677	0.507	910.058	0.475	33	0.121	R.ASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-24/3	1744.578	1744.825	-142.284	0.488	880.576	0.434	34	0.112	R.ASTAGGSGGFSGGGGSNM*LR.F
R3/RRR3-25/3	1900.960	1901.012	-26.987	0.362	881.219	0.071	28	0.074	-.RASTAGGSGGFSGGGGSNM*LR.-
R3/RRR3-17/2	1532.315	1532.672	-233.286	0.464	1004.304	0.572	17	0.183	R.ATEGPIVADKNCEK.I
R3/RRR3-17/2	1532.214	1532.672	-299.465	0.418	1008.478	0.567	18	0.182	R.ATEGPIVADKNCEK.I
R3/RRR3-17/2	1532.207	1532.672	-303.781	0.448	835.309	0.513	17	0.163	R.ATEGPIVADKNCEK.I
R3/RRR3-17/2	973.617	974.220	-1651.609	0.413	646.282	0.455	15	0.154	R.VVTSLTLLK.S
R3/RRR3-17/2	974.017	974.220	-208.617	0.394	701.125	0.425	15	0.152	R.VVTSLTLLK.S
R3/RRR3-17/2	1000.848	1001.116	-267.861	0.362	669.683	0.443	16	0.150	R.ATEGPIVADK.N
R3/RRR3-17/2	974.080	974.220	-143.368	0.404	731.244	0.349	15	0.146	R.VVTSLTLLK.S
R3/RRR3-17/2	1000.846	1001.116	-269.941	0.285	691.845	0.408	16	0.144	R.ATEGPIVADK.N
R3/RRR3-16/2	974.011	974.220	-214.652	0.328	306.077	0.305	12	0.138	-.VVTSLTLLK.-
R3/RRR3-21/2	1324.054	1324.593	-1166.140	0.492	1649.712	0.461	17	0.231	R.VLQAM*QLM*TEK.R
R3/RRR3-21/2	1324.180	1324.593	-313.066	0.517	1633.526	0.414	17	0.218	R.VLQAM*QLM*TEK.R
R3/RRR3-21/2	1323.984	1324.593	-1218.820	0.480	1576.072	0.419	17	0.213	R.VLQAM*QLM*TEK.R
R3/RRR3-21/2	945.405	946.083	-1780.476	0.429	1009.821	0.369	15	0.158	K.SIAGIVTER.D
R3/RRR3-21/2	945.914	946.083	-179.155	0.478	961.868	0.345	15	0.153	K.SIAGIVTER.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	945.484	946.083	-1696.932	0.426	907.264	0.334	14	0.149	K.SIAGIVTER.D
R3/RRR3-21/2	998.983	999.102	-118.591	0.388	993.199	0.627	14	0.144	R.LNAYIQGGY.-
R3/RRR3-21/2	998.793	999.102	-310.214	0.290	990.753	0.511	14	0.135	R.LNAYIQGGY.-
R3/RRR3-21/2	999.982	999.102	-119.575	0.461	988.524	0.539	15	0.127	R.LNAYIQGGY.-
R3/RRR3-18/3	1403.519	1403.520	-0.761	0.563	2345.281	0.333	30	0.247	K.IKSEGEAEAAAAQK.S
R3/RRR3-17/3	1403.138	1403.520	-273.664	0.537	2156.078	0.352	29	0.222	K.IKSEGEAEAAAAQK.S
R3/RRR3-17/3	1403.872	1403.520	250.938	0.597	1903.814	0.407	29	0.201	-.IKSEGEAEAAAAQK.-
R3/RRR3-18/3	1403.479	1403.520	-29.811	0.548	1774.844	0.402	28	0.182	K.IKSEGEAEAAAAQK.S
R3/RRR3-18/3	1403.528	1403.520	5.651	0.570	1926.914	0.328	28	0.178	K.IKSEGEAEAAAAQK.S
R3/RRR3-17/3	1403.326	1403.520	-139.222	0.546	1754.370	0.374	27	0.171	K.IKSEGEAEAAAAQK.S
R3/RRR3-25/2	1031.606	1032.173	-1523.874	0.350	1017.908	0.470	15	0.169	K.AVQASELVSK.H
R3/RRR3-25/2	1032.069	1032.173	-100.910	0.327	862.218	0.403	14	0.151	K.AVQASELVSK.H
R3/RRR3-26/2	1032.068	1032.173	-101.977	0.324	589.477	0.367	13	0.138	-.AVQASELVSK.-
R3/RRR3-25/3	1504.130	1504.716	-1057.855	0.500	1010.232	0.351	26	0.105	K.NKQHVVQPPTVEK.C
R3/RRR3-25/3	1247.012	1247.424	-330.656	0.449	831.639	0.390	21	0.103	R.SKAVQASELVSK.H
R3/RRR3-25/3	1504.765	1504.716	32.895	0.456	752.901	0.342	24	0.098	K.NKQHVVQPPTVEK.C
R3/RRR3-25/3	1504.153	1504.716	-1042.454	0.381	664.235	0.358	21	0.095	-.NKQHVVQPPTVEK.-
R3/RRR3-25/3	1504.723	1504.716	4.457	0.474	720.701	0.335	23	0.092	-.NKQHVVQPPTVEK.-
R3/RRR3-25/3	1504.529	1504.716	-124.568	0.428	574.338	0.337	20	0.091	-.NKQHVVQPPTVEK.-
R3/RRR3-25/3	1246.960	1247.424	-372.498	0.335	773.427	0.297	21	0.088	-.SKAVQASELVSK.-
R3/RRR3-25/2	1486.815	1487.596	-1201.511	0.354	1919.730	0.426	21	0.259	K.ATLDITADYGYGAR.G
R3/RRR3-25/2	1486.348	1487.596	-1516.639	0.333	1109.009	0.354	18	0.157	K.ATLDITADYGYGAR.G
R3/RRR3-25/2	1486.270	1487.596	-1569.523	0.276	1081.180	0.251	19	0.143	K.ATLDITADYGYGAR.G
R3/RRR3-25/2	1220.042	1220.400	-294.501	0.345	832.862	0.324	16	0.142	K.SDFVVQIGVQK.V
R3/RRR3-25/2	1168.277	1167.274	2.309	0.407	909.824	0.286	14	0.140	K.GWDEGVTQM*K.V
R3/RRR3-25/2	1220.016	1220.400	-315.281	0.286	357.357	0.287	13	0.134	K.SDFVVQIGVQK.V
R3/RRR3-2/2	1314.917	1315.458	-1175.428	0.359	829.226	0.435	14	0.154	R.FTWTIENFTR.I
R3/RRR3-3/2	1315.415	1315.458	-33.100	0.341	822.668	0.452	13	0.154	R.FTWTIENFTR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1315.262	1315.458	-149.372	0.354	939.075	0.311	15	0.146	R.FTWTIENFTR.I
R3/RRR3-3/2	1315.250	1315.458	-158.961	0.269	946.148	0.308	15	0.144	R.FTWTIENFTR.I
R3/RRR3-3/2	1512.150	1512.776	-1078.469	0.532	1729.943	0.578	22	0.271	R.LPLITISDSGNLLR.D
R3/RRR3-2/2	1511.900	1512.776	-1244.498	0.536	1537.151	0.576	21	0.243	R.LPLITISDSGNLLR.D
R3/RRR3-3/2	1512.253	1512.776	-1010.062	0.481	1538.278	0.529	22	0.232	R.LPLITISDSGNLLR.D
R3/RRR3-2/2	1512.611	1512.776	-109.324	0.493	1471.768	0.533	21	0.225	R.LPLITISDSGNLLR.D
R3/RRR3-2/2	1579.134	1577.892	153.780	0.445	1581.556	0.372	18	0.201	R.LPVLYVAYAEGLIR.A
R3/RRR3-1/2	1511.721	1512.776	-1363.379	0.305	1162.497	0.450	17	0.173	R.LPLITISDSGNLLR.D
R3/RRR3-3/2	1901.256	1903.001	-1975.632	0.409	771.543	0.584	19	0.161	K.AIAAASGDNARPASSESAQK.N
R3/RRR3-1/2	1512.352	1512.776	-281.053	0.356	578.211	0.452	15	0.144	R.LPLITISDSGNLLR.D
R3/RRR3-3/2	1872.184	1873.120	-1036.712	0.338	650.042	0.340	18	0.132	K.FNLAAVIFADM*SGTEAAK.N
R3/RRR3-24/2	1320.005	1320.493	-370.944	0.503	1951.580	0.512	17	0.288	K.SEIEYYAM*LGK.V
R3/RRR3-24/2	1320.016	1320.493	-362.501	0.495	1911.851	0.480	17	0.273	K.SEIEYYAM*LGK.V
R3/RRR3-24/2	1319.665	1320.493	-1389.376	0.396	1511.901	0.378	16	0.196	K.SEIEYYAM*LGK.V
R3/RRR3-24/2	1395.100	1394.681	300.970	0.445	1116.819	0.471	17	0.178	K.LIILANNCPPLR.K
R3/RRR3-24/2	1395.272	1394.681	-294.458	0.436	1035.103	0.452	16	0.168	K.LIILANNCPPLR.K
R3/RRR3-24/2	1393.807	1394.681	-1348.799	0.304	802.795	0.400	16	0.147	K.LIILANNCPPLR.K
R3/RRR3-24/2	1394.184	1394.681	-357.655	0.281	351.621	0.413	15	0.139	K.LIILANNCPPLR.K
R3/RRR3-20/2	1590.209	1590.716	-950.461	0.488	1425.139	0.498	24	0.212	R.EYVAEGSAPALPETR.R
R3/RRR3-20/2	1591.376	1590.716	-214.164	0.511	1246.985	0.522	23	0.199	R.EYVAEGSAPALPETR.R
R3/RRR3-18/2	1590.132	1590.716	-999.400	0.404	1304.645	0.461	23	0.192	R.EYVAEGSAPALPETR.R
R3/RRR3-20/2	1590.223	1590.716	-310.715	0.475	1162.380	0.521	22	0.191	R.EYVAEGSAPALPETR.R
R3/RRR3-19/2	1590.252	1590.716	-292.539	0.496	1144.438	0.492	22	0.184	R.EYVAEGSAPALPETR.R
R3/RRR3-18/2	1590.071	1590.716	-1037.785	0.455	1142.003	0.490	22	0.183	R.EYVAEGSAPALPETR.R
R3/RRR3-20/3	1541.566	1542.890	-1512.081	0.442	1562.368	0.463	27	0.175	R.LLELGVKPVFLTGR.T
R3/RRR3-18/2	1591.216	1590.716	-314.984	0.492	947.321	0.495	21	0.171	R.EYVAEGSAPALPETR.R
R3/RRR3-19/2	1542.450	1542.890	-286.444	0.425	1133.570	0.411	20	0.169	R.LLELGVKPVFLTGR.T
R3/RRR3-19/2	1590.201	1590.716	-955.393	0.454	867.817	0.510	20	0.167	R.EYVAEGSAPALPETR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1589.997	1590.716	-1084.344	0.433	1004.373	0.441	21	0.166	R.EYVAEGSAPALPETR.R
R3/RRR3-19/2	1590.213	1590.716	-947.994	0.455	970.272	0.420	21	0.161	R.EYVAEGSAPALPETR.R
R3/RRR3-19/2	1541.582	1542.890	-1502.090	0.403	852.441	0.437	18	0.156	R.LLELGVKPVFLTGR.T
R3/RRR3-20/2	1541.562	1542.890	-1515.135	0.409	888.509	0.407	18	0.154	R.LLELGVKPVFLTGR.T
R3/RRR3-20/2	1541.422	1542.890	-1606.221	0.372	782.133	0.396	16	0.146	R.LLELGVKPVFLTGR.T
R3/RRR3-23/2	1541.782	1542.890	-1371.897	0.386	877.383	0.348	17	0.146	R.LLELGVKPVFLTGR.T
R3/RRR3-22/2	1541.605	1542.890	-1486.659	0.309	783.686	0.390	17	0.146	R.LLELGVKPVFLTGR.T
R3/RRR3-19/2	1541.420	1542.890	-1607.255	0.335	703.531	0.278	16	0.135	R.LLELGVKPVFLTGR.T
R3/RRR3-23/2	1543.754	1542.890	-88.797	0.347	575.707	0.273	14	0.131	-.LLELGVKPVFLTGR.-
R3/RRR3-19/3	1542.042	1542.890	-1202.316	0.412	1274.476	0.389	25	0.129	R.LLELGVKPVFLTGR.T
R3/RRR3-19/3	1541.835	1542.890	-1337.315	0.404	1228.103	0.387	25	0.125	R.LLELGVKPVFLTGR.T
R3/RRR3-20/3	1541.996	1542.890	-1232.127	0.361	933.371	0.391	24	0.109	R.LLELGVKPVFLTGR.T
R3/RRR3-19/3	1541.447	1542.890	-1590.119	0.413	1024.081	0.361	24	0.109	R.LLELGVKPVFLTGR.T
R3/RRR3-19/3	1541.553	1542.890	-1521.030	0.347	1059.798	0.341	24	0.107	R.LLELGVKPVFLTGR.T
R3/RRR3-19/3	1541.615	1542.890	-1480.225	0.360	1039.177	0.344	26	0.106	R.LLELGVKPVFLTGR.T
R3/RRR3-20/3	1543.490	1542.890	-260.122	0.309	570.917	0.325	23	0.096	R.LLELGVKPVFLTGR.T
R3/RRR3-20/3	1746.814	1746.902	-51.077	0.286	931.730	0.322	27	0.096	R.EYVAEGSAPALPETRR.L
R3/RRR3-19/3	1746.913	1746.902	6.327	0.257	405.899	0.407	18	0.093	R.EYVAEGSAPALPETRR.L
R3/RRR3-19/3	1746.921	1746.902	10.743	0.265	460.065	0.382	20	0.092	R.EYVAEGSAPALPETRR.L
R3/RRR3-22/3	1541.898	1542.890	-1296.168	0.334	391.046	0.351	17	0.090	-.LLELGVKPVFLTGR.-
R3/RRR3-3/2	1763.639	1761.955	-179.708	0.508	839.115	0.518	19	0.164	R.NLTYSAPLYVDVSYR.V
R3/RRR3-3/2	1585.098	1585.658	-986.894	0.444	926.225	0.444	24	0.163	K.TSPIPQDDAQGQATR.Y
R3/RRR3-3/2	1585.232	1585.658	-269.368	0.409	713.836	0.496	22	0.158	K.TSPIPQDDAQGQATR.Y
R3/RRR3-3/2	1809.648	1809.909	-144.896	0.445	724.485	0.533	21	0.158	K.EGDATPFTDVTVDNISK.A
R3/RRR3-2/3	1916.554	1915.010	-238.396	0.509	862.517	0.597	27	0.139	R.HGSYDKLDDDGLAPPGTR.V
R3/RRR3-3/2	1584.619	1585.658	-1290.692	0.254	597.113	0.334	20	0.136	K.TSPIPQDDAQGQATR.Y
R3/RRR3-1/2	1586.163	1585.658	-313.286	0.353	293.353	0.410	13	0.134	-.TSPIPQDDAQGQATR.-
R3/RRR3-6/2	1886.052	1886.098	-24.319	0.560	2868.764	0.596	30	0.518	R.LGAAHLGLGDAASAVAAYEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1318.178	1318.372	-147.927	0.471	1474.567	0.347	16	0.186	R.GDLTQEEIQER.Q
R3/RRR3-6/2	1318.002	1318.372	-281.623	0.438	1259.137	0.281	16	0.158	R.GDLTQEEIQER.Q
R3/RRR3-6/2	1312.101	1311.469	-281.210	0.435	602.056	0.466	16	0.152	R.QVLVDLQENPR.A
R3/RRR3-6/2	1311.253	1311.469	-165.609	0.441	655.373	0.458	15	0.152	R.QVLVDLQENPR.A
R3/RRR3-6/2	1311.081	1311.469	-297.118	0.420	612.476	0.444	15	0.149	R.QVLVDLQENPR.A
R3/RRR3-2/2	1686.655	1686.844	-111.980	0.517	2150.154	0.447	21	0.301	R.YYDLSSQEIGELIR.F
R3/RRR3-2/2	1685.980	1686.844	-1108.958	0.349	1907.588	0.360	20	0.240	R.YYDLSSQEIGELIR.F
R3/RRR3-2/2	1159.130	1158.373	-210.370	0.499	1625.992	0.468	18	0.230	R.IVALSASLANAK.D
R3/RRR3-2/2	1687.722	1686.844	-72.227	0.521	1357.940	0.434	20	0.191	R.YYDLSSQEIGELIR.F
R3/RRR3-2/2	1288.104	1287.572	-364.772	0.408	935.753	0.416	16	0.156	R.VVYIAPIEALAK.E
R3/RRR3-2/2	1825.173	1825.163	5.728	0.400	704.788	0.484	17	0.148	R.LKLEGLSLSSDMVYIR.Q
R3/RRR3-1/2	1688.081	1686.844	141.027	0.362	993.033	0.324	18	0.148	R.YYDLSSQEIGELIR.F
R3/RRR3-2/2	1287.117	1287.572	-354.778	0.209	498.517	0.299	12	0.125	-.VVYIAPIEALAK.-
R3/RRR3-3/2	1487.696	1487.637	39.371	0.317	1150.794	0.317	17	0.153	R.ANQIQSDLEELVK.S
R3/RRR3-2/2	1891.387	1891.925	-815.490	0.381	613.251	0.491	18	0.143	K.SAAASEQTVEPDATPSDSK.T
R3/RRR3-17/2	1002.201	1002.150	51.053	0.283	933.356	0.243	13	0.136	K.REVQSLAAK.Y
R3/RRR3-3/3	1328.528	1328.457	53.985	0.509	1009.901	0.361	22	0.103	-.RPLSLDADDAVR.-
R3/RRR3-18/2	1617.429	1616.795	-226.762	0.546	1648.063	0.546	20	0.249	K.LSVETTANQDPLVTK.G
R3/RRR3-18/2	1745.330	1744.968	208.376	0.598	1480.059	0.589	24	0.239	K.KLSVETTANQDPLVTK.G
R3/RRR3-18/2	1744.493	1744.968	-273.061	0.578	1482.721	0.579	24	0.237	K.KLSVETTANQDPLVTK.G
R3/RRR3-18/2	1744.431	1744.968	-883.558	0.547	1510.831	0.521	24	0.227	K.KLSVETTANQDPLVTK.G
R3/RRR3-18/2	1616.348	1616.795	-277.590	0.465	1409.236	0.563	19	0.222	K.LSVETTANQDPLVTK.G
R3/RRR3-18/2	1616.216	1616.795	-980.014	0.469	1250.510	0.547	18	0.200	K.LSVETTANQDPLVTK.G
R3/RRR3-18/2	1504.845	1505.702	-1237.721	0.451	811.442	0.420	15	0.151	K.NVRPDYLSNIWK.V
R3/RRR3-18/2	1506.460	1505.702	-161.135	0.470	893.231	0.379	16	0.150	K.NVRPDYLSNIWK.V
R3/RRR3-18/2	1504.670	1505.702	-1354.877	0.411	843.749	0.380	15	0.147	K.NVRPDYLSNIWK.V
R3/RRR3-18/3	1506.862	1505.702	106.504	0.622	1024.877	0.447	27	0.123	K.NVRPDYLSNIWK.V
R3/RRR3-18/3	1745.843	1744.968	-72.039	0.435	1539.441	0.258	28	0.122	K.KLSVETTANQDPLVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/3	1505.733	1505.702	20.148	0.592	1079.510	0.414	28	0.119	K.NVRPDYLSNIWK.V
R3/RRR3-18/3	1505.001	1505.702	-1133.673	0.562	710.116	0.432	24	0.110	K.NVRPDYLSNIWK.V
R3/RRR3-15/2	1585.102	1585.768	-1054.015	0.510	1922.788	0.609	24	0.312	K.NQGNPDLIGMGALER.S
R3/RRR3-15/2	1600.953	1601.767	-1136.511	0.460	1554.586	0.529	23	0.234	K.NQGNPDLIGM*GALER.S
R3/RRR3-15/2	1601.185	1601.767	-990.755	0.521	1537.265	0.532	23	0.233	K.NQGNPDLIGM*GALER.S
R3/RRR3-15/2	977.085	977.058	27.679	0.347	669.947	0.386	13	0.145	R.WWADVSGR.E
R3/RRR3-15/2	1036.098	1036.163	-63.057	0.361	811.790	0.255	13	0.138	K.VLDIYEQR.L
R3/RRR3-15/2	976.321	977.058	-1784.542	0.257	750.687	0.277	13	0.135	R.WWADVSGR.E
R3/RRR3-15/2	1035.719	1036.163	-430.726	0.253	811.351	0.211	12	0.132	K.VLDIYEQR.L
R3/RRR3-17/2	1320.215	1320.559	-261.397	0.449	1943.964	0.493	19	0.281	R.GAVGALLVYDITK.R
R3/RRR3-17/2	1320.026	1320.559	-1164.850	0.507	1532.711	0.523	18	0.229	R.GAVGALLVYDITK.R
R3/RRR3-17/2	1320.321	1320.559	-181.256	0.495	1525.655	0.505	17	0.223	R.GAVGALLVYDITK.R
R3/RRR3-17/2	1298.068	1298.427	-277.836	0.428	1083.938	0.539	21	0.186	K.EAAAASAPLPSQGK.T
R3/RRR3-17/2	1298.161	1298.427	-206.137	0.392	927.124	0.500	20	0.167	K.EAAAASAPLPSQGK.T
R3/RRR3-3/2	1267.270	1267.543	-215.702	0.419	811.052	0.464	17	0.156	K.LVSAPVILEAVR.L
R3/RRR3-3/2	1931.075	1929.198	-63.822	0.341	693.200	0.424	15	0.137	K.LPAYSGGAAVCTFPEFLK.S
R3/RRR3-3/2	1311.364	1312.411	-1565.801	0.281	681.956	0.322	16	0.134	K.HSNVDSSDLPIK.S
R3/RRR3-3/3	1387.772	1388.547	-1282.991	0.465	783.551	0.484	21	0.113	-.CSSRPAPPPGFSK.-
R3/RRR3-3/3	1387.274	1388.547	-1643.407	0.349	616.298	0.378	19	0.096	R.CSSRPAPPPGFSK.L
R3/RRR3-3/3	1388.313	1388.547	-169.390	0.422	697.471	0.339	20	0.095	R.CSSRPAPPPGFSK.L
R3/RRR3-12/2	1306.257	1306.490	-178.802	0.538	2529.934	0.401	21	0.359	K.AFGAELVLTDAAK.G
R3/RRR3-12/2	1306.347	1306.490	-109.340	0.576	2293.989	0.398	21	0.311	K.AFGAELVLTDAAK.G
R3/RRR3-12/2	1306.100	1306.490	-298.907	0.554	2290.110	0.363	21	0.300	K.AFGAELVLTDAAK.G
R3/RRR3-12/2	1115.053	1115.310	-231.093	0.496	1516.671	0.499	19	0.226	K.IQGIGAGFVPR.N
R3/RRR3-13/2	1528.217	1528.841	-1066.176	0.393	729.493	0.378	19	0.146	K.LILTM*PASM*SM*ER.R
R3/RRR3-13/2	1528.370	1528.841	-309.357	0.389	766.300	0.361	19	0.145	K.LILTM*PASM*SM*ER.R
R3/RRR3-13/2	1514.215	1512.842	247.458	0.303	479.806	0.279	16	0.134	K.LILTMPASM*SM*ER.R
R3/RRR3-17/3	1949.758	1949.071	-160.928	0.553	2749.260	0.507	33	0.425	K.VAHATYAFNDYYQTAGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1909.548	1910.068	-798.437	0.549	2274.254	0.540	25	0.350	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-16/2	1909.482	1910.068	-833.026	0.547	2166.974	0.524	25	0.324	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-16/2	1909.613	1910.068	-239.320	0.552	2066.214	0.576	24	0.321	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-15/2	1909.486	1910.068	-831.229	0.521	2018.786	0.575	24	0.313	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-15/2	1909.418	1910.068	-867.167	0.496	1988.184	0.522	24	0.292	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-15/2	1910.299	1910.068	121.032	0.547	1962.623	0.535	24	0.291	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-16/3	1949.826	1949.071	-126.166	0.558	2129.265	0.516	31	0.285	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-17/3	1949.152	1949.071	41.727	0.528	2159.446	0.481	31	0.278	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-15/3	1949.795	1949.071	-142.181	0.541	2019.803	0.519	31	0.266	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-16/3	1949.295	1949.071	115.165	0.547	2029.895	0.504	31	0.261	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-15/3	1949.053	1949.071	-9.342	0.509	2056.854	0.459	30	0.252	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-15/3	1948.399	1949.071	-860.727	0.483	1922.619	0.504	30	0.245	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-14/3	1948.825	1949.071	-126.765	0.501	1885.999	0.461	30	0.223	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-17/3	1948.681	1949.071	-200.946	0.487	1301.044	0.459	26	0.149	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-16/2	1137.996	1138.206	-185.227	0.330	574.950	0.307	12	0.137	R.GAQCFNPDTK.V
R3/RRR3-15/2	1137.993	1138.206	-187.272	0.399	637.750	0.338	12	0.134	-.GAQCFNPDTK.-
R3/RRR3-15/2	1138.511	1138.206	268.464	0.397	788.262	0.280	13	0.134	-.GAQCFNPDTK.-
R3/RRR3-15/2	1138.845	1138.206	-318.186	0.389	592.029	0.325	12	0.132	-.GAQCFNPDTK.-
R3/RRR3-16/2	1137.819	1138.206	-341.285	0.284	618.659	0.221	12	0.130	-.GAQCFNPDTK.-
R3/RRR3-16/2	1138.027	1138.206	-157.895	0.284	691.013	0.199	12	0.128	-.GAQCFNPDTK.-
R3/RRR3-16/3	1910.739	1910.068	-173.057	0.432	748.734	0.501	24	0.117	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-17/3	1950.684	1949.071	-198.919	0.442	1103.018	0.373	29	0.115	K.VAHATYAFNDYYQTAGR.A
R3/RRR3-15/3	1910.215	1910.068	77.093	0.396	838.309	0.394	26	0.104	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-15/3	1909.358	1910.068	-898.430	0.314	567.033	0.387	21	0.096	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-15/3	1909.381	1910.068	-886.203	0.285	807.504	0.329	26	0.095	R.ASGSCDFAGAATIVTQQPK.I
R3/RRR3-16/3	1910.008	1910.068	-31.649	0.328	525.222	0.302	21	0.071	-.ASGSCDFAGAATIVTQQPK.-
R3/RRR3-4/2	1308.197	1308.492	-226.175	0.454	1230.246	0.441	19	0.183	R.NMSVIAHVDHGK.S
R3/RRR3-3/2	1041.187	1040.285	-94.499	0.437	1045.398	0.376	14	0.161	R.IRPVLTVNK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1040.085	1040.285	-193.011	0.456	843.803	0.444	13	0.160	R.IRPVLTVNK.M
R3/RRR3-5/2	1040.232	1040.285	-50.448	0.466	863.873	0.430	13	0.159	R.IRPVLTVNK.M
R3/RRR3-4/2	1307.500	1308.492	-1528.384	0.450	745.822	0.447	18	0.156	R.NMSVIAHVDHGK.S
R3/RRR3-2/2	1039.960	1040.285	-312.650	0.464	822.852	0.410	13	0.155	R.IRPVLTVNK.M
R3/RRR3-5/2	1040.191	1040.285	-89.999	0.450	842.237	0.399	13	0.154	R.IRPVLTVNK.M
R3/RRR3-2/2	1040.522	1040.285	229.028	0.505	914.516	0.367	14	0.154	R.IRPVLTVNK.M
R3/RRR3-4/2	1040.175	1040.285	-105.773	0.466	750.827	0.406	12	0.151	R.IRPVLTVNK.M
R3/RRR3-4/2	1041.130	1040.285	-149.306	0.491	842.075	0.369	13	0.150	R.IRPVLTVNK.M
R3/RRR3-1/2	1041.123	1040.285	-155.304	0.473	865.043	0.358	13	0.150	R.IRPVLTVNK.M
R3/RRR3-2/2	1041.060	1040.285	-216.470	0.444	867.951	0.341	13	0.148	R.IRPVLTVNK.M
R3/RRR3-4/2	1040.310	1040.285	24.879	0.440	870.981	0.325	13	0.147	R.IRPVLTVNK.M
R3/RRR3-5/2	1040.203	1040.285	-79.169	0.473	661.382	0.380	12	0.146	R.IRPVLTVNK.M
R3/RRR3-4/2	1307.540	1308.492	-1497.811	0.413	521.871	0.420	16	0.146	R.NMSVIAHVDHGK.S
R3/RRR3-2/2	1308.456	1308.492	-27.755	0.426	509.453	0.425	15	0.145	R.NMSVIAHVDHGK.S
R3/RRR3-1/2	1041.115	1040.285	-163.302	0.499	726.715	0.333	12	0.142	R.IRPVLTVNK.M
R3/RRR3-1/2	1325.382	1324.492	-82.550	0.268	303.333	0.310	14	0.137	R.NM*SVIAHVDHGK.S
R3/RRR3-3/2	1039.590	1040.285	-1635.244	0.430	485.430	0.412	10	0.134	-.IRPVLTVNK.-
R3/RRR3-4/3	1458.639	1458.755	-80.222	0.584	891.779	0.405	25	0.110	R.IRPVLTVNKM*DR.C
R3/RRR3-4/3	1458.888	1458.755	91.501	0.551	610.174	0.385	23	0.104	R.IRPVLTVNKM*DR.C
R3/RRR3-4/3	1457.925	1458.755	-1259.509	0.547	665.045	0.360	23	0.101	R.IRPVLTVNKM*DR.C
R3/RRR3-5/3	1458.612	1458.755	-98.229	0.523	793.913	0.330	23	0.098	R.IRPVLTVNKM*DR.C
R3/RRR3-5/3	1458.668	1458.755	-59.950	0.510	807.918	0.318	24	0.097	R.IRPVLTVNKM*DR.C
R3/RRR3-14/2	1632.242	1631.894	213.361	0.576	2404.829	0.525	25	0.375	R.LPFDDASVGSVLAVIK.K
R3/RRR3-14/2	1631.368	1631.894	-938.564	0.521	2096.439	0.482	24	0.303	R.LPFDDASVGSVLAVIK.K
R3/RRR3-14/2	1631.306	1631.894	-976.878	0.527	2006.449	0.467	23	0.282	R.LPFDDASVGSVLAVIK.K
R3/RRR3-14/2	1750.804	1749.946	-81.233	0.411	742.358	0.490	18	0.154	K.KVENLGDQFITEISR.V
R3/RRR3-14/2	1158.234	1158.290	-48.902	0.355	916.136	0.403	17	0.151	R.AVGDLAAAAGVSR.E
R3/RRR3-14/2	1751.621	1749.946	-186.114	0.272	224.034	0.349	12	0.128	-.KVENLGDQFITEISR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1288.312	1287.488	-137.101	0.478	1891.350	0.454	18	0.262	K.DASLVEIVTAIR.E
R3/RRR3-9/2	1405.320	1404.550	-164.543	0.513	1371.623	0.482	20	0.204	R.TLAIDFAPDADVR.L
R3/RRR3-9/2	1287.324	1287.488	-127.600	0.312	1361.682	0.324	16	0.174	-.DASLVEIVTAIR.-
R3/RRR3-8/2	822.882	822.932	-60.202	0.328	1155.686	0.420	13	0.171	R.LGFAASTR.H
R3/RRR3-9/2	1404.195	1404.550	-253.263	0.474	1067.581	0.448	19	0.171	R.TLAIDFAPDADVR.L
R3/RRR3-8/2	822.859	822.932	-89.218	0.331	1002.213	0.425	12	0.161	R.LGFAASTR.H
R3/RRR3-9/2	1286.620	1287.488	-1456.313	0.261	415.995	0.306	13	0.132	-.DASLVEIVTAIR.-
R3/RRR3-17/2	1479.566	1479.660	-64.018	0.396	1803.820	0.461	18	0.250	R.STNEALLVIEAYR.T
R3/RRR3-16/2	1479.004	1479.660	-1123.169	0.337	1945.645	0.353	19	0.244	R.STNEALLVIEAYR.T
R3/RRR3-16/2	1479.269	1479.660	-265.157	0.355	1798.730	0.331	18	0.219	R.STNEALLVIEAYR.T
R3/RRR3-16/2	1479.146	1479.660	-1026.711	0.326	1463.976	0.306	17	0.177	R.STNEALLVIEAYR.T
R3/RRR3-16/2	1030.845	1031.188	-334.300	0.500	1178.949	0.365	15	0.168	R.LDNLSSLIR.Q
R3/RRR3-16/2	1031.083	1031.188	-102.550	0.517	1059.943	0.367	15	0.161	R.LDNLSSLIR.Q
R3/RRR3-16/2	1031.027	1031.188	-156.706	0.524	1040.775	0.336	15	0.155	R.LDNLSSLIR.Q
R3/RRR3-17/2	1031.015	1031.188	-168.465	0.496	926.787	0.236	15	0.138	R.LDNLSSLIR.Q
R3/RRR3-17/2	1479.618	1479.660	-28.433	0.190	873.441	0.077	16	0.125	R.STNEALLVIEAYR.T
R3/RRR3-16/3	1345.353	1345.486	-99.263	0.413	1077.806	0.301	24	0.099	R.DRGPYPADQVVK.D
R3/RRR3-16/3	1345.488	1345.486	1.754	0.391	668.624	0.259	20	0.088	R.DRGPYPADQVVK.D
R3/RRR3-2/2	1118.038	1118.219	-163.018	0.479	1008.081	0.386	16	0.161	R.ELSEIAEQAK.R
R3/RRR3-3/2	1060.630	1061.133	-1420.875	0.373	1030.527	0.372	15	0.158	R.EAQWATAQR.T
R3/RRR3-2/2	1118.071	1118.219	-133.118	0.487	1012.716	0.365	16	0.158	R.ELSEIAEQAK.R
R3/RRR3-3/2	1117.898	1118.219	-288.553	0.443	763.647	0.401	14	0.150	R.ELSEIAEQAK.R
R3/RRR3-3/2	1274.344	1274.406	-49.058	0.390	559.566	0.432	16	0.148	R.ELSEIAEQAKR.R
R3/RRR3-1/2	1117.933	1118.219	-257.221	0.410	725.169	0.390	14	0.148	R.ELSEIAEQAK.R
R3/RRR3-2/2	1117.846	1118.219	-335.554	0.356	716.765	0.369	14	0.145	R.ELSEIAEQAK.R
R3/RRR3-2/2	1274.186	1274.406	-173.117	0.432	554.679	0.374	16	0.145	R.ELSEIAEQAKR.R
R3/RRR3-2/2	1274.368	1274.406	-29.554	0.385	448.242	0.419	14	0.144	R.ELSEIAEQAKR.R
R3/RRR3-2/2	1274.100	1274.406	-241.069	0.382	491.477	0.396	15	0.144	R.ELSEIAEQAKR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1273.408	1274.406	-1573.725	0.363	463.737	0.391	15	0.143	R.ELSEIAEQAKR.R
R3/RRR3-3/2	1060.408	1061.133	-1631.313	0.391	784.368	0.317	14	0.142	R.EAQWATAQR.T
R3/RRR3-10/2	1344.298	1344.539	-180.300	0.545	1337.480	0.561	20	0.217	R.LVDIGTVTAQQAK.D
R3/RRR3-11/2	1343.756	1344.539	-1330.792	0.461	1351.300	0.552	21	0.216	R.LVDIGTVTAQQAK.D
R3/RRR3-11/2	1415.272	1415.490	-154.042	0.426	1015.345	0.345	18	0.152	R.DIDSFTQQFASR.I
R3/RRR3-10/2	1343.971	1344.539	-1170.698	0.318	843.126	0.396	18	0.149	R.LVDIGTVTAQQAK.D
R3/RRR3-11/2	1168.425	1168.350	64.066	0.456	653.454	0.416	14	0.146	K.DWGFSGVMLR.-
R3/RRR3-21/2	1177.128	1177.357	-195.279	0.497	1666.845	0.399	17	0.219	R.GIGM*LQASLDR.S
R3/RRR3-21/2	1332.126	1331.497	-279.924	0.442	635.342	0.504	18	0.157	R.QALTLQSVVEDK.T
R3/RRR3-21/2	1331.094	1331.497	-303.872	0.427	482.902	0.494	16	0.150	R.QALTLQSVVEDK.T
R3/RRR3-21/2	1070.098	1069.241	-133.937	0.375	667.689	0.380	13	0.144	R.LSWALVHSR.N
R3/RRR3-21/2	1330.606	1331.497	-1425.654	0.335	409.648	0.412	15	0.140	R.QALTLQSVVEDK.T
R3/RRR3-21/2	1070.246	1069.241	4.621	0.350	564.747	0.220	12	0.131	-.LSWALVHSR.-
R3/RRR3-16/2	1487.812	1488.710	-1279.624	0.353	2058.653	0.424	22	0.281	K.AQDTFTPISAVIPK.S
R3/RRR3-16/2	1487.589	1488.710	-1430.023	0.406	1840.105	0.450	21	0.254	K.AQDTFTPISAVIPK.S
R3/RRR3-16/2	1487.534	1488.710	-1467.527	0.324	1354.668	0.435	19	0.189	K.AQDTFTPISAVIPK.S
R3/RRR3-16/2	1615.459	1615.766	-190.356	0.544	891.527	0.391	20	0.152	K.SDVANPDDLELWLK.V
R3/RRR3-16/2	1030.867	1030.202	-326.097	0.379	489.917	0.478	15	0.150	K.SAGLPWTLGK.A
R3/RRR3-16/2	1030.095	1030.202	-104.550	0.386	499.426	0.470	15	0.150	K.SAGLPWTLGK.A
R3/RRR3-16/2	1615.382	1615.766	-238.419	0.530	764.954	0.403	19	0.148	K.SDVANPDDLELWLK.V
R3/RRR3-16/2	1614.811	1615.766	-1214.016	0.405	584.811	0.383	17	0.141	K.SDVANPDDLELWLK.V
R3/RRR3-16/2	1030.088	1030.202	-111.088	0.234	530.369	0.358	13	0.135	K.SAGLPWTLGK.A
R3/RRR3-5/2	1675.003	1675.862	-1113.521	0.366	2765.077	0.566	24	0.476	K.AAVAVLGDLADTLGSSSK.D
R3/RRR3-5/2	1675.164	1675.862	-1016.643	0.377	2465.608	0.562	24	0.402	K.AAVAVLGDLADTLGSSSK.D
R3/RRR3-5/2	1336.284	1336.476	-143.632	0.356	763.334	0.348	13	0.138	R.ASAYEALNEIVR.V
R3/RRR3-5/2	1336.250	1336.476	-169.566	0.375	684.968	0.293	14	0.133	R.ASAYEALNEIVR.V
R3/RRR3-10/3	1755.910	1755.873	21.112	0.579	2381.132	0.586	33	0.366	R.TAVHQGIGHQTYAESR.G
R3/RRR3-10/3	1755.900	1755.873	15.778	0.555	2169.629	0.558	32	0.308	R.TAVHQGIGHQTYAESR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/3	1755.206	1755.873	-952.641	0.530	1941.598	0.533	31	0.255	R.TAVHQGIGHQTYAESR.G
R3/RRR3-10/3	1755.807	1755.873	-37.357	0.475	2036.961	0.481	31	0.254	R.TAVHQGIGHQTYAESR.G
R3/RRR3-9/3	1755.683	1755.873	-108.282	0.486	1906.891	0.533	29	0.252	R.TAVHQGIGHQTYAESR.G
R3/RRR3-9/3	1754.539	1755.873	-1334.017	0.483	1897.066	0.521	29	0.246	R.TAVHQGIGHQTYAESR.G
R3/RRR3-17/2	991.289	991.081	210.760	0.286	741.488	0.272	17	0.133	K.ALGGSVTGSNK.R
R3/RRR3-9/3	1774.421	1774.094	185.079	0.370	908.496	0.487	26	0.119	R.APEYLALNDKVISLVK.G
R3/RRR3-9/3	1773.575	1774.094	-859.071	0.280	544.911	0.450	22	0.097	R.APEYLALNDKVISLVK.G
R3/RRR3-18/2	1313.241	1313.502	-199.418	0.496	1697.986	0.450	19	0.236	K.FM*EVISGTGDIK.A
R3/RRR3-18/2	1257.186	1257.484	-236.999	0.444	1179.538	0.500	15	0.189	R.AM*DFLVELFR.N
R3/RRR3-18/2	1674.294	1673.805	292.830	0.483	1077.926	0.487	22	0.178	K.ENHDFLASVGLDDLK.A
R3/RRR3-19/2	1673.321	1673.805	-290.016	0.443	496.263	0.436	16	0.140	K.ENHDFLASVGLDDLK.A
R3/RRR3-18/2	1256.525	1257.484	-1563.095	0.320	577.080	0.386	13	0.139	R.AM*DFLVELFR.N
R3/RRR3-11/2	1823.699	1824.159	-253.347	0.546	2069.758	0.582	28	0.329	K.TQKPVVAFIAGLTAPPGR.R
R3/RRR3-11/2	1823.528	1824.159	-897.403	0.532	2036.145	0.578	27	0.321	K.TQKPVVAFIAGLTAPPGR.R
R3/RRR3-11/2	1823.528	1824.159	-897.336	0.502	1944.123	0.581	27	0.306	K.TQKPVVAFIAGLTAPPGR.R
R3/RRR3-12/2	1186.947	1187.325	-319.629	0.447	1390.573	0.509	20	0.212	R.EAGVTVVESPAK.I
R3/RRR3-11/2	1186.971	1187.325	-298.993	0.417	1159.859	0.527	19	0.192	R.EAGVTVVESPAK.I
R3/RRR3-12/2	1187.131	1187.325	-164.256	0.392	1095.955	0.542	18	0.187	R.EAGVTVVESPAK.I
R3/RRR3-11/2	1186.858	1187.325	-394.548	0.360	1176.441	0.446	19	0.178	R.EAGVTVVESPAK.I
R3/RRR3-11/2	1186.981	1187.325	-290.222	0.420	1049.569	0.488	18	0.176	R.EAGVTVVESPAK.I
R3/RRR3-12/2	1187.014	1187.325	-262.777	0.338	829.055	0.465	16	0.156	R.EAGVTVVESPAK.I
R3/RRR3-11/2	1084.974	1085.263	-266.502	0.338	836.492	0.246	15	0.133	R.MGHAGAIVSGGK.G
R3/RRR3-11/2	1085.157	1085.263	-97.327	0.305	762.265	0.179	15	0.128	R.MGHAGAIVSGGK.G
R3/RRR3-20/2	1369.354	1369.546	-140.521	0.543	1472.087	0.523	20	0.225	K.HLLDETISDVVK.S
R3/RRR3-20/2	1369.198	1369.546	-254.639	0.480	1530.111	0.481	20	0.222	K.HLLDETISDVVK.S
R3/RRR3-20/2	1370.195	1369.546	-256.688	0.523	1298.945	0.520	19	0.205	K.HLLDETISDVVK.S
R3/RRR3-20/2	1138.799	1139.197	-350.560	0.467	630.044	0.439	15	0.154	R.LIDDYNTER.K
R3/RRR3-20/2	1138.889	1139.197	-271.301	0.485	615.983	0.387	15	0.149	R.LIDDYNTER.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/2	1277.309	1277.493	-144.129	0.292	706.405	0.474	14	0.147	K.EGVLVEGLFWK.D
R3/RRR3-20/2	1277.124	1277.493	-289.966	0.318	640.056	0.412	14	0.142	K.EGVLVEGLFWK.D
R3/RRR3-20/2	1138.394	1139.197	-1589.039	0.346	659.337	0.245	15	0.136	R.LIDDYNTER.K
R3/RRR3-22/2	1328.009	1327.486	-359.988	0.481	1604.145	0.483	19	0.230	K.EAFELVSGEMSK.T
R3/RRR3-22/2	1344.071	1343.485	-309.300	0.557	1076.870	0.524	19	0.187	K.EAFELVSGEM*SK.T
R3/RRR3-22/2	1327.259	1327.486	-171.452	0.390	1202.010	0.340	18	0.164	K.EAFELVSGEMSK.T
R3/RRR3-22/2	1342.807	1343.485	-1253.573	0.403	1161.839	0.331	18	0.160	K.EAFELVSGEM*SK.T
R3/RRR3-22/2	1342.748	1343.485	-1297.304	0.352	1177.781	0.325	18	0.160	K.EAFELVSGEM*SK.T
R3/RRR3-22/2	1685.463	1685.902	-261.122	0.429	653.906	0.509	24	0.158	R.LDPGVTASHAFVLETK.V
R3/RRR3-22/2	1239.210	1239.405	-157.847	0.356	786.229	0.454	16	0.155	R.FQGSPAVITYR.V
R3/RRR3-22/2	1685.257	1685.902	-979.242	0.438	593.348	0.498	23	0.154	R.LDPGVTASHAFVLETK.V
R3/RRR3-22/2	1684.548	1685.902	-1401.719	0.393	661.659	0.471	24	0.153	R.LDPGVTASHAFVLETK.V
R3/RRR3-22/2	1238.553	1239.405	-1499.287	0.267	849.896	0.346	17	0.144	R.FQGSPAVITYR.V
R3/RRR3-22/2	1238.975	1239.405	-348.008	0.465	609.505	0.364	15	0.143	R.FQGSPAVITYR.V
R3/RRR3-23/2	1240.551	1239.405	118.473	0.303	438.059	0.359	12	0.136	R.FQGSPAVITYR.V
R3/RRR3-16/2	1214.863	1215.342	-394.825	0.554	1805.318	0.411	18	0.236	R.SLEGLQANVQR.L
R3/RRR3-16/2	1215.132	1215.342	-173.167	0.567	1763.780	0.401	18	0.227	R.SLEGLQANVQR.L
R3/RRR3-21/2	1214.728	1215.342	-1332.348	0.529	1733.555	0.373	18	0.218	R.SLEGLQANVQR.L
R3/RRR3-20/2	1215.096	1215.342	-202.393	0.537	1770.105	0.346	18	0.215	R.SLEGLQANVQR.L
R3/RRR3-21/2	1216.034	1215.342	-253.889	0.558	1740.656	0.361	18	0.215	R.SLEGLQANVQR.L
R3/RRR3-16/2	1215.051	1215.342	-239.987	0.551	1600.428	0.392	18	0.207	R.SLEGLQANVQR.L
R3/RRR3-20/2	1215.249	1215.342	-76.430	0.540	1697.850	0.335	18	0.204	R.SLEGLQANVQR.L
R3/RRR3-21/2	1214.435	1215.342	-1574.733	0.454	1256.632	0.391	17	0.176	R.SLEGLQANVQR.L
R3/RRR3-15/2	1215.321	1215.342	-17.087	0.494	1297.262	0.337	17	0.169	R.SLEGLQANVQR.L
R3/RRR3-20/2	1215.033	1215.342	-255.005	0.447	1435.916	0.268	18	0.169	R.SLEGLQANVQR.L
R3/RRR3-16/2	975.986	975.085	-101.753	0.435	728.927	0.414	11	0.152	K.HWQNYVK.T
R3/RRR3-16/2	974.886	975.085	-204.978	0.418	672.504	0.367	10	0.145	K.HWQNYVK.T
R3/RRR3-16/2	974.326	975.085	-1810.437	0.413	551.687	0.321	10	0.140	K.HWQNYVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1215.601	1215.342	213.769	0.342	846.136	0.230	16	0.137	R.SLEGLQANVQR.L
R3/RRR3-12/2	1216.147	1215.342	-160.237	0.397	567.750	0.251	15	0.137	R.SLEGLQANVQR.L
R3/RRR3-19/2	1214.397	1215.342	-1606.339	0.406	731.624	0.191	17	0.134	R.SLEGLQANVQR.L
R3/RRR3-16/3	1457.548	1457.659	-76.796	0.529	955.609	0.467	26	0.122	K.KYAPTIGISVDHR.R
R3/RRR3-16/3	1456.686	1457.659	-1358.962	0.441	562.100	0.437	23	0.105	K.KYAPTIGISVDHR.R
R3/RRR3-16/3	1457.918	1457.659	177.936	0.438	640.807	0.329	25	0.097	K.KYAPTIGISVDHR.R
R3/RRR3-13/2	1058.972	1059.159	-176.735	0.436	1233.635	0.483	15	0.190	R.NLNSLAVDGR.L
R3/RRR3-13/2	943.208	943.126	87.217	0.417	871.622	0.330	13	0.146	R.LTIQAAGLR.N
R3/RRR3-13/2	943.170	943.126	47.238	0.406	873.836	0.332	13	0.146	-.LTIQAAGLR.-
R3/RRR3-13/2	988.110	988.160	-51.188	0.376	807.040	0.339	14	0.145	K.ALIVSEVEK.N
R3/RRR3-13/2	942.876	943.126	-265.956	0.345	1006.644	0.272	14	0.145	R.LTIQAAGLR.N
R3/RRR3-13/2	988.029	988.160	-132.732	0.362	761.469	0.340	14	0.144	K.ALIVSEVEK.N
R3/RRR3-13/2	987.481	988.160	-1705.851	0.282	683.981	0.318	13	0.138	K.ALIVSEVEK.N
R3/RRR3-18/2	974.054	974.094	-40.803	0.448	1857.205	0.411	19	0.248	R.LSADAGAGALK.L
R3/RRR3-18/2	973.322	974.094	-1825.198	0.384	1660.015	0.336	19	0.206	R.LSADAGAGALK.L
R3/RRR3-18/2	1172.494	1173.295	-1540.527	0.498	1246.283	0.521	17	0.200	R.AAGPELVEACR.K
R3/RRR3-18/2	1172.467	1173.295	-1564.059	0.436	1101.054	0.499	16	0.181	R.AAGPELVEACR.K
R3/RRR3-18/2	1173.109	1173.295	-159.227	0.368	1069.569	0.460	16	0.171	R.AAGPELVEACR.K
R3/RRR3-18/3	1256.483	1256.417	52.548	0.400	834.436	0.495	23	0.118	R.M*LGGGGVDGAIHR.A
R3/RRR3-18/3	1255.898	1256.417	-1213.277	0.320	818.405	0.339	23	0.095	R.M*LGGGGVDGAIHR.A
R3/RRR3-18/3	1256.505	1256.417	69.940	0.387	1030.664	0.277	27	0.094	R.M*LGGGGVDGAIHR.A
R3/RRR3-15/2	1016.775	1017.188	-407.623	0.410	1781.538	0.434	18	0.241	R.AMIGQVAGGGR.T
R3/RRR3-17/3	1974.340	1975.066	-876.797	0.468	1703.871	0.574	34	0.233	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-17/3	1974.698	1975.066	-186.890	0.504	1668.668	0.565	32	0.225	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-14/3	1974.998	1975.066	-34.265	0.523	1472.896	0.595	31	0.206	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-17/3	1974.916	1975.066	-75.928	0.472	1497.548	0.581	31	0.206	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-14/2	1974.369	1975.066	-861.708	0.520	1131.681	0.574	20	0.191	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-14/3	1975.024	1975.066	-21.339	0.477	1433.273	0.549	33	0.186	R.ASGDYAIVISHNPDNGTSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1032.215	1033.188	-1916.712	0.388	1151.724	0.460	16	0.178	R.AM*IGQVAGGGR.T
R3/RRR3-15/2	1253.872	1254.504	-1305.792	0.433	1114.726	0.461	18	0.177	R.ATLSIGNVLPIR.S
R3/RRR3-14/2	1032.204	1033.188	-1927.289	0.368	1137.361	0.442	16	0.174	R.AM*IGQVAGGGR.T
R3/RRR3-14/3	1974.737	1975.066	-167.077	0.475	1238.865	0.572	30	0.171	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-16/2	1254.217	1254.504	-229.857	0.378	991.326	0.439	17	0.164	R.ATLSIGNVLPIR.S
R3/RRR3-15/2	1033.027	1033.188	-156.220	0.377	1052.802	0.388	16	0.161	R.AM*IGQVAGGGR.T
R3/RRR3-15/2	1032.403	1033.188	-1734.085	0.336	1079.158	0.361	16	0.158	R.AM*IGQVAGGGR.T
R3/RRR3-14/2	1254.169	1254.504	-268.134	0.341	987.043	0.392	18	0.158	R.ATLSIGNVLPIR.S
R3/RRR3-17/2	1254.003	1254.504	-1200.403	0.391	813.178	0.455	16	0.157	R.ATLSIGNVLPIR.S
R3/RRR3-15/2	1032.908	1033.188	-271.692	0.387	963.727	0.364	16	0.154	R.AM*IGQVAGGGR.T
R3/RRR3-15/2	1253.602	1254.504	-1521.430	0.344	863.497	0.407	16	0.153	R.ATLSIGNVLPIR.S
R3/RRR3-16/2	1254.208	1254.504	-236.790	0.340	919.609	0.375	17	0.152	R.ATLSIGNVLPIR.S
R3/RRR3-17/2	1254.239	1254.504	-212.184	0.423	810.554	0.388	16	0.150	R.ATLSIGNVLPIR.S
R3/RRR3-14/2	1254.201	1254.504	-241.965	0.405	770.613	0.406	15	0.150	R.ATLSIGNVLPIR.S
R3/RRR3-14/2	1032.774	1033.188	-401.896	0.368	825.813	0.336	15	0.144	-.AM*IGQVAGGGR.-
R3/RRR3-16/2	1254.145	1254.504	-286.981	0.251	677.129	0.276	14	0.135	R.ATLSIGNVLPIR.S
R3/RRR3-13/2	1254.206	1254.504	-238.645	0.216	699.338	0.268	15	0.134	R.ATLSIGNVLPIR.S
R3/RRR3-17/2	1254.023	1254.504	-384.351	0.273	530.993	0.252	13	0.134	R.ATLSIGNVLPIR.S
R3/RRR3-3/2	1253.663	1254.504	-1473.307	0.293	502.892	0.218	12	0.131	-.ATLSIGNVLPIR.-
R3/RRR3-20/2	1255.274	1254.504	-183.723	0.247	493.224	0.335	12	0.128	-.ATLSIGNVLPIR.-
R3/RRR3-12/3	1974.715	1975.066	-178.053	0.421	834.147	0.513	26	0.125	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-18/3	1975.036	1975.066	-15.109	0.323	382.040	0.363	21	0.097	R.ASGDYAIVISHNPDNGTSR.I
R3/RRR3-22/3	1806.137	1806.930	-995.824	0.527	1689.260	0.498	31	0.202	R.INM*SCVNHETGAVDSR.K
R3/RRR3-22/2	1215.624	1216.366	-1437.423	0.471	1675.436	0.317	16	0.202	R.LLEELERGEK.G
R3/RRR3-22/2	1216.114	1216.366	-207.962	0.523	1608.475	0.278	16	0.185	R.LLEELERGEK.G
R3/RRR3-22/2	1216.955	1216.366	-338.711	0.512	1509.524	0.311	16	0.183	R.LLEELERGEK.G
R3/RRR3-22/2	1091.077	1091.247	-156.498	0.494	1512.361	0.293	15	0.181	K.FGVLANWQR.E
R3/RRR3-22/3	1807.840	1806.930	-50.016	0.558	1358.976	0.503	29	0.163	R.INM*SCVNHETGAVDSR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/3	1806.645	1806.930	-158.278	0.526	1275.927	0.498	29	0.153	R.INM*SCVNHETGAVDSR.K
R3/RRR3-21/2	1964.548	1965.230	-858.662	0.498	1757.039	0.521	24	0.259	R.IAECLVGDETGIIVFTAR.N
R3/RRR3-21/3	1799.174	1799.070	58.135	0.427	1508.376	0.461	29	0.169	K.VDQLRPGTHGHNLLLK.V
R3/RRR3-21/2	1129.245	1129.377	-116.838	0.435	796.720	0.440	16	0.155	R.LAVDKWGIVK.A
R3/RRR3-21/3	1798.877	1799.070	-107.452	0.430	1055.661	0.503	25	0.135	K.VDQLRPGTHGHNLLLK.V
R3/RRR3-21/3	1798.776	1799.070	-163.817	0.425	973.592	0.423	26	0.114	K.VDQLRPGTHGHNLLLK.V
R3/RRR3-21/2	1422.780	1423.550	-1248.014	0.499	1301.340	0.316	18	0.165	R.DYQDDKADVILK.Y
R3/RRR3-21/2	1134.806	1135.252	-394.088	0.339	927.258	0.403	16	0.155	K.AYGELPDTLR.L
R3/RRR3-21/2	1135.162	1135.252	-79.557	0.377	641.987	0.417	14	0.146	K.AYGELPDTLR.L
R3/RRR3-21/3	1309.459	1309.439	15.454	0.434	1025.541	0.391	22	0.110	R.CEAICVDGTKR.L
R3/RRR3-18/2	1522.511	1522.773	-172.384	0.484	1983.324	0.498	20	0.288	K.FVNDLHALISPPAK.G
R3/RRR3-18/2	1522.019	1522.773	-1155.620	0.451	1877.770	0.472	21	0.265	K.FVNDLHALISPPAK.G
R3/RRR3-18/2	1522.213	1522.773	-1028.067	0.478	1681.445	0.486	20	0.240	K.FVNDLHALISPPAK.G
R3/RRR3-18/2	1559.183	1558.677	-317.843	0.496	1018.130	0.531	22	0.182	K.FVSNGQPGPAQNVDK.S
R3/RRR3-18/2	1558.993	1558.677	203.281	0.513	972.824	0.525	22	0.178	K.FVSNGQPGPAQNVDK.S
R3/RRR3-18/2	1559.175	1558.677	320.340	0.488	795.121	0.539	21	0.168	K.FVSNGQPGPAQNVDK.S
R3/RRR3-18/2	1558.153	1558.677	-981.566	0.536	790.225	0.520	22	0.167	K.FVSNGQPGPAQNVDK.S
R3/RRR3-18/2	1558.259	1558.677	-269.081	0.523	767.190	0.481	22	0.161	K.FVSNGQPGPAQNVDK.S
R3/RRR3-18/2	1558.150	1558.677	-983.218	0.498	680.821	0.439	21	0.152	K.FVSNGQPGPAQNVDK.S
R3/RRR3-18/3	1522.538	1522.773	-155.020	0.474	1055.925	0.477	29	0.128	K.FVNDLHALISPPAK.G
R3/RRR3-18/3	1705.798	1705.917	-69.779	0.467	669.183	0.495	24	0.114	K.HQELLKNEQYQM*K.L
R3/RRR3-18/3	1705.838	1705.917	-46.307	0.431	681.256	0.475	23	0.111	K.HQELLKNEQYQM*K.L
R3/RRR3-18/3	1706.191	1705.917	161.125	0.446	578.866	0.467	22	0.108	K.HQELLKNEQYQM*K.L
R3/RRR3-18/3	1522.363	1522.773	-270.006	0.435	577.753	0.452	25	0.106	K.FVNDLHALISPPAK.G
R3/RRR3-18/3	1522.724	1522.773	-32.220	0.398	567.993	0.437	26	0.104	K.FVNDLHALISPPAK.G
R3/RRR3-9/2	1423.211	1423.550	-239.039	0.498	2474.663	0.505	23	0.385	K.FIASEGDTVTPGTK.V
R3/RRR3-9/2	1423.175	1423.550	-264.252	0.474	2101.709	0.498	22	0.310	K.FIASEGDTVTPGTK.V
R3/RRR3-9/2	1423.102	1423.550	-315.457	0.455	1693.330	0.479	20	0.240	K.FIASEGDTVTPGTK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1796.199	1795.885	174.868	0.522	1326.725	0.630	22	0.226	K.SAAPAETHVAPSEDSTPK.E
R3/RRR3-9/2	1795.561	1795.885	-181.423	0.530	1167.680	0.649	20	0.211	K.SAAPAETHVAPSEDSTPK.E
R3/RRR3-9/2	1795.339	1795.885	-864.028	0.492	1167.995	0.633	20	0.208	K.SAAPAETHVAPSEDSTPK.E
R3/RRR3-8/2	1795.902	1795.885	9.367	0.459	733.177	0.575	18	0.163	K.SAAPAETHVAPSEDSTPK.E
R3/RRR3-9/2	1231.871	1232.321	-366.614	0.364	781.737	0.292	16	0.141	R.SDYKDEFVTK.H
R3/RRR3-9/2	1232.068	1232.321	-205.766	0.373	665.484	0.308	15	0.139	R.SDYKDEFVTK.H
R3/RRR3-9/2	1231.394	1232.321	-1569.650	0.354	755.423	0.277	15	0.138	R.SDYKDEFVTK.H
R3/RRR3-1/2	1797.461	1795.885	-236.950	0.319	355.431	0.443	14	0.135	K.SAAPAETHVAPSEDSTPK.E
R3/RRR3-25/2	1091.986	1092.252	-244.553	0.508	1165.807	0.335	15	0.162	K.SAQLLEQM*R.L
R3/RRR3-25/2	1091.948	1092.252	-279.432	0.472	1020.365	0.333	14	0.153	K.SAQLLEQM*R.L
R3/RRR3-25/2	1477.074	1476.696	256.912	0.380	863.435	0.391	16	0.147	K.IGVDEEIFVVDLK.K
R3/RRR3-25/3	1387.144	1387.588	-320.727	0.410	1172.154	0.448	25	0.130	R.LHM*ATDAGKDIAK.K
R3/RRR3-25/2	1092.399	1092.252	134.820	0.377	942.399	0.129	14	0.129	K.SAQLLEQM*R.L
R3/RRR3-25/3	1387.622	1387.588	25.088	0.387	864.763	0.414	24	0.107	R.LHM*ATDAGKDIAK.K
R3/RRR3-25/3	1387.942	1387.588	256.116	0.371	893.931	0.405	23	0.107	R.LHM*ATDAGKDIAK.K
R3/RRR3-13/2	1279.171	1279.421	-196.275	0.508	988.650	0.592	20	0.193	R.LVGDVDFAEVSK.V
R3/RRR3-13/2	1278.703	1279.421	-1347.844	0.406	815.681	0.545	18	0.169	R.LVGDVDFAEVSK.V
R3/RRR3-12/2	1279.144	1279.421	-217.146	0.475	736.970	0.485	18	0.160	R.LVGDVDFAEVSK.V
R3/RRR3-13/2	1278.532	1279.421	-1481.709	0.421	746.940	0.494	17	0.159	R.LVGDVDFAEVSK.V
R3/RRR3-13/2	1466.217	1466.834	-1106.159	0.325	859.855	0.458	17	0.155	R.SNIVGLPVSLLLLK.A
R3/RRR3-12/2	1466.525	1466.834	-211.274	0.354	842.453	0.440	18	0.154	R.SNIVGLPVSLLLLK.A
R3/RRR3-12/2	1279.110	1279.421	-243.953	0.395	594.235	0.496	16	0.153	R.LVGDVDFAEVSK.V
R3/RRR3-12/2	1157.064	1156.274	-182.387	0.378	632.153	0.405	14	0.141	K.ADATVSIVHSR.T
R3/RRR3-13/2	1466.209	1466.834	-1111.259	0.310	390.165	0.394	12	0.133	-.SNIVGLPVSLLLLK.-
R3/RRR3-13/2	1466.821	1466.834	-8.565	0.243	593.790	0.281	15	0.131	R.SNIVGLPVSLLLLK.A
R3/RRR3-18/2	1030.798	1031.299	-1460.353	0.451	1720.895	0.460	15	0.240	R.FGM*MAAQMK.A
R3/RRR3-18/2	1015.770	1015.299	464.833	0.452	1573.170	0.485	16	0.228	R.FGMMAAQMK.A
R3/RRR3-18/2	1779.531	1779.029	-280.550	0.578	1085.603	0.538	24	0.190	K.IWQVPETLHEEVLGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	1014.946	1015.299	-349.428	0.412	1202.712	0.454	15	0.184	R.FGMMAAQMK.A
R3/RRR3-18/2	1046.722	1047.298	-1509.732	0.475	1243.602	0.417	16	0.182	R.FGM*M*AAQMK.A
R3/RRR3-18/2	1046.732	1047.298	-1500.243	0.406	1182.883	0.431	16	0.179	R.FGM*M*AAQMK.A
R3/RRR3-18/2	1778.321	1779.029	-963.453	0.521	1106.355	0.468	24	0.179	K.IWQVPETLHEEVLGK.M
R3/RRR3-18/2	1778.323	1779.029	-962.419	0.519	970.898	0.489	23	0.172	K.IWQVPETLHEEVLGK.M
R3/RRR3-18/2	1779.488	1779.029	258.525	0.511	971.950	0.441	22	0.164	K.IWQVPETLHEEVLGK.M
R3/RRR3-18/2	1015.033	1015.299	-263.394	0.391	1018.515	0.404	13	0.162	R.FGMMAAQMK.A
R3/RRR3-18/2	1046.925	1047.298	-357.495	0.403	951.598	0.407	14	0.160	R.FGM*M*AAQMK.A
R3/RRR3-18/3	1858.769	1857.039	-145.523	0.461	524.435	0.580	25	0.121	R.WPTEM*ELEHAFHQGK.Y
R3/RRR3-18/3	1857.478	1857.039	237.180	0.456	816.633	0.502	30	0.119	R.WPTEM*ELEHAFHQGK.Y
R3/RRR3-18/3	1856.783	1857.039	-138.293	0.439	691.565	0.449	25	0.108	R.WPTEM*ELEHAFHQGK.Y
R3/RRR3-14/2	1603.251	1603.839	-993.513	0.514	1562.783	0.441	21	0.216	K.LNSSLSQVLVNCLR.Y
R3/RRR3-15/2	1295.121	1295.379	-199.719	0.414	1084.736	0.384	18	0.162	K.GSVSTESAVTQTK.F
R3/RRR3-15/2	1294.992	1295.379	-299.107	0.419	934.436	0.419	16	0.157	K.GSVSTESAVTQTK.F
R3/RRR3-14/2	1295.029	1295.379	-270.736	0.382	1045.971	0.366	17	0.156	K.GSVSTESAVTQTK.F
R3/RRR3-15/2	1294.977	1295.379	-311.307	0.396	736.006	0.448	15	0.150	K.GSVSTESAVTQTK.F
R3/RRR3-14/2	1294.895	1295.379	-374.299	0.365	857.248	0.336	16	0.144	K.GSVSTESAVTQTK.F
R3/RRR3-14/2	1294.443	1295.379	-1499.817	0.241	1032.362	0.247	17	0.141	K.GSVSTESAVTQTK.F
R3/RRR3-14/3	1173.465	1173.385	68.840	0.532	1216.478	0.393	25	0.123	K.ALKDLGLDVTK.G
R3/RRR3-3/2	1762.535	1762.040	281.851	0.578	2970.995	0.488	25	0.489	K.LVENYAELLASQGLLK.T
R3/RRR3-3/2	1762.151	1762.040	63.325	0.551	2601.349	0.462	24	0.391	K.LVENYAELLASQGLLK.T
R3/RRR3-4/2	1761.284	1762.040	-999.814	0.488	2219.342	0.408	22	0.299	K.LVENYAELLASQGLLK.T
R3/RRR3-3/2	1761.625	1762.040	-236.071	0.511	2102.558	0.459	22	0.293	K.LVENYAELLASQGLLK.T
R3/RRR3-4/2	1761.512	1762.040	-870.055	0.516	2125.100	0.407	22	0.282	K.LVENYAELLASQGLLK.T
R3/RRR3-4/2	1761.678	1762.040	-206.179	0.503	2067.990	0.376	22	0.264	K.LVENYAELLASQGLLK.T
R3/RRR3-2/2	1761.469	1762.040	-894.822	0.456	1635.196	0.430	20	0.218	K.LVENYAELLASQGLLK.T
R3/RRR3-3/2	1318.185	1318.416	-175.419	0.508	1036.226	0.442	18	0.167	K.LNSGDISPNVSSK.L
R3/RRR3-15/2	1318.114	1318.416	-229.768	0.455	1013.815	0.420	20	0.164	K.LNSGDISPNVSSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1318.081	1318.416	-254.854	0.458	913.049	0.398	17	0.153	K.LNSGDISPNVSSK.L
R3/RRR3-3/3	1494.835	1494.592	163.344	0.435	1002.312	0.470	24	0.125	R.NQKPLTSFSDSNR.T
R3/RRR3-4/3	1494.234	1494.592	-240.100	0.483	875.138	0.494	23	0.123	R.NQKPLTSFSDSNR.T
R3/RRR3-4/3	1494.819	1494.592	152.289	0.461	787.922	0.452	22	0.112	R.NQKPLTSFSDSNR.T
R3/RRR3-3/3	1494.153	1494.592	-294.565	0.419	821.863	0.440	23	0.111	R.NQKPLTSFSDSNR.T
R3/RRR3-3/3	1494.073	1494.592	-1019.494	0.408	784.848	0.436	23	0.109	R.NQKPLTSFSDSNR.T
R3/RRR3-4/3	1494.184	1494.592	-273.787	0.444	458.832	0.484	19	0.109	R.NQKPLTSFSDSNR.T
R3/RRR3-9/1	1298.765	1299.543	-1373.725	0.335	794.321	0.421	16	0.919	R.EHALLAFTLGVK.Q
R3/RRR3-9/1	1298.777	1299.543	-1363.907	0.335	692.650	0.417	15	0.916	R.EHALLAFTLGVK.Q
R3/RRR3-9/1	1298.712	1299.543	-1414.508	0.279	689.506	0.334	15	0.897	R.EHALLAFTLGVK.Q
R3/RRR3-9/2	1299.277	1299.543	-205.960	0.439	1119.939	0.501	19	0.185	R.EHALLAFTLGVK.Q
R3/RRR3-9/2	1298.607	1299.543	-1495.385	0.362	977.021	0.563	19	0.181	R.EHALLAFTLGVK.Q
R3/RRR3-9/2	1299.428	1299.543	-88.910	0.434	1007.535	0.500	19	0.177	R.EHALLAFTLGVK.Q
R3/RRR3-1/2	1299.194	1299.543	-269.679	0.428	864.358	0.530	17	0.170	R.EHALLAFTLGVK.Q
R3/RRR3-2/2	1299.512	1299.543	-24.554	0.448	699.048	0.544	16	0.164	R.EHALLAFTLGVK.Q
R3/RRR3-1/2	1299.152	1299.543	-301.919	0.447	781.764	0.505	17	0.164	R.EHALLAFTLGVK.Q
R3/RRR3-8/2	1299.656	1299.543	87.272	0.334	631.320	0.484	15	0.151	R.EHALLAFTLGVK.Q
R3/RRR3-9/2	1299.433	1299.543	-85.424	0.347	538.725	0.453	15	0.147	R.EHALLAFTLGVK.Q
R3/RRR3-1/2	1299.145	1299.543	-307.670	0.334	408.243	0.464	12	0.143	R.EHALLAFTLGVK.Q
R3/RRR3-8/2	1299.487	1299.543	-43.398	0.339	334.405	0.448	14	0.142	-.EHALLAFTLGVK.-
R3/RRR3-10/2	1299.282	1299.543	-201.907	0.262	279.114	0.406	13	0.140	R.EHALLAFTLGVK.Q
R3/RRR3-9/2	1452.909	1453.626	-1185.477	0.329	791.351	0.303	15	0.137	K.YYFTIIDAPGHR.D
R3/RRR3-9/2	1955.627	1957.220	-1842.571	0.377	720.354	0.311	19	0.135	K.YYFTIIDAPGHRDFIK.N
R3/RRR3-9/2	1955.407	1957.220	-1955.735	0.336	535.170	0.276	16	0.129	K.YYFTIIDAPGHRDFIK.N
R3/RRR3-9/3	1300.540	1299.543	-2.233	0.500	1175.194	0.439	26	0.128	R.EHALLAFTLGVK.Q
R3/RRR3-9/2	1452.660	1453.626	-1357.409	0.246	714.371	0.194	14	0.127	K.YYFTIIDAPGHR.D
R3/RRR3-9/3	1299.301	1299.543	-187.072	0.471	868.919	0.389	24	0.106	R.EHALLAFTLGVK.Q
R3/RRR3-9/3	1299.405	1299.543	-106.919	0.475	803.484	0.379	25	0.103	R.EHALLAFTLGVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	957.109	957.149	-42.613	0.563	1339.286	0.443	15	0.194	R.AAVLLLDNK.K
R3/RRR3-18/2	957.028	957.149	-127.437	0.518	1232.782	0.428	15	0.183	R.AAVLLLDNK.K
R3/RRR3-18/2	1197.045	1197.323	-233.266	0.505	1116.979	0.465	17	0.179	R.RDDADLPPVAK.R
R3/RRR3-18/2	957.379	957.149	241.053	0.512	1135.346	0.426	14	0.174	R.AAVLLLDNK.K
R3/RRR3-18/2	1349.142	1348.533	-290.641	0.510	999.905	0.410	16	0.161	K.SREPVVQLYTR.D
R3/RRR3-18/2	1196.926	1197.323	-332.820	0.480	786.463	0.475	15	0.159	R.RDDADLPPVAK.R
R3/RRR3-18/2	1348.153	1348.533	-282.772	0.425	1006.183	0.365	16	0.155	K.SREPVVQLYTR.D
R3/RRR3-18/2	1196.832	1197.323	-411.617	0.423	1048.953	0.332	16	0.153	R.RDDADLPPVAK.R
R3/RRR3-18/2	1348.315	1348.533	-162.146	0.453	929.506	0.306	16	0.144	K.SREPVVQLYTR.D
R3/RRR3-7/2	1697.326	1697.953	-961.170	0.452	2335.688	0.560	24	0.374	R.VIEVGEVDPAAYPLPK.T
R3/RRR3-7/2	1698.417	1697.953	273.965	0.525	2009.314	0.582	23	0.317	R.VIEVGEVDPAAYPLPK.T
R3/RRR3-7/2	1697.188	1697.953	-1042.767	0.409	1805.409	0.474	22	0.253	R.VIEVGEVDPAAYPLPK.T
R3/RRR3-7/2	1287.178	1287.445	-207.800	0.481	383.287	0.429	16	0.146	K.QEITAAVAELNK.A
R3/RRR3-7/2	1287.124	1287.445	-249.854	0.465	449.910	0.406	17	0.145	K.QEITAAVAELNK.A
R3/RRR3-7/2	1287.510	1287.445	51.294	0.436	478.634	0.406	17	0.145	K.QEITAAVAELNK.A
R3/RRR3-7/3	1221.820	1221.473	285.321	0.384	1018.105	0.295	19	0.095	K.KPVIVYNYPK.E
R3/RRR3-10/2	1424.221	1424.542	-225.889	0.532	2010.110	0.501	17	0.294	K.YAFEYAYLNNR.K
R3/RRR3-10/2	1423.957	1424.542	-1116.202	0.468	1895.327	0.501	17	0.276	K.YAFEYAYLNNR.K
R3/RRR3-10/2	1280.481	1281.433	-1529.654	0.360	1335.467	0.489	17	0.199	K.LADGLFLESCR.E
R3/RRR3-10/2	1280.568	1281.433	-1461.475	0.410	1213.997	0.492	16	0.189	K.LADGLFLESCR.E
R3/RRR3-10/2	1280.512	1281.433	-1504.756	0.364	1300.426	0.429	18	0.186	K.LADGLFLESCR.E
R3/RRR3-10/2	1194.207	1194.366	-133.038	0.485	1011.357	0.447	16	0.169	R.HQDVDIVVIR.E
R3/RRR3-10/2	1194.083	1194.366	-237.639	0.489	996.161	0.449	16	0.169	R.HQDVDIVVIR.E
R3/RRR3-10/2	1194.013	1194.366	-296.307	0.468	910.268	0.450	16	0.164	R.HQDVDIVVIR.E
R3/RRR3-10/2	1423.384	1424.542	-1520.161	0.280	1099.880	0.332	14	0.153	K.YAFEYAYLNNR.K
R3/RRR3-9/2	1389.175	1389.487	-225.242	0.495	2210.409	0.468	21	0.320	R.VVLDCATADPDGR.K
R3/RRR3-9/2	1388.478	1389.487	-1451.680	0.417	2206.279	0.466	21	0.319	R.VVLDCATADPDGR.K
R3/RRR3-9/2	1389.153	1389.487	-241.110	0.509	1972.997	0.505	20	0.289	R.VVLDCATADPDGR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1441.387	1441.698	-216.318	0.409	780.241	0.409	17	0.145	K.SGLVALNLDIAQVK.E
R3/RRR3-15/2	1102.197	1102.263	-60.498	0.499	1827.359	0.501	18	0.265	R.ALLEVVESGGK.N
R3/RRR3-14/2	1102.039	1102.263	-203.825	0.495	1637.917	0.535	17	0.247	R.ALLEVVESGGK.N
R3/RRR3-15/2	1102.093	1102.263	-154.489	0.474	1663.044	0.511	17	0.244	R.ALLEVVESGGK.N
R3/RRR3-14/2	1103.008	1102.263	-232.396	0.524	1683.166	0.498	17	0.243	R.ALLEVVESGGK.N
R3/RRR3-14/2	1101.638	1102.263	-1479.792	0.455	1685.512	0.458	17	0.234	R.ALLEVVESGGK.N
R3/RRR3-15/2	1101.445	1102.263	-1655.461	0.317	912.205	0.376	15	0.151	R.ALLEVVESGGK.N
R3/RRR3-14/2	921.019	921.075	-61.896	0.417	770.429	0.369	13	0.149	R.YIAGLQQK.Y
R3/RRR3-14/2	920.958	921.075	-127.974	0.389	763.509	0.357	13	0.147	R.YIAGLQQK.Y
R3/RRR3-14/2	920.940	921.075	-147.387	0.407	732.326	0.350	13	0.146	R.YIAGLQQK.Y
R3/RRR3-15/2	920.981	921.075	-103.244	0.256	710.443	0.242	12	0.134	R.YIAGLQQK.Y
R3/RRR3-14/3	1783.172	1783.099	40.908	0.380	947.080	0.354	26	0.099	R.KIASLDTHIALACAGLK.A
R3/RRR3-16/2	1722.319	1722.919	-931.654	0.559	1572.651	0.603	23	0.257	R.KLAEAPYLDSVDWSK.W
R3/RRR3-16/2	1594.125	1594.746	-1020.400	0.473	1010.281	0.537	21	0.182	K.LAEAPYLDSVDWSK.W
R3/RRR3-16/2	1350.290	1349.601	-230.549	0.490	1291.359	0.406	19	0.179	R.GAFTVVLSGGSLIK.N
R3/RRR3-16/2	1593.721	1594.746	-1274.408	0.420	964.909	0.520	21	0.174	K.LAEAPYLDSVDWSK.W
R3/RRR3-16/2	1593.937	1594.746	-1138.275	0.454	781.666	0.506	19	0.162	K.LAEAPYLDSVDWSK.W
R3/RRR3-16/2	1349.303	1349.601	-220.918	0.344	661.541	0.207	15	0.126	R.GAFTVVLSGGSLIK.N
R3/RRR3-10/2	1792.356	1791.940	232.624	0.533	1530.723	0.594	24	0.246	K.SYELPDGQVITIGNER.-
R3/RRR3-10/2	1791.389	1791.940	-868.188	0.490	1417.818	0.547	23	0.221	K.SYELPDGQVITIGNER.-
R3/RRR3-10/2	1791.216	1791.940	-965.061	0.495	1458.509	0.509	24	0.218	K.SYELPDGQVITIGNER.-
R3/RRR3-11/2	1791.416	1791.940	-853.208	0.460	1438.081	0.489	23	0.210	K.SYELPDGQVITIGNER.-
R3/RRR3-11/2	1791.446	1791.940	-276.361	0.493	1283.528	0.554	22	0.207	K.SYELPDGQVITIGNER.-
R3/RRR3-11/2	1791.395	1791.940	-864.905	0.501	1312.594	0.535	22	0.206	K.SYELPDGQVITIGNER.-
R3/RRR3-10/2	1954.664	1955.244	-810.388	0.509	1102.383	0.586	23	0.195	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-10/2	1955.762	1955.244	-246.819	0.530	1019.857	0.618	22	0.193	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-10/2	1954.551	1955.244	-868.316	0.517	903.775	0.622	21	0.184	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-10/3	1955.893	1955.244	-179.641	0.451	920.860	0.372	30	0.106	R.VAPEEHPVLLTEAPINPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1954.492	1955.244	-899.076	0.402	679.260	0.386	27	0.102	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-12/3	1954.706	1955.244	-789.144	0.390	584.448	0.399	25	0.102	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-11/3	1954.391	1955.244	-950.900	0.397	512.063	0.389	25	0.101	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-11/3	1954.754	1955.244	-251.400	0.412	585.418	0.385	26	0.101	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-12/3	1955.927	1955.244	-162.549	0.425	753.814	0.366	26	0.101	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-11/3	1954.601	1955.244	-842.649	0.414	463.472	0.382	23	0.100	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-9/3	1955.205	1955.244	-19.896	0.410	749.796	0.347	27	0.099	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-12/3	1955.325	1955.244	41.627	0.361	408.794	0.349	22	0.098	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-9/3	1954.884	1955.244	-184.212	0.398	621.248	0.330	25	0.096	R.VAPEEHPVLLTEAPINPK.S
R3/RRR3-12/2	1444.454	1443.576	-85.239	0.543	1453.331	0.495	20	0.217	R.YWLCAATEDSVK.I
R3/RRR3-12/2	1448.667	1449.588	-1329.753	0.445	1406.827	0.432	19	0.196	K.DGTTLLWDLTEGK.M
R3/RRR3-12/2	1448.780	1449.588	-1251.562	0.460	1168.525	0.433	18	0.175	K.DGTTLLWDLTEGK.M
R3/RRR3-12/2	1443.094	1443.576	-335.521	0.439	1182.678	0.417	18	0.174	R.YWLCAATEDSVK.I
R3/RRR3-12/2	1771.734	1771.992	-145.924	0.482	1025.522	0.508	19	0.174	K.LDAGAIIHSLCFSPNR.Y
R3/RRR3-12/2	1449.267	1449.588	-221.985	0.469	1101.161	0.450	17	0.172	K.DGTTLLWDLTEGK.M
R3/RRR3-12/2	1771.610	1771.992	-215.874	0.494	868.838	0.520	18	0.164	K.LDAGAIIHSLCFSPNR.Y
R3/RRR3-12/3	1771.558	1771.992	-245.433	0.530	996.213	0.607	27	0.154	K.LDAGAIIHSLCFSPNR.Y
R3/RRR3-12/2	1771.404	1771.992	-898.995	0.468	792.585	0.466	18	0.153	K.LDAGAIIHSLCFSPNR.Y
R3/RRR3-12/3	1772.156	1771.992	93.220	0.537	1041.417	0.580	30	0.151	K.LDAGAIIHSLCFSPNR.Y
R3/RRR3-12/3	1771.249	1771.992	-986.870	0.458	1092.191	0.552	28	0.148	K.LDAGAIIHSLCFSPNR.Y
R3/RRR3-19/3	1529.155	1529.724	-1028.932	0.439	1567.362	0.501	28	0.184	R.GFGHIGVTVHDVYK.A
R3/RRR3-19/2	994.534	995.116	-1595.635	0.344	679.383	0.437	13	0.150	R.TVWTFGQR.A
R3/RRR3-19/2	994.928	995.116	-190.019	0.345	616.737	0.420	13	0.147	R.TVWTFGQR.A
R3/RRR3-19/2	987.169	987.091	78.992	0.420	808.459	0.325	13	0.143	K.VSLDFYSR.V
R3/RRR3-19/2	994.644	995.116	-476.395	0.214	632.041	0.259	13	0.132	R.TVWTFGQR.A
R3/RRR3-16/2	1315.155	1315.410	-194.722	0.438	1702.701	0.338	18	0.211	K.YEDKIDAFGEK.A
R3/RRR3-16/2	1315.126	1315.410	-216.325	0.439	1510.403	0.356	17	0.193	K.YEDKIDAFGEK.A
R3/RRR3-16/2	980.451	981.128	-1714.772	0.431	1002.885	0.489	15	0.176	K.SPPNIPEVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	981.043	981.128	-87.063	0.411	1024.946	0.405	15	0.165	K.SPPNIPEVK.I
R3/RRR3-16/2	981.084	981.128	-44.254	0.427	858.965	0.417	15	0.159	K.SPPNIPEVK.I
R3/RRR3-17/2	981.105	981.128	-23.413	0.396	868.586	0.389	15	0.155	K.SPPNIPEVK.I
R3/RRR3-18/2	981.075	981.128	-53.365	0.370	1215.451	0.254	15	0.154	K.SPPNIPEVK.I
R3/RRR3-18/2	981.047	981.128	-82.196	0.397	901.460	0.358	15	0.153	K.SPPNIPEVK.I
R3/RRR3-17/2	981.022	981.128	-108.033	0.402	872.136	0.362	15	0.152	K.SPPNIPEVK.I
R3/RRR3-17/2	981.377	981.128	254.434	0.403	823.708	0.345	14	0.148	K.SPPNIPEVK.I
R3/RRR3-16/2	1063.049	1063.184	-127.569	0.250	585.358	0.443	12	0.141	K.YYALFEEK.C
R3/RRR3-16/2	1062.863	1063.184	-302.572	0.169	696.828	0.236	13	0.128	K.YYALFEEK.C
R3/RRR3-18/2	980.854	981.128	-280.062	0.360	560.303	0.253	12	0.127	-.SPPNIPEVK.-
R3/RRR3-16/3	1316.488	1315.410	59.129	0.475	1014.802	0.349	25	0.104	K.YEDKIDAFGEK.A
R3/RRR3-16/3	1315.624	1315.410	163.073	0.419	830.252	0.374	23	0.102	K.YEDKIDAFGEK.A
R3/RRR3-16/3	1315.569	1315.410	121.060	0.449	692.209	0.357	22	0.099	K.YEDKIDAFGEK.A
R3/RRR3-17/3	1315.141	1315.410	-205.534	0.367	402.114	0.337	18	0.092	-.YEDKIDAFGEK.-
R3/RRR3-15/2	1313.482	1312.540	-44.707	0.473	1778.657	0.566	21	0.277	K.LEAPVVIVTGASR.G
R3/RRR3-15/2	1628.707	1629.842	-1314.615	0.397	1784.668	0.480	22	0.253	K.WGTIDVLVNNAGITR.D
R3/RRR3-15/2	758.501	758.929	-565.953	0.490	904.424	0.278	13	0.142	K.AGVIGLTK.A
R3/RRR3-15/2	758.734	758.929	-258.693	0.483	887.677	0.254	13	0.139	K.AGVIGLTK.A
R3/RRR3-15/2	758.924	758.929	-6.632	0.454	897.062	0.233	13	0.138	K.AGVIGLTK.A
R3/RRR3-17/2	1630.170	1629.842	202.141	0.355	304.500	0.312	12	0.130	K.WGTIDVLVNNAGITR.D
R3/RRR3-12/1	963.597	964.183	-1651.106	0.241	798.309	0.400	12	0.901	R.TALAFVTLK.S
R3/RRR3-12/1	963.587	964.183	-1661.606	0.197	483.228	0.339	11	0.887	R.TALAFVTLK.S
R3/RRR3-12/1	963.543	964.183	-1707.300	0.180	679.606	0.254	12	0.881	R.TALAFVTLK.S
R3/RRR3-12/2	1689.394	1689.761	-217.755	0.513	1626.393	0.528	21	0.242	K.NGVNAEGCLFDEHAR.T
R3/RRR3-12/2	1690.288	1689.761	-281.093	0.552	1357.383	0.509	21	0.206	K.NGVNAEGCLFDEHAR.T
R3/RRR3-12/2	1689.172	1689.761	-943.630	0.527	1377.352	0.498	20	0.205	K.NGVNAEGCLFDEHAR.T
R3/RRR3-12/2	1795.393	1794.037	198.474	0.439	1683.301	0.276	22	0.193	K.IFHYGSISLITEPCR.-
R3/RRR3-12/2	963.624	964.183	-1623.567	0.379	1080.630	0.431	15	0.170	R.TALAFVTLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	964.048	964.183	-140.987	0.482	972.956	0.458	15	0.170	R.TALAFVTLK.S
R3/RRR3-12/2	963.997	964.183	-193.957	0.483	969.697	0.424	15	0.165	R.TALAFVTLK.S
R3/RRR3-12/2	1795.274	1794.037	132.470	0.451	1002.465	0.291	19	0.142	K.IFHYGSISLITEPCR.-
R3/RRR3-12/2	964.268	964.183	88.106	0.118	206.077	0.347	13	0.117	-.TALAFVTLK.-
R3/RRR3-12/3	1793.928	1794.037	-60.860	0.520	1344.184	0.242	28	0.104	-.IFHYGSISLITEPCR.-
R3/RRR3-17/2	1425.419	1424.691	-191.599	0.378	1097.607	0.451	16	0.171	R.SINTLFLTEMVR.G
R3/RRR3-17/2	1225.114	1225.375	-213.331	0.361	709.812	0.503	15	0.157	K.NVTINYPFEK.G
R3/RRR3-17/2	1225.108	1225.375	-218.428	0.453	606.857	0.507	14	0.157	K.NVTINYPFEK.G
R3/RRR3-17/2	1224.967	1225.375	-333.797	0.433	686.059	0.463	15	0.155	K.NVTINYPFEK.G
R3/RRR3-17/2	1479.050	1478.634	282.231	0.521	611.869	0.432	17	0.148	K.EIAKDWNAVFER.S
R3/RRR3-17/2	1478.168	1478.634	-315.881	0.348	431.767	0.464	17	0.144	K.EIAKDWNAVFER.S
R3/RRR3-17/2	1423.618	1424.691	-1460.655	0.269	667.567	0.353	15	0.136	R.SINTLFLTEMVR.G
R3/RRR3-17/2	1224.579	1225.375	-1470.704	0.292	665.687	0.256	14	0.135	K.NVTINYPFEK.G
R3/RRR3-17/2	1182.070	1182.353	-240.779	0.437	1385.975	0.505	17	0.210	K.FTGAFQALAQK.V
R3/RRR3-17/2	1175.054	1175.317	-224.503	0.516	918.938	0.298	17	0.143	K.AADSNTTILLR.L
R3/RRR3-17/2	1175.070	1175.317	-211.580	0.430	957.145	0.269	17	0.142	K.AADSNTTILLR.L
R3/RRR3-17/2	1174.761	1175.317	-1329.109	0.339	986.855	0.200	16	0.136	K.AADSNTTILLR.L
R3/RRR3-18/2	1181.268	1182.353	-1770.793	0.165	538.728	0.298	14	0.128	K.FTGAFQALAQK.V
R3/RRR3-17/3	1809.795	1809.143	-192.993	0.564	963.272	0.429	26	0.115	K.LIQNIVIEAIQSLPTR.A
R3/RRR3-17/3	1808.663	1809.143	-265.987	0.375	524.090	0.371	21	0.093	-.LIQNIVIEAIQSLPTR.-
R3/RRR3-17/3	1809.669	1809.143	-262.726	0.264	887.444	0.200	23	0.082	K.LIQNIVIEAIQSLPTR.A
R3/RRR3-20/2	1215.887	1216.282	-325.817	0.517	718.338	0.482	15	0.157	R.AQGSYTFADQK.T
R3/RRR3-20/2	1216.059	1216.282	-184.110	0.483	652.326	0.472	15	0.154	R.AQGSYTFADQK.T
R3/RRR3-20/2	1215.868	1216.282	-341.330	0.477	644.697	0.445	15	0.150	R.AQGSYTFADQK.T
R3/RRR3-20/2	887.928	888.004	-86.059	0.362	1106.245	0.195	13	0.141	R.NEVLSAVR.E
R3/RRR3-20/3	1760.830	1761.017	-106.853	0.490	853.731	0.585	27	0.137	K.VYFHDVVGGTKPTAIR.V
R3/RRR3-20/2	887.398	888.004	-1815.458	0.329	1203.513	0.119	13	0.136	R.NEVLSAVR.E
R3/RRR3-20/2	887.730	888.004	-308.958	0.323	1103.156	0.138	13	0.135	R.NEVLSAVR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/3	1760.542	1761.017	-270.440	0.446	1032.411	0.503	29	0.132	K.VYFHDVVGGTKPTAIR.V
R3/RRR3-20/3	1761.796	1761.017	-125.698	0.509	630.530	0.518	24	0.116	K.VYFHDVVGGTKPTAIR.V
R3/RRR3-15/2	1859.082	1859.285	-109.794	0.507	1290.084	0.597	24	0.216	R.LPLVGPLLTPPVSVASVAK.V
R3/RRR3-15/2	1859.332	1859.285	25.246	0.532	1246.475	0.578	23	0.206	R.LPLVGPLLTPPVSVASVAK.V
R3/RRR3-15/2	1586.404	1586.772	-232.509	0.483	1014.162	0.593	20	0.188	K.INGTANINAISVAAEK.G
R3/RRR3-15/2	1586.070	1586.772	-1076.608	0.448	1042.064	0.564	20	0.185	K.INGTANINAISVAAEK.G
R3/RRR3-15/2	1586.313	1586.772	-290.024	0.459	837.355	0.610	19	0.176	K.INGTANINAISVAAEK.G
R3/RRR3-15/2	962.180	962.080	104.458	0.480	881.579	0.472	15	0.167	R.ATEAELLSK.F
R3/RRR3-15/2	961.476	962.080	-1672.527	0.351	756.512	0.438	14	0.152	R.ATEAELLSK.F
R3/RRR3-15/2	961.409	962.080	-1742.304	0.313	549.794	0.325	14	0.139	R.ATEAELLSK.F
R3/RRR3-18/2	1819.021	1818.021	0.026	0.571	1487.390	0.590	24	0.238	K.AAANNIGLDGFDVIDAIK.S
R3/RRR3-12/2	1818.420	1818.021	220.469	0.568	1371.509	0.594	23	0.224	K.AAANNIGLDGFDVIDAIK.S
R3/RRR3-12/2	1817.516	1818.021	-830.244	0.513	1243.331	0.564	22	0.203	K.AAANNIGLDGFDVIDAIK.S
R3/RRR3-12/2	1818.385	1818.021	201.081	0.570	1139.509	0.575	22	0.195	K.AAANNIGLDGFDVIDAIK.S
R3/RRR3-12/2	1091.055	1091.249	-177.710	0.334	588.380	0.555	16	0.156	K.HNPGVGAALVR.L
R3/RRR3-18/2	1572.231	1572.825	-1017.243	0.391	761.425	0.459	19	0.149	K.LGAAVSCADIVVLAGR.D
R3/RRR3-12/2	1091.082	1091.249	-152.682	0.316	553.064	0.467	16	0.147	K.HNPGVGAALVR.L
R3/RRR3-12/2	1091.266	1091.249	15.976	0.410	315.628	0.447	13	0.145	K.HNPGVGAALVR.L
R3/RRR3-12/2	1090.425	1091.249	-1677.132	0.261	521.070	0.459	15	0.142	K.HNPGVGAALVR.L
R3/RRR3-18/2	1090.509	1091.249	-1599.758	0.200	287.667	0.414	11	0.133	K.HNPGVGAALVR.L
R3/RRR3-18/3	1824.541	1825.078	-845.203	0.530	1748.549	0.540	30	0.223	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-18/2	1798.318	1798.942	-906.034	0.486	1176.761	0.638	21	0.212	R.IDFAPNGQNPPHTHPR.A
R3/RRR3-19/3	1824.858	1825.078	-120.913	0.542	1673.736	0.523	29	0.207	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-19/3	1825.805	1825.078	-150.256	0.587	1636.672	0.528	29	0.203	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-18/2	1798.536	1798.942	-226.734	0.501	994.599	0.633	20	0.194	R.IDFAPNGQNPPHTHPR.A
R3/RRR3-19/2	1824.365	1825.078	-941.918	0.548	956.560	0.564	22	0.183	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-18/2	1825.477	1825.078	219.386	0.586	824.163	0.573	21	0.175	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-18/2	1824.582	1825.078	-272.915	0.571	755.426	0.602	20	0.175	K.AFM*IDKDQVDWIQAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/3	1824.332	1825.078	-959.962	0.566	1429.024	0.499	29	0.168	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-18/2	1824.428	1825.078	-907.123	0.561	700.509	0.562	20	0.166	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-18/2	1798.482	1798.942	-256.763	0.435	752.010	0.580	18	0.165	R.IDFAPNGQNPPHTHPR.A
R3/RRR3-18/2	1341.090	1341.574	-361.680	0.430	849.643	0.528	15	0.164	K.LSAVFVNGFVCK.N
R3/RRR3-19/3	1809.274	1809.079	108.395	0.385	983.761	0.476	27	0.125	K.AFMIDKDQVDWIQAK.F
R3/RRR3-18/3	1808.489	1809.079	-881.719	0.420	1078.971	0.409	26	0.119	K.AFMIDKDQVDWIQAK.F
R3/RRR3-19/3	1825.160	1825.078	44.935	0.316	685.777	0.491	20	0.113	K.AFM*IDKDQVDWIQAK.F
R3/RRR3-18/3	1809.013	1809.079	-36.258	0.421	695.848	0.460	23	0.111	K.AFMIDKDQVDWIQAK.F
R3/RRR3-7/3	1964.830	1964.189	-183.120	0.442	830.942	0.509	33	0.122	K.YVGEPM*THLESIASSAVR.A
R3/RRR3-7/3	1964.024	1964.189	-84.418	0.329	577.591	0.481	26	0.106	K.YVGEPM*THLESIASSAVR.A
R3/RRR3-7/3	1963.895	1964.189	-150.259	0.371	528.040	0.445	26	0.103	K.YVGEPM*THLESIASSAVR.A
R3/RRR3-7/3	1949.993	1948.190	-101.260	0.327	283.060	0.375	22	0.098	K.YVGEPMTHLESIASSAVR.A
R3/RRR3-13/2	1263.877	1264.326	-356.458	0.548	1740.838	0.492	20	0.251	K.FGDAVQEDVGAR.L
R3/RRR3-13/2	1263.336	1264.326	-1579.971	0.530	1737.852	0.475	20	0.247	K.FGDAVQEDVGAR.L
R3/RRR3-13/2	1360.187	1359.421	-172.883	0.508	1596.166	0.538	22	0.243	K.AEEPSASGDPLASK.S
R3/RRR3-13/2	1359.082	1359.421	-250.228	0.442	1521.380	0.507	22	0.225	K.AEEPSASGDPLASK.S
R3/RRR3-13/2	1359.006	1359.421	-306.821	0.436	1411.212	0.531	21	0.217	K.AEEPSASGDPLASK.S
R3/RRR3-13/2	1263.869	1264.326	-362.854	0.564	1455.640	0.474	20	0.212	K.FGDAVQEDVGAR.L
R3/RRR3-13/2	1070.089	1070.183	-88.514	0.302	965.455	0.284	12	0.108	R.VEWATPRPN.-
R3/RRR3-8/2	1260.142	1260.422	-223.141	0.495	2320.971	0.533	22	0.366	K.LVGVAVAAETSSR.Q
R3/RRR3-8/3	1626.755	1626.883	-78.592	0.426	1614.835	0.539	34	0.203	K.VAQGVVGAVADKGSVLR.F
R3/RRR3-8/3	1626.429	1626.883	-279.717	0.410	1074.728	0.527	31	0.140	K.VAQGVVGAVADKGSVLR.F
R3/RRR3-8/2	1113.702	1114.277	-1418.798	0.273	936.740	0.222	16	0.133	K.VAQGVVGAVADK.G
R3/RRR3-8/3	1626.145	1626.883	-1071.504	0.354	1041.048	0.425	29	0.117	K.VAQGVVGAVADKGSVLR.F
R3/RRR3-7/2	1559.507	1558.674	-107.135	0.565	2094.527	0.591	21	0.340	R.NNSTSFLIDDIYR.N
R3/RRR3-7/2	1311.345	1311.552	-158.408	0.350	362.887	0.511	15	0.141	K.VVGVPVTLNGDLK.N
R3/RRR3-7/3	1761.425	1759.984	250.672	0.388	1192.297	0.315	25	0.107	K.KFNAICHFFGYQAR.G
R3/RRR3-7/3	1761.746	1759.984	-135.848	0.311	590.286	0.362	21	0.092	K.KFNAICHFFGYQAR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1073.001	1073.228	-212.993	0.530	1703.438	0.421	18	0.229	R.SLATAAQAAIR.A
R3/RRR3-14/2	1073.059	1073.228	-158.327	0.466	1495.234	0.361	18	0.193	R.SLATAAQAAIR.A
R3/RRR3-14/2	1042.942	1043.202	-250.006	0.428	1377.092	0.408	16	0.190	R.GLVAQAQSLR.S
R3/RRR3-14/2	1347.568	1346.517	38.105	0.413	1018.733	0.602	19	0.190	R.TLTGIQIWGSGGR.G
R3/RRR3-14/2	1073.194	1073.228	-32.014	0.482	1362.417	0.411	18	0.190	R.SLATAAQAAIR.A
R3/RRR3-14/2	1347.603	1346.517	64.361	0.340	683.350	0.600	17	0.161	R.TLTGIQIWGSGGR.G
R3/RRR3-14/2	1042.446	1043.202	-1689.960	0.366	1241.192	0.193	16	0.146	R.GLVAQAQSLR.S
R3/RRR3-13/2	1465.347	1465.634	-196.321	0.460	885.689	0.497	16	0.164	R.FPYYGNYVNLSK.L
R3/RRR3-12/2	980.320	981.174	-1897.411	0.269	737.229	0.367	13	0.138	K.IAGLHAAISK.L
R3/RRR3-12/2	974.007	974.138	-135.397	0.177	456.824	0.463	14	0.135	R.YVPGIAPTR.V
R3/RRR3-12/2	974.840	974.138	-306.972	0.216	419.118	0.400	13	0.134	-.YVPGIAPTR.-
R3/RRR3-15/2	973.331	974.138	-1862.857	0.169	274.832	0.356	11	0.126	-.YVPGIAPTR.-
R3/RRR3-15/2	973.189	974.138	-2009.446	0.228	327.000	0.442	11	0.125	-.YVPGIAPTR.-
R3/RRR3-17/2	1593.262	1592.754	-309.644	0.529	961.999	0.524	25	0.178	-.M*DGAASVPSSNEVALK.Q
R3/RRR3-17/2	1592.220	1592.754	-966.314	0.453	869.493	0.501	24	0.168	-.M*DGAASVPSSNEVALK.Q
R3/RRR3-16/2	1592.164	1592.754	-1001.645	0.397	873.037	0.485	24	0.164	-.M*DGAASVPSSNEVALK.Q
R3/RRR3-17/2	1592.227	1592.754	-961.619	0.433	858.847	0.478	24	0.164	-.M*DGAASVPSSNEVALK.Q
R3/RRR3-16/2	1592.187	1592.754	-987.097	0.421	885.564	0.459	24	0.162	-.M*DGAASVPSSNEVALK.Q
R3/RRR3-16/2	1592.324	1592.754	-270.611	0.487	778.630	0.489	23	0.162	-.M*DGAASVPSSNEVALK.Q
R3/RRR3-17/2	1952.558	1951.212	177.983	0.483	691.649	0.511	20	0.156	K.QPVSVLIEANSNFQLYK.Q
R3/RRR3-17/2	1952.193	1951.212	-9.634	0.420	673.888	0.422	19	0.144	K.QPVSVLIEANSNFQLYK.Q
R3/RRR3-17/2	1577.239	1576.754	308.055	0.310	365.629	0.409	18	0.140	-.MDGAASVPSSNEVALK.Q
R3/RRR3-17/2	1121.509	1122.172	-1487.307	0.252	515.662	0.403	14	0.138	K.NSWGTGWGEK.G
R3/RRR3-17/2	1576.287	1576.754	-297.694	0.334	358.177	0.284	18	0.138	-.MDGAASVPSSNEVALK.Q
R3/RRR3-17/2	1121.322	1122.172	-1654.724	0.215	704.731	0.294	14	0.133	K.NSWGTGWGEK.G
R3/RRR3-17/2	1122.099	1122.172	-64.553	0.233	423.458	0.265	13	0.133	K.NSWGTGWGEK.G
R3/RRR3-17/2	1951.891	1951.212	-164.760	0.343	379.140	0.304	14	0.123	-.QPVSVLIEANSNFQLYK.-
R3/RRR3-17/2	1418.943	1419.648	-1204.793	0.399	1619.402	0.458	18	0.224	K.GANEVLLVIEAYK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1420.517	1419.648	-92.105	0.433	982.164	0.410	15	0.157	K.GANEVLLVIEAYK.T
R3/RRR3-17/2	1419.020	1419.648	-1150.716	0.259	907.554	0.383	15	0.147	K.GANEVLLVIEAYK.T
R3/RRR3-17/2	1140.766	1141.299	-1348.217	0.441	1030.402	0.541	17	0.144	K.VEGSTILTALH.-
R3/RRR3-17/3	1849.772	1851.084	-1253.522	0.410	1077.317	0.524	32	0.139	K.VTAVPAKEEEICGATFK.V
R3/RRR3-17/2	1418.611	1419.648	-1439.658	0.235	639.669	0.335	15	0.135	K.GANEVLLVIEAYK.T
R3/RRR3-16/2	1418.751	1419.648	-1340.618	0.323	557.691	0.341	13	0.134	-.GANEVLLVIEAYK.-
R3/RRR3-16/3	1850.638	1851.084	-241.760	0.366	950.326	0.440	30	0.115	K.VTAVPAKEEEICGATFK.V
R3/RRR3-17/2	1141.939	1141.299	-316.788	0.511	948.988	0.455	17	0.107	K.VEGSTILTALH.-
R3/RRR3-16/3	1850.176	1851.084	-1034.074	0.325	929.636	0.390	29	0.106	K.VTAVPAKEEEICGATFK.V
R3/RRR3-17/3	1849.487	1851.084	-1950.837	0.301	595.283	0.374	23	0.095	K.VTAVPAKEEEICGATFK.V
R3/RRR3-18/2	1770.579	1770.965	-219.042	0.527	928.871	0.523	22	0.171	R.VGDLGQLTPTDQVLASR.H
R3/RRR3-18/2	1770.449	1770.965	-858.955	0.483	823.913	0.522	21	0.163	R.VGDLGQLTPTDQVLASR.H
R3/RRR3-18/2	1326.073	1325.406	-252.118	0.406	489.189	0.552	17	0.157	K.QSEGLLTEYER.L
R3/RRR3-18/2	1326.137	1325.406	-203.727	0.388	384.466	0.481	15	0.148	K.QSEGLLTEYER.L
R3/RRR3-18/2	1325.172	1325.406	-177.451	0.317	316.500	0.388	14	0.140	K.QSEGLLTEYER.L
R3/RRR3-18/2	885.032	885.086	-61.992	0.305	814.920	0.247	13	0.136	R.LALLAIDR.A
R3/RRR3-18/2	884.310	885.086	-2015.080	0.208	614.705	0.278	12	0.131	R.LALLAIDR.A
R3/RRR3-10/2	1254.329	1255.383	-1642.713	0.503	1620.122	0.438	17	0.223	K.M*DYVNQALER.L
R3/RRR3-10/3	1485.755	1485.651	69.797	0.532	1923.866	0.448	31	0.215	K.SM*GHHVTVISSSAR.K
R3/RRR3-10/2	1255.567	1255.383	147.136	0.552	1347.322	0.456	16	0.197	K.M*DYVNQALER.L
R3/RRR3-10/2	1131.909	1131.333	-375.574	0.345	1211.125	0.390	16	0.172	K.HFGLM*SPGLR.G
R3/RRR3-10/2	1130.968	1131.333	-323.381	0.367	1024.875	0.415	15	0.163	K.HFGLM*SPGLR.G
R3/RRR3-10/2	1115.010	1115.333	-290.837	0.393	1106.954	0.367	16	0.163	K.HFGLMSPGLR.G
R3/RRR3-10/2	1468.257	1469.652	-1635.893	0.317	1083.396	0.382	18	0.159	K.SMGHHVTVISSSAR.K
R3/RRR3-10/2	1130.954	1131.333	-335.727	0.391	894.260	0.424	15	0.158	K.HFGLM*SPGLR.G
R3/RRR3-10/3	1486.374	1485.651	-187.276	0.546	1402.019	0.457	27	0.154	K.SM*GHHVTVISSSAR.K
R3/RRR3-10/3	1470.909	1469.652	175.199	0.538	1395.239	0.432	28	0.146	-.SMGHHVTVISSSAR.-
R3/RRR3-10/2	1485.160	1485.651	-331.855	0.295	508.588	0.448	18	0.141	K.SM*GHHVTVISSSAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1238.933	1239.383	-364.425	0.337	795.521	0.285	14	0.138	K.MDYVNQALER.L
R3/RRR3-9/3	1485.586	1485.651	-44.177	0.527	1414.427	0.385	28	0.137	K.SM*GHHVTVISSSAR.K
R3/RRR3-10/2	1484.665	1485.651	-1341.862	0.240	352.324	0.485	15	0.136	K.SM*GHHVTVISSSAR.K
R3/RRR3-10/3	1470.565	1469.652	-59.423	0.522	1248.686	0.399	27	0.127	K.SMGHHVTVISSSAR.K
R3/RRR3-10/3	1485.828	1485.651	119.482	0.491	1166.149	0.412	26	0.125	K.SM*GHHVTVISSSAR.K
R3/RRR3-9/3	1485.646	1485.651	-3.628	0.521	1188.563	0.392	27	0.122	K.SM*GHHVTVISSSAR.K
R3/RRR3-10/3	1485.791	1485.651	94.269	0.461	929.523	0.358	25	0.104	K.SM*GHHVTVISSSAR.K
R3/RRR3-10/3	1485.944	1485.651	197.214	0.444	1092.785	0.292	25	0.101	K.SM*GHHVTVISSSAR.K
R3/RRR3-10/3	1469.311	1469.652	-233.049	0.529	1023.768	0.316	25	0.099	-.SMGHHVTVISSSAR.-
R3/RRR3-7/2	1431.222	1431.617	-276.796	0.446	1388.092	0.380	18	0.185	R.GYISPYFITNQK.N
R3/RRR3-7/2	1431.169	1431.617	-313.764	0.426	1058.184	0.357	17	0.156	R.GYISPYFITNQK.N
R3/RRR3-8/2	1322.974	1323.505	-1160.866	0.415	1440.234	0.179	16	0.154	K.VCDLCSITLNK.N
R3/RRR3-14/3	1825.147	1825.058	48.788	0.475	1821.301	0.440	30	0.204	K.WGLVNHIVDDTQVLSK.A
R3/RRR3-14/2	1367.566	1367.576	-7.127	0.413	777.784	0.358	18	0.144	K.FGIFPSWGLSQK.L
R3/RRR3-14/2	1744.959	1744.917	24.164	0.348	652.212	0.420	18	0.140	R.AFCSGVDLTAAEEVFK.G
R3/RRR3-14/3	1824.466	1825.058	-875.407	0.333	853.645	0.294	23	0.091	K.WGLVNHIVDDTQVLSK.A
R3/RRR3-14/3	1825.122	1825.058	35.003	0.399	877.876	0.262	21	0.088	-.WGLVNHIVDDTQVLSK.-
R3/RRR3-18/2	1214.172	1213.323	-124.094	0.538	1619.298	0.522	20	0.241	R.AGGVDDAPLVGNK.A
R3/RRR3-18/2	1212.900	1213.323	-349.130	0.522	1414.172	0.555	19	0.223	R.AGGVDDAPLVGNK.A
R3/RRR3-18/2	1213.997	1213.323	-268.636	0.545	1297.647	0.534	19	0.206	R.AGGVDDAPLVGNK.A
R3/RRR3-18/2	1763.556	1764.013	-259.556	0.500	1253.508	0.556	22	0.204	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-19/2	1213.160	1213.323	-134.593	0.506	1366.927	0.469	19	0.199	R.AGGVDDAPLVGNK.A
R3/RRR3-19/2	1762.581	1764.013	-1383.633	0.446	1267.341	0.528	22	0.199	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-19/2	1212.450	1213.323	-1548.732	0.488	1322.605	0.485	18	0.198	R.AGGVDDAPLVGNK.A
R3/RRR3-19/2	1764.485	1764.013	268.148	0.535	1227.687	0.528	21	0.194	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-18/3	1763.543	1764.013	-267.029	0.425	1640.845	0.458	31	0.185	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-19/2	1486.255	1486.740	-327.590	0.401	971.693	0.476	22	0.169	K.SFGVLIPDQGIALR.G
R3/RRR3-18/2	1763.715	1764.013	-169.357	0.530	939.867	0.504	19	0.166	K.SGGLGDLKYPLISDVTK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1763.902	1764.013	-62.791	0.497	921.555	0.489	19	0.163	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-18/2	1486.187	1486.740	-1048.126	0.428	864.984	0.439	21	0.159	K.SFGVLIPDQGIALR.G
R3/RRR3-19/2	1486.513	1486.740	-153.249	0.413	898.851	0.382	21	0.153	K.SFGVLIPDQGIALR.G
R3/RRR3-18/3	1764.047	1764.013	19.245	0.401	1370.074	0.432	29	0.148	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-19/2	1486.157	1486.740	-1068.909	0.368	639.539	0.409	18	0.145	K.SFGVLIPDQGIALR.G
R3/RRR3-18/3	1764.013	1764.013	-0.119	0.433	1304.382	0.418	30	0.138	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-19/3	1764.080	1764.013	38.192	0.348	1195.458	0.425	28	0.130	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-19/3	1764.185	1764.013	97.736	0.283	967.391	0.256	25	0.091	K.SGGLGDLKYPLISDVTK.S
R3/RRR3-17/3	1789.566	1790.050	-271.596	0.483	785.888	0.422	28	0.108	K.KIDAAKPISEVFEDVK.A
R3/RRR3-17/3	1789.664	1790.050	-216.372	0.497	769.950	0.340	27	0.097	K.KIDAAKPISEVFEDVK.A
R3/RRR3-17/3	1789.815	1790.050	-132.007	0.478	692.749	0.340	25	0.095	K.KIDAAKPISEVFEDVK.A
R3/RRR3-14/2	1610.564	1610.883	-198.613	0.529	1654.094	0.549	21	0.251	K.IAIVGFGNFGQFLAR.T
R3/RRR3-14/2	1210.406	1210.363	35.038	0.479	1695.431	0.468	17	0.240	R.AEAFLNIFER.E
R3/RRR3-14/2	1610.387	1610.883	-308.801	0.497	1662.468	0.460	19	0.229	K.IAIVGFGNFGQFLAR.T
R3/RRR3-14/2	1210.015	1210.363	-288.644	0.473	923.485	0.456	14	0.163	R.AEAFLNIFER.E
R3/RRR3-14/2	1209.618	1210.363	-1447.293	0.416	872.048	0.373	15	0.151	R.AEAFLNIFER.E
R3/RRR3-14/2	1611.516	1610.883	-228.582	0.428	847.239	0.404	16	0.147	K.IAIVGFGNFGQFLAR.T
R3/RRR3-14/2	1009.147	1009.269	-121.640	0.373	1180.862	0.228	13	0.147	R.M*LAM*LELR.S
R3/RRR3-12/2	1472.413	1472.626	-144.988	0.449	1573.901	0.457	19	0.220	R.GQILDTVAEIQER.H
R3/RRR3-12/2	1187.593	1187.411	153.860	0.469	1038.235	0.535	17	0.184	K.KVDAIESLIAK.L
R3/RRR3-13/2	1186.948	1187.411	-391.320	0.292	548.021	0.313	13	0.133	K.KVDAIESLIAK.L
R3/RRR3-12/3	1661.724	1661.796	-43.267	0.552	864.822	0.525	28	0.128	K.TKVDELEKDNLSNR.Q
R3/RRR3-12/3	1662.786	1661.796	-6.165	0.523	624.492	0.533	25	0.120	K.TKVDELEKDNLSNR.Q
R3/RRR3-13/3	1661.734	1661.796	-37.188	0.499	896.377	0.471	28	0.119	K.TKVDELEKDNLSNR.Q
R3/RRR3-13/3	1661.672	1661.796	-74.546	0.494	619.690	0.461	24	0.110	K.TKVDELEKDNLSNR.Q
R3/RRR3-21/2	1674.526	1674.919	-235.555	0.540	840.586	0.465	20	0.158	R.SYLNLPSEVVPNTLK.K
R3/RRR3-21/2	1264.694	1264.371	255.813	0.454	426.304	0.539	15	0.156	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1264.872	1264.371	-395.477	0.434	458.700	0.522	15	0.154	K.GGAPAEFQPSFR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/2	1263.876	1264.371	-392.882	0.390	420.118	0.531	15	0.153	K.GGAPAEFQPSFR.G
R3/RRR3-20/2	1263.753	1264.371	-1284.247	0.380	497.520	0.508	16	0.153	K.GGAPAEFQPSFR.G
R3/RRR3-22/2	1264.132	1264.371	-189.797	0.408	409.597	0.537	14	0.153	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1264.044	1264.371	-259.259	0.406	465.558	0.513	15	0.153	K.GGAPAEFQPSFR.G
R3/RRR3-22/2	1264.019	1264.371	-279.121	0.387	484.284	0.490	16	0.152	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1263.787	1264.371	-1257.570	0.386	446.061	0.510	15	0.152	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1263.683	1264.371	-1339.738	0.408	469.258	0.484	15	0.151	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1264.407	1264.371	28.216	0.403	364.089	0.512	14	0.151	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1264.295	1264.371	-60.198	0.384	443.079	0.494	15	0.151	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1264.603	1264.371	184.186	0.383	373.716	0.519	14	0.151	K.GGAPAEFQPSFR.G
R3/RRR3-22/2	1264.105	1264.371	-211.593	0.369	439.373	0.483	15	0.149	K.GGAPAEFQPSFR.G
R3/RRR3-20/2	1263.490	1264.371	-1493.729	0.336	429.297	0.483	15	0.148	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1126.908	1126.328	-373.816	0.376	559.386	0.431	16	0.147	K.VDVPNLEVIK.L
R3/RRR3-21/2	1263.967	1264.371	-321.076	0.368	443.257	0.434	15	0.147	K.GGAPAEFQPSFR.G
R3/RRR3-21/2	1674.474	1674.919	-266.711	0.444	673.188	0.423	18	0.145	R.SYLNLPSEVVPNTLK.K
R3/RRR3-21/2	1127.032	1126.328	-263.401	0.399	446.019	0.396	14	0.143	K.VDVPNLEVIK.L
R3/RRR3-18/2	1456.454	1455.595	-97.230	0.584	2111.775	0.581	22	0.337	K.GVISLDTSGSSYLR.A
R3/RRR3-18/2	1455.149	1455.595	-307.752	0.497	2114.776	0.513	22	0.317	K.GVISLDTSGSSYLR.A
R3/RRR3-18/2	1455.086	1455.595	-1040.069	0.483	1849.622	0.459	21	0.257	K.GVISLDTSGSSYLR.A
R3/RRR3-18/2	1003.116	1003.180	-63.544	0.408	1332.903	0.343	14	0.174	K.AIQAFSPLR.I
R3/RRR3-18/2	1003.024	1003.180	-155.955	0.438	1285.003	0.314	14	0.166	K.AIQAFSPLR.I
R3/RRR3-17/2	1979.395	1979.268	64.045	0.396	762.676	0.399	18	0.139	K.IFVDTGAVVTFGLNALQGR.Q
R3/RRR3-7/2	1316.316	1316.486	-129.161	0.464	2209.666	0.484	19	0.324	K.SIQVIVVTDGER.I
R3/RRR3-7/2	1316.155	1316.486	-252.436	0.418	2233.162	0.428	19	0.312	K.SIQVIVVTDGER.I
R3/RRR3-6/2	1785.981	1785.934	26.489	0.493	1563.017	0.495	24	0.227	R.AVFASGSPFDPVEYNGK.I
R3/RRR3-6/2	1315.933	1316.486	-1183.825	0.422	1183.701	0.513	17	0.190	K.SIQVIVVTDGER.I
R3/RRR3-7/2	1786.386	1785.934	253.825	0.460	1209.827	0.453	22	0.180	R.AVFASGSPFDPVEYNGK.I
R3/RRR3-7/2	1801.667	1802.123	-253.435	0.445	693.271	0.511	19	0.154	R.ILGLGDLGCQGM*GIPVGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1785.237	1786.123	-1059.646	0.469	698.746	0.504	19	0.154	R.ILGLGDLGCQGMGIPVGK.L
R3/RRR3-7/2	1315.915	1316.486	-1197.612	0.324	1139.468	0.295	17	0.153	K.SIQVIVVTDGER.I
R3/RRR3-6/2	1786.077	1786.123	-25.954	0.376	698.174	0.448	18	0.146	R.ILGLGDLGCQGMGIPVGK.L
R3/RRR3-7/2	1801.410	1802.123	-953.668	0.405	606.897	0.459	19	0.146	R.ILGLGDLGCQGM*GIPVGK.L
R3/RRR3-7/2	1785.526	1786.123	-897.028	0.398	661.440	0.452	18	0.146	R.ILGLGDLGCQGMGIPVGK.L
R3/RRR3-7/2	1801.347	1802.123	-988.910	0.374	601.173	0.471	18	0.146	R.ILGLGDLGCQGM*GIPVGK.L
R3/RRR3-6/2	1801.838	1802.123	-158.416	0.366	569.071	0.220	18	0.129	R.ILGLGDLGCQGM*GIPVGK.L
R3/RRR3-13/2	1245.348	1245.368	-16.282	0.509	1880.097	0.475	20	0.266	K.SINDIAASQGIR.I
R3/RRR3-11/2	1245.173	1245.368	-156.993	0.540	1842.799	0.475	20	0.260	K.SINDIAASQGIR.I
R3/RRR3-12/2	1245.222	1245.368	-117.755	0.576	1776.888	0.490	20	0.254	K.SINDIAASQGIR.I
R3/RRR3-12/2	1245.018	1245.368	-281.414	0.487	1841.826	0.390	20	0.238	K.SINDIAASQGIR.I
R3/RRR3-11/2	1245.106	1245.368	-211.085	0.544	1586.966	0.437	19	0.217	K.SINDIAASQGIR.I
R3/RRR3-12/2	1244.518	1245.368	-1490.822	0.480	1501.011	0.416	19	0.203	K.SINDIAASQGIR.I
R3/RRR3-11/2	1610.881	1610.883	-1.490	0.485	1307.631	0.398	21	0.180	R.VLNISGVQLIGINNR.S
R3/RRR3-11/2	1346.471	1346.515	-33.245	0.410	831.648	0.542	15	0.166	R.DFYGALASAFKR.N
R3/RRR3-12/2	1610.508	1610.883	-233.515	0.449	1074.883	0.374	19	0.158	R.VLNISGVQLIGINNR.S
R3/RRR3-12/2	1610.225	1610.883	-1033.084	0.402	1174.823	0.283	20	0.152	R.VLNISGVQLIGINNR.S
R3/RRR3-11/2	1610.345	1610.883	-958.116	0.383	1151.990	0.284	20	0.151	R.VLNISGVQLIGINNR.S
R3/RRR3-11/2	1345.991	1346.515	-1135.830	0.325	771.627	0.468	15	0.151	R.DFYGALASAFKR.N
R3/RRR3-13/2	1609.892	1610.883	-1240.541	0.257	1091.198	0.214	19	0.140	R.VLNISGVQLIGINNR.S
R3/RRR3-15/2	1347.005	1347.366	-268.469	0.490	1332.518	0.368	18	0.179	K.YEDQIDSYGEK.G
R3/RRR3-14/2	1346.922	1347.366	-330.571	0.475	1197.314	0.416	18	0.177	K.YEDQIDSYGEK.G
R3/RRR3-15/2	1346.851	1347.366	-1127.923	0.430	1290.818	0.352	18	0.173	K.YEDQIDSYGEK.G
R3/RRR3-14/2	1346.979	1347.366	-288.108	0.459	1181.542	0.378	18	0.170	K.YEDQIDSYGEK.G
R3/RRR3-14/2	1346.238	1347.366	-1585.538	0.349	1265.491	0.299	18	0.163	K.YEDQIDSYGEK.G
R3/RRR3-14/2	1515.356	1515.784	-283.001	0.449	636.599	0.536	19	0.157	K.VLGGGKPADVFLWR.N
R3/RRR3-15/2	942.003	942.050	-49.925	0.336	373.466	0.431	12	0.146	K.QYAVFDAK.V
R3/RRR3-15/2	942.075	942.050	26.109	0.314	335.146	0.376	11	0.142	K.QYAVFDAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	941.969	942.050	-85.931	0.309	265.376	0.327	10	0.142	K.QYAVFDAK.V
R3/RRR3-14/2	941.893	942.050	-167.051	0.335	335.162	0.351	11	0.140	-.QYAVFDAK.-
R3/RRR3-15/2	941.816	942.050	-248.705	0.232	247.889	0.291	10	0.139	K.QYAVFDAK.V
R3/RRR3-12/2	1615.225	1614.744	298.612	0.534	1513.522	0.420	20	0.203	K.TWQGRPENVEAAQK.A
R3/RRR3-12/2	1614.342	1614.744	-249.570	0.473	1499.474	0.372	20	0.193	K.TWQGRPENVEAAQK.A
R3/RRR3-12/2	1614.352	1614.744	-243.425	0.541	1335.609	0.434	19	0.187	K.TWQGRPENVEAAQK.A
R3/RRR3-12/2	1500.400	1499.771	-248.122	0.396	709.020	0.491	21	0.156	R.TVVSIPCGPSALAVK.E
R3/RRR3-12/2	1499.370	1499.771	-268.462	0.267	592.299	0.408	19	0.139	R.TVVSIPCGPSALAVK.E
R3/RRR3-12/2	1499.320	1499.771	-302.034	0.295	638.895	0.357	20	0.138	R.TVVSIPCGPSALAVK.E
R3/RRR3-12/3	1129.408	1129.295	100.091	0.458	1530.688	0.255	21	0.121	-.AKANSLAQLGR.-
R3/RRR3-24/2	1656.422	1656.950	-925.329	0.468	1014.104	0.420	19	0.161	R.DINPQAPTHIVIIPK.V
R3/RRR3-24/2	1786.157	1786.963	-1014.201	0.468	496.875	0.552	19	0.152	K.EAALAAVPNDNPTIFDK.I
R3/RRR3-24/3	1464.148	1464.605	-313.187	0.509	1213.693	0.514	31	0.146	K.VVAKQEGLEDGYR.I
R3/RRR3-24/2	1786.310	1786.963	-928.575	0.394	508.561	0.509	18	0.145	K.EAALAAVPNDNPTIFDK.I
R3/RRR3-24/2	1656.394	1656.950	-942.567	0.477	773.149	0.358	17	0.140	R.DINPQAPTHIVIIPK.V
R3/RRR3-24/2	1656.577	1656.950	-225.912	0.489	982.338	0.281	19	0.139	R.DINPQAPTHIVIIPK.V
R3/RRR3-24/3	1464.679	1464.605	50.430	0.513	1066.122	0.498	30	0.132	K.VVAKQEGLEDGYR.I
R3/RRR3-24/3	1464.192	1464.605	-283.074	0.491	958.283	0.525	29	0.130	K.VVAKQEGLEDGYR.I
R3/RRR3-14/2	1078.428	1078.203	209.057	0.429	1110.153	0.351	15	0.159	R.LFVANVGDSR.A
R3/RRR3-15/2	1020.984	1021.195	-207.355	0.417	973.441	0.295	13	0.146	K.LLQEAYKR.E
R3/RRR3-14/2	857.922	858.021	-115.827	0.418	782.227	0.257	13	0.136	R.VGGVLAVSR.A
R3/RRR3-14/2	857.420	858.021	-1873.149	0.364	660.617	0.269	13	0.135	-.VGGVLAVSR.-
R3/RRR3-15/2	1264.590	1265.437	-1465.223	0.364	1156.478	0.480	16	0.180	K.AVTEVVDFISGK.C
R3/RRR3-15/2	1594.845	1595.887	-1284.645	0.411	901.351	0.520	21	0.170	R.IPIPVFDM*YGIGTR.K
R3/RRR3-15/2	1595.347	1595.887	-968.431	0.401	782.601	0.555	19	0.166	R.IPIPVFDM*YGIGTR.K
R3/RRR3-15/2	1265.028	1265.437	-324.775	0.353	993.738	0.439	17	0.163	K.AVTEVVDFISGK.C
R3/RRR3-15/2	1265.039	1265.437	-316.158	0.361	789.554	0.509	16	0.159	K.AVTEVVDFISGK.C
R3/RRR3-15/2	1594.428	1595.887	-1546.758	0.322	698.478	0.460	18	0.148	R.IPIPVFDM*YGIGTR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/3	1547.589	1546.748	-102.906	0.485	953.058	0.362	21	0.104	K.FHLVEAEESIFPK.G
R3/RRR3-15/3	1545.898	1546.748	-1200.149	0.383	817.029	0.333	22	0.095	K.FHLVEAEESIFPK.G
R3/RRR3-15/2	1125.165	1125.383	-194.195	0.455	1354.163	0.437	15	0.193	K.IAIDLLEPIK.R
R3/RRR3-15/2	1125.238	1125.383	-129.114	0.465	1303.580	0.452	15	0.191	K.IAIDLLEPIK.R
R3/RRR3-15/3	1944.953	1944.203	-128.887	0.526	1310.286	0.536	34	0.166	R.M*GLSDKDIVALSGGHTLGR.A
R3/RRR3-15/2	1125.034	1125.383	-311.536	0.349	822.680	0.497	13	0.159	K.IAIDLLEPIK.R
R3/RRR3-15/3	1944.166	1944.203	-19.045	0.514	1254.114	0.516	33	0.156	R.M*GLSDKDIVALSGGHTLGR.A
R3/RRR3-15/3	1592.580	1591.706	-79.280	0.428	1021.005	0.449	28	0.120	R.LAWHDAGTYDVNTK.T
R3/RRR3-15/3	1943.946	1944.203	-132.417	0.372	777.409	0.386	27	0.100	R.M*GLSDKDIVALSGGHTLGR.A
R3/RRR3-15/3	1591.267	1591.706	-276.434	0.362	753.792	0.343	26	0.095	R.LAWHDAGTYDVNTK.T
R3/RRR3-21/2	1934.513	1935.169	-858.512	0.558	1523.323	0.530	28	0.231	R.IWVFSGDADSVVPLTATR.Y
R3/RRR3-21/2	1934.148	1935.169	-1048.203	0.531	1502.663	0.487	27	0.218	R.IWVFSGDADSVVPLTATR.Y
R3/RRR3-21/2	1935.770	1935.169	-206.991	0.599	1321.582	0.546	26	0.210	R.IWVFSGDADSVVPLTATR.Y
R3/RRR3-21/2	1153.515	1154.297	-1549.209	0.390	884.431	0.426	14	0.158	K.YYNLPEVQK.A
R3/RRR3-21/2	1154.125	1154.297	-149.434	0.304	928.540	0.343	14	0.148	K.YYNLPEVQK.A
R3/RRR3-21/2	1153.961	1154.297	-291.524	0.415	740.422	0.387	13	0.148	K.YYNLPEVQK.A
R3/RRR3-19/3	1326.684	1326.492	145.194	0.439	547.213	0.455	21	0.108	R.GAGHEVPLHRPR.Q
R3/RRR3-21/3	1326.807	1326.492	237.921	0.440	938.338	0.352	23	0.103	R.GAGHEVPLHRPR.Q
R3/RRR3-19/3	1326.516	1326.492	18.255	0.394	587.399	0.358	21	0.098	R.GAGHEVPLHRPR.Q
R3/RRR3-19/3	1326.227	1326.492	-200.400	0.364	549.371	0.318	19	0.095	R.GAGHEVPLHRPR.Q
R3/RRR3-21/3	1326.409	1326.492	-62.743	0.350	660.157	0.329	20	0.095	R.GAGHEVPLHRPR.Q
R3/RRR3-12/2	855.787	856.005	-255.179	0.413	1107.960	0.421	13	0.171	K.TPAQVALR.W
R3/RRR3-12/2	855.829	856.005	-206.669	0.381	1159.044	0.362	13	0.165	K.TPAQVALR.W
R3/RRR3-12/2	1009.965	1010.126	-159.974	0.417	668.446	0.448	16	0.153	R.AIGVSNFSSK.K
R3/RRR3-12/2	1009.282	1010.126	-1832.834	0.358	611.217	0.383	15	0.144	R.AIGVSNFSSK.K
R3/RRR3-12/2	1109.083	1109.257	-157.379	0.353	839.234	0.316	14	0.141	K.REDLFITSK.L
R3/RRR3-12/2	1010.064	1010.126	-61.410	0.321	503.037	0.374	13	0.139	R.AIGVSNFSSK.K
R3/RRR3-11/2	1329.177	1329.486	-233.474	0.509	1244.742	0.469	19	0.190	K.IPATWQGIEASR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1277.590	1278.439	-1451.847	0.358	1249.059	0.301	16	0.160	R.LAYDTQGIIQR.V
R3/RRR3-12/2	1329.350	1329.486	-103.027	0.409	739.607	0.504	16	0.159	K.IPATWQGIEASR.L
R3/RRR3-12/2	1329.456	1329.486	-22.527	0.422	769.418	0.453	17	0.156	K.IPATWQGIEASR.L
R3/RRR3-11/2	1677.243	1677.832	-950.342	0.448	636.054	0.456	24	0.153	K.ILQSLEESVTDTDVK.Y
R3/RRR3-15/2	1678.563	1677.832	-160.734	0.404	510.633	0.493	15	0.144	K.ILQSLEESVTDTDVK.Y
R3/RRR3-12/2	1329.072	1329.486	-312.718	0.288	496.371	0.357	14	0.136	K.IPATWQGIEASR.L
R3/RRR3-13/3	1632.553	1632.755	-123.612	0.479	635.506	0.552	28	0.121	K.IVASEDRDLTVEER.N
R3/RRR3-13/3	1633.074	1632.755	196.150	0.460	586.355	0.436	27	0.106	K.IVASEDRDLTVEER.N
R3/RRR3-13/3	1632.359	1632.755	-242.773	0.422	410.729	0.450	24	0.106	K.IVASEDRDLTVEER.N
R3/RRR3-16/2	1427.279	1427.542	-184.486	0.538	1446.425	0.528	19	0.310	K.NLKDEPVAAEQNV.-
R3/RRR3-16/2	1427.688	1427.542	102.386	0.563	1431.214	0.548	19	0.303	K.NLKDEPVAAEQNV.-
R3/RRR3-16/2	1885.242	1886.138	-1008.826	0.512	1061.979	0.548	23	0.185	K.SGATVLPDLVAAQEWLSK.N
R3/RRR3-16/2	1885.222	1886.138	-1019.618	0.484	980.126	0.585	22	0.184	K.SGATVLPDLVAAQEWLSK.N
R3/RRR3-16/2	1480.939	1481.499	-1056.057	0.419	1255.540	0.436	17	0.182	K.AGYEYDEETFEK.I
R3/RRR3-16/2	1885.357	1886.138	-947.330	0.493	889.052	0.575	22	0.176	K.SGATVLPDLVAAQEWLSK.N
R3/RRR3-16/2	1481.267	1481.499	-157.098	0.437	918.519	0.419	15	0.155	K.AGYEYDEETFEK.I
R3/RRR3-12/2	1579.485	1578.858	-237.171	0.489	1383.707	0.524	22	0.211	R.VSAPAVTMSFAGGAALK.L
R3/RRR3-12/2	1579.552	1578.858	-194.373	0.520	1114.930	0.541	21	0.187	R.VSAPAVTMSFAGGAALK.L
R3/RRR3-12/2	1578.481	1578.858	-239.959	0.425	1166.830	0.462	19	0.176	R.VSAPAVTMSFAGGAALK.L
R3/RRR3-12/2	1167.099	1166.349	-214.493	0.439	751.989	0.537	16	0.166	R.LPTSVYSALSK.A
R3/RRR3-11/2	857.818	858.021	-236.734	0.451	1109.722	0.345	15	0.161	R.SAGLIGLAR.N
R3/RRR3-11/2	1167.122	1166.349	-194.557	0.395	828.011	0.473	16	0.160	R.LPTSVYSALSK.A
R3/RRR3-11/2	1166.117	1166.349	-199.345	0.366	853.507	0.468	16	0.160	R.LPTSVYSALSK.A
R3/RRR3-12/2	857.988	858.021	-38.331	0.400	1018.132	0.352	14	0.156	R.SAGLIGLAR.N
R3/RRR3-11/2	1166.112	1166.349	-203.440	0.270	902.332	0.353	16	0.146	R.LPTSVYSALSK.A
R3/RRR3-12/2	857.812	858.021	-244.015	0.360	882.251	0.312	14	0.145	R.SAGLIGLAR.N
R3/RRR3-11/2	857.800	858.021	-258.577	0.365	869.964	0.297	13	0.141	-.SAGLIGLAR.-
R3/RRR3-11/2	857.723	858.021	-348.673	0.350	722.307	0.294	12	0.136	-.SAGLIGLAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1525.206	1525.639	-284.625	0.463	1179.748	0.462	21	0.182	R.VDVAAPEQCPPEGR.L
R3/RRR3-15/2	1526.154	1525.639	-318.946	0.469	1081.190	0.509	20	0.182	R.VDVAAPEQCPPEGR.L
R3/RRR3-15/2	1525.242	1525.639	-260.858	0.418	1052.879	0.501	20	0.177	R.VDVAAPEQCPPEGR.L
R3/RRR3-15/3	1413.764	1413.606	112.089	0.479	1241.950	0.570	29	0.164	R.LPAAGPPSPAEHLR.E
R3/RRR3-15/3	1413.427	1413.606	-127.226	0.492	937.425	0.606	26	0.147	R.LPAAGPPSPAEHLR.E
R3/RRR3-15/3	1957.528	1956.257	138.871	0.510	1084.017	0.517	30	0.140	R.MGLSDKEIVALSGAHTLGR.S
R3/RRR3-15/3	1413.498	1413.606	-76.677	0.491	850.208	0.595	25	0.139	R.LPAAGPPSPAEHLR.E
R3/RRR3-15/3	1955.821	1956.257	-223.249	0.435	910.674	0.474	27	0.119	R.MGLSDKEIVALSGAHTLGR.S
R3/RRR3-16/2	1442.178	1441.620	-307.549	0.587	1343.399	0.527	19	0.210	R.IYNQNLINHVGR.G
R3/RRR3-16/2	1441.227	1441.620	-273.346	0.548	1400.544	0.494	19	0.209	R.IYNQNLINHVGR.G
R3/RRR3-16/2	1442.114	1441.620	343.457	0.531	1302.474	0.501	19	0.201	R.IYNQNLINHVGR.G
R3/RRR3-16/2	1396.159	1396.533	-268.226	0.463	1255.382	0.465	18	0.189	R.NNIQAYPSVSFR.Y
R3/RRR3-15/2	1441.036	1441.620	-1102.548	0.496	1336.155	0.415	19	0.187	R.IYNQNLINHVGR.G
R3/RRR3-16/2	1396.095	1396.533	-314.280	0.447	1150.602	0.465	17	0.180	R.NNIQAYPSVSFR.Y
R3/RRR3-15/2	1441.211	1441.620	-284.647	0.549	1094.912	0.463	18	0.176	R.IYNQNLINHVGR.G
R3/RRR3-16/2	1396.186	1396.533	-249.191	0.479	1165.750	0.420	17	0.173	R.NNIQAYPSVSFR.Y
R3/RRR3-15/2	1396.157	1396.533	-270.331	0.404	989.440	0.437	16	0.163	R.NNIQAYPSVSFR.Y
R3/RRR3-15/2	1441.123	1441.620	-345.495	0.486	834.411	0.410	17	0.154	R.IYNQNLINHVGR.G
R3/RRR3-16/2	1123.079	1123.330	-224.318	0.440	784.781	0.432	16	0.152	R.GALVSAGLGHIK.V
R3/RRR3-16/2	1122.451	1123.330	-1679.019	0.401	901.224	0.367	17	0.150	R.GALVSAGLGHIK.V
R3/RRR3-16/2	1397.183	1396.533	-250.941	0.354	966.298	0.326	17	0.149	R.NNIQAYPSVSFR.Y
R3/RRR3-16/2	1397.047	1396.533	-348.946	0.445	850.924	0.337	16	0.144	-.NNIQAYPSVSFR.-
R3/RRR3-15/2	1395.825	1396.533	-1226.940	0.284	492.742	0.280	12	0.133	R.NNIQAYPSVSFR.Y
R3/RRR3-8/2	1601.166	1600.839	205.267	0.526	1818.154	0.418	23	0.240	R.GLLATDAALLLNADTK.A
R3/RRR3-8/2	1282.357	1282.471	-88.948	0.416	1529.368	0.460	20	0.216	K.DLAVLSGAHTIGK.A
R3/RRR3-8/2	1038.936	1039.210	-264.405	0.496	868.937	0.444	15	0.161	K.SPELAGPVLR.L
R3/RRR3-8/2	1599.980	1600.839	-1164.968	0.370	1153.707	0.359	19	0.160	R.GLLATDAALLLNADTK.A
R3/RRR3-8/2	1039.053	1039.210	-151.489	0.480	964.454	0.395	16	0.160	K.SPELAGPVLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1600.713	1600.839	-78.754	0.385	1161.870	0.348	20	0.160	R.GLLATDAALLLNADTK.A
R3/RRR3-7/2	1039.212	1039.210	1.931	0.444	817.642	0.390	14	0.151	K.SPELAGPVLR.L
R3/RRR3-7/2	1040.097	1039.210	-109.077	0.423	960.766	0.336	15	0.151	K.SPELAGPVLR.L
R3/RRR3-8/2	1040.221	1039.210	10.521	0.490	664.040	0.412	13	0.148	K.SPELAGPVLR.L
R3/RRR3-8/2	1038.409	1039.210	-1739.801	0.330	836.997	0.310	14	0.143	K.SPELAGPVLR.L
R3/RRR3-7/2	1040.139	1039.210	-68.580	0.407	687.609	0.335	13	0.141	K.SPELAGPVLR.L
R3/RRR3-7/2	1600.622	1600.839	-136.128	0.304	493.973	0.332	14	0.131	-.GLLATDAALLLNADTK.-
R3/RRR3-6/2	1458.159	1458.513	-243.470	0.513	2086.449	0.543	23	0.323	R.VYGSSSNDVSSVTR.Q
R3/RRR3-6/2	1350.358	1349.519	-119.467	0.466	1277.070	0.379	16	0.175	R.GLAYIQDNLWR.L
R3/RRR3-6/2	1366.018	1366.591	-1155.389	0.289	696.136	0.340	14	0.133	R.TAILAEAIASHLR.Q
R3/RRR3-6/2	1348.915	1349.519	-1193.093	0.428	825.831	0.259	13	0.133	R.GLAYIQDNLWR.L
R3/RRR3-6/3	1366.961	1366.591	271.417	0.319	818.113	0.437	25	0.104	R.TAILAEAIASHLR.Q
R3/RRR3-6/3	1366.628	1366.591	26.768	0.262	897.672	0.351	26	0.094	R.TAILAEAIASHLR.Q
R3/RRR3-9/2	1305.919	1306.406	-374.609	0.421	1398.682	0.485	19	0.207	K.LGVSYNQPDGQK.L
R3/RRR3-9/2	1306.013	1306.406	-302.396	0.444	1253.607	0.472	18	0.190	K.LGVSYNQPDGQK.L
R3/RRR3-9/2	1736.362	1736.906	-891.753	0.433	872.096	0.481	22	0.162	K.YEVLPGWQSDISSVR.S
R3/RRR3-9/3	1891.577	1892.191	-855.417	0.414	1112.348	0.475	31	0.132	R.IEELVGVPVHYIGVGPGR.D
R3/RRR3-9/3	1892.171	1892.191	-10.691	0.392	884.638	0.523	30	0.124	R.IEELVGVPVHYIGVGPGR.D
R3/RRR3-4/2	1395.910	1395.690	158.651	0.520	1820.604	0.455	18	0.252	R.VTIDLLEM*VFAK.G
R3/RRR3-4/2	1396.080	1395.690	280.448	0.525	1668.777	0.533	18	0.251	R.VTIDLLEM*VFAK.G
R3/RRR3-4/2	1395.221	1395.690	-336.467	0.468	1562.853	0.397	17	0.205	R.VTIDLLEM*VFAK.G
R3/RRR3-9/2	1589.477	1589.821	-217.039	0.585	2964.622	0.640	24	0.555	K.THINIVVIGHVDSGK.S
R3/RRR3-9/2	1589.039	1589.821	-1124.910	0.593	2890.343	0.633	24	0.531	K.THINIVVIGHVDSGK.S
R3/RRR3-9/2	1589.438	1589.821	-241.463	0.591	2569.167	0.640	24	0.453	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.679	1589.821	-89.475	0.556	2530.024	0.555	35	0.377	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.277	1589.821	-974.022	0.528	2384.774	0.589	33	0.363	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.284	1589.821	-970.090	0.523	2412.326	0.556	32	0.357	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.453	1589.821	-232.303	0.537	2388.527	0.563	32	0.354	K.THINIVVIGHVDSGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/3	1589.765	1589.821	-35.175	0.537	2318.399	0.572	33	0.340	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1590.079	1589.821	163.031	0.544	2105.652	0.600	32	0.308	K.THINIVVIGHVDSGK.S
R3/RRR3-8/3	1589.802	1589.821	-12.070	0.515	2243.407	0.514	33	0.299	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.357	1589.821	-292.635	0.577	2019.824	0.552	34	0.266	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1590.699	1589.821	-76.525	0.595	1962.212	0.569	32	0.265	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.752	1589.821	-43.493	0.535	1863.007	0.571	31	0.251	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.169	1589.821	-1042.273	0.533	1736.800	0.612	32	0.244	K.THINIVVIGHVDSGK.S
R3/RRR3-1/3	1589.312	1589.821	-952.045	0.453	1912.008	0.507	31	0.239	K.THINIVVIGHVDSGK.S
R3/RRR3-10/3	1589.994	1589.821	109.214	0.505	1784.328	0.564	31	0.236	K.THINIVVIGHVDSGK.S
R3/RRR3-2/3	1589.808	1589.821	-8.142	0.521	1698.596	0.554	30	0.220	K.THINIVVIGHVDSGK.S
R3/RRR3-1/3	1589.595	1589.821	-142.626	0.465	1644.917	0.562	29	0.217	K.THINIVVIGHVDSGK.S
R3/RRR3-10/3	1590.536	1589.821	-179.645	0.511	1712.082	0.534	29	0.217	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.046	1589.821	-1120.367	0.481	1597.927	0.578	31	0.212	K.THINIVVIGHVDSGK.S
R3/RRR3-1/3	1588.854	1589.821	-1241.409	0.447	1728.908	0.498	30	0.208	K.THINIVVIGHVDSGK.S
R3/RRR3-9/3	1589.732	1589.821	-55.739	0.506	1646.222	0.523	29	0.204	K.THINIVVIGHVDSGK.S
R3/RRR3-8/3	1589.752	1589.821	-43.262	0.496	1515.902	0.527	30	0.187	K.THINIVVIGHVDSGK.S
R3/RRR3-2/2	1120.864	1121.268	-361.741	0.445	975.386	0.524	15	0.178	K.STTTGHLIYK.L
R3/RRR3-2/2	1120.529	1121.268	-1556.571	0.407	950.574	0.504	15	0.172	K.STTTGHLIYK.L
R3/RRR3-2/2	1121.122	1121.268	-130.571	0.385	959.924	0.471	15	0.168	K.STTTGHLIYK.L
R3/RRR3-8/2	1122.026	1121.268	-216.126	0.426	824.686	0.506	14	0.166	K.STTTGHLIYK.L
R3/RRR3-7/2	1120.942	1121.268	-291.592	0.417	763.473	0.527	13	0.164	K.STTTGHLIYK.L
R3/RRR3-3/2	1120.899	1121.268	-330.708	0.423	878.467	0.458	14	0.162	K.STTTGHLIYK.L
R3/RRR3-3/2	1121.181	1121.268	-78.256	0.408	850.089	0.462	14	0.161	K.STTTGHLIYK.L
R3/RRR3-3/2	1120.966	1121.268	-270.506	0.412	766.339	0.496	13	0.161	K.STTTGHLIYK.L
R3/RRR3-2/3	1589.530	1589.821	-183.187	0.394	1537.919	0.405	28	0.159	K.THINIVVIGHVDSGK.S
R3/RRR3-4/2	1120.964	1121.268	-271.817	0.406	854.667	0.445	14	0.159	K.STTTGHLIYK.L
R3/RRR3-6/2	1120.607	1121.268	-1486.427	0.401	746.098	0.491	13	0.159	K.STTTGHLIYK.L
R3/RRR3-15/2	1121.021	1121.268	-221.235	0.420	663.114	0.484	13	0.156	K.STTTGHLIYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/3	1590.227	1589.821	256.332	0.521	1221.505	0.517	28	0.153	K.THINIVVIGHVDSGK.S
R3/RRR3-11/2	1121.138	1121.268	-116.154	0.380	624.776	0.466	13	0.152	K.STTTGHLIYK.L
R3/RRR3-6/2	1121.072	1121.268	-175.792	0.357	717.092	0.444	13	0.152	K.STTTGHLIYK.L
R3/RRR3-7/2	1120.894	1121.268	-334.969	0.393	647.282	0.453	13	0.152	K.STTTGHLIYK.L
R3/RRR3-5/2	1121.035	1121.268	-208.563	0.362	709.833	0.442	13	0.152	K.STTTGHLIYK.L
R3/RRR3-4/2	1120.507	1121.268	-1576.051	0.383	685.770	0.431	13	0.151	K.STTTGHLIYK.L
R3/RRR3-1/2	1120.503	1121.268	-1579.772	0.344	726.458	0.419	14	0.151	K.STTTGHLIYK.L
R3/RRR3-1/2	1121.338	1121.268	62.716	0.392	493.108	0.475	12	0.150	K.STTTGHLIYK.L
R3/RRR3-1/2	1120.443	1121.268	-1634.058	0.364	708.452	0.412	13	0.149	K.STTTGHLIYK.L
R3/RRR3-5/2	1121.070	1121.268	-176.884	0.383	503.436	0.456	11	0.147	K.STTTGHLIYK.L
R3/RRR3-9/3	1588.842	1589.821	-1249.047	0.435	1066.098	0.497	25	0.138	K.THINIVVIGHVDSGK.S
R3/RRR3-9/2	1589.731	1589.821	-56.347	0.316	589.971	0.382	15	0.138	K.THINIVVIGHVDSGK.S
R3/RRR3-9/2	1589.362	1589.821	-289.313	0.246	298.755	0.375	12	0.133	K.THINIVVIGHVDSGK.S
R3/RRR3-9/2	1589.358	1589.821	-292.010	0.258	273.813	0.433	11	0.123	-.THINIVVIGHVDSGK.-
R3/RRR3-10/3	1589.429	1589.821	-247.327	0.372	1176.320	0.364	26	0.120	K.THINIVVIGHVDSGK.S
R3/RRR3-10/3	1590.189	1589.821	232.200	0.341	1157.034	0.363	25	0.120	K.THINIVVIGHVDSGK.S
R3/RRR3-8/3	1588.828	1589.821	-1257.728	0.401	663.976	0.506	26	0.119	K.THINIVVIGHVDSGK.S
R3/RRR3-9/2	1688.285	1688.943	-984.592	0.457	1601.083	0.362	23	0.203	R.ALFVDLEPTVIDEVK.T
R3/RRR3-9/2	1539.963	1538.597	238.549	0.389	1203.505	0.548	21	0.197	R.DAFNTFFSETSSGK.H
R3/RRR3-8/2	1539.550	1538.597	-30.189	0.425	990.458	0.526	19	0.176	R.DAFNTFFSETSSGK.H
R3/RRR3-8/2	1540.075	1538.597	311.513	0.411	1038.599	0.472	19	0.171	R.DAFNTFFSETSSGK.H
R3/RRR3-9/2	1688.306	1688.943	-972.470	0.437	1224.857	0.350	22	0.166	R.ALFVDLEPTVIDEVK.T
R3/RRR3-8/2	1539.923	1538.597	212.477	0.368	673.289	0.461	17	0.149	R.DAFNTFFSETSSGK.H
R3/RRR3-9/2	1688.586	1688.943	-212.131	0.480	882.657	0.353	19	0.145	R.ALFVDLEPTVIDEVK.T
R3/RRR3-2/2	1539.787	1538.597	123.916	0.277	225.446	0.380	12	0.136	R.DAFNTFFSETSSGK.H
R3/RRR3-8/2	1713.276	1712.969	179.901	0.537	1187.963	0.549	22	0.197	K.QTLDLGSTGLLPLEVR.F
R3/RRR3-8/2	1713.993	1712.969	14.100	0.455	860.569	0.543	19	0.169	K.QTLDLGSTGLLPLEVR.F
R3/RRR3-8/2	1200.110	1200.369	-216.449	0.432	1063.273	0.416	17	0.167	R.IYVTNSLFSR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1713.597	1712.969	-217.609	0.419	875.684	0.521	19	0.166	K.QTLDLGSTGLLPLEVR.F
R3/RRR3-8/2	1483.685	1482.689	-2.443	0.492	706.173	0.538	18	0.162	K.TMISSSWGAPAAFR.T
R3/RRR3-7/2	1713.188	1712.969	128.311	0.370	875.011	0.423	18	0.152	K.QTLDLGSTGLLPLEVR.F
R3/RRR3-7/2	1712.609	1712.969	-210.871	0.360	827.908	0.425	19	0.151	K.QTLDLGSTGLLPLEVR.F
R3/RRR3-8/2	1484.023	1482.689	225.431	0.481	484.948	0.463	16	0.146	K.TMISSSWGAPAAFR.T
R3/RRR3-8/2	1483.861	1482.689	116.209	0.378	342.606	0.335	15	0.137	K.TMISSSWGAPAAFR.T
R3/RRR3-8/2	1483.016	1482.689	221.208	0.347	363.949	0.291	15	0.133	-.TMISSSWGAPAAFR.-
R3/RRR3-14/2	1435.965	1436.615	-1152.899	0.526	973.258	0.539	20	0.181	K.AM*AAHLDELGYTK.E
R3/RRR3-14/2	1436.152	1436.615	-323.406	0.571	1007.041	0.515	20	0.179	K.AM*AAHLDELGYTK.E
R3/RRR3-14/2	1927.571	1928.268	-882.926	0.459	1088.185	0.501	21	0.176	R.AFGM*IAGGSGITPMFQVAR.A
R3/RRR3-14/2	1927.256	1928.268	-1047.484	0.491	940.125	0.544	22	0.173	R.AFGMIAGGSGITPM*FQVAR.A
R3/RRR3-14/2	1227.393	1228.377	-1621.352	0.379	1054.306	0.317	16	0.151	R.AILENPNDITK.V
R3/RRR3-14/2	1227.570	1228.377	-1476.297	0.427	967.499	0.355	15	0.151	R.AILENPNDITK.V
R3/RRR3-14/2	1227.598	1228.377	-1453.423	0.404	938.664	0.365	15	0.151	R.AILENPNDITK.V
R3/RRR3-9/2	1792.194	1792.023	95.670	0.503	1597.801	0.553	25	0.246	K.TEAIFPATLETISNVGK.V
R3/RRR3-9/2	1373.162	1373.494	-242.669	0.480	1566.696	0.521	21	0.235	R.VLQDPSSSAEALR.T
R3/RRR3-9/2	1374.092	1373.494	-293.472	0.543	1306.211	0.551	21	0.213	R.VLQDPSSSAEALR.T
R3/RRR3-9/2	1373.133	1373.494	-263.718	0.448	1347.824	0.435	21	0.193	R.VLQDPSSSAEALR.T
R3/RRR3-9/2	1446.438	1446.665	-157.156	0.460	634.672	0.568	18	0.161	K.IPGTSELQISLCK.E
R3/RRR3-9/2	1790.674	1792.023	-1315.499	0.296	1075.082	0.228	21	0.139	K.TEAIFPATLETISNVGK.V
R3/RRR3-7/2	1479.869	1478.629	162.937	0.480	1265.184	0.486	18	0.194	K.EIQDVLDDIYVR.Y
R3/RRR3-7/2	1060.164	1060.226	-59.316	0.457	954.113	0.419	16	0.162	K.ALSLVDSQVK.N
R3/RRR3-8/2	1103.110	1103.253	-129.929	0.416	781.312	0.394	15	0.150	R.VLATDEWLR.V
R3/RRR3-8/2	1060.085	1060.226	-133.816	0.329	651.707	0.406	15	0.145	K.ALSLVDSQVK.N
R3/RRR3-8/2	1060.001	1060.226	-213.526	0.295	605.509	0.373	14	0.140	K.ALSLVDSQVK.N
R3/RRR3-6/2	1026.063	1026.215	-148.634	0.471	1273.547	0.498	19	0.197	K.IGGIGTVPVGR.V
R3/RRR3-14/2	1025.995	1026.215	-214.875	0.455	1261.981	0.468	19	0.191	K.IGGIGTVPVGR.V
R3/RRR3-15/2	1026.069	1026.215	-142.309	0.482	1237.879	0.474	19	0.190	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1026.065	1026.215	-146.964	0.471	1220.405	0.454	19	0.185	K.IGGIGTVPVGR.V
R3/RRR3-16/2	1026.208	1026.215	-6.993	0.441	1178.559	0.474	19	0.185	K.IGGIGTVPVGR.V
R3/RRR3-7/2	1025.544	1026.215	-1634.600	0.426	1206.550	0.460	18	0.184	K.IGGIGTVPVGR.V
R3/RRR3-3/2	1025.597	1026.215	-1581.747	0.437	1085.162	0.492	17	0.180	K.IGGIGTVPVGR.V
R3/RRR3-6/2	1026.170	1026.215	-43.742	0.508	1115.851	0.469	18	0.180	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1261.104	1261.411	-243.844	0.471	1177.307	0.443	17	0.179	K.ANISPNAPWYK.G
R3/RRR3-11/2	1026.133	1026.215	-79.539	0.465	1041.593	0.496	18	0.179	K.IGGIGTVPVGR.V
R3/RRR3-12/2	1025.954	1026.215	-255.339	0.499	1089.142	0.474	18	0.179	K.IGGIGTVPVGR.V
R3/RRR3-2/2	1026.114	1026.215	-98.632	0.477	1034.946	0.495	17	0.178	K.IGGIGTVPVGR.V
R3/RRR3-1/2	1025.970	1026.215	-239.464	0.483	1048.784	0.481	18	0.177	K.IGGIGTVPVGR.V
R3/RRR3-1/2	1025.966	1026.215	-243.761	0.436	1070.605	0.480	17	0.177	K.IGGIGTVPVGR.V
R3/RRR3-6/2	1026.154	1026.215	-59.611	0.467	1225.804	0.408	18	0.177	K.IGGIGTVPVGR.V
R3/RRR3-15/2	1026.099	1026.215	-113.548	0.531	1058.124	0.458	18	0.174	K.IGGIGTVPVGR.V
R3/RRR3-9/2	1026.057	1026.215	-154.244	0.455	1050.042	0.452	18	0.173	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1260.886	1261.411	-1213.077	0.441	1124.844	0.426	17	0.172	K.ANISPNAPWYK.G
R3/RRR3-5/2	1025.563	1026.215	-1615.826	0.428	1040.830	0.458	17	0.172	K.IGGIGTVPVGR.V
R3/RRR3-13/2	1025.570	1026.215	-1608.890	0.471	1047.638	0.445	18	0.172	K.IGGIGTVPVGR.V
R3/RRR3-14/2	1026.081	1026.215	-130.375	0.463	992.202	0.472	17	0.172	K.IGGIGTVPVGR.V
R3/RRR3-2/2	1025.539	1026.215	-1638.546	0.384	1094.788	0.434	17	0.171	K.IGGIGTVPVGR.V
R3/RRR3-10/2	1025.580	1026.215	-1598.727	0.429	921.676	0.489	17	0.170	K.IGGIGTVPVGR.V
R3/RRR3-7/2	1025.495	1026.215	-1681.717	0.448	1021.153	0.446	17	0.169	K.IGGIGTVPVGR.V
R3/RRR3-13/2	1026.056	1026.215	-155.556	0.476	1107.417	0.413	17	0.169	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1026.201	1026.215	-13.316	0.475	822.971	0.510	16	0.168	K.IGGIGTVPVGR.V
R3/RRR3-4/2	1025.937	1026.215	-271.813	0.471	946.571	0.458	17	0.167	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1751.412	1752.026	-923.938	0.435	1146.686	0.404	22	0.167	K.AGMVVTFAPSNVTTEVK.S
R3/RRR3-10/2	1026.025	1026.215	-185.632	0.430	972.333	0.452	17	0.167	K.IGGIGTVPVGR.V
R3/RRR3-5/2	1026.026	1026.215	-184.797	0.514	875.171	0.478	17	0.167	K.IGGIGTVPVGR.V
R3/RRR3-5/2	1026.137	1026.215	-76.317	0.472	982.302	0.434	18	0.167	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1025.675	1026.215	-1505.588	0.416	879.162	0.483	17	0.167	K.IGGIGTVPVGR.V
R3/RRR3-16/2	1026.197	1026.215	-17.134	0.424	890.793	0.471	17	0.166	K.IGGIGTVPVGR.V
R3/RRR3-10/2	1026.968	1026.215	-241.019	0.468	910.226	0.459	17	0.166	K.IGGIGTVPVGR.V
R3/RRR3-15/2	1026.037	1026.215	-173.459	0.491	928.495	0.449	17	0.165	K.IGGIGTVPVGR.V
R3/RRR3-3/2	1026.018	1026.215	-191.958	0.443	895.111	0.460	17	0.165	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1026.122	1026.215	-90.636	0.475	805.541	0.479	16	0.163	K.IGGIGTVPVGR.V
R3/RRR3-13/2	1025.964	1026.215	-245.193	0.415	926.918	0.436	17	0.163	K.IGGIGTVPVGR.V
R3/RRR3-1/2	1025.606	1026.215	-1573.497	0.369	907.918	0.452	17	0.163	K.IGGIGTVPVGR.V
R3/RRR3-9/2	1026.114	1026.215	-98.870	0.483	852.865	0.459	16	0.162	K.IGGIGTVPVGR.V
R3/RRR3-9/2	1025.748	1026.215	-456.876	0.432	917.060	0.433	17	0.162	K.IGGIGTVPVGR.V
R3/RRR3-14/2	1026.177	1026.215	-37.299	0.449	800.098	0.472	16	0.162	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1751.538	1752.026	-279.163	0.464	951.466	0.456	20	0.161	K.AGMVVTFAPSNVTTEVK.S
R3/RRR3-9/2	1026.034	1026.215	-176.681	0.439	883.382	0.436	16	0.160	K.IGGIGTVPVGR.V
R3/RRR3-3/2	1025.635	1026.215	-1545.280	0.417	832.724	0.440	16	0.159	K.IGGIGTVPVGR.V
R3/RRR3-11/2	1025.560	1026.215	-1617.978	0.427	788.805	0.446	16	0.158	K.IGGIGTVPVGR.V
R3/RRR3-2/2	1025.596	1026.215	-1583.182	0.374	862.845	0.421	17	0.157	K.IGGIGTVPVGR.V
R3/RRR3-12/2	1025.812	1026.215	-393.947	0.383	682.583	0.435	15	0.152	K.IGGIGTVPVGR.V
R3/RRR3-11/2	1025.492	1026.215	-1684.946	0.382	630.464	0.429	15	0.151	K.IGGIGTVPVGR.V
R3/RRR3-12/2	1026.051	1026.215	-160.092	0.384	662.777	0.396	15	0.149	K.IGGIGTVPVGR.V
R3/RRR3-9/2	1026.472	1026.215	251.248	0.399	829.016	0.335	16	0.147	K.IGGIGTVPVGR.V
R3/RRR3-9/2	1026.200	1026.215	-14.748	0.366	509.901	0.386	14	0.146	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1750.872	1752.026	-1233.868	0.321	864.520	0.359	21	0.144	K.AGMVVTFAPSNVTTEVK.S
R3/RRR3-9/2	1026.387	1026.215	168.244	0.265	526.818	0.347	14	0.141	K.IGGIGTVPVGR.V
R3/RRR3-2/2	1026.511	1026.215	289.526	0.250	648.774	0.316	16	0.140	K.IGGIGTVPVGR.V
R3/RRR3-8/2	1026.497	1026.215	275.574	0.216	639.057	0.214	13	0.134	K.IGGIGTVPVGR.V
R3/RRR3-7/1	1279.665	1280.538	-1468.667	0.281	915.367	0.453	14	0.951	R.GLPTLVLIGPDGK.T
R3/RRR3-7/2	1517.412	1516.639	-149.806	0.463	1304.892	0.485	21	0.197	K.DNQTVQSVLGTPTR.D
R3/RRR3-7/2	1517.219	1516.639	-277.247	0.445	1165.641	0.423	19	0.173	K.DNQTVQSVLGTPTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1517.094	1516.639	300.656	0.459	1182.996	0.405	20	0.172	K.DNQTVQSVLGTPTR.D
R3/RRR3-7/2	1279.648	1280.538	-1481.373	0.273	998.169	0.473	17	0.163	R.GLPTLVLIGPDGK.T
R3/RRR3-7/2	1280.082	1280.538	-357.397	0.275	996.064	0.465	17	0.162	R.GLPTLVLIGPDGK.T
R3/RRR3-6/2	1279.528	1280.538	-1575.479	0.331	921.282	0.446	16	0.157	R.GLPTLVLIGPDGK.T
R3/RRR3-7/2	1279.651	1280.538	-1479.169	0.370	646.947	0.541	15	0.155	R.GLPTLVLIGPDGK.T
R3/RRR3-7/2	1696.496	1695.914	-247.227	0.472	590.463	0.455	18	0.146	-.MPWLAVPFSDSECR.A
R3/RRR3-6/2	1279.944	1280.538	-1249.252	0.246	405.147	0.324	11	0.130	-.GLPTLVLIGPDGK.-
R3/RRR3-8/2	1608.332	1607.833	311.539	0.546	1963.854	0.498	24	0.286	R.SPPIEEVIQSGVVPR.F
R3/RRR3-8/2	1607.458	1607.833	-234.034	0.500	2014.181	0.453	23	0.281	R.SPPIEEVIQSGVVPR.F
R3/RRR3-8/2	1607.198	1607.833	-1020.479	0.455	1723.306	0.423	22	0.231	R.SPPIEEVIQSGVVPR.F
R3/RRR3-8/3	1968.115	1968.415	-152.848	0.333	1582.760	0.317	30	0.140	R.LVELLLHPSPSVLIPALR.T
R3/RRR3-8/3	1607.861	1607.833	17.764	0.454	942.403	0.499	24	0.126	R.SPPIEEVIQSGVVPR.F
R3/RRR3-8/3	1607.423	1607.833	-255.870	0.405	933.195	0.307	24	0.095	R.SPPIEEVIQSGVVPR.F
R3/RRR3-11/2	1173.114	1173.385	-231.136	0.336	1606.950	0.448	20	0.220	K.VIAISDVTGAVK.N
R3/RRR3-10/2	1172.731	1173.385	-1413.783	0.433	1467.706	0.501	20	0.218	K.VIAISDVTGAVK.N
R3/RRR3-10/2	1747.223	1747.879	-950.329	0.455	1689.873	0.369	24	0.214	K.GGIGCSPGDLSISELER.L
R3/RRR3-10/2	1172.647	1173.385	-1485.928	0.389	1365.341	0.507	20	0.207	K.VIAISDVTGAVK.N
R3/RRR3-10/2	1173.177	1173.385	-177.690	0.427	1383.574	0.460	20	0.201	K.VIAISDVTGAVK.N
R3/RRR3-10/2	1747.239	1747.879	-941.351	0.481	1502.064	0.407	23	0.199	K.GGIGCSPGDLSISELER.L
R3/RRR3-10/2	1162.066	1162.320	-219.848	0.439	1439.843	0.416	20	0.198	K.TAVANIPYGGAK.G
R3/RRR3-10/2	1162.027	1162.320	-253.361	0.445	1408.804	0.408	20	0.194	K.TAVANIPYGGAK.G
R3/RRR3-10/2	1162.083	1162.320	-205.094	0.458	1309.311	0.459	19	0.193	K.TAVANIPYGGAK.G
R3/RRR3-11/2	1173.166	1173.385	-186.458	0.383	1168.799	0.486	18	0.184	K.VIAISDVTGAVK.N
R3/RRR3-11/2	1173.091	1173.385	-250.971	0.288	1082.371	0.352	17	0.156	K.VIAISDVTGAVK.N
R3/RRR3-9/2	1983.662	1984.152	-247.853	0.527	1780.717	0.515	23	0.260	R.ELQDEGFDVQTAGYGLLK.T
R3/RRR3-9/2	1488.361	1488.670	-208.175	0.443	1717.839	0.452	22	0.238	R.SNVIVEYPGTVPGR.A
R3/RRR3-9/2	1488.121	1488.670	-1044.132	0.376	1301.821	0.522	19	0.200	R.SNVIVEYPGTVPGR.A
R3/RRR3-9/2	1488.155	1488.670	-1021.236	0.408	1403.236	0.452	20	0.199	R.SNVIVEYPGTVPGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1758.655	1759.984	-1328.450	0.446	820.611	0.414	19	0.148	R.DAVGGLDRDPFVSLLGK.L
R3/RRR3-9/2	1759.432	1759.984	-884.653	0.461	863.522	0.385	18	0.145	R.DAVGGLDRDPFVSLLGK.L
R3/RRR3-9/2	1758.884	1759.984	-1197.410	0.431	578.555	0.440	17	0.142	R.DAVGGLDRDPFVSLLGK.L
R3/RRR3-19/2	1878.516	1878.113	215.567	0.658	3091.425	0.596	26	0.571	R.IVNAGGECLTFDQLALR.A
R3/RRR3-19/2	1877.488	1878.113	-867.698	0.620	2962.793	0.610	26	0.543	R.IVNAGGECLTFDQLALR.A
R3/RRR3-19/2	1878.670	1878.113	-236.484	0.635	2337.443	0.591	23	0.381	R.IVNAGGECLTFDQLALR.A
R3/RRR3-21/2	1183.068	1182.398	-279.902	0.417	1771.248	0.440	19	0.239	R.APLGQNTVLLR.G
R3/RRR3-19/2	1182.675	1182.398	234.732	0.521	1475.636	0.538	19	0.227	R.APLGQNTVLLR.G
R3/RRR3-19/2	1181.309	1182.398	-1773.737	0.481	1302.965	0.571	18	0.215	R.APLGQNTVLLR.G
R3/RRR3-19/2	1183.134	1182.398	-223.798	0.472	1404.935	0.513	19	0.213	R.APLGQNTVLLR.G
R3/RRR3-19/2	1182.249	1182.398	-126.720	0.491	1398.143	0.513	18	0.212	R.APLGQNTVLLR.G
R3/RRR3-18/2	1182.530	1182.398	111.758	0.469	1346.754	0.529	18	0.210	R.APLGQNTVLLR.G
R3/RRR3-19/2	1182.526	1182.398	108.755	0.415	1488.575	0.446	19	0.207	R.APLGQNTVLLR.G
R3/RRR3-19/2	1182.205	1182.398	-163.284	0.476	1321.069	0.508	18	0.203	R.APLGQNTVLLR.G
R3/RRR3-20/2	1182.612	1182.398	181.426	0.396	1324.741	0.504	18	0.201	R.APLGQNTVLLR.G
R3/RRR3-21/2	1182.012	1182.398	-327.179	0.437	1344.899	0.481	18	0.200	R.APLGQNTVLLR.G
R3/RRR3-20/2	1183.308	1182.398	-76.217	0.425	1228.143	0.480	18	0.189	R.APLGQNTVLLR.G
R3/RRR3-21/2	1183.267	1182.398	-110.780	0.426	1214.072	0.482	17	0.188	R.APLGQNTVLLR.G
R3/RRR3-21/2	1182.447	1182.398	41.355	0.429	1239.354	0.456	18	0.186	R.APLGQNTVLLR.G
R3/RRR3-21/2	1183.032	1182.398	-310.131	0.422	1033.910	0.477	17	0.174	R.APLGQNTVLLR.G
R3/RRR3-18/2	1181.781	1182.398	-1372.498	0.433	886.471	0.526	16	0.172	R.APLGQNTVLLR.G
R3/RRR3-19/2	1183.433	1182.398	29.940	0.403	856.936	0.427	14	0.156	R.APLGQNTVLLR.G
R3/RRR3-20/2	1182.731	1182.398	282.754	0.339	446.277	0.497	12	0.148	R.APLGQNTVLLR.G
R3/RRR3-8/2	1183.374	1182.398	-19.928	0.352	341.355	0.419	14	0.147	R.APLGQNTVLLR.G
R3/RRR3-19/3	1877.721	1878.113	-208.898	0.444	1383.231	0.430	29	0.147	R.IVNAGGECLTFDQLALR.A
R3/RRR3-19/2	1183.409	1182.398	9.352	0.323	633.068	0.407	13	0.145	R.APLGQNTVLLR.G
R3/RRR3-1/2	1183.532	1182.398	113.422	0.305	628.618	0.372	15	0.144	R.APLGQNTVLLR.G
R3/RRR3-18/2	1182.400	1182.398	1.697	0.302	426.060	0.375	12	0.141	R.APLGQNTVLLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1181.484	1182.398	-1624.973	0.175	629.024	0.427	13	0.139	R.APLGQNTVLLR.G
R3/RRR3-19/2	1181.514	1182.398	-1598.921	0.173	532.238	0.459	12	0.138	R.APLGQNTVLLR.G
R3/RRR3-13/2	1183.324	1182.398	-62.972	0.182	545.150	0.140	12	0.131	-.APLGQNTVLLR.-
R3/RRR3-19/3	1877.910	1878.113	-108.146	0.360	1142.705	0.299	27	0.102	R.IVNAGGECLTFDQLALR.A
R3/RRR3-9/2	1446.341	1447.533	-1519.989	0.429	1766.490	0.477	24	0.251	R.EVEAIGGNVSASASR.E
R3/RRR3-9/2	1447.083	1447.533	-311.836	0.527	1308.944	0.504	23	0.202	R.EVEAIGGNVSASASR.E
R3/RRR3-9/2	1509.496	1509.688	-127.312	0.379	550.004	0.461	18	0.146	K.QSSGGLFSWLLGEK.S
R3/RRR3-9/2	1509.280	1509.688	-270.836	0.412	450.145	0.473	16	0.145	K.QSSGGLFSWLLGEK.S
R3/RRR3-9/2	1509.336	1509.688	-233.998	0.390	388.600	0.498	15	0.144	K.QSSGGLFSWLLGEK.S
R3/RRR3-9/2	1120.014	1120.305	-260.569	0.320	853.231	0.364	14	0.144	K.SAVLMNLESR.V
R3/RRR3-6/2	1664.066	1662.865	120.695	0.462	1442.346	0.492	23	0.212	R.FDIDANGILSVAAIDK.G
R3/RRR3-6/2	1787.399	1787.993	-894.581	0.454	1090.309	0.423	20	0.164	K.LSVDNLDEVILVGGSTR.I
R3/RRR3-6/2	1012.575	1013.213	-1622.707	0.454	453.824	0.433	14	0.149	R.IPSVQELVK.K
R3/RRR3-6/2	1013.100	1013.213	-112.165	0.408	521.111	0.368	15	0.145	R.IPSVQELVK.K
R3/RRR3-6/2	1013.109	1013.213	-102.375	0.313	434.416	0.374	14	0.141	R.IPSVQELVK.K
R3/RRR3-6/2	1787.065	1787.993	-1082.062	0.357	646.815	0.293	16	0.129	K.LSVDNLDEVILVGGSTR.I
R3/RRR3-11/2	1761.244	1761.095	84.977	0.569	1429.062	0.601	24	0.237	R.VLVVTNTTVAPLYLEK.V
R3/RRR3-11/2	1276.089	1275.391	-237.047	0.438	1485.043	0.525	19	0.225	R.VSTVVDVDLGDR.S
R3/RRR3-11/2	1275.409	1275.391	14.629	0.481	1598.236	0.422	20	0.217	R.VSTVVDVDLGDR.S
R3/RRR3-11/2	1274.570	1275.391	-1432.905	0.263	1180.577	0.332	18	0.158	R.VSTVVDVDLGDR.S
R3/RRR3-11/2	1061.020	1061.213	-182.510	0.380	634.241	0.380	11	0.137	-.LGWIDESIK.-
R3/RRR3-8/3	1704.932	1704.907	14.526	0.551	1895.396	0.428	29	0.210	K.LTPHSYIGEAEFLAR.N
R3/RRR3-8/3	1704.613	1704.907	-172.831	0.493	1442.398	0.509	25	0.175	K.LTPHSYIGEAEFLAR.N
R3/RRR3-8/2	1294.944	1295.427	-374.191	0.298	735.682	0.494	17	0.149	R.THGQPASPTTLGK.E
R3/RRR3-8/2	1459.360	1459.629	-184.458	0.419	950.680	0.296	19	0.144	R.QFIEGLDLPEAAR.S
R3/RRR3-8/2	1459.303	1459.629	-224.150	0.412	705.391	0.324	18	0.139	R.QFIEGLDLPEAAR.S
R3/RRR3-7/2	1606.389	1606.759	-230.607	0.471	1033.557	0.458	16	0.166	K.FSSVCHFFGYQAR.G
R3/RRR3-7/2	1334.049	1334.458	-307.972	0.459	931.692	0.360	15	0.150	K.ASSFLLDDFYR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1334.274	1334.458	-138.251	0.230	940.957	0.323	14	0.142	K.ASSFLLDDFYR.T
R3/RRR3-7/2	1078.102	1077.320	-202.634	0.362	783.679	0.247	13	0.134	-.LTLM*EVINK.-
R3/RRR3-7/2	1333.476	1334.458	-1490.898	0.256	546.434	0.257	12	0.130	-.ASSFLLDDFYR.-
R3/RRR3-9/2	1936.176	1936.174	0.926	0.519	1487.964	0.528	25	0.225	K.GVYAYDFGDTAGLTPLM*K.M
R3/RRR3-9/2	1553.072	1552.749	208.471	0.565	1024.292	0.535	22	0.186	R.FIDIPEEVAEVYK.L
R3/RRR3-9/3	1937.366	1936.174	99.159	0.433	1566.916	0.452	30	0.174	K.GVYAYDFGDTAGLTPLM*K.M
R3/RRR3-9/2	1553.224	1552.749	306.748	0.523	983.587	0.476	22	0.173	R.FIDIPEEVAEVYK.L
R3/RRR3-9/2	1553.313	1552.749	-281.682	0.509	1016.044	0.428	22	0.168	R.FIDIPEEVAEVYK.L
R3/RRR3-9/3	1552.793	1552.749	28.132	0.540	1521.454	0.448	26	0.165	R.FIDIPEEVAEVYK.L
R3/RRR3-9/2	1259.089	1258.440	-279.631	0.415	691.344	0.534	17	0.160	K.AVEPAACPTLTK.G
R3/RRR3-9/2	1258.005	1258.440	-346.442	0.359	589.198	0.495	16	0.149	K.AVEPAACPTLTK.G
R3/RRR3-8/2	1553.401	1552.749	-224.759	0.438	455.661	0.375	16	0.141	R.FIDIPEEVAEVYK.L
R3/RRR3-3/2	1553.979	1552.749	148.075	0.424	495.935	0.340	16	0.139	R.FIDIPEEVAEVYK.L
R3/RRR3-7/2	1612.224	1612.810	-986.693	0.433	1271.619	0.560	20	0.208	K.VLEPLFSYWNSTR.Q
R3/RRR3-7/2	1613.389	1612.810	-261.632	0.523	1175.122	0.539	20	0.197	K.VLEPLFSYWNSTR.Q
R3/RRR3-7/3	1338.855	1338.538	237.701	0.628	1560.888	0.517	27	0.186	K.VGIKDHESVVVR.I
R3/RRR3-7/2	1612.337	1612.810	-294.076	0.474	1034.438	0.463	19	0.171	K.VLEPLFSYWNSTR.Q
R3/RRR3-7/3	1244.387	1244.385	1.922	0.561	1129.206	0.469	22	0.133	R.THRVETTFPR.L
R3/RRR3-7/3	1338.748	1338.538	157.467	0.575	990.336	0.488	23	0.129	K.VGIKDHESVVVR.I
R3/RRR3-7/3	1337.270	1338.538	-1700.830	0.472	810.328	0.423	21	0.108	K.VGIKDHESVVVR.I
R3/RRR3-6/3	1244.785	1244.385	322.893	0.471	677.920	0.427	18	0.106	R.THRVETTFPR.L
R3/RRR3-6/2	1650.536	1650.856	-194.767	0.509	1555.732	0.442	22	0.215	R.QFLTLNALNEFDPK.I
R3/RRR3-6/2	1651.107	1650.856	152.268	0.555	1501.050	0.439	21	0.207	R.QFLTLNALNEFDPK.I
R3/RRR3-6/2	1649.543	1650.856	-1406.377	0.311	1038.731	0.265	19	0.143	R.QFLTLNALNEFDPK.I
R3/RRR3-6/3	1340.086	1340.512	-319.020	0.454	1205.660	0.362	23	0.116	R.SIHSWDIVVQR.V
R3/RRR3-6/3	1439.090	1439.510	-292.436	0.401	983.058	0.378	26	0.107	R.CEVHAVNADPGGGR.Q
R3/RRR3-6/3	1439.681	1439.510	119.213	0.405	589.527	0.470	22	0.107	R.CEVHAVNADPGGGR.Q
R3/RRR3-6/3	1438.796	1439.510	-1194.732	0.377	680.880	0.373	23	0.098	R.CEVHAVNADPGGGR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1340.382	1340.512	-97.256	0.492	1216.828	0.221	23	0.093	R.SIHSWDIVVQR.V
R3/RRR3-6/3	1340.593	1340.512	60.166	0.457	1040.090	0.237	22	0.090	R.SIHSWDIVVQR.V
R3/RRR3-7/2	1274.089	1274.492	-317.468	0.439	1722.558	0.478	19	0.244	R.LASALVSSLGISR.G
R3/RRR3-7/2	1466.632	1466.835	-138.964	0.437	1502.715	0.517	20	0.224	K.LIFVDPALLPVLR.D
R3/RRR3-7/2	1273.300	1274.492	-1727.132	0.340	1715.301	0.386	20	0.221	R.LASALVSSLGISR.G
R3/RRR3-7/2	1275.534	1274.492	33.249	0.425	1258.586	0.564	18	0.206	R.LASALVSSLGISR.G
R3/RRR3-6/2	1307.602	1307.434	128.503	0.428	1392.009	0.321	19	0.175	R.VDAAEVFDTIAR.R
R3/RRR3-7/2	1465.807	1466.835	-1388.294	0.355	1162.109	0.437	18	0.174	K.LIFVDPALLPVLR.D
R3/RRR3-2/2	1466.586	1466.835	-170.525	0.458	897.871	0.494	17	0.166	K.LIFVDPALLPVLR.D
R3/RRR3-7/2	1466.535	1466.835	-205.679	0.408	1014.618	0.435	17	0.164	K.LIFVDPALLPVLR.D
R3/RRR3-7/2	1466.406	1466.835	-293.784	0.352	1017.702	0.415	17	0.161	K.LIFVDPALLPVLR.D
R3/RRR3-2/2	1467.286	1466.835	308.275	0.401	892.216	0.449	16	0.159	K.LIFVDPALLPVLR.D
R3/RRR3-7/2	1466.225	1466.835	-1101.560	0.357	707.606	0.417	14	0.146	K.LIFVDPALLPVLR.D
R3/RRR3-4/2	1466.185	1466.835	-1129.064	0.312	768.731	0.392	15	0.145	K.LIFVDPALLPVLR.D
R3/RRR3-1/2	1466.443	1466.835	-268.395	0.372	634.209	0.410	14	0.144	K.LIFVDPALLPVLR.D
R3/RRR3-3/2	1465.892	1466.835	-1329.579	0.215	363.240	0.328	13	0.135	K.LIFVDPALLPVLR.D
R3/RRR3-1/2	1466.536	1466.835	-205.011	0.339	364.644	0.303	11	0.133	-.LIFVDPALLPVLR.-
R3/RRR3-9/2	1466.549	1466.835	-195.742	0.227	535.227	0.220	13	0.129	-.LIFVDPALLPVLR.-
R3/RRR3-11/2	1558.570	1558.868	-192.361	0.472	1472.238	0.469	20	0.210	K.GAALNAVQIAEM*LLK.-
R3/RRR3-11/3	1997.579	1998.189	-808.001	0.435	1538.119	0.535	30	0.198	R.AHAPAAVASGAVVVDNSSAFR.M
R3/RRR3-11/2	1159.959	1160.260	-260.251	0.549	1253.302	0.494	18	0.196	R.AAEGVTIIDDR.A
R3/RRR3-11/3	1997.426	1998.189	-885.022	0.443	1555.182	0.511	29	0.193	R.AHAPAAVASGAVVVDNSSAFR.M
R3/RRR3-11/2	1159.499	1160.260	-1522.840	0.421	1174.954	0.429	17	0.176	R.AAEGVTIIDDR.A
R3/RRR3-11/2	1160.043	1160.260	-187.406	0.493	1148.041	0.431	17	0.175	R.AAEGVTIIDDR.A
R3/RRR3-12/2	1150.039	1150.306	-233.325	0.474	839.124	0.458	16	0.162	K.LIDQAVEYAK.K
R3/RRR3-12/2	1149.974	1150.306	-290.086	0.362	671.123	0.363	15	0.143	K.LIDQAVEYAK.K
R3/RRR3-12/2	1149.175	1150.306	-1859.772	0.280	645.710	0.307	14	0.136	K.LIDQAVEYAK.K
R3/RRR3-12/3	1560.298	1558.759	-296.202	0.436	952.803	0.433	27	0.113	K.KLDADGAAALDIEKK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/3	1697.922	1697.788	79.052	0.364	1020.818	0.356	28	0.103	K.KHGGSVDEQVDAALDR.L
R3/RRR3-4/2	1729.833	1729.912	-45.908	0.472	2095.239	0.440	22	0.290	R.ISEAFSGSSLISDFIR.S
R3/RRR3-4/2	1730.260	1729.912	202.124	0.518	1752.305	0.462	20	0.241	R.ISEAFSGSSLISDFIR.S
R3/RRR3-4/2	1729.714	1729.912	-114.926	0.458	1653.842	0.437	20	0.223	R.ISEAFSGSSLISDFIR.S
R3/RRR3-4/2	1027.887	1027.243	-346.577	0.446	1232.956	0.446	17	0.185	R.VLGGVIIEAR.E
R3/RRR3-4/2	1299.791	1299.414	291.294	0.396	1022.815	0.411	15	0.161	K.EAEISQFFATR.T
R3/RRR3-4/2	1027.433	1027.243	185.471	0.332	851.779	0.335	14	0.143	R.VLGGVIIEAR.E
R3/RRR3-4/2	1299.355	1299.414	-45.758	0.353	774.921	0.362	14	0.142	K.EAEISQFFATR.T
R3/RRR3-9/2	1254.417	1254.504	-69.749	0.545	1498.861	0.547	19	0.233	K.INNAVAQVLLAK.R
R3/RRR3-9/2	1254.104	1254.504	-320.184	0.463	1045.854	0.482	16	0.173	K.INNAVAQVLLAK.R
R3/RRR3-9/2	1951.055	1949.235	-92.447	0.423	846.216	0.448	16	0.149	R.FGLQCIIYM*GAQDMER.Q
R3/RRR3-9/2	1253.351	1254.504	-1722.580	0.392	411.472	0.427	15	0.143	K.INNAVAQVLLAK.R
R3/RRR3-9/3	1984.937	1984.197	-131.151	0.522	1092.547	0.526	30	0.143	R.IIAETGAGQHGVATATVCAR.F
R3/RRR3-8/2	1486.185	1486.693	-1017.646	0.442	1183.646	0.562	19	0.199	R.VADPTFLGYFIDK.G
R3/RRR3-8/2	1486.227	1486.693	-314.086	0.450	1082.034	0.558	18	0.189	R.VADPTFLGYFIDK.G
R3/RRR3-8/2	1485.736	1486.693	-1320.556	0.299	1312.797	0.428	19	0.184	R.VADPTFLGYFIDK.G
R3/RRR3-8/2	1453.240	1453.453	-147.406	0.477	732.638	0.534	18	0.160	K.NANGATYDTPDSAR.L
R3/RRR3-8/2	1091.546	1092.230	-1547.650	0.427	795.451	0.300	13	0.138	K.SLFQLQAER.I
R3/RRR3-2/2	1873.257	1873.998	-931.881	0.428	1316.512	0.366	18	0.171	K.SSSSEADFEQQLYILR.R
R3/RRR3-2/2	1899.393	1900.130	-916.995	0.500	629.148	0.571	18	0.155	K.NTGDGAGILVALPHNFFR.E
R3/RRR3-2/3	1438.882	1437.671	147.317	0.524	882.097	0.523	26	0.128	K.VAESLGHVILGWR.W
R3/RRR3-2/3	1437.437	1437.671	-163.090	0.473	829.613	0.524	25	0.124	K.VAESLGHVILGWR.W
R3/RRR3-2/3	1437.246	1437.671	-296.772	0.456	734.983	0.500	24	0.116	K.VAESLGHVILGWR.W
R3/RRR3-10/1	1039.677	1040.238	-1506.673	0.302	919.053	0.320	13	0.913	R.IIGVDLNPAK.F
R3/RRR3-10/2	1184.978	1185.304	-276.248	0.509	1715.004	0.422	16	0.230	K.FGCTDFVNPK.D
R3/RRR3-10/2	1184.952	1185.304	-298.366	0.454	1569.958	0.445	16	0.218	K.FGCTDFVNPK.D
R3/RRR3-10/2	1184.334	1185.304	-1668.721	0.407	1406.937	0.406	16	0.193	K.FGCTDFVNPK.D
R3/RRR3-10/2	1039.759	1040.238	-462.259	0.399	555.591	0.476	15	0.151	R.IIGVDLNPAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1040.110	1040.238	-123.319	0.425	581.956	0.417	16	0.149	R.IIGVDLNPAK.F
R3/RRR3-10/2	1989.940	1990.316	-189.358	0.389	375.096	0.492	21	0.141	K.GQTVAIFGLGAVGLAAMEGAR.L
R3/RRR3-9/2	1040.183	1040.238	-53.628	0.294	529.694	0.314	15	0.137	R.IIGVDLNPAK.F
R3/RRR3-8/2	1990.130	1990.316	-93.797	0.347	156.382	0.417	16	0.132	-.GQTVAIFGLGAVGLAAMEGAR.-
R3/RRR3-12/2	1826.493	1826.237	140.612	0.599	2632.657	0.621	27	0.455	K.VAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/2	1825.455	1826.237	-979.072	0.568	2515.474	0.559	26	0.404	K.VAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/2	1809.187	1810.238	-1136.776	0.544	2417.241	0.508	29	0.367	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/2	1810.434	1810.238	108.570	0.586	2284.604	0.559	27	0.356	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/2	1809.717	1810.238	-842.685	0.596	2228.655	0.563	27	0.346	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/3	1809.870	1810.238	-204.012	0.442	2277.967	0.550	34	0.337	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/2	1824.821	1826.237	-1327.702	0.445	2195.354	0.475	25	0.314	K.VAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/3	1825.864	1826.237	-204.824	0.474	2182.430	0.470	35	0.280	K.VAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/3	1811.068	1810.238	-93.884	0.521	1863.952	0.539	34	0.247	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/2	1827.632	1826.237	216.493	0.536	1350.384	0.539	23	0.207	K.VAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/3	1954.234	1954.410	-90.532	0.449	1717.267	0.414	33	0.185	R.KVAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/2	1810.350	1810.238	62.044	0.451	1427.819	0.382	21	0.183	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/2	1810.299	1810.238	34.249	0.455	1347.907	0.405	21	0.180	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/2	1809.725	1810.238	-838.487	0.343	1310.731	0.297	20	0.160	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-11/2	1810.618	1810.238	210.599	0.367	840.808	0.422	19	0.149	K.VAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/2	1826.580	1826.237	188.197	0.409	368.492	0.411	20	0.142	K.VAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/3	1954.375	1954.410	-17.791	0.480	1087.488	0.457	31	0.129	R.KVAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/3	1937.771	1938.411	-848.388	0.368	816.129	0.356	29	0.099	R.KVAILGAAGGIGQPLSLLMK.L
R3/RRR3-12/3	1953.383	1954.410	-1040.663	0.342	896.730	0.295	27	0.094	R.KVAILGAAGGIGQPLSLLM*K.L
R3/RRR3-12/3	1937.861	1938.411	-802.005	0.357	702.105	0.334	26	0.089	-.KVAILGAAGGIGQPLSLLMK.-
R3/RRR3-12/3	1825.491	1826.237	-959.341	0.283	453.383	0.364	23	0.088	-.VAILGAAGGIGQPLSLLM*K.-
R3/RRR3-11/3	1514.156	1513.812	227.404	0.589	3479.289	0.552	38	0.666	K.HLGVVGLGGLGHLGVK.F
R3/RRR3-11/3	1513.793	1513.812	-12.635	0.579	3349.581	0.559	37	0.628	K.HLGVVGLGGLGHLGVK.F
R3/RRR3-11/3	1513.879	1513.812	44.019	0.578	3275.948	0.545	36	0.597	K.HLGVVGLGGLGHLGVK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1513.256	1513.812	-1031.724	0.521	2332.665	0.570	25	0.377	K.HLGVVGLGGLGHLGVK.F
R3/RRR3-11/2	1513.606	1513.812	-137.078	0.502	2260.240	0.549	25	0.355	K.HLGVVGLGGLGHLGVK.F
R3/RRR3-11/2	1512.800	1513.812	-1334.161	0.459	2285.513	0.521	25	0.351	K.HLGVVGLGGLGHLGVK.F
R3/RRR3-2/3	1514.053	1513.812	159.128	0.496	1830.263	0.493	31	0.222	K.HLGVVGLGGLGHLGVK.F
R3/RRR3-5/2	1517.002	1517.662	-1097.376	0.300	1896.858	0.367	21	0.242	K.DIYYIAADSLSSAK.H
R3/RRR3-5/2	1486.453	1485.625	-115.860	0.561	1266.361	0.506	21	0.197	R.GVVDSNDLPLNVSR.E
R3/RRR3-5/2	1485.341	1485.625	-191.782	0.487	1282.648	0.409	21	0.181	R.GVVDSNDLPLNVSR.E
R3/RRR3-5/2	1485.312	1485.625	-210.828	0.494	1029.690	0.427	19	0.164	R.GVVDSNDLPLNVSR.E
R3/RRR3-5/2	1657.233	1657.804	-951.104	0.452	1073.523	0.369	18	0.156	R.VFISDDFDGELFPR.Y
R3/RRR3-2/2	1486.265	1485.625	-242.491	0.269	382.335	0.352	14	0.135	R.GVVDSNDLPLNVSR.E
R3/RRR3-2/2	1486.205	1485.625	-283.444	0.265	623.155	0.325	15	0.135	R.GVVDSNDLPLNVSR.E
R3/RRR3-2/2	1486.145	1485.625	-323.825	0.312	678.069	0.243	16	0.132	R.GVVDSNDLPLNVSR.E
R3/RRR3-10/2	1356.154	1356.467	-231.719	0.490	1401.587	0.501	18	0.209	K.TLEAEAAHGTVTR.H
R3/RRR3-10/2	1357.108	1356.467	-265.569	0.541	996.786	0.614	19	0.195	K.TLEAEAAHGTVTR.H
R3/RRR3-10/2	1356.152	1356.467	-232.713	0.500	984.273	0.587	19	0.188	K.TLEAEAAHGTVTR.H
R3/RRR3-10/2	1774.203	1775.079	-1060.577	0.537	1100.570	0.478	18	0.174	R.NILNGTVFREPILCK.N
R3/RRR3-10/2	1774.553	1775.079	-862.350	0.550	1200.766	0.420	19	0.172	R.NILNGTVFREPILCK.N
R3/RRR3-10/2	1775.593	1775.079	-274.139	0.555	811.438	0.538	20	0.168	R.NILNGTVFREPILCK.N
R3/RRR3-10/2	1774.433	1775.079	-930.443	0.524	1139.998	0.395	19	0.164	R.NILNGTVFREPILCK.N
R3/RRR3-10/2	1776.640	1775.079	-247.446	0.501	673.907	0.416	19	0.147	R.NILNGTVFREPILCK.N
R3/RRR3-9/2	1311.276	1311.466	-145.531	0.496	1063.765	0.466	19	0.174	K.IINQDPPALSDK.S
R3/RRR3-9/2	1295.006	1294.439	-335.315	0.362	570.321	0.465	14	0.144	R.VLYSDKDVQAR.R
R3/RRR3-9/2	1155.176	1154.362	-160.851	0.306	839.257	0.376	14	0.143	K.SVISAMEFAAK.Q
R3/RRR3-17/3	1980.788	1981.147	-181.463	0.588	2792.539	0.644	38	0.508	K.DLSVIATEVGEEGQEYLK.L
R3/RRR3-17/3	1981.089	1981.147	-29.401	0.551	2305.140	0.608	34	0.365	K.DLSVIATEVGEEGQEYLK.L
R3/RRR3-17/2	1982.265	1981.147	60.061	0.571	1570.456	0.556	21	0.238	K.DLSVIATEVGEEGQEYLK.L
R3/RRR3-17/2	1981.435	1981.147	146.224	0.571	1539.720	0.566	21	0.236	K.DLSVIATEVGEEGQEYLK.L
R3/RRR3-17/3	1980.411	1981.147	-878.993	0.382	1016.806	0.446	28	0.121	K.DLSVIATEVGEEGQEYLK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/3	1244.990	1245.408	-336.602	0.444	1009.656	0.373	20	0.108	R.AREVLLEASEK.L
R3/RRR3-17/3	1245.463	1245.408	44.855	0.497	1194.564	0.227	21	0.093	R.AREVLLEASEK.L
R3/RRR3-17/3	1245.602	1245.408	156.464	0.442	914.240	0.211	18	0.077	-.AREVLLEASEK.-
R3/RRR3-5/2	1337.175	1337.421	-184.007	0.484	1593.654	0.588	21	0.254	R.NVGSNANAVYEAK.I
R3/RRR3-6/2	1337.318	1337.421	-77.053	0.519	1570.344	0.572	21	0.248	R.NVGSNANAVYEAK.I
R3/RRR3-5/2	1488.156	1488.622	-314.337	0.461	1640.193	0.520	23	0.244	K.IDSPSGVDVTVSPSK.L
R3/RRR3-5/2	1337.149	1337.421	-203.789	0.485	1583.499	0.531	21	0.239	R.NVGSNANAVYEAK.I
R3/RRR3-6/2	1337.108	1337.421	-234.379	0.462	1500.595	0.539	21	0.230	R.NVGSNANAVYEAK.I
R3/RRR3-6/2	1337.026	1337.421	-295.656	0.467	1380.214	0.545	20	0.217	R.NVGSNANAVYEAK.I
R3/RRR3-5/2	1487.989	1488.622	-1100.670	0.391	1356.790	0.480	22	0.200	K.IDSPSGVDVTVSPSK.L
R3/RRR3-6/2	1846.072	1846.072	0.026	0.484	742.472	0.574	21	0.165	R.TGDLNYPAFAVVLSSYK.D
R3/RRR3-4/2	1570.364	1570.682	-202.918	0.528	1621.203	0.530	22	0.245	K.VFDAILDDQFGDSK.N
R3/RRR3-4/2	1386.904	1387.518	-1166.680	0.427	1500.514	0.397	19	0.199	K.VVNADEDVGDLLK.V
R3/RRR3-4/2	1313.171	1313.480	-236.693	0.376	693.626	0.352	13	0.137	K.VVFLEDYNVSK.A
R3/RRR3-8/2	1819.840	1818.148	-169.853	0.507	900.480	0.629	23	0.186	R.TSIPGIFAIGDVAAFPLK.M
R3/RRR3-9/2	1817.707	1818.148	-243.472	0.458	847.088	0.546	22	0.168	R.TSIPGIFAIGDVAAFPLK.M
R3/RRR3-8/2	1817.527	1818.148	-894.640	0.433	672.327	0.524	20	0.155	R.TSIPGIFAIGDVAAFPLK.M
R3/RRR3-8/2	1817.622	1818.148	-842.523	0.423	683.559	0.503	21	0.154	R.TSIPGIFAIGDVAAFPLK.M
R3/RRR3-9/2	1362.234	1362.468	-172.803	0.427	1015.198	0.298	17	0.145	K.SATSVEDALEIAR.S
R3/RRR3-9/2	1498.204	1499.650	-1637.518	0.308	973.834	0.245	20	0.139	K.KYEELYQQNGVK.F
R3/RRR3-9/2	1362.106	1362.468	-267.021	0.300	625.594	0.137	15	0.125	K.SATSVEDALEIAR.S
R3/RRR3-8/2	1309.375	1310.445	-1585.385	0.441	866.969	0.537	18	0.173	R.RGPEWFASFGR.K
R3/RRR3-8/2	1310.415	1310.445	-23.042	0.458	786.955	0.487	17	0.161	R.RGPEWFASFGR.K
R3/RRR3-8/2	1577.041	1576.841	127.338	0.479	642.838	0.457	21	0.150	K.AVQSGLGTAAVIVM*DK.S
R3/RRR3-8/3	1349.718	1349.518	149.202	0.389	1629.786	0.299	26	0.138	K.AREEAYAAGLLGK.N
R3/RRR3-8/2	1561.549	1560.841	-187.676	0.147	128.821	0.480	17	0.124	-.AVQSGLGTAAVIVMDK.-
R3/RRR3-8/2	1577.968	1576.841	81.252	0.034	82.972	0.513	16	0.109	-.AVQSGLGTAAVIVM*DK.-
R3/RRR3-8/2	1735.557	1735.016	-265.507	0.413	562.047	0.533	20	0.150	K.APPPPALPSAPLFTTEK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1035.899	1035.219	-309.030	0.293	882.077	0.362	16	0.145	K.VLAEAFAVSK.D
R3/RRR3-8/3	1189.427	1190.335	-1609.552	0.456	934.025	0.443	18	0.115	R.RPDYFNHIK.S
R3/RRR3-8/3	1190.314	1190.335	-17.715	0.474	1016.071	0.388	18	0.110	R.RPDYFNHIK.S
R3/RRR3-7/2	1098.976	1099.306	-301.097	0.333	888.896	0.369	14	0.148	R.DLVLQLLER.I
R3/RRR3-6/2	1497.389	1497.679	-193.837	0.286	1024.581	0.294	16	0.143	R.SFASVSAAQFPWAK.M
R3/RRR3-7/2	1497.135	1497.679	-1034.411	0.343	699.807	0.340	14	0.135	R.SFASVSAAQFPWAK.M
R3/RRR3-6/3	1506.946	1506.598	231.621	0.508	1103.014	0.452	26	0.129	R.TKNEAALEAATDSGK.Q
R3/RRR3-6/3	1506.775	1506.598	118.415	0.437	1007.966	0.350	25	0.105	R.TKNEAALEAATDSGK.Q
R3/RRR3-6/3	1506.121	1506.598	-317.222	0.460	785.612	0.345	26	0.098	R.TKNEAALEAATDSGK.Q
R3/RRR3-8/3	1506.459	1506.598	-92.468	0.380	493.928	0.338	23	0.097	R.TKNEAALEAATDSGK.Q
R3/RRR3-7/3	1506.254	1506.598	-228.918	0.352	941.789	0.188	25	0.084	R.TKNEAALEAATDSGK.Q
R3/RRR3-20/2	1537.553	1536.708	-101.100	0.524	1583.200	0.559	22	0.247	R.NDLLTDGTFALVEK.L
R3/RRR3-17/2	1448.234	1448.520	-197.626	0.501	1362.347	0.529	19	0.212	R.SPSAYLNNPAEER.S
R3/RRR3-17/2	1448.068	1448.520	-313.231	0.542	1150.421	0.548	18	0.194	R.SPSAYLNNPAEER.S
R3/RRR3-17/2	1447.607	1448.520	-1325.228	0.463	1178.942	0.479	18	0.184	R.SPSAYLNNPAEER.S
R3/RRR3-17/3	1631.677	1631.858	-111.297	0.484	1370.171	0.416	27	0.142	K.IFVNKGDLLDAGVNR.S
R3/RRR3-17/3	1631.303	1631.858	-955.947	0.267	1168.984	0.258	25	0.097	K.IFVNKGDLLDAGVNR.S
R3/RRR3-17/3	1631.379	1631.858	-294.029	0.394	968.751	0.228	25	0.087	-.IFVNKGDLLDAGVNR.-
R3/RRR3-6/2	1454.775	1453.621	106.245	0.370	1615.862	0.457	21	0.225	R.IWLDYADASAISK.G
R3/RRR3-6/2	1761.415	1761.997	-900.618	0.506	1289.127	0.536	21	0.202	K.LSFSQDSPPISIISAAK.V
R3/RRR3-6/2	1761.638	1761.997	-204.377	0.516	1047.243	0.535	21	0.180	K.LSFSQDSPPISIISAAK.V
R3/RRR3-6/2	1017.280	1017.206	72.321	0.350	717.400	0.305	12	0.135	R.FPTVQGIVR.R
R3/RRR3-6/2	1454.750	1453.621	88.909	0.167	634.697	0.241	13	0.125	R.IWLDYADASAISK.G
R3/RRR3-5/2	1933.756	1934.140	-199.166	0.534	1190.472	0.589	24	0.203	R.ALSEVAGAQLPYDSLSGVR.D
R3/RRR3-6/2	1364.146	1363.541	-290.676	0.434	968.518	0.467	18	0.166	R.ANVILPSSAFSEK.E
R3/RRR3-5/2	1270.320	1269.516	-154.271	0.380	727.375	0.508	15	0.155	R.SVVDKNLGPLVK.T
R3/RRR3-5/2	1269.273	1269.516	-191.632	0.392	680.944	0.430	15	0.146	R.SVVDKNLGPLVK.T
R3/RRR3-5/2	1364.300	1363.541	-177.028	0.358	745.309	0.332	16	0.138	R.ANVILPSSAFSEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1542.344	1542.718	-243.359	0.508	1725.437	0.430	22	0.234	R.FGPIIEQNVDPANK.G
R3/RRR3-4/2	1200.241	1200.453	-177.254	0.450	1472.516	0.371	17	0.192	K.LLDSIVALLSR.T
R3/RRR3-4/2	1102.970	1103.210	-218.195	0.429	965.303	0.587	15	0.185	R.TSGYSVSFVR.L
R3/RRR3-4/2	1103.148	1103.210	-56.228	0.411	865.914	0.541	15	0.171	R.TSGYSVSFVR.L
R3/RRR3-4/2	1200.242	1200.453	-176.131	0.355	833.986	0.358	15	0.146	K.LLDSIVALLSR.T
R3/RRR3-4/2	1200.152	1200.453	-252.046	0.384	737.832	0.235	16	0.134	K.LLDSIVALLSR.T
R3/RRR3-7/2	1646.791	1647.806	-1227.019	0.373	2634.968	0.438	24	0.397	R.TEEELIEAIATATGAK.K
R3/RRR3-7/2	1648.286	1647.806	292.028	0.503	2392.849	0.558	24	0.385	R.TEEELIEAIATATGAK.K
R3/RRR3-7/2	1647.143	1647.806	-1012.605	0.378	2232.434	0.442	23	0.316	R.TEEELIEAIATATGAK.K
R3/RRR3-7/2	1901.777	1903.124	-1237.553	0.521	1773.467	0.547	23	0.268	K.VRTEEELIEAIATATGAK.K
R3/RRR3-7/3	1648.622	1647.806	-112.047	0.420	1028.795	0.392	25	0.111	R.TEEELIEAIATATGAK.K
R3/RRR3-7/3	1648.112	1647.806	186.486	0.437	1036.199	0.364	25	0.107	R.TEEELIEAIATATGAK.K
R3/RRR3-7/2	1025.945	1026.213	-262.741	0.443	820.568	0.367	13	0.148	R.YLTVQFVR.F
R3/RRR3-7/2	1149.383	1149.322	53.943	0.420	649.780	0.407	14	0.146	K.ELFGIDLVSR.V
R3/RRR3-7/2	1149.119	1149.322	-176.828	0.353	560.519	0.309	12	0.134	K.ELFGIDLVSR.V
R3/RRR3-7/3	1503.749	1503.547	134.815	0.506	1227.869	0.333	24	0.113	R.VHCAESGEESLER.E
R3/RRR3-7/3	1503.479	1503.547	-45.215	0.498	1048.244	0.348	25	0.106	R.VHCAESGEESLER.E
R3/RRR3-10/3	1502.958	1503.547	-1060.472	0.468	988.805	0.355	22	0.104	-.VHCAESGEESLER.-
R3/RRR3-7/3	1502.945	1503.547	-1069.401	0.467	862.256	0.355	23	0.101	R.VHCAESGEESLER.E
R3/RRR3-13/2	1620.152	1620.872	-1064.691	0.487	2823.067	0.582	27	0.499	R.VVDVGGGTGFTTLGIVK.R
R3/RRR3-13/2	1621.319	1620.872	276.798	0.561	2736.141	0.573	27	0.472	R.VVDVGGGTGFTTLGIVK.R
R3/RRR3-13/2	1768.473	1768.907	-246.165	0.366	1037.321	0.454	17	0.163	R.YVSAGSIEYWPDPQR.G
R3/RRR3-7/2	1761.344	1761.957	-918.450	0.533	3006.079	0.514	26	0.516	K.YGLAADNVVDAVLVDAR.G
R3/RRR3-7/2	1762.333	1761.957	213.799	0.615	2380.641	0.552	24	0.377	K.YGLAADNVVDAVLVDAR.G
R3/RRR3-7/2	1761.228	1761.957	-984.622	0.533	2403.164	0.509	23	0.369	K.YGLAADNVVDAVLVDAR.G
R3/RRR3-8/2	1728.462	1728.972	-875.924	0.441	946.856	0.512	20	0.171	R.WQAVAPSLPDDLFIR.V
R3/RRR3-7/2	1728.177	1728.972	-1041.568	0.457	865.470	0.508	21	0.167	R.WQAVAPSLPDDLFIR.V
R3/RRR3-7/2	1728.518	1728.972	-263.047	0.453	869.997	0.480	21	0.163	R.WQAVAPSLPDDLFIR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1728.524	1728.972	-259.859	0.465	797.676	0.495	20	0.161	R.WQAVAPSLPDDLFIR.V
R3/RRR3-20/2	1116.031	1116.290	-232.865	0.555	2572.582	0.659	21	0.456	R.VVGAGGAVVACR.G
R3/RRR3-19/2	1115.950	1116.290	-305.623	0.570	2352.068	0.616	21	0.391	R.VVGAGGAVVACR.G
R3/RRR3-26/2	1117.148	1116.290	-127.200	0.547	2361.595	0.605	21	0.389	R.VVGAGGAVVACR.G
R3/RRR3-26/2	1116.102	1116.290	-168.786	0.534	2350.855	0.610	21	0.388	R.VVGAGGAVVACR.G
R3/RRR3-19/2	1116.145	1116.290	-130.386	0.564	2267.324	0.657	21	0.388	R.VVGAGGAVVACR.G
R3/RRR3-27/2	1115.939	1116.290	-315.391	0.555	2308.625	0.626	21	0.385	R.VVGAGGAVVACR.G
R3/RRR3-18/2	1115.992	1116.290	-267.981	0.562	2261.888	0.643	21	0.381	R.VVGAGGAVVACR.G
R3/RRR3-18/2	1115.944	1116.290	-310.452	0.539	2318.894	0.607	21	0.381	R.VVGAGGAVVACR.G
R3/RRR3-27/2	1115.440	1116.290	-1663.669	0.501	2242.711	0.649	20	0.379	R.VVGAGGAVVACR.G
R3/RRR3-20/2	1115.918	1116.290	-334.488	0.535	2116.048	0.679	21	0.365	R.VVGAGGAVVACR.G
R3/RRR3-19/2	1116.005	1116.290	-255.690	0.550	2186.390	0.630	21	0.362	R.VVGAGGAVVACR.G
R3/RRR3-20/2	1115.840	1116.290	-404.626	0.537	2172.108	0.616	21	0.355	R.VVGAGGAVVACR.G
R3/RRR3-26/2	1115.402	1116.290	-1697.534	0.433	2161.636	0.586	20	0.341	R.VVGAGGAVVACR.G
R3/RRR3-27/2	1115.608	1116.290	-1511.635	0.491	2111.557	0.600	21	0.338	R.VVGAGGAVVACR.G
R3/RRR3-19/2	1674.355	1673.852	-297.442	0.548	1628.798	0.592	22	0.257	R.GLVSYDFPASFWAGR.V
R3/RRR3-19/2	1673.357	1673.852	-296.669	0.518	1579.434	0.564	20	0.242	R.GLVSYDFPASFWAGR.V
R3/RRR3-19/2	1675.089	1673.852	141.901	0.579	1359.552	0.586	21	0.222	R.GLVSYDFPASFWAGR.V
R3/RRR3-20/2	1673.349	1673.852	-900.457	0.496	1341.983	0.567	21	0.216	R.GLVSYDFPASFWAGR.V
R3/RRR3-19/2	1673.154	1673.852	-1017.718	0.525	1396.541	0.538	21	0.215	R.GLVSYDFPASFWAGR.V
R3/RRR3-19/2	1673.096	1673.852	-1052.660	0.465	1371.043	0.549	21	0.215	R.GLVSYDFPASFWAGR.V
R3/RRR3-20/2	1673.214	1673.852	-981.460	0.474	1272.896	0.559	19	0.205	R.GLVSYDFPASFWAGR.V
R3/RRR3-20/2	1673.410	1673.852	-264.612	0.516	1154.803	0.587	20	0.201	R.GLVSYDFPASFWAGR.V
R3/RRR3-14/2	1117.289	1116.290	-0.944	0.398	1165.155	0.568	18	0.197	R.VVGAGGAVVACR.G
R3/RRR3-19/2	1115.733	1116.290	-1399.755	0.379	1046.184	0.567	18	0.187	R.VVGAGGAVVACR.G
R3/RRR3-20/2	1673.423	1673.852	-257.148	0.482	1025.809	0.544	19	0.181	R.GLVSYDFPASFWAGR.V
R3/RRR3-18/2	1673.409	1673.852	-265.052	0.425	1121.423	0.465	18	0.174	R.GLVSYDFPASFWAGR.V
R3/RRR3-6/2	1116.037	1116.290	-227.159	0.277	773.436	0.534	18	0.160	R.VVGAGGAVVACR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1116.899	1116.290	-351.076	0.306	390.799	0.425	15	0.145	R.VVGAGGAVVACR.G
R3/RRR3-17/2	1115.250	1116.290	-1834.667	0.274	640.393	0.383	16	0.143	R.VVGAGGAVVACR.G
R3/RRR3-18/2	1674.436	1673.852	-249.095	0.365	580.732	0.422	17	0.143	-.GLVSYDFPASFWAGR.-
R3/RRR3-19/2	1116.825	1116.290	-417.535	0.269	295.219	0.445	14	0.140	-.VVGAGGAVVACR.-
R3/RRR3-2/2	1675.289	1673.852	262.034	0.384	536.430	0.393	15	0.140	R.GLVSYDFPASFWAGR.V
R3/RRR3-4/2	1116.811	1116.290	-430.257	0.190	388.128	0.379	16	0.138	R.VVGAGGAVVACR.G
R3/RRR3-4/2	1674.928	1673.852	45.716	0.329	421.021	0.351	15	0.138	R.GLVSYDFPASFWAGR.V
R3/RRR3-1/2	1674.946	1673.852	56.826	0.399	553.447	0.356	14	0.137	R.GLVSYDFPASFWAGR.V
R3/RRR3-4/2	1116.875	1116.290	-372.131	0.158	358.974	0.411	16	0.136	R.VVGAGGAVVACR.G
R3/RRR3-19/2	1116.385	1116.290	85.477	0.203	369.330	0.347	15	0.136	-.VVGAGGAVVACR.-
R3/RRR3-7/2	1291.373	1291.478	-81.595	0.521	1095.843	0.423	15	0.167	K.VQDIVSQIFNK.T
R3/RRR3-9/2	1711.755	1710.995	-140.737	0.503	2934.843	0.485	24	0.491	R.VIYGADLAAFLQTLSK.I
R3/RRR3-9/2	1680.071	1678.863	124.282	0.476	966.867	0.558	18	0.178	R.VGYTFTTDALDALYK.K
R3/RRR3-17/2	1678.983	1678.863	71.785	0.296	155.818	0.384	11	0.126	-.VGYTFTTDALDALYK.-
R3/RRR3-7/2	1892.050	1891.160	-57.891	0.485	909.807	0.474	20	0.159	R.EGINIFLAGFVPTENLR.F
R3/RRR3-7/3	1144.017	1143.274	-225.468	0.555	1521.295	0.314	24	0.122	R.FRDESLTFK.I
R3/RRR3-7/3	1144.356	1143.274	71.982	0.550	1400.061	0.315	24	0.114	R.FRDESLTFK.I
R3/RRR3-7/3	1756.711	1756.899	-107.069	0.321	690.863	0.478	23	0.108	K.AVQGNVGQVLDQKDER.G
R3/RRR3-7/3	1756.902	1756.899	1.762	0.389	561.367	0.466	23	0.105	K.AVQGNVGQVLDQKDER.G
R3/RRR3-7/3	1756.964	1756.899	37.406	0.329	864.781	0.339	26	0.097	K.AVQGNVGQVLDQKDER.G
R3/RRR3-7/3	1144.166	1143.274	-94.941	0.404	758.022	0.172	20	0.086	R.FRDESLTFK.I
R3/RRR3-7/2	1054.874	1055.250	-357.443	0.259	799.275	0.322	12	0.135	K.APSSEILPIK.F
R3/RRR3-7/3	1836.893	1837.026	-72.334	0.445	776.673	0.458	28	0.110	R.SFLQSHGLQDTQIYAK.V
R3/RRR3-7/3	1314.764	1314.553	160.898	0.301	1044.470	0.238	21	0.087	K.CNLAGKPAIITR.V
R3/RRR3-4/2	1617.121	1617.821	-1054.875	0.463	688.520	0.538	18	0.157	R.SAPGAALWCDVQLTK.D
R3/RRR3-4/2	1668.424	1668.955	-920.140	0.416	513.177	0.531	18	0.151	R.FDPLPIVPVEDVLSK.Y
R3/RRR3-4/2	1669.228	1668.955	164.257	0.408	634.656	0.475	20	0.151	R.FDPLPIVPVEDVLSK.Y
R3/RRR3-4/2	1668.413	1668.955	-926.677	0.314	572.063	0.453	19	0.144	R.FDPLPIVPVEDVLSK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1226.978	1227.432	-371.369	0.336	992.664	0.372	15	0.151	K.GILDVLSGDLPK.S
R3/RRR3-5/2	1417.297	1416.562	-187.945	0.415	633.989	0.454	16	0.144	R.GVGAQGIELSETVR.R
R3/RRR3-5/2	1343.447	1343.468	-16.096	0.299	910.249	0.331	18	0.142	R.VNLATGDAVPETR.S
R3/RRR3-19/2	1567.243	1567.727	-310.193	0.516	2611.575	0.513	23	0.418	K.LQLNDFTGAVFEGR.L
R3/RRR3-19/2	1567.743	1567.727	10.105	0.478	2472.564	0.513	22	0.387	K.LQLNDFTGAVFEGR.L
R3/RRR3-19/2	1567.944	1567.727	138.792	0.530	1989.244	0.518	21	0.295	K.LQLNDFTGAVFEGR.L
R3/RRR3-19/2	1131.790	1132.209	-371.987	0.384	769.975	0.370	17	0.143	K.NSDVAAAVAGTR.W
R3/RRR3-6/2	1558.446	1558.759	-201.170	0.408	1552.506	0.478	19	0.220	K.TFGSSADIFAGIFPK.N
R3/RRR3-9/2	1559.916	1558.759	100.968	0.459	1161.783	0.475	18	0.179	K.TFGSSADIFAGIFPK.N
R3/RRR3-6/3	1365.310	1364.574	-194.125	0.494	1718.758	0.385	24	0.168	R.FIKEEFGQIPR.I
R3/RRR3-9/2	1560.070	1558.759	200.394	0.471	1092.802	0.436	18	0.167	K.TFGSSADIFAGIFPK.N
R3/RRR3-6/3	1724.515	1723.909	-229.196	0.497	913.241	0.609	29	0.146	R.IPVISDSIVVHDSEGR.E
R3/RRR3-6/3	1723.880	1723.909	-16.813	0.403	874.810	0.559	27	0.131	R.IPVISDSIVVHDSEGR.E
R3/RRR3-6/3	1364.082	1364.574	-361.473	0.491	1142.491	0.400	23	0.119	R.FIKEEFGQIPR.I
R3/RRR3-6/3	1364.295	1364.574	-204.994	0.501	697.221	0.368	20	0.101	R.FIKEEFGQIPR.I
R3/RRR3-11/2	1855.720	1855.084	-196.852	0.624	2597.781	0.630	25	0.462	R.HVAETLGIDLEPLYQR.I
R3/RRR3-11/2	1773.654	1773.106	-255.732	0.510	428.318	0.589	20	0.155	K.LVAPPLYVLTTQTLDK.D
R3/RRR3-15/2	1858.661	1858.206	245.470	0.630	3194.952	0.550	26	0.575	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-14/2	1859.082	1858.206	-66.557	0.599	2908.767	0.529	26	0.489	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-15/2	1857.565	1858.206	-886.034	0.543	2936.451	0.498	25	0.485	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-15/2	1857.655	1858.206	-837.153	0.566	2699.193	0.511	24	0.430	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-14/2	1856.849	1858.206	-1272.903	0.308	2050.598	0.353	22	0.258	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-12/2	1859.894	1858.206	-168.301	0.475	582.095	0.441	16	0.142	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-9/2	1859.967	1858.206	-128.601	0.433	448.489	0.425	15	0.139	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-1/2	1859.983	1858.206	-120.174	0.389	483.094	0.326	16	0.134	R.GCIVSQDLSVLNLVIVK.Q
R3/RRR3-15/3	1858.271	1858.206	35.334	0.359	1033.538	0.300	28	0.097	-.GCIVSQDLSVLNLVIVK.-
R3/RRR3-15/3	1858.982	1858.206	-120.509	0.292	744.196	0.136	25	0.078	-.GCIVSQDLSVLNLVIVK.-
R3/RRR3-5/2	1429.404	1429.644	-168.366	0.405	1212.704	0.447	20	0.180	R.AIVSVGQTDLLANK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1632.674	1631.898	-137.055	0.450	970.285	0.402	18	0.155	K.VSTPTLFLLGAQDLR.V
R3/RRR3-5/2	1631.605	1631.898	-180.143	0.419	1142.798	0.324	19	0.155	K.VSTPTLFLLGAQDLR.V
R3/RRR3-5/2	1600.597	1601.871	-1425.288	0.361	717.213	0.435	15	0.142	R.IPALFVVNISSGEVR.A
R3/RRR3-5/2	1631.145	1631.898	-1077.782	0.259	944.744	0.203	17	0.132	K.VSTPTLFLLGAQDLR.V
R3/RRR3-19/2	1793.383	1793.055	183.789	0.621	3089.980	0.587	24	0.555	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-22/2	1793.389	1793.055	187.065	0.626	2995.720	0.557	23	0.515	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1791.872	1793.055	-1221.648	0.550	2950.257	0.559	23	0.507	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-20/2	1793.449	1793.055	220.306	0.629	2852.082	0.584	23	0.489	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-16/2	1792.817	1793.055	-133.237	0.611	2696.342	0.586	23	0.452	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1793.857	1793.055	-110.295	0.620	2679.968	0.595	23	0.452	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1793.404	1793.055	195.188	0.599	2710.431	0.574	23	0.451	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1793.296	1793.055	135.118	0.640	2401.759	0.581	22	0.382	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1794.257	1793.055	113.278	0.632	2326.571	0.589	22	0.370	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-20/2	1791.888	1793.055	-1212.687	0.567	2399.542	0.539	23	0.370	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-20/2	1792.195	1793.055	-1040.800	0.590	2314.947	0.548	23	0.355	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-16/2	1794.505	1793.055	251.630	0.603	2198.484	0.587	22	0.345	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1792.391	1793.055	-930.913	0.574	2038.286	0.577	20	0.312	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1776.311	1777.055	-984.688	0.594	2051.503	0.529	22	0.300	K.AM*SIMNSFINDIFEK.L
R3/RRR3-21/2	1776.265	1777.055	-1010.907	0.561	2029.043	0.522	22	0.295	K.AM*SIMNSFINDIFEK.L
R3/RRR3-21/2	1776.306	1777.055	-987.862	0.573	1995.980	0.537	22	0.294	K.AM*SIMNSFINDIFEK.L
R3/RRR3-21/2	1777.053	1777.055	-1.438	0.544	1937.399	0.505	20	0.274	K.AMSIM*NSFINDIFEK.L
R3/RRR3-19/2	1791.848	1793.055	-1235.331	0.515	1666.492	0.510	22	0.240	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-15/2	1791.832	1793.055	-1244.088	0.489	1287.449	0.523	19	0.199	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-22/2	1793.892	1793.055	-90.977	0.545	1076.052	0.570	18	0.188	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-16/2	1794.323	1793.055	150.189	0.549	1061.435	0.543	19	0.183	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-14/2	1794.432	1793.055	210.906	0.493	1056.466	0.462	18	0.169	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-1/2	1794.795	1793.055	-145.233	0.434	747.917	0.508	16	0.158	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-2/2	1794.602	1793.055	-253.180	0.437	613.932	0.459	16	0.149	K.AM*SIM*NSFINDIFEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1793.802	1793.055	-141.422	0.386	636.508	0.431	16	0.146	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-21/2	1793.243	1793.055	105.149	0.446	542.268	0.408	16	0.143	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-18/2	1794.296	1793.055	134.838	0.295	496.751	0.329	14	0.136	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-19/2	1794.773	1793.055	-157.718	0.342	500.602	0.321	14	0.136	K.AM*SIM*NSFINDIFEK.L
R3/RRR3-19/2	1794.676	1793.055	-211.418	0.327	225.597	0.359	11	0.128	-.AM*SIM*NSFINDIFEK.-
R3/RRR3-15/2	1145.201	1144.307	-92.117	0.227	794.146	0.289	14	0.132	K.VVNAAKSAEVR.R
R3/RRR3-17/2	1455.040	1455.718	-1156.729	0.301	898.113	0.163	16	0.126	K.EICPSIGLPLVTR.I
R3/RRR3-10/2	1455.309	1455.605	-203.901	0.361	1079.007	0.090	17	0.124	K.ASNNIQSRSPKPR.K
R3/RRR3-12/2	1348.121	1347.414	-217.751	0.556	2410.030	0.633	21	0.417	K.APVTSAEVSQDSR.F
R3/RRR3-12/2	1347.055	1347.414	-267.369	0.521	2338.702	0.580	21	0.382	K.APVTSAEVSQDSR.F
R3/RRR3-12/2	1347.074	1347.414	-253.186	0.500	2353.076	0.569	21	0.382	K.APVTSAEVSQDSR.F
R3/RRR3-12/2	1125.475	1126.242	-1574.316	0.384	694.898	0.405	16	0.147	R.FITTADGSSVK.F
R3/RRR3-12/2	1125.453	1126.242	-1593.929	0.255	797.865	0.348	17	0.141	R.FITTADGSSVK.F
R3/RRR3-12/2	1126.069	1126.242	-153.374	0.435	673.826	0.327	16	0.141	R.FITTADGSSVK.F
R3/RRR3-17/2	1502.500	1501.750	-166.938	0.608	2421.996	0.620	24	0.411	K.AVASINSVLTDLVAK.G
R3/RRR3-18/2	1502.253	1501.750	-331.763	0.577	2178.459	0.609	24	0.357	K.AVASINSVLTDLVAK.G
R3/RRR3-17/2	1501.332	1501.750	-279.528	0.524	1946.880	0.605	23	0.312	K.AVASINSVLTDLVAK.G
R3/RRR3-17/2	1501.323	1501.750	-285.320	0.535	1944.132	0.575	23	0.303	K.AVASINSVLTDLVAK.G
R3/RRR3-18/2	1501.310	1501.750	-294.375	0.479	1805.120	0.547	22	0.272	K.AVASINSVLTDLVAK.G
R3/RRR3-18/2	1501.462	1501.750	-192.333	0.558	1702.954	0.580	22	0.266	K.AVASINSVLTDLVAK.G
R3/RRR3-18/2	1380.049	1379.540	-357.414	0.508	1602.155	0.591	18	0.255	K.ANNVIYGLAQCR.G
R3/RRR3-17/2	1379.251	1379.540	-210.262	0.484	1599.154	0.476	18	0.227	K.ANNVIYGLAQCR.G
R3/RRR3-17/2	1379.180	1379.540	-262.029	0.481	1627.548	0.419	18	0.217	K.ANNVIYGLAQCR.G
R3/RRR3-18/2	1379.164	1379.540	-274.017	0.497	1645.031	0.399	18	0.214	K.ANNVIYGLAQCR.G
R3/RRR3-17/2	1379.022	1379.540	-1104.274	0.452	1504.158	0.383	18	0.196	K.ANNVIYGLAQCR.G
R3/RRR3-18/2	1379.054	1379.540	-353.854	0.401	1532.364	0.353	18	0.194	K.ANNVIYGLAQCR.G
R3/RRR3-1/2	1501.954	1501.750	136.004	0.253	400.349	0.417	13	0.135	K.AVASINSVLTDLVAK.G
R3/RRR3-10/2	1563.551	1562.774	-142.862	0.515	2364.254	0.431	23	0.339	K.M*GQIGVLSGTQGEIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	893.938	894.010	-80.618	0.346	797.630	0.404	13	0.151	K.ATVNSFVR.S
R3/RRR3-10/2	894.050	894.010	45.109	0.283	796.859	0.325	13	0.142	K.ATVNSFVR.S
R3/RRR3-11/2	893.387	894.010	-1822.680	0.274	748.294	0.305	12	0.139	K.ATVNSFVR.S
R3/RRR3-11/2	893.643	894.010	-411.656	0.288	518.421	0.308	11	0.137	K.ATVNSFVR.S
R3/RRR3-4/2	1650.283	1650.815	-931.145	0.355	1148.633	0.337	20	0.156	R.ASALAALSSAFNPSSQK.N
R3/RRR3-4/2	1650.172	1650.815	-998.652	0.314	822.742	0.368	19	0.142	R.ASALAALSSAFNPSSQK.N
R3/RRR3-5/2	1873.507	1872.306	107.790	0.448	657.997	0.404	17	0.139	K.EPPQFIALFQPMVILK.G
R3/RRR3-5/2	1282.181	1282.556	-293.311	0.394	791.544	0.289	14	0.135	R.IQDFKPVPLPK.A
R3/RRR3-3/2	1651.663	1650.815	-92.410	0.312	422.638	0.323	14	0.130	R.ASALAALSSAFNPSSQK.N
R3/RRR3-4/3	1282.878	1282.556	252.176	0.457	1357.424	0.288	23	0.111	R.IQDFKPVPLPK.A
R3/RRR3-5/3	1282.616	1282.556	47.326	0.444	1173.797	0.270	22	0.099	R.IQDFKPVPLPK.A
R3/RRR3-4/3	1282.639	1282.556	65.367	0.387	1131.311	0.272	22	0.097	R.IQDFKPVPLPK.A
R3/RRR3-4/3	1282.733	1282.556	138.238	0.416	1190.903	0.204	23	0.090	R.IQDFKPVPLPK.A
R3/RRR3-12/2	1576.628	1576.843	-136.724	0.513	2134.840	0.604	24	0.348	R.MFYGPGGPYALFAGK.D
R3/RRR3-12/2	1576.500	1576.843	-218.127	0.537	1863.507	0.574	23	0.290	R.MFYGPGGPYALFAGK.D
R3/RRR3-13/2	1578.108	1576.843	168.544	0.505	1652.129	0.604	22	0.265	R.MFYGPGGPYALFAGK.D
R3/RRR3-13/2	1577.601	1576.843	-153.559	0.514	1637.994	0.607	22	0.264	R.MFYGPGGPYALFAGK.D
R3/RRR3-12/2	1167.007	1167.254	-211.782	0.458	1519.721	0.410	16	0.204	K.GQIYDVTQSR.M
R3/RRR3-12/2	1167.960	1167.254	-252.598	0.498	1250.437	0.463	16	0.189	K.GQIYDVTQSR.M
R3/RRR3-12/2	1592.059	1592.842	-1123.212	0.454	1152.297	0.526	20	0.189	R.M*FYGPGGPYALFAGK.D
R3/RRR3-13/2	1166.425	1167.254	-1572.474	0.375	1385.045	0.338	16	0.178	K.GQIYDVTQSR.M
R3/RRR3-12/2	1167.305	1167.254	44.094	0.508	1087.039	0.460	15	0.176	K.GQIYDVTQSR.M
R3/RRR3-13/2	1166.577	1167.254	-1442.023	0.413	1093.866	0.392	15	0.165	K.GQIYDVTQSR.M
R3/RRR3-14/2	1167.266	1167.254	10.006	0.469	928.331	0.378	15	0.155	K.GQIYDVTQSR.M
R3/RRR3-14/2	1167.148	1167.254	-90.700	0.457	994.439	0.335	15	0.152	K.GQIYDVTQSR.M
R3/RRR3-13/2	1166.222	1167.254	-1747.444	0.319	895.801	0.316	14	0.145	K.GQIYDVTQSR.M
R3/RRR3-18/2	1166.192	1167.254	-1773.632	0.326	895.797	0.270	15	0.142	K.GQIYDVTQSR.M
R3/RRR3-15/2	1381.587	1382.549	-1424.624	0.486	2327.726	0.523	22	0.361	R.IPTGELWAGNPAR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/2	1381.465	1382.549	-1513.023	0.456	1915.500	0.490	21	0.276	R.IPTGELWAGNPAR.F
R3/RRR3-15/2	1383.021	1382.549	342.462	0.549	1820.633	0.520	21	0.270	R.IPTGELWAGNPAR.F
R3/RRR3-15/2	1461.327	1461.706	-260.669	0.486	1110.614	0.395	19	0.166	R.KLTNEEIM*EIPK.L
R3/RRR3-17/2	1659.943	1659.866	46.202	0.491	1619.774	0.504	23	0.237	R.FDPATTPLLAAWAER.F
R3/RRR3-17/2	1659.524	1659.866	-207.066	0.500	1494.689	0.511	22	0.222	R.FDPATTPLLAAWAER.F
R3/RRR3-17/2	1659.274	1659.866	-962.625	0.464	1284.725	0.488	21	0.195	R.FDPATTPLLAAWAER.F
R3/RRR3-17/2	1658.428	1659.866	-1474.737	0.247	671.936	0.202	16	0.128	R.FDPATTPLLAAWAER.F
R3/RRR3-17/3	1815.423	1816.053	-900.135	0.333	556.542	0.300	22	0.090	K.RFDPATTPLLAAWAER.F
R3/RRR3-17/3	1815.361	1816.053	-934.461	0.259	1205.221	0.187	27	0.089	K.RFDPATTPLLAAWAER.F
R3/RRR3-17/3	1815.211	1816.053	-1017.502	0.307	806.141	0.243	25	0.086	K.RFDPATTPLLAAWAER.F
R3/RRR3-3/2	1267.405	1267.415	-7.594	0.431	1032.474	0.395	16	0.161	R.FTWTIENLSR.V
R3/RRR3-17/2	1583.630	1582.734	-66.073	0.585	2369.535	0.543	21	0.373	R.SNVGELLEYSLETK.K
R3/RRR3-17/2	1582.315	1582.734	-265.609	0.468	1987.428	0.376	20	0.255	R.SNVGELLEYSLETK.K
R3/RRR3-17/2	1581.832	1582.734	-1205.889	0.315	1209.120	0.262	19	0.152	R.SNVGELLEYSLETK.K
R3/RRR3-17/2	1582.006	1582.734	-1095.781	0.315	585.315	0.155	16	0.128	-.SNVGELLEYSLETK.-
R3/RRR3-17/3	1490.160	1490.622	-310.599	0.501	772.471	0.498	25	0.117	K.HGGIDSM*SADDLKK.L
R3/RRR3-11/2	1616.409	1616.868	-284.548	0.557	2421.075	0.507	23	0.376	K.MGQIQVLTGSQGQIR.A
R3/RRR3-12/3	1987.763	1987.161	-200.783	0.449	1151.308	0.400	25	0.121	R.TPNVFDNKYYVDLQNR.Q
R3/RRR3-11/3	1987.069	1987.161	-46.195	0.388	727.943	0.436	23	0.105	R.TPNVFDNKYYVDLQNR.Q
R3/RRR3-12/3	1987.169	1987.161	4.269	0.316	578.896	0.340	21	0.091	R.TPNVFDNKYYVDLQNR.Q
R3/RRR3-19/2	1198.893	1199.425	-1282.238	0.576	2338.819	0.466	19	0.338	R.VDIGQVLLSVR.C
R3/RRR3-16/2	1199.386	1199.425	-32.729	0.545	2200.891	0.504	19	0.325	R.VDIGQVLLSVR.C
R3/RRR3-25/2	1199.311	1199.425	-95.209	0.532	2317.410	0.435	19	0.324	R.VDIGQVLLSVR.C
R3/RRR3-25/2	1199.307	1199.425	-98.987	0.523	2064.994	0.429	19	0.280	R.VDIGQVLLSVR.C
R3/RRR3-17/2	1199.428	1199.425	2.183	0.582	1889.313	0.508	18	0.274	R.VDIGQVLLSVR.C
R3/RRR3-25/2	1199.361	1199.425	-54.167	0.514	2004.805	0.433	19	0.272	R.VDIGQVLLSVR.C
R3/RRR3-18/2	1199.383	1199.425	-35.587	0.548	1576.848	0.489	17	0.226	R.VDIGQVLLSVR.C
R3/RRR3-18/2	1199.000	1199.425	-355.833	0.441	1461.496	0.464	17	0.208	R.VDIGQVLLSVR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1198.686	1199.425	-1454.976	0.456	1229.074	0.446	18	0.184	R.VDIGQVLLSVR.C
R3/RRR3-16/2	1199.110	1199.425	-263.905	0.387	992.959	0.429	16	0.164	R.VDIGQVLLSVR.C
R3/RRR3-2/2	1199.343	1199.425	-68.868	0.374	697.387	0.431	13	0.149	R.VDIGQVLLSVR.C
R3/RRR3-15/2	1199.200	1199.425	-188.230	0.335	560.348	0.396	13	0.143	R.VDIGQVLLSVR.C
R3/RRR3-1/2	1199.007	1199.425	-349.908	0.277	688.166	0.311	14	0.138	R.VDIGQVLLSVR.C
R3/RRR3-17/3	1566.816	1567.726	-1222.495	0.429	873.867	0.432	26	0.113	R.CKPNNAVHASEALR.R
R3/RRR3-17/3	1567.595	1567.726	-83.433	0.442	745.921	0.440	24	0.110	R.CKPNNAVHASEALR.R
R3/RRR3-17/3	1567.429	1567.726	-189.480	0.437	835.915	0.410	26	0.108	R.CKPNNAVHASEALR.R
R3/RRR3-25/3	1567.075	1567.726	-1056.343	0.455	877.047	0.372	26	0.105	R.CKPNNAVHASEALR.R
R3/RRR3-25/3	1567.667	1567.726	-37.271	0.369	827.810	0.333	25	0.098	R.CKPNNAVHASEALR.R
R3/RRR3-25/3	1567.581	1567.726	-92.221	0.375	710.435	0.300	24	0.094	R.CKPNNAVHASEALR.R
R3/RRR3-10/3	1566.738	1567.726	-1272.374	0.261	750.489	0.146	23	0.084	R.CKPNNAVHASEALR.R
R3/RRR3-10/3	1566.622	1567.726	-1347.027	0.225	760.851	0.037	23	0.081	-.CKPNNAVHASEALR.-
R3/RRR3-21/2	1659.811	1659.933	-73.353	0.462	2942.955	0.511	28	0.504	R.SAAVAGAIGGVLAGAAM*AGK.Q
R3/RRR3-28/2	1496.277	1495.605	-220.002	0.549	2917.079	0.554	23	0.511	R.VCACVDSAGAVTER.G
R3/RRR3-28/2	1494.904	1495.605	-1141.117	0.461	2669.246	0.471	23	0.418	R.VCACVDSAGAVTER.G
R3/RRR3-12/2	1543.144	1543.651	-979.528	0.531	2312.583	0.480	24	0.344	K.ITGCYVVGSAGSDEK.V
R3/RRR3-12/2	1543.594	1543.651	-36.932	0.539	1864.583	0.543	24	0.284	K.ITGCYVVGSAGSDEK.V
R3/RRR3-12/2	1353.443	1352.475	-23.757	0.531	1517.469	0.564	17	0.240	K.FGFDDAFNYKK.E
R3/RRR3-12/2	1351.765	1352.475	-1269.287	0.424	1382.582	0.320	17	0.176	-.FGFDDAFNYKK.-
R3/RRR3-12/3	1352.719	1352.475	180.958	0.549	1113.600	0.445	26	0.126	K.FGFDDAFNYKK.E
R3/RRR3-12/3	1352.461	1352.475	-10.612	0.504	1055.815	0.385	26	0.111	K.FGFDDAFNYKK.E
R3/RRR3-14/2	1438.053	1438.522	-326.821	0.501	2198.792	0.514	21	0.334	R.ELAEEGYSGVEVR.V
R3/RRR3-14/2	1438.201	1438.522	-223.608	0.474	2098.722	0.472	21	0.303	R.ELAEEGYSGVEVR.V
R3/RRR3-14/3	1582.709	1582.704	3.464	0.393	618.296	0.517	23	0.111	R.ATHTQEVLGEQGRR.I
R3/RRR3-14/3	1582.603	1582.704	-63.610	0.350	396.294	0.437	19	0.098	R.ATHTQEVLGEQGRR.I
R3/RRR3-3/2	1345.959	1346.597	-1220.456	0.434	1021.869	0.380	16	0.156	R.TDAVIQVIPYVK.V
R3/RRR3-3/2	1637.576	1637.902	-199.972	0.471	567.453	0.542	19	0.155	R.IPGTELLPGDIVSIGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1345.898	1346.597	-1265.905	0.302	1220.609	0.265	18	0.153	R.TDAVIQVIPYVK.V
R3/RRR3-3/2	1637.599	1637.902	-185.764	0.455	527.003	0.507	19	0.150	R.IPGTELLPGDIVSIGR.S
R3/RRR3-2/2	1637.721	1637.902	-111.065	0.427	628.138	0.471	19	0.149	R.IPGTELLPGDIVSIGR.S
R3/RRR3-3/2	1512.497	1512.690	-128.436	0.278	840.444	0.382	15	0.142	R.NIFEYPQPTFQK.L
R3/RRR3-23/2	1647.369	1647.917	-942.635	0.515	1244.030	0.527	21	0.200	R.SGKM*ELPEWVDIVK.T
R3/RRR3-23/2	1646.739	1647.917	-1326.944	0.451	1220.012	0.502	21	0.192	R.SGKM*ELPEWVDIVK.T
R3/RRR3-23/2	1647.535	1647.917	-232.907	0.522	1098.027	0.544	20	0.190	R.SGKM*ELPEWVDIVK.T
R3/RRR3-23/2	1376.644	1375.615	20.805	0.503	849.786	0.476	18	0.166	K.M*ELPEWVDIVK.T
R3/RRR3-23/2	1375.325	1375.615	-211.349	0.430	601.656	0.404	16	0.149	K.M*ELPEWVDIVK.T
R3/RRR3-23/2	1359.378	1359.616	-175.147	0.431	797.323	0.340	17	0.147	K.MELPEWVDIVK.T
R3/RRR3-23/2	1359.074	1359.616	-1137.598	0.471	708.089	0.362	16	0.146	K.MELPEWVDIVK.T
R3/RRR3-22/2	1374.909	1375.615	-1244.846	0.421	620.484	0.336	16	0.143	K.M*ELPEWVDIVK.T
R3/RRR3-23/2	1375.248	1375.615	-267.894	0.397	552.299	0.351	15	0.143	K.M*ELPEWVDIVK.T
R3/RRR3-22/2	1375.283	1375.615	-241.981	0.307	431.910	0.348	14	0.138	-.M*ELPEWVDIVK.-
R3/RRR3-23/2	1359.294	1359.616	-237.489	0.338	666.134	0.222	16	0.135	K.MELPEWVDIVK.T
R3/RRR3-22/2	1359.153	1359.616	-341.289	0.368	470.479	0.233	14	0.132	-.MELPEWVDIVK.-
R3/RRR3-22/2	1374.654	1375.615	-1430.603	0.276	702.424	0.161	16	0.132	K.M*ELPEWVDIVK.T
R3/RRR3-23/3	1647.022	1647.917	-1154.222	0.366	1143.625	0.173	27	0.085	R.SGKM*ELPEWVDIVK.T
R3/RRR3-22/3	1648.464	1647.917	-276.085	0.317	1050.995	0.178	24	0.084	R.SGKM*ELPEWVDIVK.T
R3/RRR3-23/3	1647.405	1647.917	-920.847	0.385	1048.547	0.152	25	0.081	R.SGKM*ELPEWVDIVK.T
R3/RRR3-23/3	1647.245	1647.917	-1018.269	0.333	1170.844	0.129	26	0.081	R.SGKM*ELPEWVDIVK.T
R3/RRR3-6/2	1686.903	1687.870	-1169.536	0.363	2710.262	0.346	25	0.383	R.VVDSLDDLSLDIPSAK.S
R3/RRR3-6/2	1688.270	1687.870	237.755	0.494	2650.929	0.377	25	0.377	R.VVDSLDDLSLDIPSAK.S
R3/RRR3-6/2	1688.245	1687.870	222.819	0.567	2354.662	0.452	24	0.339	R.VVDSLDDLSLDIPSAK.S
R3/RRR3-6/2	1756.226	1755.946	160.164	0.547	1433.076	0.638	23	0.245	K.SVAPIIEEYFSTGDVK.L
R3/RRR3-6/2	1755.270	1755.946	-957.481	0.440	1348.607	0.566	22	0.216	K.SVAPIIEEYFSTGDVK.L
R3/RRR3-6/2	1755.157	1755.946	-1022.139	0.472	1102.788	0.551	21	0.189	K.SVAPIIEEYFSTGDVK.L
R3/RRR3-27/2	1375.177	1375.507	-240.978	0.510	1872.045	0.513	18	0.275	R.EGDILTLLESER.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-27/2	1374.566	1375.507	-1416.402	0.350	1473.190	0.409	18	0.198	R.EGDILTLLESER.E
R3/RRR3-27/2	1374.591	1375.507	-1397.671	0.350	1292.397	0.420	17	0.182	R.EGDILTLLESER.E
R3/RRR3-27/3	1135.352	1135.255	86.033	0.455	808.894	0.263	18	0.083	-.VKFLDDQNR.-
R3/RRR3-27/3	1135.244	1135.255	-9.569	0.514	885.102	0.270	18	0.081	-.VKFLDDQNR.-
R3/RRR3-27/3	1135.405	1135.255	132.290	0.506	981.918	0.245	18	0.079	-.VKFLDDQNR.-
R3/RRR3-8/2	1101.270	1101.315	-41.204	0.366	1229.018	0.396	15	0.174	K.NISVIAVCPK.G
R3/RRR3-7/2	1102.023	1101.315	-266.156	0.209	598.928	0.205	11	0.125	-.NISVIAVCPK.-
R3/RRR3-23/2	1867.573	1867.118	244.033	0.532	2218.521	0.568	25	0.351	K.DM*PVLQDGPPPGGFAPVR.Y
R3/RRR3-23/2	1867.594	1867.118	255.634	0.554	2005.112	0.600	26	0.321	K.DM*PVLQDGPPPGGFAPVR.Y
R3/RRR3-23/2	1866.164	1867.118	-1050.241	0.490	2082.220	0.532	25	0.314	K.DM*PVLQDGPPPGGFAPVR.Y
R3/RRR3-24/2	1866.373	1867.118	-938.077	0.495	1542.525	0.516	24	0.227	K.DM*PVLQDGPPPGGFAPVR.Y
R3/RRR3-23/2	1570.210	1570.726	-968.648	0.438	792.419	0.583	22	0.173	R.TALVPVLQAEEDER.F
R3/RRR3-23/2	1569.776	1570.726	-1246.193	0.318	661.054	0.395	20	0.142	R.TALVPVLQAEEDER.F
R3/RRR3-20/2	1662.335	1662.860	-920.417	0.494	2167.853	0.503	24	0.321	K.AITSGVLAGCSDAIAQK.I
R3/RRR3-20/2	1662.243	1662.860	-976.153	0.478	2199.950	0.455	24	0.313	K.AITSGVLAGCSDAIAQK.I
R3/RRR3-20/2	1662.258	1662.860	-966.790	0.443	2127.995	0.495	24	0.312	K.AITSGVLAGCSDAIAQK.I
R3/RRR3-20/2	983.825	984.135	-316.053	0.450	453.396	0.465	14	0.152	K.ISGVPNLQR.R
R3/RRR3-20/2	983.987	984.135	-150.137	0.394	454.530	0.438	14	0.148	K.ISGVPNLQR.R
R3/RRR3-20/2	983.957	984.135	-181.126	0.391	388.167	0.374	13	0.143	K.ISGVPNLQR.R
R3/RRR3-21/2	1351.210	1351.449	-177.565	0.484	2057.721	0.531	20	0.312	K.YGVGDAHFEVTR.F
R3/RRR3-21/2	1651.470	1651.844	-227.500	0.489	2017.851	0.441	23	0.278	K.SAWSEAYNQLVAAIK.Q
R3/RRR3-21/2	1351.148	1351.449	-223.607	0.515	1689.387	0.503	19	0.247	K.YGVGDAHFEVTR.F
R3/RRR3-21/2	1651.269	1651.844	-956.689	0.466	1773.900	0.459	22	0.246	K.SAWSEAYNQLVAAIK.Q
R3/RRR3-21/2	1351.384	1351.449	-48.346	0.463	1668.536	0.496	19	0.242	K.YGVGDAHFEVTR.F
R3/RRR3-21/2	1651.157	1651.844	-1024.825	0.415	1726.182	0.385	21	0.222	K.SAWSEAYNQLVAAIK.Q
R3/RRR3-21/3	1351.466	1351.449	12.528	0.453	785.372	0.566	21	0.129	K.YGVGDAHFEVTR.F
R3/RRR3-21/3	1351.738	1351.449	214.829	0.436	862.855	0.522	22	0.125	K.YGVGDAHFEVTR.F
R3/RRR3-21/3	1352.516	1351.449	49.814	0.457	875.926	0.503	22	0.123	K.YGVGDAHFEVTR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/3	1582.161	1581.752	259.031	0.480	695.774	0.538	26	0.121	K.TKFGFDDAFNYKK.E
R3/RRR3-12/3	1581.807	1581.752	34.543	0.506	661.803	0.502	26	0.116	K.TKFGFDDAFNYKK.E
R3/RRR3-19/2	1842.372	1842.889	-825.888	0.552	2152.914	0.501	24	0.321	R.SDVVQVDEVGYDNCDK.A
R3/RRR3-19/2	1498.286	1498.624	-225.754	0.443	1471.495	0.379	17	0.192	K.GDWLLFEYQNGR.S
R3/RRR3-19/2	1498.015	1498.624	-1076.957	0.413	1548.747	0.312	17	0.187	K.GDWLLFEYQNGR.S
R3/RRR3-8/2	1432.047	1432.514	-326.738	0.536	2002.150	0.569	20	0.314	R.VNVYYNEASCGR.F
R3/RRR3-8/2	1431.998	1432.514	-1061.369	0.520	1844.016	0.572	19	0.287	R.VNVYYNEASCGR.F
R3/RRR3-8/2	1431.969	1432.514	-1081.740	0.507	1715.571	0.571	19	0.268	R.VNVYYNEASCGR.F
R3/RRR3-9/2	1431.951	1432.514	-1094.409	0.517	1736.115	0.489	19	0.249	R.VNVYYNEASCGR.F
R3/RRR3-8/3	1919.948	1918.049	-52.752	0.369	968.238	0.467	26	0.121	K.FWEVVCDEHGIDPTGR.Y
R3/RRR3-8/3	1918.619	1918.049	-224.579	0.384	1005.628	0.452	29	0.120	K.FWEVVCDEHGIDPTGR.Y
R3/RRR3-8/3	1918.129	1918.049	41.955	0.444	701.353	0.512	26	0.116	K.FWEVVCDEHGIDPTGR.Y
R3/RRR3-23/2	1094.902	1095.363	-422.428	0.411	408.072	0.443	13	0.144	K.VKGPVRLPTK.T
R3/RRR3-23/2	1095.206	1095.363	-143.834	0.361	396.135	0.320	12	0.134	-.VKGPVRLPTK.-
R3/RRR3-23/3	868.068	868.059	10.547	0.508	818.400	0.430	16	0.111	K.GPVRLPTK.T
R3/RRR3-23/3	868.273	868.059	247.338	0.517	536.916	0.377	15	0.104	K.GPVRLPTK.T
R3/RRR3-23/3	868.266	868.059	239.197	0.450	493.518	0.269	15	0.093	-.GPVRLPTK.-
R3/RRR3-22/2	1499.189	1499.734	-1034.055	0.564	1684.156	0.610	20	0.274	K.APLLDVTQFGYFK.V
R3/RRR3-22/2	1499.432	1499.734	-202.473	0.548	1656.830	0.613	20	0.270	K.APLLDVTQFGYFK.V
R3/RRR3-22/2	1498.987	1499.734	-1169.128	0.537	1661.658	0.608	20	0.270	K.APLLDVTQFGYFK.V
R3/RRR3-22/3	969.728	969.077	-360.938	0.500	646.146	0.491	16	0.114	K.YHPGYFGK.V
R3/RRR3-22/3	969.373	969.077	306.261	0.480	809.778	0.465	17	0.114	K.YHPGYFGK.V
R3/RRR3-22/3	969.126	969.077	50.886	0.482	656.891	0.453	15	0.109	K.YHPGYFGK.V
R3/RRR3-10/2	1173.542	1174.329	-1527.779	0.453	1418.884	0.375	16	0.188	K.RDELTLEGLK.Q
R3/RRR3-9/2	1174.130	1174.329	-170.038	0.439	1311.448	0.389	16	0.181	K.RDELTLEGLK.Q
R3/RRR3-10/2	1174.195	1174.329	-114.555	0.458	1427.354	0.332	16	0.180	K.RDELTLEGLK.Q
R3/RRR3-9/2	1174.094	1174.329	-201.119	0.485	1338.754	0.330	16	0.172	K.RDELTLEGLK.Q
R3/RRR3-9/2	1173.596	1174.329	-1481.388	0.452	1309.815	0.312	16	0.168	K.RDELTLEGLK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1173.906	1174.329	-361.770	0.413	865.251	0.346	14	0.148	K.RDELTLEGLK.Q
R3/RRR3-9/2	1018.162	1018.143	18.686	0.422	836.897	0.340	14	0.146	-.DELTLEGLK.-
R3/RRR3-9/2	1018.355	1018.143	208.405	0.413	886.726	0.306	14	0.142	-.DELTLEGLK.-
R3/RRR3-1/2	1790.316	1790.906	-890.525	0.487	1591.955	0.609	23	0.258	R.LSSDDGYLESLTSAGFK.V
R3/RRR3-1/2	1451.933	1452.638	-1177.672	0.430	898.783	0.537	17	0.170	R.AIISGTSSIYNLGR.K
R3/RRR3-2/2	1453.151	1452.638	-335.811	0.367	883.844	0.413	18	0.153	R.AIISGTSSIYNLGR.K
R3/RRR3-2/2	1453.375	1452.638	-181.258	0.385	750.287	0.419	17	0.147	R.AIISGTSSIYNLGR.K
R3/RRR3-3/2	1545.439	1544.732	-189.870	0.451	1195.240	0.198	19	0.139	R.SNQEELGSVLNLLK.Y
R3/RRR3-8/2	1835.499	1836.018	-829.781	0.583	2594.020	0.471	23	0.393	R.MTNFYTNFQVDEIGR.V
R3/RRR3-8/2	1835.296	1836.018	-941.082	0.543	2535.354	0.497	23	0.392	R.MTNFYTNFQVDEIGR.V
R3/RRR3-8/2	1852.310	1852.017	158.259	0.582	2259.446	0.539	22	0.348	R.M*TNFYTNFQVDEIGR.V
R3/RRR3-8/2	1851.403	1852.017	-874.376	0.539	2108.963	0.562	21	0.327	R.M*TNFYTNFQVDEIGR.V
R3/RRR3-8/2	1204.043	1204.356	-260.688	0.466	2020.785	0.433	18	0.278	R.AAELTTLLESR.M
R3/RRR3-8/2	1853.418	1852.017	216.892	0.618	1779.291	0.532	20	0.261	R.M*TNFYTNFQVDEIGR.V
R3/RRR3-8/2	1204.034	1204.356	-267.910	0.538	1802.275	0.429	17	0.242	R.AAELTTLLESR.M
R3/RRR3-8/2	1204.224	1204.356	-109.563	0.500	1768.694	0.362	17	0.222	R.AAELTTLLESR.M
R3/RRR3-8/3	1204.171	1204.356	-153.351	0.419	1104.234	0.246	24	0.092	R.AAELTTLLESR.M
R3/RRR3-13/2	1756.547	1756.962	-237.242	0.507	1878.508	0.600	25	0.297	R.GMGDAADLVALSGGHTVGK.-
R3/RRR3-14/2	1772.284	1772.962	-949.257	0.553	1841.180	0.602	28	0.294	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-13/2	1772.322	1772.962	-927.683	0.544	1701.641	0.627	26	0.278	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-14/2	1772.581	1772.962	-215.618	0.567	1592.376	0.631	26	0.263	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-14/2	1773.406	1772.962	251.471	0.555	1448.843	0.605	25	0.236	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-14/3	1773.724	1772.962	-134.309	0.476	986.487	0.572	34	0.146	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-13/3	1772.756	1772.962	-116.426	0.449	891.333	0.560	33	0.137	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-14/3	1772.526	1772.962	-246.370	0.428	787.190	0.542	32	0.127	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-13/3	1772.853	1772.962	-61.515	0.401	657.689	0.521	30	0.118	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-13/3	1772.251	1772.962	-968.419	0.405	831.414	0.464	32	0.117	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-14/3	1756.869	1756.962	-52.980	0.349	334.795	0.570	28	0.116	R.GMGDAADLVALSGGHTVGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/3	1773.083	1772.962	68.381	0.376	615.956	0.486	29	0.112	R.GM*GDAADLVALSGGHTVGK.-
R3/RRR3-14/3	1756.511	1756.962	-257.608	0.242	279.132	0.441	24	0.103	R.GMGDAADLVALSGGHTVGK.-
R3/RRR3-13/3	1756.787	1756.962	-99.921	0.200	409.556	0.396	28	0.099	R.GMGDAADLVALSGGHTVGK.-
R3/RRR3-13/3	1756.923	1756.962	-22.141	0.303	236.019	0.406	22	0.096	-.GMGDAADLVALSGGHTVGK.-
R3/RRR3-9/3	1664.003	1663.769	140.925	0.520	2509.935	0.399	31	0.310	R.FHLPGETEEEFATR.L
R3/RRR3-9/2	1270.286	1270.500	-169.311	0.448	1456.585	0.377	18	0.192	R.LANNLEELILK.E
R3/RRR3-9/2	1270.234	1270.500	-209.994	0.522	1407.187	0.383	18	0.188	R.LANNLEELILK.E
R3/RRR3-9/2	1270.416	1270.500	-66.365	0.489	1475.793	0.345	18	0.187	R.LANNLEELILK.E
R3/RRR3-9/3	1663.821	1663.769	31.663	0.496	1825.489	0.329	27	0.170	R.FHLPGETEEEFATR.L
R3/RRR3-10/3	1797.885	1797.946	-34.167	0.513	2382.097	0.428	35	0.295	K.YFRPAEVDSLQGDATK.A
R3/RRR3-10/3	1797.688	1797.946	-144.097	0.555	2256.189	0.424	34	0.268	K.YFRPAEVDSLQGDATK.A
R3/RRR3-10/3	1797.750	1797.946	-109.460	0.567	1965.120	0.437	33	0.222	K.YFRPAEVDSLQGDATK.A
R3/RRR3-10/2	1047.942	1048.220	-266.923	0.469	1322.977	0.394	17	0.184	K.VFLGNLSAAR.D
R3/RRR3-10/2	1047.840	1048.220	-364.165	0.358	1116.591	0.273	15	0.149	K.VFLGNLSAAR.D
R3/RRR3-14/2	1706.308	1705.894	243.350	0.615	2812.168	0.525	25	0.473	R.YVFTGASWVTNAFNK.V
R3/RRR3-7/2	1752.599	1752.904	-174.273	0.525	2327.229	0.485	23	0.345	R.SFGTDLDTATNELVIR.V
R3/RRR3-7/2	1752.005	1752.904	-1087.083	0.496	1468.518	0.456	20	0.205	R.SFGTDLDTATNELVIR.V
R3/RRR3-7/2	1495.225	1495.706	-322.923	0.352	1286.510	0.383	19	0.176	R.FSNLVFEPLWSR.N
R3/RRR3-1/2	1754.117	1752.904	121.967	0.395	344.336	0.366	14	0.134	R.SFGTDLDTATNELVIR.V
R3/RRR3-1/2	1754.563	1752.904	-194.594	0.375	118.148	0.337	12	0.114	-.SFGTDLDTATNELVIR.-
R3/RRR3-26/2	1631.291	1631.683	-241.498	0.547	2084.661	0.578	26	0.330	K.GSPAADEEQSTAAAAVR.F
R3/RRR3-26/2	1631.211	1631.683	-290.523	0.554	1682.523	0.584	24	0.264	K.GSPAADEEQSTAAAAVR.F
R3/RRR3-26/2	1631.238	1631.683	-273.780	0.534	1569.746	0.571	24	0.245	K.GSPAADEEQSTAAAAVR.F
R3/RRR3-26/3	1631.714	1631.683	18.742	0.411	912.479	0.411	26	0.107	K.GSPAADEEQSTAAAAVR.F
R3/RRR3-26/2	1494.297	1494.718	-282.729	0.371	859.739	0.411	19	0.088	R.SEPRPSLAQLLSPV.-
R3/RRR3-26/2	1494.857	1494.718	93.404	0.382	636.998	0.456	17	0.046	R.SEPRPSLAQLLSPV.-
R3/RRR3-26/2	1494.265	1494.718	-303.957	0.335	590.985	0.411	16	0.038	R.SEPRPSLAQLLSPV.-
R3/RRR3-27/2	1122.981	1123.284	-270.347	0.505	1112.265	0.455	16	0.178	R.VCGNPHGLIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-27/2	1122.503	1123.284	-1591.464	0.456	1003.771	0.472	16	0.173	R.VCGNPHGLIR.K
R3/RRR3-27/2	1123.139	1123.284	-129.901	0.459	1055.195	0.425	16	0.169	R.VCGNPHGLIR.K
R3/RRR3-27/2	975.745	976.120	-385.726	0.369	982.948	0.311	11	0.149	K.YGLM*CCR.Q
R3/RRR3-27/2	975.329	976.120	-1841.954	0.413	937.116	0.293	11	0.146	K.YGLM*CCR.Q
R3/RRR3-27/2	1122.331	1123.284	-1745.199	0.396	739.095	0.334	14	0.141	-.VCGNPHGLIR.-
R3/RRR3-27/2	975.796	976.120	-332.504	0.250	916.605	0.285	11	0.140	K.YGLM*CCR.Q
R3/RRR3-25/2	1275.065	1275.396	-259.803	0.452	1117.396	0.599	22	0.200	R.HGGSGGPADPVPVK.L
R3/RRR3-25/3	1544.422	1544.740	-206.414	0.542	976.680	0.468	29	0.124	R.LRHGGSGGPADPVPVK.L
R3/RRR3-25/3	1544.989	1544.740	161.568	0.391	1028.641	0.373	26	0.109	R.LRHGGSGGPADPVPVK.L
R3/RRR3-25/3	1544.604	1544.740	-88.440	0.505	839.916	0.401	27	0.106	R.LRHGGSGGPADPVPVK.L
R3/RRR3-25/3	1275.154	1275.396	-190.135	0.325	750.107	0.308	20	0.093	R.HGGSGGPADPVPVK.L
R3/RRR3-26/3	1274.642	1275.396	-1379.812	0.315	563.780	0.363	19	0.093	-.HGGSGGPADPVPVK.-
R3/RRR3-23/3	1275.857	1275.396	363.155	0.327	897.575	0.278	21	0.093	R.HGGSGGPADPVPVK.L
R3/RRR3-25/3	1275.452	1275.396	44.472	0.365	722.576	0.330	21	0.093	-.HGGSGGPADPVPVK.-
R3/RRR3-25/3	1275.403	1275.396	6.171	0.377	1031.752	0.235	23	0.091	R.HGGSGGPADPVPVK.L
R3/RRR3-27/3	1275.395	1275.396	-0.165	0.274	762.413	0.078	21	0.081	-.HGGSGGPADPVPVK.-
R3/RRR3-8/2	1746.534	1746.901	-210.841	0.465	2279.638	0.467	23	0.333	R.VTGSLADGAATIQSALDR.M
R3/RRR3-8/2	1903.448	1904.153	-898.704	0.477	1738.238	0.497	24	0.250	R.SALDYLELQPDLSALVR.G
R3/RRR3-8/3	1903.206	1904.153	-1026.491	0.320	2240.165	0.243	32	0.210	R.SALDYLELQPDLSALVR.G
R3/RRR3-8/2	1904.513	1904.153	189.545	0.567	1296.364	0.500	23	0.197	R.SALDYLELQPDLSALVR.G
R3/RRR3-8/2	1902.895	1904.153	-1190.371	0.422	1376.413	0.391	23	0.184	R.SALDYLELQPDLSALVR.G
R3/RRR3-15/2	1772.315	1772.894	-893.421	0.484	2127.613	0.524	21	0.320	R.GFTVSTVEEEVAYNAR.L
R3/RRR3-15/2	1771.671	1772.894	-1258.083	0.348	2155.942	0.445	21	0.302	R.GFTVSTVEEEVAYNAR.L
R3/RRR3-15/2	1772.262	1772.894	-923.431	0.474	1996.274	0.512	21	0.293	R.GFTVSTVEEEVAYNAR.L
R3/RRR3-15/2	1208.057	1208.456	-331.375	0.399	1461.180	0.383	17	0.193	R.MAFTGDALLIR.A
R3/RRR3-15/2	1225.093	1224.455	-296.067	0.365	652.220	0.390	13	0.141	R.M*AFTGDALLIR.A
R3/RRR3-23/2	1205.512	1206.380	-1553.888	0.509	1199.622	0.545	19	0.201	R.KGHAVGDIPGVR.F
R3/RRR3-22/2	1207.152	1206.380	-189.120	0.478	1161.083	0.530	19	0.194	R.KGHAVGDIPGVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1206.174	1206.380	-171.205	0.515	1022.758	0.555	18	0.187	R.KGHAVGDIPGVR.F
R3/RRR3-22/2	1205.945	1206.380	-361.500	0.486	914.445	0.529	17	0.174	R.KGHAVGDIPGVR.F
R3/RRR3-22/2	1206.202	1206.380	-147.550	0.517	911.881	0.519	17	0.173	R.KGHAVGDIPGVR.F
R3/RRR3-23/2	1078.108	1078.207	-91.944	0.407	616.398	0.563	16	0.163	K.GHAVGDIPGVR.F
R3/RRR3-23/2	1077.929	1078.207	-258.702	0.367	625.693	0.567	16	0.161	K.GHAVGDIPGVR.F
R3/RRR3-22/2	1077.991	1078.207	-200.308	0.404	558.151	0.558	15	0.159	K.GHAVGDIPGVR.F
R3/RRR3-23/2	1078.237	1078.207	28.319	0.366	736.011	0.445	16	0.153	K.GHAVGDIPGVR.F
R3/RRR3-22/2	1077.814	1078.207	-365.511	0.358	521.564	0.516	14	0.151	K.GHAVGDIPGVR.F
R3/RRR3-22/2	1077.365	1078.207	-1714.509	0.324	483.864	0.518	15	0.150	K.GHAVGDIPGVR.F
R3/RRR3-28/2	1078.047	1078.207	-148.622	0.333	254.197	0.459	11	0.136	-.GHAVGDIPGVR.-
R3/RRR3-22/3	1205.619	1206.380	-1464.647	0.466	1045.297	0.417	24	0.118	R.KGHAVGDIPGVR.F
R3/RRR3-23/3	1205.634	1206.380	-1451.985	0.426	883.776	0.455	22	0.118	R.KGHAVGDIPGVR.F
R3/RRR3-28/3	1206.395	1206.380	13.171	0.461	1035.879	0.418	25	0.117	R.KGHAVGDIPGVR.F
R3/RRR3-22/3	1206.148	1206.380	-192.232	0.506	1128.987	0.378	25	0.115	R.KGHAVGDIPGVR.F
R3/RRR3-23/3	1206.367	1206.380	-10.882	0.491	796.668	0.427	23	0.111	R.KGHAVGDIPGVR.F
R3/RRR3-23/3	1206.623	1206.380	201.904	0.466	907.778	0.409	25	0.111	R.KGHAVGDIPGVR.F
R3/RRR3-19/3	1205.996	1206.380	-318.653	0.423	992.454	0.380	24	0.110	R.KGHAVGDIPGVR.F
R3/RRR3-22/3	1206.641	1206.380	217.578	0.468	996.369	0.376	24	0.109	R.KGHAVGDIPGVR.F
R3/RRR3-20/3	1206.164	1206.380	-179.135	0.408	653.948	0.400	22	0.105	R.KGHAVGDIPGVR.F
R3/RRR3-24/3	1206.173	1206.380	-172.130	0.432	1230.900	0.283	25	0.104	R.KGHAVGDIPGVR.F
R3/RRR3-28/3	1205.872	1206.380	-1254.166	0.421	991.684	0.306	23	0.100	R.KGHAVGDIPGVR.F
R3/RRR3-28/3	1206.352	1206.380	-22.605	0.420	696.086	0.327	23	0.099	R.KGHAVGDIPGVR.F
R3/RRR3-20/3	1206.095	1206.380	-237.009	0.354	506.945	0.321	19	0.097	-.KGHAVGDIPGVR.-
R3/RRR3-21/3	1206.901	1206.380	-397.745	0.429	911.015	0.223	24	0.089	R.KGHAVGDIPGVR.F
R3/RRR3-19/3	1206.033	1206.380	-288.492	0.315	919.990	0.144	23	0.083	R.KGHAVGDIPGVR.F
R3/RRR3-21/3	1207.207	1206.380	-143.128	0.356	686.595	0.172	20	0.081	-.KGHAVGDIPGVR.-
R3/RRR3-20/2	1335.193	1334.500	-230.405	0.466	1750.266	0.386	19	0.226	R.IEVTDPASFQVK.E
R3/RRR3-20/2	1334.086	1334.500	-310.900	0.406	1155.802	0.351	17	0.162	R.IEVTDPASFQVK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	945.038	945.100	-66.412	0.380	967.668	0.283	13	0.145	R.LAVDKWGR.I
R3/RRR3-21/2	945.058	945.100	-44.516	0.341	801.772	0.316	13	0.143	R.LAVDKWGR.I
R3/RRR3-21/2	944.797	945.100	-321.463	0.340	845.617	0.311	12	0.143	R.LAVDKWGR.I
R3/RRR3-20/2	1333.949	1334.500	-1166.001	0.241	683.835	0.126	13	0.125	R.IEVTDPASFQVK.E
R3/RRR3-22/3	1866.246	1867.012	-949.035	0.514	2072.363	0.518	30	0.275	R.HDVESAIPYHAELTQR.G
R3/RRR3-22/3	1866.955	1867.012	-30.542	0.546	1611.806	0.559	29	0.212	R.HDVESAIPYHAELTQR.G
R3/RRR3-22/3	1866.290	1867.012	-925.198	0.540	1495.206	0.590	27	0.206	R.HDVESAIPYHAELTQR.G
R3/RRR3-21/3	1867.081	1867.012	37.331	0.463	1480.951	0.529	28	0.186	R.HDVESAIPYHAELTQR.G
R3/RRR3-21/3	1866.312	1867.012	-913.280	0.454	1316.690	0.513	26	0.163	R.HDVESAIPYHAELTQR.G
R3/RRR3-21/2	1465.636	1464.604	22.254	0.442	796.731	0.431	15	0.152	R.LSYLWADDPEVR.A
R3/RRR3-22/2	1464.178	1464.604	-291.806	0.391	845.297	0.368	15	0.146	R.LSYLWADDPEVR.A
R3/RRR3-22/2	1464.053	1464.604	-1062.383	0.343	815.356	0.345	15	0.142	R.LSYLWADDPEVR.A
R3/RRR3-23/2	1224.683	1225.420	-1421.992	0.429	1789.706	0.502	20	0.260	R.VLLINEGPNAGK.L
R3/RRR3-23/2	1226.217	1225.420	-165.511	0.545	1377.842	0.490	17	0.204	R.VLLINEGPNAGK.L
R3/RRR3-23/2	1225.127	1225.420	-239.612	0.459	1101.164	0.545	17	0.189	R.VLLINEGPNAGK.L
R3/RRR3-23/2	1131.964	1132.206	-214.445	0.423	1227.602	0.394	17	0.175	R.VLVDGPSSDSR.L
R3/RRR3-23/2	1131.541	1132.206	-1476.285	0.335	1031.052	0.398	16	0.160	R.VLVDGPSSDSR.L
R3/RRR3-23/2	1131.359	1132.206	-1637.662	0.336	1043.795	0.360	16	0.156	R.VLVDGPSSDSR.L
R3/RRR3-23/2	1131.375	1132.206	-1623.896	0.289	1091.930	0.327	16	0.153	R.VLVDGPSSDSR.L
R3/RRR3-21/2	1316.230	1316.443	-162.378	0.425	2027.999	0.411	24	0.273	R.ATGGEVGASSALAPK.I
R3/RRR3-21/2	1315.667	1316.443	-1354.086	0.356	1791.808	0.400	23	0.235	R.ATGGEVGASSALAPK.I
R3/RRR3-21/2	1316.174	1316.443	-204.990	0.410	1622.966	0.401	22	0.213	R.ATGGEVGASSALAPK.I
R3/RRR3-23/2	1473.389	1472.624	-160.099	0.565	1936.713	0.546	20	0.295	R.AFVVHELEDDLGK.G
R3/RRR3-23/2	1471.625	1472.624	-1362.837	0.445	1977.221	0.455	20	0.276	R.AFVVHELEDDLGK.G
R3/RRR3-23/2	1472.086	1472.624	-1048.019	0.513	1977.845	0.444	20	0.273	R.AFVVHELEDDLGK.G
R3/RRR3-23/2	1325.267	1324.511	-184.552	0.405	592.899	0.552	17	0.157	K.QIPLSGPNSVVGR.A
R3/RRR3-23/2	1324.570	1324.511	44.128	0.334	520.249	0.484	16	0.145	K.QIPLSGPNSVVGR.A
R3/RRR3-23/2	1323.663	1324.511	-1400.851	0.298	316.208	0.468	13	0.138	K.QIPLSGPNSVVGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/3	1472.164	1472.624	-313.852	0.381	418.139	0.546	22	0.110	R.AFVVHELEDDLGK.G
R3/RRR3-23/3	1472.203	1472.624	-287.272	0.312	445.705	0.438	22	0.098	R.AFVVHELEDDLGK.G
R3/RRR3-15/2	1421.078	1421.622	-1090.204	0.509	1796.815	0.571	21	0.279	K.LPGLFIWSADSSK.V
R3/RRR3-15/2	1422.124	1421.622	-351.403	0.541	1686.176	0.577	21	0.264	K.LPGLFIWSADSSK.V
R3/RRR3-15/2	1422.353	1421.622	-189.601	0.545	1590.884	0.574	21	0.251	K.LPGLFIWSADSSK.V
R3/RRR3-15/2	1421.077	1421.622	-1090.290	0.507	1528.144	0.605	21	0.250	K.LPGLFIWSADSSK.V
R3/RRR3-15/2	1421.033	1421.622	-1121.773	0.503	1486.521	0.543	20	0.229	K.LPGLFIWSADSSK.V
R3/RRR3-15/2	1420.955	1421.622	-1176.807	0.512	1195.100	0.600	18	0.208	K.LPGLFIWSADSSK.V
R3/RRR3-15/2	1338.004	1338.404	-299.375	0.442	1201.867	0.487	17	0.189	K.VSSYGFEYETR.G
R3/RRR3-14/2	1421.857	1421.622	165.624	0.444	1047.474	0.561	17	0.186	K.LPGLFIWSADSSK.V
R3/RRR3-15/2	1337.596	1338.404	-1355.319	0.358	1056.795	0.522	17	0.179	K.VSSYGFEYETR.G
R3/RRR3-15/2	1337.574	1338.404	-1372.185	0.391	1181.542	0.443	17	0.178	K.VSSYGFEYETR.G
R3/RRR3-19/2	1299.963	1299.585	291.915	0.545	1791.685	0.588	19	0.283	R.TLINNLIIGVTK.G
R3/RRR3-18/2	1299.133	1299.585	-348.575	0.469	1148.433	0.457	17	0.178	R.TLINNLIIGVTK.G
R3/RRR3-19/3	1501.115	1501.669	-1038.487	0.482	1456.728	0.506	25	0.175	K.SLSHVAVNFSQPSK.N
R3/RRR3-18/2	1298.632	1299.585	-1508.462	0.418	1137.756	0.400	16	0.167	R.TLINNLIIGVTK.G
R3/RRR3-19/3	1502.004	1501.669	224.027	0.521	1491.105	0.425	26	0.156	K.SLSHVAVNFSQPSK.N
R3/RRR3-18/2	1298.932	1299.585	-1276.330	0.449	699.048	0.410	16	0.148	R.TLINNLIIGVTK.G
R3/RRR3-19/2	1298.738	1299.585	-1425.849	0.345	628.103	0.446	15	0.147	R.TLINNLIIGVTK.G
R3/RRR3-18/3	1501.212	1501.669	-305.332	0.397	941.472	0.411	21	0.110	-.SLSHVAVNFSQPSK.-
R3/RRR3-13/2	1767.861	1766.927	-37.441	0.557	1775.568	0.577	21	0.276	R.GLLTSDQTLFESPETK.R
R3/RRR3-13/2	1766.631	1766.927	-168.038	0.464	1612.966	0.496	21	0.232	R.GLLTSDQTLFESPETK.R
R3/RRR3-13/2	1304.263	1305.420	-1658.531	0.347	1022.924	0.463	17	0.168	R.TSNVFDGVYFR.E
R3/RRR3-13/2	1305.335	1305.420	-65.528	0.454	853.878	0.441	15	0.156	R.TSNVFDGVYFR.E
R3/RRR3-18/2	1174.392	1174.374	15.366	0.518	1800.128	0.476	17	0.256	K.LSELGILSWR.L
R3/RRR3-18/2	1173.387	1174.374	-1698.270	0.445	1663.444	0.535	17	0.251	K.LSELGILSWR.L
R3/RRR3-18/2	1174.320	1174.374	-46.460	0.568	1666.720	0.421	17	0.224	K.LSELGILSWR.L
R3/RRR3-18/2	1704.403	1704.776	-219.214	0.534	1437.514	0.477	19	0.207	R.LNADDWENDENLKK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1229.062	1229.385	-263.713	0.445	1683.114	0.463	17	0.237	R.ISAM*IYEETR.G
R3/RRR3-25/2	1326.237	1326.527	-219.498	0.489	1400.381	0.492	19	0.209	R.DNIQGITKPAIR.R
R3/RRR3-25/2	1326.380	1326.527	-111.565	0.470	1201.882	0.398	17	0.172	R.DNIQGITKPAIR.R
R3/RRR3-25/2	1326.599	1326.527	54.305	0.414	1264.470	0.349	18	0.169	R.DNIQGITKPAIR.R
R3/RRR3-24/2	1326.037	1326.527	-370.587	0.443	1015.457	0.458	17	0.169	R.DNIQGITKPAIR.R
R3/RRR3-24/2	1327.040	1326.527	-368.370	0.448	982.618	0.438	17	0.165	R.DNIQGITKPAIR.R
R3/RRR3-25/2	1326.173	1326.527	-267.794	0.423	988.142	0.394	17	0.159	R.DNIQGITKPAIR.R
R3/RRR3-24/2	1327.430	1326.527	-73.291	0.407	907.300	0.423	16	0.157	R.DNIQGITKPAIR.R
R3/RRR3-23/2	1327.187	1326.527	-257.164	0.369	864.672	0.400	16	0.152	R.DNIQGITKPAIR.R
R3/RRR3-25/2	1326.218	1326.527	-233.811	0.451	893.891	0.374	16	0.151	R.DNIQGITKPAIR.R
R3/RRR3-25/2	1228.754	1229.385	-1331.352	0.341	879.250	0.386	15	0.150	R.ISAM*IYEETR.G
R3/RRR3-25/2	1327.389	1326.527	-104.655	0.366	900.146	0.287	15	0.141	-.DNIQGITKPAIR.-
R3/RRR3-25/2	1260.251	1260.466	-170.853	0.479	1802.264	0.528	18	0.268	R.FTTFALSGFIR.A
R3/RRR3-25/2	1260.958	1260.466	391.537	0.499	1318.322	0.571	17	0.217	R.FTTFALSGFIR.A
R3/RRR3-26/2	1260.307	1260.466	-126.449	0.439	1376.220	0.524	18	0.212	R.FTTFALSGFIR.A
R3/RRR3-25/2	1260.049	1260.466	-331.791	0.425	1398.849	0.507	18	0.211	R.FTTFALSGFIR.A
R3/RRR3-25/2	1260.013	1260.466	-360.466	0.433	1233.078	0.550	17	0.203	R.FTTFALSGFIR.A
R3/RRR3-25/2	1260.178	1260.466	-228.964	0.409	1272.857	0.516	17	0.199	R.FTTFALSGFIR.A
R3/RRR3-25/2	1674.261	1674.796	-919.565	0.506	1394.477	0.418	20	0.190	R.AQGDADSALDRLWQK.R
R3/RRR3-26/2	1260.310	1260.466	-123.826	0.427	1047.072	0.525	16	0.182	R.FTTFALSGFIR.A
R3/RRR3-25/2	1259.980	1260.466	-386.809	0.445	1029.109	0.498	17	0.178	R.FTTFALSGFIR.A
R3/RRR3-25/2	1674.290	1674.796	-902.584	0.485	1092.294	0.427	18	0.166	R.AQGDADSALDRLWQK.R
R3/RRR3-25/2	1675.273	1674.796	285.131	0.520	1183.834	0.384	19	0.165	R.AQGDADSALDRLWQK.R
R3/RRR3-26/2	1260.039	1260.466	-339.567	0.304	329.277	0.366	13	0.141	R.FTTFALSGFIR.A
R3/RRR3-26/2	1674.265	1674.796	-917.442	0.365	878.129	0.294	17	0.138	R.AQGDADSALDRLWQK.R
R3/RRR3-10/2	1886.237	1885.236	0.545	0.611	1850.099	0.599	28	0.296	R.QAIPFLESLVVADVAALK.D
R3/RRR3-10/2	1884.705	1885.236	-814.873	0.576	1837.444	0.576	28	0.287	R.QAIPFLESLVVADVAALK.D
R3/RRR3-10/2	1885.828	1885.236	-217.342	0.597	1874.359	0.524	28	0.277	R.QAIPFLESLVVADVAALK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1884.601	1885.236	-870.472	0.499	1932.448	0.447	33	0.225	R.QAIPFLESLVVADVAALK.D
R3/RRR3-10/3	1884.290	1885.236	-1035.919	0.449	1739.450	0.398	31	0.182	R.QAIPFLESLVVADVAALK.D
R3/RRR3-10/2	1397.204	1397.473	-193.189	0.411	1025.650	0.470	18	0.169	K.DGTGTLTVFTNDR.G
R3/RRR3-14/3	1569.758	1570.729	-1259.436	0.511	1907.842	0.552	34	0.249	R.SPSGVIHLTDTSVTR.F
R3/RRR3-14/3	1570.814	1570.729	54.076	0.506	1711.776	0.571	34	0.223	R.SPSGVIHLTDTSVTR.F
R3/RRR3-14/3	1570.690	1570.729	-24.961	0.407	1305.935	0.478	29	0.149	R.SPSGVIHLTDTSVTR.F
R3/RRR3-14/3	1570.749	1570.729	12.338	0.400	1005.390	0.505	27	0.131	R.SPSGVIHLTDTSVTR.F
R3/RRR3-14/3	1813.980	1813.994	-7.541	0.383	1101.766	0.346	24	0.106	R.SRSPSGVIHLTDTSVTR.F
R3/RRR3-18/2	1772.446	1772.978	-867.106	0.486	1261.995	0.561	23	0.206	R.NQDVSLTELPATVSAVK.N
R3/RRR3-18/2	1771.683	1772.978	-1299.470	0.371	1136.720	0.454	21	0.173	R.NQDVSLTELPATVSAVK.N
R3/RRR3-18/2	1771.732	1772.978	-1271.308	0.382	571.662	0.413	17	0.139	R.NQDVSLTELPATVSAVK.N
R3/RRR3-18/3	1771.594	1772.978	-1349.856	0.385	929.688	0.305	27	0.092	-.NQDVSLTELPATVSAVK.-
R3/RRR3-17/2	1518.081	1518.721	-1083.772	0.496	1905.507	0.538	23	0.284	K.AAAVGANSQAAQSMLK.Q
R3/RRR3-16/3	1534.975	1534.721	166.511	0.508	1864.855	0.552	29	0.251	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-17/2	1517.704	1518.721	-1333.077	0.415	1598.091	0.506	23	0.232	K.AAAVGANSQAAQSMLK.Q
R3/RRR3-17/3	1533.789	1534.721	-1263.327	0.495	1669.369	0.546	30	0.215	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-16/2	1535.824	1534.721	67.176	0.544	1318.786	0.559	20	0.210	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-17/2	1536.150	1534.721	280.050	0.525	1055.256	0.576	19	0.188	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-16/2	1536.092	1534.721	242.678	0.526	1065.745	0.546	20	0.185	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-17/2	1007.984	1008.110	-125.428	0.446	893.753	0.491	14	0.169	R.TTIFSPEGR.L
R3/RRR3-17/2	1536.109	1534.721	253.435	0.516	781.253	0.545	19	0.166	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-17/2	1007.847	1008.110	-261.992	0.325	830.518	0.379	14	0.149	R.TTIFSPEGR.L
R3/RRR3-16/2	1535.926	1534.721	134.291	0.362	425.870	0.519	17	0.148	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-17/2	1536.061	1534.721	222.357	0.355	391.463	0.476	18	0.145	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-16/2	1007.513	1008.110	-1589.480	0.303	610.890	0.353	13	0.141	R.TTIFSPEGR.L
R3/RRR3-19/2	1535.819	1534.721	64.226	0.258	232.612	0.459	17	0.141	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-15/2	1535.907	1534.721	121.618	0.272	153.982	0.343	14	0.140	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-17/2	1007.869	1008.110	-239.512	0.309	674.861	0.248	13	0.136	R.TTIFSPEGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1007.898	1008.110	-211.444	0.291	680.988	0.227	13	0.134	R.TTIFSPEGR.L
R3/RRR3-16/2	1007.768	1008.110	-340.740	0.302	498.634	0.271	11	0.134	-.TTIFSPEGR.-
R3/RRR3-16/3	1533.651	1534.721	-1353.852	0.372	742.412	0.450	24	0.107	K.AAAVGANSQAAQSM*LK.Q
R3/RRR3-11/2	1325.468	1325.538	-52.801	0.522	1744.061	0.540	19	0.264	R.YSGNFLVNLLGK.W
R3/RRR3-11/2	1324.802	1325.538	-1314.251	0.508	1593.467	0.565	19	0.249	R.YSGNFLVNLLGK.W
R3/RRR3-11/2	1324.966	1325.538	-1189.338	0.509	1371.766	0.583	18	0.225	R.YSGNFLVNLLGK.W
R3/RRR3-11/2	1165.159	1165.278	-102.624	0.469	1351.056	0.449	18	0.196	K.TWIEVSGSSAK.D
R3/RRR3-11/2	1165.132	1165.278	-125.639	0.371	1125.031	0.368	17	0.162	K.TWIEVSGSSAK.D
R3/RRR3-6/2	1775.524	1775.041	273.307	0.571	2120.846	0.573	22	0.337	K.IPIDYSWAQELGLIR.K
R3/RRR3-6/2	1413.908	1413.514	279.561	0.477	1228.662	0.466	19	0.185	R.FGGALDGAAEEFTK.A
R3/RRR3-24/2	937.865	937.977	-118.944	0.417	904.015	0.310	13	0.147	R.ASLNDFDR.F
R3/RRR3-24/2	937.374	937.977	-1714.748	0.354	761.180	0.341	13	0.144	R.ASLNDFDR.F
R3/RRR3-24/2	1212.440	1213.324	-1558.541	0.356	743.976	0.314	14	0.141	R.ASLNDFDRFK.-
R3/RRR3-24/2	937.684	937.977	-312.607	0.348	888.788	0.257	13	0.140	R.ASLNDFDR.F
R3/RRR3-23/2	1213.060	1213.324	-218.075	0.353	658.037	0.322	13	0.139	R.ASLNDFDRFK.-
R3/RRR3-23/2	1212.451	1213.324	-1549.843	0.347	737.947	0.282	14	0.138	R.ASLNDFDRFK.-
R3/RRR3-24/2	1213.041	1213.324	-234.227	0.384	603.625	0.279	13	0.137	R.ASLNDFDRFK.-
R3/RRR3-23/2	1212.559	1213.324	-1460.242	0.355	486.866	0.282	12	0.135	-.ASLNDFDRFK.-
R3/RRR3-24/2	1213.130	1213.324	-160.635	0.362	605.648	0.236	13	0.134	R.ASLNDFDRFK.-
R3/RRR3-28/2	1484.359	1484.624	-179.042	0.452	1849.848	0.414	20	0.246	R.SPCSLYACEAGLR.A
R3/RRR3-28/2	1484.074	1484.624	-1047.309	0.429	1778.120	0.393	20	0.231	R.SPCSLYACEAGLR.A
R3/RRR3-28/2	1483.935	1484.624	-1141.219	0.411	1810.229	0.329	20	0.220	R.SPCSLYACEAGLR.A
R3/RRR3-28/2	993.861	994.080	-221.083	0.312	921.797	0.256	15	0.141	R.AWCGSGVTR.C
R3/RRR3-28/2	993.424	994.080	-1671.921	0.308	871.093	0.260	15	0.140	R.AWCGSGVTR.C
R3/RRR3-28/2	993.418	994.080	-1678.217	0.220	636.013	0.182	13	0.130	R.AWCGSGVTR.C
R3/RRR3-28/2	993.427	994.080	-1668.464	0.199	673.868	0.190	13	0.130	R.AWCGSGVTR.C
R3/RRR3-22/2	1484.087	1484.624	-1038.390	0.202	764.265	0.048	18	0.125	R.SPCSLYACEAGLR.A
R3/RRR3-15/2	943.845	944.071	-240.193	0.470	1576.252	0.410	15	0.211	R.SAVQAALQR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	943.799	944.071	-289.242	0.486	1552.258	0.421	15	0.211	R.SAVQAALQR.E
R3/RRR3-14/2	944.974	944.071	-102.177	0.538	1520.182	0.426	15	0.208	R.SAVQAALQR.E
R3/RRR3-12/2	943.986	944.071	-89.444	0.438	1487.511	0.413	15	0.202	R.SAVQAALQR.E
R3/RRR3-13/2	943.570	944.071	-1595.334	0.445	1310.580	0.402	14	0.183	R.SAVQAALQR.E
R3/RRR3-13/2	943.950	944.071	-128.359	0.508	1319.265	0.386	14	0.180	R.SAVQAALQR.E
R3/RRR3-12/2	1027.067	1027.243	-171.735	0.454	1140.547	0.411	15	0.171	R.EIALAAGLIR.I
R3/RRR3-12/2	1026.631	1027.243	-1574.430	0.374	981.614	0.251	14	0.140	R.EIALAAGLIR.I
R3/RRR3-21/2	1994.235	1994.193	20.898	0.615	1658.052	0.646	28	0.278	R.VVIGLYGDDVPQTAENFR.A
R3/RRR3-20/2	1993.497	1994.193	-853.686	0.563	1527.714	0.603	27	0.248	R.VVIGLYGDDVPQTAENFR.A
R3/RRR3-21/2	1993.636	1994.193	-783.369	0.590	1242.148	0.637	26	0.222	R.VVIGLYGDDVPQTAENFR.A
R3/RRR3-20/2	1993.559	1994.193	-822.460	0.589	1305.414	0.606	26	0.222	R.VVIGLYGDDVPQTAENFR.A
R3/RRR3-20/2	1994.044	1994.193	-75.254	0.622	1111.608	0.654	25	0.212	R.VVIGLYGDDVPQTAENFR.A
R3/RRR3-21/2	1993.673	1994.193	-765.054	0.579	1171.005	0.602	25	0.206	R.VVIGLYGDDVPQTAENFR.A
R3/RRR3-20/2	1408.793	1409.611	-1294.647	0.400	868.461	0.543	15	0.166	K.VYFDISIGNPVGK.N
R3/RRR3-20/2	1408.592	1409.611	-1438.078	0.378	678.127	0.439	14	0.144	-.VYFDISIGNPVGK.-
R3/RRR3-11/2	1084.792	1085.234	-408.871	0.331	840.166	0.543	15	0.165	K.YGVSGYPTLK.F
R3/RRR3-11/2	1084.824	1085.234	-379.627	0.335	780.117	0.532	14	0.160	K.YGVSGYPTLK.F
R3/RRR3-11/2	970.484	971.134	-1705.701	0.409	609.435	0.429	12	0.149	K.HLAPIYEK.L
R3/RRR3-11/2	970.354	971.134	-1840.561	0.365	632.732	0.353	12	0.142	K.HLAPIYEK.L
R3/RRR3-11/2	970.889	971.134	-253.490	0.326	508.885	0.292	11	0.137	K.HLAPIYEK.L
R3/RRR3-20/3	1771.627	1772.938	-1308.261	0.436	1850.051	0.496	28	0.230	R.KENLSKPDDVLSAAER.Y
R3/RRR3-20/3	1773.905	1772.938	-18.651	0.520	1642.403	0.486	30	0.192	R.KENLSKPDDVLSAAER.Y
R3/RRR3-20/2	1547.529	1546.685	-101.335	0.492	620.992	0.465	17	0.148	R.SILEEVESEHM*AR.A
R3/RRR3-13/2	1456.171	1456.625	-312.665	0.507	1961.406	0.525	21	0.294	R.NDVFQYLASSLAK.L
R3/RRR3-13/2	1456.226	1456.625	-274.482	0.528	1858.618	0.483	21	0.266	R.NDVFQYLASSLAK.L
R3/RRR3-13/2	1457.221	1456.625	-278.243	0.553	1765.953	0.499	20	0.255	R.NDVFQYLASSLAK.L
R3/RRR3-13/2	1153.026	1153.267	-209.466	0.463	1113.620	0.371	16	0.164	K.YVVNDSTNIK.S
R3/RRR3-13/2	1152.948	1153.267	-277.975	0.454	1009.188	0.398	16	0.162	K.YVVNDSTNIK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1152.817	1153.267	-391.329	0.377	998.294	0.339	15	0.152	K.YVVNDSTNIK.S
R3/RRR3-12/2	1158.077	1158.244	-144.589	0.510	1539.225	0.442	19	0.215	K.VASDDLDPAVR.E
R3/RRR3-12/2	1158.069	1158.244	-151.357	0.519	1547.390	0.421	19	0.211	K.VASDDLDPAVR.E
R3/RRR3-12/2	1157.459	1158.244	-1546.680	0.408	1462.565	0.345	19	0.187	K.VASDDLDPAVR.E
R3/RRR3-12/2	1108.036	1108.229	-175.097	0.460	1016.744	0.494	16	0.174	R.VAEEGLPHGAK.I
R3/RRR3-10/2	1654.315	1654.974	-1006.143	0.467	2178.862	0.452	23	0.308	K.ETLIAGGPFVLPLAQK.H
R3/RRR3-10/2	1655.366	1654.974	237.230	0.569	2002.029	0.514	22	0.294	K.ETLIAGGPFVLPLAQK.H
R3/RRR3-10/2	1656.032	1654.974	35.073	0.557	1939.994	0.495	22	0.278	K.ETLIAGGPFVLPLAQK.H
R3/RRR3-10/2	1423.171	1423.575	-284.740	0.452	1317.208	0.460	20	0.192	R.AGGTM*TGVLSAANEK.A
R3/RRR3-10/2	1423.154	1423.575	-296.874	0.435	1050.563	0.465	19	0.169	R.AGGTM*TGVLSAANEK.A
R3/RRR3-17/2	1294.417	1295.467	-1588.288	0.389	1172.392	0.551	17	0.194	R.VNQSFVIATSTK.L
R3/RRR3-17/2	1294.662	1295.467	-1398.090	0.362	1303.334	0.474	18	0.193	R.VNQSFVIATSTK.L
R3/RRR3-17/2	1295.353	1295.467	-88.056	0.443	1068.996	0.568	17	0.190	R.VNQSFVIATSTK.L
R3/RRR3-17/2	1451.020	1451.653	-1128.798	0.450	1104.229	0.466	19	0.175	K.RVNQSFVIATSTK.L
R3/RRR3-20/2	1294.839	1295.467	-1261.169	0.301	711.977	0.430	16	0.147	R.VNQSFVIATSTK.L
R3/RRR3-19/2	1295.043	1295.467	-328.404	0.350	751.197	0.405	15	0.147	R.VNQSFVIATSTK.L
R3/RRR3-18/2	1729.435	1728.967	271.317	0.561	1060.299	0.589	24	0.197	K.IWQVPETLSEEVLGK.M
R3/RRR3-18/2	1728.475	1728.967	-285.437	0.514	1121.249	0.549	24	0.194	K.IWQVPETLSEEVLGK.M
R3/RRR3-18/2	1728.288	1728.967	-974.555	0.487	1082.928	0.562	24	0.193	K.IWQVPETLSEEVLGK.M
R3/RRR3-18/3	1728.806	1728.967	-93.252	0.448	1255.528	0.417	28	0.131	K.IWQVPETLSEEVLGK.M
R3/RRR3-11/2	1933.416	1933.152	137.127	0.570	1691.789	0.643	24	0.281	R.SFLQAVSTVTEEAPSPLR.V
R3/RRR3-11/2	1932.527	1933.152	-843.429	0.493	1681.148	0.602	24	0.268	R.SFLQAVSTVTEEAPSPLR.V
R3/RRR3-11/2	1589.435	1589.856	-265.652	0.474	1691.480	0.350	19	0.210	K.LSWVDIFEEIPIK.V
R3/RRR3-11/2	1931.843	1933.152	-1198.709	0.324	1329.179	0.392	22	0.178	R.SFLQAVSTVTEEAPSPLR.V
R3/RRR3-14/2	1499.762	1499.777	-10.091	0.505	2038.370	0.487	21	0.297	K.LLLLTDVSGILADR.N
R3/RRR3-14/2	1488.522	1487.725	-137.249	0.500	953.290	0.434	19	0.162	R.VDVLSEALPFIQR.F
R3/RRR3-14/2	1487.462	1487.725	-177.763	0.434	964.067	0.415	19	0.160	R.VDVLSEALPFIQR.F
R3/RRR3-14/2	1486.894	1487.725	-1235.455	0.345	927.860	0.322	19	0.146	R.VDVLSEALPFIQR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1506.298	1506.601	-201.388	0.527	1867.469	0.606	23	0.302	K.LASLSQGAAGESSTAR.E
R3/RRR3-10/2	1357.161	1356.553	-289.646	0.470	1879.187	0.567	21	0.292	R.GVAIGVGQSEILGR.I
R3/RRR3-10/2	1356.528	1356.553	-18.693	0.414	1390.054	0.457	19	0.198	R.GVAIGVGQSEILGR.I
R3/RRR3-7/3	1584.307	1584.675	-232.941	0.491	2077.969	0.516	29	0.267	K.HQLDDKWDGVNTR.L
R3/RRR3-2/3	1584.024	1584.675	-1045.427	0.433	1492.010	0.512	26	0.179	K.HQLDDKWDGVNTR.L
R3/RRR3-7/2	1380.608	1380.656	-35.261	0.410	869.621	0.428	17	0.154	R.IVGFEVKPYSIK.H
R3/RRR3-7/3	1584.253	1584.675	-266.799	0.452	1298.364	0.467	24	0.148	K.HQLDDKWDGVNTR.L
R3/RRR3-3/3	1584.279	1584.675	-250.450	0.442	1105.336	0.512	24	0.141	K.HQLDDKWDGVNTR.L
R3/RRR3-2/3	1584.896	1584.675	140.041	0.476	1132.663	0.487	24	0.138	K.HQLDDKWDGVNTR.L
R3/RRR3-7/3	1584.930	1584.675	161.359	0.477	1210.916	0.431	25	0.131	K.HQLDDKWDGVNTR.L
R3/RRR3-2/3	1584.943	1584.675	169.701	0.396	893.777	0.388	22	0.107	K.HQLDDKWDGVNTR.L
R3/RRR3-8/3	1585.143	1584.675	296.430	0.362	691.613	0.292	20	0.093	K.HQLDDKWDGVNTR.L
R3/RRR3-11/2	1088.214	1088.283	-63.525	0.523	1650.236	0.597	19	0.266	R.VVGVLLGTSSR.G
R3/RRR3-11/2	1087.317	1088.283	-1813.673	0.476	1644.251	0.564	19	0.256	R.VVGVLLGTSSR.G
R3/RRR3-12/2	1087.997	1088.283	-263.961	0.425	1501.649	0.539	17	0.229	R.VVGVLLGTSSR.G
R3/RRR3-11/3	1973.999	1974.338	-172.225	0.469	1016.180	0.527	32	0.135	K.VVVHPLVLLSIVDHYNR.V
R3/RRR3-11/2	1087.458	1088.283	-1683.171	0.251	613.913	0.267	13	0.132	R.VVGVLLGTSSR.G
R3/RRR3-9/2	1828.135	1829.048	-1049.515	0.558	1320.470	0.600	24	0.223	R.GIYAYGFEKPSAIQQR.A
R3/RRR3-9/2	1828.580	1829.048	-256.956	0.557	1325.275	0.597	24	0.223	R.GIYAYGFEKPSAIQQR.A
R3/RRR3-9/2	1828.445	1829.048	-879.253	0.572	1314.915	0.580	24	0.218	R.GIYAYGFEKPSAIQQR.A
R3/RRR3-9/3	1828.596	1829.048	-248.089	0.442	1396.523	0.558	28	0.183	R.GIYAYGFEKPSAIQQR.A
R3/RRR3-10/3	1828.858	1829.048	-104.151	0.421	1337.963	0.530	29	0.167	R.GIYAYGFEKPSAIQQR.A
R3/RRR3-9/3	1829.717	1829.048	-181.724	0.406	1258.483	0.537	28	0.161	R.GIYAYGFEKPSAIQQR.A
R3/RRR3-10/2	925.531	926.138	-1742.246	0.219	652.702	0.408	13	0.139	R.AVLPIISGR.-
R3/RRR3-10/3	1828.843	1829.048	-112.386	0.428	1165.354	0.470	27	0.137	R.GIYAYGFEKPSAIQQR.A
R3/RRR3-10/2	925.982	926.138	-169.393	0.205	446.518	0.379	12	0.134	R.AVLPIISGR.-
R3/RRR3-10/2	925.616	926.138	-1649.228	0.191	504.449	0.255	12	0.130	R.AVLPIISGR.-
R3/RRR3-9/3	1829.640	1829.048	-223.689	0.462	999.650	0.489	25	0.129	R.GIYAYGFEKPSAIQQR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1669.748	1669.904	-93.682	0.472	2307.212	0.462	23	0.335	R.VVGQAEAVSAVAEAVLR.S
R3/RRR3-4/2	1669.853	1669.904	-30.840	0.437	2314.342	0.433	22	0.327	R.VVGQAEAVSAVAEAVLR.S
R3/RRR3-4/2	1669.469	1669.904	-261.717	0.470	1724.933	0.416	21	0.226	R.VVGQAEAVSAVAEAVLR.S
R3/RRR3-9/2	1587.276	1586.775	-315.534	0.407	607.345	0.318	15	0.116	-.EAGVSAARVRAELEK.-
R3/RRR3-17/2	1205.001	1204.357	-296.246	0.467	1557.406	0.505	18	0.229	R.YVDIGIPANNK.G
R3/RRR3-17/2	1203.969	1204.357	-323.246	0.407	1550.445	0.427	18	0.211	R.YVDIGIPANNK.G
R3/RRR3-11/2	1205.202	1204.357	-129.285	0.422	1496.944	0.451	17	0.210	R.YVDIGIPANNK.G
R3/RRR3-17/2	1203.326	1204.357	-1692.952	0.355	1466.844	0.452	18	0.206	R.YVDIGIPANNK.G
R3/RRR3-10/2	1203.940	1204.357	-347.254	0.396	1184.699	0.430	16	0.176	R.YVDIGIPANNK.G
R3/RRR3-17/2	1465.868	1464.730	94.416	0.485	758.300	0.472	19	0.161	K.QSIGCLFWLLAR.M
R3/RRR3-12/2	1465.602	1464.730	-87.517	0.445	614.985	0.488	16	0.155	K.QSIGCLFWLLAR.M
R3/RRR3-16/2	1465.724	1464.730	-4.395	0.401	504.823	0.432	15	0.146	K.QSIGCLFWLLAR.M
R3/RRR3-11/2	1203.878	1204.357	-399.445	0.377	759.301	0.336	16	0.144	R.YVDIGIPANNK.G
R3/RRR3-14/2	1465.997	1464.730	182.352	0.454	375.929	0.385	14	0.139	-.QSIGCLFWLLAR.-
R3/RRR3-9/2	1465.761	1464.730	21.166	0.356	569.147	0.350	14	0.139	K.QSIGCLFWLLAR.M
R3/RRR3-11/2	1466.047	1464.730	217.171	0.368	323.673	0.384	11	0.138	K.QSIGCLFWLLAR.M
R3/RRR3-14/2	1466.159	1464.730	293.648	0.353	441.948	0.267	14	0.136	K.QSIGCLFWLLAR.M
R3/RRR3-10/2	1203.347	1204.357	-1675.218	0.287	623.932	0.224	15	0.134	R.YVDIGIPANNK.G
R3/RRR3-15/2	1204.388	1204.357	25.454	0.315	715.771	0.203	16	0.134	R.YVDIGIPANNK.G
R3/RRR3-9/2	1116.995	1117.278	-253.929	0.423	2003.089	0.506	20	0.297	K.ALESAGLALGSK.S
R3/RRR3-9/2	1298.079	1298.471	-302.829	0.499	1745.323	0.556	22	0.269	R.LLAGESGIGPIDR.F
R3/RRR3-9/2	1298.151	1298.471	-246.600	0.487	1446.834	0.592	20	0.236	R.LLAGESGIGPIDR.F
R3/RRR3-9/2	1298.128	1298.471	-264.619	0.448	1401.717	0.512	20	0.213	R.LLAGESGIGPIDR.F
R3/RRR3-13/2	1212.815	1212.424	323.188	0.529	1912.761	0.519	23	0.285	K.VLVIGGGDGGVLR.E
R3/RRR3-13/2	1212.246	1212.424	-147.521	0.428	1772.978	0.511	21	0.259	K.VLVIGGGDGGVLR.E
R3/RRR3-13/2	1212.335	1212.424	-74.089	0.410	1325.142	0.444	18	0.190	K.VLVIGGGDGGVLR.E
R3/RRR3-13/2	1356.220	1356.595	-277.298	0.347	916.588	0.358	16	0.145	R.VSLHIGDGVAFLK.N
R3/RRR3-11/2	1212.579	1212.424	127.769	0.350	775.328	0.390	15	0.145	K.VLVIGGGDGGVLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/3	1356.868	1356.595	201.970	0.486	955.620	0.436	25	0.116	R.VSLHIGDGVAFLK.N
R3/RRR3-13/3	1356.825	1356.595	169.897	0.466	1058.619	0.396	26	0.114	R.VSLHIGDGVAFLK.N
R3/RRR3-13/3	1356.704	1356.595	80.705	0.527	890.411	0.403	24	0.106	-.VSLHIGDGVAFLK.-
R3/RRR3-5/2	1937.298	1938.085	-925.091	0.527	1788.507	0.554	24	0.273	K.AGIDNTSVLQATDEFISR.Q
R3/RRR3-23/2	1257.221	1256.479	-205.545	0.564	1905.927	0.346	17	0.233	R.ALDWAIANLLR.R
R3/RRR3-23/2	1255.851	1256.479	-1299.737	0.444	1878.427	0.340	17	0.232	R.ALDWAIANLLR.R
R3/RRR3-23/2	1244.748	1245.385	-1319.000	0.445	1152.106	0.505	18	0.186	R.IGVAM*DYSASSK.R
R3/RRR3-23/2	1256.152	1256.479	-260.985	0.410	1339.945	0.302	15	0.166	R.ALDWAIANLLR.R
R3/RRR3-11/2	1616.199	1615.641	-273.979	0.507	2638.730	0.479	26	0.412	R.LDFSSGQSTGTASNSR.L
R3/RRR3-11/2	1616.104	1615.641	287.464	0.560	2439.784	0.512	25	0.378	R.LDFSSGQSTGTASNSR.L
R3/RRR3-11/2	1615.372	1615.641	-166.870	0.457	2052.345	0.431	23	0.281	R.LDFSSGQSTGTASNSR.L
R3/RRR3-11/2	1073.000	1072.283	-264.797	0.526	1757.389	0.398	17	0.230	K.ISQATLALVR.N
R3/RRR3-11/2	1072.987	1072.283	-276.668	0.487	1353.844	0.420	17	0.192	K.ISQATLALVR.N
R3/RRR3-11/2	1072.968	1072.283	-294.930	0.541	1293.455	0.350	17	0.172	K.ISQATLALVR.N
R3/RRR3-11/2	1272.623	1273.418	-1414.798	0.327	1032.997	0.394	17	0.157	K.GLIDINQDSLGK.A
R3/RRR3-12/2	1860.268	1859.933	180.626	0.574	1675.417	0.608	21	0.268	R.DAGVNFFDNAEVYANGR.A
R3/RRR3-12/2	1859.394	1859.933	-829.917	0.522	1502.876	0.488	20	0.214	R.DAGVNFFDNAEVYANGR.A
R3/RRR3-12/2	1219.058	1219.330	-224.333	0.373	815.060	0.294	15	0.139	K.LFWGGQGPNDK.G
R3/RRR3-12/2	1218.893	1219.330	-359.668	0.324	876.281	0.212	16	0.134	K.LFWGGQGPNDK.G
R3/RRR3-12/2	1219.664	1219.330	274.292	0.247	691.886	0.173	14	0.128	K.LFWGGQGPNDK.G
R3/RRR3-17/2	901.331	902.074	-1938.718	0.366	1010.101	0.256	13	0.144	R.LSVQIVSR.I
R3/RRR3-17/2	901.506	902.074	-1744.538	0.403	976.335	0.256	13	0.143	-.LSVQIVSR.-
R3/RRR3-16/2	1081.785	1082.191	-376.280	0.400	1102.358	0.187	13	0.139	R.LYQFEPER.L
R3/RRR3-16/2	1081.934	1082.191	-237.828	0.351	789.386	0.188	11	0.130	R.LYQFEPER.L
R3/RRR3-16/2	901.821	902.074	-280.643	0.338	685.224	0.219	11	0.124	-.LSVQIVSR.-
R3/RRR3-9/2	1230.288	1230.436	-120.876	0.482	1059.773	0.498	17	0.180	K.TLNDQIVVLSK.R
R3/RRR3-9/2	1230.228	1230.436	-169.848	0.555	1134.049	0.450	17	0.177	K.TLNDQIVVLSK.R
R3/RRR3-9/2	1230.292	1230.436	-117.194	0.485	1049.181	0.455	17	0.172	K.TLNDQIVVLSK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1295.121	1295.500	-293.689	0.191	888.224	0.103	13	0.122	K.AAIDIVELCYK.A
R3/RRR3-22/2	1306.332	1306.450	-90.127	0.467	1205.356	0.554	17	0.200	R.TGEIVVFNVDGR.E
R3/RRR3-22/2	1307.320	1306.450	-99.518	0.527	1173.728	0.506	17	0.189	R.TGEIVVFNVDGR.E
R3/RRR3-22/2	1234.130	1233.350	-179.331	0.398	323.935	0.462	16	0.149	R.QESAEVDILTK.G
R3/RRR3-22/2	1233.049	1233.350	-244.924	0.366	292.820	0.457	14	0.145	R.QESAEVDILTK.G
R3/RRR3-22/2	1233.018	1233.350	-270.648	0.334	288.292	0.459	14	0.144	R.QESAEVDILTK.G
R3/RRR3-21/2	1234.355	1233.350	3.411	0.303	224.356	0.474	13	0.142	R.QESAEVDILTK.G
R3/RRR3-13/2	1165.029	1165.324	-254.074	0.447	1112.235	0.486	18	0.181	R.SKGTAEVVFAR.R
R3/RRR3-13/2	949.792	950.074	-297.020	0.359	964.400	0.316	14	0.148	K.GTAEVVFAR.R
R3/RRR3-13/2	949.595	950.074	-506.086	0.274	688.310	0.203	12	0.130	K.GTAEVVFAR.R
R3/RRR3-18/2	1650.683	1649.825	-86.605	0.452	1666.650	0.585	25	0.262	R.CSYTVWPGALPGGGAR.L
R3/RRR3-18/2	1884.255	1885.070	-966.078	0.503	1438.919	0.545	26	0.222	R.LDPGQSWSISVAAGTPAAR.I
R3/RRR3-18/2	1648.846	1649.825	-1204.105	0.314	1530.025	0.485	25	0.217	R.CSYTVWPGALPGGGAR.L
R3/RRR3-18/2	1884.491	1885.070	-840.564	0.510	1350.094	0.541	26	0.211	R.LDPGQSWSISVAAGTPAAR.I
R3/RRR3-18/2	1648.792	1649.825	-1236.966	0.320	1480.722	0.467	24	0.208	R.CSYTVWPGALPGGGAR.L
R3/RRR3-17/2	1649.467	1649.825	-217.979	0.472	1370.038	0.500	23	0.206	R.CSYTVWPGALPGGGAR.L
R3/RRR3-18/2	1884.488	1885.070	-842.255	0.520	1241.634	0.565	25	0.204	R.LDPGQSWSISVAAGTPAAR.I
R3/RRR3-17/2	1649.246	1649.825	-960.461	0.436	1348.273	0.504	23	0.204	R.CSYTVWPGALPGGGAR.L
R3/RRR3-17/2	1885.526	1885.070	242.687	0.568	1099.677	0.591	24	0.196	R.LDPGQSWSISVAAGTPAAR.I
R3/RRR3-17/2	1884.509	1885.070	-831.006	0.537	1083.613	0.558	24	0.188	R.LDPGQSWSISVAAGTPAAR.I
R3/RRR3-17/2	1883.980	1885.070	-1112.833	0.477	1130.858	0.538	23	0.188	R.LDPGQSWSISVAAGTPAAR.I
R3/RRR3-17/2	1648.599	1649.825	-1354.304	0.310	683.452	0.463	17	0.145	-.CSYTVWPGALPGGGAR.-
R3/RRR3-8/2	1239.999	1240.388	-314.150	0.484	1703.512	0.582	19	0.268	K.YGVTESTLLTR.N
R3/RRR3-7/2	1240.210	1240.388	-144.096	0.545	1541.018	0.587	19	0.249	K.YGVTESTLLTR.N
R3/RRR3-8/2	1240.029	1240.388	-290.544	0.538	1565.095	0.578	18	0.248	K.YGVTESTLLTR.N
R3/RRR3-8/2	1867.903	1869.154	-1208.409	0.558	1478.445	0.517	26	0.222	R.LPIYVVQPQDGLDAIAR.N
R3/RRR3-7/2	1868.373	1869.154	-955.745	0.559	1481.958	0.491	26	0.216	R.LPIYVVQPQDGLDAIAR.N
R3/RRR3-7/2	1240.040	1240.388	-281.359	0.491	1273.377	0.570	18	0.213	K.YGVTESTLLTR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1240.078	1240.388	-250.842	0.529	1189.043	0.594	18	0.210	K.YGVTESTLLTR.N
R3/RRR3-8/2	1869.850	1869.154	-162.953	0.581	1290.788	0.531	25	0.204	R.LPIYVVQPQDGLDAIAR.N
R3/RRR3-8/2	1869.518	1869.154	195.385	0.623	1235.063	0.556	25	0.204	R.LPIYVVQPQDGLDAIAR.N
R3/RRR3-8/2	1240.255	1240.388	-107.763	0.520	1084.115	0.520	17	0.186	K.YGVTESTLLTR.N
R3/RRR3-9/2	1239.795	1240.388	-1288.918	0.378	755.470	0.476	15	0.157	K.YGVTESTLLTR.N
R3/RRR3-12/2	1240.824	1240.388	352.796	0.222	380.621	0.405	15	0.138	K.YGVTESTLLTR.N
R3/RRR3-4/2	1442.242	1441.652	-284.784	0.548	1641.574	0.483	21	0.235	K.LLVSEDLQPLGEK.L
R3/RRR3-4/2	1441.000	1441.652	-1149.902	0.425	1769.223	0.306	21	0.211	K.LLVSEDLQPLGEK.L
R3/RRR3-4/2	1441.315	1441.652	-234.423	0.455	1416.013	0.458	19	0.203	K.LLVSEDLQPLGEK.L
R3/RRR3-4/2	1490.190	1490.705	-1019.172	0.417	662.431	0.378	19	0.143	K.EVM*DGSKPAAELVK.L
R3/RRR3-4/2	1490.159	1490.705	-1040.309	0.412	578.682	0.387	19	0.142	K.EVM*DGSKPAAELVK.L
R3/RRR3-24/2	1242.217	1242.366	-119.617	0.523	1138.599	0.580	17	0.202	K.HQYLPADAQAK.Q
R3/RRR3-24/2	1242.125	1242.366	-193.948	0.493	1202.770	0.541	17	0.200	K.HQYLPADAQAK.Q
R3/RRR3-24/2	1242.029	1242.366	-271.938	0.489	893.681	0.541	15	0.173	K.HQYLPADAQAK.Q
R3/RRR3-24/2	1231.050	1231.426	-306.488	0.469	865.283	0.390	18	0.154	R.EALGALPLYQR.T
R3/RRR3-24/2	1231.176	1231.426	-203.131	0.415	620.527	0.367	16	0.143	R.EALGALPLYQR.T
R3/RRR3-24/2	1230.538	1231.426	-1538.703	0.328	551.044	0.315	15	0.137	R.EALGALPLYQR.T
R3/RRR3-26/2	1051.216	1051.246	-28.681	0.398	945.284	0.393	13	0.158	R.FAWM*VQPR.N
R3/RRR3-26/2	1030.836	1030.202	-356.395	0.417	863.381	0.341	15	0.147	K.AFLNSPVGPK.T
R3/RRR3-26/2	1050.774	1051.246	-450.496	0.314	587.381	0.250	12	0.135	R.FAWM*VQPR.N
R3/RRR3-26/2	1050.660	1051.246	-1514.375	0.238	506.321	0.260	11	0.133	R.FAWM*VQPR.N
R3/RRR3-26/2	1030.994	1030.202	-202.195	0.372	718.684	0.188	14	0.130	K.AFLNSPVGPK.T
R3/RRR3-9/3	1468.844	1468.637	141.478	0.522	1490.555	0.479	26	0.169	R.VTSHSLQELQPTK.S
R3/RRR3-9/3	1468.676	1468.637	26.325	0.513	1498.015	0.474	26	0.169	R.VTSHSLQELQPTK.S
R3/RRR3-9/2	1469.937	1468.637	204.352	0.444	802.270	0.517	18	0.162	R.VTSHSLQELQPTK.S
R3/RRR3-9/2	1319.256	1318.547	-221.124	0.424	936.052	0.394	20	0.158	K.FTVLLLPSGSQR.V
R3/RRR3-9/2	1317.769	1318.547	-1353.320	0.373	942.780	0.323	19	0.148	K.FTVLLLPSGSQR.V
R3/RRR3-9/2	1318.178	1318.547	-280.750	0.343	841.234	0.294	19	0.141	K.FTVLLLPSGSQR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/3	1469.769	1468.637	90.241	0.421	962.063	0.399	23	0.110	R.VTSHSLQELQPTK.S
R3/RRR3-9/3	1469.327	1468.637	-211.964	0.318	299.476	0.345	20	0.100	R.VTSHSLQELQPTK.S
R3/RRR3-10/2	1594.115	1594.836	-1082.464	0.480	1834.439	0.477	22	0.258	R.LPGYLGEYLALTGAR.L
R3/RRR3-10/2	1294.445	1295.424	-1533.204	0.331	1566.556	0.356	19	0.198	R.SVVTGDVYEGIR.A
R3/RRR3-10/2	1594.194	1594.836	-1033.104	0.538	1343.251	0.447	20	0.190	R.LPGYLGEYLALTGAR.L
R3/RRR3-10/2	1593.452	1594.836	-1500.756	0.380	1339.447	0.365	21	0.177	R.LPGYLGEYLALTGAR.L
R3/RRR3-10/2	1294.440	1295.424	-1536.899	0.297	1432.448	0.271	19	0.170	R.SVVTGDVYEGIR.A
R3/RRR3-8/2	1596.006	1594.836	106.893	0.389	833.039	0.500	16	0.159	R.LPGYLGEYLALTGAR.L
R3/RRR3-11/2	1595.887	1594.836	32.252	0.338	1013.444	0.410	18	0.158	R.LPGYLGEYLALTGAR.L
R3/RRR3-10/2	1294.418	1295.424	-1553.951	0.361	1125.010	0.281	17	0.150	R.SVVTGDVYEGIR.A
R3/RRR3-10/2	1472.499	1471.768	-183.061	0.618	2448.487	0.567	21	0.394	K.TNMVMVFGEITTK.A
R3/RRR3-10/2	1472.263	1471.768	337.504	0.604	2225.223	0.536	21	0.338	K.TNMVMVFGEITTK.A
R3/RRR3-9/2	1472.336	1471.768	-294.513	0.603	2193.974	0.547	21	0.337	K.TNMVMVFGEITTK.A
R3/RRR3-10/2	1503.188	1503.767	-1053.378	0.523	2227.134	0.473	21	0.320	K.TNM*VM*VFGEITTK.A
R3/RRR3-10/2	1487.368	1487.767	-269.223	0.474	2078.716	0.536	20	0.317	-.TNMVM*VFGEITTK.-
R3/RRR3-10/2	1487.606	1487.767	-108.769	0.512	2147.734	0.491	20	0.311	K.TNMVM*VFGEITTK.A
R3/RRR3-10/2	1504.198	1503.767	287.523	0.521	2000.035	0.465	20	0.279	K.TNM*VM*VFGEITTK.A
R3/RRR3-9/2	1503.144	1503.767	-1082.569	0.524	1889.122	0.468	20	0.263	K.TNM*VM*VFGEITTK.A
R3/RRR3-9/2	1470.407	1471.768	-1610.145	0.407	1346.635	0.421	18	0.187	K.TNMVMVFGEITTK.A
R3/RRR3-11/2	1503.098	1503.767	-1113.801	0.314	1139.311	0.356	17	0.160	K.TNM*VM*VFGEITTK.A
R3/RRR3-4/2	1472.794	1471.768	17.823	0.345	711.656	0.315	14	0.137	K.TNMVMVFGEITTK.A
R3/RRR3-10/2	1226.132	1226.404	-222.939	0.488	1249.623	0.552	19	0.207	R.IPAEALDVIER.S
R3/RRR3-10/2	1202.690	1203.324	-1362.888	0.375	734.024	0.380	16	0.143	K.IVSIEEDGNVK.L
R3/RRR3-8/2	1259.981	1260.374	-313.152	0.484	992.106	0.522	15	0.179	K.SKFDNLYGCR.H
R3/RRR3-8/2	1260.156	1260.374	-173.975	0.518	1128.116	0.448	16	0.177	K.SKFDNLYGCR.H
R3/RRR3-8/2	905.356	906.083	-1912.654	0.412	996.666	0.424	15	0.164	R.ATDVMLAGK.V
R3/RRR3-8/2	1260.069	1260.374	-243.073	0.520	927.745	0.443	15	0.163	K.SKFDNLYGCR.H
R3/RRR3-8/2	905.367	906.083	-1900.324	0.406	876.493	0.437	14	0.158	-.ATDVMLAGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/3	1594.195	1593.934	164.223	0.436	1906.848	0.345	30	0.183	K.IILITPPPIYEPAR.I
R3/RRR3-17/2	1465.257	1465.678	-288.081	0.415	404.074	0.484	16	0.145	K.ELNHPVIDIWTK.M
R3/RRR3-17/2	1594.402	1593.934	294.295	0.382	615.796	0.400	19	0.141	K.IILITPPPIYEPAR.I
R3/RRR3-10/3	1563.900	1562.755	92.521	0.462	2179.482	0.364	32	0.236	K.AVAHQPVSVAIEAGGR.E
R3/RRR3-10/2	1792.517	1791.894	-210.829	0.545	852.812	0.499	20	0.163	K.VVSIDGFEDVPQNDEK.S
R3/RRR3-10/2	1791.122	1791.894	-992.182	0.470	821.788	0.480	22	0.161	K.VVSIDGFEDVPQNDEK.S
R3/RRR3-10/2	1791.390	1791.894	-842.080	0.495	717.451	0.479	21	0.156	K.VVSIDGFEDVPQNDEK.S
R3/RRR3-11/2	1791.127	1791.894	-989.034	0.461	660.565	0.503	20	0.155	K.VVSIDGFEDVPQNDEK.S
R3/RRR3-10/3	1562.524	1562.755	-148.428	0.413	1728.283	0.270	30	0.143	K.AVAHQPVSVAIEAGGR.E
R3/RRR3-10/3	1562.432	1562.755	-207.444	0.427	1478.576	0.255	28	0.119	-.AVAHQPVSVAIEAGGR.-
R3/RRR3-19/2	1629.367	1629.749	-235.471	0.495	1742.784	0.478	20	0.249	R.VNIYYDELDSELR.F
R3/RRR3-18/2	1619.298	1619.762	-287.821	0.339	515.589	0.509	17	0.143	R.LGHATGATPAEFYQR.R
R3/RRR3-9/2	1573.209	1573.773	-997.154	0.495	1656.219	0.570	22	0.259	K.VNQIGTLTESIQAAK.D
R3/RRR3-9/2	1998.745	1999.212	-234.038	0.541	1736.127	0.482	23	0.245	K.TQDIQIVGDDLTVTNPIR.I
R3/RRR3-22/2	1219.978	1220.357	-311.176	0.462	873.337	0.535	20	0.175	K.LNPAADAGSIYK.T
R3/RRR3-22/2	1219.623	1220.357	-1425.582	0.445	740.325	0.532	19	0.167	K.LNPAADAGSIYK.T
R3/RRR3-21/2	1219.995	1220.357	-297.322	0.412	872.003	0.484	20	0.166	K.LNPAADAGSIYK.T
R3/RRR3-21/2	1219.514	1220.357	-1515.365	0.318	841.880	0.437	20	0.156	K.LNPAADAGSIYK.T
R3/RRR3-21/2	1220.079	1220.357	-228.059	0.388	703.074	0.461	19	0.156	K.LNPAADAGSIYK.T
R3/RRR3-22/2	1219.633	1220.357	-1417.138	0.354	611.228	0.457	17	0.150	K.LNPAADAGSIYK.T
R3/RRR3-23/2	1219.866	1220.357	-403.544	0.342	653.258	0.450	17	0.150	K.LNPAADAGSIYK.T
R3/RRR3-12/2	1657.255	1657.850	-965.497	0.550	2209.345	0.660	32	0.383	K.GLPLGSGLGSSAASAAAAAK.A
R3/RRR3-12/2	1658.145	1657.850	178.203	0.578	2074.920	0.670	32	0.359	K.GLPLGSGLGSSAASAAAAAK.A
R3/RRR3-12/2	1657.466	1657.850	-232.735	0.580	1865.306	0.678	30	0.322	K.GLPLGSGLGSSAASAAAAAK.A
R3/RRR3-24/2	1170.246	1170.256	-8.852	0.344	1006.666	0.385	17	0.156	K.LQGFAEDYAR.Q
R3/RRR3-10/2	1298.761	1299.414	-1276.309	0.507	1584.014	0.578	19	0.252	K.DDGTLASFIGFR.V
R3/RRR3-10/2	1299.254	1299.414	-123.318	0.405	846.233	0.594	15	0.173	K.DDGTLASFIGFR.V
R3/RRR3-10/2	1118.958	1119.295	-302.285	0.383	935.648	0.420	16	0.156	K.TAVAAIPYGGAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1118.918	1119.295	-338.406	0.385	873.264	0.402	16	0.151	K.TAVAAIPYGGAK.G
R3/RRR3-21/2	1335.317	1334.500	-137.134	0.488	891.197	0.361	18	0.148	R.IEVTEPASFNVK.E
R3/RRR3-23/2	1307.175	1307.502	-251.095	0.458	1231.236	0.505	19	0.195	R.LM*GSLTNTQGLR.F
R3/RRR3-23/2	1307.237	1307.502	-203.691	0.454	998.740	0.474	18	0.171	R.LM*GSLTNTQGLR.F
R3/RRR3-23/2	1307.031	1307.502	-362.034	0.432	929.454	0.467	18	0.165	R.LM*GSLTNTQGLR.F
R3/RRR3-23/2	747.676	747.908	-311.810	0.351	882.557	0.369	12	0.152	R.FGVVVAR.F
R3/RRR3-23/2	747.856	747.908	-70.253	0.371	798.206	0.376	11	0.149	R.FGVVVAR.F
R3/RRR3-23/2	747.582	747.908	-437.138	0.378	773.636	0.359	11	0.147	R.FGVVVAR.F
R3/RRR3-24/2	747.462	747.908	-598.062	0.424	641.507	0.386	10	0.147	R.FGVVVAR.F
R3/RRR3-17/2	1164.194	1164.336	-122.480	0.498	1786.187	0.470	17	0.251	R.SIGAAVIYNQK.K
R3/RRR3-17/2	1164.156	1164.336	-155.088	0.447	1637.961	0.383	16	0.214	-.SIGAAVIYNQK.-
R3/RRR3-16/2	1163.924	1164.336	-355.090	0.355	1200.455	0.441	16	0.178	R.SIGAAVIYNQK.K
R3/RRR3-16/2	1903.746	1903.081	-176.322	0.516	760.551	0.546	23	0.166	K.DYTDPPPAPLFDVGELR.L
R3/RRR3-16/2	1902.783	1903.081	-157.172	0.421	670.142	0.490	26	0.155	K.DYTDPPPAPLFDVGELR.L
R3/RRR3-17/2	1164.290	1164.336	-39.920	0.299	1302.635	0.220	16	0.153	R.SIGAAVIYNQK.K
R3/RRR3-17/3	1903.001	1903.081	-41.866	0.380	931.055	0.420	27	0.108	K.DYTDPPPAPLFDVGELR.L
R3/RRR3-14/2	1546.111	1545.639	306.734	0.538	1531.000	0.412	22	0.206	K.FNDLSTNHNNQLK.T
R3/RRR3-13/2	1545.298	1545.639	-221.342	0.553	1377.745	0.482	20	0.204	K.FNDLSTNHNNQLK.T
R3/RRR3-13/2	1544.595	1545.639	-1327.387	0.476	1288.086	0.401	20	0.180	K.FNDLSTNHNNQLK.T
R3/RRR3-14/2	1545.436	1545.639	-131.323	0.519	1151.250	0.425	20	0.174	K.FNDLSTNHNNQLK.T
R3/RRR3-13/2	1545.247	1545.639	-254.232	0.531	994.162	0.462	18	0.168	K.FNDLSTNHNNQLK.T
R3/RRR3-14/2	1544.526	1545.639	-1372.234	0.428	980.255	0.373	19	0.156	K.FNDLSTNHNNQLK.T
R3/RRR3-14/3	1674.989	1673.812	106.230	0.502	1323.151	0.395	30	0.131	K.KFNDLSTNHNNQLK.T
R3/RRR3-13/3	1674.902	1673.812	54.042	0.497	1076.681	0.452	28	0.126	K.KFNDLSTNHNNQLK.T
R3/RRR3-14/3	1673.224	1673.812	-951.644	0.454	969.323	0.478	27	0.124	K.KFNDLSTNHNNQLK.T
R3/RRR3-13/3	1673.814	1673.812	1.227	0.454	713.966	0.493	23	0.116	K.KFNDLSTNHNNQLK.T
R3/RRR3-14/3	1674.783	1673.812	-16.904	0.453	744.959	0.437	24	0.109	K.KFNDLSTNHNNQLK.T
R3/RRR3-13/3	1673.647	1673.812	-98.849	0.472	894.877	0.375	26	0.105	K.KFNDLSTNHNNQLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1523.264	1523.630	-240.861	0.503	1661.441	0.479	20	0.236	K.VLSDNFEQLNTSR.A
R3/RRR3-13/2	1523.313	1523.630	-208.301	0.510	1612.298	0.500	20	0.235	K.VLSDNFEQLNTSR.A
R3/RRR3-13/2	1523.287	1523.630	-225.586	0.525	1529.922	0.470	20	0.217	K.VLSDNFEQLNTSR.A
R3/RRR3-14/2	1523.171	1523.630	-301.886	0.466	1504.559	0.481	20	0.217	K.VLSDNFEQLNTSR.A
R3/RRR3-14/2	1523.169	1523.630	-303.172	0.540	1488.709	0.479	21	0.216	K.VLSDNFEQLNTSR.A
R3/RRR3-14/2	1523.068	1523.630	-1028.454	0.500	1280.456	0.406	19	0.179	K.VLSDNFEQLNTSR.A
R3/RRR3-14/2	898.146	898.085	67.737	0.287	755.465	0.321	14	0.140	K.AVGAPLTLR.M
R3/RRR3-14/2	898.203	898.085	131.391	0.214	560.944	0.315	11	0.132	K.AVGAPLTLR.M
R3/RRR3-14/2	898.187	898.085	113.536	0.204	598.317	0.190	11	0.128	K.AVGAPLTLR.M
R3/RRR3-14/2	1498.072	1497.677	264.590	0.433	1262.371	0.469	17	0.189	R.EQIQSYVFDVIR.A
R3/RRR3-14/2	1498.176	1497.677	333.792	0.420	1126.144	0.454	16	0.174	R.EQIQSYVFDVIR.A
R3/RRR3-14/2	934.128	934.117	11.389	0.492	902.380	0.266	15	0.141	K.YLAGLGIAR.Q
R3/RRR3-14/2	933.961	934.117	-168.208	0.449	868.822	0.266	15	0.141	K.YLAGLGIAR.Q
R3/RRR3-14/2	934.116	934.117	-1.718	0.464	856.946	0.269	15	0.141	K.YLAGLGIAR.Q
R3/RRR3-9/2	1978.407	1979.049	-832.843	0.528	1743.917	0.652	26	0.290	K.TVGGGDDAFNTFFSETGAGK.H
R3/RRR3-9/2	1978.421	1979.049	-825.783	0.569	1686.560	0.679	27	0.290	K.TVGGGDDAFNTFFSETGAGK.H
R3/RRR3-9/2	1979.182	1979.049	67.021	0.575	1635.214	0.656	24	0.273	K.TVGGGDDAFNTFFSETGAGK.H
R3/RRR3-9/2	1702.413	1702.929	-893.355	0.533	1514.745	0.514	23	0.223	R.AVFVDLEPTVIDEVR.T
R3/RRR3-14/2	1703.622	1702.929	-180.829	0.564	1411.014	0.543	24	0.219	R.AVFVDLEPTVIDEVR.T
R3/RRR3-2/2	1978.639	1979.049	-208.014	0.536	1187.429	0.660	23	0.216	K.TVGGGDDAFNTFFSETGAGK.H
R3/RRR3-9/2	1703.436	1702.929	-290.424	0.576	1272.264	0.570	23	0.210	R.AVFVDLEPTVIDEVR.T
R3/RRR3-8/2	1702.626	1702.929	-178.741	0.531	1382.516	0.511	22	0.208	R.AVFVDLEPTVIDEVR.T
R3/RRR3-9/2	1702.450	1702.929	-282.681	0.548	1262.226	0.530	23	0.201	R.AVFVDLEPTVIDEVR.T
R3/RRR3-9/2	1702.515	1702.929	-243.980	0.560	1226.992	0.517	23	0.195	R.AVFVDLEPTVIDEVR.T
R3/RRR3-15/2	1702.317	1702.929	-949.937	0.464	1107.895	0.487	20	0.178	R.AVFVDLEPTVIDEVR.T
R3/RRR3-3/2	1703.125	1702.929	114.979	0.519	1109.550	0.477	21	0.178	R.AVFVDLEPTVIDEVR.T
R3/RRR3-1/2	1702.339	1702.929	-936.979	0.440	975.783	0.510	20	0.173	R.AVFVDLEPTVIDEVR.T
R3/RRR3-11/2	1702.506	1702.929	-249.591	0.457	1064.618	0.427	20	0.166	R.AVFVDLEPTVIDEVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1701.860	1702.929	-1219.762	0.350	1037.428	0.436	20	0.165	R.AVFVDLEPTVIDEVR.T
R3/RRR3-7/2	1703.529	1702.929	-235.641	0.526	857.588	0.496	19	0.164	R.AVFVDLEPTVIDEVR.T
R3/RRR3-10/2	1702.258	1702.929	-985.070	0.387	1126.900	0.344	21	0.159	R.AVFVDLEPTVIDEVR.T
R3/RRR3-2/2	1702.434	1702.929	-291.889	0.460	910.133	0.411	18	0.154	R.AVFVDLEPTVIDEVR.T
R3/RRR3-1/2	1702.755	1702.929	-102.724	0.480	571.370	0.497	17	0.153	R.AVFVDLEPTVIDEVR.T
R3/RRR3-8/2	1701.638	1702.929	-1350.730	0.386	843.455	0.412	19	0.153	R.AVFVDLEPTVIDEVR.T
R3/RRR3-10/2	1702.205	1702.929	-1016.389	0.357	903.603	0.366	20	0.150	R.AVFVDLEPTVIDEVR.T
R3/RRR3-20/2	1701.580	1702.929	-1384.810	0.311	1100.131	0.293	20	0.150	R.AVFVDLEPTVIDEVR.T
R3/RRR3-14/2	1701.720	1702.929	-1302.243	0.331	797.316	0.410	18	0.149	R.AVFVDLEPTVIDEVR.T
R3/RRR3-7/2	1702.186	1702.929	-1027.118	0.336	971.112	0.330	19	0.148	R.AVFVDLEPTVIDEVR.T
R3/RRR3-9/3	1702.465	1702.929	-273.409	0.504	1189.011	0.507	30	0.146	R.AVFVDLEPTVIDEVR.T
R3/RRR3-9/3	1703.008	1702.929	46.320	0.497	1104.304	0.510	27	0.140	R.AVFVDLEPTVIDEVR.T
R3/RRR3-7/2	1702.170	1702.929	-1036.982	0.310	597.044	0.325	16	0.138	R.AVFVDLEPTVIDEVR.T
R3/RRR3-13/2	1702.274	1702.929	-975.495	0.379	710.528	0.267	18	0.136	R.AVFVDLEPTVIDEVR.T
R3/RRR3-6/2	1702.765	1702.929	-97.115	0.342	533.991	0.319	15	0.135	-.AVFVDLEPTVIDEVR.-
R3/RRR3-1/2	1701.318	1702.929	-2129.077	0.333	613.787	0.255	15	0.133	R.AVFVDLEPTVIDEVR.T
R3/RRR3-9/3	1979.195	1979.049	73.880	0.469	654.235	0.484	27	0.109	K.TVGGGDDAFNTFFSETGAGK.H
R3/RRR3-9/3	1979.541	1979.049	248.844	0.425	695.918	0.477	28	0.109	K.TVGGGDDAFNTFFSETGAGK.H
R3/RRR3-1/2	1747.483	1746.982	-286.396	0.585	2072.061	0.456	25	0.289	K.NEILAESEFAAPTIIK.L
R3/RRR3-1/2	1746.365	1746.982	-929.132	0.447	1715.620	0.336	23	0.209	K.NEILAESEFAAPTIIK.L
R3/RRR3-2/2	1746.546	1746.982	-250.658	0.415	1631.954	0.312	22	0.195	K.NEILAESEFAAPTIIK.L
R3/RRR3-2/2	1758.502	1758.010	280.409	0.425	672.261	0.498	16	0.147	K.GAIEILGPYGISYTFR.R
R3/RRR3-23/2	1651.411	1651.889	-290.083	0.495	1083.603	0.550	21	0.187	K.LIGATNPLQAEPGTIR.G
R3/RRR3-23/2	1651.193	1651.889	-1030.068	0.540	950.239	0.600	19	0.184	K.LIGATNPLQAEPGTIR.G
R3/RRR3-23/2	943.304	944.111	-1920.856	0.398	1259.025	0.370	14	0.172	R.GLVGEIISR.F
R3/RRR3-20/2	1032.797	1033.154	-346.708	0.427	1561.972	0.339	15	0.195	R.GLEECGLVR.E
R3/RRR3-20/2	1032.766	1033.154	-377.424	0.295	1524.491	0.146	14	0.158	R.GLEECGLVR.E
R3/RRR3-20/2	1351.430	1351.620	-140.988	0.395	595.346	0.494	16	0.149	R.ALGFPEGM*M*PLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-20/2	1032.820	1033.154	-324.414	0.329	1318.260	0.165	13	0.147	R.GLEECGLVR.E
R3/RRR3-16/2	965.081	965.045	37.729	0.328	878.236	0.396	14	0.150	K.GGYSAISGPR.V
R3/RRR3-16/2	964.838	965.045	-215.805	0.323	444.109	0.433	11	0.138	K.GGYSAISGPR.V
R3/RRR3-12/2	1368.289	1368.518	-167.564	0.466	1638.261	0.446	20	0.226	K.YIGLSEASASTIR.R
R3/RRR3-12/2	1367.421	1368.518	-1537.785	0.370	1380.862	0.389	18	0.185	K.YIGLSEASASTIR.R
R3/RRR3-12/2	1444.467	1445.688	-1542.304	0.403	741.075	0.610	14	0.165	R.ELGIGIVAYSPLGR.G
R3/RRR3-12/2	1367.464	1368.518	-1506.310	0.292	1225.050	0.194	17	0.144	K.YIGLSEASASTIR.R
R3/RRR3-12/2	1444.723	1445.688	-1364.400	0.259	635.092	0.467	12	0.138	R.ELGIGIVAYSPLGR.G
R3/RRR3-14/3	1297.769	1296.548	170.694	0.496	1395.013	0.537	26	0.174	K.HITGGMMGGHAVK.L
R3/RRR3-14/3	1297.733	1296.548	143.244	0.528	1268.602	0.506	26	0.153	K.HITGGMMGGHAVK.L
R3/RRR3-14/3	1296.218	1296.548	-255.810	0.447	1101.052	0.466	24	0.130	K.HITGGMMGGHAVK.L
R3/RRR3-24/3	1122.058	1122.261	-181.869	0.561	851.239	0.426	18	0.112	K.KHFSVNAYR.V
R3/RRR3-14/3	1122.282	1122.261	18.468	0.533	746.089	0.427	18	0.110	K.KHFSVNAYR.V
R3/RRR3-15/3	1122.168	1122.261	-83.327	0.516	525.779	0.327	15	0.099	K.KHFSVNAYR.V
R3/RRR3-24/3	1122.731	1122.261	419.555	0.563	606.777	0.368	16	0.098	-.KHFSVNAYR.-
R3/RRR3-24/3	1122.600	1122.261	302.959	0.532	474.200	0.352	14	0.097	-.KHFSVNAYR.-
R3/RRR3-14/3	1123.354	1122.261	83.300	0.547	487.130	0.404	15	0.094	-.KHFSVNAYR.-
R3/RRR3-14/3	1122.758	1122.261	443.754	0.546	640.023	0.317	16	0.094	-.KHFSVNAYR.-
R3/RRR3-13/3	1123.077	1122.261	-164.424	0.488	419.293	0.291	14	0.093	-.KHFSVNAYR.-
R3/RRR3-24/3	1122.381	1122.261	107.153	0.601	766.702	0.277	17	0.089	-.KHFSVNAYR.-
R3/RRR3-19/2	1948.327	1949.023	-873.352	0.562	1476.743	0.581	22	0.235	K.YGLDTSQFTYNPSDPSR.Y
R3/RRR3-19/2	1360.189	1360.414	-166.131	0.465	687.158	0.356	16	0.139	R.YQQNGAPPAEER.N
R3/RRR3-18/2	1334.343	1334.546	-152.466	0.370	875.671	0.350	17	0.146	R.GAVGALLVYDISR.R
R3/RRR3-18/2	1334.159	1334.546	-291.060	0.298	584.083	0.394	12	0.136	-.GAVGALLVYDISR.-
R3/RRR3-16/2	1334.221	1334.546	-244.063	0.358	664.152	0.320	13	0.134	R.GAVGALLVYDISR.R
R3/RRR3-18/2	1334.062	1334.546	-364.228	0.262	668.293	0.316	14	0.134	-.GAVGALLVYDISR.-
R3/RRR3-5/2	1731.480	1731.934	-263.163	0.544	2070.347	0.467	23	0.294	K.LNSELLNNLGNFINR.V
R3/RRR3-5/2	1253.262	1253.470	-166.140	0.341	674.365	0.368	13	0.139	K.LLNPTELIDPK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-2/2	1731.164	1731.934	-1025.768	0.377	854.269	0.301	18	0.138	K.LNSELLNNLGNFINR.V
R3/RRR3-5/2	1252.823	1253.470	-1318.417	0.282	440.408	0.260	11	0.126	-.LLNPTELIDPK.-
R3/RRR3-9/3	1867.492	1866.102	209.718	0.426	1810.652	0.359	28	0.178	K.TKELILNYANQLCER.L
R3/RRR3-9/2	1559.927	1559.710	139.740	0.476	999.447	0.520	18	0.176	K.HYKGDHTYVPVSR.K
R3/RRR3-9/3	1560.642	1559.710	-43.794	0.430	584.434	0.496	23	0.113	K.HYKGDHTYVPVSR.K
R3/RRR3-14/3	1559.299	1559.710	-264.277	0.456	538.252	0.470	22	0.110	K.HYKGDHTYVPVSR.K
R3/RRR3-8/3	1558.816	1559.710	-1218.951	0.449	871.834	0.402	27	0.108	K.HYKGDHTYVPVSR.K
R3/RRR3-9/3	1560.593	1559.710	-74.981	0.443	531.898	0.434	23	0.107	K.HYKGDHTYVPVSR.K
R3/RRR3-9/3	1559.736	1559.710	16.389	0.446	602.943	0.426	23	0.106	K.HYKGDHTYVPVSR.K
R3/RRR3-9/3	1559.050	1559.710	-1067.985	0.325	419.022	0.389	21	0.102	K.HYKGDHTYVPVSR.K
R3/RRR3-14/3	1559.699	1559.710	-7.043	0.413	714.186	0.364	25	0.100	K.HYKGDHTYVPVSR.K
R3/RRR3-14/3	1560.049	1559.710	217.811	0.420	550.158	0.363	22	0.100	K.HYKGDHTYVPVSR.K
R3/RRR3-19/2	1596.336	1595.847	306.901	0.520	558.770	0.582	22	0.168	R.VIPNFMLQGGDFTR.G
R3/RRR3-21/2	1269.950	1269.300	-276.275	0.450	861.855	0.440	18	0.159	R.GNGTGGESIYGEK.-
R3/RRR3-19/2	1612.334	1611.847	303.366	0.359	376.100	0.576	20	0.154	R.VIPNFM*LQGGDFTR.G
R3/RRR3-21/2	1269.423	1269.300	97.549	0.425	690.133	0.444	16	0.151	R.GNGTGGESIYGEK.-
R3/RRR3-19/2	1595.189	1595.847	-1042.898	0.454	556.378	0.435	21	0.150	R.VIPNFMLQGGDFTR.G
R3/RRR3-21/2	1269.828	1269.300	-373.011	0.401	828.847	0.382	17	0.149	R.GNGTGGESIYGEK.-
R3/RRR3-19/2	1611.213	1611.847	-1017.058	0.327	360.096	0.524	20	0.149	R.VIPNFM*LQGGDFTR.G
R3/RRR3-22/2	1269.519	1269.300	173.346	0.345	769.190	0.397	17	0.148	R.GNGTGGESIYGEK.-
R3/RRR3-22/2	1268.955	1269.300	-272.922	0.400	495.099	0.439	17	0.148	R.GNGTGGESIYGEK.-
R3/RRR3-22/2	1268.972	1269.300	-259.024	0.394	471.199	0.439	16	0.147	R.GNGTGGESIYGEK.-
R3/RRR3-19/2	1594.861	1595.847	-1249.239	0.334	547.420	0.426	21	0.146	R.VIPNFMLQGGDFTR.G
R3/RRR3-22/2	1268.985	1269.300	-248.987	0.370	446.856	0.434	16	0.146	R.GNGTGGESIYGEK.-
R3/RRR3-22/2	1268.839	1269.300	-364.038	0.386	422.898	0.386	15	0.143	R.GNGTGGESIYGEK.-
R3/RRR3-22/2	1269.863	1269.300	-344.750	0.362	660.654	0.361	16	0.142	R.GNGTGGESIYGEK.-
R3/RRR3-21/2	1268.989	1269.300	-245.899	0.373	432.341	0.364	15	0.141	R.GNGTGGESIYGEK.-
R3/RRR3-20/2	1269.086	1269.300	-168.699	0.294	373.011	0.301	15	0.139	R.GNGTGGESIYGEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1610.368	1611.847	-1543.644	0.215	256.763	0.336	19	0.138	R.VIPNFM*LQGGDFTR.G
R3/RRR3-22/2	1268.528	1269.300	-1400.543	0.237	475.938	0.334	17	0.138	R.GNGTGGESIYGEK.-
R3/RRR3-22/2	1268.429	1269.300	-1479.225	0.219	361.906	0.326	15	0.137	R.GNGTGGESIYGEK.-
R3/RRR3-11/2	1602.202	1602.815	-1009.753	0.480	2472.407	0.472	23	0.372	R.AVNITINSIGTELTR.D
R3/RRR3-11/2	1603.406	1602.815	-255.930	0.559	2189.562	0.495	23	0.322	R.AVNITINSIGTELTR.D
R3/RRR3-11/2	1601.687	1602.815	-1332.282	0.393	1639.140	0.434	21	0.222	R.AVNITINSIGTELTR.D
R3/RRR3-10/2	1602.013	1602.815	-1127.951	0.363	1627.857	0.386	21	0.210	R.AVNITINSIGTELTR.D
R3/RRR3-20/2	1117.137	1117.275	-123.584	0.443	950.135	0.469	16	0.168	K.LEVSDVVVEK.A
R3/RRR3-20/2	1117.064	1117.275	-189.246	0.508	760.744	0.385	16	0.150	K.LEVSDVVVEK.A
R3/RRR3-20/2	1116.890	1117.275	-345.049	0.389	823.492	0.343	16	0.147	K.LEVSDVVVEK.A
R3/RRR3-20/2	926.887	927.080	-208.327	0.487	664.055	0.346	12	0.141	-.HLDTIISK.-
R3/RRR3-20/2	926.516	927.080	-1693.217	0.481	592.209	0.354	11	0.137	-.HLDTIISK.-
R3/RRR3-6/2	1212.345	1212.424	-65.605	0.513	2017.205	0.446	21	0.281	K.DAGIIAGLNVLR.I
R3/RRR3-6/2	1213.174	1212.424	-206.751	0.585	1853.591	0.439	20	0.252	K.DAGIIAGLNVLR.I
R3/RRR3-6/2	1397.152	1396.613	-330.430	0.477	1868.615	0.372	17	0.239	K.FEELNIDLFKK.T
R3/RRR3-6/2	1395.711	1396.613	-1366.785	0.417	1452.536	0.327	17	0.182	K.FEELNIDLFKK.T
R3/RRR3-6/2	1211.875	1212.424	-1282.444	0.455	953.821	0.355	15	0.149	K.DAGIIAGLNVLR.I
R3/RRR3-19/2	1353.677	1352.434	180.026	0.395	1348.395	0.467	17	0.197	K.FEIWDTAGQER.Y
R3/RRR3-19/2	1072.443	1072.280	151.885	0.302	1312.429	0.406	18	0.181	K.LVLLGDVGTGK.S
R3/RRR3-19/2	1072.950	1072.280	-309.199	0.453	1185.122	0.418	18	0.177	K.LVLLGDVGTGK.S
R3/RRR3-19/2	1072.833	1072.280	-418.336	0.408	1074.713	0.474	17	0.176	K.LVLLGDVGTGK.S
R3/RRR3-20/2	1072.387	1072.280	100.173	0.273	498.181	0.310	13	0.133	-.LVLLGDVGTGK.-
R3/RRR3-23/2	1308.230	1308.590	-276.146	0.518	1005.283	0.483	18	0.175	K.IPYDFLISLVK.D
R3/RRR3-23/2	1308.184	1308.590	-310.972	0.489	983.168	0.417	18	0.164	K.IPYDFLISLVK.D
R3/RRR3-23/2	1309.199	1308.590	-299.602	0.533	864.072	0.431	18	0.160	K.IPYDFLISLVK.D
R3/RRR3-23/2	1351.367	1351.607	-178.179	0.444	600.831	0.448	15	0.147	R.LPICELTYTLK.C
R3/RRR3-8/2	1466.232	1465.678	-305.092	0.542	1707.589	0.523	21	0.254	K.FLGNSLEVYPLGR.T
R3/RRR3-8/2	1465.370	1465.678	-210.856	0.498	1255.435	0.435	19	0.183	K.FLGNSLEVYPLGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1464.433	1465.678	-1537.663	0.362	1313.643	0.402	19	0.181	K.FLGNSLEVYPLGR.T
R3/RRR3-8/2	933.185	933.089	102.258	0.489	971.200	0.449	13	0.168	K.VNNLIFGR.T
R3/RRR3-8/2	932.964	933.089	-134.857	0.560	945.447	0.406	13	0.160	K.VNNLIFGR.T
R3/RRR3-8/2	932.616	933.089	-508.932	0.537	864.861	0.435	12	0.159	K.VNNLIFGR.T
R3/RRR3-8/2	1799.523	1800.992	-1375.981	0.365	1223.386	0.395	20	0.168	K.VTSGLAEGAAVIQEALDR.M
R3/RRR3-23/2	1716.223	1716.868	-961.288	0.550	2243.276	0.612	23	0.374	R.VPDEVIDKVQEETSK.S
R3/RRR3-23/2	1716.306	1716.868	-912.732	0.578	2190.445	0.613	23	0.363	R.VPDEVIDKVQEETSK.S
R3/RRR3-23/3	1717.293	1716.868	248.380	0.442	936.754	0.529	30	0.130	R.VPDEVIDKVQEETSK.S
R3/RRR3-23/3	1716.832	1716.868	-21.018	0.465	679.404	0.551	25	0.122	R.VPDEVIDKVQEETSK.S
R3/RRR3-23/3	1717.057	1716.868	110.116	0.437	564.751	0.455	24	0.106	R.VPDEVIDKVQEETSK.S
R3/RRR3-25/2	1586.290	1586.752	-292.576	0.523	2379.851	0.543	23	0.376	K.AGGAYTM*NTASAVTVR.S
R3/RRR3-25/2	1586.369	1586.752	-242.240	0.518	1908.470	0.544	22	0.288	K.AGGAYTM*NTASAVTVR.S
R3/RRR3-25/2	1586.267	1586.752	-307.245	0.526	1863.368	0.546	21	0.280	K.AGGAYTM*NTASAVTVR.S
R3/RRR3-25/2	1570.093	1570.753	-1060.503	0.515	1863.411	0.527	22	0.276	K.AGGAYTMNTASAVTVR.S
R3/RRR3-15/2	1744.668	1743.942	-157.521	0.489	656.020	0.498	19	0.152	R.ELNAGLAEKDWLLDR.M
R3/RRR3-15/2	983.938	984.133	-198.737	0.341	755.993	0.299	11	0.136	R.GFYQSLLR.E
R3/RRR3-24/2	1059.763	1060.187	-400.851	0.402	1093.233	0.292	13	0.152	K.FTNFVEFR.T
R3/RRR3-24/2	1060.116	1060.187	-66.364	0.367	766.332	0.395	11	0.147	K.FTNFVEFR.T
R3/RRR3-24/2	965.220	965.104	120.797	0.476	1076.831	0.358	13	0.134	R.M*GELEKLE.-
R3/RRR3-10/2	1486.246	1486.779	-1034.657	0.344	2383.643	0.474	21	0.355	K.SEMIMVFGEITTK.A
R3/RRR3-10/2	1502.601	1502.779	-118.821	0.434	1293.777	0.414	18	0.183	-.SEM*IMVFGEITTK.-
R3/RRR3-10/2	1503.381	1502.779	-265.353	0.266	606.161	0.227	14	0.129	K.SEMIM*VFGEITTK.A
R3/RRR3-11/2	1118.155	1118.223	-60.729	0.361	1216.183	0.353	17	0.167	R.SVGTLGEADLR.G
R3/RRR3-10/2	1117.881	1118.223	-306.848	0.457	1105.336	0.393	17	0.166	R.SVGTLGEADLR.G
R3/RRR3-10/2	1118.004	1118.223	-196.644	0.423	1298.388	0.307	17	0.166	R.SVGTLGEADLR.G
R3/RRR3-15/2	1118.007	1118.223	-193.577	0.453	1122.812	0.374	17	0.165	R.SVGTLGEADLR.G
R3/RRR3-26/2	1117.801	1118.223	-378.505	0.295	306.138	0.271	14	0.139	R.SVGTLGEADLR.G
R3/RRR3-29/3	1706.294	1705.962	195.626	0.203	993.715	0.161	27	0.075	-.MATKRSVGTLGEADLR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-25/2	1377.053	1377.546	-359.570	0.525	1944.399	0.510	21	0.285	K.GTDPVAIDLGSM*GK.G
R3/RRR3-25/2	1377.201	1377.546	-251.426	0.454	1513.833	0.518	20	0.226	K.GTDPVAIDLGSM*GK.G
R3/RRR3-25/2	1376.450	1377.546	-1527.475	0.390	817.346	0.447	16	0.152	K.GTDPVAIDLGSM*GK.G
R3/RRR3-24/2	1376.554	1377.546	-1451.312	0.279	591.597	0.345	17	0.136	K.GTDPVAIDLGSM*GK.G
R3/RRR3-5/3	1243.791	1244.491	-1370.674	0.140	936.026	0.207	19	0.075	-.MLVSAGLHYPR.A
R3/RRR3-5/2	1361.246	1360.580	-246.323	0.528	1052.383	0.536	19	0.187	K.FTEQALPVDLVK.R
R3/RRR3-5/2	1359.596	1360.580	-1463.696	0.432	919.078	0.515	19	0.172	K.FTEQALPVDLVK.R
R3/RRR3-5/2	1361.331	1360.580	-183.800	0.544	882.493	0.490	18	0.167	K.FTEQALPVDLVK.R
R3/RRR3-5/2	1350.120	1349.514	-292.607	0.460	558.866	0.432	19	0.147	R.QTLINADGIFEK.T
R3/RRR3-17/2	925.875	926.138	-284.857	0.414	998.468	0.409	12	0.162	R.SQLIVLPR.N
R3/RRR3-16/2	925.913	926.138	-243.720	0.442	1127.813	0.331	13	0.160	R.SQLIVLPR.N
R3/RRR3-17/2	926.231	926.138	100.580	0.422	973.898	0.382	12	0.157	R.SQLIVLPR.N
R3/RRR3-16/2	925.935	926.138	-220.707	0.426	818.313	0.401	11	0.152	R.SQLIVLPR.N
R3/RRR3-16/2	925.902	926.138	-256.286	0.437	898.108	0.368	11	0.151	R.SQLIVLPR.N
R3/RRR3-17/3	1501.264	1501.626	-241.341	0.407	712.201	0.486	21	0.112	K.NTAETVPFEHVTR.I
R3/RRR3-17/3	1501.529	1501.626	-64.802	0.383	632.361	0.461	21	0.106	K.NTAETVPFEHVTR.I
R3/RRR3-17/3	1501.537	1501.626	-59.298	0.347	446.209	0.368	17	0.092	-.NTAETVPFEHVTR.-
R3/RRR3-25/2	1499.006	1499.673	-1115.881	0.421	851.728	0.501	19	0.166	R.LM*GFFPNDSEVAR.Y
R3/RRR3-26/2	1498.883	1499.673	-1197.902	0.462	860.751	0.473	19	0.163	R.LM*GFFPNDSEVAR.Y
R3/RRR3-25/2	1499.042	1499.673	-1091.760	0.442	772.924	0.499	18	0.161	R.LM*GFFPNDSEVAR.Y
R3/RRR3-26/2	1498.589	1499.673	-1395.037	0.361	899.230	0.448	19	0.160	R.LM*GFFPNDSEVAR.Y
R3/RRR3-26/2	1499.180	1499.673	-330.095	0.439	720.324	0.431	18	0.152	R.LM*GFFPNDSEVAR.Y
R3/RRR3-25/2	1353.709	1354.536	-1353.387	0.402	391.029	0.522	12	0.146	K.VVGNFSALDYLR.L
R3/RRR3-25/2	1501.122	1499.673	299.593	0.341	354.551	0.364	16	0.141	R.LM*GFFPNDSEVAR.Y
R3/RRR3-26/2	1353.467	1354.536	-1533.105	0.290	628.809	0.354	14	0.137	K.VVGNFSALDYLR.L
R3/RRR3-26/2	1354.247	1354.536	-213.602	0.271	592.993	0.358	14	0.136	K.VVGNFSALDYLR.L
R3/RRR3-26/2	1353.629	1354.536	-1412.803	0.212	340.118	0.327	12	0.132	K.VVGNFSALDYLR.L
R3/RRR3-5/2	1359.159	1359.512	-261.024	0.369	750.129	0.380	16	0.142	K.GLLTLSPYHSDR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/3	1036.492	1036.253	231.737	0.446	634.043	0.474	20	0.110	R.IAQGLVHLGK.G
R3/RRR3-5/3	1036.258	1036.253	4.848	0.436	604.675	0.459	20	0.108	R.IAQGLVHLGK.G
R3/RRR3-5/3	1036.255	1036.253	2.278	0.461	518.849	0.389	19	0.103	R.IAQGLVHLGK.G
R3/RRR3-20/2	1720.295	1719.902	228.956	0.518	1313.255	0.512	19	0.200	R.TGGTITM*SNFFNAWR.N
R3/RRR3-20/2	1720.379	1719.902	277.980	0.497	1157.182	0.488	18	0.181	R.TGGTITM*SNFFNAWR.N
R3/RRR3-20/2	1200.142	1199.342	-167.678	0.462	896.551	0.392	13	0.155	K.TFNQYWAIR.T
R3/RRR3-20/2	1199.419	1199.342	63.738	0.420	694.413	0.343	12	0.142	K.TFNQYWAIR.T
R3/RRR3-20/2	1199.361	1199.342	15.965	0.318	367.948	0.287	13	0.140	K.TFNQYWAIR.T
R3/RRR3-20/2	1199.270	1199.342	-60.807	0.340	886.187	0.264	13	0.140	K.TFNQYWAIR.T
R3/RRR3-19/2	1199.387	1199.342	37.402	0.259	503.420	0.296	12	0.136	K.TFNQYWAIR.T
R3/RRR3-9/2	1232.185	1231.381	-159.145	0.549	1416.302	0.451	17	0.202	R.SIVQELLGDTR.I
R3/RRR3-9/2	1759.449	1760.067	-922.710	0.511	1097.066	0.553	22	0.189	R.ISQAITNVVIPTFDIK.L
R3/RRR3-9/2	1230.568	1231.381	-1477.476	0.324	951.472	0.464	18	0.163	R.SIVQELLGDTR.I
R3/RRR3-9/2	1230.453	1231.381	-1571.348	0.384	532.152	0.389	15	0.143	R.SIVQELLGDTR.I
R3/RRR3-9/2	1092.878	1093.215	-308.826	0.444	1772.902	0.474	18	0.251	K.IGYDNAAAVAK.K
R3/RRR3-9/2	1093.004	1093.215	-193.412	0.494	1726.395	0.490	18	0.249	K.IGYDNAAAVAK.K
R3/RRR3-9/2	1092.412	1093.215	-1655.701	0.381	1576.909	0.446	17	0.218	K.IGYDNAAAVAK.K
R3/RRR3-9/2	1167.261	1166.306	-38.664	0.539	607.424	0.490	16	0.155	R.LLGDASVSFEK.N
R3/RRR3-9/2	1165.982	1166.306	-278.648	0.404	699.566	0.428	17	0.150	R.LLGDASVSFEK.N
R3/RRR3-8/2	1655.323	1655.984	-1006.417	0.542	2258.025	0.591	21	0.369	K.TPLQQLMNDALIVAK.Q
R3/RRR3-8/2	1655.612	1655.984	-225.526	0.575	2072.212	0.609	22	0.338	K.TPLQQLMNDALIVAK.Q
R3/RRR3-15/2	1454.845	1454.636	144.195	0.444	1316.636	0.468	19	0.193	K.SAYGGATGVWTPMR.E
R3/RRR3-15/2	1185.747	1186.345	-1351.385	0.443	617.462	0.508	16	0.158	R.HSGIIDIQFR.R
R3/RRR3-15/2	1185.397	1186.345	-1648.633	0.403	549.921	0.484	16	0.152	R.HSGIIDIQFR.R
R3/RRR3-15/2	1454.430	1454.636	-141.813	0.358	701.436	0.326	16	0.136	K.SAYGGATGVWTPMR.E
R3/RRR3-10/2	1250.153	1250.384	-185.259	0.562	1841.309	0.403	19	0.240	R.AFDEGWGGVIAK.T
R3/RRR3-10/2	1249.823	1250.384	-1253.302	0.437	1760.400	0.297	19	0.208	R.AFDEGWGGVIAK.T
R3/RRR3-10/2	1249.370	1250.384	-1617.429	0.426	1688.058	0.313	19	0.203	R.AFDEGWGGVIAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1410.166	1410.661	-352.299	0.449	1198.314	0.467	17	0.183	R.ILIGSIMEEYNK.A
R3/RRR3-9/2	1418.260	1418.534	-193.515	0.525	1406.018	0.598	19	0.232	R.GPLLDEDGPSYVR.V
R3/RRR3-9/2	1418.209	1418.534	-229.523	0.493	1414.322	0.566	19	0.225	R.GPLLDEDGPSYVR.V
R3/RRR3-9/2	1417.606	1418.534	-1363.725	0.492	1324.806	0.588	19	0.220	R.GPLLDEDGPSYVR.V
R3/RRR3-9/2	1047.870	1048.217	-332.257	0.369	1092.842	0.377	15	0.161	R.ALFVQADGVK.L
R3/RRR3-9/2	1047.787	1048.217	-411.859	0.313	595.067	0.307	13	0.122	-.ALFVQADGVK.-
R3/RRR3-18/2	1634.951	1634.686	162.684	0.568	2288.662	0.572	27	0.368	R.ASDFDSLGSDGGPGPVR.S
R3/RRR3-18/2	1634.153	1634.686	-940.786	0.484	2180.387	0.560	27	0.343	R.ASDFDSLGSDGGPGPVR.S
R3/RRR3-18/2	1636.298	1634.686	-237.541	0.564	1860.936	0.568	24	0.287	R.ASDFDSLGSDGGPGPVR.S
R3/RRR3-22/2	1339.147	1339.543	-296.285	0.499	2304.058	0.538	20	0.357	R.FSQVVSNALDMK.L
R3/RRR3-22/2	1355.527	1355.542	-11.702	0.451	2183.186	0.509	20	0.324	R.FSQVVSNALDM*K.L
R3/RRR3-23/2	1355.076	1355.542	-345.021	0.518	2122.156	0.501	20	0.311	R.FSQVVSNALDM*K.L
R3/RRR3-22/2	1355.987	1355.542	328.979	0.492	2147.932	0.476	20	0.308	R.FSQVVSNALDM*K.L
R3/RRR3-22/2	1354.659	1355.542	-1394.551	0.495	2104.144	0.467	20	0.297	R.FSQVVSNALDM*K.L
R3/RRR3-22/2	1339.856	1339.543	234.152	0.520	1981.022	0.521	19	0.292	R.FSQVVSNALDMK.L
R3/RRR3-22/2	1355.136	1355.542	-301.096	0.542	1939.035	0.472	20	0.272	R.FSQVVSNALDM*K.L
R3/RRR3-22/2	1339.158	1339.543	-288.237	0.534	1801.003	0.526	19	0.266	R.FSQVVSNALDMK.L
R3/RRR3-23/2	1355.132	1355.542	-303.536	0.527	1719.703	0.509	19	0.250	R.FSQVVSNALDM*K.L
R3/RRR3-23/2	1355.158	1355.542	-284.196	0.489	1737.938	0.455	20	0.240	R.FSQVVSNALDM*K.L
R3/RRR3-22/2	1356.100	1355.542	-326.975	0.546	1532.526	0.540	18	0.233	R.FSQVVSNALDM*K.L
R3/RRR3-22/2	1355.035	1355.542	-1115.865	0.528	1593.259	0.486	19	0.228	R.FSQVVSNALDM*K.L
R3/RRR3-22/3	1355.456	1355.542	-64.193	0.472	1162.839	0.364	24	0.114	R.FSQVVSNALDM*K.L
R3/RRR3-22/3	1355.482	1355.542	-44.817	0.473	812.290	0.321	21	0.093	-.FSQVVSNALDM*K.-
R3/RRR3-12/2	1787.522	1788.978	-1378.164	0.381	1360.756	0.479	20	0.199	K.TPSLIFEYVNNTDFK.V
R3/RRR3-12/2	1427.542	1426.680	-97.055	0.493	1280.103	0.453	18	0.188	K.ILQNLCGGPNIVK.L
R3/RRR3-12/2	1426.448	1426.680	-163.393	0.409	844.513	0.366	16	0.145	K.ILQNLCGGPNIVK.L
R3/RRR3-12/2	1788.326	1788.978	-926.570	0.409	726.400	0.430	16	0.145	K.TPSLIFEYVNNTDFK.V
R3/RRR3-13/2	1500.251	1499.693	-295.236	0.568	1319.189	0.520	20	0.206	R.SIGISNYDIFLTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1499.006	1499.693	-1129.010	0.410	1375.708	0.405	20	0.189	R.SIGISNYDIFLTR.D
R3/RRR3-13/2	1499.382	1499.693	-207.624	0.517	1133.959	0.469	19	0.179	R.SIGISNYDIFLTR.D
R3/RRR3-13/2	897.672	898.085	-461.707	0.539	1070.046	0.366	13	0.161	K.TPAQLVLR.W
R3/RRR3-13/2	898.004	898.085	-90.138	0.539	1061.638	0.367	13	0.160	K.TPAQLVLR.W
R3/RRR3-13/2	898.150	898.085	72.780	0.578	1023.171	0.328	13	0.151	K.TPAQLVLR.W
R3/RRR3-13/2	897.928	898.085	-174.958	0.208	847.108	0.128	12	0.128	K.TPAQLVLR.W
R3/RRR3-19/2	947.851	948.058	-218.897	0.448	1183.962	0.517	15	0.194	R.SPAAEAVFR.N
R3/RRR3-19/2	947.872	948.058	-196.029	0.474	1088.325	0.506	14	0.184	R.SPAAEAVFR.N
R3/RRR3-19/3	1233.371	1233.359	10.153	0.451	1352.284	0.407	24	0.134	R.HREPLPDSGPK.K
R3/RRR3-19/3	1233.365	1233.359	5.388	0.539	1313.034	0.402	24	0.131	R.HREPLPDSGPK.K
R3/RRR3-19/3	1233.496	1233.359	111.546	0.504	1003.987	0.370	21	0.108	R.HREPLPDSGPK.K
R3/RRR3-20/2	920.104	920.092	12.294	0.472	1021.598	0.445	13	0.170	R.AAGFVWLR.Q
R3/RRR3-20/3	1581.913	1582.651	-1101.852	0.449	1380.122	0.527	27	0.169	R.SGAEVHTGHELCER.K
R3/RRR3-20/2	919.680	920.092	-449.659	0.440	1049.994	0.402	13	0.165	R.AAGFVWLR.Q
R3/RRR3-22/2	1731.549	1730.893	-199.373	0.549	1032.420	0.470	20	0.169	R.DVQEACVHDGYVLPK.L
R3/RRR3-22/2	1013.614	1014.161	-1530.388	0.390	762.933	0.331	14	0.141	R.NIVEQAAIR.D
R3/RRR3-11/2	1192.056	1192.303	-208.051	0.497	1301.767	0.515	19	0.205	K.VLAPYSAEDAR.G
R3/RRR3-11/2	1191.476	1192.303	-1538.694	0.420	1184.216	0.531	19	0.195	K.VLAPYSAEDAR.G
R3/RRR3-11/2	1786.307	1786.045	147.177	0.519	1040.971	0.522	22	0.180	K.SNYM*SAGQISVPIVFR.G
R3/RRR3-11/2	1192.142	1192.303	-135.631	0.477	1035.390	0.461	19	0.174	K.VLAPYSAEDAR.G
R3/RRR3-11/2	1769.498	1770.046	-877.061	0.434	817.592	0.545	19	0.166	K.SNYMSAGQISVPIVFR.G
R3/RRR3-11/2	1785.322	1786.045	-968.188	0.444	564.038	0.487	17	0.147	K.SNYM*SAGQISVPIVFR.G
R3/RRR3-11/2	1769.705	1770.046	-193.137	0.407	837.213	0.380	19	0.146	K.SNYMSAGQISVPIVFR.G
R3/RRR3-12/2	1191.978	1192.303	-273.804	0.336	809.822	0.325	16	0.143	K.VLAPYSAEDAR.G
R3/RRR3-14/2	1059.075	1059.198	-116.834	0.456	1592.097	0.308	17	0.192	K.ILESAAELGR.G
R3/RRR3-14/2	1059.022	1059.198	-167.131	0.473	1358.372	0.347	17	0.178	K.ILESAAELGR.G
R3/RRR3-14/2	1058.998	1059.198	-189.449	0.382	1248.258	0.241	16	0.153	K.ILESAAELGR.G
R3/RRR3-14/2	1182.782	1183.207	-360.609	0.345	708.234	0.417	15	0.145	K.DAFSSSGPETGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1183.076	1183.207	-110.694	0.396	528.959	0.435	14	0.143	K.DAFSSSGPETGK.G
R3/RRR3-14/2	1183.871	1183.207	-284.366	0.452	509.822	0.402	14	0.141	K.DAFSSSGPETGK.G
R3/RRR3-24/2	1562.246	1562.620	-239.866	0.367	673.291	0.486	20	0.153	R.QSGTTPGYSYSTANK.N
R3/RRR3-24/2	1562.240	1562.620	-243.864	0.336	642.623	0.449	19	0.147	R.QSGTTPGYSYSTANK.N
R3/RRR3-24/2	923.137	923.088	53.237	0.399	882.997	0.311	13	0.146	R.ADLISYLK.E
R3/RRR3-24/2	922.893	923.088	-212.479	0.407	884.351	0.289	13	0.144	R.ADLISYLK.E
R3/RRR3-24/2	922.363	923.088	-1875.462	0.378	913.869	0.277	13	0.143	R.ADLISYLK.E
R3/RRR3-24/2	1562.155	1562.620	-298.506	0.362	460.771	0.445	17	0.142	R.QSGTTPGYSYSTANK.N
R3/RRR3-19/2	1563.226	1562.620	-252.248	0.275	302.124	0.364	14	0.134	R.QSGTTPGYSYSTANK.N
R3/RRR3-5/2	1459.855	1458.599	175.319	0.478	1754.863	0.536	17	0.265	K.YNVESWLDYLR.S
R3/RRR3-5/2	1458.668	1458.599	47.122	0.496	1291.754	0.459	16	0.191	K.YNVESWLDYLR.S
R3/RRR3-5/3	1758.686	1758.869	-104.060	0.345	1595.323	0.279	26	0.133	K.TSHVFYSQADGFSSPK.E
R3/RRR3-19/3	1852.179	1851.949	124.360	0.586	2393.172	0.499	31	0.335	R.SNNIHHDLDTQCPTAK.T
R3/RRR3-11/2	1558.539	1558.671	-84.734	0.531	1154.888	0.551	20	0.195	R.GCSANVFLDNAAYR.Q
R3/RRR3-11/2	1315.087	1314.477	-297.237	0.341	337.963	0.550	15	0.149	R.QHAFWVPVSSR.Y
R3/RRR3-11/2	1314.156	1314.477	-244.528	0.272	242.438	0.524	13	0.141	R.QHAFWVPVSSR.Y
R3/RRR3-11/2	1314.325	1314.477	-115.383	0.280	263.307	0.558	11	0.140	R.QHAFWVPVSSR.Y
R3/RRR3-3/2	1492.174	1490.749	285.402	0.507	811.603	0.556	18	0.170	R.TYIGPM*TPPLVER.I
R3/RRR3-3/2	1158.808	1159.280	-408.536	0.463	1012.902	0.373	16	0.155	R.RFPAAPTEGGR.L
R3/RRR3-10/2	1243.999	1244.337	-272.098	0.473	1172.428	0.388	19	0.169	R.VSSEQEAAPAVR.A
R3/RRR3-10/3	1220.165	1219.503	-277.875	0.364	944.155	0.421	20	0.108	R.FPAPPPLVRPK.A
R3/RRR3-19/2	1282.155	1282.339	-143.584	0.438	673.969	0.505	15	0.155	R.VTSGELEDEFR.V
R3/RRR3-19/3	1457.793	1457.517	190.381	0.412	865.664	0.379	22	0.102	K.CYECGEAGHFAR.E
R3/RRR3-19/3	1457.319	1457.517	-135.955	0.349	849.719	0.232	22	0.085	K.CYECGEAGHFAR.E
R3/RRR3-11/2	1991.409	1992.243	-923.441	0.477	1401.372	0.552	24	0.218	R.LGLPDAGLISYGEMVDQGR.L
R3/RRR3-11/2	1255.098	1254.458	-287.348	0.447	456.339	0.459	15	0.146	K.INEGIPAGILEK.I
R3/RRR3-11/2	1254.120	1254.458	-270.292	0.389	431.270	0.345	15	0.138	K.INEGIPAGILEK.I
R3/RRR3-11/2	1254.291	1254.458	-133.010	0.321	394.776	0.317	14	0.134	-.INEGIPAGILEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1930.944	1929.204	-135.477	0.557	2099.370	0.620	26	0.347	R.NLADPSSLAVATTNLISLK.G
R3/RRR3-7/2	820.540	820.959	-512.643	0.407	863.491	0.478	13	0.164	R.VGVVFSGR.Q
R3/RRR3-7/2	820.415	820.959	-1887.345	0.343	879.828	0.403	13	0.154	R.VGVVFSGR.Q
R3/RRR3-7/2	1297.227	1297.526	-231.013	0.336	665.949	0.464	19	0.150	K.VVGVPVSLNGDLK.N
R3/RRR3-7/2	1297.207	1297.526	-246.307	0.370	548.877	0.474	19	0.149	K.VVGVPVSLNGDLK.N
R3/RRR3-7/2	820.322	820.959	-2001.141	0.323	669.959	0.383	11	0.143	R.VGVVFSGR.Q
R3/RRR3-7/2	1296.470	1297.526	-1590.684	0.267	465.367	0.333	16	0.134	K.VVGVPVSLNGDLK.N
R3/RRR3-18/2	1569.320	1569.615	-188.619	0.433	1303.844	0.491	20	0.196	K.GSYGVNYGGGDGYFR.F
R3/RRR3-18/2	1343.537	1343.548	-8.440	0.378	1264.926	0.367	18	0.171	R.VNCPALLTVNGGK.G
R3/RRR3-18/2	1343.280	1343.548	-199.760	0.387	1196.222	0.374	18	0.167	R.VNCPALLTVNGGK.G
R3/RRR3-18/2	1344.194	1343.548	-264.021	0.376	946.154	0.298	16	0.143	-.VNCPALLTVNGGK.-
R3/RRR3-26/2	1486.251	1486.719	-316.000	0.391	1139.785	0.375	19	0.163	R.GIM*QPVPVSDALSR.F
R3/RRR3-25/2	1486.300	1486.719	-283.039	0.393	909.272	0.406	18	0.154	R.GIM*QPVPVSDALSR.F
R3/RRR3-25/2	1485.504	1486.719	-1495.766	0.278	1060.885	0.233	19	0.141	R.GIM*QPVPVSDALSR.F
R3/RRR3-25/2	1038.230	1039.148	-1852.451	0.251	686.184	0.332	15	0.138	R.FAGGAPEM*SR.A
R3/RRR3-26/2	1039.019	1039.148	-124.002	0.233	358.390	0.366	11	0.134	R.FAGGAPEM*SR.A
R3/RRR3-25/2	1038.815	1039.148	-320.737	0.271	688.868	0.247	14	0.134	R.FAGGAPEM*SR.A
R3/RRR3-26/2	1038.818	1039.148	-318.379	0.245	674.868	0.249	13	0.132	R.FAGGAPEM*SR.A
R3/RRR3-25/2	1485.499	1486.719	-1498.986	0.203	654.430	0.087	16	0.125	R.GIM*QPVPVSDALSR.F
R3/RRR3-13/2	1260.705	1261.452	-1389.422	0.382	1135.495	0.585	20	0.195	R.AFTVGIGGPVGTGK.T
R3/RRR3-13/2	1443.263	1443.626	-252.176	0.301	412.705	0.403	14	0.137	K.YSLAAVTNDIFTK.E
R3/RRR3-13/2	1443.700	1443.626	51.087	0.229	385.909	0.336	14	0.132	K.YSLAAVTNDIFTK.E
R3/RRR3-13/2	1443.452	1443.626	-121.262	0.254	722.937	0.261	14	0.131	K.YSLAAVTNDIFTK.E
R3/RRR3-15/2	1588.247	1588.791	-975.147	0.428	1630.549	0.387	21	0.211	R.DNVQAYWPNVIIR.Y
R3/RRR3-14/2	1588.369	1588.791	-266.601	0.497	1617.893	0.396	21	0.211	R.DNVQAYWPNVIIR.Y
R3/RRR3-14/2	1588.315	1588.791	-300.604	0.477	1460.551	0.425	20	0.200	R.DNVQAYWPNVIIR.Y
R3/RRR3-13/2	1588.539	1588.791	-159.592	0.507	1333.346	0.415	19	0.185	R.DNVQAYWPNVIIR.Y
R3/RRR3-15/2	1588.487	1588.791	-192.047	0.513	1303.426	0.421	19	0.184	R.DNVQAYWPNVIIR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1588.263	1588.791	-965.270	0.469	1295.001	0.410	19	0.182	R.DNVQAYWPNVIIR.Y
R3/RRR3-14/2	1807.935	1808.027	-51.374	0.493	605.319	0.611	19	0.166	R.EIPLNYATFQPGTTVR.D
R3/RRR3-15/2	1807.513	1808.027	-840.394	0.466	773.285	0.506	20	0.161	R.EIPLNYATFQPGTTVR.D
R3/RRR3-15/2	1807.412	1808.027	-896.395	0.451	753.000	0.499	20	0.159	R.EIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1806.893	1808.027	-1184.636	0.398	794.578	0.478	21	0.158	R.EIPLNYATFQPGTTVR.D
R3/RRR3-15/2	1588.155	1588.791	-1033.409	0.385	1067.399	0.348	17	0.155	R.DNVQAYWPNVIIR.Y
R3/RRR3-14/2	1808.758	1808.027	-149.503	0.505	441.974	0.566	17	0.155	R.EIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1807.303	1808.027	-956.810	0.432	669.338	0.496	19	0.154	R.EIPLNYATFQPGTTVR.D
R3/RRR3-15/2	1807.335	1808.027	-939.247	0.420	671.444	0.477	19	0.152	R.EIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1808.148	1808.027	66.657	0.514	384.754	0.540	16	0.150	R.EIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1808.279	1808.027	139.574	0.493	407.636	0.506	16	0.147	R.EIPLNYATFQPGTTVR.D
R3/RRR3-12/2	1590.005	1588.791	134.864	0.389	285.127	0.298	12	0.137	R.DNVQAYWPNVIIR.Y
R3/RRR3-11/2	1589.648	1588.791	-90.470	0.376	536.222	0.269	12	0.130	-.DNVQAYWPNVIIR.-
R3/RRR3-1/2	1589.250	1588.791	289.548	0.349	794.316	0.121	17	0.127	R.DNVQAYWPNVIIR.Y
R3/RRR3-14/3	1807.909	1808.027	-65.740	0.459	980.957	0.406	27	0.112	R.EIPLNYATFQPGTTVR.D
R3/RRR3-14/3	1807.870	1808.027	-87.278	0.404	721.621	0.404	25	0.101	R.EIPLNYATFQPGTTVR.D
R3/RRR3-16/2	1143.634	1144.346	-1501.892	0.429	2064.254	0.629	22	0.339	K.VAVITGAASGIGK.A
R3/RRR3-16/2	1144.145	1144.346	-176.848	0.514	1948.506	0.682	22	0.337	K.VAVITGAASGIGK.A
R3/RRR3-13/2	1144.046	1144.346	-263.336	0.465	2070.872	0.595	22	0.331	K.VAVITGAASGIGK.A
R3/RRR3-15/2	1144.369	1144.346	19.407	0.502	2009.212	0.617	22	0.327	K.VAVITGAASGIGK.A
R3/RRR3-16/2	1144.197	1144.346	-130.827	0.510	1973.905	0.624	22	0.323	K.VAVITGAASGIGK.A
R3/RRR3-15/2	1144.172	1144.346	-152.981	0.499	1967.702	0.628	22	0.323	K.VAVITGAASGIGK.A
R3/RRR3-13/2	1144.971	1144.346	-328.567	0.521	1829.721	0.645	21	0.304	K.VAVITGAASGIGK.A
R3/RRR3-13/2	1144.128	1144.346	-191.619	0.397	1943.537	0.585	21	0.303	K.VAVITGAASGIGK.A
R3/RRR3-15/2	1143.722	1144.346	-1424.700	0.358	1846.730	0.566	20	0.281	K.VAVITGAASGIGK.A
R3/RRR3-22/2	1715.341	1714.900	257.914	0.438	477.341	0.496	23	0.151	K.LDPGATASHNFILETK.V
R3/RRR3-22/2	1715.492	1714.900	-238.851	0.420	265.198	0.555	19	0.149	K.LDPGATASHNFILETK.V
R3/RRR3-22/2	1254.039	1253.432	-314.245	0.407	732.614	0.386	15	0.145	K.FQGSPAIITYR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-22/2	1253.335	1253.432	-77.527	0.223	636.949	0.104	13	0.126	-.FQGSPAIITYR.-
R3/RRR3-15/2	1930.007	1930.151	-74.833	0.409	2026.443	0.534	26	0.699	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-15/2	1930.261	1930.151	57.302	0.408	1828.998	0.561	26	0.562	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-15/2	1930.346	1930.151	101.255	0.444	1713.123	0.597	25	0.490	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-16/2	1930.299	1930.151	77.218	0.465	1681.003	0.526	26	0.453	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-15/2	1929.530	1930.151	-842.391	0.395	1571.134	0.512	25	0.395	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-16/2	1930.073	1930.151	-40.574	0.461	1537.156	0.559	25	0.377	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-15/2	1730.382	1730.852	-272.033	0.496	2097.731	0.575	23	0.329	R.SGTALCSYIASTAQSGR.I
R3/RRR3-15/2	1730.406	1730.852	-258.515	0.537	2023.393	0.569	23	0.313	R.SGTALCSYIASTAQSGR.I
R3/RRR3-16/2	1730.632	1730.852	-127.600	0.516	2091.220	0.521	23	0.310	R.SGTALCSYIASTAQSGR.I
R3/RRR3-16/2	1731.417	1730.852	-252.070	0.570	1931.869	0.611	23	0.309	R.SGTALCSYIASTAQSGR.I
R3/RRR3-15/2	1929.487	1930.151	-864.683	0.377	1386.579	0.522	24	0.301	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-15/2	1729.809	1730.852	-1184.269	0.487	1943.584	0.562	22	0.297	R.SGTALCSYIASTAQSGR.I
R3/RRR3-16/2	1730.272	1730.852	-915.625	0.526	1755.040	0.572	22	0.269	R.SGTALCSYIASTAQSGR.I
R3/RRR3-15/2	1929.289	1930.151	-967.898	0.359	1304.110	0.508	24	0.261	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-16/2	1929.258	1930.151	-983.842	0.342	1207.598	0.461	23	0.215	R.ISGIPSGTVNLLAFNGNPSA.-
R3/RRR3-18/2	907.366	906.874	543.373	0.218	1154.945	0.165	15	0.136	R.DGCGGNGGGR.W
R3/RRR3-17/2	907.263	907.859	-1765.047	0.211	815.402	0.236	14	0.131	R.DGCGGDGGGR.W
R3/RRR3-17/2	907.019	907.859	-2034.415	0.167	563.913	0.249	12	0.127	R.DGCGGDGGGR.W
R3/RRR3-23/2	1745.514	1745.956	-254.103	0.394	1087.515	0.457	18	0.165	R.TGDSYLSAIGVYVRPF.-
R3/RRR3-23/2	1211.907	1212.339	-357.802	0.471	688.341	0.501	14	0.154	K.NNSSIVGFFAR.T
R3/RRR3-23/2	1745.253	1745.956	-978.972	0.367	987.470	0.498	18	0.137	R.TGDSYLSAIGVYVRPF.-
R3/RRR3-23/2	1745.560	1745.956	-227.723	0.393	891.307	0.487	17	0.106	R.TGDSYLSAIGVYVRPF.-
R3/RRR3-25/2	1208.993	1209.399	-336.575	0.352	855.046	0.335	18	0.143	R.GTVGVM*VTATTR.C
R3/RRR3-16/3	1343.351	1343.513	-121.103	0.468	685.916	0.485	22	0.114	R.LDEALATGLFHR.I
R3/RRR3-25/3	1343.241	1343.513	-202.875	0.446	790.393	0.444	22	0.110	R.LDEALATGLFHR.I
R3/RRR3-16/3	1343.358	1343.513	-115.907	0.468	693.679	0.451	22	0.110	R.LDEALATGLFHR.I
R3/RRR3-25/3	1343.895	1343.513	285.095	0.386	736.064	0.385	22	0.101	R.LDEALATGLFHR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1366.157	1366.613	-334.998	0.387	764.570	0.493	16	0.158	R.VLGSWASPFVM*R.V
R3/RRR3-16/2	1307.957	1308.509	-1190.015	0.420	777.124	0.475	16	0.158	K.SELLLASNPVHK.K
R3/RRR3-17/2	1350.739	1350.614	93.217	0.269	873.041	0.482	14	0.155	R.VLGSWASPFVMR.V
R3/RRR3-16/2	1308.079	1308.509	-329.530	0.388	853.753	0.355	18	0.149	K.SELLLASNPVHK.K
R3/RRR3-17/2	1307.659	1308.509	-1418.838	0.405	491.195	0.474	15	0.149	K.SELLLASNPVHK.K
R3/RRR3-16/2	1350.481	1350.614	-98.695	0.398	550.437	0.456	14	0.146	R.VLGSWASPFVMR.V
R3/RRR3-17/2	1308.383	1308.509	-96.162	0.395	500.080	0.374	16	0.143	K.SELLLASNPVHK.K
R3/RRR3-17/2	1308.137	1308.509	-284.776	0.406	624.854	0.346	17	0.143	K.SELLLASNPVHK.K
R3/RRR3-17/2	1366.391	1366.613	-163.256	0.309	238.535	0.315	14	0.140	R.VLGSWASPFVM*R.V
R3/RRR3-16/2	1307.718	1308.509	-1372.990	0.339	664.228	0.306	14	0.136	-.SELLLASNPVHK.-
R3/RRR3-16/2	1365.946	1366.613	-1224.318	0.333	359.858	0.358	11	0.135	R.VLGSWASPFVM*R.V
R3/RRR3-8/3	1727.331	1727.927	-927.111	0.508	1108.268	0.549	26	0.150	R.RVQEHM*TLASNPTAR.R
R3/RRR3-8/2	1198.087	1198.396	-258.407	0.361	547.686	0.448	15	0.143	K.LPEAPLTPGFR.Q
R3/RRR3-8/3	1727.724	1727.927	-118.038	0.475	1012.092	0.430	25	0.118	R.RVQEHM*TLASNPTAR.R
R3/RRR3-8/3	1728.027	1727.927	57.664	0.460	761.826	0.499	23	0.117	R.RVQEHM*TLASNPTAR.R
R3/RRR3-2/2	1874.614	1875.067	-242.481	0.522	2301.176	0.488	23	0.342	K.ILLLDEATSALDVESER.I
R3/RRR3-2/2	1874.549	1875.067	-812.103	0.449	1484.306	0.446	21	0.205	K.ILLLDEATSALDVESER.I
R3/RRR3-10/2	1333.289	1333.515	-169.575	0.524	1094.433	0.541	19	0.189	K.SVGGQPIVFDSVK.G
R3/RRR3-10/2	1333.225	1333.515	-217.796	0.372	947.822	0.500	19	0.168	K.SVGGQPIVFDSVK.G
R3/RRR3-10/2	1623.323	1623.832	-932.656	0.407	924.695	0.523	20	0.165	K.AGSGVATLGLPDSPGVPK.G
R3/RRR3-12/2	1454.998	1455.600	-1104.338	0.491	1501.762	0.386	20	0.197	K.FQAELQTQPGAHK.Y
R3/RRR3-12/2	1348.621	1347.628	-5.412	0.287	798.654	0.266	16	0.133	K.SVATILTYPLIR.C
R3/RRR3-12/3	1505.734	1504.676	38.565	0.363	1039.661	0.481	27	0.129	R.LAAALSSPAHPAGGAGR.N
R3/RRR3-11/3	1504.689	1504.676	8.729	0.375	700.996	0.509	24	0.115	R.LAAALSSPAHPAGGAGR.N
R3/RRR3-11/3	1314.916	1314.518	303.716	0.408	921.627	0.406	22	0.107	R.VSIAHQTAFALR.L
R3/RRR3-12/3	1504.947	1504.676	180.796	0.393	617.125	0.441	24	0.104	R.LAAALSSPAHPAGGAGR.N
R3/RRR3-12/3	1504.482	1504.676	-129.333	0.376	629.451	0.430	24	0.102	R.LAAALSSPAHPAGGAGR.N
R3/RRR3-10/2	1630.309	1630.910	-984.985	0.514	1147.505	0.589	21	0.200	R.ELLGGNGILADFLVAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1102.769	1103.294	-1387.121	0.346	933.404	0.319	19	0.145	K.LATLGLAGGTTK.G
R3/RRR3-15/2	1103.182	1103.296	-103.284	0.318	1350.263	0.397	16	0.183	K.VAVSFTHTIK.A
R3/RRR3-15/2	1441.165	1441.698	-1066.597	0.498	1100.538	0.496	22	0.183	K.ITPTVLQSAGLNVK.Q
R3/RRR3-15/2	1442.530	1441.698	-116.842	0.511	938.099	0.471	22	0.168	K.ITPTVLQSAGLNVK.Q
R3/RRR3-15/2	1103.127	1103.296	-153.234	0.350	1017.635	0.434	15	0.164	K.VAVSFTHTIK.A
R3/RRR3-15/2	1441.144	1441.698	-1081.566	0.387	895.801	0.443	20	0.159	K.ITPTVLQSAGLNVK.Q
R3/RRR3-15/2	1102.984	1103.296	-283.685	0.332	1004.505	0.286	15	0.146	K.VAVSFTHTIK.A
R3/RRR3-10/2	1666.159	1665.871	173.452	0.537	1324.948	0.581	21	0.217	K.GFAIGNGLTDPAIQYK.A
R3/RRR3-9/2	1665.273	1665.871	-962.613	0.504	1403.011	0.493	21	0.206	K.GFAIGNGLTDPAIQYK.A
R3/RRR3-9/2	1665.270	1665.871	-964.306	0.466	1412.334	0.448	20	0.198	K.GFAIGNGLTDPAIQYK.A
R3/RRR3-10/2	1696.541	1696.923	-226.003	0.476	743.078	0.512	20	0.161	R.NLEVGIPELLENDIK.V
R3/RRR3-9/2	1697.409	1696.923	286.823	0.504	684.219	0.485	20	0.156	R.NLEVGIPELLENDIK.V
R3/RRR3-10/2	1696.804	1696.923	-70.686	0.432	701.758	0.470	19	0.153	R.NLEVGIPELLENDIK.V
R3/RRR3-9/2	1696.735	1696.923	-111.459	0.442	648.150	0.468	19	0.152	R.NLEVGIPELLENDIK.V
R3/RRR3-9/2	1696.441	1696.923	-285.342	0.452	599.253	0.426	18	0.146	R.NLEVGIPELLENDIK.V
R3/RRR3-10/2	1696.102	1696.923	-1076.930	0.416	553.127	0.416	18	0.144	R.NLEVGIPELLENDIK.V
R3/RRR3-5/2	1785.466	1784.987	268.837	0.524	853.840	0.597	19	0.175	K.QSGVELGNSILFFGCR.N
R3/RRR3-5/3	1713.503	1713.871	-215.271	0.423	1471.415	0.383	27	0.144	R.ALHTIVQEQGSLDSSK.T
R3/RRR3-13/2	1734.617	1733.021	-233.721	0.559	1403.594	0.517	19	0.212	K.TM*M*ALSDLLWEDM*K.S
R3/RRR3-13/3	1979.952	1980.189	-119.935	0.462	1308.851	0.371	29	0.126	K.NVNYLPNVLSIM*DAEDR.G
R3/RRR3-19/2	1015.740	1016.174	-428.048	0.304	778.107	0.362	16	0.145	K.LVLVGDGGTGK.T
R3/RRR3-18/2	1016.126	1016.174	-46.885	0.374	754.036	0.259	15	0.137	K.LVLVGDGGTGK.T
R3/RRR3-16/2	1016.093	1016.174	-79.542	0.360	667.659	0.238	16	0.136	K.LVLVGDGGTGK.T
R3/RRR3-19/2	1015.892	1016.174	-277.815	0.340	568.903	0.231	14	0.135	K.LVLVGDGGTGK.T
R3/RRR3-16/2	1017.175	1016.174	1.672	0.323	476.355	0.256	13	0.134	-.LVLVGDGGTGK.-
R3/RRR3-17/2	1015.208	1016.174	-1941.712	0.219	907.282	0.177	16	0.133	K.LVLVGDGGTGK.T
R3/RRR3-19/2	1015.616	1016.174	-1538.040	0.223	448.828	0.270	12	0.133	-.LVLVGDGGTGK.-
R3/RRR3-18/2	1015.817	1016.174	-352.443	0.286	617.471	0.158	14	0.131	K.LVLVGDGGTGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1016.196	1016.174	22.397	0.369	670.967	0.217	13	0.129	-.LVLVGDGGTGK.-
R3/RRR3-14/1	1129.658	1130.320	-1475.319	0.218	720.154	0.452	15	0.922	K.VAVITGGASGIGK.A
R3/RRR3-14/2	1129.651	1130.320	-1481.355	0.426	2242.883	0.512	22	0.338	K.VAVITGGASGIGK.A
R3/RRR3-14/2	1129.582	1130.320	-1543.338	0.445	2198.248	0.519	22	0.332	K.VAVITGGASGIGK.A
R3/RRR3-14/2	1129.639	1130.320	-1492.318	0.464	2158.148	0.519	22	0.324	K.VAVITGGASGIGK.A
R3/RRR3-16/2	1130.140	1130.320	-159.214	0.437	2023.404	0.565	21	0.313	K.VAVITGGASGIGK.A
R3/RRR3-16/2	1329.134	1328.497	-273.922	0.559	1906.178	0.595	19	0.304	K.VIIADVQDELGR.S
R3/RRR3-16/2	1327.580	1328.497	-1448.456	0.407	1931.270	0.473	19	0.273	K.VIIADVQDELGR.S
R3/RRR3-16/2	1327.756	1328.497	-1315.108	0.403	1805.538	0.477	19	0.255	K.VIIADVQDELGR.S
R3/RRR3-16/2	1129.869	1130.320	-399.927	0.405	1736.297	0.499	20	0.250	K.VAVITGGASGIGK.A
R3/RRR3-15/2	1129.591	1130.320	-1535.522	0.417	1686.756	0.514	19	0.246	K.VAVITGGASGIGK.A
R3/RRR3-16/2	1328.208	1328.497	-217.697	0.399	779.403	0.395	14	0.146	-.VIIADVQDELGR.-
R3/RRR3-16/2	1328.314	1328.497	-138.226	0.231	564.330	0.375	12	0.134	-.VIIADVQDELGR.-
R3/RRR3-14/2	1130.610	1130.320	257.020	0.140	393.161	0.321	14	0.129	-.VAVITGGASGIGK.-
R3/RRR3-21/2	1440.300	1440.710	-285.848	0.476	1043.916	0.466	19	0.171	K.QALVDQLGLELIK.D
R3/RRR3-21/2	1424.570	1423.726	-109.376	0.429	564.057	0.518	19	0.153	K.QSLAGIPLLVLGNK.I
R3/RRR3-21/2	1423.330	1423.726	-278.675	0.412	787.666	0.391	21	0.149	K.QSLAGIPLLVLGNK.I
R3/RRR3-25/2	1802.681	1801.036	-197.686	0.383	1063.505	0.210	18	0.134	K.VFVRADLNVPLDDAQK.I
R3/RRR3-25/2	1802.766	1801.036	-150.271	0.291	1047.660	0.162	18	0.131	K.VFVRADLNVPLDDAQK.I
R3/RRR3-15/2	1441.575	1441.698	-85.239	0.494	1249.288	0.410	22	0.179	K.VTPTVLQSAGLNLK.Q
R3/RRR3-15/2	1440.953	1441.698	-1214.856	0.421	1259.181	0.388	22	0.176	K.VTPTVLQSAGLNLK.Q
R3/RRR3-15/2	1441.106	1441.698	-1108.272	0.433	861.751	0.425	20	0.156	K.VTPTVLQSAGLNLK.Q
R3/RRR3-15/2	1441.887	1441.698	131.565	0.467	874.221	0.431	18	0.156	K.VTPTVLQSAGLNLK.Q
R3/RRR3-10/2	1949.684	1948.249	223.398	0.572	2039.055	0.625	22	0.337	R.VGYTLYNTVLFFDPLGK.Y
R3/RRR3-6/2	1420.944	1421.581	-1155.016	0.455	1091.289	0.500	20	0.182	R.IVTNVGQDNAVYK.A
R3/RRR3-6/2	1420.746	1421.581	-1295.303	0.446	1013.140	0.499	19	0.175	R.IVTNVGQDNAVYK.A
R3/RRR3-6/2	1822.783	1823.127	-188.923	0.462	855.586	0.496	19	0.160	K.GSLVDLNLPSITIPNLR.M
R3/RRR3-6/2	1420.650	1421.581	-1363.044	0.354	859.396	0.469	18	0.159	R.IVTNVGQDNAVYK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1822.558	1823.127	-863.351	0.440	724.577	0.520	18	0.156	K.GSLVDLNLPSITIPNLR.M
R3/RRR3-6/2	1822.516	1823.127	-886.346	0.434	704.932	0.515	18	0.154	K.GSLVDLNLPSITIPNLR.M
R3/RRR3-5/2	1421.190	1421.581	-275.390	0.427	623.991	0.396	15	0.141	-.IVTNVGQDNAVYK.-
R3/RRR3-24/2	1060.168	1060.231	-59.893	0.423	679.657	0.359	14	0.142	R.AAFNLSPLAR.E
R3/RRR3-24/2	1059.575	1060.231	-1567.424	0.354	617.452	0.307	12	0.134	R.AAFNLSPLAR.E
R3/RRR3-24/3	1218.575	1218.433	116.127	0.442	1271.855	0.422	23	0.132	-.ALGHVVPAQLGR.-
R3/RRR3-24/3	1218.286	1218.433	-121.274	0.418	1256.934	0.365	23	0.119	-.ALGHVVPAQLGR.-
R3/RRR3-24/3	1217.875	1218.433	-1283.123	0.368	906.298	0.330	22	0.096	-.ALGHVVPAQLGR.-
R3/RRR3-18/2	916.032	916.099	-73.528	0.436	1067.284	0.401	13	0.165	K.AADVLLWK.D
R3/RRR3-18/2	1294.334	1294.485	-116.787	0.474	617.952	0.455	15	0.151	R.TDINQALHLLR.E
R3/RRR3-18/2	1294.215	1294.485	-209.130	0.433	554.278	0.365	14	0.140	R.TDINQALHLLR.E
R3/RRR3-18/2	1294.320	1294.485	-127.761	0.389	548.084	0.327	14	0.138	R.TDINQALHLLR.E
R3/RRR3-15/2	1115.129	1115.350	-199.127	0.451	1160.721	0.441	16	0.178	K.VAVSFTHIIK.S
R3/RRR3-2/2	1264.123	1263.425	-239.388	0.334	1150.113	0.392	17	0.166	K.SAEPAFSVLVSR.F
R3/RRR3-15/2	1114.556	1115.350	-1614.126	0.388	860.751	0.451	15	0.158	K.VAVSFTHIIK.S
R3/RRR3-2/2	1263.294	1263.425	-103.568	0.240	568.517	0.186	13	0.127	-.SAEPAFSVLVSR.-
R3/RRR3-9/2	1702.835	1702.978	-84.025	0.512	1052.509	0.499	20	0.176	R.GFIVTTWAPQVDVLR.H
R3/RRR3-9/2	1733.955	1733.902	30.532	0.465	954.400	0.523	20	0.171	R.AAPDLDALFPDGFVER.T
R3/RRR3-9/2	1702.573	1702.978	-238.075	0.427	730.552	0.436	17	0.147	R.GFIVTTWAPQVDVLR.H
R3/RRR3-12/2	1205.916	1206.288	-309.322	0.440	1033.197	0.544	20	0.185	R.VIGSGTNLDSSR.F
R3/RRR3-12/2	1205.996	1206.288	-243.311	0.417	743.839	0.480	17	0.156	R.VIGSGTNLDSSR.F
R3/RRR3-12/2	834.787	834.943	-187.458	0.344	691.300	0.351	12	0.143	K.LSGFPASR.V
R3/RRR3-12/2	834.857	834.943	-102.675	0.289	796.078	0.325	13	0.142	K.LSGFPASR.V
R3/RRR3-12/2	834.321	834.943	-1949.442	0.291	547.334	0.312	11	0.135	-.LSGFPASR.-
R3/RRR3-10/2	1114.263	1114.314	-45.888	0.476	1090.875	0.467	15	0.177	K.APLLIGCDVR.S
R3/RRR3-10/2	1113.536	1114.314	-1601.642	0.344	1193.501	0.417	15	0.174	K.APLLIGCDVR.S
R3/RRR3-10/2	1113.664	1114.314	-1485.690	0.421	1102.377	0.432	15	0.171	K.APLLIGCDVR.S
R3/RRR3-10/3	1501.321	1501.601	-186.882	0.448	1118.071	0.385	27	0.115	-.M*PGSLDHEEQDVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/3	1501.744	1501.601	95.671	0.416	1010.004	0.372	26	0.108	-.M*PGSLDHEEQDVK.T
R3/RRR3-10/3	1501.849	1501.601	165.367	0.413	939.542	0.363	26	0.104	-.M*PGSLDHEEQDVK.T
R3/RRR3-11/3	1501.009	1501.601	-1064.119	0.392	697.227	0.394	21	0.102	-.M*PGSLDHEEQDVK.T
R3/RRR3-11/3	1502.242	1501.601	-239.988	0.268	624.495	0.264	21	0.089	-.M*PGSLDHEEQDVK.T
R3/RRR3-24/2	1052.204	1052.163	39.259	0.427	666.690	0.368	14	0.142	-.LYSLEEAAR.-
R3/RRR3-24/3	1735.630	1736.732	-1214.519	0.463	1228.226	0.450	29	0.137	K.DAKEEFDDAGHSESAK.E
R3/RRR3-24/3	1736.310	1736.732	-243.858	0.462	942.846	0.435	28	0.115	K.DAKEEFDDAGHSESAK.E
R3/RRR3-24/3	1736.486	1736.732	-141.772	0.446	863.849	0.451	26	0.114	K.DAKEEFDDAGHSESAK.E
R3/RRR3-21/2	1673.808	1672.880	-43.650	0.446	422.010	0.547	20	0.159	R.IIPNFM*CQGGDFTR.X
R3/RRR3-22/2	1673.213	1672.880	199.567	0.338	368.177	0.589	18	0.154	R.IIPNFM*CQGGDFTR.X
R3/RRR3-22/2	1657.047	1656.881	100.591	0.464	319.828	0.508	18	0.154	R.IIPNFMCQGGDFTR.X
R3/RRR3-21/2	1657.268	1656.881	234.519	0.409	332.825	0.500	17	0.151	R.IIPNFMCQGGDFTR.X
R3/RRR3-21/2	1673.086	1672.880	123.548	0.321	434.813	0.527	19	0.151	R.IIPNFM*CQGGDFTR.X
R3/RRR3-22/2	1672.958	1672.880	46.786	0.340	361.648	0.508	18	0.150	R.IIPNFM*CQGGDFTR.X
R3/RRR3-22/2	1673.139	1672.880	155.084	0.310	350.670	0.533	18	0.149	R.IIPNFM*CQGGDFTR.X
R3/RRR3-22/2	1658.408	1656.881	-285.980	0.454	290.566	0.502	18	0.149	-.IIPNFMCQGGDFTR.-
R3/RRR3-22/2	1674.126	1672.880	146.947	0.355	306.169	0.485	17	0.149	R.IIPNFM*CQGGDFTR.X
R3/RRR3-21/2	1672.991	1672.880	66.252	0.359	273.433	0.446	18	0.149	R.IIPNFM*CQGGDFTR.X
R3/RRR3-21/2	1673.305	1672.880	254.507	0.283	373.039	0.533	18	0.148	R.IIPNFM*CQGGDFTR.X
R3/RRR3-22/2	1674.436	1672.880	-266.360	0.308	372.986	0.482	18	0.147	R.IIPNFM*CQGGDFTR.X
R3/RRR3-21/2	1656.521	1656.881	-217.715	0.335	242.446	0.410	17	0.147	R.IIPNFMCQGGDFTR.X
R3/RRR3-22/2	1656.370	1656.881	-915.009	0.340	321.881	0.422	18	0.147	R.IIPNFMCQGGDFTR.X
R3/RRR3-21/2	1658.316	1656.881	263.018	0.481	340.153	0.428	19	0.146	-.IIPNFMCQGGDFTR.-
R3/RRR3-21/2	1673.389	1672.880	-294.257	0.285	377.904	0.480	18	0.146	R.IIPNFM*CQGGDFTR.X
R3/RRR3-22/2	1656.544	1656.881	-204.335	0.308	329.742	0.431	18	0.146	R.IIPNFMCQGGDFTR.X
R3/RRR3-21/2	1672.412	1672.880	-280.885	0.293	240.434	0.384	18	0.146	R.IIPNFM*CQGGDFTR.X
R3/RRR3-21/2	1364.926	1365.620	-1245.061	0.342	972.158	0.304	16	0.145	R.VVM*ELFADTVPK.T
R3/RRR3-22/2	1673.542	1672.880	-202.560	0.321	315.944	0.406	17	0.145	R.IIPNFM*CQGGDFTR.X

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1365.814	1365.620	142.536	0.400	726.311	0.359	16	0.144	R.VVM*ELFADTVPK.T
R3/RRR3-21/2	1364.925	1365.620	-1245.510	0.313	676.686	0.359	15	0.140	R.VVM*ELFADTVPK.T
R3/RRR3-20/2	1349.343	1349.621	-206.484	0.327	536.076	0.357	14	0.137	-.VVMELFADTVPK.-
R3/RRR3-21/2	1350.040	1349.621	311.559	0.282	706.191	0.188	17	0.132	R.VVMELFADTVPK.T
R3/RRR3-21/2	1625.254	1625.757	-927.555	0.538	1994.238	0.629	23	0.328	R.YVCQDQFTGQPGPK.C
R3/RRR3-23/2	1625.197	1625.757	-962.770	0.517	1880.233	0.620	22	0.304	R.YVCQDQFTGQPGPK.C
R3/RRR3-20/2	1625.309	1625.757	-276.813	0.533	1889.361	0.606	22	0.302	R.YVCQDQFTGQPGPK.C
R3/RRR3-23/2	1625.241	1625.757	-935.548	0.525	1864.745	0.612	22	0.300	R.YVCQDQFTGQPGPK.C
R3/RRR3-21/2	1625.187	1625.757	-968.727	0.531	1828.470	0.631	22	0.299	R.YVCQDQFTGQPGPK.C
R3/RRR3-22/2	1626.371	1625.757	-238.314	0.587	1748.269	0.634	22	0.288	R.YVCQDQFTGQPGPK.C
R3/RRR3-22/2	1626.330	1625.757	-263.389	0.555	1737.707	0.633	22	0.286	R.YVCQDQFTGQPGPK.C
R3/RRR3-21/2	1625.207	1625.757	-956.360	0.533	1654.138	0.612	22	0.268	R.YVCQDQFTGQPGPK.C
R3/RRR3-22/2	1625.347	1625.757	-253.304	0.508	1589.626	0.622	21	0.260	R.YVCQDQFTGQPGPK.C
R3/RRR3-23/2	1625.094	1625.757	-1026.494	0.516	1532.619	0.602	20	0.247	R.YVCQDQFTGQPGPK.C
R3/RRR3-20/2	1625.288	1625.757	-289.623	0.515	1479.000	0.597	20	0.239	R.YVCQDQFTGQPGPK.C
R3/RRR3-16/2	1089.091	1089.356	-243.347	0.476	900.353	0.220	14	0.132	-.IFIVQSLLR.-
R3/RRR3-13/2	1785.562	1786.020	-257.249	0.510	1003.403	0.523	18	0.172	R.TGNTFLGSLLWVDYAK.W
R3/RRR3-7/2	957.986	958.054	-71.138	0.459	1394.469	0.306	15	0.173	K.DLAGGLQQR.R
R3/RRR3-17/2	1057.607	1058.254	-1561.775	0.404	643.996	0.439	14	0.148	K.LSGIVGVPTSK.R
R3/RRR3-17/2	1057.465	1058.254	-1696.756	0.302	624.396	0.396	13	0.140	K.LSGIVGVPTSK.R
R3/RRR3-17/2	1058.025	1058.254	-216.933	0.404	542.408	0.394	13	0.137	-.LSGIVGVPTSK.-
R3/RRR3-17/3	1085.651	1085.279	343.776	0.452	679.492	0.448	19	0.108	K.TPIKDALAAGK.E
R3/RRR3-17/3	1084.842	1085.279	-404.152	0.460	447.758	0.444	16	0.105	K.TPIKDALAAGK.E
R3/RRR3-17/3	1085.599	1085.279	295.747	0.396	865.381	0.380	21	0.103	K.TPIKDALAAGK.E
R3/RRR3-16/3	1084.787	1085.279	-454.878	0.389	311.698	0.379	14	0.096	-.TPIKDALAAGK.-
R3/RRR3-1/2	1340.703	1339.372	247.551	0.483	1301.870	0.568	20	0.213	K.GEGM*SAVADSGEGR.G
R3/RRR3-2/2	1324.541	1323.373	127.507	0.347	1107.227	0.319	18	0.152	K.GEGMSAVADSGEGR.G
R3/RRR3-8/3	1914.055	1914.066	-5.717	0.370	1163.395	0.429	29	0.125	R.LGM*EKGEGM*SAVADSGEGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1587.294	1587.755	-291.773	0.510	2077.021	0.582	26	0.328	K.LAFGSLGDSFSATSVK.A
R3/RRR3-20/2	1587.925	1587.755	107.283	0.517	2013.861	0.577	25	0.315	K.LAFGSLGDSFSATSVK.A
R3/RRR3-20/2	1587.228	1587.755	-965.360	0.468	2006.828	0.572	25	0.312	K.LAFGSLGDSFSATSVK.A
R3/RRR3-19/2	1587.386	1587.755	-233.214	0.500	1940.832	0.566	25	0.299	K.LAFGSLGDSFSATSVK.A
R3/RRR3-20/2	1587.253	1587.755	-949.068	0.470	1920.976	0.565	25	0.295	K.LAFGSLGDSFSATSVK.A
R3/RRR3-19/2	1587.343	1587.755	-260.757	0.493	1746.439	0.582	24	0.272	K.LAFGSLGDSFSATSVK.A
R3/RRR3-2/2	1588.516	1587.755	-151.270	0.495	1926.319	0.440	24	0.261	K.LAFGSLGDSFSATSVK.A
R3/RRR3-3/2	1587.502	1587.755	-160.159	0.401	1757.682	0.422	24	0.234	K.LAFGSLGDSFSATSVK.A
R3/RRR3-3/2	1587.544	1587.755	-133.470	0.373	1104.114	0.255	20	0.144	K.LAFGSLGDSFSATSVK.A
R3/RRR3-3/2	1619.985	1618.847	85.207	0.372	691.219	0.332	16	0.132	R.TVATEILAAPSSAVCK.R
R3/RRR3-9/2	1753.040	1754.018	-1131.419	0.505	1101.709	0.566	22	0.191	K.IQLLDLPGIIEGASEGK.G
R3/RRR3-9/3	1206.762	1206.395	305.466	0.431	1127.996	0.248	21	0.093	R.IKEIEAEM*AR.T
R3/RRR3-9/3	1207.395	1206.395	-0.331	0.366	702.867	0.225	18	0.084	-.IKEIEAEM*AR.-
R3/RRR3-23/2	1250.131	1249.355	-179.386	0.509	956.501	0.428	15	0.160	K.GIEDLSSPQFR.A
R3/RRR3-23/2	1249.166	1249.355	-151.590	0.417	905.994	0.434	15	0.158	K.GIEDLSSPQFR.A
R3/RRR3-23/2	1248.908	1249.355	-358.573	0.423	840.661	0.441	14	0.155	K.GIEDLSSPQFR.A
R3/RRR3-23/3	1974.229	1974.293	-32.790	0.400	949.002	0.412	25	0.110	R.AVVQDILNKHPGAQELLK.A
R3/RRR3-23/3	1973.677	1974.293	-821.167	0.227	774.412	0.106	22	0.073	R.AVVQDILNKHPGAQELLK.A
R3/RRR3-11/2	1900.702	1901.151	-236.899	0.544	2139.537	0.546	25	0.332	K.ANVVVASLEETLEIVASR.K
R3/RRR3-7/2	1437.754	1438.605	-1291.135	0.406	1340.580	0.506	18	0.203	R.TTDVLDGFTDLLK.A
R3/RRR3-7/2	1758.529	1757.924	-225.069	0.510	1461.446	0.375	18	0.186	R.AGLTEELLQEQIEQR.T
R3/RRR3-7/2	1438.202	1438.605	-280.561	0.435	1207.912	0.450	18	0.181	R.TTDVLDGFTDLLK.A
R3/RRR3-7/2	1437.711	1438.605	-1321.321	0.385	1152.487	0.398	18	0.168	R.TTDVLDGFTDLLK.A
R3/RRR3-9/3	1599.015	1598.869	91.178	0.443	1303.294	0.485	25	0.150	R.TPFYLYSKPQVVR.N
R3/RRR3-9/2	1127.270	1127.316	-40.905	0.284	1139.180	0.205	15	0.141	R.DLTLIIEPGR.S
R3/RRR3-9/3	1599.111	1598.869	151.353	0.355	1498.514	0.327	26	0.131	R.TPFYLYSKPQVVR.N
R3/RRR3-14/2	1455.427	1455.640	-146.596	0.440	1393.269	0.356	17	0.180	K.SQIQSYVFDVIR.A
R3/RRR3-14/2	1455.514	1455.640	-87.199	0.390	1215.874	0.385	16	0.170	K.SQIQSYVFDVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1405.933	1404.635	212.784	0.213	954.840	0.177	16	0.128	R.EVTGSDLKTVVKK.L
R3/RRR3-5/2	1899.697	1899.178	-253.974	0.531	1412.051	0.568	21	0.221	K.LALGTLALEDALSTGSPIR.T
R3/RRR3-5/2	1675.633	1675.821	-112.205	0.445	1522.254	0.497	20	0.220	R.GLQGSEAAEIASEWVK.Q
R3/RRR3-5/2	1675.147	1675.821	-1002.474	0.319	1464.588	0.416	20	0.196	R.GLQGSEAAEIASEWVK.Q
R3/RRR3-8/2	1740.752	1741.879	-1225.567	0.338	1330.339	0.479	21	0.193	R.EVAAFAQFGSDLDAATK.Q
R3/RRR3-8/2	1740.859	1741.879	-1164.023	0.386	944.080	0.497	20	0.165	R.EVAAFAQFGSDLDAATK.Q
R3/RRR3-8/2	1740.782	1741.879	-1208.385	0.364	702.338	0.388	17	0.139	R.EVAAFAQFGSDLDAATK.Q
R3/RRR3-14/2	1176.226	1176.347	-103.219	0.417	675.069	0.370	13	0.140	R.SINDLITPFR.H
R3/RRR3-14/2	1613.053	1613.794	-1082.507	0.338	919.866	0.237	18	0.134	K.ILNENDLITPDLSR.V
R3/RRR3-10/2	1691.176	1691.903	-1024.610	0.487	2177.997	0.503	26	0.324	K.FVAPDVSILESDSAIK.S
R3/RRR3-9/2	1691.650	1691.903	-150.516	0.487	1937.993	0.533	25	0.290	K.FVAPDVSILESDSAIK.S
R3/RRR3-10/2	1691.489	1691.903	-245.498	0.490	1835.223	0.531	25	0.274	K.FVAPDVSILESDSAIK.S
R3/RRR3-9/2	1691.614	1691.903	-171.654	0.466	1225.074	0.469	21	0.185	K.FVAPDVSILESDSAIK.S
R3/RRR3-9/2	1690.951	1691.903	-1157.903	0.309	1119.934	0.411	20	0.165	K.FVAPDVSILESDSAIK.S
R3/RRR3-15/2	1537.028	1536.841	121.748	0.518	2004.066	0.598	21	0.319	R.ALALQENPGLVILGK.Q
R3/RRR3-14/2	1537.337	1536.841	323.537	0.489	1786.311	0.601	20	0.283	R.ALALQENPGLVILGK.Q
R3/RRR3-15/2	1536.473	1536.841	-240.384	0.382	1749.170	0.518	20	0.254	R.ALALQENPGLVILGK.Q
R3/RRR3-15/2	1536.374	1536.841	-304.711	0.449	1666.013	0.516	20	0.243	R.ALALQENPGLVILGK.Q
R3/RRR3-14/2	1535.620	1536.841	-1450.914	0.338	1203.466	0.482	17	0.181	R.ALALQENPGLVILGK.Q
R3/RRR3-14/2	1535.528	1536.841	-1511.122	0.311	1047.225	0.408	16	0.158	R.ALALQENPGLVILGK.Q
R3/RRR3-10/3	1315.278	1314.473	-149.101	0.507	1287.576	0.490	22	0.150	R.HLAYHEYGVPK.D
R3/RRR3-10/2	1819.300	1820.124	-1005.551	0.366	762.020	0.411	17	0.143	K.LFPASSVISFNPAILSR.E
R3/RRR3-10/2	1819.581	1820.124	-850.969	0.415	723.963	0.329	19	0.136	K.LFPASSVISFNPAILSR.E
R3/RRR3-13/2	1366.032	1365.514	-353.822	0.316	1152.367	0.473	16	0.177	K.EPYTATIVSVER.L
R3/RRR3-13/2	1365.286	1365.514	-167.664	0.263	801.709	0.466	14	0.150	K.EPYTATIVSVER.L
R3/RRR3-13/2	1366.281	1365.514	-170.857	0.299	792.440	0.432	14	0.148	K.EPYTATIVSVER.L
R3/RRR3-13/2	911.433	911.037	435.631	0.233	793.263	0.237	12	0.132	R.LYSIASTR.Y
R3/RRR3-13/2	911.755	911.037	-310.485	0.191	565.206	0.197	11	0.128	R.LYSIASTR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1364.416	1365.514	-1542.159	0.177	715.909	0.196	14	0.128	K.EPYTATIVSVER.L
R3/RRR3-22/3	1774.444	1774.999	-879.144	0.507	1382.939	0.405	28	0.141	R.IIKDFIVQGGDPTGTGR.G
R3/RRR3-22/3	1909.198	1910.121	-1010.155	0.461	629.019	0.514	24	0.112	R.LGSVQTDKSDRPIHEVK.I
R3/RRR3-22/3	1910.110	1910.121	-6.136	0.457	871.986	0.420	27	0.109	R.LGSVQTDKSDRPIHEVK.I
R3/RRR3-13/2	1102.078	1102.268	-172.711	0.435	928.817	0.422	13	0.160	R.ILDITHAYR.A
R3/RRR3-13/2	1101.722	1102.268	-1407.888	0.426	803.483	0.349	13	0.146	R.ILDITHAYR.A
R3/RRR3-14/2	1102.071	1102.268	-179.378	0.284	591.068	0.316	12	0.137	R.ILDITHAYR.A
R3/RRR3-13/2	1696.603	1696.928	-191.933	0.334	650.283	0.358	18	0.134	R.ADLPEFAPGAVTGPVVR.L
R3/RRR3-14/2	1102.208	1102.268	-54.498	0.331	663.881	0.155	12	0.113	-.ILDITHAYR.-
R3/RRR3-8/2	1232.141	1232.409	-218.076	0.438	876.729	0.465	16	0.160	K.NTVEGITGIISK.T
R3/RRR3-8/2	1231.971	1232.409	-356.148	0.394	830.538	0.359	16	0.145	K.NTVEGITGIISK.T
R3/RRR3-5/2	1607.220	1607.700	-299.887	0.497	1473.626	0.559	20	0.230	K.VSSSYDASSQTFSLK.F
R3/RRR3-5/2	1606.492	1607.700	-1378.521	0.281	993.826	0.372	17	0.149	K.VSSSYDASSQTFSLK.F
R3/RRR3-5/2	964.733	965.088	-369.202	0.398	807.986	0.291	12	0.141	K.SLNIFQSR.L
R3/RRR3-5/2	964.801	965.088	-298.237	0.417	787.310	0.292	12	0.141	K.SLNIFQSR.L
R3/RRR3-5/2	964.984	965.088	-108.876	0.408	784.212	0.276	12	0.137	-.SLNIFQSR.-
R3/RRR3-10/2	1246.977	1247.425	-360.798	0.430	872.263	0.531	17	0.171	K.FTAEIIPVNSR.V
R3/RRR3-10/2	1674.193	1672.970	133.713	0.427	876.582	0.433	17	0.151	R.EFDLIVMPGGLPGAQK.F
R3/RRR3-10/2	1247.034	1247.425	-314.439	0.352	575.064	0.396	14	0.141	K.FTAEIIPVNSR.V
R3/RRR3-10/2	1674.450	1672.970	287.757	0.387	491.065	0.312	15	0.130	R.EFDLIVMPGGLPGAQK.F
R3/RRR3-14/2	1550.205	1550.695	-316.840	0.485	1332.231	0.333	19	0.171	R.ESELIQENYLGVR.N
R3/RRR3-14/2	1298.211	1298.467	-198.301	0.466	985.481	0.464	19	0.170	K.VVLNPDEVADVK.Y
R3/RRR3-14/2	1298.127	1298.467	-263.204	0.425	878.248	0.467	17	0.162	K.VVLNPDEVADVK.Y
R3/RRR3-14/2	1298.226	1298.467	-186.698	0.411	862.309	0.440	18	0.158	K.VVLNPDEVADVK.Y
R3/RRR3-14/2	1549.767	1550.695	-1248.141	0.353	1347.543	0.216	19	0.155	R.ESELIQENYLGVR.N
R3/RRR3-14/2	1550.393	1550.695	-195.739	0.490	1036.961	0.335	18	0.151	R.ESELIQENYLGVR.N
R3/RRR3-4/2	1412.275	1412.614	-240.110	0.454	1530.902	0.490	18	0.222	K.LVQIENPLAEGTK.Y
R3/RRR3-4/2	1413.221	1412.614	-278.416	0.456	1350.825	0.544	18	0.212	K.LVQIENPLAEGTK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1002.393	1003.263	-1871.386	0.257	733.874	0.281	14	0.135	K.ILLAFQAVK.Q
R3/RRR3-4/2	1002.513	1003.263	-1750.375	0.279	631.854	0.270	13	0.133	K.ILLAFQAVK.Q
R3/RRR3-7/2	1768.447	1769.034	-900.360	0.495	804.902	0.548	20	0.169	K.QLLQWPIEEIETLR.R
R3/RRR3-7/2	1768.601	1769.034	-245.732	0.392	320.520	0.438	13	0.137	K.QLLQWPIEEIETLR.R
R3/RRR3-21/3	1309.122	1309.455	-255.439	0.435	1315.062	0.354	24	0.120	R.RLDYGHVYASK.S
R3/RRR3-21/3	1309.334	1309.455	-92.970	0.438	1215.777	0.261	24	0.098	R.RLDYGHVYASK.S
R3/RRR3-1/2	1774.931	1774.009	-44.052	0.457	1121.055	0.459	18	0.171	R.DTLTDAIQLQIVSSLR.V
R3/RRR3-2/2	971.900	972.164	-272.816	0.402	964.337	0.385	15	0.156	R.LVILEAASR.A
R3/RRR3-14/2	1070.924	1071.249	-304.068	0.371	864.683	0.444	15	0.156	K.IVAISLDDPK.A
R3/RRR3-14/2	1303.818	1304.386	-1206.094	0.308	748.571	0.340	15	0.138	K.ASLVNDVDDVEK.H
R3/RRR3-14/2	1304.085	1304.386	-231.019	0.261	502.401	0.347	12	0.131	-.ASLVNDVDDVEK.-
R3/RRR3-4/2	1607.609	1607.833	-139.801	0.431	1922.204	0.358	20	0.242	R.SVEQLGYITVLTQR.N
R3/RRR3-4/2	1607.300	1607.833	-956.808	0.317	1856.896	0.230	19	0.205	R.SVEQLGYITVLTQR.N
R3/RRR3-4/3	1611.019	1611.697	-1044.705	0.429	930.729	0.388	30	0.106	K.YIAEHGGSTNAFTSR.E
R3/RRR3-4/3	1611.276	1611.697	-262.021	0.364	747.482	0.377	28	0.098	K.YIAEHGGSTNAFTSR.E
R3/RRR3-5/2	1209.093	1209.379	-237.220	0.481	1828.704	0.635	20	0.305	R.VPAGAAALYYGR.G
R3/RRR3-4/2	1720.274	1720.822	-902.513	0.393	1263.829	0.413	23	0.178	R.TLSFAIADGSQPGNEGR.E
R3/RRR3-4/2	1268.252	1268.444	-152.012	0.405	766.315	0.446	18	0.154	R.EADGTLRPLPAK.H
R3/RRR3-4/2	1267.930	1268.444	-1198.227	0.420	421.979	0.457	16	0.146	R.EADGTLRPLPAK.H
R3/RRR3-9/2	1786.632	1786.063	-242.019	0.505	903.225	0.498	20	0.165	R.DIQAWETIPLGPFLGK.S
R3/RRR3-9/2	1786.330	1786.063	149.583	0.469	804.949	0.523	20	0.163	R.DIQAWETIPLGPFLGK.S
R3/RRR3-9/2	1785.630	1786.063	-243.457	0.423	633.989	0.511	18	0.152	R.DIQAWETIPLGPFLGK.S
R3/RRR3-11/2	1113.524	1113.289	211.155	0.308	1114.352	0.262	15	0.147	K.ILSADEPVLR.D
R3/RRR3-11/2	1113.483	1113.289	174.437	0.347	944.797	0.269	14	0.141	-.ILSADEPVLR.-
R3/RRR3-24/3	1717.302	1717.776	-276.893	0.528	2187.948	0.479	29	0.279	K.HGYIGEFEELDDHR.S
R3/RRR3-24/3	1717.363	1717.776	-241.379	0.535	2059.822	0.462	28	0.249	K.HGYIGEFEELDDHR.S
R3/RRR3-8/2	1488.313	1487.747	-292.339	0.375	1262.235	0.433	18	0.179	R.GAVAGLIAELMEGQK.G
R3/RRR3-8/2	1331.739	1330.600	104.293	0.425	823.623	0.522	17	0.166	K.VYTLGPLQLVAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1330.288	1330.600	-235.765	0.488	865.282	0.485	17	0.164	K.VYTLGPLQLVAR.K
R3/RRR3-8/2	1330.446	1330.600	-116.378	0.359	547.168	0.450	13	0.143	K.VYTLGPLQLVAR.K
R3/RRR3-16/2	1711.054	1711.896	-1080.256	0.455	1019.714	0.463	22	0.168	K.TEGVFSFLPASQATGAK.F
R3/RRR3-16/2	1711.476	1711.896	-246.136	0.513	855.195	0.489	23	0.163	K.TEGVFSFLPASQATGAK.F
R3/RRR3-16/2	1711.429	1711.896	-273.901	0.487	864.903	0.488	22	0.162	K.TEGVFSFLPASQATGAK.F
R3/RRR3-16/2	1132.209	1132.249	-36.076	0.469	824.966	0.422	18	0.155	K.AGNSVGLEVASK.Y
R3/RRR3-16/2	1132.004	1132.249	-217.249	0.376	801.855	0.433	17	0.153	K.AGNSVGLEVASK.Y
R3/RRR3-16/2	1132.350	1132.249	88.706	0.464	752.414	0.434	17	0.153	K.AGNSVGLEVASK.Y
R3/RRR3-16/2	1832.245	1831.959	156.192	0.459	767.980	0.493	20	0.156	R.VESGTQPDIDLATITDR.M
R3/RRR3-16/2	1731.455	1730.900	-257.439	0.346	640.273	0.365	14	0.132	K.INEALEFAQEELAPR.G
R3/RRR3-16/2	1831.043	1831.959	-1049.720	0.251	483.504	0.326	16	0.130	R.VESGTQPDIDLATITDR.M
R3/RRR3-16/2	1830.709	1831.959	-1232.827	0.230	543.438	0.236	16	0.127	R.VESGTQPDIDLATITDR.M
R3/RRR3-17/2	1667.287	1667.847	-938.392	0.426	1742.014	0.453	20	0.241	K.TNQNVEQVFFTIAR.D
R3/RRR3-8/2	1540.511	1539.800	-188.570	0.496	2032.412	0.534	21	0.310	R.AFQTLLTYIGNVAK.N
R3/RRR3-14/1	1151.606	1152.279	-1456.983	0.339	1068.263	0.310	14	0.930	R.AALYLASDEAK.Y
R3/RRR3-14/2	1844.625	1845.008	-208.059	0.547	2175.571	0.413	26	0.296	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/3	1845.786	1845.008	-120.509	0.552	1986.176	0.545	37	0.262	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/2	1152.040	1152.279	-208.051	0.500	1478.326	0.458	17	0.210	R.AALYLASDEAK.Y
R3/RRR3-14/2	1151.615	1152.279	-1449.169	0.492	1448.625	0.435	17	0.202	R.AALYLASDEAK.Y
R3/RRR3-14/2	1845.338	1845.008	179.368	0.539	1227.707	0.545	24	0.201	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/3	1845.216	1845.008	113.383	0.568	1665.648	0.500	33	0.198	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/2	1152.129	1152.279	-130.245	0.520	1419.907	0.431	16	0.197	R.AALYLASDEAK.Y
R3/RRR3-14/3	1844.488	1845.008	-826.342	0.564	1601.391	0.483	32	0.185	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/3	1845.470	1845.008	250.999	0.565	1468.925	0.498	31	0.173	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/3	1845.961	1845.008	-25.285	0.522	1318.667	0.473	32	0.151	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/3	1846.722	1845.008	-155.288	0.522	700.680	0.524	32	0.121	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/3	1845.719	1845.008	-156.931	0.471	677.372	0.501	31	0.117	K.YVNGHNLVVDGGFTSHK.G
R3/RRR3-14/3	1846.072	1845.008	34.606	0.482	673.095	0.457	31	0.111	K.YVNGHNLVVDGGFTSHK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1230.284	1230.393	-88.931	0.507	1056.839	0.398	18	0.164	K.LIDENVGTQLK.E
R3/RRR3-8/2	1101.188	1101.323	-123.151	0.293	670.129	0.396	14	0.142	K.FITASPPVLR.E
R3/RRR3-8/2	1100.445	1101.323	-1711.928	0.316	563.221	0.255	13	0.133	-.FITASPPVLR.-
R3/RRR3-8/2	1101.162	1101.323	-147.059	0.303	430.925	0.343	12	0.128	-.FITASPPVLR.-
R3/RRR3-6/2	1243.327	1243.392	-52.153	0.271	1227.465	0.320	17	0.159	R.KESEPPSAAAKK.R
R3/RRR3-27/2	1115.920	1115.219	-268.766	0.299	916.427	0.237	15	0.137	K.ESEPPSAAAKK.R
R3/RRR3-27/2	1116.103	1115.219	-103.843	0.275	980.335	0.158	15	0.132	K.ESEPPSAAAKK.R
R3/RRR3-28/2	1115.922	1115.219	-267.010	0.294	951.660	0.085	16	0.127	K.ESEPPSAAAKK.R
R3/RRR3-28/2	1115.677	1115.219	411.465	0.269	775.599	0.083	14	0.126	K.ESEPPSAAAKK.R
R3/RRR3-28/2	1115.776	1115.219	-398.285	0.265	808.289	0.066	15	0.125	K.ESEPPSAAAKK.R
R3/RRR3-4/2	1464.058	1464.649	-1089.475	0.376	1339.028	0.540	20	0.208	R.LPPISADGDVPNLR.A
R3/RRR3-4/2	1119.095	1119.295	-180.041	0.395	1414.861	0.231	15	0.163	R.VFVQEVLER.E
R3/RRR3-10/2	1925.714	1926.157	-231.151	0.444	1151.002	0.401	19	0.164	K.SIALDVEELADNLQLGPK.F
R3/RRR3-10/2	1925.967	1926.157	-99.210	0.455	1012.443	0.467	18	0.163	K.SIALDVEELADNLQLGPK.F
R3/RRR3-10/2	1925.462	1926.157	-883.087	0.385	747.124	0.477	15	0.147	K.SIALDVEELADNLQLGPK.F
R3/RRR3-10/3	1927.794	1926.157	-189.023	0.539	1024.027	0.516	30	0.136	K.SIALDVEELADNLQLGPK.F
R3/RRR3-10/3	1381.705	1381.646	43.002	0.401	451.485	0.524	21	0.111	K.LPWVVYHELPK.S
R3/RRR3-10/3	1381.415	1381.646	-167.710	0.409	361.710	0.494	19	0.109	K.LPWVVYHELPK.S
R3/RRR3-10/3	1381.752	1381.646	76.894	0.369	311.922	0.407	18	0.103	K.LPWVVYHELPK.S
R3/RRR3-10/3	1926.025	1926.157	-68.796	0.279	864.562	0.235	23	0.084	-.SIALDVEELADNLQLGPK.-
R3/RRR3-13/2	1313.465	1313.522	-43.775	0.372	1390.312	0.382	19	0.185	K.VLDVGCGIGGPLR.E
R3/RRR3-13/2	1682.721	1682.900	-106.421	0.417	1296.157	0.433	20	0.184	R.IKDEIELGNGLPDIR.S
R3/RRR3-13/2	1313.611	1313.522	68.263	0.356	1132.346	0.381	17	0.163	K.VLDVGCGIGGPLR.E
R3/RRR3-13/2	1313.823	1313.522	229.845	0.301	847.578	0.313	18	0.141	K.VLDVGCGIGGPLR.E
R3/RRR3-13/2	1241.071	1240.476	-326.999	0.452	1205.303	0.372	18	0.169	R.DVAWAPVLGLAK.A
R3/RRR3-13/2	1241.230	1240.476	-198.428	0.386	1052.182	0.339	17	0.154	R.DVAWAPVLGLAK.A
R3/RRR3-14/2	1240.012	1240.476	-375.068	0.368	976.452	0.343	16	0.150	R.DVAWAPVLGLAK.A
R3/RRR3-13/2	1463.421	1463.568	-100.867	0.385	883.382	0.348	16	0.143	K.YGTILASCSYDGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1240.090	1240.476	-312.448	0.241	599.369	0.256	13	0.130	R.DVAWAPVLGLAK.A
R3/RRR3-10/2	949.744	950.074	-348.214	0.466	898.995	0.382	13	0.155	K.VELFSQAR.D
R3/RRR3-10/2	957.899	958.182	-296.807	0.373	303.165	0.474	13	0.148	K.GLPIVGVFR.S
R3/RRR3-10/2	949.965	950.074	-115.109	0.426	584.949	0.346	12	0.142	K.VELFSQAR.D
R3/RRR3-10/2	957.499	958.182	-1762.846	0.289	250.907	0.360	12	0.138	-.GLPIVGVFR.-
R3/RRR3-10/2	957.928	958.182	-265.867	0.329	191.844	0.403	11	0.137	-.GLPIVGVFR.-
R3/RRR3-19/2	1679.383	1679.861	-285.470	0.456	761.884	0.510	20	0.161	R.EALGIHQGTVPSWQR.C
R3/RRR3-19/2	1679.343	1679.861	-906.867	0.425	703.539	0.471	20	0.153	R.EALGIHQGTVPSWQR.C
R3/RRR3-19/2	1679.407	1679.861	-270.885	0.444	615.543	0.461	19	0.149	R.EALGIHQGTVPSWQR.C
R3/RRR3-25/2	1265.456	1265.482	-20.764	0.259	866.779	0.263	14	0.136	R.LLYKPESWTK.R
R3/RRR3-17/2	1265.028	1265.482	-360.102	0.266	560.995	0.199	12	0.129	-.LLYKPESWTK.-
R3/RRR3-15/2	1479.725	1480.688	-1330.637	0.392	675.812	0.430	20	0.147	R.EIEEALLEHLGVK.R
R3/RRR3-15/3	1693.882	1692.896	-8.437	0.325	1036.918	0.389	23	0.111	K.KVNEILSHYPSNYK.Q
R3/RRR3-15/3	1692.973	1692.896	45.510	0.404	1049.419	0.366	23	0.109	K.KVNEILSHYPSNYK.Q
R3/RRR3-15/3	1693.338	1692.896	261.547	0.300	645.669	0.258	19	0.086	K.KVNEILSHYPSNYK.Q
R3/RRR3-4/2	1219.950	1220.466	-1246.436	0.447	718.035	0.343	15	0.140	-.M*LGPNYVPGKK.-
R3/RRR3-4/2	1220.087	1220.466	-311.831	0.412	639.974	0.287	14	0.133	-.M*LGPNYVPGKK.-
R3/RRR3-10/2	1145.704	1145.295	358.363	0.368	1032.059	0.459	16	0.169	K.VAGNFHFAPGK.S
R3/RRR3-10/2	1146.050	1145.295	-214.160	0.400	881.180	0.494	16	0.165	K.VAGNFHFAPGK.S
R3/RRR3-10/2	1145.454	1145.295	139.532	0.367	931.524	0.396	16	0.155	K.VAGNFHFAPGK.S
R3/RRR3-10/3	1708.031	1707.871	93.710	0.508	1156.714	0.402	25	0.122	R.KINSNQFSVTEHFR.E
R3/RRR3-22/3	1429.354	1429.511	-110.133	0.550	2060.430	0.511	30	0.253	K.DCRPVESSEPPR.Y
R3/RRR3-22/3	1429.046	1429.511	-326.320	0.541	1616.488	0.482	27	0.181	K.DCRPVESSEPPR.Y
R3/RRR3-22/3	1429.587	1429.511	53.166	0.554	1321.245	0.481	27	0.149	K.DCRPVESSEPPR.Y
R3/RRR3-23/3	1430.054	1429.511	-320.611	0.545	1211.627	0.481	26	0.140	K.DCRPVESSEPPR.Y
R3/RRR3-23/3	1429.488	1429.511	-16.592	0.509	1307.534	0.447	27	0.139	K.DCRPVESSEPPR.Y
R3/RRR3-23/3	1429.283	1429.511	-160.123	0.484	763.418	0.425	22	0.109	K.DCRPVESSEPPR.Y
R3/RRR3-22/3	1429.154	1429.511	-250.734	0.496	972.735	0.376	23	0.108	K.DCRPVESSEPPR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/3	1429.700	1429.511	132.677	0.451	686.748	0.418	21	0.103	-.DCRPVESSEPPR.-
R3/RRR3-5/2	1349.898	1348.573	241.752	0.344	1242.456	0.247	17	0.151	K.FIIDTLVNGLSR.L
R3/RRR3-5/3	1379.676	1379.549	92.273	0.346	1014.119	0.258	22	0.090	K.SVHYPHEVIAAR.K
R3/RRR3-5/3	1378.640	1379.549	-1388.781	0.305	160.486	0.382	17	0.063	-.SVHYPHEVIAAR.-
R3/RRR3-16/2	1616.689	1617.659	-1221.920	0.412	941.114	0.465	18	0.163	K.NSWGADWGDNGYFK.M
R3/RRR3-16/2	1616.050	1617.659	-2239.519	0.363	1032.204	0.383	19	0.158	K.NSWGADWGDNGYFK.M
R3/RRR3-23/2	1617.204	1617.659	-282.289	0.374	239.029	0.414	13	0.140	K.NSWGADWGDNGYFK.M
R3/RRR3-16/2	1616.087	1617.659	-2216.664	0.335	541.603	0.349	17	0.138	K.NSWGADWGDNGYFK.M
R3/RRR3-17/2	1617.034	1617.659	-1007.533	0.336	475.715	0.276	18	0.136	K.NSWGADWGDNGYFK.M
R3/RRR3-17/3	1401.044	1401.549	-1077.313	0.499	1190.356	0.296	26	0.103	K.DWREDGIVSPVK.D
R3/RRR3-17/3	1401.570	1401.549	15.050	0.512	964.219	0.334	25	0.101	K.DWREDGIVSPVK.D
R3/RRR3-17/3	1401.265	1401.549	-203.561	0.493	881.872	0.335	24	0.100	K.DWREDGIVSPVK.D
R3/RRR3-16/3	1402.478	1401.549	-50.872	0.517	750.800	0.340	22	0.099	K.DWREDGIVSPVK.D
R3/RRR3-16/3	1400.631	1401.549	-1373.575	0.395	859.273	0.239	22	0.088	K.DWREDGIVSPVK.D
R3/RRR3-6/2	1939.589	1940.232	-849.511	0.517	991.596	0.589	24	0.186	R.VILSGAAPLATHVEEYLR.V
R3/RRR3-6/3	1419.627	1418.540	61.776	0.367	782.122	0.508	29	0.115	R.AAADGRPSVGPTYR.S
R3/RRR3-6/3	1417.509	1418.540	-1437.160	0.356	512.441	0.562	25	0.114	R.AAADGRPSVGPTYR.S
R3/RRR3-2/3	1418.582	1418.540	29.499	0.310	249.432	0.392	18	0.100	R.AAADGRPSVGPTYR.S
R3/RRR3-4/3	1419.361	1418.540	-126.479	0.291	265.731	0.391	18	0.096	-.AAADGRPSVGPTYR.-
R3/RRR3-3/2	1673.812	1672.925	-67.987	0.537	1418.584	0.525	22	0.216	R.GVEVLDPLGLGVM*DNK.S
R3/RRR3-3/2	921.928	922.103	-191.121	0.360	632.617	0.379	13	0.141	R.LALSVFSGK.F
R3/RRR3-9/2	1330.851	1331.604	-1321.434	0.342	1234.680	0.353	16	0.166	R.EGLVLLMDAIEK.A
R3/RRR3-9/2	1398.365	1398.607	-173.562	0.426	825.515	0.423	17	0.150	K.IGM*DVAASEFLTK.D
R3/RRR3-9/2	1330.846	1331.604	-1324.842	0.350	728.458	0.474	13	0.150	R.EGLVLLMDAIEK.A
R3/RRR3-9/2	1331.210	1331.604	-296.764	0.253	540.475	0.306	12	0.131	R.EGLVLLMDAIEK.A
R3/RRR3-13/2	1189.508	1189.348	134.982	0.323	908.507	0.390	14	0.150	K.HQQWYVLSK.T
R3/RRR3-13/3	1448.528	1447.581	-36.956	0.421	1141.443	0.382	25	0.116	K.TLHLHALDGANER.L
R3/RRR3-13/3	1447.574	1447.581	-5.220	0.450	1176.108	0.317	25	0.107	K.TLHLHALDGANER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/3	1447.598	1447.581	11.273	0.421	933.504	0.327	24	0.099	K.TLHLHALDGANER.L
R3/RRR3-7/2	1628.157	1628.804	-1014.712	0.492	1542.687	0.405	18	0.204	R.LSQLYDQIEDYLK.K
R3/RRR3-7/2	1628.187	1628.804	-996.496	0.423	1042.682	0.407	16	0.160	R.LSQLYDQIEDYLK.K
R3/RRR3-8/2	1689.863	1688.866	-1.928	0.419	574.052	0.479	15	0.142	R.STQGILNDLWNSLAR.Y
R3/RRR3-13/2	1344.379	1344.496	-87.486	0.376	1094.189	0.292	15	0.148	R.VLDTLQEIQER.H
R3/RRR3-12/2	993.919	994.126	-209.614	0.326	901.484	0.239	13	0.138	R.ISEFQTLR.E
R3/RRR3-12/2	993.912	994.126	-216.391	0.259	971.995	0.134	12	0.130	R.ISEFQTLR.E
R3/RRR3-13/2	1594.811	1594.877	-41.504	0.461	1145.512	0.492	20	0.182	R.NIEGVSLPVLTPNLK.G
R3/RRR3-13/2	1793.451	1794.039	-888.217	0.328	854.505	0.365	18	0.141	R.LATSGLSVVEATSFVSPK.W
R3/RRR3-13/2	1793.410	1794.039	-911.245	0.303	645.144	0.142	17	0.122	R.LATSGLSVVEATSFVSPK.W
R3/RRR3-10/2	1753.230	1753.845	-924.167	0.391	947.723	0.475	18	0.160	R.YDATADDLIDVIEGSR.I
R3/RRR3-10/2	1480.438	1480.774	-227.566	0.474	1110.434	0.375	19	0.160	K.IQLLDLPGIIEGAK.D
R3/RRR3-5/2	1730.468	1728.925	-265.298	0.557	1906.850	0.554	23	0.292	R.SALEAVVAADEELAALR.A
R3/RRR3-7/2	1348.314	1347.502	-139.717	0.470	1175.465	0.442	16	0.178	R.DNIDNIQIVFR.E
R3/RRR3-7/2	1348.001	1347.502	371.432	0.401	868.766	0.315	15	0.143	R.DNIDNIQIVFR.E
R3/RRR3-7/2	1347.553	1347.502	37.923	0.274	569.345	0.122	12	0.122	-.DNIDNIQIVFR.-
R3/RRR3-14/2	1236.168	1236.399	-187.751	0.486	2141.751	0.447	19	0.302	R.VYVLSVEGDVR.E
R3/RRR3-14/2	1235.890	1236.399	-1225.030	0.360	1200.023	0.283	15	0.154	R.VYVLSVEGDVR.E
R3/RRR3-14/2	1235.465	1236.399	-1570.127	0.378	968.358	0.222	16	0.137	R.VYVLSVEGDVR.E
R3/RRR3-3/2	1356.432	1357.580	-1588.154	0.490	1450.903	0.542	19	0.226	K.IPSVNDIPLNFK.V
R3/RRR3-2/2	1358.733	1357.580	113.304	0.463	1104.389	0.454	17	0.174	K.IPSVNDIPLNFK.V
R3/RRR3-2/2	1357.434	1357.580	-107.841	0.417	913.415	0.450	15	0.159	K.IPSVNDIPLNFK.V
R3/RRR3-3/2	1318.258	1317.519	-198.443	0.382	1330.432	0.255	18	0.159	K.YVANVLGLPQSR.V
R3/RRR3-2/2	1358.456	1357.580	-91.446	0.294	509.077	0.300	12	0.132	K.IPSVNDIPLNFK.V
R3/RRR3-13/2	1622.025	1621.773	155.828	0.358	1019.039	0.382	17	0.155	K.SLAEFFTDFGYAPR.E
R3/RRR3-13/2	1014.826	1015.101	-272.014	0.365	830.634	0.336	12	0.144	R.SYIEFAER.L
R3/RRR3-13/2	1014.773	1015.101	-324.271	0.392	734.584	0.267	12	0.137	R.SYIEFAER.L
R3/RRR3-13/2	1622.264	1621.773	303.052	0.294	681.219	0.246	18	0.132	K.SLAEFFTDFGYAPR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1622.100	1621.773	201.939	0.320	682.219	0.230	16	0.130	K.SLAEFFTDFGYAPR.E
R3/RRR3-4/2	1420.336	1420.636	-211.938	0.484	2166.620	0.412	19	0.295	R.VNDQYITNVLLK.I
R3/RRR3-4/2	1420.353	1420.636	-199.609	0.482	1394.252	0.399	17	0.188	R.VNDQYITNVLLK.I
R3/RRR3-4/2	1420.494	1420.636	-100.381	0.479	1079.781	0.366	17	0.159	R.VNDQYITNVLLK.I
R3/RRR3-2/2	1808.789	1809.077	-159.451	0.529	1943.286	0.549	23	0.295	R.LTQMNTDLFGGVDAVVK.Y
R3/RRR3-3/2	1823.901	1825.076	-1196.183	0.514	1731.045	0.557	23	0.264	R.LTQM*NTDLFGGVDAVVK.Y
R3/RRR3-2/2	1825.366	1825.076	159.291	0.565	1560.167	0.530	22	0.232	R.LTQM*NTDLFGGVDAVVK.Y
R3/RRR3-8/3	1845.952	1847.019	-1123.130	0.420	1082.074	0.400	25	0.115	K.DKSQHAADYEAIISAVK.G
R3/RRR3-8/3	1870.412	1871.082	-895.175	0.422	960.747	0.377	26	0.105	K.IADILGQLLASEENVER.D
R3/RRR3-8/3	1870.673	1871.082	-219.175	0.458	983.652	0.341	26	0.101	-.IADILGQLLASEENVER.-
R3/RRR3-8/2	1973.324	1972.074	127.355	0.490	1857.722	0.564	22	0.284	R.SGGDDDILDDLDEM*IFGK.K
R3/RRR3-8/2	1973.221	1972.074	75.054	0.375	581.948	0.452	15	0.138	R.SGGDDDILDDLDEM*IFGK.K
R3/RRR3-11/2	1215.731	1216.323	-1313.221	0.427	1257.259	0.355	16	0.170	R.LLLEEENEAR.I
R3/RRR3-11/2	1527.182	1525.820	237.980	0.429	826.061	0.417	16	0.147	K.TVFNILGPLLNPAR.V
R3/RRR3-9/2	1577.440	1576.693	-160.870	0.548	1333.874	0.394	19	0.178	R.TTGAGSNWLAQDLNK.G
R3/RRR3-9/2	1577.243	1576.693	-285.870	0.489	1107.233	0.268	19	0.143	R.TTGAGSNWLAQDLNK.G
R3/RRR3-9/2	1576.606	1576.693	-55.340	0.522	889.399	0.335	19	0.142	R.TTGAGSNWLAQDLNK.G
R3/RRR3-1/3	1430.273	1430.632	-251.779	0.448	1374.246	0.349	24	0.127	R.VTGKDEGLTLLQR.Q
R3/RRR3-1/3	1430.274	1430.632	-251.265	0.440	999.109	0.337	23	0.102	-.VTGKDEGLTLLQR.-
R3/RRR3-2/3	1430.362	1430.632	-189.234	0.444	994.646	0.282	22	0.094	-.VTGKDEGLTLLQR.-
R3/RRR3-2/3	1430.314	1430.632	-222.881	0.370	883.739	0.203	22	0.084	-.VTGKDEGLTLLQR.-
R3/RRR3-13/2	1828.200	1828.016	101.286	0.456	641.899	0.499	20	0.150	R.AGAEEVLPLGPLNDFER.A
R3/RRR3-13/2	952.048	952.048	0.050	0.436	1074.290	0.283	12	0.149	K.YGNANVWK.T
R3/RRR3-12/2	951.401	952.048	-1736.503	0.372	849.522	0.313	13	0.145	K.YGNANVWK.T
R3/RRR3-12/2	951.368	952.048	-1771.053	0.360	865.993	0.279	13	0.142	K.YGNANVWK.T
R3/RRR3-12/2	951.206	952.048	-1941.904	0.380	931.544	0.267	12	0.142	K.YGNANVWK.T
R3/RRR3-13/2	951.925	952.048	-129.985	0.416	823.218	0.276	12	0.141	K.YGNANVWK.T
R3/RRR3-12/3	1613.922	1613.898	14.965	0.351	1156.159	0.201	23	0.087	R.LM*QCKPLPEPEVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1210.215	1210.365	-123.994	0.579	1578.695	0.671	21	0.274	K.APSAAVAQPAAAGK.V
R3/RRR3-14/2	1210.313	1210.365	-43.258	0.527	1505.496	0.647	21	0.257	K.APSAAVAQPAAAGK.V
R3/RRR3-14/2	1210.026	1210.365	-280.850	0.563	1331.092	0.615	20	0.227	K.APSAAVAQPAAAGK.V
R3/RRR3-17/2	1250.242	1250.426	-147.445	0.541	1985.014	0.510	17	0.293	K.ALEVYQAQLSK.S
R3/RRR3-17/2	1249.912	1250.426	-1215.206	0.463	1738.297	0.401	17	0.228	K.ALEVYQAQLSK.S
R3/RRR3-17/2	1249.582	1250.426	-1479.881	0.421	1601.951	0.323	17	0.195	K.ALEVYQAQLSK.S
R3/RRR3-3/2	1485.419	1485.753	-225.484	0.364	1434.981	0.477	19	0.206	R.LAVGEALTNLVWAK.V
R3/RRR3-3/2	1676.408	1676.932	-911.887	0.477	1697.294	0.271	19	0.192	R.IPYLQESETIELLK.Q
R3/RRR3-27/2	1304.108	1304.437	-253.266	0.510	1826.464	0.578	22	0.287	K.NVAAGAAGGPYISR.A
R3/RRR3-27/2	1304.164	1304.437	-210.164	0.514	1785.316	0.578	22	0.280	K.NVAAGAAGGPYISR.A
R3/RRR3-27/2	1304.000	1304.437	-335.725	0.487	1826.671	0.543	22	0.277	K.NVAAGAAGGPYISR.A
R3/RRR3-7/2	1755.204	1754.961	138.772	0.548	1835.674	0.567	24	0.284	K.EGVAFYNSLIDDVIAK.G
R3/RRR3-7/2	1755.452	1754.961	280.408	0.566	1583.683	0.577	23	0.249	K.EGVAFYNSLIDDVIAK.G
R3/RRR3-7/2	1755.292	1754.961	189.197	0.535	1609.523	0.553	23	0.246	K.EGVAFYNSLIDDVIAK.G
R3/RRR3-2/2	1754.289	1754.961	-955.853	0.350	682.112	0.416	16	0.142	K.EGVAFYNSLIDDVIAK.G
R3/RRR3-6/2	1000.619	1001.162	-1546.837	0.515	1231.733	0.458	17	0.188	R.IGAATALEVR.A
R3/RRR3-6/2	1001.130	1001.162	-31.872	0.535	1226.187	0.442	17	0.185	R.IGAATALEVR.A
R3/RRR3-6/2	1231.259	1231.464	-166.623	0.423	992.106	0.536	19	0.180	R.ITVGTTILDAVK.A
R3/RRR3-7/2	1232.459	1231.464	-4.432	0.410	978.895	0.496	18	0.172	R.ITVGTTILDAVK.A
R3/RRR3-6/2	1230.924	1231.464	-1254.839	0.448	734.340	0.475	16	0.156	R.ITVGTTILDAVK.A
R3/RRR3-6/2	1230.533	1231.464	-1573.733	0.334	624.536	0.440	16	0.146	R.ITVGTTILDAVK.A
R3/RRR3-15/2	1206.808	1206.350	380.490	0.312	944.505	0.258	15	0.138	K.DTNYAIM*YAK.D
R3/RRR3-15/2	1531.235	1530.899	220.274	0.301	782.464	0.162	16	0.128	K.MAIDEFM*LTMALK.E
R3/RRR3-15/2	1530.710	1530.899	-123.993	0.258	793.757	0.147	16	0.127	K.MAIDEFM*LTMALK.E
R3/RRR3-16/2	1530.868	1530.899	-20.328	0.275	720.207	0.099	16	0.125	K.MAIDEFM*LTMALK.E
R3/RRR3-16/3	1567.656	1567.772	-73.979	0.479	2100.709	0.428	31	0.243	R.LPLRDVLDDAGVGAR.V
R3/RRR3-16/3	1567.353	1567.772	-268.270	0.499	1709.946	0.440	31	0.185	R.LPLRDVLDDAGVGAR.V
R3/RRR3-16/2	1567.282	1567.772	-313.310	0.421	1061.081	0.347	20	0.153	R.LPLRDVLDDAGVGAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-15/3	1567.021	1567.772	-1120.996	0.448	1031.258	0.439	25	0.122	R.LPLRDVLDDAGVGAR.V
R3/RRR3-16/3	1567.418	1567.772	-226.664	0.395	1163.100	0.384	26	0.119	R.LPLRDVLDDAGVGAR.V
R3/RRR3-13/3	1567.054	1567.772	-1099.760	0.359	553.238	0.298	19	0.083	-.LPLRDVLDDAGVGAR.-
R3/RRR3-9/2	1498.341	1498.619	-186.033	0.422	781.058	0.422	20	0.153	R.DLPSFFTDLADTR.L
R3/RRR3-9/2	1498.323	1498.619	-197.720	0.397	728.961	0.435	20	0.151	R.DLPSFFTDLADTR.L
R3/RRR3-9/2	1224.092	1223.319	-185.902	0.212	892.901	0.234	15	0.131	R.LFASDGEAAWR.H
R3/RRR3-8/2	1401.923	1402.577	-1183.526	0.384	1128.619	0.381	18	0.165	R.IIEVEPQYTGPR.V
R3/RRR3-8/3	1871.284	1872.927	-1952.486	0.546	1078.599	0.591	33	0.156	R.SHEVKDEGYEIEHDGK.L
R3/RRR3-8/2	1402.251	1402.577	-233.357	0.411	778.602	0.369	16	0.145	R.IIEVEPQYTGPR.V
R3/RRR3-8/2	1401.944	1402.577	-1168.312	0.346	705.232	0.402	16	0.145	R.IIEVEPQYTGPR.V
R3/RRR3-13/2	988.243	989.156	-1941.729	0.371	776.574	0.270	13	0.137	K.HLDHVVIR.L
R3/RRR3-13/2	1606.985	1607.700	-1070.824	0.395	1010.885	0.243	18	0.136	K.GASFLEDNTPDEAIK.M
R3/RRR3-10/2	1099.996	1100.334	-307.607	0.295	926.166	0.400	17	0.151	K.IGSVALADLLK.K
R3/RRR3-10/3	1849.750	1851.180	-1317.742	0.390	1258.538	0.425	28	0.133	K.LLVDKDPGLVGNLLVER.L
R3/RRR3-7/2	1143.187	1143.275	-77.928	0.378	946.722	0.489	15	0.165	R.APLLAQGETSR.A
R3/RRR3-11/2	980.102	980.140	-38.302	0.335	665.884	0.379	12	0.135	-.DGIYTALVK.-
R3/RRR3-11/2	979.732	980.140	-417.224	0.279	602.833	0.229	13	0.122	-.DGIYTALVK.-
R3/RRR3-7/2	1197.429	1197.368	50.756	0.357	937.575	0.486	16	0.163	R.GYLLHGPPGTGK.S
R3/RRR3-7/2	1028.139	1028.231	-89.268	0.381	740.504	0.296	13	0.138	R.LQLQTLVGR.H
R3/RRR3-7/2	1028.194	1028.231	-35.439	0.321	495.404	0.298	13	0.136	R.LQLQTLVGR.H
R3/RRR3-6/2	1614.184	1614.734	-963.422	0.485	2073.146	0.429	20	0.285	K.AVFDELQYSADDIK.A
R3/RRR3-20/2	1259.137	1258.490	-280.689	0.585	1911.491	0.521	19	0.282	R.SIVGATLEVIQK.K
R3/RRR3-20/2	1259.355	1258.490	-107.295	0.590	1783.583	0.540	19	0.268	R.SIVGATLEVIQK.K
R3/RRR3-19/2	1259.433	1258.490	-45.167	0.543	1625.394	0.532	18	0.244	R.SIVGATLEVIQK.K
R3/RRR3-19/2	1258.562	1258.490	57.921	0.517	1004.638	0.492	15	0.171	R.SIVGATLEVIQK.K
R3/RRR3-20/2	1258.250	1258.490	-191.170	0.345	643.394	0.337	16	0.140	R.SIVGATLEVIQK.K
R3/RRR3-6/2	1048.907	1048.217	-297.143	0.417	1486.031	0.407	16	0.201	R.VNDFVAAALK.Q
R3/RRR3-6/2	1049.265	1048.217	45.437	0.424	1316.072	0.433	15	0.188	R.VNDFVAAALK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/2	1519.018	1518.743	181.629	0.427	822.496	0.395	16	0.148	R.KFVFAEQAFFQR.W
R3/RRR3-12/2	1694.603	1692.976	-220.626	0.385	515.984	0.381	14	0.134	R.DFVPAIYDTTVIIPK.D
R3/RRR3-13/2	1692.553	1692.976	-250.986	0.238	831.242	0.180	17	0.127	R.DFVPAIYDTTVIIPK.D
R3/RRR3-13/3	1566.630	1565.740	-70.085	0.455	1172.767	0.427	31	0.125	K.AM*GNEHALVISNHR.S
R3/RRR3-13/3	1565.965	1565.740	144.310	0.410	887.424	0.326	27	0.097	K.AM*GNEHALVISNHR.S
R3/RRR3-13/3	1565.614	1565.740	-80.649	0.421	983.315	0.276	28	0.093	K.AM*GNEHALVISNHR.S
R3/RRR3-8/2	1404.571	1403.560	7.966	0.426	974.209	0.431	19	0.161	R.EIESAVGGALELSK.L
R3/RRR3-8/2	990.000	989.153	-155.224	0.409	543.321	0.521	15	0.154	K.LAPAYAVAGR.I
R3/RRR3-8/2	1404.809	1403.560	177.569	0.393	476.832	0.355	16	0.136	R.EIESAVGGALELSK.L
R3/RRR3-7/2	990.140	989.153	-12.874	0.343	389.047	0.354	13	0.131	-.LAPAYAVAGR.-
R3/RRR3-16/2	1710.007	1710.696	-990.558	0.409	2012.858	0.419	23	0.271	R.SSSAADAASASAASSPSER.S
R3/RRR3-21/2	1447.241	1447.616	-260.281	0.456	1818.389	0.527	22	0.272	K.TVTLQSELVGNASK.V
R3/RRR3-4/2	1232.443	1232.414	23.981	0.342	932.645	0.369	16	0.148	R.FALGVSNPSALR.E
R3/RRR3-17/3	1811.321	1811.887	-866.720	0.531	1842.862	0.526	27	0.238	K.HKEAEENGDQYYLSK.L
R3/RRR3-2/2	1295.148	1294.436	-222.498	0.461	1209.296	0.526	17	0.195	K.GVADFLQEVTSK.K
R3/RRR3-1/2	1910.437	1910.226	110.631	0.438	488.782	0.469	16	0.139	R.GM*VLPFTPLSLSFDNVR.Y
R3/RRR3-19/2	1189.192	1188.268	-64.720	0.530	1752.995	0.555	18	0.265	R.FDDSFSAASLK.A
R3/RRR3-20/2	1187.973	1188.268	-249.476	0.521	1753.576	0.548	18	0.264	R.FDDSFSAASLK.A
R3/RRR3-20/2	1187.894	1188.268	-316.179	0.518	1717.195	0.541	18	0.257	R.FDDSFSAASLK.A
R3/RRR3-2/2	1187.848	1188.268	-354.638	0.476	1687.638	0.557	18	0.257	R.FDDSFSAASLK.A
R3/RRR3-6/2	1187.824	1188.268	-375.261	0.441	1748.724	0.518	18	0.255	R.FDDSFSAASLK.A
R3/RRR3-17/2	1188.104	1188.268	-138.359	0.443	1661.683	0.564	18	0.254	R.FDDSFSAASLK.A
R3/RRR3-14/2	1188.262	1188.268	-5.009	0.434	1873.489	0.413	18	0.246	R.FDDSFSAASLK.A
R3/RRR3-20/2	1187.997	1188.268	-228.653	0.475	1625.300	0.523	18	0.240	R.FDDSFSAASLK.A
R3/RRR3-1/2	1187.992	1188.268	-233.498	0.414	1494.465	0.504	17	0.219	R.FDDSFSAASLK.A
R3/RRR3-17/2	1188.077	1188.268	-161.652	0.371	1519.830	0.483	17	0.216	R.FDDSFSAASLK.A
R3/RRR3-4/2	1187.999	1188.268	-227.003	0.434	1480.019	0.497	17	0.216	R.FDDSFSAASLK.A
R3/RRR3-4/2	1187.855	1188.268	-349.276	0.468	1445.537	0.484	17	0.210	R.FDDSFSAASLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1187.958	1188.268	-262.363	0.437	1412.880	0.501	17	0.210	R.FDDSFSAASLK.A
R3/RRR3-2/2	1188.095	1188.268	-146.295	0.430	1442.657	0.481	17	0.209	R.FDDSFSAASLK.A
R3/RRR3-10/2	1188.028	1188.268	-202.779	0.465	1252.679	0.550	17	0.204	R.FDDSFSAASLK.A
R3/RRR3-19/2	1187.955	1188.268	-264.940	0.451	1370.611	0.460	17	0.198	R.FDDSFSAASLK.A
R3/RRR3-10/2	1187.786	1188.268	-407.021	0.461	1119.929	0.571	17	0.197	R.FDDSFSAASLK.A
R3/RRR3-2/2	1187.432	1188.268	-1551.358	0.412	1252.658	0.495	16	0.192	R.FDDSFSAASLK.A
R3/RRR3-14/2	1188.021	1188.268	-209.067	0.350	1238.182	0.429	16	0.179	R.FDDSFSAASLK.A
R3/RRR3-14/2	1188.016	1188.268	-213.293	0.359	1301.753	0.319	16	0.167	R.FDDSFSAASLK.A
R3/RRR3-13/2	1188.026	1188.268	-204.635	0.321	890.284	0.399	15	0.153	R.FDDSFSAASLK.A
R3/RRR3-15/2	1188.097	1188.268	-144.955	0.467	783.857	0.396	14	0.150	R.FDDSFSAASLK.A
R3/RRR3-5/2	1187.856	1188.268	-348.452	0.348	579.072	0.403	15	0.147	R.FDDSFSAASLK.A
R3/RRR3-18/2	1187.742	1188.268	-1288.812	0.351	514.786	0.397	13	0.144	R.FDDSFSAASLK.A
R3/RRR3-5/2	1330.290	1329.569	-210.270	0.472	1168.811	0.461	17	0.180	R.ALVEGPFLDVLR.S
R3/RRR3-5/2	1387.961	1386.686	198.779	0.454	831.810	0.459	16	0.156	R.LMTLAGVYGFWK.Y
R3/RRR3-5/2	1328.904	1329.569	-1256.941	0.269	777.718	0.312	15	0.138	R.ALVEGPFLDVLR.S
R3/RRR3-5/2	1328.669	1329.569	-1434.921	0.310	689.332	0.292	15	0.136	R.ALVEGPFLDVLR.S
R3/RRR3-5/2	1328.689	1329.569	-1419.694	0.280	641.010	0.133	14	0.127	R.ALVEGPFLDVLR.S
R3/RRR3-17/2	1524.124	1524.703	-1038.988	0.439	1807.383	0.516	22	0.266	K.GVNPWIEVDGGVGPK.N
R3/RRR3-17/2	1524.139	1524.703	-1029.017	0.411	1435.256	0.459	20	0.203	K.GVNPWIEVDGGVGPK.N
R3/RRR3-7/2	1812.542	1812.018	-263.282	0.466	2273.036	0.262	22	0.272	K.NVWNEFTQEVYILR.E
R3/RRR3-9/2	1828.788	1827.097	-169.490	0.485	1727.880	0.549	20	0.261	K.IISYAQGFQLMQEAAR.E
R3/RRR3-5/2	1321.076	1321.547	-357.706	0.385	763.506	0.469	16	0.152	K.VYTAGSIIDLLR.F
R3/RRR3-5/3	1958.810	1959.232	-216.221	0.388	1092.940	0.386	28	0.112	R.AIAPEVLDSDFLGLQTLR.H
R3/RRR3-3/2	1480.384	1479.750	-247.672	0.519	899.407	0.523	20	0.174	R.AQVQIPLEVVNLR.A
R3/RRR3-3/2	1479.290	1479.750	-311.255	0.421	914.491	0.490	20	0.168	R.AQVQIPLEVVNLR.A
R3/RRR3-3/2	1479.393	1479.750	-241.962	0.397	896.055	0.494	19	0.166	R.AQVQIPLEVVNLR.A
R3/RRR3-2/2	1479.779	1479.750	19.724	0.360	1037.702	0.350	18	0.154	R.AQVQIPLEVVNLR.A
R3/RRR3-3/2	1560.387	1560.884	-319.895	0.480	765.534	0.345	18	0.142	R.M*LLVTDVQDIIKR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-3/2	1561.642	1560.884	-155.541	0.428	433.872	0.380	15	0.136	-.M*LLVTDVQDIIKR.-
R3/RRR3-5/2	1627.218	1627.864	-1014.696	0.526	1820.878	0.499	22	0.264	R.SNIISELKPLAAENK.Q
R3/RRR3-16/2	1698.021	1698.942	-1134.983	0.378	1967.063	0.411	23	0.264	R.NVQAALVNLDLADTIK.V
R3/RRR3-9/1	949.509	950.070	-1649.816	0.242	585.609	0.051	10	0.939	-.GFEVIDAAK.-
R3/RRR3-9/1	949.479	950.070	-1681.461	0.192	700.777	0.111	11	0.932	-.GFEVIDAAK.-
R3/RRR3-9/1	949.512	950.070	-1646.457	0.288	917.364	0.241	12	0.925	R.GFEVIDAAK.A
R3/RRR3-7/1	949.475	950.070	-1685.013	0.312	895.730	0.163	12	0.922	R.GFEVIDAAK.A
R3/RRR3-8/1	949.500	950.070	-1658.728	0.271	788.681	0.181	11	0.922	-.GFEVIDAAK.-
R3/RRR3-8/1	949.389	950.070	-1776.279	0.265	672.049	0.187	11	0.915	-.GFEVIDAAK.-
R3/RRR3-8/1	949.456	950.070	-1705.874	0.298	704.511	0.245	11	0.913	-.GFEVIDAAK.-
R3/RRR3-8/2	1393.255	1393.607	-253.054	0.502	2545.126	0.507	22	0.395	R.VVSCADILAFAAR.D
R3/RRR3-9/2	1393.261	1393.607	-249.011	0.503	2290.238	0.440	21	0.321	R.VVSCADILAFAAR.D
R3/RRR3-8/2	1393.166	1393.607	-317.489	0.480	2191.498	0.471	21	0.313	R.VVSCADILAFAAR.D
R3/RRR3-7/2	1394.168	1393.607	-315.505	0.483	2111.026	0.477	20	0.300	R.VVSCADILAFAAR.D
R3/RRR3-9/2	1394.431	1393.607	-126.755	0.518	1951.672	0.506	20	0.282	R.VVSCADILAFAAR.D
R3/RRR3-8/2	1394.123	1393.607	-348.010	0.558	1839.766	0.530	19	0.270	R.VVSCADILAFAAR.D
R3/RRR3-9/2	1394.181	1393.607	-306.281	0.553	1835.484	0.472	19	0.254	R.VVSCADILAFAAR.D
R3/RRR3-7/2	1393.227	1393.607	-273.448	0.455	1686.969	0.459	18	0.231	R.VVSCADILAFAAR.D
R3/RRR3-7/2	1392.969	1393.607	-1179.091	0.418	1307.837	0.374	17	0.175	R.VVSCADILAFAAR.D
R3/RRR3-9/2	949.466	950.070	-1695.296	0.372	1167.338	0.405	14	0.172	R.GFEVIDAAK.A
R3/RRR3-8/2	949.476	950.070	-1684.704	0.377	1093.186	0.435	14	0.171	R.GFEVIDAAK.A
R3/RRR3-9/2	949.978	950.070	-97.772	0.406	1237.458	0.359	14	0.170	R.GFEVIDAAK.A
R3/RRR3-9/2	950.062	950.070	-8.455	0.350	1144.028	0.399	14	0.169	R.GFEVIDAAK.A
R3/RRR3-10/2	949.811	950.070	-274.133	0.356	1119.154	0.403	14	0.168	R.GFEVIDAAK.A
R3/RRR3-10/2	949.862	950.070	-220.110	0.351	1107.880	0.398	14	0.166	R.GFEVIDAAK.A
R3/RRR3-10/2	1394.973	1393.607	263.256	0.341	1074.555	0.415	16	0.163	R.VVSCADILAFAAR.D
R3/RRR3-1/2	950.133	950.070	65.770	0.361	1002.162	0.396	13	0.160	R.GFEVIDAAK.A
R3/RRR3-10/2	1394.742	1393.607	97.036	0.296	1147.347	0.349	16	0.159	R.VVSCADILAFAAR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1394.995	1393.607	278.787	0.302	970.237	0.372	16	0.152	R.VVSCADILAFAAR.D
R3/RRR3-8/2	949.943	950.070	-134.896	0.417	875.908	0.380	13	0.152	-.GFEVIDAAK.-
R3/RRR3-1/2	949.975	950.070	-100.479	0.333	917.483	0.337	13	0.148	-.GFEVIDAAK.-
R3/RRR3-7/2	950.363	950.070	308.344	0.343	671.821	0.344	15	0.145	R.GFEVIDAAK.A
R3/RRR3-8/2	1394.684	1393.607	55.692	0.339	957.473	0.300	16	0.144	R.VVSCADILAFAAR.D
R3/RRR3-10/2	949.292	950.070	-1879.528	0.362	732.215	0.386	12	0.141	-.GFEVIDAAK.-
R3/RRR3-8/2	949.459	950.070	-1702.659	0.268	755.134	0.319	12	0.140	-.GFEVIDAAK.-
R3/RRR3-7/2	950.042	950.070	-30.364	0.311	885.650	0.200	13	0.135	-.GFEVIDAAK.-
R3/RRR3-9/2	1394.644	1393.607	26.371	0.246	546.111	0.298	12	0.133	R.VVSCADILAFAAR.D
R3/RRR3-16/3	1468.493	1468.556	-42.832	0.611	2088.816	0.388	28	0.217	R.HYNDISELSPHR.L
R3/RRR3-16/3	1468.178	1468.556	-258.121	0.562	1975.864	0.381	28	0.198	R.HYNDISELSPHR.L
R3/RRR3-17/3	1468.838	1468.556	192.367	0.551	1573.513	0.314	26	0.133	R.HYNDISELSPHR.L
R3/RRR3-16/3	1468.339	1468.556	-148.151	0.541	1308.810	0.336	23	0.118	R.HYNDISELSPHR.L
R3/RRR3-3/2	1271.963	1272.436	-373.058	0.401	1318.903	0.456	18	0.191	K.AAVVGGNVLTSQR.V
R3/RRR3-3/2	1272.807	1272.436	292.467	0.457	1114.461	0.473	17	0.176	K.AAVVGGNVLTSQR.V
R3/RRR3-3/2	1363.890	1364.486	-1173.889	0.293	729.257	0.386	14	0.138	K.LIEQGFGEDSIR.T
R3/RRR3-1/2	1273.401	1272.436	-27.750	0.307	563.895	0.163	13	0.110	-.AAVVGGNVLTSQR.-
R3/RRR3-5/2	1074.971	1075.286	-293.469	0.394	655.370	0.400	13	0.146	R.VVLNIFDVR.T
R3/RRR3-5/2	1075.278	1075.286	-7.015	0.445	782.065	0.343	13	0.143	-.VVLNIFDVR.-
R3/RRR3-5/2	1221.171	1221.343	-141.330	0.416	617.110	0.400	14	0.143	K.STYTGFELFR.I
R3/RRR3-24/2	1523.165	1523.713	-1019.225	0.470	1909.937	0.450	22	0.264	R.LSYGAISDLSGIQAK.K
R3/RRR3-24/2	1523.124	1523.713	-1046.423	0.433	1838.417	0.417	21	0.244	R.LSYGAISDLSGIQAK.K
R3/RRR3-24/2	1522.835	1523.713	-1236.687	0.348	1739.376	0.374	21	0.221	R.LSYGAISDLSGIQAK.K
R3/RRR3-24/3	1523.618	1523.713	-62.376	0.456	1597.999	0.339	29	0.145	R.LSYGAISDLSGIQAK.K
R3/RRR3-10/2	1423.014	1421.620	277.083	0.507	1970.147	0.420	20	0.266	R.FLDLDTGIIATNK.Q
R3/RRR3-10/2	1420.775	1421.620	-1302.773	0.358	864.852	0.296	17	0.139	R.FLDLDTGIIATNK.Q
R3/RRR3-11/2	1089.319	1089.309	9.036	0.367	758.982	0.291	13	0.138	R.INEPILYVK.M
R3/RRR3-11/2	1089.010	1089.309	-276.082	0.330	622.973	0.257	12	0.133	R.INEPILYVK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/3	1819.528	1819.015	-268.267	0.411	1082.097	0.358	26	0.108	R.VHNAALSAQPALVQNER.K
R3/RRR3-11/3	1820.603	1819.015	-226.884	0.422	866.916	0.419	27	0.108	R.VHNAALSAQPALVQNER.K
R3/RRR3-24/2	1259.323	1259.439	-92.228	0.391	1887.496	0.437	21	0.257	R.FPGVNGLGISAAR.V
R3/RRR3-23/2	1259.347	1259.439	-73.559	0.454	1599.681	0.454	20	0.223	R.FPGVNGLGISAAR.V
R3/RRR3-23/2	1259.295	1259.439	-115.175	0.448	1510.862	0.498	20	0.222	R.FPGVNGLGISAAR.V
R3/RRR3-23/2	1259.101	1259.439	-269.028	0.292	1154.074	0.402	18	0.166	R.FPGVNGLGISAAR.V
R3/RRR3-1/2	1403.203	1403.554	-250.562	0.407	695.162	0.385	16	0.144	R.YFDLPFCSPEK.V
R3/RRR3-1/2	1260.040	1260.336	-235.791	0.291	989.750	0.301	17	0.143	K.SEALGEVLNGDR.L
R3/RRR3-18/2	1694.039	1694.966	-1140.985	0.477	1863.850	0.465	20	0.260	K.GLLDLTCQTVADM*IK.G
R3/RRR3-18/2	1694.584	1694.966	-225.984	0.474	918.840	0.494	17	0.163	K.GLLDLTCQTVADM*IK.G
R3/RRR3-10/2	1207.930	1208.300	-306.576	0.372	995.323	0.306	16	0.146	K.VDFGDIDGLEK.I
R3/RRR3-10/2	1741.325	1740.938	223.269	0.484	713.083	0.412	15	0.140	K.AFSDVLEHDLPQLQK.Q
R3/RRR3-10/2	1459.024	1458.596	294.496	0.437	1820.316	0.469	21	0.256	R.EADPLDSQVVTVGK.F
R3/RRR3-10/2	1458.042	1458.596	-1068.695	0.368	1525.958	0.535	20	0.229	R.EADPLDSQVVTVGK.F
R3/RRR3-10/2	1457.708	1458.596	-1298.911	0.304	1361.721	0.383	19	0.181	R.EADPLDSQVVTVGK.F
R3/RRR3-10/2	1683.467	1683.843	-224.267	0.545	1446.913	0.608	23	0.239	R.VFFANTGTEANEAAIK.F
R3/RRR3-10/2	1683.377	1683.843	-277.520	0.562	1387.121	0.575	23	0.225	R.VFFANTGTEANEAAIK.F
R3/RRR3-2/2	1787.693	1789.087	-1343.585	0.387	1624.357	0.354	21	0.201	R.M*LAISALNTLLQGSPDK.A
R3/RRR3-2/2	1773.812	1773.088	-155.969	0.537	1273.415	0.520	19	0.195	R.MLAISALNTLLQGSPDK.A
R3/RRR3-2/2	1772.472	1773.088	-914.272	0.412	1417.157	0.388	21	0.186	R.MLAISALNTLLQGSPDK.A
R3/RRR3-2/2	1787.335	1789.087	-2105.873	0.388	1209.641	0.328	19	0.158	R.M*LAISALNTLLQGSPDK.A
R3/RRR3-2/2	1108.435	1109.218	-1613.320	0.330	796.983	0.287	16	0.136	K.NAVTSVAFSGR.A
R3/RRR3-15/2	1591.385	1590.801	-261.787	0.490	1857.748	0.454	21	0.257	R.LDLVFADAPFPAEGK.S
R3/RRR3-2/2	1018.966	1018.148	-179.048	0.510	1458.439	0.455	16	0.208	R.GGAWVVVDSK.I
R3/RRR3-2/2	1017.866	1018.148	-277.637	0.464	1013.221	0.505	14	0.176	R.GGAWVVVDSK.I
R3/RRR3-2/2	1017.993	1018.148	-153.120	0.473	1123.275	0.417	15	0.171	R.GGAWVVVDSK.I
R3/RRR3-24/2	1343.355	1343.551	-146.613	0.536	1641.534	0.543	20	0.251	R.TPEGTIIELTIR.G
R3/RRR3-24/2	1343.369	1343.551	-136.403	0.538	1461.091	0.554	19	0.230	R.TPEGTIIELTIR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1342.772	1343.551	-1329.032	0.494	1431.553	0.534	19	0.222	R.TPEGTIIELTIR.G
R3/RRR3-23/2	1344.470	1343.551	-60.797	0.353	434.290	0.493	13	0.144	R.TPEGTIIELTIR.G
R3/RRR3-4/2	1134.050	1134.265	-190.622	0.371	1164.211	0.356	18	0.164	K.LSSAIEASISR.G
R3/RRR3-4/2	1197.309	1197.406	-81.563	0.492	1046.880	0.394	18	0.163	K.IPADLIINAEK.A
R3/RRR3-4/2	1197.381	1197.406	-20.820	0.443	1048.937	0.393	18	0.163	K.IPADLIINAEK.A
R3/RRR3-4/2	1133.951	1134.265	-278.097	0.383	1121.996	0.272	18	0.151	K.LSSAIEASISR.G
R3/RRR3-4/2	1134.068	1134.265	-174.857	0.325	673.338	0.236	16	0.134	K.LSSAIEASISR.G
R3/RRR3-4/2	1416.264	1416.607	-242.978	0.296	552.341	0.407	14	0.136	-.GADPAIVLNNLYR.-
R3/RRR3-18/2	1146.935	1147.307	-325.442	0.267	932.353	0.172	13	0.132	R.CSVIERRAR.F
R3/RRR3-17/2	1147.947	1147.307	-314.596	0.312	922.049	0.149	13	0.130	R.CSVIERRAR.F
R3/RRR3-18/2	1146.962	1147.307	-301.737	0.270	905.350	0.088	13	0.126	R.CSVIERRAR.F
R3/RRR3-4/2	1417.021	1416.607	292.598	0.136	504.943	0.243	15	0.125	R.GADPAIVLNNLYR.H
R3/RRR3-23/2	1550.090	1549.706	248.523	0.508	1537.111	0.573	21	0.242	R.TLSDPLFFGYSSSK.N
R3/RRR3-23/2	1549.174	1549.706	-991.443	0.462	1602.819	0.476	21	0.227	R.TLSDPLFFGYSSSK.N
R3/RRR3-23/2	1549.297	1549.706	-264.789	0.464	1328.079	0.529	20	0.207	R.TLSDPLFFGYSSSK.N
R3/RRR3-22/2	1549.496	1549.706	-135.404	0.415	1322.941	0.516	20	0.203	R.TLSDPLFFGYSSSK.N
R3/RRR3-23/2	1550.268	1549.706	-283.183	0.489	1197.328	0.535	19	0.195	R.TLSDPLFFGYSSSK.N
R3/RRR3-23/2	1548.431	1549.706	-1473.622	0.339	1132.803	0.491	18	0.178	R.TLSDPLFFGYSSSK.N
R3/RRR3-23/2	1549.061	1549.706	-1064.548	0.405	1120.815	0.464	19	0.176	R.TLSDPLFFGYSSSK.N
R3/RRR3-22/2	1550.131	1549.706	275.134	0.380	937.249	0.515	19	0.170	R.TLSDPLFFGYSSSK.N
R3/RRR3-22/2	1548.955	1549.706	-1133.864	0.310	938.778	0.449	17	0.158	R.TLSDPLFFGYSSSK.N
R3/RRR3-8/2	1944.835	1945.335	-257.838	0.519	1450.458	0.598	23	0.234	R.LPAPVTTSAVELVALPLPR.V
R3/RRR3-8/2	1946.991	1945.335	-176.997	0.395	948.110	0.499	18	0.163	R.LPAPVTTSAVELVALPLPR.V
R3/RRR3-8/2	1945.063	1945.335	-140.159	0.452	829.148	0.446	18	0.149	R.LPAPVTTSAVELVALPLPR.V
R3/RRR3-5/2	1863.163	1862.027	73.363	0.396	501.974	0.452	17	0.139	K.SEGLHNEVCQILNGYK.Q
R3/RRR3-5/2	1452.794	1451.798	-2.495	0.324	715.397	0.337	13	0.134	K.YLDIFMPPLITK.W
R3/RRR3-5/2	879.672	878.995	-368.715	0.274	889.262	0.110	13	0.126	K.ISDFGIAR.I
R3/RRR3-9/2	1478.556	1477.862	-207.573	0.312	1007.585	0.059	17	0.121	K.LNM*PKKGLSTMLK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1603.164	1603.708	-965.844	0.532	1489.608	0.583	23	0.240	K.AGDTVGVGYFVDSCR.A
R3/RRR3-11/2	1603.290	1603.708	-261.447	0.509	1386.140	0.600	22	0.230	K.AGDTVGVGYFVDSCR.A
R3/RRR3-11/2	1603.411	1603.708	-186.136	0.522	1418.210	0.499	22	0.211	K.AGDTVGVGYFVDSCR.A
R3/RRR3-10/2	1934.459	1934.179	145.154	0.588	1526.010	0.545	25	0.232	K.LITELIGSPDDSSLGFLR.S
R3/RRR3-10/2	1933.422	1934.179	-911.558	0.503	1529.773	0.510	26	0.226	K.LITELIGSPDDSSLGFLR.S
R3/RRR3-10/2	1934.644	1934.179	240.639	0.559	1392.528	0.559	24	0.220	K.LITELIGSPDDSSLGFLR.S
R3/RRR3-10/3	1933.414	1934.179	-916.002	0.337	815.687	0.396	27	0.098	K.LITELIGSPDDSSLGFLR.S
R3/RRR3-3/2	1725.822	1725.918	-56.089	0.472	1680.791	0.468	21	0.235	R.EAEFLASTIVSSLTEK.Q
R3/RRR3-11/2	1214.538	1215.298	-1453.830	0.481	1640.049	0.504	21	0.239	R.AVAGGGAAGEEAVR.A
R3/RRR3-11/2	1214.749	1215.298	-1279.410	0.445	1421.670	0.479	21	0.208	R.AVAGGGAAGEEAVR.A
R3/RRR3-11/2	1215.226	1215.298	-59.807	0.489	1330.826	0.499	20	0.202	R.AVAGGGAAGEEAVR.A
R3/RRR3-10/2	1910.447	1909.045	211.066	0.595	1149.131	0.631	22	0.207	R.DSGAFSWEIAPVEISSGR.G
R3/RRR3-2/2	1513.153	1513.764	-1067.801	0.416	1130.864	0.625	20	0.202	K.VPTGVSGTALAASLLR.D
R3/RRR3-1/2	1514.111	1513.764	229.684	0.334	664.964	0.362	17	0.136	K.VPTGVSGTALAASLLR.D
R3/RRR3-14/2	1794.400	1794.001	223.147	0.526	1350.057	0.600	24	0.225	R.DIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1793.361	1794.001	-917.346	0.476	1544.667	0.494	24	0.224	R.DIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1793.637	1794.001	-203.256	0.485	1396.998	0.551	24	0.219	R.DIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1794.356	1794.001	198.793	0.541	1110.914	0.602	22	0.201	R.DIPLNYATFQPGTTVR.D
R3/RRR3-13/2	1794.189	1794.001	105.049	0.474	1093.915	0.509	21	0.181	R.DIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1794.403	1794.001	224.784	0.524	863.424	0.559	21	0.174	R.DIPLNYATFQPGTTVR.D
R3/RRR3-13/2	1793.283	1794.001	-960.603	0.399	1121.213	0.451	20	0.173	R.DIPLNYATFQPGTTVR.D
R3/RRR3-13/2	1793.546	1794.001	-254.261	0.440	936.909	0.478	19	0.164	R.DIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1794.239	1794.001	133.297	0.473	767.838	0.485	18	0.156	R.DIPLNYATFQPGTTVR.D
R3/RRR3-14/2	1792.722	1794.001	-1274.795	0.305	864.620	0.376	19	0.147	R.DIPLNYATFQPGTTVR.D
R3/RRR3-14/3	1793.782	1794.001	-122.262	0.364	915.792	0.378	28	0.101	R.DIPLNYATFQPGTTVR.D
R3/RRR3-2/2	1788.532	1788.938	-227.591	0.490	1682.892	0.456	21	0.230	R.SGGAAASAQIIDLLEDTR.I
R3/RRR3-12/2	1412.047	1412.527	-341.164	0.547	1512.809	0.545	20	0.234	K.IVASYQTTNGETK.S
R3/RRR3-26/2	1539.294	1539.711	-271.521	0.484	1614.454	0.531	20	0.242	R.FLFCQSSPASAPAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-26/2	1540.779	1539.711	44.690	0.473	1264.142	0.574	18	0.208	R.FLFCQSSPASAPAR.E
R3/RRR3-26/2	1540.337	1539.711	-243.358	0.455	1057.513	0.573	18	0.189	R.FLFCQSSPASAPAR.E
R3/RRR3-26/2	1540.865	1539.711	100.468	0.393	611.798	0.446	14	0.143	R.FLFCQSSPASAPAR.E
R3/RRR3-12/2	1353.968	1353.465	-367.645	0.512	1290.659	0.607	19	0.222	R.DNVQAYPGVSFR.Y
R3/RRR3-12/2	1353.081	1353.465	-284.275	0.460	1104.577	0.510	18	0.185	R.DNVQAYPGVSFR.Y
R3/RRR3-13/2	1352.999	1353.465	-345.375	0.426	911.663	0.531	17	0.173	R.DNVQAYPGVSFR.Y
R3/RRR3-12/2	1352.462	1353.465	-1484.996	0.341	921.352	0.379	17	0.152	R.DNVQAYPGVSFR.Y
R3/RRR3-13/2	1352.473	1353.465	-1476.836	0.260	539.239	0.330	13	0.134	-.DNVQAYPGVSFR.-
R3/RRR3-12/2	1353.499	1353.465	25.726	0.293	555.663	0.240	13	0.132	R.DNVQAYPGVSFR.Y
R3/RRR3-22/3	1383.532	1382.670	-100.285	0.499	1822.503	0.421	28	0.190	R.CKQLGITALHIK.I
R3/RRR3-22/3	1382.594	1382.670	-55.677	0.450	1130.560	0.420	24	0.122	R.CKQLGITALHIK.I
R3/RRR3-22/3	1383.436	1382.670	-170.253	0.520	894.327	0.430	22	0.110	-.CKQLGITALHIK.-
R3/RRR3-5/2	1587.447	1587.888	-278.556	0.412	1060.149	0.402	21	0.161	K.LLVFQSTLPSLGVGR.L
R3/RRR3-5/3	1581.683	1581.799	-73.169	0.418	1063.464	0.355	26	0.107	R.LTTHAIPASQSLVSR.W
R3/RRR3-4/3	1581.388	1581.799	-260.392	0.386	800.323	0.341	24	0.094	-.LTTHAIPASQSLVSR.-
R3/RRR3-5/2	1239.960	1240.434	-383.279	0.458	1302.497	0.599	19	0.220	R.VPATNILLGEGR.G
R3/RRR3-5/2	1240.248	1240.434	-150.410	0.472	1314.938	0.575	19	0.217	R.VPATNILLGEGR.G
R3/RRR3-5/2	1240.396	1240.434	-31.153	0.425	1179.118	0.595	18	0.205	R.VPATNILLGEGR.G
R3/RRR3-25/2	1531.193	1531.645	-296.066	0.497	1804.589	0.419	21	0.238	R.AGDCALIHSGSWEK.A
R3/RRR3-25/2	1531.158	1531.645	-318.943	0.498	1668.843	0.469	22	0.234	R.AGDCALIHSGSWEK.A
R3/RRR3-24/2	1531.192	1531.645	-297.186	0.523	1678.856	0.456	22	0.231	R.AGDCALIHSGSWEK.A
R3/RRR3-25/2	1531.154	1531.645	-321.742	0.517	1448.229	0.471	20	0.207	R.AGDCALIHSGSWEK.A
R3/RRR3-24/2	1531.192	1531.645	-296.626	0.489	1439.507	0.464	20	0.205	R.AGDCALIHSGSWEK.A
R3/RRR3-25/2	1531.297	1531.645	-227.924	0.481	1403.659	0.442	20	0.197	R.AGDCALIHSGSWEK.A
R3/RRR3-24/2	1532.125	1531.645	314.009	0.531	1407.323	0.425	20	0.193	R.AGDCALIHSGSWEK.A
R3/RRR3-25/2	1531.276	1531.645	-241.839	0.458	1273.949	0.404	20	0.178	R.AGDCALIHSGSWEK.A
R3/RRR3-25/3	1530.820	1531.645	-1196.094	0.424	1486.217	0.461	29	0.164	R.AGDCALIHSGSWEK.A
R3/RRR3-25/2	1531.331	1531.645	-205.691	0.372	1620.613	0.142	21	0.162	R.AGDCALIHSGSWEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/3	1532.747	1531.645	66.283	0.550	1499.031	0.439	29	0.157	R.AGDCALIHSGSWEK.A
R3/RRR3-20/3	1531.296	1531.645	-228.892	0.443	1409.792	0.422	28	0.147	R.AGDCALIHSGSWEK.A
R3/RRR3-1/3	1531.168	1531.645	-312.752	0.390	1499.002	0.367	28	0.144	R.AGDCALIHSGSWEK.A
R3/RRR3-23/2	1531.831	1531.645	121.682	0.315	735.138	0.282	17	0.137	R.AGDCALIHSGSWEK.A
R3/RRR3-23/3	1530.994	1531.645	-1081.758	0.423	1164.654	0.411	27	0.126	R.AGDCALIHSGSWEK.A
R3/RRR3-24/3	1531.758	1531.645	73.800	0.449	1125.814	0.415	26	0.125	R.AGDCALIHSGSWEK.A
R3/RRR3-23/3	1531.327	1531.645	-208.619	0.408	1155.940	0.397	26	0.124	R.AGDCALIHSGSWEK.A
R3/RRR3-22/3	1532.241	1531.645	-264.629	0.434	1115.547	0.395	26	0.120	R.AGDCALIHSGSWEK.A
R3/RRR3-17/3	1531.575	1531.645	-46.104	0.472	1122.523	0.375	27	0.116	R.AGDCALIHSGSWEK.A
R3/RRR3-25/3	1530.959	1531.645	-1104.455	0.425	1115.254	0.364	26	0.115	R.AGDCALIHSGSWEK.A
R3/RRR3-20/3	1531.513	1531.645	-86.878	0.414	1059.484	0.361	26	0.112	R.AGDCALIHSGSWEK.A
R3/RRR3-19/3	1531.146	1531.645	-327.150	0.395	1044.609	0.356	24	0.112	R.AGDCALIHSGSWEK.A
R3/RRR3-21/3	1531.509	1531.645	-88.916	0.401	1146.408	0.325	26	0.110	R.AGDCALIHSGSWEK.A
R3/RRR3-19/3	1530.885	1531.645	-1153.335	0.414	1247.036	0.298	27	0.110	R.AGDCALIHSGSWEK.A
R3/RRR3-26/3	1531.557	1531.645	-57.496	0.452	1109.538	0.331	26	0.108	R.AGDCALIHSGSWEK.A
R3/RRR3-25/3	1531.543	1531.645	-67.090	0.453	1011.248	0.351	25	0.108	R.AGDCALIHSGSWEK.A
R3/RRR3-20/3	1531.332	1531.645	-205.020	0.412	1026.324	0.338	25	0.107	R.AGDCALIHSGSWEK.A
R3/RRR3-27/3	1532.964	1531.645	208.241	0.415	871.888	0.371	25	0.107	R.AGDCALIHSGSWEK.A
R3/RRR3-24/3	1530.841	1531.645	-1182.161	0.415	1113.784	0.314	26	0.107	R.AGDCALIHSGSWEK.A
R3/RRR3-22/3	1531.642	1531.645	-2.096	0.401	827.345	0.370	23	0.106	R.AGDCALIHSGSWEK.A
R3/RRR3-27/3	1531.267	1531.645	-247.846	0.403	1236.155	0.271	26	0.105	R.AGDCALIHSGSWEK.A
R3/RRR3-24/3	1531.849	1531.645	133.501	0.373	952.266	0.334	25	0.105	R.AGDCALIHSGSWEK.A
R3/RRR3-25/3	1531.166	1531.645	-313.712	0.405	851.747	0.349	23	0.104	R.AGDCALIHSGSWEK.A
R3/RRR3-23/3	1531.171	1531.645	-310.833	0.411	852.692	0.349	25	0.103	R.AGDCALIHSGSWEK.A
R3/RRR3-22/3	1531.569	1531.645	-50.181	0.466	866.104	0.345	23	0.102	R.AGDCALIHSGSWEK.A
R3/RRR3-26/3	1531.700	1531.645	36.033	0.444	1138.585	0.283	27	0.102	R.AGDCALIHSGSWEK.A
R3/RRR3-3/3	1531.699	1531.645	35.314	0.401	827.664	0.315	22	0.099	R.AGDCALIHSGSWEK.A
R3/RRR3-26/3	1531.810	1531.645	107.847	0.422	1043.343	0.279	25	0.099	R.AGDCALIHSGSWEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-27/3	1531.879	1531.645	153.040	0.404	889.554	0.291	23	0.097	R.AGDCALIHSGSWEK.A
R3/RRR3-24/3	1531.029	1531.645	-1058.942	0.387	898.168	0.283	23	0.097	R.AGDCALIHSGSWEK.A
R3/RRR3-19/3	1531.844	1531.645	130.264	0.416	886.836	0.287	24	0.097	R.AGDCALIHSGSWEK.A
R3/RRR3-6/3	1533.106	1531.645	301.181	0.371	694.167	0.201	24	0.090	-.AGDCALIHSGSWEK.-
R3/RRR3-4/2	1390.594	1391.596	-1443.747	0.348	865.755	0.418	18	0.153	R.WSSFVPDLVAAAK.S
R3/RRR3-4/2	1355.392	1356.505	-1564.261	0.336	931.982	0.334	15	0.146	K.LLSEEIFDFSR.G
R3/RRR3-4/2	1391.260	1391.596	-242.153	0.299	465.137	0.337	14	0.134	R.WSSFVPDLVAAAK.S
R3/RRR3-4/2	1390.399	1391.596	-1584.579	0.232	732.379	0.176	17	0.128	R.WSSFVPDLVAAAK.S
R3/RRR3-4/2	1355.501	1356.505	-1482.841	0.232	488.181	0.355	10	0.128	-.LLSEEIFDFSR.-
R3/RRR3-3/2	1853.269	1852.980	156.072	0.465	1232.082	0.399	21	0.170	R.SSSSDAPLVAFGSSDGVIR.V
R3/RRR3-2/2	1853.426	1852.980	241.407	0.444	1017.907	0.399	22	0.156	R.SSSSDAPLVAFGSSDGVIR.V
R3/RRR3-3/2	1877.295	1876.230	34.722	0.428	618.260	0.554	17	0.151	R.LASFQYAPSIPPFIVPK.Q
R3/RRR3-2/2	1852.427	1852.980	-840.903	0.348	608.163	0.176	18	0.124	-.SSSSDAPLVAFGSSDGVIR.-
R3/RRR3-18/3	1859.499	1859.081	225.566	0.471	1434.331	0.549	32	0.186	R.AAHGGPAFEPHATVVGAIR.L
R3/RRR3-18/3	1859.362	1859.081	151.602	0.413	1213.203	0.453	30	0.137	R.AAHGGPAFEPHATVVGAIR.L
R3/RRR3-18/3	1858.654	1859.081	-230.540	0.377	667.876	0.418	27	0.101	R.AAHGGPAFEPHATVVGAIR.L
R3/RRR3-27/2	1300.282	1299.502	-169.737	0.475	1326.990	0.582	17	0.217	R.LLAQAALTVGADR.A
R3/RRR3-27/2	1299.464	1299.502	-28.889	0.259	353.260	0.360	14	0.134	R.LLAQAALTVGADR.A
R3/RRR3-27/2	1298.592	1299.502	-1475.226	0.248	571.865	0.314	16	0.133	R.LLAQAALTVGADR.A
R3/RRR3-3/3	1281.592	1281.443	116.101	0.531	1569.122	0.506	23	0.185	K.HVVDDGLELRK.A
R3/RRR3-3/3	1281.852	1281.443	319.955	0.535	1473.481	0.520	23	0.177	K.HVVDDGLELRK.A
R3/RRR3-3/3	1280.598	1281.443	-1445.628	0.471	1127.708	0.486	22	0.135	K.HVVDDGLELRK.A
R3/RRR3-1/3	1281.352	1281.443	-71.351	0.455	917.120	0.437	21	0.114	K.HVVDDGLELRK.A
R3/RRR3-6/2	1361.134	1360.535	-295.817	0.509	1588.610	0.489	19	0.230	R.NLSQQCLNALAK.A
R3/RRR3-6/2	1360.172	1360.535	-268.301	0.495	1512.239	0.470	19	0.217	R.NLSQQCLNALAK.A
R3/RRR3-6/2	1359.703	1360.535	-1352.014	0.464	1528.546	0.429	19	0.210	R.NLSQQCLNALAK.A
R3/RRR3-2/2	1360.364	1360.535	-126.329	0.379	905.637	0.320	17	0.145	R.NLSQQCLNALAK.A
R3/RRR3-17/2	1643.517	1643.908	-238.658	0.483	1281.296	0.591	23	0.215	K.NLVAPVIGEANLAAYK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-16/2	1264.696	1264.453	193.466	0.498	1598.087	0.500	19	0.234	K.DIGNAVYALISK.E
R3/RRR3-16/2	1263.978	1264.453	-376.771	0.444	1170.213	0.511	17	0.189	K.DIGNAVYALISK.E
R3/RRR3-16/2	1263.393	1264.453	-1635.237	0.303	833.885	0.463	16	0.154	K.DIGNAVYALISK.E
R3/RRR3-23/2	1597.281	1597.684	-252.970	0.486	1713.357	0.448	22	0.234	K.VSDSGELNSLM*DDAK.Y
R3/RRR3-22/2	1597.162	1597.684	-955.874	0.516	1414.832	0.495	20	0.208	K.VSDSGELNSLM*DDAK.Y
R3/RRR3-23/2	1597.069	1597.684	-1014.347	0.500	1386.794	0.466	20	0.199	K.VSDSGELNSLM*DDAK.Y
R3/RRR3-22/2	1598.339	1597.684	-216.800	0.524	1366.805	0.476	20	0.199	K.VSDSGELNSLM*DDAK.Y
R3/RRR3-22/2	1597.154	1597.684	-960.708	0.485	1196.546	0.479	19	0.183	K.VSDSGELNSLM*DDAK.Y
R3/RRR3-23/2	1597.180	1597.684	-944.287	0.471	1135.922	0.450	19	0.174	K.VSDSGELNSLM*DDAK.Y
R3/RRR3-2/2	1390.276	1390.563	-206.922	0.436	839.375	0.496	17	0.163	K.VGESPEEIAAFLK.S
R3/RRR3-2/2	1390.266	1390.563	-214.321	0.446	859.945	0.396	18	0.152	K.VGESPEEIAAFLK.S
R3/RRR3-3/2	1391.153	1390.563	-295.770	0.288	764.519	0.356	16	0.141	K.VGESPEEIAAFLK.S
R3/RRR3-2/3	1849.715	1849.848	-72.065	0.554	876.267	0.561	33	0.135	K.TEDESRPLEDGTGEASR.S
R3/RRR3-2/2	1390.248	1390.563	-227.446	0.219	579.247	0.155	15	0.128	K.VGESPEEIAAFLK.S
R3/RRR3-2/3	1850.014	1849.848	89.959	0.483	728.941	0.552	29	0.124	K.TEDESRPLEDGTGEASR.S
R3/RRR3-6/2	1208.478	1209.420	-1611.572	0.460	1312.854	0.571	21	0.217	K.VPGATDLGLIPR.K
R3/RRR3-6/2	1208.573	1209.420	-1533.035	0.468	1129.995	0.505	20	0.187	K.VPGATDLGLIPR.K
R3/RRR3-6/2	1208.281	1209.420	-1775.688	0.390	1050.056	0.545	20	0.185	K.VPGATDLGLIPR.K
R3/RRR3-5/2	1209.163	1209.420	-213.006	0.321	522.980	0.441	14	0.142	K.VPGATDLGLIPR.K
R3/RRR3-12/3	1076.181	1076.234	-49.685	0.548	1956.790	0.341	27	0.179	K.HVGHLGGALSK.N
R3/RRR3-13/3	1076.344	1076.234	102.864	0.491	1606.499	0.291	25	0.129	K.HVGHLGGALSK.N
R3/RRR3-13/3	1076.090	1076.234	-133.659	0.512	1447.681	0.342	24	0.128	K.HVGHLGGALSK.N
R3/RRR3-12/3	1076.892	1076.234	-317.971	0.512	1332.683	0.346	24	0.120	K.HVGHLGGALSK.N
R3/RRR3-13/3	1076.731	1076.234	462.723	0.487	1393.500	0.301	25	0.114	K.HVGHLGGALSK.N
R3/RRR3-12/3	1076.608	1076.234	348.227	0.460	1066.508	0.280	22	0.097	K.HVGHLGGALSK.N
R3/RRR3-2/2	1516.350	1515.734	-253.990	0.477	814.200	0.445	19	0.154	K.QALEDSTLVGLLQK.I
R3/RRR3-2/3	1653.959	1653.903	33.703	0.357	830.262	0.418	24	0.103	K.KPAEGEVHLYPVSVK.T
R3/RRR3-17/2	1607.052	1607.786	-1082.741	0.524	1560.395	0.497	23	0.228	R.YAVGPGQCSSLLAQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1607.208	1607.786	-984.820	0.502	1154.255	0.473	20	0.180	R.YAVGPGQCSSLLAQR.I
R3/RRR3-17/2	1049.955	1050.233	-265.945	0.526	1268.783	0.579	16	0.215	R.SLGAAIIYNK.D
R3/RRR3-17/2	1050.056	1050.233	-169.374	0.515	1102.763	0.518	16	0.188	R.SLGAAIIYNK.D
R3/RRR3-18/2	1049.878	1050.233	-339.201	0.421	1226.956	0.463	15	0.186	R.SLGAAIIYNK.D
R3/RRR3-18/2	1049.895	1050.233	-322.753	0.389	1209.919	0.442	15	0.180	R.SLGAAIIYNK.D
R3/RRR3-15/2	1535.644	1534.734	-58.650	0.488	1394.069	0.541	22	0.218	R.VSTTVTVDEALTGLK.T
R3/RRR3-29/2	1095.237	1095.280	-39.306	0.348	1146.709	0.248	14	0.148	K.LSKLNVHQR.A
R3/RRR3-29/2	1094.195	1095.280	-1912.044	0.328	773.529	0.185	12	0.129	K.LSKLNVHQR.A
R3/RRR3-12/2	741.666	740.957	-393.989	0.119	897.926	0.148	11	0.123	K.KLLAAPK.R
R3/RRR3-16/2	1700.539	1700.920	-224.752	0.528	1503.847	0.512	23	0.223	R.NLAGNSAIFVAPNGLNK.G
R3/RRR3-12/2	1834.350	1835.005	-904.991	0.448	1500.930	0.511	21	0.220	K.NGVEEVLGLGQLSDFEK.E
R3/RRR3-12/2	1835.679	1835.005	-177.791	0.350	800.193	0.412	19	0.147	K.NGVEEVLGLGQLSDFEK.E
R3/RRR3-12/2	1835.017	1835.005	6.498	0.388	540.898	0.406	20	0.141	K.NGVEEVLGLGQLSDFEK.E
R3/RRR3-12/2	1835.511	1835.005	-269.593	0.309	473.755	0.382	17	0.136	K.NGVEEVLGLGQLSDFEK.E
R3/RRR3-21/2	1552.422	1552.713	-187.912	0.497	1539.560	0.495	19	0.223	K.DFNLAEHPDIPGVK.N
R3/RRR3-21/2	1551.303	1552.713	-1557.711	0.308	608.122	0.366	14	0.134	-.DFNLAEHPDIPGVK.-
R3/RRR3-10/2	1445.167	1445.685	-1053.562	0.503	1859.409	0.354	19	0.231	R.LPDFSLDVAQIVK.V
R3/RRR3-10/2	1444.846	1445.685	-1276.663	0.438	1714.493	0.326	19	0.208	R.LPDFSLDVAQIVK.V
R3/RRR3-24/2	1307.712	1308.470	-1348.372	0.472	1513.394	0.494	17	0.221	K.GVAFVNNFNIGR.F
R3/RRR3-6/2	1955.928	1955.302	-191.524	0.567	1473.685	0.516	21	0.216	K.LMSTTYLVALCQAVDLR.H
R3/RRR3-6/2	1970.882	1971.301	-213.203	0.533	1486.952	0.499	22	0.216	K.LM*STTYLVALCQAVDLR.H
R3/RRR3-2/2	1956.203	1955.302	-50.860	0.463	1219.698	0.371	18	0.163	K.LMSTTYLVALCQAVDLR.H
R3/RRR3-6/2	1954.728	1955.302	-807.605	0.423	1029.636	0.367	18	0.152	K.LMSTTYLVALCQAVDLR.H
R3/RRR3-6/2	1954.313	1955.302	-1020.659	0.382	1031.834	0.354	18	0.151	K.LMSTTYLVALCQAVDLR.H
R3/RRR3-6/2	1970.539	1971.301	-896.958	0.443	799.620	0.400	19	0.147	K.LM*STTYLVALCQAVDLR.H
R3/RRR3-17/2	966.887	967.190	-314.562	0.477	1520.313	0.490	15	0.223	K.AILLQGVPR.N
R3/RRR3-18/2	966.615	967.190	-1635.263	0.514	1494.811	0.497	15	0.222	K.AILLQGVPR.N
R3/RRR3-18/2	967.023	967.190	-174.105	0.530	1433.870	0.481	15	0.212	K.AILLQGVPR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-18/2	966.569	967.190	-1682.462	0.445	1324.914	0.405	14	0.185	K.AILLQGVPR.N
R3/RRR3-9/2	1891.938	1891.158	-116.591	0.583	1158.679	0.573	24	0.201	R.FIQYNIFGNVFEVTAK.Y
R3/RRR3-9/2	1892.342	1891.158	97.530	0.552	580.634	0.562	20	0.160	R.FIQYNIFGNVFEVTAK.Y
R3/RRR3-9/2	1892.397	1891.158	126.706	0.512	607.535	0.504	21	0.155	R.FIQYNIFGNVFEVTAK.Y
R3/RRR3-10/2	1891.988	1891.158	-90.250	0.375	412.941	0.373	20	0.140	R.FIQYNIFGNVFEVTAK.Y
R3/RRR3-24/2	1675.426	1675.950	-912.348	0.455	1571.820	0.476	20	0.223	K.YLIGEIDASTIPVKR.T
R3/RRR3-23/2	1459.249	1459.672	-290.526	0.485	1759.160	0.399	20	0.231	K.LYVQAVQPADLNK.N
R3/RRR3-2/2	973.049	972.164	-118.606	0.396	1151.714	0.372	14	0.165	R.VAILETVAR.Y
R3/RRR3-3/2	1157.102	1157.259	-136.246	0.396	850.783	0.273	15	0.138	-.ISQDDVPQVR.-
R3/RRR3-12/3	1997.111	1996.257	-73.551	0.391	561.160	0.662	30	0.131	R.VSPVGFGASPLGHVFGDVPR.D
R3/RRR3-12/3	1997.204	1996.257	-26.650	0.311	614.969	0.583	33	0.117	R.VSPVGFGASPLGHVFGDVPR.D
R3/RRR3-12/3	1997.033	1996.257	-112.639	0.307	523.747	0.597	31	0.116	R.VSPVGFGASPLGHVFGDVPR.D
R3/RRR3-16/3	1581.993	1581.717	175.009	0.480	1660.476	0.437	29	0.178	K.NHAVHISQIGEGYR.A
R3/RRR3-17/3	1581.423	1581.717	-186.449	0.523	1367.168	0.554	29	0.175	K.NHAVHISQIGEGYR.A
R3/RRR3-17/3	1581.592	1581.717	-79.366	0.538	1399.119	0.526	27	0.172	K.NHAVHISQIGEGYR.A
R3/RRR3-17/3	1580.401	1581.717	-1469.889	0.316	609.487	0.332	22	0.093	K.NHAVHISQIGEGYR.A
R3/RRR3-9/2	1762.251	1762.985	-986.690	0.488	775.664	0.625	24	0.177	K.LLEATGISTVPGSGFGQK.E
R3/RRR3-9/2	1762.221	1762.985	-1004.077	0.436	873.113	0.569	25	0.175	K.LLEATGISTVPGSGFGQK.E
R3/RRR3-9/2	1764.356	1762.985	210.847	0.484	700.804	0.556	22	0.162	K.LLEATGISTVPGSGFGQK.E
R3/RRR3-5/2	1460.082	1458.752	226.695	0.377	782.633	0.175	15	0.124	-.MQAKAIADAAVAVAK.-
R3/RRR3-5/2	1459.597	1458.752	-106.667	0.291	547.040	0.161	14	0.120	-.MQAKAIADAAVAVAK.-
R3/RRR3-5/2	1459.270	1458.752	-331.466	0.301	571.661	0.224	14	0.120	-.MQAKAIADAAVAVAK.-
R3/RRR3-9/2	1550.183	1548.766	269.991	0.511	1207.672	0.560	19	0.199	R.APLSALLGELSASYR.R
R3/RRR3-22/2	1585.042	1585.739	-1074.139	0.477	1297.101	0.554	22	0.209	K.STGFGLIYDNLDAAK.K
R3/RRR3-21/2	1585.388	1585.739	-222.078	0.486	969.427	0.552	20	0.180	K.STGFGLIYDNLDAAK.K
R3/RRR3-22/2	1584.963	1585.739	-1124.404	0.448	1071.674	0.485	21	0.176	K.STGFGLIYDNLDAAK.K
R3/RRR3-21/2	1585.055	1585.739	-1066.019	0.430	1020.335	0.514	20	0.176	K.STGFGLIYDNLDAAK.K
R3/RRR3-22/2	1585.211	1585.739	-967.206	0.480	961.041	0.533	19	0.175	K.STGFGLIYDNLDAAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1584.535	1585.739	-1395.306	0.317	852.201	0.378	18	0.147	K.STGFGLIYDNLDAAK.K
R3/RRR3-13/2	1586.219	1585.739	303.300	0.364	106.414	0.452	12	0.128	-.STGFGLIYDNLDAAK.-
R3/RRR3-7/2	1457.223	1456.542	-219.765	0.453	1359.360	0.530	18	0.210	R.SFGFNTAVEEAQR.A
R3/RRR3-20/2	1238.921	1238.372	-365.318	0.452	1379.765	0.523	17	0.212	K.YSGNDLLGVTAK.V
R3/RRR3-1/3	1513.612	1513.593	12.601	0.509	1516.791	0.471	26	0.170	K.VLYHEDPNSPDAR.I
R3/RRR3-8/3	1512.529	1513.593	-1369.217	0.422	1507.825	0.412	25	0.156	K.VLYHEDPNSPDAR.I
R3/RRR3-8/3	1513.957	1513.593	241.142	0.505	1310.443	0.458	24	0.147	K.VLYHEDPNSPDAR.I
R3/RRR3-8/3	1513.494	1513.593	-66.029	0.470	1326.659	0.364	23	0.129	-.VLYHEDPNSPDAR.-
R3/RRR3-1/3	1513.199	1513.593	-261.567	0.454	1122.834	0.385	23	0.118	-.VLYHEDPNSPDAR.-
R3/RRR3-2/3	1514.613	1513.593	13.159	0.479	989.219	0.391	22	0.110	-.VLYHEDPNSPDAR.-
R3/RRR3-1/3	1513.512	1513.593	-54.137	0.436	817.665	0.420	20	0.110	-.VLYHEDPNSPDAR.-
R3/RRR3-2/3	1513.251	1513.593	-226.726	0.457	693.940	0.423	21	0.108	K.VLYHEDPNSPDAR.I
R3/RRR3-2/3	1513.198	1513.593	-262.296	0.452	797.047	0.403	22	0.108	K.VLYHEDPNSPDAR.I
R3/RRR3-7/3	1513.272	1513.593	-212.767	0.439	930.048	0.383	23	0.108	-.VLYHEDPNSPDAR.-
R3/RRR3-4/3	1513.581	1513.593	-8.269	0.463	697.135	0.401	23	0.106	K.VLYHEDPNSPDAR.I
R3/RRR3-4/3	1514.390	1513.593	-134.914	0.453	673.765	0.399	23	0.105	K.VLYHEDPNSPDAR.I
R3/RRR3-3/3	1513.948	1513.593	234.957	0.430	657.114	0.414	21	0.104	-.VLYHEDPNSPDAR.-
R3/RRR3-3/3	1513.448	1513.593	-96.369	0.432	794.735	0.359	23	0.101	-.VLYHEDPNSPDAR.-
R3/RRR3-3/3	1513.178	1513.593	-275.407	0.423	638.962	0.340	20	0.097	-.VLYHEDPNSPDAR.-
R3/RRR3-5/3	1513.950	1513.593	236.533	0.403	472.795	0.313	19	0.092	-.VLYHEDPNSPDAR.-
R3/RRR3-9/2	1996.445	1997.149	-856.105	0.519	1059.282	0.580	21	0.188	K.GFIDFDSDPWPVISDSAK.D
R3/RRR3-9/2	1996.258	1997.149	-950.454	0.418	890.449	0.339	18	0.140	K.GFIDFDSDPWPVISDSAK.D
R3/RRR3-10/3	1305.587	1305.594	-5.694	0.491	1610.789	0.437	24	0.172	R.HVVLITNVKPGK.L
R3/RRR3-15/3	1305.777	1305.594	140.440	0.316	791.154	0.254	20	0.086	R.HVVLITNVKPGK.L
R3/RRR3-4/2	1645.150	1645.790	-1000.064	0.395	1337.949	0.512	21	0.202	K.TVGAVAEVIEEEAEAK.L
R3/RRR3-24/2	1345.324	1345.486	-120.460	0.462	1191.894	0.566	18	0.203	R.HLVDQYLEATR.G
R3/RRR3-24/2	1345.265	1345.486	-164.607	0.422	1031.839	0.477	17	0.174	R.HLVDQYLEATR.G
R3/RRR3-23/2	1344.373	1345.486	-1576.535	0.283	638.964	0.316	14	0.137	R.HLVDQYLEATR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1345.469	1345.486	-12.249	0.319	476.194	0.257	13	0.134	R.HLVDQYLEATR.G
R3/RRR3-23/2	1345.442	1345.486	-32.816	0.242	473.034	0.258	13	0.130	-.HLVDQYLEATR.-
R3/RRR3-24/3	1346.030	1345.486	-339.806	0.423	1162.400	0.205	22	0.089	R.HLVDQYLEATR.G
R3/RRR3-14/3	1607.411	1606.808	-248.141	0.463	1377.013	0.509	28	0.167	K.ALAHQPVSVAIEASGR.N
R3/RRR3-14/3	1606.030	1606.808	-1110.463	0.400	1091.482	0.292	26	0.099	K.ALAHQPVSVAIEASGR.N
R3/RRR3-14/3	1606.339	1606.808	-292.972	0.364	644.597	0.314	22	0.089	-.ALAHQPVSVAIEASGR.-
R3/RRR3-21/2	1830.464	1831.128	-911.527	0.537	1395.353	0.516	27	0.215	K.IFEVAPSASQMFSFLR.N
R3/RRR3-21/2	1830.519	1831.128	-881.334	0.535	1389.829	0.512	27	0.213	K.IFEVAPSASQMFSFLR.N
R3/RRR3-21/2	1846.529	1847.127	-867.807	0.565	1263.697	0.531	25	0.203	K.IFEVAPSASQM*FSFLR.N
R3/RRR3-21/2	1846.363	1847.127	-958.269	0.554	1306.728	0.475	25	0.196	K.IFEVAPSASQM*FSFLR.N
R3/RRR3-21/2	1846.757	1847.127	-201.205	0.527	1242.036	0.483	24	0.191	K.IFEVAPSASQM*FSFLR.N
R3/RRR3-13/2	1560.037	1558.804	149.855	0.459	1485.478	0.477	20	0.212	R.LFYGPGGPYALFAGK.D
R3/RRR3-13/2	1558.634	1558.804	-109.081	0.455	1326.153	0.475	20	0.195	R.LFYGPGGPYALFAGK.D
R3/RRR3-14/2	1558.244	1558.804	-1003.666	0.271	1074.511	0.346	17	0.152	R.LFYGPGGPYALFAGK.D
R3/RRR3-15/2	1560.299	1558.804	318.305	0.360	553.679	0.396	14	0.136	-.LFYGPGGPYALFAGK.-
R3/RRR3-13/2	1558.168	1558.804	-1053.140	0.319	638.820	0.206	15	0.128	R.LFYGPGGPYALFAGK.D
R3/RRR3-4/3	1948.829	1950.056	-1146.237	0.471	865.684	0.599	30	0.140	R.YGAIWTGDNSADWDHLK.S
R3/RRR3-4/3	1949.755	1950.056	-155.025	0.463	523.922	0.563	25	0.116	R.YGAIWTGDNSADWDHLK.S
R3/RRR3-5/2	1494.403	1494.678	-184.720	0.487	907.117	0.588	21	0.181	R.LPATGEPIGQLQGGR.E
R3/RRR3-5/2	1494.229	1494.678	-301.424	0.482	933.121	0.571	21	0.180	R.LPATGEPIGQLQGGR.E
R3/RRR3-21/2	1186.637	1187.411	-1499.363	0.438	1558.431	0.448	19	0.217	K.AVVVLGSSEVVK.G
R3/RRR3-12/2	1265.052	1264.413	-286.346	0.509	1456.596	0.480	19	0.213	R.LTSQFAGADVVR.T
R3/RRR3-7/2	1546.509	1545.806	-193.143	0.543	748.543	0.579	22	0.173	K.LWPFVDQAATAVVK.E
R3/RRR3-20/2	1829.534	1828.960	-233.934	0.545	1190.976	0.545	21	0.194	R.VVGNSVSEFQSGFSDIR.T
R3/RRR3-20/2	1828.392	1828.960	-860.261	0.502	1015.930	0.528	20	0.176	R.VVGNSVSEFQSGFSDIR.T
R3/RRR3-1/2	1613.496	1612.682	-115.851	0.385	224.682	0.536	14	0.139	K.ANDGM*AEENGDAVM*R.N
R3/RRR3-10/2	1586.210	1586.689	-302.702	0.486	1079.176	0.582	21	0.193	K.GGLGNDAVILNSQDGR.S
R3/RRR3-10/2	1586.139	1586.689	-980.225	0.481	1016.407	0.572	21	0.186	K.GGLGNDAVILNSQDGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-10/2	1586.377	1586.689	-197.396	0.483	797.890	0.550	19	0.166	K.GGLGNDAVILNSQDGR.S
R3/RRR3-4/2	1474.250	1474.602	-239.484	0.510	1642.388	0.397	20	0.215	K.IQSNETSNVVQVR.T
R3/RRR3-4/2	1474.212	1474.602	-265.070	0.518	1462.591	0.428	19	0.201	K.IQSNETSNVVQVR.T
R3/RRR3-6/2	1258.906	1258.526	302.797	0.464	856.082	0.599	19	0.181	R.IPSSLCGIIGLK.T
R3/RRR3-6/2	1258.354	1258.526	-137.056	0.348	564.639	0.457	17	0.146	R.IPSSLCGIIGLK.T
R3/RRR3-4/3	1849.362	1849.909	-838.926	0.492	2166.048	0.083	28	0.141	K.EEEM*KEEEEHEEKK.E
R3/RRR3-4/3	1849.932	1849.909	12.463	0.515	1754.104	0.260	27	0.141	K.EEEM*KEEEEHEEKK.E
R3/RRR3-3/2	1502.717	1501.774	-38.099	0.374	765.979	0.290	16	0.134	-.ATPDMAVTLLEIAR.-
R3/RRR3-3/2	1503.108	1501.774	223.057	0.259	609.042	0.143	16	0.125	K.ATPDMAVTLLEIAR.I
R3/RRR3-3/3	1312.471	1312.505	-26.094	0.410	719.906	0.439	19	0.105	R.SFSRPVLHAAAR.V
R3/RRR3-4/3	1312.826	1312.505	244.605	0.356	897.126	0.389	20	0.103	R.SFSRPVLHAAAR.V
R3/RRR3-8/2	1473.114	1472.671	301.570	0.427	417.932	0.598	19	0.156	R.VAPAPPAGEPALPER.A
R3/RRR3-8/2	1472.241	1472.671	-292.786	0.367	447.196	0.569	19	0.152	R.VAPAPPAGEPALPER.A
R3/RRR3-8/2	1472.239	1472.671	-294.283	0.380	390.928	0.569	18	0.150	R.VAPAPPAGEPALPER.A
R3/RRR3-18/2	1363.766	1364.526	-1294.478	0.515	1296.707	0.520	18	0.202	R.IAASFDELEAVAK.Q
R3/RRR3-18/2	1364.303	1364.526	-163.566	0.213	595.154	0.200	13	0.125	R.IAASFDELEAVAK.Q
R3/RRR3-26/2	1591.466	1591.830	-229.308	0.387	1156.889	0.561	18	0.201	K.TLIIDYKPTIVNNS.-
R3/RRR3-21/2	1544.154	1544.817	-1079.745	0.394	1386.651	0.494	17	0.203	K.VIGEVLDIFNPTVK.M
R3/RRR3-10/3	1299.187	1299.420	-179.879	0.525	1034.594	0.567	22	0.146	R.HLSTLTGYHNR.T
R3/RRR3-11/3	1299.201	1299.420	-169.417	0.451	1156.270	0.475	23	0.134	R.HLSTLTGYHNR.T
R3/RRR3-10/3	1299.574	1299.420	118.358	0.483	1037.156	0.500	23	0.131	R.HLSTLTGYHNR.T
R3/RRR3-10/3	1300.636	1299.420	166.082	0.501	593.733	0.484	20	0.113	R.HLSTLTGYHNR.T
R3/RRR3-11/3	1298.263	1299.420	-1666.961	0.411	581.767	0.477	18	0.110	R.HLSTLTGYHNR.T
R3/RRR3-11/3	1298.456	1299.420	-1517.635	0.403	647.818	0.373	18	0.097	-.HLSTLTGYHNR.-
R3/RRR3-4/2	1875.694	1876.167	-252.525	0.450	678.908	0.598	21	0.164	K.IGGDPQIIQEFMQLASK.S
R3/RRR3-13/2	1380.896	1380.611	206.623	0.444	1381.263	0.493	18	0.205	K.VSYIDAILGTTVK.V
R3/RRR3-17/2	1938.403	1938.130	141.258	0.558	1219.175	0.525	21	0.192	K.YNVGQINSTQLTDAVWK.N
R3/RRR3-9/2	1311.019	1311.380	-276.025	0.571	1327.102	0.500	18	0.202	K.AGNEQFVTETSK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1393.144	1393.529	-277.331	0.509	1543.982	0.438	19	0.213	R.GFVISDWQGLDR.I
R3/RRR3-5/2	1394.114	1393.529	-298.567	0.553	1462.079	0.442	19	0.204	R.GFVISDWQGLDR.I
R3/RRR3-5/2	1394.053	1393.529	-342.758	0.534	1503.255	0.389	19	0.197	R.GFVISDWQGLDR.I
R3/RRR3-6/2	1392.536	1393.529	-1435.756	0.367	1466.488	0.353	18	0.187	R.GFVISDWQGLDR.I
R3/RRR3-6/2	1392.458	1393.529	-1491.758	0.357	1554.702	0.267	19	0.180	R.GFVISDWQGLDR.I
R3/RRR3-11/2	1415.079	1415.531	-320.447	0.531	1447.826	0.462	21	0.207	R.SPNELLNSEGGLGK.Q
R3/RRR3-11/2	1414.951	1415.531	-1119.758	0.490	1183.136	0.413	20	0.173	R.SPNELLNSEGGLGK.Q
R3/RRR3-6/2	1443.290	1443.623	-231.303	0.454	1368.332	0.480	17	0.202	K.SIDTETFLEFLK.T
R3/RRR3-6/2	1443.443	1443.623	-124.741	0.356	953.788	0.411	15	0.155	K.SIDTETFLEFLK.T
R3/RRR3-5/2	1787.939	1787.050	-62.015	0.518	832.037	0.581	20	0.176	R.LDQLIYIPLPDDKSR.M
R3/RRR3-5/2	1786.437	1787.050	-905.618	0.473	924.271	0.465	21	0.165	R.LDQLIYIPLPDDKSR.M
R3/RRR3-4/2	1787.717	1787.050	-186.397	0.534	973.324	0.421	21	0.160	R.LDQLIYIPLPDDKSR.M
R3/RRR3-4/2	1787.504	1787.050	255.037	0.538	772.869	0.488	19	0.159	R.LDQLIYIPLPDDKSR.M
R3/RRR3-5/2	1787.507	1787.050	256.543	0.528	840.379	0.403	20	0.151	R.LDQLIYIPLPDDKSR.M
R3/RRR3-2/2	1788.327	1787.050	155.783	0.505	629.328	0.480	17	0.151	R.LDQLIYIPLPDDKSR.M
R3/RRR3-2/2	1786.739	1787.050	-174.233	0.407	555.066	0.305	17	0.136	R.LDQLIYIPLPDDKSR.M
R3/RRR3-4/2	1785.743	1787.050	-1295.340	0.275	634.833	0.167	17	0.129	R.LDQLIYIPLPDDKSR.M
R3/RRR3-12/2	1548.262	1548.766	-974.076	0.430	1564.678	0.421	21	0.212	R.IPSFTKEQSELIR.G
R3/RRR3-14/2	1427.749	1426.704	32.014	0.480	913.714	0.577	17	0.179	R.IATVLM*YLSDVGK.G
R3/RRR3-14/2	1410.353	1410.704	-249.466	0.314	1093.291	0.261	16	0.144	R.IATVLMYLSDVGK.G
R3/RRR3-17/2	1573.445	1572.764	-203.129	0.476	1317.324	0.502	20	0.201	R.M*TLFNIFGDDASPK.V
R3/RRR3-17/2	1571.778	1572.764	-1267.727	0.394	1324.897	0.397	21	0.182	R.M*TLFNIFGDDASPK.V
R3/RRR3-17/2	1557.984	1556.765	141.172	0.462	1118.133	0.411	17	0.165	R.MTLFNIFGDDASPK.V
R3/RRR3-15/2	1556.968	1556.765	130.727	0.390	465.812	0.324	14	0.134	R.MTLFNIFGDDASPK.V
R3/RRR3-20/2	1616.617	1616.760	-88.961	0.498	1333.941	0.494	21	0.201	K.GQQPLQGDITAANFR.T
R3/RRR3-1/2	1972.636	1972.224	209.316	0.513	1138.956	0.498	21	0.179	R.IVTSFTSLVDSADFLEVK.N
R3/RRR3-13/2	1828.583	1828.059	-260.839	0.515	1351.040	0.484	22	0.199	R.ELGDFPLPIALVENSGR.C
R3/RRR3-17/2	1587.178	1586.726	285.760	0.488	1173.794	0.527	25	0.194	K.DLALPVSGVSAEENGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1586.338	1586.726	-245.408	0.491	1137.641	0.528	24	0.190	K.DLALPVSGVSAEENGK.A
R3/RRR3-17/2	1586.403	1586.726	-204.339	0.478	1035.294	0.492	23	0.175	K.DLALPVSGVSAEENGK.A
R3/RRR3-7/2	1226.134	1226.408	-223.638	0.432	1188.752	0.537	19	0.195	R.GIPSLVAIGADGR.T
R3/RRR3-7/2	1226.144	1226.408	-215.748	0.426	1194.510	0.523	20	0.194	R.GIPSLVAIGADGR.T
R3/RRR3-7/2	1226.046	1226.408	-296.155	0.449	1128.281	0.500	20	0.185	R.GIPSLVAIGADGR.T
R3/RRR3-7/2	1225.717	1226.408	-1383.234	0.297	886.595	0.394	16	0.149	R.GIPSLVAIGADGR.T
R3/RRR3-12/2	1322.283	1322.404	-92.281	0.487	1323.489	0.492	18	0.202	K.FDSGYYSNLQK.K
R3/RRR3-12/2	1612.799	1612.810	-6.955	0.456	1170.132	0.526	18	0.188	R.GFGFITFADPAVVDR.V
R3/RRR3-5/2	1562.165	1560.768	255.145	0.405	356.205	0.543	15	0.144	K.LPLEIGSVSEISCR.R
R3/RRR3-22/2	1123.971	1124.229	-230.240	0.399	1102.328	0.547	18	0.189	K.GISSSAVPYSR.N
R3/RRR3-22/2	1123.840	1124.229	-347.601	0.461	1087.488	0.480	18	0.180	K.GISSSAVPYSR.N
R3/RRR3-22/2	1123.817	1124.229	-368.090	0.429	822.626	0.494	16	0.163	K.GISSSAVPYSR.N
R3/RRR3-26/2	1188.575	1189.384	-1526.895	0.452	1424.583	0.459	18	0.204	K.LSAGIASILESK.L
R3/RRR3-26/2	1189.105	1189.384	-235.647	0.408	1252.750	0.446	18	0.185	K.LSAGIASILESK.L
R3/RRR3-26/2	1188.527	1189.384	-1567.235	0.459	923.799	0.454	17	0.163	K.LSAGIASILESK.L
R3/RRR3-12/2	1935.498	1936.189	-876.357	0.479	1163.821	0.519	22	0.185	R.VCGLAAVGSFADLIVADEK.Q
R3/RRR3-5/3	1961.927	1961.162	-119.865	0.484	764.709	0.549	32	0.124	R.IVLTDGASHAVDSSELAFK.L
R3/RRR3-4/2	1004.856	1005.109	-252.963	0.268	827.891	0.226	13	0.131	R.LGASLDWSR.E
R3/RRR3-21/3	1886.459	1885.022	231.981	0.149	1028.331	0.104	25	0.070	R.LEEGNLDPDELNLERK.L
R3/RRR3-20/2	1277.010	1277.363	-277.528	0.361	1414.839	0.451	18	0.200	R.EAAVETVLDSSR.Y
R3/RRR3-20/2	1277.135	1277.363	-179.524	0.339	961.630	0.459	17	0.162	R.EAAVETVLDSSR.Y
R3/RRR3-14/2	1532.305	1532.633	-215.069	0.409	1443.411	0.444	21	0.202	K.SVEGPYSGDPIEGPK.V
R3/RRR3-14/2	1532.211	1532.633	-276.292	0.470	1054.406	0.509	19	0.177	K.SVEGPYSGDPIEGPK.V
R3/RRR3-26/2	1314.125	1314.473	-266.056	0.392	1350.412	0.476	18	0.198	K.AIADILSNVNGAR.D
R3/RRR3-25/2	1314.278	1314.473	-149.204	0.377	824.419	0.434	16	0.152	K.AIADILSNVNGAR.D
R3/RRR3-26/2	1314.539	1314.473	49.866	0.334	459.661	0.485	16	0.144	K.AIADILSNVNGAR.D
R3/RRR3-17/2	1517.421	1517.708	-189.906	0.438	1345.410	0.474	21	0.199	R.VVYAPVLEVGEEGR.L
R3/RRR3-17/2	1516.855	1517.708	-1225.662	0.359	1381.747	0.182	21	0.152	R.VVYAPVLEVGEEGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1217.043	1217.266	-183.861	0.465	1377.422	0.468	16	0.202	R.DLGYLDDSYR.A
R3/RRR3-14/2	1218.194	1217.266	-59.662	0.490	1047.468	0.551	15	0.188	R.DLGYLDDSYR.A
R3/RRR3-14/2	1217.112	1217.266	-127.114	0.385	1290.277	0.394	16	0.180	R.DLGYLDDSYR.A
R3/RRR3-15/3	1925.237	1926.061	-950.320	0.440	729.100	0.575	30	0.127	K.GGRPIQM*STDHDPNVER.G
R3/RRR3-15/3	1925.255	1926.061	-940.867	0.440	558.979	0.534	27	0.115	K.GGRPIQM*STDHDPNVER.G
R3/RRR3-15/3	1925.820	1926.061	-125.765	0.438	653.795	0.512	28	0.114	K.GGRPIQM*STDHDPNVER.G
R3/RRR3-4/2	1487.425	1486.698	-183.447	0.427	1469.446	0.418	17	0.200	R.WIELGAFYPFSR.D
R3/RRR3-23/2	1235.302	1235.486	-149.129	0.528	1433.709	0.464	18	0.207	R.KVVGCSCVVVK.D
R3/RRR3-23/2	1235.682	1235.486	159.267	0.448	1395.657	0.370	17	0.184	R.KVVGCSCVVVK.D
R3/RRR3-23/2	1235.159	1235.486	-265.818	0.541	915.354	0.432	16	0.160	R.KVVGCSCVVVK.D
R3/RRR3-22/2	1235.116	1235.486	-300.126	0.391	915.921	0.332	15	0.147	R.KVVGCSCVVVK.D
R3/RRR3-15/3	1736.959	1737.725	-1019.427	0.331	310.765	0.576	22	0.108	R.GYGDSYQNDRDYQR.K
R3/RRR3-15/3	1737.460	1737.725	-152.968	0.324	220.531	0.537	19	0.104	R.GYGDSYQNDRDYQR.K
R3/RRR3-18/2	1975.874	1975.188	-159.848	0.506	859.572	0.538	19	0.165	R.IYDADPTVLDALANQNIK.V
R3/RRR3-18/2	1976.193	1975.188	2.069	0.476	872.983	0.528	19	0.165	R.IYDADPTVLDALANQNIK.V
R3/RRR3-18/2	1975.940	1975.188	-126.134	0.419	395.213	0.436	16	0.137	R.IYDADPTVLDALANQNIK.V
R3/RRR3-10/2	1388.420	1388.509	-64.164	0.477	1653.904	0.360	20	0.209	K.LADQIDQSAGITR.L
R3/RRR3-15/2	1712.522	1711.895	-218.103	0.502	1201.708	0.508	21	0.191	R.QVVSTLYSLEDTISR.R
R3/RRR3-15/2	1712.971	1711.895	44.415	0.479	1031.516	0.532	19	0.179	R.QVVSTLYSLEDTISR.R
R3/RRR3-14/2	1542.814	1543.661	-1200.753	0.462	1194.082	0.513	24	0.192	K.LLAESQPEGDGATVR.R
R3/RRR3-8/2	1159.104	1159.230	-108.864	0.360	1303.207	0.477	16	0.194	R.SAVDYFEATR.A
R3/RRR3-8/2	1158.455	1159.230	-1537.107	0.350	1303.113	0.454	15	0.189	R.SAVDYFEATR.A
R3/RRR3-8/2	1159.000	1159.230	-199.407	0.424	1271.086	0.429	16	0.185	R.SAVDYFEATR.A
R3/RRR3-21/3	1554.885	1553.788	61.993	0.466	1427.015	0.441	24	0.155	R.LPLRDVLADTGIGGR.A
R3/RRR3-15/3	1553.370	1553.788	-270.370	0.401	1190.356	0.248	23	0.096	-.LPLRDVLADTGIGGR.-
R3/RRR3-8/3	1499.650	1499.653	-1.692	0.457	490.011	0.536	22	0.115	R.HTSKPEAEYPALR.F
R3/RRR3-8/3	1499.516	1499.653	-91.589	0.434	492.442	0.519	20	0.111	R.HTSKPEAEYPALR.F
R3/RRR3-8/3	1499.752	1499.653	66.517	0.431	350.538	0.503	20	0.109	R.HTSKPEAEYPALR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	1550.384	1550.781	-257.101	0.519	1148.258	0.509	21	0.188	R.LLSSTNQPSFLSKK.D
R3/RRR3-7/2	1551.438	1550.781	-222.203	0.579	1053.852	0.538	20	0.185	R.LLSSTNQPSFLSKK.D
R3/RRR3-7/2	1550.101	1550.781	-1087.293	0.479	1090.087	0.434	19	0.169	R.LLSSTNQPSFLSKK.D
R3/RRR3-8/2	1448.938	1449.677	-1203.936	0.407	1221.536	0.498	18	0.186	R.ASASAVAFGLGLLSGK.G
R3/RRR3-7/2	1978.282	1978.234	24.223	0.458	824.016	0.547	19	0.164	R.ELTAPFVDDGLIEVVGFR.D
R3/RRR3-7/2	1978.229	1978.234	-2.699	0.388	622.877	0.488	18	0.146	R.ELTAPFVDDGLIEVVGFR.D
R3/RRR3-7/2	1977.708	1978.234	-773.891	0.311	311.090	0.438	15	0.135	R.ELTAPFVDDGLIEVVGFR.D
R3/RRR3-27/2	1109.009	1109.257	-224.293	0.549	1374.460	0.458	17	0.201	R.YIEATGIVSR.A
R3/RRR3-27/2	1108.236	1109.257	-1829.042	0.412	1389.101	0.387	17	0.188	R.YIEATGIVSR.A
R3/RRR3-27/2	1109.098	1109.257	-143.799	0.502	1188.087	0.427	17	0.179	R.YIEATGIVSR.A
R3/RRR3-1/2	1790.073	1788.971	57.344	0.499	957.866	0.497	19	0.166	R.AADLLNDESPLLTQCK.A
R3/RRR3-12/2	1088.883	1089.181	-274.428	0.503	1616.131	0.375	17	0.209	K.LGGELTVDER.N
R3/RRR3-1/2	1893.121	1892.187	-35.158	0.438	368.718	0.497	17	0.139	R.FIVSGGAPLSVAVEEFLR.V
R3/RRR3-5/2	1234.187	1234.347	-129.423	0.441	1579.289	0.375	20	0.204	R.AAGGFGGITVNNR.A
R3/RRR3-24/2	1274.277	1274.446	-133.230	0.557	1510.720	0.415	18	0.204	K.LNNETVTIELK.N
R3/RRR3-24/2	1274.237	1274.446	-164.558	0.493	907.142	0.358	16	0.150	K.LNNETVTIELK.N
R3/RRR3-25/2	1274.091	1274.446	-278.932	0.291	282.462	0.366	10	0.117	-.LNNETVTIELK.-
R3/RRR3-24/3	1577.053	1577.785	-1102.101	0.438	1417.655	0.440	31	0.148	K.RGEEVLKAEEM*AAK.Y
R3/RRR3-14/3	1561.400	1561.786	-248.199	0.509	1210.062	0.428	25	0.132	K.RGEEVLKAEEMAAK.Y
R3/RRR3-14/3	1561.323	1561.786	-297.498	0.484	1212.842	0.423	26	0.131	K.RGEEVLKAEEMAAK.Y
R3/RRR3-14/3	1577.649	1577.785	-87.012	0.398	1147.197	0.350	31	0.109	K.RGEEVLKAEEM*AAK.Y
R3/RRR3-14/3	1577.474	1577.785	-197.857	0.399	1132.737	0.351	31	0.109	K.RGEEVLKAEEM*AAK.Y
R3/RRR3-24/3	1578.142	1577.785	226.294	0.480	1148.572	0.319	30	0.105	K.RGEEVLKAEEM*AAK.Y
R3/RRR3-16/3	1577.776	1577.785	-5.873	0.419	1015.693	0.311	29	0.099	K.RGEEVLKAEEM*AAK.Y
R3/RRR3-14/3	1577.328	1577.785	-290.673	0.430	966.473	0.266	28	0.093	K.RGEEVLKAEEM*AAK.Y
R3/RRR3-26/2	1058.356	1059.243	-1788.106	0.399	214.794	0.477	13	0.150	R.EKVHFAISK.W
R3/RRR3-26/2	1058.834	1059.243	-387.442	0.276	211.070	0.345	13	0.142	R.EKVHFAISK.W
R3/RRR3-26/2	1058.208	1059.243	-1929.050	0.308	167.829	0.399	12	0.140	-.EKVHFAISK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-19/2	1160.868	1161.204	-290.423	0.458	1775.361	0.293	20	0.209	R.GGEGEEVGSLAR.R
R3/RRR3-19/2	1161.098	1161.204	-92.332	0.442	1699.833	0.308	20	0.204	R.GGEGEEVGSLAR.R
R3/RRR3-9/2	1628.341	1628.764	-260.432	0.473	1113.129	0.517	21	0.184	R.GDELLTSYPGLGSYR.V
R3/RRR3-14/3	1919.089	1918.183	-49.235	0.369	571.991	0.574	23	0.115	R.VATNPAIIVGLHPCGGNAR.Q
R3/RRR3-14/3	1917.882	1918.183	-157.729	0.298	425.733	0.428	22	0.090	-.VATNPAIIVGLHPCGGNAR.-
R3/RRR3-21/2	1148.206	1147.304	-85.691	0.529	987.206	0.526	18	0.182	K.IGSLVDVQTSK.D
R3/RRR3-22/2	1147.110	1147.304	-169.346	0.465	1076.768	0.488	18	0.180	K.IGSLVDVQTSK.D
R3/RRR3-22/2	1146.858	1147.304	-389.626	0.353	927.255	0.448	18	0.162	K.IGSLVDVQTSK.D
R3/RRR3-22/2	1146.431	1147.304	-1638.774	0.364	747.368	0.411	17	0.151	K.IGSLVDVQTSK.D
R3/RRR3-21/2	1146.581	1147.304	-1507.215	0.328	776.169	0.412	16	0.150	K.IGSLVDVQTSK.D
R3/RRR3-21/2	1146.550	1147.304	-1534.593	0.303	769.605	0.422	16	0.149	K.IGSLVDVQTSK.D
R3/RRR3-1/2	1883.069	1884.165	-1116.818	0.431	708.477	0.558	22	0.158	K.GPDVVGSFGLLQPLADGLK.L
R3/RRR3-13/3	1671.520	1671.792	-163.287	0.476	1411.743	0.433	29	0.150	R.TPGAGATEVFVHDVDR.H
R3/RRR3-13/3	1671.781	1671.792	-6.607	0.392	691.822	0.464	22	0.106	R.TPGAGATEVFVHDVDR.H
R3/RRR3-18/2	1161.951	1161.375	-366.652	0.463	1427.208	0.432	18	0.200	K.LLFLGLDNAGK.T
R3/RRR3-19/2	1161.385	1161.375	8.264	0.455	1291.053	0.439	18	0.189	K.LLFLGLDNAGK.T
R3/RRR3-19/2	1161.198	1161.375	-153.690	0.564	1320.885	0.424	18	0.187	K.LLFLGLDNAGK.T
R3/RRR3-19/2	1160.998	1161.375	-325.824	0.447	1288.273	0.405	17	0.181	K.LLFLGLDNAGK.T
R3/RRR3-18/2	1161.225	1161.375	-129.963	0.389	1292.973	0.362	17	0.174	K.LLFLGLDNAGK.T
R3/RRR3-18/2	1161.209	1161.375	-143.672	0.440	1257.284	0.372	18	0.174	K.LLFLGLDNAGK.T
R3/RRR3-9/2	1374.530	1374.569	-28.380	0.416	1189.792	0.492	16	0.186	R.YATNAVTAFIFR.E
R3/RRR3-8/2	1374.493	1374.569	-55.282	0.403	1191.581	0.389	17	0.170	R.YATNAVTAFIFR.E
R3/RRR3-8/2	1373.960	1374.569	-1174.196	0.351	866.511	0.491	16	0.162	R.YATNAVTAFIFR.E
R3/RRR3-8/2	1374.531	1374.569	-27.400	0.452	778.084	0.480	16	0.159	R.YATNAVTAFIFR.E
R3/RRR3-9/2	1375.157	1374.569	-300.190	0.394	695.772	0.410	16	0.148	R.YATNAVTAFIFR.E
R3/RRR3-9/2	1373.718	1374.569	-1351.054	0.410	667.635	0.434	14	0.147	R.YATNAVTAFIFR.E
R3/RRR3-8/2	1247.434	1246.480	-37.455	0.375	1141.287	0.510	16	0.184	R.ALLVGINYPGTK.A
R3/RRR3-8/2	1247.284	1246.480	-157.611	0.319	1116.917	0.441	16	0.170	R.ALLVGINYPGTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/2	1246.846	1246.480	294.433	0.266	586.509	0.500	15	0.146	R.ALLVGINYPGTK.A
R3/RRR3-15/2	1247.218	1246.480	-211.022	0.295	475.828	0.433	13	0.140	R.ALLVGINYPGTK.A
R3/RRR3-8/2	1247.227	1246.480	-203.953	0.229	543.876	0.395	15	0.137	R.ALLVGINYPGTK.A
R3/RRR3-23/3	1320.092	1319.531	-333.497	0.504	1603.354	0.367	24	0.151	K.YSDRIPVIVEK.A
R3/RRR3-4/2	1943.816	1944.307	-253.375	0.444	1066.262	0.492	23	0.174	K.LLVFQSVLPSLGVGSLSAR.E
R3/RRR3-5/2	1944.417	1944.307	56.696	0.459	807.335	0.496	23	0.159	K.LLVFQSVLPSLGVGSLSAR.E
R3/RRR3-2/2	1944.116	1944.307	-98.599	0.295	518.011	0.221	17	0.127	K.LLVFQSVLPSLGVGSLSAR.E
R3/RRR3-4/3	1943.555	1944.307	-904.324	0.276	1054.838	0.278	26	0.091	K.LLVFQSVLPSLGVGSLSAR.E
R3/RRR3-7/2	1333.620	1333.518	76.420	0.436	1080.436	0.509	16	0.177	K.AGLINAIAVGDYR.S
R3/RRR3-13/3	1951.777	1951.175	-204.359	0.451	1254.678	0.473	30	0.145	K.SSAGYQAPLHAEPIKPQR.Y
R3/RRR3-13/3	1950.621	1951.175	-799.239	0.401	1076.130	0.489	27	0.133	K.SSAGYQAPLHAEPIKPQR.Y
R3/RRR3-13/3	1950.867	1951.175	-158.295	0.444	1262.376	0.381	29	0.126	K.SSAGYQAPLHAEPIKPQR.Y
R3/RRR3-7/2	1147.238	1147.309	-62.391	0.480	1153.981	0.496	18	0.185	K.FAGVLTSAPAGR.R
R3/RRR3-7/2	1587.425	1587.754	-207.447	0.523	1543.724	0.385	23	0.201	R.NCPEFAFSFLGAAR.L
R3/RRR3-7/2	1587.156	1587.754	-1009.914	0.487	1302.683	0.415	22	0.184	R.NCPEFAFSFLGAAR.L
R3/RRR3-7/2	1586.305	1587.754	-1548.502	0.420	1551.175	0.239	22	0.174	R.NCPEFAFSFLGAAR.L
R3/RRR3-9/2	1435.208	1435.650	-309.383	0.457	1380.765	0.432	22	0.195	R.VQLAQLGSATGVYK.T
R3/RRR3-9/2	1435.233	1435.650	-291.549	0.416	773.577	0.431	19	0.152	R.VQLAQLGSATGVYK.T
R3/RRR3-9/2	1434.428	1435.650	-1553.781	0.267	418.735	0.370	15	0.134	R.VQLAQLGSATGVYK.T
R3/RRR3-9/2	1361.268	1361.528	-191.543	0.495	1421.720	0.420	17	0.197	R.LIQENQAEFLR.L
R3/RRR3-5/2	1747.457	1746.944	-279.324	0.470	877.561	0.529	17	0.165	K.NWNFTEQGLPADLIK.R
R3/RRR3-22/2	1898.595	1898.064	-247.931	0.511	637.685	0.513	23	0.158	K.IFTQFWDEEGIANAQK.S
R3/RRR3-22/2	1898.101	1898.064	19.183	0.553	695.551	0.503	22	0.158	K.IFTQFWDEEGIANAQK.S
R3/RRR3-2/2	1657.231	1655.834	240.213	0.458	754.731	0.497	19	0.156	R.SQHTADVVSLLSEIR.I
R3/RRR3-6/2	1291.308	1291.561	-196.232	0.529	1355.099	0.442	19	0.194	R.TLATDVLFGLLK.E
R3/RRR3-14/2	1659.381	1659.735	-213.946	0.485	985.899	0.517	19	0.173	K.SGGLESEKDYPYTGR.D
R3/RRR3-14/2	1659.128	1659.735	-971.713	0.474	968.309	0.520	19	0.173	K.SGGLESEKDYPYTGR.D
R3/RRR3-14/3	1659.728	1659.735	-4.479	0.508	1286.448	0.498	28	0.154	K.SGGLESEKDYPYTGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/3	1659.446	1659.735	-175.026	0.467	1139.303	0.531	28	0.148	K.SGGLESEKDYPYTGR.D
R3/RRR3-15/3	1659.512	1659.735	-134.736	0.518	1219.073	0.495	28	0.147	K.SGGLESEKDYPYTGR.D
R3/RRR3-15/3	1658.509	1659.735	-1346.294	0.459	1072.055	0.503	26	0.137	K.SGGLESEKDYPYTGR.D
R3/RRR3-14/3	1659.158	1659.735	-953.476	0.472	1048.066	0.477	26	0.130	K.SGGLESEKDYPYTGR.D
R3/RRR3-13/3	1659.484	1659.735	-152.114	0.325	719.573	0.323	21	0.094	K.SGGLESEKDYPYTGR.D
R3/RRR3-4/2	1996.117	1995.258	-71.005	0.404	625.090	0.519	15	0.145	R.YVNLGPIVDFCVVDLDR.Q
R3/RRR3-24/2	1339.251	1338.535	-212.794	0.537	1161.666	0.482	20	0.185	K.VSGVEIVPDPVAR.G
R3/RRR3-25/2	1338.333	1338.535	-150.822	0.508	1132.220	0.454	20	0.178	K.VSGVEIVPDPVAR.G
R3/RRR3-24/2	1338.278	1338.535	-192.272	0.462	1092.269	0.441	20	0.173	K.VSGVEIVPDPVAR.G
R3/RRR3-25/2	1338.182	1338.535	-264.292	0.498	965.405	0.426	19	0.162	K.VSGVEIVPDPVAR.G
R3/RRR3-24/2	1337.601	1338.535	-1450.328	0.373	1137.893	0.337	20	0.160	K.VSGVEIVPDPVAR.G
R3/RRR3-25/2	1337.997	1338.535	-1152.407	0.381	953.744	0.376	19	0.155	K.VSGVEIVPDPVAR.G
R3/RRR3-23/2	1337.695	1338.535	-1379.383	0.326	512.791	0.329	15	0.137	K.VSGVEIVPDPVAR.G
R3/RRR3-23/2	1337.616	1338.535	-1438.961	0.297	647.061	0.330	14	0.136	-.VSGVEIVPDPVAR.-
R3/RRR3-12/2	1249.099	1249.357	-206.588	0.467	878.544	0.529	16	0.172	K.TGFTGGLNYYR.C
R3/RRR3-12/2	1249.468	1249.357	89.406	0.531	921.986	0.463	17	0.166	K.TGFTGGLNYYR.C
R3/RRR3-12/2	1249.074	1249.357	-227.176	0.466	762.881	0.459	16	0.157	K.TGFTGGLNYYR.C
R3/RRR3-9/3	1785.707	1785.979	-152.229	0.407	666.690	0.539	28	0.118	R.LEYQSRPSISGVSSFK.N
R3/RRR3-9/3	1785.932	1785.979	-26.341	0.450	527.188	0.493	27	0.110	R.LEYQSRPSISGVSSFK.N
R3/RRR3-9/3	1785.822	1785.979	-87.944	0.311	371.206	0.377	20	0.094	R.LEYQSRPSISGVSSFK.N
R3/RRR3-13/2	1267.918	1268.491	-1243.913	0.392	1613.701	0.334	18	0.199	R.IVVAGNQIAVQR.T
R3/RRR3-13/2	1268.152	1268.491	-267.688	0.379	1453.567	0.413	17	0.197	R.IVVAGNQIAVQR.T
R3/RRR3-23/3	1442.214	1442.517	-210.855	0.425	1174.309	0.487	25	0.140	R.ALAADHDASASAVSR.R
R3/RRR3-23/3	1441.848	1442.517	-1160.911	0.426	813.632	0.384	23	0.098	-.ALAADHDASASAVSR.-
R3/RRR3-13/3	1596.501	1596.764	-164.959	0.462	1004.328	0.516	26	0.133	K.TAGKDLASDKTTYPK.L
R3/RRR3-13/3	1596.745	1596.764	-11.902	0.481	826.130	0.509	25	0.121	K.TAGKDLASDKTTYPK.L
R3/RRR3-1/2	1542.546	1541.620	-48.459	0.474	569.548	0.502	19	0.156	R.ISAEDETSGM*DLTR.H
R3/RRR3-1/2	1542.478	1541.620	-92.357	0.463	424.760	0.519	19	0.155	R.ISAEDETSGM*DLTR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-11/2	1542.921	1541.620	195.644	0.460	430.887	0.500	19	0.153	R.ISAEDETSGM*DLTR.H
R3/RRR3-11/2	1542.955	1541.620	217.303	0.393	305.157	0.468	18	0.148	R.ISAEDETSGM*DLTR.H
R3/RRR3-11/2	1543.048	1541.620	277.594	0.302	238.025	0.486	18	0.146	R.ISAEDETSGM*DLTR.H
R3/RRR3-4/2	1542.811	1541.620	123.997	0.350	250.839	0.317	17	0.143	R.ISAEDETSGM*DLTR.H
R3/RRR3-6/2	1542.985	1541.620	236.898	0.319	182.568	0.314	14	0.139	-.ISAEDETSGM*DLTR.-
R3/RRR3-5/2	1543.064	1541.620	288.382	0.188	124.174	0.348	14	0.139	R.ISAEDETSGM*DLTR.H
R3/RRR3-16/2	1608.167	1608.731	-975.478	0.395	1151.668	0.487	19	0.178	K.SAVSVVEGENAFDGVK.Q
R3/RRR3-7/2	1933.628	1934.210	-820.154	0.425	595.686	0.524	15	0.145	K.FPGGNYVMGNYLLNAFR.W
R3/RRR3-9/3	1783.001	1783.021	-11.036	0.488	666.486	0.509	29	0.116	R.FAVEVIDAVVGEIGAHR.V
R3/RRR3-9/3	1782.655	1783.021	-205.855	0.431	665.898	0.503	28	0.113	R.FAVEVIDAVVGEIGAHR.V
R3/RRR3-9/3	1783.247	1783.021	126.970	0.408	563.648	0.424	27	0.102	R.FAVEVIDAVVGEIGAHR.V
R3/RRR3-17/2	1472.274	1471.638	-247.955	0.426	804.410	0.529	19	0.163	R.SSAPDLPSLLLDSR.I
R3/RRR3-12/2	1244.855	1245.408	-1251.222	0.415	1227.854	0.465	18	0.185	K.NSLSGTIPASLGK.I
R3/RRR3-11/2	1245.190	1245.408	-175.280	0.403	1251.207	0.445	19	0.184	K.NSLSGTIPASLGK.I
R3/RRR3-7/3	1360.984	1360.414	-316.685	0.481	1285.875	0.439	21	0.139	K.HDNEGKEFVER.I
R3/RRR3-7/3	1359.557	1360.414	-1369.999	0.488	1331.292	0.423	22	0.138	K.HDNEGKEFVER.I
R3/RRR3-9/3	1359.769	1360.414	-1213.653	0.302	845.626	0.239	20	0.086	K.HDNEGKEFVER.I
R3/RRR3-7/2	1738.324	1737.936	224.218	0.471	1203.788	0.457	19	0.181	R.WPNVIVQFEDFQSK.W
R3/RRR3-20/3	1772.615	1772.935	-181.189	0.480	902.286	0.508	26	0.124	K.TSQKPVSPEDGEEIKK.K
R3/RRR3-12/2	1520.899	1519.688	139.784	0.303	328.230	0.530	18	0.143	R.QALNNLQATVSGFR.F
R3/RRR3-12/2	1520.867	1519.688	118.373	0.335	350.676	0.490	17	0.142	R.QALNNLQATVSGFR.F
R3/RRR3-7/2	1452.214	1452.591	-260.992	0.453	437.469	0.478	17	0.143	-.SEPIPEVNDQPVK.-
R3/RRR3-28/3	1706.983	1707.819	-1078.424	0.406	856.859	0.533	25	0.125	K.CM*SYCSGHSGPCCK.W
R3/RRR3-28/3	1707.354	1707.819	-273.230	0.393	723.467	0.500	25	0.113	K.CM*SYCSGHSGPCCK.W
R3/RRR3-19/2	1082.417	1082.232	171.638	0.365	992.979	0.516	17	0.175	R.YGSLTGLSGVK.V
R3/RRR3-21/2	1081.958	1082.232	-253.665	0.364	778.802	0.525	16	0.163	R.YGSLTGLSGVK.V
R3/RRR3-20/2	1082.066	1082.232	-153.614	0.358	841.785	0.486	16	0.161	R.YGSLTGLSGVK.V
R3/RRR3-23/2	1083.005	1082.232	-209.895	0.348	640.340	0.404	15	0.146	R.YGSLTGLSGVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-23/2	1083.301	1082.232	63.562	0.286	710.356	0.394	15	0.144	R.YGSLTGLSGVK.V
R3/RRR3-21/2	1081.764	1082.232	-434.236	0.189	598.345	0.311	15	0.133	R.YGSLTGLSGVK.V
R3/RRR3-11/2	1681.739	1680.820	-47.936	0.359	233.622	0.453	17	0.144	R.DTFVGTYNYM*APER.I
R3/RRR3-11/2	1681.834	1680.820	8.413	0.310	223.091	0.438	16	0.140	R.DTFVGTYNYM*APER.I
R3/RRR3-11/2	1681.182	1680.820	215.975	0.272	252.124	0.326	15	0.136	R.DTFVGTYNYM*APER.I
R3/RRR3-3/2	1020.815	1021.152	-331.048	0.354	719.810	0.522	13	0.157	R.ALGSTPGVYR.V
R3/RRR3-3/2	1020.317	1021.152	-1803.470	0.232	563.912	0.426	14	0.138	R.ALGSTPGVYR.V
R3/RRR3-3/2	1020.789	1021.152	-356.604	0.301	491.910	0.284	13	0.135	R.ALGSTPGVYR.V
R3/RRR3-7/2	1568.456	1568.712	-164.159	0.362	911.316	0.514	16	0.163	K.NNCM*LGM*GSGQPNR.L
R3/RRR3-6/2	1138.718	1138.296	372.496	0.291	443.713	0.547	14	0.142	K.AIVSEYAVTGK.D
R3/RRR3-3/2	1760.116	1760.027	50.738	0.414	486.782	0.490	21	0.144	K.SFASSGIPAPTLLSAALR.V
R3/RRR3-2/2	1326.789	1327.555	-1335.353	0.427	1049.231	0.469	16	0.170	R.VGQIIAQLLSER.L
R3/RRR3-7/3	1831.064	1830.975	49.165	0.430	1158.992	0.456	25	0.132	R.FGELTTEYGKPPGYDR.V
R3/RRR3-24/3	1926.376	1925.291	44.445	0.491	1658.522	0.317	28	0.146	R.RYLQMIQKNSIFNLR.S
R3/RRR3-24/3	1926.811	1925.291	-249.359	0.453	1502.395	0.242	28	0.114	R.RYLQMIQKNSIFNLR.S
R3/RRR3-24/3	1926.338	1925.291	24.711	0.418	1291.038	0.133	25	0.084	R.RYLQMIQKNSIFNLR.S
R3/RRR3-24/3	1432.638	1432.567	50.105	0.441	759.331	0.520	26	0.121	R.VTGGGHTSQVYAVR.Q
R3/RRR3-23/3	1432.373	1432.567	-135.673	0.414	607.565	0.546	26	0.118	R.VTGGGHTSQVYAVR.Q
R3/RRR3-23/3	1432.987	1432.567	294.498	0.414	661.106	0.496	27	0.113	R.VTGGGHTSQVYAVR.Q
R3/RRR3-24/3	1432.337	1432.567	-160.679	0.442	561.754	0.467	25	0.109	R.VTGGGHTSQVYAVR.Q
R3/RRR3-23/3	1432.658	1432.567	64.205	0.410	379.478	0.458	23	0.108	R.VTGGGHTSQVYAVR.Q
R3/RRR3-24/3	1432.578	1432.567	7.673	0.431	684.309	0.429	28	0.107	R.VTGGGHTSQVYAVR.Q
R3/RRR3-1/2	1289.329	1288.353	-18.575	0.430	617.673	0.476	18	0.146	K.ISASGGNGLAGGGGGR.V
R3/RRR3-15/3	1819.179	1819.141	20.748	0.519	936.973	0.487	29	0.125	K.LPNNAVAPSLFFFRPK.N
R3/RRR3-15/3	1818.655	1819.141	-268.060	0.481	863.809	0.473	27	0.118	K.LPNNAVAPSLFFFRPK.N
R3/RRR3-15/3	1819.249	1819.141	59.311	0.422	526.736	0.384	21	0.096	K.LPNNAVAPSLFFFRPK.N
R3/RRR3-5/2	1776.805	1777.014	-117.668	0.472	1249.231	0.448	23	0.186	K.TMEINPENAIMDELR.K
R3/RRR3-5/2	1792.922	1793.013	-51.109	0.407	1358.683	0.268	21	0.162	K.TMEINPENAIM*DELR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1776.368	1777.014	-929.499	0.407	875.522	0.386	20	0.150	K.TMEINPENAIMDELR.K
R3/RRR3-19/2	1260.127	1260.376	-198.173	0.435	1366.833	0.414	18	0.189	R.LGGGQQEVCGVR.E
R3/RRR3-19/2	1259.985	1260.376	-311.402	0.466	1158.287	0.492	17	0.185	R.LGGGQQEVCGVR.E
R3/RRR3-24/3	1786.294	1786.786	-276.000	0.379	571.704	0.520	25	0.107	K.DGEEESSGVVDYDKEK.K
R3/RRR3-9/3	1692.821	1692.808	7.615	0.400	873.114	0.509	29	0.122	R.SFDVNKPGSEVDEIR.G
R3/RRR3-9/3	1693.889	1692.808	47.473	0.383	379.489	0.507	24	0.108	R.SFDVNKPGSEVDEIR.G
R3/RRR3-9/3	1692.447	1692.808	-213.970	0.340	433.898	0.513	25	0.106	R.SFDVNKPGSEVDEIR.G
R3/RRR3-7/2	1064.668	1065.334	-1569.702	0.344	604.507	0.540	17	0.156	K.AVKPVLVGGPK.M
R3/RRR3-7/2	1065.185	1065.334	-140.302	0.317	672.556	0.522	18	0.156	K.AVKPVLVGGPK.M
R3/RRR3-7/2	1064.639	1065.334	-1597.115	0.309	558.087	0.475	17	0.148	K.AVKPVLVGGPK.M
R3/RRR3-6/2	1065.044	1065.334	-272.753	0.285	511.367	0.459	16	0.144	K.AVKPVLVGGPK.M
R3/RRR3-6/3	1065.219	1065.334	-108.673	0.435	957.534	0.377	22	0.107	K.AVKPVLVGGPK.M
R3/RRR3-1/3	1065.615	1065.334	264.584	0.378	827.969	0.375	20	0.103	K.AVKPVLVGGPK.M
R3/RRR3-4/3	1065.387	1065.334	49.506	0.361	704.691	0.265	19	0.092	K.AVKPVLVGGPK.M
R3/RRR3-6/3	1065.235	1065.334	-93.240	0.402	749.376	0.312	19	0.092	-.AVKPVLVGGPK.-
R3/RRR3-7/3	1065.507	1065.334	162.571	0.356	786.660	0.240	19	0.090	K.AVKPVLVGGPK.M
R3/RRR3-6/3	1065.440	1065.334	99.837	0.342	661.524	0.284	18	0.088	-.AVKPVLVGGPK.-
R3/RRR3-2/3	1065.686	1065.334	331.087	0.347	590.148	0.286	18	0.086	-.AVKPVLVGGPK.-
R3/RRR3-2/3	1065.341	1065.334	6.411	0.333	625.073	0.298	18	0.084	-.AVKPVLVGGPK.-
R3/RRR3-4/3	1065.251	1065.334	-78.412	0.367	579.778	0.250	17	0.079	-.AVKPVLVGGPK.-
R3/RRR3-25/2	1320.197	1320.516	-242.482	0.461	939.538	0.501	15	0.168	R.TLADNPVVIYSK.S
R3/RRR3-25/2	1320.068	1320.516	-340.171	0.297	1038.122	0.269	16	0.144	-.TLADNPVVIYSK.-
R3/RRR3-8/2	1083.632	1083.222	379.455	0.464	734.524	0.507	12	0.158	K.YSLVSNFPR.V
R3/RRR3-8/2	1390.959	1390.528	310.316	0.448	1384.626	0.405	18	0.189	K.IVFANGSQDPWR.H
R3/RRR3-8/2	1390.128	1390.528	-288.502	0.416	1012.271	0.388	16	0.157	K.IVFANGSQDPWR.H
R3/RRR3-22/2	1394.649	1395.573	-1383.475	0.397	771.467	0.523	20	0.161	R.GAAAAAAPAVQHM*GR.-
R3/RRR3-22/2	1395.101	1395.573	-339.540	0.415	823.462	0.459	21	0.157	R.GAAAAAAPAVQHM*GR.-
R3/RRR3-22/2	1394.959	1395.573	-1160.230	0.409	567.245	0.478	17	0.147	R.GAAAAAAPAVQHM*GR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/3	1636.461	1636.793	-203.297	0.427	1248.013	0.441	26	0.136	K.FVQKHEYGTNIGSR.M
R3/RRR3-9/3	1636.597	1636.793	-120.014	0.498	982.150	0.484	25	0.126	K.FVQKHEYGTNIGSR.M
R3/RRR3-9/3	1636.339	1636.793	-278.060	0.445	993.677	0.427	25	0.116	K.FVQKHEYGTNIGSR.M
R3/RRR3-17/2	1827.010	1828.100	-1147.467	0.411	465.657	0.466	18	0.143	K.GLLTDQTLPLLTDSALR.D
R3/RRR3-17/2	1827.353	1828.100	-958.908	0.335	301.829	0.445	15	0.136	K.GLLTDQTLPLLTDSALR.D
R3/RRR3-17/2	1826.480	1828.100	-1988.207	0.275	404.315	0.412	16	0.134	K.GLLTDQTLPLLTDSALR.D
R3/RRR3-12/2	1947.915	1946.190	-141.777	0.365	772.321	0.516	18	0.151	K.VAVEPSGAIGLAAALSDEFK.Q
R3/RRR3-20/2	1602.247	1602.813	-980.228	0.378	456.153	0.500	15	0.140	R.VGPETVTDPAFLVTR.N
R3/RRR3-7/2	1418.544	1417.675	-92.751	0.466	926.667	0.482	17	0.164	K.LGSILNVPESFLK.R
R3/RRR3-13/2	1508.669	1507.674	-2.890	0.535	1184.484	0.442	18	0.177	R.GWLEWNGADFALK.T
R3/RRR3-13/2	1508.095	1507.674	280.449	0.410	812.588	0.341	18	0.144	R.GWLEWNGADFALK.T
R3/RRR3-12/2	1508.524	1507.674	-99.312	0.382	556.435	0.282	17	0.135	R.GWLEWNGADFALK.T
R3/RRR3-20/2	1503.694	1503.685	5.813	0.387	1384.298	0.395	19	0.186	R.ALEWITANGGITTR.D
R3/RRR3-14/2	1503.106	1503.685	-1053.761	0.328	1171.240	0.252	18	0.148	R.ALEWITANGGITTR.D
R3/RRR3-16/2	1503.448	1503.685	-158.201	0.278	798.156	0.135	16	0.125	R.ALEWITANGGITTR.D
R3/RRR3-14/2	1279.051	1279.427	-295.369	0.420	980.135	0.496	17	0.172	K.GVVTDIIHDPGR.G
R3/RRR3-14/2	1278.648	1279.427	-1395.874	0.425	917.543	0.505	18	0.171	K.GVVTDIIHDPGR.G
R3/RRR3-15/2	1279.216	1279.427	-165.736	0.430	862.113	0.514	17	0.168	K.GVVTDIIHDPGR.G
R3/RRR3-15/2	1278.785	1279.427	-1288.491	0.414	883.974	0.449	17	0.160	K.GVVTDIIHDPGR.G
R3/RRR3-17/2	1279.212	1279.427	-169.182	0.458	751.310	0.493	16	0.160	K.GVVTDIIHDPGR.G
R3/RRR3-15/2	1279.318	1279.427	-85.714	0.398	735.245	0.463	16	0.155	K.GVVTDIIHDPGR.G
R3/RRR3-17/2	1278.332	1279.427	-1644.286	0.308	812.986	0.394	16	0.148	K.GVVTDIIHDPGR.G
R3/RRR3-19/2	1438.137	1437.661	331.381	0.488	1076.734	0.470	18	0.176	R.VVFELYDDIVPK.T
R3/RRR3-19/2	1436.736	1437.661	-1344.374	0.346	1122.698	0.426	18	0.170	R.VVFELYDDIVPK.T
R3/RRR3-19/2	1437.230	1437.661	-301.111	0.470	1013.850	0.393	17	0.159	R.VVFELYDDIVPK.T
R3/RRR3-10/2	1961.012	1961.207	-99.747	0.461	812.695	0.493	16	0.153	R.GLTHFDVDNFVQEVLVK.D
R3/RRR3-13/2	1567.263	1567.769	-963.517	0.494	908.397	0.486	21	0.166	R.SRPSELALPVSDPAK.A
R3/RRR3-13/2	1567.280	1567.769	-312.920	0.486	944.868	0.450	21	0.163	R.SRPSELALPVSDPAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/2	1568.330	1567.769	-280.937	0.494	870.332	0.468	21	0.162	R.SRPSELALPVSDPAK.A
R3/RRR3-13/3	1567.750	1567.769	-11.849	0.246	1170.023	0.257	28	0.092	R.SRPSELALPVSDPAK.A
R3/RRR3-22/2	1258.434	1258.450	-12.610	0.446	1228.985	0.443	18	0.182	R.EVVGLSGQTVLR.A
R3/RRR3-2/2	1361.867	1362.472	-1181.656	0.388	493.889	0.460	15	0.140	R.TTVANAATAAQTNK.K
R3/RRR3-21/2	1345.049	1345.529	-358.158	0.363	467.675	0.508	16	0.146	R.NSPVPSFSGLLAR.A
R3/RRR3-22/2	1345.093	1345.529	-325.104	0.374	559.867	0.413	18	0.143	R.NSPVPSFSGLLAR.A
R3/RRR3-13/3	1916.189	1916.121	35.416	0.429	1185.149	0.448	30	0.131	R.VTAEFNHINNLDLVCR.A
R3/RRR3-23/2	935.208	935.102	113.885	0.559	1303.299	0.412	15	0.185	-.SGLFVGINK.-
R3/RRR3-23/2	934.436	935.102	-1788.798	0.414	1443.312	0.327	15	0.182	K.SGLFVGINK.X
R3/RRR3-23/2	934.964	935.102	-147.861	0.470	1261.467	0.407	15	0.181	-.SGLFVGINK.-
R3/RRR3-27/2	935.976	935.102	-135.274	0.295	487.414	0.236	13	0.135	K.SGLFVGINK.X
R3/RRR3-12/2	1720.198	1720.910	-998.000	0.406	1507.014	0.345	18	0.187	K.NLSLGTEAFWLGQQR.K
R3/RRR3-25/2	955.915	956.035	-125.664	0.341	805.616	0.521	13	0.087	R.GPAAAEGIVGN.-
R3/RRR3-25/2	955.919	956.035	-122.333	0.251	559.458	0.399	11	0.035	R.GPAAAEGIVGN.-
R3/RRR3-7/2	1102.211	1102.266	-50.833	0.374	1246.717	0.429	17	0.180	K.AALLSSLGVDR.V
R3/RRR3-18/3	1578.909	1578.700	132.856	0.404	752.748	0.508	24	0.116	R.VSGSHSCGASLVSTTK.A
R3/RRR3-18/3	1579.704	1578.700	2.308	0.343	942.824	0.447	26	0.115	R.VSGSHSCGASLVSTTK.A
R3/RRR3-18/3	1579.778	1578.700	49.391	0.445	775.686	0.472	24	0.113	R.VSGSHSCGASLVSTTK.A
R3/RRR3-6/2	1732.167	1732.916	-1012.733	0.395	528.315	0.493	18	0.147	K.DGAPGLWPFGPVDFEK.M
R3/RRR3-6/2	1732.613	1732.916	-175.294	0.343	487.299	0.396	17	0.137	K.DGAPGLWPFGPVDFEK.M
R3/RRR3-6/2	1732.270	1732.916	-952.665	0.301	547.706	0.385	18	0.137	K.DGAPGLWPFGPVDFEK.M
R3/RRR3-6/2	982.993	983.187	-197.807	0.454	455.487	0.457	14	0.150	R.IPAVQDLVK.K
R3/RRR3-6/2	983.050	983.187	-139.632	0.428	470.651	0.425	14	0.147	R.IPAVQDLVK.K
R3/RRR3-15/2	1726.767	1726.997	-133.983	0.421	1385.811	0.387	23	0.185	K.QGPGTAILLGPNFLAEK.G
R3/RRR3-15/2	1726.536	1726.997	-268.100	0.444	1135.261	0.435	21	0.171	K.QGPGTAILLGPNFLAEK.G
R3/RRR3-15/2	1727.468	1726.997	273.114	0.485	912.345	0.520	20	0.168	K.QGPGTAILLGPNFLAEK.G
R3/RRR3-12/2	1394.196	1394.595	-286.782	0.441	1331.051	0.408	18	0.184	R.AVVDSAYEVISLK.G
R3/RRR3-12/2	1394.353	1394.595	-173.739	0.394	1193.246	0.422	17	0.174	R.AVVDSAYEVISLK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1324.180	1324.508	-248.410	0.477	1062.351	0.467	17	0.173	K.SELLLSSNPVHK.K
R3/RRR3-17/2	1324.271	1324.508	-179.513	0.495	1073.844	0.434	17	0.169	K.SELLLSSNPVHK.K
R3/RRR3-17/2	1324.199	1324.508	-233.982	0.487	1063.273	0.437	17	0.169	K.SELLLSSNPVHK.K
R3/RRR3-11/3	1624.636	1624.772	-84.159	0.483	737.835	0.484	25	0.115	K.LVLHHWSDDDCVK.I
R3/RRR3-11/3	1625.535	1624.772	-146.515	0.469	715.871	0.437	26	0.108	K.LVLHHWSDDDCVK.I
R3/RRR3-26/2	1081.533	1081.207	301.739	0.323	326.245	0.486	14	0.142	-.VPAQPDALNR.-
R3/RRR3-26/2	1081.357	1081.207	138.971	0.260	269.639	0.294	12	0.135	-.VPAQPDALNR.-
R3/RRR3-26/2	1081.672	1081.207	430.513	0.184	123.016	0.372	11	0.114	-.VPAQPDALNR.-
R3/RRR3-6/2	1507.539	1507.715	-117.082	0.448	551.364	0.474	19	0.148	K.FTPSVIEPSFGIGR.I
R3/RRR3-16/2	1100.203	1099.288	-76.968	0.413	1414.270	0.376	16	0.189	K.YGGIM*LWSR.Y
R3/RRR3-29/2	1476.214	1474.788	289.325	0.357	1783.011	0.172	17	0.182	K.KMEEELILLEVK.Y
R3/RRR3-25/2	1476.232	1474.788	301.680	0.357	1248.705	0.205	16	0.147	K.KMEEELILLEVK.Y
R3/RRR3-11/2	1476.200	1474.788	279.707	0.357	1382.708	0.142	16	0.145	K.KMEEELILLEVK.Y
R3/RRR3-9/2	1475.613	1474.788	-119.200	0.289	1274.839	0.161	16	0.144	K.KMEEELILLEVK.Y
R3/RRR3-17/2	1476.121	1474.788	226.389	0.339	1345.690	0.090	16	0.137	K.KMEEELILLEVK.Y
R3/RRR3-13/2	1475.666	1474.788	-83.270	0.300	1025.024	0.191	15	0.136	K.KMEEELILLEVK.Y
R3/RRR3-24/2	1476.005	1474.788	147.022	0.333	1144.115	0.133	15	0.135	-.KMEEELILLEVK.-
R3/RRR3-25/2	1476.156	1474.788	249.690	0.321	1120.524	0.141	16	0.135	K.KMEEELILLEVK.Y
R3/RRR3-6/2	1476.228	1474.788	298.529	0.353	1021.137	0.165	15	0.133	-.KMEEELILLEVK.-
R3/RRR3-9/2	1476.249	1474.788	312.873	0.351	1205.082	0.102	15	0.133	-.KMEEELILLEVK.-
R3/RRR3-10/2	1476.234	1474.788	303.089	0.333	1079.795	0.122	15	0.131	K.KMEEELILLEVK.Y
R3/RRR3-18/2	1476.018	1474.788	156.062	0.300	1125.685	0.092	16	0.130	K.KMEEELILLEVK.Y
R3/RRR3-11/2	1476.145	1474.788	242.393	0.327	1129.799	0.092	15	0.130	-.KMEEELILLEVK.-
R3/RRR3-17/2	1476.100	1474.788	211.545	0.349	1098.215	0.103	16	0.129	K.KMEEELILLEVK.Y
R3/RRR3-6/2	1476.215	1474.788	289.823	0.375	891.642	0.140	15	0.128	-.KMEEELILLEVK.-
R3/RRR3-21/2	1475.739	1474.788	-33.652	0.304	770.982	0.101	14	0.126	-.KMEEELILLEVK.-
R3/RRR3-4/2	1187.151	1186.343	-162.603	0.513	1342.599	0.400	16	0.186	K.GNINIEELRK.A
R3/RRR3-4/2	1186.139	1186.343	-172.445	0.429	1089.113	0.373	15	0.162	K.GNINIEELRK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1187.422	1186.343	66.238	0.431	854.823	0.330	14	0.144	-.GNINIEELRK.-
R3/RRR3-3/2	1856.543	1855.104	237.224	0.402	750.198	0.477	19	0.151	K.M*TPFQPLDFSEASLVR.G
R3/RRR3-10/2	1627.617	1627.867	-154.406	0.313	1198.888	0.429	19	0.171	R.GVAALDALAVSAVVAGSR.N
R3/RRR3-10/2	1627.438	1627.867	-264.639	0.180	690.288	0.057	16	0.120	R.GVAALDALAVSAVVAGSR.N
R3/RRR3-13/3	1228.156	1228.339	-149.709	0.474	692.424	0.473	21	0.112	R.IPESGTPYAHR.S
R3/RRR3-13/3	1228.076	1228.339	-214.921	0.436	624.103	0.439	20	0.106	R.IPESGTPYAHR.S
R3/RRR3-13/3	1228.396	1228.339	46.624	0.471	653.006	0.386	21	0.102	R.IPESGTPYAHR.S
R3/RRR3-13/3	1227.948	1228.339	-319.487	0.375	491.813	0.330	17	0.096	R.IPESGTPYAHR.S
R3/RRR3-8/2	1618.402	1618.862	-285.484	0.433	766.458	0.486	18	0.154	R.AVTQPGSEHKPIVVR.N
R3/RRR3-11/3	1246.576	1246.397	143.426	0.471	1009.908	0.465	22	0.124	R.HDDVILATHPK.S
R3/RRR3-12/3	1246.149	1246.397	-200.063	0.491	820.219	0.477	19	0.118	R.HDDVILATHPK.S
R3/RRR3-11/3	1246.258	1246.397	-112.216	0.479	1077.816	0.408	22	0.117	R.HDDVILATHPK.S
R3/RRR3-11/3	1246.128	1246.397	-216.425	0.358	494.771	0.356	15	0.096	R.HDDVILATHPK.S
R3/RRR3-12/3	1246.291	1246.397	-85.245	0.427	797.213	0.295	18	0.092	-.HDDVILATHPK.-
R3/RRR3-14/2	1474.871	1474.728	97.409	0.363	1387.093	0.372	17	0.181	R.LISQVVSSITASLR.F
R3/RRR3-10/2	1474.506	1474.728	-150.760	0.337	825.164	0.420	16	0.150	R.LISQVVSSITASLR.F
R3/RRR3-8/2	1475.613	1474.728	-78.212	0.427	939.822	0.357	17	0.149	R.LISQVVSSITASLR.F
R3/RRR3-8/2	1474.313	1474.728	-282.492	0.284	800.906	0.271	16	0.136	R.LISQVVSSITASLR.F
R3/RRR3-2/2	1474.498	1474.728	-156.740	0.245	735.798	0.271	15	0.133	R.LISQVVSSITASLR.F
R3/RRR3-2/2	1474.599	1474.728	-87.731	0.310	489.428	0.297	13	0.133	R.LISQVVSSITASLR.F
R3/RRR3-9/3	1475.037	1474.728	210.235	0.388	1496.108	0.332	28	0.133	R.LISQVVSSITASLR.F
R3/RRR3-2/2	1475.558	1474.728	-115.886	0.291	737.540	0.262	14	0.133	R.LISQVVSSITASLR.F
R3/RRR3-14/2	1474.480	1474.728	-168.948	0.233	952.632	0.174	16	0.132	R.LISQVVSSITASLR.F
R3/RRR3-6/2	1475.254	1474.728	-322.398	0.272	242.645	0.360	11	0.123	-.LISQVVSSITASLR.-
R3/RRR3-9/3	1474.198	1474.728	-1040.838	0.371	960.162	0.320	25	0.098	R.LISQVVSSITASLR.F
R3/RRR3-9/3	1474.373	1474.728	-241.466	0.315	1065.359	0.264	27	0.093	R.LISQVVSSITASLR.F
R3/RRR3-5/2	1991.933	1992.260	-165.074	0.407	514.673	0.457	17	0.137	R.RIITSEDTVSAILSSITGK.Y
R3/RRR3-2/2	965.255	965.130	130.254	0.351	457.060	0.447	12	0.143	R.IPFGFIDR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-9/2	1097.283	1096.305	-20.041	0.374	1378.816	0.372	17	0.182	K.AGPGILGVNLGK.N
R3/RRR3-9/2	1097.172	1096.305	-121.369	0.384	993.340	0.389	16	0.156	K.AGPGILGVNLGK.N
R3/RRR3-4/2	1613.152	1611.777	233.115	0.499	1011.359	0.429	18	0.161	K.FSTGSWETLETKPK.E
R3/RRR3-11/2	1336.249	1336.645	-297.294	0.349	509.354	0.495	18	0.148	K.AIPLIDISPLVGK.I
R3/RRR3-11/2	1335.708	1336.645	-1454.307	0.292	327.659	0.513	16	0.142	K.AIPLIDISPLVGK.I
R3/RRR3-11/2	1336.724	1336.645	59.023	0.329	325.086	0.449	14	0.137	-.AIPLIDISPLVGK.-
R3/RRR3-25/2	980.681	981.045	-371.812	0.384	1139.070	0.448	14	0.175	R.SNVDVFSGR.G
R3/RRR3-7/3	1495.095	1494.726	247.419	0.512	1373.502	0.370	26	0.131	R.NDRPLFGHVLVAR.D
R3/RRR3-5/3	1966.646	1965.159	248.732	0.373	1843.998	0.135	31	0.124	K.HLASIAKGHPEDAIDSFR.R
R3/RRR3-16/2	1213.071	1213.319	-205.355	0.429	609.082	0.476	14	0.146	K.SAAAVDPVEPEK.V
R3/RRR3-10/2	1153.849	1154.301	-393.420	0.316	1025.155	0.470	16	0.166	R.HLISSGALEAR.L
R3/RRR3-5/2	1165.205	1164.376	-147.067	0.503	1173.533	0.416	16	0.174	K.LLVNYLSDVK.Y
R3/RRR3-13/2	1872.763	1873.058	-158.123	0.415	622.586	0.472	20	0.146	R.FSPNPQNPVIVSSGWDK.L
R3/RRR3-22/3	1647.889	1647.860	17.407	0.487	1101.435	0.445	27	0.127	R.TVNRPYGGVLSGTAVR.E
R3/RRR3-23/3	1647.577	1647.860	-172.757	0.404	1005.648	0.356	25	0.106	-.TVNRPYGGVLSGTAVR.-
R3/RRR3-22/3	1647.383	1647.860	-290.503	0.411	1047.098	0.323	27	0.102	R.TVNRPYGGVLSGTAVR.E
R3/RRR3-23/3	1647.972	1647.860	68.001	0.404	832.792	0.295	25	0.092	R.TVNRPYGGVLSGTAVR.E
R3/RRR3-4/2	1380.434	1379.584	-108.793	0.408	528.036	0.434	15	0.140	K.IAAEPLNPSELPK.M
R3/RRR3-26/2	1247.122	1247.385	-212.020	0.486	813.930	0.463	15	0.159	R.HLAHLEELER.Q
R3/RRR3-26/3	1246.927	1247.385	-368.727	0.522	872.622	0.397	21	0.108	R.HLAHLEELER.Q
R3/RRR3-26/3	1247.407	1247.385	17.008	0.524	917.835	0.351	22	0.102	R.HLAHLEELER.Q
R3/RRR3-25/3	1247.134	1247.385	-202.555	0.526	527.133	0.320	21	0.102	R.HLAHLEELER.Q
R3/RRR3-25/3	1247.316	1247.385	-55.580	0.413	335.745	0.321	20	0.102	-.HLAHLEELER.-
R3/RRR3-25/3	1246.892	1247.385	-396.575	0.476	620.555	0.358	20	0.102	R.HLAHLEELER.Q
R3/RRR3-26/3	1247.145	1247.385	-193.129	0.514	1042.385	0.328	24	0.101	R.HLAHLEELER.Q
R3/RRR3-25/3	1246.806	1247.385	-1270.289	0.433	535.332	0.344	19	0.097	-.HLAHLEELER.-
R3/RRR3-25/3	1247.116	1247.385	-216.548	0.448	420.483	0.345	19	0.096	-.HLAHLEELER.-
R3/RRR3-25/3	1246.794	1247.385	-1280.318	0.453	460.389	0.348	19	0.095	-.HLAHLEELER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-26/3	1246.824	1247.385	-1256.131	0.299	351.062	0.347	20	0.070	-.HLAHLEELER.-
R3/RRR3-17/2	1300.034	1300.400	-282.784	0.279	480.646	0.510	17	0.142	R.QPIGTAAQGAEEK.D
R3/RRR3-17/2	1299.994	1300.400	-313.685	0.237	441.219	0.424	16	0.135	R.QPIGTAAQGAEEK.D
R3/RRR3-1/2	1290.533	1289.422	86.087	0.348	534.630	0.495	13	0.144	R.HELPQTNQPPK.Y
R3/RRR3-7/3	1316.645	1316.448	150.718	0.502	1330.572	0.387	22	0.131	K.YGKDEAIQHVR.D
R3/RRR3-14/2	1456.295	1455.680	-265.305	0.440	1163.785	0.432	17	0.171	R.FAFASLGDTVSLVK.K
R3/RRR3-9/2	1128.384	1128.387	-2.345	0.261	570.358	0.519	14	0.142	K.VPILTIGSLSK.R
R3/RRR3-23/2	887.724	888.087	-409.574	0.399	364.268	0.405	13	0.146	R.VLTVISQK.Q
R3/RRR3-23/2	887.662	888.087	-479.948	0.365	377.247	0.362	13	0.143	R.VLTVISQK.Q
R3/RRR3-6/3	1403.234	1403.651	-298.643	0.520	843.099	0.442	24	0.113	R.TKEAIVSWVNKK.L
R3/RRR3-8/2	1096.856	1097.242	-352.356	0.373	586.245	0.480	13	0.152	R.SHCASFLFK.N
R3/RRR3-9/2	1096.509	1097.242	-1585.198	0.312	517.956	0.432	12	0.144	R.SHCASFLFK.N
R3/RRR3-8/2	1096.231	1097.242	-1839.355	0.304	419.456	0.456	11	0.143	R.SHCASFLFK.N
R3/RRR3-8/2	1097.056	1097.242	-170.265	0.291	374.142	0.376	11	0.139	R.SHCASFLFK.N
R3/RRR3-7/2	1096.981	1097.242	-238.360	0.246	520.635	0.368	12	0.137	R.SHCASFLFK.N
R3/RRR3-17/2	1548.087	1546.697	253.036	0.418	502.569	0.450	18	0.143	R.FGTICVFCGSNAGR.R
R3/RRR3-13/2	1723.090	1723.862	-1031.995	0.415	691.110	0.475	18	0.146	R.TSGFVLESSTPGDAVQK.T
R3/RRR3-7/2	1313.492	1314.513	-1543.503	0.342	680.143	0.485	14	0.149	R.KGADILVEALER.C
R3/RRR3-7/2	1313.935	1314.513	-1204.355	0.313	880.601	0.369	15	0.146	R.KGADILVEALER.C
R3/RRR3-23/2	1131.922	1132.209	-254.475	0.420	844.553	0.473	16	0.163	R.NITVNEAQSR.R
R3/RRR3-24/2	1131.871	1132.209	-299.918	0.426	724.508	0.432	15	0.151	-.NITVNEAQSR.-
R3/RRR3-23/2	1131.345	1132.209	-1652.617	0.288	852.726	0.301	16	0.141	R.NITVNEAQSR.R
R3/RRR3-23/3	1795.211	1794.993	121.486	0.365	1178.915	0.428	27	0.126	K.TQRPAQENISLGPQVR.E
R3/RRR3-13/2	1031.118	1031.187	-66.449	0.410	893.633	0.472	14	0.164	K.FTDVPINPK.V
R3/RRR3-13/2	1030.925	1031.187	-254.940	0.326	608.106	0.438	12	0.144	K.FTDVPINPK.V
R3/RRR3-5/2	1200.773	1200.410	302.977	0.410	1462.936	0.335	17	0.185	R.LLNLETLDLR.G
R3/RRR3-5/2	1200.750	1200.410	283.915	0.365	1166.856	0.298	15	0.155	R.LLNLETLDLR.G
R3/RRR3-21/2	1077.041	1077.215	-162.289	0.467	465.268	0.406	15	0.143	-.SALPGALEYR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-21/2	1076.993	1077.215	-206.974	0.270	397.257	0.349	14	0.134	-.SALPGALEYR.-
R3/RRR3-8/2	1895.444	1894.192	133.737	0.322	807.677	0.476	19	0.152	-.MAEVEVAAAAAAAGVLHRR.I
R3/RRR3-8/2	1895.276	1894.192	44.406	0.293	805.977	0.474	19	0.150	-.MAEVEVAAAAAAAGVLHRR.I
R3/RRR3-8/2	1895.444	1894.192	133.414	0.293	781.068	0.393	19	0.142	-.MAEVEVAAAAAAAGVLHRR.I
R3/RRR3-9/2	1895.517	1894.192	171.906	0.321	681.450	0.354	19	0.137	-.MAEVEVAAAAAAAGVLHRR.I
R3/RRR3-9/2	1895.190	1894.192	-0.879	0.218	650.592	0.339	17	0.132	-.MAEVEVAAAAAAAGVLHRR.I
R3/RRR3-7/2	1039.440	1039.254	179.795	0.539	1072.665	0.426	17	0.171	R.LGVEPVIGVR.A
R3/RRR3-13/2	1039.459	1039.254	198.284	0.428	804.201	0.440	16	0.158	R.LGVEPVIGVR.A
R3/RRR3-13/2	1038.929	1039.254	-313.196	0.351	790.744	0.377	15	0.148	R.LGVEPVIGVR.A
R3/RRR3-7/2	1038.540	1039.254	-1654.935	0.399	694.917	0.361	15	0.145	R.LGVEPVIGVR.A
R3/RRR3-12/3	1793.288	1792.011	154.660	0.436	1741.848	0.216	31	0.130	R.VGQM*ETQINLVGSSRR.K
R3/RRR3-12/3	1793.756	1792.011	-142.845	0.334	1241.893	0.174	27	0.088	R.VGQM*ETQINLVGSSRR.K
R3/RRR3-9/3	1560.428	1560.718	-186.262	0.492	1040.627	0.427	28	0.119	R.IRVEPQM*SGGGQER.G
R3/RRR3-18/2	1521.130	1520.674	300.422	0.486	1338.478	0.378	23	0.181	K.FQLSGGQPPNAFTR.A
R3/RRR3-18/2	1520.331	1520.674	-226.266	0.458	943.920	0.468	21	0.167	K.FQLSGGQPPNAFTR.A
R3/RRR3-18/2	1521.213	1520.674	-303.723	0.535	792.669	0.490	19	0.160	K.FQLSGGQPPNAFTR.A
R3/RRR3-13/2	1543.169	1542.673	322.076	0.464	652.663	0.442	19	0.147	R.SLVAATPSDPDLEAR.G
R3/RRR3-13/2	1541.670	1542.673	-1303.379	0.304	660.498	0.356	18	0.137	R.SLVAATPSDPDLEAR.G
R3/RRR3-15/3	1478.368	1478.678	-210.585	0.364	877.919	0.475	26	0.116	R.VTALDLAASGVHPAR.I
R3/RRR3-15/3	1478.452	1478.678	-153.307	0.368	567.824	0.478	25	0.106	R.VTALDLAASGVHPAR.I
R3/RRR3-15/3	1478.839	1478.678	109.019	0.361	364.109	0.418	20	0.096	-.VTALDLAASGVHPAR.-
R3/RRR3-14/3	1992.980	1993.073	-46.458	0.474	964.396	0.443	31	0.117	K.NEEKENEEVSSTAGLVEK.L
R3/RRR3-14/2	1539.766	1539.671	61.974	0.353	1093.599	0.439	18	0.169	R.SLALEWGTDYDIR.V
R3/RRR3-14/2	1539.169	1539.671	-978.319	0.336	530.100	0.315	14	0.133	R.SLALEWGTDYDIR.V
R3/RRR3-14/2	1539.520	1539.671	-98.267	0.292	670.914	0.293	15	0.133	R.SLALEWGTDYDIR.V
R3/RRR3-16/2	843.892	843.994	-121.888	0.356	1264.262	0.379	15	0.174	K.VALVTGAGR.G
R3/RRR3-6/3	1688.242	1688.845	-952.267	0.460	1191.167	0.420	31	0.126	K.AAQEM*TGSHLDEVKR.M
R3/RRR3-6/3	1688.804	1688.845	-24.072	0.380	989.102	0.302	29	0.097	K.AAQEM*TGSHLDEVKR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-6/3	1688.846	1688.845	0.505	0.386	662.105	0.333	26	0.095	K.AAQEM*TGSHLDEVKR.M
R3/RRR3-19/3	1688.984	1688.845	82.493	0.394	790.035	0.222	25	0.086	K.AAQEM*TGSHLDEVKR.M
R3/RRR3-17/2	941.045	941.150	-111.646	0.467	1028.986	0.419	13	0.167	R.ILLITDPR.T
R3/RRR3-18/2	941.035	941.150	-122.316	0.469	1136.703	0.377	13	0.167	R.ILLITDPR.T
R3/RRR3-16/2	940.521	941.150	-1736.608	0.443	1093.842	0.385	13	0.166	R.ILLITDPR.T
R3/RRR3-15/2	940.766	941.150	-409.713	0.459	1105.420	0.377	13	0.165	R.ILLITDPR.T
R3/RRR3-14/2	940.547	941.150	-1708.832	0.434	1098.796	0.377	13	0.165	R.ILLITDPR.T
R3/RRR3-11/2	941.327	941.150	188.584	0.511	1030.736	0.387	13	0.162	R.ILLITDPR.T
R3/RRR3-18/2	940.682	941.150	-499.037	0.437	1122.923	0.352	13	0.162	R.ILLITDPR.T
R3/RRR3-14/2	941.011	941.150	-148.342	0.438	1098.365	0.359	13	0.162	R.ILLITDPR.T
R3/RRR3-10/2	940.923	941.150	-241.654	0.416	959.682	0.412	12	0.161	R.ILLITDPR.T
R3/RRR3-11/2	940.633	941.150	-1617.041	0.469	1039.132	0.372	13	0.161	R.ILLITDPR.T
R3/RRR3-15/2	941.123	941.150	-28.505	0.473	998.594	0.394	12	0.161	R.ILLITDPR.T
R3/RRR3-16/2	941.183	941.150	35.630	0.537	1014.821	0.386	12	0.160	R.ILLITDPR.T
R3/RRR3-14/2	941.022	941.150	-135.979	0.506	954.971	0.396	12	0.159	R.ILLITDPR.T
R3/RRR3-11/2	940.578	941.150	-1676.234	0.481	1098.223	0.339	13	0.159	R.ILLITDPR.T
R3/RRR3-10/2	940.283	941.150	-1991.092	0.450	929.670	0.396	12	0.158	R.ILLITDPR.T
R3/RRR3-12/2	941.224	941.150	78.685	0.357	981.153	0.385	12	0.158	R.ILLITDPR.T
R3/RRR3-12/2	940.511	941.150	-1748.083	0.433	970.034	0.377	12	0.157	R.ILLITDPR.T
R3/RRR3-17/2	941.064	941.150	-91.087	0.502	931.682	0.384	12	0.156	R.ILLITDPR.T
R3/RRR3-17/2	940.946	941.150	-216.925	0.503	1082.341	0.329	13	0.156	R.ILLITDPR.T
R3/RRR3-10/2	940.471	941.150	-1790.989	0.468	967.507	0.364	12	0.156	R.ILLITDPR.T
R3/RRR3-18/2	940.547	941.150	-1709.484	0.411	962.959	0.364	12	0.155	R.ILLITDPR.T
R3/RRR3-13/2	940.936	941.150	-228.118	0.474	970.631	0.362	12	0.155	R.ILLITDPR.T
R3/RRR3-13/2	941.067	941.150	-87.834	0.462	909.935	0.377	12	0.155	R.ILLITDPR.T
R3/RRR3-12/2	941.469	941.150	340.192	0.467	980.760	0.342	12	0.153	R.ILLITDPR.T
R3/RRR3-13/2	941.107	941.150	-45.419	0.482	840.491	0.368	11	0.150	R.ILLITDPR.T
R3/RRR3-4/2	1427.130	1427.549	-294.148	0.400	833.764	0.450	15	0.153	R.NPVYQNAGNFFR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-5/2	1690.429	1690.967	-912.146	0.353	884.790	0.468	15	0.153	R.LTAAWLQDLLAVGYR.Q
R3/RRR3-18/2	1238.262	1237.518	-207.308	0.427	827.602	0.465	18	0.162	K.LPFAPVPLVQR.M
R3/RRR3-18/2	1237.139	1237.518	-307.255	0.374	697.347	0.507	17	0.159	K.LPFAPVPLVQR.M
R3/RRR3-18/2	1237.200	1237.518	-257.957	0.362	643.744	0.527	17	0.158	K.LPFAPVPLVQR.M
R3/RRR3-19/2	1237.242	1237.518	-224.005	0.358	418.686	0.396	13	0.141	K.LPFAPVPLVQR.M
R3/RRR3-19/2	1237.449	1237.518	-56.062	0.282	393.873	0.355	13	0.137	K.LPFAPVPLVQR.M
R3/RRR3-21/2	1282.934	1283.330	-309.362	0.403	502.870	0.442	15	0.140	K.GDGTGGKSIYGDR.F
R3/RRR3-13/2	1156.339	1157.213	-1624.837	0.339	988.826	0.456	17	0.162	R.DSSVSYASAAAK.V
R3/RRR3-19/2	1114.951	1114.146	-175.329	0.398	1334.678	0.366	15	0.179	R.FGFDEDDIR.V
R3/RRR3-19/2	1113.873	1114.146	-246.067	0.336	961.644	0.294	13	0.144	R.FGFDEDDIR.V
R3/RRR3-10/3	1625.606	1624.868	-161.836	0.473	1004.937	0.433	25	0.118	R.YLNAIQTNAPHLLR.Y
R3/RRR3-10/3	1624.618	1624.868	-154.888	0.463	765.951	0.361	25	0.100	R.YLNAIQTNAPHLLR.Y
R3/RRR3-10/3	1624.784	1624.868	-52.125	0.394	705.637	0.253	25	0.089	R.YLNAIQTNAPHLLR.Y
R3/RRR3-12/3	1317.357	1317.458	-76.707	0.458	742.933	0.448	19	0.110	K.FEHHEM*FPAR.T
R3/RRR3-12/3	1317.445	1317.458	-9.649	0.483	764.212	0.404	20	0.106	K.FEHHEM*FPAR.T
R3/RRR3-12/3	1317.510	1317.458	39.976	0.423	849.787	0.381	20	0.103	K.FEHHEM*FPAR.T
R3/RRR3-11/2	1384.373	1384.516	-103.354	0.389	556.747	0.453	13	0.144	K.LTYIFDEETPR.W
R3/RRR3-11/2	1384.097	1384.516	-303.028	0.337	483.448	0.386	14	0.139	K.LTYIFDEETPR.W
R3/RRR3-1/2	1221.832	1221.343	401.570	0.318	1064.634	0.437	17	0.165	R.ETTQLTAVTTR.T
R3/RRR3-12/2	1449.012	1448.620	271.645	0.507	1027.303	0.426	16	0.165	K.NLYISCDPYM*R.N
R3/RRR3-12/2	1448.151	1448.620	-324.333	0.468	1059.572	0.392	16	0.162	K.NLYISCDPYM*R.N
R3/RRR3-12/2	1448.030	1448.620	-1100.987	0.413	1002.703	0.385	16	0.158	K.NLYISCDPYM*R.N
R3/RRR3-4/2	1576.259	1575.874	245.251	0.308	880.855	0.448	17	0.151	K.LLILGSPGAGTSTIFK.Q
R3/RRR3-4/2	1577.219	1575.874	219.174	0.304	373.368	0.343	15	0.131	K.LLILGSPGAGTSTIFK.Q
R3/RRR3-19/2	1198.125	1197.371	-206.384	0.365	1072.808	0.435	14	0.166	R.SLPNNHVFLR.C
R3/RRR3-15/2	1176.219	1176.347	-109.466	0.533	1086.278	0.413	17	0.167	K.IGAGIEAFEIR.N
R3/RRR3-26/2	1333.932	1333.497	326.923	0.503	1144.527	0.411	19	0.170	R.NLNM*GNAASIPSK.C
R3/RRR3-27/2	1333.173	1333.497	-243.942	0.439	971.461	0.421	19	0.162	R.NLNM*GNAASIPSK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-26/2	1333.981	1333.497	364.083	0.497	914.915	0.414	18	0.157	R.NLNM*GNAASIPSK.C
R3/RRR3-26/2	1333.089	1333.497	-307.055	0.413	930.034	0.363	19	0.153	R.NLNM*GNAASIPSK.C
R3/RRR3-27/2	1333.871	1333.497	281.318	0.429	793.914	0.418	17	0.152	R.NLNM*GNAASIPSK.C
R3/RRR3-27/2	1332.517	1333.497	-1489.912	0.347	946.080	0.356	19	0.152	R.NLNM*GNAASIPSK.C
R3/RRR3-26/2	1333.006	1333.497	-369.072	0.404	917.863	0.357	19	0.151	R.NLNM*GNAASIPSK.C
R3/RRR3-26/2	1334.022	1333.497	-356.860	0.444	762.506	0.387	17	0.148	R.NLNM*GNAASIPSK.C
R3/RRR3-27/2	1332.479	1333.497	-1518.807	0.305	771.982	0.335	18	0.143	R.NLNM*GNAASIPSK.C
R3/RRR3-26/2	1332.515	1333.497	-1491.477	0.289	819.313	0.295	18	0.140	R.NLNM*GNAASIPSK.C
R3/RRR3-4/2	1316.369	1317.562	-1670.623	0.393	1041.193	0.418	15	0.161	K.AALQFIQGLSLR.S
R3/RRR3-9/2	1438.329	1438.693	-253.381	0.428	703.988	0.455	15	0.151	K.TFVLTPEQYIVK.L
R3/RRR3-9/2	1438.398	1438.693	-205.362	0.341	761.349	0.403	16	0.147	K.TFVLTPEQYIVK.L
R3/RRR3-20/2	1438.351	1438.693	-238.396	0.391	513.283	0.390	12	0.134	-.TFVLTPEQYIVK.-
R3/RRR3-25/2	1429.056	1429.560	-1055.244	0.519	1065.489	0.416	19	0.165	K.YSPAAHDVVEVNK.A
R3/RRR3-25/2	1429.027	1429.560	-1075.400	0.507	1111.596	0.337	20	0.157	K.YSPAAHDVVEVNK.A
R3/RRR3-9/2	1399.502	1399.578	-54.382	0.490	966.642	0.433	14	0.160	K.LLQYVYWSNGR.E
R3/RRR3-9/2	1399.898	1399.578	229.269	0.432	724.659	0.374	13	0.141	-.LLQYVYWSNGR.-
R3/RRR3-7/2	1141.085	1141.346	-229.362	0.370	677.843	0.470	16	0.153	R.AQPTLGLITAR.A
R3/RRR3-7/2	1141.145	1141.346	-176.777	0.355	528.903	0.468	16	0.149	R.AQPTLGLITAR.A
R3/RRR3-6/2	1141.202	1141.346	-126.235	0.370	399.613	0.421	14	0.143	R.AQPTLGLITAR.A
R3/RRR3-7/2	1141.197	1141.346	-130.849	0.290	444.156	0.348	14	0.137	R.AQPTLGLITAR.A
R3/RRR3-10/2	1637.623	1637.814	-116.903	0.386	1263.103	0.375	20	0.172	K.FAFVDVSPEELQQK.E
R3/RRR3-11/2	1218.025	1218.384	-295.893	0.395	1007.401	0.442	17	0.166	R.YIDIGIPANNK.G
R3/RRR3-11/2	1217.463	1218.384	-1582.583	0.262	916.930	0.266	16	0.139	R.YIDIGIPANNK.G
R3/RRR3-11/2	1217.922	1218.384	-380.564	0.261	594.808	0.319	13	0.134	R.YIDIGIPANNK.G
R3/RRR3-10/3	1840.004	1839.990	7.970	0.392	948.396	0.438	26	0.112	R.GFANTDGIGKPAQGGSPHK.S
R3/RRR3-17/2	1130.147	1130.317	-150.113	0.420	773.629	0.450	15	0.154	R.VLVTPTSDLGK.I
R3/RRR3-17/2	1131.399	1130.317	72.872	0.394	697.063	0.402	16	0.147	R.VLVTPTSDLGK.I
R3/RRR3-17/2	1129.588	1130.317	-1534.549	0.288	672.396	0.283	15	0.135	R.VLVTPTSDLGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-12/2	1351.543	1351.490	38.899	0.435	1257.285	0.384	17	0.175	K.FGFNDAFNYKK.E
R3/RRR3-12/3	1526.510	1525.694	-120.729	0.384	1334.972	0.365	26	0.125	K.STSLHDKHPTFVR.K
R3/RRR3-12/3	1526.491	1525.694	-133.123	0.263	519.372	0.287	19	0.080	-.STSLHDKHPTFVR.-
R3/RRR3-10/2	1079.991	1080.259	-249.366	0.369	1208.418	0.392	16	0.172	K.AILQSYLSGK.H
R3/RRR3-10/2	1079.763	1080.259	-460.781	0.300	748.252	0.394	14	0.144	K.AILQSYLSGK.H
R3/RRR3-16/2	940.986	941.151	-175.995	0.311	634.385	0.456	13	0.148	K.IPFPLTPR.F
R3/RRR3-16/2	941.144	941.151	-7.755	0.383	545.310	0.407	12	0.146	K.IPFPLTPR.F
R3/RRR3-16/2	940.969	941.151	-194.215	0.321	547.046	0.404	12	0.143	K.IPFPLTPR.F
R3/RRR3-5/2	1128.956	1129.250	-261.759	0.388	988.856	0.444	16	0.163	K.SPAGANQWVAK.N
R3/RRR3-4/2	1230.957	1231.335	-307.505	0.462	1277.057	0.380	19	0.176	K.TTAGIEPEDVAK.R
R3/RRR3-4/2	1231.020	1231.335	-255.970	0.477	735.335	0.429	16	0.151	K.TTAGIEPEDVAK.R
R3/RRR3-4/2	1231.030	1231.335	-248.210	0.461	728.808	0.405	15	0.145	-.TTAGIEPEDVAK.-
R3/RRR3-10/2	1218.234	1218.427	-159.158	0.417	502.611	0.412	16	0.143	R.YAPGIEIISVR.V
R3/RRR3-4/2	1974.585	1974.287	151.319	0.492	890.766	0.396	18	0.144	K.QFIAGLTELTPDTVQVLK.A
R3/RRR3-13/2	1562.936	1562.834	65.599	0.418	1214.972	0.393	19	0.171	K.LFNIIEPDVAVFGK.K
R3/RRR3-13/2	1561.950	1562.834	-1209.559	0.323	894.110	0.325	15	0.142	-.LFNIIEPDVAVFGK.-
R3/RRR3-13/2	1561.677	1562.834	-1385.074	0.344	509.628	0.244	13	0.124	-.LFNIIEPDVAVFGK.-
R3/RRR3-20/3	1464.526	1464.645	-81.864	0.442	977.986	0.433	24	0.116	K.KGEEVPLSEYKGK.V
R3/RRR3-20/3	1463.339	1464.645	-1581.117	0.461	619.832	0.464	22	0.108	K.KGEEVPLSEYKGK.V
R3/RRR3-7/3	1648.264	1648.827	-951.037	0.471	997.541	0.410	27	0.113	R.LRPNSSGSQTVQM*AR.A
R3/RRR3-7/3	1648.550	1648.827	-168.334	0.459	529.007	0.319	22	0.087	-.LRPNSSGSQTVQM*AR.-
R3/RRR3-21/2	828.938	828.978	-48.389	0.368	362.393	0.398	11	0.146	R.TPPSWLK.I
R3/RRR3-21/2	828.894	828.978	-101.863	0.376	230.472	0.355	9	0.144	R.TPPSWLK.I
R3/RRR3-21/2	828.324	828.978	-2002.652	0.292	376.803	0.378	11	0.141	R.TPPSWLK.I
R3/RRR3-18/3	1538.434	1538.734	-195.518	0.419	1003.638	0.435	26	0.118	R.KIENVATGPNNRPK.L
R3/RRR3-18/3	1538.686	1538.734	-31.011	0.458	932.689	0.441	25	0.116	R.KIENVATGPNNRPK.L
R3/RRR3-18/3	1538.976	1538.734	157.784	0.459	1030.419	0.387	26	0.112	R.KIENVATGPNNRPK.L
R3/RRR3-18/3	1540.204	1538.734	306.073	0.336	1296.816	0.160	26	0.089	R.KIENVATGPNNRPK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1987.629	1988.292	-839.266	0.408	639.907	0.418	16	0.135	R.ESSPLSIVSGTPNIMDLVK.C
R3/RRR3-11/2	1473.979	1473.612	249.478	0.399	792.539	0.448	17	0.150	K.AVSTGYTDLVAYGR.L
R3/RRR3-2/2	1592.934	1591.787	92.342	0.327	1050.853	0.411	18	0.159	K.IAYDDGDVEVLLLR.D
R3/RRR3-23/2	1258.297	1258.472	-138.867	0.400	1304.475	0.363	16	0.176	K.FNLFM*QQVSK.S
R3/RRR3-22/2	1257.800	1258.472	-1333.112	0.385	1337.732	0.330	16	0.173	K.FNLFM*QQVSK.S
R3/RRR3-22/2	1258.103	1258.472	-293.527	0.439	1161.536	0.351	16	0.164	K.FNLFM*QQVSK.S
R3/RRR3-22/2	1258.163	1258.472	-245.927	0.346	1078.666	0.348	16	0.158	K.FNLFM*QQVSK.S
R3/RRR3-23/2	1257.485	1258.472	-1584.455	0.333	429.511	0.338	11	0.133	-.FNLFM*QQVSK.-
R3/RRR3-23/2	1257.659	1258.472	-1445.216	0.309	681.398	0.236	12	0.131	-.FNLFM*QQVSK.-
R3/RRR3-3/2	1560.183	1559.744	282.622	0.323	1229.635	0.352	17	0.164	R.IIEETADQFFAFK.V
R3/RRR3-6/3	1358.848	1359.514	-1229.613	0.395	753.885	0.455	21	0.108	K.TNQIVITNDKGR.L
R3/RRR3-6/3	1359.548	1359.514	24.926	0.392	649.444	0.368	21	0.097	K.TNQIVITNDKGR.L
R3/RRR3-11/2	1302.150	1302.461	-239.355	0.385	606.620	0.440	17	0.149	R.QALSLDEALWR.V
R3/RRR3-11/2	1303.084	1302.461	-290.391	0.391	491.986	0.445	16	0.147	R.QALSLDEALWR.V
R3/RRR3-11/2	1302.260	1302.461	-155.094	0.341	461.824	0.373	15	0.140	R.QALSLDEALWR.V
R3/RRR3-5/2	1591.495	1591.790	-186.145	0.502	987.929	0.415	22	0.161	K.LISGDLQPTSGTVFR.S
R3/RRR3-5/2	1591.412	1591.790	-238.317	0.480	992.525	0.356	21	0.152	K.LISGDLQPTSGTVFR.S
R3/RRR3-5/2	1592.549	1591.790	-152.040	0.384	601.146	0.358	18	0.138	K.LISGDLQPTSGTVFR.S
R3/RRR3-19/3	1495.515	1495.567	-34.812	0.363	771.803	0.459	24	0.109	R.SCYNCGEAGHIAR.D
R3/RRR3-19/3	1495.793	1495.567	151.944	0.342	580.221	0.506	23	0.108	R.SCYNCGEAGHIAR.D
R3/RRR3-19/3	1495.327	1495.567	-160.706	0.364	643.479	0.480	24	0.108	R.SCYNCGEAGHIAR.D
R3/RRR3-17/2	1357.839	1358.570	-1278.764	0.432	686.518	0.437	17	0.148	K.VYGPAM*STNVM*R.I
R3/RRR3-6/2	1844.586	1844.232	192.119	0.423	1678.972	0.201	20	0.176	R.FQIIKGLAEGLLYLHK.H
R3/RRR3-6/2	1844.469	1844.232	128.870	0.377	860.719	0.117	15	0.117	-.FQIIKGLAEGLLYLHK.-
R3/RRR3-20/2	1287.619	1288.474	-1444.818	0.364	1033.794	0.430	17	0.165	R.VQVDYTQPIPK.D
R3/RRR3-20/2	1288.144	1288.474	-257.070	0.507	797.604	0.437	15	0.154	R.VQVDYTQPIPK.D
R3/RRR3-16/2	1272.360	1273.509	-1693.862	0.352	861.032	0.455	15	0.155	R.LLQINNGVFVR.V
R3/RRR3-2/2	1872.401	1872.151	133.944	0.354	659.893	0.414	15	0.136	K.QVIEISEDYLPVGLPAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-1/2	1314.320	1314.513	-147.522	0.407	702.883	0.429	13	0.143	R.LAGQLLSDLIDR.N
R3/RRR3-14/2	1034.035	1034.230	-189.996	0.471	782.791	0.427	14	0.156	R.LEALLFEAK.G
R3/RRR3-13/2	1034.181	1034.230	-48.139	0.384	775.352	0.383	13	0.148	R.LEALLFEAK.G
R3/RRR3-13/2	1034.140	1034.230	-87.803	0.281	522.786	0.338	12	0.137	R.LEALLFEAK.G
R3/RRR3-13/2	1033.481	1034.230	-1697.392	0.272	561.409	0.323	13	0.137	R.LEALLFEAK.G
R3/RRR3-6/2	1673.707	1673.851	-86.511	0.454	859.018	0.421	19	0.151	R.KYGLLGKEEAHDNAK.R
R3/RRR3-5/2	974.887	975.083	-201.838	0.473	917.545	0.423	13	0.160	K.HGESYLLR.V
R3/RRR3-14/2	1487.841	1487.637	136.965	0.497	848.014	0.408	21	0.152	K.QDEGLANAVETVLK.N
R3/RRR3-1/2	1821.247	1821.106	77.740	0.388	712.518	0.441	16	0.143	R.LAYYGISTNLVTYLTK.K
R3/RRR3-16/2	1344.144	1344.451	-229.053	0.391	1049.439	0.416	16	0.162	R.ALANYIDESGYK.A
R3/RRR3-12/2	1132.011	1132.297	-254.130	0.451	599.293	0.404	15	0.148	R.LQQAPPPPQR.Q
R3/RRR3-12/2	1132.031	1132.297	-236.496	0.408	571.390	0.335	15	0.142	R.LQQAPPPPQR.Q
R3/RRR3-12/2	1131.910	1132.297	-342.959	0.444	603.420	0.315	15	0.141	R.LQQAPPPPQR.Q
R3/RRR3-12/2	1132.912	1132.297	-340.926	0.457	610.596	0.293	15	0.139	R.LQQAPPPPQR.Q
R3/RRR3-12/2	1133.037	1132.297	-230.991	0.411	514.554	0.290	14	0.139	R.LQQAPPPPQR.Q
R3/RRR3-12/3	1132.009	1132.297	-255.711	0.381	891.745	0.370	19	0.099	-.LQQAPPPPQR.-
R3/RRR3-12/3	1132.081	1132.297	-191.939	0.323	694.558	0.293	17	0.089	R.LQQAPPPPQR.Q
R3/RRR3-8/2	1075.198	1074.250	-48.466	0.488	664.443	0.383	13	0.140	-.IVCTLGPASR.-
R3/RRR3-8/2	1073.804	1074.250	-416.475	0.378	688.612	0.312	14	0.136	-.IVCTLGPASR.-
R3/RRR3-8/2	1073.907	1074.250	-319.983	0.444	652.706	0.313	13	0.129	-.IVCTLGPASR.-
R3/RRR3-11/2	1152.068	1152.325	-223.881	0.502	1454.184	0.302	16	0.176	K.VLQENNPIPK.L
R3/RRR3-11/2	1152.202	1152.325	-107.603	0.502	1143.516	0.396	15	0.169	K.VLQENNPIPK.L
R3/RRR3-11/2	1152.120	1152.325	-178.493	0.460	997.168	0.365	14	0.154	K.VLQENNPIPK.L
R3/RRR3-10/2	1994.619	1994.233	193.811	0.440	799.638	0.416	19	0.146	K.GYNNIFAIGDITDIPEIK.Q
R3/RRR3-10/2	1994.822	1994.233	-207.001	0.422	676.625	0.365	18	0.136	K.GYNNIFAIGDITDIPEIK.Q
R3/RRR3-7/2	968.674	969.119	-460.348	0.473	820.211	0.396	13	0.152	R.FTDFALVR.K
R3/RRR3-7/2	1622.385	1622.803	-258.445	0.390	813.140	0.439	19	0.154	R.ELGQWGLDNYLSVK.Q
R3/RRR3-8/2	1622.177	1622.803	-1005.244	0.292	345.575	0.331	17	0.136	R.ELGQWGLDNYLSVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1622.072	1622.803	-1070.148	0.168	154.179	0.287	13	0.134	R.ELGQWGLDNYLSVK.Q
R3/RRR3-13/2	1512.857	1512.735	81.124	0.409	1308.417	0.350	18	0.171	K.TLRENVALSSFFK.I
R3/RRR3-18/2	1110.610	1111.275	-1504.108	0.427	1069.764	0.408	15	0.167	R.FFLQDATLR.Q
R3/RRR3-18/2	1111.819	1111.275	-411.045	0.531	967.017	0.413	15	0.163	R.FFLQDATLR.Q
R3/RRR3-18/2	1110.417	1111.275	-1678.582	0.242	1095.532	0.143	14	0.135	R.FFLQDATLR.Q
R3/RRR3-17/2	1110.783	1111.275	-443.945	0.330	525.995	0.239	12	0.135	R.FFLQDATLR.Q
R3/RRR3-7/3	1373.159	1373.542	-280.173	0.488	937.294	0.397	21	0.106	-.IYAHSSIGQLQR.-
R3/RRR3-7/3	1373.485	1373.542	-41.560	0.501	1060.525	0.289	22	0.097	-.IYAHSSIGQLQR.-
R3/RRR3-7/3	1372.727	1373.542	-1326.263	0.429	804.456	0.321	20	0.094	-.IYAHSSIGQLQR.-
R3/RRR3-16/3	1374.386	1373.542	-114.003	0.378	1369.318	0.118	25	0.084	K.IYAHSSIGQLQR.A
R3/RRR3-4/3	1764.365	1765.007	-933.887	0.372	871.739	0.408	24	0.105	R.VLQLINVTDTGVHAQR.Y
R3/RRR3-4/3	1764.744	1765.007	-149.493	0.351	655.489	0.351	21	0.091	R.VLQLINVTDTGVHAQR.Y
R3/RRR3-11/2	1176.948	1177.289	-290.408	0.250	654.112	0.466	12	0.140	K.GYDPEVIDIR.S
R3/RRR3-24/2	1370.156	1370.577	-307.988	0.385	1037.976	0.414	17	0.162	K.TPIQNLKDAIEK.L
R3/RRR3-24/2	1369.891	1370.577	-1234.528	0.391	727.657	0.423	16	0.148	K.TPIQNLKDAIEK.L
R3/RRR3-4/3	1165.048	1165.367	-275.153	0.475	1003.902	0.400	18	0.113	R.HISILKDNPK.I
R3/RRR3-4/3	1165.000	1165.367	-316.151	0.455	1085.099	0.338	18	0.106	R.HISILKDNPK.I
R3/RRR3-4/3	1165.694	1165.367	281.466	0.474	1060.702	0.342	18	0.106	R.HISILKDNPK.I
R3/RRR3-18/2	1183.433	1183.466	-27.894	0.371	689.753	0.442	14	0.146	K.TPIGILNITLK.Q
R3/RRR3-4/2	1023.482	1023.188	287.955	0.394	840.271	0.423	12	0.153	-.GKDLEM*WK.-
R3/RRR3-7/2	1506.828	1507.670	-1226.261	0.324	1452.035	0.261	18	0.168	K.IFEVGDVVTLDGSR.D
R3/RRR3-13/3	1402.011	1400.737	196.209	0.375	1026.190	0.327	23	0.101	R.LIHILPPKAIER.K
R3/RRR3-13/3	1400.910	1400.737	123.518	0.327	910.080	0.269	22	0.090	R.LIHILPPKAIER.K
R3/RRR3-13/3	1401.425	1400.737	-223.195	0.399	823.859	0.259	23	0.090	R.LIHILPPKAIER.K
R3/RRR3-11/2	1309.367	1309.452	-65.232	0.350	1177.709	0.374	15	0.165	R.TLEEIQWSFR.-
R3/RRR3-4/2	1178.566	1178.320	209.163	0.307	787.499	0.412	14	0.147	K.YTSDPGLVLGR.Q
R3/RRR3-8/2	1177.635	1178.320	-1435.344	0.216	703.702	0.228	13	0.129	K.YTSDPGLVLGR.Q
R3/RRR3-4/2	1178.565	1178.320	208.540	0.237	788.762	0.168	15	0.129	K.YTSDPGLVLGR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-14/3	1512.401	1512.650	-165.004	0.490	822.557	0.398	23	0.105	K.LAIRDHESDTNLK.N
R3/RRR3-14/3	1512.086	1512.650	-1037.754	0.398	698.691	0.355	23	0.096	K.LAIRDHESDTNLK.N
R3/RRR3-9/2	1242.288	1242.490	-163.271	0.461	602.976	0.383	17	0.146	R.LATNLENLILK.E
R3/RRR3-9/2	1242.384	1242.490	-85.503	0.450	711.400	0.329	18	0.144	R.LATNLENLILK.E
R3/RRR3-9/2	1241.801	1242.490	-1364.036	0.380	529.084	0.364	16	0.142	R.LATNLENLILK.E
R3/RRR3-12/2	1141.910	1142.292	-335.559	0.384	1010.805	0.410	16	0.163	K.TIFHLNPSGR.F
R3/RRR3-10/2	1143.113	1142.292	-157.407	0.382	1075.846	0.377	17	0.163	K.TIFHLNPSGR.F
R3/RRR3-9/2	1141.576	1142.292	-1508.353	0.399	1066.208	0.378	16	0.162	K.TIFHLNPSGR.F
R3/RRR3-9/2	1142.146	1142.292	-128.382	0.360	1020.175	0.349	16	0.155	K.TIFHLNPSGR.F
R3/RRR3-9/2	1142.289	1142.292	-2.745	0.375	888.576	0.364	15	0.151	K.TIFHLNPSGR.F
R3/RRR3-12/2	1142.152	1142.292	-122.914	0.324	582.339	0.342	13	0.139	-.TIFHLNPSGR.-
R3/RRR3-13/2	1141.372	1142.292	-1687.229	0.335	583.294	0.345	12	0.136	-.TIFHLNPSGR.-
R3/RRR3-22/2	1142.952	1142.292	-298.296	0.274	341.858	0.381	10	0.133	-.TIFHLNPSGR.-
R3/RRR3-4/2	1032.508	1033.246	-1687.845	0.383	878.881	0.410	15	0.155	K.TFASGIIVPK.K
R3/RRR3-4/2	1033.002	1033.246	-237.004	0.409	832.644	0.414	14	0.153	K.TFASGIIVPK.K
R3/RRR3-4/2	1032.442	1033.246	-1751.872	0.244	618.559	0.379	12	0.136	K.TFASGIIVPK.K
R3/RRR3-11/2	1627.994	1627.860	82.757	0.547	1252.451	0.346	16	0.163	R.IFEDMCAQMYYR.G
R3/RRR3-11/2	1628.285	1627.860	262.079	0.329	487.936	0.371	12	0.134	R.IFEDMCAQMYYR.G
R3/RRR3-2/2	1548.237	1547.885	228.054	0.428	709.018	0.418	17	0.148	R.M*SINVVRLGILCR.L
R3/RRR3-2/2	1548.388	1547.885	-322.241	0.416	365.873	0.323	14	0.134	-.M*SINVVRLGILCR.-
R3/RRR3-2/2	1547.403	1547.885	-312.555	0.325	525.116	0.282	15	0.133	R.M*SINVVRLGILCR.L
R3/RRR3-10/3	1489.662	1489.612	33.886	0.436	1217.244	0.365	25	0.118	K.FKNEPESGPQLDK.F
R3/RRR3-10/3	1488.965	1489.612	-1109.044	0.393	1039.495	0.348	23	0.104	K.FKNEPESGPQLDK.F
R3/RRR3-27/2	1087.271	1087.210	56.236	0.464	911.567	0.405	14	0.158	R.GYISYQSLR.R
R3/RRR3-27/2	1086.822	1087.210	-358.313	0.408	1024.877	0.356	14	0.157	R.GYISYQSLR.R
R3/RRR3-28/2	1086.889	1087.210	-296.560	0.371	967.353	0.349	14	0.153	R.GYISYQSLR.R
R3/RRR3-27/2	1087.117	1087.210	-85.664	0.480	892.835	0.347	14	0.150	R.GYISYQSLR.R
R3/RRR3-28/2	1086.394	1087.210	-1676.818	0.301	931.765	0.349	14	0.149	R.GYISYQSLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1593.999	1592.898	63.734	0.400	650.544	0.412	15	0.138	R.RGPHM*ARLAAAAVVR.S
R3/RRR3-5/3	1420.058	1420.599	-1088.453	0.463	1019.633	0.388	21	0.111	R.DRDLIISPHPTR.N
R3/RRR3-5/3	1420.304	1420.599	-208.095	0.483	846.795	0.399	19	0.106	R.DRDLIISPHPTR.N
R3/RRR3-6/3	1420.700	1420.599	70.994	0.467	771.847	0.374	19	0.100	R.DRDLIISPHPTR.N
R3/RRR3-17/3	1584.968	1584.795	110.024	0.407	895.018	0.419	23	0.107	R.TPEFLLEVEELHK.V
R3/RRR3-9/2	1702.127	1700.912	126.915	0.422	678.727	0.401	17	0.140	K.VFDILGPDFDALSYK.M
R3/RRR3-5/3	1457.375	1456.764	-267.470	0.550	1093.889	0.339	23	0.106	-.RPLVLQLVHQPR.-
R3/RRR3-9/2	1262.970	1263.453	-383.205	0.291	654.764	0.444	13	0.138	R.LAAAAAASSM*RAR.V
R3/RRR3-5/2	1020.317	1021.149	-1800.290	0.418	927.316	0.402	14	0.158	R.YADLLNSPK.K
R3/RRR3-5/2	1021.120	1021.149	-28.251	0.419	685.067	0.427	13	0.150	R.YADLLNSPK.K
R3/RRR3-5/2	1020.340	1021.149	-1777.931	0.356	653.305	0.362	12	0.141	R.YADLLNSPK.K
R3/RRR3-9/2	1146.024	1146.321	-259.570	0.376	948.676	0.412	14	0.156	R.ITEGVNLPFR.V
R3/RRR3-8/2	1162.970	1163.353	-330.746	0.395	808.556	0.424	15	0.153	R.VFVNAWALSR.D
R3/RRR3-8/2	1162.756	1163.353	-1377.685	0.280	392.860	0.286	11	0.108	-.VFVNAWALSR.-
R3/RRR3-10/3	1514.231	1513.637	-268.949	0.406	843.593	0.419	23	0.107	K.YPGIHNPLDETTR.I
R3/RRR3-10/3	1513.982	1513.637	228.765	0.382	962.541	0.174	22	0.082	-.YPGIHNPLDETTR.-
R3/RRR3-10/3	1514.036	1513.637	264.298	0.365	626.822	0.250	20	0.074	-.YPGIHNPLDETTR.-
R3/RRR3-16/3	1620.478	1621.916	-1509.337	0.337	1065.989	0.397	24	0.110	R.VLM*IRTAM*SHHHR.C
R3/RRR3-17/2	922.425	923.048	-1765.302	0.374	916.758	0.411	12	0.100	K.ISEYGVRV.-
R3/RRR3-16/2	1108.804	1109.171	-331.996	0.373	1033.162	0.403	17	0.162	K.YDSAISPEAR.Q
R3/RRR3-16/2	1109.078	1109.171	-84.188	0.449	898.065	0.429	16	0.160	K.YDSAISPEAR.Q
R3/RRR3-22/2	1031.186	1032.136	-1897.318	0.261	725.853	0.445	12	0.144	K.HGWDYVVR.K
R3/RRR3-14/2	1383.254	1383.577	-234.260	0.475	764.100	0.393	18	0.144	K.SSSVFIPHGPGAVK.D
R3/RRR3-13/2	1124.241	1123.286	-39.926	0.399	850.021	0.412	15	0.155	R.VPTDIFFQR.X
R3/RRR3-13/2	1122.971	1123.286	-281.362	0.298	489.715	0.470	12	0.142	R.VPTDIFFQR.X
R3/RRR3-12/2	1020.696	1020.124	-420.332	0.415	830.109	0.408	15	0.152	R.ALAGAAEGFGR.R
R3/RRR3-12/2	1020.303	1020.124	176.267	0.325	647.710	0.416	15	0.144	R.ALAGAAEGFGR.R
R3/RRR3-12/2	1020.214	1020.124	88.195	0.345	548.143	0.329	14	0.132	-.ALAGAAEGFGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-4/2	1417.448	1417.575	-89.992	0.370	1003.843	0.217	17	0.135	-.M*AAVANGGAAPEWR.-
R3/RRR3-4/2	1264.593	1264.645	-41.401	0.340	696.563	0.427	14	0.146	R.TVVVTIIFMIK.L
R3/RRR3-4/2	1264.976	1264.645	262.338	0.372	676.797	0.392	14	0.144	R.TVVVTIIFMIK.L
R3/RRR3-4/2	1264.945	1264.645	237.565	0.356	490.737	0.369	12	0.137	R.TVVVTIIFMIK.L
R3/RRR3-16/2	765.899	766.007	-140.854	0.391	571.303	0.400	11	0.146	R.LPVVIPK.I
R3/RRR3-16/2	765.888	766.007	-155.404	0.425	475.378	0.369	10	0.143	R.LPVVIPK.I
R3/RRR3-17/2	1409.614	1410.684	-1472.646	0.343	729.878	0.426	17	0.144	R.SIGPVEGLALNLVK.D
R3/RRR3-17/2	1203.044	1203.371	-272.507	0.408	909.685	0.407	19	0.157	R.ASPTTALTLATR.A
R3/RRR3-16/2	1203.040	1203.371	-275.357	0.354	950.272	0.319	18	0.147	R.ASPTTALTLATR.A
R3/RRR3-16/2	1202.868	1203.371	-1252.960	0.304	825.291	0.175	18	0.131	R.ASPTTALTLATR.A
R3/RRR3-4/2	1037.133	1037.198	-62.522	0.198	1090.032	0.349	15	0.151	R.VVVQGAGPGPR.Y
R3/RRR3-4/2	1036.627	1037.198	-1519.563	0.173	908.558	0.339	14	0.139	R.VVVQGAGPGPR.Y
R3/RRR3-2/2	1038.059	1037.198	-133.471	0.194	740.966	0.118	14	0.126	R.VVVQGAGPGPR.Y
R3/RRR3-2/2	1431.201	1431.702	-1051.609	0.463	1151.306	0.331	17	0.156	R.GIPIYAISQVLEK.I
R3/RRR3-2/2	1431.146	1431.702	-1090.405	0.284	1000.346	0.293	16	0.142	R.GIPIYAISQVLEK.I
R3/RRR3-3/2	1058.139	1057.226	-82.456	0.414	759.375	0.362	14	0.143	R.LDLAGELLGR.E
R3/RRR3-18/2	1044.125	1044.227	-98.220	0.425	946.981	0.400	16	0.157	K.VLVLGDAATGK.T
R3/RRR3-18/2	1043.372	1044.227	-1783.276	0.359	783.122	0.442	14	0.152	K.VLVLGDAATGK.T
R3/RRR3-18/2	1043.703	1044.227	-1464.919	0.273	1005.167	0.310	16	0.147	K.VLVLGDAATGK.T
R3/RRR3-19/2	1043.844	1044.227	-367.905	0.290	588.114	0.270	13	0.133	K.VLVLGDAATGK.T
R3/RRR3-7/2	1543.237	1541.731	-320.968	0.380	1366.479	0.303	18	0.169	-.ESDLAAAVAVAPVATR.-
R3/RRR3-6/2	1542.903	1541.731	111.921	0.270	935.191	0.181	16	0.130	-.ESDLAAAVAVAPVATR.-
R3/RRR3-5/2	1233.391	1234.387	-1623.196	0.376	1452.340	0.290	17	0.176	R.LLQYGEQNIR.R
R3/RRR3-5/2	1234.091	1234.387	-240.253	0.449	1125.076	0.261	16	0.148	R.LLQYGEQNIR.R
R3/RRR3-7/2	1104.422	1104.155	242.938	0.272	691.849	0.429	12	0.141	-.HSVEAEEFR.-
R3/RRR3-19/2	1197.283	1197.234	41.763	0.433	1121.519	0.372	18	0.165	R.FEDGSISDQAK.R
R3/RRR3-19/2	1198.166	1197.234	-56.367	0.480	1036.902	0.407	17	0.164	-.FEDGSISDQAK.-
R3/RRR3-19/2	1197.160	1197.234	-62.040	0.438	813.432	0.419	16	0.154	R.FEDGSISDQAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	1155.501	1156.359	-1612.453	0.421	733.385	0.401	14	0.146	R.TPLLVAWAER.V
R3/RRR3-1/2	1306.186	1305.523	-258.714	0.422	1512.422	0.249	18	0.172	R.M*TSLPDVDIAVK.Y
R3/RRR3-5/2	1306.403	1305.523	-92.131	0.381	1304.313	0.124	18	0.139	R.M*TSLPDVDIAVK.Y
R3/RRR3-11/2	1306.226	1305.523	-228.243	0.439	1088.227	0.197	16	0.136	R.M*TSLPDVDIAVK.Y
R3/RRR3-3/2	1306.503	1305.523	-15.654	0.367	1069.401	0.069	16	0.124	R.M*TSLPDVDIAVK.Y
R3/RRR3-21/2	1476.161	1477.516	-1600.427	0.226	276.454	0.346	12	0.133	R.GEEETRGEAGGKEK.E
R3/RRR3-27/2	1476.348	1477.516	-1473.338	0.293	467.781	0.264	13	0.131	R.GEEETRGEAGGKEK.E
R3/RRR3-24/2	1476.838	1477.516	-1139.905	0.221	546.704	0.226	14	0.129	R.GEEETRGEAGGKEK.E
R3/RRR3-3/2	1476.496	1477.516	-1372.687	0.209	584.150	0.126	14	0.126	R.GEEETRGEAGGKEK.E
R3/RRR3-20/2	1476.428	1477.516	-1418.775	0.229	816.036	0.066	14	0.122	R.GEEETRGEAGGKEK.E
R3/RRR3-9/3	1445.004	1445.479	-330.130	0.420	1143.788	0.366	26	0.115	K.AGHQTSAESWGTGR.A
R3/RRR3-9/3	1444.672	1445.479	-1254.579	0.362	744.448	0.370	22	0.101	K.AGHQTSAESWGTGR.A
R3/RRR3-10/3	1446.127	1445.479	-244.066	0.463	580.296	0.386	19	0.100	K.AGHQTSAESWGTGR.A
R3/RRR3-10/3	1445.795	1445.479	219.314	0.361	881.138	0.310	24	0.097	K.AGHQTSAESWGTGR.A
R3/RRR3-25/3	1445.561	1445.479	57.110	0.404	769.990	0.315	22	0.096	K.AGHQTSAESWGTGR.A
R3/RRR3-10/3	1445.465	1445.479	-9.844	0.403	474.509	0.412	18	0.095	-.AGHQTSAESWGTGR.-
R3/RRR3-9/3	1445.701	1445.479	154.033	0.423	584.973	0.361	19	0.094	-.AGHQTSAESWGTGR.-
R3/RRR3-25/3	1444.798	1445.479	-1167.269	0.372	962.499	0.258	24	0.093	K.AGHQTSAESWGTGR.A
R3/RRR3-7/3	1445.381	1445.479	-68.421	0.398	584.911	0.292	20	0.090	-.AGHQTSAESWGTGR.-
R3/RRR3-26/3	1445.465	1445.479	-9.717	0.355	704.282	0.204	20	0.073	-.AGHQTSAESWGTGR.-
R3/RRR3-14/2	1497.262	1497.679	-278.816	0.378	938.274	0.403	19	0.154	K.IDWSGAPFVVSYR.G
R3/RRR3-12/3	1671.360	1671.744	-230.588	0.386	803.311	0.408	22	0.104	K.IGHVETEPDTAASESK.T
R3/RRR3-12/3	1671.436	1671.744	-184.868	0.393	1086.676	0.282	27	0.097	K.IGHVETEPDTAASESK.T
R3/RRR3-12/3	1670.999	1671.744	-1047.395	0.346	694.479	0.318	23	0.091	K.IGHVETEPDTAASESK.T
R3/RRR3-9/3	1990.709	1991.228	-765.308	0.441	962.179	0.377	24	0.104	R.GAQDDKCLPIQYLEAIR.G
R3/RRR3-8/2	1719.493	1718.932	-256.168	0.491	1163.922	0.350	18	0.157	R.TTLFLNLANDPTIER.I
R3/RRR3-10/2	1445.640	1445.642	-1.661	0.354	621.171	0.409	15	0.139	R.ENIDPSVIGPIYK.Y
R3/RRR3-17/2	872.060	872.004	63.726	0.465	1195.917	0.351	13	0.166	K.LAEQLAAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-17/2	872.057	872.004	60.637	0.445	967.465	0.334	12	0.150	K.LAEQLAAR.K
R3/RRR3-23/3	1029.413	1030.120	-1663.138	0.463	1698.459	0.138	20	0.101	K.EQEVRNVR.L
R3/RRR3-24/3	1029.859	1030.120	-254.800	0.444	1581.062	0.150	19	0.097	K.EQEVRNVR.L
R3/RRR3-12/3	1718.413	1718.851	-255.553	0.468	1044.527	0.367	28	0.108	K.RLTSSDADVQAEAAKR.W
R3/RRR3-19/2	1697.913	1697.782	77.186	0.413	1160.204	0.357	19	0.159	K.DGDGIVSLSETYDGLR.A
R3/RRR3-15/3	1356.810	1356.509	222.869	0.439	800.430	0.394	23	0.103	K.QDPQFLLEHTK.K
R3/RRR3-15/3	1356.250	1356.509	-191.134	0.352	732.200	0.350	21	0.095	K.QDPQFLLEHTK.K
R3/RRR3-17/2	1057.517	1058.254	-1647.235	0.262	704.415	0.433	14	0.142	K.VVLLGDTGVGK.S
R3/RRR3-18/2	1057.695	1058.254	-1477.835	0.267	362.028	0.425	10	0.100	-.VVLLGDTGVGK.-
R3/RRR3-10/2	1613.107	1612.870	147.302	0.374	1139.436	0.345	19	0.157	R.EVFSAVLM*SSDILGK.S
R3/RRR3-24/2	1622.401	1621.908	305.139	0.469	1007.695	0.362	17	0.150	R.RAFDFRLGIGEVIK.G
R3/RRR3-18/2	1344.641	1345.575	-1443.007	0.400	1036.671	0.388	17	0.159	K.SALRPLQFVSAR.-
R3/RRR3-18/2	1345.408	1345.575	-125.003	0.382	525.395	0.367	14	0.137	K.SALRPLQFVSAR.-
R3/RRR3-18/3	1346.198	1345.575	-281.146	0.521	931.510	0.483	25	0.123	K.SALRPLQFVSAR.-
R3/RRR3-18/3	1345.672	1345.575	71.858	0.436	820.002	0.468	23	0.113	K.SALRPLQFVSAR.-
R3/RRR3-22/3	1611.620	1611.800	-112.175	0.415	1011.370	0.385	25	0.109	K.KIM*TSTVDVKDDSR.S
R3/RRR3-22/3	1611.524	1611.800	-172.013	0.370	927.481	0.368	25	0.102	K.KIM*TSTVDVKDDSR.S
R3/RRR3-11/2	989.077	989.148	-72.059	0.286	1139.296	0.355	14	0.159	R.VTVISTSPGK.R
R3/RRR3-10/2	988.558	989.148	-1613.579	0.216	864.950	0.141	13	0.127	R.VTVISTSPGK.R
R3/RRR3-10/2	1594.244	1593.841	253.621	0.355	741.282	0.402	14	0.140	K.TTCSSILSILLASAR.Q
R3/RRR3-10/2	1594.312	1593.841	296.155	0.380	888.701	0.325	16	0.140	K.TTCSSILSILLASAR.Q
R3/RRR3-12/2	950.104	950.074	32.460	0.382	786.955	0.406	14	0.151	R.TPIAAYASR.D
R3/RRR3-12/2	949.645	950.074	-452.554	0.396	770.155	0.367	13	0.146	R.TPIAAYASR.D
R3/RRR3-6/2	964.229	965.088	-1934.408	0.289	1160.940	0.330	14	0.158	R.AGVANYTLR.A
R3/RRR3-6/2	964.888	965.088	-207.736	0.290	1037.995	0.267	14	0.144	R.AGVANYTLR.A
R3/RRR3-11/2	1000.987	1001.202	-214.983	0.410	1008.983	0.380	15	0.159	K.VTVLQDVVK.G
R3/RRR3-11/2	1000.306	1001.202	-1901.177	0.304	683.836	0.325	13	0.137	-.VTVLQDVVK.-
R3/RRR3-14/2	1469.738	1468.591	100.582	0.367	746.578	0.405	16	0.143	K.SSQGSNELLEYLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-13/3	1507.395	1507.652	-171.392	0.519	1496.954	0.250	25	0.113	R.KQM*DQTDQVIER.S
R3/RRR3-13/3	1507.449	1507.652	-134.837	0.438	1136.980	0.250	24	0.094	-.KQM*DQTDQVIER.-
R3/RRR3-13/3	1507.217	1507.652	-289.729	0.495	1076.220	0.214	24	0.088	R.KQM*DQTDQVIER.S
R3/RRR3-13/2	1406.100	1405.581	-343.130	0.422	999.929	0.380	17	0.155	-.GLLASDQVLFADR.-
R3/RRR3-8/3	1451.762	1451.691	49.107	0.531	1091.073	0.335	23	0.106	R.DLKPENFLFLSK.S
R3/RRR3-8/3	1451.451	1451.691	-165.986	0.482	764.406	0.245	20	0.086	-.DLKPENFLFLSK.-
R3/RRR3-24/2	1605.130	1604.894	147.610	0.330	1352.746	0.285	18	0.163	-.M*LSTQALLGAIGVGEK.S
R3/RRR3-24/2	1604.451	1604.894	-276.614	0.272	956.942	0.083	16	0.124	-.M*LSTQALLGAIGVGEK.-
R3/RRR3-10/2	1102.004	1102.308	-276.493	0.319	1071.148	0.373	14	0.158	K.VLLQQEPFK.S
R3/RRR3-9/2	1101.939	1102.308	-335.954	0.274	439.224	0.267	10	0.127	-.VLLQQEPFK.-
R3/RRR3-12/2	999.224	1000.174	-1957.088	0.267	611.546	0.421	12	0.139	K.GNVISTPAIK.G
R3/RRR3-12/2	999.794	1000.174	-381.727	0.305	550.946	0.401	11	0.137	K.GNVISTPAIK.G
R3/RRR3-17/3	1236.905	1237.347	-359.045	0.449	712.721	0.367	20	0.100	K.VRDGEAYVATR.K
R3/RRR3-17/3	1237.512	1237.347	133.247	0.453	1028.170	0.311	22	0.098	-.VRDGEAYVATR.-
R3/RRR3-17/3	1236.966	1237.347	-308.843	0.390	850.902	0.284	20	0.092	K.VRDGEAYVATR.K
R3/RRR3-20/2	1144.151	1143.315	-144.209	0.408	1159.419	0.351	15	0.172	K.VSGAEVILNQI.-
R3/RRR3-8/2	1130.302	1131.331	-1800.882	0.331	971.908	0.384	17	0.154	R.VAGM*VTPAAAAR.S
R3/RRR3-17/2	1130.595	1131.331	-1540.510	0.387	782.976	0.372	17	0.147	R.VAGM*VTPAAAAR.S
R3/RRR3-17/2	1130.963	1131.331	-326.321	0.335	575.678	0.275	16	0.135	R.VAGM*VTPAAAAR.S
R3/RRR3-16/2	1130.651	1131.331	-1490.946	0.271	605.864	0.306	15	0.135	R.VAGM*VTPAAAAR.S
R3/RRR3-5/2	1616.389	1616.840	-279.704	0.449	1244.010	0.318	21	0.162	K.FQQLSPEIVQIEGK.D
R3/RRR3-25/2	982.114	982.244	-132.596	0.465	938.628	0.373	13	0.156	K.LAVLKFYK.V
R3/RRR3-25/2	981.519	982.244	-1762.055	0.409	795.183	0.413	13	0.155	K.LAVLKFYK.V
R3/RRR3-25/2	982.161	982.244	-84.720	0.458	737.244	0.389	13	0.152	K.LAVLKFYK.V
R3/RRR3-24/2	982.036	982.244	-212.400	0.520	746.068	0.385	13	0.152	K.LAVLKFYK.V
R3/RRR3-24/2	981.509	982.244	-1772.302	0.387	792.892	0.368	13	0.150	K.LAVLKFYK.V
R3/RRR3-24/2	982.093	982.244	-154.167	0.384	892.236	0.333	13	0.149	K.LAVLKFYK.V
R3/RRR3-8/2	1231.829	1231.381	365.014	0.454	816.322	0.364	15	0.151	R.LHFHDCFVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-8/2	1231.180	1231.381	-164.048	0.410	764.376	0.281	14	0.141	R.LHFHDCFVR.-
R3/RRR3-9/2	1230.931	1231.381	-366.894	0.389	864.308	0.200	15	0.136	R.LHFHDCFVR.-
R3/RRR3-10/2	1230.974	1231.381	-331.969	0.376	632.844	0.233	13	0.136	R.LHFHDCFVR.-
R3/RRR3-9/2	1230.513	1231.381	-1522.915	0.323	612.987	0.225	13	0.135	R.LHFHDCFVR.-
R3/RRR3-8/2	1231.050	1231.381	-269.589	0.386	625.086	0.188	13	0.133	R.LHFHDCFVR.-
R3/RRR3-9/3	1231.051	1231.381	-268.804	0.434	853.738	0.412	20	0.107	R.LHFHDCFVR.-
R3/RRR3-12/3	1231.059	1231.381	-262.089	0.398	819.804	0.414	18	0.107	R.LHFHDCFVR.-
R3/RRR3-10/3	1231.163	1231.381	-177.785	0.407	680.028	0.366	18	0.100	R.LHFHDCFVR.-
R3/RRR3-10/3	1231.205	1231.381	-143.321	0.360	709.095	0.377	18	0.100	R.LHFHDCFVR.-
R3/RRR3-8/3	1231.442	1231.381	49.840	0.418	977.537	0.341	21	0.100	R.LHFHDCFVR.-
R3/RRR3-9/3	1231.780	1231.381	324.761	0.363	713.508	0.354	18	0.098	R.LHFHDCFVR.-
R3/RRR3-8/3	1231.527	1231.381	119.181	0.420	735.705	0.337	19	0.098	R.LHFHDCFVR.-
R3/RRR3-11/3	1230.960	1231.381	-342.825	0.357	925.125	0.248	19	0.089	R.LHFHDCFVR.-
R3/RRR3-11/2	1194.927	1195.503	-1323.113	0.318	1474.637	0.212	15	0.164	R.FM*KIKVVGTR.-
R3/RRR3-29/2	1195.206	1195.503	-249.031	0.358	1236.775	0.270	14	0.155	R.FM*KIKVVGTR.-
R3/RRR3-6/2	1088.525	1089.231	-1572.304	0.430	1112.201	0.356	15	0.160	K.GWAGVQAFPR.K
R3/RRR3-6/2	1088.183	1089.231	-1887.614	0.338	939.765	0.339	14	0.147	K.GWAGVQAFPR.K
R3/RRR3-17/2	1095.781	1095.209	-391.865	0.270	691.714	0.406	13	0.139	R.TVSDGM*AELR.L
R3/RRR3-6/2	1144.186	1144.305	-104.184	0.395	870.882	0.377	18	0.150	R.FDLSGIAPAPR.G
R3/RRR3-4/2	1435.413	1435.561	-103.261	0.442	927.101	0.341	16	0.144	K.FGEDGGIQELLEK.A
R3/RRR3-4/2	1392.566	1392.587	-15.440	0.378	1066.423	0.367	16	0.156	K.NVAYSIIAAGWAR.V
R3/RRR3-4/2	1392.535	1392.587	-37.861	0.346	628.993	0.434	15	0.143	K.NVAYSIIAAGWAR.V
R3/RRR3-7/2	944.730	944.152	-448.558	0.355	612.906	0.385	13	0.143	K.SVVFGPLPK.T
R3/RRR3-7/2	944.077	944.152	-79.643	0.300	570.542	0.389	12	0.138	-.SVVFGPLPK.-
R3/RRR3-27/2	975.795	976.070	-282.078	0.404	686.341	0.348	11	0.144	R.FYQAQYR.N
R3/RRR3-27/2	975.251	976.070	-1870.111	0.309	562.317	0.378	10	0.140	R.FYQAQYR.N
R3/RRR3-6/2	1463.486	1463.621	-92.413	0.292	1100.460	0.336	20	0.152	R.ATGGADAAAALAAYLR.G
R3/RRR3-23/2	1131.472	1131.225	219.059	0.327	834.547	0.398	16	0.150	R.NITVNQAQSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-24/2	1131.452	1131.225	201.100	0.335	816.664	0.379	16	0.148	R.NITVNQAQSR.G
R3/RRR3-24/2	1131.919	1131.225	-270.809	0.435	583.836	0.385	14	0.144	R.NITVNQAQSR.G
R3/RRR3-12/2	1127.034	1127.233	-177.143	0.446	733.973	0.365	13	0.144	R.QVQAADPELR.V
R3/RRR3-12/2	1126.570	1127.233	-1480.516	0.409	832.956	0.277	14	0.139	R.QVQAADPELR.V
R3/RRR3-15/2	1127.277	1127.233	38.926	0.412	708.826	0.257	14	0.136	R.QVQAADPELR.V
R3/RRR3-15/2	1127.031	1127.233	-179.642	0.350	581.456	0.233	13	0.134	R.QVQAADPELR.V
R3/RRR3-12/2	1127.139	1127.233	-83.708	0.386	542.255	0.256	12	0.133	-.QVQAADPELR.-
R3/RRR3-12/3	1707.693	1707.909	-127.027	0.388	1074.210	0.351	26	0.105	R.AGRPEVPVAEGSAEPLK.G
R3/RRR3-9/2	1020.946	1021.066	-117.179	0.464	755.963	0.350	14	0.146	K.FGDPTEQAR.A
R3/RRR3-9/2	1020.828	1021.066	-233.413	0.419	725.089	0.347	14	0.145	K.FGDPTEQAR.A
R3/RRR3-9/2	1020.358	1021.066	-1678.966	0.367	779.075	0.330	14	0.144	K.FGDPTEQAR.A
R3/RRR3-19/2	1271.966	1272.390	-334.554	0.357	726.514	0.390	16	0.146	K.VLTPISQDDQR.Q
R3/RRR3-19/2	1272.125	1272.390	-209.201	0.292	719.343	0.390	16	0.144	K.VLTPISQDDQR.Q
R3/RRR3-19/2	1272.129	1272.390	-205.928	0.327	781.855	0.333	17	0.143	K.VLTPISQDDQR.Q
R3/RRR3-13/2	1085.159	1085.239	-73.633	0.310	686.850	0.402	14	0.140	K.LGLVGDLANGR.T
R3/RRR3-9/2	1626.584	1626.838	-156.763	0.444	1069.223	0.341	18	0.152	K.GSSQVIAQYYQLIR.H
R3/RRR3-8/2	907.038	907.006	35.756	0.395	854.337	0.384	12	0.151	K.TFATVDPR.T
R3/RRR3-8/2	906.998	907.006	-8.249	0.322	973.057	0.300	13	0.146	K.TFATVDPR.T
R3/RRR3-21/3	1020.229	1021.210	-1947.310	0.342	869.996	0.374	18	0.097	K.CPLIAM*GSR.G
R3/RRR3-17/3	1138.811	1139.333	-1341.029	0.445	910.519	0.368	20	0.103	R.KHTAASVVLGR.D
R3/RRR3-17/3	1138.864	1139.333	-413.498	0.355	779.175	0.196	19	0.072	-.KHTAASVVLGR.-
R3/RRR3-9/2	1157.964	1158.373	-354.592	0.361	673.531	0.385	15	0.141	K.LTLAGDVTIVR.E
R3/RRR3-21/2	1257.520	1258.450	-1538.694	0.339	1454.657	0.225	16	0.164	K.NILLLDSEGKR.V
R3/RRR3-14/2	1459.678	1459.669	6.324	0.349	1260.130	0.302	18	0.161	R.SPWSTLDIIAEVK.Q
R3/RRR3-14/2	1460.981	1459.669	214.488	0.248	393.835	0.297	14	0.131	R.SPWSTLDIIAEVK.Q
R3/RRR3-13/2	977.820	977.099	-285.814	0.428	1061.433	0.351	15	0.157	R.DVAGAVAAFR.A
R3/RRR3-13/2	977.150	977.099	52.675	0.385	841.565	0.309	14	0.142	R.DVAGAVAAFR.A
R3/RRR3-13/2	977.009	977.099	-92.060	0.418	874.941	0.285	14	0.141	R.DVAGAVAAFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R3/RRR3-7/2	976.892	977.099	-212.265	-0.037	502.758	0.064	10	0.123	-.DVAGAVAAFR.-
R4/RRR4-2/2	1846.640	1847.062	-229.049	0.659	3692.661	0.636	29	0.757	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/2	1846.524	1847.062	-835.104	0.640	3335.747	0.635	28	0.646	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/1	1436.739	1437.534	-1252.880	0.158	979.753	0.138	17	0.538	R.AAEEANVYDDLVK.Y
R4/RRR4-2/2	1846.419	1847.062	-892.178	0.629	2785.826	0.643	26	0.501	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/2	1565.256	1565.711	-291.892	0.593	2716.604	0.538	24	0.440	R.SQALEAHAASFASFK.V
R4/RRR4-2/2	1565.309	1565.711	-258.091	0.582	2635.203	0.582	24	0.440	R.SQALEAHAASFASFK.V
R4/RRR4-2/2	1566.325	1565.711	-247.293	0.588	2552.967	0.591	24	0.426	R.SQALEAHAASFASFK.V
R4/RRR4-2/2	1842.542	1843.120	-858.971	0.587	2407.935	0.550	24	0.380	K.FNLNVQAVNVLLDNIR.S
R4/RRR4-2/2	1842.652	1843.120	-254.794	0.579	2483.535	0.482	24	0.370	K.FNLNVQAVNVLLDNIR.S
R4/RRR4-1/3	1674.037	1673.876	96.051	0.544	2610.908	0.379	34	0.365	R.RPITADSALM*NPNTR.I
R4/RRR4-2/2	1778.457	1779.076	-912.779	0.556	2315.664	0.545	27	0.361	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-2/2	1778.434	1779.076	-926.009	0.563	2285.096	0.543	27	0.355	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-1/2	1564.941	1565.711	-1134.486	0.502	2402.551	0.454	23	0.346	R.SQALEAHAASFASFK.V
R4/RRR4-2/2	1842.092	1843.120	-1104.041	0.563	2278.831	0.506	23	0.339	K.FNLNVQAVNVLLDNIR.S
R4/RRR4-2/2	1633.294	1632.740	-273.960	0.529	2154.969	0.565	20	0.339	K.EVCFACVDAEEFR.L
R4/RRR4-2/2	1633.359	1632.740	-234.146	0.524	2112.660	0.556	20	0.328	K.EVCFACVDAEEFR.L
R4/RRR4-2/2	1694.963	1694.979	-9.143	0.481	2167.653	0.515	23	0.324	R.AHM*GIFTELGVLYAR.Y
R4/RRR4-2/2	1694.607	1694.979	-219.900	0.504	2108.078	0.543	23	0.323	R.AHM*GIFTELGVLYAR.Y
R4/RRR4-1/2	1438.096	1437.534	-305.016	0.558	2123.863	0.535	20	0.323	R.AAEEANVYDDLVK.Y
R4/RRR4-1/2	1566.469	1565.711	-155.275	0.585	2027.419	0.565	22	0.315	R.SQALEAHAASFASFK.V
R4/RRR4-2/2	1778.735	1779.076	-192.087	0.552	2075.926	0.534	25	0.314	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-2/2	1695.850	1694.979	-76.065	0.542	1891.503	0.611	22	0.308	R.AHM*GIFTELGVLYAR.Y
R4/RRR4-2/3	1673.687	1673.876	-113.515	0.524	2347.310	0.354	32	0.288	R.RPITADSALM*NPNTR.I
R4/RRR4-2/2	1696.558	1694.979	-248.586	0.545	1855.650	0.563	21	0.287	R.AHM*GIFTELGVLYAR.Y
R4/RRR4-2/3	1847.130	1847.062	36.807	0.602	1986.622	0.508	33	0.286	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/2	1505.882	1506.591	-1138.327	0.454	2075.690	0.411	20	0.278	R.GQCDDELINVTNK.N
R4/RRR4-2/2	1480.209	1480.648	-297.413	0.520	1751.084	0.564	20	0.275	R.GKLNAYESLELSR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1225.602	1226.403	-1473.872	0.418	1861.070	0.506	18	0.273	K.VDGELIFAYAK.I
R4/RRR4-1/2	1842.491	1843.120	-886.771	0.498	2026.523	0.424	22	0.272	K.FNLNVQAVNVLLDNIR.S
R4/RRR4-2/2	1295.022	1295.424	-310.729	0.470	1854.251	0.497	18	0.271	K.LNAYESLELSR.L
R4/RRR4-2/2	1226.136	1226.403	-218.545	0.515	1878.010	0.478	18	0.269	K.VDGELIFAYAK.I
R4/RRR4-2/2	1226.118	1226.403	-233.227	0.582	1782.546	0.515	18	0.267	K.VDGELIFAYAK.I
R4/RRR4-2/2	1584.476	1584.801	-205.901	0.530	1744.652	0.527	19	0.263	R.ALQHYTELPDIKR.V
R4/RRR4-2/2	1480.291	1480.648	-241.650	0.509	1766.505	0.509	20	0.262	R.GKLNAYESLELSR.L
R4/RRR4-2/2	1327.236	1326.567	-250.605	0.495	1815.688	0.475	18	0.260	K.IIYAFISNWAK.L
R4/RRR4-1/2	1451.805	1450.619	129.064	0.570	1693.204	0.540	20	0.260	R.EGLVSEAIESFIR.A
R4/RRR4-2/2	1437.155	1437.534	-264.238	0.464	1866.445	0.436	20	0.255	R.AAEEANVYDDLVK.Y
R4/RRR4-2/2	1584.250	1584.801	-981.858	0.515	1668.094	0.514	19	0.249	R.ALQHYTELPDIKR.V
R4/RRR4-2/2	1303.547	1304.480	-1487.464	0.468	1769.122	0.454	19	0.248	K.LKQFQGAVDAAR.K
R4/RRR4-2/2	1632.143	1632.740	-981.328	0.420	1798.230	0.435	19	0.245	K.EVCFACVDAEEFR.L
R4/RRR4-2/2	1438.008	1437.534	331.070	0.538	1639.090	0.507	20	0.244	R.AAEEANVYDDLVK.Y
R4/RRR4-1/3	1848.110	1847.062	26.121	0.572	1776.024	0.507	31	0.244	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/2	1555.349	1555.715	-236.207	0.484	1835.857	0.405	22	0.242	K.EAAELAAESPQGLLR.T
R4/RRR4-2/2	1450.832	1450.619	147.210	0.552	1648.081	0.497	19	0.241	R.EGLVSEAIESFIR.A
R4/RRR4-2/2	1507.238	1506.591	-234.892	0.552	1735.045	0.453	19	0.241	R.GQCDDELINVTNK.N
R4/RRR4-1/3	1846.622	1847.062	-239.070	0.549	1775.990	0.498	32	0.240	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/2	1362.046	1361.482	-320.878	0.592	1597.448	0.495	20	0.238	R.VEEDAVWSQVAK.A
R4/RRR4-2/3	1846.856	1847.062	-111.555	0.527	1879.444	0.447	32	0.237	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/2	1140.700	1141.346	-1447.042	0.461	1593.763	0.495	17	0.236	R.GNLQIVVQAAK.E
R4/RRR4-2/2	1140.348	1141.346	-1757.245	0.439	1508.819	0.536	17	0.235	R.GNLQIVVQAAK.E
R4/RRR4-2/2	1361.361	1361.482	-89.092	0.553	1521.163	0.518	19	0.235	R.VEEDAVWSQVAK.A
R4/RRR4-2/2	1506.042	1506.591	-1031.626	0.451	1811.721	0.386	19	0.235	R.GQCDDELINVTNK.N
R4/RRR4-1/2	1565.153	1565.711	-998.845	0.433	1828.007	0.381	21	0.234	R.SQALEAHAASFASFK.V
R4/RRR4-2/2	1304.038	1304.480	-339.564	0.458	1673.634	0.450	18	0.234	K.LKQFQGAVDAAR.K
R4/RRR4-1/2	1326.708	1326.567	106.626	0.507	1842.810	0.359	18	0.233	K.IIYAFISNWAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1437.222	1437.534	-217.456	0.531	1569.163	0.487	20	0.231	R.AAEEANVYDDLVK.Y
R4/RRR4-2/2	1140.705	1141.346	-1442.743	0.445	1535.892	0.501	17	0.230	R.GNLQIVVQAAK.E
R4/RRR4-2/2	1295.262	1295.424	-125.022	0.489	1615.339	0.456	17	0.230	K.LNAYESLELSR.L
R4/RRR4-2/2	1326.293	1326.567	-207.211	0.481	1679.222	0.419	18	0.229	K.IIYAFISNWAK.L
R4/RRR4-2/2	1450.250	1450.619	-254.760	0.510	1583.551	0.472	19	0.228	R.EGLVSEAIESFIR.A
R4/RRR4-1/2	1437.087	1437.534	-311.790	0.490	1583.696	0.462	20	0.227	R.AAEEANVYDDLVK.Y
R4/RRR4-2/2	1480.125	1480.648	-1032.153	0.518	1439.363	0.513	19	0.223	R.GKLNAYESLELSR.L
R4/RRR4-2/2	1555.594	1555.715	-77.653	0.490	1639.989	0.416	22	0.221	K.EAAELAAESPQGLLR.T
R4/RRR4-1/2	1736.495	1736.941	-257.397	0.516	1364.497	0.532	22	0.218	K.VVGNENPSTLICFASK.T
R4/RRR4-2/2	1303.633	1304.480	-1420.965	0.438	1606.559	0.403	18	0.216	K.LKQFQGAVDAAR.K
R4/RRR4-2/2	1450.194	1450.619	-293.691	0.486	1446.710	0.471	19	0.214	R.EGLVSEAIESFIR.A
R4/RRR4-2/2	1629.317	1628.849	287.989	0.510	1432.733	0.473	21	0.212	R.QLIDQVVSTALPESK.S
R4/RRR4-2/2	1736.443	1736.941	-287.865	0.485	1180.402	0.586	21	0.210	K.VVGNENPSTLICFASK.T
R4/RRR4-2/2	1423.155	1423.580	-299.701	0.345	2038.873	0.159	18	0.210	K.GNMQLFSVDQQR.S
R4/RRR4-2/2	1736.514	1736.941	-246.818	0.511	1177.495	0.575	21	0.208	K.VVGNENPSTLICFASK.T
R4/RRR4-2/2	1532.183	1532.748	-1024.668	0.493	1299.300	0.506	18	0.208	K.SHQM*PEQVVFWK.W
R4/RRR4-2/2	1737.120	1736.941	103.425	0.594	1199.432	0.559	21	0.207	K.VVGNENPSTLICFASK.T
R4/RRR4-2/2	1555.074	1555.715	-1058.385	0.392	1692.639	0.325	21	0.206	K.EAAELAAESPQGLLR.T
R4/RRR4-1/3	1846.748	1847.062	-170.335	0.525	1603.464	0.487	31	0.206	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/2	1537.261	1537.749	-318.393	0.547	1176.092	0.531	23	0.205	K.RANLPGAENLVVQR.F
R4/RRR4-1/2	1141.350	1141.346	3.260	0.439	1350.276	0.471	16	0.204	R.GNLQIVVQAAK.E
R4/RRR4-1/2	1627.925	1628.849	-1185.283	0.335	1483.850	0.392	22	0.198	R.QLIDQVVSTALPESK.S
R4/RRR4-1/2	1736.510	1736.941	-248.934	0.528	1076.210	0.564	20	0.197	K.VVGNENPSTLICFASK.T
R4/RRR4-2/2	1440.100	1439.579	-334.160	0.492	1359.624	0.420	17	0.194	K.GNM*QLFSVDQQR.S
R4/RRR4-1/2	1628.317	1628.849	-943.405	0.435	1271.680	0.456	21	0.193	R.QLIDQVVSTALPESK.S
R4/RRR4-2/2	1512.289	1512.637	-230.707	0.446	1253.400	0.458	19	0.193	K.EYSEQLGVDACIK.L
R4/RRR4-1/2	1344.129	1344.448	-238.256	0.503	1108.330	0.500	17	0.192	R.LYDEELYEAAK.I
R4/RRR4-2/2	1069.922	1070.306	-359.624	0.493	944.040	0.560	14	0.192	K.YGLIYVITK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1537.449	1537.749	-195.874	0.565	1017.779	0.524	22	0.191	K.RANLPGAENLVVQR.F
R4/RRR4-2/2	1070.035	1070.306	-253.745	0.461	995.639	0.536	14	0.190	K.YGLIYVITK.L
R4/RRR4-2/2	1538.275	1537.749	-309.428	0.571	909.009	0.554	21	0.189	K.RANLPGAENLVVQR.F
R4/RRR4-2/3	1304.595	1304.480	88.386	0.543	1748.517	0.397	28	0.188	K.LKQFQGAVDAAR.K
R4/RRR4-1/3	1673.885	1673.876	4.884	0.522	1856.836	0.338	30	0.186	R.RPITADSALM*NPNTR.I
R4/RRR4-1/2	1736.231	1736.941	-987.726	0.506	925.182	0.572	19	0.186	K.VVGNENPSTLICFASK.T
R4/RRR4-2/3	1532.125	1532.748	-1062.595	0.507	1780.387	0.369	26	0.186	K.SHQM*PEQVVFWK.W
R4/RRR4-1/2	1436.528	1437.534	-1400.310	0.384	1321.413	0.397	18	0.186	R.AAEEANVYDDLVK.Y
R4/RRR4-2/2	1372.852	1373.496	-1200.828	0.447	1309.040	0.389	18	0.186	R.ADDATHFLDVIR.A
R4/RRR4-2/2	1099.025	1099.261	-215.079	0.532	951.184	0.502	14	0.184	K.VANVELYYK.A
R4/RRR4-1/2	1373.260	1373.496	-172.664	0.423	1275.767	0.399	17	0.184	R.ADDATHFLDVIR.A
R4/RRR4-2/2	1098.878	1099.261	-349.814	0.499	944.218	0.506	14	0.184	K.VANVELYYK.A
R4/RRR4-2/2	1424.042	1423.580	325.289	0.446	1576.192	0.270	17	0.183	K.GNMQLFSVDQQR.S
R4/RRR4-1/2	1326.007	1326.567	-1180.464	0.472	1257.796	0.405	15	0.183	K.IIYAFISNWAK.L
R4/RRR4-2/2	1512.358	1512.637	-185.037	0.447	1210.173	0.415	19	0.182	K.EYSEQLGVDACIK.L
R4/RRR4-2/2	1373.111	1373.496	-280.842	0.415	1359.218	0.354	17	0.182	R.ADDATHFLDVIR.A
R4/RRR4-1/2	1344.221	1344.448	-169.653	0.459	1055.413	0.459	17	0.181	R.LYDEELYEAAK.I
R4/RRR4-1/2	1372.391	1373.496	-1538.104	0.364	1334.521	0.353	17	0.180	R.ADDATHFLDVIR.A
R4/RRR4-2/2	1345.399	1344.448	-36.821	0.500	1026.504	0.454	17	0.179	R.LYDEELYEAAK.I
R4/RRR4-2/2	1098.477	1099.261	-1628.837	0.403	918.500	0.506	14	0.179	K.VANVELYYK.A
R4/RRR4-2/2	1450.284	1450.619	-231.707	0.475	1003.048	0.490	16	0.178	R.EGLVSEAIESFIR.A
R4/RRR4-2/2	1438.653	1439.579	-1343.075	0.443	1248.234	0.374	17	0.177	K.GNM*QLFSVDQQR.S
R4/RRR4-2/2	1226.072	1226.403	-270.684	0.433	1058.937	0.435	16	0.176	K.VDGELIFAYAK.I
R4/RRR4-1/2	1098.409	1099.261	-1691.025	0.366	980.024	0.468	14	0.175	K.VANVELYYK.A
R4/RRR4-1/2	1070.307	1070.306	1.074	0.469	1025.907	0.429	14	0.175	K.YGLIYVITK.L
R4/RRR4-2/2	1381.203	1381.563	-261.113	0.419	831.304	0.503	19	0.173	R.ANLPGAENLVVQR.F
R4/RRR4-2/2	1381.192	1381.563	-269.005	0.371	944.904	0.468	20	0.173	R.ANLPGAENLVVQR.F
R4/RRR4-2/2	1373.233	1373.496	-192.193	0.511	1102.206	0.400	17	0.172	R.ADDATHFLDVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1361.647	1361.482	121.694	0.431	1158.267	0.371	18	0.172	R.VEEDAVWSQVAK.A
R4/RRR4-2/2	1111.551	1112.260	-1541.606	0.433	826.243	0.478	14	0.172	R.FQELFAQTK.Y
R4/RRR4-1/2	1631.723	1632.740	-1239.851	0.221	1559.581	0.209	19	0.171	K.EVCFACVDAEEFR.L
R4/RRR4-2/2	928.676	928.091	-448.402	0.389	1139.285	0.373	12	0.171	K.HELLEMR.R
R4/RRR4-2/2	970.079	970.190	-113.984	0.382	821.149	0.500	13	0.170	R.IAAYIYKK.A
R4/RRR4-2/2	1450.352	1450.619	-184.253	0.431	879.216	0.474	17	0.170	R.EGLVSEAIESFIR.A
R4/RRR4-2/2	1345.725	1344.448	205.927	0.433	996.326	0.411	17	0.170	R.LYDEELYEAAK.I
R4/RRR4-2/2	1439.088	1439.579	-342.818	0.466	1339.125	0.299	17	0.170	K.GNM*QLFSVDQQR.S
R4/RRR4-3/2	1450.027	1450.619	-1100.946	0.344	808.079	0.512	16	0.167	R.EGLVSEAIESFIR.A
R4/RRR4-2/2	1112.061	1112.260	-178.867	0.451	957.571	0.395	14	0.166	R.FQELFAQTK.Y
R4/RRR4-1/3	1480.281	1480.648	-248.774	0.481	1640.998	0.371	28	0.165	R.GKLNAYESLELSR.L
R4/RRR4-2/2	1294.379	1295.424	-1584.551	0.311	1191.049	0.333	15	0.164	K.LNAYESLELSR.L
R4/RRR4-2/2	1111.984	1112.260	-248.467	0.517	807.858	0.415	14	0.164	R.FQELFAQTK.Y
R4/RRR4-2/2	1784.453	1785.026	-884.120	0.467	759.810	0.451	20	0.162	R.SLLPVEPLVDECEKR.N
R4/RRR4-2/2	862.469	862.996	-1776.226	0.423	654.138	0.436	13	0.162	K.VVAAFAER.R
R4/RRR4-2/2	1784.478	1785.026	-869.698	0.454	731.025	0.455	20	0.161	R.SLLPVEPLVDECEKR.N
R4/RRR4-2/2	862.262	862.996	-2016.479	0.409	642.737	0.436	13	0.161	K.VVAAFAER.R
R4/RRR4-2/2	862.857	862.996	-161.636	0.385	680.125	0.422	13	0.159	K.VVAAFAER.R
R4/RRR4-1/2	1381.385	1381.563	-128.749	0.450	736.675	0.414	18	0.158	R.ANLPGAENLVVQR.F
R4/RRR4-2/2	1380.719	1381.563	-1339.504	0.367	759.605	0.403	19	0.157	R.ANLPGAENLVVQR.F
R4/RRR4-1/2	1382.525	1381.563	-27.242	0.475	640.706	0.425	17	0.156	R.ANLPGAENLVVQR.F
R4/RRR4-1/2	1343.975	1344.448	-353.525	0.400	777.503	0.367	17	0.155	R.LYDEELYEAAK.I
R4/RRR4-1/2	1098.491	1099.261	-1616.221	0.306	746.594	0.415	13	0.155	K.VANVELYYK.A
R4/RRR4-1/2	1140.608	1141.346	-1527.773	0.333	749.754	0.415	14	0.154	R.GNLQIVVQAAK.E
R4/RRR4-2/2	1148.878	1148.250	-325.318	0.391	710.105	0.381	14	0.154	K.VLQPENEYR.R
R4/RRR4-1/2	1372.273	1373.496	-1624.513	0.353	891.651	0.346	15	0.152	R.ADDATHFLDVIR.A
R4/RRR4-1/2	1780.356	1779.076	158.268	0.385	784.849	0.421	17	0.152	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-1/2	1381.070	1381.563	-357.682	0.381	525.631	0.399	17	0.151	R.ANLPGAENLVVQR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	862.708	862.996	-335.234	0.317	532.292	0.391	12	0.150	K.VVAAFAER.R
R4/RRR4-1/2	862.392	862.996	-1865.116	0.318	614.105	0.372	12	0.150	K.VVAAFAER.R
R4/RRR4-2/2	1674.036	1673.876	95.511	0.319	255.887	0.492	17	0.149	R.RPITADSALM*NPNTR.I
R4/RRR4-1/2	1970.382	1971.293	-972.381	0.446	781.961	0.392	19	0.149	K.KFNLNVQAVNVLLDNIR.S
R4/RRR4-2/2	1674.302	1673.876	255.022	0.303	244.018	0.506	17	0.148	R.RPITADSALM*NPNTR.I
R4/RRR4-1/2	1112.069	1112.260	-172.040	0.367	827.776	0.294	14	0.148	-.FQELFAQTK.-
R4/RRR4-1/2	1627.662	1628.849	-1347.579	0.309	664.020	0.405	16	0.146	R.QLIDQVVSTALPESK.S
R4/RRR4-1/2	1361.938	1361.482	335.807	0.338	788.604	0.315	16	0.146	R.VEEDAVWSQVAK.A
R4/RRR4-2/3	1516.928	1516.749	118.389	0.508	1983.447	0.172	27	0.145	K.SHQMPEQVVFWK.W
R4/RRR4-2/2	1784.511	1785.026	-851.432	0.358	481.527	0.378	17	0.144	R.SLLPVEPLVDECEKR.N
R4/RRR4-1/2	1673.346	1673.876	-917.580	0.275	210.845	0.452	16	0.144	R.RPITADSALM*NPNTR.I
R4/RRR4-2/2	1325.415	1326.567	-1628.460	0.244	552.437	0.339	15	0.142	K.IIYAFISNWAK.L
R4/RRR4-1/2	1098.447	1099.261	-1656.301	0.261	740.300	0.271	13	0.142	K.VANVELYYK.A
R4/RRR4-2/3	1778.747	1779.076	-185.417	0.450	1145.885	0.468	29	0.141	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-2/2	1147.745	1148.250	-1315.590	0.342	609.474	0.252	13	0.140	K.VLQPENEYR.R
R4/RRR4-2/3	1778.345	1779.076	-976.254	0.442	1018.621	0.493	27	0.136	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-2/3	1480.045	1480.648	-1086.071	0.458	1363.408	0.369	26	0.133	R.GKLNAYESLELSR.L
R4/RRR4-2/2	1449.826	1450.619	-1240.018	0.185	627.297	0.111	14	0.132	R.EGLVSEAIESFIR.A
R4/RRR4-2/3	1673.775	1673.876	-60.841	0.524	1503.834	0.306	29	0.129	R.RPITADSALM*NPNTR.I
R4/RRR4-2/3	1584.936	1584.801	85.306	0.534	1111.911	0.436	25	0.128	R.ALQHYTELPDIKR.V
R4/RRR4-2/3	1780.085	1779.076	5.040	0.480	979.548	0.462	30	0.125	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-1/2	1111.933	1112.260	-294.395	0.316	515.442	0.299	11	0.122	-.FQELFAQTK.-
R4/RRR4-2/3	1930.124	1930.109	7.440	0.440	957.807	0.456	25	0.121	K.VDELVKDRIESQNEVR.A
R4/RRR4-1/3	1779.309	1779.076	131.414	0.440	919.788	0.463	30	0.120	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-2/3	1930.096	1930.109	-7.119	0.450	894.746	0.470	24	0.120	K.VDELVKDRIESQNEVR.A
R4/RRR4-2/3	1480.340	1480.648	-208.443	0.510	1376.162	0.314	27	0.119	R.GKLNAYESLELSR.L
R4/RRR4-1/3	1480.650	1480.648	1.222	0.459	1266.167	0.347	26	0.118	R.GKLNAYESLELSR.L
R4/RRR4-2/3	1842.190	1843.120	-1050.787	0.488	1198.910	0.364	28	0.118	K.FNLNVQAVNVLLDNIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/3	1480.606	1480.648	-28.547	0.502	1205.843	0.353	26	0.115	R.GKLNAYESLELSR.L
R4/RRR4-2/3	1450.826	1450.619	143.657	0.514	1393.189	0.278	25	0.112	R.EGLVSEAIESFIR.A
R4/RRR4-2/3	1373.509	1373.496	9.563	0.484	725.916	0.460	25	0.111	R.ADDATHFLDVIR.A
R4/RRR4-2/3	1929.975	1930.109	-69.829	0.426	894.504	0.425	25	0.110	K.VDELVKDRIESQNEVR.A
R4/RRR4-1/3	1779.167	1779.076	51.322	0.434	760.488	0.452	27	0.109	K.LHVIELGAQPGKPGFSK.K
R4/RRR4-1/3	1373.636	1373.496	102.350	0.437	605.651	0.474	23	0.109	R.ADDATHFLDVIR.A
R4/RRR4-1/3	1373.125	1373.496	-271.041	0.465	686.922	0.453	24	0.109	R.ADDATHFLDVIR.A
R4/RRR4-2/3	1584.959	1584.801	100.136	0.484	1054.447	0.367	26	0.108	R.ALQHYTELPDIKR.V
R4/RRR4-2/3	1584.928	1584.801	80.439	0.518	1021.451	0.372	25	0.108	R.ALQHYTELPDIKR.V
R4/RRR4-1/3	1539.690	1539.755	-42.322	0.468	927.081	0.392	29	0.107	K.LPDARPLINVCDR.F
R4/RRR4-2/3	1373.739	1373.496	177.476	0.454	645.029	0.467	23	0.106	-.ADDATHFLDVIR.-
R4/RRR4-2/3	1539.427	1539.755	-214.003	0.413	971.613	0.383	30	0.105	K.LPDARPLINVCDR.F
R4/RRR4-2/3	1450.010	1450.619	-1113.001	0.370	1137.451	0.326	25	0.103	R.EGLVSEAIESFIR.A
R4/RRR4-2/3	1303.711	1304.480	-1360.597	0.439	1267.562	0.279	26	0.102	K.LKQFQGAVDAAR.K
R4/RRR4-2/3	1428.601	1428.615	-9.318	0.404	772.258	0.416	21	0.102	R.ALQHYTELPDIK.R
R4/RRR4-2/3	1429.409	1428.615	-144.519	0.450	761.168	0.414	20	0.102	R.ALQHYTELPDIK.R
R4/RRR4-2/3	1539.441	1539.755	-204.815	0.434	690.687	0.407	27	0.102	K.LPDARPLINVCDR.F
R4/RRR4-1/3	1373.394	1373.496	-74.548	0.481	681.579	0.399	23	0.101	R.ADDATHFLDVIR.A
R4/RRR4-2/3	1374.668	1373.496	125.875	0.428	681.377	0.404	24	0.101	R.ADDATHFLDVIR.A
R4/RRR4-2/3	1673.888	1673.876	6.749	0.465	1409.651	0.223	27	0.101	R.RPITADSALM*NPNTR.I
R4/RRR4-1/3	1539.539	1539.755	-140.623	0.409	706.835	0.403	28	0.101	K.LPDARPLINVCDR.F
R4/RRR4-1/3	1304.818	1304.480	260.088	0.510	808.042	0.376	24	0.100	K.LKQFQGAVDAAR.K
R4/RRR4-2/3	1845.987	1847.062	-1127.121	0.414	1106.155	0.295	28	0.098	K.YKEAAELAAESPQGLLR.T
R4/RRR4-2/3	1515.912	1516.749	-1214.964	0.440	1697.421	0.109	24	0.098	K.SHQMPEQVVFWK.W
R4/RRR4-2/3	1450.913	1450.619	203.773	0.467	1252.710	0.256	25	0.097	-.EGLVSEAIESFIR.-
R4/RRR4-2/3	1539.582	1539.755	-112.944	0.379	965.675	0.339	30	0.097	K.LPDARPLINVCDR.F
R4/RRR4-2/3	1305.269	1304.480	-162.157	0.506	795.181	0.391	23	0.096	-.LKQFQGAVDAAR.-
R4/RRR4-2/3	1429.598	1428.615	-11.410	0.425	925.287	0.362	22	0.095	-.ALQHYTELPDIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/3	1842.689	1843.120	-234.398	0.478	916.303	0.333	27	0.094	K.FNLNVQAVNVLLDNIR.S
R4/RRR4-1/3	1479.911	1480.648	-1177.258	0.440	1022.100	0.285	23	0.092	R.GKLNAYESLELSR.L
R4/RRR4-1/3	1930.198	1930.109	46.069	0.380	776.089	0.337	22	0.091	K.VDELVKDRIESQNEVR.A
R4/RRR4-1/3	1539.394	1539.755	-235.483	0.396	834.693	0.299	28	0.090	K.LPDARPLINVCDR.F
R4/RRR4-2/3	1842.256	1843.120	-1014.561	0.367	657.606	0.270	24	0.083	K.FNLNVQAVNVLLDNIR.S
R4/RRR4-2/3	1584.881	1584.801	50.545	0.329	649.246	0.241	21	0.077	-.ALQHYTELPDIKR.-
R4/RRR4-1/3	1584.160	1584.801	-1038.883	0.310	680.679	0.155	21	0.071	-.ALQHYTELPDIKR.-
R4/RRR4-1/3	1304.709	1304.480	175.792	0.407	450.415	0.299	20	0.042	-.LKQFQGAVDAAR.-
R4/RRR4-7/2	1446.210	1446.542	-230.412	0.559	2333.853	0.429	20	0.325	K.SPEDATNLIDDKK.I
R4/RRR4-7/2	1489.287	1489.700	-277.761	0.548	1821.927	0.572	21	0.288	K.VVVADNVHDFVFK.S
R4/RRR4-7/2	1489.236	1489.700	-312.300	0.513	1607.204	0.575	20	0.258	K.VVVADNVHDFVFK.S
R4/RRR4-7/2	1489.144	1489.700	-1047.772	0.540	1573.736	0.576	20	0.255	K.VVVADNVHDFVFK.S
R4/RRR4-7/3	1881.347	1881.000	185.038	0.510	1566.795	0.595	32	0.245	R.SDYDFGHTLHANHLPR.G
R4/RRR4-7/2	1877.273	1878.071	-960.606	0.482	1643.361	0.503	21	0.241	K.SVYYGAAEEFKDKEIK.F
R4/RRR4-7/3	1881.099	1881.000	52.869	0.521	1429.965	0.611	31	0.228	R.SDYDFGHTLHANHLPR.G
R4/RRR4-7/2	1522.242	1522.730	-321.454	0.424	1266.020	0.549	19	0.211	K.AHVEPDQIVSWLK.Q
R4/RRR4-7/2	1522.453	1522.730	-182.121	0.449	1322.805	0.497	19	0.207	K.AHVEPDQIVSWLK.Q
R4/RRR4-7/2	1522.307	1522.730	-278.653	0.446	1301.544	0.485	19	0.203	K.AHVEPDQIVSWLK.Q
R4/RRR4-7/2	1446.114	1446.542	-297.060	0.520	1369.974	0.450	19	0.202	K.SPEDATNLIDDKK.I
R4/RRR4-7/2	1279.337	1279.464	-99.398	0.476	1425.976	0.416	17	0.201	R.TADEIVDFIKK.N
R4/RRR4-7/2	1279.097	1279.464	-287.700	0.532	1361.419	0.441	16	0.199	R.TADEIVDFIKK.N
R4/RRR4-7/2	1446.237	1446.542	-211.190	0.568	1369.718	0.435	19	0.198	K.SPEDATNLIDDKK.I
R4/RRR4-7/3	1522.701	1522.730	-18.913	0.481	1992.973	0.311	29	0.198	K.AHVEPDQIVSWLK.Q
R4/RRR4-7/2	1877.352	1878.071	-918.304	0.473	1276.702	0.493	18	0.196	K.SVYYGAAEEFKDKEIK.F
R4/RRR4-7/2	1880.505	1881.110	-856.214	0.530	1129.426	0.535	19	0.196	K.NVLVEFYAPWCGHCK.K
R4/RRR4-7/2	1880.544	1881.110	-835.493	0.478	1104.031	0.542	19	0.194	K.NVLVEFYAPWCGHCK.K
R4/RRR4-7/2	975.467	976.063	-1640.882	0.457	1528.998	0.326	15	0.193	K.SDEDVVIAK.M
R4/RRR4-7/2	1196.145	1196.377	-194.443	0.453	1263.441	0.413	15	0.187	K.YEIQGFPTLK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1279.115	1279.464	-273.434	0.463	1329.718	0.387	16	0.186	R.TADEIVDFIKK.N
R4/RRR4-7/2	1195.948	1196.377	-359.300	0.349	1404.647	0.354	16	0.186	K.YEIQGFPTLK.I
R4/RRR4-7/2	1507.404	1507.625	-147.145	0.433	1000.192	0.530	18	0.185	K.SVYYGAAEEFKDK.E
R4/RRR4-7/2	1151.129	1151.291	-141.314	0.534	1092.600	0.428	16	0.179	R.TADEIVDFIK.K
R4/RRR4-7/2	1196.075	1196.377	-253.314	0.437	1153.654	0.414	15	0.179	K.YEIQGFPTLK.I
R4/RRR4-7/3	1446.618	1446.542	52.921	0.563	1364.363	0.508	28	0.174	K.SPEDATNLIDDKK.I
R4/RRR4-7/2	1151.089	1151.291	-175.888	0.508	1120.537	0.385	16	0.173	R.TADEIVDFIK.K
R4/RRR4-7/2	975.948	976.063	-117.815	0.469	1308.423	0.309	15	0.173	K.SDEDVVIAK.M
R4/RRR4-7/2	1877.462	1878.071	-859.493	0.524	1027.971	0.476	17	0.173	K.SVYYGAAEEFKDKEIK.F
R4/RRR4-7/2	975.315	976.063	-1797.177	0.388	1322.526	0.302	15	0.172	K.SDEDVVIAK.M
R4/RRR4-7/2	1539.137	1537.781	231.995	0.533	890.832	0.425	21	0.168	R.LFKPFDELVVDSK.D
R4/RRR4-7/2	1453.158	1452.591	-298.821	0.429	493.523	0.563	18	0.167	K.SEPIPEVNNEPVK.V
R4/RRR4-7/2	1717.405	1717.990	-925.907	0.481	661.696	0.546	19	0.167	K.AAQELSKHDPPIVLAK.V
R4/RRR4-7/2	1150.700	1151.291	-1387.225	0.379	1021.775	0.387	15	0.166	R.TADEIVDFIK.K
R4/RRR4-7/2	965.923	966.070	-152.248	0.429	778.040	0.402	16	0.162	K.FIDASSTPK.V
R4/RRR4-7/2	1105.566	1105.229	305.480	0.368	832.578	0.422	14	0.162	K.NIQEYKGPR.E
R4/RRR4-7/2	1384.411	1384.643	-168.354	0.420	550.202	0.486	19	0.161	K.LAPILDEVATTLK.S
R4/RRR4-7/2	1537.308	1537.781	-308.348	0.473	777.503	0.390	20	0.158	R.LFKPFDELVVDSK.D
R4/RRR4-7/2	990.063	990.181	-119.660	0.379	460.666	0.483	13	0.158	K.HDPPIVLAK.V
R4/RRR4-7/2	1385.210	1384.643	-313.656	0.365	548.355	0.491	18	0.158	K.LAPILDEVATTLK.S
R4/RRR4-7/2	965.851	966.070	-227.051	0.409	668.259	0.385	16	0.157	K.FIDASSTPK.V
R4/RRR4-7/2	1104.491	1105.229	-1578.509	0.335	699.541	0.440	14	0.157	K.NIQEYKGPR.E
R4/RRR4-7/2	1453.216	1452.591	-259.127	0.410	377.448	0.496	16	0.156	K.SEPIPEVNNEPVK.V
R4/RRR4-7/2	989.539	990.181	-1664.132	0.387	446.995	0.444	13	0.155	K.HDPPIVLAK.V
R4/RRR4-7/2	1279.314	1279.464	-117.680	0.341	308.530	0.471	15	0.154	R.EAEGIVEYLKK.Q
R4/RRR4-7/2	1453.144	1452.591	-309.019	0.392	471.940	0.435	18	0.154	K.SEPIPEVNNEPVK.V
R4/RRR4-7/2	1537.665	1537.781	-75.692	0.466	807.300	0.345	20	0.153	R.LFKPFDELVVDSK.D
R4/RRR4-7/2	1279.156	1279.464	-241.552	0.378	301.154	0.413	15	0.153	R.EAEGIVEYLKK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1278.693	1279.464	-1389.314	0.345	350.676	0.421	16	0.153	R.EAEGIVEYLKK.Q
R4/RRR4-7/2	1452.168	1452.591	-292.280	0.368	345.949	0.451	16	0.152	K.SEPIPEVNNEPVK.V
R4/RRR4-7/2	989.560	990.181	-1643.311	0.344	316.259	0.463	11	0.151	K.HDPPIVLAK.V
R4/RRR4-7/2	1522.705	1522.730	-16.211	0.317	514.552	0.418	15	0.147	K.AHVEPDQIVSWLK.Q
R4/RRR4-7/2	1104.737	1105.229	-446.375	0.308	746.257	0.314	14	0.146	K.NIQEYKGPR.E
R4/RRR4-1/2	966.216	966.070	152.047	0.315	663.376	0.280	15	0.145	K.FIDASSTPK.V
R4/RRR4-7/2	965.739	966.070	-343.969	0.396	423.608	0.366	13	0.139	-.FIDASSTPK.-
R4/RRR4-7/2	885.986	885.986	-0.499	0.294	975.035	0.171	14	0.138	K.FFQSSAAK.A
R4/RRR4-7/2	1279.529	1279.464	51.039	0.240	698.576	0.224	14	0.137	R.EAEGIVEYLKK.Q
R4/RRR4-7/2	1384.413	1384.643	-166.762	0.307	273.641	0.317	13	0.136	-.LAPILDEVATTLK.-
R4/RRR4-7/2	1279.918	1279.464	355.891	0.234	468.421	0.281	11	0.136	R.EAEGIVEYLKK.Q
R4/RRR4-7/3	1539.005	1537.781	146.166	0.530	1319.044	0.390	25	0.135	-.LFKPFDELVVDSK.-
R4/RRR4-1/2	965.924	966.070	-150.980	0.405	443.847	0.294	13	0.132	-.FIDASSTPK.-
R4/RRR4-7/3	1881.033	1881.000	17.332	0.481	978.002	0.494	28	0.132	R.SDYDFGHTLHANHLPR.G
R4/RRR4-7/3	1901.904	1901.154	-131.856	0.453	830.710	0.541	29	0.131	K.VVTFDKNPDNHPYLLK.F
R4/RRR4-2/3	1446.234	1446.542	-213.867	0.526	1058.031	0.459	24	0.130	K.SPEDATNLIDDKK.I
R4/RRR4-7/3	1446.478	1446.542	-44.584	0.520	1028.148	0.450	24	0.126	K.SPEDATNLIDDKK.I
R4/RRR4-7/2	1490.469	1489.700	-154.978	0.273	103.328	0.310	12	0.124	-.VVVADNVHDFVFK.-
R4/RRR4-7/3	1446.723	1446.542	125.276	0.522	1219.881	0.379	27	0.122	K.SPEDATNLIDDKK.I
R4/RRR4-7/3	1902.828	1901.154	-172.168	0.492	774.109	0.506	28	0.120	K.VVTFDKNPDNHPYLLK.F
R4/RRR4-7/2	1627.424	1627.775	-216.191	0.437	795.414	0.572	20	0.120	K.EKAESAPAEPLKDEL.-
R4/RRR4-1/3	1446.432	1446.542	-76.328	0.520	942.465	0.427	22	0.115	K.SPEDATNLIDDKK.I
R4/RRR4-1/3	1446.030	1446.542	-1049.006	0.443	1001.257	0.404	23	0.114	K.SPEDATNLIDDKK.I
R4/RRR4-7/2	1627.266	1627.775	-929.644	0.449	631.076	0.573	18	0.114	K.EKAESAPAEPLKDEL.-
R4/RRR4-7/2	1370.335	1370.487	-111.471	0.430	1192.607	0.382	19	0.114	K.AESAPAEPLKDEL.-
R4/RRR4-7/3	1522.320	1522.730	-270.214	0.467	1496.794	0.241	25	0.112	K.AHVEPDQIVSWLK.Q
R4/RRR4-7/2	1627.339	1627.775	-268.417	0.435	863.131	0.514	21	0.111	K.EKAESAPAEPLKDEL.-
R4/RRR4-7/3	1522.703	1522.730	-17.346	0.443	1452.424	0.235	26	0.107	K.AHVEPDQIVSWLK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1901.237	1901.154	43.455	0.433	679.152	0.462	27	0.107	K.VVTFDKNPDNHPYLLK.F
R4/RRR4-7/3	1537.872	1537.781	59.494	0.462	957.321	0.369	22	0.103	R.LFKPFDELVVDSK.D
R4/RRR4-2/3	1445.404	1446.542	-1483.882	0.434	699.925	0.388	22	0.101	K.SPEDATNLIDDKK.I
R4/RRR4-6/3	1446.129	1446.542	-286.144	0.418	846.374	0.365	21	0.101	K.SPEDATNLIDDKK.I
R4/RRR4-2/3	1446.125	1446.542	-289.320	0.422	684.143	0.351	20	0.096	K.SPEDATNLIDDKK.I
R4/RRR4-6/3	1446.559	1446.542	11.535	0.412	936.332	0.306	22	0.095	K.SPEDATNLIDDKK.I
R4/RRR4-7/3	1537.358	1537.781	-275.814	0.444	961.812	0.325	23	0.094	-.LFKPFDELVVDSK.-
R4/RRR4-7/2	1370.225	1370.487	-192.079	0.429	849.700	0.409	17	0.090	K.AESAPAEPLKDEL.-
R4/RRR4-7/2	1522.877	1522.730	97.313	0.296	170.508	0.380	10	0.084	-.AHVEPDQIVSWLK.-
R4/RRR4-7/2	1370.240	1370.487	-180.997	0.403	704.848	0.343	16	0.080	K.AESAPAEPLKDEL.-
R4/RRR4-3/2	1886.356	1885.881	252.511	0.580	2430.992	0.618	28	0.407	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1885.345	1885.881	-817.195	0.598	2173.114	0.633	27	0.361	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1885.385	1885.881	-263.630	0.592	2152.609	0.645	26	0.360	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1800.695	1800.047	-196.272	0.580	2216.246	0.585	24	0.357	R.LFHETTATALAYGIYK.T
R4/RRR4-3/2	1886.459	1885.881	-224.474	0.635	2099.285	0.648	26	0.351	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1886.231	1885.881	186.514	0.595	1954.456	0.659	26	0.330	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1885.735	1885.881	-77.304	0.587	2009.000	0.619	27	0.327	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/3	1789.391	1789.969	-884.218	0.557	2338.814	0.408	32	0.314	K.FKDEYKIDVYQNAR.A
R4/RRR4-3/2	1742.337	1741.919	240.285	0.577	1934.109	0.591	23	0.310	R.GPSIDQLAYCINSFR.D
R4/RRR4-3/2	1469.184	1469.645	-315.025	0.496	2120.452	0.477	23	0.305	R.FIGTAGAASSTM*NPK.N
R4/RRR4-3/2	1469.101	1469.645	-1054.446	0.480	2137.453	0.464	23	0.303	R.FIGTAGAASSTM*NPK.N
R4/RRR4-3/2	1741.807	1741.919	-64.712	0.576	1730.936	0.596	21	0.279	R.GPSIDQLAYCINSFR.D
R4/RRR4-3/2	1469.294	1469.645	-240.005	0.497	1882.536	0.497	22	0.273	R.FIGTAGAASSTM*NPK.N
R4/RRR4-3/2	1793.545	1794.215	-934.181	0.475	1950.542	0.429	23	0.264	R.VFTPTQLMAMVLSNLK.G
R4/RRR4-3/3	1789.650	1789.969	-178.438	0.545	2008.719	0.448	31	0.261	K.FKDEYKIDVYQNAR.A
R4/RRR4-3/2	1799.364	1800.047	-937.896	0.498	1757.640	0.486	23	0.253	R.LFHETTATALAYGIYK.T
R4/RRR4-3/2	1567.865	1567.796	44.308	0.500	1650.504	0.525	21	0.250	R.GCALECAILSPTFK.V
R4/RRR4-3/2	1567.481	1567.796	-201.260	0.503	1611.367	0.499	21	0.239	R.GCALECAILSPTFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1885.753	1885.881	-68.148	0.520	1322.012	0.606	22	0.225	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1740.793	1741.919	-1224.905	0.525	1460.725	0.508	20	0.222	R.GPSIDQLAYCINSFR.D
R4/RRR4-3/2	1540.908	1541.811	-1238.391	0.319	1670.475	0.395	21	0.217	R.AVLDAATIAGLCPLR.L
R4/RRR4-3/2	1295.206	1294.482	-213.508	0.477	1488.767	0.451	20	0.216	K.HANPVLLSSDLK.K
R4/RRR4-3/2	1542.339	1541.811	-306.707	0.430	1638.152	0.382	20	0.212	R.AVLDAATIAGLCPLR.L
R4/RRR4-3/3	1423.683	1422.655	19.546	0.535	2036.741	0.321	28	0.208	K.HANPVLLSSDLKK.K
R4/RRR4-3/2	1604.085	1604.783	-1061.539	0.417	1774.061	0.273	19	0.204	K.VINQCSEAEVWLR.E
R4/RRR4-3/2	1566.934	1567.796	-1191.334	0.367	1489.226	0.410	20	0.203	R.GCALECAILSPTFK.V
R4/RRR4-3/2	1294.059	1294.482	-327.991	0.442	1074.165	0.500	17	0.187	K.HANPVLLSSDLK.K
R4/RRR4-3/2	1358.962	1359.511	-1143.369	0.438	1052.649	0.467	17	0.179	R.GIDVVLNEESKR.E
R4/RRR4-2/3	1422.176	1422.655	-337.711	0.480	1869.247	0.306	26	0.177	K.HANPVLLSSDLKK.K
R4/RRR4-3/2	1323.364	1323.522	-119.406	0.462	949.524	0.473	16	0.175	K.ILTDFFGKEPR.R
R4/RRR4-3/2	1604.007	1604.783	-1110.443	0.322	1599.696	0.206	18	0.174	K.VINQCSEAEVWLR.E
R4/RRR4-3/3	1422.801	1422.655	103.374	0.543	1746.949	0.349	26	0.173	K.HANPVLLSSDLKK.K
R4/RRR4-3/2	1598.145	1598.760	-1013.301	0.469	935.977	0.462	19	0.172	K.AVEKEYEM*ALQDR.V
R4/RRR4-3/2	1293.564	1294.482	-1487.302	0.373	1085.375	0.418	17	0.172	K.HANPVLLSSDLK.K
R4/RRR4-3/2	1422.138	1422.655	-1069.589	0.447	862.462	0.495	17	0.170	K.HANPVLLSSDLKK.K
R4/RRR4-3/2	1481.241	1481.638	-268.855	0.494	699.924	0.510	18	0.167	R.VSEGPDGFPLVHAR.Y
R4/RRR4-3/2	1681.156	1681.870	-1022.779	0.455	632.135	0.532	18	0.163	K.ISTYTVGPFNPGKGDK.A
R4/RRR4-3/2	1237.274	1237.377	-84.075	0.363	709.370	0.491	16	0.161	R.ETPAIVCFGDK.Q
R4/RRR4-3/3	1885.747	1885.881	-71.337	0.496	1276.111	0.481	32	0.160	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1481.082	1481.638	-1053.227	0.415	737.979	0.448	18	0.159	R.VSEGPDGFPLVHAR.Y
R4/RRR4-3/2	1040.504	1041.183	-1618.982	0.382	917.470	0.350	14	0.157	K.IQQQDALPK.H
R4/RRR4-3/2	1382.248	1381.558	-225.219	0.318	949.736	0.400	16	0.156	K.ISTYTVGPFNPGK.G
R4/RRR4-3/3	1887.200	1885.881	169.543	0.469	1238.185	0.483	33	0.156	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/2	1681.413	1681.870	-273.111	0.455	587.989	0.495	17	0.156	K.ISTYTVGPFNPGKGDK.A
R4/RRR4-3/2	1040.709	1041.183	-456.896	0.447	1052.533	0.285	15	0.156	K.IQQQDALPK.H
R4/RRR4-3/2	1480.881	1481.638	-1190.120	0.422	623.321	0.457	17	0.156	R.VSEGPDGFPLVHAR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1041.136	1041.183	-45.347	0.469	889.210	0.335	14	0.155	K.IQQQDALPK.H
R4/RRR4-3/2	936.446	937.077	-1745.995	0.330	525.093	0.506	10	0.155	R.DIAAFPFR.V
R4/RRR4-3/2	1348.274	1347.479	-152.434	0.380	942.856	0.345	15	0.153	K.NAVESYVYDMR.N
R4/RRR4-3/2	1007.707	1008.067	-357.710	0.390	662.336	0.379	12	0.153	K.YSDPELQR.D
R4/RRR4-3/2	1682.355	1681.870	288.880	0.490	462.938	0.513	15	0.153	K.ISTYTVGPFNPGKGDK.A
R4/RRR4-3/2	1007.912	1008.067	-153.801	0.373	647.174	0.371	12	0.152	K.YSDPELQR.D
R4/RRR4-3/2	1135.975	1136.240	-233.627	0.387	619.167	0.398	13	0.151	R.KYSDPELQR.D
R4/RRR4-3/2	1008.072	1008.067	4.723	0.377	537.174	0.397	11	0.151	K.YSDPELQR.D
R4/RRR4-3/2	936.472	937.077	-1718.098	0.327	444.715	0.504	9	0.151	R.DIAAFPFR.V
R4/RRR4-3/3	1886.694	1885.881	-99.076	0.522	1224.798	0.465	33	0.149	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/3	1789.938	1789.969	-17.218	0.568	1263.312	0.455	30	0.148	K.FKDEYKIDVYQNAR.A
R4/RRR4-3/2	975.050	975.083	-34.169	0.359	907.357	0.278	13	0.147	K.ILSHAYDR.S
R4/RRR4-3/2	1322.765	1323.522	-1332.288	0.289	703.852	0.366	14	0.145	K.ILTDFFGKEPR.R
R4/RRR4-9/2	1041.881	1041.183	-290.686	0.204	589.383	0.156	11	0.133	K.IQQQDALPK.H
R4/RRR4-2/2	1541.146	1541.811	-1083.521	0.235	855.053	0.178	15	0.132	-.AVLDAATIAGLCPLR.-
R4/RRR4-1/3	1481.129	1481.638	-1021.956	0.410	1164.032	0.417	26	0.128	R.VSEGPDGFPLVHAR.Y
R4/RRR4-2/3	1885.529	1885.881	-187.254	0.471	981.215	0.450	31	0.124	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/3	1885.930	1885.881	26.149	0.406	977.903	0.428	30	0.120	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/3	1481.522	1481.638	-78.652	0.377	808.703	0.481	24	0.118	R.VSEGPDGFPLVHAR.Y
R4/RRR4-3/3	1541.351	1541.811	-299.565	0.336	1123.671	0.393	27	0.116	R.AVLDAATIAGLCPLR.L
R4/RRR4-3/3	1886.258	1885.881	200.719	0.489	912.615	0.430	30	0.115	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/3	1800.736	1800.047	-173.022	0.522	1221.786	0.329	26	0.111	R.LFHETTATALAYGIYK.T
R4/RRR4-3/3	1799.722	1800.047	-181.045	0.462	1078.828	0.372	25	0.111	R.LFHETTATALAYGIYK.T
R4/RRR4-2/3	1885.318	1885.881	-831.306	0.462	615.133	0.467	26	0.110	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-1/3	1422.926	1422.655	191.260	0.481	1383.813	0.270	24	0.110	K.HANPVLLSSDLKK.K
R4/RRR4-3/3	1885.359	1885.881	-809.760	0.403	685.382	0.443	27	0.108	K.APADAAADGAENGAPNSEEK.S
R4/RRR4-3/3	1542.681	1541.811	-84.225	0.491	853.653	0.416	25	0.106	R.AVLDAATIAGLCPLR.L
R4/RRR4-1/3	1481.159	1481.638	-324.180	0.398	874.355	0.367	24	0.101	R.VSEGPDGFPLVHAR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1799.976	1800.047	-39.501	0.450	1125.733	0.310	24	0.100	R.LFHETTATALAYGIYK.T
R4/RRR4-3/3	1481.782	1481.638	97.978	0.353	859.906	0.371	26	0.100	R.VSEGPDGFPLVHAR.Y
R4/RRR4-3/3	1481.042	1481.638	-1080.670	0.329	595.667	0.403	22	0.099	R.VSEGPDGFPLVHAR.Y
R4/RRR4-3/3	1422.772	1422.655	82.723	0.458	1236.727	0.261	23	0.098	K.HANPVLLSSDLKK.K
R4/RRR4-2/3	1481.762	1481.638	84.470	0.373	645.634	0.369	22	0.096	R.VSEGPDGFPLVHAR.Y
R4/RRR4-2/3	1884.907	1885.881	-1050.520	0.401	548.392	0.362	26	0.093	-.APADAAADGAENGAPNSEEK.-
R4/RRR4-3/3	1541.654	1541.811	-102.111	0.361	915.325	0.330	24	0.093	R.AVLDAATIAGLCPLR.L
R4/RRR4-2/3	1480.964	1481.638	-1133.803	0.289	627.528	0.337	23	0.092	R.VSEGPDGFPLVHAR.Y
R4/RRR4-1/3	1480.888	1481.638	-1184.956	0.245	683.437	0.265	22	0.086	R.VSEGPDGFPLVHAR.Y
R4/RRR4-3/3	1886.412	1885.881	-249.020	0.391	693.721	0.259	25	0.083	-.APADAAADGAENGAPNSEEK.-
R4/RRR4-3/2	1435.409	1434.684	-192.191	0.575	2576.235	0.522	23	0.405	K.TNM*ASVLLEAGLAK.L
R4/RRR4-3/2	1434.075	1434.684	-1125.536	0.524	2439.811	0.518	23	0.376	K.TNM*ASVLLEAGLAK.L
R4/RRR4-3/2	1434.291	1434.684	-274.631	0.521	2189.819	0.497	22	0.323	K.TNM*ASVLLEAGLAK.L
R4/RRR4-3/2	1273.445	1274.359	-1507.722	0.467	1890.105	0.471	16	0.267	R.DVEIEVEAVDR.T
R4/RRR4-3/2	1547.322	1547.738	-269.400	0.583	1851.627	0.439	20	0.253	R.KAALQNLEQFQEK.A
R4/RRR4-3/2	1213.038	1213.324	-236.650	0.514	1660.370	0.506	17	0.249	K.FYVQTVGDQR.V
R4/RRR4-3/2	1547.226	1547.738	-979.793	0.593	1838.667	0.419	20	0.245	R.KAALQNLEQFQEK.A
R4/RRR4-3/2	1212.417	1213.324	-1577.657	0.438	1810.665	0.382	17	0.236	K.FYVQTVGDQR.V
R4/RRR4-3/2	1385.525	1385.588	-45.387	0.458	1536.800	0.524	18	0.234	K.DLALELVENGLAK.Y
R4/RRR4-3/2	1212.930	1213.324	-326.208	0.484	1719.764	0.405	17	0.231	K.FYVQTVGDQR.V
R4/RRR4-3/2	1286.226	1286.503	-215.760	0.428	1587.888	0.452	18	0.224	R.VASIQQQLASLK.L
R4/RRR4-3/2	1419.967	1419.565	284.489	0.552	1572.326	0.380	17	0.204	K.AALQNLEQFQEK.A
R4/RRR4-3/2	1058.111	1058.254	-135.107	0.437	1140.737	0.544	16	0.199	K.VVVTEVLGGGK.F
R4/RRR4-3/2	1286.160	1286.503	-267.557	0.387	1295.130	0.460	18	0.196	R.VASIQQQLASLK.L
R4/RRR4-3/2	1420.112	1419.565	-319.569	0.570	1411.907	0.407	17	0.194	K.AALQNLEQFQEK.A
R4/RRR4-3/2	1420.032	1419.565	329.915	0.563	1450.506	0.379	17	0.192	K.AALQNLEQFQEK.A
R4/RRR4-3/2	1462.311	1461.595	-194.970	0.491	1193.950	0.466	19	0.191	K.ETCSIAFSFSGVR.C
R4/RRR4-3/2	1286.162	1286.503	-265.843	0.380	1145.937	0.450	16	0.181	R.VASIQQQLASLK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1728.901	1729.977	-1204.437	0.417	759.599	0.551	23	0.174	K.ESPVMHITDLTTVSAK.K
R4/RRR4-3/2	1058.120	1058.254	-126.312	0.392	766.669	0.531	16	0.171	K.VVVTEVLGGGK.F
R4/RRR4-1/2	1285.599	1286.503	-1485.564	0.429	966.069	0.446	15	0.169	R.VASIQQQLASLK.L
R4/RRR4-3/2	1647.259	1647.726	-284.348	0.437	803.659	0.488	22	0.168	R.ISTVDGQPTTNTADAR.V
R4/RRR4-3/2	1469.176	1469.753	-1076.847	0.448	1203.821	0.356	18	0.168	K.LKDAPVIGAFNPVK.G
R4/RRR4-3/2	1729.498	1729.977	-277.481	0.440	526.652	0.576	21	0.168	K.ESPVMHITDLTTVSAK.K
R4/RRR4-3/2	1242.831	1242.384	360.600	0.426	641.937	0.506	16	0.167	K.QVTVEMEYSR.R
R4/RRR4-3/2	1647.386	1647.726	-207.031	0.470	809.113	0.461	22	0.166	R.ISTVDGQPTTNTADAR.V
R4/RRR4-3/2	1647.094	1647.726	-993.828	0.448	688.944	0.503	21	0.165	R.ISTVDGQPTTNTADAR.V
R4/RRR4-3/2	1044.857	1045.238	-365.872	0.505	679.030	0.430	15	0.164	R.IPDANVLM*R.A
R4/RRR4-3/2	1327.198	1326.479	-212.605	0.497	748.802	0.439	17	0.162	R.TGTFLGSLWESK.T
R4/RRR4-3/2	1045.002	1045.238	-227.216	0.536	525.833	0.426	14	0.159	R.IPDANVLM*R.A
R4/RRR4-3/2	1326.293	1326.479	-140.559	0.472	758.734	0.412	16	0.157	R.TGTFLGSLWESK.T
R4/RRR4-3/2	944.981	945.102	-128.348	0.564	737.000	0.352	14	0.156	R.RVNLSSIR.A
R4/RRR4-3/2	1326.355	1326.479	-93.844	0.475	729.119	0.397	16	0.154	R.TGTFLGSLWESK.T
R4/RRR4-3/3	1547.851	1547.738	73.349	0.445	1544.642	0.369	27	0.154	R.KAALQNLEQFQEK.A
R4/RRR4-3/2	1044.834	1045.238	-388.144	0.442	521.660	0.365	14	0.153	R.IPDANVLM*R.A
R4/RRR4-3/2	944.884	945.102	-231.636	0.509	785.759	0.315	13	0.151	R.RVNLSSIR.A
R4/RRR4-4/2	1262.948	1263.473	-1210.708	0.393	706.487	0.356	13	0.148	K.ARDFLPFLQR.N
R4/RRR4-3/2	1524.022	1522.687	221.040	0.334	779.232	0.338	18	0.148	R.SHYFDLLLAAESR.A
R4/RRR4-3/2	1460.979	1461.595	-1109.538	0.309	912.184	0.322	16	0.148	K.ETCSIAFSFSGVR.C
R4/RRR4-3/2	1273.941	1274.359	-329.134	0.326	1091.514	0.228	16	0.147	R.DVEIEVEAVDR.T
R4/RRR4-3/2	944.960	945.102	-150.248	0.517	978.616	0.241	14	0.147	R.RVNLSSIR.A
R4/RRR4-3/2	1241.355	1242.384	-1639.609	0.311	416.974	0.335	14	0.144	K.QVTVEMEYSR.R
R4/RRR4-3/2	1418.003	1418.685	-1189.446	0.396	658.495	0.299	19	0.144	K.TNMASVLLEAGLAK.L
R4/RRR4-3/2	1523.096	1522.687	269.728	0.250	567.019	0.342	15	0.139	R.SHYFDLLLAAESR.A
R4/RRR4-5/2	1286.070	1286.503	-337.264	0.238	465.531	0.301	13	0.138	R.VASIQQQLASLK.L
R4/RRR4-3/2	1385.087	1385.588	-1086.886	0.259	505.580	0.355	13	0.138	K.DLALELVENGLAK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1523.209	1522.687	-314.579	0.207	718.793	0.277	18	0.137	R.SHYFDLLLAAESR.A
R4/RRR4-3/3	1469.626	1469.753	-86.662	0.500	1380.658	0.379	31	0.137	K.LKDAPVIGAFNPVK.G
R4/RRR4-3/2	1273.589	1274.359	-1394.305	0.277	758.394	0.205	14	0.135	R.DVEIEVEAVDR.T
R4/RRR4-3/2	1386.245	1385.588	-248.240	0.189	587.956	0.212	13	0.131	-.DLALELVENGLAK.-
R4/RRR4-3/2	1462.278	1461.595	-217.247	0.253	652.649	0.169	14	0.131	K.ETCSIAFSFSGVR.C
R4/RRR4-3/2	1263.361	1263.473	-88.347	0.334	724.595	0.200	12	0.131	-.ARDFLPFLQR.-
R4/RRR4-3/3	1470.262	1469.753	-335.243	0.491	1226.141	0.387	25	0.126	K.LKDAPVIGAFNPVK.G
R4/RRR4-3/3	1921.231	1921.211	10.820	0.367	1278.078	0.336	27	0.118	K.LSSFGLDRIPDANVLM*R.A
R4/RRR4-3/3	1248.742	1248.330	330.694	0.470	944.361	0.394	18	0.107	R.RDEKPDNFAR.E
R4/RRR4-3/3	1502.116	1502.659	-1030.297	0.518	1119.684	0.324	24	0.103	R.HSAIVEYVFSGHR.F
R4/RRR4-3/3	1968.126	1968.171	-23.269	0.423	871.099	0.407	23	0.102	R.CPGKDEPYSNEAIALM*R.R
R4/RRR4-3/3	1548.168	1547.738	278.559	0.479	1243.659	0.278	24	0.101	R.KAALQNLEQFQEK.A
R4/RRR4-3/3	1418.593	1418.685	-65.009	0.510	1106.834	0.314	26	0.100	-.TNMASVLLEAGLAK.-
R4/RRR4-4/3	1502.950	1502.659	194.478	0.461	1034.430	0.334	23	0.099	-.HSAIVEYVFSGHR.-
R4/RRR4-3/3	1248.123	1248.330	-166.197	0.434	960.588	0.347	18	0.098	R.RDEKPDNFAR.E
R4/RRR4-3/3	1921.290	1921.211	41.599	0.313	1002.206	0.317	26	0.094	K.LSSFGLDRIPDANVLM*R.A
R4/RRR4-3/3	1547.557	1547.738	-116.990	0.428	1065.956	0.268	24	0.090	R.KAALQNLEQFQEK.A
R4/RRR4-3/3	1469.655	1469.753	-66.916	0.424	773.564	0.322	25	0.087	-.LKDAPVIGAFNPVK.-
R4/RRR4-4/3	1502.658	1502.659	-0.670	0.440	739.938	0.295	19	0.076	-.HSAIVEYVFSGHR.-
R4/RRR4-3/3	1920.604	1921.211	-839.206	0.298	765.538	0.187	24	0.073	-.LSSFGLDRIPDANVLM*R.-
R4/RRR4-6/2	1967.543	1968.236	-862.706	0.610	2305.580	0.567	25	0.367	R.VQQLLQDFFNGKELCK.S
R4/RRR4-6/2	1967.460	1968.236	-905.433	0.640	2115.236	0.587	24	0.338	R.VQQLLQDFFNGKELCK.S
R4/RRR4-6/2	1412.749	1413.562	-1287.035	0.431	2153.339	0.569	21	0.337	K.SSVHDVVLVGGSTR.I
R4/RRR4-6/2	1437.190	1437.625	-303.334	0.558	2339.173	0.453	19	0.332	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1438.172	1437.625	-315.556	0.615	2180.554	0.531	19	0.332	-.VQQLLQDFFNGK.-
R4/RRR4-6/2	1436.527	1437.625	-1464.660	0.488	2247.642	0.493	19	0.330	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1437.207	1437.625	-291.404	0.579	2180.625	0.492	19	0.317	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1968.497	1968.236	133.252	0.617	1992.419	0.580	24	0.315	R.VQQLLQDFFNGKELCK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1438.109	1437.625	337.432	0.581	2119.817	0.493	19	0.308	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1310.118	1309.490	-285.187	0.467	1933.427	0.578	20	0.305	R.EIAEAYLGTTIK.N
R4/RRR4-6/2	1438.247	1437.625	-263.697	0.630	2036.011	0.527	18	0.302	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1412.702	1413.562	-1320.098	0.496	1795.317	0.574	20	0.282	K.SSVHDVVLVGGSTR.I
R4/RRR4-6/2	1438.049	1437.625	295.897	0.597	1851.645	0.516	18	0.273	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1309.179	1309.490	-238.444	0.412	1847.756	0.480	19	0.264	R.EIAEAYLGTTIK.N
R4/RRR4-6/2	1413.193	1413.562	-261.700	0.486	1749.539	0.526	21	0.263	K.SSVHDVVLVGGSTR.I
R4/RRR4-6/2	1676.271	1676.683	-246.120	0.458	1822.967	0.485	23	0.261	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-5/2	1437.274	1437.625	-244.708	0.526	1917.915	0.429	19	0.259	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1215.662	1216.436	-1464.069	0.505	1711.180	0.519	21	0.259	K.DAGVIAGLNVMR.I
R4/RRR4-5/2	1676.179	1676.683	-899.521	0.476	1693.647	0.536	22	0.256	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-3/2	1438.555	1437.625	-48.650	0.606	1802.616	0.467	18	0.251	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1196.520	1197.277	-1472.960	0.517	1722.479	0.484	18	0.250	R.FSDASVQSDIK.L
R4/RRR4-6/2	1197.150	1197.277	-106.529	0.512	1678.820	0.490	18	0.246	R.FSDASVQSDIK.L
R4/RRR4-6/2	1233.049	1232.436	-314.662	0.541	1820.918	0.415	20	0.244	K.DAGVIAGLNVM*R.I
R4/RRR4-6/2	1216.167	1216.436	-221.846	0.534	1585.134	0.516	20	0.242	K.DAGVIAGLNVMR.I
R4/RRR4-6/2	1232.176	1232.436	-210.948	0.559	1625.130	0.499	19	0.241	K.DAGVIAGLNVM*R.I
R4/RRR4-6/2	1216.060	1216.436	-310.568	0.551	1543.445	0.532	20	0.241	K.DAGVIAGLNVMR.I
R4/RRR4-6/2	1232.090	1232.436	-281.517	0.476	1784.806	0.419	20	0.241	K.DAGVIAGLNVM*R.I
R4/RRR4-6/2	1676.299	1676.683	-229.463	0.543	1575.601	0.529	22	0.240	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/2	1197.003	1197.277	-229.183	0.545	1610.064	0.479	18	0.235	R.FSDASVQSDIK.L
R4/RRR4-6/2	1596.188	1596.874	-1059.044	0.503	1663.199	0.404	22	0.222	K.MREIAEAYLGTTIK.N
R4/RRR4-6/2	1676.157	1676.683	-912.973	0.456	1388.437	0.535	21	0.219	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-5/2	1676.281	1676.683	-240.275	0.474	1352.202	0.528	21	0.214	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/2	1308.655	1309.490	-1406.437	0.326	1493.605	0.457	17	0.211	R.EIAEAYLGTTIK.N
R4/RRR4-5/2	1437.283	1437.625	-238.147	0.528	1385.333	0.468	17	0.206	R.VQQLLQDFFNGK.E
R4/RRR4-1/2	1676.205	1676.683	-285.865	0.448	1391.283	0.469	22	0.206	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-5/2	1197.074	1197.277	-169.540	0.424	1408.032	0.437	18	0.204	R.FSDASVQSDIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1582.448	1582.844	-250.641	0.484	1321.405	0.435	21	0.195	K.QFAAEEISSM*VLIK.M
R4/RRR4-6/2	1613.392	1612.873	-298.903	0.553	1096.416	0.497	23	0.192	K.M*REIAEAYLGTTIK.N
R4/RRR4-6/2	1374.966	1375.492	-1113.250	0.478	1145.754	0.494	16	0.192	K.NALENYAYNM*R.N
R4/RRR4-6/3	1804.050	1804.019	17.537	0.467	1610.416	0.432	30	0.191	K.M*DKSSVHDVVLVGGSTR.I
R4/RRR4-6/2	1374.933	1375.492	-1137.231	0.457	1125.732	0.476	16	0.187	K.NALENYAYNM*R.N
R4/RRR4-6/2	1374.916	1375.492	-1149.891	0.443	1109.557	0.480	16	0.186	K.NALENYAYNM*R.N
R4/RRR4-6/2	1566.242	1566.844	-1025.979	0.536	1152.981	0.399	22	0.177	K.QFAAEEISSMVLIK.M
R4/RRR4-6/2	1566.299	1566.844	-989.515	0.519	1150.124	0.382	22	0.173	K.QFAAEEISSMVLIK.M
R4/RRR4-6/2	1566.438	1566.844	-260.172	0.517	1177.743	0.353	22	0.170	K.QFAAEEISSMVLIK.M
R4/RRR4-6/2	1682.334	1681.830	-296.104	0.437	609.577	0.535	21	0.169	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-6/2	1540.893	1541.757	-1213.375	0.433	1066.408	0.377	18	0.166	R.ARFEELNMDLFR.K
R4/RRR4-5/2	1681.350	1681.830	-286.884	0.384	618.498	0.527	21	0.166	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-5/2	1681.359	1681.830	-281.057	0.411	614.728	0.500	21	0.164	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-6/3	1669.583	1669.929	-208.174	0.530	1621.631	0.370	26	0.164	R.ARFEELNMDLFRK.C
R4/RRR4-6/3	1542.365	1541.757	-254.716	0.540	1573.574	0.388	25	0.162	R.ARFEELNMDLFR.K
R4/RRR4-6/2	1612.270	1612.873	-996.927	0.496	600.852	0.439	21	0.160	K.M*REIAEAYLGTTIK.N
R4/RRR4-6/3	1557.527	1557.756	-147.693	0.492	1672.878	0.336	23	0.160	R.ARFEELNM*DLFR.K
R4/RRR4-5/2	1567.754	1566.844	-57.527	0.517	762.524	0.416	19	0.158	K.QFAAEEISSMVLIK.M
R4/RRR4-6/2	1295.158	1295.492	-258.146	0.458	666.375	0.400	15	0.157	R.M*VNHFVQEFK.R
R4/RRR4-5/2	1681.210	1681.830	-966.961	0.351	560.551	0.466	20	0.157	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-1/2	1197.286	1197.277	8.119	0.273	1034.958	0.331	16	0.156	R.FSDASVQSDIK.L
R4/RRR4-1/2	1682.382	1681.830	-267.204	0.431	489.061	0.451	19	0.156	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-2/2	1681.344	1681.830	-290.307	0.367	503.421	0.468	19	0.156	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-6/2	1582.221	1582.844	-1028.683	0.463	686.365	0.411	18	0.155	K.QFAAEEISSM*VLIK.M
R4/RRR4-1/2	1437.299	1437.625	-227.241	0.394	780.478	0.386	15	0.154	R.VQQLLQDFFNGK.E
R4/RRR4-6/2	1613.405	1612.873	-290.780	0.483	486.625	0.390	20	0.152	K.M*REIAEAYLGTTIK.N
R4/RRR4-6/2	1295.062	1295.492	-333.137	0.463	547.437	0.380	14	0.152	R.M*VNHFVQEFK.R
R4/RRR4-6/2	1295.155	1295.492	-260.700	0.446	558.647	0.375	14	0.151	R.M*VNHFVQEFK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1670.327	1669.929	238.542	0.507	1486.701	0.380	25	0.151	R.ARFEELNMDLFRK.C
R4/RRR4-1/2	1681.093	1681.830	-1036.436	0.363	341.948	0.443	16	0.150	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-2/2	1197.363	1197.277	72.130	0.282	725.057	0.379	15	0.150	R.FSDASVQSDIK.L
R4/RRR4-6/3	1540.945	1541.757	-1179.097	0.444	1430.717	0.392	23	0.149	-.ARFEELNMDLFR.-
R4/RRR4-6/3	1676.939	1676.683	153.491	0.390	818.851	0.618	31	0.148	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/2	1680.764	1681.830	-1233.104	0.245	359.978	0.460	17	0.146	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-1/2	1680.951	1681.830	-1121.599	0.291	308.390	0.395	15	0.145	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-6/2	1681.117	1681.830	-1022.366	0.245	399.873	0.413	17	0.144	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-4/2	1681.402	1681.830	-255.855	0.357	239.153	0.354	13	0.143	K.NAVVTVPAYFNDSQR.Q
R4/RRR4-6/2	1197.835	1197.277	-369.773	0.268	313.002	0.295	12	0.142	R.FSDASVQSDIK.L
R4/RRR4-5/3	1677.524	1676.683	-95.008	0.457	712.308	0.594	30	0.137	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/3	1677.757	1676.683	44.463	0.420	889.517	0.546	32	0.137	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/3	1677.748	1676.683	38.990	0.441	749.466	0.582	30	0.136	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/2	1356.997	1357.571	-1164.062	0.317	1003.685	0.178	16	0.136	K.ELEGICNPIIAK.M
R4/RRR4-6/3	1541.299	1541.757	-297.748	0.544	1477.055	0.322	24	0.130	R.ARFEELNMDLFR.K
R4/RRR4-5/3	1676.318	1676.683	-218.074	0.383	618.853	0.592	26	0.130	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-5/3	1676.918	1676.683	140.570	0.481	698.729	0.559	29	0.129	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/3	1670.082	1669.929	91.880	0.514	1382.993	0.332	23	0.126	-.ARFEELNMDLFRK.-
R4/RRR4-6/3	1869.818	1869.109	-156.022	0.430	850.748	0.511	29	0.125	R.FSDASVQSDIKLWPFK.V
R4/RRR4-6/3	1969.013	1968.236	-113.589	0.474	640.828	0.523	26	0.118	R.VQQLLQDFFNGKELCK.S
R4/RRR4-8/3	1676.266	1676.683	-249.415	0.374	676.137	0.501	27	0.116	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-7/3	1675.911	1676.683	-1060.105	0.348	519.352	0.521	23	0.113	K.ATAGDTHLGGEDFDNR.M
R4/RRR4-6/3	1869.300	1869.109	102.556	0.399	644.041	0.499	26	0.110	R.FSDASVQSDIKLWPFK.V
R4/RRR4-6/3	1451.054	1451.678	-1122.640	0.521	604.964	0.470	21	0.109	R.M*VNHFVQEFKR.K
R4/RRR4-6/3	1869.059	1869.109	-27.036	0.418	561.460	0.506	24	0.109	R.FSDASVQSDIKLWPFK.V
R4/RRR4-6/3	1969.022	1968.236	-109.018	0.440	468.019	0.490	25	0.108	R.VQQLLQDFFNGKELCK.S
R4/RRR4-6/3	1451.761	1451.678	57.480	0.470	373.336	0.500	17	0.106	R.M*VNHFVQEFKR.K
R4/RRR4-6/3	1969.302	1968.236	33.684	0.407	411.015	0.473	24	0.105	R.VQQLLQDFFNGKELCK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1967.455	1968.236	-907.589	0.427	609.495	0.446	27	0.105	R.VQQLLQDFFNGKELCK.S
R4/RRR4-6/3	1566.904	1566.844	38.466	0.486	986.281	0.352	26	0.101	K.QFAAEEISSMVLIK.M
R4/RRR4-6/3	1970.056	1968.236	-91.279	0.396	450.931	0.422	25	0.100	R.VQQLLQDFFNGKELCK.S
R4/RRR4-6/3	1558.175	1557.756	269.966	0.455	1054.625	0.319	21	0.099	R.ARFEELNM*DLFR.K
R4/RRR4-6/3	1969.522	1968.236	146.044	0.419	493.147	0.403	25	0.099	R.VQQLLQDFFNGKELCK.S
R4/RRR4-6/3	1451.018	1451.678	-1147.476	0.418	562.180	0.372	20	0.094	R.M*VNHFVQEFKR.K
R4/RRR4-3/3	1676.414	1676.683	-160.656	0.363	526.279	0.360	24	0.088	-.ATAGDTHLGGEDFDNR.-
R4/RRR4-6/3	1686.944	1685.929	8.722	0.482	787.952	0.259	24	0.085	R.ARFEELNM*DLFRK.C
R4/RRR4-16/3	1863.712	1862.190	-256.871	0.338	1057.385	0.180	23	0.075	-.M*NPINTVFDAKRLIGR.-
R4/RRR4-5/2	1968.483	1969.179	-864.223	0.635	3413.250	0.593	26	0.646	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1556.058	1556.618	-1005.784	0.484	3348.375	0.520	24	0.595	K.DEAYFAANAAAQASR.R
R4/RRR4-5/2	1556.102	1556.618	-977.037	0.484	3195.422	0.528	24	0.557	K.DEAYFAANAAAQASR.R
R4/RRR4-5/2	1968.514	1969.179	-848.287	0.620	3066.383	0.581	26	0.544	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1968.602	1969.179	-803.593	0.628	3115.035	0.536	26	0.536	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1556.092	1556.618	-983.731	0.476	3099.009	0.487	24	0.514	K.DEAYFAANAAAQASR.R
R4/RRR4-5/2	1807.517	1808.137	-899.277	0.545	2828.761	0.595	25	0.487	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-1/2	1807.616	1808.137	-843.821	0.537	2573.502	0.552	24	0.412	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/2	1808.459	1808.137	178.536	0.599	2297.228	0.657	23	0.393	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/2	1807.499	1808.137	-908.972	0.562	2324.102	0.573	23	0.368	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-1/2	1809.535	1808.137	220.718	0.582	2206.379	0.636	22	0.367	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/2	1808.337	1808.137	110.909	0.593	2279.837	0.590	23	0.365	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/2	1791.773	1792.138	-204.220	0.567	2304.991	0.574	23	0.365	K.GMLTGPVTILNWSFVR.N
R4/RRR4-4/2	1808.140	1808.137	1.630	0.553	2175.681	0.627	23	0.359	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-1/2	1807.497	1808.137	-910.396	0.545	2262.677	0.578	23	0.359	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-2/2	1808.354	1808.137	120.048	0.579	2171.907	0.591	23	0.346	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-2/2	1807.751	1808.137	-214.492	0.517	2134.585	0.562	22	0.330	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-1/3	1969.099	1969.179	-40.554	0.549	1921.823	0.576	34	0.304	K.KISEDEYVSAIKEEISK.V
R4/RRR4-4/3	1969.123	1969.179	-28.709	0.571	1922.197	0.570	36	0.299	K.KISEDEYVSAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/3	1969.095	1969.179	-42.793	0.579	1832.782	0.585	35	0.287	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/3	1977.286	1978.201	-971.067	0.540	1938.246	0.496	30	0.281	R.KAEHAFYLDWAVHSFR.I
R4/RRR4-5/2	1809.108	1808.137	-16.238	0.545	1830.242	0.559	22	0.280	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/3	1739.761	1740.015	-146.265	0.471	1877.455	0.530	36	0.269	K.YTEVKPALTNM*VSAAK.L
R4/RRR4-5/3	1969.223	1969.179	22.587	0.583	1603.746	0.602	34	0.251	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1486.363	1486.653	-195.604	0.505	1792.889	0.422	20	0.242	R.IPSTEEIADRINK.M
R4/RRR4-5/2	1486.295	1486.653	-241.250	0.487	1703.325	0.433	19	0.233	R.IPSTEEIADRINK.M
R4/RRR4-5/2	1254.249	1254.368	-95.334	0.497	1597.551	0.472	18	0.233	K.ISEDEYVSAIK.E
R4/RRR4-5/2	1739.538	1740.015	-275.009	0.549	1276.737	0.581	23	0.222	K.YTEVKPALTNM*VSAAK.L
R4/RRR4-2/3	1969.781	1969.179	-202.523	0.516	1539.075	0.549	32	0.219	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/3	1808.054	1808.137	-46.186	0.516	1781.842	0.435	30	0.216	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/2	1486.245	1486.653	-275.281	0.482	1570.342	0.413	18	0.212	R.IPSTEEIADRINK.M
R4/RRR4-5/2	1659.347	1659.826	-289.581	0.501	1266.170	0.537	22	0.209	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1969.160	1969.179	-9.869	0.554	1425.190	0.571	33	0.208	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1659.528	1659.826	-180.137	0.530	1330.574	0.500	22	0.207	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1739.474	1740.015	-888.232	0.574	1131.318	0.571	22	0.205	K.YTEVKPALTNM*VSAAK.L
R4/RRR4-5/2	1841.481	1841.006	258.930	0.544	1341.076	0.481	21	0.203	K.ISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1739.427	1740.015	-915.708	0.508	1121.819	0.559	22	0.201	K.YTEVKPALTNM*VSAAK.L
R4/RRR4-5/2	1840.436	1841.006	-855.563	0.506	1364.155	0.461	21	0.201	K.ISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1867.419	1868.188	-949.752	0.542	933.765	0.600	24	0.197	R.KYTEVKPALTNM*VSAAK.L
R4/RRR4-4/2	1659.291	1659.826	-928.009	0.500	1212.795	0.482	21	0.192	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1867.557	1868.188	-875.862	0.531	850.153	0.589	24	0.189	R.KYTEVKPALTNM*VSAAK.L
R4/RRR4-3/2	1660.243	1659.826	251.577	0.455	1039.965	0.540	19	0.188	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1194.249	1194.362	-94.998	0.514	1241.234	0.403	17	0.185	R.SDEKLLSVFR.E
R4/RRR4-5/2	1659.372	1659.826	-274.967	0.475	1080.803	0.499	20	0.185	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1867.616	1868.188	-844.235	0.527	843.346	0.563	24	0.184	R.KYTEVKPALTNM*VSAAK.L
R4/RRR4-5/3	1724.103	1724.015	50.724	0.460	1438.417	0.502	32	0.184	K.YTEVKPALTNMVSAAK.L
R4/RRR4-5/2	1659.427	1659.826	-241.166	0.483	859.954	0.550	19	0.179	K.YGAGIGPGVYDIHSPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1131.018	1131.218	-177.602	0.489	867.692	0.491	17	0.179	R.IPSTEEIADR.I
R4/RRR4-4/2	1659.353	1659.826	-286.186	0.475	921.520	0.527	18	0.178	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-2/2	1130.821	1131.218	-352.384	0.485	860.253	0.482	17	0.177	R.IPSTEEIADR.I
R4/RRR4-4/2	1130.485	1131.218	-1538.206	0.470	814.605	0.490	17	0.176	R.IPSTEEIADR.I
R4/RRR4-3/2	1130.934	1131.218	-252.532	0.487	851.857	0.470	17	0.175	R.IPSTEEIADR.I
R4/RRR4-2/2	1806.723	1808.137	-1340.023	0.351	1136.167	0.431	18	0.175	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/2	1021.984	1022.181	-194.094	0.442	1088.930	0.388	14	0.172	K.SWLAFAAQK.V
R4/RRR4-5/2	1194.093	1194.362	-226.358	0.500	1112.103	0.377	16	0.172	R.SDEKLLSVFR.E
R4/RRR4-1/2	1130.471	1131.218	-1549.921	0.457	854.847	0.448	17	0.171	R.IPSTEEIADR.I
R4/RRR4-5/2	1194.231	1194.362	-110.173	0.507	1124.915	0.369	16	0.171	R.SDEKLLSVFR.E
R4/RRR4-2/2	1132.155	1131.218	-56.409	0.507	766.681	0.455	17	0.170	R.IPSTEEIADR.I
R4/RRR4-3/2	1659.523	1659.826	-183.236	0.433	936.097	0.473	18	0.170	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1130.954	1131.218	-234.556	0.480	856.196	0.422	17	0.168	R.IPSTEEIADR.I
R4/RRR4-5/2	1195.344	1194.362	-15.632	0.439	1048.811	0.361	16	0.166	R.SDEKLLSVFR.E
R4/RRR4-3/2	1130.498	1131.218	-1526.166	0.415	766.913	0.435	17	0.165	R.IPSTEEIADR.I
R4/RRR4-1/2	1193.902	1194.362	-387.092	0.393	970.559	0.394	15	0.165	R.SDEKLLSVFR.E
R4/RRR4-5/2	1707.792	1707.951	-93.316	0.369	1186.462	0.347	19	0.164	K.LDSEIKSWLAFAAQK.V
R4/RRR4-2/3	1969.843	1969.179	-171.283	0.505	1126.738	0.553	30	0.164	K.KISEDEYVSAIKEEISK.V
R4/RRR4-1/2	1132.019	1131.218	-176.147	0.490	601.287	0.460	15	0.164	R.IPSTEEIADR.I
R4/RRR4-4/2	1022.199	1022.181	17.594	0.454	1006.595	0.368	13	0.163	K.SWLAFAAQK.V
R4/RRR4-4/2	1131.851	1131.218	-325.020	0.498	687.397	0.424	16	0.163	R.IPSTEEIADR.I
R4/RRR4-5/2	1021.627	1022.181	-1526.235	0.411	1058.838	0.336	14	0.162	K.SWLAFAAQK.V
R4/RRR4-4/2	1131.118	1131.218	-88.609	0.431	668.818	0.434	16	0.162	R.IPSTEEIADR.I
R4/RRR4-5/2	1840.559	1841.006	-243.775	0.585	1053.478	0.403	19	0.162	K.ISEDEYVSAIKEEISK.V
R4/RRR4-5/2	1131.081	1131.218	-121.520	0.468	741.779	0.409	16	0.162	R.IPSTEEIADR.I
R4/RRR4-5/2	1021.619	1022.181	-1533.917	0.398	1155.095	0.297	14	0.161	K.SWLAFAAQK.V
R4/RRR4-2/2	1130.830	1131.218	-344.152	0.397	661.678	0.420	16	0.160	R.IPSTEEIADR.I
R4/RRR4-1/2	1131.222	1131.218	3.614	0.448	657.924	0.406	16	0.160	R.IPSTEEIADR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/3	1739.670	1740.015	-198.740	0.463	1246.077	0.499	30	0.160	K.YTEVKPALTNM*VSAAK.L
R4/RRR4-6/2	1809.421	1808.137	157.532	0.509	701.595	0.470	18	0.159	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-1/2	1022.091	1022.181	-88.538	0.393	1118.193	0.295	14	0.159	K.SWLAFAAQK.V
R4/RRR4-4/2	942.811	943.123	-331.620	0.410	370.471	0.475	12	0.159	K.VVEVNALAK.A
R4/RRR4-2/2	1659.739	1659.826	-52.863	0.374	805.043	0.439	17	0.158	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-3/2	943.058	943.123	-69.148	0.409	426.390	0.436	13	0.157	K.VVEVNALAK.A
R4/RRR4-1/2	943.018	943.123	-111.477	0.372	492.244	0.400	14	0.155	K.VVEVNALAK.A
R4/RRR4-5/2	1658.857	1659.826	-1191.007	0.360	892.875	0.374	18	0.154	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1194.953	1194.362	-343.923	0.372	749.957	0.387	13	0.154	R.SDEKLLSVFR.E
R4/RRR4-5/3	1659.948	1659.826	73.190	0.443	832.699	0.610	28	0.154	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1740.395	1740.015	219.115	0.484	1272.910	0.470	32	0.153	K.YTEVKPALTNM*VSAAK.L
R4/RRR4-5/2	1659.557	1659.826	-162.796	0.383	626.124	0.427	18	0.153	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-3/3	1659.088	1659.826	-1051.151	0.412	820.563	0.609	28	0.152	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-1/2	942.902	943.123	-234.849	0.345	357.973	0.394	12	0.152	K.VVEVNALAK.A
R4/RRR4-2/2	942.483	943.123	-1745.010	0.346	324.450	0.416	11	0.152	K.VVEVNALAK.A
R4/RRR4-3/2	942.977	943.123	-154.589	0.342	667.591	0.331	15	0.151	K.VVEVNALAK.A
R4/RRR4-3/2	1808.966	1808.137	-94.751	0.399	815.982	0.367	17	0.150	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-2/2	942.500	943.123	-1726.661	0.309	388.975	0.389	12	0.150	K.VVEVNALAK.A
R4/RRR4-2/2	1807.384	1808.137	-973.047	0.368	558.344	0.447	15	0.150	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/2	1809.904	1808.137	-128.932	0.411	461.000	0.436	16	0.149	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-9/3	1660.131	1659.826	183.808	0.443	818.440	0.597	28	0.149	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1659.649	1659.826	-107.163	0.369	394.887	0.406	17	0.148	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-4/2	942.483	943.123	-1745.010	0.305	325.308	0.367	11	0.148	K.VVEVNALAK.A
R4/RRR4-7/2	942.866	943.123	-272.646	0.320	293.323	0.386	10	0.148	K.VVEVNALAK.A
R4/RRR4-5/3	1556.053	1556.618	-1008.865	0.428	1424.938	0.385	26	0.148	K.DEAYFAANAAAQASR.R
R4/RRR4-3/2	943.028	943.123	-100.440	0.300	439.447	0.316	13	0.147	K.VVEVNALAK.A
R4/RRR4-4/2	1021.794	1022.181	-380.698	0.297	987.854	0.241	13	0.146	K.SWLAFAAQK.V
R4/RRR4-5/3	1660.930	1659.826	62.495	0.471	710.892	0.609	26	0.146	K.YGAGIGPGVYDIHSPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/3	1659.174	1659.826	-999.183	0.427	719.499	0.610	27	0.146	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1131.221	1131.218	2.532	0.347	602.417	0.275	14	0.145	R.IPSTEEIADR.I
R4/RRR4-5/3	1659.706	1659.826	-72.864	0.465	802.377	0.581	29	0.144	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-4/2	1193.589	1194.362	-1490.323	0.353	494.381	0.337	11	0.144	R.SDEKLLSVFR.E
R4/RRR4-5/3	1659.993	1659.826	100.626	0.445	781.933	0.584	29	0.143	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1267.978	1268.556	-1248.876	0.386	879.403	0.297	13	0.143	K.MAQSMTSRPMK.G
R4/RRR4-5/2	1661.018	1659.826	115.388	0.284	209.914	0.409	12	0.142	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-4/2	1194.104	1194.362	-217.025	0.373	561.563	0.271	12	0.141	R.SDEKLLSVFR.E
R4/RRR4-3/3	1660.889	1659.826	37.506	0.464	695.056	0.596	28	0.141	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-3/3	1659.257	1659.826	-948.660	0.430	634.848	0.610	26	0.141	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-25/2	1131.372	1131.218	135.858	0.256	645.628	0.235	15	0.141	-.IPSTEEIADR.-
R4/RRR4-5/3	1659.820	1659.826	-3.815	0.447	615.358	0.609	25	0.140	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-8/3	1660.047	1659.826	133.369	0.400	890.227	0.536	27	0.140	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-6/3	1659.978	1659.826	91.775	0.427	667.285	0.598	27	0.140	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-10/3	1660.102	1659.826	166.554	0.434	668.835	0.596	27	0.140	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-7/2	1659.704	1659.826	-74.184	0.279	329.445	0.369	13	0.139	-.YGAGIGPGVYDIHSPR.-
R4/RRR4-1/2	1659.410	1659.826	-251.498	0.294	695.951	0.297	15	0.139	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1660.499	1659.826	-197.736	0.478	596.183	0.603	25	0.138	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-6/3	1658.554	1659.826	-1373.940	0.402	531.870	0.607	24	0.136	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/2	1022.950	1022.181	-226.586	0.365	1056.259	0.108	14	0.135	K.SWLAFAAQK.V
R4/RRR4-2/3	1659.130	1659.826	-1025.332	0.401	565.784	0.593	23	0.135	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-10/3	1659.863	1659.826	22.297	0.463	687.556	0.564	27	0.134	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-1/2	1659.316	1659.826	-912.942	0.256	502.474	0.257	13	0.133	-.YGAGIGPGVYDIHSPR.-
R4/RRR4-1/3	1659.053	1659.826	-1072.427	0.398	497.919	0.591	22	0.132	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-8/3	1660.809	1659.826	-10.595	0.378	775.875	0.529	26	0.132	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1660.715	1659.826	-67.438	0.436	528.757	0.579	24	0.131	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-4/3	1969.338	1969.179	81.151	0.451	951.581	0.489	28	0.131	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/3	1991.747	1992.176	-215.841	0.516	821.605	0.535	34	0.130	K.IQEELDIDVLVHGEPER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/3	1659.963	1659.826	82.372	0.470	552.556	0.570	24	0.130	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1658.603	1659.826	-1344.668	0.413	627.974	0.557	26	0.130	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-4/3	1659.292	1659.826	-927.500	0.414	616.603	0.545	25	0.128	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1659.187	1659.826	-990.873	0.407	514.562	0.558	24	0.127	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-2/3	1659.804	1659.826	-13.774	0.406	540.954	0.555	25	0.127	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-1/3	1660.617	1659.826	-126.278	0.433	494.620	0.554	23	0.126	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-4/3	1659.758	1659.826	-41.326	0.430	529.401	0.543	25	0.125	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1194.564	1194.362	169.606	0.572	1246.901	0.376	21	0.123	R.SDEKLLSVFR.E
R4/RRR4-5/3	1868.470	1868.188	151.607	0.487	914.543	0.466	31	0.121	R.KYTEVKPALTNM*VSAAK.L
R4/RRR4-5/3	1993.683	1992.176	-248.027	0.474	599.839	0.550	29	0.120	K.IQEELDIDVLVHGEPER.N
R4/RRR4-10/3	1659.714	1659.826	-67.774	0.454	429.604	0.516	22	0.120	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1659.595	1659.826	-139.930	0.372	517.423	0.510	25	0.119	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1992.215	1992.176	19.561	0.466	596.583	0.535	30	0.117	K.IQEELDIDVLVHGEPER.N
R4/RRR4-5/3	1194.691	1194.362	275.813	0.533	1305.392	0.319	21	0.114	R.SDEKLLSVFR.E
R4/RRR4-2/3	1659.810	1659.826	-9.790	0.370	340.421	0.436	19	0.113	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-6/3	1659.647	1659.826	-108.499	0.375	571.570	0.446	24	0.112	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-9/3	1659.964	1659.826	82.925	0.339	487.106	0.424	23	0.110	K.YGAGIGPGVYDIHSPR.I
R4/RRR4-5/3	1194.507	1194.362	121.798	0.431	1254.221	0.317	21	0.109	R.SDEKLLSVFR.E
R4/RRR4-7/3	1660.135	1659.826	186.463	0.315	327.583	0.484	19	0.109	-.YGAGIGPGVYDIHSPR.-
R4/RRR4-5/3	1868.256	1868.188	36.512	0.467	762.599	0.436	30	0.107	R.KYTEVKPALTNM*VSAAK.L
R4/RRR4-1/3	1195.044	1194.362	-266.812	0.393	1149.452	0.328	20	0.105	R.SDEKLLSVFR.E
R4/RRR4-5/3	1849.544	1850.028	-262.259	0.368	908.643	0.395	24	0.103	K.AEHAFYLDWAVHSFR.I
R4/RRR4-5/3	1851.610	1852.188	-854.870	0.475	544.597	0.429	27	0.100	R.KYTEVKPALTNMVSAAK.L
R4/RRR4-5/3	1807.635	1808.137	-833.626	0.418	768.869	0.400	25	0.100	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/3	1852.165	1852.188	-12.343	0.430	512.204	0.418	26	0.098	R.KYTEVKPALTNMVSAAK.L
R4/RRR4-3/3	1968.956	1969.179	-113.685	0.379	698.531	0.360	23	0.097	K.KISEDEYVSAIKEEISK.V
R4/RRR4-5/3	1722.755	1724.015	-1315.738	0.281	469.572	0.393	21	0.094	-.YTEVKPALTNMVSAAK.-
R4/RRR4-4/3	1968.710	1969.179	-238.797	0.278	591.297	0.317	22	0.093	K.KISEDEYVSAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/3	1194.607	1194.362	205.574	0.336	675.652	0.351	17	0.092	R.SDEKLLSVFR.E
R4/RRR4-5/3	1808.286	1808.137	82.805	0.378	707.469	0.340	27	0.091	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-1/3	1740.680	1740.015	-193.068	0.275	845.252	0.301	24	0.090	-.YTEVKPALTNM*VSAAK.-
R4/RRR4-5/3	1723.550	1724.015	-270.739	0.347	670.387	0.269	25	0.087	K.YTEVKPALTNMVSAAK.L
R4/RRR4-5/3	1807.974	1808.137	-90.680	0.323	923.523	0.271	27	0.086	K.GM*LTGPVTILNWSFVR.N
R4/RRR4-5/3	1851.066	1850.028	20.490	0.210	767.979	0.236	21	0.075	K.AEHAFYLDWAVHSFR.I
R4/RRR4-3/2	1979.767	1980.162	-199.917	0.619	2249.363	0.532	25	0.343	K.VSEDDKLVEYDALLVDR.F
R4/RRR4-3/2	1979.496	1980.162	-844.013	0.610	2079.267	0.573	24	0.327	K.VSEDDKLVEYDALLVDR.F
R4/RRR4-1/2	1646.351	1646.869	-924.593	0.423	1816.132	0.493	21	0.261	K.LLVAGDLQSFGEQLR.N
R4/RRR4-3/3	1980.125	1980.162	-18.842	0.460	1854.623	0.490	31	0.256	K.VSEDDKLVEYDALLVDR.F
R4/RRR4-3/2	1860.537	1860.958	-226.614	0.597	1686.468	0.516	22	0.250	K.DITADDKQELDEALQR.E
R4/RRR4-3/2	1861.277	1860.958	172.306	0.620	1743.592	0.480	23	0.247	K.DITADDKQELDEALQR.E
R4/RRR4-3/2	1861.644	1860.958	-169.064	0.614	1670.667	0.510	23	0.247	K.DITADDKQELDEALQR.E
R4/RRR4-4/2	1269.013	1268.444	-341.218	0.504	1525.740	0.537	21	0.239	K.LADLEAAPAAVAR.L
R4/RRR4-4/2	1268.132	1268.444	-246.934	0.450	1622.774	0.490	21	0.238	K.LADLEAAPAAVAR.L
R4/RRR4-3/2	1915.546	1914.112	227.379	0.574	1499.292	0.519	22	0.227	K.NQTVDLVFTAHPTQSVR.R
R4/RRR4-3/2	1268.100	1268.444	-272.623	0.474	1421.165	0.457	20	0.209	K.LADLEAAPAAVAR.L
R4/RRR4-3/2	1187.393	1188.293	-1605.207	0.395	1208.208	0.537	17	0.204	R.TPPTPQDEM*R.A
R4/RRR4-3/3	1980.075	1980.162	-44.071	0.441	1623.773	0.466	30	0.204	K.VSEDDKLVEYDALLVDR.F
R4/RRR4-4/2	1267.447	1268.444	-1580.353	0.398	1410.816	0.435	19	0.202	K.LADLEAAPAAVAR.L
R4/RRR4-3/3	1647.825	1646.869	-26.951	0.521	1502.724	0.506	30	0.198	K.LLVAGDLQSFGEQLR.N
R4/RRR4-3/2	1267.536	1268.444	-1510.308	0.349	1440.663	0.353	19	0.188	K.LADLEAAPAAVAR.L
R4/RRR4-3/3	1743.554	1742.932	-217.403	0.491	1593.901	0.436	30	0.187	R.INGKQEVM*IGYSDSGK.D
R4/RRR4-1/2	1646.691	1646.869	-108.526	0.360	1324.532	0.418	19	0.187	K.LLVAGDLQSFGEQLR.N
R4/RRR4-3/2	1914.723	1914.112	-203.383	0.562	939.528	0.539	18	0.178	K.NQTVDLVFTAHPTQSVR.R
R4/RRR4-3/2	1316.230	1316.491	-198.842	0.490	1399.763	0.306	16	0.177	K.RQDWLLSELR.G
R4/RRR4-3/2	1113.865	1114.299	-391.022	0.420	1229.623	0.366	14	0.176	R.LSAAWQM*YK.A
R4/RRR4-3/2	1187.951	1188.293	-288.721	0.397	836.999	0.522	15	0.175	R.TPPTPQDEM*R.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1188.028	1188.293	-224.394	0.350	1013.051	0.461	16	0.174	R.TPPTPQDEM*R.A
R4/RRR4-3/2	1915.002	1914.112	-57.197	0.539	880.145	0.532	18	0.173	K.NQTVDLVFTAHPTQSVR.R
R4/RRR4-3/2	1023.939	1023.168	-224.095	0.530	948.061	0.431	11	0.173	K.HYIEFWK.K
R4/RRR4-3/2	1067.893	1068.169	-259.185	0.436	940.801	0.440	15	0.173	R.HQSIDAQLR.L
R4/RRR4-3/2	1067.784	1068.169	-361.147	0.444	1175.324	0.346	15	0.171	R.HQSIDAQLR.L
R4/RRR4-3/2	1113.944	1114.299	-319.771	0.503	1042.521	0.395	14	0.171	R.LSAAWQM*YK.A
R4/RRR4-3/2	1120.032	1120.237	-183.935	0.403	560.191	0.567	17	0.169	K.GDPGIAALYDK.L
R4/RRR4-3/2	1113.977	1114.299	-290.305	0.490	1027.574	0.388	14	0.169	R.LSAAWQM*YK.A
R4/RRR4-3/2	1067.982	1068.169	-175.474	0.486	728.142	0.466	14	0.168	R.HQSIDAQLR.L
R4/RRR4-3/2	1491.256	1490.733	-320.580	0.503	620.983	0.484	17	0.165	R.AIPWIFAWTQTR.F
R4/RRR4-3/2	975.864	976.154	-297.992	0.428	940.945	0.374	13	0.163	R.SIVFKEPR.F
R4/RRR4-4/2	1491.095	1490.733	243.740	0.455	690.316	0.438	18	0.162	R.AIPWIFAWTQTR.F
R4/RRR4-3/2	975.686	976.154	-480.882	0.389	829.900	0.404	12	0.160	R.SIVFKEPR.F
R4/RRR4-3/2	1316.259	1316.491	-176.699	0.389	1135.712	0.293	15	0.159	K.RQDWLLSELR.G
R4/RRR4-3/2	1316.617	1316.491	95.726	0.460	1143.814	0.289	15	0.158	K.RQDWLLSELR.G
R4/RRR4-3/2	1023.887	1023.168	-275.047	0.455	896.651	0.329	11	0.156	K.HYIEFWK.K
R4/RRR4-1/2	1490.051	1490.733	-1132.015	0.333	638.710	0.419	17	0.154	R.AIPWIFAWTQTR.F
R4/RRR4-3/2	1023.021	1023.168	-143.631	0.347	907.181	0.318	11	0.154	K.HYIEFWK.K
R4/RRR4-4/2	1022.376	1023.168	-1758.164	0.475	843.198	0.309	11	0.152	K.HYIEFWK.K
R4/RRR4-3/2	1067.420	1068.169	-1642.849	0.337	607.783	0.401	13	0.152	R.HQSIDAQLR.L
R4/RRR4-4/2	1023.088	1023.168	-78.160	0.396	835.495	0.304	11	0.151	K.HYIEFWK.K
R4/RRR4-4/2	1490.057	1490.733	-1127.655	0.324	536.025	0.407	17	0.151	R.AIPWIFAWTQTR.F
R4/RRR4-3/2	1330.098	1330.447	-262.945	0.386	394.062	0.472	15	0.151	K.QEVM*IGYSDSGK.D
R4/RRR4-3/2	1201.063	1200.373	-258.990	0.430	718.007	0.352	16	0.151	K.RKPSGGIESLR.A
R4/RRR4-1/2	1490.093	1490.733	-1103.307	0.361	640.006	0.357	17	0.150	R.AIPWIFAWTQTR.F
R4/RRR4-3/2	1119.537	1120.237	-1522.844	0.278	433.743	0.497	16	0.150	K.GDPGIAALYDK.L
R4/RRR4-3/2	1344.466	1345.551	-1555.207	0.377	751.676	0.362	13	0.149	R.LFSIDWYMNR.I
R4/RRR4-3/2	1490.072	1490.733	-1117.455	0.318	654.351	0.354	18	0.149	R.AIPWIFAWTQTR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1022.606	1023.168	-1531.957	0.389	850.822	0.267	11	0.148	K.HYIEFWK.K
R4/RRR4-3/2	1489.716	1490.733	-1357.711	0.313	523.928	0.348	17	0.147	R.AIPWIFAWTQTR.F
R4/RRR4-3/2	1193.812	1194.319	-1266.568	0.395	870.932	0.275	14	0.145	K.SREEVFDALK.N
R4/RRR4-3/2	1200.050	1200.373	-269.921	0.428	643.506	0.316	15	0.145	K.RKPSGGIESLR.A
R4/RRR4-1/2	1022.727	1023.168	-432.666	0.298	827.684	0.244	11	0.144	K.HYIEFWK.K
R4/RRR4-3/2	1200.285	1200.373	-73.711	0.412	561.024	0.320	14	0.144	K.RKPSGGIESLR.A
R4/RRR4-4/2	1489.995	1490.733	-1169.693	0.271	556.592	0.296	17	0.143	R.AIPWIFAWTQTR.F
R4/RRR4-3/2	976.106	976.154	-49.686	0.464	797.372	0.250	12	0.143	R.SIVFKEPR.F
R4/RRR4-3/2	1194.177	1194.319	-119.610	0.370	732.697	0.239	14	0.140	K.SREEVFDALK.N
R4/RRR4-3/2	1097.822	1098.300	-436.249	0.168	383.640	0.282	13	0.137	R.LSAAWQMYK.A
R4/RRR4-3/3	1860.596	1860.958	-195.093	0.516	1202.836	0.433	30	0.136	K.DITADDKQELDEALQR.E
R4/RRR4-3/2	1361.204	1361.550	-255.405	0.289	813.213	0.111	14	0.131	-.LFSIDWYM*NR.-
R4/RRR4-3/2	1193.543	1194.319	-1492.329	0.320	598.552	0.188	13	0.129	-.SREEVFDALK.-
R4/RRR4-3/3	1979.969	1980.162	-97.872	0.385	908.147	0.444	24	0.114	K.VSEDDKLVEYDALLVDR.F
R4/RRR4-4/3	1860.391	1860.958	-844.715	0.451	1031.634	0.385	27	0.110	K.DITADDKQELDEALQR.E
R4/RRR4-3/3	1742.780	1742.932	-87.425	0.463	905.193	0.416	24	0.108	R.INGKQEVM*IGYSDSGK.D
R4/RRR4-3/3	1832.426	1832.114	171.124	0.465	864.758	0.410	25	0.105	R.IRDPSFEVM*PQPALSK.E
R4/RRR4-3/3	1860.401	1860.958	-839.083	0.456	918.029	0.378	25	0.102	K.DITADDKQELDEALQR.E
R4/RRR4-3/3	1832.142	1832.114	15.276	0.448	905.222	0.371	26	0.100	R.IRDPSFEVM*PQPALSK.E
R4/RRR4-3/3	1831.790	1832.114	-177.420	0.436	790.557	0.384	23	0.097	R.IRDPSFEVM*PQPALSK.E
R4/RRR4-3/3	1194.102	1194.319	-182.483	0.485	1129.964	0.288	22	0.097	K.SREEVFDALK.N
R4/RRR4-3/3	1194.155	1194.319	-137.720	0.469	675.984	0.283	18	0.087	K.SREEVFDALK.N
R4/RRR4-1/3	1648.035	1646.869	101.096	0.340	597.702	0.284	22	0.080	-.LLVAGDLQSFGEQLR.-
R4/RRR4-3/3	1193.570	1194.319	-1469.585	0.442	1278.955	0.096	21	0.072	-.SREEVFDALK.-
R4/RRR4-4/2	1569.103	1569.783	-1073.891	0.598	2413.240	0.466	22	0.352	K.YLLQSGLQEYLNK.Q
R4/RRR4-4/2	1569.314	1569.783	-299.641	0.618	2252.466	0.463	22	0.321	K.YLLQSGLQEYLNK.Q
R4/RRR4-4/2	1569.486	1569.783	-189.925	0.596	2275.106	0.439	22	0.318	K.YLLQSGLQEYLNK.Q
R4/RRR4-4/3	1993.922	1994.066	-72.011	0.524	2015.980	0.501	38	0.297	K.SEGHDTIVLAGAEYGSGSSR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1570.994	1569.783	134.625	0.554	1990.909	0.480	21	0.285	K.YLLQSGLQEYLNK.Q
R4/RRR4-4/2	1528.208	1528.563	-233.352	0.429	1902.513	0.514	22	0.280	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/2	1499.825	1498.684	94.482	0.552	1825.462	0.519	20	0.272	R.SDETVAMIEAYLR.A
R4/RRR4-2/2	1569.235	1569.783	-989.692	0.507	2017.856	0.418	20	0.271	K.YLLQSGLQEYLNK.Q
R4/RRR4-4/2	1499.574	1498.684	-73.124	0.562	1757.528	0.521	20	0.263	R.SDETVAMIEAYLR.A
R4/RRR4-4/2	1545.201	1545.656	-295.288	0.486	1571.430	0.558	19	0.249	K.M*FVDYNEPQTER.V
R4/RRR4-4/2	1545.187	1545.656	-304.403	0.485	1664.848	0.509	20	0.249	K.M*FVDYNEPQTER.V
R4/RRR4-4/2	1498.271	1498.684	-276.259	0.407	1846.487	0.362	20	0.234	R.SDETVAMIEAYLR.A
R4/RRR4-4/2	1280.123	1280.431	-241.189	0.477	1493.057	0.522	18	0.232	K.FVEFYGEGM*GK.L
R4/RRR4-4/2	1280.170	1280.431	-204.645	0.469	1535.568	0.472	18	0.225	K.FVEFYGEGM*GK.L
R4/RRR4-4/2	1527.566	1528.563	-1311.646	0.426	1560.800	0.473	21	0.225	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/2	1724.239	1724.761	-885.100	0.590	1598.710	0.431	23	0.222	R.NCDNFQVNQNDVEK.I
R4/RRR4-4/2	1545.013	1545.656	-1066.073	0.482	1266.579	0.580	18	0.220	K.M*FVDYNEPQTER.V
R4/RRR4-4/2	1724.180	1724.761	-919.855	0.611	1631.784	0.406	23	0.218	R.NCDNFQVNQNDVEK.I
R4/RRR4-4/2	1529.067	1529.656	-1042.596	0.503	1257.187	0.517	19	0.208	K.MFVDYNEPQTER.V
R4/RRR4-4/2	1724.294	1724.761	-271.715	0.625	1512.729	0.416	23	0.208	R.NCDNFQVNQNDVEK.I
R4/RRR4-4/2	1280.024	1280.431	-318.781	0.397	1251.659	0.509	17	0.202	K.FVEFYGEGM*GK.L
R4/RRR4-4/2	1528.079	1528.563	-317.823	0.446	1267.785	0.485	19	0.196	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/2	1289.161	1289.421	-201.972	0.375	1451.799	0.367	17	0.192	K.FDFHGQPAELK.H
R4/RRR4-4/2	1294.121	1293.453	-257.207	0.348	1103.132	0.519	17	0.189	K.FYSLPALNDPR.I
R4/RRR4-4/2	1515.671	1514.683	-7.892	0.497	1220.225	0.448	18	0.188	R.SDETVAM*IEAYLR.A
R4/RRR4-4/2	1529.177	1529.656	-314.312	0.511	899.292	0.554	17	0.186	K.MFVDYNEPQTER.V
R4/RRR4-4/2	1566.334	1565.896	280.647	0.503	823.924	0.554	19	0.181	R.SNLVGM*GIIPLCFK.A
R4/RRR4-4/2	1551.073	1549.897	113.936	0.516	898.094	0.495	18	0.174	R.SNLVGMGIIPLCFK.A
R4/RRR4-1/2	1292.775	1293.453	-1301.539	0.369	904.503	0.474	17	0.172	K.FYSLPALNDPR.I
R4/RRR4-4/2	1514.140	1514.683	-1022.234	0.342	1252.953	0.331	18	0.170	R.SDETVAM*IEAYLR.A
R4/RRR4-4/2	1202.800	1203.326	-1272.881	0.499	693.337	0.431	16	0.163	K.IIDWENTSPK.L
R4/RRR4-3/2	1515.558	1514.683	-82.863	0.452	855.899	0.438	16	0.163	R.SDETVAM*IEAYLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1565.286	1565.896	-1031.617	0.439	594.363	0.518	17	0.162	R.SNLVGM*GIIPLCFK.A
R4/RRR4-3/2	1292.839	1293.453	-1251.945	0.397	595.949	0.499	14	0.161	K.FYSLPALNDPR.I
R4/RRR4-4/2	1118.199	1117.278	-70.581	0.401	779.633	0.415	19	0.161	K.TSLAPGSGVVTK.Y
R4/RRR4-4/2	1118.078	1117.278	-179.110	0.375	640.601	0.453	18	0.160	K.TSLAPGSGVVTK.Y
R4/RRR4-4/2	1514.415	1514.683	-177.517	0.441	1084.414	0.330	17	0.159	R.SDETVAM*IEAYLR.A
R4/RRR4-4/2	1141.583	1142.375	-1574.410	0.431	501.006	0.448	15	0.158	K.LAEIPFKPAR.V
R4/RRR4-4/2	914.609	915.112	-1648.594	0.471	568.875	0.389	13	0.158	R.ILLESAIR.N
R4/RRR4-4/2	814.326	815.059	-2135.559	0.452	947.510	0.340	12	0.157	-.GPMLLGVK.-
R4/RRR4-4/2	1116.982	1117.278	-265.442	0.347	600.379	0.449	17	0.156	K.TSLAPGSGVVTK.Y
R4/RRR4-4/2	1645.588	1645.881	-178.612	0.441	464.019	0.516	17	0.156	K.NILTTLPKPGGGEYGK.F
R4/RRR4-4/2	914.681	915.112	-473.066	0.487	595.282	0.348	13	0.154	R.ILLESAIR.N
R4/RRR4-4/2	1646.425	1645.881	-277.650	0.485	448.529	0.505	16	0.153	K.NILTTLPKPGGGEYGK.F
R4/RRR4-4/2	915.077	915.112	-38.549	0.464	573.538	0.345	13	0.153	R.ILLESAIR.N
R4/RRR4-4/2	1202.545	1203.326	-1485.332	0.435	670.415	0.365	15	0.153	K.IIDWENTSPK.L
R4/RRR4-3/2	914.849	915.112	-288.558	0.460	579.454	0.335	13	0.152	R.ILLESAIR.N
R4/RRR4-4/2	1292.900	1293.453	-1204.536	0.248	904.151	0.355	16	0.152	K.FYSLPALNDPR.I
R4/RRR4-3/2	915.179	915.112	73.031	0.501	593.191	0.319	13	0.151	R.ILLESAIR.N
R4/RRR4-4/2	1292.575	1293.453	-1456.897	0.218	871.007	0.375	16	0.151	K.FYSLPALNDPR.I
R4/RRR4-4/2	1289.207	1289.421	-166.256	0.374	1031.428	0.269	16	0.150	K.FDFHGQPAELK.H
R4/RRR4-4/2	814.959	815.059	-123.736	0.430	817.686	0.303	12	0.149	K.GPMLLGVK.A
R4/RRR4-4/3	1528.368	1528.563	-128.273	0.475	1170.659	0.494	29	0.149	K.AGEDADSLGLTGHER.Y
R4/RRR4-3/2	1293.368	1293.453	-65.187	0.331	697.237	0.360	14	0.149	K.FYSLPALNDPR.I
R4/RRR4-4/2	1142.247	1142.375	-113.150	0.396	576.003	0.314	16	0.148	K.LAEIPFKPAR.V
R4/RRR4-4/2	1142.224	1142.375	-132.661	0.382	447.573	0.329	14	0.147	K.LAEIPFKPAR.V
R4/RRR4-1/2	915.008	915.112	-114.555	0.434	501.634	0.272	12	0.147	R.ILLESAIR.N
R4/RRR4-4/2	1644.687	1645.881	-1337.947	0.370	550.078	0.403	18	0.146	K.NILTTLPKPGGGEYGK.F
R4/RRR4-2/2	915.061	915.112	-56.613	0.388	628.547	0.264	13	0.146	R.ILLESAIR.N
R4/RRR4-4/2	1564.806	1565.896	-1339.824	0.271	511.230	0.444	16	0.146	R.SNLVGM*GIIPLCFK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1292.516	1293.453	-1502.527	0.243	763.251	0.323	15	0.145	K.FYSLPALNDPR.I
R4/RRR4-3/2	914.637	915.112	-521.681	0.370	510.465	0.222	12	0.144	R.ILLESAIR.N
R4/RRR4-1/2	914.543	915.112	-1720.873	0.317	501.978	0.209	12	0.143	R.ILLESAIR.N
R4/RRR4-3/2	1202.212	1203.326	-1764.080	0.338	888.567	0.199	16	0.140	K.IIDWENTSPK.L
R4/RRR4-4/2	830.957	831.059	-122.530	0.310	684.066	0.239	11	0.139	-.GPM*LLGVK.-
R4/RRR4-2/2	1293.444	1293.453	-6.873	0.208	524.672	0.252	12	0.137	K.FYSLPALNDPR.I
R4/RRR4-4/3	1528.814	1528.563	164.759	0.485	1150.934	0.446	28	0.135	K.AGEDADSLGLTGHER.Y
R4/RRR4-3/2	1117.342	1117.278	57.571	0.398	314.831	0.404	13	0.132	-.TSLAPGSGVVTK.-
R4/RRR4-1/3	1657.464	1657.972	-912.530	0.344	1788.384	0.188	27	0.130	K.KACELGLEVKPWVK.T
R4/RRR4-4/3	1528.207	1528.563	-233.801	0.468	971.341	0.482	28	0.130	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/2	831.165	831.059	127.923	0.270	692.420	0.211	11	0.130	-.GPM*LLGVK.-
R4/RRR4-4/3	1766.560	1766.957	-225.597	0.519	688.255	0.528	26	0.122	R.SPNAVQSNM*ELEFKR.N
R4/RRR4-3/2	1118.012	1117.278	-238.257	0.315	296.968	0.363	13	0.121	-.TSLAPGSGVVTK.-
R4/RRR4-4/3	1993.747	1994.066	-160.079	0.470	1009.717	0.415	30	0.115	K.SEGHDTIVLAGAEYGSGSSR.D
R4/RRR4-4/3	1658.269	1657.972	179.954	0.504	1171.380	0.360	25	0.114	K.KACELGLEVKPWVK.T
R4/RRR4-2/3	1528.518	1528.563	-29.495	0.457	897.331	0.412	25	0.111	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/3	1387.356	1386.580	-161.715	0.456	623.436	0.490	23	0.111	K.DM*TM*SPPGPHGVK.N
R4/RRR4-1/3	1528.905	1528.563	224.090	0.433	540.503	0.467	23	0.109	K.AGEDADSLGLTGHER.Y
R4/RRR4-7/2	1118.130	1117.278	-132.344	0.276	305.088	0.392	12	0.109	-.TSLAPGSGVVTK.-
R4/RRR4-2/3	1528.020	1528.563	-1012.950	0.399	645.342	0.425	22	0.105	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/3	1767.406	1766.957	254.792	0.473	457.577	0.458	23	0.105	R.SPNAVQSNM*ELEFKR.N
R4/RRR4-2/3	1528.044	1528.563	-997.310	0.397	666.055	0.419	23	0.104	K.AGEDADSLGLTGHER.Y
R4/RRR4-3/3	1766.525	1766.957	-245.563	0.459	586.319	0.444	24	0.104	R.SPNAVQSNM*ELEFKR.N
R4/RRR4-1/3	1528.489	1528.563	-48.840	0.386	748.343	0.401	24	0.104	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/3	1657.535	1657.972	-263.942	0.518	1006.015	0.358	25	0.104	K.KACELGLEVKPWVK.T
R4/RRR4-1/3	1528.676	1528.563	74.069	0.390	729.559	0.392	24	0.102	K.AGEDADSLGLTGHER.Y
R4/RRR4-4/3	1386.521	1386.580	-42.424	0.354	481.902	0.471	21	0.102	K.DM*TM*SPPGPHGVK.N
R4/RRR4-4/3	1766.586	1766.957	-210.831	0.446	567.617	0.421	24	0.101	R.SPNAVQSNM*ELEFKR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1766.391	1766.957	-889.513	0.438	517.421	0.422	21	0.100	R.SPNAVQSNM*ELEFKR.N
R4/RRR4-4/3	1386.633	1386.580	38.504	0.369	629.846	0.422	24	0.099	K.DM*TM*SPPGPHGVK.N
R4/RRR4-5/3	1528.462	1528.563	-66.384	0.357	510.758	0.394	20	0.097	-.AGEDADSLGLTGHER.-
R4/RRR4-4/3	1656.521	1657.972	-1483.574	0.408	1081.446	0.291	24	0.096	K.KACELGLEVKPWVK.T
R4/RRR4-5/3	1527.903	1528.563	-1089.956	0.333	521.499	0.321	21	0.095	K.AGEDADSLGLTGHER.Y
R4/RRR4-3/2	1117.945	1117.278	-298.397	0.254	211.120	0.377	11	0.095	-.TSLAPGSGVVTK.-
R4/RRR4-3/3	1386.617	1386.580	26.849	0.380	305.430	0.433	18	0.091	-.DM*TM*SPPGPHGVK.-
R4/RRR4-3/3	1766.829	1766.957	-72.866	0.405	519.269	0.358	22	0.091	-.SPNAVQSNM*ELEFKR.-
R4/RRR4-4/3	1570.363	1569.783	-268.263	0.290	1195.178	0.151	24	0.075	K.YLLQSGLQEYLNK.Q
R4/RRR4-1/3	1658.448	1657.972	287.794	0.333	1465.106	0.049	25	0.074	K.KACELGLEVKPWVK.T
R4/RRR4-4/2	1846.366	1847.057	-918.596	0.612	2703.133	0.590	25	0.459	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/2	1846.494	1847.057	-849.308	0.597	2687.489	0.582	25	0.453	R.KPEEITKEEYAAFYK.S
R4/RRR4-4/2	1847.326	1847.057	145.837	0.612	2242.481	0.579	25	0.360	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/2	1846.520	1847.057	-834.708	0.615	2178.100	0.562	24	0.341	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/3	1321.465	1321.463	1.508	0.601	2082.397	0.505	25	0.302	K.HFSVEGQLEFK.A
R4/RRR4-5/2	1846.594	1847.057	-251.664	0.609	1892.971	0.584	23	0.301	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/2	1569.542	1569.786	-155.985	0.570	1919.612	0.445	20	0.265	K.IKEVSHEWSLVNK.Q
R4/RRR4-5/2	1837.751	1838.052	-164.066	0.591	1646.133	0.556	23	0.258	K.HSEFISYPISLWTEK.T
R4/RRR4-5/3	1321.454	1321.463	-6.830	0.615	1863.012	0.505	25	0.255	K.HFSVEGQLEFK.A
R4/RRR4-4/2	1839.439	1838.052	211.027	0.567	1508.371	0.555	22	0.240	K.HSEFISYPISLWTEK.T
R4/RRR4-4/2	1839.415	1838.052	197.717	0.602	1407.827	0.526	22	0.221	K.HSEFISYPISLWTEK.T
R4/RRR4-5/2	1356.748	1357.621	-1384.738	0.438	1813.495	0.307	18	0.216	K.VIKEVLGDKVEK.V
R4/RRR4-5/2	1274.254	1273.421	-131.503	0.538	1327.890	0.494	18	0.208	K.SDLVNNLGTIAR.S
R4/RRR4-2/2	1529.127	1528.689	286.840	0.535	1425.612	0.438	22	0.205	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	1543.323	1542.675	-228.766	0.558	1232.480	0.503	19	0.201	K.SLTNDWEEHLAVK.H
R4/RRR4-5/2	1529.189	1528.689	327.743	0.533	1332.872	0.447	22	0.199	K.GIVDSEDLPLNISR.Q
R4/RRR4-4/2	1528.300	1528.689	-255.369	0.488	1448.038	0.393	22	0.198	K.GIVDSEDLPLNISR.Q
R4/RRR4-4/3	1321.371	1321.463	-69.236	0.593	1572.352	0.486	24	0.197	K.HFSVEGQLEFK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1273.182	1273.421	-188.640	0.463	1333.653	0.437	18	0.197	K.SDLVNNLGTIAR.S
R4/RRR4-4/2	1528.265	1528.689	-278.367	0.497	1383.620	0.411	22	0.196	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	1837.713	1838.052	-184.790	0.525	1258.555	0.477	20	0.195	K.HSEFISYPISLWTEK.T
R4/RRR4-5/2	1837.427	1838.052	-887.149	0.592	1077.498	0.548	20	0.195	K.HSEFISYPISLWTEK.T
R4/RRR4-5/2	1584.374	1584.710	-212.483	0.549	1226.737	0.490	18	0.195	K.SGDELTSLKDYVTR.M
R4/RRR4-5/2	1542.366	1542.675	-200.886	0.538	1276.675	0.454	19	0.194	K.SLTNDWEEHLAVK.H
R4/RRR4-1/3	1584.896	1584.710	117.986	0.517	1409.853	0.539	27	0.194	K.SGDELTSLKDYVTR.M
R4/RRR4-4/2	1528.444	1528.689	-161.061	0.517	1280.985	0.442	22	0.194	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	1585.296	1584.710	-262.097	0.568	1255.124	0.458	19	0.191	K.SGDELTSLKDYVTR.M
R4/RRR4-4/2	1273.100	1273.421	-253.087	0.457	1364.945	0.392	17	0.189	K.SDLVNNLGTIAR.S
R4/RRR4-6/2	1528.251	1528.689	-287.984	0.483	1275.704	0.420	21	0.188	K.GIVDSEDLPLNISR.Q
R4/RRR4-3/2	1529.522	1528.689	-110.036	0.464	1361.319	0.380	22	0.188	K.GIVDSEDLPLNISR.Q
R4/RRR4-1/2	1529.239	1528.689	-295.564	0.538	1294.131	0.415	21	0.188	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	949.455	950.026	-1659.660	0.353	1346.825	0.383	15	0.187	K.SGDELTSLK.D
R4/RRR4-5/2	1272.593	1273.421	-1440.904	0.409	1379.940	0.363	18	0.186	K.SDLVNNLGTIAR.S
R4/RRR4-5/3	1847.041	1847.057	-8.930	0.589	1315.794	0.560	31	0.186	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/2	1528.183	1528.689	-988.718	0.460	1334.116	0.379	21	0.185	K.GIVDSEDLPLNISR.Q
R4/RRR4-4/2	1542.245	1542.675	-279.417	0.536	1237.109	0.422	19	0.185	K.SLTNDWEEHLAVK.H
R4/RRR4-5/2	949.704	950.026	-339.978	0.409	1360.637	0.355	15	0.185	K.SGDELTSLK.D
R4/RRR4-6/2	1273.182	1273.421	-188.255	0.473	1285.506	0.398	17	0.184	K.SDLVNNLGTIAR.S
R4/RRR4-6/3	1846.703	1847.057	-192.119	0.533	1254.996	0.569	28	0.184	R.KPEEITKEEYAAFYK.S
R4/RRR4-6/2	1528.257	1528.689	-283.496	0.462	1327.517	0.374	21	0.184	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	1528.286	1528.689	-265.065	0.478	1248.638	0.403	21	0.183	K.GIVDSEDLPLNISR.Q
R4/RRR4-2/3	1846.558	1847.057	-271.303	0.563	1309.038	0.548	29	0.183	R.KPEEITKEEYAAFYK.S
R4/RRR4-1/2	1528.357	1528.689	-218.108	0.513	1309.303	0.380	21	0.183	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	1584.257	1584.710	-286.459	0.507	1082.185	0.483	17	0.181	K.SGDELTSLKDYVTR.M
R4/RRR4-6/2	1528.341	1528.689	-229.005	0.480	1250.680	0.384	21	0.180	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	1541.783	1542.675	-1230.383	0.517	1145.974	0.425	18	0.178	K.SLTNDWEEHLAVK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1542.052	1542.675	-1055.492	0.505	1147.837	0.418	18	0.177	K.SLTNDWEEHLAVK.H
R4/RRR4-5/3	1846.610	1847.057	-242.751	0.571	1296.987	0.535	30	0.176	R.KPEEITKEEYAAFYK.S
R4/RRR4-4/2	1542.246	1542.675	-278.861	0.533	1057.223	0.443	18	0.176	K.SLTNDWEEHLAVK.H
R4/RRR4-5/2	1321.152	1321.463	-236.190	0.464	839.280	0.502	16	0.175	K.HFSVEGQLEFK.A
R4/RRR4-5/2	1274.166	1273.421	-201.082	0.456	1024.456	0.443	16	0.174	K.SDLVNNLGTIAR.S
R4/RRR4-5/2	1836.519	1838.052	-1929.471	0.460	985.603	0.461	18	0.172	K.HSEFISYPISLWTEK.T
R4/RRR4-5/2	1321.061	1321.463	-304.604	0.471	859.587	0.471	16	0.172	K.HFSVEGQLEFK.A
R4/RRR4-4/2	1272.608	1273.421	-1428.668	0.398	1197.350	0.356	17	0.171	K.SDLVNNLGTIAR.S
R4/RRR4-5/3	1528.898	1528.689	136.602	0.494	1584.158	0.404	29	0.171	K.GIVDSEDLPLNISR.Q
R4/RRR4-4/3	1846.714	1847.057	-186.350	0.533	1222.427	0.544	29	0.171	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/2	949.580	950.026	-470.894	0.375	1172.418	0.351	15	0.170	K.SGDELTSLK.D
R4/RRR4-5/2	1966.224	1966.225	-0.349	0.535	493.552	0.588	20	0.169	K.KHSEFISYPISLWTEK.T
R4/RRR4-3/2	1528.802	1528.689	73.871	0.494	1028.267	0.404	20	0.169	K.GIVDSEDLPLNISR.Q
R4/RRR4-4/3	1846.950	1847.057	-57.953	0.588	1161.798	0.561	30	0.168	R.KPEEITKEEYAAFYK.S
R4/RRR4-6/2	1273.207	1273.421	-168.922	0.435	1032.173	0.401	16	0.168	K.SDLVNNLGTIAR.S
R4/RRR4-5/2	1261.634	1262.437	-1433.137	0.489	1036.639	0.379	17	0.167	K.KAVENSPFLEK.L
R4/RRR4-1/3	1846.722	1847.057	-181.774	0.517	1161.674	0.551	29	0.166	R.KPEEITKEEYAAFYK.S
R4/RRR4-1/2	1584.534	1584.710	-111.006	0.508	941.591	0.440	17	0.166	K.SGDELTSLKDYVTR.M
R4/RRR4-5/2	1261.567	1262.437	-1486.786	0.474	1029.436	0.363	17	0.164	K.KAVENSPFLEK.L
R4/RRR4-4/2	1081.822	1082.191	-341.295	0.419	784.422	0.439	14	0.164	R.APFDLFDTR.K
R4/RRR4-4/2	1262.105	1262.437	-263.635	0.520	894.402	0.409	16	0.164	K.KAVENSPFLEK.L
R4/RRR4-1/2	1527.492	1528.689	-1443.084	0.364	1245.476	0.282	21	0.164	K.GIVDSEDLPLNISR.Q
R4/RRR4-3/2	1527.662	1528.689	-1331.360	0.338	1312.652	0.254	21	0.164	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/2	1134.042	1134.264	-195.806	0.469	801.785	0.417	15	0.163	K.AVENSPFLEK.L
R4/RRR4-1/2	1273.376	1273.421	-35.250	0.453	834.487	0.423	16	0.162	K.SDLVNNLGTIAR.S
R4/RRR4-5/3	1528.109	1528.689	-1037.449	0.457	1450.248	0.429	28	0.162	K.GIVDSEDLPLNISR.Q
R4/RRR4-4/2	1320.957	1321.463	-1143.267	0.394	807.261	0.421	16	0.161	K.HFSVEGQLEFK.A
R4/RRR4-6/2	1272.849	1273.421	-1238.902	0.365	892.154	0.411	15	0.161	K.SDLVNNLGTIAR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1133.882	1134.264	-337.935	0.446	639.440	0.450	14	0.161	K.AVENSPFLEK.L
R4/RRR4-5/2	1135.090	1134.264	-153.558	0.513	587.481	0.449	14	0.160	K.AVENSPFLEK.L
R4/RRR4-4/2	1134.023	1134.264	-213.408	0.445	689.983	0.418	15	0.159	K.AVENSPFLEK.L
R4/RRR4-5/2	1356.725	1357.621	-1401.637	0.458	1078.157	0.337	16	0.159	-.VIKEVLGDKVEK.-
R4/RRR4-5/2	1272.504	1273.421	-1511.050	0.404	1040.003	0.335	16	0.159	-.SDLVNNLGTIAR.-
R4/RRR4-5/2	1321.135	1321.463	-249.075	0.418	837.394	0.385	16	0.158	K.HFSVEGQLEFK.A
R4/RRR4-4/2	1133.900	1134.264	-321.409	0.431	637.873	0.432	14	0.158	K.AVENSPFLEK.L
R4/RRR4-2/3	1846.142	1847.057	-1040.678	0.485	1247.059	0.490	27	0.158	R.KPEEITKEEYAAFYK.S
R4/RRR4-4/3	1321.387	1321.463	-57.283	0.531	1413.708	0.437	25	0.157	K.HFSVEGQLEFK.A
R4/RRR4-4/2	1082.078	1082.191	-104.506	0.424	786.688	0.365	14	0.156	R.APFDLFDTR.K
R4/RRR4-4/2	1262.071	1262.437	-290.611	0.453	873.773	0.349	15	0.154	K.KAVENSPFLEK.L
R4/RRR4-4/2	1261.394	1262.437	-1624.044	0.459	853.004	0.342	15	0.152	K.KAVENSPFLEK.L
R4/RRR4-4/2	1082.185	1082.191	-5.500	0.356	738.853	0.411	13	0.152	-.APFDLFDTR.-
R4/RRR4-1/2	1274.549	1273.421	100.711	0.362	762.556	0.366	15	0.152	K.SDLVNNLGTIAR.S
R4/RRR4-4/2	1321.098	1321.463	-276.700	0.340	606.792	0.406	15	0.152	K.HFSVEGQLEFK.A
R4/RRR4-4/3	1847.262	1847.057	110.971	0.571	1086.336	0.529	29	0.151	R.KPEEITKEEYAAFYK.S
R4/RRR4-4/2	1133.505	1134.264	-1556.359	0.357	535.974	0.427	13	0.150	-.AVENSPFLEK.-
R4/RRR4-5/2	1262.065	1262.437	-295.560	0.515	709.962	0.373	14	0.150	K.KAVENSPFLEK.L
R4/RRR4-3/2	1272.195	1273.421	-1755.050	0.238	248.402	0.215	15	0.147	K.SDLVNNLGTIAR.S
R4/RRR4-6/3	1584.792	1584.710	52.054	0.506	1167.175	0.479	25	0.146	K.SGDELTSLKDYVTR.M
R4/RRR4-2/3	1584.968	1584.710	163.634	0.469	1143.081	0.473	25	0.142	K.SGDELTSLKDYVTR.M
R4/RRR4-5/3	1527.983	1528.689	-1120.108	0.477	1389.286	0.381	27	0.140	K.GIVDSEDLPLNISR.Q
R4/RRR4-5/3	1892.496	1893.065	-831.276	0.485	1049.894	0.494	26	0.138	R.M*KEGQNDIYYITGESK.K
R4/RRR4-4/3	1584.547	1584.710	-103.133	0.467	1111.520	0.471	27	0.137	K.SGDELTSLKDYVTR.M
R4/RRR4-6/3	1847.091	1847.057	18.512	0.555	974.623	0.510	27	0.137	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/2	1836.615	1838.052	-1330.992	0.227	640.796	0.190	17	0.134	K.HSEFISYPISLWTEK.T
R4/RRR4-1/3	1846.807	1847.057	-135.624	0.532	896.176	0.509	26	0.132	R.KPEEITKEEYAAFYK.S
R4/RRR4-4/3	1584.771	1584.710	38.960	0.516	980.281	0.485	26	0.131	K.SGDELTSLKDYVTR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/3	1847.041	1847.057	-8.731	0.519	844.222	0.509	26	0.129	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/3	1584.817	1584.710	67.930	0.484	1004.320	0.466	27	0.128	K.SGDELTSLKDYVTR.M
R4/RRR4-6/3	1846.812	1847.057	-133.237	0.499	991.814	0.461	26	0.127	R.KPEEITKEEYAAFYK.S
R4/RRR4-1/3	1846.197	1847.057	-1010.306	0.526	802.948	0.510	24	0.127	R.KPEEITKEEYAAFYK.S
R4/RRR4-2/3	1846.746	1847.057	-169.043	0.496	835.365	0.500	26	0.126	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/3	1569.698	1569.786	-56.606	0.478	755.141	0.518	24	0.122	K.IKEVSHEWSLVNK.Q
R4/RRR4-5/3	1142.398	1142.204	170.117	0.435	667.108	0.538	21	0.120	K.LGIHEDSTNR.N
R4/RRR4-5/3	1585.835	1584.710	79.081	0.521	860.947	0.466	24	0.120	K.SGDELTSLKDYVTR.M
R4/RRR4-2/3	1584.499	1584.710	-133.272	0.455	1011.390	0.410	24	0.117	K.SGDELTSLKDYVTR.M
R4/RRR4-5/3	1838.051	1838.052	-0.781	0.506	924.421	0.436	25	0.115	K.HSEFISYPISLWTEK.T
R4/RRR4-5/3	1357.506	1357.621	-85.026	0.454	954.315	0.426	26	0.114	K.VIKEVLGDKVEK.V
R4/RRR4-4/3	1838.658	1838.052	-214.768	0.449	924.701	0.429	25	0.113	K.HSEFISYPISLWTEK.T
R4/RRR4-4/3	1584.588	1584.710	-77.052	0.508	951.917	0.411	27	0.113	K.SGDELTSLKDYVTR.M
R4/RRR4-5/3	1141.712	1142.204	-432.198	0.463	499.212	0.502	19	0.110	K.LGIHEDSTNR.N
R4/RRR4-5/3	1838.437	1838.052	210.202	0.428	935.573	0.400	26	0.108	K.HSEFISYPISLWTEK.T
R4/RRR4-5/3	1569.956	1569.786	108.346	0.521	695.650	0.446	23	0.107	K.IKEVSHEWSLVNK.Q
R4/RRR4-5/3	1366.328	1366.550	-162.796	0.548	900.757	0.380	21	0.103	K.RAPFDLFDTRK.K
R4/RRR4-3/3	1845.942	1847.057	-1149.336	0.409	900.046	0.351	24	0.103	R.KPEEITKEEYAAFYK.S
R4/RRR4-5/3	1142.147	1142.204	-50.461	0.452	448.345	0.413	18	0.100	K.LGIHEDSTNR.N
R4/RRR4-5/3	1365.578	1366.550	-1448.239	0.501	966.325	0.341	22	0.099	K.RAPFDLFDTRK.K
R4/RRR4-5/3	1569.532	1569.786	-162.274	0.452	704.835	0.397	23	0.098	K.IKEVSHEWSLVNK.Q
R4/RRR4-1/3	1584.903	1584.710	122.504	0.354	762.487	0.360	20	0.097	-.SGDELTSLKDYVTR.-
R4/RRR4-5/3	1358.270	1357.621	-259.041	0.410	629.418	0.361	22	0.092	K.VIKEVLGDKVEK.V
R4/RRR4-6/3	1968.038	1966.225	-95.012	0.297	1067.619	0.261	24	0.090	K.KHSEFISYPISLWTEK.T
R4/RRR4-4/3	1968.059	1966.225	-84.653	0.307	560.024	0.355	21	0.089	K.KHSEFISYPISLWTEK.T
R4/RRR4-5/3	1366.156	1366.550	-289.183	0.511	822.509	0.304	20	0.089	K.RAPFDLFDTRK.K
R4/RRR4-5/3	1966.927	1966.225	-151.898	0.358	667.797	0.308	23	0.087	K.KHSEFISYPISLWTEK.T
R4/RRR4-4/3	1965.505	1966.225	-877.748	0.407	824.943	0.244	24	0.081	K.KHSEFISYPISLWTEK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/3	1584.283	1584.710	-270.311	0.381	587.208	0.357	18	0.076	-.SGDELTSLKDYVTR.-
R4/RRR4-5/3	1891.658	1893.065	-1275.816	0.333	690.351	0.217	21	0.071	-.M*KEGQNDIYYITGESK.-
R4/RRR4-4/3	1838.013	1838.052	-21.364	0.306	526.352	0.272	17	0.064	-.HSEFISYPISLWTEK.-
R4/RRR4-5/1	963.497	964.097	-1665.828	0.290	1006.311	0.172	12	0.544	R.FQELGLEK.G
R4/RRR4-4/1	963.554	964.097	-1606.326	0.322	979.306	0.148	12	0.521	R.FQELGLEK.G
R4/RRR4-4/1	963.590	964.097	-1568.337	0.335	994.159	0.135	12	0.518	R.FQELGLEK.G
R4/RRR4-4/1	963.552	964.097	-1607.916	0.288	963.401	0.116	12	0.506	R.FQELGLEK.G
R4/RRR4-4/3	1926.635	1927.150	-788.948	0.527	2533.797	0.592	36	0.481	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/1	963.490	964.097	-1673.529	0.330	792.680	0.187	11	0.479	R.FQELGLEK.G
R4/RRR4-5/1	963.483	964.097	-1680.466	0.291	732.415	0.157	11	0.468	-.FQELGLEK.-
R4/RRR4-4/3	1927.493	1927.150	178.163	0.547	2321.981	0.581	36	0.410	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-4/3	1927.470	1927.150	166.255	0.556	2047.860	0.574	35	0.334	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-1/3	1927.232	1927.150	42.487	0.491	1829.018	0.587	33	0.294	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-4/2	1864.425	1864.118	165.579	0.580	1714.958	0.588	22	0.277	K.MFDLIEQYNLNGHIR.W
R4/RRR4-1/3	1927.318	1927.150	87.367	0.547	1762.202	0.561	35	0.264	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/3	1926.142	1927.150	-1045.638	0.486	1890.979	0.495	35	0.260	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/2	1234.620	1235.414	-1457.652	0.480	1647.395	0.505	19	0.246	K.NLTGLVELYGR.N
R4/RRR4-5/2	1235.095	1235.414	-259.586	0.540	1653.135	0.441	18	0.230	K.NLTGLVELYGR.N
R4/RRR4-4/2	1268.312	1268.491	-141.290	0.448	1404.553	0.515	18	0.220	R.IKQQGLNITPR.I
R4/RRR4-4/2	1234.640	1235.414	-1441.862	0.450	1436.422	0.474	17	0.214	K.NLTGLVELYGR.N
R4/RRR4-4/2	1267.701	1268.491	-1415.847	0.402	1307.400	0.535	16	0.211	R.IKQQGLNITPR.I
R4/RRR4-1/2	1235.600	1235.414	150.855	0.449	1352.448	0.494	17	0.210	K.NLTGLVELYGR.N
R4/RRR4-4/2	1417.558	1416.712	-109.399	0.526	1205.654	0.548	19	0.210	R.LMTLTGVYGFWK.Y
R4/RRR4-4/2	1234.456	1235.414	-1591.247	0.411	1289.599	0.517	17	0.207	K.NLTGLVELYGR.N
R4/RRR4-5/2	1254.273	1254.456	-146.776	0.480	1457.957	0.434	16	0.207	K.ASALLVEFFEK.C
R4/RRR4-5/2	1268.253	1268.491	-188.021	0.450	1271.808	0.506	17	0.205	R.IKQQGLNITPR.I
R4/RRR4-5/2	1234.575	1235.414	-1494.598	0.389	1330.881	0.489	17	0.205	K.NLTGLVELYGR.N
R4/RRR4-5/2	1268.186	1268.491	-240.745	0.384	1298.917	0.504	16	0.204	R.IKQQGLNITPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1016.145	1016.177	-31.160	0.420	1863.064	0.223	17	0.204	R.SLSALQGALR.K
R4/RRR4-4/2	1747.632	1747.949	-182.075	0.470	1042.546	0.593	24	0.201	R.TM*ASTVPLAVEGEPSNK.-
R4/RRR4-5/2	1926.523	1927.150	-847.456	0.501	931.445	0.630	22	0.197	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-4/2	1926.553	1927.150	-831.364	0.492	916.697	0.635	22	0.197	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/2	1926.744	1927.150	-211.392	0.527	952.420	0.598	23	0.195	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/2	1926.649	1927.150	-781.500	0.525	949.646	0.602	22	0.194	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-4/2	1927.474	1927.150	168.611	0.529	921.412	0.607	22	0.193	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-4/2	1417.252	1416.712	-325.743	0.514	925.117	0.565	19	0.193	R.LMTLTGVYGFWK.Y
R4/RRR4-4/2	1255.097	1254.456	-287.349	0.514	1173.496	0.480	16	0.192	K.ASALLVEFFEK.C
R4/RRR4-1/3	1926.504	1927.150	-856.877	0.431	1433.542	0.508	27	0.192	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-4/2	1416.421	1416.712	-206.473	0.467	1031.362	0.523	18	0.190	R.LMTLTGVYGFWK.Y
R4/RRR4-5/2	1748.077	1747.949	73.480	0.509	923.612	0.572	23	0.189	R.TM*ASTVPLAVEGEPSNK.-
R4/RRR4-4/2	1206.187	1205.349	-134.356	0.457	1222.469	0.441	17	0.189	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1747.398	1747.949	-889.925	0.504	820.520	0.607	23	0.189	R.TM*ASTVPLAVEGEPSNK.-
R4/RRR4-4/2	1225.628	1226.406	-1455.360	0.375	953.619	0.560	18	0.187	R.VVHGIDVFDPK.F
R4/RRR4-4/2	1926.537	1927.150	-839.760	0.538	796.030	0.624	21	0.187	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/2	1267.799	1268.491	-1338.673	0.441	1136.103	0.468	16	0.186	R.IKQQGLNITPR.I
R4/RRR4-4/2	1206.064	1205.349	-236.293	0.450	1277.887	0.403	17	0.186	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1205.102	1205.349	-204.986	0.478	1034.121	0.490	18	0.186	K.SIGNGVQFLNR.H
R4/RRR4-5/2	1253.754	1254.456	-1361.872	0.433	1400.452	0.351	16	0.185	K.ASALLVEFFEK.C
R4/RRR4-5/2	1226.128	1226.406	-227.533	0.411	788.899	0.595	16	0.183	R.VVHGIDVFDPK.F
R4/RRR4-4/2	1204.521	1205.349	-1521.521	0.448	1099.862	0.449	17	0.182	K.SIGNGVQFLNR.H
R4/RRR4-5/3	1415.267	1415.574	-218.157	0.538	1429.900	0.511	26	0.182	K.TKYPNSDLYWK.K
R4/RRR4-4/2	1433.058	1432.712	242.588	0.543	1019.498	0.471	18	0.181	R.LM*TLTGVYGFWK.Y
R4/RRR4-5/2	1015.485	1016.177	-1670.563	0.380	1571.921	0.233	17	0.179	R.SLSALQGALR.K
R4/RRR4-4/2	1268.095	1268.491	-313.369	0.435	923.870	0.511	15	0.179	R.IKQQGLNITPR.I
R4/RRR4-5/2	1747.367	1747.949	-908.229	0.483	813.630	0.546	22	0.177	R.TM*ASTVPLAVEGEPSNK.-
R4/RRR4-4/2	1253.819	1254.456	-1309.851	0.477	1283.984	0.354	16	0.176	K.ASALLVEFFEK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1205.006	1205.349	-285.272	0.461	860.993	0.488	17	0.176	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1205.094	1205.349	-211.490	0.444	886.667	0.483	16	0.175	K.SIGNGVQFLNR.H
R4/RRR4-2/2	1016.216	1016.177	38.722	0.464	1528.865	0.234	17	0.174	R.SLSALQGALR.K
R4/RRR4-5/2	1747.282	1747.949	-956.904	0.470	752.256	0.549	21	0.174	R.TM*ASTVPLAVEGEPSNK.-
R4/RRR4-5/2	1205.559	1205.349	175.332	0.367	1208.489	0.358	17	0.173	K.SIGNGVQFLNR.H
R4/RRR4-5/2	1226.063	1226.406	-280.372	0.384	749.671	0.537	16	0.172	R.VVHGIDVFDPK.F
R4/RRR4-4/2	1747.307	1747.949	-942.455	0.477	667.436	0.568	20	0.172	R.TM*ASTVPLAVEGEPSNK.-
R4/RRR4-5/2	1015.418	1016.177	-1737.354	0.400	1510.863	0.221	16	0.172	R.SLSALQGALR.K
R4/RRR4-4/2	1432.446	1432.712	-185.959	0.463	879.768	0.459	17	0.170	R.LM*TLTGVYGFWK.Y
R4/RRR4-5/2	1194.287	1193.444	-131.983	0.474	642.757	0.511	15	0.170	R.NKPIIFSM*AR.L
R4/RRR4-4/2	1015.483	1016.177	-1673.220	0.398	1482.919	0.223	16	0.170	R.SLSALQGALR.K
R4/RRR4-4/2	1433.230	1432.712	-336.722	0.541	902.238	0.440	18	0.170	R.LM*TLTGVYGFWK.Y
R4/RRR4-5/2	1204.640	1205.349	-1422.783	0.443	929.711	0.420	17	0.169	K.SIGNGVQFLNR.H
R4/RRR4-5/2	1015.529	1016.177	-1627.692	0.426	1473.892	0.221	16	0.168	R.SLSALQGALR.K
R4/RRR4-1/2	1015.930	1016.177	-243.758	0.415	1444.421	0.229	16	0.168	R.SLSALQGALR.K
R4/RRR4-5/2	1206.092	1205.349	-213.548	0.416	978.853	0.398	17	0.168	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1415.499	1416.712	-1568.505	0.294	939.076	0.460	17	0.168	R.LMTLTGVYGFWK.Y
R4/RRR4-4/2	1416.245	1415.574	-233.472	0.449	799.208	0.458	16	0.167	K.TKYPNSDLYWK.K
R4/RRR4-1/2	1016.150	1016.177	-25.979	0.437	1460.108	0.217	16	0.166	R.SLSALQGALR.K
R4/RRR4-1/2	1206.164	1205.349	-153.544	0.427	789.391	0.450	16	0.166	K.SIGNGVQFLNR.H
R4/RRR4-5/2	1193.093	1193.444	-294.872	0.359	739.508	0.475	16	0.165	R.NKPIIFSM*AR.L
R4/RRR4-3/2	1206.073	1205.349	-229.287	0.443	805.507	0.429	17	0.165	K.SIGNGVQFLNR.H
R4/RRR4-5/2	1432.073	1432.712	-1147.753	0.441	816.599	0.432	18	0.165	R.LM*TLTGVYGFWK.Y
R4/RRR4-4/2	1205.536	1205.349	155.632	0.438	980.360	0.377	17	0.165	K.SIGNGVQFLNR.H
R4/RRR4-1/2	1205.435	1205.349	71.951	0.457	840.151	0.413	17	0.164	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1226.115	1226.406	-237.921	0.366	694.898	0.500	15	0.164	R.VVHGIDVFDPK.F
R4/RRR4-4/2	1015.484	1016.177	-1672.254	0.381	1347.141	0.242	16	0.164	R.SLSALQGALR.K
R4/RRR4-5/2	1205.537	1205.349	156.851	0.385	728.806	0.461	15	0.163	K.SIGNGVQFLNR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1193.117	1193.444	-275.472	0.364	651.021	0.481	15	0.163	R.NKPIIFSM*AR.L
R4/RRR4-4/2	1389.996	1390.518	-1098.815	0.417	484.733	0.488	21	0.163	R.LLPDATGTTCGQR.L
R4/RRR4-4/2	1226.046	1226.406	-294.157	0.350	687.290	0.494	15	0.163	R.VVHGIDVFDPK.F
R4/RRR4-5/2	1390.008	1390.518	-1089.821	0.352	430.667	0.555	20	0.163	R.LLPDATGTTCGQR.L
R4/RRR4-2/2	1204.952	1205.349	-330.400	0.413	687.249	0.437	16	0.161	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1731.596	1731.949	-204.458	0.486	611.549	0.498	20	0.161	R.TMASTVPLAVEGEPSNK.-
R4/RRR4-5/2	1432.545	1432.712	-116.889	0.434	910.941	0.372	18	0.161	R.LM*TLTGVYGFWK.Y
R4/RRR4-5/2	1417.498	1416.712	-151.382	0.357	596.190	0.492	16	0.161	R.LMTLTGVYGFWK.Y
R4/RRR4-5/2	1225.560	1226.406	-1510.587	0.329	911.728	0.385	17	0.160	R.VVHGIDVFDPK.F
R4/RRR4-4/2	1262.601	1263.425	-1448.622	0.429	758.440	0.432	16	0.160	-.LKDGAFEDVLR.-
R4/RRR4-5/2	1415.318	1415.574	-182.066	0.475	754.924	0.413	16	0.160	K.TKYPNSDLYWK.K
R4/RRR4-5/2	1415.182	1415.574	-278.376	0.463	729.025	0.416	16	0.159	K.TKYPNSDLYWK.K
R4/RRR4-4/2	1206.189	1205.349	-133.036	0.454	783.662	0.384	17	0.159	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1390.957	1390.518	316.214	0.382	521.065	0.458	21	0.159	R.LLPDATGTTCGQR.L
R4/RRR4-1/2	1205.175	1205.349	-144.730	0.443	640.646	0.431	15	0.159	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1205.957	1205.349	-325.860	0.462	818.881	0.382	16	0.159	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1193.116	1193.444	-275.523	0.316	629.321	0.471	15	0.159	R.NKPIIFSM*AR.L
R4/RRR4-5/2	1159.837	1160.408	-1358.160	0.422	1087.126	0.294	14	0.158	R.YLEM*LYALK.Y
R4/RRR4-1/2	1017.170	1016.177	-6.333	0.454	1446.050	0.178	16	0.158	R.SLSALQGALR.K
R4/RRR4-5/2	1177.188	1177.445	-219.104	0.383	597.597	0.423	15	0.157	R.NKPIIFSMAR.L
R4/RRR4-4/2	1390.053	1390.518	-335.552	0.386	480.939	0.434	21	0.157	R.LLPDATGTTCGQR.L
R4/RRR4-5/2	1193.140	1193.444	-255.969	0.342	641.916	0.427	15	0.157	R.NKPIIFSM*AR.L
R4/RRR4-5/2	1159.659	1160.408	-1512.198	0.410	771.562	0.366	14	0.156	R.YLEM*LYALK.Y
R4/RRR4-1/2	1205.019	1205.349	-273.889	0.424	643.204	0.408	15	0.156	K.SIGNGVQFLNR.H
R4/RRR4-1/2	1206.360	1205.349	9.377	0.426	691.459	0.384	16	0.156	K.SIGNGVQFLNR.H
R4/RRR4-4/2	1177.184	1177.445	-222.329	0.382	598.585	0.396	15	0.155	R.NKPIIFSMAR.L
R4/RRR4-4/2	1254.349	1254.456	-86.054	0.352	1055.062	0.310	14	0.155	K.ASALLVEFFEK.C
R4/RRR4-4/2	1159.799	1160.408	-1390.930	0.342	764.845	0.368	14	0.155	R.YLEM*LYALK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1138.906	1139.329	-372.192	0.397	977.204	0.305	14	0.155	R.AM*ENEM*LLR.I
R4/RRR4-5/2	1416.174	1416.712	-1089.310	0.478	702.172	0.416	14	0.154	R.LMTLTGVYGFWK.Y
R4/RRR4-4/2	1160.122	1160.408	-247.465	0.363	725.828	0.364	14	0.154	R.YLEM*LYALK.Y
R4/RRR4-5/2	1262.916	1263.425	-1197.845	0.383	673.806	0.399	15	0.154	K.LKDGAFEDVLR.S
R4/RRR4-5/2	1389.939	1390.518	-1139.380	0.350	457.929	0.419	21	0.154	R.LLPDATGTTCGQR.L
R4/RRR4-5/2	1263.319	1263.425	-83.892	0.425	735.887	0.366	16	0.154	K.LKDGAFEDVLR.S
R4/RRR4-5/2	1160.069	1160.408	-292.543	0.349	727.177	0.358	14	0.153	R.YLEM*LYALK.Y
R4/RRR4-5/2	1176.607	1177.445	-1566.359	0.273	534.369	0.473	14	0.153	R.NKPIIFSMAR.L
R4/RRR4-4/2	1234.874	1235.414	-1251.420	0.351	559.988	0.440	13	0.152	K.NLTGLVELYGR.N
R4/RRR4-2/2	1016.444	1016.177	263.604	0.395	1262.383	0.194	16	0.152	R.SLSALQGALR.K
R4/RRR4-4/2	1262.694	1263.425	-1374.725	0.385	633.143	0.382	15	0.152	K.LKDGAFEDVLR.S
R4/RRR4-5/2	1144.146	1144.408	-230.247	0.422	691.315	0.334	14	0.152	R.YLEMLYALK.Y
R4/RRR4-4/2	1177.108	1177.445	-287.040	0.404	666.379	0.326	16	0.151	R.NKPIIFSMAR.L
R4/RRR4-1/2	1226.102	1226.406	-248.708	0.305	765.349	0.356	16	0.151	R.VVHGIDVFDPK.F
R4/RRR4-5/2	1138.951	1139.329	-332.295	0.423	824.741	0.306	14	0.151	R.AM*ENEM*LLR.I
R4/RRR4-5/2	1390.185	1390.518	-240.755	0.274	445.752	0.448	20	0.150	R.LLPDATGTTCGQR.L
R4/RRR4-4/2	1262.637	1263.425	-1419.975	0.375	600.875	0.360	15	0.150	K.LKDGAFEDVLR.S
R4/RRR4-4/2	1415.226	1415.574	-247.136	0.413	653.847	0.356	15	0.149	K.TKYPNSDLYWK.K
R4/RRR4-5/2	1177.282	1177.445	-138.799	0.344	623.551	0.331	15	0.149	R.NKPIIFSMAR.L
R4/RRR4-1/2	1262.922	1263.425	-1193.283	0.388	623.651	0.361	14	0.149	K.LKDGAFEDVLR.S
R4/RRR4-1/2	1193.114	1193.444	-277.217	0.307	462.736	0.384	13	0.149	R.NKPIIFSM*AR.L
R4/RRR4-4/2	1177.139	1177.445	-260.197	0.368	514.235	0.306	14	0.147	R.NKPIIFSMAR.L
R4/RRR4-2/2	1205.265	1205.349	-69.851	0.330	632.283	0.342	14	0.147	-.SIGNGVQFLNR.-
R4/RRR4-5/2	1262.441	1263.425	-1576.146	0.382	771.881	0.284	16	0.146	K.LKDGAFEDVLR.S
R4/RRR4-5/3	1584.086	1584.816	-1095.310	0.537	992.529	0.543	28	0.146	K.M*GVTHCTIAHALEK.T
R4/RRR4-1/2	1234.417	1235.414	-1623.036	0.336	537.756	0.366	14	0.146	-.NLTGLVELYGR.-
R4/RRR4-5/2	1143.499	1144.408	-1674.669	0.264	626.150	0.361	12	0.146	-.YLEMLYALK.-
R4/RRR4-4/2	1015.550	1016.177	-1606.438	0.334	987.874	0.210	16	0.145	R.SLSALQGALR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1138.932	1139.329	-349.071	0.384	941.552	0.222	14	0.144	R.AM*ENEM*LLR.I
R4/RRR4-5/2	1144.266	1144.408	-124.506	0.348	690.641	0.259	14	0.143	-.YLEMLYALK.-
R4/RRR4-5/2	1254.086	1254.456	-295.781	0.388	630.471	0.295	14	0.143	K.ASALLVEFFEK.C
R4/RRR4-4/2	1144.089	1144.408	-280.342	0.378	665.341	0.232	14	0.143	R.YLEMLYALK.Y
R4/RRR4-4/2	1160.054	1160.408	-305.951	0.330	838.679	0.221	14	0.143	R.YLEM*LYALK.Y
R4/RRR4-4/2	1138.912	1139.329	-367.353	0.399	748.139	0.253	13	0.143	R.AM*ENEM*LLR.I
R4/RRR4-4/2	1415.610	1416.712	-1489.675	0.230	291.592	0.316	12	0.143	R.LMTLTGVYGFWK.Y
R4/RRR4-4/2	1144.173	1144.408	-206.592	0.336	702.564	0.214	14	0.142	R.YLEMLYALK.Y
R4/RRR4-1/2	1431.478	1432.712	-1564.682	0.215	531.234	0.253	17	0.141	R.LM*TLTGVYGFWK.Y
R4/RRR4-4/3	1415.545	1415.574	-21.037	0.501	1057.048	0.503	22	0.140	K.TKYPNSDLYWK.K
R4/RRR4-4/2	964.903	964.097	-202.023	0.401	958.055	0.166	14	0.140	R.FQELGLEK.G
R4/RRR4-4/2	1143.483	1144.408	-1688.933	0.281	739.351	0.175	14	0.139	R.YLEMLYALK.Y
R4/RRR4-5/2	1263.978	1263.425	-354.298	0.237	372.232	0.335	11	0.139	-.LKDGAFEDVLR.-
R4/RRR4-4/2	1138.277	1139.329	-1808.149	0.334	887.151	0.172	14	0.138	R.AM*ENEM*LLR.I
R4/RRR4-24/2	1733.403	1731.949	262.431	0.304	254.884	0.329	14	0.138	-.TMASTVPLAVEGEPSNK.-
R4/RRR4-5/3	1585.552	1584.816	-167.425	0.556	889.821	0.539	26	0.137	K.M*GVTHCTIAHALEK.T
R4/RRR4-4/2	1415.480	1416.712	-1581.933	0.237	562.582	0.213	13	0.137	R.LMTLTGVYGFWK.Y
R4/RRR4-5/2	963.436	964.097	-1728.853	0.305	961.150	0.120	14	0.137	R.FQELGLEK.G
R4/RRR4-1/2	964.311	964.097	222.561	0.313	805.738	0.116	13	0.135	-.FQELGLEK.-
R4/RRR4-4/2	964.814	964.097	-294.426	0.338	930.783	0.101	14	0.135	R.FQELGLEK.G
R4/RRR4-3/2	963.953	964.097	-149.765	0.335	779.361	0.147	13	0.134	-.FQELGLEK.-
R4/RRR4-1/2	1255.609	1254.456	121.733	0.340	534.857	0.239	12	0.134	-.ASALLVEFFEK.-
R4/RRR4-1/2	963.941	964.097	-162.468	0.285	796.161	0.132	13	0.134	-.FQELGLEK.-
R4/RRR4-2/2	963.841	964.097	-266.650	0.330	806.143	0.137	13	0.134	-.FQELGLEK.-
R4/RRR4-2/2	1226.101	1226.406	-249.907	0.246	897.314	0.106	16	0.134	R.VVHGIDVFDPK.F
R4/RRR4-5/2	963.990	964.097	-111.275	0.256	1039.448	0.071	14	0.134	R.FQELGLEK.G
R4/RRR4-4/2	1227.017	1226.406	-318.172	0.152	562.581	0.186	12	0.134	R.VVHGIDVFDPK.F
R4/RRR4-1/2	963.517	964.097	-1644.841	0.315	853.201	0.117	13	0.133	-.FQELGLEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	963.972	964.097	-129.694	0.321	647.602	0.116	12	0.133	-.FQELGLEK.-
R4/RRR4-5/2	1417.541	1416.712	-121.147	0.253	878.458	0.086	15	0.132	R.LMTLTGVYGFWK.Y
R4/RRR4-4/3	1415.071	1415.574	-1065.726	0.479	1075.709	0.468	24	0.132	K.TKYPNSDLYWK.K
R4/RRR4-5/3	1879.786	1880.117	-176.851	0.460	846.094	0.526	27	0.131	K.M*FDLIEQYNLNGHIR.W
R4/RRR4-3/3	1926.958	1927.150	-99.992	0.402	1095.807	0.437	26	0.131	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/3	1415.672	1415.574	68.867	0.491	1217.201	0.411	24	0.129	K.TKYPNSDLYWK.K
R4/RRR4-5/3	1584.473	1584.816	-217.225	0.570	864.844	0.511	25	0.129	K.M*GVTHCTIAHALEK.T
R4/RRR4-4/3	1583.943	1584.816	-1186.313	0.537	888.547	0.503	28	0.128	K.M*GVTHCTIAHALEK.T
R4/RRR4-4/3	1415.158	1415.574	-295.261	0.487	967.498	0.477	22	0.127	K.TKYPNSDLYWK.K
R4/RRR4-5/3	1415.332	1415.574	-172.082	0.492	922.801	0.485	22	0.126	K.TKYPNSDLYWK.K
R4/RRR4-4/3	1568.728	1568.817	-57.149	0.495	946.404	0.472	28	0.125	K.MGVTHCTIAHALEK.T
R4/RRR4-4/3	1584.755	1584.816	-39.066	0.480	782.029	0.511	26	0.124	K.M*GVTHCTIAHALEK.T
R4/RRR4-4/3	1263.756	1263.425	263.258	0.512	1555.988	0.263	25	0.119	K.LKDGAFEDVLR.S
R4/RRR4-4/3	1881.016	1880.117	-54.137	0.469	736.080	0.495	26	0.119	K.M*FDLIEQYNLNGHIR.W
R4/RRR4-4/3	1863.705	1864.118	-221.834	0.403	459.970	0.547	22	0.117	K.MFDLIEQYNLNGHIR.W
R4/RRR4-4/3	1584.301	1584.816	-959.186	0.476	836.736	0.460	26	0.116	K.M*GVTHCTIAHALEK.T
R4/RRR4-5/3	1879.486	1880.117	-870.300	0.414	696.695	0.471	24	0.113	K.M*FDLIEQYNLNGHIR.W
R4/RRR4-4/3	1864.930	1864.118	-100.987	0.422	584.013	0.488	24	0.112	K.MFDLIEQYNLNGHIR.W
R4/RRR4-4/3	1863.288	1864.118	-984.908	0.374	472.836	0.491	22	0.110	K.MFDLIEQYNLNGHIR.W
R4/RRR4-4/3	1864.113	1864.118	-2.478	0.413	490.481	0.482	24	0.110	K.MFDLIEQYNLNGHIR.W
R4/RRR4-4/3	1880.208	1880.117	48.434	0.461	722.484	0.440	25	0.109	K.M*FDLIEQYNLNGHIR.W
R4/RRR4-4/3	1879.835	1880.117	-150.370	0.351	439.862	0.467	20	0.106	K.M*FDLIEQYNLNGHIR.W
R4/RRR4-4/3	1568.675	1568.817	-90.986	0.464	748.790	0.403	24	0.103	K.MGVTHCTIAHALEK.T
R4/RRR4-3/3	1926.763	1927.150	-201.802	0.267	804.381	0.391	24	0.103	R.IGDSLSAHPNELVAVFTR.L
R4/RRR4-5/3	1263.561	1263.425	108.214	0.532	1334.422	0.264	23	0.102	K.LKDGAFEDVLR.S
R4/RRR4-4/3	1880.438	1880.117	171.194	0.355	433.599	0.379	21	0.099	K.M*FDLIEQYNLNGHIR.W
R4/RRR4-4/3	1263.248	1263.425	-140.510	0.489	1351.979	0.234	23	0.098	K.LKDGAFEDVLR.S
R4/RRR4-4/3	1268.767	1268.491	218.504	0.450	1226.671	0.255	22	0.096	R.IKQQGLNITPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/3	1194.630	1193.444	155.730	0.451	1056.328	0.302	23	0.096	R.NKPIIFSM*AR.L
R4/RRR4-2/3	1263.630	1263.425	162.710	0.449	1263.185	0.226	21	0.093	-.LKDGAFEDVLR.-
R4/RRR4-4/3	1262.814	1263.425	-1279.347	0.510	1079.314	0.247	22	0.088	K.LKDGAFEDVLR.S
R4/RRR4-4/3	1268.190	1268.491	-238.293	0.406	1248.401	0.207	23	0.088	R.IKQQGLNITPR.I
R4/RRR4-5/3	1193.414	1193.444	-25.343	0.419	827.951	0.280	20	0.088	R.NKPIIFSM*AR.L
R4/RRR4-5/3	1193.416	1193.444	-23.804	0.362	782.818	0.287	20	0.087	R.NKPIIFSM*AR.L
R4/RRR4-5/3	1267.610	1268.491	-1488.353	0.395	694.777	0.239	19	0.086	R.IKQQGLNITPR.I
R4/RRR4-2/3	1267.920	1268.491	-1242.618	0.467	655.564	0.332	18	0.086	-.IKQQGLNITPR.-
R4/RRR4-1/3	1262.871	1263.425	-1234.353	0.469	1328.910	0.192	22	0.086	-.LKDGAFEDVLR.-
R4/RRR4-4/3	1268.734	1268.491	192.164	0.452	1338.033	0.175	23	0.086	R.IKQQGLNITPR.I
R4/RRR4-5/3	1263.065	1263.425	-285.789	0.493	1249.356	0.178	22	0.083	K.LKDGAFEDVLR.S
R4/RRR4-1/3	1263.311	1263.425	-90.639	0.441	1015.297	0.234	19	0.083	-.LKDGAFEDVLR.-
R4/RRR4-2/3	1268.576	1268.491	67.684	0.376	1000.847	0.204	21	0.082	R.IKQQGLNITPR.I
R4/RRR4-2/3	1262.277	1263.425	-1706.627	0.409	1157.857	0.176	20	0.082	K.LKDGAFEDVLR.S
R4/RRR4-5/3	1268.723	1268.491	183.625	0.502	978.088	0.233	21	0.082	-.IKQQGLNITPR.-
R4/RRR4-5/3	1264.455	1263.425	23.992	0.516	1253.050	0.180	23	0.081	-.LKDGAFEDVLR.-
R4/RRR4-5/3	1268.680	1268.491	149.902	0.406	921.345	0.232	19	0.081	-.IKQQGLNITPR.-
R4/RRR4-5/3	1177.176	1177.445	-229.466	0.383	737.633	0.231	17	0.080	-.NKPIIFSMAR.-
R4/RRR4-5/3	1177.175	1177.445	-230.246	0.425	941.677	0.183	18	0.078	R.NKPIIFSMAR.L
R4/RRR4-5/3	1414.189	1415.574	-1692.084	0.255	254.277	0.404	15	0.077	-.TKYPNSDLYWK.-
R4/RRR4-4/2	1814.454	1815.062	-888.530	0.539	2203.403	0.531	25	0.333	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1813.949	1815.062	-1168.148	0.457	2251.662	0.490	25	0.328	K.AYLPVIESFGFSSQLR.A
R4/RRR4-3/2	1814.442	1815.062	-895.284	0.496	2213.796	0.487	25	0.321	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1814.565	1815.062	-274.662	0.534	2028.985	0.554	23	0.310	K.AYLPVIESFGFSSQLR.A
R4/RRR4-1/2	1815.976	1815.062	-47.371	0.552	1893.466	0.593	25	0.302	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1815.506	1815.062	245.506	0.595	1935.419	0.574	23	0.300	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1819.514	1819.945	-237.510	0.536	1909.881	0.568	22	0.297	K.NATLTNEKESDACPIR.A
R4/RRR4-4/2	1819.314	1819.945	-899.549	0.543	1939.894	0.538	23	0.293	K.NATLTNEKESDACPIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1814.432	1815.062	-900.619	0.525	1926.706	0.547	25	0.293	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1814.538	1815.062	-842.133	0.541	1923.797	0.532	24	0.287	K.AYLPVIESFGFSSQLR.A
R4/RRR4-1/2	1815.469	1815.062	225.009	0.577	1840.593	0.572	23	0.286	K.AYLPVIESFGFSSQLR.A
R4/RRR4-3/2	1815.478	1815.062	230.065	0.593	1880.569	0.545	24	0.284	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1815.487	1815.062	235.257	0.603	1874.416	0.541	25	0.283	K.AYLPVIESFGFSSQLR.A
R4/RRR4-3/2	1815.838	1815.062	-123.298	0.605	1785.138	0.584	24	0.282	K.AYLPVIESFGFSSQLR.A
R4/RRR4-3/2	1814.613	1815.062	-247.935	0.501	1875.651	0.498	23	0.270	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/3	1820.300	1819.945	195.481	0.441	1951.844	0.494	34	0.268	K.NATLTNEKESDACPIR.A
R4/RRR4-4/3	1815.042	1815.062	-11.044	0.480	1873.987	0.519	32	0.267	K.AYLPVIESFGFSSQLR.A
R4/RRR4-2/2	1815.170	1815.062	60.126	0.552	1706.284	0.559	23	0.264	K.AYLPVIESFGFSSQLR.A
R4/RRR4-2/2	1814.043	1815.062	-1116.253	0.434	1796.837	0.502	23	0.260	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1815.477	1815.062	229.324	0.612	1616.030	0.582	22	0.256	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1820.310	1819.945	201.138	0.557	1635.970	0.528	21	0.246	K.NATLTNEKESDACPIR.A
R4/RRR4-4/2	1389.367	1388.586	-157.443	0.566	1629.812	0.506	17	0.244	R.GFVQFCYEPIK.Q
R4/RRR4-4/2	1347.270	1347.588	-236.973	0.508	1445.363	0.586	18	0.241	R.VIYASQLTAKPR.L
R4/RRR4-4/2	1347.297	1347.588	-216.703	0.467	1486.964	0.559	19	0.239	R.VIYASQLTAKPR.L
R4/RRR4-2/2	1816.202	1815.062	77.619	0.505	1434.345	0.565	22	0.232	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1425.208	1425.569	-254.168	0.516	1473.361	0.495	20	0.224	R.LWGENFFDPATK.K
R4/RRR4-3/2	1813.694	1815.062	-1309.334	0.370	1638.840	0.422	23	0.221	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1388.081	1388.586	-1087.276	0.477	1537.518	0.455	17	0.221	R.GFVQFCYEPIK.Q
R4/RRR4-4/2	1425.321	1425.569	-174.517	0.515	1499.670	0.467	20	0.220	R.LWGENFFDPATK.K
R4/RRR4-4/2	1425.361	1425.569	-146.595	0.490	1440.679	0.454	20	0.212	R.LWGENFFDPATK.K
R4/RRR4-2/2	1346.962	1347.588	-1211.003	0.450	1190.478	0.581	17	0.211	R.VIYASQLTAKPR.L
R4/RRR4-3/3	1820.314	1819.945	203.148	0.506	1566.657	0.525	35	0.209	K.NATLTNEKESDACPIR.A
R4/RRR4-4/2	1652.267	1651.841	258.571	0.530	1637.453	0.377	18	0.207	K.ILSEEFGWDKDLAK.K
R4/RRR4-3/2	1425.414	1425.569	-109.311	0.502	1337.156	0.485	18	0.207	R.LWGENFFDPATK.K
R4/RRR4-4/2	1624.150	1623.846	187.738	0.583	1116.240	0.564	21	0.205	R.NCDPEGPLMLYVSK.M
R4/RRR4-4/2	1387.741	1388.586	-1333.432	0.394	1373.186	0.466	16	0.204	R.GFVQFCYEPIK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1347.271	1347.588	-236.064	0.463	1051.904	0.586	17	0.201	R.VIYASQLTAKPR.L
R4/RRR4-4/2	1624.412	1623.846	-268.147	0.544	1080.255	0.556	21	0.200	R.NCDPEGPLMLYVSK.M
R4/RRR4-4/2	1623.182	1623.846	-1028.534	0.502	1191.132	0.511	21	0.200	R.NCDPEGPLMLYVSK.M
R4/RRR4-4/2	1504.330	1503.774	-296.144	0.612	966.776	0.568	20	0.196	R.RVIYASQLTAKPR.L
R4/RRR4-3/2	1653.448	1651.841	-238.187	0.519	1381.916	0.435	17	0.195	K.ILSEEFGWDKDLAK.K
R4/RRR4-4/2	1554.374	1553.742	-237.931	0.455	1250.825	0.447	21	0.193	R.LWGENFFDPATKK.W
R4/RRR4-4/2	1640.236	1639.845	238.663	0.534	1112.196	0.503	21	0.192	R.NCDPEGPLM*LYVSK.M
R4/RRR4-1/2	1651.310	1651.841	-929.825	0.499	1504.970	0.355	18	0.191	K.ILSEEFGWDKDLAK.K
R4/RRR4-4/2	1651.389	1651.841	-274.369	0.515	1431.425	0.366	18	0.186	K.ILSEEFGWDKDLAK.K
R4/RRR4-3/3	1820.010	1819.945	35.673	0.478	1256.688	0.560	29	0.182	K.NATLTNEKESDACPIR.A
R4/RRR4-4/2	1867.179	1868.098	-1030.841	0.524	1306.011	0.556	21	0.181	K.GLKEQM*TPLSDFEDKL.-
R4/RRR4-4/2	1639.244	1639.845	-979.699	0.495	1166.716	0.419	21	0.181	R.NCDPEGPLM*LYVSK.M
R4/RRR4-3/2	1424.562	1425.569	-1413.534	0.514	916.629	0.516	16	0.180	R.LWGENFFDPATK.K
R4/RRR4-4/2	1652.296	1651.841	276.425	0.492	1339.707	0.367	18	0.180	K.ILSEEFGWDKDLAK.K
R4/RRR4-3/2	1651.380	1651.841	-280.079	0.525	1377.603	0.355	18	0.179	K.ILSEEFGWDKDLAK.K
R4/RRR4-1/2	1652.540	1651.841	-182.899	0.501	1310.572	0.379	17	0.178	K.ILSEEFGWDKDLAK.K
R4/RRR4-1/2	1426.213	1425.569	-250.727	0.389	993.271	0.473	16	0.175	R.LWGENFFDPATK.K
R4/RRR4-3/3	1504.299	1503.774	-317.199	0.531	1525.010	0.442	28	0.173	R.RVIYASQLTAKPR.L
R4/RRR4-4/2	1639.426	1639.845	-256.364	0.510	990.453	0.441	20	0.173	R.NCDPEGPLM*LYVSK.M
R4/RRR4-1/3	1820.718	1819.945	-125.362	0.459	1260.881	0.530	32	0.170	K.NATLTNEKESDACPIR.A
R4/RRR4-2/2	1424.282	1425.569	-1610.754	0.347	1056.560	0.407	17	0.170	R.LWGENFFDPATK.K
R4/RRR4-2/2	1425.212	1425.569	-251.504	0.433	861.627	0.470	16	0.169	R.LWGENFFDPATK.K
R4/RRR4-4/2	1120.971	1120.219	-221.791	0.445	907.354	0.440	15	0.169	K.EGALAEENMR.G
R4/RRR4-4/2	1552.626	1553.742	-1366.967	0.458	979.324	0.406	19	0.167	R.LWGENFFDPATKK.W
R4/RRR4-3/2	1347.312	1347.588	-205.614	0.437	852.000	0.451	15	0.164	R.VIYASQLTAKPR.L
R4/RRR4-4/2	1503.135	1503.774	-1093.571	0.546	769.637	0.443	19	0.164	R.RVIYASQLTAKPR.L
R4/RRR4-4/2	1426.715	1425.569	102.413	0.467	841.458	0.437	15	0.163	R.LWGENFFDPATK.K
R4/RRR4-9/2	1816.207	1815.062	80.181	0.379	806.917	0.470	18	0.163	K.AYLPVIESFGFSSQLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1813.839	1815.062	-1228.835	0.314	1136.832	0.338	20	0.163	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1553.383	1553.742	-232.171	0.453	908.484	0.396	18	0.162	R.LWGENFFDPATKK.W
R4/RRR4-3/2	1388.095	1388.586	-354.813	0.425	866.843	0.436	13	0.161	-.GFVQFCYEPIK.-
R4/RRR4-4/3	1503.294	1503.774	-320.302	0.503	1529.299	0.400	27	0.160	R.RVIYASQLTAKPR.L
R4/RRR4-3/2	1639.243	1639.845	-980.297	0.423	922.824	0.392	18	0.160	R.NCDPEGPLM*LYVSK.M
R4/RRR4-2/2	1651.350	1651.841	-298.250	0.481	1272.819	0.291	17	0.160	K.ILSEEFGWDKDLAK.K
R4/RRR4-4/3	1814.873	1815.062	-104.447	0.484	1166.238	0.523	27	0.159	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/2	1120.058	1120.219	-143.922	0.450	900.787	0.357	15	0.158	K.EGALAEENMR.G
R4/RRR4-3/2	890.903	891.049	-164.518	0.395	582.243	0.424	11	0.156	K.FSVSPVVR.V
R4/RRR4-4/2	1120.001	1120.219	-195.528	0.384	766.894	0.391	14	0.155	K.EGALAEENMR.G
R4/RRR4-10/2	1816.579	1815.062	-266.674	0.388	834.641	0.375	20	0.155	K.AYLPVIESFGFSSQLR.A
R4/RRR4-3/2	1425.124	1425.569	-313.463	0.371	814.236	0.384	15	0.155	R.LWGENFFDPATK.K
R4/RRR4-4/3	1814.673	1815.062	-214.975	0.423	1469.138	0.393	28	0.155	K.AYLPVIESFGFSSQLR.A
R4/RRR4-2/2	1425.449	1425.569	-84.400	0.406	797.054	0.385	14	0.153	R.LWGENFFDPATK.K
R4/RRR4-4/2	744.821	744.863	-56.484	0.335	352.544	0.437	9	0.152	-.FFAFGR.-
R4/RRR4-4/2	890.932	891.049	-132.493	0.355	558.712	0.383	11	0.151	K.FSVSPVVR.V
R4/RRR4-1/2	1553.209	1553.742	-990.208	0.369	752.045	0.371	16	0.150	R.LWGENFFDPATKK.W
R4/RRR4-1/2	1388.175	1388.586	-296.493	0.350	913.749	0.320	14	0.150	R.GFVQFCYEPIK.Q
R4/RRR4-4/2	1543.786	1544.772	-1290.093	0.440	737.668	0.352	17	0.149	K.RGFVQFCYEPIK.Q
R4/RRR4-2/2	1553.479	1553.742	-170.287	0.409	705.116	0.357	16	0.148	R.LWGENFFDPATKK.W
R4/RRR4-1/2	1425.586	1425.569	11.972	0.358	728.111	0.350	14	0.148	R.LWGENFFDPATK.K
R4/RRR4-4/2	744.430	744.863	-583.147	0.318	337.770	0.306	9	0.147	-.FFAFGR.-
R4/RRR4-3/2	744.293	744.863	-2115.082	0.272	345.124	0.405	9	0.147	-.FFAFGR.-
R4/RRR4-3/2	890.868	891.049	-204.244	0.286	452.291	0.385	10	0.147	K.FSVSPVVR.V
R4/RRR4-4/2	744.739	744.863	-167.297	0.334	349.607	0.406	9	0.146	-.FFAFGR.-
R4/RRR4-4/2	841.911	841.930	-22.921	0.358	741.567	0.310	10	0.146	-.FGVDEFK.-
R4/RRR4-3/2	890.596	891.049	-510.192	0.300	583.673	0.363	11	0.146	-.FSVSPVVR.-
R4/RRR4-2/2	744.750	744.863	-151.841	0.327	293.099	0.412	8	0.146	-.FFAFGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	744.281	744.863	-2132.226	0.245	356.977	0.268	9	0.146	R.FFAFGR.V
R4/RRR4-2/2	744.949	744.863	116.592	0.346	289.694	0.377	8	0.146	-.FFAFGR.-
R4/RRR4-5/2	891.042	891.049	-7.985	0.257	518.699	0.357	11	0.145	K.FSVSPVVR.V
R4/RRR4-3/2	744.672	744.863	-256.919	0.307	342.566	0.196	9	0.145	-.FFAFGR.-
R4/RRR4-4/3	1819.508	1819.945	-241.085	0.441	1191.811	0.460	28	0.144	K.NATLTNEKESDACPIR.A
R4/RRR4-5/2	891.115	891.049	74.317	0.290	430.153	0.418	10	0.143	-.FSVSPVVR.-
R4/RRR4-7/2	891.020	891.049	-32.719	0.241	702.692	0.287	11	0.142	K.FSVSPVVR.V
R4/RRR4-3/2	744.318	744.863	-2081.289	0.204	347.283	0.294	9	0.141	-.FFAFGR.-
R4/RRR4-3/2	1813.618	1815.062	-1351.447	0.303	576.356	0.271	16	0.139	K.AYLPVIESFGFSSQLR.A
R4/RRR4-1/2	1553.554	1553.742	-121.653	0.347	447.723	0.287	14	0.138	-.LWGENFFDPATKK.-
R4/RRR4-4/3	1814.996	1815.062	-36.139	0.347	1100.107	0.465	23	0.138	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/3	1821.159	1819.945	117.604	0.466	1208.621	0.436	31	0.137	K.NATLTNEKESDACPIR.A
R4/RRR4-4/2	841.878	841.930	-62.188	0.257	676.272	0.242	10	0.137	-.FGVDEFK.-
R4/RRR4-1/2	841.992	841.930	73.781	0.217	738.482	0.204	10	0.136	K.FGVDEFK.M
R4/RRR4-4/2	1063.960	1064.217	-242.076	0.246	853.699	0.219	13	0.136	-.GVQYLNEIK.-
R4/RRR4-1/2	841.866	841.930	-76.587	0.237	708.888	0.158	10	0.135	-.FGVDEFK.-
R4/RRR4-2/3	1819.793	1819.945	-83.813	0.397	918.752	0.504	28	0.131	K.NATLTNEKESDACPIR.A
R4/RRR4-3/3	1503.025	1503.774	-1167.300	0.496	1250.172	0.397	24	0.130	R.RVIYASQLTAKPR.L
R4/RRR4-3/3	1503.907	1503.774	88.803	0.501	1166.203	0.422	24	0.129	R.RVIYASQLTAKPR.L
R4/RRR4-2/2	744.429	744.863	-584.628	0.239	222.932	0.352	7	0.126	-.FFAFGR.-
R4/RRR4-3/3	1815.303	1815.062	133.328	0.406	1079.281	0.420	25	0.124	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/3	1814.032	1815.062	-1122.409	0.384	884.872	0.468	24	0.121	K.AYLPVIESFGFSSQLR.A
R4/RRR4-4/3	1503.816	1503.774	28.112	0.421	1278.997	0.340	24	0.118	R.RVIYASQLTAKPR.L
R4/RRR4-2/3	1819.956	1819.945	5.804	0.401	850.921	0.460	27	0.118	K.NATLTNEKESDACPIR.A
R4/RRR4-1/3	1819.246	1819.945	-937.009	0.385	880.917	0.447	25	0.117	K.NATLTNEKESDACPIR.A
R4/RRR4-2/3	1819.464	1819.945	-265.518	0.410	821.886	0.453	25	0.115	K.NATLTNEKESDACPIR.A
R4/RRR4-3/3	1819.869	1819.945	-41.828	0.387	837.927	0.440	26	0.113	K.NATLTNEKESDACPIR.A
R4/RRR4-4/3	1503.857	1503.774	54.978	0.470	1076.484	0.360	24	0.108	R.RVIYASQLTAKPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1570.700	1569.715	-9.848	0.393	782.609	0.415	16	0.105	K.EQM*TPLSDFEDKL.-
R4/RRR4-1/2	1569.275	1569.715	-281.683	0.389	787.359	0.381	16	0.101	K.EQM*TPLSDFEDKL.-
R4/RRR4-3/2	1569.176	1569.715	-984.013	0.339	574.066	0.219	14	0.101	-.EQM*TPLSDFEDKL.-
R4/RRR4-3/2	1569.422	1569.715	-187.338	0.411	933.127	0.357	17	0.098	K.EQM*TPLSDFEDKL.-
R4/RRR4-4/2	1569.328	1569.715	-247.735	0.410	848.885	0.332	16	0.093	K.EQM*TPLSDFEDKL.-
R4/RRR4-1/3	1814.011	1815.062	-1133.761	0.362	715.356	0.283	23	0.088	K.AYLPVIESFGFSSQLR.A
R4/RRR4-1/3	1814.487	1815.062	-870.505	0.384	687.628	0.242	26	0.086	K.AYLPVIESFGFSSQLR.A
R4/RRR4-3/2	1570.311	1569.715	-258.340	0.422	811.715	0.251	16	0.086	K.EQM*TPLSDFEDKL.-
R4/RRR4-2/2	1592.342	1592.644	-190.506	0.528	2655.879	0.561	23	0.441	R.TQDLENELSTANEK.F
R4/RRR4-1/2	1612.295	1611.732	-271.757	0.569	2109.316	0.528	20	0.319	K.VSQLSDELEAYQTK.A
R4/RRR4-1/2	1387.995	1388.509	-1094.224	0.425	1732.169	0.428	19	0.236	R.TIANQEEQISVR.E
R4/RRR4-1/2	1202.539	1203.328	-1492.060	0.400	1861.124	0.345	18	0.232	K.TAALEEQALTR.E
R4/RRR4-2/2	1203.185	1203.328	-118.918	0.415	1948.450	0.283	19	0.228	K.TAALEEQALTR.E
R4/RRR4-1/2	1161.035	1161.248	-183.450	0.487	1561.523	0.445	18	0.222	R.GLELQSAAESR.S
R4/RRR4-1/2	1388.151	1388.509	-258.924	0.453	1553.140	0.435	18	0.217	R.TIANQEEQISVR.E
R4/RRR4-1/2	1202.659	1203.328	-1391.429	0.384	1845.507	0.288	18	0.217	K.TAALEEQALTR.E
R4/RRR4-1/2	1536.174	1536.663	-319.256	0.347	1571.688	0.389	19	0.206	K.LSSISSEKEEVAEK.L
R4/RRR4-1/2	1163.080	1162.315	-203.023	0.434	1156.050	0.542	17	0.201	R.TSLEASLLEAK.Q
R4/RRR4-1/2	1507.198	1507.625	-284.208	0.449	1463.426	0.409	20	0.201	K.INELQASLDSTTSK.N
R4/RRR4-1/2	1160.789	1161.248	-396.341	0.370	1303.126	0.461	18	0.197	R.GLELQSAAESR.S
R4/RRR4-1/2	1536.190	1536.663	-308.812	0.364	1605.775	0.308	20	0.194	K.LSSISSEKEEVAEK.L
R4/RRR4-1/2	1202.811	1203.328	-1264.624	0.433	1486.200	0.327	17	0.189	K.TAALEEQALTR.E
R4/RRR4-1/2	1388.296	1388.509	-153.772	0.424	1218.467	0.388	18	0.178	R.TIANQEEQISVR.E
R4/RRR4-2/2	1357.182	1357.535	-260.502	0.433	999.937	0.441	17	0.171	R.SLELESLLHTSK.S
R4/RRR4-1/2	1101.270	1101.318	-44.094	0.402	986.874	0.428	16	0.171	K.VLALEESLVK.L
R4/RRR4-2/2	1202.921	1203.328	-339.202	0.360	1319.292	0.275	17	0.167	K.TAALEEQALTR.E
R4/RRR4-2/2	1161.209	1162.315	-1819.094	0.334	805.990	0.410	14	0.154	R.TSLEASLLEAK.Q
R4/RRR4-1/2	1073.867	1074.253	-360.356	0.352	1081.528	0.282	15	0.153	K.LALVNTEVSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1101.698	1101.318	346.005	0.275	742.743	0.379	14	0.148	K.VLALEESLVK.L
R4/RRR4-1/2	1535.852	1536.663	-1182.998	0.301	898.468	0.304	19	0.147	K.LSSISSEKEEVAEK.L
R4/RRR4-1/2	1077.967	1078.157	-177.142	0.284	663.382	0.413	12	0.147	K.SHLTEFESK.L
R4/RRR4-1/2	1009.341	1010.123	-1770.680	0.380	773.971	0.305	12	0.146	-.YNITLEEK.-
R4/RRR4-2/3	1416.874	1416.602	192.509	0.523	1685.618	0.294	24	0.144	R.RIEELELEKEK.L
R4/RRR4-2/2	1536.105	1536.663	-1017.533	0.222	182.675	0.295	14	0.141	K.LSSISSEKEEVAEK.L
R4/RRR4-1/2	1009.764	1010.123	-356.254	0.272	1053.822	0.133	13	0.138	-.YNITLEEK.-
R4/RRR4-2/2	1058.884	1059.155	-256.996	0.297	1027.137	0.127	14	0.134	K.LQLEEAEAR.V
R4/RRR4-2/3	1322.245	1322.452	-157.066	0.471	548.412	0.543	18	0.118	K.TIEHLTEVHSR.G
R4/RRR4-1/3	1322.678	1322.452	171.229	0.520	426.464	0.513	16	0.110	K.TIEHLTEVHSR.G
R4/RRR4-2/3	1322.326	1322.452	-95.529	0.467	642.723	0.445	18	0.105	K.TIEHLTEVHSR.G
R4/RRR4-1/3	1322.424	1322.452	-21.500	0.489	393.867	0.477	15	0.105	K.TIEHLTEVHSR.G
R4/RRR4-1/3	1322.414	1322.452	-28.861	0.477	542.043	0.455	18	0.105	K.TIEHLTEVHSR.G
R4/RRR4-2/3	1426.606	1425.529	53.921	0.523	892.357	0.391	22	0.102	-.AIDHQQVEESLR.-
R4/RRR4-2/3	1425.059	1425.529	-330.927	0.502	977.240	0.337	21	0.099	K.AIDHQQVEESLR.S
R4/RRR4-25/3	1317.798	1318.502	-1296.578	0.300	1368.936	0.233	26	0.098	K.RTSLEASLLEAK.Q
R4/RRR4-6/3	1317.970	1318.502	-1165.842	0.351	923.167	0.342	24	0.096	K.RTSLEASLLEAK.Q
R4/RRR4-1/3	1416.066	1416.602	-1088.149	0.460	1258.227	0.244	22	0.095	R.RIEELELEKEK.L
R4/RRR4-2/3	1319.641	1318.502	105.563	0.404	444.346	0.279	20	0.094	K.RTSLEASLLEAK.Q
R4/RRR4-1/3	1425.658	1425.529	90.714	0.447	932.429	0.300	22	0.090	-.AIDHQQVEESLR.-
R4/RRR4-1/3	1317.859	1318.502	-1250.112	0.336	601.509	0.286	22	0.089	K.RTSLEASLLEAK.Q
R4/RRR4-1/3	1425.139	1425.529	-274.723	0.491	821.128	0.290	22	0.089	K.AIDHQQVEESLR.S
R4/RRR4-4/3	1317.445	1318.502	-1565.554	0.284	728.051	0.284	23	0.086	K.RTSLEASLLEAK.Q
R4/RRR4-2/3	1425.411	1425.529	-83.338	0.483	792.685	0.317	21	0.085	-.AIDHQQVEESLR.-
R4/RRR4-2/3	1527.253	1527.660	-267.057	0.400	673.678	0.272	21	0.085	K.FKEVEADLEQYR.S
R4/RRR4-1/3	1425.334	1425.529	-137.330	0.522	609.995	0.351	18	0.082	-.AIDHQQVEESLR.-
R4/RRR4-2/3	1527.516	1527.660	-94.840	0.439	1202.148	0.180	24	0.082	K.FKEVEADLEQYR.S
R4/RRR4-2/3	1416.191	1416.602	-291.112	0.499	1144.225	0.198	20	0.081	-.RIEELELEKEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/3	1416.981	1416.602	268.057	0.468	1168.507	0.167	20	0.078	R.RIEELELEKEK.L
R4/RRR4-9/3	1318.037	1318.502	-353.943	0.297	824.064	0.163	22	0.078	K.RTSLEASLLEAK.Q
R4/RRR4-2/3	1527.520	1527.660	-91.954	0.473	1020.686	0.197	21	0.078	K.FKEVEADLEQYR.S
R4/RRR4-1/3	1415.397	1416.602	-1562.658	0.472	917.003	0.197	19	0.074	-.RIEELELEKEK.-
R4/RRR4-2/2	1459.444	1459.670	-155.504	0.510	2407.509	0.609	26	0.403	K.LVAEAGIGTVASGVSK.G
R4/RRR4-2/2	1459.354	1459.670	-217.514	0.510	2160.919	0.612	25	0.355	K.LVAEAGIGTVASGVSK.G
R4/RRR4-2/2	1907.661	1907.199	242.888	0.566	1862.522	0.530	26	0.281	R.FGVTPTFLVNAEQIEIK.I
R4/RRR4-2/2	1907.489	1907.199	152.470	0.573	1755.745	0.567	25	0.275	R.FGVTPTFLVNAEQIEIK.I
R4/RRR4-2/2	1906.575	1907.199	-854.332	0.527	1917.814	0.482	26	0.275	R.FGVTPTFLVNAEQIEIK.I
R4/RRR4-2/2	1202.382	1202.343	32.828	0.491	1691.379	0.493	19	0.250	R.NGSQLLVLSDR.S
R4/RRR4-2/2	1676.231	1676.807	-943.392	0.500	1726.015	0.444	23	0.238	K.ASDSANLDSTAELLLR.S
R4/RRR4-2/2	1521.330	1521.699	-243.179	0.450	1477.281	0.438	19	0.209	K.VFTDEGLEVLGWR.T
R4/RRR4-2/2	1218.893	1219.321	-352.235	0.515	1470.138	0.429	18	0.209	K.VLCDEADAAVR.N
R4/RRR4-2/2	1677.366	1676.807	-263.623	0.551	1472.667	0.437	22	0.206	K.ASDSANLDSTAELLLR.S
R4/RRR4-2/2	1275.960	1276.379	-328.997	0.380	1473.392	0.425	19	0.205	K.GLQNGDTATSAIK.Q
R4/RRR4-2/2	1521.360	1521.699	-222.974	0.421	1466.100	0.420	19	0.204	K.VFTDEGLEVLGWR.T
R4/RRR4-2/2	1676.178	1676.807	-974.758	0.493	1633.967	0.326	21	0.197	K.ASDSANLDSTAELLLR.S
R4/RRR4-2/2	1276.049	1276.379	-258.835	0.455	1272.728	0.457	18	0.194	K.GLQNGDTATSAIK.Q
R4/RRR4-2/2	1276.129	1276.379	-196.167	0.435	1041.623	0.536	19	0.191	K.GLQNGDTATSAIK.Q
R4/RRR4-2/2	1522.960	1521.699	172.074	0.529	1111.731	0.505	17	0.190	K.VFTDEGLEVLGWR.T
R4/RRR4-2/2	1218.450	1219.321	-1539.800	0.446	1243.301	0.430	18	0.189	K.VLCDEADAAVR.N
R4/RRR4-2/2	1852.502	1852.985	-261.304	0.534	871.420	0.574	20	0.183	K.SVASANPYGSWLQQSTR.S
R4/RRR4-2/2	1852.439	1852.985	-837.131	0.480	853.764	0.575	20	0.181	K.SVASANPYGSWLQQSTR.S
R4/RRR4-2/2	1852.604	1852.985	-206.304	0.518	813.319	0.554	19	0.175	K.SVASANPYGSWLQQSTR.S
R4/RRR4-2/2	1143.968	1144.303	-293.964	0.401	1238.828	0.337	18	0.172	K.IGGLTLDELGR.E
R4/RRR4-2/3	1508.617	1508.705	-58.289	0.356	1744.002	0.324	32	0.166	K.IAQGAKPGEGGQLPGK.K
R4/RRR4-2/2	1979.210	1980.190	-1003.468	0.396	1095.154	0.393	21	0.165	K.GQM*EAWDGPALLLFSDGR.T
R4/RRR4-2/2	1049.067	1049.245	-170.584	0.417	843.810	0.420	15	0.161	-.YLLSSAGLPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/3	1906.832	1907.199	-193.188	0.459	1799.058	0.269	29	0.161	R.FGVTPTFLVNAEQIEIK.I
R4/RRR4-2/2	1980.454	1980.190	133.645	0.439	684.403	0.494	21	0.160	K.GQM*EAWDGPALLLFSDGR.T
R4/RRR4-2/2	1218.382	1219.321	-1595.558	0.367	1121.087	0.309	17	0.160	K.VLCDEADAAVR.N
R4/RRR4-2/2	1156.059	1156.273	-185.405	0.444	890.230	0.399	13	0.158	-.TFQIYNVDR.-
R4/RRR4-2/2	1276.824	1276.379	350.137	0.344	611.294	0.463	17	0.155	K.GLQNGDTATSAIK.Q
R4/RRR4-1/2	1616.466	1615.762	-184.103	0.410	919.899	0.352	16	0.153	K.YPEVIDFYDYYK.G
R4/RRR4-2/3	1508.686	1508.705	-12.394	0.352	1452.230	0.407	33	0.153	K.IAQGAKPGEGGQLPGK.K
R4/RRR4-2/2	1144.204	1144.303	-86.954	0.405	844.877	0.357	15	0.150	-.IGGLTLDELGR.-
R4/RRR4-2/2	1049.057	1049.245	-180.273	0.350	682.883	0.341	14	0.147	K.YLLSSAGLPK.W
R4/RRR4-2/2	1173.184	1173.368	-157.632	0.355	710.252	0.328	16	0.145	R.VNAPAGQM*QLK.G
R4/RRR4-2/2	1401.384	1401.654	-193.390	0.399	1272.836	0.081	19	0.131	K.GM*AGGELVVVPVEK.T
R4/RRR4-2/2	1144.707	1144.303	353.327	0.363	536.153	0.246	13	0.128	-.IGGLTLDELGR.-
R4/RRR4-2/3	1508.779	1508.705	49.686	0.353	1296.317	0.333	31	0.117	K.IAQGAKPGEGGQLPGK.K
R4/RRR4-2/3	1636.362	1636.877	-928.600	0.443	727.315	0.495	28	0.114	K.IAQGAKPGEGGQLPGKK.V
R4/RRR4-2/3	1713.085	1713.864	-1041.496	0.477	754.384	0.466	24	0.111	R.ICHTNNCPVGVASQR.E
R4/RRR4-2/3	1636.870	1636.877	-4.542	0.452	858.775	0.431	30	0.109	K.IAQGAKPGEGGQLPGKK.V
R4/RRR4-2/3	1713.586	1713.864	-163.066	0.472	728.566	0.451	25	0.107	R.ICHTNNCPVGVASQR.E
R4/RRR4-2/3	1713.505	1713.864	-210.340	0.500	629.503	0.445	22	0.102	R.ICHTNNCPVGVASQR.E
R4/RRR4-4/2	1971.474	1971.200	139.634	0.663	3497.381	0.653	27	0.703	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/2	1970.874	1971.200	-166.030	0.631	3214.238	0.628	26	0.607	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/2	1970.074	1971.200	-1082.349	0.556	2848.134	0.634	25	0.512	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/3	1961.255	1961.210	23.147	0.572	2620.411	0.525	35	0.460	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/3	1971.194	1971.200	-2.840	0.610	2538.609	0.567	37	0.455	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/3	1961.394	1961.210	94.214	0.600	2438.878	0.534	34	0.411	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/3	1971.368	1971.200	85.663	0.604	2255.187	0.557	36	0.370	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/2	1969.700	1969.312	197.755	0.611	2431.582	0.492	23	0.359	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/2	1969.476	1969.312	83.515	0.611	2302.360	0.510	23	0.342	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/3	1960.401	1961.210	-925.595	0.541	2013.639	0.554	33	0.316	R.LGATFSSHPNELIALFSR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/3	1970.572	1971.200	-828.706	0.564	2041.729	0.538	36	0.308	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-5/3	1961.424	1961.210	109.381	0.483	1989.042	0.544	32	0.308	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/3	1960.966	1961.210	-124.919	0.514	2040.157	0.503	33	0.297	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/3	1961.147	1961.210	-32.010	0.567	2027.530	0.506	33	0.294	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/3	1970.622	1971.200	-803.149	0.554	1968.141	0.535	34	0.292	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/2	1969.615	1969.312	154.623	0.631	2106.060	0.465	23	0.292	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/3	1960.744	1961.210	-238.268	0.527	2003.843	0.489	34	0.280	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-1/3	1973.011	1971.200	-95.797	0.570	1722.069	0.603	34	0.274	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-5/2	1840.335	1841.009	-912.426	0.535	1608.104	0.578	23	0.256	R.DLANLVIVCGDHGNQSK.D
R4/RRR4-5/3	1971.719	1971.200	-244.580	0.563	1786.734	0.530	33	0.253	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/2	1840.411	1841.009	-871.275	0.551	1564.806	0.585	23	0.253	R.DLANLVIVCGDHGNQSK.D
R4/RRR4-4/2	1840.373	1841.009	-891.650	0.535	1425.174	0.567	22	0.231	R.DLANLVIVCGDHGNQSK.D
R4/RRR4-4/2	1840.377	1841.009	-889.786	0.536	1481.259	0.536	22	0.230	R.DLANLVIVCGDHGNQSK.D
R4/RRR4-2/3	1960.540	1961.210	-854.523	0.515	1701.520	0.471	31	0.216	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/3	1457.340	1457.610	-185.899	0.461	1857.255	0.416	28	0.215	K.TKYPNSDIYLDK.F
R4/RRR4-5/2	1839.566	1841.009	-1331.985	0.503	1271.681	0.574	20	0.214	R.DLANLVIVCGDHGNQSK.D
R4/RRR4-4/2	1541.393	1541.768	-244.144	0.482	1631.660	0.372	19	0.209	K.LGVTQCTIAHALEK.T
R4/RRR4-4/3	1969.845	1971.200	-1198.867	0.495	1677.297	0.458	32	0.205	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/2	1968.493	1969.312	-926.852	0.438	1723.677	0.305	21	0.203	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/2	1241.252	1241.462	-169.523	0.494	1440.873	0.385	18	0.197	R.IKQQGLDITPK.I
R4/RRR4-4/2	1541.233	1541.768	-998.617	0.493	1416.868	0.413	18	0.195	K.LGVTQCTIAHALEK.T
R4/RRR4-4/2	1241.124	1241.462	-273.123	0.463	1283.348	0.419	17	0.190	R.IKQQGLDITPK.I
R4/RRR4-3/2	1968.715	1969.312	-813.622	0.472	1339.011	0.422	19	0.189	K.LFQDKESLYPLLNFLK.A
R4/RRR4-1/3	1961.465	1961.210	130.727	0.490	1340.219	0.535	28	0.188	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-1/2	1241.254	1241.462	-168.536	0.461	1364.111	0.343	17	0.182	R.IKQQGLDITPK.I
R4/RRR4-3/3	1961.512	1961.210	154.599	0.548	1473.331	0.472	30	0.181	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-5/2	1240.737	1241.462	-1394.810	0.495	1215.876	0.383	17	0.178	R.IKQQGLDITPK.I
R4/RRR4-5/2	1242.365	1241.462	-78.408	0.492	1381.081	0.316	17	0.177	R.IKQQGLDITPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1961.670	1961.210	235.452	0.514	836.626	0.550	20	0.176	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/2	1241.116	1241.462	-279.833	0.476	1341.765	0.312	17	0.174	R.IKQQGLDITPK.I
R4/RRR4-1/3	1961.030	1961.210	-92.043	0.520	1496.482	0.439	29	0.174	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/2	1253.733	1254.418	-1347.734	0.479	913.531	0.440	17	0.171	K.VIGTEHTDILR.V
R4/RRR4-5/2	1961.684	1961.210	242.690	0.477	768.894	0.542	19	0.170	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-1/2	1241.382	1241.462	-64.958	0.425	1110.791	0.373	16	0.169	R.IKQQGLDITPK.I
R4/RRR4-5/2	1960.353	1961.210	-949.999	0.501	645.381	0.573	18	0.168	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/2	1254.104	1254.418	-251.258	0.473	931.783	0.401	18	0.167	K.VIGTEHTDILR.V
R4/RRR4-4/2	1388.071	1388.546	-342.735	0.392	603.857	0.524	20	0.167	R.LLPDAVGTTCGQR.V
R4/RRR4-5/2	1253.656	1254.418	-1409.834	0.463	877.182	0.416	17	0.166	K.VIGTEHTDILR.V
R4/RRR4-5/2	1254.078	1254.418	-271.864	0.411	838.802	0.436	17	0.166	K.VIGTEHTDILR.V
R4/RRR4-4/3	1970.971	1971.200	-116.426	0.514	1227.087	0.519	30	0.165	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/2	1275.964	1275.477	382.185	0.437	844.549	0.420	17	0.164	K.NM*TGLVEM*YGK.N
R4/RRR4-4/2	1387.958	1388.546	-1147.093	0.411	681.101	0.451	21	0.163	R.LLPDAVGTTCGQR.V
R4/RRR4-5/2	1387.668	1388.546	-1357.325	0.332	725.341	0.473	21	0.162	R.LLPDAVGTTCGQR.V
R4/RRR4-4/2	1541.203	1541.768	-1018.179	0.495	1013.757	0.401	16	0.162	K.LGVTQCTIAHALEK.T
R4/RRR4-1/2	1960.769	1961.210	-225.270	0.407	621.286	0.525	19	0.161	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-5/2	1253.552	1254.418	-1493.069	0.449	749.989	0.422	16	0.161	K.VIGTEHTDILR.V
R4/RRR4-4/2	1254.084	1254.418	-266.981	0.422	701.313	0.443	15	0.160	K.VIGTEHTDILR.V
R4/RRR4-5/2	1242.228	1241.462	-188.905	0.495	1104.089	0.314	16	0.159	R.IKQQGLDITPK.I
R4/RRR4-1/2	1388.237	1388.546	-222.660	0.381	685.280	0.419	20	0.158	R.LLPDAVGTTCGQR.V
R4/RRR4-2/2	1241.112	1241.462	-283.089	0.431	746.072	0.373	15	0.154	R.IKQQGLDITPK.I
R4/RRR4-4/2	1243.215	1243.479	-212.687	0.450	743.321	0.370	16	0.154	K.NMTGLVEMYGK.N
R4/RRR4-4/2	1124.001	1124.271	-241.018	0.303	373.652	0.425	16	0.152	K.YAPFEDILR.A
R4/RRR4-4/2	1274.944	1275.477	-1206.566	0.420	801.496	0.338	16	0.151	K.NM*TGLVEM*YGK.N
R4/RRR4-1/2	1961.056	1961.210	-78.518	0.403	443.425	0.468	17	0.150	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-1/2	1388.045	1388.546	-1084.040	0.375	564.319	0.351	19	0.150	R.LLPDAVGTTCGQR.V
R4/RRR4-5/2	1088.921	1089.291	-341.319	0.251	256.224	0.133	13	0.149	R.ALENEMLLR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1968.430	1969.312	-958.915	0.390	769.627	0.368	17	0.148	K.LFQDKESLYPLLNFLK.A
R4/RRR4-5/2	1124.007	1124.271	-235.243	0.287	371.431	0.257	16	0.147	K.YAPFEDILR.A
R4/RRR4-5/2	1387.539	1388.546	-1450.632	0.254	617.324	0.370	20	0.147	R.LLPDAVGTTCGQR.V
R4/RRR4-1/2	1960.470	1961.210	-889.926	0.350	236.433	0.497	14	0.146	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/2	1124.088	1124.271	-162.685	0.236	370.247	0.384	16	0.145	K.YAPFEDILR.A
R4/RRR4-1/2	1090.142	1089.291	-136.977	0.352	370.740	0.254	13	0.144	-.ALENEMLLR.-
R4/RRR4-4/2	1105.013	1105.291	-251.960	0.409	826.703	0.251	13	0.144	R.ALENEM*LLR.I
R4/RRR4-10/2	1970.249	1969.312	-32.104	0.319	713.884	0.354	16	0.144	K.LFQDKESLYPLLNFLK.A
R4/RRR4-1/2	1090.078	1089.291	-196.290	0.391	556.741	0.226	13	0.142	R.ALENEMLLR.I
R4/RRR4-3/2	1968.938	1969.312	-190.570	0.386	490.065	0.333	17	0.142	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/2	1959.942	1961.210	-1160.783	0.303	223.664	0.391	14	0.142	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/2	1960.169	1961.210	-1044.094	0.249	365.735	0.397	17	0.141	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/2	1961.479	1961.210	137.412	0.236	262.223	0.418	16	0.141	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-3/2	1960.456	1961.210	-897.302	0.270	285.728	0.399	15	0.141	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/2	1104.850	1105.291	-399.938	0.415	813.355	0.217	13	0.140	R.ALENEM*LLR.I
R4/RRR4-1/2	1387.864	1388.546	-1215.099	0.266	491.722	0.260	16	0.140	R.LLPDAVGTTCGQR.V
R4/RRR4-4/2	1959.838	1961.210	-1213.947	0.363	517.712	0.329	17	0.140	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-5/2	1105.128	1105.291	-147.127	0.347	786.508	0.198	13	0.140	R.ALENEM*LLR.I
R4/RRR4-4/2	1124.010	1124.271	-232.737	0.135	306.163	0.242	15	0.139	K.YAPFEDILR.A
R4/RRR4-1/3	1961.404	1961.210	99.083	0.443	985.166	0.497	25	0.138	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-1/3	1969.455	1969.312	73.096	0.394	1587.876	0.286	28	0.137	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/2	1124.046	1124.271	-200.161	0.132	319.068	0.303	15	0.137	K.YAPFEDILR.A
R4/RRR4-5/2	1104.558	1105.291	-1573.023	0.284	657.833	0.143	12	0.136	R.ALENEM*LLR.I
R4/RRR4-4/2	1104.705	1105.291	-1439.150	0.308	726.125	0.137	12	0.135	-.ALENEM*LLR.-
R4/RRR4-5/3	1960.408	1961.210	-921.844	0.442	968.518	0.465	24	0.130	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-5/2	1123.535	1124.271	-1549.137	0.216	264.997	0.368	14	0.130	-.YAPFEDILR.-
R4/RRR4-3/3	1961.581	1961.210	189.704	0.398	1066.010	0.432	25	0.129	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-4/3	1457.368	1457.610	-166.362	0.445	1234.880	0.391	25	0.126	K.TKYPNSDIYLDK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1960.601	1961.210	-822.928	0.470	1006.635	0.438	26	0.125	R.LGATFSSHPNELIALFSR.Y
R4/RRR4-5/2	1105.584	1105.291	266.008	0.358	510.981	0.218	11	0.125	-.ALENEM*LLR.-
R4/RRR4-5/3	1969.213	1969.312	-50.189	0.384	1282.064	0.339	29	0.119	K.LFQDKESLYPLLNFLK.A
R4/RRR4-5/3	1970.680	1971.200	-773.583	0.461	856.206	0.453	26	0.118	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/3	1968.770	1969.312	-785.496	0.341	1154.731	0.364	26	0.116	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/3	1969.067	1969.312	-124.902	0.340	991.495	0.375	24	0.109	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/3	1241.721	1241.462	209.015	0.542	1207.696	0.313	24	0.105	R.IKQQGLDITPK.I
R4/RRR4-6/3	1971.379	1971.200	91.066	0.349	517.771	0.420	24	0.103	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-5/3	1241.555	1241.462	74.729	0.469	1239.358	0.275	24	0.100	R.IKQQGLDITPK.I
R4/RRR4-1/3	1969.133	1969.312	-91.135	0.352	1116.794	0.287	26	0.098	K.LFQDKESLYPLLNFLK.A
R4/RRR4-5/3	1240.884	1241.462	-1275.513	0.499	1017.694	0.313	22	0.098	R.IKQQGLDITPK.I
R4/RRR4-4/3	1970.145	1971.200	-1046.085	0.343	935.934	0.307	23	0.097	R.HQLLAEFDALIEADKEK.Y
R4/RRR4-4/3	1241.637	1241.462	141.137	0.502	1139.247	0.281	23	0.097	R.IKQQGLDITPK.I
R4/RRR4-5/3	1457.213	1457.610	-272.877	0.457	972.690	0.327	23	0.096	K.TKYPNSDIYLDK.F
R4/RRR4-4/3	1241.353	1241.462	-88.149	0.513	1091.153	0.265	23	0.089	-.IKQQGLDITPK.-
R4/RRR4-3/3	1241.854	1241.462	316.359	0.498	905.665	0.265	21	0.089	R.IKQQGLDITPK.I
R4/RRR4-2/3	1241.630	1241.462	135.221	0.463	840.324	0.257	20	0.088	R.IKQQGLDITPK.I
R4/RRR4-4/3	1970.812	1971.200	-197.229	0.454	613.822	0.351	22	0.087	-.HQLLAEFDALIEADKEK.-
R4/RRR4-1/3	1969.019	1969.312	-149.343	0.358	948.142	0.226	26	0.084	K.LFQDKESLYPLLNFLK.A
R4/RRR4-5/3	1968.768	1969.312	-786.430	0.346	1169.372	0.184	28	0.084	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/3	1242.459	1241.462	-2.239	0.452	1251.686	0.174	23	0.083	-.IKQQGLDITPK.-
R4/RRR4-4/3	1970.040	1969.312	-138.203	0.285	960.872	0.199	22	0.082	K.LFQDKESLYPLLNFLK.A
R4/RRR4-4/3	1242.671	1241.462	168.903	0.495	1363.955	0.151	23	0.082	-.IKQQGLDITPK.-
R4/RRR4-3/3	1242.275	1241.462	-150.964	0.511	736.109	0.267	20	0.082	-.IKQQGLDITPK.-
R4/RRR4-3/3	1241.642	1241.462	145.426	0.494	923.144	0.245	21	0.078	-.IKQQGLDITPK.-
R4/RRR4-2/3	1241.835	1241.462	301.427	0.474	904.411	0.208	21	0.077	-.IKQQGLDITPK.-
R4/RRR4-1/3	1241.870	1241.462	329.073	0.474	698.121	0.237	20	0.076	-.IKQQGLDITPK.-
R4/RRR4-2/3	1241.451	1241.462	-9.144	0.453	893.502	0.134	21	0.066	-.IKQQGLDITPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1803.253	1803.946	-941.305	0.541	1754.531	0.515	22	0.259	K.NATLTNEKEADACPIR.A
R4/RRR4-2/3	1803.670	1803.946	-153.598	0.350	2038.747	0.377	32	0.240	K.NATLTNEKEADACPIR.A
R4/RRR4-4/2	1804.361	1803.946	231.076	0.519	1707.228	0.448	22	0.236	K.NATLTNEKEADACPIR.A
R4/RRR4-4/3	1802.636	1803.946	-1285.417	0.483	1350.075	0.446	32	0.156	K.NATLTNEKEADACPIR.A
R4/RRR4-6/2	1600.057	1599.899	99.353	0.465	2297.414	0.413	27	0.314	K.VILGPATVGGIQAGAFK.I
R4/RRR4-7/2	1619.248	1619.792	-956.629	0.512	1991.338	0.526	22	0.298	K.IGDTAGTIDNIIQCK.L
R4/RRR4-6/2	1599.385	1599.899	-949.295	0.472	2013.736	0.486	26	0.290	K.VILGPATVGGIQAGAFK.I
R4/RRR4-7/2	1599.452	1599.899	-280.369	0.423	2147.840	0.404	25	0.286	K.VILGPATVGGIQAGAFK.I
R4/RRR4-7/2	1619.357	1619.792	-269.892	0.508	1833.772	0.522	22	0.273	K.IGDTAGTIDNIIQCK.L
R4/RRR4-7/2	1818.283	1817.977	168.771	0.532	1650.172	0.600	25	0.268	R.ETPSVAGIINPGSDGFQK.L
R4/RRR4-7/2	1528.288	1528.729	-289.499	0.442	1545.175	0.622	24	0.259	R.VVAIIAEGVPESDTK.Q
R4/RRR4-6/2	1599.308	1599.899	-997.494	0.454	1715.269	0.520	23	0.254	K.VILGPATVGGIQAGAFK.I
R4/RRR4-7/2	1528.323	1528.729	-266.580	0.406	1613.044	0.550	24	0.249	R.VVAIIAEGVPESDTK.Q
R4/RRR4-7/2	1817.217	1817.977	-971.398	0.483	1501.351	0.585	24	0.244	R.ETPSVAGIINPGSDGFQK.L
R4/RRR4-7/2	1817.431	1817.977	-853.256	0.471	1472.306	0.565	24	0.235	R.ETPSVAGIINPGSDGFQK.L
R4/RRR4-7/2	1627.312	1627.907	-983.187	0.335	1839.141	0.380	23	0.235	K.DLVSSLVSGLLTIGPR.F
R4/RRR4-7/2	1620.260	1619.792	289.296	0.543	1467.165	0.506	21	0.223	K.IGDTAGTIDNIIQCK.L
R4/RRR4-1/2	1528.813	1528.729	55.130	0.459	1312.301	0.561	22	0.219	R.VVAIIAEGVPESDTK.Q
R4/RRR4-1/2	1599.560	1599.899	-212.150	0.460	1503.214	0.460	23	0.215	K.VILGPATVGGIQAGAFK.I
R4/RRR4-7/2	1659.680	1658.920	-144.784	0.485	1230.477	0.537	23	0.208	K.VQKPVVAWVSGTCAR.L
R4/RRR4-7/2	1528.291	1528.729	-287.415	0.418	1182.223	0.527	22	0.199	R.VVAIIAEGVPESDTK.Q
R4/RRR4-7/2	1248.497	1249.396	-1525.592	0.377	1414.681	0.415	16	0.199	K.TTQALFYNYK.Q
R4/RRR4-7/2	1249.205	1249.396	-153.938	0.505	1144.081	0.498	15	0.194	K.TTQALFYNYK.Q
R4/RRR4-7/2	1248.904	1249.396	-395.141	0.381	1320.572	0.415	15	0.190	K.TTQALFYNYK.Q
R4/RRR4-5/2	1818.863	1817.977	-63.182	0.482	1007.608	0.553	20	0.186	R.ETPSVAGIINPGSDGFQK.L
R4/RRR4-7/2	1273.963	1274.464	-1181.788	0.495	1387.320	0.354	16	0.186	R.MLDFDFLCGR.E
R4/RRR4-6/2	1619.311	1619.792	-298.404	0.455	1006.836	0.530	19	0.185	K.IGDTAGTIDNIIQCK.L
R4/RRR4-7/2	1563.164	1563.696	-982.998	0.474	1155.589	0.439	18	0.180	K.SGGM*SNEM*YNTIAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	992.903	993.055	-154.092	0.466	1350.693	0.329	17	0.180	R.FGGAIDDAAR.Y
R4/RRR4-7/2	1657.893	1658.920	-1226.188	0.426	1015.694	0.489	21	0.180	K.VQKPVVAWVSGTCAR.L
R4/RRR4-7/2	1563.134	1563.696	-1002.129	0.481	1085.583	0.448	18	0.177	K.SGGM*SNEM*YNTIAR.V
R4/RRR4-7/2	1563.027	1563.696	-1070.974	0.459	1061.271	0.419	17	0.169	K.SGGM*SNEM*YNTIAR.V
R4/RRR4-7/2	992.706	993.055	-353.310	0.393	1227.399	0.313	17	0.168	R.FGGAIDDAAR.Y
R4/RRR4-7/2	1290.331	1290.464	-103.539	0.395	1090.941	0.354	13	0.163	R.M*LDFDFLCGR.E
R4/RRR4-7/2	1835.280	1836.033	-957.969	0.426	762.038	0.477	23	0.162	K.DAGAVVPTSYEALETAIK.E
R4/RRR4-7/2	1309.572	1310.526	-1496.889	0.436	1023.982	0.337	17	0.158	K.LYRPGSVGFVSK.S
R4/RRR4-7/2	1289.902	1290.464	-1214.223	0.382	910.142	0.384	13	0.158	R.M*LDFDFLCGR.E
R4/RRR4-3/2	1599.720	1599.899	-112.325	0.319	939.783	0.405	19	0.158	K.VILGPATVGGIQAGAFK.I
R4/RRR4-7/2	1187.177	1187.332	-130.422	0.392	605.527	0.433	14	0.156	K.YAHTHFPSVK.Y
R4/RRR4-7/2	1187.988	1187.332	-290.080	0.465	553.166	0.397	15	0.155	K.YAHTHFPSVK.Y
R4/RRR4-7/2	1310.334	1310.526	-147.411	0.467	909.958	0.351	16	0.154	K.LYRPGSVGFVSK.S
R4/RRR4-7/2	1310.133	1310.526	-301.164	0.436	849.125	0.321	16	0.149	K.LYRPGSVGFVSK.S
R4/RRR4-7/3	1659.552	1658.920	-222.490	0.430	1353.980	0.417	31	0.146	K.VQKPVVAWVSGTCAR.L
R4/RRR4-6/2	992.387	993.055	-1686.129	0.343	554.341	0.390	14	0.142	-.FGGAIDDAAR.-
R4/RRR4-1/2	1619.656	1619.792	-84.182	0.311	474.252	0.432	13	0.141	-.IGDTAGTIDNIIQCK.-
R4/RRR4-7/3	1310.533	1310.526	5.585	0.465	1260.123	0.438	26	0.141	K.LYRPGSVGFVSK.S
R4/RRR4-7/2	1187.277	1187.332	-45.747	0.284	631.825	0.231	16	0.140	K.YAHTHFPSVK.Y
R4/RRR4-7/3	1660.123	1658.920	122.964	0.443	1349.135	0.392	32	0.138	K.VQKPVVAWVSGTCAR.L
R4/RRR4-6/2	992.455	993.055	-1617.792	0.340	319.245	0.325	12	0.121	-.FGGAIDDAAR.-
R4/RRR4-7/3	1636.860	1635.868	-5.013	0.442	636.908	0.497	25	0.111	R.SAAASSM*SALKQPTIR.V
R4/RRR4-7/3	1884.030	1884.210	-95.609	0.294	1204.770	0.308	27	0.105	R.AGKDLVSSLVSGLLTIGPR.F
R4/RRR4-7/3	1884.280	1884.210	37.056	0.361	1171.289	0.308	25	0.103	R.AGKDLVSSLVSGLLTIGPR.F
R4/RRR4-7/3	1310.764	1310.526	182.126	0.334	314.227	0.372	20	0.096	K.LYRPGSVGFVSK.S
R4/RRR4-7/3	1634.988	1635.868	-1153.347	0.396	587.445	0.382	24	0.093	R.SAAASSM*SALKQPTIR.V
R4/RRR4-7/3	1310.741	1310.526	164.615	0.430	719.317	0.340	24	0.092	K.LYRPGSVGFVSK.S
R4/RRR4-7/3	1426.492	1426.557	-46.067	0.425	977.001	0.284	26	0.089	R.APTHIISTISDDR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1636.202	1635.868	204.695	0.401	416.919	0.372	21	0.082	-.SAAASSM*SALKQPTIR.-
R4/RRR4-7/3	1426.528	1426.557	-20.446	0.369	890.289	0.195	26	0.077	R.APTHIISTISDDR.G
R4/RRR4-2/2	1634.156	1633.746	251.772	0.527	1949.685	0.547	21	0.297	R.TALTYIDADGNWHR.A
R4/RRR4-4/2	1633.347	1633.746	-245.167	0.493	1905.532	0.522	21	0.283	R.TALTYIDADGNWHR.A
R4/RRR4-1/2	1634.054	1633.746	189.223	0.505	1921.294	0.503	21	0.280	R.TALTYIDADGNWHR.A
R4/RRR4-4/2	1940.508	1940.229	144.449	0.566	1893.948	0.515	27	0.278	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/2	1559.531	1559.743	-136.653	0.457	1865.477	0.526	22	0.278	K.IDQSALTGESLPVTK.G
R4/RRR4-2/2	1559.247	1559.743	-319.400	0.413	1993.355	0.459	22	0.277	K.IDQSALTGESLPVTK.G
R4/RRR4-2/2	1990.294	1991.233	-977.478	0.479	2023.070	0.436	25	0.275	R.TENQDAIDAAMVGMLADPK.E
R4/RRR4-2/2	1560.396	1559.743	-223.595	0.463	1718.802	0.554	21	0.264	K.IDQSALTGESLPVTK.G
R4/RRR4-2/2	1633.069	1633.746	-1029.728	0.481	1727.408	0.527	21	0.260	R.TALTYIDADGNWHR.A
R4/RRR4-2/2	1407.448	1407.643	-139.153	0.543	1795.662	0.482	20	0.258	K.GVDKDHVLLLAAR.A
R4/RRR4-4/2	1492.128	1492.742	-1084.981	0.500	1717.386	0.494	19	0.249	K.LSVDKNLVEVFTK.G
R4/RRR4-2/2	1397.955	1398.451	-355.639	0.546	1462.874	0.591	21	0.246	K.NPGDEVFSGSTCK.Q
R4/RRR4-2/2	1633.265	1633.746	-295.480	0.477	1605.230	0.525	20	0.243	R.TALTYIDADGNWHR.A
R4/RRR4-3/2	1559.311	1559.743	-277.850	0.457	1671.655	0.482	21	0.240	K.IDQSALTGESLPVTK.G
R4/RRR4-1/2	1633.363	1633.746	-234.970	0.456	1634.111	0.494	20	0.239	R.TALTYIDADGNWHR.A
R4/RRR4-2/2	1559.344	1559.743	-256.880	0.439	1651.535	0.472	21	0.235	K.IDQSALTGESLPVTK.G
R4/RRR4-3/2	1559.074	1559.743	-1073.731	0.352	1723.497	0.433	21	0.233	K.IDQSALTGESLPVTK.G
R4/RRR4-2/2	1407.598	1407.643	-32.237	0.525	1555.204	0.498	19	0.232	K.GVDKDHVLLLAAR.A
R4/RRR4-1/2	1559.245	1559.743	-320.579	0.423	1628.819	0.469	21	0.231	K.IDQSALTGESLPVTK.G
R4/RRR4-3/2	1398.150	1398.451	-216.002	0.483	1371.548	0.548	21	0.225	K.NPGDEVFSGSTCK.Q
R4/RRR4-2/2	1492.264	1492.742	-321.430	0.514	1404.281	0.539	19	0.225	K.LSVDKNLVEVFTK.G
R4/RRR4-2/2	1407.199	1407.643	-317.021	0.511	1526.663	0.463	20	0.221	K.GVDKDHVLLLAAR.A
R4/RRR4-2/2	1491.911	1492.742	-1231.054	0.522	1446.148	0.506	19	0.221	K.LSVDKNLVEVFTK.G
R4/RRR4-4/2	1493.394	1492.742	-233.790	0.558	1328.658	0.551	19	0.220	K.LSVDKNLVEVFTK.G
R4/RRR4-1/2	1492.458	1492.742	-190.950	0.507	1427.563	0.499	19	0.218	K.LSVDKNLVEVFTK.G
R4/RRR4-2/2	1939.643	1940.229	-819.946	0.545	1462.866	0.491	24	0.217	R.WGEQEAAILVPGDIISIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1492.415	1492.742	-219.669	0.525	1388.933	0.508	19	0.216	K.LSVDKNLVEVFTK.G
R4/RRR4-4/2	1493.318	1492.742	-284.800	0.540	1362.330	0.515	20	0.216	K.LSVDKNLVEVFTK.G
R4/RRR4-2/2	1493.348	1492.742	-264.789	0.569	1303.106	0.532	19	0.213	K.LSVDKNLVEVFTK.G
R4/RRR4-1/2	1492.386	1492.742	-239.281	0.515	1367.343	0.498	19	0.212	K.LSVDKNLVEVFTK.G
R4/RRR4-2/2	1915.530	1915.182	182.456	0.559	1316.052	0.532	23	0.211	R.LGM*GTNM*YPSSALLGQNK.D
R4/RRR4-2/2	1430.801	1429.649	106.314	0.469	1321.486	0.513	18	0.211	R.KVHAVIDKYAER.G
R4/RRR4-4/2	1398.185	1398.451	-190.865	0.514	1221.005	0.543	21	0.210	K.NPGDEVFSGSTCK.Q
R4/RRR4-1/2	1940.602	1940.229	193.086	0.584	1371.365	0.492	24	0.207	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/2	1633.208	1633.746	-944.179	0.441	1355.355	0.490	19	0.207	R.TALTYIDADGNWHR.A
R4/RRR4-2/2	1940.237	1940.229	4.316	0.572	1400.448	0.468	25	0.205	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/2	1914.321	1915.182	-974.816	0.532	1331.909	0.488	24	0.204	R.LGM*GTNM*YPSSALLGQNK.D
R4/RRR4-1/2	1914.443	1915.182	-910.800	0.559	1276.063	0.515	22	0.202	R.LGM*GTNM*YPSSALLGQNK.D
R4/RRR4-4/2	1939.614	1940.229	-835.235	0.553	1347.105	0.466	25	0.201	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-3/3	1429.443	1429.649	-144.687	0.570	1707.674	0.448	27	0.200	R.KVHAVIDKYAER.G
R4/RRR4-3/2	1492.060	1492.742	-1130.737	0.436	1330.248	0.457	19	0.199	K.LSVDKNLVEVFTK.G
R4/RRR4-1/2	1163.975	1163.370	-340.164	0.488	1284.657	0.458	18	0.199	K.M*ITGDQLAIGK.E
R4/RRR4-2/2	1163.194	1163.370	-152.190	0.445	1467.704	0.374	18	0.197	K.M*ITGDQLAIGK.E
R4/RRR4-4/2	1559.215	1559.743	-982.938	0.410	1295.782	0.455	19	0.193	K.IDQSALTGESLPVTK.G
R4/RRR4-4/2	1940.740	1940.229	-252.452	0.610	1163.937	0.502	24	0.191	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/2	1939.686	1940.229	-797.709	0.524	1158.911	0.492	24	0.190	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/3	1407.506	1407.643	-97.750	0.555	1804.214	0.376	28	0.188	K.GVDKDHVLLLAAR.A
R4/RRR4-1/3	1408.732	1407.643	62.906	0.580	1614.551	0.449	27	0.187	K.GVDKDHVLLLAAR.A
R4/RRR4-2/2	1398.041	1398.451	-294.313	0.473	1046.087	0.499	20	0.187	K.NPGDEVFSGSTCK.Q
R4/RRR4-2/2	1914.272	1915.182	-1000.489	0.515	1135.161	0.488	22	0.186	R.LGM*GTNM*YPSSALLGQNK.D
R4/RRR4-3/2	1633.056	1633.746	-1037.834	0.443	1185.023	0.453	18	0.185	R.TALTYIDADGNWHR.A
R4/RRR4-3/3	1407.643	1407.643	-0.411	0.546	1663.880	0.416	27	0.183	K.GVDKDHVLLLAAR.A
R4/RRR4-1/3	1430.847	1429.649	138.432	0.596	1791.223	0.371	28	0.181	R.KVHAVIDKYAER.G
R4/RRR4-2/2	1914.438	1915.182	-913.233	0.533	1071.258	0.487	21	0.180	R.LGM*GTNM*YPSSALLGQNK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1505.519	1504.698	-119.028	0.425	1329.511	0.368	17	0.179	K.GAPEQILTLCNCK.E
R4/RRR4-1/3	1429.490	1429.649	-111.407	0.589	1609.217	0.434	28	0.179	R.KVHAVIDKYAER.G
R4/RRR4-3/2	1939.786	1940.229	-229.222	0.527	1178.227	0.418	22	0.175	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/2	1939.660	1940.229	-811.228	0.477	1012.535	0.454	21	0.171	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-4/2	1643.617	1642.829	-129.289	0.507	1206.018	0.352	23	0.171	K.DASLEALPVDELIEK.A
R4/RRR4-3/2	1939.800	1940.229	-221.583	0.545	1086.821	0.414	23	0.169	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/3	1408.216	1407.643	-304.586	0.522	1599.363	0.397	26	0.168	K.GVDKDHVLLLAAR.A
R4/RRR4-2/2	1163.066	1163.370	-262.530	0.470	1126.389	0.361	16	0.168	K.M*ITGDQLAIGK.E
R4/RRR4-2/2	1398.126	1398.451	-232.907	0.403	946.753	0.443	17	0.168	K.NPGDEVFSGSTCK.Q
R4/RRR4-2/2	1907.762	1908.145	-201.494	0.485	984.603	0.447	19	0.166	K.ADGFAGVFPEHKYEIVK.R
R4/RRR4-1/2	1642.334	1642.829	-302.496	0.394	1035.111	0.371	22	0.165	K.DASLEALPVDELIEK.A
R4/RRR4-2/2	1026.534	1027.156	-1584.956	0.448	711.510	0.453	15	0.165	K.LGDIVPADAR.L
R4/RRR4-4/2	1558.915	1559.743	-1176.492	0.332	1044.261	0.407	17	0.165	K.IDQSALTGESLPVTK.G
R4/RRR4-4/3	1407.616	1407.643	-19.329	0.542	1496.376	0.427	26	0.165	K.GVDKDHVLLLAAR.A
R4/RRR4-3/3	1429.887	1429.649	166.696	0.559	1494.021	0.432	26	0.164	R.KVHAVIDKYAER.G
R4/RRR4-3/2	1492.332	1492.742	-275.471	0.418	860.860	0.445	16	0.164	K.LSVDKNLVEVFTK.G
R4/RRR4-2/3	1429.691	1429.649	29.655	0.588	1584.512	0.398	27	0.163	R.KVHAVIDKYAER.G
R4/RRR4-4/3	1407.963	1407.643	227.338	0.556	1554.258	0.396	26	0.161	K.GVDKDHVLLLAAR.A
R4/RRR4-1/2	1642.076	1642.829	-1070.980	0.336	960.960	0.381	21	0.161	K.DASLEALPVDELIEK.A
R4/RRR4-3/2	1633.164	1633.746	-971.493	0.412	821.134	0.447	16	0.161	R.TALTYIDADGNWHR.A
R4/RRR4-3/2	1026.394	1027.156	-1722.354	0.438	735.868	0.413	15	0.161	K.LGDIVPADAR.L
R4/RRR4-3/2	1491.563	1492.742	-1465.451	0.367	881.268	0.399	17	0.159	K.LSVDKNLVEVFTK.G
R4/RRR4-1/3	1429.367	1429.649	-197.760	0.516	1507.717	0.411	26	0.159	R.KVHAVIDKYAER.G
R4/RRR4-2/2	1146.942	1147.371	-374.545	0.415	673.463	0.439	15	0.159	K.MITGDQLAIGK.E
R4/RRR4-4/2	1643.312	1642.829	294.700	0.471	933.634	0.367	21	0.159	K.DASLEALPVDELIEK.A
R4/RRR4-1/2	1162.990	1163.370	-328.029	0.500	883.675	0.373	16	0.159	K.M*ITGDQLAIGK.E
R4/RRR4-3/2	1026.387	1027.156	-1728.926	0.416	716.333	0.399	15	0.158	K.LGDIVPADAR.L
R4/RRR4-4/2	1026.943	1027.156	-208.715	0.409	643.944	0.405	15	0.157	K.LGDIVPADAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1643.657	1642.829	-105.226	0.497	856.642	0.386	20	0.157	K.DASLEALPVDELIEK.A
R4/RRR4-2/3	1407.201	1407.643	-315.464	0.536	1564.347	0.381	27	0.157	K.GVDKDHVLLLAAR.A
R4/RRR4-2/2	1940.837	1940.229	-202.476	0.519	834.640	0.435	19	0.157	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-1/2	1162.571	1163.370	-1552.333	0.415	982.573	0.321	16	0.156	K.M*ITGDQLAIGK.E
R4/RRR4-2/2	1146.909	1147.371	-403.380	0.288	767.300	0.405	16	0.154	K.MITGDQLAIGK.E
R4/RRR4-1/2	1026.406	1027.156	-1710.166	0.325	787.883	0.363	16	0.154	K.LGDIVPADAR.L
R4/RRR4-4/2	1162.883	1163.370	-419.659	0.485	1023.913	0.292	17	0.154	K.M*ITGDQLAIGK.E
R4/RRR4-2/2	1940.122	1940.229	-55.131	0.382	819.513	0.408	18	0.153	R.WGEQEAAILVPGDIISIK.L
R4/RRR4-3/2	1027.052	1027.156	-102.118	0.460	657.886	0.379	15	0.153	-.LGDIVPADAR.-
R4/RRR4-2/2	1027.753	1027.156	-393.441	0.539	646.912	0.391	15	0.153	-.LGDIVPADAR.-
R4/RRR4-1/2	1026.496	1027.156	-1622.348	0.379	585.271	0.392	14	0.151	-.LGDIVPADAR.-
R4/RRR4-3/2	1642.513	1642.829	-193.184	0.414	763.197	0.329	20	0.149	K.DASLEALPVDELIEK.A
R4/RRR4-4/2	1026.945	1027.156	-206.330	0.431	556.150	0.362	14	0.149	-.LGDIVPADAR.-
R4/RRR4-3/2	1642.145	1642.829	-1028.884	0.353	777.542	0.321	20	0.148	K.DASLEALPVDELIEK.A
R4/RRR4-1/2	1641.440	1642.829	-1459.864	0.281	780.465	0.325	19	0.147	K.DASLEALPVDELIEK.A
R4/RRR4-1/2	1027.065	1027.156	-89.003	0.369	539.450	0.400	13	0.147	-.LGDIVPADAR.-
R4/RRR4-4/2	1641.483	1642.829	-1433.347	0.304	650.485	0.354	18	0.146	K.DASLEALPVDELIEK.A
R4/RRR4-2/2	1642.231	1642.829	-976.119	0.352	720.424	0.295	19	0.144	K.DASLEALPVDELIEK.A
R4/RRR4-2/2	1276.415	1275.394	16.632	0.306	747.405	0.351	14	0.144	K.ADGFAGVFPEHK.Y
R4/RRR4-3/2	1642.397	1642.829	-264.018	0.382	582.614	0.331	17	0.144	K.DASLEALPVDELIEK.A
R4/RRR4-2/2	1026.951	1027.156	-200.964	0.411	568.333	0.375	14	0.144	-.LGDIVPADAR.-
R4/RRR4-2/2	1642.202	1642.829	-993.657	0.325	677.144	0.295	18	0.143	K.DASLEALPVDELIEK.A
R4/RRR4-4/3	1406.999	1407.643	-1172.217	0.533	1473.346	0.366	26	0.142	K.GVDKDHVLLLAAR.A
R4/RRR4-3/2	1162.997	1163.370	-321.921	0.466	763.452	0.269	15	0.142	K.M*ITGDQLAIGK.E
R4/RRR4-4/2	1026.852	1027.156	-297.206	0.437	506.554	0.423	13	0.140	-.LGDIVPADAR.-
R4/RRR4-2/3	1429.787	1429.649	96.446	0.572	1496.962	0.350	27	0.137	R.KVHAVIDKYAER.G
R4/RRR4-1/2	1275.595	1275.394	157.643	0.347	618.706	0.288	13	0.137	K.ADGFAGVFPEHK.Y
R4/RRR4-13/2	1941.195	1940.229	-17.762	0.369	348.492	0.368	13	0.137	-.WGEQEAAILVPGDIISIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1642.058	1642.829	-1082.102	0.247	586.338	0.216	15	0.135	K.DASLEALPVDELIEK.A
R4/RRR4-2/3	1407.850	1407.643	147.520	0.540	1425.521	0.336	26	0.128	K.GVDKDHVLLLAAR.A
R4/RRR4-1/3	1839.396	1840.094	-926.091	0.440	1062.754	0.446	30	0.127	K.KHIVGM*TGDGVNDAPALK.K
R4/RRR4-2/3	1429.797	1429.649	103.639	0.551	1370.231	0.344	26	0.124	R.KVHAVIDKYAER.G
R4/RRR4-2/3	1839.529	1840.094	-853.442	0.466	1033.984	0.438	31	0.123	K.KHIVGM*TGDGVNDAPALK.K
R4/RRR4-2/3	1839.546	1840.094	-844.449	0.452	1317.512	0.332	33	0.120	K.KHIVGM*TGDGVNDAPALK.K
R4/RRR4-2/3	1407.359	1407.643	-202.549	0.499	1191.953	0.365	23	0.117	-.GVDKDHVLLLAAR.-
R4/RRR4-3/3	1633.675	1633.746	-43.260	0.386	567.988	0.517	25	0.114	R.TALTYIDADGNWHR.A
R4/RRR4-3/3	1493.125	1492.742	257.217	0.457	996.294	0.408	25	0.114	K.LSVDKNLVEVFTK.G
R4/RRR4-1/3	1493.872	1492.742	87.146	0.493	984.040	0.409	26	0.114	K.LSVDKNLVEVFTK.G
R4/RRR4-1/3	1492.818	1492.742	51.202	0.457	810.754	0.440	23	0.112	K.LSVDKNLVEVFTK.G
R4/RRR4-4/3	1632.864	1633.746	-1155.799	0.351	491.783	0.479	23	0.107	R.TALTYIDADGNWHR.A
R4/RRR4-2/3	1840.562	1840.094	254.650	0.503	1068.558	0.358	30	0.107	K.KHIVGM*TGDGVNDAPALK.K
R4/RRR4-4/3	1633.312	1633.746	-266.244	0.339	455.923	0.480	23	0.107	R.TALTYIDADGNWHR.A
R4/RRR4-4/3	1633.949	1633.746	124.559	0.355	582.415	0.455	26	0.105	R.TALTYIDADGNWHR.A
R4/RRR4-3/3	1633.652	1633.746	-57.650	0.334	376.447	0.441	22	0.103	R.TALTYIDADGNWHR.A
R4/RRR4-4/3	1492.575	1492.742	-111.949	0.374	760.448	0.394	23	0.102	K.LSVDKNLVEVFTK.G
R4/RRR4-2/3	1492.250	1492.742	-330.550	0.464	845.602	0.371	23	0.102	K.LSVDKNLVEVFTK.G
R4/RRR4-1/3	1493.069	1492.742	219.710	0.448	741.745	0.387	23	0.101	K.LSVDKNLVEVFTK.G
R4/RRR4-3/3	1492.435	1492.742	-206.098	0.399	867.372	0.363	24	0.101	K.LSVDKNLVEVFTK.G
R4/RRR4-3/3	1633.561	1633.746	-113.529	0.309	444.278	0.418	23	0.100	R.TALTYIDADGNWHR.A
R4/RRR4-3/3	1492.719	1492.742	-15.479	0.451	757.902	0.374	22	0.100	K.LSVDKNLVEVFTK.G
R4/RRR4-2/3	1492.886	1492.742	96.963	0.430	944.120	0.329	25	0.098	K.LSVDKNLVEVFTK.G
R4/RRR4-2/3	1633.899	1633.746	94.214	0.335	423.981	0.339	21	0.097	R.TALTYIDADGNWHR.A
R4/RRR4-3/3	1429.571	1429.649	-55.003	0.530	737.902	0.359	21	0.097	R.KVHAVIDKYAER.G
R4/RRR4-2/3	1634.117	1633.746	227.831	0.316	361.362	0.360	21	0.096	-.TALTYIDADGNWHR.-
R4/RRR4-2/3	1492.621	1492.742	-81.185	0.372	694.602	0.344	22	0.095	K.LSVDKNLVEVFTK.G
R4/RRR4-2/3	1633.174	1633.746	-965.423	0.331	348.033	0.486	20	0.095	-.TALTYIDADGNWHR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1844.365	1844.098	145.142	0.544	2478.166	0.517	25	0.381	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/2	1431.139	1431.767	-1140.457	0.602	2225.286	0.610	20	0.365	R.IVSQLLTLMDGLK.Q
R4/RRR4-4/2	1432.254	1431.767	341.205	0.565	2248.842	0.568	21	0.356	R.IVSQLLTLMDGLK.Q
R4/RRR4-4/2	1846.217	1846.969	-951.896	0.514	2103.248	0.565	23	0.328	K.YTQGFSGADITEICQR.A
R4/RRR4-4/2	1447.215	1447.766	-1074.730	0.489	2049.433	0.480	21	0.294	R.IVSQLLTLM*DGLK.Q
R4/RRR4-4/2	1846.492	1846.969	-259.303	0.527	1840.385	0.561	22	0.284	K.YTQGFSGADITEICQR.A
R4/RRR4-4/2	1431.192	1431.767	-1103.287	0.470	1900.131	0.521	20	0.282	R.IVSQLLTLMDGLK.Q
R4/RRR4-4/2	1843.189	1844.098	-1038.552	0.450	2196.874	0.365	23	0.281	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/2	1843.564	1844.098	-834.586	0.487	2087.270	0.415	24	0.279	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/2	1846.353	1846.969	-877.953	0.512	1717.508	0.549	22	0.263	K.YTQGFSGADITEICQR.A
R4/RRR4-4/2	1328.748	1329.521	-1338.913	0.417	1852.260	0.424	19	0.250	K.LAEDVDLELIAK.D
R4/RRR4-4/2	1329.184	1329.521	-254.383	0.508	1855.833	0.417	19	0.250	K.LAEDVDLELIAK.D
R4/RRR4-4/2	1447.403	1447.766	-251.187	0.462	1656.260	0.508	19	0.245	R.IVSQLLTLM*DGLK.Q
R4/RRR4-4/2	1431.390	1431.767	-264.019	0.467	1521.086	0.561	19	0.242	R.IVSQLLTLMDGLK.Q
R4/RRR4-4/2	1843.857	1844.098	-131.252	0.493	1762.886	0.409	24	0.233	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/2	1843.520	1844.098	-858.249	0.502	1609.006	0.422	22	0.216	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/2	1843.534	1844.098	-850.671	0.497	1486.566	0.437	23	0.208	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/2	1565.387	1565.746	-230.547	0.496	1381.508	0.483	18	0.207	K.AIANECQANFISVK.G
R4/RRR4-3/2	1847.394	1846.969	230.531	0.523	1172.828	0.580	18	0.205	K.YTQGFSGADITEICQR.A
R4/RRR4-4/2	1564.760	1565.746	-1273.192	0.427	1421.728	0.448	19	0.204	K.AIANECQANFISVK.G
R4/RRR4-4/2	1158.979	1159.360	-329.350	0.444	1368.157	0.456	19	0.204	K.GILLYGPPGSGK.T
R4/RRR4-4/2	1952.553	1953.165	-827.829	0.520	1237.440	0.518	21	0.200	K.GPELLTM*WFGESEANVR.E
R4/RRR4-4/2	1953.353	1953.165	96.666	0.559	1191.959	0.494	21	0.191	K.GPELLTM*WFGESEANVR.E
R4/RRR4-4/2	1565.348	1565.746	-255.426	0.506	1188.315	0.489	17	0.190	K.AIANECQANFISVK.G
R4/RRR4-4/2	1252.080	1252.437	-285.792	0.415	1143.096	0.485	18	0.189	K.GVLFYGPPGCGK.T
R4/RRR4-1/2	1188.139	1188.316	-149.175	0.473	1490.157	0.323	19	0.188	K.TALGTSNPSALR.E
R4/RRR4-3/2	1188.010	1188.316	-258.744	0.404	1387.562	0.339	19	0.183	K.TALGTSNPSALR.E
R4/RRR4-3/2	1447.354	1447.766	-285.371	0.399	1219.425	0.429	17	0.183	R.IVSQLLTLM*DGLK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1952.535	1953.165	-837.431	0.494	998.690	0.513	20	0.180	K.GPELLTM*WFGESEANVR.E
R4/RRR4-1/2	1188.113	1188.316	-171.746	0.508	1198.638	0.375	19	0.176	K.TALGTSNPSALR.E
R4/RRR4-3/2	1188.106	1188.316	-177.415	0.438	1013.255	0.429	19	0.174	K.TALGTSNPSALR.E
R4/RRR4-2/2	1188.100	1188.316	-182.363	0.443	1166.333	0.360	18	0.171	K.TALGTSNPSALR.E
R4/RRR4-4/2	1447.214	1447.766	-1075.577	0.484	1073.395	0.411	17	0.171	R.IVSQLLTLM*DGLK.Q
R4/RRR4-1/2	1187.851	1188.316	-392.465	0.479	1141.922	0.368	18	0.170	K.TALGTSNPSALR.E
R4/RRR4-4/2	1801.152	1801.033	66.372	0.508	828.023	0.462	20	0.167	R.LDQLIYIPLPDEQSR.L
R4/RRR4-4/2	1801.372	1801.033	188.503	0.526	841.593	0.455	20	0.166	R.LDQLIYIPLPDEQSR.L
R4/RRR4-4/2	1800.614	1801.033	-233.680	0.441	797.633	0.457	20	0.164	R.LDQLIYIPLPDEQSR.L
R4/RRR4-4/2	1584.092	1584.750	-1049.508	0.389	917.782	0.430	18	0.163	R.LGDVVSVHQCQDVK.Y
R4/RRR4-3/2	1187.788	1188.316	-1290.308	0.452	752.465	0.433	17	0.162	K.TALGTSNPSALR.E
R4/RRR4-4/2	1299.131	1299.412	-217.292	0.378	549.271	0.490	16	0.158	R.EIDIGVPDEVGR.L
R4/RRR4-4/2	958.867	959.079	-221.490	0.407	898.128	0.342	15	0.157	K.DVDLNALAK.Y
R4/RRR4-4/2	1299.070	1299.412	-263.861	0.365	482.340	0.535	15	0.156	-.EIDIGVPDEVGR.-
R4/RRR4-4/2	968.863	969.160	-307.539	0.320	814.377	0.380	12	0.155	R.ELVELPLR.H
R4/RRR4-2/2	1188.107	1188.316	-176.694	0.421	906.517	0.350	16	0.155	K.TALGTSNPSALR.E
R4/RRR4-4/2	968.936	969.160	-231.698	0.317	841.942	0.349	13	0.154	R.ELVELPLR.H
R4/RRR4-4/2	968.576	969.160	-1640.738	0.320	789.900	0.363	12	0.153	R.ELVELPLR.H
R4/RRR4-4/2	1075.732	1076.143	-382.608	0.412	759.156	0.350	15	0.152	K.LAGESESNLR.K
R4/RRR4-4/2	1075.488	1076.143	-1542.752	0.339	740.884	0.368	14	0.150	K.LAGESESNLR.K
R4/RRR4-4/2	958.446	959.079	-1708.793	0.337	773.167	0.320	14	0.149	K.DVDLNALAK.Y
R4/RRR4-4/2	958.449	959.079	-1705.466	0.321	834.255	0.309	14	0.149	K.DVDLNALAK.Y
R4/RRR4-2/2	1187.299	1188.316	-1703.946	0.371	508.731	0.352	15	0.147	K.TALGTSNPSALR.E
R4/RRR4-2/2	1253.463	1252.437	20.844	0.264	659.220	0.432	15	0.147	K.GVLFYGPPGCGK.T
R4/RRR4-3/2	969.011	969.160	-154.100	0.313	904.999	0.237	13	0.145	R.ELVELPLR.H
R4/RRR4-4/2	1584.342	1584.750	-258.005	0.358	497.736	0.328	17	0.142	R.LGDVVSVHQCQDVK.Y
R4/RRR4-4/2	1299.042	1299.412	-285.922	0.273	370.881	0.386	13	0.141	R.EIDIGVPDEVGR.L
R4/RRR4-3/2	1800.882	1801.033	-84.073	0.344	526.138	0.330	16	0.141	R.LDQLIYIPLPDEQSR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1800.414	1801.033	-901.783	0.332	367.167	0.320	13	0.137	R.LDQLIYIPLPDEQSR.L
R4/RRR4-3/2	968.906	969.160	-262.539	0.258	594.839	0.164	11	0.137	-.ELVELPLR.-
R4/RRR4-3/2	958.758	959.079	-335.171	0.260	784.134	0.169	13	0.136	K.DVDLNALAK.Y
R4/RRR4-4/3	1649.875	1649.830	27.515	0.501	1169.614	0.387	24	0.122	K.YAIRENIEKDIER.E
R4/RRR4-3/2	968.793	969.160	-379.977	0.224	504.328	0.183	9	0.119	-.ELVELPLR.-
R4/RRR4-4/3	1843.625	1844.098	-257.157	0.396	1008.179	0.313	28	0.095	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/3	1584.811	1584.750	38.688	0.345	998.851	0.283	23	0.088	R.LGDVVSVHQCQDVK.Y
R4/RRR4-4/3	1584.294	1584.750	-288.663	0.375	644.081	0.300	21	0.081	-.LGDVVSVHQCQDVK.-
R4/RRR4-4/3	1843.455	1844.098	-894.019	0.338	806.005	0.253	27	0.081	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-4/3	1844.122	1844.098	13.198	0.316	790.391	0.130	26	0.073	K.NAPSIIFIDEIDSIAPK.R
R4/RRR4-2/2	1938.760	1939.113	-182.548	0.593	3093.945	0.568	25	0.543	K.TGSEATQEAALDSLYLLR.Q
R4/RRR4-2/2	1885.492	1886.184	-900.119	0.540	2784.329	0.586	26	0.476	R.LLAALALGDLFQNEGLAR.S
R4/RRR4-2/2	1938.557	1939.113	-805.248	0.543	2746.398	0.545	25	0.449	K.TGSEATQEAALDSLYLLR.Q
R4/RRR4-2/2	1886.515	1886.184	175.517	0.584	2686.287	0.566	26	0.444	R.LLAALALGDLFQNEGLAR.S
R4/RRR4-1/2	1939.033	1939.113	-41.208	0.578	2667.776	0.513	24	0.417	K.TGSEATQEAALDSLYLLR.Q
R4/RRR4-2/2	1937.364	1939.113	-1941.023	0.346	2196.948	0.412	23	0.294	K.TGSEATQEAALDSLYLLR.Q
R4/RRR4-2/3	1859.303	1858.169	72.158	0.523	1917.464	0.479	31	0.265	K.VSLKNESLVDGLLTGALK.N
R4/RRR4-2/2	1216.038	1216.414	-310.372	0.472	1600.607	0.439	16	0.223	K.ALNALLSNFPR.L
R4/RRR4-2/2	1154.468	1155.372	-1654.196	0.423	1488.684	0.487	16	0.222	R.LIEALLNNVR.I
R4/RRR4-2/3	1858.300	1858.169	70.649	0.454	1941.211	0.365	31	0.219	K.VSLKNESLVDGLLTGALK.N
R4/RRR4-2/2	1568.873	1567.857	10.566	0.558	1125.297	0.560	21	0.203	K.ALANLALAWPNTIAK.E
R4/RRR4-2/2	1787.569	1786.087	270.781	0.523	1073.349	0.575	21	0.200	R.QAIQPLVEILSTGMER.E
R4/RRR4-2/2	1802.506	1802.086	233.692	0.472	1075.332	0.547	20	0.193	R.QAIQPLVEILSTGM*ER.E
R4/RRR4-2/2	1216.329	1216.414	-70.826	0.418	1341.105	0.374	16	0.184	K.ALNALLSNFPR.L
R4/RRR4-2/2	1802.909	1802.086	-98.646	0.476	894.721	0.577	18	0.183	R.QAIQPLVEILSTGM*ER.E
R4/RRR4-1/2	1888.030	1886.184	-81.944	0.496	1021.431	0.523	21	0.183	R.LLAALALGDLFQNEGLAR.S
R4/RRR4-1/2	1154.989	1155.372	-333.244	0.502	1183.904	0.385	15	0.176	R.LIEALLNNVR.I
R4/RRR4-2/2	1567.320	1567.857	-983.637	0.357	960.489	0.512	19	0.175	K.ALANLALAWPNTIAK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1231.215	1231.509	-239.620	0.427	778.030	0.507	17	0.172	K.VVQPLFSLLSK.A
R4/RRR4-2/2	1904.907	1903.210	-159.761	0.604	786.484	0.526	20	0.172	K.IFSTENVVPVLWEQLK.V
R4/RRR4-2/2	1219.862	1219.443	344.205	0.371	1004.137	0.441	18	0.171	K.VGGCALLVCAAK.E
R4/RRR4-2/2	959.927	960.112	-193.058	0.486	1089.422	0.374	13	0.171	K.APFLVQER.V
R4/RRR4-1/2	1787.276	1786.087	106.414	0.460	742.016	0.537	19	0.170	R.QAIQPLVEILSTGMER.E
R4/RRR4-2/2	1216.174	1216.414	-198.288	0.365	973.450	0.440	16	0.169	K.ALNALLSNFPR.L
R4/RRR4-2/2	1219.670	1219.443	186.655	0.421	929.528	0.422	19	0.167	K.VGGCALLVCAAK.E
R4/RRR4-2/2	1902.434	1903.210	-936.639	0.448	730.531	0.506	19	0.165	K.IFSTENVVPVLWEQLK.V
R4/RRR4-2/2	1902.492	1903.210	-905.977	0.479	690.238	0.507	19	0.164	K.IFSTENVVPVLWEQLK.V
R4/RRR4-1/2	1903.037	1903.210	-91.398	0.463	820.013	0.461	20	0.164	K.IFSTENVVPVLWEQLK.V
R4/RRR4-2/2	1154.641	1155.372	-1504.010	0.386	828.304	0.428	14	0.162	R.LIEALLNNVR.I
R4/RRR4-2/2	960.079	960.112	-33.873	0.465	1103.551	0.311	13	0.161	K.APFLVQER.V
R4/RRR4-1/2	1567.945	1567.857	56.409	0.378	676.628	0.518	17	0.161	K.ALANLALAWPNTIAK.E
R4/RRR4-2/2	960.051	960.112	-63.206	0.448	1209.792	0.271	13	0.161	K.APFLVQER.V
R4/RRR4-1/2	959.983	960.112	-134.888	0.394	1182.692	0.273	13	0.160	K.APFLVQER.V
R4/RRR4-2/2	1174.091	1174.291	-170.669	0.439	830.992	0.394	16	0.160	K.NYTLHEAVAR.A
R4/RRR4-1/2	1232.102	1231.509	-330.870	0.322	491.724	0.559	15	0.159	K.VVQPLFSLLSK.A
R4/RRR4-1/2	1154.926	1155.372	-387.328	0.390	808.838	0.406	14	0.159	R.LIEALLNNVR.I
R4/RRR4-1/2	959.889	960.112	-232.734	0.440	1053.710	0.303	13	0.158	K.APFLVQER.V
R4/RRR4-2/2	1801.122	1802.086	-1093.669	0.340	736.432	0.483	17	0.157	R.QAIQPLVEILSTGM*ER.E
R4/RRR4-1/2	1155.216	1155.372	-135.727	0.342	1035.419	0.316	14	0.156	R.LIEALLNNVR.I
R4/RRR4-2/2	1232.987	1233.399	-334.406	0.429	646.194	0.394	17	0.156	K.LLGPGNETYIR.A
R4/RRR4-2/3	1706.987	1705.983	2.387	0.458	1452.945	0.405	29	0.156	R.SNAALHSIPVLSNLLR.S
R4/RRR4-2/2	1857.212	1858.169	-1057.146	0.403	610.784	0.492	18	0.153	K.VSLKNESLVDGLLTGALK.N
R4/RRR4-1/2	1233.267	1233.399	-106.983	0.414	679.686	0.346	16	0.150	K.LLGPGNETYIR.A
R4/RRR4-2/2	1232.416	1233.399	-1613.551	0.272	811.090	0.354	18	0.150	K.LLGPGNETYIR.A
R4/RRR4-2/2	982.868	982.119	-256.318	0.372	734.859	0.339	12	0.148	K.LTLGNNPPR.L
R4/RRR4-2/2	1706.221	1705.983	140.101	0.430	556.886	0.460	16	0.148	R.SNAALHSIPVLSNLLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/3	1706.407	1705.983	249.534	0.442	1386.408	0.408	30	0.148	R.SNAALHSIPVLSNLLR.S
R4/RRR4-1/2	1730.174	1728.924	144.884	0.359	695.316	0.428	16	0.146	R.YFAAQALASLVCNGSR.G
R4/RRR4-2/2	982.240	982.119	123.452	0.359	725.240	0.329	12	0.146	-.LTLGNNPPR.-
R4/RRR4-1/2	1231.069	1231.509	-358.299	0.271	454.697	0.438	14	0.146	K.VVQPLFSLLSK.A
R4/RRR4-2/2	982.401	982.119	287.570	0.289	525.082	0.371	11	0.144	K.LTLGNNPPR.L
R4/RRR4-2/2	920.888	921.115	-247.244	0.343	776.949	0.300	13	0.144	-.VYVLDALK.-
R4/RRR4-2/2	1567.093	1567.857	-1128.631	0.305	638.376	0.391	15	0.143	K.ALANLALAWPNTIAK.E
R4/RRR4-2/2	1232.413	1233.399	-1616.337	0.335	594.355	0.241	17	0.142	K.LLGPGNETYIR.A
R4/RRR4-1/2	1857.001	1858.169	-1171.197	0.364	283.336	0.416	13	0.137	K.VSLKNESLVDGLLTGALK.N
R4/RRR4-2/2	920.904	921.115	-230.355	0.290	572.586	0.331	12	0.135	-.VYVLDALK.-
R4/RRR4-2/3	1857.748	1858.169	-227.390	0.375	1313.284	0.289	26	0.111	K.VSLKNESLVDGLLTGALK.N
R4/RRR4-1/3	1705.770	1705.983	-124.945	0.440	977.180	0.350	28	0.101	R.SNAALHSIPVLSNLLR.S
R4/RRR4-2/3	1807.287	1806.059	126.264	0.420	821.475	0.402	25	0.099	R.HNEAALGTVNQLVAVLR.L
R4/RRR4-2/3	1938.613	1939.113	-258.609	0.315	907.979	0.342	24	0.090	K.TGSEATQEAALDSLYLLR.Q
R4/RRR4-2/3	1705.659	1705.983	-190.527	0.356	880.801	0.240	24	0.081	-.SNAALHSIPVLSNLLR.-
R4/RRR4-1/2	1646.551	1646.909	-218.290	0.543	2169.445	0.519	24	0.327	R.LDQPIILTGYSALNK.L
R4/RRR4-1/2	1647.376	1646.909	284.163	0.585	1947.159	0.513	24	0.289	R.LDQPIILTGYSALNK.L
R4/RRR4-1/2	1646.095	1646.909	-1105.555	0.508	1856.768	0.552	23	0.286	R.LDQPIILTGYSALNK.L
R4/RRR4-1/2	1281.149	1281.483	-261.723	0.493	1833.423	0.494	18	0.266	K.IIEEGPVTVAPR.E
R4/RRR4-1/2	1281.195	1281.483	-225.972	0.448	1745.869	0.476	18	0.249	K.IIEEGPVTVAPR.E
R4/RRR4-1/2	1744.481	1744.874	-225.969	0.474	1796.702	0.442	20	0.245	R.EDAFFEAVTNLACEK.K
R4/RRR4-1/2	1391.816	1390.610	148.614	0.466	1429.089	0.565	18	0.233	R.EIIVVANDITFR.A
R4/RRR4-1/2	1280.525	1281.483	-1533.520	0.366	1668.992	0.439	18	0.229	K.IIEEGPVTVAPR.E
R4/RRR4-1/2	1149.913	1149.282	-321.831	0.550	1632.057	0.403	17	0.221	K.TAQALLDFNR.E
R4/RRR4-1/3	1803.186	1803.135	28.062	0.592	1811.607	0.433	31	0.219	R.HVEPPLSALLELDKLK.V
R4/RRR4-1/2	1430.525	1429.691	-116.367	0.516	1505.404	0.454	18	0.217	R.EGLPLFILANWR.-
R4/RRR4-1/2	1205.104	1205.216	-93.431	0.442	1734.354	0.316	18	0.211	R.VGWSDDGSPER.G
R4/RRR4-1/3	1803.288	1803.135	84.889	0.533	1787.316	0.412	32	0.206	R.HVEPPLSALLELDKLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1255.934	1256.347	-329.954	0.479	1254.955	0.509	19	0.205	K.DNVTDLHASGVK.T
R4/RRR4-1/2	1181.180	1181.357	-150.676	0.355	1330.089	0.455	18	0.197	K.VVEFCTALGGK.T
R4/RRR4-1/2	1429.725	1429.691	23.840	0.452	1239.808	0.488	16	0.196	R.EGLPLFILANWR.-
R4/RRR4-1/2	1205.001	1205.216	-178.585	0.403	1468.368	0.350	17	0.191	R.VGWSDDGSPER.G
R4/RRR4-1/2	1905.281	1905.095	98.024	0.545	965.022	0.577	22	0.191	K.TVTANTATVSDYVGYLTK.G
R4/RRR4-1/2	1904.752	1905.095	-180.665	0.482	818.036	0.602	20	0.182	K.TVTANTATVSDYVGYLTK.G
R4/RRR4-1/2	1021.031	1021.195	-160.699	0.436	1024.760	0.475	17	0.182	R.TVGIGAYLAR.L
R4/RRR4-1/2	1204.296	1205.216	-1598.665	0.357	1491.326	0.265	17	0.177	R.VGWSDDGSPER.G
R4/RRR4-1/2	993.944	994.123	-180.476	0.482	920.859	0.460	15	0.175	K.ATELVFADK.H
R4/RRR4-2/3	1802.894	1803.135	-134.411	0.523	1571.229	0.413	30	0.174	R.HVEPPLSALLELDKLK.V
R4/RRR4-2/2	1905.644	1905.095	-237.569	0.449	408.639	0.571	20	0.162	K.TVTANTATVSDYVGYLTK.G
R4/RRR4-1/3	1487.839	1487.772	45.325	0.464	1614.166	0.356	27	0.161	K.KLPLIYLAANSGAR.I
R4/RRR4-1/2	1905.497	1905.095	211.743	0.482	652.801	0.505	19	0.160	K.TVTANTATVSDYVGYLTK.G
R4/RRR4-1/2	993.607	994.123	-1530.212	0.363	831.618	0.357	15	0.155	K.ATELVFADK.H
R4/RRR4-1/2	1073.268	1073.179	82.979	0.338	1065.773	0.296	15	0.154	R.LDLDDPSAVK.R
R4/RRR4-1/2	1712.047	1710.935	65.535	0.444	779.152	0.419	16	0.152	K.FDSGIINDFPANMLR.V
R4/RRR4-1/2	1308.132	1307.436	-233.206	0.403	732.439	0.408	15	0.152	R.AGQVWFPDSATK.T
R4/RRR4-1/2	1726.811	1726.935	-72.026	0.446	605.922	0.445	16	0.151	K.FDSGIINDFPANM*LR.V
R4/RRR4-2/2	1905.457	1905.095	190.318	0.263	202.074	0.488	17	0.144	K.TVTANTATVSDYVGYLTK.G
R4/RRR4-1/2	1180.448	1181.357	-1621.939	0.233	621.451	0.383	13	0.140	-.VVEFCTALGGK.-
R4/RRR4-2/2	1428.783	1429.691	-1339.261	0.261	642.252	0.312	13	0.139	R.EGLPLFILANWR.-
R4/RRR4-2/2	1428.781	1429.691	-1340.548	0.268	329.644	0.349	11	0.138	R.EGLPLFILANWR.-
R4/RRR4-1/2	1073.287	1073.179	101.572	0.325	672.097	0.241	13	0.138	R.LDLDDPSAVK.R
R4/RRR4-1/3	1488.061	1487.772	194.901	0.460	1231.820	0.298	24	0.105	K.KLPLIYLAANSGAR.I
R4/RRR4-5/3	1562.222	1561.804	268.215	0.392	1153.568	0.198	24	0.082	-.HVEPPLSALLELDK.-
R4/RRR4-5/3	1563.091	1561.804	184.253	0.340	855.123	0.102	23	0.064	-.HVEPPLSALLELDK.-
R4/RRR4-9/2	1667.474	1666.881	-244.775	0.595	3178.463	0.494	27	0.530	R.GLLYLGMGVSGGEEGAR.N
R4/RRR4-9/2	1997.808	1997.392	209.007	0.597	2984.573	0.560	28	0.510	R.IGLAGLAVMGQNLALNIAEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1683.432	1682.880	-267.256	0.604	3049.418	0.517	26	0.507	R.GLLYLGM*GVSGGEEGAR.N
R4/RRR4-9/2	1996.616	1997.392	-891.905	0.562	2925.266	0.571	28	0.501	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-8/2	1667.585	1666.881	-177.651	0.615	2996.664	0.522	26	0.495	R.GLLYLGMGVSGGEEGAR.N
R4/RRR4-9/2	1682.226	1682.880	-986.247	0.539	3068.001	0.454	26	0.487	R.GLLYLGM*GVSGGEEGAR.N
R4/RRR4-8/2	1997.661	1997.392	134.984	0.598	2715.305	0.568	28	0.449	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-9/2	1665.752	1666.881	-1281.556	0.437	3042.580	0.357	27	0.444	R.GLLYLGMGVSGGEEGAR.N
R4/RRR4-8/2	1682.469	1682.880	-244.850	0.551	2917.817	0.438	26	0.443	R.GLLYLGM*GVSGGEEGAR.N
R4/RRR4-8/2	1997.466	1997.392	37.414	0.584	2681.855	0.566	28	0.441	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-9/2	1682.298	1682.880	-943.411	0.574	2835.828	0.466	26	0.435	R.GLLYLGM*GVSGGEEGAR.N
R4/RRR4-9/2	1681.554	1682.880	-1387.396	0.454	2897.391	0.411	26	0.431	R.GLLYLGM*GVSGGEEGAR.N
R4/RRR4-9/2	1996.289	1997.392	-1056.421	0.582	2553.438	0.606	27	0.428	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-8/2	1666.414	1666.881	-280.785	0.521	2772.726	0.459	25	0.420	R.GLLYLGMGVSGGEEGAR.N
R4/RRR4-9/2	1666.357	1666.881	-916.946	0.523	2800.214	0.427	26	0.414	R.GLLYLGMGVSGGEEGAR.N
R4/RRR4-8/2	1996.791	1997.392	-803.960	0.558	2486.698	0.557	27	0.395	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-8/2	1682.478	1682.880	-239.755	0.515	2666.989	0.441	26	0.391	R.GLLYLGM*GVSGGEEGAR.N
R4/RRR4-8/2	1667.879	1666.881	-1.293	0.488	2355.886	0.397	25	0.317	R.GLLYLGMGVSGGEEGAR.N
R4/RRR4-9/2	1216.146	1216.371	-185.607	0.563	1845.444	0.436	18	0.253	K.GWSLNLGELAR.I
R4/RRR4-8/3	1996.821	1997.392	-789.178	0.481	1797.884	0.445	36	0.224	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-8/2	1110.159	1110.292	-119.619	0.507	1401.935	0.494	17	0.218	R.LPANLVQAQR.D
R4/RRR4-9/2	1109.860	1110.292	-389.817	0.484	1305.542	0.535	17	0.217	R.LPANLVQAQR.D
R4/RRR4-9/2	1215.697	1216.371	-1381.139	0.503	1654.605	0.378	18	0.216	K.GWSLNLGELAR.I
R4/RRR4-9/2	1563.189	1563.780	-1020.855	0.483	1415.806	0.432	21	0.203	R.FLSGLKDERVEAAK.V
R4/RRR4-9/2	1554.181	1553.697	312.310	0.481	1306.359	0.450	21	0.197	K.VFQGDFSSNLPVDK.A
R4/RRR4-8/2	1110.095	1110.292	-177.420	0.470	1073.676	0.498	15	0.189	R.LPANLVQAQR.D
R4/RRR4-9/2	1762.321	1762.978	-943.160	0.484	903.578	0.549	24	0.185	K.VAAQVPDSGPCVTYIGK.G
R4/RRR4-9/2	1414.006	1414.646	-1163.298	0.467	1234.791	0.404	18	0.183	K.ICSYAQGM*NIIK.A
R4/RRR4-9/2	1554.306	1553.697	-252.514	0.523	1101.867	0.460	20	0.182	K.VFQGDFSSNLPVDK.A
R4/RRR4-8/3	1998.263	1997.392	-64.655	0.385	1668.849	0.387	35	0.181	R.IGLAGLAVMGQNLALNIAEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1110.327	1110.292	32.132	0.505	1115.162	0.428	16	0.181	R.LPANLVQAQR.D
R4/RRR4-8/2	1763.268	1762.978	164.524	0.497	846.020	0.539	24	0.180	K.VAAQVPDSGPCVTYIGK.G
R4/RRR4-9/2	1415.080	1414.646	307.605	0.529	1068.236	0.451	17	0.179	K.ICSYAQGM*NIIK.A
R4/RRR4-8/2	1762.433	1762.978	-879.743	0.480	863.533	0.511	24	0.176	K.VAAQVPDSGPCVTYIGK.G
R4/RRR4-9/2	1413.922	1414.646	-1223.030	0.470	1114.112	0.417	17	0.176	K.ICSYAQGM*NIIK.A
R4/RRR4-8/2	1762.414	1762.978	-890.034	0.444	780.108	0.533	23	0.174	K.VAAQVPDSGPCVTYIGK.G
R4/RRR4-9/2	1215.559	1216.371	-1495.316	0.442	1171.454	0.366	17	0.173	K.GWSLNLGELAR.I
R4/RRR4-1/2	1216.134	1216.371	-195.979	0.469	1097.426	0.380	17	0.170	K.GWSLNLGELAR.I
R4/RRR4-9/2	1259.060	1259.308	-197.660	0.367	905.343	0.453	15	0.169	R.DYFGAHTYER.V
R4/RRR4-9/2	1763.233	1762.978	144.598	0.508	677.165	0.523	22	0.169	K.VAAQVPDSGPCVTYIGK.G
R4/RRR4-9/2	1258.595	1259.308	-1365.681	0.363	760.065	0.495	14	0.166	R.DYFGAHTYER.V
R4/RRR4-9/2	1762.355	1762.978	-923.689	0.498	716.616	0.494	22	0.166	K.VAAQVPDSGPCVTYIGK.G
R4/RRR4-8/2	943.247	944.067	-1935.640	0.408	764.681	0.416	12	0.161	K.AQLIEDVR.Q
R4/RRR4-9/2	1572.390	1571.736	-220.741	0.461	530.691	0.498	18	0.159	R.NGPSLM*PGGSFEAYK.Y
R4/RRR4-9/2	1381.290	1381.566	-200.733	0.462	816.251	0.368	19	0.158	R.DRLPANLVQAQR.D
R4/RRR4-8/2	1572.451	1571.736	-182.190	0.413	463.011	0.504	17	0.156	R.NGPSLM*PGGSFEAYK.Y
R4/RRR4-9/2	1581.331	1581.776	-281.956	0.410	382.317	0.522	15	0.156	R.VDMPGSFHTEWFK.I
R4/RRR4-8/2	1571.215	1571.736	-971.244	0.360	603.275	0.469	19	0.156	R.NGPSLM*PGGSFEAYK.Y
R4/RRR4-8/2	1259.019	1259.308	-230.731	0.371	644.394	0.423	14	0.156	R.DYFGAHTYER.V
R4/RRR4-8/2	1258.493	1259.308	-1446.735	0.325	706.504	0.428	14	0.156	R.DYFGAHTYER.V
R4/RRR4-8/2	944.008	944.067	-62.788	0.413	736.367	0.364	12	0.154	K.AQLIEDVR.Q
R4/RRR4-8/2	1570.651	1571.736	-1331.500	0.295	782.816	0.405	21	0.154	R.NGPSLM*PGGSFEAYK.Y
R4/RRR4-8/2	1381.279	1381.566	-208.358	0.443	448.398	0.387	18	0.154	R.DRLPANLVQAQR.D
R4/RRR4-7/2	1111.252	1110.292	-35.765	0.332	520.093	0.455	13	0.153	R.LPANLVQAQR.D
R4/RRR4-9/2	1258.482	1259.308	-1455.796	0.372	691.130	0.371	14	0.152	R.DYFGAHTYER.V
R4/RRR4-9/2	1381.293	1381.566	-198.251	0.432	490.339	0.363	18	0.152	R.DRLPANLVQAQR.D
R4/RRR4-9/2	1571.173	1571.736	-998.233	0.355	603.683	0.410	19	0.151	R.NGPSLM*PGGSFEAYK.Y
R4/RRR4-9/2	1381.303	1381.566	-191.247	0.455	457.900	0.344	18	0.150	R.DRLPANLVQAQR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1259.104	1259.308	-163.133	0.285	852.169	0.330	15	0.150	R.DYFGAHTYER.V
R4/RRR4-9/2	943.532	944.067	-1632.186	0.374	805.426	0.308	12	0.149	K.AQLIEDVR.Q
R4/RRR4-9/2	1597.069	1597.775	-1071.641	0.372	547.850	0.417	15	0.148	R.VDM*PGSFHTEWFK.I
R4/RRR4-9/2	944.218	944.067	159.998	0.403	814.564	0.300	12	0.148	-.AQLIEDVR.-
R4/RRR4-8/2	1381.411	1381.566	-112.350	0.449	726.131	0.298	18	0.147	R.DRLPANLVQAQR.D
R4/RRR4-8/2	1053.047	1053.196	-141.686	0.269	362.727	0.524	13	0.146	-.GFPISVYNR.-
R4/RRR4-9/2	1571.357	1571.736	-242.158	0.345	405.838	0.408	16	0.146	R.NGPSLM*PGGSFEAYK.Y
R4/RRR4-9/2	1582.122	1581.776	219.656	0.420	405.125	0.364	15	0.145	R.VDMPGSFHTEWFK.I
R4/RRR4-8/2	1052.402	1053.196	-1709.456	0.244	252.223	0.436	12	0.144	K.GFPISVYNR.T
R4/RRR4-9/2	1064.859	1065.205	-325.231	0.454	803.390	0.221	15	0.142	R.FLSGLKDER.V
R4/RRR4-9/2	943.381	944.067	-1793.121	0.301	789.553	0.195	12	0.139	K.AQLIEDVR.Q
R4/RRR4-9/3	1996.759	1997.392	-820.290	0.425	1528.376	0.303	31	0.136	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-9/2	1064.416	1065.205	-1685.675	0.343	920.054	0.132	15	0.135	R.FLSGLKDER.V
R4/RRR4-9/2	1064.850	1065.205	-333.857	0.306	587.320	0.179	13	0.134	-.FLSGLKDER.-
R4/RRR4-9/3	1382.572	1381.566	4.630	0.545	1252.883	0.272	25	0.099	R.DRLPANLVQAQR.D
R4/RRR4-8/3	1382.246	1381.566	-232.271	0.528	1068.806	0.319	24	0.098	-.DRLPANLVQAQR.-
R4/RRR4-9/3	1997.553	1997.392	80.986	0.412	945.548	0.333	28	0.097	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-9/3	1381.578	1381.566	8.665	0.508	1198.730	0.251	24	0.092	-.DRLPANLVQAQR.-
R4/RRR4-9/3	1382.515	1381.566	-37.215	0.500	769.712	0.322	20	0.085	-.DRLPANLVQAQR.-
R4/RRR4-8/3	1380.569	1381.566	-1450.693	0.419	778.798	0.304	21	0.085	-.DRLPANLVQAQR.-
R4/RRR4-8/3	1996.258	1997.392	-1072.115	0.289	699.889	0.272	30	0.084	R.IGLAGLAVMGQNLALNIAEK.G
R4/RRR4-8/3	1381.240	1381.566	-236.917	0.463	821.701	0.212	20	0.071	-.DRLPANLVQAQR.-
R4/RRR4-7/2	1706.193	1705.010	107.577	0.593	2255.635	0.542	23	0.346	K.SALGILM*NLGLIEESK.I
R4/RRR4-7/2	1688.320	1689.011	-1004.370	0.444	1962.819	0.518	22	0.289	K.SALGILMNLGLIEESK.I
R4/RRR4-7/2	1604.264	1603.761	-311.125	0.456	1629.085	0.492	22	0.238	K.GFLTINSQPAVNGER.S
R4/RRR4-7/2	1688.463	1689.011	-919.734	0.472	1543.703	0.539	20	0.236	K.SALGILMNLGLIEESK.I
R4/RRR4-7/2	1846.639	1845.946	-166.924	0.545	1320.107	0.573	23	0.221	R.SDSTSVGWGGPGGYVYQK.A
R4/RRR4-7/2	1604.154	1603.761	245.414	0.521	1388.519	0.473	20	0.206	K.GFLTINSQPAVNGER.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1199.165	1199.381	-180.476	0.448	1482.141	0.406	16	0.205	K.LQEEWAVPVK.S
R4/RRR4-7/2	1889.138	1889.052	45.587	0.524	1302.664	0.497	21	0.202	K.LTSSPWSELDGLQPETK.I
R4/RRR4-7/2	1604.263	1603.761	-311.583	0.472	1309.819	0.468	21	0.199	K.GFLTINSQPAVNGER.S
R4/RRR4-7/2	1845.304	1845.946	-892.784	0.473	1255.636	0.498	23	0.198	R.SDSTSVGWGGPGGYVYQK.A
R4/RRR4-7/2	1330.128	1330.433	-230.178	0.452	1199.786	0.477	17	0.194	R.TLGWDQYPHGR.W
R4/RRR4-7/2	1199.100	1199.381	-234.704	0.453	1413.497	0.366	16	0.191	K.LQEEWAVPVK.S
R4/RRR4-7/2	1330.038	1330.433	-297.393	0.485	1174.638	0.467	17	0.191	R.TLGWDQYPHGR.W
R4/RRR4-7/2	1604.277	1603.761	-302.880	0.475	1171.592	0.479	21	0.190	K.GFLTINSQPAVNGER.S
R4/RRR4-7/2	1327.255	1327.553	-225.695	0.482	1208.745	0.435	18	0.188	K.KLQEEWAVPVK.S
R4/RRR4-7/2	1845.047	1845.946	-1032.529	0.499	971.979	0.570	20	0.187	R.SDSTSVGWGGPGGYVYQK.A
R4/RRR4-7/2	1889.452	1889.052	211.921	0.551	1141.238	0.476	20	0.182	K.LTSSPWSELDGLQPETK.I
R4/RRR4-7/2	1323.064	1323.391	-247.416	0.353	1341.885	0.360	16	0.180	K.TEEGLDNLFER.M
R4/RRR4-7/2	1604.236	1603.761	297.146	0.522	1002.563	0.463	20	0.175	K.GFLTINSQPAVNGER.S
R4/RRR4-7/2	1185.038	1185.359	-271.068	0.475	1156.152	0.379	18	0.175	K.SNGIQNVLALR.G
R4/RRR4-7/2	1889.303	1889.052	133.135	0.490	985.830	0.499	18	0.174	K.LTSSPWSELDGLQPETK.I
R4/RRR4-7/2	1326.622	1327.553	-1460.299	0.449	1026.464	0.412	17	0.171	K.KLQEEWAVPVK.S
R4/RRR4-7/2	1165.100	1165.313	-183.230	0.447	1178.116	0.353	14	0.171	K.AYLEFFCSK.E
R4/RRR4-7/2	1604.260	1603.761	311.719	0.527	910.258	0.457	19	0.168	K.GFLTINSQPAVNGER.S
R4/RRR4-7/2	989.889	990.133	-247.017	0.466	936.524	0.397	15	0.167	K.IDDALTTIK.S
R4/RRR4-7/2	1165.051	1165.313	-225.695	0.425	1220.656	0.313	14	0.167	K.AYLEFFCSK.E
R4/RRR4-5/2	1705.741	1705.010	-158.264	0.345	1073.001	0.404	18	0.165	K.SALGILM*NLGLIEESK.I
R4/RRR4-26/2	989.965	990.133	-170.070	0.425	925.354	0.383	15	0.164	K.IDDALTTIK.S
R4/RRR4-7/2	1184.632	1185.359	-1462.006	0.476	918.784	0.384	17	0.162	K.SNGIQNVLALR.G
R4/RRR4-7/2	1327.142	1327.553	-310.774	0.506	870.681	0.405	16	0.162	K.KLQEEWAVPVK.S
R4/RRR4-26/2	990.098	990.133	-35.133	0.399	928.889	0.378	14	0.162	K.IDDALTTIK.S
R4/RRR4-7/2	1198.668	1199.381	-1433.242	0.408	945.732	0.389	14	0.161	-.LQEEWAVPVK.-
R4/RRR4-7/2	1185.220	1185.359	-117.622	0.537	838.211	0.385	17	0.159	K.SNGIQNVLALR.G
R4/RRR4-7/2	1324.901	1324.550	265.997	0.467	611.707	0.442	18	0.159	K.AFPSLTYIAVNK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1363.246	1363.608	-266.079	0.413	635.032	0.473	14	0.157	K.TLHLYTLNMEK.S
R4/RRR4-7/2	989.810	990.133	-327.192	0.431	674.431	0.401	13	0.157	K.IDDALTTIK.S
R4/RRR4-7/2	1164.705	1165.313	-1384.841	0.372	1072.281	0.298	13	0.156	K.AYLEFFCSK.E
R4/RRR4-7/2	990.080	990.133	-53.931	0.469	819.765	0.346	14	0.155	K.IDDALTTIK.S
R4/RRR4-26/2	989.953	990.133	-181.946	0.404	651.923	0.395	13	0.155	K.IDDALTTIK.S
R4/RRR4-7/3	1889.652	1889.052	-212.471	0.461	1542.957	0.359	31	0.155	K.LTSSPWSELDGLQPETK.I
R4/RRR4-7/2	1886.671	1887.045	-198.685	0.468	544.337	0.437	18	0.151	R.NPSYGALTDYQFTRPR.G
R4/RRR4-7/2	1887.477	1887.045	229.593	0.480	497.313	0.443	17	0.149	R.NPSYGALTDYQFTRPR.G
R4/RRR4-7/2	1886.403	1887.045	-873.009	0.448	523.980	0.421	18	0.149	R.NPSYGALTDYQFTRPR.G
R4/RRR4-7/2	1323.618	1324.550	-1463.614	0.316	470.001	0.383	17	0.146	K.AFPSLTYIAVNK.D
R4/RRR4-7/2	1704.970	1705.010	-23.976	0.281	183.791	0.342	14	0.140	-.SALGILM*NLGLIEESK.-
R4/RRR4-7/3	1854.439	1856.163	-2014.358	0.497	845.274	0.513	28	0.127	R.VKEDVRPIFWANRPK.S
R4/RRR4-7/3	1327.703	1327.553	112.991	0.518	1623.708	0.239	25	0.125	-.KLQEEWAVPVK.-
R4/RRR4-9/2	1705.983	1705.010	-15.852	0.278	260.578	0.388	11	0.124	-.SALGILM*NLGLIEESK.-
R4/RRR4-7/3	1855.874	1856.163	-156.468	0.498	984.870	0.391	29	0.109	R.VKEDVRPIFWANRPK.S
R4/RRR4-7/3	1856.108	1856.163	-29.995	0.526	561.566	0.405	26	0.094	-.VKEDVRPIFWANRPK.-
R4/RRR4-7/3	1327.582	1327.553	21.284	0.519	1307.036	0.217	24	0.091	-.KLQEEWAVPVK.-
R4/RRR4-7/2	1295.498	1296.501	-1550.860	0.441	1875.093	0.593	21	0.299	K.VVAAGANPVQITR.G
R4/RRR4-7/2	1295.664	1296.501	-1421.767	0.436	1927.182	0.560	21	0.298	K.VVAAGANPVQITR.G
R4/RRR4-7/2	1295.768	1296.501	-1341.526	0.477	1693.429	0.594	20	0.274	K.VVAAGANPVQITR.G
R4/RRR4-7/2	1183.298	1183.423	-105.396	0.544	1805.025	0.508	20	0.268	K.LADLVGVTLGPK.G
R4/RRR4-7/2	1183.909	1183.423	411.744	0.521	1835.489	0.441	20	0.254	K.LADLVGVTLGPK.G
R4/RRR4-7/2	1183.248	1183.423	-147.618	0.555	1707.748	0.455	20	0.241	K.LADLVGVTLGPK.G
R4/RRR4-7/2	1286.019	1285.472	-353.462	0.537	1629.277	0.468	17	0.234	R.DLINVLEEAIR.G
R4/RRR4-7/2	1284.354	1285.472	-1653.735	0.390	1709.896	0.398	17	0.226	R.DLINVLEEAIR.G
R4/RRR4-7/2	1285.121	1285.472	-273.585	0.419	1660.997	0.409	17	0.223	R.DLINVLEEAIR.G
R4/RRR4-7/2	1284.940	1285.472	-1196.086	0.386	1701.090	0.383	17	0.221	R.DLINVLEEAIR.G
R4/RRR4-7/2	1284.707	1285.472	-1377.568	0.424	1553.915	0.446	17	0.220	R.DLINVLEEAIR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1321.128	1321.504	-285.498	0.446	1446.800	0.496	17	0.219	-.NVVLESKYGSPK.-
R4/RRR4-7/2	1284.597	1285.472	-1463.466	0.417	1584.826	0.394	17	0.212	R.DLINVLEEAIR.G
R4/RRR4-7/2	1542.299	1542.670	-240.984	0.499	1460.839	0.373	21	0.194	R.EVELEDPVENIGAK.L
R4/RRR4-7/2	1245.891	1246.383	-395.507	0.547	882.239	0.536	18	0.187	R.CCLEHAASVAK.T
R4/RRR4-7/2	1043.949	1044.187	-228.889	0.505	1078.825	0.423	17	0.179	K.IVNDGVTVAR.E
R4/RRR4-7/2	1543.506	1542.670	-106.342	0.550	1203.173	0.406	20	0.178	R.EVELEDPVENIGAK.L
R4/RRR4-7/2	1089.073	1088.240	-153.863	0.419	1029.815	0.463	16	0.178	R.KGVVTLEEGR.S
R4/RRR4-7/2	1043.898	1044.187	-277.575	0.466	1233.416	0.343	17	0.174	K.IVNDGVTVAR.E
R4/RRR4-7/2	1245.977	1246.383	-326.400	0.517	785.830	0.491	17	0.173	R.CCLEHAASVAK.T
R4/RRR4-7/2	1043.504	1044.187	-1617.964	0.455	1012.076	0.412	17	0.172	K.IVNDGVTVAR.E
R4/RRR4-7/2	960.885	960.067	-189.871	0.519	1000.932	0.394	14	0.168	K.GVVTLEEGR.S
R4/RRR4-7/2	1245.946	1246.383	-351.073	0.526	643.352	0.486	17	0.168	R.CCLEHAASVAK.T
R4/RRR4-7/2	1506.091	1506.638	-1030.210	0.324	1037.855	0.407	19	0.166	R.GYISPYFVTDSEK.M
R4/RRR4-7/2	1174.516	1175.274	-1501.389	0.379	811.018	0.459	16	0.163	K.NAGVNGSVVTEK.V
R4/RRR4-7/2	1937.262	1938.040	-920.748	0.453	672.574	0.544	18	0.161	K.ESTTIVGDGSTQEEVTKR.V
R4/RRR4-7/2	1230.175	1230.396	-180.604	0.409	926.338	0.386	14	0.157	K.LRVEDALNATK.A
R4/RRR4-7/2	1175.674	1175.274	341.416	0.385	625.647	0.448	15	0.155	K.NAGVNGSVVTEK.V
R4/RRR4-7/2	1505.516	1506.638	-1413.402	0.285	932.590	0.368	18	0.153	R.GYISPYFVTDSEK.M
R4/RRR4-7/2	1174.458	1175.274	-1550.773	0.370	672.190	0.420	15	0.153	K.NAGVNGSVVTEK.V
R4/RRR4-7/2	1542.218	1542.670	-293.473	0.501	945.946	0.364	18	0.153	-.EVELEDPVENIGAK.-
R4/RRR4-7/2	959.370	960.067	-1773.573	0.408	885.149	0.318	14	0.152	K.GVVTLEEGR.S
R4/RRR4-7/2	743.759	743.875	-155.500	0.448	967.958	0.224	11	0.143	K.VGAEIVR.R
R4/RRR4-9/2	1322.689	1321.504	139.904	0.282	476.231	0.309	15	0.138	-.NVVLESKYGSPK.-
R4/RRR4-7/2	1174.384	1175.274	-1614.154	0.269	376.763	0.349	13	0.134	-.NAGVNGSVVTEK.-
R4/RRR4-7/3	1230.085	1230.396	-254.135	0.499	1371.985	0.326	24	0.123	-.LRVEDALNATK.-
R4/RRR4-7/3	1230.668	1230.396	221.140	0.506	1220.261	0.350	24	0.116	K.LRVEDALNATK.A
R4/RRR4-7/3	1632.049	1631.723	200.137	0.486	638.923	0.506	24	0.114	R.VDAIKDNLENDEQK.V
R4/RRR4-7/3	1631.210	1631.723	-930.857	0.463	883.706	0.417	25	0.108	R.VDAIKDNLENDEQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1630.828	1631.723	-1165.989	0.432	552.563	0.454	23	0.102	R.VDAIKDNLENDEQK.V
R4/RRR4-5/3	1800.634	1801.027	-218.861	0.569	2306.267	0.525	30	0.374	R.FVREELGCVYLTGEK.L
R4/RRR4-5/2	1465.292	1465.683	-267.352	0.489	2050.828	0.568	24	0.323	K.KVLTTGPAGGLHSAR.F
R4/RRR4-2/2	1707.232	1707.826	-936.588	0.516	1822.998	0.563	23	0.282	R.EVNSVNDNPVIDVHR.G
R4/RRR4-5/3	1800.981	1801.027	-25.169	0.528	1782.145	0.569	30	0.273	R.FVREELGCVYLTGEK.L
R4/RRR4-3/2	1707.386	1707.826	-258.415	0.565	1620.175	0.587	23	0.262	R.EVNSVNDNPVIDVHR.G
R4/RRR4-6/2	1707.348	1707.826	-280.866	0.537	1588.802	0.575	22	0.254	R.EVNSVNDNPVIDVHR.G
R4/RRR4-5/2	1707.430	1707.826	-232.808	0.529	1568.327	0.579	23	0.253	R.EVNSVNDNPVIDVHR.G
R4/RRR4-1/2	1707.449	1707.826	-221.619	0.538	1617.614	0.552	23	0.252	R.EVNSVNDNPVIDVHR.G
R4/RRR4-1/2	1707.310	1707.826	-890.864	0.533	1561.663	0.577	22	0.251	R.EVNSVNDNPVIDVHR.G
R4/RRR4-8/2	1707.298	1707.826	-897.898	0.504	1521.644	0.573	24	0.246	R.EVNSVNDNPVIDVHR.G
R4/RRR4-6/2	1708.227	1707.826	235.551	0.546	1426.691	0.609	22	0.243	R.EVNSVNDNPVIDVHR.G
R4/RRR4-5/2	1707.410	1707.826	-244.786	0.526	1461.993	0.547	22	0.232	R.EVNSVNDNPVIDVHR.G
R4/RRR4-6/2	1337.355	1337.510	-116.326	0.460	1546.424	0.480	21	0.226	K.VLTTGPAGGLHSAR.F
R4/RRR4-6/2	1378.303	1377.528	-163.326	0.516	1385.872	0.547	20	0.225	R.VAFETGTAPITNR.I
R4/RRR4-5/2	1377.115	1377.528	-300.385	0.456	1423.589	0.534	20	0.225	R.VAFETGTAPITNR.I
R4/RRR4-5/2	1337.124	1337.510	-289.408	0.432	1456.911	0.510	21	0.223	K.VLTTGPAGGLHSAR.F
R4/RRR4-2/2	1708.326	1707.826	293.232	0.549	1289.297	0.575	22	0.221	R.EVNSVNDNPVIDVHR.G
R4/RRR4-2/2	1707.309	1707.826	-891.510	0.516	1340.234	0.551	21	0.220	R.EVNSVNDNPVIDVHR.G
R4/RRR4-5/2	1707.303	1707.826	-895.099	0.494	1297.958	0.568	21	0.219	R.EVNSVNDNPVIDVHR.G
R4/RRR4-1/2	1707.366	1707.826	-270.250	0.526	1340.342	0.536	21	0.216	R.EVNSVNDNPVIDVHR.G
R4/RRR4-6/3	1464.919	1465.683	-1207.903	0.520	1501.778	0.557	29	0.215	K.KVLTTGPAGGLHSAR.F
R4/RRR4-6/2	1707.247	1707.826	-927.615	0.496	1281.530	0.540	20	0.210	R.EVNSVNDNPVIDVHR.G
R4/RRR4-5/3	1465.404	1465.683	-190.808	0.524	1520.290	0.540	30	0.210	K.KVLTTGPAGGLHSAR.F
R4/RRR4-3/2	1707.438	1707.826	-227.859	0.489	1271.115	0.532	22	0.210	R.EVNSVNDNPVIDVHR.G
R4/RRR4-5/2	1399.003	1398.534	336.012	0.533	1176.198	0.557	17	0.207	R.EELGCVYLTGEK.L
R4/RRR4-1/2	1377.045	1377.528	-351.792	0.479	1329.984	0.488	19	0.206	R.VAFETGTAPITNR.I
R4/RRR4-5/2	1337.264	1337.510	-184.269	0.416	1346.538	0.486	20	0.206	K.VLTTGPAGGLHSAR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1377.081	1377.528	-325.199	0.436	1420.416	0.440	20	0.205	R.VAFETGTAPITNR.I
R4/RRR4-6/2	1377.143	1377.528	-280.464	0.467	1426.579	0.431	20	0.204	R.VAFETGTAPITNR.I
R4/RRR4-5/2	1337.179	1337.510	-248.467	0.404	1318.705	0.491	20	0.204	K.VLTTGPAGGLHSAR.F
R4/RRR4-1/2	1377.111	1377.528	-303.854	0.459	1375.043	0.446	20	0.202	R.VAFETGTAPITNR.I
R4/RRR4-1/2	1377.031	1377.528	-361.754	0.455	1263.452	0.491	19	0.201	R.VAFETGTAPITNR.I
R4/RRR4-2/2	1377.998	1377.528	342.111	0.486	1203.242	0.505	19	0.199	R.VAFETGTAPITNR.I
R4/RRR4-6/3	1465.938	1465.683	174.206	0.565	1382.818	0.554	29	0.195	K.KVLTTGPAGGLHSAR.F
R4/RRR4-8/2	1707.053	1707.826	-1042.121	0.528	1027.382	0.571	19	0.195	R.EVNSVNDNPVIDVHR.G
R4/RRR4-8/2	1707.228	1707.826	-938.813	0.508	1031.397	0.543	21	0.192	R.EVNSVNDNPVIDVHR.G
R4/RRR4-5/2	1377.066	1377.528	-336.405	0.436	1179.074	0.483	19	0.192	R.VAFETGTAPITNR.I
R4/RRR4-8/2	1377.332	1377.528	-142.551	0.441	1165.141	0.478	19	0.190	R.VAFETGTAPITNR.I
R4/RRR4-1/2	1337.133	1337.510	-282.905	0.376	1167.564	0.453	20	0.184	K.VLTTGPAGGLHSAR.F
R4/RRR4-5/2	1377.209	1377.528	-232.266	0.401	1148.650	0.437	19	0.182	R.VAFETGTAPITNR.I
R4/RRR4-6/3	1465.967	1465.683	194.623	0.544	1377.136	0.517	29	0.181	K.KVLTTGPAGGLHSAR.F
R4/RRR4-5/2	1398.073	1398.534	-330.825	0.374	1157.351	0.429	17	0.179	R.EELGCVYLTGEK.L
R4/RRR4-1/2	1624.470	1624.865	-243.868	0.443	999.177	0.478	19	0.178	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1252.035	1252.485	-360.220	0.545	890.715	0.482	16	0.175	K.VNEVDPLLKPK.Q
R4/RRR4-4/2	1377.201	1377.528	-237.779	0.410	1061.242	0.418	20	0.174	R.VAFETGTAPITNR.I
R4/RRR4-1/2	1252.163	1252.485	-257.808	0.466	883.519	0.477	16	0.173	K.VNEVDPLLKPK.Q
R4/RRR4-5/2	1625.115	1624.865	154.100	0.493	919.432	0.467	18	0.171	R.TSPQWLGPQIEVIR.A
R4/RRR4-3/2	1625.611	1624.865	-156.630	0.524	817.032	0.485	19	0.171	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1251.780	1252.485	-1366.073	0.542	780.881	0.490	15	0.170	K.VNEVDPLLKPK.Q
R4/RRR4-5/2	1624.534	1624.865	-204.593	0.486	863.699	0.465	19	0.170	R.TSPQWLGPQIEVIR.A
R4/RRR4-5/2	1624.926	1624.865	37.704	0.494	793.842	0.490	18	0.169	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1625.720	1624.865	-89.366	0.484	677.576	0.514	18	0.168	R.TSPQWLGPQIEVIR.A
R4/RRR4-1/3	1465.295	1465.683	-265.648	0.487	1240.244	0.528	28	0.168	K.KVLTTGPAGGLHSAR.F
R4/RRR4-6/2	1624.352	1624.865	-934.327	0.422	757.903	0.487	19	0.168	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1625.304	1624.865	270.921	0.518	785.978	0.482	18	0.168	R.TSPQWLGPQIEVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1624.408	1624.865	-282.167	0.460	857.614	0.451	19	0.168	R.TSPQWLGPQIEVIR.A
R4/RRR4-1/2	1624.461	1624.865	-249.523	0.497	726.870	0.484	19	0.167	R.TSPQWLGPQIEVIR.A
R4/RRR4-2/2	1624.464	1624.865	-247.638	0.488	846.984	0.452	19	0.167	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1624.322	1624.865	-952.660	0.442	815.210	0.433	19	0.163	R.TSPQWLGPQIEVIR.A
R4/RRR4-5/2	1252.153	1252.485	-265.926	0.539	998.124	0.380	16	0.163	K.VNEVDPLLKPK.Q
R4/RRR4-1/2	1625.519	1624.865	-213.733	0.403	761.469	0.446	18	0.162	R.TSPQWLGPQIEVIR.A
R4/RRR4-3/2	1624.298	1624.865	-967.977	0.444	685.628	0.458	18	0.162	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1625.237	1624.865	229.423	0.509	808.026	0.424	19	0.162	R.TSPQWLGPQIEVIR.A
R4/RRR4-5/2	1624.661	1624.865	-125.749	0.464	675.626	0.455	17	0.160	R.TSPQWLGPQIEVIR.A
R4/RRR4-4/2	1624.470	1624.865	-244.095	0.419	810.139	0.402	19	0.159	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1624.239	1624.865	-1003.968	0.483	764.220	0.414	19	0.159	R.TSPQWLGPQIEVIR.A
R4/RRR4-5/2	1625.155	1624.865	178.958	0.506	723.871	0.443	17	0.159	R.TSPQWLGPQIEVIR.A
R4/RRR4-8/2	1625.492	1624.865	-230.082	0.493	635.305	0.443	18	0.159	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/3	1800.284	1801.027	-971.090	0.416	1498.345	0.396	27	0.159	R.FVREELGCVYLTGEK.L
R4/RRR4-2/2	1624.496	1624.865	-227.962	0.471	701.893	0.428	18	0.158	R.TSPQWLGPQIEVIR.A
R4/RRR4-8/2	1625.478	1624.865	-238.896	0.484	726.368	0.414	19	0.158	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1624.633	1624.865	-143.310	0.421	561.709	0.465	17	0.158	R.TSPQWLGPQIEVIR.A
R4/RRR4-1/2	1625.509	1624.865	-219.685	0.348	742.239	0.423	18	0.158	R.TSPQWLGPQIEVIR.A
R4/RRR4-7/2	1624.304	1624.865	-963.751	0.446	614.039	0.447	17	0.158	R.TSPQWLGPQIEVIR.A
R4/RRR4-4/2	1624.451	1624.865	-255.478	0.439	733.945	0.412	18	0.157	R.TSPQWLGPQIEVIR.A
R4/RRR4-6/2	1108.198	1108.226	-25.920	0.355	864.607	0.375	14	0.157	K.ITAFEEELR.E
R4/RRR4-4/2	1624.418	1624.865	-276.060	0.448	724.885	0.411	18	0.157	R.TSPQWLGPQIEVIR.A
R4/RRR4-5/2	1252.105	1252.485	-304.267	0.484	782.852	0.409	14	0.157	K.VNEVDPLLKPK.Q
R4/RRR4-1/2	1625.010	1624.865	89.389	0.486	707.985	0.404	19	0.157	R.TSPQWLGPQIEVIR.A
R4/RRR4-1/3	1466.027	1465.683	235.580	0.543	1121.186	0.534	28	0.157	K.KVLTTGPAGGLHSAR.F
R4/RRR4-2/2	1626.101	1624.865	145.197	0.452	530.550	0.448	17	0.157	R.TSPQWLGPQIEVIR.A
R4/RRR4-1/2	935.249	935.102	157.998	0.460	870.429	0.335	13	0.156	K.VFLAISER.K
R4/RRR4-5/2	1251.927	1252.485	-1248.555	0.486	946.559	0.350	15	0.156	K.VNEVDPLLKPK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1041.859	1041.138	-268.951	0.384	362.835	0.445	12	0.155	R.NPSLDYGFK.G
R4/RRR4-5/2	1088.186	1088.280	-85.917	0.452	593.400	0.394	15	0.155	R.KTAEAVDILK.L
R4/RRR4-5/2	934.998	935.102	-111.452	0.500	911.306	0.311	13	0.154	K.VFLAISER.K
R4/RRR4-7/2	1624.310	1624.865	-960.281	0.387	547.436	0.434	16	0.154	R.TSPQWLGPQIEVIR.A
R4/RRR4-5/2	934.453	935.102	-1770.028	0.456	911.279	0.306	13	0.154	K.VFLAISER.K
R4/RRR4-5/3	1801.293	1801.027	148.061	0.485	1173.049	0.504	27	0.153	R.FVREELGCVYLTGEK.L
R4/RRR4-6/2	1398.581	1398.534	33.913	0.369	997.526	0.308	16	0.152	R.EELGCVYLTGEK.L
R4/RRR4-6/2	872.993	873.032	-45.106	0.317	907.587	0.318	13	0.152	K.ALLTAIDR.E
R4/RRR4-5/2	1088.196	1088.280	-77.140	0.505	662.746	0.355	15	0.152	R.KTAEAVDILK.L
R4/RRR4-1/2	934.530	935.102	-1687.475	0.416	933.296	0.284	13	0.152	K.VFLAISER.K
R4/RRR4-6/2	1624.543	1624.865	-198.939	0.374	654.099	0.360	18	0.151	R.TSPQWLGPQIEVIR.A
R4/RRR4-8/2	1624.293	1624.865	-971.070	0.411	493.654	0.394	16	0.150	R.TSPQWLGPQIEVIR.A
R4/RRR4-5/2	1041.042	1041.138	-92.866	0.364	307.429	0.378	11	0.150	R.NPSLDYGFK.G
R4/RRR4-1/3	1465.714	1465.683	21.241	0.470	1139.125	0.503	27	0.150	K.KVLTTGPAGGLHSAR.F
R4/RRR4-2/2	1623.615	1624.865	-1390.302	0.299	598.753	0.378	18	0.150	R.TSPQWLGPQIEVIR.A
R4/RRR4-2/2	960.365	960.107	269.372	0.330	950.699	0.275	15	0.150	K.TAEAVDILK.L
R4/RRR4-6/2	1040.995	1041.138	-137.916	0.361	455.354	0.337	13	0.149	R.NPSLDYGFK.G
R4/RRR4-3/2	1377.168	1377.528	-262.234	0.371	859.302	0.307	17	0.149	R.VAFETGTAPITNR.I
R4/RRR4-5/2	934.531	935.102	-1686.163	0.450	939.658	0.263	13	0.149	K.VFLAISER.K
R4/RRR4-5/2	872.986	873.032	-53.381	0.323	797.156	0.321	12	0.149	K.ALLTAIDR.E
R4/RRR4-1/2	959.718	960.107	-406.342	0.302	1161.475	0.204	15	0.149	K.TAEAVDILK.L
R4/RRR4-6/2	873.035	873.032	3.280	0.338	779.274	0.318	12	0.149	K.ALLTAIDR.E
R4/RRR4-1/2	959.974	960.107	-138.524	0.366	978.516	0.252	15	0.149	K.TAEAVDILK.L
R4/RRR4-3/2	1040.349	1041.138	-1725.141	0.244	340.931	0.495	12	0.149	R.NPSLDYGFK.G
R4/RRR4-3/2	1040.946	1041.138	-185.206	0.346	304.865	0.337	11	0.148	R.NPSLDYGFK.G
R4/RRR4-5/2	959.690	960.107	-435.697	0.323	952.268	0.255	15	0.147	K.TAEAVDILK.L
R4/RRR4-3/2	1040.422	1041.138	-1655.119	0.272	370.401	0.383	12	0.147	R.NPSLDYGFK.G
R4/RRR4-4/2	1377.246	1377.528	-205.323	0.396	669.527	0.332	16	0.147	R.VAFETGTAPITNR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1378.301	1377.528	-164.748	0.374	891.949	0.267	18	0.147	R.VAFETGTAPITNR.I
R4/RRR4-5/2	872.393	873.032	-1885.209	0.321	651.241	0.312	12	0.146	K.ALLTAIDR.E
R4/RRR4-8/2	1040.784	1041.138	-341.459	0.292	266.372	0.299	11	0.145	-.NPSLDYGFK.-
R4/RRR4-5/3	1465.891	1465.683	142.139	0.531	976.115	0.536	25	0.144	K.KVLTTGPAGGLHSAR.F
R4/RRR4-2/2	1376.607	1377.528	-1399.627	0.274	965.938	0.223	18	0.144	R.VAFETGTAPITNR.I
R4/RRR4-3/2	1623.851	1624.865	-1243.976	0.284	535.839	0.276	17	0.144	R.TSPQWLGPQIEVIR.A
R4/RRR4-2/3	1466.067	1465.683	262.757	0.490	1062.192	0.500	27	0.142	K.KVLTTGPAGGLHSAR.F
R4/RRR4-6/2	1109.039	1108.226	-169.419	0.306	719.339	0.241	13	0.141	K.ITAFEEELR.E
R4/RRR4-2/2	1107.813	1108.226	-374.291	0.307	493.990	0.277	11	0.141	K.ITAFEEELR.E
R4/RRR4-2/2	1088.003	1088.280	-254.731	0.348	782.129	0.229	15	0.140	-.KTAEAVDILK.-
R4/RRR4-8/2	1377.063	1377.528	-338.273	0.285	803.810	0.195	17	0.139	R.VAFETGTAPITNR.I
R4/RRR4-16/2	1041.240	1041.138	97.761	0.169	547.187	0.227	13	0.137	R.NPSLDYGFK.G
R4/RRR4-1/2	1108.231	1108.226	4.352	0.176	841.629	0.237	13	0.137	K.ITAFEEELR.E
R4/RRR4-5/2	1088.067	1088.280	-196.203	0.464	415.661	0.404	13	0.137	-.KTAEAVDILK.-
R4/RRR4-8/3	1465.884	1465.683	137.253	0.501	942.458	0.506	26	0.134	K.KVLTTGPAGGLHSAR.F
R4/RRR4-1/3	1800.863	1801.027	-90.949	0.433	1470.509	0.322	27	0.132	R.FVREELGCVYLTGEK.L
R4/RRR4-4/3	1465.640	1465.683	-29.257	0.500	826.061	0.439	24	0.113	K.KVLTTGPAGGLHSAR.F
R4/RRR4-6/3	1252.662	1252.485	142.045	0.482	821.695	0.400	20	0.105	K.VNEVDPLLKPK.Q
R4/RRR4-6/3	1252.714	1252.485	183.529	0.435	646.072	0.438	18	0.102	-.VNEVDPLLKPK.-
R4/RRR4-2/3	1252.383	1252.485	-81.849	0.335	782.363	0.392	20	0.100	K.VNEVDPLLKPK.Q
R4/RRR4-6/3	1252.962	1252.485	381.810	0.452	590.186	0.357	18	0.096	K.VNEVDPLLKPK.Q
R4/RRR4-5/3	1088.882	1088.280	-365.912	0.480	1200.231	0.258	23	0.096	R.KTAEAVDILK.L
R4/RRR4-2/3	1252.200	1252.485	-228.380	0.348	532.053	0.384	17	0.094	-.VNEVDPLLKPK.-
R4/RRR4-1/3	1253.715	1252.485	184.212	0.429	492.983	0.407	17	0.090	-.VNEVDPLLKPK.-
R4/RRR4-2/3	1252.530	1252.485	35.755	0.381	576.834	0.370	18	0.085	-.VNEVDPLLKPK.-
R4/RRR4-1/3	1089.132	1088.280	-135.824	0.420	1084.560	0.214	21	0.082	-.KTAEAVDILK.-
R4/RRR4-1/3	1252.200	1252.485	-228.380	0.308	581.770	0.267	18	0.082	-.VNEVDPLLKPK.-
R4/RRR4-4/2	1569.434	1569.746	-199.683	0.634	2632.744	0.551	22	0.429	R.KYQAFAQTLQQSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1569.549	1569.746	-126.498	0.628	2608.801	0.553	22	0.425	R.KYQAFAQTLQQSR.G
R4/RRR4-4/2	1569.390	1569.746	-227.618	0.596	2416.473	0.544	22	0.382	R.KYQAFAQTLQQSR.G
R4/RRR4-4/2	1441.174	1441.574	-278.368	0.557	2038.998	0.523	19	0.307	K.YQAFAQTLQQSR.G
R4/RRR4-4/2	1440.639	1441.574	-1346.851	0.508	2016.601	0.521	19	0.302	K.YQAFAQTLQQSR.G
R4/RRR4-4/2	1440.642	1441.574	-1345.149	0.527	1999.704	0.514	19	0.298	K.YQAFAQTLQQSR.G
R4/RRR4-4/2	1352.576	1353.503	-1429.020	0.429	1884.275	0.428	19	0.256	K.LAEDVDLEHIAK.D
R4/RRR4-4/2	1352.344	1353.503	-1601.284	0.282	914.050	0.270	16	0.143	K.LAEDVDLEHIAK.D
R4/RRR4-4/3	1553.905	1553.736	109.544	0.393	751.552	0.449	24	0.106	R.LGDVVSVHQCPDVK.Y
R4/RRR4-4/3	1553.211	1553.736	-984.540	0.394	592.819	0.469	21	0.104	R.LGDVVSVHQCPDVK.Y
R4/RRR4-4/3	1554.515	1553.736	-142.301	0.415	547.954	0.377	20	0.086	-.LGDVVSVHQCPDVK.-
R4/RRR4-10/2	1917.704	1918.175	-246.418	0.647	3036.535	0.600	25	0.544	K.SLVEEDKLELATSLIEK.A
R4/RRR4-10/3	1918.573	1918.175	207.804	0.517	2879.376	0.505	36	0.538	K.SLVEEDKLELATSLIEK.A
R4/RRR4-10/1	1042.628	1043.282	-1590.833	0.194	717.269	0.260	12	0.484	-.IGVIESLLAK.-
R4/RRR4-10/2	1918.610	1918.175	227.271	0.637	2736.855	0.599	24	0.468	K.SLVEEDKLELATSLIEK.A
R4/RRR4-10/2	1918.624	1918.175	234.480	0.624	2696.808	0.585	24	0.454	K.SLVEEDKLELATSLIEK.A
R4/RRR4-10/1	1042.561	1043.282	-1655.409	0.168	504.519	0.273	11	0.437	-.IGVIESLLAK.-
R4/RRR4-10/3	1919.175	1918.175	-0.046	0.543	2430.435	0.483	34	0.385	K.SLVEEDKLELATSLIEK.A
R4/RRR4-10/3	1752.056	1752.048	4.212	0.496	2451.618	0.440	33	0.373	K.LAATLPDGGVLLLENVR.F
R4/RRR4-10/2	1390.273	1389.578	-220.572	0.499	2111.482	0.486	22	0.307	K.ELDYLVGAVANPK.K
R4/RRR4-10/2	1389.217	1389.578	-260.841	0.429	2151.092	0.457	22	0.304	K.ELDYLVGAVANPK.K
R4/RRR4-10/2	1803.445	1804.016	-873.615	0.498	1855.249	0.586	27	0.295	K.M*SHISTGGGASLELLEGK.T
R4/RRR4-10/2	1390.168	1389.578	-296.244	0.505	1952.317	0.523	21	0.293	K.ELDYLVGAVANPK.K
R4/RRR4-10/2	1920.449	1921.103	-863.716	0.547	1734.212	0.594	23	0.277	K.LASVADLYVNDAFGTAHR.A
R4/RRR4-10/2	1920.333	1921.103	-924.147	0.528	1566.036	0.602	22	0.255	K.LASVADLYVNDAFGTAHR.A
R4/RRR4-10/2	1573.681	1574.758	-1324.093	0.383	1798.742	0.482	23	0.254	K.GVTTIIGGGDSVAAVEK.A
R4/RRR4-10/2	1920.513	1921.103	-830.026	0.528	1408.347	0.583	22	0.231	K.LASVADLYVNDAFGTAHR.A
R4/RRR4-10/3	1751.960	1752.048	-50.717	0.459	1656.422	0.461	29	0.209	K.LAATLPDGGVLLLENVR.F
R4/RRR4-10/2	1043.147	1043.282	-130.003	0.537	1218.808	0.477	17	0.199	K.IGVIESLLAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1774.340	1774.908	-886.260	0.529	997.252	0.553	21	0.194	R.FYKEEEKNDPEFAK.K
R4/RRR4-10/2	1043.208	1043.282	-71.430	0.524	1212.383	0.422	17	0.187	K.IGVIESLLAK.V
R4/RRR4-10/2	1043.256	1043.282	-24.952	0.484	1207.912	0.412	17	0.185	K.IGVIESLLAK.V
R4/RRR4-10/2	1149.890	1150.261	-324.287	0.351	1058.280	0.472	17	0.178	R.SVGTLTESDLK.G
R4/RRR4-10/2	1752.555	1752.048	-282.633	0.507	747.922	0.565	23	0.178	K.LAATLPDGGVLLLENVR.F
R4/RRR4-10/2	1774.291	1774.908	-913.749	0.570	865.009	0.522	19	0.178	R.FYKEEEKNDPEFAK.K
R4/RRR4-10/2	1527.421	1526.800	-248.622	0.486	911.772	0.500	22	0.178	K.GVSLLLPTDVVVADK.F
R4/RRR4-10/2	1771.504	1771.029	268.856	0.499	994.215	0.468	18	0.172	K.TVIWNGPM*GVFEFEK.F
R4/RRR4-10/2	1774.352	1774.908	-879.216	0.489	795.308	0.482	19	0.168	R.FYKEEEKNDPEFAK.K
R4/RRR4-10/2	1750.897	1752.048	-1232.312	0.443	689.768	0.532	22	0.168	K.LAATLPDGGVLLLENVR.F
R4/RRR4-10/2	1751.595	1752.048	-259.861	0.473	673.032	0.527	22	0.168	K.LAATLPDGGVLLLENVR.F
R4/RRR4-10/3	1918.052	1918.175	-64.646	0.466	1600.790	0.376	28	0.167	K.SLVEEDKLELATSLIEK.A
R4/RRR4-10/3	1390.734	1389.578	112.008	0.418	1819.247	0.291	26	0.166	K.ELDYLVGAVANPK.K
R4/RRR4-10/2	1093.014	1093.258	-224.103	0.396	1076.746	0.365	16	0.165	K.FAAGTDAIAKK.L
R4/RRR4-10/2	1786.715	1788.016	-1291.964	0.377	1263.451	0.301	23	0.163	K.MSHISTGGGASLELLEGK.T
R4/RRR4-10/2	1072.550	1073.313	-1648.576	0.411	413.597	0.494	14	0.161	K.YSLKPLVPR.L
R4/RRR4-10/2	1075.059	1075.286	-212.016	0.417	554.394	0.473	17	0.161	K.KPFAAIVGGSK.V
R4/RRR4-10/2	1150.071	1150.261	-165.717	0.416	807.117	0.411	16	0.160	R.SVGTLTESDLK.G
R4/RRR4-10/2	1075.056	1075.286	-214.066	0.362	744.908	0.431	18	0.160	K.KPFAAIVGGSK.V
R4/RRR4-10/2	1526.339	1526.800	-302.462	0.412	808.819	0.413	21	0.159	K.GVSLLLPTDVVVADK.F
R4/RRR4-10/2	1073.113	1073.313	-186.957	0.367	536.545	0.461	15	0.158	K.YSLKPLVPR.L
R4/RRR4-10/2	1092.548	1093.258	-1570.101	0.451	1115.413	0.295	16	0.156	K.FAAGTDAIAKK.L
R4/RRR4-10/3	1389.603	1389.578	17.779	0.377	1674.341	0.312	25	0.153	K.ELDYLVGAVANPK.K
R4/RRR4-10/2	1388.982	1389.578	-1152.682	0.341	1080.013	0.296	16	0.153	K.ELDYLVGAVANPK.K
R4/RRR4-10/2	1074.704	1075.286	-1476.092	0.353	676.421	0.370	18	0.152	K.KPFAAIVGGSK.V
R4/RRR4-10/2	1073.171	1073.313	-132.983	0.342	435.663	0.410	14	0.152	K.YSLKPLVPR.L
R4/RRR4-10/2	1526.335	1526.800	-305.512	0.380	842.622	0.322	20	0.148	K.GVSLLLPTDVVVADK.F
R4/RRR4-10/2	1573.667	1574.758	-1332.585	0.229	907.883	0.289	18	0.140	K.GVTTIIGGGDSVAAVEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1575.667	1574.758	-58.170	0.404	611.564	0.333	17	0.139	K.GVTTIIGGGDSVAAVEK.A
R4/RRR4-10/3	1774.681	1774.908	-128.372	0.462	1034.583	0.499	24	0.138	R.FYKEEEKNDPEFAK.K
R4/RRR4-10/3	1775.589	1774.908	-179.954	0.470	1036.526	0.496	25	0.137	R.FYKEEEKNDPEFAK.K
R4/RRR4-10/3	1774.465	1774.908	-250.517	0.454	1054.016	0.479	24	0.134	R.FYKEEEKNDPEFAK.K
R4/RRR4-10/2	1804.079	1804.016	35.289	0.277	362.395	0.358	14	0.134	K.M*SHISTGGGASLELLEGK.T
R4/RRR4-10/2	1149.325	1150.261	-1690.042	0.265	852.723	0.117	17	0.133	R.SVGTLTESDLK.G
R4/RRR4-10/3	1921.452	1921.103	182.514	0.372	937.978	0.490	32	0.125	K.LASVADLYVNDAFGTAHR.A
R4/RRR4-10/3	1075.406	1075.286	112.346	0.412	1346.326	0.338	23	0.122	K.KPFAAIVGGSK.V
R4/RRR4-10/3	1775.733	1774.908	-98.648	0.444	811.740	0.476	23	0.116	R.FYKEEEKNDPEFAK.K
R4/RRR4-10/3	1075.430	1075.286	134.203	0.399	1186.552	0.304	23	0.102	K.KPFAAIVGGSK.V
R4/RRR4-10/3	1921.629	1921.103	-247.324	0.369	652.216	0.430	29	0.099	K.LASVADLYVNDAFGTAHR.A
R4/RRR4-10/3	1920.669	1921.103	-226.475	0.343	680.892	0.382	29	0.093	K.LASVADLYVNDAFGTAHR.A
R4/RRR4-10/3	1803.819	1804.016	-109.256	0.424	1090.780	0.281	28	0.092	K.M*SHISTGGGASLELLEGK.T
R4/RRR4-10/3	1075.516	1075.286	214.449	0.376	980.360	0.243	20	0.084	K.KPFAAIVGGSK.V
R4/RRR4-2/3	1917.195	1918.175	-1035.957	0.321	643.080	0.261	23	0.083	K.SLVEEDKLELATSLIEK.A
R4/RRR4-10/3	1074.718	1075.286	-1463.383	0.327	1035.700	0.198	21	0.079	K.KPFAAIVGGSK.V
R4/RRR4-10/3	1803.076	1804.016	-1078.804	0.348	920.565	0.222	22	0.077	-.M*SHISTGGGASLELLEGK.-
R4/RRR4-10/3	1389.183	1389.578	-285.491	0.203	682.659	0.128	21	0.072	-.ELDYLVGAVANPK.-
R4/RRR4-2/2	1559.390	1558.757	-236.380	0.548	1928.974	0.575	20	0.304	K.LVYELFTDTLTSR.L
R4/RRR4-2/2	1558.620	1558.757	-88.343	0.488	1939.949	0.505	20	0.285	K.LVYELFTDTLTSR.L
R4/RRR4-2/2	1558.488	1558.757	-173.197	0.444	1958.361	0.431	20	0.267	K.LVYELFTDTLTSR.L
R4/RRR4-26/2	1649.083	1648.774	187.568	0.530	1862.685	0.366	20	0.234	K.VLNDM*IQDDSEQPK.K
R4/RRR4-26/2	1648.358	1648.774	-253.188	0.492	1780.090	0.333	20	0.217	K.VLNDM*IQDDSEQPK.K
R4/RRR4-2/2	1095.796	1096.219	-386.999	0.476	1313.916	0.512	14	0.211	R.HDNVQLLEK.L
R4/RRR4-2/2	1674.333	1674.788	-272.437	0.419	1336.461	0.486	22	0.203	K.AIENTAASISDVPEEK.L
R4/RRR4-3/2	1096.068	1096.219	-137.689	0.472	1236.699	0.506	14	0.203	R.HDNVQLLEK.L
R4/RRR4-2/2	1228.124	1227.392	-219.088	0.486	1322.768	0.464	19	0.202	K.IIGLDGSEAPVR.V
R4/RRR4-2/2	1095.909	1096.219	-283.170	0.487	1252.479	0.489	14	0.202	R.HDNVQLLEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1226.919	1227.392	-386.654	0.482	1334.785	0.443	19	0.199	K.IIGLDGSEAPVR.V
R4/RRR4-2/2	1557.644	1558.757	-1360.914	0.343	1586.491	0.336	19	0.198	K.LVYELFTDTLTSR.L
R4/RRR4-26/2	1648.142	1648.774	-993.498	0.495	1583.991	0.339	19	0.196	K.VLNDM*IQDDSEQPK.K
R4/RRR4-2/2	1508.499	1508.761	-174.324	0.454	1201.275	0.466	21	0.193	R.LTEPSFLESLM*PK.K
R4/RRR4-3/2	1095.893	1096.219	-298.257	0.440	1184.412	0.458	14	0.190	R.HDNVQLLEK.L
R4/RRR4-3/2	1674.501	1674.788	-172.092	0.441	1228.200	0.446	22	0.187	K.AIENTAASISDVPEEK.L
R4/RRR4-2/2	1835.682	1836.147	-254.491	0.508	991.892	0.521	23	0.185	R.FINVPIGASWVEVTM*R.T
R4/RRR4-3/2	1226.573	1227.392	-1487.778	0.446	1251.951	0.406	19	0.185	K.IIGLDGSEAPVR.V
R4/RRR4-3/2	1226.383	1227.392	-1643.253	0.361	1378.606	0.351	19	0.184	K.IIGLDGSEAPVR.V
R4/RRR4-3/2	1226.385	1227.392	-1641.753	0.355	1411.947	0.330	19	0.183	K.IIGLDGSEAPVR.V
R4/RRR4-2/2	1095.486	1096.219	-1586.343	0.368	1008.628	0.496	14	0.180	R.HDNVQLLEK.L
R4/RRR4-2/2	1310.976	1310.485	375.852	0.455	525.023	0.536	17	0.167	K.LTTGHGLLQVDR.A
R4/RRR4-2/2	1236.956	1237.409	-367.534	0.404	909.406	0.397	19	0.163	R.LGSM*ETGTGLVR.A
R4/RRR4-2/2	1508.030	1508.761	-1151.903	0.362	866.963	0.417	18	0.161	R.LTEPSFLESLM*PK.K
R4/RRR4-2/2	1508.469	1508.761	-194.213	0.408	718.337	0.453	17	0.160	R.LTEPSFLESLM*PK.K
R4/RRR4-3/2	1508.664	1508.761	-64.826	0.377	725.558	0.451	17	0.159	R.LTEPSFLESLM*PK.K
R4/RRR4-2/2	1499.428	1499.647	-146.458	0.466	1075.042	0.328	17	0.159	K.DAFEENYKELIK.W
R4/RRR4-2/2	1492.292	1492.762	-315.845	0.413	1074.678	0.302	20	0.158	R.LTEPSFLESLMPK.K
R4/RRR4-2/2	1310.005	1309.495	-375.310	0.348	638.093	0.465	16	0.158	K.LADFVPLTNYR.L
R4/RRR4-2/2	1056.047	1056.153	-100.821	0.368	1207.080	0.267	13	0.157	R.AFEYAQQAK.E
R4/RRR4-2/2	1237.214	1237.409	-158.451	0.408	782.825	0.387	18	0.157	R.LGSM*ETGTGLVR.A
R4/RRR4-3/2	1493.111	1492.762	234.555	0.398	732.132	0.414	17	0.156	R.LTEPSFLESLMPK.K
R4/RRR4-2/2	1236.862	1237.409	-1254.112	0.425	841.265	0.344	19	0.155	R.LGSM*ETGTGLVR.A
R4/RRR4-2/2	1309.797	1310.485	-1292.196	0.377	608.445	0.419	17	0.154	K.LTTGHGLLQVDR.A
R4/RRR4-2/2	1309.247	1309.495	-189.803	0.357	504.031	0.453	15	0.154	K.LADFVPLTNYR.L
R4/RRR4-2/2	894.873	894.952	-87.853	0.313	664.665	0.396	12	0.151	R.TSAFDTPR.R
R4/RRR4-2/2	894.878	894.952	-82.654	0.241	624.005	0.447	12	0.148	R.TSAFDTPR.R
R4/RRR4-3/2	1309.915	1310.485	-1202.163	0.327	632.632	0.360	16	0.146	K.LTTGHGLLQVDR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1308.883	1309.495	-1234.915	0.316	415.516	0.415	13	0.146	K.LADFVPLTNYR.L
R4/RRR4-2/2	1492.310	1492.762	-303.863	0.353	658.945	0.337	16	0.146	R.LTEPSFLESLMPK.K
R4/RRR4-2/2	1499.141	1499.647	-1007.136	0.442	651.677	0.341	15	0.145	K.DAFEENYKELIK.W
R4/RRR4-2/2	894.265	894.952	-1891.331	0.243	512.580	0.263	12	0.140	R.TSAFDTPR.R
R4/RRR4-2/2	1499.163	1499.647	-323.789	0.423	812.414	0.245	16	0.139	K.DAFEENYKELIK.W
R4/RRR4-1/2	1227.120	1227.392	-222.560	0.314	780.622	0.202	17	0.139	K.IIGLDGSEAPVR.V
R4/RRR4-1/2	1226.351	1227.392	-1669.753	0.277	454.928	0.296	15	0.138	-.IIGLDGSEAPVR.-
R4/RRR4-2/3	1403.080	1403.608	-1092.679	0.526	903.112	0.434	25	0.114	K.FKLEDGAEIKPR.V
R4/RRR4-3/3	1626.741	1626.750	-5.511	0.517	617.274	0.489	24	0.113	R.IYDNKFESQYYR.I
R4/RRR4-3/3	1403.708	1403.608	71.504	0.469	868.860	0.429	23	0.111	K.FKLEDGAEIKPR.V
R4/RRR4-3/3	1402.945	1403.608	-1189.393	0.421	835.278	0.384	23	0.101	K.FKLEDGAEIKPR.V
R4/RRR4-2/3	1626.244	1626.750	-929.107	0.409	542.359	0.415	22	0.099	R.IYDNKFESQYYR.I
R4/RRR4-2/3	1403.852	1403.608	174.061	0.493	634.883	0.385	22	0.099	K.FKLEDGAEIKPR.V
R4/RRR4-2/3	1670.353	1670.761	-245.057	0.390	995.880	0.340	24	0.098	K.WDEHNQEAISEALK.Q
R4/RRR4-2/3	1626.044	1626.750	-1052.558	0.391	426.870	0.400	19	0.097	R.IYDNKFESQYYR.I
R4/RRR4-2/3	1402.696	1403.608	-1367.669	0.436	824.319	0.333	25	0.095	K.FKLEDGAEIKPR.V
R4/RRR4-3/3	1403.532	1403.608	-54.497	0.415	662.401	0.338	23	0.093	K.FKLEDGAEIKPR.V
R4/RRR4-3/3	1627.743	1626.750	-4.643	0.352	469.526	0.355	20	0.093	R.IYDNKFESQYYR.I
R4/RRR4-2/3	1670.631	1670.761	-78.251	0.396	756.027	0.191	24	0.077	K.WDEHNQEAISEALK.Q
R4/RRR4-1/2	1954.419	1954.172	126.507	0.575	3845.347	0.561	27	0.766	R.SPVYAQFSEALNGLSTIR.A
R4/RRR4-1/2	1953.684	1954.172	-250.779	0.600	3261.755	0.564	26	0.588	R.SPVYAQFSEALNGLSTIR.A
R4/RRR4-1/2	1953.605	1954.172	-804.560	0.537	3268.094	0.526	26	0.573	R.SPVYAQFSEALNGLSTIR.A
R4/RRR4-1/2	1486.677	1485.708	-20.557	0.554	2942.139	0.581	23	0.515	K.ILVLDEATAAVDVR.T
R4/RRR4-1/2	1485.426	1485.708	-190.123	0.387	2847.676	0.429	22	0.430	K.ILVLDEATAAVDVR.T
R4/RRR4-2/2	1487.442	1487.641	-133.810	0.505	2379.207	0.455	22	0.343	R.LASLAENSLNAVER.V
R4/RRR4-1/2	1486.692	1487.641	-1314.271	0.390	2361.929	0.422	21	0.328	R.LASLAENSLNAVER.V
R4/RRR4-1/2	1486.971	1487.641	-1125.961	0.485	2221.089	0.480	22	0.323	R.LASLAENSLNAVER.V
R4/RRR4-1/2	1954.709	1954.172	-237.744	0.533	2110.626	0.527	26	0.317	R.SPVYAQFSEALNGLSTIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1486.678	1487.641	-1324.084	0.406	1805.338	0.477	20	0.256	R.LASLAENSLNAVER.V
R4/RRR4-1/2	1202.503	1201.352	126.498	0.511	1691.337	0.465	17	0.243	R.LEDLLLAEER.L
R4/RRR4-1/2	1201.443	1201.352	75.961	0.480	1756.875	0.312	17	0.212	R.LEDLLLAEER.L
R4/RRR4-1/2	1643.349	1642.705	-217.225	0.518	1431.393	0.467	18	0.210	K.LDSWDETETLYNR.F
R4/RRR4-1/2	1201.091	1201.352	-217.495	0.435	1551.083	0.374	16	0.205	R.LEDLLLAEER.L
R4/RRR4-1/2	1357.214	1357.538	-239.296	0.497	1391.307	0.439	18	0.204	K.RLEDLLLAEER.L
R4/RRR4-1/2	1358.810	1357.538	200.610	0.441	1330.007	0.441	18	0.198	K.RLEDLLLAEER.L
R4/RRR4-1/2	1851.173	1851.007	89.579	0.518	1137.409	0.518	24	0.195	R.HDLDLLPGGDLTEIGER.G
R4/RRR4-1/2	1357.516	1357.538	-16.290	0.434	1276.996	0.404	17	0.186	K.RLEDLLLAEER.L
R4/RRR4-1/2	1643.214	1642.705	-299.726	0.486	1138.465	0.462	17	0.183	K.LDSWDETETLYNR.F
R4/RRR4-2/2	1941.783	1941.343	227.081	0.477	396.505	0.550	21	0.162	R.LLLPNPPLDPELPAISIK.N
R4/RRR4-1/2	1941.521	1941.343	91.906	0.399	429.291	0.576	21	0.162	R.LLLPNPPLDPELPAISIK.N
R4/RRR4-1/2	844.933	844.941	-8.783	0.387	829.053	0.398	12	0.161	R.HANIFSR.I
R4/RRR4-1/2	1941.701	1941.343	184.969	0.446	435.241	0.530	21	0.159	R.LLLPNPPLDPELPAISIK.N
R4/RRR4-2/2	1357.313	1357.538	-165.942	0.417	960.707	0.356	15	0.158	K.RLEDLLLAEER.L
R4/RRR4-1/2	1400.009	1400.603	-1142.029	0.427	958.011	0.379	15	0.156	K.DAVITLQNVLEGK.H
R4/RRR4-1/2	844.954	844.941	15.706	0.297	832.801	0.403	12	0.156	R.HANIFSR.I
R4/RRR4-1/2	1753.753	1754.109	-203.760	0.400	524.037	0.471	21	0.155	K.VLGIIPQAPVLFSGSVR.F
R4/RRR4-1/2	1122.736	1123.198	-412.392	0.277	991.941	0.315	16	0.152	K.TLVFGDGEER.L
R4/RRR4-1/2	1941.676	1941.343	171.918	0.370	400.928	0.474	20	0.151	R.LLLPNPPLDPELPAISIK.N
R4/RRR4-1/2	1753.533	1754.109	-901.315	0.355	429.660	0.450	19	0.148	K.VLGIIPQAPVLFSGSVR.F
R4/RRR4-2/2	1941.970	1941.343	-192.775	0.350	222.498	0.511	16	0.148	R.LLLPNPPLDPELPAISIK.N
R4/RRR4-1/2	1753.331	1754.109	-1017.058	0.324	467.173	0.462	19	0.148	K.VLGIIPQAPVLFSGSVR.F
R4/RRR4-1/2	1786.427	1787.094	-936.327	0.499	780.107	0.380	16	0.147	R.VLVTNQLHFLPYVDK.I
R4/RRR4-2/2	1357.136	1357.538	-296.959	0.395	823.616	0.291	15	0.146	K.RLEDLLLAEER.L
R4/RRR4-1/2	1400.055	1400.603	-1108.585	0.391	515.665	0.383	14	0.144	K.DAVITLQNVLEGK.H
R4/RRR4-1/2	1487.966	1488.672	-1150.223	0.271	825.833	0.277	15	0.137	R.DNILFGSPFQPPR.Y
R4/RRR4-1/2	1123.192	1123.198	-4.972	0.226	737.075	0.168	15	0.133	K.TLVFGDGEER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1786.427	1787.094	-936.053	0.405	687.296	0.249	15	0.131	-.VLVTNQLHFLPYVDK.-
R4/RRR4-1/3	1850.942	1851.007	-35.305	0.442	1201.409	0.389	29	0.124	R.HDLDLLPGGDLTEIGER.G
R4/RRR4-1/3	1680.843	1679.815	16.847	0.530	929.287	0.413	26	0.112	K.VQDIRDDEISWFR.S
R4/RRR4-2/3	1503.477	1503.753	-184.215	0.415	850.033	0.443	24	0.111	R.APM*VFFHTNPLGR.I
R4/RRR4-1/3	1940.594	1941.343	-903.969	0.370	1164.077	0.341	27	0.108	R.LLLPNPPLDPELPAISIK.N
R4/RRR4-2/3	1503.940	1503.753	124.795	0.437	851.151	0.419	24	0.107	R.APM*VFFHTNPLGR.I
R4/RRR4-2/3	1503.470	1503.753	-188.613	0.429	669.522	0.447	22	0.105	R.APM*VFFHTNPLGR.I
R4/RRR4-1/3	1487.871	1487.641	155.427	0.427	1075.189	0.333	25	0.102	R.LASLAENSLNAVER.V
R4/RRR4-1/3	1487.167	1487.754	-1070.085	0.322	1017.074	0.337	25	0.098	R.APMVFFHTNPLGR.I
R4/RRR4-1/3	1954.455	1954.172	145.134	0.386	395.142	0.432	22	0.092	-.SPVYAQFSEALNGLSTIR.-
R4/RRR4-2/3	1954.109	1954.172	-32.752	0.312	1136.791	0.255	26	0.091	R.SPVYAQFSEALNGLSTIR.A
R4/RRR4-1/3	1850.695	1851.007	-169.476	0.353	606.296	0.352	24	0.089	R.HDLDLLPGGDLTEIGER.G
R4/RRR4-1/3	1850.678	1851.007	-178.409	0.384	654.424	0.316	25	0.086	R.HDLDLLPGGDLTEIGER.G
R4/RRR4-1/3	1953.602	1954.172	-806.197	0.361	493.903	0.364	21	0.084	-.SPVYAQFSEALNGLSTIR.-
R4/RRR4-1/3	1487.400	1487.641	-161.851	0.390	864.665	0.276	23	0.084	R.LASLAENSLNAVER.V
R4/RRR4-7/2	1983.441	1983.204	119.656	0.620	2693.082	0.598	26	0.459	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-7/2	1745.192	1745.940	-1004.262	0.539	2566.319	0.610	26	0.437	R.HMDGFGVNTYTFVTR.D
R4/RRR4-7/2	1745.189	1745.940	-1006.439	0.504	2613.079	0.580	26	0.435	R.HMDGFGVNTYTFVTR.D
R4/RRR4-7/2	1982.611	1983.204	-805.634	0.559	2652.205	0.550	26	0.431	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-7/2	1982.473	1983.204	-875.602	0.564	2604.402	0.570	26	0.428	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-8/2	1982.419	1983.204	-903.357	0.548	2586.717	0.562	26	0.421	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-8/2	1982.413	1983.204	-906.139	0.534	2609.971	0.538	26	0.417	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-7/2	1746.042	1745.940	58.720	0.548	2377.362	0.595	26	0.392	R.HMDGFGVNTYTFVTR.D
R4/RRR4-7/3	1984.085	1983.204	-60.211	0.563	2101.492	0.513	34	0.317	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-7/2	1539.724	1540.785	-1342.241	0.550	1900.356	0.526	20	0.284	R.GPILLEDYHLIEK.L
R4/RRR4-7/2	1540.293	1540.785	-320.469	0.581	1831.478	0.557	20	0.282	R.GPILLEDYHLIEK.L
R4/RRR4-3/2	1539.653	1540.785	-1388.823	0.493	1932.561	0.501	20	0.281	R.GPILLEDYHLIEK.L
R4/RRR4-6/2	1540.391	1540.785	-256.226	0.556	1895.624	0.510	20	0.278	R.GPILLEDYHLIEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1540.266	1540.785	-988.910	0.552	1821.053	0.498	20	0.264	R.GPILLEDYHLIEK.L
R4/RRR4-1/2	1540.348	1540.785	-284.450	0.535	1831.459	0.490	20	0.264	R.GPILLEDYHLIEK.L
R4/RRR4-7/2	1540.346	1540.785	-285.564	0.574	1790.533	0.494	20	0.259	R.GPILLEDYHLIEK.L
R4/RRR4-6/2	1540.394	1540.785	-254.397	0.532	1699.619	0.506	19	0.250	R.GPILLEDYHLIEK.L
R4/RRR4-6/2	1544.428	1543.855	-277.736	0.543	1472.635	0.570	21	0.239	R.LGPNYLM*LPVNAPK.C
R4/RRR4-5/2	1540.467	1540.785	-206.856	0.517	1690.108	0.458	19	0.236	R.GPILLEDYHLIEK.L
R4/RRR4-7/2	1528.684	1527.856	-113.220	0.555	1457.328	0.575	19	0.236	R.LGPNYLMLPVNAPK.C
R4/RRR4-6/2	1543.345	1543.855	-981.525	0.505	1594.862	0.505	20	0.236	R.LGPNYLM*LPVNAPK.C
R4/RRR4-8/2	1527.516	1527.856	-223.438	0.522	1468.403	0.523	20	0.226	R.LGPNYLMLPVNAPK.C
R4/RRR4-1/2	1539.696	1540.785	-1360.475	0.487	1489.237	0.489	19	0.222	R.GPILLEDYHLIEK.L
R4/RRR4-7/2	1527.357	1527.856	-327.592	0.508	1393.533	0.524	19	0.218	R.LGPNYLMLPVNAPK.C
R4/RRR4-3/2	1539.725	1540.785	-1342.161	0.451	1573.679	0.428	19	0.217	R.GPILLEDYHLIEK.L
R4/RRR4-8/2	1543.398	1543.855	-296.960	0.462	1462.115	0.479	19	0.215	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1544.384	1543.855	-305.887	0.504	1610.735	0.411	19	0.214	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1527.297	1527.856	-1023.923	0.521	1342.198	0.526	18	0.212	R.LGPNYLMLPVNAPK.C
R4/RRR4-1/2	1543.644	1543.855	-137.486	0.524	1350.151	0.510	19	0.210	R.LGPNYLM*LPVNAPK.C
R4/RRR4-8/2	1544.509	1543.855	-225.084	0.555	1228.942	0.553	19	0.209	R.LGPNYLM*LPVNAPK.C
R4/RRR4-2/2	1539.530	1540.785	-1468.940	0.414	1445.431	0.448	20	0.208	R.GPILLEDYHLIEK.L
R4/RRR4-7/2	1761.244	1761.939	-965.398	0.520	1065.794	0.588	24	0.206	R.HM*DGFGVNTYTFVTR.D
R4/RRR4-7/2	1124.508	1125.303	-1601.039	0.449	1338.028	0.476	18	0.205	R.SPGAQTPVIVR.F
R4/RRR4-1/2	1544.299	1543.855	287.766	0.592	1183.423	0.548	19	0.203	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1125.104	1125.303	-177.229	0.510	1260.172	0.480	18	0.201	R.SPGAQTPVIVR.F
R4/RRR4-7/2	1761.288	1761.939	-940.348	0.579	1140.479	0.521	25	0.200	R.HM*DGFGVNTYTFVTR.D
R4/RRR4-7/2	1762.392	1761.939	257.657	0.588	846.370	0.622	23	0.198	R.HM*DGFGVNTYTFVTR.D
R4/RRR4-8/2	1124.620	1125.303	-1501.483	0.486	1268.000	0.466	18	0.198	R.SPGAQTPVIVR.F
R4/RRR4-2/2	1125.221	1125.303	-73.296	0.526	1223.777	0.481	18	0.198	R.SPGAQTPVIVR.F
R4/RRR4-6/2	1125.128	1125.303	-156.332	0.475	1194.262	0.485	18	0.196	R.SPGAQTPVIVR.F
R4/RRR4-3/2	1125.136	1125.303	-148.931	0.524	1095.733	0.519	18	0.196	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1125.084	1125.303	-195.624	0.501	1195.689	0.476	18	0.195	R.SPGAQTPVIVR.F
R4/RRR4-1/2	1124.593	1125.303	-1525.579	0.457	1181.981	0.488	17	0.195	R.SPGAQTPVIVR.F
R4/RRR4-6/2	1544.181	1543.855	211.671	0.481	1208.461	0.488	19	0.194	R.LGPNYLM*LPVNAPK.C
R4/RRR4-2/2	1539.462	1540.785	-1513.543	0.385	1348.073	0.420	19	0.193	R.GPILLEDYHLIEK.L
R4/RRR4-10/2	1125.167	1125.303	-121.832	0.462	1185.863	0.463	18	0.191	R.SPGAQTPVIVR.F
R4/RRR4-9/2	1125.101	1125.303	-180.277	0.500	1173.395	0.468	17	0.191	R.SPGAQTPVIVR.F
R4/RRR4-2/2	1543.276	1543.855	-1026.632	0.476	1173.557	0.487	18	0.190	R.LGPNYLM*LPVNAPK.C
R4/RRR4-1/2	1124.444	1125.303	-1658.623	0.452	1155.753	0.470	17	0.189	R.SPGAQTPVIVR.F
R4/RRR4-1/2	1124.663	1125.303	-1462.560	0.493	1193.198	0.448	18	0.189	R.SPGAQTPVIVR.F
R4/RRR4-7/2	1543.699	1543.855	-101.513	0.536	1097.656	0.499	19	0.188	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1543.393	1543.855	-300.372	0.527	1110.636	0.500	18	0.188	R.LGPNYLM*LPVNAPK.C
R4/RRR4-3/2	1070.970	1071.168	-185.502	0.488	1181.008	0.440	15	0.188	R.VFAYADTQR.Y
R4/RRR4-2/2	1527.505	1527.856	-230.413	0.486	902.494	0.561	20	0.187	R.LGPNYLMLPVNAPK.C
R4/RRR4-2/2	1071.012	1071.168	-145.369	0.468	1134.014	0.457	15	0.187	R.VFAYADTQR.Y
R4/RRR4-4/2	1125.120	1125.303	-163.407	0.502	1010.117	0.508	17	0.187	R.SPGAQTPVIVR.F
R4/RRR4-5/2	1543.743	1543.855	-72.839	0.479	1038.556	0.521	18	0.187	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1272.997	1273.287	-228.582	0.412	1474.203	0.326	15	0.187	R.DEEVDYYPSR.H
R4/RRR4-2/2	1540.463	1540.785	-209.320	0.475	1145.553	0.470	18	0.187	R.GPILLEDYHLIEK.L
R4/RRR4-1/2	970.897	970.107	-216.854	0.413	1105.311	0.473	15	0.187	R.FAGELAHPK.V
R4/RRR4-8/2	1124.567	1125.303	-1548.587	0.515	1136.780	0.453	18	0.186	R.SPGAQTPVIVR.F
R4/RRR4-6/2	1125.057	1125.303	-219.897	0.477	1155.086	0.446	18	0.186	R.SPGAQTPVIVR.F
R4/RRR4-1/2	970.712	970.107	-408.110	0.414	1212.091	0.426	14	0.186	R.FAGELAHPK.V
R4/RRR4-2/2	1072.138	1071.168	-27.934	0.530	920.325	0.512	15	0.185	R.VFAYADTQR.Y
R4/RRR4-7/2	969.909	970.107	-204.452	0.465	1066.946	0.473	14	0.185	R.FAGELAHPK.V
R4/RRR4-7/2	1125.249	1125.303	-48.160	0.450	1152.961	0.442	17	0.184	R.SPGAQTPVIVR.F
R4/RRR4-8/2	1544.351	1543.855	321.689	0.560	923.865	0.555	17	0.184	R.LGPNYLM*LPVNAPK.C
R4/RRR4-10/2	1125.232	1125.303	-63.394	0.494	1023.166	0.482	17	0.183	R.SPGAQTPVIVR.F
R4/RRR4-5/2	1071.422	1071.168	238.193	0.488	888.913	0.513	15	0.183	R.VFAYADTQR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1125.091	1125.303	-188.984	0.509	979.438	0.491	17	0.183	R.SPGAQTPVIVR.F
R4/RRR4-3/2	1543.920	1543.855	42.238	0.513	1111.826	0.468	18	0.182	R.LGPNYLM*LPVNAPK.C
R4/RRR4-5/2	1124.515	1125.303	-1595.368	0.476	1094.244	0.441	18	0.182	R.SPGAQTPVIVR.F
R4/RRR4-6/2	970.085	970.107	-22.669	0.415	1155.880	0.418	14	0.181	R.FAGELAHPK.V
R4/RRR4-6/2	1124.941	1125.303	-322.880	0.505	1035.896	0.460	17	0.181	R.SPGAQTPVIVR.F
R4/RRR4-7/2	1603.457	1603.755	-186.360	0.508	1317.487	0.359	20	0.180	K.LFVQVIDPEEEER.F
R4/RRR4-4/2	1125.041	1125.303	-233.612	0.490	970.177	0.474	17	0.179	R.SPGAQTPVIVR.F
R4/RRR4-2/2	1124.895	1125.303	-363.818	0.477	1055.446	0.444	17	0.179	R.SPGAQTPVIVR.F
R4/RRR4-3/2	1124.742	1125.303	-1392.353	0.495	1116.750	0.410	18	0.178	R.SPGAQTPVIVR.F
R4/RRR4-7/2	1125.080	1125.303	-198.563	0.497	1005.503	0.451	17	0.177	R.SPGAQTPVIVR.F
R4/RRR4-9/2	1124.583	1125.303	-1533.866	0.444	1068.064	0.425	18	0.177	R.SPGAQTPVIVR.F
R4/RRR4-4/2	1125.135	1125.303	-149.584	0.493	934.880	0.471	17	0.177	R.SPGAQTPVIVR.F
R4/RRR4-6/2	1071.093	1071.168	-70.256	0.451	961.766	0.448	15	0.176	R.VFAYADTQR.Y
R4/RRR4-7/2	969.881	970.107	-232.861	0.515	895.370	0.469	14	0.176	R.FAGELAHPK.V
R4/RRR4-1/2	1070.854	1071.168	-293.454	0.513	929.204	0.451	15	0.175	R.VFAYADTQR.Y
R4/RRR4-2/2	1544.252	1543.855	257.884	0.532	880.557	0.514	17	0.175	R.LGPNYLM*LPVNAPK.C
R4/RRR4-9/2	1125.007	1125.303	-264.528	0.466	1067.378	0.415	17	0.175	R.SPGAQTPVIVR.F
R4/RRR4-7/2	969.952	970.107	-160.010	0.466	919.932	0.458	14	0.174	R.FAGELAHPK.V
R4/RRR4-7/2	1070.916	1071.168	-236.159	0.414	923.274	0.462	14	0.174	R.VFAYADTQR.Y
R4/RRR4-5/2	1124.857	1125.303	-397.791	0.499	860.072	0.472	17	0.174	R.SPGAQTPVIVR.F
R4/RRR4-1/2	1542.703	1543.855	-1399.155	0.434	1052.557	0.436	18	0.174	R.LGPNYLM*LPVNAPK.C
R4/RRR4-10/2	1125.074	1125.303	-204.658	0.503	975.745	0.437	17	0.173	R.SPGAQTPVIVR.F
R4/RRR4-3/2	1070.991	1071.168	-165.263	0.475	897.370	0.445	15	0.173	R.VFAYADTQR.Y
R4/RRR4-5/2	1071.005	1071.168	-152.457	0.422	784.751	0.493	14	0.172	R.VFAYADTQR.Y
R4/RRR4-11/2	1125.303	1125.303	-0.502	0.496	840.229	0.474	16	0.172	R.SPGAQTPVIVR.F
R4/RRR4-7/2	1104.514	1105.188	-1519.503	0.423	858.043	0.468	13	0.172	R.SHVQEYWR.V
R4/RRR4-2/2	1124.382	1125.303	-1713.595	0.426	922.039	0.441	17	0.171	R.SPGAQTPVIVR.F
R4/RRR4-7/2	1070.960	1071.168	-194.306	0.497	894.000	0.432	15	0.171	R.VFAYADTQR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1272.974	1273.287	-246.860	0.385	1344.053	0.283	15	0.169	R.DEEVDYYPSR.H
R4/RRR4-6/2	970.161	970.107	56.714	0.438	764.781	0.477	13	0.169	R.FAGELAHPK.V
R4/RRR4-3/2	1543.185	1543.855	-1085.562	0.444	925.389	0.447	17	0.168	R.LGPNYLM*LPVNAPK.C
R4/RRR4-1/2	970.098	970.107	-8.912	0.444	886.182	0.421	14	0.168	R.FAGELAHPK.V
R4/RRR4-2/2	1071.048	1071.168	-111.984	0.489	787.446	0.440	14	0.167	R.VFAYADTQR.Y
R4/RRR4-8/2	1070.429	1071.168	-1629.081	0.402	1008.488	0.377	15	0.167	R.VFAYADTQR.Y
R4/RRR4-3/2	969.609	970.107	-514.644	0.373	978.128	0.387	15	0.166	R.FAGELAHPK.V
R4/RRR4-1/2	1071.029	1071.168	-129.476	0.434	883.693	0.403	15	0.166	R.VFAYADTQR.Y
R4/RRR4-7/2	1603.430	1603.755	-203.009	0.482	1167.639	0.331	19	0.165	K.LFVQVIDPEEEER.F
R4/RRR4-7/2	1543.459	1543.855	-257.920	0.456	850.718	0.444	17	0.164	R.LGPNYLM*LPVNAPK.C
R4/RRR4-3/2	1071.324	1071.168	146.330	0.392	879.257	0.409	13	0.164	R.VFAYADTQR.Y
R4/RRR4-2/2	1542.601	1543.855	-1466.078	0.391	1077.703	0.366	17	0.164	R.LGPNYLM*LPVNAPK.C
R4/RRR4-9/2	1070.961	1071.168	-193.963	0.429	899.210	0.381	15	0.164	R.VFAYADTQR.Y
R4/RRR4-7/2	988.868	989.110	-245.229	0.443	738.739	0.434	12	0.163	R.FSTVIHER.G
R4/RRR4-8/2	970.126	970.107	19.611	0.390	750.046	0.441	13	0.163	R.FAGELAHPK.V
R4/RRR4-7/2	988.854	989.110	-259.224	0.456	664.715	0.455	11	0.163	R.FSTVIHER.G
R4/RRR4-7/2	1104.935	1105.188	-228.999	0.463	912.282	0.394	12	0.162	-.SHVQEYWR.-
R4/RRR4-5/2	1070.981	1071.168	-174.410	0.441	756.751	0.410	14	0.162	R.VFAYADTQR.Y
R4/RRR4-2/2	969.948	970.107	-163.545	0.359	1086.654	0.319	14	0.161	R.FAGELAHPK.V
R4/RRR4-1/2	1071.101	1071.168	-62.368	0.441	787.640	0.408	13	0.161	R.VFAYADTQR.Y
R4/RRR4-6/2	1070.988	1071.168	-168.236	0.431	870.252	0.370	15	0.161	R.VFAYADTQR.Y
R4/RRR4-8/2	1104.905	1105.188	-256.043	0.329	808.954	0.442	12	0.161	R.SHVQEYWR.V
R4/RRR4-9/2	1071.027	1071.168	-131.534	0.412	753.914	0.405	14	0.161	R.VFAYADTQR.Y
R4/RRR4-5/2	1124.498	1125.303	-1609.981	0.466	749.385	0.412	16	0.161	R.SPGAQTPVIVR.F
R4/RRR4-7/2	970.068	970.107	-40.339	0.413	887.985	0.370	14	0.161	R.FAGELAHPK.V
R4/RRR4-4/2	1543.507	1543.855	-226.738	0.487	877.401	0.416	17	0.161	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1105.100	1105.188	-79.062	0.405	747.524	0.442	12	0.160	-.SHVQEYWR.-
R4/RRR4-16/2	1125.083	1125.303	-196.386	0.422	713.865	0.398	16	0.158	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	970.017	970.107	-92.976	0.372	929.176	0.340	13	0.157	R.FAGELAHPK.V
R4/RRR4-7/2	1603.338	1603.755	-260.522	0.460	1022.913	0.328	18	0.156	K.LFVQVIDPEEEER.F
R4/RRR4-6/2	969.167	970.107	-2007.615	0.337	1023.174	0.299	14	0.156	R.FAGELAHPK.V
R4/RRR4-3/2	969.462	970.107	-1701.374	0.362	722.811	0.377	13	0.155	R.FAGELAHPK.V
R4/RRR4-1/2	989.296	989.110	188.660	0.361	489.469	0.426	11	0.155	R.FSTVIHER.G
R4/RRR4-7/2	988.418	989.110	-1717.179	0.415	510.438	0.424	10	0.154	R.FSTVIHER.G
R4/RRR4-1/2	989.112	989.110	2.276	0.382	644.028	0.388	11	0.154	R.FSTVIHER.G
R4/RRR4-3/2	969.284	970.107	-1886.235	0.307	746.744	0.380	13	0.154	R.FAGELAHPK.V
R4/RRR4-1/2	989.017	989.110	-93.789	0.370	490.073	0.429	10	0.153	R.FSTVIHER.G
R4/RRR4-6/2	1070.976	1071.168	-179.785	0.434	725.753	0.337	14	0.153	R.VFAYADTQR.Y
R4/RRR4-7/2	970.020	970.107	-89.567	0.395	889.433	0.308	14	0.153	R.FAGELAHPK.V
R4/RRR4-7/2	970.119	970.107	12.922	0.353	903.564	0.307	14	0.153	R.FAGELAHPK.V
R4/RRR4-16/2	1125.313	1125.303	8.855	0.427	636.525	0.344	16	0.152	R.SPGAQTPVIVR.F
R4/RRR4-2/2	989.093	989.110	-17.034	0.398	519.089	0.393	10	0.152	R.FSTVIHER.G
R4/RRR4-10/2	1543.455	1543.855	-259.903	0.374	657.077	0.392	15	0.150	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1543.774	1543.855	-52.851	0.242	1091.231	0.248	16	0.149	R.LGPNYLM*LPVNAPK.C
R4/RRR4-2/2	988.536	989.110	-1596.708	0.397	415.397	0.353	10	0.149	R.FSTVIHER.G
R4/RRR4-16/2	1125.166	1125.303	-122.267	0.381	564.863	0.349	16	0.149	-.SPGAQTPVIVR.-
R4/RRR4-5/3	1541.229	1540.785	289.187	0.395	880.112	0.579	22	0.149	R.GPILLEDYHLIEK.L
R4/RRR4-11/2	1071.854	1071.168	-293.866	0.367	436.610	0.369	11	0.148	-.VFAYADTQR.-
R4/RRR4-7/2	1071.193	1071.168	23.247	0.340	758.063	0.284	13	0.148	R.VFAYADTQR.Y
R4/RRR4-2/2	1543.428	1543.855	-277.995	0.323	1327.650	0.143	17	0.147	R.LGPNYLM*LPVNAPK.C
R4/RRR4-2/2	1526.875	1527.856	-1301.254	0.213	406.776	0.432	18	0.147	R.LGPNYLMLPVNAPK.C
R4/RRR4-7/2	1071.207	1071.168	36.506	0.300	663.550	0.299	12	0.146	R.VFAYADTQR.Y
R4/RRR4-7/2	1070.867	1071.168	-281.674	0.191	226.192	0.344	10	0.146	R.VFAYADTQR.Y
R4/RRR4-9/2	1528.988	1527.856	86.274	0.315	781.487	0.278	16	0.144	R.LGPNYLMLPVNAPK.C
R4/RRR4-7/2	1071.141	1071.168	-24.988	0.264	539.986	0.338	12	0.142	-.VFAYADTQR.-
R4/RRR4-2/2	988.308	989.110	-1828.618	0.313	493.867	0.276	10	0.142	-.FSTVIHER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1529.247	1527.856	256.714	0.328	583.727	0.319	13	0.141	R.LGPNYLMLPVNAPK.C
R4/RRR4-4/2	988.887	989.110	-226.529	0.315	545.662	0.211	11	0.141	R.FSTVIHER.G
R4/RRR4-7/2	1070.872	1071.168	-276.985	0.205	475.946	0.253	11	0.141	-.VFAYADTQR.-
R4/RRR4-3/2	1528.709	1527.856	-96.559	0.365	825.893	0.228	16	0.139	R.LGPNYLMLPVNAPK.C
R4/RRR4-15/2	1539.891	1540.785	-1233.485	0.280	683.772	0.253	14	0.139	R.GPILLEDYHLIEK.L
R4/RRR4-7/2	1544.561	1543.855	-190.911	0.351	841.500	0.211	15	0.137	R.LGPNYLM*LPVNAPK.C
R4/RRR4-7/2	1543.358	1543.855	-323.226	0.402	552.195	0.290	13	0.137	-.LGPNYLM*LPVNAPK.-
R4/RRR4-7/3	1770.595	1769.943	-197.127	0.483	1139.767	0.444	28	0.133	K.ATIHKQNDFKQPGER.Y
R4/RRR4-4/3	1541.208	1540.785	275.606	0.402	842.310	0.520	22	0.133	R.GPILLEDYHLIEK.L
R4/RRR4-1/3	1541.086	1540.785	195.783	0.416	838.169	0.505	22	0.129	R.GPILLEDYHLIEK.L
R4/RRR4-7/3	1540.178	1540.785	-1046.530	0.429	774.464	0.517	22	0.128	R.GPILLEDYHLIEK.L
R4/RRR4-7/3	1540.397	1540.785	-252.657	0.406	818.828	0.490	22	0.125	R.GPILLEDYHLIEK.L
R4/RRR4-2/3	1540.416	1540.785	-240.135	0.393	859.944	0.475	22	0.124	R.GPILLEDYHLIEK.L
R4/RRR4-7/3	1952.887	1952.248	-185.403	0.372	1173.665	0.389	27	0.124	R.DGIKFPDVIHAFKPNPR.S
R4/RRR4-6/3	1540.744	1540.785	-26.480	0.396	794.873	0.487	23	0.123	R.GPILLEDYHLIEK.L
R4/RRR4-6/3	1540.802	1540.785	11.187	0.431	708.339	0.502	22	0.122	R.GPILLEDYHLIEK.L
R4/RRR4-1/3	1541.008	1540.785	145.380	0.416	780.077	0.485	22	0.122	R.GPILLEDYHLIEK.L
R4/RRR4-2/3	1540.665	1540.785	-78.097	0.435	615.261	0.513	20	0.122	R.GPILLEDYHLIEK.L
R4/RRR4-7/3	1127.192	1126.293	-89.582	0.514	1153.894	0.381	22	0.117	R.RFAGELAHPK.V
R4/RRR4-7/3	1952.106	1952.248	-72.926	0.342	1221.062	0.338	27	0.116	R.DGIKFPDVIHAFKPNPR.S
R4/RRR4-8/3	1540.793	1540.785	5.108	0.363	886.667	0.421	23	0.115	R.GPILLEDYHLIEK.L
R4/RRR4-3/3	1540.465	1540.785	-208.176	0.389	799.321	0.433	22	0.114	R.GPILLEDYHLIEK.L
R4/RRR4-6/3	1539.510	1540.785	-1481.931	0.343	886.395	0.411	23	0.113	R.GPILLEDYHLIEK.L
R4/RRR4-5/3	1541.409	1540.785	-244.428	0.358	612.464	0.447	18	0.112	R.GPILLEDYHLIEK.L
R4/RRR4-2/3	1540.789	1540.785	2.843	0.418	839.735	0.414	22	0.112	R.GPILLEDYHLIEK.L
R4/RRR4-4/3	1541.205	1540.785	273.462	0.335	538.924	0.449	19	0.111	R.GPILLEDYHLIEK.L
R4/RRR4-3/3	1951.960	1952.248	-147.919	0.377	888.210	0.416	26	0.110	R.DGIKFPDVIHAFKPNPR.S
R4/RRR4-7/3	1541.022	1540.785	154.198	0.439	557.232	0.433	19	0.110	R.GPILLEDYHLIEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1770.783	1769.943	-90.488	0.495	938.525	0.410	25	0.109	K.ATIHKQNDFKQPGER.Y
R4/RRR4-9/3	1540.859	1540.785	48.374	0.289	526.815	0.424	18	0.108	R.GPILLEDYHLIEK.L
R4/RRR4-8/3	1541.303	1540.785	-313.436	0.401	609.015	0.404	20	0.107	R.GPILLEDYHLIEK.L
R4/RRR4-3/3	1540.157	1540.785	-1060.019	0.358	521.655	0.386	18	0.105	R.GPILLEDYHLIEK.L
R4/RRR4-7/3	1982.460	1983.204	-882.532	0.413	1151.559	0.311	26	0.103	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-9/3	1540.843	1540.785	38.124	0.286	459.808	0.378	18	0.102	-.GPILLEDYHLIEK.-
R4/RRR4-8/3	1540.643	1540.785	-92.641	0.334	722.098	0.356	22	0.101	R.GPILLEDYHLIEK.L
R4/RRR4-4/3	1540.453	1540.785	-215.927	0.307	538.479	0.330	18	0.101	R.GPILLEDYHLIEK.L
R4/RRR4-7/3	1982.252	1983.204	-987.689	0.383	884.887	0.367	23	0.099	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-3/3	1951.969	1952.248	-143.214	0.326	621.001	0.375	23	0.095	R.DGIKFPDVIHAFKPNPR.S
R4/RRR4-1/3	1540.420	1540.785	-237.750	0.367	695.438	0.282	21	0.095	R.GPILLEDYHLIEK.L
R4/RRR4-3/3	1540.243	1540.785	-1004.276	0.246	526.185	0.303	19	0.095	-.GPILLEDYHLIEK.-
R4/RRR4-7/3	1126.804	1126.293	-434.820	0.473	1004.614	0.316	21	0.090	-.RFAGELAHPK.-
R4/RRR4-4/3	1952.663	1952.248	213.394	0.328	753.511	0.303	23	0.089	R.DGIKFPDVIHAFKPNPR.S
R4/RRR4-2/3	1983.100	1983.204	-52.709	0.355	754.218	0.330	22	0.089	R.AIWVNYLSQCDESLGVK.I
R4/RRR4-4/3	1952.027	1952.248	-113.479	0.326	642.286	0.279	22	0.087	R.DGIKFPDVIHAFKPNPR.S
R4/RRR4-7/3	1125.975	1126.293	-283.070	0.479	829.071	0.318	19	0.087	-.RFAGELAHPK.-
R4/RRR4-7/3	1951.337	1952.248	-981.972	0.275	801.200	0.277	24	0.087	R.DGIKFPDVIHAFKPNPR.S
R4/RRR4-7/3	1126.850	1126.293	-393.894	0.404	646.218	0.287	17	0.087	-.RFAGELAHPK.-
R4/RRR4-5/3	1125.765	1126.293	-1361.518	0.426	819.852	0.187	19	0.082	R.RFAGELAHPK.V
R4/RRR4-5/3	1126.731	1126.293	389.976	0.411	781.751	0.292	18	0.076	-.RFAGELAHPK.-
R4/RRR4-3/3	1125.715	1126.293	-1406.280	0.405	789.991	0.235	17	0.075	-.RFAGELAHPK.-
R4/RRR4-2/3	1126.968	1126.293	-289.556	0.375	645.622	0.234	17	0.073	-.RFAGELAHPK.-
R4/RRR4-7/3	1901.596	1902.181	-835.715	0.434	2442.022	0.470	39	0.389	K.AAVEEGIVPGGGVALLYASK.E
R4/RRR4-7/2	1418.229	1418.685	-322.152	0.402	2429.526	0.423	21	0.340	R.GISMAVDAVVTNLK.G
R4/RRR4-7/2	1418.389	1418.685	-209.035	0.421	2048.912	0.429	20	0.278	R.GISMAVDAVVTNLK.G
R4/RRR4-7/2	1321.129	1321.461	-252.227	0.519	1782.306	0.550	19	0.276	R.NVVIEQSYGSPK.V
R4/RRR4-7/2	1434.566	1434.684	-82.376	0.396	2068.037	0.379	20	0.267	R.GISM*AVDAVVTNLK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1322.119	1321.461	-259.354	0.542	1646.673	0.562	18	0.260	R.NVVIEQSYGSPK.V
R4/RRR4-7/3	1902.265	1902.181	44.429	0.488	1732.234	0.529	36	0.251	K.AAVEEGIVPGGGVALLYASK.E
R4/RRR4-7/2	1433.921	1434.684	-1233.072	0.468	1781.572	0.405	21	0.236	R.GISM*AVDAVVTNLK.G
R4/RRR4-7/2	1387.280	1386.576	-214.517	0.514	1372.540	0.584	19	0.234	R.GYISPYFVTNPK.T
R4/RRR4-7/2	1901.444	1902.181	-916.135	0.476	1367.268	0.599	28	0.232	K.AAVEEGIVPGGGVALLYASK.E
R4/RRR4-7/2	1386.101	1386.576	-344.194	0.492	1379.842	0.540	19	0.224	R.GYISPYFVTNPK.T
R4/RRR4-7/2	1146.397	1147.218	-1592.791	0.398	1668.832	0.400	19	0.222	K.IGGASEAEVGEK.K
R4/RRR4-7/2	1386.864	1386.576	208.206	0.497	1231.235	0.571	18	0.215	R.GYISPYFVTNPK.T
R4/RRR4-7/2	1901.001	1902.181	-1149.821	0.441	1259.772	0.571	26	0.213	K.AAVEEGIVPGGGVALLYASK.E
R4/RRR4-7/2	1196.722	1197.453	-1450.613	0.486	1356.242	0.462	17	0.205	K.IGVQIIQNALK.T
R4/RRR4-7/2	1196.715	1197.453	-1456.043	0.530	1333.672	0.461	17	0.203	K.IGVQIIQNALK.T
R4/RRR4-7/2	1902.065	1902.181	-60.934	0.482	1073.389	0.560	25	0.195	K.AAVEEGIVPGGGVALLYASK.E
R4/RRR4-7/3	1534.233	1534.699	-304.307	0.379	1911.840	0.306	30	0.188	K.GRNVVIEQSYGSPK.V
R4/RRR4-7/2	1031.987	1031.142	-150.391	0.501	1218.409	0.409	16	0.184	R.GVEELADAVK.V
R4/RRR4-7/2	1587.239	1586.679	-278.284	0.553	1079.760	0.491	18	0.184	R.SAIELSTSDYDKEK.L
R4/RRR4-7/2	1030.919	1031.142	-216.580	0.472	1116.741	0.405	16	0.176	-.GVEELADAVK.-
R4/RRR4-7/2	1146.351	1147.218	-1633.441	0.368	1096.988	0.412	17	0.171	K.IGGASEAEVGEK.K
R4/RRR4-7/2	1586.388	1586.679	-184.429	0.498	960.781	0.465	17	0.171	R.SAIELSTSDYDKEK.L
R4/RRR4-7/2	1032.003	1031.142	-134.491	0.530	882.046	0.421	15	0.166	R.GVEELADAVK.V
R4/RRR4-7/2	1586.300	1586.679	-239.548	0.507	773.348	0.479	16	0.162	R.SAIELSTSDYDKEK.L
R4/RRR4-7/3	1861.496	1862.072	-848.916	0.486	1405.168	0.423	31	0.156	K.VTVSKDDTVILDGAGDKK.S
R4/RRR4-7/2	1535.499	1535.724	-146.367	0.460	772.953	0.392	19	0.156	K.ELDKLLTANFDQK.I
R4/RRR4-7/2	843.910	844.034	-146.984	0.350	845.201	0.325	15	0.152	K.LSGGVAVLK.I
R4/RRR4-7/2	843.911	844.034	-146.114	0.479	833.311	0.284	15	0.149	K.LSGGVAVLK.I
R4/RRR4-7/2	1434.108	1434.684	-1102.374	0.317	916.915	0.287	18	0.147	R.GISM*AVDAVVTNLK.G
R4/RRR4-7/2	843.843	844.034	-227.233	0.368	513.262	0.326	12	0.145	K.LSGGVAVLK.I
R4/RRR4-7/2	1203.958	1204.316	-297.927	0.415	764.854	0.315	15	0.145	K.DRVTDALNATK.A
R4/RRR4-7/3	1861.854	1862.072	-117.496	0.508	1069.710	0.479	27	0.136	K.VTVSKDDTVILDGAGDKK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1435.233	1434.684	-314.972	0.284	600.820	0.149	14	0.131	R.GISM*AVDAVVTNLK.G
R4/RRR4-7/3	1861.996	1862.072	-40.947	0.469	990.866	0.445	27	0.121	K.VTVSKDDTVILDGAGDKK.S
R4/RRR4-7/3	1546.275	1546.665	-253.121	0.435	804.927	0.415	28	0.103	K.IGGASEAEVGEKKDR.V
R4/RRR4-7/3	1546.588	1546.665	-49.654	0.377	749.791	0.311	26	0.086	K.IGGASEAEVGEKKDR.V
R4/RRR4-14/2	1368.134	1367.556	-309.670	0.554	1992.688	0.623	22	0.331	K.FDVGNVVM*VTGGR.N
R4/RRR4-14/2	1366.906	1367.556	-1211.132	0.505	1819.006	0.556	21	0.282	K.FDVGNVVM*VTGGR.N
R4/RRR4-14/2	1368.369	1367.556	-137.106	0.600	1733.072	0.588	21	0.280	K.FDVGNVVM*VTGGR.N
R4/RRR4-14/3	1901.373	1900.185	99.107	0.503	1837.609	0.522	32	0.265	R.TDKTYPAGFM*DVISIPK.T
R4/RRR4-14/2	1351.158	1351.557	-296.188	0.438	1351.777	0.547	18	0.218	K.FDVGNVVMVTGGR.N
R4/RRR4-14/2	1350.870	1351.557	-1252.363	0.455	1451.968	0.482	18	0.215	K.FDVGNVVMVTGGR.N
R4/RRR4-15/2	949.151	949.129	23.141	0.418	1065.145	0.573	15	0.200	R.LGNVFTIGK.G
R4/RRR4-15/2	949.315	949.129	196.864	0.452	1040.847	0.543	15	0.195	R.LGNVFTIGK.G
R4/RRR4-14/2	1899.610	1900.185	-831.632	0.473	1088.745	0.548	22	0.194	R.TDKTYPAGFM*DVISIPK.T
R4/RRR4-13/2	948.942	949.129	-197.228	0.487	987.480	0.546	15	0.194	R.LGNVFTIGK.G
R4/RRR4-14/2	949.010	949.129	-125.223	0.508	959.671	0.534	15	0.191	R.LGNVFTIGK.G
R4/RRR4-15/2	949.269	949.129	148.248	0.461	1073.822	0.488	15	0.189	R.LGNVFTIGK.G
R4/RRR4-14/2	948.543	949.129	-1676.679	0.454	910.550	0.544	14	0.186	R.LGNVFTIGK.G
R4/RRR4-14/2	949.040	949.129	-93.612	0.486	889.088	0.477	14	0.176	R.LGNVFTIGK.G
R4/RRR4-14/2	1104.895	1105.334	-398.635	0.412	941.325	0.429	14	0.170	R.EVISILM*QR.H
R4/RRR4-14/2	1090.043	1089.334	-267.733	0.445	1140.646	0.351	14	0.169	R.EVISILMQR.H
R4/RRR4-14/2	1483.478	1483.818	-229.741	0.547	1156.802	0.358	17	0.167	K.SRECLPLILIIR.N
R4/RRR4-14/3	1483.517	1483.818	-203.664	0.540	1688.506	0.350	25	0.164	K.SRECLPLILIIR.N
R4/RRR4-14/2	1883.513	1884.186	-890.729	0.469	791.367	0.487	20	0.164	R.TDKTYPAGFMDVISIPK.T
R4/RRR4-14/2	1127.214	1126.333	-105.426	0.419	699.736	0.468	14	0.163	K.GNKPWVSLPK.G
R4/RRR4-14/2	1126.994	1126.333	-301.325	0.462	546.641	0.488	14	0.162	K.GNKPWVSLPK.G
R4/RRR4-14/2	1484.394	1483.818	-286.100	0.552	1004.385	0.377	16	0.160	K.SRECLPLILIIR.N
R4/RRR4-14/2	1548.432	1548.805	-242.086	0.475	948.673	0.361	19	0.158	K.IDLETNKIVDFIK.F
R4/RRR4-14/3	1215.635	1216.454	-1501.025	0.534	1724.910	0.324	25	0.156	R.TIRYPDPIIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1483.750	1483.818	-45.931	0.529	1013.601	0.344	16	0.156	K.SRECLPLILIIR.N
R4/RRR4-14/2	767.344	767.896	-2028.888	0.382	538.664	0.444	10	0.156	R.HVLVDGK.V
R4/RRR4-14/2	1540.214	1539.820	256.317	0.466	396.320	0.502	16	0.155	K.TYPAGFMDVISIPK.T
R4/RRR4-14/2	1126.447	1126.333	101.344	0.405	563.327	0.414	15	0.155	K.GNKPWVSLPK.G
R4/RRR4-14/2	767.858	767.896	-49.368	0.352	591.127	0.420	10	0.153	R.HVLVDGK.V
R4/RRR4-14/2	987.431	988.120	-1715.484	0.380	967.159	0.251	13	0.148	K.LSIIEEQR.K
R4/RRR4-14/2	1482.946	1483.818	-1266.072	0.499	885.078	0.331	15	0.148	K.SRECLPLILIIR.N
R4/RRR4-14/2	987.848	988.120	-276.530	0.462	1016.549	0.242	13	0.148	K.LSIIEEQR.K
R4/RRR4-14/3	1483.603	1483.818	-145.100	0.561	1689.087	0.303	25	0.148	K.SRECLPLILIIR.N
R4/RRR4-14/2	1555.417	1555.820	-259.673	0.329	231.504	0.405	16	0.146	K.TYPAGFM*DVISIPK.T
R4/RRR4-1/2	949.086	949.129	-44.843	0.247	432.204	0.384	11	0.144	R.LGNVFTIGK.G
R4/RRR4-14/3	1883.812	1884.186	-198.831	0.439	1403.503	0.382	28	0.144	R.TDKTYPAGFMDVISIPK.T
R4/RRR4-14/2	1350.726	1351.557	-1359.639	0.341	768.229	0.308	15	0.143	K.FDVGNVVMVTGGR.N
R4/RRR4-14/2	987.917	988.120	-206.612	0.521	949.407	0.228	13	0.143	K.LSIIEEQR.K
R4/RRR4-14/2	1451.204	1451.655	-311.795	0.363	734.194	0.304	19	0.142	K.LGGAFAPKPSSGPHK.A
R4/RRR4-14/2	1547.641	1548.805	-1402.857	0.406	932.521	0.242	18	0.142	K.IDLETNKIVDFIK.F
R4/RRR4-14/2	1451.119	1451.655	-1061.644	0.329	593.048	0.344	18	0.142	K.LGGAFAPKPSSGPHK.A
R4/RRR4-10/2	988.822	988.120	-302.260	0.293	544.951	0.242	12	0.142	K.LSIIEEQR.K
R4/RRR4-15/2	1105.745	1105.334	373.111	0.308	598.477	0.202	12	0.138	R.EVISILM*QR.H
R4/RRR4-14/2	988.012	988.120	-110.057	0.278	786.808	0.171	12	0.137	K.LSIIEEQR.K
R4/RRR4-15/2	1105.976	1105.334	-324.295	0.288	1009.450	0.116	14	0.136	R.EVISILM*QR.H
R4/RRR4-14/2	1104.967	1105.334	-332.680	0.154	828.814	0.164	12	0.133	R.EVISILM*QR.H
R4/RRR4-14/3	1900.053	1900.185	-69.460	0.447	1030.190	0.473	25	0.132	R.TDKTYPAGFM*DVISIPK.T
R4/RRR4-14/3	1475.397	1475.626	-155.865	0.464	860.257	0.492	24	0.122	K.ANDTIKIDLETNK.I
R4/RRR4-14/3	1483.153	1483.818	-1126.145	0.528	1464.412	0.295	24	0.122	-.SRECLPLILIIR.-
R4/RRR4-14/3	1483.289	1483.818	-1033.675	0.559	1396.923	0.291	25	0.112	-.SRECLPLILIIR.-
R4/RRR4-14/3	1483.412	1483.818	-274.619	0.557	1439.282	0.276	24	0.112	-.SRECLPLILIIR.-
R4/RRR4-14/3	1884.081	1884.186	-55.414	0.382	1434.809	0.220	28	0.104	R.TDKTYPAGFMDVISIPK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/3	1216.796	1216.454	281.317	0.496	1013.853	0.351	22	0.103	R.TIRYPDPIIK.A
R4/RRR4-14/3	1216.597	1216.454	117.725	0.437	1216.173	0.285	23	0.100	R.TIRYPDPIIK.A
R4/RRR4-14/3	1476.987	1475.626	244.525	0.480	608.753	0.416	21	0.099	K.ANDTIKIDLETNK.I
R4/RRR4-14/3	1475.294	1475.626	-225.837	0.417	741.123	0.396	22	0.098	K.ANDTIKIDLETNK.I
R4/RRR4-14/3	1216.432	1216.454	-18.593	0.418	805.831	0.294	19	0.089	R.TIRYPDPIIK.A
R4/RRR4-14/3	1216.642	1216.454	154.855	0.352	922.343	0.266	21	0.086	R.TIRYPDPIIK.A
R4/RRR4-3/2	1646.276	1645.938	205.818	0.533	3129.042	0.429	24	0.495	K.IFM*VGSGALGCEFLK.N
R4/RRR4-3/2	1645.417	1645.938	-927.200	0.522	3016.835	0.430	24	0.468	K.IFM*VGSGALGCEFLK.N
R4/RRR4-3/3	1975.119	1974.290	-86.644	0.539	2532.057	0.498	36	0.425	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1631.006	1629.939	41.617	0.572	2625.158	0.520	24	0.414	K.IFMVGSGALGCEFLK.N
R4/RRR4-3/3	1973.808	1974.290	-245.128	0.516	2466.537	0.499	35	0.408	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-1/2	1974.388	1974.290	49.634	0.536	2526.532	0.497	28	0.382	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1974.436	1974.290	74.189	0.604	2382.658	0.563	28	0.376	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1570.440	1570.728	-184.119	0.584	2345.323	0.536	24	0.365	R.YDAQISVFGSNLQK.K
R4/RRR4-3/2	1570.192	1570.728	-980.979	0.543	2239.167	0.499	24	0.333	R.YDAQISVFGSNLQK.K
R4/RRR4-3/3	1974.360	1974.290	35.396	0.516	2165.571	0.486	34	0.322	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1570.250	1570.728	-305.466	0.575	2143.364	0.492	24	0.314	R.YDAQISVFGSNLQK.K
R4/RRR4-3/3	1883.808	1882.198	-207.638	0.445	2115.374	0.473	29	0.307	K.FDRPPLLHLAFQALDK.F
R4/RRR4-3/2	1975.605	1974.290	159.794	0.569	2169.121	0.472	28	0.307	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1973.705	1974.290	-805.672	0.557	2098.749	0.486	27	0.299	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/3	1975.029	1974.290	-132.398	0.497	1982.640	0.488	35	0.280	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1973.670	1974.290	-822.993	0.529	1864.526	0.514	26	0.272	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1803.273	1804.100	-1016.225	0.490	1760.137	0.494	24	0.256	K.M*AEAVDKVIVPDFQPK.Q
R4/RRR4-3/2	1973.226	1974.290	-1049.037	0.508	1785.057	0.491	26	0.255	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1291.904	1292.380	-369.385	0.504	1613.296	0.440	20	0.227	R.FPIAGSSDDVQR.L
R4/RRR4-3/2	1292.018	1292.380	-280.464	0.476	1570.485	0.421	20	0.218	R.FPIAGSSDDVQR.L
R4/RRR4-3/2	1292.212	1292.380	-129.959	0.500	1457.330	0.466	19	0.216	R.FPIAGSSDDVQR.L
R4/RRR4-3/2	1645.059	1645.938	-1145.621	0.443	1576.931	0.386	19	0.205	K.IFM*VGSGALGCEFLK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1447.724	1448.566	-1275.985	0.414	1617.027	0.318	19	0.198	R.RFPIAGSSDDVQR.L
R4/RRR4-3/3	1974.512	1974.290	112.780	0.542	1233.844	0.589	30	0.192	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1448.223	1448.566	-237.532	0.421	1434.056	0.355	18	0.187	R.RFPIAGSSDDVQR.L
R4/RRR4-3/2	1080.079	1080.223	-133.152	0.456	1232.415	0.414	15	0.186	K.LHVEALQNR.A
R4/RRR4-3/2	1249.484	1248.362	97.930	0.468	1002.297	0.489	17	0.183	K.LTVTDDDVIEK.S
R4/RRR4-3/2	1448.011	1448.566	-1077.113	0.419	1405.244	0.319	18	0.178	R.RFPIAGSSDDVQR.L
R4/RRR4-3/2	1079.971	1080.223	-233.385	0.484	1025.598	0.432	15	0.177	K.LHVEALQNR.A
R4/RRR4-3/2	1319.290	1319.447	-119.218	0.471	932.374	0.438	16	0.172	R.LKFEDYFSNR.V
R4/RRR4-3/2	1282.147	1282.342	-152.370	0.451	1265.801	0.337	16	0.172	R.APEIDEDLHSR.Q
R4/RRR4-3/2	1079.977	1080.223	-227.829	0.444	1067.114	0.386	14	0.170	K.LHVEALQNR.A
R4/RRR4-3/2	1974.203	1974.290	-44.381	0.499	970.949	0.488	20	0.170	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/2	1247.411	1248.362	-1568.635	0.365	1153.278	0.363	18	0.170	K.LTVTDDDVIEK.S
R4/RRR4-3/3	1883.226	1882.198	15.167	0.403	1542.690	0.403	26	0.169	K.FDRPPLLHLAFQALDK.F
R4/RRR4-3/2	1124.565	1125.265	-1516.472	0.386	781.271	0.478	16	0.167	K.LLHHFASGSR.A
R4/RRR4-3/2	1125.033	1125.265	-206.407	0.375	864.340	0.442	16	0.166	K.LLHHFASGSR.A
R4/RRR4-3/2	1320.278	1319.447	-128.031	0.488	867.860	0.382	16	0.161	R.LKFEDYFSNR.V
R4/RRR4-3/2	1124.475	1125.265	-1596.949	0.317	718.299	0.493	15	0.161	K.LLHHFASGSR.A
R4/RRR4-3/2	1051.807	1052.160	-336.368	0.390	623.587	0.459	14	0.160	R.SEFEGLLEK.T
R4/RRR4-3/2	957.992	958.053	-63.917	0.471	1117.264	0.299	13	0.160	R.DWNIGQPK.S
R4/RRR4-3/2	1247.434	1248.362	-1549.761	0.335	992.573	0.354	17	0.159	K.LTVTDDDVIEK.S
R4/RRR4-3/2	1319.222	1319.447	-170.548	0.470	729.283	0.379	14	0.154	R.LKFEDYFSNR.V
R4/RRR4-3/2	1052.120	1052.160	-37.659	0.345	601.910	0.432	13	0.152	-.SEFEGLLEK.-
R4/RRR4-3/2	958.011	958.053	-43.211	0.411	935.292	0.304	12	0.151	-.DWNIGQPK.-
R4/RRR4-3/2	1079.503	1080.223	-1598.035	0.338	1074.916	0.237	15	0.150	K.LHVEALQNR.A
R4/RRR4-3/2	1474.627	1473.697	-47.543	0.436	681.705	0.367	17	0.150	R.AETFGIPIPDWVK.N
R4/RRR4-3/2	1474.352	1473.697	-234.485	0.411	416.089	0.428	14	0.149	R.AETFGIPIPDWVK.N
R4/RRR4-3/2	1079.532	1080.223	-1570.544	0.371	728.856	0.305	13	0.147	K.LHVEALQNR.A
R4/RRR4-3/2	1051.549	1052.160	-1535.957	0.306	460.141	0.342	12	0.144	R.SEFEGLLEK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1079.401	1080.223	-1692.900	0.352	727.851	0.293	11	0.143	K.LHVEALQNR.A
R4/RRR4-2/2	1571.251	1570.728	-304.726	0.333	508.835	0.335	16	0.141	-.YDAQISVFGSNLQK.-
R4/RRR4-3/2	1474.804	1473.697	72.508	0.398	428.797	0.282	15	0.141	R.AETFGIPIPDWVK.N
R4/RRR4-2/2	1789.532	1788.101	241.406	0.395	688.413	0.338	16	0.139	K.MAEAVDKVIVPDFQPK.Q
R4/RRR4-1/2	1473.888	1473.697	130.204	0.310	481.936	0.272	15	0.139	R.AETFGIPIPDWVK.N
R4/RRR4-3/2	1473.231	1473.697	-317.272	0.302	524.275	0.226	16	0.138	R.AETFGIPIPDWVK.N
R4/RRR4-3/3	1124.770	1125.265	-441.675	0.379	705.252	0.427	19	0.104	K.LLHHFASGSR.A
R4/RRR4-1/3	1125.333	1125.265	60.795	0.362	381.724	0.407	16	0.101	K.LLHHFASGSR.A
R4/RRR4-3/3	1125.303	1125.265	33.868	0.383	883.829	0.374	22	0.100	K.LLHHFASGSR.A
R4/RRR4-3/3	1124.904	1125.265	-321.869	0.378	481.226	0.403	16	0.099	K.LLHHFASGSR.A
R4/RRR4-2/3	1125.476	1125.265	188.068	0.373	376.669	0.356	15	0.098	K.LLHHFASGSR.A
R4/RRR4-1/3	1124.839	1125.265	-379.686	0.345	578.768	0.315	19	0.092	K.LLHHFASGSR.A
R4/RRR4-3/3	1124.994	1125.265	-241.688	0.297	855.556	0.330	19	0.092	K.LLHHFASGSR.A
R4/RRR4-2/3	1973.317	1974.290	-1002.709	0.406	942.637	0.265	27	0.089	R.LFASNVLVSGLNGLGAEIAK.N
R4/RRR4-3/3	1974.593	1974.290	153.699	0.328	828.440	0.244	28	0.085	-.LFASNVLVSGLNGLGAEIAK.-
R4/RRR4-3/3	1804.089	1804.100	-6.095	0.340	1301.881	0.175	30	0.085	K.M*AEAVDKVIVPDFQPK.Q
R4/RRR4-3/3	1974.060	1974.290	-116.802	0.284	696.685	0.145	25	0.080	-.LFASNVLVSGLNGLGAEIAK.-
R4/RRR4-3/3	1974.772	1974.290	245.105	0.394	694.494	0.318	26	0.077	-.LFASNVLVSGLNGLGAEIAK.-
R4/RRR4-3/3	1804.030	1804.100	-39.384	0.321	1251.487	0.091	29	0.070	K.M*AEAVDKVIVPDFQPK.Q
R4/RRR4-19/3	1915.905	1915.135	-120.060	0.586	3226.851	0.460	38	0.610	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/3	1914.930	1915.135	-107.142	0.600	3040.128	0.451	37	0.538	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/3	1916.032	1915.135	-53.723	0.599	2954.826	0.475	37	0.525	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/2	1914.623	1915.135	-791.717	0.639	2599.151	0.562	26	0.421	K.VKDELVLDGNDIELVSR.S
R4/RRR4-19/2	1914.580	1915.135	-814.565	0.629	2585.432	0.562	26	0.419	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/2	1914.552	1915.135	-828.901	0.629	2516.627	0.562	26	0.404	K.VKDELVLDGNDIELVSR.S
R4/RRR4-19/2	1915.457	1915.135	168.711	0.628	2472.573	0.558	26	0.394	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/2	1914.575	1915.135	-817.125	0.612	2463.073	0.549	26	0.389	K.VKDELVLDGNDIELVSR.S
R4/RRR4-19/2	1915.711	1915.135	-221.813	0.641	2410.329	0.563	26	0.383	K.VKDELVLDGNDIELVSR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1582.419	1582.827	-258.318	0.512	2372.453	0.566	22	0.377	R.TAISHVQNLITGVTK.G
R4/RRR4-18/3	1915.008	1915.135	-66.283	0.568	2446.446	0.462	34	0.369	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/2	1583.160	1582.827	211.005	0.560	2147.846	0.626	22	0.356	R.TAISHVQNLITGVTK.G
R4/RRR4-18/2	1845.325	1844.996	178.772	0.522	2004.022	0.515	25	0.342	K.FLDGIYVSDKGTITEDA.-
R4/RRR4-18/2	1582.434	1582.827	-248.799	0.552	1977.539	0.601	21	0.317	R.TAISHVQNLITGVTK.G
R4/RRR4-18/2	1844.966	1844.996	-16.366	0.532	1877.163	0.561	25	0.315	K.FLDGIYVSDKGTITEDA.-
R4/RRR4-18/2	1583.427	1582.827	-252.818	0.531	1893.559	0.603	22	0.305	R.TAISHVQNLITGVTK.G
R4/RRR4-18/2	1374.253	1374.675	-308.317	0.560	2018.653	0.496	20	0.294	R.KVDMLEGVTILR.S
R4/RRR4-18/2	1373.736	1374.675	-1416.189	0.523	2050.630	0.451	20	0.286	R.KVDMLEGVTILR.S
R4/RRR4-18/2	1374.242	1374.675	-315.803	0.548	1939.685	0.497	20	0.283	R.KVDMLEGVTILR.S
R4/RRR4-18/2	1513.257	1512.695	-289.947	0.580	1743.744	0.571	22	0.277	K.HLNLDFQLLEGGR.K
R4/RRR4-19/2	1844.492	1844.996	-818.301	0.484	1784.494	0.522	24	0.276	K.FLDGIYVSDKGTITEDA.-
R4/RRR4-18/2	1845.389	1844.996	213.133	0.549	1748.855	0.559	24	0.270	K.FLDGIYVSDKGTITEDA.-
R4/RRR4-19/2	1513.417	1512.695	-183.937	0.558	1723.041	0.543	22	0.266	K.HLNLDFQLLEGGR.K
R4/RRR4-18/2	1582.164	1582.827	-1054.038	0.475	1585.299	0.622	21	0.264	R.TAISHVQNLITGVTK.G
R4/RRR4-19/2	1512.538	1512.695	-104.067	0.519	1733.300	0.502	22	0.256	K.HLNLDFQLLEGGR.K
R4/RRR4-18/2	1512.396	1512.695	-198.228	0.545	1596.216	0.555	21	0.252	K.HLNLDFQLLEGGR.K
R4/RRR4-19/2	1512.373	1512.695	-213.613	0.510	1560.021	0.542	21	0.244	K.HLNLDFQLLEGGR.K
R4/RRR4-18/2	1511.495	1512.695	-1459.734	0.462	1510.191	0.538	21	0.237	K.HLNLDFQLLEGGR.K
R4/RRR4-23/2	1582.380	1582.827	-283.162	0.472	1445.339	0.572	20	0.234	R.TAISHVQNLITGVTK.G
R4/RRR4-18/2	1261.777	1262.502	-1370.785	0.481	1772.344	0.392	18	0.233	K.VDM*LEGVTILR.S
R4/RRR4-19/2	1390.475	1390.675	-143.811	0.508	1401.619	0.443	19	0.205	R.KVDM*LEGVTILR.S
R4/RRR4-18/2	1321.219	1321.509	-219.868	0.463	1462.585	0.410	17	0.203	R.KLQVDAWFGTR.R
R4/RRR4-18/2	1320.494	1321.509	-1530.683	0.412	1417.911	0.411	17	0.199	R.KLQVDAWFGTR.R
R4/RRR4-19/2	1391.178	1390.675	-357.777	0.497	1040.833	0.489	19	0.186	R.KVDM*LEGVTILR.S
R4/RRR4-18/2	1156.497	1157.297	-1561.624	0.491	1203.650	0.398	16	0.181	K.FLDGIYVSDK.G
R4/RRR4-18/2	1390.233	1390.675	-318.829	0.468	1021.356	0.467	19	0.181	R.KVDM*LEGVTILR.S
R4/RRR4-19/2	1390.208	1390.675	-336.449	0.480	964.706	0.476	19	0.179	R.KVDM*LEGVTILR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1390.242	1390.675	-311.781	0.467	1076.193	0.431	19	0.178	R.KVDM*LEGVTILR.S
R4/RRR4-18/2	1284.624	1285.470	-1441.610	0.380	1278.240	0.364	17	0.178	R.KFLDGIYVSDK.G
R4/RRR4-18/2	1194.100	1193.336	-198.364	0.488	852.760	0.500	16	0.178	K.LQVDAWFGTR.R
R4/RRR4-18/2	1156.335	1157.297	-1702.562	0.469	1050.753	0.433	16	0.177	K.FLDGIYVSDK.G
R4/RRR4-19/2	1844.736	1844.996	-141.477	0.438	1407.295	0.497	22	0.177	K.FLDGIYVSDKGTITEDA.-
R4/RRR4-18/2	1390.123	1390.675	-1119.377	0.437	994.252	0.449	19	0.176	R.KVDM*LEGVTILR.S
R4/RRR4-18/2	1193.050	1193.336	-240.820	0.450	850.633	0.484	16	0.174	K.LQVDAWFGTR.R
R4/RRR4-18/2	1321.263	1321.509	-186.408	0.465	1082.020	0.416	15	0.173	R.KLQVDAWFGTR.R
R4/RRR4-18/2	1261.641	1262.502	-1479.138	0.348	1476.190	0.226	16	0.169	K.VDM*LEGVTILR.S
R4/RRR4-18/2	1156.731	1157.297	-1358.506	0.464	1109.040	0.357	16	0.168	K.FLDGIYVSDK.G
R4/RRR4-19/2	1582.222	1582.827	-1017.242	0.488	510.678	0.548	20	0.168	R.TAISHVQNLITGVTK.G
R4/RRR4-19/2	1845.687	1844.996	-168.071	0.465	1314.400	0.519	22	0.165	K.FLDGIYVSDKGTITEDA.-
R4/RRR4-18/2	856.929	856.990	-71.241	0.367	576.222	0.501	12	0.163	K.VVTVEGPR.G
R4/RRR4-18/2	856.860	856.990	-151.836	0.370	526.680	0.496	12	0.162	K.VVTVEGPR.G
R4/RRR4-19/2	1321.244	1321.509	-200.960	0.451	707.290	0.459	13	0.159	R.KLQVDAWFGTR.R
R4/RRR4-19/2	1156.798	1157.297	-432.742	0.409	847.517	0.369	15	0.157	K.FLDGIYVSDK.G
R4/RRR4-18/2	856.919	856.990	-82.958	0.364	344.397	0.483	10	0.157	K.VVTVEGPR.G
R4/RRR4-19/2	856.936	856.990	-63.096	0.389	338.964	0.459	10	0.156	K.VVTVEGPR.G
R4/RRR4-19/2	856.828	856.990	-189.566	0.385	336.026	0.452	10	0.156	K.VVTVEGPR.G
R4/RRR4-19/2	856.945	856.990	-52.665	0.335	374.240	0.465	11	0.156	K.VVTVEGPR.G
R4/RRR4-25/2	856.992	856.990	2.484	0.318	467.604	0.458	12	0.156	K.VVTVEGPR.G
R4/RRR4-18/2	1511.541	1512.695	-1428.990	0.315	973.204	0.356	16	0.156	K.HLNLDFQLLEGGR.K
R4/RRR4-18/2	1285.277	1285.470	-150.761	0.348	941.656	0.339	16	0.154	R.KFLDGIYVSDK.G
R4/RRR4-18/3	1913.542	1915.135	-1883.038	0.443	1452.220	0.391	27	0.154	K.VKDELVLDGNDIELVSR.S
R4/RRR4-23/2	857.106	856.990	136.619	0.323	363.050	0.436	11	0.154	K.VVTVEGPR.G
R4/RRR4-18/2	856.859	856.990	-153.408	0.342	489.488	0.410	12	0.151	-.VVTVEGPR.-
R4/RRR4-18/2	857.451	856.990	539.093	0.283	542.044	0.371	12	0.149	K.VVTVEGPR.G
R4/RRR4-18/2	856.660	856.990	-386.266	0.302	298.295	0.446	10	0.149	-.VVTVEGPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1261.453	1262.502	-1628.636	0.360	935.661	0.304	14	0.148	K.VDM*LEGVTILR.S
R4/RRR4-18/3	1914.563	1915.135	-823.372	0.507	1253.066	0.449	29	0.147	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/2	1192.896	1193.336	-370.484	0.316	827.442	0.288	15	0.146	K.LQVDAWFGTR.R
R4/RRR4-19/2	1157.095	1157.297	-175.398	0.374	862.283	0.259	15	0.145	K.FLDGIYVSDK.G
R4/RRR4-21/2	856.925	856.990	-76.242	0.292	351.796	0.257	11	0.145	-.VVTVEGPR.-
R4/RRR4-25/2	856.815	856.990	-204.287	0.222	471.325	0.272	11	0.142	K.VVTVEGPR.G
R4/RRR4-18/2	1320.630	1321.509	-1427.338	0.298	676.647	0.308	13	0.142	R.KLQVDAWFGTR.R
R4/RRR4-19/3	1915.570	1915.135	227.976	0.453	1346.753	0.386	26	0.141	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/3	1641.036	1640.868	103.056	0.478	881.622	0.556	23	0.139	K.HLNLDFQLLEGGRK.L
R4/RRR4-20/3	1913.825	1915.135	-1210.513	0.469	1187.731	0.440	27	0.139	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/3	1390.196	1390.675	-344.960	0.439	1814.653	0.217	26	0.136	R.KVDM*LEGVTILR.S
R4/RRR4-18/3	1914.972	1915.135	-84.890	0.415	1295.014	0.362	27	0.129	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/3	1582.341	1582.827	-307.745	0.503	1120.636	0.425	30	0.126	R.TAISHVQNLITGVTK.G
R4/RRR4-19/3	1582.413	1582.827	-262.003	0.434	1175.480	0.399	31	0.123	R.TAISHVQNLITGVTK.G
R4/RRR4-21/3	1583.026	1582.827	126.633	0.433	1272.081	0.364	31	0.123	R.TAISHVQNLITGVTK.G
R4/RRR4-18/3	1583.793	1582.827	-21.199	0.454	1120.792	0.400	30	0.120	R.TAISHVQNLITGVTK.G
R4/RRR4-19/3	1582.480	1582.827	-219.864	0.447	1076.337	0.391	30	0.115	R.TAISHVQNLITGVTK.G
R4/RRR4-19/3	1583.082	1582.827	161.780	0.468	934.773	0.416	29	0.113	R.TAISHVQNLITGVTK.G
R4/RRR4-18/3	1640.516	1640.868	-214.847	0.438	670.725	0.522	20	0.112	-.HLNLDFQLLEGGRK.-
R4/RRR4-18/3	1640.807	1640.868	-37.065	0.384	724.996	0.449	22	0.105	K.HLNLDFQLLEGGRK.L
R4/RRR4-18/3	1915.484	1915.135	182.827	0.366	869.842	0.356	22	0.103	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/3	1915.397	1915.135	137.579	0.398	713.640	0.374	24	0.101	K.VKDELVLDGNDIELVSR.S
R4/RRR4-17/3	1583.139	1582.827	197.968	0.432	794.286	0.370	28	0.100	R.TAISHVQNLITGVTK.G
R4/RRR4-21/3	1582.741	1582.827	-54.128	0.426	563.476	0.381	24	0.100	R.TAISHVQNLITGVTK.G
R4/RRR4-18/3	1390.192	1390.675	-348.264	0.423	1493.604	0.188	25	0.099	R.KVDM*LEGVTILR.S
R4/RRR4-19/3	1915.160	1915.135	13.603	0.409	926.593	0.320	27	0.098	K.VKDELVLDGNDIELVSR.S
R4/RRR4-24/3	1915.224	1915.135	46.877	0.421	793.233	0.335	25	0.097	K.VKDELVLDGNDIELVSR.S
R4/RRR4-18/3	1583.802	1582.827	-15.517	0.382	786.834	0.299	27	0.092	R.TAISHVQNLITGVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/3	1511.864	1512.695	-1214.856	0.383	893.753	0.351	21	0.091	-.HLNLDFQLLEGGR.-
R4/RRR4-24/3	1582.515	1582.827	-197.693	0.326	760.487	0.249	23	0.088	R.TAISHVQNLITGVTK.G
R4/RRR4-14/3	1583.563	1582.827	-166.751	0.340	478.294	0.324	22	0.085	-.TAISHVQNLITGVTK.-
R4/RRR4-18/3	1374.471	1374.675	-148.648	0.469	1291.308	0.178	25	0.083	-.KVDMLEGVTILR.-
R4/RRR4-18/3	1374.317	1374.675	-261.050	0.369	1497.435	0.089	26	0.081	-.KVDMLEGVTILR.-
R4/RRR4-19/3	1390.509	1390.675	-119.559	0.443	1180.471	0.172	23	0.080	-.KVDM*LEGVTILR.-
R4/RRR4-18/3	1374.417	1374.675	-188.073	0.434	1065.520	0.202	23	0.079	-.KVDMLEGVTILR.-
R4/RRR4-18/3	1390.395	1390.675	-201.860	0.456	979.571	0.150	23	0.074	-.KVDM*LEGVTILR.-
R4/RRR4-18/3	1512.588	1512.695	-71.088	0.380	707.211	0.200	19	0.068	-.HLNLDFQLLEGGR.-
R4/RRR4-18/3	1916.577	1915.135	231.657	0.239	456.196	0.265	19	0.051	-.VKDELVLDGNDIELVSR.-
R4/RRR4-19/3	1389.834	1390.675	-1328.360	0.368	723.409	0.096	19	0.051	-.KVDM*LEGVTILR.-
R4/RRR4-6/2	1582.284	1582.844	-988.572	0.487	1031.385	0.408	22	0.171	K.QFSAEEISSMVLIK.M
R4/RRR4-6/2	1582.504	1582.844	-215.210	0.540	1062.568	0.407	21	0.171	K.QFSAEEISSMVLIK.M
R4/RRR4-6/2	1583.436	1582.844	-258.307	0.539	737.498	0.377	19	0.152	K.QFSAEEISSMVLIK.M
R4/RRR4-6/2	1582.464	1582.844	-240.748	0.378	958.163	0.295	21	0.151	K.QFSAEEISSMVLIK.M
R4/RRR4-15/2	1803.825	1804.124	-166.006	0.610	3956.056	0.569	28	0.802	K.NFMIDFLM*GGVSAAVSK.T
R4/RRR4-15/2	1820.395	1820.123	149.931	0.623	3771.641	0.646	27	0.782	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-15/2	1803.584	1804.124	-856.624	0.581	3785.527	0.573	28	0.748	K.NFMIDFLM*GGVSAAVSK.T
R4/RRR4-15/2	1819.654	1820.123	-258.498	0.574	3697.986	0.603	27	0.736	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-14/2	1819.443	1820.123	-926.079	0.566	3622.181	0.602	27	0.711	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-15/2	1803.204	1804.124	-1068.040	0.574	3525.453	0.590	27	0.675	K.NFMIDFLM*GGVSAAVSK.T
R4/RRR4-14/2	1818.949	1820.123	-1198.876	0.507	3495.633	0.575	26	0.659	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-15/3	1803.493	1804.124	-906.980	0.465	2885.198	0.469	34	0.522	K.NFMIDFLM*GGVSAAVSK.T
R4/RRR4-15/2	1819.225	1820.123	-1046.727	0.539	2787.819	0.586	24	0.473	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-1/2	1819.476	1820.123	-907.826	0.520	2786.909	0.570	25	0.467	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-14/2	1819.466	1820.123	-913.888	0.548	2704.717	0.600	25	0.459	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-15/2	1803.453	1804.124	-929.124	0.466	2639.725	0.507	25	0.410	K.NFM*IDFLMGGVSAAVSK.T
R4/RRR4-15/2	1803.239	1804.124	-1048.328	0.533	2390.042	0.587	25	0.387	K.NFM*IDFLMGGVSAAVSK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1803.420	1804.124	-947.608	0.547	2117.010	0.633	24	0.350	K.NFM*IDFLMGGVSAAVSK.T
R4/RRR4-15/2	1499.726	1498.745	-12.704	0.557	2140.373	0.552	20	0.332	R.GFNISCVGIIVYR.G
R4/RRR4-15/2	1498.336	1498.745	-273.713	0.448	2013.485	0.470	20	0.285	R.GFNISCVGIIVYR.G
R4/RRR4-14/2	1498.453	1498.745	-195.415	0.439	1537.716	0.460	18	0.219	R.GFNISCVGIIVYR.G
R4/RRR4-15/2	1226.855	1227.413	-1273.422	0.500	1535.990	0.437	17	0.216	K.SSMDAFSQILK.N
R4/RRR4-14/2	1498.275	1498.745	-314.747	0.336	1717.908	0.321	18	0.208	R.GFNISCVGIIVYR.G
R4/RRR4-14/2	1243.053	1243.412	-289.359	0.472	1410.430	0.434	17	0.203	K.SSM*DAFSQILK.N
R4/RRR4-14/2	1243.303	1243.412	-87.621	0.400	1302.936	0.467	16	0.198	K.SSM*DAFSQILK.N
R4/RRR4-15/2	1361.629	1361.590	28.759	0.516	1432.984	0.404	17	0.198	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	1242.662	1243.412	-1412.567	0.409	1360.936	0.402	17	0.192	K.SSM*DAFSQILK.N
R4/RRR4-14/2	1345.050	1345.591	-1148.458	0.493	1429.099	0.354	18	0.189	K.LLIQNQDEMIK.S
R4/RRR4-15/2	1228.122	1227.413	-237.433	0.512	1231.616	0.446	15	0.188	K.SSMDAFSQILK.N
R4/RRR4-15/2	1242.834	1243.412	-1273.762	0.359	1397.284	0.364	17	0.188	K.SSM*DAFSQILK.N
R4/RRR4-15/2	1345.140	1345.591	-336.198	0.502	1317.084	0.391	17	0.187	K.LLIQNQDEMIK.S
R4/RRR4-15/2	1361.219	1361.590	-273.451	0.546	1377.885	0.363	17	0.184	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	1344.666	1345.591	-1435.422	0.458	1264.117	0.389	18	0.184	K.LLIQNQDEMIK.S
R4/RRR4-15/2	1345.214	1345.591	-280.568	0.518	1288.112	0.382	17	0.182	K.LLIQNQDEMIK.S
R4/RRR4-14/2	1243.924	1243.412	-393.490	0.416	1324.626	0.362	16	0.181	K.SSM*DAFSQILK.N
R4/RRR4-14/2	1423.408	1423.598	-133.722	0.471	1119.620	0.433	19	0.181	R.TIKDEGFASLWR.G
R4/RRR4-15/2	1294.006	1294.482	-369.069	0.443	1253.320	0.377	19	0.180	K.TLKSDGIAGLYR.G
R4/RRR4-15/2	1362.127	1361.590	-341.133	0.514	1371.661	0.333	17	0.179	K.LLIQNQDEM*IK.S
R4/RRR4-14/2	1360.665	1361.590	-1418.954	0.507	1260.050	0.367	17	0.178	K.LLIQNQDEM*IK.S
R4/RRR4-13/2	1821.407	1820.123	156.368	0.465	844.284	0.564	18	0.177	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-14/2	1424.296	1423.598	-212.553	0.500	871.215	0.489	18	0.176	R.TIKDEGFASLWR.G
R4/RRR4-14/2	1423.205	1423.598	-277.323	0.416	1079.656	0.412	19	0.175	R.TIKDEGFASLWR.G
R4/RRR4-14/2	1360.686	1361.590	-1403.726	0.486	1326.530	0.320	17	0.174	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	1599.138	1599.763	-1018.961	0.382	1038.863	0.447	20	0.174	R.LSEPYKGIGDCFGR.T
R4/RRR4-15/2	1448.144	1447.661	334.671	0.475	813.814	0.479	20	0.174	R.YFPTQALNFAFK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1423.202	1423.598	-279.216	0.426	1127.734	0.385	19	0.173	R.TIKDEGFASLWR.G
R4/RRR4-15/2	1423.191	1423.598	-286.961	0.441	995.326	0.436	18	0.173	R.TIKDEGFASLWR.G
R4/RRR4-15/2	1599.063	1599.763	-1066.328	0.396	999.814	0.455	20	0.173	R.LSEPYKGIGDCFGR.T
R4/RRR4-14/2	1226.426	1227.413	-1624.626	0.452	1162.152	0.382	15	0.173	K.SSMDAFSQILK.N
R4/RRR4-15/2	951.923	952.046	-129.921	0.485	839.776	0.456	15	0.172	K.SDGIAGLYR.G
R4/RRR4-15/2	1423.264	1423.598	-235.675	0.454	1079.942	0.393	19	0.172	R.TIKDEGFASLWR.G
R4/RRR4-13/2	1362.101	1361.590	-359.746	0.502	1194.870	0.353	17	0.171	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	1293.638	1294.482	-1429.388	0.420	986.867	0.427	18	0.170	K.TLKSDGIAGLYR.G
R4/RRR4-15/2	1361.980	1361.590	286.843	0.517	1342.799	0.298	17	0.170	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	1447.215	1447.661	-309.439	0.387	875.674	0.444	20	0.168	R.YFPTQALNFAFK.D
R4/RRR4-1/2	1362.515	1361.590	-55.549	0.532	1236.359	0.328	17	0.168	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	951.541	952.046	-1586.408	0.442	879.241	0.416	15	0.168	K.SDGIAGLYR.G
R4/RRR4-15/2	881.831	881.950	-134.832	0.443	677.836	0.487	12	0.167	K.GIGDCFGR.T
R4/RRR4-15/2	1447.206	1447.661	-315.702	0.433	752.416	0.465	19	0.167	R.YFPTQALNFAFK.D
R4/RRR4-15/2	1294.181	1294.482	-232.882	0.455	1018.401	0.398	17	0.167	K.TLKSDGIAGLYR.G
R4/RRR4-14/2	1361.124	1361.590	-343.273	0.503	1179.278	0.331	17	0.166	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	1599.371	1599.763	-245.552	0.441	816.638	0.478	18	0.166	R.LSEPYKGIGDCFGR.T
R4/RRR4-2/2	1820.877	1820.123	-135.611	0.459	1014.605	0.431	18	0.166	K.NFM*IDFLM*GGVSAAVSK.T
R4/RRR4-15/2	1423.166	1423.598	-304.861	0.449	986.693	0.388	18	0.166	R.TIKDEGFASLWR.G
R4/RRR4-15/2	1422.931	1423.598	-1175.432	0.443	895.835	0.421	17	0.165	R.TIKDEGFASLWR.G
R4/RRR4-14/2	1227.174	1227.413	-195.213	0.387	1081.977	0.365	15	0.165	K.SSMDAFSQILK.N
R4/RRR4-15/2	1447.083	1447.661	-1093.795	0.397	728.335	0.465	19	0.165	R.YFPTQALNFAFK.D
R4/RRR4-15/2	951.265	952.046	-1878.525	0.422	714.689	0.448	14	0.165	K.SDGIAGLYR.G
R4/RRR4-15/2	1423.140	1423.598	-323.019	0.435	1028.718	0.365	18	0.164	R.TIKDEGFASLWR.G
R4/RRR4-15/2	1758.723	1758.932	-119.298	0.475	368.633	0.576	19	0.163	K.SSM*DAFSQILKNEGSK.S
R4/RRR4-14/2	1345.123	1345.591	-348.308	0.474	1226.380	0.291	17	0.163	K.LLIQNQDEMIK.S
R4/RRR4-15/2	1361.201	1361.590	-286.587	0.490	1214.830	0.296	17	0.163	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	952.042	952.046	-4.773	0.480	769.041	0.404	14	0.162	K.SDGIAGLYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1758.330	1758.932	-913.759	0.517	383.200	0.544	19	0.161	K.SSM*DAFSQILKNEGSK.S
R4/RRR4-15/2	1424.176	1423.598	-297.165	0.468	772.451	0.428	16	0.161	R.TIKDEGFASLWR.G
R4/RRR4-14/2	881.731	881.950	-248.573	0.324	698.333	0.473	12	0.160	K.GIGDCFGR.T
R4/RRR4-14/2	1447.308	1447.661	-244.619	0.424	584.216	0.450	18	0.160	R.YFPTQALNFAFK.D
R4/RRR4-15/2	1447.102	1447.661	-1080.920	0.411	738.241	0.413	19	0.160	R.YFPTQALNFAFK.D
R4/RRR4-1/2	1362.024	1361.590	319.286	0.502	1191.475	0.288	17	0.160	K.LLIQNQDEM*IK.S
R4/RRR4-1/2	952.059	952.046	12.846	0.391	430.451	0.462	13	0.159	K.SDGIAGLYR.G
R4/RRR4-15/3	1804.034	1804.124	-50.211	0.348	1535.117	0.380	29	0.159	K.NFMIDFLM*GGVSAAVSK.T
R4/RRR4-1/2	1423.134	1423.598	-327.064	0.373	824.558	0.390	17	0.158	R.TIKDEGFASLWR.G
R4/RRR4-15/2	1211.137	1211.351	-177.681	0.371	496.683	0.458	16	0.158	R.QFNGLVDVYR.K
R4/RRR4-2/2	1361.331	1361.590	-190.955	0.447	1310.740	0.215	17	0.156	K.LLIQNQDEM*IK.S
R4/RRR4-15/2	1210.613	1211.351	-1439.934	0.358	366.200	0.479	14	0.156	R.QFNGLVDVYR.K
R4/RRR4-15/2	951.706	952.046	-358.946	0.434	607.615	0.383	13	0.155	K.SDGIAGLYR.G
R4/RRR4-14/2	881.979	881.950	33.302	0.317	602.378	0.439	12	0.155	K.GIGDCFGR.T
R4/RRR4-2/2	951.812	952.046	-247.380	0.344	258.510	0.381	12	0.154	K.SDGIAGLYR.G
R4/RRR4-15/2	1086.057	1085.345	-266.011	0.407	603.723	0.397	14	0.153	R.MMMTSGEAVK.Y
R4/RRR4-15/2	1243.686	1243.412	221.135	0.338	921.129	0.311	16	0.152	K.SSM*DAFSQILK.N
R4/RRR4-13/2	1360.512	1361.590	-1532.326	0.387	1145.366	0.227	17	0.152	K.LLIQNQDEM*IK.S
R4/RRR4-1/2	951.791	952.046	-269.254	0.331	383.996	0.346	13	0.151	K.SDGIAGLYR.G
R4/RRR4-14/2	952.093	952.046	48.853	0.365	582.584	0.348	13	0.151	K.SDGIAGLYR.G
R4/RRR4-15/2	1211.030	1211.351	-265.958	0.284	397.709	0.470	15	0.151	R.QFNGLVDVYR.K
R4/RRR4-15/2	881.698	881.950	-285.798	0.329	623.611	0.369	12	0.151	K.GIGDCFGR.T
R4/RRR4-13/2	1803.649	1804.124	-263.909	0.366	725.681	0.396	18	0.150	K.NFMIDFLM*GGVSAAVSK.T
R4/RRR4-14/2	881.376	881.950	-1790.910	0.279	639.162	0.404	12	0.150	K.GIGDCFGR.T
R4/RRR4-2/2	951.274	952.046	-1868.854	0.320	229.838	0.400	12	0.150	-.SDGIAGLYR.-
R4/RRR4-15/2	1212.327	1211.351	-20.361	0.295	320.651	0.473	13	0.150	R.QFNGLVDVYR.K
R4/RRR4-15/2	881.708	881.950	-274.686	0.279	623.358	0.366	12	0.148	K.GIGDCFGR.T
R4/RRR4-3/2	1361.536	1361.590	-39.762	0.431	1032.528	0.228	16	0.146	K.LLIQNQDEM*IK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1446.581	1447.661	-1442.123	0.256	426.290	0.329	16	0.144	R.YFPTQALNFAFK.D
R4/RRR4-1/2	1446.765	1447.661	-1314.575	0.238	461.260	0.342	15	0.143	R.YFPTQALNFAFK.D
R4/RRR4-14/2	1424.214	1423.598	-270.507	0.307	614.118	0.277	15	0.142	R.TIKDEGFASLWR.G
R4/RRR4-15/2	1085.047	1085.345	-275.060	0.316	476.696	0.321	13	0.142	-.MMMTSGEAVK.-
R4/RRR4-15/2	1100.900	1101.344	-404.233	0.399	847.332	0.219	15	0.140	-.MMM*TSGEAVK.-
R4/RRR4-15/2	1100.730	1101.344	-1470.789	0.246	707.434	0.271	14	0.140	R.MMM*TSGEAVK.Y
R4/RRR4-14/2	1447.481	1447.661	-124.816	0.201	369.511	0.329	13	0.139	R.YFPTQALNFAFK.D
R4/RRR4-13/2	1244.395	1243.412	-13.456	0.296	738.554	0.218	14	0.139	K.SSM*DAFSQILK.N
R4/RRR4-3/2	1361.984	1361.590	289.989	0.376	1184.429	0.119	16	0.139	K.LLIQNQDEM*IK.S
R4/RRR4-13/2	951.809	952.046	-249.696	0.206	201.173	0.372	12	0.132	-.SDGIAGLYR.-
R4/RRR4-13/2	951.863	952.046	-192.957	0.153	141.617	0.305	11	0.128	-.SDGIAGLYR.-
R4/RRR4-27/2	951.566	952.046	-505.938	0.231	125.755	0.412	11	0.125	-.SDGIAGLYR.-
R4/RRR4-12/2	951.507	952.046	-1622.237	0.119	150.232	0.318	12	0.125	-.SDGIAGLYR.-
R4/RRR4-11/2	951.717	952.046	-347.364	0.311	180.827	0.478	11	0.124	-.SDGIAGLYR.-
R4/RRR4-15/3	1498.515	1498.745	-153.542	0.465	1283.599	0.286	27	0.107	R.GFNISCVGIIVYR.G
R4/RRR4-5/2	951.897	952.046	-157.192	0.201	106.724	0.416	10	0.099	-.SDGIAGLYR.-
R4/RRR4-15/3	1803.596	1804.124	-849.497	0.369	510.973	0.402	24	0.090	-.NFM*IDFLMGGVSAAVSK.-
R4/RRR4-29/2	951.376	952.046	-1761.452	0.189	94.430	0.354	10	0.090	-.SDGIAGLYR.-
R4/RRR4-15/3	1294.563	1294.482	62.920	0.415	1021.360	0.278	22	0.090	K.TLKSDGIAGLYR.G
R4/RRR4-27/2	951.582	952.046	-489.332	0.217	103.203	0.405	10	0.088	-.SDGIAGLYR.-
R4/RRR4-15/3	1294.223	1294.482	-200.720	0.372	851.248	0.279	20	0.085	K.TLKSDGIAGLYR.G
R4/RRR4-15/3	1294.322	1294.482	-124.224	0.412	801.319	0.276	20	0.084	K.TLKSDGIAGLYR.G
R4/RRR4-6/2	1496.212	1496.694	-322.873	0.575	2777.607	0.588	22	0.477	K.SQIHEIVLVGGSTR.I
R4/RRR4-6/2	1496.402	1496.694	-195.929	0.556	2606.404	0.575	22	0.432	K.SQIHEIVLVGGSTR.I
R4/RRR4-5/2	1496.170	1496.694	-1021.821	0.509	2540.207	0.522	22	0.398	K.SQIHEIVLVGGSTR.I
R4/RRR4-5/2	1155.997	1156.317	-278.195	0.506	2062.255	0.452	20	0.290	K.DAGVIAGLNVAR.I
R4/RRR4-5/3	1385.215	1385.612	-287.031	0.475	2337.603	0.303	29	0.250	K.M*KETAEAYLGKK.I
R4/RRR4-6/2	1537.066	1537.620	-1014.149	0.506	1607.223	0.506	19	0.238	K.NGHVEIIANDQGNR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1652.722	1652.835	-68.727	0.547	1970.445	0.406	27	0.233	R.ARFEELNNDLFRK.T
R4/RRR4-6/2	1536.795	1537.620	-1190.717	0.412	1681.400	0.441	20	0.231	K.NGHVEIIANDQGNR.I
R4/RRR4-6/2	1523.630	1523.776	-96.265	0.422	1666.078	0.367	21	0.214	K.VFSPEEVSAM*ILGK.M
R4/RRR4-6/2	1537.059	1537.620	-1018.296	0.466	1354.391	0.508	19	0.211	K.NGHVEIIANDQGNR.I
R4/RRR4-5/3	1653.562	1652.835	-166.134	0.536	1882.426	0.355	26	0.196	R.ARFEELNNDLFRK.T
R4/RRR4-5/2	1156.031	1156.317	-248.532	0.402	1479.277	0.376	17	0.196	K.DAGVIAGLNVAR.I
R4/RRR4-6/2	1523.727	1524.663	-1273.809	0.488	1325.162	0.404	19	0.190	R.ARFEELNNDLFR.K
R4/RRR4-6/2	1144.080	1144.305	-196.977	0.429	948.167	0.466	19	0.177	K.FDLSGIPAAPR.G
R4/RRR4-6/2	1510.343	1509.645	-200.281	0.470	535.550	0.602	19	0.176	R.ITPSWVAFTDSER.L
R4/RRR4-6/2	1143.783	1144.305	-1334.598	0.425	859.070	0.503	18	0.174	-.FDLSGIPAAPR.-
R4/RRR4-5/2	1523.756	1523.776	-13.575	0.354	971.905	0.476	18	0.171	K.VFSPEEVSAM*ILGK.M
R4/RRR4-5/2	1144.005	1144.305	-263.239	0.441	748.980	0.517	17	0.171	-.FDLSGIPAAPR.-
R4/RRR4-6/2	1143.913	1144.305	-343.856	0.433	984.364	0.416	19	0.170	-.FDLSGIPAAPR.-
R4/RRR4-6/3	1502.652	1502.783	-87.691	0.406	1614.604	0.392	27	0.169	K.IVNKDGKPYIQVK.I
R4/RRR4-6/2	1524.242	1524.663	-276.692	0.401	1158.368	0.350	19	0.169	R.ARFEELNNDLFR.K
R4/RRR4-5/2	1523.646	1524.663	-1327.637	0.442	1123.500	0.360	18	0.168	R.ARFEELNNDLFR.K
R4/RRR4-5/2	1524.594	1523.776	-119.814	0.425	871.365	0.470	17	0.167	K.VFSPEEVSAM*ILGK.M
R4/RRR4-5/2	1893.794	1894.077	-150.225	0.455	772.622	0.438	23	0.161	K.INDAVVTVPAYFNDAQR.Q
R4/RRR4-5/2	1510.182	1509.645	-307.077	0.387	509.056	0.504	18	0.160	R.ITPSWVAFTDSER.L
R4/RRR4-6/3	1385.618	1385.612	4.648	0.475	1854.378	0.284	28	0.159	K.M*KETAEAYLGKK.I
R4/RRR4-5/2	1143.664	1144.305	-1439.439	0.425	560.431	0.487	15	0.158	-.FDLSGIPAAPR.-
R4/RRR4-5/2	1144.128	1144.305	-155.341	0.406	880.399	0.358	18	0.158	K.FDLSGIPAAPR.G
R4/RRR4-6/2	1509.227	1509.645	-277.660	0.344	542.180	0.483	19	0.157	R.ITPSWVAFTDSER.L
R4/RRR4-6/2	1509.267	1509.645	-251.288	0.378	360.827	0.541	15	0.157	R.ITPSWVAFTDSER.L
R4/RRR4-6/2	1552.324	1552.665	-219.867	0.460	523.302	0.435	19	0.157	R.EAEEFAEEDKKVK.E
R4/RRR4-6/2	1553.230	1552.665	-280.751	0.512	420.532	0.433	19	0.157	R.EAEEFAEEDKKVK.E
R4/RRR4-5/2	1894.279	1894.077	106.867	0.479	494.041	0.477	20	0.155	K.INDAVVTVPAYFNDAQR.Q
R4/RRR4-6/3	1537.501	1537.620	-77.302	0.421	1614.337	0.336	27	0.153	K.NGHVEIIANDQGNR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1894.521	1894.077	234.943	0.457	508.973	0.438	20	0.151	K.INDAVVTVPAYFNDAQR.Q
R4/RRR4-5/2	1509.159	1509.645	-322.699	0.330	510.193	0.387	18	0.149	R.ITPSWVAFTDSER.L
R4/RRR4-5/2	1228.039	1227.305	-216.711	0.390	769.323	0.307	14	0.146	-.DYFEGKEPNK.-
R4/RRR4-5/2	1227.262	1227.305	-35.078	0.380	735.947	0.305	13	0.145	R.DYFEGKEPNK.G
R4/RRR4-6/2	1551.504	1552.665	-1396.681	0.332	341.994	0.297	17	0.144	R.EAEEFAEEDKKVK.E
R4/RRR4-6/2	1227.177	1227.305	-104.222	0.378	758.157	0.282	13	0.143	-.DYFEGKEPNK.-
R4/RRR4-6/2	1226.344	1227.305	-1603.470	0.353	584.860	0.358	12	0.142	-.DYFEGKEPNK.-
R4/RRR4-6/2	1228.232	1227.305	-59.174	0.439	727.140	0.340	13	0.142	-.DYFEGKEPNK.-
R4/RRR4-5/2	1226.935	1227.305	-302.327	0.271	667.523	0.294	13	0.142	R.DYFEGKEPNK.G
R4/RRR4-6/3	1537.973	1537.620	230.689	0.470	1531.957	0.329	26	0.141	K.NGHVEIIANDQGNR.I
R4/RRR4-6/3	1385.799	1385.612	135.584	0.496	1391.086	0.390	26	0.139	K.M*KETAEAYLGKK.I
R4/RRR4-6/2	1506.774	1507.777	-1333.240	0.250	967.567	0.221	16	0.139	K.VFSPEEVSAMILGK.M
R4/RRR4-5/3	1652.334	1652.835	-911.287	0.491	1397.964	0.366	24	0.136	R.ARFEELNNDLFRK.T
R4/RRR4-5/3	1384.863	1385.612	-1266.383	0.437	1591.726	0.301	26	0.135	K.M*KETAEAYLGKK.I
R4/RRR4-6/3	1653.706	1652.835	-78.496	0.553	1474.675	0.332	25	0.133	R.ARFEELNNDLFRK.T
R4/RRR4-6/3	1652.697	1652.835	-83.841	0.558	1431.637	0.345	24	0.133	R.ARFEELNNDLFRK.T
R4/RRR4-6/3	1502.810	1502.783	18.272	0.427	1325.520	0.364	25	0.128	K.IVNKDGKPYIQVK.I
R4/RRR4-5/3	1652.701	1652.835	-81.841	0.484	1387.237	0.327	24	0.124	R.ARFEELNNDLFRK.T
R4/RRR4-5/2	1970.453	1970.856	-205.460	0.443	919.291	0.525	24	0.122	R.TGGAPGGGADGEGGGDDEHDEL.-
R4/RRR4-6/2	1970.532	1970.856	-165.065	0.469	971.760	0.519	24	0.122	R.TGGAPGGGADGEGGGDDEHDEL.-
R4/RRR4-5/3	1370.418	1369.612	-142.208	0.499	924.213	0.456	23	0.121	K.MKETAEAYLGKK.I
R4/RRR4-6/2	1971.149	1970.856	148.912	0.486	791.414	0.545	22	0.118	R.TGGAPGGGADGEGGGDDEHDEL.-
R4/RRR4-5/3	1369.420	1369.612	-140.658	0.494	1135.885	0.385	23	0.118	K.MKETAEAYLGKK.I
R4/RRR4-6/3	1502.236	1502.783	-1032.659	0.323	1423.298	0.291	26	0.117	K.IVNKDGKPYIQVK.I
R4/RRR4-6/2	1970.184	1970.856	-851.421	0.450	787.670	0.513	23	0.115	R.TGGAPGGGADGEGGGDDEHDEL.-
R4/RRR4-5/2	1970.128	1970.856	-880.032	0.445	907.353	0.494	24	0.115	R.TGGAPGGGADGEGGGDDEHDEL.-
R4/RRR4-6/3	1369.675	1369.612	45.748	0.533	997.486	0.404	23	0.114	K.MKETAEAYLGKK.I
R4/RRR4-6/3	1385.747	1385.612	97.950	0.513	1264.805	0.329	25	0.113	K.M*KETAEAYLGKK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1969.829	1970.856	-1032.323	0.408	800.029	0.474	23	0.110	R.TGGAPGGGADGEGGGDDEHDEL.-
R4/RRR4-5/3	1524.397	1524.663	-174.549	0.514	1106.533	0.361	23	0.110	R.ARFEELNNDLFR.K
R4/RRR4-6/3	1368.977	1369.612	-1198.156	0.495	925.207	0.394	23	0.108	K.MKETAEAYLGKK.I
R4/RRR4-6/3	1369.483	1369.612	-94.787	0.493	818.866	0.390	21	0.104	K.MKETAEAYLGKK.I
R4/RRR4-5/3	1385.003	1385.612	-1164.947	0.455	1166.851	0.307	23	0.104	K.M*KETAEAYLGKK.I
R4/RRR4-6/3	1524.514	1524.663	-97.918	0.549	1102.195	0.318	23	0.101	R.ARFEELNNDLFR.K
R4/RRR4-5/3	1369.167	1369.612	-326.060	0.405	794.702	0.368	21	0.100	K.MKETAEAYLGKK.I
R4/RRR4-5/3	1503.132	1502.783	232.819	0.401	924.205	0.333	23	0.096	K.IVNKDGKPYIQVK.I
R4/RRR4-5/3	1537.672	1537.620	33.783	0.439	854.963	0.346	25	0.096	K.NGHVEIIANDQGNR.I
R4/RRR4-6/3	1524.735	1524.663	47.841	0.537	1208.207	0.262	23	0.095	R.ARFEELNNDLFR.K
R4/RRR4-5/3	1502.384	1502.783	-266.669	0.339	639.422	0.299	19	0.088	K.IVNKDGKPYIQVK.I
R4/RRR4-5/3	1524.211	1524.663	-297.472	0.482	866.360	0.256	22	0.085	R.ARFEELNNDLFR.K
R4/RRR4-6/3	1525.990	1524.663	215.170	0.542	1018.824	0.318	22	0.085	-.ARFEELNNDLFR.-
R4/RRR4-5/3	1537.590	1537.620	-19.487	0.453	905.901	0.244	24	0.083	K.NGHVEIIANDQGNR.I
R4/RRR4-5/3	1537.377	1537.620	-158.421	0.364	1179.061	0.184	28	0.082	K.NGHVEIIANDQGNR.I
R4/RRR4-5/3	1502.938	1502.783	103.687	0.365	862.735	0.205	23	0.081	K.IVNKDGKPYIQVK.I
R4/RRR4-5/3	1524.153	1524.663	-993.268	0.454	736.359	0.202	20	0.075	-.ARFEELNNDLFR.-
R4/RRR4-6/2	1718.439	1717.987	263.790	0.567	2238.908	0.603	26	0.370	K.KVPVVVGNCTGFAVNR.T
R4/RRR4-6/2	1635.325	1635.906	-970.134	0.425	2041.293	0.487	22	0.292	R.ASDLDIASILGMGFPK.F
R4/RRR4-6/2	1652.122	1651.906	131.167	0.538	1674.062	0.576	23	0.265	R.ASDLDIASILGM*GFPK.F
R4/RRR4-6/2	1250.189	1249.443	-203.665	0.587	1613.629	0.528	17	0.249	R.LWALEIANYR.K
R4/RRR4-6/2	1250.148	1249.443	-236.383	0.612	1647.819	0.508	17	0.248	R.LWALEIANYR.K
R4/RRR4-6/3	1717.627	1717.987	-210.406	0.521	1711.599	0.523	34	0.244	K.KVPVVVGNCTGFAVNR.T
R4/RRR4-1/2	1653.380	1651.906	287.466	0.490	1472.938	0.597	22	0.244	R.ASDLDIASILGM*GFPK.F
R4/RRR4-6/2	1651.023	1651.906	-1143.817	0.396	1597.126	0.530	22	0.240	R.ASDLDIASILGM*GFPK.F
R4/RRR4-6/2	1651.455	1651.906	-273.873	0.480	1381.403	0.569	21	0.226	R.ASDLDIASILGM*GFPK.F
R4/RRR4-5/2	1651.623	1651.906	-171.692	0.497	1363.845	0.571	20	0.224	R.ASDLDIASILGM*GFPK.F
R4/RRR4-5/2	1934.918	1933.198	-145.197	0.479	1374.974	0.562	20	0.220	R.GGLVFWADTIGAPYIHSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1174.987	1175.424	-373.311	0.390	1552.657	0.421	18	0.214	K.M*IAANLEGLVK.R
R4/RRR4-6/2	1628.354	1628.769	-255.844	0.469	1211.812	0.575	25	0.214	R.SLPLSAPNATQQASSR.S
R4/RRR4-6/2	1310.249	1309.540	-222.270	0.494	1112.654	0.605	19	0.212	K.VPGVTDVQLKPR.K
R4/RRR4-6/2	1086.027	1085.194	-154.633	0.426	1293.506	0.532	16	0.212	K.DIYAAAFGTR.N
R4/RRR4-6/2	1628.280	1628.769	-301.272	0.521	1145.957	0.567	25	0.208	R.SLPLSAPNATQQASSR.S
R4/RRR4-6/2	1634.759	1635.906	-1317.312	0.327	1554.579	0.410	20	0.207	R.ASDLDIASILGMGFPK.F
R4/RRR4-5/2	1531.411	1530.739	-214.875	0.513	1347.217	0.486	19	0.206	R.GLVDALCSPDELIK.M
R4/RRR4-5/2	1651.185	1651.906	-1045.085	0.419	1216.003	0.542	20	0.202	R.ASDLDIASILGM*GFPK.F
R4/RRR4-6/2	1248.362	1249.443	-1671.697	0.424	1209.651	0.511	14	0.199	R.LWALEIANYR.K
R4/RRR4-5/2	1628.386	1628.769	-235.913	0.506	1000.256	0.582	24	0.199	R.SLPLSAPNATQQASSR.S
R4/RRR4-5/2	1628.183	1628.769	-977.022	0.505	1021.947	0.573	24	0.198	R.SLPLSAPNATQQASSR.S
R4/RRR4-5/2	1627.809	1628.769	-1207.556	0.423	1043.329	0.545	25	0.193	R.SLPLSAPNATQQASSR.S
R4/RRR4-6/2	1531.377	1530.739	-236.706	0.536	1251.146	0.463	19	0.193	R.GLVDALCSPDELIK.M
R4/RRR4-6/2	1531.144	1530.739	265.592	0.507	1265.698	0.432	19	0.188	R.GLVDALCSPDELIK.M
R4/RRR4-5/2	1248.683	1249.443	-1413.978	0.351	1368.218	0.368	15	0.185	R.LWALEIANYR.K
R4/RRR4-5/2	1650.662	1651.906	-1363.252	0.311	1244.802	0.446	19	0.184	R.ASDLDIASILGM*GFPK.F
R4/RRR4-6/2	1530.334	1530.739	-265.030	0.465	1314.407	0.389	19	0.184	R.GLVDALCSPDELIK.M
R4/RRR4-6/2	1629.156	1628.769	238.190	0.518	816.669	0.560	21	0.181	R.SLPLSAPNATQQASSR.S
R4/RRR4-6/3	1456.118	1456.709	-1096.477	0.528	1555.249	0.437	28	0.180	K.TSPQAILDLITVGK.M
R4/RRR4-6/2	1084.678	1085.194	-1401.903	0.387	902.390	0.501	15	0.175	K.DIYAAAFGTR.N
R4/RRR4-5/2	1456.354	1456.709	-244.528	0.478	875.204	0.460	20	0.170	K.TSPQAILDLITVGK.M
R4/RRR4-6/2	1456.286	1456.709	-291.706	0.429	922.076	0.440	21	0.170	K.TSPQAILDLITVGK.M
R4/RRR4-6/2	1090.918	1091.264	-318.120	0.460	944.118	0.405	15	0.168	R.VM*DENVVIR.A
R4/RRR4-6/2	1174.741	1175.424	-1436.894	0.396	914.612	0.416	17	0.166	K.M*IAANLEGLVK.R
R4/RRR4-5/2	1174.663	1175.424	-1504.010	0.339	934.335	0.394	16	0.161	K.M*IAANLEGLVK.R
R4/RRR4-5/2	1456.213	1456.709	-341.915	0.395	688.901	0.450	20	0.161	K.TSPQAILDLITVGK.M
R4/RRR4-1/2	1628.291	1628.769	-294.428	0.435	687.647	0.440	21	0.158	R.SLPLSAPNATQQASSR.S
R4/RRR4-5/2	1456.559	1456.709	-103.359	0.425	755.118	0.407	19	0.158	K.TSPQAILDLITVGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1456.088	1456.709	-1117.217	0.422	499.380	0.475	17	0.157	K.TSPQAILDLITVGK.M
R4/RRR4-5/2	1090.897	1091.264	-337.206	0.380	790.190	0.374	14	0.156	R.VM*DENVVIR.A
R4/RRR4-5/2	1634.530	1635.906	-1458.471	0.324	1009.992	0.340	18	0.154	R.ASDLDIASILGMGFPK.F
R4/RRR4-6/2	1455.727	1456.709	-1365.946	0.377	706.174	0.343	20	0.150	K.TSPQAILDLITVGK.M
R4/RRR4-1/2	1249.263	1249.443	-144.032	0.319	785.956	0.358	13	0.150	R.LWALEIANYR.K
R4/RRR4-6/2	1085.054	1085.194	-129.608	0.342	830.971	0.324	15	0.150	K.DIYAAAFGTR.N
R4/RRR4-5/2	1934.976	1933.198	-114.884	0.378	597.929	0.489	16	0.149	R.GGLVFWADTIGAPYIHSK.L
R4/RRR4-4/2	1457.946	1456.709	162.448	0.363	627.039	0.369	17	0.148	K.TSPQAILDLITVGK.M
R4/RRR4-6/2	886.937	887.059	-138.059	0.287	932.223	0.292	15	0.146	K.AIVLTGAGGK.F
R4/RRR4-3/2	1456.219	1456.709	-337.710	0.427	553.814	0.323	17	0.144	K.TSPQAILDLITVGK.M
R4/RRR4-5/2	1455.593	1456.709	-1458.598	0.307	602.716	0.300	16	0.141	K.TSPQAILDLITVGK.M
R4/RRR4-6/2	1174.460	1175.424	-1677.532	0.256	545.732	0.331	12	0.139	-.M*IAANLEGLVK.-
R4/RRR4-6/3	1456.654	1456.709	-38.221	0.457	1434.064	0.356	27	0.138	K.TSPQAILDLITVGK.M
R4/RRR4-8/2	1091.104	1091.264	-147.053	0.295	762.074	0.071	13	0.129	-.VM*DENVVIR.-
R4/RRR4-6/3	1651.968	1651.906	37.786	0.483	1020.814	0.461	26	0.127	R.ASDLDIASILGM*GFPK.F
R4/RRR4-2/2	1176.537	1175.424	96.203	0.276	651.042	0.121	14	0.126	-.M*IAANLEGLVK.-
R4/RRR4-6/2	1456.632	1456.709	-53.174	0.230	233.348	0.394	11	0.126	-.TSPQAILDLITVGK.-
R4/RRR4-5/3	1160.536	1160.353	158.701	0.465	757.526	0.483	21	0.116	K.ALVHAFFAQR.L
R4/RRR4-6/3	1160.130	1160.353	-192.523	0.433	687.967	0.496	20	0.115	K.ALVHAFFAQR.L
R4/RRR4-6/3	1160.743	1160.353	337.306	0.442	833.117	0.459	21	0.114	K.ALVHAFFAQR.L
R4/RRR4-5/3	1159.887	1160.353	-402.837	0.432	783.856	0.468	21	0.113	K.ALVHAFFAQR.L
R4/RRR4-6/3	1651.151	1651.906	-1066.174	0.350	1237.314	0.336	28	0.113	R.ASDLDIASILGM*GFPK.F
R4/RRR4-5/3	1160.760	1160.353	351.857	0.467	477.055	0.490	19	0.110	K.ALVHAFFAQR.L
R4/RRR4-6/3	1160.281	1160.353	-61.596	0.433	679.905	0.426	20	0.104	K.ALVHAFFAQR.L
R4/RRR4-6/3	1205.583	1205.304	232.647	0.478	896.574	0.355	21	0.098	R.TDRLGSLSEAR.S
R4/RRR4-6/3	1205.389	1205.304	71.181	0.431	808.689	0.272	22	0.085	R.TDRLGSLSEAR.S
R4/RRR4-10/2	1318.249	1318.495	-187.671	0.530	2052.147	0.480	22	0.296	K.CDVIASGIVNAAK.Q
R4/RRR4-10/2	1318.138	1318.495	-271.841	0.482	1897.927	0.467	21	0.269	K.CDVIASGIVNAAK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1292.220	1292.616	-307.478	0.520	1607.280	0.508	18	0.241	K.AILVNIFGGIM*K.C
R4/RRR4-10/3	1619.865	1619.824	25.608	0.537	1896.202	0.400	30	0.216	R.LNIHEYQGAELM*GK.Y
R4/RRR4-10/2	1474.343	1474.642	-203.344	0.491	1431.276	0.492	21	0.216	R.GAAAGSVEEVKNTLK.N
R4/RRR4-10/2	1686.547	1685.857	-184.511	0.485	1517.641	0.456	23	0.216	K.GITDDDAAKVVDGLAPK.T
R4/RRR4-10/2	1474.226	1474.642	-283.173	0.479	1481.856	0.452	20	0.211	R.GAAAGSVEEVKNTLK.N
R4/RRR4-10/2	1474.274	1474.642	-249.861	0.481	1200.312	0.483	20	0.192	R.GAAAGSVEEVKNTLK.N
R4/RRR4-10/2	1018.591	1019.284	-1666.693	0.468	1168.611	0.438	16	0.187	K.M*LGQILVTK.Q
R4/RRR4-10/2	1317.995	1318.495	-1142.028	0.381	1299.625	0.410	18	0.186	K.CDVIASGIVNAAK.Q
R4/RRR4-10/2	1182.473	1183.255	-1511.269	0.461	1166.628	0.374	17	0.175	K.LNFDDNAAFR.Q
R4/RRR4-10/2	1096.184	1095.277	-85.514	0.456	962.823	0.471	15	0.175	K.SGLQGGVHIVK.A
R4/RRR4-10/2	1245.176	1245.444	-216.383	0.449	786.787	0.538	17	0.175	R.NTAGPLIIACSK.G
R4/RRR4-10/3	1604.734	1603.825	-56.324	0.522	1528.790	0.437	28	0.174	R.LNIHEYQGAELMGK.Y
R4/RRR4-10/2	1002.555	1003.285	-1730.701	0.421	932.496	0.454	14	0.173	K.MLGQILVTK.Q
R4/RRR4-10/2	1019.007	1019.284	-272.361	0.507	1134.813	0.362	16	0.172	K.M*LGQILVTK.Q
R4/RRR4-10/2	1094.473	1095.277	-1653.590	0.421	877.160	0.453	15	0.167	K.SGLQGGVHIVK.A
R4/RRR4-10/2	817.928	817.995	-82.871	0.481	398.218	0.484	11	0.165	K.VPIDVFK.G
R4/RRR4-10/2	817.923	817.995	-88.559	0.417	356.394	0.513	11	0.164	K.VPIDVFK.G
R4/RRR4-10/2	1018.550	1019.284	-1707.270	0.424	1009.087	0.348	15	0.163	K.M*LGQILVTK.Q
R4/RRR4-10/2	1003.158	1003.285	-126.764	0.455	894.344	0.376	15	0.162	K.MLGQILVTK.Q
R4/RRR4-10/2	818.550	818.943	-481.281	0.457	805.413	0.402	11	0.162	K.YGINVPR.G
R4/RRR4-10/2	1390.264	1389.622	-257.914	0.434	906.209	0.401	17	0.162	K.NVFPSEKEIVVK.S
R4/RRR4-10/2	1003.106	1003.285	-178.034	0.443	808.423	0.399	14	0.161	K.MLGQILVTK.Q
R4/RRR4-10/2	1531.225	1531.607	-250.403	0.481	793.484	0.433	19	0.161	R.DTTQEDPREVAAAK.A
R4/RRR4-10/2	818.617	818.943	-400.328	0.368	657.510	0.470	10	0.160	K.YGINVPR.G
R4/RRR4-10/2	818.943	818.943	-0.390	0.463	759.245	0.393	11	0.160	K.YGINVPR.G
R4/RRR4-10/2	1094.616	1095.277	-1522.394	0.378	781.983	0.410	14	0.155	K.SGLQGGVHIVK.A
R4/RRR4-10/2	1390.296	1389.622	-234.835	0.462	825.975	0.373	16	0.154	K.NVFPSEKEIVVK.S
R4/RRR4-10/2	1531.323	1531.607	-186.103	0.426	577.181	0.430	18	0.153	R.DTTQEDPREVAAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	817.928	817.995	-82.272	0.353	371.605	0.388	11	0.152	K.VPIDVFK.G
R4/RRR4-10/2	1531.235	1531.607	-243.925	0.407	547.284	0.348	18	0.146	R.DTTQEDPREVAAAK.A
R4/RRR4-11/2	1183.550	1183.255	249.765	0.214	261.125	0.345	13	0.138	-.LNFDDNAAFR.-
R4/RRR4-10/3	1619.779	1619.824	-28.134	0.540	1190.246	0.404	27	0.126	R.LNIHEYQGAELM*GK.Y
R4/RRR4-10/3	1619.513	1619.824	-192.571	0.533	1232.171	0.372	27	0.122	R.LNIHEYQGAELM*GK.Y
R4/RRR4-10/3	1602.725	1603.825	-1314.125	0.373	1009.611	0.332	25	0.099	R.LNIHEYQGAELMGK.Y
R4/RRR4-6/2	1427.339	1427.588	-175.128	0.488	2256.282	0.570	21	0.358	K.STVHDVVLVGGSTR.I
R4/RRR4-6/2	1427.184	1427.588	-284.014	0.498	2166.618	0.548	21	0.334	K.STVHDVVLVGGSTR.I
R4/RRR4-6/2	1427.260	1427.588	-230.812	0.486	2058.319	0.588	21	0.328	K.STVHDVVLVGGSTR.I
R4/RRR4-6/2	1248.062	1248.435	-300.020	0.527	1685.474	0.482	20	0.246	K.DAGVISGLNVM*R.I
R4/RRR4-6/2	1248.027	1248.435	-328.282	0.579	1451.533	0.529	20	0.231	K.DAGVISGLNVM*R.I
R4/RRR4-6/2	1249.104	1248.435	-265.757	0.541	1354.677	0.451	20	0.204	K.DAGVISGLNVM*R.I
R4/RRR4-6/2	1544.579	1544.752	-112.635	0.480	1439.391	0.421	20	0.202	K.M*KETAEAYLGSTVK.N
R4/RRR4-6/2	1584.245	1583.788	289.226	0.564	1218.148	0.409	22	0.181	-.QFSAEEISSMVLNK.-
R4/RRR4-6/2	1583.206	1583.788	-1002.690	0.457	897.085	0.423	20	0.165	K.QFSAEEISSMVLNK.M
R4/RRR4-6/2	1599.870	1599.788	51.502	0.528	886.646	0.376	20	0.158	K.QFSAEEISSM*VLNK.M
R4/RRR4-6/2	1599.223	1599.788	-981.272	0.447	736.319	0.366	19	0.152	K.QFSAEEISSM*VLNK.M
R4/RRR4-5/2	1584.674	1583.788	-72.288	0.481	686.772	0.363	18	0.149	K.QFSAEEISSMVLNK.M
R4/RRR4-6/3	1528.404	1528.753	-229.005	0.428	902.205	0.389	25	0.104	K.MKETAEAYLGSTVK.N
R4/RRR4-6/3	1529.288	1528.753	-305.051	0.487	1150.907	0.311	28	0.102	K.MKETAEAYLGSTVK.N
R4/RRR4-6/3	1527.985	1528.753	-1160.732	0.448	1320.834	0.235	30	0.097	K.MKETAEAYLGSTVK.N
R4/RRR4-6/3	1545.506	1544.752	-159.871	0.514	1120.139	0.278	26	0.094	K.M*KETAEAYLGSTVK.N
R4/RRR4-8/2	1842.629	1842.085	-248.618	0.657	2817.125	0.651	26	0.520	-.HVAEADIIFVSVNTPTK.-
R4/RRR4-8/3	1682.242	1682.979	-1035.992	0.570	2497.215	0.534	32	0.432	K.CPAIEVVVVDISKPR.I
R4/RRR4-8/3	1682.815	1682.979	-98.129	0.574	1990.654	0.538	31	0.303	K.CPAIEVVVVDISKPR.I
R4/RRR4-8/2	1476.316	1476.699	-260.629	0.536	1898.614	0.557	22	0.293	R.IITTNLWSAELSK.L
R4/RRR4-7/3	1683.404	1682.979	252.653	0.531	2000.456	0.513	31	0.293	K.CPAIEVVVVDISKPR.I
R4/RRR4-8/3	1682.500	1682.979	-285.895	0.587	1940.891	0.534	32	0.288	K.CPAIEVVVVDISKPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1476.259	1476.699	-299.122	0.513	1991.720	0.488	22	0.287	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1620.324	1619.796	-292.097	0.602	1753.274	0.551	24	0.273	K.FLNASVGFGGSCFQK.D
R4/RRR4-1/2	1477.997	1476.699	202.409	0.575	1867.765	0.502	22	0.272	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1620.146	1619.796	217.146	0.604	1731.824	0.528	24	0.263	K.FLNASVGFGGSCFQK.D
R4/RRR4-5/2	1075.155	1075.246	-84.909	0.497	1809.642	0.458	17	0.254	K.LAANAFLAQR.I
R4/RRR4-7/2	1477.315	1476.699	-261.198	0.556	1700.075	0.514	21	0.253	R.IITTNLWSAELSK.L
R4/RRR4-1/2	1355.546	1354.450	71.390	0.469	1649.865	0.522	18	0.248	K.AADLTYWESAAR.M
R4/RRR4-8/2	1074.705	1075.246	-1437.811	0.506	1724.430	0.476	17	0.248	K.LAANAFLAQR.I
R4/RRR4-8/2	1355.096	1354.450	-261.897	0.531	1654.086	0.507	18	0.246	K.AADLTYWESAAR.M
R4/RRR4-1/2	1477.345	1476.699	-240.474	0.572	1678.354	0.495	21	0.245	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1476.424	1476.699	-187.053	0.507	1788.846	0.437	21	0.244	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1074.538	1075.246	-1594.594	0.451	1732.280	0.455	17	0.243	K.LAANAFLAQR.I
R4/RRR4-9/2	1476.406	1476.699	-199.246	0.476	1659.501	0.452	21	0.233	R.IITTNLWSAELSK.L
R4/RRR4-7/2	1075.050	1075.246	-183.089	0.583	1678.186	0.442	17	0.232	K.LAANAFLAQR.I
R4/RRR4-8/2	1075.033	1075.246	-198.467	0.590	1608.932	0.471	17	0.232	K.LAANAFLAQR.I
R4/RRR4-7/2	1075.235	1075.246	-10.432	0.557	1565.553	0.463	17	0.226	K.LAANAFLAQR.I
R4/RRR4-6/2	1075.370	1075.246	115.266	0.538	1638.098	0.424	17	0.224	K.LAANAFLAQR.I
R4/RRR4-5/2	1074.955	1075.246	-271.150	0.483	1602.708	0.435	17	0.224	K.LAANAFLAQR.I
R4/RRR4-8/2	1353.768	1354.450	-1245.975	0.436	1638.434	0.418	18	0.222	K.AADLTYWESAAR.M
R4/RRR4-9/2	1476.319	1476.699	-258.389	0.445	1589.212	0.435	20	0.221	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1354.055	1354.450	-291.938	0.505	1560.363	0.440	18	0.219	K.AADLTYWESAAR.M
R4/RRR4-4/2	1477.891	1476.699	130.017	0.585	1401.991	0.509	20	0.217	R.IITTNLWSAELSK.L
R4/RRR4-9/2	1476.461	1476.699	-161.507	0.512	1415.380	0.503	19	0.217	R.IITTNLWSAELSK.L
R4/RRR4-3/2	1075.360	1075.246	105.931	0.492	1546.385	0.416	17	0.213	K.LAANAFLAQR.I
R4/RRR4-2/2	1476.748	1476.699	33.445	0.491	1509.510	0.431	20	0.211	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1272.075	1272.453	-298.222	0.401	1281.062	0.538	20	0.211	R.VVSSM*FNTVSGK.K
R4/RRR4-5/2	1075.117	1075.246	-120.329	0.462	1509.930	0.411	17	0.209	K.LAANAFLAQR.I
R4/RRR4-4/2	1476.431	1476.699	-182.076	0.448	1400.476	0.452	19	0.205	R.IITTNLWSAELSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1475.990	1476.699	-1161.380	0.385	1513.187	0.399	20	0.205	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1272.024	1272.453	-338.660	0.401	1104.592	0.590	19	0.204	R.VVSSM*FNTVSGK.K
R4/RRR4-1/2	1354.348	1354.450	-75.270	0.490	1303.922	0.485	17	0.203	K.AADLTYWESAAR.M
R4/RRR4-6/2	1075.246	1075.246	-0.297	0.485	1415.044	0.422	17	0.203	K.LAANAFLAQR.I
R4/RRR4-15/2	1075.947	1075.246	-278.296	0.478	1376.570	0.417	16	0.197	K.LAANAFLAQR.I
R4/RRR4-7/2	1476.159	1476.699	-1046.621	0.439	1403.471	0.410	19	0.197	R.IITTNLWSAELSK.L
R4/RRR4-6/2	1075.300	1075.246	50.030	0.479	1251.439	0.452	16	0.194	K.LAANAFLAQR.I
R4/RRR4-8/2	1255.853	1256.454	-1278.774	0.334	1264.539	0.474	19	0.194	R.VVSSMFNTVSGK.K
R4/RRR4-5/2	1477.398	1476.699	-204.664	0.553	1131.776	0.509	18	0.193	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1256.001	1256.454	-361.422	0.514	941.634	0.554	18	0.190	R.VVSSMFNTVSGK.K
R4/RRR4-10/2	1074.948	1075.246	-277.985	0.468	1259.026	0.416	16	0.188	K.LAANAFLAQR.I
R4/RRR4-8/2	1271.841	1272.453	-1271.730	0.357	954.086	0.574	18	0.187	R.VVSSM*FNTVSGK.K
R4/RRR4-6/2	1074.857	1075.246	-362.530	0.374	1331.587	0.375	16	0.185	K.LAANAFLAQR.I
R4/RRR4-8/2	980.083	980.228	-148.362	0.441	1163.872	0.426	15	0.183	K.IAILGFAFK.K
R4/RRR4-2/2	1476.265	1476.699	-295.139	0.389	1235.926	0.392	20	0.181	R.IITTNLWSAELSK.L
R4/RRR4-7/2	1475.676	1476.699	-1375.192	0.376	1377.419	0.330	20	0.180	R.IITTNLWSAELSK.L
R4/RRR4-8/2	979.876	980.228	-360.435	0.425	1240.273	0.373	15	0.179	K.IAILGFAFK.K
R4/RRR4-8/2	1497.487	1496.646	-106.258	0.467	865.582	0.515	20	0.179	K.QVSVVWDAYEATK.G
R4/RRR4-8/3	1801.235	1802.046	-1008.494	0.452	1353.834	0.515	28	0.179	R.IFDNM*QKPAFVFDGR.N
R4/RRR4-8/2	1625.272	1625.799	-942.009	0.477	632.409	0.569	22	0.175	R.ETPAIDVCHGLLGDK.A
R4/RRR4-6/2	1475.680	1476.699	-1372.616	0.356	1228.201	0.363	19	0.175	R.IITTNLWSAELSK.L
R4/RRR4-6/2	1477.894	1476.699	132.502	0.481	912.300	0.493	16	0.174	R.IITTNLWSAELSK.L
R4/RRR4-10/2	1476.183	1476.699	-1030.514	0.423	1147.651	0.393	18	0.174	R.IITTNLWSAELSK.L
R4/RRR4-1/2	1353.860	1354.450	-1177.702	0.393	1268.934	0.315	17	0.169	K.AADLTYWESAAR.M
R4/RRR4-8/2	1625.318	1625.799	-296.849	0.426	566.814	0.516	21	0.164	R.ETPAIDVCHGLLGDK.A
R4/RRR4-8/2	1625.382	1625.799	-257.366	0.433	488.707	0.505	20	0.160	R.ETPAIDVCHGLLGDK.A
R4/RRR4-8/2	1496.907	1496.646	174.824	0.355	701.432	0.452	18	0.158	K.QVSVVWDAYEATK.G
R4/RRR4-8/2	1476.345	1476.699	-240.388	0.416	1054.369	0.313	18	0.157	R.IITTNLWSAELSK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1354.205	1354.450	-181.151	0.428	684.132	0.372	15	0.151	K.AADLTYWESAAR.M
R4/RRR4-8/2	1199.598	1200.322	-1441.623	0.358	913.009	0.300	15	0.150	R.NLFFSTDVEK.H
R4/RRR4-2/2	1353.890	1354.450	-1155.610	0.373	626.823	0.377	15	0.150	K.AADLTYWESAAR.M
R4/RRR4-8/2	1199.910	1200.322	-344.747	0.348	809.515	0.323	14	0.149	R.NLFFSTDVEK.H
R4/RRR4-8/2	1199.537	1200.322	-1492.731	0.311	990.748	0.251	15	0.147	R.NLFFSTDVEK.H
R4/RRR4-8/2	1075.957	1075.246	-269.304	0.296	531.119	0.361	12	0.147	K.LAANAFLAQR.I
R4/RRR4-8/3	1786.096	1786.047	27.508	0.512	927.913	0.555	29	0.143	R.IFDNMQKPAFVFDGR.N
R4/RRR4-8/2	1496.969	1496.646	216.447	0.362	422.204	0.327	15	0.143	K.QVSVVWDAYEATK.G
R4/RRR4-8/2	1475.284	1476.699	-1642.293	0.293	714.144	0.283	15	0.143	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1496.136	1496.646	-1011.941	0.323	540.865	0.322	16	0.142	K.QVSVVWDAYEATK.G
R4/RRR4-5/2	1354.355	1354.450	-69.936	0.290	557.351	0.275	14	0.140	K.AADLTYWESAAR.M
R4/RRR4-8/2	1227.146	1227.394	-202.401	0.364	747.089	0.288	14	0.140	R.HLQPTSPTAFK.Q
R4/RRR4-7/2	1200.352	1200.322	25.030	0.233	890.540	0.117	14	0.133	R.NLFFSTDVEK.H
R4/RRR4-8/2	1075.411	1075.246	153.629	0.254	521.860	0.207	12	0.133	-.LAANAFLAQR.-
R4/RRR4-8/2	1075.192	1075.246	-50.516	0.273	355.294	0.410	11	0.132	-.LAANAFLAQR.-
R4/RRR4-8/3	1786.146	1786.047	55.474	0.510	770.184	0.552	28	0.131	R.IFDNMQKPAFVFDGR.N
R4/RRR4-8/3	1476.749	1476.699	33.788	0.469	906.374	0.388	24	0.104	R.IITTNLWSAELSK.L
R4/RRR4-8/3	1785.837	1786.047	-117.904	0.360	664.609	0.293	24	0.086	R.IFDNMQKPAFVFDGR.N
R4/RRR4-8/3	1476.558	1476.699	-96.247	0.328	773.718	0.189	21	0.075	R.IITTNLWSAELSK.L
R4/RRR4-8/2	1911.450	1911.020	225.688	0.622	3190.544	0.535	28	0.556	R.TGELIAHVAEGDAEDINR.A
R4/RRR4-8/2	1910.389	1911.020	-856.344	0.587	3081.112	0.490	28	0.508	R.TGELIAHVAEGDAEDINR.A
R4/RRR4-8/3	1910.866	1911.020	-80.747	0.508	2879.380	0.444	35	0.507	R.TGELIAHVAEGDAEDINR.A
R4/RRR4-8/2	1910.334	1911.020	-885.338	0.574	2915.660	0.507	27	0.474	R.TGELIAHVAEGDAEDINR.A
R4/RRR4-8/2	1481.217	1481.550	-225.380	0.530	2476.432	0.568	25	0.402	K.YGVDSGANLVTGGDR.L
R4/RRR4-8/2	1482.055	1481.550	-334.632	0.546	2036.851	0.564	24	0.318	K.YGVDSGANLVTGGDR.L
R4/RRR4-8/3	1910.170	1911.020	-971.118	0.462	2223.445	0.419	31	0.308	R.TGELIAHVAEGDAEDINR.A
R4/RRR4-8/2	1481.125	1481.550	-287.310	0.476	1976.262	0.548	24	0.303	K.YGVDSGANLVTGGDR.L
R4/RRR4-8/2	1818.242	1818.879	-902.974	0.573	1718.654	0.553	23	0.266	K.NGVEQGPQIDDEQFNK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1818.370	1818.879	-832.346	0.568	1675.379	0.574	23	0.266	K.NGVEQGPQIDDEQFNK.I
R4/RRR4-8/2	1818.252	1818.879	-897.785	0.566	1656.003	0.560	23	0.259	K.NGVEQGPQIDDEQFNK.I
R4/RRR4-8/2	1672.451	1672.947	-297.122	0.538	1721.767	0.437	22	0.234	K.IAQEEIFGPVQSILK.F
R4/RRR4-8/2	1465.340	1464.645	-209.356	0.515	1316.989	0.604	21	0.231	K.TAEQTPLSALFASK.L
R4/RRR4-8/2	1379.207	1378.599	-284.927	0.501	1717.219	0.332	18	0.210	K.GIDSLKNYLQVK.A
R4/RRR4-8/2	1673.492	1672.947	-272.208	0.559	1439.958	0.457	21	0.208	K.IAQEEIFGPVQSILK.F
R4/RRR4-8/2	1465.062	1464.645	285.176	0.498	1179.401	0.553	20	0.206	K.TAEQTPLSALFASK.L
R4/RRR4-2/2	1465.278	1464.645	-251.312	0.476	1146.044	0.546	20	0.201	K.TAEQTPLSALFASK.L
R4/RRR4-8/2	1464.094	1464.645	-1062.605	0.429	1186.281	0.510	20	0.197	K.TAEQTPLSALFASK.L
R4/RRR4-8/2	1400.313	1399.655	-244.872	0.517	1029.698	0.561	19	0.195	K.VGPALACGNTVVLK.T
R4/RRR4-8/2	1673.504	1672.947	-265.476	0.570	1220.744	0.451	20	0.186	K.IAQEEIFGPVQSILK.F
R4/RRR4-8/3	1464.797	1464.645	103.963	0.564	1344.082	0.532	27	0.185	K.TAEQTPLSALFASK.L
R4/RRR4-8/2	1398.625	1399.655	-1455.855	0.442	842.839	0.553	18	0.178	K.VGPALACGNTVVLK.T
R4/RRR4-8/2	1097.935	1098.188	-231.128	0.356	1098.794	0.442	18	0.178	K.IAFTGSTDTGK.I
R4/RRR4-1/2	1464.267	1464.645	-259.011	0.376	957.815	0.485	18	0.173	K.TAEQTPLSALFASK.L
R4/RRR4-8/2	1377.630	1378.599	-1433.693	0.433	1410.863	0.258	17	0.170	-.GIDSLKNYLQVK.-
R4/RRR4-8/2	1399.254	1399.655	-287.408	0.468	889.349	0.458	18	0.167	K.VGPALACGNTVVLK.T
R4/RRR4-1/2	1674.599	1672.947	-208.419	0.555	1211.329	0.360	19	0.166	K.IAQEEIFGPVQSILK.F
R4/RRR4-8/2	1377.765	1378.599	-1334.911	0.453	1274.021	0.309	16	0.166	K.GIDSLKNYLQVK.A
R4/RRR4-8/2	1248.257	1248.413	-125.904	0.448	1042.815	0.352	16	0.164	K.FNDLNEVIKR.A
R4/RRR4-2/2	1674.032	1672.947	51.006	0.511	1195.826	0.336	18	0.162	K.IAQEEIFGPVQSILK.F
R4/RRR4-7/2	1673.627	1672.947	-191.714	0.519	912.884	0.420	18	0.161	K.IAQEEIFGPVQSILK.F
R4/RRR4-7/2	1674.244	1672.947	177.952	0.506	1260.974	0.301	19	0.161	K.IAQEEIFGPVQSILK.F
R4/RRR4-8/2	1098.147	1098.188	-37.753	0.325	907.628	0.406	17	0.160	K.IAFTGSTDTGK.I
R4/RRR4-8/2	1175.032	1175.318	-243.471	0.405	815.029	0.403	14	0.158	R.KAFDEGPWPK.M
R4/RRR4-1/2	1463.505	1464.645	-1467.026	0.318	841.353	0.422	17	0.157	K.TAEQTPLSALFASK.L
R4/RRR4-8/2	1091.546	1092.227	-1544.285	0.381	1354.482	0.196	14	0.157	K.FNDLNEVIK.R
R4/RRR4-8/2	1174.612	1175.318	-1456.445	0.452	534.306	0.466	12	0.156	R.KAFDEGPWPK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1092.017	1092.227	-192.578	0.438	1230.281	0.232	14	0.155	K.FNDLNEVIK.R
R4/RRR4-8/2	1098.209	1098.188	18.996	0.382	720.920	0.404	15	0.154	K.IAFTGSTDTGK.I
R4/RRR4-8/2	1091.445	1092.227	-1637.424	0.369	1416.779	0.155	14	0.154	K.FNDLNEVIK.R
R4/RRR4-8/2	1248.053	1248.413	-289.559	0.460	857.120	0.347	14	0.153	K.FNDLNEVIKR.A
R4/RRR4-7/2	1673.425	1672.947	286.763	0.475	845.468	0.385	17	0.153	K.IAQEEIFGPVQSILK.F
R4/RRR4-21/2	1481.916	1481.550	247.893	0.448	558.759	0.459	16	0.153	K.YGVDSGANLVTGGDR.L
R4/RRR4-8/3	1820.394	1818.879	-267.467	0.516	1257.251	0.463	26	0.152	K.NGVEQGPQIDDEQFNK.I
R4/RRR4-8/2	884.294	885.086	-2033.116	0.372	690.213	0.347	13	0.151	K.IVLELAAR.S
R4/RRR4-8/2	884.653	885.086	-491.753	0.426	619.010	0.337	13	0.151	K.IVLELAAR.S
R4/RRR4-8/2	1175.102	1175.318	-184.276	0.413	651.614	0.384	13	0.151	R.KAFDEGPWPK.M
R4/RRR4-8/3	1672.763	1672.947	-110.210	0.380	1463.401	0.374	26	0.148	K.IAQEEIFGPVQSILK.F
R4/RRR4-8/3	1175.271	1175.318	-40.079	0.541	1353.285	0.427	22	0.148	R.KAFDEGPWPK.M
R4/RRR4-8/2	1247.620	1248.413	-1441.384	0.457	780.396	0.335	13	0.147	-.FNDLNEVIKR.-
R4/RRR4-21/2	1482.009	1481.550	310.666	0.329	241.137	0.373	16	0.146	K.YGVDSGANLVTGGDR.L
R4/RRR4-9/2	1465.131	1464.645	332.295	0.293	483.008	0.383	14	0.142	K.TAEQTPLSALFASK.L
R4/RRR4-7/2	885.001	885.086	-96.858	0.313	615.507	0.253	13	0.142	K.IVLELAAR.S
R4/RRR4-3/2	1674.177	1672.947	137.956	0.426	675.057	0.334	15	0.141	K.IAQEEIFGPVQSILK.F
R4/RRR4-6/2	1673.481	1672.947	-279.234	0.402	799.474	0.217	16	0.133	K.IAQEEIFGPVQSILK.F
R4/RRR4-8/3	1175.391	1175.318	62.737	0.505	1083.968	0.465	19	0.133	R.KAFDEGPWPK.M
R4/RRR4-17/2	1043.443	1043.151	280.369	0.195	941.965	0.073	13	0.127	R.IYDEFVEK.A
R4/RRR4-8/3	1464.715	1464.645	47.545	0.463	1230.322	0.387	26	0.126	K.TAEQTPLSALFASK.L
R4/RRR4-8/3	1175.290	1175.318	-23.827	0.534	1067.835	0.428	20	0.123	R.KAFDEGPWPK.M
R4/RRR4-8/3	1378.291	1378.599	-223.788	0.474	832.133	0.483	26	0.119	K.GIDSLKNYLQVK.A
R4/RRR4-8/3	1378.859	1378.599	189.470	0.534	841.890	0.467	26	0.118	K.GIDSLKNYLQVK.A
R4/RRR4-8/3	1378.534	1378.599	-46.826	0.535	767.164	0.410	26	0.105	K.GIDSLKNYLQVK.A
R4/RRR4-8/3	1818.646	1818.879	-128.501	0.425	620.085	0.375	26	0.092	K.NGVEQGPQIDDEQFNK.I
R4/RRR4-4/2	1832.721	1833.143	-230.989	0.519	2837.854	0.504	25	0.455	R.NGVTATDLVLTVTQMLR.K
R4/RRR4-4/2	1833.095	1833.143	-26.357	0.465	2396.118	0.551	22	0.375	R.NGVTATDLVLTVTQMLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1515.348	1515.630	-186.143	0.522	1682.571	0.529	20	0.258	K.M*FVDYNQPEAER.V
R4/RRR4-4/2	1657.289	1656.768	-290.015	0.565	1645.189	0.547	21	0.255	K.SDWLSCLDNDVGFK.G
R4/RRR4-4/2	1558.249	1558.589	-219.110	0.501	1524.021	0.549	22	0.240	K.SGEDADTLGLTGHER.F
R4/RRR4-4/2	1518.085	1516.656	283.531	0.616	1437.422	0.477	20	0.214	R.SDDTVAM*IESYLR.A
R4/RRR4-4/2	1517.471	1516.656	-122.118	0.520	1362.013	0.477	19	0.207	R.SDDTVAM*IESYLR.A
R4/RRR4-4/2	1516.242	1516.656	-273.542	0.515	1453.847	0.420	20	0.204	R.SDDTVAM*IESYLR.A
R4/RRR4-4/2	1558.062	1558.589	-983.352	0.502	1195.186	0.527	22	0.203	K.SGEDADTLGLTGHER.F
R4/RRR4-4/2	1516.289	1516.656	-242.769	0.479	1404.432	0.428	19	0.201	R.SDDTVAM*IESYLR.A
R4/RRR4-4/2	1558.099	1558.589	-315.942	0.502	1164.206	0.528	22	0.200	K.SGEDADTLGLTGHER.F
R4/RRR4-4/2	1655.977	1656.768	-1084.466	0.411	1345.377	0.391	19	0.187	K.SDWLSCLDNDVGFK.G
R4/RRR4-4/2	1850.464	1849.143	174.359	0.493	1149.756	0.464	18	0.179	R.NGVTATDLVLTVTQM*LR.K
R4/RRR4-4/2	1849.009	1849.143	-72.362	0.403	1120.894	0.471	18	0.178	R.NGVTATDLVLTVTQM*LR.K
R4/RRR4-4/2	1655.262	1656.768	-2124.111	0.357	1109.823	0.408	19	0.171	K.SDWLSCLDNDVGFK.G
R4/RRR4-4/2	1616.470	1616.793	-200.766	0.440	779.314	0.473	21	0.168	R.DIWPSTEEIAEVVK.S
R4/RRR4-4/2	1291.219	1291.437	-169.221	0.447	808.705	0.468	17	0.166	K.VAEFSFHGTPAK.L
R4/RRR4-4/2	1537.252	1537.843	-1037.525	0.414	644.885	0.533	17	0.164	R.SNLAGM*GIIPLCFK.S
R4/RRR4-1/2	1617.428	1616.793	-226.838	0.449	841.123	0.416	22	0.164	R.DIWPSTEEIAEVVK.S
R4/RRR4-4/2	1015.513	1016.174	-1640.196	0.363	680.241	0.500	16	0.164	K.TSLAPGSGVVK.K
R4/RRR4-1/2	1616.993	1616.793	123.830	0.405	823.358	0.396	21	0.159	R.DIWPSTEEIAEVVK.S
R4/RRR4-4/2	1537.518	1537.843	-212.114	0.442	532.269	0.518	16	0.159	R.SNLAGM*GIIPLCFK.S
R4/RRR4-4/2	1172.377	1173.300	-1645.638	0.433	800.415	0.388	16	0.159	K.ILDWENSAPK.Q
R4/RRR4-4/2	1616.309	1616.793	-300.777	0.412	792.227	0.391	21	0.158	R.DIWPSTEEIAEVVK.S
R4/RRR4-4/2	1536.995	1537.843	-1205.462	0.351	725.057	0.464	18	0.158	R.SNLAGM*GIIPLCFK.S
R4/RRR4-3/2	1617.244	1616.793	279.161	0.427	661.358	0.415	20	0.157	R.DIWPSTEEIAEVVK.S
R4/RRR4-4/2	1173.100	1173.300	-171.022	0.520	806.476	0.361	16	0.156	K.ILDWENSAPK.Q
R4/RRR4-3/2	951.966	952.086	-126.506	0.307	762.398	0.377	14	0.152	K.LSVFDAATK.Y
R4/RRR4-4/2	951.586	952.086	-1581.123	0.308	586.680	0.390	13	0.149	K.LSVFDAATK.Y
R4/RRR4-4/2	952.183	952.086	102.275	0.304	486.238	0.386	12	0.146	K.LSVFDAATK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1658.221	1656.768	273.739	0.365	533.904	0.415	14	0.146	K.SDWLSCLDNDVGFK.G
R4/RRR4-3/2	1281.409	1282.426	-1578.995	0.187	975.832	0.345	15	0.145	K.YYSLPALSDPR.I
R4/RRR4-3/2	1616.260	1616.793	-951.504	0.301	389.772	0.344	15	0.142	R.DIWPSTEEIAEVVK.S
R4/RRR4-1/2	1516.929	1516.656	180.514	0.336	872.397	0.264	15	0.141	R.SDDTVAM*IESYLR.A
R4/RRR4-4/2	1015.648	1016.174	-1506.408	0.295	413.574	0.410	13	0.141	-.TSLAPGSGVVK.-
R4/RRR4-4/2	1657.473	1656.768	-178.735	0.378	638.796	0.294	16	0.140	K.SDWLSCLDNDVGFK.G
R4/RRR4-4/2	1015.507	1016.174	-1646.355	0.249	347.828	0.310	12	0.138	-.TSLAPGSGVVK.-
R4/RRR4-3/2	1016.063	1016.174	-108.826	0.274	383.027	0.315	13	0.111	-.TSLAPGSGVVK.-
R4/RRR4-4/3	1671.593	1671.998	-243.374	0.483	1178.564	0.316	27	0.105	K.KACELGLEVKPWIK.T
R4/RRR4-4/3	1672.093	1671.998	56.988	0.495	969.055	0.309	25	0.093	K.KACELGLEVKPWIK.T
R4/RRR4-4/3	1673.046	1671.998	28.708	0.511	985.398	0.296	25	0.091	K.KACELGLEVKPWIK.T
R4/RRR4-4/2	1807.882	1807.103	-122.418	0.521	2357.087	0.517	23	0.359	K.NTLLIMTSNVGSSVIEK.G
R4/RRR4-4/3	1892.649	1893.091	-234.097	0.460	2309.579	0.470	32	0.356	R.HAQLPDEAKELDKELR.Q
R4/RRR4-4/2	1160.939	1160.260	-277.433	0.575	1813.995	0.552	18	0.282	K.AIDLIDEAGSR.V
R4/RRR4-4/2	1031.013	1030.160	-143.171	0.557	2001.510	0.391	16	0.262	K.TAIAEGLAQR.I
R4/RRR4-4/2	1611.642	1610.834	-119.243	0.553	1593.411	0.560	22	0.253	K.VPEPTVDETIQILR.G
R4/RRR4-4/3	1960.364	1960.225	71.217	0.449	1873.925	0.450	33	0.244	K.NPNRPIASFIFSGPTGVGK.S
R4/RRR4-4/2	1160.060	1160.260	-172.839	0.546	1545.036	0.509	18	0.236	K.AIDLIDEAGSR.V
R4/RRR4-4/2	1159.318	1160.260	-1679.487	0.411	1656.215	0.418	18	0.225	K.AIDLIDEAGSR.V
R4/RRR4-4/2	1609.884	1610.834	-1214.537	0.495	1314.222	0.577	20	0.223	K.VPEPTVDETIQILR.G
R4/RRR4-4/2	1609.826	1610.834	-1250.783	0.444	1384.153	0.516	21	0.217	K.VPEPTVDETIQILR.G
R4/RRR4-4/2	1159.982	1159.315	-287.900	0.577	1452.860	0.462	17	0.216	R.VLELSLEEAR.Q
R4/RRR4-4/2	1159.072	1159.315	-210.380	0.476	1529.961	0.429	17	0.216	R.VLELSLEEAR.Q
R4/RRR4-4/2	1160.107	1159.315	-179.797	0.562	1459.497	0.445	17	0.213	R.VLELSLEEAR.Q
R4/RRR4-4/2	1030.077	1030.160	-80.898	0.471	1481.836	0.433	16	0.211	K.TAIAEGLAQR.I
R4/RRR4-4/2	1398.279	1398.547	-192.078	0.508	1410.120	0.458	21	0.209	R.VLESLGADPNNIR.T
R4/RRR4-4/2	1398.280	1398.547	-191.377	0.481	1323.783	0.481	21	0.206	R.VLESLGADPNNIR.T
R4/RRR4-4/2	1421.113	1421.446	-234.826	0.459	1230.727	0.481	20	0.195	K.EGDSAIVDVDSEGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1398.308	1398.547	-171.409	0.501	1222.305	0.468	20	0.194	R.VLESLGADPNNIR.T
R4/RRR4-4/2	1513.071	1513.695	-1076.554	0.470	1189.236	0.474	20	0.192	K.M*PTLEEYGTNLTK.L
R4/RRR4-4/2	1476.505	1477.689	-1483.879	0.312	1219.626	0.368	18	0.170	R.GSGFVAVEIPFTPR.A
R4/RRR4-4/2	1477.547	1477.689	-96.339	0.411	1046.602	0.415	18	0.169	R.GSGFVAVEIPFTPR.A
R4/RRR4-4/3	1960.788	1960.225	-223.402	0.443	1369.604	0.434	29	0.157	K.NPNRPIASFIFSGPTGVGK.S
R4/RRR4-4/3	1207.643	1208.349	-1417.026	0.528	1282.718	0.434	21	0.143	K.HIEKDPALER.R
R4/RRR4-4/3	1208.023	1208.349	-270.533	0.530	1199.874	0.440	21	0.137	K.HIEKDPALER.R
R4/RRR4-4/3	1960.269	1960.225	22.690	0.429	1322.296	0.386	28	0.137	K.NPNRPIASFIFSGPTGVGK.S
R4/RRR4-4/2	1610.461	1610.834	-231.849	0.347	674.349	0.238	16	0.136	K.VPEPTVDETIQILR.G
R4/RRR4-4/3	1260.823	1260.419	321.213	0.492	1373.668	0.364	24	0.135	K.AKDIDLQVTEK.F
R4/RRR4-4/2	1476.511	1477.689	-1479.727	0.209	796.301	0.197	17	0.134	R.GSGFVAVEIPFTPR.A
R4/RRR4-4/2	1476.483	1477.689	-1498.661	0.202	653.318	0.209	16	0.133	R.GSGFVAVEIPFTPR.A
R4/RRR4-4/3	1208.441	1208.349	76.219	0.539	1118.198	0.361	21	0.111	K.HIEKDPALER.R
R4/RRR4-4/3	1766.785	1766.034	-141.316	0.441	993.721	0.336	26	0.098	R.RRPYTVVLFDEIEK.A
R4/RRR4-7/1	1030.604	1031.142	-1496.890	0.174	1138.081	0.191	13	0.628	K.AIDDAEGLVK.V
R4/RRR4-7/1	1030.531	1031.142	-1567.449	0.142	925.923	0.249	12	0.543	K.AIDDAEGLVK.V
R4/RRR4-7/2	1834.579	1836.033	-1341.612	0.514	2424.717	0.565	28	0.390	R.VPYTAGIGLESVGVETDK.A
R4/RRR4-7/2	1835.331	1836.033	-929.857	0.530	2009.771	0.608	26	0.326	R.VPYTAGIGLESVGVETDK.A
R4/RRR4-7/2	1947.564	1948.118	-800.455	0.552	2024.932	0.580	28	0.319	K.LASPSEVSVDLSDGGSTVVK.G
R4/RRR4-7/2	1836.387	1836.033	193.310	0.599	1826.040	0.573	26	0.287	R.VPYTAGIGLESVGVETDK.A
R4/RRR4-7/2	1947.493	1948.118	-836.822	0.520	1710.628	0.606	26	0.277	K.LASPSEVSVDLSDGGSTVVK.G
R4/RRR4-7/2	1595.413	1595.726	-196.662	0.535	1616.351	0.526	23	0.247	K.AEEDGVACVEFIAGK.E
R4/RRR4-7/2	1948.728	1948.118	-200.840	0.572	1326.700	0.583	24	0.222	K.LASPSEVSVDLSDGGSTVVK.G
R4/RRR4-7/2	1576.316	1575.823	314.060	0.526	1439.828	0.500	21	0.219	K.IVSSTGALCLSEIPK.K
R4/RRR4-7/2	1595.359	1595.726	-230.820	0.517	1191.118	0.557	21	0.207	K.AEEDGVACVEFIAGK.E
R4/RRR4-7/2	1726.215	1726.996	-1035.275	0.481	1344.770	0.448	22	0.199	K.FSNLEVDLPAM*M*AQK.D
R4/RRR4-7/2	1130.887	1131.305	-370.552	0.384	1225.982	0.426	17	0.185	K.NIIIATGSDVK.S
R4/RRR4-7/2	1726.295	1726.996	-988.700	0.533	1136.137	0.459	21	0.184	K.FSNLEVDLPAM*M*AQK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1726.443	1726.996	-902.379	0.537	1178.531	0.435	21	0.182	K.FSNLEVDLPAM*M*AQK.D
R4/RRR4-7/2	1452.038	1451.603	299.877	0.507	1059.149	0.454	18	0.178	R.TCHAHPTVSEALK.E
R4/RRR4-7/2	1451.057	1451.603	-1068.692	0.468	1023.195	0.466	18	0.177	R.TCHAHPTVSEALK.E
R4/RRR4-7/2	1130.919	1131.305	-342.393	0.372	1242.780	0.367	17	0.176	K.NIIIATGSDVK.S
R4/RRR4-7/2	1316.826	1316.529	226.439	0.445	1217.322	0.377	19	0.175	K.GKNIIIATGSDVK.S
R4/RRR4-7/2	1130.432	1131.305	-1661.642	0.353	1344.786	0.306	17	0.173	K.NIIIATGSDVK.S
R4/RRR4-7/2	1575.007	1575.823	-1155.920	0.283	1380.086	0.294	20	0.170	K.IVSSTGALCLSEIPK.K
R4/RRR4-7/2	1451.050	1451.603	-1073.591	0.428	906.759	0.468	17	0.169	R.TCHAHPTVSEALK.E
R4/RRR4-7/2	1030.545	1031.142	-1553.956	0.401	871.633	0.415	17	0.165	K.AIDDAEGLVK.V
R4/RRR4-7/2	1030.912	1031.142	-224.064	0.445	799.712	0.412	16	0.162	K.AIDDAEGLVK.V
R4/RRR4-7/2	1186.586	1187.368	-1506.237	0.426	269.404	0.518	15	0.161	K.SLPGVTIDEKK.I
R4/RRR4-7/2	1030.917	1031.142	-218.481	0.434	804.584	0.373	17	0.158	K.AIDDAEGLVK.V
R4/RRR4-7/2	1132.964	1133.234	-239.327	0.424	460.887	0.461	15	0.154	K.VVGVDTSGDGVK.L
R4/RRR4-7/2	1132.413	1133.234	-1613.434	0.322	759.939	0.404	18	0.154	K.VVGVDTSGDGVK.L
R4/RRR4-7/2	1186.918	1187.368	-380.499	0.349	226.332	0.430	14	0.151	K.SLPGVTIDEKK.I
R4/RRR4-7/2	1187.110	1187.368	-218.097	0.366	286.643	0.357	16	0.151	K.SLPGVTIDEKK.I
R4/RRR4-7/2	1132.470	1133.234	-1562.538	0.273	420.303	0.403	15	0.144	K.VVGVDTSGDGVK.L
R4/RRR4-7/2	918.007	918.075	-73.836	0.374	896.817	0.293	13	0.143	-.FPLLANSR.-
R4/RRR4-7/2	1574.720	1575.823	-1339.080	0.254	1330.074	0.102	20	0.142	K.IVSSTGALCLSEIPK.K
R4/RRR4-7/2	918.803	918.075	-296.710	0.458	802.785	0.232	12	0.137	-.FPLLANSR.-
R4/RRR4-7/3	1202.291	1202.431	-116.625	0.486	1424.822	0.331	24	0.128	-.VGKFPLLANSR.-
R4/RRR4-1/2	918.964	918.075	-121.190	0.352	545.581	0.193	10	0.123	-.FPLLANSR.-
R4/RRR4-7/3	1451.555	1451.603	-33.547	0.411	1152.408	0.337	23	0.108	R.TCHAHPTVSEALK.E
R4/RRR4-7/3	1451.376	1451.603	-156.800	0.427	1008.720	0.339	24	0.100	R.TCHAHPTVSEALK.E
R4/RRR4-7/3	1451.274	1451.603	-227.930	0.434	916.809	0.318	23	0.092	R.TCHAHPTVSEALK.E
R4/RRR4-7/3	1202.151	1202.431	-233.050	0.478	1050.283	0.230	22	0.083	-.VGKFPLLANSR.-
R4/RRR4-7/3	1202.184	1202.431	-205.546	0.388	924.444	0.166	19	0.069	-.VGKFPLLANSR.-
R4/RRR4-7/2	1272.538	1272.473	51.224	0.446	1743.932	0.353	18	0.220	R.DLITILEDAIR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1272.174	1272.473	-235.659	0.486	1121.210	0.450	16	0.183	R.DLITILEDAIR.G
R4/RRR4-7/2	1273.330	1272.473	-112.848	0.429	1017.679	0.386	16	0.166	R.DLITILEDAIR.G
R4/RRR4-8/2	1271.420	1272.473	-1619.712	0.314	1107.624	0.339	15	0.162	R.DLITILEDAIR.G
R4/RRR4-7/2	1016.069	1016.174	-102.920	0.413	686.004	0.438	15	0.159	K.IVNDGVTVAK.E
R4/RRR4-7/2	949.828	949.046	-230.301	0.379	458.341	0.452	12	0.156	K.VLANDNFR.Y
R4/RRR4-7/2	1016.118	1016.174	-55.079	0.423	521.078	0.427	14	0.154	K.IVNDGVTVAK.E
R4/RRR4-7/2	1617.736	1617.737	-0.425	0.472	644.369	0.393	20	0.153	K.VDAIIETLENDEQK.V
R4/RRR4-8/2	1271.769	1272.473	-1344.025	0.350	542.932	0.401	13	0.149	R.DLITILEDAIR.G
R4/RRR4-7/2	948.960	949.046	-90.394	0.362	403.268	0.328	11	0.147	K.VLANDNFR.Y
R4/RRR4-7/2	948.895	949.046	-159.561	0.316	485.411	0.340	12	0.146	K.VLANDNFR.Y
R4/RRR4-6/2	1272.025	1272.473	-353.212	0.364	353.450	0.317	13	0.145	R.DLITILEDAIR.G
R4/RRR4-7/2	1272.155	1272.473	-250.580	0.314	692.762	0.281	14	0.142	R.DLITILEDAIR.G
R4/RRR4-7/2	1618.168	1617.737	267.501	0.188	282.865	0.311	19	0.138	K.VDAIIETLENDEQK.V
R4/RRR4-22/2	1930.448	1931.131	-874.337	0.629	3799.578	0.679	31	0.817	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-22/2	1930.521	1931.131	-836.315	0.645	3541.302	0.675	30	0.729	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-22/2	1913.669	1914.037	-193.151	0.615	3387.363	0.600	27	0.645	K.M*NVEYELEDGGSLSPEK.E
R4/RRR4-22/2	1912.677	1914.037	-1237.818	0.539	3407.337	0.576	27	0.640	K.M*NVEYELEDGGSLSPEK.E
R4/RRR4-22/2	1930.610	1931.131	-789.853	0.620	3074.527	0.666	28	0.585	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-22/1	1219.569	1220.313	-1435.022	0.216	879.208	0.351	16	0.583	K.LNPAVDDGGSFK.T
R4/RRR4-22/1	1219.575	1220.313	-1429.995	0.189	727.672	0.290	15	0.491	K.LNPAVDDGGSFK.T
R4/RRR4-22/3	1931.012	1931.131	-61.739	0.513	2317.810	0.702	37	0.490	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-22/3	1931.210	1931.131	40.973	0.594	2355.540	0.670	35	0.482	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-21/2	1668.232	1668.849	-971.947	0.478	2150.372	0.602	22	0.444	K.M*IEDYLVAHPTEYA.-
R4/RRR4-22/1	1219.574	1220.313	-1430.699	0.149	611.328	0.174	14	0.441	K.LNPAVDDGGSFK.T
R4/RRR4-22/3	1931.261	1931.131	67.884	0.505	2219.518	0.660	36	0.434	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-22/2	1669.202	1668.849	212.199	0.554	2094.035	0.618	22	0.415	K.M*IEDYLVAHPTEYA.-
R4/RRR4-22/2	1338.924	1339.455	-1146.944	0.513	2400.226	0.592	24	0.395	K.VEGDGGAGTVTTM*K.L
R4/RRR4-22/3	1950.176	1951.170	-1025.657	0.536	2364.032	0.510	34	0.393	R.DNAAHVIKSEVLDVPAGSK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1338.975	1339.455	-359.689	0.473	2193.342	0.620	23	0.362	K.VEGDGGAGTVTTM*K.L
R4/RRR4-22/2	1653.059	1652.849	127.053	0.557	1924.999	0.635	21	0.358	K.MIEDYLVAHPTEYA.-
R4/RRR4-22/3	1950.374	1951.170	-923.762	0.511	2109.646	0.519	33	0.332	R.DNAAHVIKSEVLDVPAGSK.V
R4/RRR4-23/3	1931.041	1931.131	-46.521	0.498	1883.022	0.615	34	0.322	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-21/2	1669.607	1668.849	-145.349	0.568	1755.087	0.672	21	0.318	K.M*IEDYLVAHPTEYA.-
R4/RRR4-23/3	1930.362	1931.131	-919.099	0.481	1848.780	0.616	34	0.315	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-22/2	1323.029	1323.456	-323.308	0.475	1797.902	0.606	23	0.292	K.VEGDGGAGTVTTMK.L
R4/RRR4-22/2	1669.191	1668.849	205.745	0.600	1651.035	0.673	21	0.285	K.M*IEDYLVAHPTEYA.-
R4/RRR4-22/2	1338.995	1339.455	-344.871	0.505	1790.805	0.544	21	0.273	K.VEGDGGAGTVTTM*K.L
R4/RRR4-23/3	1930.694	1931.131	-226.884	0.468	1757.738	0.559	35	0.266	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-22/2	1652.373	1652.849	-288.951	0.437	1607.962	0.564	20	0.250	K.MIEDYLVAHPTEYA.-
R4/RRR4-22/2	1669.794	1668.849	-32.926	0.593	1536.288	0.639	20	0.242	K.M*IEDYLVAHPTEYA.-
R4/RRR4-22/2	1949.799	1951.170	-1219.506	0.503	1454.999	0.597	22	0.238	R.DNAAHVIKSEVLDVPAGSK.V
R4/RRR4-22/2	1950.655	1951.170	-779.164	0.578	1356.404	0.635	22	0.237	R.DNAAHVIKSEVLDVPAGSK.V
R4/RRR4-22/2	1652.206	1652.849	-997.645	0.404	1489.745	0.570	19	0.227	K.MIEDYLVAHPTEYA.-
R4/RRR4-22/2	1323.160	1323.456	-223.895	0.469	1220.562	0.561	19	0.209	K.VEGDGGAGTVTTMK.L
R4/RRR4-22/2	1147.868	1148.285	-365.070	0.454	1360.684	0.482	19	0.209	K.IEAAGAGSCLAK.M
R4/RRR4-22/2	1147.928	1148.285	-312.362	0.473	1195.881	0.509	18	0.200	K.IEAAGAGSCLAK.M
R4/RRR4-21/2	1147.981	1148.285	-265.953	0.477	1212.536	0.494	18	0.198	K.IEAAGAGSCLAK.M
R4/RRR4-23/2	1147.917	1148.285	-321.751	0.472	1181.857	0.504	18	0.197	K.IEAAGAGSCLAK.M
R4/RRR4-23/2	1148.058	1148.285	-198.641	0.461	1219.302	0.485	18	0.197	K.IEAAGAGSCLAK.M
R4/RRR4-23/2	1149.016	1148.285	-234.812	0.492	1186.500	0.494	18	0.196	K.IEAAGAGSCLAK.M
R4/RRR4-22/2	1147.971	1148.285	-274.381	0.470	1178.557	0.477	18	0.192	K.IEAAGAGSCLAK.M
R4/RRR4-21/2	1148.100	1148.285	-162.162	0.425	1191.272	0.455	18	0.188	K.IEAAGAGSCLAK.M
R4/RRR4-21/2	1286.247	1286.565	-247.407	0.466	1102.567	0.460	18	0.185	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1323.191	1323.456	-200.294	0.407	994.764	0.541	17	0.184	K.VEGDGGAGTVTTMK.L
R4/RRR4-21/2	1147.977	1148.285	-269.794	0.408	1145.273	0.449	18	0.184	K.IEAAGAGSCLAK.M
R4/RRR4-22/2	1286.189	1286.565	-293.301	0.485	1073.109	0.457	18	0.183	K.LILDGYFGM*LK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1286.138	1286.565	-332.534	0.480	1107.379	0.444	18	0.183	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1270.258	1270.565	-242.280	0.503	957.329	0.488	18	0.182	K.LILDGYFGMLK.M
R4/RRR4-22/2	1271.261	1270.565	-240.259	0.548	956.859	0.485	18	0.182	K.LILDGYFGMLK.M
R4/RRR4-23/2	1286.207	1286.565	-278.923	0.459	1149.135	0.422	18	0.182	K.LILDGYFGM*LK.M
R4/RRR4-21/2	1287.586	1286.565	16.440	0.474	966.217	0.493	17	0.182	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1270.137	1270.565	-338.603	0.500	899.625	0.474	18	0.177	K.LILDGYFGMLK.M
R4/RRR4-22/2	1287.222	1286.565	-267.004	0.526	952.448	0.456	17	0.175	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1094.246	1094.279	-30.391	0.418	1334.544	0.307	16	0.174	K.VCAGFIDAIK.V
R4/RRR4-23/2	1286.114	1286.565	-351.770	0.431	988.040	0.402	17	0.169	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1101.945	1102.220	-250.397	0.407	1223.408	0.288	17	0.163	K.SEVLDVPAGSK.V
R4/RRR4-22/2	1101.935	1102.220	-259.288	0.398	1091.945	0.332	16	0.162	K.SEVLDVPAGSK.V
R4/RRR4-23/2	1269.860	1270.565	-1346.913	0.418	768.439	0.367	17	0.156	K.LILDGYFGMLK.M
R4/RRR4-23/2	1102.629	1102.220	372.029	0.381	946.365	0.339	15	0.155	K.SEVLDVPAGSK.V
R4/RRR4-24/2	1668.267	1668.849	-950.937	0.464	1199.232	0.506	19	0.154	K.M*IEDYLVAHPTEYA.-
R4/RRR4-21/2	1220.136	1220.313	-146.166	0.358	598.033	0.423	16	0.154	K.LNPAVDDGGSFK.T
R4/RRR4-23/2	1080.275	1079.252	21.357	0.445	564.696	0.362	14	0.151	K.VFSDAPAM*PK.V
R4/RRR4-22/2	1063.093	1063.252	-150.137	0.308	712.617	0.360	15	0.151	K.VFSDAPAMPK.V
R4/RRR4-22/2	1078.423	1079.252	-1700.788	0.260	635.622	0.415	15	0.151	K.VFSDAPAM*PK.V
R4/RRR4-22/2	1064.015	1063.252	-223.191	0.407	428.428	0.393	12	0.150	K.VFSDAPAMPK.V
R4/RRR4-22/2	1093.733	1094.279	-1418.171	0.296	1157.968	0.225	16	0.150	K.VCAGFIDAIK.V
R4/RRR4-22/2	1078.843	1079.252	-379.797	0.359	720.935	0.323	15	0.150	K.VFSDAPAM*PK.V
R4/RRR4-23/2	1102.271	1102.220	46.584	0.422	1001.438	0.277	15	0.149	K.SEVLDVPAGSK.V
R4/RRR4-22/2	1078.365	1079.252	-1755.151	0.306	699.425	0.337	15	0.149	K.VFSDAPAM*PK.V
R4/RRR4-27/2	1102.289	1102.220	62.578	0.298	1169.289	0.210	15	0.149	K.SEVLDVPAGSK.V
R4/RRR4-21/2	1078.323	1079.252	-1793.596	0.327	632.683	0.338	14	0.148	K.VFSDAPAM*PK.V
R4/RRR4-22/2	1286.168	1286.565	-309.679	0.320	783.734	0.300	15	0.147	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1093.618	1094.279	-1524.007	0.297	1026.175	0.247	15	0.147	K.VCAGFIDAIK.V
R4/RRR4-23/2	1078.448	1079.252	-1677.588	0.263	605.794	0.349	14	0.146	K.VFSDAPAM*PK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1078.610	1079.252	-1526.931	0.241	594.171	0.366	14	0.146	K.VFSDAPAM*PK.V
R4/RRR4-22/2	1219.975	1220.313	-278.460	0.296	642.918	0.338	16	0.146	K.LNPAVDDGGSFK.T
R4/RRR4-21/2	1078.982	1079.252	-250.501	0.379	394.577	0.355	12	0.145	-.VFSDAPAM*PK.-
R4/RRR4-23/2	1101.891	1102.220	-299.522	0.325	821.259	0.288	14	0.144	-.SEVLDVPAGSK.-
R4/RRR4-21/2	1219.964	1220.313	-287.093	0.270	468.497	0.379	14	0.144	K.LNPAVDDGGSFK.T
R4/RRR4-22/2	1220.067	1220.313	-202.773	0.299	428.271	0.325	14	0.143	K.LNPAVDDGGSFK.T
R4/RRR4-22/2	1219.673	1220.313	-1349.232	0.270	381.919	0.366	13	0.143	K.LNPAVDDGGSFK.T
R4/RRR4-22/2	1285.932	1286.565	-1273.284	0.200	625.651	0.332	14	0.142	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1269.848	1270.565	-1356.085	0.216	335.321	0.320	11	0.141	K.LILDGYFGMLK.M
R4/RRR4-21/2	1219.806	1220.313	-1239.376	0.258	522.425	0.300	15	0.141	K.LNPAVDDGGSFK.T
R4/RRR4-21/2	1286.073	1286.565	-383.674	0.241	534.496	0.266	13	0.141	K.LILDGYFGM*LK.M
R4/RRR4-22/2	1219.916	1220.313	-326.447	0.212	377.851	0.398	13	0.140	K.LNPAVDDGGSFK.T
R4/RRR4-22/2	1079.029	1079.252	-206.918	0.264	735.090	0.192	15	0.139	K.VFSDAPAM*PK.V
R4/RRR4-21/3	1930.424	1931.131	-886.913	0.368	896.010	0.442	27	0.116	K.SHVTETKIEAAGAGSCLAK.M
R4/RRR4-10/3	1451.315	1450.816	344.433	0.558	3449.503	0.456	32	0.694	K.FLKPAVAGFLMQK.E
R4/RRR4-10/3	1449.892	1450.816	-1331.467	0.520	3253.181	0.449	31	0.616	K.FLKPAVAGFLMQK.E
R4/RRR4-10/3	1450.720	1450.816	-66.861	0.561	3090.549	0.410	29	0.532	K.FLKPAVAGFLMQK.E
R4/RRR4-10/3	1466.936	1466.816	81.850	0.542	2705.665	0.384	28	0.396	K.FLKPAVAGFLM*QK.E
R4/RRR4-10/3	1467.625	1466.816	-130.338	0.544	2564.355	0.443	28	0.391	K.FLKPAVAGFLM*QK.E
R4/RRR4-10/3	1735.035	1736.049	-1163.986	0.562	2597.372	0.375	35	0.368	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1547.212	1546.705	-319.669	0.527	2328.196	0.528	24	0.356	K.GATTIIGGGDSVAAVEK.A
R4/RRR4-10/3	1466.967	1466.816	103.382	0.586	2416.483	0.442	27	0.351	K.FLKPAVAGFLM*QK.E
R4/RRR4-10/3	1736.357	1736.049	177.678	0.585	2493.818	0.391	34	0.349	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/3	1735.525	1736.049	-880.586	0.497	2516.186	0.365	33	0.344	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1546.270	1546.705	-282.015	0.478	2247.774	0.507	24	0.334	K.GATTIIGGGDSVAAVEK.A
R4/RRR4-10/2	1547.135	1546.705	279.070	0.515	2026.741	0.559	24	0.313	K.GATTIIGGGDSVAAVEK.A
R4/RRR4-10/2	1735.474	1736.049	-910.412	0.539	1252.149	0.561	26	0.216	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1735.586	1736.049	-267.619	0.538	1072.362	0.545	25	0.197	K.LAAALPEGGVLLLENVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1736.588	1736.049	-266.196	0.572	1174.686	0.503	26	0.197	K.LAAALPEGGVLLLENVR.F
R4/RRR4-9/2	1735.394	1736.049	-956.383	0.484	965.122	0.558	24	0.190	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1737.119	1736.049	40.625	0.552	959.053	0.514	24	0.183	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1735.500	1736.049	-895.018	0.500	876.974	0.531	23	0.180	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1735.606	1736.049	-256.047	0.507	736.778	0.527	21	0.171	K.LAAALPEGGVLLLENVR.F
R4/RRR4-2/2	1735.507	1736.049	-891.205	0.467	822.805	0.461	22	0.166	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1451.811	1450.816	-3.678	0.525	677.148	0.454	20	0.164	K.FLKPAVAGFLMQK.E
R4/RRR4-1/2	1734.780	1736.049	-1311.727	0.383	812.214	0.453	21	0.162	K.LAAALPEGGVLLLENVR.F
R4/RRR4-1/2	1735.458	1736.049	-919.662	0.444	754.286	0.435	21	0.159	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1466.273	1466.816	-1055.692	0.440	767.428	0.390	20	0.158	K.FLKPAVAGFLM*QK.E
R4/RRR4-2/2	1735.455	1736.049	-921.216	0.407	716.339	0.415	21	0.155	K.LAAALPEGGVLLLENVR.F
R4/RRR4-10/2	1466.332	1466.816	-331.216	0.487	512.742	0.424	18	0.155	K.FLKPAVAGFLM*QK.E
R4/RRR4-10/2	1466.387	1466.816	-293.380	0.452	579.105	0.359	19	0.150	K.FLKPAVAGFLM*QK.E
R4/RRR4-16/2	1735.067	1736.049	-1145.963	0.292	327.863	0.349	14	0.140	K.LAAALPEGGVLLLENVR.F
R4/RRR4-5/2	1709.677	1708.894	-127.230	0.507	2147.654	0.501	21	0.317	R.DVWWQDVVTSFPTK.C
R4/RRR4-5/2	1247.361	1247.334	21.535	0.460	1962.727	0.502	19	0.288	K.DIVDAGLAESEK.Q
R4/RRR4-5/2	1248.005	1247.334	-264.161	0.495	1766.251	0.508	19	0.262	K.DIVDAGLAESEK.Q
R4/RRR4-5/2	1246.353	1247.334	-1593.838	0.333	1766.786	0.398	18	0.230	K.DIVDAGLAESEK.Q
R4/RRR4-5/2	1382.151	1381.644	-358.022	0.488	1278.024	0.566	18	0.218	K.VTIFYTAPTLVR.S
R4/RRR4-5/2	1211.006	1211.310	-251.910	0.504	1460.439	0.412	19	0.206	R.VDDVINVSGHR.I
R4/RRR4-5/2	1211.268	1211.310	-34.227	0.509	1362.849	0.420	19	0.199	R.VDDVINVSGHR.I
R4/RRR4-5/2	1225.958	1226.315	-291.781	0.484	1224.432	0.477	17	0.198	K.TNICYNAVDR.N
R4/RRR4-5/2	1225.909	1226.315	-332.042	0.505	1220.086	0.453	17	0.194	K.TNICYNAVDR.N
R4/RRR4-5/2	1708.881	1708.894	-7.638	0.321	1507.806	0.342	19	0.190	R.DVWWQDVVTSFPTK.C
R4/RRR4-5/2	1226.054	1226.315	-213.367	0.483	1129.183	0.454	16	0.186	K.TNICYNAVDR.N
R4/RRR4-5/2	1582.190	1582.785	-1010.994	0.467	970.516	0.527	21	0.184	R.VLGSVGEPINPSAWR.W
R4/RRR4-5/2	1382.360	1381.644	-206.601	0.441	987.198	0.528	16	0.184	K.VTIFYTAPTLVR.S
R4/RRR4-5/2	1538.192	1538.727	-1000.989	0.429	1179.289	0.462	18	0.183	R.IGTAEVESALVSHPK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1210.700	1211.310	-1333.342	0.484	1055.495	0.461	18	0.183	R.VDDVINVSGHR.I
R4/RRR4-5/2	1062.211	1062.246	-33.036	0.444	1060.320	0.470	13	0.182	K.GPVQISWFK.G
R4/RRR4-5/2	1473.102	1473.594	-335.057	0.414	1056.722	0.472	20	0.179	R.HVESM*SELPSGAGR.I
R4/RRR4-5/2	1061.997	1062.246	-235.260	0.468	967.186	0.483	13	0.179	K.GPVQISWFK.G
R4/RRR4-5/2	1062.027	1062.246	-206.893	0.484	950.919	0.439	13	0.171	K.GPVQISWFK.G
R4/RRR4-2/2	1133.287	1132.251	31.805	0.323	1073.210	0.251	16	0.150	R.NQIGAFAAPDK.I
R4/RRR4-5/2	1581.566	1582.785	-1407.447	0.326	496.586	0.464	16	0.148	R.VLGSVGEPINPSAWR.W
R4/RRR4-5/2	1131.413	1132.251	-1629.468	0.325	840.180	0.305	14	0.146	R.NQIGAFAAPDK.I
R4/RRR4-5/2	1131.943	1132.251	-272.750	0.335	892.507	0.287	14	0.146	R.NQIGAFAAPDK.I
R4/RRR4-5/2	1109.838	1109.294	-412.551	0.406	1219.127	0.159	14	0.143	R.VCQLANYLK.S
R4/RRR4-5/2	1581.613	1582.785	-1377.679	0.286	484.006	0.376	16	0.141	R.VLGSVGEPINPSAWR.W
R4/RRR4-2/2	1133.244	1132.251	-6.548	0.328	585.832	0.256	14	0.139	R.NQIGAFAAPDK.I
R4/RRR4-5/2	1707.449	1708.894	-1436.269	0.161	630.438	0.082	14	0.127	R.DVWWQDVVTSFPTK.C
R4/RRR4-5/3	1211.171	1211.310	-115.365	0.508	956.310	0.476	23	0.126	R.VDDVINVSGHR.I
R4/RRR4-5/3	1211.595	1211.310	236.495	0.481	947.581	0.476	24	0.125	R.VDDVINVSGHR.I
R4/RRR4-5/3	1512.791	1512.683	71.407	0.522	781.600	0.488	25	0.117	K.CAEAAVVAVEHEVK.G
R4/RRR4-5/3	1538.953	1538.727	146.728	0.440	834.641	0.466	25	0.115	R.IGTAEVESALVSHPK.C
R4/RRR4-5/3	1210.842	1211.310	-387.502	0.470	985.090	0.383	23	0.107	R.VDDVINVSGHR.I
R4/RRR4-5/3	1537.780	1538.727	-1270.339	0.374	762.200	0.430	24	0.104	R.IGTAEVESALVSHPK.C
R4/RRR4-5/3	1538.727	1538.727	-0.177	0.349	627.581	0.421	24	0.096	-.IGTAEVESALVSHPK.-
R4/RRR4-5/3	1019.629	1019.224	398.367	0.391	937.506	0.323	19	0.094	K.IHWAPGLPK.T
R4/RRR4-5/3	1019.229	1019.224	4.989	0.386	853.804	0.315	18	0.090	K.IHWAPGLPK.T
R4/RRR4-4/3	1538.901	1538.727	113.436	0.301	725.628	0.297	24	0.085	R.IGTAEVESALVSHPK.C
R4/RRR4-5/3	1019.004	1019.224	-216.332	0.369	738.474	0.230	16	0.081	K.IHWAPGLPK.T
R4/RRR4-22/1	1177.614	1178.320	-1452.668	0.307	595.545	0.569	15	0.618	K.LNPAAGVGSTYK.T
R4/RRR4-22/2	1923.481	1924.095	-841.476	0.612	3099.648	0.595	26	0.560	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-22/2	1924.535	1924.095	229.180	0.639	3074.279	0.600	26	0.555	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-22/2	1923.594	1924.095	-782.869	0.606	3099.633	0.583	26	0.554	K.LKVEYELEDGSSLSPEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/1	1177.620	1178.320	-1447.775	0.258	506.282	0.508	14	0.534	K.LNPAAGVGSTYK.T
R4/RRR4-22/2	1638.271	1638.823	-949.975	0.451	2328.999	0.555	22	0.504	K.M*IEDYLVAHPAEYA.-
R4/RRR4-22/2	1978.433	1979.086	-838.031	0.601	2616.597	0.695	26	0.479	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/1	1177.592	1178.320	-1471.827	0.207	355.989	0.388	12	0.456	K.LNPAAGVGSTYK.T
R4/RRR4-22/2	1979.594	1979.086	-249.290	0.593	2258.819	0.670	26	0.392	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/2	1682.450	1682.764	-186.925	0.532	2507.530	0.484	23	0.377	K.VEYELEDGSSLSPEK.E
R4/RRR4-22/2	1639.215	1638.823	239.971	0.536	2015.348	0.591	20	0.372	K.M*IEDYLVAHPAEYA.-
R4/RRR4-22/2	1682.343	1682.764	-250.908	0.543	2410.216	0.509	23	0.367	K.VEYELEDGSSLSPEK.E
R4/RRR4-20/2	1638.105	1638.823	-1051.422	0.359	1954.291	0.555	20	0.364	K.M*IEDYLVAHPAEYA.-
R4/RRR4-19/2	1639.114	1638.823	178.286	0.520	1925.662	0.633	20	0.361	K.M*IEDYLVAHPAEYA.-
R4/RRR4-21/2	1637.976	1638.823	-1130.888	0.366	1966.203	0.529	20	0.356	K.M*IEDYLVAHPAEYA.-
R4/RRR4-21/2	1637.947	1638.823	-1148.399	0.459	1931.495	0.575	20	0.348	K.M*IEDYLVAHPAEYA.-
R4/RRR4-20/2	1638.205	1638.823	-990.446	0.433	1850.526	0.609	21	0.341	K.M*IEDYLVAHPAEYA.-
R4/RRR4-22/2	1638.372	1638.823	-275.771	0.490	1893.536	0.587	20	0.335	K.M*IEDYLVAHPAEYA.-
R4/RRR4-21/2	1639.282	1638.823	281.189	0.542	1904.132	0.587	20	0.330	K.M*IEDYLVAHPAEYA.-
R4/RRR4-22/2	1978.453	1979.086	-827.749	0.587	1889.740	0.688	25	0.330	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/3	1978.551	1979.086	-778.210	0.480	1874.060	0.610	37	0.312	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/2	1682.314	1682.764	-268.306	0.497	2108.352	0.458	22	0.296	K.VEYELEDGSSLSPEK.E
R4/RRR4-22/3	1978.376	1979.086	-866.932	0.490	1728.804	0.576	36	0.265	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-21/3	1979.114	1979.086	14.524	0.507	1592.788	0.582	33	0.244	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/2	1207.902	1208.295	-326.147	0.479	1584.714	0.506	20	0.239	K.LEATGDGSCVAK.L
R4/RRR4-22/2	1269.684	1270.454	-1398.497	0.448	1593.173	0.423	19	0.219	R.VAVCDAASHVLK.S
R4/RRR4-22/2	1270.048	1270.454	-320.406	0.465	1547.967	0.440	19	0.218	R.VAVCDAASHVLK.S
R4/RRR4-21/3	1978.869	1979.086	-109.929	0.513	1539.638	0.545	34	0.218	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/2	1270.182	1270.454	-214.629	0.486	1497.389	0.441	19	0.214	R.VAVCDAASHVLK.S
R4/RRR4-22/3	1979.144	1979.086	29.279	0.541	1449.894	0.564	34	0.211	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/2	1207.975	1208.295	-265.718	0.448	1438.711	0.449	19	0.209	K.LEATGDGSCVAK.L
R4/RRR4-22/2	1207.955	1208.295	-282.244	0.459	1375.074	0.477	19	0.209	K.LEATGDGSCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1084.067	1083.240	-160.557	0.479	1241.000	0.482	16	0.199	K.AFM*DASSLPK.A
R4/RRR4-21/2	1271.132	1270.454	-253.768	0.453	1286.137	0.461	18	0.197	R.VAVCDAASHVLK.S
R4/RRR4-20/2	1083.272	1083.240	29.772	0.458	1195.091	0.491	16	0.197	K.AFM*DASSLPK.A
R4/RRR4-21/2	1083.681	1083.240	407.573	0.390	1138.973	0.510	16	0.194	K.AFM*DASSLPK.A
R4/RRR4-22/3	1979.997	1979.086	-44.876	0.517	1257.965	0.588	32	0.193	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-21/3	1979.294	1979.086	105.270	0.529	1320.422	0.564	32	0.193	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/2	1531.377	1531.755	-247.740	0.526	1246.247	0.448	21	0.193	K.EKDIVDGYYGMLK.M
R4/RRR4-21/2	1269.938	1270.454	-1197.296	0.467	1359.387	0.407	18	0.193	R.VAVCDAASHVLK.S
R4/RRR4-22/2	1178.199	1178.320	-102.631	0.459	916.615	0.554	20	0.189	K.LNPAAGVGSTYK.T
R4/RRR4-21/2	1269.667	1270.454	-1411.437	0.414	1366.892	0.373	18	0.187	R.VAVCDAASHVLK.S
R4/RRR4-22/3	1978.558	1979.086	-774.401	0.499	1336.613	0.542	34	0.187	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/3	1923.472	1924.095	-846.261	0.458	1496.572	0.475	31	0.185	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-22/2	1178.048	1178.320	-231.519	0.423	889.350	0.544	20	0.184	K.LNPAAGVGSTYK.T
R4/RRR4-22/3	1923.763	1924.095	-173.254	0.473	1668.886	0.401	32	0.183	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-21/2	1177.919	1178.320	-341.517	0.413	885.893	0.535	20	0.182	K.LNPAAGVGSTYK.T
R4/RRR4-21/2	1179.023	1178.320	-252.928	0.406	805.010	0.571	19	0.182	K.LNPAAGVGSTYK.T
R4/RRR4-22/2	1177.570	1178.320	-1490.633	0.374	899.326	0.537	20	0.181	K.LNPAAGVGSTYK.T
R4/RRR4-21/3	1923.931	1924.095	-85.704	0.435	1556.405	0.434	31	0.179	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-20/2	1177.261	1178.320	-1753.835	0.342	755.946	0.588	19	0.177	K.LNPAAGVGSTYK.T
R4/RRR4-21/2	1083.041	1083.240	-184.675	0.457	1173.747	0.385	15	0.176	K.AFM*DASSLPK.A
R4/RRR4-21/2	1178.904	1178.320	-353.694	0.412	794.001	0.522	19	0.176	K.LNPAAGVGSTYK.T
R4/RRR4-19/2	1177.567	1178.320	-1492.716	0.342	836.229	0.532	19	0.175	K.LNPAAGVGSTYK.T
R4/RRR4-19/2	1177.443	1178.320	-1598.834	0.353	699.609	0.580	18	0.174	K.LNPAAGVGSTYK.T
R4/RRR4-20/2	1178.091	1178.320	-194.512	0.401	744.395	0.519	19	0.173	K.LNPAAGVGSTYK.T
R4/RRR4-22/2	1178.095	1178.320	-191.602	0.369	669.428	0.567	18	0.173	K.LNPAAGVGSTYK.T
R4/RRR4-19/2	1084.064	1083.240	-163.381	0.389	896.637	0.474	14	0.172	K.AFM*DASSLPK.A
R4/RRR4-23/2	1177.865	1178.320	-387.581	0.366	760.627	0.505	19	0.170	K.LNPAAGVGSTYK.T
R4/RRR4-22/2	1547.378	1547.755	-244.352	0.504	1000.026	0.406	20	0.169	K.EKDIVDGYYGM*LK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1547.105	1547.755	-1069.500	0.469	875.390	0.431	20	0.167	K.EKDIVDGYYGM*LK.M
R4/RRR4-22/2	1178.997	1178.320	-274.222	0.427	591.454	0.496	18	0.166	K.LNPAAGVGSTYK.T
R4/RRR4-19/2	1083.058	1083.240	-169.072	0.406	1067.199	0.359	15	0.166	K.AFM*DASSLPK.A
R4/RRR4-22/3	1924.008	1924.095	-45.514	0.478	1345.522	0.475	30	0.165	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-22/2	1066.720	1067.241	-1430.325	0.377	631.510	0.502	14	0.164	K.AFMDASSLPK.A
R4/RRR4-22/2	1290.221	1290.467	-191.439	0.350	1184.128	0.317	16	0.164	K.DIVDGYYGM*LK.M
R4/RRR4-22/3	1979.008	1979.086	-39.207	0.486	1024.905	0.581	31	0.163	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-20/2	1084.138	1083.240	-94.705	0.345	959.470	0.377	15	0.162	K.AFM*DASSLPK.A
R4/RRR4-19/2	1547.800	1547.755	29.334	0.450	974.318	0.359	19	0.160	K.EKDIVDGYYGM*LK.M
R4/RRR4-22/2	1546.685	1547.755	-1342.341	0.480	988.804	0.353	19	0.160	K.EKDIVDGYYGM*LK.M
R4/RRR4-22/2	977.322	978.036	-1759.162	0.317	1049.519	0.349	14	0.159	-.SDVLEAESK.-
R4/RRR4-19/2	1177.567	1178.320	-1492.820	0.305	642.876	0.437	18	0.156	K.LNPAAGVGSTYK.T
R4/RRR4-21/2	1980.942	1979.086	-72.599	0.395	313.992	0.582	18	0.155	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-19/2	1083.878	1083.240	-335.110	0.330	742.232	0.390	14	0.155	K.AFM*DASSLPK.A
R4/RRR4-22/2	1067.117	1067.241	-116.183	0.401	583.701	0.405	13	0.154	K.AFMDASSLPK.A
R4/RRR4-19/3	1978.388	1979.086	-860.707	0.413	1096.812	0.523	31	0.154	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-22/2	1178.069	1178.320	-213.327	0.314	532.970	0.434	15	0.152	K.LNPAAGVGSTYK.T
R4/RRR4-20/3	1978.846	1979.086	-121.346	0.492	997.672	0.553	32	0.152	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-20/2	1083.556	1083.240	292.365	0.287	617.018	0.403	13	0.151	K.AFM*DASSLPK.A
R4/RRR4-19/3	1978.725	1979.086	-182.890	0.418	1000.400	0.541	29	0.150	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-19/2	1547.875	1547.755	77.820	0.434	685.061	0.339	18	0.149	K.EKDIVDGYYGM*LK.M
R4/RRR4-21/2	1623.852	1622.823	18.050	0.421	923.963	0.552	18	0.148	K.MIEDYLVAHPAEYA.-
R4/RRR4-18/2	1177.895	1178.320	-361.585	0.267	531.350	0.389	16	0.148	K.LNPAAGVGSTYK.T
R4/RRR4-22/2	1066.990	1067.241	-236.110	0.241	563.922	0.363	13	0.145	K.AFMDASSLPK.A
R4/RRR4-19/2	1547.466	1547.755	-186.738	0.422	407.456	0.343	15	0.145	K.EKDIVDGYYGM*LK.M
R4/RRR4-22/2	1290.093	1290.467	-291.013	0.347	481.487	0.386	12	0.144	K.DIVDGYYGM*LK.M
R4/RRR4-22/2	1622.388	1622.823	-268.859	0.371	939.067	0.515	16	0.143	-.MIEDYLVAHPAEYA.-
R4/RRR4-21/2	1623.668	1622.823	-95.813	0.427	668.249	0.532	16	0.143	K.MIEDYLVAHPAEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1082.211	1083.240	-1880.605	0.270	553.738	0.286	12	0.142	K.AFM*DASSLPK.A
R4/RRR4-22/2	1289.915	1290.467	-1207.015	0.301	479.506	0.311	12	0.139	K.DIVDGYYGM*LK.M
R4/RRR4-22/2	1083.148	1083.240	-85.071	0.155	486.947	0.289	13	0.137	-.AFM*DASSLPK.-
R4/RRR4-22/2	1177.205	1178.320	-1801.449	0.154	534.056	0.266	14	0.137	K.LNPAAGVGSTYK.T
R4/RRR4-17/2	1083.815	1083.240	-393.647	0.141	511.577	0.253	12	0.137	K.AFM*DASSLPK.A
R4/RRR4-21/3	1925.936	1924.095	-83.008	0.488	990.229	0.429	27	0.118	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-21/2	1623.570	1622.823	-156.601	0.337	756.783	0.337	17	0.117	K.MIEDYLVAHPAEYA.-
R4/RRR4-22/3	1270.709	1270.454	201.742	0.459	572.462	0.517	24	0.116	R.VAVCDAASHVLK.S
R4/RRR4-15/3	1980.073	1979.086	-6.568	0.313	248.697	0.406	23	0.107	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-15/3	1980.270	1979.086	93.038	0.312	318.365	0.435	25	0.107	K.SHSTETKLEATGDGSCVAK.L
R4/RRR4-21/3	1270.534	1270.454	63.291	0.377	381.517	0.470	20	0.106	R.VAVCDAASHVLK.S
R4/RRR4-21/3	1270.698	1270.454	192.494	0.390	365.198	0.460	20	0.105	R.VAVCDAASHVLK.S
R4/RRR4-21/3	1923.340	1924.095	-915.070	0.420	991.606	0.365	29	0.105	K.LKVEYELEDGSSLSPEK.E
R4/RRR4-22/3	1270.519	1270.454	51.150	0.282	291.948	0.366	17	0.099	R.VAVCDAASHVLK.S
R4/RRR4-22/3	1270.544	1270.454	70.952	0.382	512.241	0.382	23	0.098	R.VAVCDAASHVLK.S
R4/RRR4-21/3	1270.399	1270.454	-42.957	0.335	281.297	0.344	17	0.096	-.VAVCDAASHVLK.-
R4/RRR4-20/3	1270.657	1270.454	160.702	0.306	377.449	0.355	19	0.090	-.VAVCDAASHVLK.-
R4/RRR4-10/2	1760.352	1760.969	-921.402	0.631	2951.934	0.533	24	0.494	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/2	1760.529	1760.969	-250.823	0.640	2944.420	0.498	24	0.476	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/2	1760.430	1760.969	-876.710	0.620	2697.817	0.548	24	0.441	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/2	1761.314	1760.969	196.475	0.570	2682.558	0.463	23	0.404	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/3	1778.002	1777.908	53.077	0.570	2460.361	0.479	33	0.390	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-10/2	1436.141	1436.569	-299.039	0.551	2189.894	0.562	20	0.343	R.AFAEASM*TTAYEK.K
R4/RRR4-10/3	1778.612	1777.908	-167.223	0.603	2343.784	0.452	32	0.343	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-10/2	1322.085	1321.453	-279.179	0.599	2049.380	0.626	22	0.343	K.LEAACVGTVESGK.M
R4/RRR4-10/2	1321.098	1321.453	-269.100	0.535	2064.901	0.594	22	0.334	K.LEAACVGTVESGK.M
R4/RRR4-10/2	1321.061	1321.453	-297.097	0.556	2001.691	0.618	22	0.331	K.LEAACVGTVESGK.M
R4/RRR4-9/2	1320.927	1321.453	-1158.216	0.495	2058.218	0.568	22	0.324	K.LEAACVGTVESGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1436.097	1436.569	-329.741	0.543	2073.306	0.556	20	0.321	R.AFAEASM*TTAYEK.K
R4/RRR4-10/2	1436.254	1436.569	-220.332	0.540	2028.261	0.546	20	0.311	R.AFAEASM*TTAYEK.K
R4/RRR4-10/2	1798.326	1798.934	-896.907	0.504	1897.520	0.514	23	0.278	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/2	1777.387	1777.908	-858.358	0.534	1936.910	0.482	25	0.276	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-9/3	1777.755	1777.908	-86.277	0.535	2036.562	0.455	31	0.275	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-9/2	1799.683	1798.934	-140.120	0.552	1899.737	0.501	23	0.274	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/2	1485.086	1485.622	-1037.279	0.382	2109.884	0.355	19	0.268	K.DIFQEVYEAGWK.S
R4/RRR4-9/2	1799.565	1798.934	-205.512	0.564	1904.812	0.472	22	0.265	K.GGETSTNSIASIFAWTR.G
R4/RRR4-9/2	1800.149	1798.934	119.664	0.519	1823.924	0.475	22	0.256	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/2	1798.522	1798.934	-230.071	0.525	1733.860	0.503	22	0.251	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/2	1420.171	1420.570	-281.364	0.512	1627.747	0.520	19	0.246	R.AFAEASMTTAYEK.K
R4/RRR4-10/2	1778.340	1777.908	243.201	0.577	1725.518	0.474	24	0.244	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-10/3	1777.083	1777.908	-1030.205	0.531	2024.959	0.389	31	0.241	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-10/2	1777.510	1777.908	-224.594	0.565	1639.024	0.482	24	0.236	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-9/2	1777.373	1777.908	-866.631	0.528	1523.540	0.520	23	0.231	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-10/3	1760.463	1760.969	-858.132	0.556	1843.275	0.419	29	0.218	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/2	1799.606	1798.934	-182.920	0.539	1464.786	0.507	19	0.217	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/2	1056.414	1057.226	-1719.768	0.429	1576.580	0.342	17	0.202	-.ATDAVLKGPGK.-
R4/RRR4-10/2	1253.369	1252.505	-108.882	0.602	1031.273	0.553	18	0.199	R.LIDDMVAYALK.S
R4/RRR4-10/2	1057.004	1057.226	-210.193	0.509	1380.686	0.398	17	0.194	-.ATDAVLKGPGK.-
R4/RRR4-10/2	1269.096	1268.505	-322.645	0.497	1026.275	0.519	18	0.191	R.LIDDM*VAYALK.S
R4/RRR4-10/2	1269.094	1268.505	-324.383	0.503	1113.081	0.483	18	0.191	R.LIDDM*VAYALK.S
R4/RRR4-10/2	1484.770	1485.622	-1250.911	0.333	1756.064	0.195	18	0.187	K.DIFQEVYEAGWK.S
R4/RRR4-10/2	1252.109	1252.505	-317.370	0.539	1078.559	0.469	18	0.186	R.LIDDMVAYALK.S
R4/RRR4-10/3	1798.726	1798.934	-116.242	0.468	1662.037	0.404	30	0.186	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/3	1761.110	1760.969	80.040	0.543	1452.771	0.468	29	0.175	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/2	1268.151	1268.505	-279.440	0.484	990.843	0.432	18	0.174	R.LIDDM*VAYALK.S
R4/RRR4-10/2	993.594	994.045	-455.703	0.397	792.383	0.524	12	0.173	R.HAFGDQYR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/3	1761.192	1760.969	127.066	0.580	1465.122	0.453	30	0.171	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/2	994.036	994.045	-8.882	0.380	621.057	0.537	12	0.167	R.HAFGDQYR.C
R4/RRR4-10/2	1057.943	1057.226	-268.335	0.494	1302.105	0.282	17	0.166	-.ATDAVLKGPGK.-
R4/RRR4-10/2	1419.601	1420.570	-1391.133	0.337	1146.961	0.305	19	0.160	R.AFAEASMTTAYEK.K
R4/RRR4-10/2	994.056	994.045	10.825	0.327	618.500	0.502	12	0.160	R.HAFGDQYR.C
R4/RRR4-9/2	1498.006	1496.694	209.268	0.372	473.245	0.462	17	0.150	K.DLALLIHGSSNVTR.S
R4/RRR4-10/2	1133.932	1134.216	-250.676	0.348	891.011	0.259	17	0.147	K.CATITPDEAR.V
R4/RRR4-9/3	1777.809	1777.908	-55.903	0.471	1450.050	0.370	26	0.146	R.DATDDKVTVEAAEATLK.Y
R4/RRR4-9/2	1762.276	1760.969	174.552	0.543	915.276	0.280	22	0.146	R.FKDIFQEVYEAGWK.S
R4/RRR4-10/2	1133.880	1134.216	-297.119	0.334	688.341	0.229	15	0.140	K.CATITPDEAR.V
R4/RRR4-10/3	1594.559	1594.755	-123.025	0.616	1001.962	0.510	28	0.140	K.SKFEAAGIWYEHR.L
R4/RRR4-1/2	1800.011	1798.934	42.607	0.330	545.630	0.248	18	0.136	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/3	1595.416	1594.755	-212.556	0.595	914.228	0.516	26	0.134	K.SKFEAAGIWYEHR.L
R4/RRR4-9/2	1134.135	1134.216	-70.885	0.366	534.372	0.229	13	0.132	-.CATITPDEAR.-
R4/RRR4-10/3	1594.305	1594.755	-282.819	0.562	933.310	0.499	27	0.131	K.SKFEAAGIWYEHR.L
R4/RRR4-9/3	1799.830	1798.934	-57.940	0.413	581.446	0.395	24	0.094	K.GGETSTNSIASIFAWTR.G
R4/RRR4-10/3	1798.757	1798.934	-99.087	0.303	708.347	0.195	24	0.077	K.GGETSTNSIASIFAWTR.G
R4/RRR4-8/2	1842.544	1841.100	241.637	0.648	2904.750	0.589	27	0.508	K.HVAEANIIFVSVNTPTK.T
R4/RRR4-8/2	1841.560	1841.100	250.343	0.632	2730.222	0.657	26	0.494	K.HVAEANIIFVSVNTPTK.T
R4/RRR4-8/2	1094.097	1094.374	-254.208	0.340	1158.500	0.442	16	0.179	K.IAVLGFAFKK.D
R4/RRR4-7/2	966.017	966.201	-190.636	0.420	1154.406	0.378	15	0.175	K.IAVLGFAFK.K
R4/RRR4-7/2	966.043	966.201	-163.762	0.431	1144.298	0.378	15	0.174	K.IAVLGFAFK.K
R4/RRR4-8/2	965.919	966.201	-293.075	0.464	992.261	0.406	15	0.171	K.IAVLGFAFK.K
R4/RRR4-7/2	966.137	966.201	-66.673	0.507	990.174	0.384	15	0.168	K.IAVLGFAFK.K
R4/RRR4-8/2	965.582	966.201	-1681.645	0.388	1015.895	0.375	15	0.166	K.IAVLGFAFK.K
R4/RRR4-8/2	965.689	966.201	-1570.140	0.398	973.458	0.354	15	0.162	K.IAVLGFAFK.K
R4/RRR4-10/2	1832.317	1832.134	99.990	0.569	2736.187	0.638	24	0.488	R.MFVADGGELLMAQSYAK.N
R4/RRR4-11/2	1531.330	1531.695	-239.272	0.481	2018.813	0.467	22	0.285	K.LIFGADSPAIQENR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1449.171	1449.629	-317.048	0.511	1795.046	0.559	22	0.279	R.VATVQCLSGTGSLR.V
R4/RRR4-11/2	1449.284	1449.629	-238.963	0.524	1730.614	0.548	22	0.267	R.VATVQCLSGTGSLR.V
R4/RRR4-10/2	1574.794	1574.798	-2.302	0.499	1796.204	0.502	23	0.262	R.VGALSIVCGSADVAVR.V
R4/RRR4-10/2	1575.090	1574.798	185.657	0.518	1720.747	0.539	22	0.261	R.VGALSIVCGSADVAVR.V
R4/RRR4-11/2	1449.130	1449.629	-345.445	0.511	1783.915	0.481	22	0.256	R.VATVQCLSGTGSLR.V
R4/RRR4-10/2	1450.139	1449.629	-338.535	0.537	1538.764	0.548	22	0.243	R.VATVQCLSGTGSLR.V
R4/RRR4-10/2	1531.249	1531.695	-292.298	0.487	1691.182	0.475	21	0.242	K.LIFGADSPAIQENR.V
R4/RRR4-11/2	1449.197	1449.629	-298.624	0.488	1632.390	0.498	21	0.241	R.VATVQCLSGTGSLR.V
R4/RRR4-10/2	1531.896	1531.695	131.508	0.533	1709.971	0.455	21	0.239	K.LIFGADSPAIQENR.V
R4/RRR4-10/2	1574.455	1574.798	-218.643	0.495	1641.283	0.490	22	0.238	R.VGALSIVCGSADVAVR.V
R4/RRR4-10/2	1531.320	1531.695	-245.430	0.520	1653.193	0.462	21	0.234	K.LIFGADSPAIQENR.V
R4/RRR4-11/2	1530.975	1531.695	-1126.867	0.424	1608.182	0.482	21	0.233	K.LIFGADSPAIQENR.V
R4/RRR4-11/2	1531.892	1531.695	128.870	0.508	1662.893	0.446	22	0.232	K.LIFGADSPAIQENR.V
R4/RRR4-10/2	1449.221	1449.629	-282.314	0.479	1441.738	0.513	21	0.223	R.VATVQCLSGTGSLR.V
R4/RRR4-10/3	1709.403	1708.979	248.990	0.498	1933.440	0.375	30	0.217	R.VKEYLPITGLADFNK.L
R4/RRR4-10/2	1708.590	1708.979	-228.279	0.533	1402.861	0.488	24	0.215	R.VKEYLPITGLADFNK.L
R4/RRR4-11/2	1574.356	1574.798	-281.806	0.462	1337.401	0.503	21	0.207	R.VGALSIVCGSADVAVR.V
R4/RRR4-10/2	1709.178	1708.979	116.793	0.560	1215.826	0.467	23	0.193	R.VKEYLPITGLADFNK.L
R4/RRR4-10/2	1707.611	1708.979	-1390.531	0.448	1247.486	0.436	23	0.189	R.VKEYLPITGLADFNK.L
R4/RRR4-11/2	948.430	949.089	-1754.271	0.436	904.196	0.528	15	0.184	K.VNLGVGAYR.D
R4/RRR4-10/2	949.046	949.089	-45.813	0.496	926.073	0.503	15	0.183	K.VNLGVGAYR.D
R4/RRR4-11/2	1481.012	1481.674	-1125.945	0.363	1288.428	0.357	20	0.177	K.EYLPITGLADFNK.L
R4/RRR4-10/2	948.927	949.089	-170.716	0.456	926.041	0.472	15	0.177	K.VNLGVGAYR.D
R4/RRR4-10/2	1481.803	1481.674	87.038	0.456	1042.220	0.450	19	0.177	K.EYLPITGLADFNK.L
R4/RRR4-10/2	1481.511	1481.674	-110.544	0.455	1029.137	0.453	19	0.177	K.EYLPITGLADFNK.L
R4/RRR4-11/2	948.316	949.089	-1875.199	0.416	896.985	0.487	15	0.176	K.VNLGVGAYR.D
R4/RRR4-11/2	948.436	949.089	-1747.805	0.431	789.572	0.480	14	0.170	K.VNLGVGAYR.D
R4/RRR4-10/2	948.425	949.089	-1759.573	0.411	687.597	0.515	14	0.170	K.VNLGVGAYR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1558.655	1558.807	-97.846	0.459	619.760	0.549	21	0.170	R.TIPHLADAIHAAVTK.L
R4/RRR4-10/2	1454.658	1454.697	-26.564	0.529	702.884	0.485	20	0.169	R.TEEGKPLVLNVVR.R
R4/RRR4-11/2	848.883	848.969	-101.483	0.510	1093.860	0.357	13	0.168	R.VGGEFLAR.H
R4/RRR4-10/2	1558.347	1558.807	-296.172	0.446	586.288	0.548	21	0.168	R.TIPHLADAIHAAVTK.L
R4/RRR4-11/2	1077.002	1077.302	-278.706	0.433	843.313	0.415	17	0.165	K.VFTLAGLTVR.S
R4/RRR4-11/2	848.478	848.969	-580.901	0.488	1157.752	0.318	13	0.165	R.VGGEFLAR.H
R4/RRR4-10/2	848.787	848.969	-215.019	0.563	1056.341	0.347	13	0.163	R.VGGEFLAR.H
R4/RRR4-10/2	848.557	848.969	-486.915	0.512	1077.047	0.325	13	0.162	R.VGGEFLAR.H
R4/RRR4-11/2	848.138	848.969	-2165.765	0.486	1135.863	0.301	13	0.161	R.VGGEFLAR.H
R4/RRR4-10/2	1076.897	1077.302	-376.851	0.424	450.178	0.482	15	0.161	K.VFTLAGLTVR.S
R4/RRR4-11/2	1454.318	1454.697	-261.035	0.440	668.911	0.447	19	0.161	R.TEEGKPLVLNVVR.R
R4/RRR4-11/2	1076.885	1077.302	-388.224	0.362	585.914	0.497	14	0.160	K.VFTLAGLTVR.S
R4/RRR4-10/2	1077.173	1077.302	-119.872	0.440	844.734	0.370	17	0.160	K.VFTLAGLTVR.S
R4/RRR4-10/2	1481.198	1481.674	-322.840	0.375	906.035	0.385	18	0.159	K.EYLPITGLADFNK.L
R4/RRR4-10/2	848.531	848.969	-517.953	0.501	1010.281	0.318	13	0.158	R.VGGEFLAR.H
R4/RRR4-11/2	1454.221	1454.697	-328.408	0.470	532.658	0.450	18	0.158	R.TEEGKPLVLNVVR.R
R4/RRR4-11/2	1454.382	1454.697	-217.248	0.438	526.655	0.405	17	0.152	R.TEEGKPLVLNVVR.R
R4/RRR4-11/2	1708.428	1708.979	-910.778	0.486	871.371	0.339	20	0.151	R.VKEYLPITGLADFNK.L
R4/RRR4-1/2	1531.660	1531.695	-22.751	0.380	467.648	0.396	14	0.145	K.LIFGADSPAIQENR.V
R4/RRR4-11/2	1708.471	1708.979	-885.314	0.463	985.584	0.244	21	0.143	R.VKEYLPITGLADFNK.L
R4/RRR4-11/2	1077.180	1077.302	-113.165	0.230	488.074	0.343	13	0.141	K.VFTLAGLTVR.S
R4/RRR4-10/2	1289.637	1289.444	150.112	0.373	1105.818	0.147	15	0.136	-.AEQM*LINNPSR.-
R4/RRR4-11/3	1708.941	1708.979	-22.190	0.505	1055.559	0.452	26	0.128	R.VKEYLPITGLADFNK.L
R4/RRR4-11/3	1531.869	1531.695	113.678	0.494	1139.772	0.334	25	0.106	K.LIFGADSPAIQENR.V
R4/RRR4-11/3	1531.459	1531.695	-154.436	0.403	987.595	0.299	23	0.091	K.LIFGADSPAIQENR.V
R4/RRR4-11/3	1708.574	1708.979	-237.605	0.441	860.124	0.273	26	0.085	R.VKEYLPITGLADFNK.L
R4/RRR4-13/2	1985.596	1986.176	-798.133	0.641	2305.222	0.625	24	0.386	K.THNSFILQQFENPANPK.I
R4/RRR4-13/2	1691.658	1690.041	-226.873	0.611	2377.140	0.553	24	0.374	K.AFGAELILTDPLLGMK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1986.280	1986.176	52.234	0.608	1887.878	0.620	23	0.310	K.THNSFILQQFENPANPK.I
R4/RRR4-13/2	1688.405	1688.864	-272.922	0.522	1825.892	0.655	26	0.309	K.VDGLVSGIGTGGTITGAGR.Y
R4/RRR4-13/2	1690.190	1690.041	88.404	0.536	1988.788	0.533	22	0.298	K.AFGAELILTDPLLGMK.G
R4/RRR4-13/2	1688.310	1688.864	-923.298	0.496	1691.163	0.648	25	0.285	K.VDGLVSGIGTGGTITGAGR.Y
R4/RRR4-13/2	1357.228	1357.512	-210.156	0.485	1822.944	0.528	19	0.274	R.IGYSMITDAEEK.G
R4/RRR4-13/2	1357.163	1357.512	-257.980	0.478	1814.572	0.476	19	0.259	R.IGYSMITDAEEK.G
R4/RRR4-13/3	1818.112	1818.064	26.754	0.436	1742.197	0.534	31	0.253	K.DVTELIGNTPLVYLNR.V
R4/RRR4-13/2	1689.296	1688.864	256.093	0.541	1496.937	0.607	24	0.249	K.VDGLVSGIGTGGTITGAGR.Y
R4/RRR4-13/2	1818.425	1818.064	199.528	0.516	1570.239	0.467	21	0.223	K.DVTELIGNTPLVYLNR.V
R4/RRR4-13/2	1705.324	1706.040	-1009.051	0.432	1426.719	0.529	19	0.219	K.AFGAELILTDPLLGM*K.G
R4/RRR4-13/2	1373.084	1373.511	-311.845	0.401	1407.256	0.487	17	0.211	R.IGYSM*ITDAEEK.G
R4/RRR4-13/2	1817.385	1818.064	-926.306	0.441	1434.215	0.424	20	0.199	K.DVTELIGNTPLVYLNR.V
R4/RRR4-13/2	1372.428	1373.511	-1522.418	0.371	1414.161	0.417	18	0.198	R.IGYSM*ITDAEEK.G
R4/RRR4-13/2	1818.262	1818.064	109.180	0.518	1333.337	0.451	20	0.195	K.DVTELIGNTPLVYLNR.V
R4/RRR4-13/3	1985.848	1986.176	-165.803	0.524	1419.306	0.508	32	0.187	K.THNSFILQQFENPANPK.I
R4/RRR4-13/2	1613.110	1613.841	-1076.397	0.374	1096.387	0.492	27	0.184	K.EGLLVGISSGAAAAAAVR.L
R4/RRR4-13/2	1688.643	1690.041	-1423.914	0.333	1344.903	0.382	20	0.182	K.AFGAELILTDPLLGMK.G
R4/RRR4-13/2	1373.128	1373.511	-279.736	0.433	1089.993	0.444	18	0.180	R.IGYSM*ITDAEEK.G
R4/RRR4-13/2	1704.827	1706.040	-1302.146	0.366	1213.218	0.420	19	0.178	K.AFGAELILTDPLLGM*K.G
R4/RRR4-13/2	1474.299	1474.642	-233.497	0.484	701.352	0.536	16	0.172	K.IHYETTGPEIWK.S
R4/RRR4-13/2	1474.098	1474.642	-1050.327	0.475	803.297	0.492	17	0.171	K.IHYETTGPEIWK.S
R4/RRR4-13/2	1475.197	1474.642	-302.491	0.526	757.045	0.493	16	0.168	K.IHYETTGPEIWK.S
R4/RRR4-13/2	1285.975	1285.513	359.928	0.327	1097.129	0.376	17	0.166	R.YLSSVLFQSIK.K
R4/RRR4-13/2	1285.872	1285.513	280.069	0.336	920.295	0.437	16	0.164	R.YLSSVLFQSIK.K
R4/RRR4-13/2	1285.247	1285.513	-208.303	0.366	1115.247	0.339	17	0.164	R.YLSSVLFQSIK.K
R4/RRR4-13/3	1817.901	1818.064	-89.625	0.492	1166.204	0.534	28	0.163	K.DVTELIGNTPLVYLNR.V
R4/RRR4-13/2	1214.461	1215.382	-1585.990	0.415	1091.531	0.330	18	0.161	K.GAVQKAEELAAK.T
R4/RRR4-13/2	1397.209	1397.645	-312.978	0.427	1035.323	0.342	17	0.160	K.LFVVVFPSFGER.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1474.325	1474.642	-215.305	0.474	709.446	0.439	16	0.159	K.IHYETTGPEIWK.S
R4/RRR4-13/2	1413.395	1413.686	-206.655	0.369	961.663	0.362	16	0.157	R.YLSSVLFQSIKK.E
R4/RRR4-13/2	1214.214	1215.382	-1790.304	0.441	516.233	0.435	17	0.156	K.GAVQKAEELAAK.T
R4/RRR4-13/2	1214.377	1215.382	-1655.466	0.436	727.616	0.355	17	0.151	K.GAVQKAEELAAK.T
R4/RRR4-13/2	1514.163	1514.815	-1094.062	0.354	568.670	0.438	18	0.151	R.LVLTM*PASM*SM*ER.R
R4/RRR4-13/2	1397.210	1397.645	-312.189	0.376	849.718	0.318	16	0.149	K.LFVVVFPSFGER.Y
R4/RRR4-13/2	1413.278	1413.686	-290.014	0.459	890.921	0.326	15	0.149	R.YLSSVLFQSIKK.E
R4/RRR4-13/2	1612.768	1613.841	-1289.041	0.288	461.979	0.494	22	0.148	K.EGLLVGISSGAAAAAAVR.L
R4/RRR4-13/2	1397.187	1397.645	-328.844	0.392	824.040	0.289	16	0.145	K.LFVVVFPSFGER.Y
R4/RRR4-13/2	1413.177	1413.686	-1071.520	0.419	794.779	0.304	15	0.144	R.YLSSVLFQSIKK.E
R4/RRR4-13/2	1397.274	1397.645	-266.259	0.356	721.322	0.296	15	0.143	K.LFVVVFPSFGER.Y
R4/RRR4-13/3	1986.437	1986.176	131.857	0.449	1241.365	0.395	31	0.129	K.THNSFILQQFENPANPK.I
R4/RRR4-14/2	1795.510	1795.025	271.015	0.555	3001.242	0.595	27	0.532	K.LTVSTVSSSGVGLTSTAVK.K
R4/RRR4-15/2	1794.546	1795.025	-267.628	0.494	2611.507	0.519	26	0.409	K.LTVSTVSSSGVGLTSTAVK.K
R4/RRR4-14/2	1794.696	1795.025	-183.762	0.478	2506.740	0.558	26	0.401	K.LTVSTVSSSGVGLTSTAVK.K
R4/RRR4-15/2	1794.420	1795.025	-897.017	0.463	2408.249	0.579	26	0.388	K.LTVSTVSSSGVGLTSTAVK.K
R4/RRR4-14/2	1794.417	1795.025	-898.997	0.505	2372.338	0.582	26	0.382	K.LTVSTVSSSGVGLTSTAVK.K
R4/RRR4-14/2	1530.422	1530.747	-212.774	0.531	2259.240	0.543	22	0.351	K.KGGLYTLDVSSVYK.Y
R4/RRR4-14/2	1530.449	1530.747	-195.330	0.518	2283.406	0.520	22	0.348	K.KGGLYTLDVSSVYK.Y
R4/RRR4-15/2	1795.345	1795.025	178.838	0.512	2099.221	0.551	24	0.320	K.LTVSTVSSSGVGLTSTAVK.K
R4/RRR4-14/2	1402.393	1402.574	-129.178	0.510	1850.218	0.582	19	0.293	K.GGLYTLDVSSVYK.Y
R4/RRR4-14/2	1402.102	1402.574	-337.559	0.482	1859.919	0.573	19	0.291	K.GGLYTLDVSSVYK.Y
R4/RRR4-14/2	1402.464	1402.574	-78.973	0.453	1692.730	0.612	19	0.276	K.GGLYTLDVSSVYK.Y
R4/RRR4-15/2	1766.484	1766.977	-279.781	0.549	1704.302	0.558	24	0.267	R.RLSTNENTLTVGGLYK.V
R4/RRR4-14/2	1297.443	1297.436	5.604	0.487	1369.852	0.555	18	0.225	K.SVLTISGEFDTK.A
R4/RRR4-14/2	1147.098	1147.309	-184.612	0.434	1553.960	0.430	17	0.216	K.GPGLFSDIGKR.A
R4/RRR4-14/2	1611.459	1610.790	-206.176	0.515	1288.771	0.535	21	0.212	R.LSTNENTLTVGGLYK.V
R4/RRR4-14/2	1610.377	1610.790	-257.559	0.509	1313.176	0.524	20	0.210	R.LSTNENTLTVGGLYK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1610.253	1610.790	-957.334	0.478	1397.209	0.479	20	0.208	R.LSTNENTLTVGGLYK.V
R4/RRR4-15/2	991.002	991.123	-122.265	0.477	1026.709	0.605	17	0.206	K.GPGLFSDIGK.K
R4/RRR4-15/2	961.439	962.083	-1715.317	0.402	1646.622	0.299	15	0.199	K.SSVVAELTR.R
R4/RRR4-14/2	1148.097	1147.309	-185.517	0.473	1284.228	0.465	16	0.198	K.GPGLFSDIGKR.A
R4/RRR4-15/2	1610.360	1610.790	-267.978	0.497	1098.818	0.520	20	0.192	R.LSTNENTLTVGGLYK.V
R4/RRR4-14/2	1296.683	1297.436	-1356.443	0.377	1126.760	0.509	18	0.190	K.SVLTISGEFDTK.A
R4/RRR4-15/2	1297.022	1297.436	-320.351	0.370	1052.568	0.543	17	0.189	K.SVLTISGEFDTK.A
R4/RRR4-15/2	961.942	962.083	-146.323	0.453	1610.299	0.268	15	0.188	K.SSVVAELTR.R
R4/RRR4-15/2	961.846	962.083	-246.390	0.421	1557.053	0.268	15	0.184	K.SSVVAELTR.R
R4/RRR4-14/2	1146.434	1147.309	-1640.692	0.450	1059.367	0.438	16	0.176	K.GPGLFSDIGKR.A
R4/RRR4-15/2	1610.320	1610.790	-292.847	0.450	956.488	0.491	19	0.176	R.LSTNENTLTVGGLYK.V
R4/RRR4-14/3	1530.745	1530.747	-1.137	0.517	1788.726	0.326	28	0.171	K.KGGLYTLDVSSVYK.Y
R4/RRR4-14/2	961.970	962.083	-117.300	0.355	1413.188	0.211	14	0.163	K.SSVVAELTR.R
R4/RRR4-15/2	1296.279	1297.436	-1668.746	0.371	863.485	0.412	17	0.161	K.SVLTISGEFDTK.A
R4/RRR4-15/2	1296.468	1297.436	-1522.406	0.346	837.327	0.440	15	0.160	K.SVLTISGEFDTK.A
R4/RRR4-14/2	1389.196	1389.539	-247.625	0.489	1044.860	0.334	17	0.158	K.VSGVYHLDDKQK.S
R4/RRR4-15/2	1389.192	1389.539	-250.181	0.454	1084.944	0.285	18	0.154	K.VSGVYHLDDKQK.S
R4/RRR4-14/3	1530.547	1530.747	-130.730	0.486	1633.086	0.335	27	0.154	K.KGGLYTLDVSSVYK.Y
R4/RRR4-14/2	1389.168	1389.539	-267.460	0.454	910.135	0.330	17	0.153	K.VSGVYHLDDKQK.S
R4/RRR4-14/3	1530.461	1530.747	-187.497	0.508	1795.247	0.246	28	0.145	K.KGGLYTLDVSSVYK.Y
R4/RRR4-14/2	1296.543	1297.436	-1464.242	0.309	550.428	0.360	13	0.143	K.SVLTISGEFDTK.A
R4/RRR4-15/2	1118.339	1118.269	62.885	0.370	1002.201	0.211	15	0.143	K.SSVVAELTRR.L
R4/RRR4-14/2	1117.853	1118.269	-373.230	0.324	922.123	0.164	14	0.136	K.SSVVAELTRR.L
R4/RRR4-14/2	1117.300	1118.269	-1767.523	0.193	1046.607	0.062	14	0.130	K.SSVVAELTRR.L
R4/RRR4-14/3	1147.613	1147.309	265.843	0.381	580.534	0.531	21	0.115	K.GPGLFSDIGKR.A
R4/RRR4-15/3	1147.065	1147.309	-213.395	0.342	547.695	0.530	20	0.112	K.GPGLFSDIGKR.A
R4/RRR4-15/3	1147.217	1147.309	-80.654	0.320	473.518	0.546	19	0.111	K.GPGLFSDIGKR.A
R4/RRR4-14/3	1147.469	1147.309	140.075	0.314	671.168	0.482	22	0.107	K.GPGLFSDIGKR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/3	1147.485	1147.309	153.678	0.355	642.215	0.445	21	0.103	K.GPGLFSDIGKR.A
R4/RRR4-14/3	1147.713	1147.309	353.030	0.340	639.260	0.447	21	0.103	K.GPGLFSDIGKR.A
R4/RRR4-15/3	1530.325	1530.747	-276.321	0.372	1352.140	0.191	27	0.091	K.KGGLYTLDVSSVYK.Y
R4/RRR4-15/3	1530.416	1530.747	-216.663	0.401	921.692	0.299	22	0.085	-.KGGLYTLDVSSVYK.-
R4/RRR4-15/1	1131.629	1132.377	-1549.676	0.269	781.721	0.416	14	0.622	K.SGLLLVTGPFK.I
R4/RRR4-16/2	1740.465	1740.890	-244.851	0.584	2044.905	0.567	24	0.321	K.KTEGELFETEKEATK.N
R4/RRR4-16/2	1739.919	1740.890	-1136.082	0.596	2011.058	0.563	23	0.314	K.KTEGELFETEKEATK.N
R4/RRR4-15/2	1310.969	1311.466	-380.077	0.455	1884.606	0.550	20	0.289	R.VNQSYVIATSTK.V
R4/RRR4-15/2	1311.153	1311.466	-239.299	0.481	1782.838	0.563	19	0.278	R.VNQSYVIATSTK.V
R4/RRR4-15/2	1311.072	1311.466	-301.696	0.473	1801.037	0.545	20	0.276	R.VNQSYVIATSTK.V
R4/RRR4-15/2	1740.316	1740.890	-907.034	0.577	1705.201	0.572	22	0.270	K.KTEGELFETEKEATK.N
R4/RRR4-15/2	1311.130	1311.466	-257.232	0.479	1681.561	0.574	19	0.267	R.VNQSYVIATSTK.V
R4/RRR4-15/3	1210.654	1211.350	-1404.905	0.493	1748.736	0.419	26	0.200	K.AEKPDAAAAAAPK.F
R4/RRR4-15/2	1059.989	1060.183	-184.074	0.476	1131.854	0.506	16	0.195	K.VDISGVNVEK.F
R4/RRR4-15/3	1211.589	1211.350	197.994	0.530	1778.543	0.394	27	0.194	K.AEKPDAAAAAAPK.F
R4/RRR4-15/2	1059.917	1060.183	-252.356	0.424	1121.877	0.515	16	0.194	K.VDISGVNVEK.F
R4/RRR4-15/2	1060.018	1060.183	-156.810	0.494	1097.460	0.492	16	0.191	K.VDISGVNVEK.F
R4/RRR4-16/2	1612.210	1612.717	-937.186	0.511	1158.581	0.488	19	0.190	K.TEGELFETEKEATK.N
R4/RRR4-16/2	1612.991	1612.717	170.288	0.562	1030.039	0.512	18	0.184	K.TEGELFETEKEATK.N
R4/RRR4-15/2	1131.920	1132.377	-405.152	0.441	1064.747	0.494	14	0.183	K.SGLLLVTGPFK.I
R4/RRR4-15/2	1131.899	1132.377	-424.197	0.438	1107.164	0.437	14	0.177	K.SGLLLVTGPFK.I
R4/RRR4-16/2	1613.283	1612.717	-269.617	0.565	966.088	0.485	18	0.175	K.TEGELFETEKEATK.N
R4/RRR4-15/2	1211.143	1211.350	-171.210	0.442	667.370	0.532	20	0.171	K.AEKPDAAAAAAPK.F
R4/RRR4-15/2	1131.400	1132.377	-1753.288	0.397	1149.809	0.382	14	0.170	K.SGLLLVTGPFK.I
R4/RRR4-15/2	1498.492	1498.793	-201.538	0.436	974.834	0.433	22	0.170	R.SSITPGTVLILLAGR.F
R4/RRR4-16/2	1208.102	1208.348	-203.464	0.422	506.956	0.534	15	0.166	K.FYPADDVKPR.Q
R4/RRR4-15/2	1210.584	1211.350	-1462.725	0.442	584.263	0.508	19	0.165	K.AEKPDAAAAAAPK.F
R4/RRR4-16/2	956.016	956.118	-106.952	0.362	898.451	0.399	15	0.162	K.AIEAVPDLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	955.665	956.118	-475.070	0.391	925.760	0.374	15	0.161	K.AIEAVPDLK.T
R4/RRR4-16/2	1131.874	1132.377	-1332.307	0.363	874.855	0.388	14	0.157	K.SGLLLVTGPFK.I
R4/RRR4-15/2	1210.892	1211.350	-379.538	0.377	668.896	0.433	18	0.156	K.AEKPDAAAAAAPK.F
R4/RRR4-16/2	1207.398	1208.348	-1619.199	0.391	505.077	0.392	15	0.153	K.FYPADDVKPR.Q
R4/RRR4-15/2	1497.767	1498.793	-1356.298	0.335	728.162	0.403	20	0.152	R.SSITPGTVLILLAGR.F
R4/RRR4-16/3	1211.428	1211.350	64.914	0.471	1505.574	0.376	24	0.152	K.AEKPDAAAAAAPK.F
R4/RRR4-16/2	1132.242	1132.377	-119.881	0.474	882.756	0.349	13	0.151	K.SGLLLVTGPFK.I
R4/RRR4-16/2	1132.027	1132.377	-310.801	0.412	778.196	0.364	13	0.150	K.SGLLLVTGPFK.I
R4/RRR4-15/2	1498.310	1498.793	-322.830	0.323	831.676	0.351	21	0.150	R.SSITPGTVLILLAGR.F
R4/RRR4-20/3	1211.590	1211.350	198.600	0.461	1413.759	0.401	25	0.148	K.AEKPDAAAAAAPK.F
R4/RRR4-16/2	1207.975	1208.348	-309.302	0.367	408.996	0.390	14	0.148	-.FYPADDVKPR.-
R4/RRR4-16/2	956.183	956.118	67.979	0.403	534.445	0.377	12	0.144	-.AIEAVPDLK.-
R4/RRR4-15/2	925.037	925.114	-83.003	0.399	871.995	0.201	13	0.140	K.INGVPIRR.V
R4/RRR4-16/3	1740.250	1740.890	-944.822	0.546	1068.966	0.492	29	0.139	K.KTEGELFETEKEATK.N
R4/RRR4-13/2	1131.908	1132.377	-415.432	0.271	518.438	0.290	12	0.138	-.SGLLLVTGPFK.-
R4/RRR4-15/3	1498.592	1498.793	-134.049	0.371	1772.322	0.221	29	0.138	R.SSITPGTVLILLAGR.F
R4/RRR4-16/3	1740.373	1740.890	-874.370	0.523	1252.183	0.425	30	0.137	K.KTEGELFETEKEATK.N
R4/RRR4-15/2	924.934	925.114	-195.133	0.334	646.319	0.163	12	0.136	K.INGVPIRR.V
R4/RRR4-20/3	1211.730	1211.350	314.372	0.538	1196.731	0.408	24	0.128	K.AEKPDAAAAAAPK.F
R4/RRR4-16/2	1208.783	1208.348	361.034	0.097	239.198	0.386	11	0.124	-.FYPADDVKPR.-
R4/RRR4-15/3	1741.019	1740.890	74.423	0.459	1014.472	0.437	28	0.121	K.KTEGELFETEKEATK.N
R4/RRR4-15/3	1741.220	1740.890	190.331	0.448	911.457	0.430	27	0.114	K.KTEGELFETEKEATK.N
R4/RRR4-14/3	1211.516	1211.350	137.673	0.430	1054.066	0.389	24	0.113	K.AEKPDAAAAAAPK.F
R4/RRR4-16/3	1741.076	1740.890	107.332	0.489	882.573	0.427	28	0.112	K.KTEGELFETEKEATK.N
R4/RRR4-19/3	1741.079	1740.890	108.914	0.483	801.335	0.413	26	0.106	K.KTEGELFETEKEATK.N
R4/RRR4-15/3	1740.513	1740.890	-216.889	0.465	1028.917	0.351	27	0.104	K.KTEGELFETEKEATK.N
R4/RRR4-15/3	1498.369	1498.793	-283.971	0.401	1396.489	0.216	27	0.099	R.SSITPGTVLILLAGR.F
R4/RRR4-16/3	1311.723	1311.420	231.977	0.488	1019.669	0.289	20	0.092	K.KTEGELFETEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/3	1310.959	1311.420	-352.632	0.421	787.099	0.244	19	0.078	-.KTEGELFETEK.-
R4/RRR4-25/2	1264.259	1264.456	-156.269	0.493	1938.563	0.551	19	0.296	R.LQAALSTGLFSR.I
R4/RRR4-24/2	1608.895	1609.806	-1190.855	0.443	1837.254	0.499	22	0.265	K.LDISGHTVSAVGPDIK.H
R4/RRR4-26/2	1264.307	1264.456	-118.399	0.528	1709.070	0.555	19	0.265	R.LQAALSTGLFSR.I
R4/RRR4-24/2	1264.356	1264.456	-78.981	0.519	1736.343	0.536	20	0.264	R.LQAALSTGLFSR.I
R4/RRR4-25/2	1609.619	1609.806	-116.198	0.489	1856.717	0.472	23	0.261	K.LDISGHTVSAVGPDIK.H
R4/RRR4-25/2	1264.182	1264.456	-217.488	0.503	1611.135	0.590	19	0.261	R.LQAALSTGLFSR.I
R4/RRR4-12/2	1312.138	1312.497	-274.204	0.466	1702.767	0.544	20	0.260	R.VLVGVVASPEADR.D
R4/RRR4-14/2	1263.625	1264.456	-1453.359	0.525	1678.730	0.551	19	0.260	R.LQAALSTGLFSR.I
R4/RRR4-23/2	1312.310	1312.497	-142.897	0.497	1703.837	0.541	20	0.259	R.VLVGVVASPEADR.D
R4/RRR4-14/2	1312.134	1312.497	-277.284	0.455	1672.423	0.555	21	0.259	R.VLVGVVASPEADR.D
R4/RRR4-14/2	1265.294	1264.456	-128.563	0.517	1637.736	0.553	19	0.255	R.LQAALSTGLFSR.I
R4/RRR4-15/2	1263.742	1264.456	-1360.603	0.519	1607.199	0.544	19	0.249	R.LQAALSTGLFSR.I
R4/RRR4-24/2	1264.261	1264.456	-154.816	0.547	1518.378	0.581	19	0.248	R.LQAALSTGLFSR.I
R4/RRR4-25/2	1265.699	1264.456	192.442	0.497	1603.878	0.532	19	0.246	R.LQAALSTGLFSR.I
R4/RRR4-15/2	1312.117	1312.497	-290.444	0.499	1643.489	0.512	20	0.245	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1609.459	1609.806	-216.246	0.452	1732.090	0.465	22	0.243	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/2	1609.387	1609.806	-261.065	0.452	1556.985	0.547	21	0.240	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/2	1263.680	1264.456	-1409.696	0.514	1514.853	0.552	19	0.240	R.LQAALSTGLFSR.I
R4/RRR4-24/2	1313.103	1312.497	-301.042	0.506	1443.307	0.587	20	0.240	R.VLVGVVASPEADR.D
R4/RRR4-24/2	1264.151	1264.456	-241.804	0.512	1547.913	0.534	19	0.240	R.LQAALSTGLFSR.I
R4/RRR4-19/2	1312.678	1312.497	137.893	0.505	1490.916	0.562	20	0.239	R.VLVGVVASPEADR.D
R4/RRR4-13/2	1264.081	1264.456	-297.317	0.434	1684.734	0.471	18	0.239	R.LQAALSTGLFSR.I
R4/RRR4-25/2	1311.626	1312.497	-1430.975	0.373	1734.906	0.446	21	0.239	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1263.661	1264.456	-1424.250	0.506	1440.302	0.573	18	0.236	R.LQAALSTGLFSR.I
R4/RRR4-15/2	1311.591	1312.497	-1457.711	0.394	1547.540	0.527	20	0.235	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1610.211	1609.806	252.246	0.521	1562.912	0.513	23	0.235	K.LDISGHTVSAVGPDIK.H
R4/RRR4-14/2	1263.529	1264.456	-1529.536	0.446	1637.699	0.469	19	0.234	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1312.070	1312.497	-326.381	0.432	1454.197	0.563	20	0.234	R.VLVGVVASPEADR.D
R4/RRR4-26/2	1312.157	1312.497	-260.390	0.451	1430.176	0.570	20	0.233	R.VLVGVVASPEADR.D
R4/RRR4-23/2	1313.011	1312.497	-371.466	0.524	1434.655	0.561	20	0.233	R.VLVGVVASPEADR.D
R4/RRR4-14/2	1312.166	1312.497	-252.830	0.464	1452.938	0.556	20	0.233	R.VLVGVVASPEADR.D
R4/RRR4-20/2	1312.268	1312.497	-175.184	0.421	1486.478	0.546	19	0.233	R.VLVGVVASPEADR.D
R4/RRR4-22/2	1264.126	1264.456	-261.857	0.492	1375.859	0.581	18	0.231	R.LQAALSTGLFSR.I
R4/RRR4-25/2	1263.635	1264.456	-1444.917	0.513	1385.432	0.559	18	0.227	R.LQAALSTGLFSR.I
R4/RRR4-17/2	1312.179	1312.497	-243.124	0.422	1488.849	0.519	19	0.227	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1609.355	1609.806	-280.850	0.469	1457.107	0.542	20	0.227	K.LDISGHTVSAVGPDIK.H
R4/RRR4-25/2	1312.130	1312.497	-280.457	0.461	1471.497	0.521	20	0.227	R.VLVGVVASPEADR.D
R4/RRR4-26/2	1311.406	1312.497	-1599.642	0.379	1536.334	0.496	20	0.227	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1312.168	1312.497	-251.804	0.464	1376.595	0.556	20	0.225	R.VLVGVVASPEADR.D
R4/RRR4-21/2	1264.033	1264.456	-335.492	0.522	1383.409	0.553	17	0.224	R.LQAALSTGLFSR.I
R4/RRR4-13/2	1312.205	1312.497	-223.338	0.444	1418.552	0.522	19	0.221	R.VLVGVVASPEADR.D
R4/RRR4-12/2	1312.061	1312.497	-333.662	0.438	1450.611	0.491	20	0.218	R.VLVGVVASPEADR.D
R4/RRR4-23/2	1263.431	1264.456	-1607.472	0.448	1428.851	0.496	18	0.217	R.LQAALSTGLFSR.I
R4/RRR4-23/2	1264.073	1264.456	-304.099	0.437	1307.752	0.537	18	0.214	R.LQAALSTGLFSR.I
R4/RRR4-26/2	1312.143	1312.497	-270.564	0.443	1241.402	0.566	19	0.213	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1312.237	1312.497	-199.167	0.477	1263.547	0.545	19	0.211	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1263.675	1264.456	-1413.674	0.496	1309.281	0.516	19	0.211	R.LQAALSTGLFSR.I
R4/RRR4-13/2	1312.183	1312.497	-239.950	0.417	1300.065	0.538	18	0.211	R.VLVGVVASPEADR.D
R4/RRR4-27/2	1312.152	1312.497	-264.030	0.406	1285.929	0.540	19	0.211	R.VLVGVVASPEADR.D
R4/RRR4-24/2	1312.146	1312.497	-268.137	0.463	1306.751	0.522	19	0.210	R.VLVGVVASPEADR.D
R4/RRR4-22/2	1312.169	1312.497	-250.964	0.442	1350.674	0.496	19	0.209	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1609.295	1609.806	-941.547	0.434	1356.021	0.500	21	0.208	K.LDISGHTVSAVGPDIK.H
R4/RRR4-26/2	1264.272	1264.456	-145.518	0.509	1272.776	0.515	18	0.207	R.LQAALSTGLFSR.I
R4/RRR4-14/2	1312.154	1312.497	-262.070	0.439	1278.347	0.518	19	0.207	R.VLVGVVASPEADR.D
R4/RRR4-23/2	1264.216	1264.456	-190.656	0.412	1248.240	0.527	17	0.205	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1049.031	1049.270	-228.375	0.500	1418.007	0.424	16	0.202	R.LGVM*LTATAR.C
R4/RRR4-14/2	1609.267	1609.806	-959.138	0.420	1414.370	0.436	22	0.202	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/2	1265.287	1264.456	-134.080	0.447	1211.577	0.516	17	0.200	R.LQAALSTGLFSR.I
R4/RRR4-3/2	1312.263	1312.497	-178.637	0.425	1215.025	0.512	18	0.199	R.VLVGVVASPEADR.D
R4/RRR4-1/2	1312.217	1312.497	-214.379	0.411	1255.910	0.485	19	0.198	R.VLVGVVASPEADR.D
R4/RRR4-23/2	1049.173	1049.270	-92.741	0.446	1382.499	0.416	16	0.198	R.LGVM*LTATAR.C
R4/RRR4-1/2	1312.191	1312.497	-234.071	0.436	1194.103	0.504	18	0.196	R.VLVGVVASPEADR.D
R4/RRR4-3/2	1049.908	1049.270	-345.967	0.455	1497.705	0.360	16	0.196	R.LGVM*LTATAR.C
R4/RRR4-17/2	1264.070	1264.456	-305.843	0.455	1040.400	0.562	16	0.195	R.LQAALSTGLFSR.I
R4/RRR4-1/2	1311.986	1312.497	-1155.471	0.359	1257.189	0.478	18	0.195	R.VLVGVVASPEADR.D
R4/RRR4-24/2	1312.251	1312.497	-188.155	0.441	1180.554	0.499	18	0.194	R.VLVGVVASPEADR.D
R4/RRR4-17/2	1311.717	1312.497	-1361.431	0.372	1231.220	0.481	18	0.194	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1110.080	1110.271	-172.459	0.433	1331.385	0.414	15	0.193	K.WMAAYPQSR.V
R4/RRR4-24/2	1609.106	1609.806	-1059.673	0.476	1303.342	0.447	21	0.193	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/2	1110.092	1110.271	-161.427	0.393	1305.542	0.430	14	0.193	K.WMAAYPQSR.V
R4/RRR4-15/2	1050.105	1049.270	-157.602	0.542	1366.126	0.404	16	0.193	R.LGVM*LTATAR.C
R4/RRR4-23/2	1610.571	1609.806	-145.854	0.518	1212.947	0.486	20	0.192	K.LDISGHTVSAVGPDIK.H
R4/RRR4-22/2	1311.593	1312.497	-1456.403	0.390	1286.464	0.439	19	0.192	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1048.987	1049.270	-270.753	0.536	1353.649	0.403	16	0.192	R.LGVM*LTATAR.C
R4/RRR4-25/2	1048.986	1049.270	-272.038	0.493	1317.827	0.413	16	0.192	R.LGVM*LTATAR.C
R4/RRR4-15/2	1109.979	1110.271	-263.366	0.438	1095.441	0.505	14	0.191	K.WMAAYPQSR.V
R4/RRR4-19/2	1312.264	1312.497	-177.983	0.397	1271.751	0.433	19	0.190	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1048.465	1049.270	-1727.097	0.396	1372.959	0.378	16	0.189	R.LGVM*LTATAR.C
R4/RRR4-17/2	1263.951	1264.456	-1193.861	0.440	1013.108	0.531	16	0.187	R.LQAALSTGLFSR.I
R4/RRR4-22/2	1312.131	1312.497	-279.991	0.461	1221.903	0.436	18	0.186	R.VLVGVVASPEADR.D
R4/RRR4-13/2	1311.596	1312.497	-1453.878	0.365	960.792	0.556	17	0.185	R.VLVGVVASPEADR.D
R4/RRR4-26/2	1048.523	1049.270	-1670.834	0.393	1385.167	0.345	16	0.184	R.LGVM*LTATAR.C
R4/RRR4-24/2	1048.767	1049.270	-1437.192	0.395	1428.021	0.326	16	0.184	R.LGVM*LTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1048.429	1049.270	-1761.139	0.324	1460.825	0.308	16	0.183	R.LGVM*LTATAR.C
R4/RRR4-14/2	1048.512	1049.270	-1681.361	0.427	1311.095	0.369	16	0.183	R.LGVM*LTATAR.C
R4/RRR4-27/2	1311.960	1312.497	-1174.904	0.331	1232.686	0.417	19	0.183	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1754.346	1754.945	-914.009	0.489	1001.458	0.499	20	0.182	R.EELEKWM*AAYPQSR.V
R4/RRR4-25/2	1048.910	1049.270	-344.312	0.358	1392.763	0.327	16	0.181	R.LGVM*LTATAR.C
R4/RRR4-23/2	1048.886	1049.270	-367.082	0.433	1274.867	0.377	15	0.181	R.LGVM*LTATAR.C
R4/RRR4-25/2	1264.930	1264.456	375.692	0.465	980.685	0.496	16	0.180	R.LQAALSTGLFSR.I
R4/RRR4-15/2	1125.985	1126.270	-253.869	0.351	1084.211	0.457	15	0.180	K.WM*AAYPQSR.V
R4/RRR4-21/2	1312.494	1312.497	-2.389	0.456	1010.880	0.472	17	0.178	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1032.947	1033.271	-314.773	0.495	1084.780	0.422	15	0.176	R.LGVMLTATAR.C
R4/RRR4-15/2	1033.017	1033.271	-246.719	0.497	1067.235	0.425	15	0.176	R.LGVMLTATAR.C
R4/RRR4-24/2	1049.078	1049.270	-183.315	0.472	1224.794	0.369	15	0.176	R.LGVM*LTATAR.C
R4/RRR4-25/2	1032.973	1033.271	-289.163	0.476	1052.282	0.426	15	0.175	R.LGVMLTATAR.C
R4/RRR4-13/2	1049.381	1049.270	105.625	0.424	1202.055	0.366	16	0.175	R.LGVM*LTATAR.C
R4/RRR4-24/2	1127.131	1126.270	-124.019	0.419	811.489	0.506	14	0.175	K.WM*AAYPQSR.V
R4/RRR4-25/2	1126.046	1126.270	-199.381	0.347	990.841	0.462	14	0.175	K.WM*AAYPQSR.V
R4/RRR4-24/2	1049.091	1049.270	-170.825	0.381	1239.278	0.353	15	0.175	R.LGVM*LTATAR.C
R4/RRR4-25/2	1126.022	1126.270	-220.805	0.443	807.737	0.493	14	0.174	K.WM*AAYPQSR.V
R4/RRR4-24/2	1126.104	1126.270	-147.726	0.379	929.786	0.466	14	0.174	K.WM*AAYPQSR.V
R4/RRR4-25/2	1032.575	1033.271	-1646.708	0.429	1020.140	0.403	15	0.170	R.LGVMLTATAR.C
R4/RRR4-27/2	1311.628	1312.497	-1429.386	0.375	976.104	0.434	17	0.169	R.VLVGVVASPEADR.D
R4/RRR4-15/2	1263.994	1264.456	-366.208	0.357	794.948	0.492	18	0.169	R.LQAALSTGLFSR.I
R4/RRR4-15/2	1125.997	1126.270	-243.210	0.447	829.042	0.441	14	0.168	K.WM*AAYPQSR.V
R4/RRR4-24/2	1133.875	1133.194	-282.327	0.500	960.159	0.389	16	0.166	R.NTDQLEGSLR.E
R4/RRR4-24/2	1125.967	1126.270	-270.075	0.384	687.417	0.480	13	0.165	K.WM*AAYPQSR.V
R4/RRR4-25/2	1109.753	1110.271	-1371.993	0.356	884.897	0.416	14	0.165	K.WMAAYPQSR.V
R4/RRR4-19/2	1311.998	1312.497	-381.458	0.393	1032.799	0.372	17	0.164	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1109.563	1110.271	-1543.817	0.362	977.469	0.371	14	0.163	K.WMAAYPQSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	1126.007	1126.270	-234.727	0.392	796.833	0.424	13	0.163	K.WM*AAYPQSR.V
R4/RRR4-19/2	1133.001	1133.194	-170.699	0.444	804.275	0.392	16	0.162	R.NTDQLEGSLR.E
R4/RRR4-24/2	1109.708	1110.271	-1412.540	0.360	835.418	0.401	13	0.160	K.WMAAYPQSR.V
R4/RRR4-15/2	1132.448	1133.194	-1546.675	0.384	799.831	0.389	16	0.160	R.NTDQLEGSLR.E
R4/RRR4-21/2	1133.017	1133.194	-157.081	0.424	751.967	0.392	16	0.160	R.NTDQLEGSLR.E
R4/RRR4-16/2	1312.093	1312.497	-308.646	0.331	808.442	0.441	15	0.160	R.VLVGVVASPEADR.D
R4/RRR4-20/2	1312.100	1312.497	-303.419	0.368	565.716	0.488	16	0.160	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1531.016	1531.733	-1124.917	0.343	1466.326	0.174	18	0.160	K.DLYYDVLQFINK.L
R4/RRR4-27/2	1133.013	1133.194	-160.539	0.478	792.376	0.369	16	0.158	R.NTDQLEGSLR.E
R4/RRR4-15/2	1126.104	1126.270	-148.161	0.333	822.825	0.386	14	0.158	K.WM*AAYPQSR.V
R4/RRR4-27/2	1134.054	1133.194	-123.684	0.464	718.508	0.378	16	0.158	R.NTDQLEGSLR.E
R4/RRR4-15/2	1033.260	1033.271	-10.381	0.377	765.231	0.396	14	0.158	R.LGVMLTATAR.C
R4/RRR4-12/2	1134.010	1133.194	-162.557	0.406	674.816	0.386	16	0.158	R.NTDQLEGSLR.E
R4/RRR4-2/2	1132.973	1133.194	-195.558	0.363	723.729	0.379	16	0.157	R.NTDQLEGSLR.E
R4/RRR4-24/2	921.909	922.014	-114.296	0.399	744.923	0.361	12	0.157	R.CVFPDQR.L
R4/RRR4-28/2	1132.999	1133.194	-172.860	0.390	802.572	0.352	16	0.157	R.NTDQLEGSLR.E
R4/RRR4-20/2	1132.928	1133.194	-235.444	0.415	671.211	0.374	15	0.156	R.NTDQLEGSLR.E
R4/RRR4-24/2	921.796	922.014	-236.640	0.383	831.898	0.336	12	0.156	R.CVFPDQR.L
R4/RRR4-26/2	1132.335	1133.194	-1646.522	0.418	668.020	0.368	15	0.155	R.NTDQLEGSLR.E
R4/RRR4-1/2	1132.988	1133.194	-182.480	0.470	698.680	0.366	15	0.155	R.NTDQLEGSLR.E
R4/RRR4-21/2	1132.917	1133.194	-245.389	0.455	735.506	0.348	16	0.155	R.NTDQLEGSLR.E
R4/RRR4-25/2	921.645	922.014	-401.009	0.426	604.124	0.365	11	0.155	R.CVFPDQR.L
R4/RRR4-2/2	1132.826	1133.194	-326.145	0.445	743.763	0.344	16	0.155	R.NTDQLEGSLR.E
R4/RRR4-25/2	1132.879	1133.194	-278.901	0.472	761.491	0.341	16	0.155	R.NTDQLEGSLR.E
R4/RRR4-25/2	1247.200	1246.509	-248.330	0.385	789.409	0.388	16	0.154	K.GRLGVMLTATAR.C
R4/RRR4-20/2	1312.242	1312.497	-194.781	0.332	975.046	0.318	16	0.154	R.VLVGVVASPEADR.D
R4/RRR4-25/2	1127.244	1126.270	-22.994	0.328	523.817	0.393	14	0.154	K.WM*AAYPQSR.V
R4/RRR4-25/2	1126.856	1126.270	-368.302	0.434	457.588	0.363	13	0.153	K.WM*AAYPQSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	1531.208	1531.733	-999.078	0.357	1294.925	0.206	17	0.153	K.DLYYDVLQFINK.L
R4/RRR4-19/2	1133.000	1133.194	-172.212	0.480	658.500	0.351	15	0.153	R.NTDQLEGSLR.E
R4/RRR4-12/2	1134.211	1133.194	15.263	0.481	636.683	0.352	15	0.153	R.NTDQLEGSLR.E
R4/RRR4-14/2	1133.039	1133.194	-137.627	0.424	757.787	0.323	16	0.153	R.NTDQLEGSLR.E
R4/RRR4-17/2	1132.845	1133.194	-309.063	0.335	685.028	0.353	15	0.153	R.NTDQLEGSLR.E
R4/RRR4-24/2	1132.876	1133.194	-281.820	0.476	783.947	0.323	16	0.153	R.NTDQLEGSLR.E
R4/RRR4-15/2	921.456	922.014	-1695.539	0.399	736.400	0.327	11	0.152	R.CVFPDQR.L
R4/RRR4-18/2	1132.762	1133.194	-382.693	0.385	678.125	0.337	15	0.152	R.NTDQLEGSLR.E
R4/RRR4-25/2	921.907	922.014	-115.757	0.387	523.019	0.359	10	0.152	R.CVFPDQR.L
R4/RRR4-20/2	1132.283	1133.194	-1692.879	0.423	762.630	0.311	16	0.152	R.NTDQLEGSLR.E
R4/RRR4-1/2	1048.949	1049.270	-307.414	0.362	832.442	0.318	14	0.152	R.LGVM*LTATAR.C
R4/RRR4-15/2	1132.337	1133.194	-1645.331	0.355	761.564	0.311	16	0.151	R.NTDQLEGSLR.E
R4/RRR4-13/2	1048.957	1049.270	-299.825	0.348	912.693	0.288	15	0.151	R.LGVM*LTATAR.C
R4/RRR4-14/2	1132.434	1133.194	-1559.453	0.399	766.749	0.303	16	0.151	R.NTDQLEGSLR.E
R4/RRR4-12/2	1133.113	1133.194	-72.137	0.438	626.414	0.326	15	0.151	R.NTDQLEGSLR.E
R4/RRR4-15/2	1133.179	1133.194	-13.140	0.450	670.928	0.325	15	0.151	R.NTDQLEGSLR.E
R4/RRR4-20/2	1133.013	1133.194	-160.755	0.495	731.991	0.316	16	0.151	R.NTDQLEGSLR.E
R4/RRR4-19/2	1132.419	1133.194	-1572.231	0.368	606.211	0.319	15	0.150	R.NTDQLEGSLR.E
R4/RRR4-23/2	1132.930	1133.194	-233.607	0.423	773.398	0.294	16	0.150	R.NTDQLEGSLR.E
R4/RRR4-2/2	1132.790	1133.194	-357.500	0.358	648.421	0.315	15	0.150	R.NTDQLEGSLR.E
R4/RRR4-14/2	1049.022	1049.270	-237.130	0.361	653.934	0.346	13	0.150	R.LGVM*LTATAR.C
R4/RRR4-1/2	1132.394	1133.194	-1594.106	0.337	585.249	0.315	15	0.150	R.NTDQLEGSLR.E
R4/RRR4-26/2	1132.890	1133.194	-269.712	0.374	510.184	0.314	14	0.149	R.NTDQLEGSLR.E
R4/RRR4-15/2	1132.971	1133.194	-197.720	0.351	565.833	0.321	14	0.149	R.NTDQLEGSLR.E
R4/RRR4-25/2	1133.045	1133.194	-132.439	0.439	694.799	0.292	16	0.149	R.NTDQLEGSLR.E
R4/RRR4-24/2	1132.919	1133.194	-243.335	0.459	771.046	0.288	16	0.149	R.NTDQLEGSLR.E
R4/RRR4-1/2	1132.381	1133.194	-1605.801	0.397	796.033	0.276	16	0.149	R.NTDQLEGSLR.E
R4/RRR4-15/2	921.337	922.014	-1825.459	0.297	745.614	0.311	12	0.149	R.CVFPDQR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	921.935	922.014	-85.341	0.401	525.917	0.304	10	0.148	R.CVFPDQR.L
R4/RRR4-28/2	1132.269	1133.194	-1705.227	0.298	704.022	0.295	16	0.148	R.NTDQLEGSLR.E
R4/RRR4-24/2	1132.938	1133.194	-226.905	0.334	821.197	0.264	16	0.148	R.NTDQLEGSLR.E
R4/RRR4-25/2	1133.190	1133.194	-3.848	0.518	673.545	0.313	15	0.148	R.NTDQLEGSLR.E
R4/RRR4-13/2	1264.137	1264.456	-252.557	0.352	898.815	0.272	16	0.148	R.LQAALSTGLFSR.I
R4/RRR4-14/2	1132.199	1133.194	-1767.622	0.288	727.791	0.285	16	0.148	R.NTDQLEGSLR.E
R4/RRR4-25/2	1126.477	1126.270	184.479	0.276	428.136	0.307	13	0.147	K.WM*AAYPQSR.V
R4/RRR4-21/2	1132.858	1133.194	-297.820	0.480	716.247	0.280	16	0.147	R.NTDQLEGSLR.E
R4/RRR4-24/2	1132.758	1133.194	-385.829	0.425	644.889	0.279	15	0.147	R.NTDQLEGSLR.E
R4/RRR4-15/2	921.851	922.014	-177.390	0.325	489.679	0.292	10	0.147	R.CVFPDQR.L
R4/RRR4-24/2	921.937	922.014	-83.216	0.390	410.044	0.326	9	0.146	-.CVFPDQR.-
R4/RRR4-23/2	1132.421	1133.194	-1570.498	0.382	804.680	0.234	16	0.145	R.NTDQLEGSLR.E
R4/RRR4-22/2	1132.338	1133.194	-1644.356	0.348	825.051	0.229	16	0.145	R.NTDQLEGSLR.E
R4/RRR4-23/2	1609.359	1609.806	-278.567	0.383	943.061	0.260	20	0.145	K.LDISGHTVSAVGPDIK.H
R4/RRR4-1/2	1263.750	1264.456	-1354.200	0.304	701.069	0.268	17	0.144	-.LQAALSTGLFSR.-
R4/RRR4-24/2	1033.109	1033.271	-156.865	0.337	794.272	0.242	15	0.144	-.LGVMLTATAR.-
R4/RRR4-24/2	1264.071	1264.456	-305.358	0.278	545.212	0.271	15	0.144	R.LQAALSTGLFSR.I
R4/RRR4-23/2	921.925	922.014	-96.099	0.314	404.902	0.267	9	0.143	-.CVFPDQR.-
R4/RRR4-22/2	1132.413	1133.194	-1577.754	0.322	892.517	0.197	16	0.143	R.NTDQLEGSLR.E
R4/RRR4-17/2	1311.658	1312.497	-1406.110	0.255	614.966	0.313	14	0.143	R.VLVGVVASPEADR.D
R4/RRR4-13/2	1048.801	1049.270	-449.063	0.313	755.512	0.232	14	0.143	R.LGVM*LTATAR.C
R4/RRR4-25/2	1109.205	1110.271	-1868.287	0.260	725.570	0.247	13	0.143	K.WMAAYPQSR.V
R4/RRR4-25/3	1910.720	1911.131	-216.022	0.434	1044.396	0.513	27	0.143	R.REELEKWM*AAYPQSR.V
R4/RRR4-23/2	1132.843	1133.194	-310.901	0.448	729.478	0.236	15	0.143	R.NTDQLEGSLR.E
R4/RRR4-15/3	1608.891	1609.806	-1193.759	0.445	1053.861	0.508	30	0.142	K.LDISGHTVSAVGPDIK.H
R4/RRR4-26/2	1132.202	1133.194	-1764.805	0.332	697.601	0.202	15	0.142	R.NTDQLEGSLR.E
R4/RRR4-26/2	1048.348	1049.270	-1838.589	0.268	784.998	0.195	15	0.141	R.LGVM*LTATAR.C
R4/RRR4-14/2	921.967	922.014	-50.545	0.366	574.654	0.190	10	0.141	R.CVFPDQR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1049.647	1049.270	360.235	0.245	621.197	0.237	13	0.141	-.LGVM*LTATAR.-
R4/RRR4-2/2	1610.540	1609.806	-165.242	0.314	426.649	0.328	15	0.141	K.LDISGHTVSAVGPDIK.H
R4/RRR4-25/2	1247.143	1246.509	-293.893	0.353	473.986	0.320	13	0.140	K.GRLGVMLTATAR.C
R4/RRR4-25/2	1263.388	1264.456	-1641.348	0.233	491.827	0.284	12	0.140	-.LQAALSTGLFSR.-
R4/RRR4-26/2	921.649	922.014	-396.756	0.382	423.297	0.250	9	0.139	-.CVFPDQR.-
R4/RRR4-2/2	1610.028	1609.806	138.510	0.323	385.289	0.310	14	0.139	K.LDISGHTVSAVGPDIK.H
R4/RRR4-24/3	1609.719	1609.806	-54.134	0.478	964.433	0.518	29	0.138	K.LDISGHTVSAVGPDIK.H
R4/RRR4-25/3	1910.537	1911.131	-836.962	0.483	735.407	0.582	21	0.137	R.REELEKWM*AAYPQSR.V
R4/RRR4-1/2	921.933	922.014	-88.130	0.365	418.431	0.295	8	0.137	-.CVFPDQR.-
R4/RRR4-24/3	1611.147	1609.806	212.613	0.490	858.773	0.540	27	0.136	K.LDISGHTVSAVGPDIK.H
R4/RRR4-25/3	1910.602	1911.131	-803.001	0.448	938.581	0.515	26	0.135	R.REELEKWM*AAYPQSR.V
R4/RRR4-23/3	1609.310	1609.806	-308.636	0.415	1155.520	0.437	28	0.134	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/3	1610.190	1609.806	239.125	0.460	929.978	0.498	29	0.130	K.LDISGHTVSAVGPDIK.H
R4/RRR4-23/3	1609.696	1609.806	-68.625	0.419	941.097	0.493	28	0.130	K.LDISGHTVSAVGPDIK.H
R4/RRR4-14/3	1610.866	1609.806	37.303	0.500	892.007	0.479	27	0.124	K.LDISGHTVSAVGPDIK.H
R4/RRR4-24/3	1609.824	1609.806	11.354	0.396	792.486	0.487	26	0.120	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/3	1911.064	1911.131	-35.506	0.447	741.079	0.496	23	0.119	R.REELEKWM*AAYPQSR.V
R4/RRR4-25/3	1910.744	1911.131	-203.236	0.419	720.532	0.499	23	0.118	R.REELEKWM*AAYPQSR.V
R4/RRR4-15/3	1610.910	1609.806	64.891	0.465	854.335	0.459	28	0.118	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/3	1911.195	1911.131	33.492	0.403	749.622	0.497	23	0.117	-.REELEKWM*AAYPQSR.-
R4/RRR4-1/3	1610.090	1609.806	177.202	0.424	767.708	0.444	26	0.111	K.LDISGHTVSAVGPDIK.H
R4/RRR4-15/3	1910.420	1911.131	-898.153	0.393	645.426	0.476	20	0.111	R.REELEKWM*AAYPQSR.V
R4/RRR4-25/2	1262.112	1262.508	-314.953	0.280	112.658	0.398	13	0.095	-.GRLGVM*LTATAR.-
R4/RRR4-24/3	1910.567	1911.131	-821.280	0.371	829.088	0.289	24	0.090	R.REELEKWM*AAYPQSR.V
R4/RRR4-1/2	1649.244	1649.735	-298.630	0.531	4024.227	0.454	25	0.772	R.ALEDDETSATALDGLK.Q
R4/RRR4-1/2	1650.473	1649.735	-159.390	0.521	2167.837	0.468	23	0.309	R.ALEDDETSATALDGLK.Q
R4/RRR4-1/2	1459.271	1458.725	-312.085	0.537	1858.823	0.481	19	0.266	K.VTSLLDQLIQLSK.T
R4/RRR4-1/2	1929.424	1930.237	-942.637	0.499	1499.249	0.497	21	0.221	R.NPEIVLQSIGYLLNTVR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1555.270	1555.758	-314.470	0.518	1256.138	0.514	21	0.206	K.LLDVLNTPSEAVQR.A
R4/RRR4-1/2	1556.247	1555.758	315.042	0.600	1219.820	0.523	21	0.205	K.LLDVLNTPSEAVQR.A
R4/RRR4-1/2	1555.394	1555.758	-234.547	0.521	1135.898	0.487	20	0.190	K.LLDVLNTPSEAVQR.A
R4/RRR4-1/2	1696.432	1696.970	-908.990	0.491	1210.717	0.452	23	0.189	K.SAGLQAIDEIVPTLLR.A
R4/RRR4-2/2	1696.447	1696.970	-899.961	0.488	1063.357	0.472	22	0.181	K.SAGLQAIDEIVPTLLR.A
R4/RRR4-1/2	1696.688	1696.970	-166.666	0.467	1082.818	0.429	22	0.175	K.SAGLQAIDEIVPTLLR.A
R4/RRR4-1/2	1458.261	1458.725	-319.354	0.391	1297.898	0.326	17	0.171	K.VTSLLDQLIQLSK.T
R4/RRR4-1/2	1448.189	1449.634	-1693.226	0.382	947.318	0.458	16	0.165	K.SNDLAQALVGVYAK.E
R4/RRR4-1/2	1449.136	1449.674	-1064.110	0.408	518.350	0.539	16	0.161	R.QSSVELLGDLLFK.V
R4/RRR4-1/2	1696.085	1696.970	-1114.406	0.392	919.380	0.382	20	0.157	K.SAGLQAIDEIVPTLLR.A
R4/RRR4-1/2	1923.198	1924.228	-1058.499	0.390	750.271	0.484	17	0.157	K.ENVPLLFPIFESYLNK.K
R4/RRR4-1/2	1205.177	1205.428	-208.732	0.394	952.711	0.358	16	0.156	R.EGVVIFTGALAK.H
R4/RRR4-1/2	1293.321	1293.580	-200.660	0.451	456.266	0.461	15	0.153	K.EVVVPITGPLIR.I
R4/RRR4-1/2	1069.961	1070.181	-206.617	0.343	888.724	0.323	15	0.151	R.ALADPNVDVR.G
R4/RRR4-1/2	1655.042	1655.851	-1096.848	0.399	851.146	0.366	17	0.149	K.SSDPDTLLSM*FNAIK.A
R4/RRR4-1/2	1457.657	1458.725	-1423.186	0.327	813.922	0.350	16	0.148	K.VTSLLDQLIQLSK.T
R4/RRR4-1/2	857.103	857.033	81.694	0.359	802.361	0.303	13	0.147	-.AIIDVLGR.-
R4/RRR4-1/2	1069.709	1070.181	-442.564	0.292	588.022	0.333	14	0.143	R.ALADPNVDVR.G
R4/RRR4-1/2	1448.452	1449.674	-1538.229	0.266	509.380	0.334	16	0.140	R.QSSVELLGDLLFK.V
R4/RRR4-5/2	1640.057	1639.852	125.597	0.369	363.643	0.350	15	0.140	K.SSDPDTLLSMFNAIK.A
R4/RRR4-1/2	1449.206	1449.674	-323.545	0.231	243.990	0.394	13	0.139	R.QSSVELLGDLLFK.V
R4/RRR4-2/2	857.207	857.033	203.234	0.329	553.632	0.228	10	0.136	-.AIIDVLGR.-
R4/RRR4-1/2	1205.191	1205.428	-197.148	0.231	705.251	0.276	14	0.135	R.EGVVIFTGALAK.H
R4/RRR4-1/3	1030.031	1030.248	-211.371	0.419	1217.438	0.189	21	0.084	R.HTLPHLLAK.A
R4/RRR4-1/3	1030.706	1030.248	445.551	0.463	1134.845	0.200	20	0.083	R.HTLPHLLAK.A
R4/RRR4-6/2	1879.448	1880.002	-829.726	0.526	2720.988	0.439	25	0.405	K.SWEDLTSDKDAIETIR.A
R4/RRR4-6/2	1879.298	1880.002	-909.536	0.517	2419.629	0.439	24	0.344	K.SWEDLTSDKDAIETIR.A
R4/RRR4-6/2	1856.462	1855.901	-237.466	0.619	2188.622	0.555	24	0.342	R.TAWWDGSAVYGNNEER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1879.519	1880.002	-257.939	0.550	2246.184	0.462	24	0.320	K.SWEDLTSDKDAIETIR.A
R4/RRR4-6/2	1633.306	1633.915	-988.350	0.441	1668.811	0.437	21	0.229	R.NSWAGVSILQALFVK.E
R4/RRR4-6/2	1633.828	1633.915	-53.627	0.489	1337.813	0.473	19	0.200	R.NSWAGVSILQALFVK.E
R4/RRR4-6/2	1628.164	1628.720	-958.308	0.506	1079.829	0.557	18	0.198	R.FFTSNFNEETYTK.K
R4/RRR4-6/2	1751.494	1752.050	-890.900	0.466	1337.305	0.447	24	0.196	K.DTFGHIGGPILGGLVGLK.K
R4/RRR4-6/2	1021.956	1022.181	-221.415	0.418	945.320	0.494	14	0.178	R.ANWYGLLGK.K
R4/RRR4-1/2	1456.268	1455.770	343.565	0.421	528.931	0.675	15	0.177	K.VPVPIGLLYLNTR.R
R4/RRR4-6/2	1455.344	1455.770	-293.577	0.367	813.724	0.542	17	0.173	K.VPVPIGLLYLNTR.R
R4/RRR4-1/2	1456.887	1455.770	81.215	0.441	582.094	0.592	16	0.172	K.VPVPIGLLYLNTR.R
R4/RRR4-6/2	1131.060	1131.222	-143.496	0.391	1117.377	0.378	17	0.170	K.ENGVALSGDIR.N
R4/RRR4-6/2	1455.366	1455.770	-278.009	0.412	558.865	0.590	16	0.169	K.VPVPIGLLYLNTR.R
R4/RRR4-6/2	1627.622	1628.720	-1292.774	0.429	698.496	0.505	17	0.165	R.FFTSNFNEETYTK.K
R4/RRR4-1/2	1456.430	1455.770	-234.092	0.451	494.920	0.548	15	0.163	K.VPVPIGLLYLNTR.R
R4/RRR4-6/2	1021.502	1022.181	-1649.158	0.366	949.948	0.379	15	0.162	R.ANWYGLLGK.K
R4/RRR4-6/2	1521.283	1521.700	-274.977	0.386	719.448	0.426	17	0.155	R.SDRIDLAALEVYR.D
R4/RRR4-6/2	1456.046	1455.770	190.157	0.324	758.955	0.373	18	0.152	K.VPVPIGLLYLNTR.R
R4/RRR4-6/2	1454.590	1455.770	-1502.868	0.320	351.432	0.474	13	0.148	K.VPVPIGLLYLNTR.R
R4/RRR4-6/2	1131.060	1131.222	-143.280	0.401	686.401	0.334	15	0.147	K.ENGVALSGDIR.N
R4/RRR4-6/3	1456.640	1455.770	-89.410	0.437	1647.055	0.301	24	0.147	K.VPVPIGLLYLNTR.R
R4/RRR4-6/3	1455.261	1455.770	-1040.038	0.384	1563.658	0.336	25	0.146	K.VPVPIGLLYLNTR.R
R4/RRR4-6/2	1521.253	1521.700	-294.943	0.363	747.884	0.316	16	0.143	R.SDRIDLAALEVYR.D
R4/RRR4-6/2	1130.405	1131.222	-1611.750	0.286	621.977	0.312	15	0.142	K.ENGVALSGDIR.N
R4/RRR4-6/3	1454.689	1454.695	-4.437	0.562	1113.394	0.468	24	0.137	K.VHTIDWTVELLK.T
R4/RRR4-6/3	1522.041	1521.700	224.376	0.511	1303.326	0.398	24	0.136	-.SDRIDLAALEVYR.-
R4/RRR4-6/2	1274.143	1274.409	-209.350	0.292	814.603	0.163	13	0.133	-.TTEGLRDVINR.-
R4/RRR4-6/2	1274.098	1274.409	-245.105	0.349	601.137	0.156	13	0.131	-.TTEGLRDVINR.-
R4/RRR4-6/2	1273.953	1274.409	-359.405	0.298	540.597	0.175	12	0.131	-.TTEGLRDVINR.-
R4/RRR4-6/3	1455.126	1454.695	297.211	0.535	1129.051	0.438	23	0.130	K.VHTIDWTVELLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1455.532	1455.770	-163.502	0.382	1594.826	0.248	25	0.125	K.VPVPIGLLYLNTR.R
R4/RRR4-6/3	1521.108	1521.700	-1049.548	0.472	1109.454	0.396	22	0.118	-.SDRIDLAALEVYR.-
R4/RRR4-6/3	1881.775	1880.002	-121.197	0.512	852.376	0.472	28	0.118	K.SWEDLTSDKDAIETIR.A
R4/RRR4-6/3	1881.052	1880.002	26.607	0.522	980.802	0.431	30	0.117	K.SWEDLTSDKDAIETIR.A
R4/RRR4-6/3	1521.724	1521.700	15.873	0.500	1172.872	0.353	23	0.111	-.SDRIDLAALEVYR.-
R4/RRR4-6/3	1994.714	1993.381	167.126	0.409	818.402	0.454	30	0.108	K.IKDTFGHIGGPILGGLVGLK.K
R4/RRR4-6/3	1454.220	1454.695	-327.491	0.402	800.306	0.280	20	0.077	-.VHTIDWTVELLK.-
R4/RRR4-8/2	1967.653	1968.196	-786.495	0.568	3544.459	0.539	27	0.660	K.EYVFVANSDNLGAIVDIK.I
R4/RRR4-8/2	1967.637	1968.196	-794.591	0.567	3141.142	0.562	26	0.555	K.EYVFVANSDNLGAIVDIK.I
R4/RRR4-8/2	1967.531	1968.196	-848.648	0.563	3153.013	0.514	26	0.537	K.EYVFVANSDNLGAIVDIK.I
R4/RRR4-8/2	1476.251	1476.704	-307.997	0.516	2138.658	0.338	18	0.264	K.IFNTNNLWVNLK.A
R4/RRR4-8/2	1359.266	1359.592	-240.737	0.491	2025.769	0.377	20	0.261	R.IVTEDFLPLPSK.G
R4/RRR4-8/2	1359.272	1359.592	-236.322	0.506	1906.515	0.381	20	0.246	R.IVTEDFLPLPSK.G
R4/RRR4-8/2	1452.298	1452.636	-233.493	0.557	1763.222	0.444	22	0.244	K.VSGDVWFGSGVTLK.G
R4/RRR4-8/2	1451.993	1452.636	-1135.209	0.515	1727.597	0.432	22	0.237	K.VSGDVWFGSGVTLK.G
R4/RRR4-7/2	1477.576	1476.704	-86.974	0.461	1975.696	0.279	19	0.228	K.IFNTNNLWVNLK.A
R4/RRR4-8/2	1476.624	1476.704	-54.195	0.535	1781.272	0.343	19	0.219	K.IFNTNNLWVNLK.A
R4/RRR4-7/2	1360.046	1359.592	334.654	0.463	1662.681	0.389	19	0.219	R.IVTEDFLPLPSK.G
R4/RRR4-8/2	1477.304	1476.704	-271.892	0.547	1459.010	0.409	18	0.201	K.IFNTNNLWVNLK.A
R4/RRR4-2/2	1477.380	1476.704	-220.247	0.403	1533.480	0.273	17	0.181	K.IFNTNNLWVNLK.A
R4/RRR4-8/2	1477.872	1476.704	114.029	0.527	1217.783	0.381	17	0.175	K.IFNTNNLWVNLK.A
R4/RRR4-8/2	1631.460	1630.780	-196.519	0.510	613.181	0.565	20	0.172	R.TNPSNPSIELGPEFK.K
R4/RRR4-8/2	1632.388	1630.780	-240.885	0.492	613.544	0.557	20	0.171	R.TNPSNPSIELGPEFK.K
R4/RRR4-8/2	958.873	959.122	-260.370	0.416	741.343	0.440	15	0.163	K.LDTLLAQGK.E
R4/RRR4-8/2	1758.351	1758.953	-913.607	0.458	546.164	0.520	19	0.161	R.TNPSNPSIELGPEFKK.V
R4/RRR4-8/2	790.928	790.933	-5.899	0.463	749.611	0.385	11	0.158	K.VANFLAR.F
R4/RRR4-8/2	959.229	959.122	111.544	0.460	590.855	0.403	15	0.158	K.LDTLLAQGK.E
R4/RRR4-8/2	1758.377	1758.953	-898.762	0.445	484.723	0.500	18	0.156	R.TNPSNPSIELGPEFKK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1758.378	1758.953	-898.553	0.454	350.164	0.546	16	0.156	R.TNPSNPSIELGPEFKK.V
R4/RRR4-7/2	1360.480	1359.592	-82.850	0.293	970.120	0.350	16	0.155	R.IVTEDFLPLPSK.G
R4/RRR4-8/2	1478.142	1476.704	296.734	0.448	1077.791	0.296	16	0.154	K.IFNTNNLWVNLK.A
R4/RRR4-8/2	790.844	790.933	-112.879	0.460	743.390	0.340	11	0.153	K.VANFLAR.F
R4/RRR4-8/2	957.921	958.157	-247.793	0.374	1058.497	0.259	12	0.150	K.M*EIIPNPK.E
R4/RRR4-5/2	1359.053	1359.592	-1135.904	0.342	805.506	0.330	15	0.148	R.IVTEDFLPLPSK.G
R4/RRR4-8/2	1477.874	1476.704	115.354	0.494	806.621	0.309	17	0.147	K.IFNTNNLWVNLK.A
R4/RRR4-8/2	1359.693	1359.592	74.594	0.403	867.866	0.277	15	0.144	-.IVTEDFLPLPSK.-
R4/RRR4-8/2	1359.600	1359.592	5.618	0.330	758.997	0.245	15	0.140	R.IVTEDFLPLPSK.G
R4/RRR4-1/2	1476.118	1476.704	-1077.920	0.309	1225.958	0.098	17	0.139	K.IFNTNNLWVNLK.A
R4/RRR4-8/2	1358.958	1359.592	-1206.529	0.290	615.976	0.252	13	0.137	R.IVTEDFLPLPSK.G
R4/RRR4-8/3	1813.029	1812.164	-74.766	0.491	1309.137	0.389	28	0.135	R.LVEAEALKM*EIIPNPK.E
R4/RRR4-8/2	958.031	958.157	-132.106	0.328	791.947	0.132	11	0.129	-.M*EIIPNPK.-
R4/RRR4-8/3	1811.946	1812.164	-120.894	0.391	1348.997	0.238	28	0.100	R.LVEAEALKM*EIIPNPK.E
R4/RRR4-8/3	1571.021	1570.769	160.917	0.404	1030.742	0.273	25	0.088	-.SGKLEIPDGAVLENK.-
R4/RRR4-18/2	1901.759	1902.048	-152.557	0.504	2007.800	0.564	27	0.385	K.FLDGIYVSDKGTITEDQ.-
R4/RRR4-18/2	1901.288	1902.048	-928.639	0.496	1870.779	0.539	26	0.322	K.FLDGIYVSDKGTITEDQ.-
R4/RRR4-18/2	1900.705	1902.048	-1236.383	0.434	1634.197	0.515	25	0.243	K.FLDGIYVSDKGTITEDQ.-
R4/RRR4-11/2	1593.048	1593.752	-1072.660	0.417	1630.240	0.458	21	0.231	K.YVFTIDDDCFVAK.D
R4/RRR4-10/2	1593.271	1593.752	-302.743	0.432	1623.423	0.456	21	0.230	K.YVFTIDDDCFVAK.D
R4/RRR4-11/2	1593.177	1593.752	-991.727	0.429	1599.445	0.466	21	0.229	K.YVFTIDDDCFVAK.D
R4/RRR4-10/2	1593.788	1593.752	22.462	0.427	1569.710	0.480	21	0.229	K.YVFTIDDDCFVAK.D
R4/RRR4-10/2	1593.186	1593.752	-985.726	0.419	1593.083	0.468	21	0.229	K.YVFTIDDDCFVAK.D
R4/RRR4-10/2	1239.156	1239.397	-194.808	0.501	1592.311	0.436	17	0.224	K.CYLSLAEQVR.E
R4/RRR4-10/2	1239.035	1239.397	-292.951	0.504	1546.656	0.424	17	0.216	K.CYLSLAEQVR.E
R4/RRR4-11/2	1502.304	1502.609	-203.961	0.519	1146.049	0.576	19	0.211	R.VPEGFDYELYNR.N
R4/RRR4-10/2	1181.194	1181.324	-109.834	0.470	1529.145	0.396	15	0.206	K.DINALEQHIK.N
R4/RRR4-10/2	1503.217	1502.609	-261.259	0.545	1068.067	0.564	19	0.203	R.VPEGFDYELYNR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1502.090	1502.609	-1014.533	0.518	1122.494	0.544	19	0.202	R.VPEGFDYELYNR.N
R4/RRR4-11/2	1181.137	1181.324	-158.456	0.471	1488.620	0.390	15	0.201	K.DINALEQHIK.N
R4/RRR4-10/2	1123.910	1123.348	-390.064	0.568	938.036	0.582	17	0.199	R.YVDAVMTVPK.G
R4/RRR4-10/2	1502.415	1502.609	-129.624	0.470	1069.458	0.553	19	0.199	R.VPEGFDYELYNR.N
R4/RRR4-10/2	1502.405	1502.609	-136.470	0.511	1021.481	0.569	18	0.198	R.VPEGFDYELYNR.N
R4/RRR4-11/2	1180.612	1181.324	-1454.333	0.510	1423.349	0.395	15	0.196	K.DINALEQHIK.N
R4/RRR4-11/2	1502.087	1502.609	-1016.083	0.525	1039.948	0.523	18	0.191	R.VPEGFDYELYNR.N
R4/RRR4-11/2	1180.553	1181.324	-1504.186	0.485	1393.309	0.374	15	0.189	K.DINALEQHIK.N
R4/RRR4-11/2	1138.922	1139.347	-374.284	0.547	870.528	0.550	16	0.188	R.YVDAVM*TVPK.G
R4/RRR4-9/2	1503.956	1502.609	231.561	0.480	958.319	0.536	18	0.188	R.VPEGFDYELYNR.N
R4/RRR4-10/2	1138.992	1139.347	-312.988	0.511	873.574	0.545	16	0.187	R.YVDAVM*TVPK.G
R4/RRR4-10/2	1122.949	1123.348	-356.272	0.490	934.452	0.524	16	0.186	R.YVDAVMTVPK.G
R4/RRR4-11/2	1138.532	1139.347	-1599.281	0.474	827.036	0.553	16	0.184	R.YVDAVM*TVPK.G
R4/RRR4-10/2	1180.534	1181.324	-1520.286	0.463	1383.223	0.352	15	0.184	K.DINALEQHIK.N
R4/RRR4-10/2	1181.223	1181.324	-85.576	0.481	1248.585	0.384	15	0.180	K.DINALEQHIK.N
R4/RRR4-11/2	1138.530	1139.347	-1600.466	0.450	822.061	0.523	16	0.179	R.YVDAVM*TVPK.G
R4/RRR4-10/2	1138.419	1139.347	-1698.169	0.417	853.861	0.512	16	0.177	R.YVDAVM*TVPK.G
R4/RRR4-10/2	1503.252	1502.609	-238.447	0.404	736.912	0.571	16	0.176	R.VPEGFDYELYNR.N
R4/RRR4-11/2	1122.788	1123.348	-1392.704	0.323	995.876	0.457	16	0.173	R.YVDAVMTVPK.G
R4/RRR4-11/2	1240.928	1241.456	-1234.758	0.442	788.826	0.493	15	0.169	K.VICDHLSLGVK.T
R4/RRR4-10/2	1242.119	1241.456	-271.918	0.463	965.688	0.409	17	0.168	K.VICDHLSLGVK.T
R4/RRR4-11/2	1122.907	1123.348	-393.139	0.394	742.623	0.479	15	0.167	R.YVDAVMTVPK.G
R4/RRR4-11/2	1238.580	1239.397	-1470.884	0.371	698.933	0.508	14	0.165	K.CYLSLAEQVR.E
R4/RRR4-10/2	1138.490	1139.347	-1636.012	0.429	827.165	0.409	16	0.164	R.YVDAVM*TVPK.G
R4/RRR4-10/2	1241.263	1241.456	-155.909	0.415	821.197	0.421	16	0.162	K.VICDHLSLGVK.T
R4/RRR4-11/2	1239.195	1239.397	-162.789	0.368	814.028	0.415	15	0.160	K.CYLSLAEQVR.E
R4/RRR4-10/2	1730.380	1731.026	-954.343	0.449	608.303	0.476	19	0.159	K.GTLFPMCGMNLAFDR.D
R4/RRR4-11/2	1118.068	1118.311	-217.658	0.407	612.822	0.433	14	0.157	K.ASNPFVNLKK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1007.921	1008.167	-245.026	0.387	413.503	0.451	11	0.156	R.CFGYM*VSK.K
R4/RRR4-11/2	989.812	990.138	-329.975	0.385	530.554	0.415	14	0.156	K.ASNPFVNLK.K
R4/RRR4-10/2	1117.661	1118.311	-1480.486	0.397	673.650	0.392	15	0.155	K.ASNPFVNLKK.E
R4/RRR4-10/2	1118.968	1118.311	-306.987	0.405	524.811	0.423	13	0.154	K.ASNPFVNLKK.E
R4/RRR4-10/2	991.795	992.167	-376.905	0.392	453.660	0.451	11	0.153	-.CFGYMVSK.-
R4/RRR4-10/2	1731.166	1731.026	80.937	0.420	631.490	0.412	19	0.153	K.GTLFPMCGMNLAFDR.D
R4/RRR4-10/2	989.496	990.138	-1664.328	0.337	561.597	0.402	14	0.153	K.ASNPFVNLK.K
R4/RRR4-10/2	1118.023	1118.311	-258.295	0.349	669.144	0.375	15	0.152	K.ASNPFVNLKK.E
R4/RRR4-11/2	1118.086	1118.311	-201.557	0.359	548.479	0.418	13	0.152	K.ASNPFVNLKK.E
R4/RRR4-1/2	1139.153	1139.347	-170.747	0.329	503.306	0.413	13	0.152	R.YVDAVM*TVPK.G
R4/RRR4-11/2	992.390	992.167	225.146	0.371	579.433	0.344	13	0.151	R.CFGYMVSK.K
R4/RRR4-10/2	1240.358	1241.456	-1695.908	0.328	570.626	0.413	14	0.150	K.VICDHLSLGVK.T
R4/RRR4-10/2	991.605	992.167	-1580.469	0.317	436.739	0.356	12	0.149	R.CFGYMVSK.K
R4/RRR4-11/2	1118.065	1118.311	-220.286	0.369	593.550	0.341	14	0.148	K.ASNPFVNLKK.E
R4/RRR4-10/2	1007.356	1008.167	-1803.094	0.298	453.553	0.348	12	0.148	R.CFGYM*VSK.K
R4/RRR4-10/2	1007.534	1008.167	-1624.990	0.342	468.600	0.307	12	0.147	R.CFGYM*VSK.K
R4/RRR4-10/2	1479.807	1479.656	102.715	0.361	879.961	0.281	17	0.147	R.YDDM*WAGWCMK.V
R4/RRR4-10/2	990.055	990.138	-83.550	0.376	451.161	0.343	13	0.146	-.ASNPFVNLK.-
R4/RRR4-11/2	1592.481	1593.752	-1430.323	0.238	857.100	0.308	17	0.145	K.YVFTIDDDCFVAK.D
R4/RRR4-1/2	1138.981	1139.347	-322.021	0.278	697.244	0.284	14	0.144	R.YVDAVM*TVPK.G
R4/RRR4-1/2	1138.382	1139.347	-1731.675	0.216	372.546	0.389	12	0.144	R.YVDAVM*TVPK.G
R4/RRR4-10/2	1747.780	1747.026	-140.935	0.377	535.443	0.380	16	0.143	-.GTLFPMCGM*NLAFDR.-
R4/RRR4-11/2	1732.145	1731.026	68.380	0.395	534.073	0.338	17	0.143	K.GTLFPMCGMNLAFDR.D
R4/RRR4-11/2	989.851	990.138	-290.628	0.417	450.328	0.372	13	0.142	-.ASNPFVNLK.-
R4/RRR4-11/2	1731.835	1731.026	-111.038	0.366	388.731	0.325	15	0.140	K.GTLFPMCGMNLAFDR.D
R4/RRR4-10/2	989.561	990.138	-1598.643	0.255	489.415	0.273	13	0.137	-.ASNPFVNLK.-
R4/RRR4-10/2	1479.859	1479.656	137.543	0.315	683.358	0.226	15	0.137	R.YDDM*WAGWCMK.V
R4/RRR4-10/2	1502.225	1502.609	-256.134	0.174	59.755	0.477	10	0.083	-.VPEGFDYELYNR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1499.196	1499.734	-1029.395	0.493	2429.006	0.593	22	0.397	R.VPTVDVSVVDLTVR.I
R4/RRR4-10/2	1499.415	1499.734	-213.744	0.517	2321.542	0.646	22	0.394	R.VPTVDVSVVDLTVR.I
R4/RRR4-10/2	1499.310	1499.734	-283.907	0.518	2266.153	0.662	23	0.389	R.VPTVDVSVVDLTVR.I
R4/RRR4-1/2	1499.276	1499.734	-306.942	0.512	2255.217	0.663	23	0.387	R.VPTVDVSVVDLTVR.I
R4/RRR4-1/2	1499.338	1499.734	-264.956	0.490	2313.595	0.631	22	0.387	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1500.070	1499.734	224.080	0.521	2220.938	0.656	22	0.378	R.VPTVDVSVVDLTVR.I
R4/RRR4-1/2	1499.486	1499.734	-165.804	0.517	2244.367	0.622	22	0.371	R.VPTVDVSVVDLTVR.I
R4/RRR4-13/2	1500.497	1499.734	-159.001	0.543	2145.790	0.661	22	0.366	R.VPTVDVSVVDLTVR.I
R4/RRR4-12/2	1500.339	1499.734	-264.535	0.526	2156.074	0.656	22	0.366	R.VPTVDVSVVDLTVR.I
R4/RRR4-3/2	1499.403	1499.734	-221.340	0.502	2145.615	0.658	22	0.364	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1499.430	1499.734	-203.535	0.494	2173.623	0.632	21	0.360	R.VPTVDVSVVDLTVR.I
R4/RRR4-2/2	1499.227	1499.734	-1008.140	0.500	2175.440	0.622	21	0.357	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1499.559	1499.734	-117.297	0.504	1991.240	0.652	21	0.334	R.VPTVDVSVVDLTVR.I
R4/RRR4-13/2	1499.210	1499.734	-1020.075	0.472	2117.056	0.576	22	0.332	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1499.775	1499.734	27.135	0.455	2098.962	0.539	21	0.317	R.VPTVDVSVVDLTVR.I
R4/RRR4-16/2	1499.638	1499.734	-64.385	0.519	1865.580	0.616	21	0.303	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1757.522	1757.017	-282.392	0.567	1751.614	0.625	21	0.291	K.TLLFGEKEVTVFGCR.N
R4/RRR4-12/2	1499.108	1499.734	-1088.178	0.457	1891.994	0.543	20	0.285	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/3	1499.567	1499.734	-112.243	0.426	2345.176	0.328	30	0.278	R.VPTVDVSVVDLTVR.I
R4/RRR4-15/2	1498.974	1499.734	-1178.206	0.451	1706.634	0.592	20	0.272	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1762.462	1762.859	-225.956	0.533	1652.107	0.578	20	0.263	K.LVSWYDNEWGYSSR.V
R4/RRR4-11/2	1757.498	1757.017	274.299	0.586	1598.254	0.595	21	0.261	K.TLLFGEKEVTVFGCR.N
R4/RRR4-11/2	1762.320	1762.859	-876.118	0.506	1641.630	0.556	19	0.255	K.LVSWYDNEWGYSSR.V
R4/RRR4-25/2	1499.148	1499.734	-1061.198	0.476	1697.234	0.519	20	0.252	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1762.340	1762.859	-864.714	0.531	1585.409	0.570	19	0.251	K.LVSWYDNEWGYSSR.V
R4/RRR4-11/2	1756.541	1757.017	-271.815	0.574	1453.244	0.613	20	0.247	K.TLLFGEKEVTVFGCR.N
R4/RRR4-16/2	1499.481	1499.734	-169.234	0.508	1426.014	0.584	19	0.235	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1762.533	1762.859	-185.448	0.525	1447.849	0.536	19	0.227	K.LVSWYDNEWGYSSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1499.508	1499.734	-151.186	0.449	1275.049	0.584	20	0.219	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1762.095	1762.859	-1003.801	0.487	1387.977	0.534	18	0.219	K.LVSWYDNEWGYSSR.V
R4/RRR4-11/2	1763.233	1762.859	212.718	0.534	1157.289	0.591	17	0.209	K.LVSWYDNEWGYSSR.V
R4/RRR4-11/3	1499.778	1499.734	29.208	0.446	2022.379	0.317	29	0.207	R.VPTVDVSVVDLTVR.I
R4/RRR4-2/2	1499.094	1499.734	-1097.499	0.440	1155.945	0.573	18	0.204	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/3	1499.621	1499.734	-75.989	0.436	1866.722	0.371	27	0.204	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1499.489	1499.734	-164.334	0.470	1073.079	0.571	19	0.199	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1162.565	1162.320	210.989	0.436	1370.052	0.409	17	0.194	K.AGIALNDNFVK.-
R4/RRR4-9/2	1162.289	1162.320	-26.821	0.452	1398.301	0.390	16	0.192	K.AGIALNDNFVK.-
R4/RRR4-11/2	1162.469	1162.320	128.221	0.417	1319.353	0.401	17	0.189	K.AGIALNDNFVK.-
R4/RRR4-10/2	1162.152	1162.320	-145.241	0.471	1217.344	0.443	16	0.188	K.AGIALNDNFVK.-
R4/RRR4-10/2	1162.144	1162.320	-152.195	0.468	1182.072	0.454	16	0.188	K.AGIALNDNFVK.-
R4/RRR4-11/2	1162.140	1162.320	-155.567	0.432	1288.581	0.396	17	0.186	K.AGIALNDNFVK.-
R4/RRR4-10/2	1162.089	1162.320	-200.036	0.441	1334.548	0.379	16	0.185	K.AGIALNDNFVK.-
R4/RRR4-11/2	1162.390	1162.320	60.291	0.497	1300.298	0.390	17	0.185	K.AGIALNDNFVK.-
R4/RRR4-11/2	1162.092	1162.320	-196.980	0.460	1182.057	0.407	17	0.180	K.AGIALNDNFVK.-
R4/RRR4-11/2	1161.687	1162.320	-1410.044	0.427	1134.012	0.425	16	0.179	K.AGIALNDNFVK.-
R4/RRR4-10/2	1133.987	1134.226	-210.607	0.436	1100.691	0.423	14	0.178	K.YDTVHGQWK.H
R4/RRR4-11/2	1435.292	1435.607	-220.393	0.460	1067.694	0.442	22	0.178	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	1307.249	1306.513	-202.549	0.453	1149.411	0.410	18	0.178	K.DAPMFVVGVNEK.E
R4/RRR4-11/2	1435.241	1435.607	-256.145	0.467	864.844	0.506	22	0.177	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	928.994	929.139	-157.048	0.425	1035.585	0.430	15	0.176	K.KVVISAPSK.D
R4/RRR4-11/2	1161.738	1162.320	-1366.140	0.457	1122.269	0.406	16	0.176	K.AGIALNDNFVK.-
R4/RRR4-2/2	1162.147	1162.320	-149.877	0.427	1298.373	0.335	16	0.175	K.AGIALNDNFVK.-
R4/RRR4-10/2	1133.945	1134.226	-247.974	0.434	907.506	0.472	14	0.175	K.YDTVHGQWK.H
R4/RRR4-11/2	1133.991	1134.226	-207.907	0.423	1023.644	0.427	14	0.174	K.YDTVHGQWK.H
R4/RRR4-11/2	1133.936	1134.226	-256.074	0.428	910.263	0.462	14	0.173	K.YDTVHGQWK.H
R4/RRR4-12/2	1162.135	1162.320	-159.571	0.436	1112.863	0.394	16	0.173	K.AGIALNDNFVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1435.126	1435.607	-336.275	0.426	760.500	0.499	20	0.169	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	1161.887	1162.320	-373.943	0.382	1113.730	0.367	15	0.168	K.AGIALNDNFVK.-
R4/RRR4-11/2	1307.093	1306.513	-321.910	0.368	1170.609	0.347	18	0.168	K.DAPMFVVGVNEK.E
R4/RRR4-11/2	833.824	833.958	-161.023	0.420	952.559	0.384	13	0.166	K.IGINGFGR.I
R4/RRR4-10/2	1435.069	1435.607	-1074.882	0.437	730.957	0.469	20	0.165	R.AASFNIIPSSTGAAK.A
R4/RRR4-2/2	1435.426	1435.607	-126.632	0.440	735.843	0.476	19	0.165	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	1162.582	1162.320	225.519	0.397	908.169	0.399	15	0.163	K.AGIALNDNFVK.-
R4/RRR4-11/2	1133.886	1134.226	-300.033	0.388	855.139	0.410	13	0.162	K.YDTVHGQWK.H
R4/RRR4-17/2	1162.088	1162.320	-200.668	0.419	902.473	0.392	14	0.160	K.AGIALNDNFVK.-
R4/RRR4-27/2	833.544	833.958	-497.889	0.389	946.968	0.347	13	0.160	K.IGINGFGR.I
R4/RRR4-10/2	833.956	833.958	-2.292	0.402	774.229	0.397	12	0.160	K.IGINGFGR.I
R4/RRR4-11/2	928.223	929.139	-2070.053	0.388	886.653	0.373	15	0.160	K.KVVISAPSK.D
R4/RRR4-27/2	833.728	833.958	-276.322	0.429	851.541	0.373	12	0.160	K.IGINGFGR.I
R4/RRR4-9/2	1162.167	1162.320	-132.386	0.382	999.280	0.346	15	0.160	K.AGIALNDNFVK.-
R4/RRR4-11/2	833.481	833.958	-574.460	0.374	776.102	0.394	12	0.159	K.IGINGFGR.I
R4/RRR4-11/2	1435.152	1435.607	-318.268	0.436	564.172	0.464	19	0.159	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	833.540	833.958	-502.885	0.391	753.233	0.394	12	0.159	K.IGINGFGR.I
R4/RRR4-10/2	833.869	833.958	-106.835	0.450	770.690	0.381	12	0.159	K.IGINGFGR.I
R4/RRR4-10/2	1435.331	1435.607	-192.664	0.422	649.295	0.446	19	0.159	R.AASFNIIPSSTGAAK.A
R4/RRR4-1/2	1162.130	1162.320	-163.997	0.340	1078.568	0.309	15	0.158	K.AGIALNDNFVK.-
R4/RRR4-11/2	1435.423	1435.607	-128.764	0.446	526.157	0.472	18	0.158	R.AASFNIIPSSTGAAK.A
R4/RRR4-10/2	1133.906	1134.226	-282.535	0.410	777.641	0.379	14	0.158	K.YDTVHGQWK.H
R4/RRR4-11/2	1435.074	1435.607	-1071.722	0.401	755.673	0.406	19	0.157	R.AASFNIIPSSTGAAK.A
R4/RRR4-15/2	1435.427	1435.607	-125.608	0.405	616.302	0.419	20	0.156	R.AASFNIIPSSTGAAK.A
R4/RRR4-10/2	1435.341	1435.607	-186.350	0.403	681.701	0.401	20	0.155	R.AASFNIIPSSTGAAK.A
R4/RRR4-10/2	833.841	833.958	-141.198	0.413	769.335	0.350	12	0.155	K.IGINGFGR.I
R4/RRR4-15/2	1435.402	1435.607	-143.608	0.458	546.932	0.425	19	0.155	R.AASFNIIPSSTGAAK.A
R4/RRR4-26/2	834.012	833.958	65.238	0.347	904.752	0.323	12	0.155	K.IGINGFGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1162.146	1162.320	-150.720	0.434	1062.483	0.304	14	0.155	K.AGIALNDNFVK.-
R4/RRR4-2/2	1436.084	1435.607	332.792	0.448	556.922	0.460	18	0.154	-.AASFNIIPSSTGAAK.-
R4/RRR4-5/2	1161.759	1162.320	-1348.200	0.405	778.745	0.372	14	0.154	K.AGIALNDNFVK.-
R4/RRR4-11/2	928.542	929.139	-1725.191	0.326	627.038	0.447	12	0.154	K.KVVISAPSK.D
R4/RRR4-12/2	1161.583	1162.320	-1499.976	0.341	1038.802	0.284	15	0.154	K.AGIALNDNFVK.-
R4/RRR4-9/2	1162.259	1162.320	-52.841	0.336	872.658	0.341	14	0.153	K.AGIALNDNFVK.-
R4/RRR4-1/2	1161.780	1162.320	-1330.154	0.361	1021.639	0.295	14	0.153	K.AGIALNDNFVK.-
R4/RRR4-27/2	833.989	833.958	37.200	0.391	621.707	0.346	11	0.151	K.IGINGFGR.I
R4/RRR4-11/2	1435.184	1435.607	-295.568	0.416	520.748	0.395	18	0.151	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	1161.536	1162.320	-1540.513	0.338	927.011	0.294	15	0.151	K.AGIALNDNFVK.-
R4/RRR4-9/2	834.186	833.958	274.524	0.363	781.060	0.308	12	0.151	K.IGINGFGR.I
R4/RRR4-7/2	1498.720	1499.734	-1348.165	0.294	919.500	0.293	20	0.150	R.VPTVDVSVVDLTVR.I
R4/RRR4-11/2	1499.201	1499.734	-1026.125	0.347	471.645	0.408	16	0.150	R.VPTVDVSVVDLTVR.I
R4/RRR4-16/2	1161.427	1162.320	-1634.691	0.331	881.816	0.306	14	0.150	K.AGIALNDNFVK.-
R4/RRR4-1/2	833.913	833.958	-53.533	0.317	722.651	0.330	11	0.150	K.IGINGFGR.I
R4/RRR4-18/2	1435.350	1435.607	-179.610	0.391	424.526	0.408	16	0.149	R.AASFNIIPSSTGAAK.A
R4/RRR4-17/2	1435.404	1435.607	-141.817	0.414	360.149	0.398	16	0.149	R.AASFNIIPSSTGAAK.A
R4/RRR4-2/2	833.860	833.958	-117.554	0.356	689.837	0.316	11	0.149	K.IGINGFGR.I
R4/RRR4-9/2	1435.167	1435.607	-307.601	0.325	501.645	0.397	17	0.149	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	1134.820	1134.226	-358.479	0.373	809.652	0.301	13	0.149	K.YDTVHGQWK.H
R4/RRR4-28/2	833.622	833.958	-404.431	0.288	497.372	0.371	10	0.149	K.IGINGFGR.I
R4/RRR4-15/2	1162.050	1162.320	-233.548	0.410	744.015	0.325	14	0.149	K.AGIALNDNFVK.-
R4/RRR4-11/2	1434.706	1435.607	-1328.952	0.352	416.991	0.373	17	0.148	R.AASFNIIPSSTGAAK.A
R4/RRR4-9/2	834.140	833.958	219.349	0.282	549.417	0.352	10	0.148	K.IGINGFGR.I
R4/RRR4-11/2	1134.646	1134.226	371.351	0.373	955.526	0.256	13	0.148	K.YDTVHGQWK.H
R4/RRR4-9/2	1435.176	1435.607	-301.371	0.329	302.656	0.442	13	0.147	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	834.391	833.958	520.682	0.325	634.340	0.274	12	0.147	K.IGINGFGR.I
R4/RRR4-23/2	833.536	833.958	-508.029	0.293	724.170	0.292	11	0.146	K.IGINGFGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1435.127	1435.607	-335.507	0.307	334.090	0.338	16	0.146	R.AASFNIIPSSTGAAK.A
R4/RRR4-11/2	1762.549	1762.859	-176.416	0.319	408.926	0.408	15	0.146	K.LVSWYDNEWGYSSR.V
R4/RRR4-1/2	834.031	833.958	87.844	0.379	825.088	0.243	12	0.145	K.IGINGFGR.I
R4/RRR4-28/2	833.857	833.958	-121.226	0.315	451.172	0.304	9	0.145	K.IGINGFGR.I
R4/RRR4-3/2	1435.487	1435.607	-83.639	0.375	384.887	0.326	16	0.145	R.AASFNIIPSSTGAAK.A
R4/RRR4-2/2	1161.605	1162.320	-1481.503	0.269	855.104	0.243	14	0.143	K.AGIALNDNFVK.-
R4/RRR4-16/2	1162.276	1162.320	-38.409	0.364	576.448	0.327	12	0.143	-.AGIALNDNFVK.-
R4/RRR4-23/2	833.881	833.958	-92.150	0.297	705.308	0.240	11	0.143	K.IGINGFGR.I
R4/RRR4-11/2	1322.343	1322.512	-128.596	0.364	681.495	0.276	17	0.143	K.DAPM*FVVGVNEK.E
R4/RRR4-1/2	833.586	833.958	-447.190	0.336	731.733	0.232	11	0.143	K.IGINGFGR.I
R4/RRR4-11/3	1304.103	1303.487	-295.573	0.562	1208.525	0.443	27	0.142	K.AAIKEESEGKLK.G
R4/RRR4-9/2	1435.278	1435.607	-230.035	0.347	407.774	0.389	15	0.141	-.AASFNIIPSSTGAAK.-
R4/RRR4-13/2	1435.148	1435.607	-321.170	0.261	320.823	0.355	13	0.141	-.AASFNIIPSSTGAAK.-
R4/RRR4-11/2	928.530	929.139	-1738.267	0.325	549.182	0.249	12	0.141	K.KVVISAPSK.D
R4/RRR4-3/2	1162.347	1162.320	23.004	0.373	766.797	0.271	13	0.140	-.AGIALNDNFVK.-
R4/RRR4-18/2	1434.697	1435.607	-1335.532	0.329	259.498	0.413	14	0.139	-.AASFNIIPSSTGAAK.-
R4/RRR4-10/2	834.712	833.958	-294.918	0.238	719.667	0.167	11	0.139	K.IGINGFGR.I
R4/RRR4-10/2	834.464	833.958	-593.885	0.262	850.849	0.110	12	0.136	K.IGINGFGR.I
R4/RRR4-11/2	1321.674	1322.512	-1394.922	0.234	624.521	0.168	18	0.136	K.DAPM*FVVGVNEK.E
R4/RRR4-11/2	834.445	833.958	585.356	0.247	748.715	0.051	12	0.135	K.IGINGFGR.I
R4/RRR4-11/3	1292.729	1292.463	206.403	0.561	1174.062	0.416	24	0.126	R.LEKPASYDQIK.A
R4/RRR4-11/3	1292.288	1292.463	-136.026	0.527	1123.871	0.410	25	0.121	R.LEKPASYDQIK.A
R4/RRR4-12/3	1292.413	1292.463	-38.246	0.479	1004.645	0.416	23	0.117	R.LEKPASYDQIK.A
R4/RRR4-17/2	1435.293	1435.607	-219.881	0.319	240.808	0.371	12	0.114	-.AASFNIIPSSTGAAK.-
R4/RRR4-11/3	1292.719	1292.463	198.449	0.518	951.709	0.405	23	0.112	R.LEKPASYDQIK.A
R4/RRR4-11/3	1763.569	1762.859	-165.005	0.477	834.935	0.460	25	0.112	-.LVSWYDNEWGYSSR.-
R4/RRR4-9/3	1292.654	1292.463	148.448	0.467	770.525	0.427	21	0.111	R.LEKPASYDQIK.A
R4/RRR4-11/3	1762.534	1762.859	-184.865	0.451	776.278	0.462	25	0.111	K.LVSWYDNEWGYSSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/3	1292.670	1292.463	161.091	0.434	521.925	0.433	19	0.109	R.LEKPASYDQIK.A
R4/RRR4-23/3	1292.545	1292.463	63.919	0.374	335.673	0.376	16	0.109	R.LEKPASYDQIK.A
R4/RRR4-9/3	1291.485	1292.463	-1536.302	0.478	667.367	0.424	20	0.109	R.LEKPASYDQIK.A
R4/RRR4-7/3	1292.221	1292.463	-187.908	0.404	549.021	0.422	18	0.108	R.LEKPASYDQIK.A
R4/RRR4-10/3	1292.025	1292.463	-339.960	0.521	739.084	0.426	22	0.105	-.LEKPASYDQIK.-
R4/RRR4-16/3	1292.469	1292.463	4.810	0.386	479.272	0.336	18	0.103	R.LEKPASYDQIK.A
R4/RRR4-16/3	1292.889	1292.463	330.671	0.423	471.183	0.410	17	0.103	-.LEKPASYDQIK.-
R4/RRR4-3/3	1292.426	1292.463	-28.157	0.415	589.279	0.369	19	0.103	R.LEKPASYDQIK.A
R4/RRR4-3/3	1291.972	1292.463	-380.985	0.449	488.775	0.413	18	0.103	-.LEKPASYDQIK.-
R4/RRR4-12/3	1292.160	1292.463	-235.388	0.420	580.604	0.353	19	0.101	R.LEKPASYDQIK.A
R4/RRR4-24/3	1292.597	1292.463	104.267	0.422	653.755	0.358	21	0.101	R.LEKPASYDQIK.A
R4/RRR4-10/3	1292.761	1292.463	231.685	0.443	723.100	0.347	22	0.100	R.LEKPASYDQIK.A
R4/RRR4-11/3	1292.826	1292.463	281.962	0.505	925.126	0.357	23	0.100	-.LEKPASYDQIK.-
R4/RRR4-13/3	1292.848	1292.463	298.862	0.426	692.923	0.337	21	0.099	R.LEKPASYDQIK.A
R4/RRR4-10/3	1499.334	1499.734	-268.069	0.416	1150.867	0.284	23	0.098	R.VPTVDVSVVDLTVR.I
R4/RRR4-12/3	1292.357	1292.463	-82.017	0.341	847.712	0.283	19	0.092	-.LEKPASYDQIK.-
R4/RRR4-11/3	1292.962	1292.463	387.611	0.456	892.975	0.274	21	0.092	R.LEKPASYDQIK.A
R4/RRR4-11/3	1292.816	1292.463	274.293	0.479	776.246	0.329	20	0.090	-.LEKPASYDQIK.-
R4/RRR4-7/3	1291.916	1292.463	-1200.868	0.370	572.000	0.363	18	0.086	-.LEKPASYDQIK.-
R4/RRR4-7/2	1183.265	1183.426	-136.545	0.526	2405.901	0.542	22	0.379	R.LAVQLVAGGGGIK.S
R4/RRR4-7/2	1183.982	1183.426	-375.754	0.560	2442.620	0.504	22	0.373	R.LAVQLVAGGGGIK.S
R4/RRR4-7/2	1183.357	1183.426	-58.004	0.539	2351.625	0.506	22	0.356	R.LAVQLVAGGGGIK.S
R4/RRR4-6/3	1719.661	1719.960	-174.665	0.463	1879.025	0.582	30	0.307	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-6/2	1718.965	1719.960	-1164.390	0.339	1946.446	0.430	23	0.261	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-6/2	1651.327	1651.796	-284.685	0.533	1372.093	0.545	22	0.222	K.FPSAISESGEITVEGK.V
R4/RRR4-6/2	1719.547	1719.960	-240.780	0.355	1597.688	0.446	21	0.219	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-6/2	1651.392	1651.796	-245.527	0.515	1341.509	0.524	22	0.214	K.FPSAISESGEITVEGK.V
R4/RRR4-6/3	1540.209	1540.767	-1014.454	0.431	1835.372	0.402	29	0.209	K.HAVM*AIGVDEEPKK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1650.630	1651.796	-1316.515	0.459	1259.291	0.510	22	0.202	K.FPSAISESGEITVEGK.V
R4/RRR4-6/3	1540.774	1540.767	4.849	0.524	1804.752	0.388	31	0.196	K.HAVM*AIGVDEEPKK.S
R4/RRR4-7/2	1719.474	1719.960	-283.371	0.328	1330.438	0.388	20	0.181	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-6/2	922.195	922.103	100.091	0.450	567.737	0.464	15	0.164	K.YVGVSLVGK.T
R4/RRR4-7/2	1605.623	1605.899	-172.154	0.471	708.664	0.472	20	0.163	K.IGEIPAIEEFVFLK.-
R4/RRR4-7/2	919.926	920.131	-222.880	0.418	741.068	0.374	15	0.157	K.TLAILGFGK.V
R4/RRR4-6/3	1164.815	1164.379	375.071	0.464	1888.393	0.242	25	0.157	R.NKYVGVSLVGK.T
R4/RRR4-7/2	919.471	920.131	-1810.788	0.366	660.549	0.377	14	0.154	K.TLAILGFGK.V
R4/RRR4-6/2	919.661	920.131	-512.507	0.386	677.889	0.345	14	0.152	K.TLAILGFGK.V
R4/RRR4-6/2	1143.525	1144.260	-1522.271	0.407	763.635	0.375	14	0.151	-.GGVIDEDALVR.-
R4/RRR4-6/2	919.977	920.131	-167.903	0.369	651.673	0.352	14	0.151	K.TLAILGFGK.V
R4/RRR4-7/2	920.102	920.131	-31.086	0.424	673.342	0.335	14	0.151	K.TLAILGFGK.V
R4/RRR4-6/2	920.049	920.131	-89.109	0.431	651.505	0.323	14	0.150	K.TLAILGFGK.V
R4/RRR4-3/2	1145.109	1144.260	-132.648	0.313	1002.094	0.262	14	0.147	R.GGVIDEDALVR.A
R4/RRR4-6/3	1164.830	1164.379	388.310	0.482	1873.440	0.215	23	0.147	R.NKYVGVSLVGK.T
R4/RRR4-7/2	1719.618	1719.960	-199.617	0.351	838.612	0.324	20	0.146	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-6/3	1668.816	1668.940	-74.320	0.476	1101.886	0.509	31	0.146	R.KHAVM*AIGVDEEPKK.S
R4/RRR4-6/2	1144.126	1144.260	-117.780	0.467	719.636	0.305	14	0.142	-.GGVIDEDALVR.-
R4/RRR4-6/3	1719.426	1719.960	-894.848	0.450	1215.982	0.449	29	0.142	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-6/2	1143.562	1144.260	-1489.245	0.402	776.193	0.258	14	0.141	R.GGVIDEDALVR.A
R4/RRR4-6/2	921.913	922.103	-207.459	0.364	485.059	0.397	14	0.140	-.YVGVSLVGK.-
R4/RRR4-1/2	1145.174	1144.260	-75.013	0.328	894.862	0.203	14	0.139	-.GGVIDEDALVR.-
R4/RRR4-6/2	1718.338	1719.960	-2113.973	0.228	440.148	0.337	16	0.136	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-1/2	1145.224	1144.260	-31.711	0.295	516.529	0.220	13	0.135	-.GGVIDEDALVR.-
R4/RRR4-3/2	1145.110	1144.260	-131.578	0.273	626.582	0.228	13	0.133	-.GGVIDEDALVR.-
R4/RRR4-6/2	921.830	922.103	-297.529	0.337	348.858	0.389	12	0.126	-.YVGVSLVGK.-
R4/RRR4-6/3	1540.695	1540.767	-46.527	0.425	1338.504	0.348	29	0.124	K.HAVM*AIGVDEEPKK.S
R4/RRR4-6/3	1826.452	1827.014	-857.648	0.465	1019.328	0.424	29	0.118	K.GLGM*HVIAHDPYASADR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1827.723	1827.014	-159.601	0.456	1125.043	0.366	31	0.112	K.GLGM*HVIAHDPYASADR.A
R4/RRR4-7/3	1668.765	1668.940	-105.028	0.436	669.431	0.443	26	0.103	R.KHAVM*AIGVDEEPKK.S
R4/RRR4-7/3	1540.158	1540.767	-1047.518	0.250	1067.865	0.327	24	0.098	K.HAVM*AIGVDEEPKK.S
R4/RRR4-6/3	1668.499	1668.940	-264.649	0.439	666.540	0.403	26	0.098	R.KHAVM*AIGVDEEPKK.S
R4/RRR4-6/3	1826.409	1827.014	-881.601	0.424	831.762	0.351	29	0.094	K.GLGM*HVIAHDPYASADR.A
R4/RRR4-6/3	1719.096	1719.960	-1087.853	0.394	746.925	0.362	27	0.093	R.ALDSGIVAQAALDVFTK.E
R4/RRR4-8/2	1522.212	1522.682	-309.476	0.517	3100.754	0.569	25	0.550	R.IEEELGAAAVYAGTK.F
R4/RRR4-8/2	1523.531	1522.682	-99.379	0.631	2950.172	0.638	25	0.542	R.IEEELGAAAVYAGTK.F
R4/RRR4-8/2	1522.191	1522.682	-322.993	0.497	2696.705	0.512	24	0.428	R.IEEELGAAAVYAGTK.F
R4/RRR4-8/2	1514.452	1514.829	-249.296	0.481	2607.577	0.485	22	0.398	K.LGANAILAVSLALCK.A
R4/RRR4-8/2	1514.457	1514.829	-245.899	0.484	2416.654	0.548	23	0.382	K.LGANAILAVSLALCK.A
R4/RRR4-8/2	1998.380	1999.112	-869.429	0.499	2073.935	0.620	25	0.341	R.GNPTVEVDICCSDGTFAR.A
R4/RRR4-8/3	1574.764	1574.758	3.637	0.451	1830.930	0.472	29	0.242	K.VNQIGSVTESIEAVK.M
R4/RRR4-1/2	1575.002	1574.758	155.272	0.548	1444.444	0.562	22	0.234	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1574.349	1574.758	-260.576	0.490	1479.359	0.506	23	0.225	K.VNQIGSVTESIEAVK.M
R4/RRR4-2/2	1574.166	1574.758	-1014.437	0.488	1450.660	0.519	22	0.224	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1573.941	1574.758	-1157.870	0.445	1484.553	0.500	23	0.224	K.VNQIGSVTESIEAVK.M
R4/RRR4-7/2	1574.408	1574.758	-222.771	0.517	1440.929	0.510	22	0.221	K.VNQIGSVTESIEAVK.M
R4/RRR4-5/2	1574.260	1574.758	-317.521	0.493	1350.414	0.532	22	0.217	K.VNQIGSVTESIEAVK.M
R4/RRR4-3/2	1574.223	1574.758	-978.001	0.452	1406.499	0.505	22	0.216	K.VNQIGSVTESIEAVK.M
R4/RRR4-7/2	1574.246	1574.758	-963.676	0.463	1422.124	0.492	23	0.216	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1872.551	1872.241	165.776	0.593	1174.722	0.607	22	0.215	K.LAMQEFMILPTGASSFK.E
R4/RRR4-7/2	1574.442	1574.758	-201.303	0.499	1369.890	0.507	22	0.213	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1581.140	1581.839	-1077.409	0.398	1418.613	0.497	21	0.212	K.AVDNVNSIIGPALIGK.D
R4/RRR4-1/2	1573.767	1574.758	-1268.939	0.399	1418.625	0.485	21	0.212	K.VNQIGSVTESIEAVK.M
R4/RRR4-4/2	1574.534	1574.758	-142.505	0.509	1301.743	0.525	21	0.210	K.VNQIGSVTESIEAVK.M
R4/RRR4-3/2	1574.483	1574.758	-175.014	0.493	1260.221	0.516	21	0.205	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1871.350	1872.241	-1013.698	0.506	1170.907	0.562	22	0.205	K.LAMQEFMILPTGASSFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1871.450	1872.241	-960.259	0.495	1073.038	0.598	22	0.203	K.LAMQEFMILPTGASSFK.E
R4/RRR4-7/2	1574.259	1574.758	-318.221	0.491	1220.654	0.525	21	0.203	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1191.122	1190.397	-231.445	0.567	1482.323	0.401	16	0.203	K.MGVEVYHNLK.S
R4/RRR4-8/2	1189.924	1190.397	-399.293	0.518	1499.303	0.388	16	0.202	K.MGVEVYHNLK.S
R4/RRR4-2/2	1575.238	1574.758	305.570	0.537	1214.900	0.523	21	0.202	K.VNQIGSVTESIEAVK.M
R4/RRR4-2/2	1574.201	1574.758	-991.781	0.510	1141.427	0.553	20	0.201	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1553.832	1552.802	19.336	0.526	1342.948	0.448	22	0.201	K.IPLYQHIANLAGNK.Q
R4/RRR4-8/2	1554.039	1552.802	152.876	0.563	1176.228	0.501	22	0.198	K.IPLYQHIANLAGNK.Q
R4/RRR4-8/2	1573.901	1574.758	-1183.571	0.404	1254.469	0.477	21	0.195	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1581.285	1581.839	-985.325	0.338	1375.118	0.438	21	0.194	K.AVDNVNSIIGPALIGK.D
R4/RRR4-8/2	1553.494	1552.802	-199.210	0.482	1442.737	0.355	20	0.188	K.IPLYQHIANLAGNK.Q
R4/RRR4-9/2	1574.173	1574.758	-1009.765	0.423	1242.415	0.441	20	0.188	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1513.452	1514.829	-1575.231	0.302	1465.187	0.356	19	0.187	K.LGANAILAVSLALCK.A
R4/RRR4-8/2	1189.707	1190.397	-1424.586	0.475	1285.859	0.395	16	0.186	K.MGVEVYHNLK.S
R4/RRR4-8/2	1680.398	1680.975	-941.417	0.499	834.598	0.530	22	0.179	K.KIPLYQHIANLAGNK.Q
R4/RRR4-8/2	1791.577	1791.983	-227.478	0.484	669.730	0.587	24	0.177	R.AAVPSGASTGVYEALELR.D
R4/RRR4-8/2	1205.592	1206.397	-1500.965	0.505	1019.253	0.424	16	0.174	K.M*GVEVYHNLK.S
R4/RRR4-8/2	1791.372	1791.983	-902.303	0.470	579.778	0.572	22	0.170	R.AAVPSGASTGVYEALELR.D
R4/RRR4-7/2	1791.553	1791.983	-240.875	0.478	611.041	0.553	23	0.170	R.AAVPSGASTGVYEALELR.D
R4/RRR4-7/2	1791.265	1791.983	-962.233	0.493	615.404	0.541	23	0.169	R.AAVPSGASTGVYEALELR.D
R4/RRR4-1/2	1792.368	1791.983	215.408	0.471	593.619	0.575	20	0.168	R.AAVPSGASTGVYEALELR.D
R4/RRR4-1/2	1573.521	1574.758	-1425.848	0.397	913.868	0.458	18	0.168	K.VNQIGSVTESIEAVK.M
R4/RRR4-8/2	1205.518	1206.397	-1562.808	0.503	986.087	0.378	16	0.166	K.M*GVEVYHNLK.S
R4/RRR4-8/2	1680.403	1680.975	-938.572	0.488	802.407	0.439	22	0.164	K.KIPLYQHIANLAGNK.Q
R4/RRR4-8/2	1206.046	1206.397	-291.310	0.488	1090.808	0.337	16	0.164	K.M*GVEVYHNLK.S
R4/RRR4-8/2	1680.568	1680.975	-243.086	0.481	678.226	0.465	20	0.161	K.KIPLYQHIANLAGNK.Q
R4/RRR4-8/2	1790.673	1791.983	-1294.236	0.365	571.769	0.452	23	0.155	R.AAVPSGASTGVYEALELR.D
R4/RRR4-9/2	1573.502	1574.758	-1438.159	0.325	925.641	0.312	18	0.150	K.VNQIGSVTESIEAVK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	902.436	903.095	-1843.680	0.426	832.567	0.305	13	0.150	K.ACNALLLK.V
R4/RRR4-8/3	1791.969	1791.983	-7.838	0.430	1104.223	0.500	33	0.144	R.AAVPSGASTGVYEALELR.D
R4/RRR4-2/2	1790.534	1791.983	-1372.084	0.299	135.256	0.369	15	0.144	R.AAVPSGASTGVYEALELR.D
R4/RRR4-8/3	1792.853	1791.983	-72.916	0.474	867.466	0.498	31	0.124	R.AAVPSGASTGVYEALELR.D
R4/RRR4-1/2	1790.617	1791.983	-1325.182	0.232	118.864	0.381	14	0.121	-.AAVPSGASTGVYEALELR.-
R4/RRR4-8/3	1791.645	1791.983	-189.071	0.434	860.970	0.443	30	0.112	R.AAVPSGASTGVYEALELR.D
R4/RRR4-1/3	1576.137	1574.758	241.300	0.310	620.571	0.260	22	0.076	-.VNQIGSVTESIEAVK.-
R4/RRR4-3/2	1433.026	1433.508	-337.280	0.504	2144.112	0.429	20	0.296	R.WSNEVQEAVQSR.A
R4/RRR4-3/2	1433.042	1433.508	-326.255	0.507	2156.677	0.372	20	0.281	R.WSNEVQEAVQSR.A
R4/RRR4-4/2	1171.225	1171.408	-157.079	0.519	1927.538	0.392	17	0.252	R.SPLAQCLLIR.Y
R4/RRR4-3/2	1245.129	1245.534	-325.835	0.529	1627.322	0.520	19	0.247	R.SIATLAITTLLK.T
R4/RRR4-4/2	1172.174	1171.408	-201.030	0.559	1533.323	0.450	17	0.221	R.SPLAQCLLIR.Y
R4/RRR4-4/2	1402.406	1402.619	-151.963	0.452	1570.957	0.441	17	0.219	R.IIDSTLLTQIER.Y
R4/RRR4-3/2	1171.063	1171.408	-295.945	0.505	1544.183	0.378	17	0.205	R.SPLAQCLLIR.Y
R4/RRR4-3/2	1344.023	1343.507	-360.982	0.414	1325.261	0.466	19	0.201	K.VEATEVFFATTK.L
R4/RRR4-4/2	1172.346	1171.408	-53.640	0.555	1364.250	0.428	16	0.199	R.SPLAQCLLIR.Y
R4/RRR4-3/2	1161.136	1161.291	-133.769	0.458	1175.820	0.432	18	0.185	R.AITELNGVTSR.E
R4/RRR4-3/2	1170.685	1171.408	-1476.810	0.442	1143.747	0.402	15	0.176	R.SPLAQCLLIR.Y
R4/RRR4-3/2	1160.913	1161.291	-326.797	0.430	1008.382	0.421	19	0.173	R.AITELNGVTSR.E
R4/RRR4-3/2	1935.752	1936.214	-239.087	0.427	926.959	0.540	17	0.172	K.ELSPSADEVIIVTSSLM*K.D
R4/RRR4-3/2	1160.443	1161.291	-1597.040	0.365	907.582	0.379	18	0.160	R.AITELNGVTSR.E
R4/RRR4-3/2	1402.215	1402.619	-289.071	0.394	1345.706	0.231	17	0.160	R.IIDSTLLTQIER.Y
R4/RRR4-3/2	1015.947	1015.189	-239.114	0.391	835.032	0.370	15	0.158	R.VILENATVR.A
R4/RRR4-3/2	1366.423	1366.587	-119.765	0.373	584.737	0.440	19	0.156	K.LLSSIPEFAGFGK.L
R4/RRR4-3/2	899.066	899.113	-52.241	0.430	599.022	0.383	13	0.156	K.IVVVEAIR.S
R4/RRR4-3/2	1366.238	1366.587	-255.997	0.382	527.609	0.440	18	0.154	K.LLSSIPEFAGFGK.L
R4/RRR4-3/2	1016.046	1015.189	-140.640	0.390	742.700	0.352	15	0.153	R.VILENATVR.A
R4/RRR4-4/2	1244.645	1245.534	-1521.755	0.321	937.593	0.327	17	0.152	R.SIATLAITTLLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1786.451	1786.962	-848.451	0.459	335.461	0.491	18	0.152	R.SLPYDSPGQTFVAFEK.L
R4/RRR4-3/2	898.908	899.113	-228.637	0.487	645.786	0.333	13	0.152	K.IVVVEAIR.S
R4/RRR4-1/2	1402.036	1402.619	-1131.907	0.487	1176.311	0.264	16	0.152	R.IIDSTLLTQIER.Y
R4/RRR4-3/2	1015.125	1015.189	-63.214	0.446	737.808	0.318	15	0.151	R.VILENATVR.A
R4/RRR4-3/2	1343.568	1343.507	46.055	0.324	642.684	0.366	15	0.146	K.VEATEVFFATTK.L
R4/RRR4-3/2	1366.164	1366.587	-310.232	0.331	405.185	0.372	15	0.145	K.LLSSIPEFAGFGK.L
R4/RRR4-4/2	899.038	899.113	-83.701	0.307	467.473	0.288	11	0.143	K.IVVVEAIR.S
R4/RRR4-3/2	898.377	899.113	-1937.939	0.389	614.320	0.283	12	0.143	-.IVVVEAIR.-
R4/RRR4-4/2	1245.223	1245.534	-250.592	0.311	675.619	0.278	16	0.141	R.SIATLAITTLLK.T
R4/RRR4-3/2	1245.323	1245.534	-169.755	0.308	761.346	0.264	16	0.141	R.SIATLAITTLLK.T
R4/RRR4-3/2	1365.895	1366.587	-1242.173	0.236	348.135	0.364	15	0.141	K.LLSSIPEFAGFGK.L
R4/RRR4-3/2	1342.948	1343.507	-1163.931	0.287	480.774	0.300	13	0.138	K.VEATEVFFATTK.L
R4/RRR4-3/2	1197.474	1198.313	-1539.882	0.252	615.328	0.260	11	0.135	-.VFHDPQLDAR.-
R4/RRR4-3/2	1197.849	1198.313	-388.679	0.282	932.038	0.144	13	0.133	R.VFHDPQLDAR.R
R4/RRR4-2/2	1170.628	1171.408	-1525.620	0.451	579.150	0.242	13	0.114	-.SPLAQCLLIR.-
R4/RRR4-8/2	1984.329	1985.085	-887.926	0.559	2653.818	0.628	26	0.462	R.GNPTVEVDVCCSDGTFAR.A
R4/RRR4-8/2	1984.387	1985.085	-858.530	0.541	2477.466	0.643	26	0.429	R.GNPTVEVDVCCSDGTFAR.A
R4/RRR4-8/2	1493.221	1492.656	-292.198	0.567	2520.174	0.572	23	0.410	R.IEEELGAAAVYAGAK.F
R4/RRR4-8/2	1492.151	1492.656	-1011.198	0.479	2439.932	0.563	23	0.390	R.IEEELGAAAVYAGAK.F
R4/RRR4-8/2	1984.424	1985.085	-839.573	0.571	2068.781	0.644	24	0.347	R.GNPTVEVDVCCSDGTFAR.A
R4/RRR4-8/2	1581.933	1581.839	59.664	0.519	1977.675	0.557	25	0.306	K.AVDNVNSVIAPALIGK.D
R4/RRR4-8/2	1902.327	1902.953	-857.398	0.548	1902.598	0.561	23	0.296	K.TYDLNFKEENNDGSQK.I
R4/RRR4-7/2	1492.059	1492.656	-1073.543	0.431	1976.754	0.452	22	0.274	R.IEEELGAAAVYAGAK.F
R4/RRR4-8/2	1871.649	1872.241	-853.166	0.547	1681.526	0.599	24	0.272	K.LAMQEFM*ILPTGAASFK.E
R4/RRR4-8/2	1491.698	1492.656	-1316.427	0.394	1924.683	0.424	23	0.259	R.IEEELGAAAVYAGAK.F
R4/RRR4-7/2	1492.222	1492.656	-291.491	0.457	1773.694	0.480	22	0.253	R.IEEELGAAAVYAGAK.F
R4/RRR4-8/2	1580.898	1581.839	-1231.540	0.359	1784.796	0.463	22	0.247	K.AVDNVNSVIAPALIGK.D
R4/RRR4-7/2	1492.310	1492.656	-232.237	0.500	1616.012	0.502	21	0.238	R.IEEELGAAAVYAGAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1887.126	1888.241	-1124.250	0.588	1460.556	0.552	25	0.233	K.LAM*QEFM*ILPTGAASFK.E
R4/RRR4-8/2	1856.458	1856.242	116.958	0.550	1398.615	0.574	23	0.230	K.LAMQEFMILPTGAASFK.E
R4/RRR4-8/2	1888.468	1888.241	120.580	0.613	1487.965	0.523	25	0.228	K.LAM*QEFM*ILPTGAASFK.E
R4/RRR4-2/2	1492.255	1492.656	-269.167	0.456	1640.725	0.435	21	0.225	R.IEEELGAAAVYAGAK.F
R4/RRR4-8/2	1873.276	1872.241	18.426	0.582	1285.855	0.592	22	0.222	K.LAM*QEFMILPTGAASFK.E
R4/RRR4-8/2	1855.471	1856.242	-957.112	0.524	1336.484	0.556	25	0.221	K.LAMQEFMILPTGAASFK.E
R4/RRR4-8/2	1871.765	1872.241	-255.114	0.555	1192.883	0.597	23	0.215	K.LAMQEFM*ILPTGAASFK.E
R4/RRR4-8/3	1492.462	1492.656	-130.005	0.449	1732.568	0.447	29	0.212	R.IEEELGAAAVYAGAK.F
R4/RRR4-2/2	1491.951	1492.656	-1145.837	0.385	1676.487	0.351	21	0.210	R.IEEELGAAAVYAGAK.F
R4/RRR4-8/3	1492.827	1492.656	115.461	0.477	1867.545	0.378	29	0.208	R.IEEELGAAAVYAGAK.F
R4/RRR4-8/2	1888.485	1888.241	129.461	0.595	1175.110	0.551	23	0.203	K.LAM*QEFM*ILPTGAASFK.E
R4/RRR4-7/2	1581.367	1581.839	-298.906	0.410	1606.499	0.332	22	0.198	K.AVDNVNSVIAPALIGK.D
R4/RRR4-8/2	1871.330	1872.241	-1024.601	0.504	1125.262	0.546	21	0.197	K.LAM*QEFMILPTGAASFK.E
R4/RRR4-8/3	1492.389	1492.656	-179.359	0.489	1761.946	0.390	30	0.194	R.IEEELGAAAVYAGAK.F
R4/RRR4-1/2	1581.187	1581.839	-1047.410	0.381	1445.555	0.351	21	0.187	K.AVDNVNSVIAPALIGK.D
R4/RRR4-7/2	1581.394	1581.839	-281.868	0.427	1126.380	0.478	20	0.184	K.AVDNVNSVIAPALIGK.D
R4/RRR4-8/2	1855.810	1856.242	-233.393	0.524	850.261	0.527	21	0.176	K.LAMQEFMILPTGAASFK.E
R4/RRR4-8/2	1870.853	1872.241	-1280.225	0.415	901.734	0.498	19	0.171	K.LAMQEFM*ILPTGAASFK.E
R4/RRR4-8/2	1855.011	1856.242	-1206.181	0.402	750.834	0.413	20	0.155	K.LAMQEFMILPTGAASFK.E
R4/RRR4-8/2	918.954	919.094	-153.035	0.510	770.125	0.341	13	0.151	-.SCNALLLK.-
R4/RRR4-6/2	1856.490	1856.242	133.839	0.434	468.486	0.462	16	0.150	K.LAMQEFMILPTGAASFK.E
R4/RRR4-8/2	918.952	919.094	-155.566	0.499	746.034	0.317	13	0.145	-.SCNALLLK.-
R4/RRR4-8/2	1857.923	1856.242	-172.038	0.428	531.068	0.311	15	0.136	K.LAMQEFMILPTGAASFK.E
R4/RRR4-9/2	919.646	919.094	-489.483	0.312	198.015	0.197	12	0.127	-.SCNALLLK.-
R4/RRR4-8/3	1902.802	1902.953	-79.449	0.404	559.006	0.536	29	0.114	K.TYDLNFKEENNDGSQK.I
R4/RRR4-8/3	1903.889	1902.953	-33.615	0.432	389.568	0.531	25	0.109	K.TYDLNFKEENNDGSQK.I
R4/RRR4-8/3	1903.375	1902.953	222.393	0.380	547.679	0.500	26	0.106	K.TYDLNFKEENNDGSQK.I
R4/RRR4-8/3	1887.532	1888.241	-908.271	0.309	1045.177	0.276	27	0.087	K.LAM*QEFM*ILPTGAASFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1240.229	1240.477	-200.562	0.537	2417.448	0.442	18	0.346	R.ALNILADILQR.S
R4/RRR4-7/2	1239.711	1240.477	-1429.050	0.503	2114.524	0.435	18	0.292	R.ALNILADILQR.S
R4/RRR4-7/2	1239.755	1240.477	-1393.842	0.461	1833.203	0.400	17	0.242	R.ALNILADILQR.S
R4/RRR4-7/2	1250.971	1251.372	-321.965	0.438	1419.829	0.538	16	0.226	K.YIETHYTAPR.M
R4/RRR4-7/2	1251.096	1251.372	-221.427	0.506	1374.236	0.547	16	0.226	K.YIETHYTAPR.M
R4/RRR4-7/2	1188.336	1189.344	-1695.247	0.442	1200.823	0.474	17	0.193	R.IDAVDATTVKR.V
R4/RRR4-7/2	1189.025	1189.344	-269.335	0.455	1258.783	0.435	18	0.192	R.IDAVDATTVKR.V
R4/RRR4-7/2	1211.550	1212.469	-1588.184	0.449	1231.364	0.446	16	0.191	R.RIPIPELFAR.I
R4/RRR4-7/2	1213.327	1212.469	-117.621	0.470	1223.070	0.436	16	0.189	R.RIPIPELFAR.I
R4/RRR4-7/2	1211.585	1212.469	-1559.540	0.433	1247.737	0.419	16	0.187	R.RIPIPELFAR.I
R4/RRR4-7/2	1159.224	1159.295	-61.429	0.425	982.434	0.545	14	0.186	K.HDDIVEMATK.L
R4/RRR4-7/2	942.144	942.095	52.098	0.487	1249.874	0.385	13	0.183	K.VLDKDVPR.A
R4/RRR4-7/2	1056.762	1057.209	-424.814	0.414	688.077	0.527	14	0.170	K.HMGSELVQR.V
R4/RRR4-7/2	1057.019	1057.209	-180.884	0.428	771.942	0.443	15	0.165	K.HMGSELVQR.V
R4/RRR4-7/2	941.767	942.095	-348.694	0.481	1051.615	0.347	13	0.164	K.VLDKDVPR.A
R4/RRR4-7/2	1056.177	1056.282	-100.113	0.336	649.439	0.457	15	0.157	R.IPIPELFAR.I
R4/RRR4-7/2	960.944	961.052	-112.201	0.423	669.279	0.345	13	0.152	R.VTEEDVIR.A
R4/RRR4-7/2	960.425	961.052	-1698.643	0.400	739.916	0.313	13	0.150	R.VTEEDVIR.A
R4/RRR4-7/2	960.803	961.052	-259.401	0.409	567.707	0.332	12	0.149	R.VTEEDVIR.A
R4/RRR4-7/2	1056.008	1056.282	-260.942	0.226	312.162	0.328	11	0.139	R.IPIPELFAR.I
R4/RRR4-7/2	960.868	961.205	-351.319	0.424	718.205	0.219	15	0.139	R.MVITAAGAVK.H
R4/RRR4-7/2	960.961	961.205	-254.071	0.426	857.737	0.212	15	0.138	-.MVITAAGAVK.-
R4/RRR4-7/3	1998.776	1998.184	-204.363	0.513	905.938	0.411	29	0.107	K.SSIQLHLDGSTAVVEDIGR.Q
R4/RRR4-7/3	1212.419	1212.469	-41.174	0.406	994.033	0.384	21	0.106	R.RIPIPELFAR.I
R4/RRR4-7/3	1998.863	1998.184	-160.711	0.530	801.975	0.356	27	0.092	K.SSIQLHLDGSTAVVEDIGR.Q
R4/RRR4-7/3	1212.729	1212.469	214.769	0.378	1028.628	0.279	21	0.090	R.RIPIPELFAR.I
R4/RRR4-7/3	1212.593	1212.469	102.261	0.366	882.832	0.299	20	0.088	R.RIPIPELFAR.I
R4/RRR4-9/2	1505.784	1504.744	26.620	0.538	1835.078	0.568	21	0.288	K.ECILSGLLSVDGLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/3	1626.696	1626.798	-63.128	0.496	2119.379	0.453	34	0.287	R.FRGEDKPPAHLGSSK.D
R4/RRR4-9/3	1626.942	1626.798	88.710	0.513	2127.519	0.446	34	0.285	R.FRGEDKPPAHLGSSK.D
R4/RRR4-9/2	1504.424	1504.744	-213.277	0.395	1752.794	0.454	21	0.243	K.ECILSGLLSVDGLK.V
R4/RRR4-9/2	1505.146	1504.744	267.902	0.476	1484.354	0.502	20	0.224	K.ECILSGLLSVDGLK.V
R4/RRR4-9/3	1626.544	1626.798	-156.850	0.457	1704.719	0.459	32	0.210	R.FRGEDKPPAHLGSSK.D
R4/RRR4-9/2	1865.429	1864.003	229.156	0.507	1178.547	0.458	19	0.184	R.NFFIYVQDYNEADPK.T
R4/RRR4-9/2	1038.259	1038.243	15.569	0.336	1299.609	0.389	15	0.183	K.SPLM*GLFEK.R
R4/RRR4-9/2	1096.947	1097.224	-252.889	0.412	1154.626	0.385	13	0.172	R.DYNVDM*VPK.F
R4/RRR4-9/2	1090.944	1091.261	-291.575	0.459	586.384	0.516	15	0.168	K.VPATDM*EALK.S
R4/RRR4-9/2	1291.405	1292.456	-1593.130	0.300	1085.944	0.365	15	0.161	K.VVCDPSYLPNK.V
R4/RRR4-9/2	1090.947	1091.261	-288.544	0.454	465.576	0.453	14	0.158	K.VPATDM*EALK.S
R4/RRR4-9/2	1091.074	1091.261	-171.693	0.437	491.816	0.425	14	0.155	K.VPATDM*EALK.S
R4/RRR4-9/2	1072.445	1073.180	-1623.393	0.311	632.443	0.384	15	0.149	K.AVDGSYVFSK.G
R4/RRR4-9/2	1038.357	1038.243	110.488	0.304	740.362	0.346	13	0.147	K.SPLM*GLFEK.R
R4/RRR4-9/2	1072.556	1073.180	-1519.117	0.311	395.506	0.295	12	0.139	-.AVDGSYVFSK.-
R4/RRR4-9/2	1199.334	1198.418	-70.196	0.359	742.868	0.287	13	0.139	-.M*KLYAESLAR.-
R4/RRR4-9/2	1292.011	1292.456	-345.474	0.320	722.375	0.227	12	0.133	K.VVCDPSYLPNK.V
R4/RRR4-9/3	1805.390	1805.970	-877.468	0.480	1430.904	0.322	28	0.128	R.DDRYLNEPAIDTVKR.M
R4/RRR4-9/3	1805.295	1805.970	-930.720	0.474	1385.030	0.334	27	0.127	R.DDRYLNEPAIDTVKR.M
R4/RRR4-9/3	1469.546	1469.732	-126.477	0.481	1139.055	0.343	24	0.108	K.IHKVPATDM*EALK.S
R4/RRR4-9/3	1805.608	1805.970	-201.238	0.419	1184.143	0.321	24	0.107	R.DDRYLNEPAIDTVKR.M
R4/RRR4-9/3	1469.809	1469.732	52.850	0.476	1101.899	0.338	25	0.105	K.IHKVPATDM*EALK.S
R4/RRR4-9/3	1470.033	1469.732	205.385	0.466	849.942	0.303	23	0.089	K.IHKVPATDM*EALK.S
R4/RRR4-7/2	1568.378	1567.722	-220.349	0.600	2291.076	0.638	26	0.391	K.IAVFAGGVDTSATETK.G
R4/RRR4-7/2	1445.192	1445.561	-255.821	0.489	2429.294	0.433	22	0.346	K.NEEGGNSVATVVLR.G
R4/RRR4-7/2	1445.264	1445.561	-205.572	0.510	2236.154	0.462	22	0.320	K.NEEGGNSVATVVLR.G
R4/RRR4-7/2	1773.351	1773.968	-914.164	0.579	1925.473	0.606	23	0.313	K.GTVLIHSAEQLENYAK.T
R4/RRR4-7/2	1773.673	1773.968	-166.818	0.593	1902.202	0.609	23	0.310	K.GTVLIHSAEQLENYAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1566.667	1567.722	-1316.188	0.407	2090.483	0.479	25	0.299	K.IAVFAGGVDTSATETK.G
R4/RRR4-7/2	1566.722	1567.722	-1280.662	0.412	1920.821	0.513	24	0.282	K.IAVFAGGVDTSATETK.G
R4/RRR4-7/2	1228.786	1229.387	-1306.992	0.447	1900.568	0.506	17	0.280	K.FAESFEM*VPR.T
R4/RRR4-7/2	1289.152	1289.457	-237.589	0.558	1990.156	0.416	18	0.267	K.TEEAKVEELIK.A
R4/RRR4-7/2	1289.006	1289.457	-350.838	0.515	2004.668	0.360	18	0.254	K.TEEAKVEELIK.A
R4/RRR4-7/2	1229.054	1229.387	-271.371	0.518	1750.875	0.458	17	0.248	K.FAESFEM*VPR.T
R4/RRR4-7/2	1289.387	1289.457	-54.943	0.526	1890.879	0.358	17	0.237	K.TEEAKVEELIK.A
R4/RRR4-7/2	1259.927	1260.341	-329.394	0.479	1315.299	0.493	18	0.208	K.NPANFNVDNVR.V
R4/RRR4-7/2	1259.447	1260.341	-1508.148	0.437	1232.245	0.489	17	0.198	K.NPANFNVDNVR.V
R4/RRR4-1/2	1230.199	1229.387	-153.181	0.423	1155.556	0.453	16	0.186	K.FAESFEM*VPR.T
R4/RRR4-7/2	1182.065	1182.352	-243.473	0.459	1015.420	0.438	18	0.176	K.HLSGLDEAVLK.N
R4/RRR4-7/2	1182.119	1182.352	-197.475	0.442	889.778	0.473	17	0.173	K.HLSGLDEAVLK.N
R4/RRR4-7/2	1182.218	1182.352	-113.053	0.440	833.036	0.413	17	0.163	K.HLSGLDEAVLK.N
R4/RRR4-7/2	1288.283	1288.469	-144.612	0.435	911.616	0.372	15	0.158	K.TVEILEDLVEK.G
R4/RRR4-7/2	1425.164	1425.656	-345.756	0.332	585.970	0.464	20	0.152	R.IIPGAAATEIELAR.R
R4/RRR4-7/2	1321.108	1321.373	-201.444	0.348	1026.880	0.296	17	0.152	R.GSTDSILDDLER.A
R4/RRR4-7/2	1288.151	1288.469	-247.564	0.356	643.969	0.373	14	0.148	K.TVEILEDLVEK.G
R4/RRR4-7/2	1288.061	1288.469	-317.636	0.322	796.919	0.308	14	0.144	K.TVEILEDLVEK.G
R4/RRR4-7/2	1321.490	1321.373	88.795	0.352	949.420	0.238	16	0.142	R.GSTDSILDDLER.A
R4/RRR4-7/2	1209.015	1209.331	-261.945	0.303	742.941	0.305	14	0.142	K.ETGLDQYAIAK.F
R4/RRR4-7/2	1209.027	1209.331	-251.917	0.261	764.975	0.283	14	0.139	K.ETGLDQYAIAK.F
R4/RRR4-7/2	1320.669	1321.373	-1293.888	0.301	1019.403	0.145	16	0.135	R.GSTDSILDDLER.A
R4/RRR4-16/2	1282.126	1281.503	-295.106	0.494	1567.615	0.473	18	0.229	K.NM*GLLLAEFEK.I
R4/RRR4-16/2	1281.227	1281.503	-216.092	0.486	1451.900	0.477	17	0.217	K.NM*GLLLAEFEK.I
R4/RRR4-16/2	1627.269	1627.778	-930.094	0.470	1307.087	0.511	22	0.208	K.EKITIDPDDPAAVSR.Y
R4/RRR4-16/2	1315.998	1316.479	-366.902	0.480	1605.103	0.329	18	0.200	K.IEEELELEIAK.S
R4/RRR4-16/2	1264.882	1265.504	-1285.907	0.444	1363.400	0.402	17	0.193	K.NMGLLLAEFEK.I
R4/RRR4-16/2	1627.354	1627.778	-261.267	0.495	1127.385	0.509	21	0.193	K.EKITIDPDDPAAVSR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1370.288	1370.490	-147.752	0.463	1057.803	0.523	20	0.192	K.ITIDPDDPAAVSR.Y
R4/RRR4-15/2	1251.257	1251.414	-125.700	0.416	1107.542	0.487	16	0.188	R.TYLNTLQEIR.I
R4/RRR4-16/2	1072.058	1072.194	-127.411	0.458	1036.817	0.506	15	0.187	R.TPVNGDDLLK.G
R4/RRR4-16/2	1370.106	1370.490	-281.100	0.485	959.033	0.533	19	0.186	K.ITIDPDDPAAVSR.Y
R4/RRR4-16/2	1072.153	1072.194	-37.983	0.498	1006.520	0.508	15	0.186	R.TPVNGDDLLK.G
R4/RRR4-16/2	1315.401	1316.479	-1585.104	0.431	1303.172	0.353	18	0.180	K.IEEELELEIAK.S
R4/RRR4-16/2	1281.097	1281.503	-318.089	0.471	923.909	0.480	15	0.175	K.NM*GLLLAEFEK.I
R4/RRR4-16/2	1315.375	1316.479	-1604.682	0.372	1319.523	0.312	18	0.173	K.IEEELELEIAK.S
R4/RRR4-16/2	1370.021	1370.490	-343.855	0.445	861.775	0.474	19	0.171	K.ITIDPDDPAAVSR.Y
R4/RRR4-16/2	1071.670	1072.194	-1426.117	0.426	951.667	0.416	15	0.167	R.TPVNGDDLLK.G
R4/RRR4-15/2	1370.106	1370.490	-281.726	0.398	680.260	0.519	16	0.164	K.ITIDPDDPAAVSR.Y
R4/RRR4-16/2	967.969	968.174	-211.945	0.403	677.385	0.401	12	0.156	K.GIFFEVKK.K
R4/RRR4-16/2	968.179	968.174	5.614	0.380	656.026	0.396	12	0.154	K.GIFFEVKK.K
R4/RRR4-15/2	1251.163	1251.414	-200.962	0.361	658.649	0.431	13	0.153	R.TYLNTLQEIR.I
R4/RRR4-16/2	968.123	968.174	-52.814	0.380	630.900	0.384	12	0.153	K.GIFFEVKK.K
R4/RRR4-16/2	1265.385	1265.504	-94.205	0.393	641.400	0.400	13	0.151	K.NMGLLLAEFEK.I
R4/RRR4-16/2	1234.169	1234.513	-279.225	0.535	986.607	0.299	16	0.150	K.KFETALGVLKK.E
R4/RRR4-16/2	1263.304	1262.352	-38.148	0.313	118.721	0.533	14	0.147	-.QKADLLSDSER.-
R4/RRR4-16/3	1627.854	1627.778	47.105	0.449	1231.163	0.452	24	0.145	K.EKITIDPDDPAAVSR.Y
R4/RRR4-16/2	1234.203	1234.513	-251.341	0.496	993.991	0.246	16	0.143	K.KFETALGVLKK.E
R4/RRR4-16/3	1230.629	1230.435	158.567	0.467	1100.837	0.419	22	0.123	R.IKYTIDTFTK.G
R4/RRR4-16/3	1230.527	1230.435	75.299	0.431	857.723	0.385	20	0.101	R.IKYTIDTFTK.G
R4/RRR4-4/2	1860.541	1860.057	260.753	0.607	2418.672	0.598	25	0.400	R.AYLPVQELLNGEEIDR.W
R4/RRR4-4/2	1241.149	1241.379	-185.715	0.521	1917.294	0.547	20	0.294	K.IDNPIGATNIGR.A
R4/RRR4-5/2	1241.200	1241.379	-145.066	0.497	1949.086	0.518	20	0.290	K.IDNPIGATNIGR.A
R4/RRR4-5/2	1241.005	1241.379	-302.155	0.526	1907.174	0.519	20	0.285	K.IDNPIGATNIGR.A
R4/RRR4-4/2	1240.691	1241.379	-1364.862	0.441	1899.721	0.517	21	0.282	K.IDNPIGATNIGR.A
R4/RRR4-4/2	1242.341	1241.379	-31.006	0.526	1763.933	0.509	20	0.262	K.IDNPIGATNIGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1241.351	1241.379	-23.140	0.446	1743.580	0.507	21	0.258	K.IDNPIGATNIGR.A
R4/RRR4-4/2	1406.663	1406.561	72.626	0.492	1794.902	0.459	17	0.253	R.DYLTFFCLGNR.E
R4/RRR4-4/2	1859.979	1860.057	-42.367	0.548	1402.384	0.550	23	0.227	R.AYLPVQELLNGEEIDR.W
R4/RRR4-4/2	1859.351	1860.057	-920.544	0.548	1425.110	0.525	23	0.223	R.AYLPVQELLNGEEIDR.W
R4/RRR4-4/2	1950.647	1951.170	-783.435	0.528	1474.681	0.508	20	0.222	R.LEGPIAWDVLYNFEQR.W
R4/RRR4-4/2	1241.149	1241.379	-186.208	0.465	1402.329	0.508	19	0.218	K.IDNPIGATNIGR.A
R4/RRR4-4/2	1880.472	1880.989	-809.025	0.455	1009.169	0.617	23	0.198	R.SIDGGAAFGFPDTPEEAAK.A
R4/RRR4-4/2	1288.206	1287.449	-189.386	0.444	1306.473	0.450	17	0.197	R.SIQDAYIHAIR.R
R4/RRR4-4/2	1288.105	1287.449	-268.199	0.434	1343.681	0.434	16	0.196	R.SIQDAYIHAIR.R
R4/RRR4-4/2	1288.224	1287.449	-175.317	0.425	1390.604	0.397	16	0.193	R.SIQDAYIHAIR.R
R4/RRR4-5/2	1859.431	1860.057	-877.573	0.411	1419.845	0.374	23	0.190	R.AYLPVQELLNGEEIDR.W
R4/RRR4-4/2	1508.361	1508.695	-222.217	0.441	1170.936	0.434	19	0.181	R.IVSFVGGLDLCDGR.Y
R4/RRR4-4/2	1880.253	1880.989	-925.743	0.448	784.634	0.599	20	0.177	R.SIDGGAAFGFPDTPEEAAK.A
R4/RRR4-4/2	1201.009	1201.378	-308.491	0.452	1046.144	0.428	15	0.174	-.M*ITNEPINPR.-
R4/RRR4-4/2	1880.238	1880.989	-933.825	0.457	701.738	0.590	20	0.172	R.SIDGGAAFGFPDTPEEAAK.A
R4/RRR4-4/2	1200.958	1201.378	-350.813	0.476	1215.354	0.309	16	0.166	-.M*ITNEPINPR.-
R4/RRR4-4/2	1406.235	1406.561	-232.522	0.407	861.806	0.425	15	0.162	R.DYLTFFCLGNR.E
R4/RRR4-4/2	1463.272	1462.633	-247.556	0.425	532.770	0.465	18	0.160	K.YPGVPYTFFSQR.Q
R4/RRR4-4/2	1463.390	1462.633	-166.380	0.408	611.578	0.433	19	0.159	K.YPGVPYTFFSQR.Q
R4/RRR4-1/2	1952.547	1951.170	193.473	0.452	745.394	0.476	17	0.159	R.LEGPIAWDVLYNFEQR.W
R4/RRR4-4/2	1463.343	1462.633	-198.514	0.377	505.243	0.427	18	0.155	K.YPGVPYTFFSQR.Q
R4/RRR4-4/2	1147.996	1147.372	-328.981	0.314	914.179	0.348	13	0.153	R.VLMLVWDDR.T
R4/RRR4-3/2	1950.842	1951.170	-168.802	0.374	499.720	0.413	17	0.146	R.LEGPIAWDVLYNFEQR.W
R4/RRR4-5/2	1463.037	1462.633	277.035	0.310	397.286	0.314	16	0.145	K.YPGVPYTFFSQR.Q
R4/RRR4-5/2	1462.081	1462.633	-1064.403	0.371	471.535	0.272	17	0.144	K.YPGVPYTFFSQR.Q
R4/RRR4-4/2	1185.150	1185.379	-193.457	0.345	706.057	0.289	13	0.142	-.MITNEPINPR.W
R4/RRR4-4/2	1510.109	1508.695	275.291	0.427	406.966	0.284	15	0.137	R.IVSFVGGLDLCDGR.Y
R4/RRR4-3/2	1147.761	1147.372	339.372	0.145	559.102	0.097	12	0.125	-.VLMLVWDDR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/3	1819.884	1820.000	-63.928	0.394	815.471	0.508	27	0.122	K.IVVVDHELPNQGSQQR.R
R4/RRR4-4/3	1819.944	1820.000	-30.928	0.486	818.697	0.491	28	0.121	K.IVVVDHELPNQGSQQR.R
R4/RRR4-5/3	1821.007	1820.000	3.952	0.436	796.453	0.461	27	0.113	K.IVVVDHELPNQGSQQR.R
R4/RRR4-5/3	1820.680	1820.000	-176.204	0.430	774.534	0.466	27	0.113	K.IVVVDHELPNQGSQQR.R
R4/RRR4-5/3	1819.156	1820.000	-1016.609	0.375	600.357	0.469	23	0.103	-.IVVVDHELPNQGSQQR.-
R4/RRR4-4/3	1950.787	1951.170	-196.994	0.326	978.728	0.265	24	0.084	R.LEGPIAWDVLYNFEQR.W
R4/RRR4-4/3	1951.037	1951.170	-68.385	0.297	532.222	0.371	22	0.083	-.LEGPIAWDVLYNFEQR.-
R4/RRR4-14/3	1529.394	1529.764	-242.386	0.533	2589.215	0.576	34	0.485	K.VKIQLGEGSAAQVTK.N
R4/RRR4-15/3	1529.621	1529.764	-93.349	0.518	2170.189	0.522	31	0.337	K.VKIQLGEGSAAQVTK.N
R4/RRR4-15/2	1460.185	1460.637	-310.169	0.556	2053.060	0.474	20	0.292	K.NM*LANEGIGSFYK.G
R4/RRR4-15/3	1529.395	1529.764	-241.545	0.539	1963.955	0.520	30	0.289	K.VKIQLGEGSAAQVTK.N
R4/RRR4-15/2	1459.939	1460.637	-1166.306	0.477	2044.953	0.450	20	0.285	K.NM*LANEGIGSFYK.G
R4/RRR4-14/2	1461.375	1460.637	-179.888	0.564	1953.718	0.457	20	0.272	K.NM*LANEGIGSFYK.G
R4/RRR4-15/2	1461.242	1460.637	-271.234	0.566	1927.389	0.469	20	0.272	K.NM*LANEGIGSFYK.G
R4/RRR4-15/2	1329.201	1328.581	-287.172	0.573	1488.766	0.584	20	0.248	R.IIADEGVLALWK.G
R4/RRR4-15/2	1302.215	1302.459	-188.383	0.526	1615.060	0.498	22	0.241	K.IQLGEGSAAQVTK.N
R4/RRR4-14/2	1329.505	1328.581	-57.798	0.591	1478.809	0.551	20	0.238	R.IIADEGVLALWK.G
R4/RRR4-15/2	1303.012	1302.459	-343.966	0.532	1469.917	0.533	21	0.232	K.IQLGEGSAAQVTK.N
R4/RRR4-14/2	1302.323	1302.459	-104.977	0.506	1601.787	0.456	22	0.229	K.IQLGEGSAAQVTK.N
R4/RRR4-15/2	1329.073	1328.581	371.194	0.522	1412.547	0.537	20	0.227	R.IIADEGVLALWK.G
R4/RRR4-14/2	1328.316	1328.581	-200.351	0.546	1449.417	0.479	20	0.218	R.IIADEGVLALWK.G
R4/RRR4-15/2	1302.175	1302.459	-218.665	0.477	1281.492	0.525	20	0.210	K.IQLGEGSAAQVTK.N
R4/RRR4-14/2	1328.268	1328.581	-236.307	0.557	1293.037	0.513	19	0.210	R.IIADEGVLALWK.G
R4/RRR4-14/2	1327.968	1328.581	-1218.458	0.513	1346.923	0.484	19	0.209	R.IIADEGVLALWK.G
R4/RRR4-14/2	1301.606	1302.459	-1427.975	0.436	1403.064	0.460	21	0.208	K.IQLGEGSAAQVTK.N
R4/RRR4-14/2	1327.479	1328.581	-1588.851	0.401	1519.484	0.403	19	0.207	R.IIADEGVLALWK.G
R4/RRR4-15/2	1328.193	1328.581	-293.105	0.453	1239.964	0.500	18	0.201	R.IIADEGVLALWK.G
R4/RRR4-14/2	1302.078	1302.459	-293.906	0.519	1189.235	0.500	20	0.198	K.IQLGEGSAAQVTK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1301.700	1302.459	-1355.635	0.405	1297.674	0.440	20	0.194	K.IQLGEGSAAQVTK.N
R4/RRR4-15/2	1328.101	1328.581	-362.728	0.488	1252.362	0.444	19	0.193	R.IIADEGVLALWK.G
R4/RRR4-15/2	1744.337	1744.890	-892.871	0.550	736.802	0.609	22	0.186	K.QQQQQQTAAAATGVWK.T
R4/RRR4-15/2	1347.141	1347.523	-284.630	0.488	1197.018	0.426	19	0.185	R.M*QADSTLPIAQR.R
R4/RRR4-14/2	1348.030	1347.523	-367.367	0.533	1049.820	0.478	18	0.184	R.M*QADSTLPIAQR.R
R4/RRR4-15/2	1745.340	1744.890	258.602	0.547	569.804	0.650	21	0.183	K.QQQQQQTAAAATGVWK.T
R4/RRR4-15/3	1528.935	1529.764	-1199.490	0.475	1344.335	0.513	27	0.177	K.VKIQLGEGSAAQVTK.N
R4/RRR4-15/2	1744.524	1744.890	-210.312	0.559	565.758	0.612	20	0.177	K.QQQQQQTAAAATGVWK.T
R4/RRR4-15/2	1328.291	1328.581	-219.619	0.465	996.052	0.454	17	0.175	R.IIADEGVLALWK.G
R4/RRR4-15/2	1410.155	1409.607	-320.871	0.463	880.544	0.477	16	0.173	K.FYTGFPVYCVR.I
R4/RRR4-15/2	1347.421	1347.523	-76.394	0.489	892.361	0.453	17	0.170	R.M*QADSTLPIAQR.R
R4/RRR4-15/2	1410.458	1409.607	-105.349	0.410	662.463	0.544	14	0.169	K.FYTGFPVYCVR.I
R4/RRR4-15/2	1347.060	1347.523	-345.000	0.461	994.058	0.402	18	0.168	R.M*QADSTLPIAQR.R
R4/RRR4-14/2	1347.184	1347.523	-252.540	0.489	950.317	0.408	17	0.166	R.M*QADSTLPIAQR.R
R4/RRR4-14/2	1347.109	1347.523	-308.905	0.472	1001.813	0.383	18	0.165	R.M*QADSTLPIAQR.R
R4/RRR4-14/2	1327.707	1328.581	-1415.949	0.371	1019.383	0.378	17	0.164	R.IIADEGVLALWK.G
R4/RRR4-15/2	1208.897	1209.420	-1263.828	0.434	704.002	0.451	16	0.163	K.NDGKPLPLVQK.A
R4/RRR4-14/2	1209.128	1209.420	-242.479	0.433	536.558	0.473	16	0.161	K.NDGKPLPLVQK.A
R4/RRR4-14/2	1650.513	1650.944	-262.126	0.516	902.014	0.410	19	0.159	K.AIEKNDGKPLPLVQK.A
R4/RRR4-14/2	1209.297	1209.420	-102.320	0.420	512.005	0.453	16	0.159	K.NDGKPLPLVQK.A
R4/RRR4-14/2	991.901	992.115	-217.076	0.417	710.841	0.384	13	0.157	K.NAFHALYR.I
R4/RRR4-15/2	1209.077	1209.420	-284.919	0.409	500.465	0.433	16	0.157	K.NDGKPLPLVQK.A
R4/RRR4-15/2	1327.919	1328.581	-1255.568	0.389	813.012	0.374	17	0.156	R.IIADEGVLALWK.G
R4/RRR4-15/2	1209.187	1209.420	-193.358	0.404	406.747	0.458	14	0.155	K.NDGKPLPLVQK.A
R4/RRR4-14/2	1410.137	1409.607	-334.073	0.436	612.727	0.422	14	0.155	K.FYTGFPVYCVR.I
R4/RRR4-14/2	1209.161	1209.420	-214.829	0.400	510.003	0.399	16	0.154	K.NDGKPLPLVQK.A
R4/RRR4-14/2	1410.253	1409.607	-251.567	0.367	783.589	0.370	15	0.153	K.FYTGFPVYCVR.I
R4/RRR4-15/2	1409.329	1409.607	-197.782	0.362	494.931	0.470	12	0.152	K.FYTGFPVYCVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	991.970	992.115	-146.707	0.391	779.609	0.283	13	0.148	K.NAFHALYR.I
R4/RRR4-15/2	991.409	992.115	-1725.952	0.403	841.577	0.257	13	0.147	K.NAFHALYR.I
R4/RRR4-14/2	992.072	992.115	-43.888	0.367	731.977	0.269	13	0.146	K.NAFHALYR.I
R4/RRR4-15/2	1409.796	1409.607	134.994	0.318	708.326	0.325	14	0.146	K.FYTGFPVYCVR.I
R4/RRR4-15/2	991.508	992.115	-1625.757	0.354	671.114	0.251	13	0.144	K.NAFHALYR.I
R4/RRR4-14/2	992.098	992.115	-17.230	0.335	766.263	0.226	13	0.142	K.NAFHALYR.I
R4/RRR4-14/2	1409.943	1409.607	239.012	0.243	558.329	0.209	13	0.137	K.FYTGFPVYCVR.I
R4/RRR4-15/3	1650.983	1650.944	23.900	0.422	950.588	0.346	28	0.100	K.AIEKNDGKPLPLVQK.A
R4/RRR4-14/3	1650.694	1650.944	-151.885	0.431	598.081	0.401	23	0.099	K.AIEKNDGKPLPLVQK.A
R4/RRR4-15/3	1651.035	1650.944	55.490	0.426	715.234	0.376	25	0.097	K.AIEKNDGKPLPLVQK.A
R4/RRR4-15/3	1650.258	1650.944	-1024.575	0.427	819.871	0.351	26	0.096	K.AIEKNDGKPLPLVQK.A
R4/RRR4-14/3	1650.750	1650.944	-117.836	0.406	607.113	0.310	24	0.090	K.AIEKNDGKPLPLVQK.A
R4/RRR4-14/3	1650.929	1650.944	-9.138	0.447	506.204	0.382	23	0.086	-.AIEKNDGKPLPLVQK.-
R4/RRR4-9/2	1711.490	1711.936	-261.658	0.608	2462.742	0.594	25	0.410	K.KLEEVYGTFEAPSLK.K
R4/RRR4-9/2	1711.379	1711.936	-912.641	0.593	1767.732	0.604	21	0.287	K.KLEEVYGTFEAPSLK.K
R4/RRR4-9/2	1711.348	1711.936	-930.830	0.548	1765.792	0.573	21	0.277	K.KLEEVYGTFEAPSLK.K
R4/RRR4-9/2	1349.276	1349.557	-208.944	0.488	1731.261	0.554	20	0.268	R.KGPLIVYGTEGSK.I
R4/RRR4-9/2	1887.454	1886.970	256.949	0.584	1596.737	0.566	23	0.253	K.TM*ISDSDYAEFDNFSK.W
R4/RRR4-9/2	1349.031	1349.557	-1134.722	0.485	1617.066	0.547	20	0.252	R.KGPLIVYGTEGSK.I
R4/RRR4-9/2	1886.436	1886.970	-816.094	0.526	1600.191	0.549	24	0.250	K.TM*ISDSDYAEFDNFSK.W
R4/RRR4-9/2	1886.296	1886.970	-890.215	0.528	1248.658	0.589	22	0.219	K.TM*ISDSDYAEFDNFSK.W
R4/RRR4-9/2	1886.394	1886.970	-838.180	0.517	1251.046	0.562	22	0.213	K.TM*ISDSDYAEFDNFSK.W
R4/RRR4-4/3	1446.546	1446.680	-92.488	0.407	1890.027	0.396	31	0.209	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/2	1349.238	1349.557	-237.807	0.478	1179.908	0.546	18	0.203	R.KGPLIVYGTEGSK.I
R4/RRR4-9/2	1446.505	1446.680	-121.006	0.544	1139.515	0.529	22	0.201	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/2	1446.403	1446.680	-191.697	0.524	1163.200	0.514	22	0.199	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/2	1221.160	1221.385	-184.745	0.414	1013.584	0.522	17	0.185	K.GPLIVYGTEGSK.I
R4/RRR4-9/3	1839.824	1840.109	-155.537	0.480	1459.453	0.481	30	0.182	K.KLEEVYGTFEAPSLKK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/3	1797.944	1797.132	-105.124	0.397	1575.712	0.436	38	0.180	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-13/2	1446.525	1446.680	-107.293	0.480	966.038	0.473	20	0.176	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/2	1222.094	1221.385	-238.303	0.518	1008.503	0.456	17	0.176	K.GPLIVYGTEGSK.I
R4/RRR4-9/2	1445.731	1446.680	-1352.016	0.471	918.496	0.482	20	0.175	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/3	1796.745	1797.132	-215.962	0.396	1475.225	0.456	38	0.173	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-13/2	1798.069	1797.132	-35.586	0.407	969.614	0.492	20	0.172	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-9/2	1282.643	1283.416	-1386.563	0.399	388.345	0.577	18	0.168	R.NLPGVDVANVER.L
R4/RRR4-9/2	1797.249	1797.132	65.358	0.420	989.535	0.441	21	0.167	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-9/3	1447.033	1446.680	244.764	0.391	1616.887	0.380	28	0.166	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/2	1283.114	1283.416	-236.226	0.391	480.130	0.517	19	0.165	R.NLPGVDVANVER.L
R4/RRR4-9/2	1056.900	1056.329	-406.570	0.398	888.048	0.419	14	0.164	K.KGFILPRPK.M
R4/RRR4-10/2	1283.175	1283.416	-188.602	0.382	452.345	0.509	19	0.163	R.NLPGVDVANVER.L
R4/RRR4-10/3	1446.600	1446.680	-55.033	0.424	1609.830	0.374	29	0.162	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/2	1228.153	1228.420	-218.784	0.408	776.468	0.427	15	0.161	R.FVIWTESAFK.K
R4/RRR4-13/2	1798.735	1797.132	-221.331	0.462	832.169	0.458	19	0.159	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-13/2	1446.399	1446.680	-194.322	0.504	688.576	0.456	17	0.159	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/2	1796.493	1797.132	-915.133	0.334	1068.839	0.350	21	0.158	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-10/2	1283.350	1283.416	-51.958	0.366	367.800	0.459	17	0.157	R.NLPGVDVANVER.L
R4/RRR4-10/2	1283.060	1283.416	-278.032	0.330	418.738	0.477	18	0.157	R.NLPGVDVANVER.L
R4/RRR4-9/3	1797.306	1797.132	96.991	0.444	1412.726	0.426	37	0.156	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-9/2	1227.951	1228.420	-383.438	0.332	791.194	0.396	15	0.155	R.FVIWTESAFK.K
R4/RRR4-9/2	1795.919	1797.132	-1236.325	0.307	1027.599	0.342	20	0.153	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-2/2	1284.380	1283.416	-28.084	0.320	361.810	0.380	17	0.151	R.NLPGVDVANVER.L
R4/RRR4-1/3	1446.685	1446.680	3.621	0.430	1377.252	0.416	27	0.150	R.LNLLDLAPGGHLGR.F
R4/RRR4-11/2	1283.398	1283.416	-14.368	0.296	297.922	0.347	15	0.148	R.NLPGVDVANVER.L
R4/RRR4-9/2	1282.501	1283.416	-1497.553	0.258	325.460	0.354	17	0.148	R.NLPGVDVANVER.L
R4/RRR4-9/2	1056.897	1056.329	-409.815	0.302	666.601	0.365	13	0.147	K.KGFILPRPK.M
R4/RRR4-1/2	1283.455	1283.416	30.850	0.246	321.481	0.292	16	0.146	R.NLPGVDVANVER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/3	1446.885	1446.680	142.483	0.386	1511.152	0.355	28	0.146	R.LNLLDLAPGGHLGR.F
R4/RRR4-2/2	1283.325	1283.416	-70.754	0.348	275.417	0.317	14	0.145	-.NLPGVDVANVER.-
R4/RRR4-1/2	1796.818	1797.132	-175.300	0.282	783.381	0.383	17	0.145	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-1/2	1283.887	1283.416	368.333	0.223	302.623	0.282	15	0.145	R.NLPGVDVANVER.L
R4/RRR4-13/2	1283.138	1283.416	-217.042	0.212	308.329	0.285	15	0.144	R.NLPGVDVANVER.L
R4/RRR4-2/2	1283.123	1283.416	-229.068	0.316	255.605	0.382	14	0.143	-.NLPGVDVANVER.-
R4/RRR4-1/3	1446.860	1446.680	125.222	0.404	1337.169	0.397	26	0.141	R.LNLLDLAPGGHLGR.F
R4/RRR4-2/3	1446.237	1446.680	-306.991	0.438	1504.441	0.336	27	0.140	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/3	1447.709	1446.680	20.194	0.409	1403.805	0.364	27	0.137	R.LNLLDLAPGGHLGR.F
R4/RRR4-7/2	1796.472	1797.132	-926.866	0.220	672.833	0.255	16	0.132	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-4/3	1446.684	1446.680	3.367	0.443	1342.457	0.360	26	0.131	R.LNLLDLAPGGHLGR.F
R4/RRR4-8/3	1446.837	1446.680	109.103	0.413	1370.554	0.346	27	0.130	R.LNLLDLAPGGHLGR.F
R4/RRR4-3/3	1446.378	1446.680	-209.444	0.456	1109.647	0.425	25	0.129	R.LNLLDLAPGGHLGR.F
R4/RRR4-6/3	1446.155	1446.680	-1057.211	0.484	1180.645	0.399	25	0.127	R.LNLLDLAPGGHLGR.F
R4/RRR4-13/3	1446.944	1446.680	183.093	0.346	1291.775	0.347	26	0.125	R.LNLLDLAPGGHLGR.F
R4/RRR4-7/3	1446.451	1446.680	-158.773	0.418	1103.713	0.406	25	0.124	R.LNLLDLAPGGHLGR.F
R4/RRR4-11/3	1446.650	1446.680	-20.754	0.435	1036.962	0.412	24	0.122	R.LNLLDLAPGGHLGR.F
R4/RRR4-12/3	1446.966	1446.680	198.702	0.367	1280.509	0.331	25	0.121	R.LNLLDLAPGGHLGR.F
R4/RRR4-13/3	1446.490	1446.680	-131.598	0.466	1057.101	0.394	23	0.119	R.LNLLDLAPGGHLGR.F
R4/RRR4-10/3	1446.464	1446.680	-149.248	0.431	1161.695	0.359	24	0.118	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/3	1446.738	1446.680	40.434	0.387	1279.105	0.322	26	0.117	R.LNLLDLAPGGHLGR.F
R4/RRR4-13/3	1446.430	1446.680	-173.250	0.403	1116.210	0.354	25	0.114	R.LNLLDLAPGGHLGR.F
R4/RRR4-7/3	1446.410	1446.680	-187.092	0.427	1021.808	0.373	24	0.113	R.LNLLDLAPGGHLGR.F
R4/RRR4-6/3	1446.870	1446.680	132.203	0.438	907.005	0.390	24	0.111	R.LNLLDLAPGGHLGR.F
R4/RRR4-10/3	1447.052	1446.680	258.214	0.352	1079.821	0.340	24	0.110	R.LNLLDLAPGGHLGR.F
R4/RRR4-3/3	1446.467	1446.680	-147.598	0.300	1227.946	0.294	26	0.109	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/3	1840.146	1840.109	20.046	0.449	806.212	0.443	24	0.108	K.KLEEVYGTFEAPSLKK.K
R4/RRR4-2/3	1446.966	1446.680	198.448	0.357	985.336	0.351	24	0.108	R.LNLLDLAPGGHLGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1446.145	1446.680	-1064.331	0.372	1035.000	0.330	24	0.106	R.LNLLDLAPGGHLGR.F
R4/RRR4-12/3	1446.639	1446.680	-28.371	0.371	948.857	0.337	23	0.105	R.LNLLDLAPGGHLGR.F
R4/RRR4-1/3	1446.452	1446.680	-157.884	0.304	918.469	0.335	23	0.103	R.LNLLDLAPGGHLGR.F
R4/RRR4-9/3	1840.946	1840.109	-88.835	0.493	833.718	0.415	25	0.103	-.KLEEVYGTFEAPSLKK.-
R4/RRR4-6/3	1446.367	1446.680	-216.937	0.429	1120.643	0.291	25	0.102	R.LNLLDLAPGGHLGR.F
R4/RRR4-5/3	1446.178	1446.680	-1041.448	0.384	986.584	0.288	24	0.098	R.LNLLDLAPGGHLGR.F
R4/RRR4-8/3	1796.439	1797.132	-945.361	0.337	697.587	0.296	27	0.088	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-13/3	1797.039	1797.132	-52.000	0.262	722.307	0.227	28	0.082	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-7/3	1796.183	1797.132	-1088.335	0.222	895.070	0.160	30	0.077	R.VAVASALAATSVPSLVLAR.G
R4/RRR4-6/2	1315.868	1316.355	-370.939	0.504	2130.447	0.552	20	0.333	R.YDYENVDAGAAK.E
R4/RRR4-6/3	1985.940	1986.216	-139.470	0.509	2095.362	0.496	34	0.311	K.NKDNLGGDKLVTVEDIVR.Q
R4/RRR4-6/2	1489.233	1489.609	-252.860	0.506	1923.647	0.397	19	0.253	R.VYIEQYEKDSSK.T
R4/RRR4-6/2	1743.391	1743.940	-890.967	0.551	1637.167	0.532	24	0.251	K.DNLGGDKLVTVEDIVR.Q
R4/RRR4-6/2	1489.277	1489.609	-223.256	0.471	1515.599	0.453	18	0.217	R.VYIEQYEKDSSK.T
R4/RRR4-6/3	1985.949	1986.216	-134.660	0.501	1628.791	0.457	31	0.201	K.NKDNLGGDKLVTVEDIVR.Q
R4/RRR4-6/3	1986.336	1986.216	60.547	0.506	1539.988	0.465	30	0.190	K.NKDNLGGDKLVTVEDIVR.Q
R4/RRR4-6/2	1032.078	1032.133	-53.812	0.500	1213.749	0.441	17	0.189	K.GATIVVSGDGR.Y
R4/RRR4-6/2	1555.323	1555.755	-278.484	0.323	1466.832	0.342	23	0.188	R.DSQDALAPLVDVALK.L
R4/RRR4-6/2	1306.123	1306.511	-297.877	0.479	764.146	0.585	20	0.185	R.SM*PTSAALDVVAK.N
R4/RRR4-6/2	1555.201	1555.755	-1001.772	0.349	1163.551	0.385	21	0.172	R.DSQDALAPLVDVALK.L
R4/RRR4-6/2	1306.018	1306.511	-378.618	0.417	709.763	0.504	20	0.169	R.SM*PTSAALDVVAK.N
R4/RRR4-6/2	1032.005	1032.133	-124.644	0.368	1071.361	0.398	16	0.168	K.GATIVVSGDGR.Y
R4/RRR4-6/2	1306.065	1306.511	-342.700	0.441	635.853	0.484	19	0.164	R.SM*PTSAALDVVAK.N
R4/RRR4-6/2	1554.607	1555.755	-1385.781	0.342	1257.837	0.274	22	0.162	R.DSQDALAPLVDVALK.L
R4/RRR4-6/2	1291.027	1290.512	-376.369	0.415	487.216	0.477	18	0.159	R.SMPTSAALDVVAK.N
R4/RRR4-6/2	1110.625	1111.273	-1488.542	0.397	616.986	0.398	13	0.154	K.FFEVPTGWK.F
R4/RRR4-6/2	1111.051	1111.273	-200.519	0.400	386.960	0.367	11	0.147	K.FFEVPTGWK.F
R4/RRR4-6/2	1633.437	1633.787	-215.171	0.326	637.428	0.413	19	0.147	K.ATTPFDGQKPGTSGLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1289.990	1290.512	-1182.955	0.356	423.007	0.354	17	0.147	R.SMPTSAALDVVAK.N
R4/RRR4-6/2	887.880	888.044	-184.660	0.468	1026.282	0.219	13	0.145	K.DAVQIITK.M
R4/RRR4-6/2	887.350	888.044	-1915.040	0.394	512.245	0.265	12	0.144	K.DAVQIITK.M
R4/RRR4-6/2	1633.370	1633.787	-256.107	0.302	530.445	0.411	17	0.142	K.ATTPFDGQKPGTSGLR.K
R4/RRR4-5/2	1555.830	1555.755	48.428	0.337	774.454	0.243	17	0.137	R.DSQDALAPLVDVALK.L
R4/RRR4-6/2	1555.836	1555.755	52.678	0.272	435.670	0.317	14	0.137	R.DSQDALAPLVDVALK.L
R4/RRR4-6/2	1112.015	1111.273	-232.826	0.457	469.944	0.297	11	0.129	-.FFEVPTGWK.-
R4/RRR4-6/3	1761.324	1761.960	-931.919	0.442	995.822	0.355	28	0.101	K.KATTPFDGQKPGTSGLR.K
R4/RRR4-8/1	975.551	976.154	-1648.131	0.298	791.958	0.289	15	0.526	K.IGLFGGAGVGK.T
R4/RRR4-8/1	975.653	976.154	-1543.173	0.237	544.862	0.374	13	0.484	K.IGLFGGAGVGK.T
R4/RRR4-8/1	975.488	976.154	-1713.380	0.186	542.546	0.291	13	0.455	K.IGLFGGAGVGK.T
R4/RRR4-8/2	1707.855	1709.007	-1263.943	0.559	2420.486	0.623	23	0.410	R.LVLEVAQHLGENMVR.T
R4/RRR4-8/2	1709.580	1709.007	-250.778	0.576	2119.853	0.622	22	0.351	R.LVLEVAQHLGENMVR.T
R4/RRR4-8/2	1475.292	1474.791	-339.427	0.545	2355.484	0.453	20	0.336	K.TVLIM*ELINNVAK.A
R4/RRR4-8/2	1475.157	1474.791	248.506	0.567	2258.343	0.469	20	0.323	K.TVLIM*ELINNVAK.A
R4/RRR4-8/2	1493.261	1493.647	-258.819	0.533	2253.399	0.460	23	0.321	R.FTQANSEVSALLGR.I
R4/RRR4-8/2	1458.339	1458.792	-311.780	0.549	2239.497	0.403	20	0.299	K.TVLIMELINNVAK.A
R4/RRR4-8/2	1458.289	1458.792	-1033.839	0.567	2213.299	0.414	20	0.298	K.TVLIMELINNVAK.A
R4/RRR4-8/2	1474.436	1474.791	-241.804	0.480	2071.004	0.392	19	0.271	K.TVLIM*ELINNVAK.A
R4/RRR4-8/2	1458.417	1458.792	-257.783	0.484	1832.841	0.446	20	0.253	K.TVLIMELINNVAK.A
R4/RRR4-8/2	1857.278	1857.040	128.467	0.560	1260.196	0.604	24	0.227	R.M*LSPHVLGEDHYNTAR.G
R4/RRR4-8/2	1723.535	1725.007	-1438.379	0.498	1242.190	0.599	22	0.221	R.LVLEVAQHLGENM*VR.T
R4/RRR4-8/2	1390.614	1391.516	-1372.234	0.518	1124.295	0.623	23	0.219	K.AHGGFSVFAGVGER.T
R4/RRR4-8/2	1391.117	1391.516	-287.504	0.513	1207.586	0.584	23	0.218	K.AHGGFSVFAGVGER.T
R4/RRR4-8/2	1400.213	1400.608	-282.489	0.457	1413.885	0.508	18	0.217	R.VGLTGLTVAEHFR.D
R4/RRR4-8/3	1840.661	1841.041	-207.317	0.491	1562.526	0.522	31	0.212	R.MLSPHVLGEDHYNTAR.G
R4/RRR4-8/2	1279.080	1279.446	-286.716	0.428	1328.925	0.516	19	0.212	R.TIAM*DGTEGLVR.G
R4/RRR4-8/2	1865.464	1866.064	-860.361	0.494	1329.434	0.527	20	0.210	R.DAEGQDVLLFIDNIFR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1279.049	1279.446	-311.611	0.433	1336.636	0.496	19	0.209	R.TIAM*DGTEGLVR.G
R4/RRR4-8/2	1391.313	1391.516	-146.575	0.499	1173.493	0.550	24	0.208	K.AHGGFSVFAGVGER.T
R4/RRR4-15/2	1493.934	1493.647	192.710	0.513	1445.602	0.439	21	0.207	R.FTQANSEVSALLGR.I
R4/RRR4-8/2	1724.534	1725.007	-274.617	0.513	1095.846	0.578	21	0.204	R.LVLEVAQHLGENM*VR.T
R4/RRR4-8/2	1857.307	1857.040	143.891	0.526	1045.020	0.586	23	0.202	R.M*LSPHVLGEDHYNTAR.G
R4/RRR4-8/2	1410.181	1410.644	-329.026	0.408	1202.150	0.536	20	0.202	R.VLNTGSPITVPVGR.A
R4/RRR4-8/2	1410.293	1410.644	-249.911	0.413	1167.157	0.482	20	0.190	R.VLNTGSPITVPVGR.A
R4/RRR4-8/2	1400.372	1400.608	-168.446	0.474	1006.335	0.544	17	0.188	R.VGLTGLTVAEHFR.D
R4/RRR4-8/2	1410.219	1410.644	-302.190	0.446	1129.545	0.456	20	0.183	R.VLNTGSPITVPVGR.A
R4/RRR4-8/2	1400.571	1400.608	-26.279	0.483	911.736	0.546	16	0.182	R.VGLTGLTVAEHFR.D
R4/RRR4-8/2	1279.049	1279.446	-310.845	0.417	1109.522	0.449	18	0.181	R.TIAM*DGTEGLVR.G
R4/RRR4-8/2	976.023	976.154	-134.992	0.439	1173.248	0.415	17	0.181	K.IGLFGGAGVGK.T
R4/RRR4-8/2	976.053	976.154	-104.129	0.471	1134.510	0.419	17	0.179	K.IGLFGGAGVGK.T
R4/RRR4-12/2	976.195	976.154	42.253	0.410	998.501	0.457	15	0.174	K.IGLFGGAGVGK.T
R4/RRR4-8/2	1411.176	1410.644	-332.872	0.420	975.950	0.459	18	0.172	R.VLNTGSPITVPVGR.A
R4/RRR4-8/2	1174.176	1174.374	-169.718	0.451	763.696	0.496	14	0.170	K.VVDLLAPYQR.G
R4/RRR4-8/2	1263.022	1263.447	-337.214	0.466	1119.690	0.380	17	0.170	R.TIAMDGTEGLVR.G
R4/RRR4-8/2	975.893	976.154	-268.877	0.399	977.976	0.401	16	0.166	K.IGLFGGAGVGK.T
R4/RRR4-5/2	1494.841	1493.647	130.344	0.401	867.098	0.452	18	0.165	R.FTQANSEVSALLGR.I
R4/RRR4-8/2	1175.226	1174.374	-126.123	0.388	671.760	0.478	14	0.162	K.VVDLLAPYQR.G
R4/RRR4-8/2	1175.245	1174.374	-110.390	0.404	670.339	0.440	13	0.157	K.VVDLLAPYQR.G
R4/RRR4-8/3	1840.542	1841.041	-271.990	0.491	1313.518	0.464	30	0.157	R.MLSPHVLGEDHYNTAR.G
R4/RRR4-15/2	1493.336	1493.647	-208.793	0.442	728.842	0.417	17	0.155	R.FTQANSEVSALLGR.I
R4/RRR4-8/2	975.754	976.154	-411.083	0.287	815.984	0.400	14	0.153	K.IGLFGGAGVGK.T
R4/RRR4-8/2	1174.431	1174.374	48.309	0.367	773.936	0.351	14	0.151	K.VVDLLAPYQR.G
R4/RRR4-8/3	1856.517	1857.040	-822.744	0.498	1216.421	0.457	29	0.144	R.M*LSPHVLGEDHYNTAR.G
R4/RRR4-8/3	1856.742	1857.040	-161.382	0.481	1162.647	0.473	28	0.144	R.M*LSPHVLGEDHYNTAR.G
R4/RRR4-15/2	1492.748	1493.647	-1275.639	0.282	793.789	0.290	17	0.142	R.FTQANSEVSALLGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	975.373	976.154	-1831.717	0.274	782.359	0.279	14	0.142	-.IGLFGGAGVGK.-
R4/RRR4-7/2	1493.574	1493.647	-48.580	0.310	878.736	0.253	16	0.141	-.FTQANSEVSALLGR.-
R4/RRR4-8/3	1857.834	1857.040	-111.300	0.515	1001.262	0.510	27	0.139	R.M*LSPHVLGEDHYNTAR.G
R4/RRR4-1/2	1410.380	1410.644	-187.565	0.280	633.089	0.225	16	0.136	R.VLNTGSPITVPVGR.A
R4/RRR4-6/2	1174.013	1174.374	-308.342	0.273	583.496	0.203	11	0.135	K.VVDLLAPYQR.G
R4/RRR4-8/2	1411.074	1410.644	305.372	0.241	760.751	0.202	16	0.135	R.VLNTGSPITVPVGR.A
R4/RRR4-8/3	1708.592	1709.007	-243.944	0.433	709.610	0.589	31	0.133	R.LVLEVAQHLGENMVR.T
R4/RRR4-8/3	1724.155	1725.007	-1077.126	0.389	922.788	0.517	30	0.130	R.LVLEVAQHLGENM*VR.T
R4/RRR4-8/3	1708.625	1709.007	-224.269	0.449	715.951	0.567	29	0.130	R.LVLEVAQHLGENMVR.T
R4/RRR4-8/3	1401.718	1400.608	78.637	0.471	987.927	0.485	27	0.129	R.VGLTGLTVAEHFR.D
R4/RRR4-8/3	1493.498	1493.647	-99.705	0.438	1353.522	0.349	27	0.127	R.FTQANSEVSALLGR.I
R4/RRR4-8/3	1725.112	1725.007	61.348	0.487	762.765	0.526	30	0.125	R.LVLEVAQHLGENM*VR.T
R4/RRR4-8/3	1400.773	1400.608	118.198	0.447	1027.684	0.452	27	0.124	R.VGLTGLTVAEHFR.D
R4/RRR4-8/3	1411.488	1410.644	-111.093	0.389	868.284	0.492	24	0.121	R.VLNTGSPITVPVGR.A
R4/RRR4-8/3	1841.112	1841.041	38.822	0.522	911.040	0.461	27	0.120	R.MLSPHVLGEDHYNTAR.G
R4/RRR4-8/3	1400.364	1400.608	-174.621	0.421	973.617	0.422	26	0.113	R.VGLTGLTVAEHFR.D
R4/RRR4-8/3	1708.490	1709.007	-890.902	0.375	504.450	0.493	27	0.107	R.LVLEVAQHLGENMVR.T
R4/RRR4-8/3	1493.299	1493.647	-233.281	0.376	1291.326	0.282	26	0.105	R.FTQANSEVSALLGR.I
R4/RRR4-8/3	1474.608	1474.791	-124.505	0.395	1215.157	0.279	25	0.099	K.TVLIM*ELINNVAK.A
R4/RRR4-8/3	1410.688	1410.644	31.313	0.341	828.380	0.391	24	0.099	R.VLNTGSPITVPVGR.A
R4/RRR4-8/3	1475.165	1474.791	254.015	0.467	911.379	0.325	23	0.093	K.TVLIM*ELINNVAK.A
R4/RRR4-8/3	1493.105	1493.647	-1035.694	0.381	948.187	0.281	24	0.087	R.FTQANSEVSALLGR.I
R4/RRR4-8/3	1410.463	1410.644	-128.579	0.392	734.443	0.295	24	0.086	R.VLNTGSPITVPVGR.A
R4/RRR4-6/3	1740.325	1740.944	-933.103	0.575	2776.056	0.480	32	0.483	R.NIIHFNTLANQAVER.A
R4/RRR4-6/2	1741.302	1740.944	206.326	0.602	2318.856	0.592	24	0.379	R.NIIHFNTLANQAVER.A
R4/RRR4-6/2	1562.276	1562.774	-319.626	0.489	2511.228	0.434	23	0.360	R.TTLVANTSNM*PVAAR.E
R4/RRR4-6/2	1562.232	1562.774	-989.722	0.499	2390.199	0.496	22	0.357	R.TTLVANTSNM*PVAAR.E
R4/RRR4-6/2	1741.335	1740.944	225.096	0.607	2177.400	0.587	24	0.351	R.NIIHFNTLANQAVER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1518.687	1519.635	-1286.018	0.420	2181.086	0.574	24	0.344	K.FEDPAEGEDVLVAK.F
R4/RRR4-6/2	1545.995	1546.775	-1154.646	0.399	2293.094	0.478	23	0.333	R.TTLVANTSNMPVAAR.E
R4/RRR4-6/2	1519.128	1519.635	-994.853	0.460	2138.496	0.536	24	0.327	K.FEDPAEGEDVLVAK.F
R4/RRR4-6/2	1519.182	1519.635	-298.649	0.527	2058.962	0.545	24	0.318	K.FEDPAEGEDVLVAK.F
R4/RRR4-6/2	1740.370	1740.944	-907.358	0.521	2062.610	0.549	23	0.318	R.NIIHFNTLANQAVER.A
R4/RRR4-6/2	1563.261	1562.774	312.237	0.508	2072.362	0.457	22	0.289	R.TTLVANTSNM*PVAAR.E
R4/RRR4-6/2	1605.284	1605.769	-303.147	0.539	1807.289	0.563	22	0.282	K.DALAESDKITLETAK.L
R4/RRR4-6/3	1740.930	1740.944	-8.209	0.523	2095.390	0.395	29	0.258	R.NIIHFNTLANQAVER.A
R4/RRR4-6/2	1605.334	1605.769	-271.486	0.539	1707.389	0.511	22	0.253	K.DALAESDKITLETAK.L
R4/RRR4-6/2	1812.245	1813.024	-984.721	0.535	1484.936	0.582	24	0.243	R.LAEM*PADSGYPAYLAAR.L
R4/RRR4-6/2	1796.464	1797.025	-871.734	0.562	1337.062	0.601	24	0.232	R.LAEMPADSGYPAYLAAR.L
R4/RRR4-6/2	1472.429	1472.623	-131.848	0.482	1526.436	0.439	20	0.216	R.EDDLNEIVQLVGK.D
R4/RRR4-6/2	1811.804	1813.024	-1229.184	0.514	1344.221	0.526	24	0.215	R.LAEM*PADSGYPAYLAAR.L
R4/RRR4-6/2	1546.066	1546.775	-1108.582	0.339	1685.198	0.340	20	0.208	R.TTLVANTSNMPVAAR.E
R4/RRR4-6/2	1200.735	1201.310	-1315.551	0.560	1208.324	0.473	17	0.197	K.LYDDLTTGFR.N
R4/RRR4-6/2	1605.387	1605.769	-238.912	0.536	1165.574	0.517	20	0.196	K.DALAESDKITLETAK.L
R4/RRR4-6/2	1200.805	1201.310	-1257.458	0.536	1097.162	0.505	17	0.195	K.LYDDLTTGFR.N
R4/RRR4-6/2	1472.181	1472.623	-300.948	0.440	1485.869	0.360	19	0.194	R.EDDLNEIVQLVGK.D
R4/RRR4-5/2	1202.127	1201.310	-152.939	0.519	1035.386	0.529	16	0.194	K.LYDDLTTGFR.N
R4/RRR4-6/3	1605.595	1605.769	-108.377	0.482	1517.869	0.487	31	0.191	K.DALAESDKITLETAK.L
R4/RRR4-6/2	1472.221	1472.623	-273.912	0.401	1335.999	0.400	19	0.188	R.EDDLNEIVQLVGK.D
R4/RRR4-6/2	1734.692	1734.930	-137.394	0.442	1136.698	0.476	16	0.179	R.EASIYTGITIAEYFR.D
R4/RRR4-6/3	1605.776	1605.769	4.177	0.537	1543.963	0.427	31	0.173	K.DALAESDKITLETAK.L
R4/RRR4-5/2	1201.253	1201.310	-48.068	0.351	1129.752	0.379	16	0.170	K.LYDDLTTGFR.N
R4/RRR4-6/3	1605.935	1605.769	103.898	0.541	1418.077	0.452	30	0.166	K.DALAESDKITLETAK.L
R4/RRR4-6/2	1578.745	1578.795	-31.999	0.423	399.730	0.451	17	0.154	K.HFPSVNWLISYSK.Y
R4/RRR4-6/2	901.963	902.052	-99.448	0.385	796.965	0.345	11	0.153	R.MGDLFYR.L
R4/RRR4-6/2	1578.377	1578.795	-265.418	0.440	360.290	0.430	16	0.152	K.HFPSVNWLISYSK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1577.610	1578.795	-1388.935	0.258	346.265	0.332	16	0.141	K.HFPSVNWLISYSK.Y
R4/RRR4-6/3	1741.104	1740.944	92.000	0.475	1331.637	0.397	25	0.140	R.NIIHFNTLANQAVER.A
R4/RRR4-6/2	901.774	902.052	-309.238	0.341	620.615	0.237	10	0.139	-.MGDLFYR.-
R4/RRR4-6/3	1562.611	1562.774	-104.955	0.455	1159.338	0.426	27	0.130	R.TTLVANTSNM*PVAAR.E
R4/RRR4-6/3	1562.406	1562.774	-236.267	0.446	702.099	0.491	22	0.111	R.TTLVANTSNM*PVAAR.E
R4/RRR4-5/3	1741.643	1740.944	-173.268	0.420	1144.353	0.328	27	0.106	R.NIIHFNTLANQAVER.A
R4/RRR4-6/3	1578.152	1578.795	-1044.196	0.321	1450.565	0.181	25	0.095	K.HFPSVNWLISYSK.Y
R4/RRR4-6/3	1578.834	1578.795	25.070	0.399	1025.560	0.131	24	0.072	K.HFPSVNWLISYSK.Y
R4/RRR4-6/3	1578.184	1578.795	-1023.694	0.346	950.624	0.119	22	0.071	-.HFPSVNWLISYSK.-
R4/RRR4-5/2	1996.572	1997.232	-834.097	0.643	3079.480	0.589	27	0.552	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/2	1996.449	1997.232	-895.843	0.648	2519.272	0.614	25	0.426	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/2	1996.730	1997.232	-754.684	0.640	2481.302	0.607	24	0.414	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/3	1996.578	1997.232	-831.065	0.629	2190.616	0.562	38	0.351	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/2	1869.597	1869.059	-247.913	0.592	1893.478	0.545	23	0.288	K.ISEEEYISAIKEEISK.V
R4/RRR4-1/3	1998.088	1997.232	-72.596	0.580	1908.452	0.533	36	0.274	K.KISEEEYISAIKEEISK.V
R4/RRR4-1/3	1997.409	1997.232	88.592	0.560	1895.948	0.538	37	0.274	K.KISEEEYISAIKEEISK.V
R4/RRR4-2/3	1998.447	1997.232	107.539	0.541	1718.605	0.574	35	0.258	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/2	1282.139	1282.422	-221.031	0.484	1884.162	0.407	17	0.251	K.ISEEEYISAIK.E
R4/RRR4-3/3	1997.291	1997.232	29.380	0.552	1829.995	0.503	35	0.246	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/3	1997.240	1997.232	3.818	0.588	1747.983	0.541	36	0.246	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/2	1868.518	1869.059	-827.634	0.597	1612.644	0.529	22	0.244	K.ISEEEYISAIKEEISK.V
R4/RRR4-5/2	1868.416	1869.059	-882.199	0.598	1530.558	0.486	22	0.223	K.ISEEEYISAIKEEISK.V
R4/RRR4-2/3	1996.467	1997.232	-886.949	0.523	1513.190	0.573	34	0.222	K.KISEEEYISAIKEEISK.V
R4/RRR4-4/3	1999.172	1997.232	-30.237	0.550	1588.308	0.543	34	0.221	K.KISEEEYISAIKEEISK.V
R4/RRR4-4/3	1997.757	1997.232	-238.818	0.598	1421.676	0.510	34	0.183	K.KISEEEYISAIKEEISK.V
R4/RRR4-3/3	1997.132	1997.232	-50.622	0.520	1434.125	0.477	31	0.176	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/3	1997.557	1997.232	163.057	0.581	1214.592	0.487	31	0.152	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/3	1996.669	1997.232	-785.129	0.434	1113.308	0.441	28	0.133	K.KISEEEYISAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1997.218	1997.232	-7.217	0.502	1079.011	0.444	28	0.131	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/3	1868.717	1869.059	-183.959	0.493	717.159	0.478	29	0.114	K.ISEEEYISAIKEEISK.V
R4/RRR4-5/3	1410.473	1410.594	-86.304	0.450	1322.137	0.305	23	0.114	K.KISEEEYISAIK.E
R4/RRR4-5/3	1868.728	1869.059	-177.865	0.415	543.935	0.486	27	0.110	K.ISEEEYISAIKEEISK.V
R4/RRR4-5/3	1868.884	1869.059	-94.124	0.386	413.514	0.497	23	0.109	K.ISEEEYISAIKEEISK.V
R4/RRR4-6/3	1997.105	1997.232	-64.141	0.373	829.085	0.395	26	0.108	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/3	1996.916	1997.232	-158.967	0.382	958.874	0.369	29	0.108	K.KISEEEYISAIKEEISK.V
R4/RRR4-5/3	1997.629	1997.232	199.090	0.467	730.757	0.418	28	0.108	K.KISEEEYISAIKEEISK.V
R4/RRR4-4/3	1869.776	1869.059	-151.965	0.425	454.067	0.438	24	0.103	K.ISEEEYISAIKEEISK.V
R4/RRR4-2/3	1996.954	1997.232	-139.835	0.402	801.188	0.354	27	0.101	K.KISEEEYISAIKEEISK.V
R4/RRR4-4/3	1868.865	1869.059	-104.542	0.288	394.991	0.360	22	0.097	K.ISEEEYISAIKEEISK.V
R4/RRR4-6/3	1869.471	1869.059	220.663	0.387	432.350	0.334	24	0.096	K.ISEEEYISAIKEEISK.V
R4/RRR4-4/3	1869.269	1869.059	112.416	0.359	505.072	0.360	25	0.096	K.ISEEEYISAIKEEISK.V
R4/RRR4-6/3	1869.579	1869.059	-257.877	0.371	271.742	0.383	20	0.094	-.ISEEEYISAIKEEISK.-
R4/RRR4-1/3	1996.093	1997.232	-1075.086	0.312	726.141	0.242	24	0.091	K.KISEEEYISAIKEEISK.V
R4/RRR4-23/1	1549.829	1548.681	95.985	0.462	1088.607	0.610	18	1.000	R.AWSAADAVASWVGEK.K
R4/RRR4-23/1	1549.870	1548.681	122.684	0.450	921.728	0.611	17	0.863	R.AWSAADAVASWVGEK.K
R4/RRR4-23/1	1549.838	1548.681	101.830	0.420	860.600	0.529	17	0.732	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1548.297	1548.681	-248.828	0.453	2933.525	0.566	25	0.498	R.AWSAADAVASWVGEK.K
R4/RRR4-23/3	1384.720	1384.522	143.088	0.584	2443.415	0.599	30	0.437	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1384.669	1384.522	106.751	0.580	2363.373	0.605	30	0.417	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1385.537	1384.522	10.806	0.597	2320.587	0.619	29	0.416	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1548.238	1548.681	-286.955	0.432	2727.649	0.458	24	0.409	R.AWSAADAVASWVGEK.K
R4/RRR4-23/3	1384.789	1384.522	193.080	0.554	2334.214	0.584	30	0.397	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1384.605	1384.522	59.801	0.511	2312.282	0.577	30	0.388	R.RADGVGPVSWDPK.V
R4/RRR4-22/3	1384.702	1384.522	130.224	0.558	2244.229	0.598	30	0.381	R.RADGVGPVSWDPK.V
R4/RRR4-1/2	1549.394	1548.681	-185.829	0.530	2264.837	0.589	23	0.362	R.AWSAADAVASWVGEK.K
R4/RRR4-22/2	1548.205	1548.681	-308.472	0.463	2393.902	0.489	23	0.353	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1549.306	1548.681	-242.581	0.524	2165.064	0.597	23	0.346	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1549.239	1548.681	-285.821	0.544	2096.437	0.588	23	0.332	R.AWSAADAVASWVGEK.K
R4/RRR4-22/2	1549.241	1548.681	-284.793	0.532	2097.003	0.582	23	0.330	R.AWSAADAVASWVGEK.K
R4/RRR4-22/2	1676.434	1676.854	-251.427	0.578	2063.339	0.570	24	0.320	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/3	1383.724	1384.522	-1303.158	0.495	1989.275	0.585	28	0.316	R.RADGVGPVSWDPK.V
R4/RRR4-13/2	1549.345	1548.681	-217.208	0.514	2099.560	0.533	22	0.314	R.AWSAADAVASWVGEK.K
R4/RRR4-16/2	1548.216	1548.681	-301.194	0.410	2161.841	0.460	23	0.303	R.AWSAADAVASWVGEK.K
R4/RRR4-19/2	1548.346	1548.681	-216.874	0.463	2146.788	0.467	23	0.303	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1549.378	1548.681	-196.104	0.580	1968.942	0.566	22	0.303	R.AWSAADAVASWVGEK.K
R4/RRR4-4/2	1549.747	1548.681	42.772	0.560	1987.324	0.550	22	0.301	R.AWSAADAVASWVGEK.K
R4/RRR4-13/2	1548.204	1548.681	-308.788	0.392	2165.880	0.435	23	0.296	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1548.307	1548.681	-242.500	0.430	1962.622	0.513	21	0.286	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1548.203	1548.681	-309.658	0.508	1929.257	0.521	23	0.285	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1548.176	1548.681	-975.000	0.520	1817.213	0.578	22	0.284	R.AWSAADAVASWVGEK.K
R4/RRR4-7/2	1549.753	1548.681	46.564	0.495	1780.651	0.594	21	0.282	R.AWSAADAVASWVGEK.K
R4/RRR4-24/2	1549.124	1548.681	287.010	0.566	1849.852	0.554	22	0.281	R.AWSAADAVASWVGEK.K
R4/RRR4-16/2	1548.189	1548.681	-318.756	0.427	1932.156	0.508	21	0.280	R.AWSAADAVASWVGEK.K
R4/RRR4-24/2	1548.170	1548.681	-978.642	0.454	1916.529	0.496	22	0.275	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1548.245	1548.681	-282.367	0.495	1761.727	0.574	22	0.275	R.AWSAADAVASWVGEK.K
R4/RRR4-1/2	1548.764	1548.681	54.104	0.522	1860.117	0.517	21	0.272	R.AWSAADAVASWVGEK.K
R4/RRR4-2/2	1548.854	1548.681	111.847	0.518	1838.360	0.519	22	0.270	R.AWSAADAVASWVGEK.K
R4/RRR4-24/2	1549.018	1548.681	218.106	0.523	1874.464	0.499	22	0.270	R.AWSAADAVASWVGEK.K
R4/RRR4-12/2	1548.427	1548.681	-164.201	0.481	1893.671	0.488	21	0.269	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1547.945	1548.681	-1124.479	0.377	2035.703	0.406	23	0.269	R.AWSAADAVASWVGEK.K
R4/RRR4-25/2	1548.149	1548.681	-992.416	0.454	1910.043	0.474	22	0.268	R.AWSAADAVASWVGEK.K
R4/RRR4-21/2	1548.975	1548.681	190.605	0.531	1785.569	0.534	22	0.267	R.AWSAADAVASWVGEK.K
R4/RRR4-18/2	1548.264	1548.681	-270.185	0.431	1937.691	0.453	22	0.267	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1548.538	1548.681	-92.476	0.475	1804.278	0.517	21	0.265	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1548.351	1548.681	-213.394	0.486	1803.125	0.497	22	0.260	R.AWSAADAVASWVGEK.K
R4/RRR4-25/2	1548.405	1548.681	-178.594	0.494	1739.533	0.515	21	0.255	R.AWSAADAVASWVGEK.K
R4/RRR4-22/3	1384.762	1384.522	174.118	0.576	1629.099	0.605	26	0.253	R.RADGVGPVSWDPK.V
R4/RRR4-16/2	1548.461	1548.681	-142.532	0.478	1784.313	0.480	21	0.252	R.AWSAADAVASWVGEK.K
R4/RRR4-1/2	1676.342	1676.854	-904.400	0.485	1715.454	0.505	23	0.251	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1677.280	1676.854	255.153	0.593	1541.433	0.583	22	0.248	R.AWSAADAVASWVGEKK.N
R4/RRR4-21/2	1547.796	1548.681	-1221.648	0.368	1837.549	0.422	22	0.245	R.AWSAADAVASWVGEK.K
R4/RRR4-19/2	1547.583	1548.681	-1359.634	0.319	1960.857	0.347	23	0.243	R.AWSAADAVASWVGEK.K
R4/RRR4-21/2	1676.402	1676.854	-270.348	0.504	1658.206	0.503	23	0.243	R.AWSAADAVASWVGEKK.N
R4/RRR4-3/2	1548.406	1548.681	-178.041	0.418	1804.048	0.424	22	0.242	R.AWSAADAVASWVGEK.K
R4/RRR4-21/2	1547.973	1548.681	-1106.821	0.367	1827.356	0.408	22	0.241	R.AWSAADAVASWVGEK.K
R4/RRR4-19/2	1547.760	1548.681	-1245.013	0.337	1869.049	0.382	22	0.239	R.AWSAADAVASWVGEK.K
R4/RRR4-25/2	1547.884	1548.681	-1164.152	0.386	1736.552	0.451	22	0.239	R.AWSAADAVASWVGEK.K
R4/RRR4-6/2	1548.596	1548.681	-55.234	0.462	1670.983	0.478	21	0.238	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1676.358	1676.854	-296.722	0.544	1403.120	0.599	22	0.236	R.AWSAADAVASWVGEKK.N
R4/RRR4-3/2	1548.943	1548.681	169.583	0.494	1608.069	0.472	21	0.229	R.AWSAADAVASWVGEK.K
R4/RRR4-24/2	1676.748	1676.854	-63.426	0.536	1485.277	0.523	22	0.227	R.AWSAADAVASWVGEKK.N
R4/RRR4-20/2	1548.263	1548.681	-270.422	0.487	1518.560	0.506	20	0.226	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1405.196	1405.579	-273.558	0.495	1618.696	0.437	18	0.226	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1384.442	1384.522	-57.858	0.580	1565.200	0.561	26	0.223	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1548.061	1548.681	-1049.655	0.375	1626.443	0.435	21	0.223	R.AWSAADAVASWVGEK.K
R4/RRR4-21/2	1676.393	1676.854	-275.973	0.532	1494.314	0.496	22	0.221	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/3	1384.632	1384.522	79.431	0.532	1532.658	0.567	26	0.221	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1384.715	1384.522	139.773	0.544	1518.081	0.563	25	0.219	R.RADGVGPVSWDPK.V
R4/RRR4-2/3	1383.368	1384.522	-1561.843	0.500	1634.670	0.518	26	0.218	R.RADGVGPVSWDPK.V
R4/RRR4-12/2	1548.058	1548.681	-1051.634	0.402	1560.113	0.438	21	0.216	R.AWSAADAVASWVGEK.K
R4/RRR4-23/3	1548.674	1548.681	-4.603	0.500	1692.949	0.473	27	0.215	R.AWSAADAVASWVGEK.K
R4/RRR4-1/3	1384.574	1384.522	37.784	0.497	1379.530	0.603	25	0.213	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1548.467	1548.681	-138.578	0.431	1558.441	0.425	20	0.213	R.AWSAADAVASWVGEK.K
R4/RRR4-20/2	1547.328	1548.681	-1525.156	0.350	1601.640	0.402	20	0.212	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1405.143	1405.579	-311.734	0.541	1435.467	0.456	16	0.209	K.VCGHYTQVVWR.K
R4/RRR4-9/2	1548.247	1548.681	-281.180	0.383	1509.496	0.435	19	0.209	R.AWSAADAVASWVGEK.K
R4/RRR4-19/3	1384.539	1384.522	12.317	0.552	1433.102	0.570	26	0.207	R.RADGVGPVSWDPK.V
R4/RRR4-15/2	1548.202	1548.681	-310.212	0.369	1524.408	0.412	20	0.207	R.AWSAADAVASWVGEK.K
R4/RRR4-18/2	1548.252	1548.681	-278.095	0.418	1498.863	0.419	20	0.205	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1405.905	1405.579	231.948	0.601	1350.279	0.476	16	0.204	K.VCGHYTQVVWR.K
R4/RRR4-22/2	1677.238	1676.854	229.610	0.573	1234.291	0.537	20	0.203	R.AWSAADAVASWVGEKK.N
R4/RRR4-18/2	1547.294	1548.681	-1547.425	0.330	1631.329	0.336	21	0.203	R.AWSAADAVASWVGEK.K
R4/RRR4-26/2	1143.025	1143.274	-218.261	0.514	950.812	0.609	18	0.202	K.VASFAQSYAAK.R
R4/RRR4-3/3	1384.696	1384.522	126.246	0.545	1395.807	0.566	24	0.202	R.RADGVGPVSWDPK.V
R4/RRR4-6/2	1548.370	1548.681	-201.688	0.373	1545.409	0.378	20	0.202	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1406.162	1405.579	-297.750	0.539	1358.339	0.454	16	0.202	K.VCGHYTQVVWR.K
R4/RRR4-25/2	1142.933	1143.274	-299.051	0.501	1032.279	0.575	18	0.201	K.VASFAQSYAAK.R
R4/RRR4-23/2	1677.394	1676.854	-275.152	0.545	1086.569	0.588	19	0.201	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1406.240	1405.579	-241.924	0.525	1371.062	0.443	16	0.201	K.VCGHYTQVVWR.K
R4/RRR4-3/2	1143.006	1143.274	-235.404	0.482	1016.313	0.579	18	0.200	K.VASFAQSYAAK.R
R4/RRR4-20/2	1547.839	1548.681	-1193.771	0.330	1550.104	0.363	21	0.200	R.AWSAADAVASWVGEK.K
R4/RRR4-24/2	1142.736	1143.274	-1350.179	0.492	1060.396	0.555	18	0.199	K.VASFAQSYAAK.R
R4/RRR4-15/2	1548.346	1548.681	-217.111	0.383	1389.069	0.436	20	0.199	R.AWSAADAVASWVGEK.K
R4/RRR4-11/2	1143.061	1143.274	-186.442	0.443	996.221	0.586	18	0.198	K.VASFAQSYAAK.R
R4/RRR4-19/2	1143.174	1143.274	-87.354	0.508	971.218	0.580	18	0.198	K.VASFAQSYAAK.R
R4/RRR4-24/2	1676.459	1676.854	-236.160	0.480	1426.117	0.422	21	0.198	R.AWSAADAVASWVGEKK.N
R4/RRR4-2/2	1143.146	1143.274	-112.097	0.521	948.525	0.583	18	0.198	K.VASFAQSYAAK.R
R4/RRR4-23/2	1143.319	1143.274	39.129	0.533	945.534	0.582	18	0.198	K.VASFAQSYAAK.R
R4/RRR4-23/2	1143.079	1143.274	-170.801	0.458	1028.518	0.561	18	0.197	K.VASFAQSYAAK.R
R4/RRR4-23/2	1228.003	1228.336	-271.355	0.411	1304.495	0.455	18	0.197	R.ADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-27/2	1143.009	1143.274	-232.725	0.504	988.580	0.562	18	0.196	K.VASFAQSYAAK.R
R4/RRR4-1/3	1383.958	1384.522	-1133.609	0.520	1360.711	0.565	25	0.196	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1547.958	1548.681	-1116.402	0.349	1414.890	0.409	20	0.195	R.AWSAADAVASWVGEK.K
R4/RRR4-13/2	1143.004	1143.274	-236.582	0.504	1003.911	0.551	18	0.195	K.VASFAQSYAAK.R
R4/RRR4-22/2	1143.031	1143.274	-212.797	0.452	1038.338	0.546	18	0.195	K.VASFAQSYAAK.R
R4/RRR4-23/2	1676.260	1676.854	-953.382	0.485	1263.280	0.477	20	0.194	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1142.993	1143.274	-246.225	0.510	970.599	0.558	18	0.194	K.VASFAQSYAAK.R
R4/RRR4-20/2	1143.048	1143.274	-198.226	0.456	904.300	0.592	18	0.194	K.VASFAQSYAAK.R
R4/RRR4-22/2	1142.994	1143.274	-245.797	0.449	1003.570	0.553	18	0.194	K.VASFAQSYAAK.R
R4/RRR4-20/3	1384.005	1384.522	-1099.334	0.452	1323.534	0.569	25	0.193	R.RADGVGPVSWDPK.V
R4/RRR4-29/2	1143.041	1143.274	-204.012	0.474	999.270	0.541	18	0.192	K.VASFAQSYAAK.R
R4/RRR4-9/2	1143.068	1143.274	-180.871	0.479	1002.491	0.539	18	0.192	K.VASFAQSYAAK.R
R4/RRR4-20/3	1384.071	1384.522	-326.574	0.508	1442.739	0.526	26	0.192	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1548.137	1548.681	-1000.016	0.357	1414.208	0.388	20	0.192	R.AWSAADAVASWVGEK.K
R4/RRR4-29/2	1143.046	1143.274	-199.619	0.463	922.210	0.566	18	0.191	K.VASFAQSYAAK.R
R4/RRR4-1/2	1143.084	1143.274	-166.730	0.474	853.993	0.591	17	0.191	K.VASFAQSYAAK.R
R4/RRR4-17/2	1676.809	1676.854	-26.769	0.476	1187.055	0.481	21	0.190	R.AWSAADAVASWVGEKK.N
R4/RRR4-12/2	1547.952	1548.681	-1120.282	0.315	1460.740	0.359	19	0.190	R.AWSAADAVASWVGEK.K
R4/RRR4-17/2	1144.013	1143.274	-228.668	0.518	849.865	0.569	18	0.190	K.VASFAQSYAAK.R
R4/RRR4-22/2	1227.987	1228.336	-284.819	0.483	1121.501	0.491	17	0.189	R.ADGVGPVSWDPK.V
R4/RRR4-15/2	1143.074	1143.274	-175.300	0.465	947.121	0.542	18	0.189	K.VASFAQSYAAK.R
R4/RRR4-17/3	1384.737	1384.522	155.420	0.535	1392.639	0.537	26	0.189	R.RADGVGPVSWDPK.V
R4/RRR4-19/2	1142.489	1143.274	-1567.054	0.445	902.515	0.557	18	0.188	K.VASFAQSYAAK.R
R4/RRR4-2/2	1142.986	1143.274	-252.333	0.473	963.094	0.526	18	0.188	K.VASFAQSYAAK.R
R4/RRR4-23/2	1142.755	1143.274	-1333.549	0.429	931.018	0.546	18	0.188	K.VASFAQSYAAK.R
R4/RRR4-9/2	1143.013	1143.274	-228.868	0.452	955.913	0.530	18	0.187	K.VASFAQSYAAK.R
R4/RRR4-23/2	1677.358	1676.854	-296.253	0.408	1222.179	0.455	20	0.187	R.AWSAADAVASWVGEKK.N
R4/RRR4-22/2	1405.031	1405.579	-1105.705	0.487	1260.204	0.420	16	0.187	K.VCGHYTQVVWR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1675.212	1676.854	-2180.601	0.391	1474.074	0.341	20	0.187	R.AWSAADAVASWVGEKK.N
R4/RRR4-2/2	1142.427	1143.274	-1621.475	0.453	973.229	0.521	18	0.187	K.VASFAQSYAAK.R
R4/RRR4-23/2	1584.966	1585.607	-1037.960	0.435	1209.246	0.443	18	0.186	K.NYHYDTNTCDPGK.V
R4/RRR4-7/2	1143.028	1143.274	-215.475	0.459	944.445	0.523	18	0.186	K.VASFAQSYAAK.R
R4/RRR4-23/2	1142.579	1143.274	-1488.062	0.400	968.826	0.528	18	0.186	K.VASFAQSYAAK.R
R4/RRR4-25/2	1143.183	1143.274	-79.749	0.445	945.156	0.524	18	0.186	K.VASFAQSYAAK.R
R4/RRR4-15/3	1384.453	1384.522	-49.765	0.482	1408.683	0.519	26	0.185	R.RADGVGPVSWDPK.V
R4/RRR4-17/2	1143.015	1143.274	-226.832	0.463	819.482	0.565	17	0.185	K.VASFAQSYAAK.R
R4/RRR4-2/3	1384.652	1384.522	94.417	0.532	1245.415	0.572	24	0.184	R.RADGVGPVSWDPK.V
R4/RRR4-1/3	1384.138	1384.522	-278.128	0.494	1208.074	0.581	23	0.184	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1142.462	1143.274	-1591.097	0.412	896.858	0.540	18	0.184	K.VASFAQSYAAK.R
R4/RRR4-28/2	1143.391	1143.274	103.055	0.478	795.962	0.555	18	0.184	K.VASFAQSYAAK.R
R4/RRR4-20/2	1142.604	1143.274	-1465.848	0.393	934.955	0.529	18	0.184	K.VASFAQSYAAK.R
R4/RRR4-5/2	1143.116	1143.274	-138.448	0.485	921.559	0.509	18	0.183	K.VASFAQSYAAK.R
R4/RRR4-29/2	1142.426	1143.274	-1622.119	0.431	900.033	0.531	17	0.183	K.VASFAQSYAAK.R
R4/RRR4-14/2	1142.429	1143.274	-1620.079	0.376	913.471	0.536	18	0.182	K.VASFAQSYAAK.R
R4/RRR4-3/2	1142.424	1143.274	-1623.944	0.415	907.984	0.522	18	0.182	K.VASFAQSYAAK.R
R4/RRR4-22/2	1142.563	1143.274	-1501.799	0.368	961.997	0.513	18	0.182	K.VASFAQSYAAK.R
R4/RRR4-23/2	1676.555	1676.854	-178.453	0.390	1364.597	0.363	19	0.181	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1143.003	1143.274	-237.547	0.415	978.128	0.487	18	0.181	K.VASFAQSYAAK.R
R4/RRR4-5/2	1142.304	1143.274	-1729.798	0.433	952.076	0.481	18	0.179	K.VASFAQSYAAK.R
R4/RRR4-27/2	1142.635	1143.274	-1438.806	0.432	880.185	0.506	18	0.179	K.VASFAQSYAAK.R
R4/RRR4-23/2	1549.509	1548.681	-111.461	0.502	951.208	0.503	19	0.178	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1713.170	1713.780	-942.347	0.476	947.384	0.492	20	0.178	K.KNYHYDTNTCDPGK.V
R4/RRR4-13/2	1142.454	1143.274	-1597.645	0.341	981.189	0.489	18	0.178	K.VASFAQSYAAK.R
R4/RRR4-16/3	1384.654	1384.522	95.876	0.564	1306.607	0.535	25	0.177	R.RADGVGPVSWDPK.V
R4/RRR4-26/2	1143.042	1143.274	-203.797	0.460	773.156	0.525	17	0.177	K.VASFAQSYAAK.R
R4/RRR4-26/2	1144.041	1143.274	-204.583	0.487	809.308	0.501	18	0.177	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	1677.350	1676.854	296.603	0.526	953.163	0.500	19	0.176	R.AWSAADAVASWVGEKK.N
R4/RRR4-25/2	1142.931	1143.274	-301.301	0.446	691.752	0.549	16	0.176	K.VASFAQSYAAK.R
R4/RRR4-23/2	1585.160	1585.607	-282.897	0.383	1196.231	0.390	18	0.176	K.NYHYDTNTCDPGK.V
R4/RRR4-22/2	1227.795	1228.336	-1258.935	0.406	1043.681	0.443	17	0.175	R.ADGVGPVSWDPK.V
R4/RRR4-9/2	1548.431	1548.681	-161.670	0.453	1035.348	0.469	17	0.175	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1585.078	1585.607	-967.596	0.361	1064.861	0.455	17	0.175	K.NYHYDTNTCDPGK.V
R4/RRR4-1/2	1142.442	1143.274	-1608.164	0.413	936.265	0.463	18	0.175	K.VASFAQSYAAK.R
R4/RRR4-23/2	1677.572	1676.854	-168.200	0.453	1066.727	0.442	20	0.175	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1585.071	1585.607	-971.694	0.421	1108.204	0.412	18	0.174	K.NYHYDTNTCDPGK.V
R4/RRR4-27/2	1142.391	1143.274	-1653.036	0.396	756.596	0.517	18	0.174	K.VASFAQSYAAK.R
R4/RRR4-23/2	1228.024	1228.336	-254.700	0.406	1212.915	0.358	18	0.173	R.ADGVGPVSWDPK.V
R4/RRR4-22/3	1383.735	1384.522	-1295.583	0.490	1126.910	0.577	23	0.173	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1714.193	1713.780	242.016	0.534	868.180	0.481	20	0.173	K.KNYHYDTNTCDPGK.V
R4/RRR4-19/2	1142.424	1143.274	-1623.729	0.385	722.866	0.519	17	0.172	K.VASFAQSYAAK.R
R4/RRR4-19/3	1384.690	1384.522	122.002	0.556	1288.376	0.523	25	0.171	R.RADGVGPVSWDPK.V
R4/RRR4-1/2	1142.558	1143.274	-1506.521	0.383	798.341	0.487	18	0.171	K.VASFAQSYAAK.R
R4/RRR4-8/2	1144.156	1143.274	-103.544	0.492	595.842	0.524	16	0.171	K.VASFAQSYAAK.R
R4/RRR4-22/2	1227.633	1228.336	-1390.948	0.355	1042.049	0.416	17	0.170	R.ADGVGPVSWDPK.V
R4/RRR4-23/2	1384.124	1384.522	-288.338	0.461	585.154	0.520	20	0.170	R.RADGVGPVSWDPK.V
R4/RRR4-20/2	1142.346	1143.274	-1692.865	0.368	735.655	0.509	17	0.170	K.VASFAQSYAAK.R
R4/RRR4-17/2	1142.492	1143.274	-1564.478	0.399	745.273	0.484	17	0.169	K.VASFAQSYAAK.R
R4/RRR4-11/2	1143.212	1143.274	-54.472	0.374	862.531	0.453	17	0.169	K.VASFAQSYAAK.R
R4/RRR4-15/2	1142.963	1143.274	-272.798	0.441	777.165	0.463	17	0.169	K.VASFAQSYAAK.R
R4/RRR4-23/2	1713.100	1713.780	-983.338	0.539	917.076	0.438	20	0.168	K.KNYHYDTNTCDPGK.V
R4/RRR4-25/2	1676.158	1676.854	-1014.652	0.461	1396.507	0.263	23	0.167	R.AWSAADAVASWVGEKK.N
R4/RRR4-28/2	1143.017	1143.274	-225.225	0.434	767.882	0.451	17	0.167	K.VASFAQSYAAK.R
R4/RRR4-13/2	1142.408	1143.274	-1638.329	0.352	805.524	0.452	18	0.166	K.VASFAQSYAAK.R
R4/RRR4-14/2	1142.338	1143.274	-1699.629	0.333	923.656	0.416	18	0.166	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1142.466	1143.274	-1587.126	0.358	775.842	0.461	17	0.166	K.VASFAQSYAAK.R
R4/RRR4-14/2	1547.922	1548.681	-1139.683	0.292	1082.967	0.379	19	0.166	R.AWSAADAVASWVGEK.K
R4/RRR4-22/2	1675.264	1676.854	-2149.033	0.485	907.508	0.438	20	0.165	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1585.139	1585.607	-296.109	0.432	1015.511	0.391	17	0.164	K.NYHYDTNTCDPGK.V
R4/RRR4-23/2	1143.096	1143.274	-156.017	0.392	424.240	0.504	17	0.164	K.VASFAQSYAAK.R
R4/RRR4-23/2	1383.701	1384.522	-1320.071	0.438	664.628	0.447	21	0.164	R.RADGVGPVSWDPK.V
R4/RRR4-21/2	1384.251	1384.522	-196.412	0.435	513.456	0.490	19	0.164	R.RADGVGPVSWDPK.V
R4/RRR4-21/3	1384.485	1384.522	-26.948	0.452	1090.786	0.560	23	0.164	R.RADGVGPVSWDPK.V
R4/RRR4-21/3	1384.259	1384.522	-190.406	0.522	1156.362	0.539	24	0.163	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1584.959	1585.607	-1042.677	0.413	1006.708	0.385	17	0.163	K.NYHYDTNTCDPGK.V
R4/RRR4-20/2	1384.191	1384.522	-240.117	0.426	566.019	0.457	20	0.162	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1143.082	1143.274	-168.337	0.403	412.586	0.466	17	0.162	K.VASFAQSYAAK.R
R4/RRR4-23/2	1383.695	1384.522	-1324.058	0.415	593.753	0.451	20	0.162	R.RADGVGPVSWDPK.V
R4/RRR4-3/3	1384.334	1384.522	-136.003	0.418	1203.236	0.514	24	0.161	R.RADGVGPVSWDPK.V
R4/RRR4-17/2	1549.002	1548.681	208.149	0.403	854.172	0.413	19	0.161	R.AWSAADAVASWVGEK.K
R4/RRR4-21/2	1676.325	1676.854	-914.927	0.461	1039.726	0.353	21	0.160	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1227.903	1228.336	-353.739	0.337	989.537	0.367	16	0.160	-.ADGVGPVSWDPK.-
R4/RRR4-23/2	1143.075	1143.274	-174.550	0.319	438.288	0.493	17	0.159	K.VASFAQSYAAK.R
R4/RRR4-23/2	1675.540	1676.854	-1385.068	0.376	893.176	0.416	17	0.159	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1676.158	1676.854	-1014.726	0.396	952.279	0.386	18	0.159	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1548.343	1548.681	-218.614	0.344	852.378	0.417	17	0.159	R.AWSAADAVASWVGEK.K
R4/RRR4-20/2	1385.230	1384.522	-211.211	0.402	551.491	0.423	20	0.159	R.RADGVGPVSWDPK.V
R4/RRR4-8/2	1143.034	1143.274	-210.869	0.288	618.091	0.469	17	0.158	K.VASFAQSYAAK.R
R4/RRR4-5/2	1142.472	1143.274	-1581.973	0.424	615.602	0.412	16	0.158	K.VASFAQSYAAK.R
R4/RRR4-23/2	1677.890	1676.854	21.555	0.473	959.900	0.372	20	0.158	R.AWSAADAVASWVGEKK.N
R4/RRR4-22/2	1384.146	1384.522	-272.677	0.412	579.529	0.411	20	0.158	R.RADGVGPVSWDPK.V
R4/RRR4-20/2	1228.203	1228.336	-108.421	0.329	979.163	0.345	17	0.158	R.ADGVGPVSWDPK.V
R4/RRR4-23/2	1143.096	1143.274	-156.231	0.336	779.784	0.381	17	0.157	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1143.376	1143.274	89.456	0.312	922.348	0.331	18	0.156	K.VASFAQSYAAK.R
R4/RRR4-24/2	1384.171	1384.522	-254.096	0.401	474.471	0.416	18	0.156	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1548.624	1548.681	-36.860	0.468	1124.123	0.529	27	0.156	R.AWSAADAVASWVGEK.K
R4/RRR4-1/2	1676.471	1676.854	-228.928	0.468	658.590	0.465	16	0.156	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1142.157	1143.274	-1858.872	0.239	969.567	0.340	17	0.156	K.VASFAQSYAAK.R
R4/RRR4-23/2	1384.248	1384.522	-198.270	0.407	562.659	0.381	20	0.155	R.RADGVGPVSWDPK.V
R4/RRR4-21/2	1383.709	1384.522	-1314.046	0.356	578.172	0.394	20	0.155	R.RADGVGPVSWDPK.V
R4/RRR4-1/2	1384.180	1384.522	-247.637	0.407	469.447	0.403	18	0.155	R.RADGVGPVSWDPK.V
R4/RRR4-6/2	1144.198	1143.274	-66.516	0.349	771.636	0.354	17	0.155	K.VASFAQSYAAK.R
R4/RRR4-17/2	1547.965	1548.681	-1112.126	0.299	1168.580	0.260	18	0.155	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1677.978	1676.854	74.236	0.453	565.451	0.457	17	0.155	R.AWSAADAVASWVGEKK.N
R4/RRR4-19/2	1384.047	1384.522	-343.908	0.370	561.926	0.373	20	0.154	R.RADGVGPVSWDPK.V
R4/RRR4-15/3	1384.442	1384.522	-57.725	0.520	928.437	0.575	22	0.153	R.RADGVGPVSWDPK.V
R4/RRR4-24/2	1384.329	1384.522	-139.797	0.442	391.298	0.386	17	0.153	R.RADGVGPVSWDPK.V
R4/RRR4-22/2	1384.100	1384.522	-305.769	0.434	510.554	0.406	19	0.153	-.RADGVGPVSWDPK.-
R4/RRR4-22/2	1385.156	1384.522	-265.053	0.429	489.838	0.359	19	0.153	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1384.148	1384.522	-270.907	0.350	502.678	0.366	19	0.152	R.RADGVGPVSWDPK.V
R4/RRR4-1/2	1383.674	1384.522	-1339.209	0.353	489.619	0.363	19	0.152	R.RADGVGPVSWDPK.V
R4/RRR4-18/2	1384.457	1384.522	-46.748	0.384	442.434	0.361	18	0.152	R.RADGVGPVSWDPK.V
R4/RRR4-19/2	1384.173	1384.522	-253.123	0.408	412.886	0.423	17	0.152	-.RADGVGPVSWDPK.-
R4/RRR4-19/2	1383.862	1384.522	-1202.953	0.393	485.144	0.357	18	0.152	R.RADGVGPVSWDPK.V
R4/RRR4-2/3	1383.962	1384.522	-1130.687	0.494	937.698	0.570	24	0.152	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1384.223	1384.522	-216.937	0.400	502.551	0.400	18	0.151	-.RADGVGPVSWDPK.-
R4/RRR4-16/3	1384.532	1384.522	7.409	0.539	1124.784	0.504	23	0.150	R.RADGVGPVSWDPK.V
R4/RRR4-19/3	1384.532	1384.522	7.276	0.485	1272.353	0.459	26	0.150	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1142.320	1143.274	-1715.626	0.298	854.638	0.284	18	0.150	K.VASFAQSYAAK.R
R4/RRR4-17/3	1384.218	1384.522	-220.264	0.523	902.202	0.567	21	0.150	R.RADGVGPVSWDPK.V
R4/RRR4-16/2	1384.411	1384.522	-80.534	0.447	531.675	0.320	19	0.149	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1383.893	1384.522	-1180.897	0.395	316.505	0.411	15	0.149	-.RADGVGPVSWDPK.-
R4/RRR4-23/2	1678.413	1676.854	-263.605	0.430	338.195	0.455	14	0.149	R.AWSAADAVASWVGEKK.N
R4/RRR4-18/2	1384.166	1384.522	-258.254	0.383	510.949	0.303	19	0.149	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	1384.181	1384.522	-247.195	0.374	358.587	0.377	16	0.148	-.RADGVGPVSWDPK.-
R4/RRR4-23/2	1227.502	1228.336	-1498.622	0.304	970.265	0.269	16	0.148	R.ADGVGPVSWDPK.V
R4/RRR4-1/2	1547.920	1548.681	-1141.108	0.267	1072.779	0.231	18	0.148	R.AWSAADAVASWVGEK.K
R4/RRR4-1/2	1384.069	1384.522	-328.511	0.398	354.575	0.298	16	0.148	R.RADGVGPVSWDPK.V
R4/RRR4-3/2	1384.423	1384.522	-71.866	0.342	363.328	0.289	16	0.148	R.RADGVGPVSWDPK.V
R4/RRR4-24/2	1384.143	1384.522	-274.446	0.386	426.515	0.292	17	0.147	R.RADGVGPVSWDPK.V
R4/RRR4-5/2	1548.976	1548.681	191.079	0.376	573.528	0.377	15	0.147	R.AWSAADAVASWVGEK.K
R4/RRR4-21/2	1384.165	1384.522	-258.785	0.420	576.095	0.314	20	0.147	-.RADGVGPVSWDPK.-
R4/RRR4-23/2	1548.035	1548.681	-1066.123	0.307	444.104	0.388	15	0.147	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1675.808	1676.854	-1224.404	0.359	561.590	0.339	19	0.147	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	789.441	789.897	-578.745	0.280	682.209	0.357	11	0.146	R.VVCAANR.G
R4/RRR4-23/2	1678.334	1676.854	286.873	0.373	409.782	0.354	16	0.145	R.AWSAADAVASWVGEKK.N
R4/RRR4-23/2	1405.626	1405.579	33.395	0.337	285.783	0.280	12	0.144	K.VCGHYTQVVWR.K
R4/RRR4-21/2	1227.949	1228.336	-316.136	0.303	572.069	0.328	14	0.144	R.ADGVGPVSWDPK.V
R4/RRR4-18/2	1384.080	1384.522	-320.193	0.332	413.932	0.249	17	0.144	-.RADGVGPVSWDPK.-
R4/RRR4-23/2	1228.000	1228.336	-273.848	0.283	789.543	0.290	14	0.143	R.ADGVGPVSWDPK.V
R4/RRR4-23/2	1547.930	1548.681	-1134.377	0.292	713.459	0.304	15	0.143	R.AWSAADAVASWVGEK.K
R4/RRR4-18/2	1676.312	1676.854	-922.238	0.425	316.907	0.355	14	0.143	R.AWSAADAVASWVGEKK.N
R4/RRR4-11/3	1384.393	1384.522	-93.147	0.457	878.766	0.544	21	0.143	R.RADGVGPVSWDPK.V
R4/RRR4-23/2	790.004	789.897	135.515	0.251	508.175	0.352	10	0.142	R.VVCAANR.G
R4/RRR4-23/2	1548.293	1548.681	-251.518	0.265	551.738	0.229	17	0.141	R.AWSAADAVASWVGEK.K
R4/RRR4-23/2	1384.063	1384.522	-332.758	0.367	320.049	0.277	15	0.141	-.RADGVGPVSWDPK.-
R4/RRR4-20/2	1384.043	1384.522	-347.006	0.366	322.403	0.268	15	0.141	-.RADGVGPVSWDPK.-
R4/RRR4-14/2	1678.277	1676.854	253.105	0.430	387.402	0.375	14	0.140	-.AWSAADAVASWVGEKK.-
R4/RRR4-23/2	1384.149	1384.522	-270.199	0.344	351.555	0.277	16	0.139	-.RADGVGPVSWDPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1228.252	1228.336	-68.344	0.345	600.765	0.248	14	0.138	-.ADGVGPVSWDPK.-
R4/RRR4-18/3	1384.637	1384.522	83.144	0.408	668.562	0.586	22	0.138	R.RADGVGPVSWDPK.V
R4/RRR4-5/2	1547.950	1548.681	-1121.787	0.236	759.897	0.179	16	0.137	R.AWSAADAVASWVGEK.K
R4/RRR4-20/3	1384.375	1384.522	-106.813	0.494	925.462	0.511	23	0.137	R.RADGVGPVSWDPK.V
R4/RRR4-20/2	1228.018	1228.336	-259.287	0.258	723.777	0.198	14	0.136	R.ADGVGPVSWDPK.V
R4/RRR4-16/2	1676.541	1676.854	-187.072	0.456	638.819	0.303	18	0.134	-.AWSAADAVASWVGEKK.-
R4/RRR4-23/3	1383.984	1384.522	-1114.479	0.474	729.306	0.543	20	0.133	R.RADGVGPVSWDPK.V
R4/RRR4-15/3	1384.325	1384.522	-142.902	0.459	718.872	0.553	19	0.133	-.RADGVGPVSWDPK.-
R4/RRR4-12/3	1384.283	1384.522	-173.421	0.479	732.770	0.538	21	0.132	R.RADGVGPVSWDPK.V
R4/RRR4-6/2	1143.135	1143.274	-121.523	0.268	358.683	0.285	13	0.130	-.VASFAQSYAAK.-
R4/RRR4-18/3	1384.134	1384.522	-281.313	0.412	399.324	0.569	18	0.127	R.RADGVGPVSWDPK.V
R4/RRR4-16/3	1384.540	1384.522	13.378	0.525	643.316	0.533	20	0.127	R.RADGVGPVSWDPK.V
R4/RRR4-17/3	1384.257	1384.522	-191.866	0.492	727.850	0.525	20	0.126	-.RADGVGPVSWDPK.-
R4/RRR4-24/3	1384.580	1384.522	42.161	0.471	999.092	0.439	24	0.125	R.RADGVGPVSWDPK.V
R4/RRR4-18/3	1384.279	1384.522	-176.075	0.429	688.464	0.519	21	0.123	-.RADGVGPVSWDPK.-
R4/RRR4-22/3	1405.910	1405.579	235.638	0.548	1263.941	0.367	24	0.121	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1713.462	1713.780	-186.193	0.535	993.518	0.438	30	0.120	K.KNYHYDTNTCDPGK.V
R4/RRR4-13/3	1384.653	1384.522	95.080	0.328	298.885	0.395	21	0.114	R.RADGVGPVSWDPK.V
R4/RRR4-27/3	1384.801	1384.522	202.096	0.497	583.882	0.486	21	0.113	-.RADGVGPVSWDPK.-
R4/RRR4-23/3	1405.724	1405.579	103.062	0.567	1271.696	0.333	24	0.113	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1384.477	1384.522	-32.519	0.474	968.150	0.383	22	0.112	R.RADGVGPVSWDPK.V
R4/RRR4-13/3	1384.795	1384.522	197.986	0.286	309.543	0.383	21	0.112	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1405.420	1405.579	-113.969	0.534	1280.396	0.319	24	0.111	K.VCGHYTQVVWR.K
R4/RRR4-13/3	1384.797	1384.522	199.444	0.342	371.497	0.394	21	0.111	R.RADGVGPVSWDPK.V
R4/RRR4-22/3	1405.471	1405.579	-77.507	0.514	1074.488	0.363	23	0.110	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1384.452	1384.522	-50.826	0.459	909.141	0.377	23	0.109	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1549.394	1548.681	-185.759	0.477	836.246	0.430	21	0.109	-.AWSAADAVASWVGEK.-
R4/RRR4-23/3	1585.705	1585.607	61.869	0.341	877.345	0.433	29	0.108	K.NYHYDTNTCDPGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/3	1405.392	1405.579	-133.965	0.541	946.393	0.377	22	0.107	K.VCGHYTQVVWR.K
R4/RRR4-22/3	1713.933	1713.780	89.565	0.476	564.446	0.475	24	0.107	K.KNYHYDTNTCDPGK.V
R4/RRR4-23/3	1548.249	1548.681	-279.686	0.405	888.578	0.392	23	0.106	R.AWSAADAVASWVGEK.K
R4/RRR4-21/3	1384.714	1384.522	139.110	0.361	568.373	0.376	20	0.106	R.RADGVGPVSWDPK.V
R4/RRR4-23/3	1405.908	1405.579	234.332	0.559	1230.183	0.311	24	0.106	K.VCGHYTQVVWR.K
R4/RRR4-27/3	1384.363	1384.522	-114.906	0.424	432.027	0.405	20	0.105	-.RADGVGPVSWDPK.-
R4/RRR4-27/3	1384.407	1384.522	-83.462	0.341	365.985	0.426	19	0.105	-.RADGVGPVSWDPK.-
R4/RRR4-23/3	1406.502	1405.579	-55.166	0.547	1074.653	0.344	22	0.103	-.VCGHYTQVVWR.-
R4/RRR4-23/3	1585.187	1585.607	-265.406	0.387	741.158	0.413	25	0.103	K.NYHYDTNTCDPGK.V
R4/RRR4-23/3	1713.908	1713.780	75.207	0.494	720.628	0.412	26	0.103	K.KNYHYDTNTCDPGK.V
R4/RRR4-23/3	1585.680	1585.607	46.234	0.390	852.797	0.388	28	0.102	K.NYHYDTNTCDPGK.V
R4/RRR4-21/3	1405.150	1405.579	-306.513	0.522	852.327	0.349	21	0.101	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1384.584	1384.522	45.212	0.445	522.746	0.370	19	0.101	-.RADGVGPVSWDPK.-
R4/RRR4-21/3	1406.205	1405.579	-266.885	0.540	789.601	0.353	21	0.101	K.VCGHYTQVVWR.K
R4/RRR4-25/3	1405.341	1405.579	-170.038	0.481	561.169	0.330	17	0.101	K.VCGHYTQVVWR.K
R4/RRR4-19/3	1405.535	1405.579	-31.771	0.472	651.511	0.342	19	0.101	K.VCGHYTQVVWR.K
R4/RRR4-24/3	1406.488	1405.579	-64.959	0.469	586.215	0.329	18	0.100	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1585.681	1585.607	47.161	0.345	702.733	0.407	25	0.100	K.NYHYDTNTCDPGK.V
R4/RRR4-22/3	1548.570	1548.681	-71.729	0.372	381.385	0.383	21	0.099	R.AWSAADAVASWVGEK.K
R4/RRR4-19/3	1406.515	1405.579	-46.286	0.475	506.558	0.364	18	0.099	-.VCGHYTQVVWR.-
R4/RRR4-18/3	1405.620	1405.579	28.987	0.476	596.772	0.317	18	0.099	K.VCGHYTQVVWR.K
R4/RRR4-18/3	1405.966	1405.579	275.992	0.477	665.471	0.321	19	0.098	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1713.827	1713.780	27.632	0.463	668.735	0.392	26	0.098	K.KNYHYDTNTCDPGK.V
R4/RRR4-24/3	1406.415	1405.579	-117.066	0.496	825.523	0.355	22	0.098	-.VCGHYTQVVWR.-
R4/RRR4-3/3	1405.285	1405.579	-210.036	0.453	524.086	0.333	18	0.097	-.VCGHYTQVVWR.-
R4/RRR4-25/3	1405.609	1405.579	20.756	0.505	902.582	0.339	21	0.097	-.VCGHYTQVVWR.-
R4/RRR4-14/3	1406.163	1405.579	-297.194	0.426	621.010	0.343	19	0.097	-.VCGHYTQVVWR.-
R4/RRR4-14/3	1405.009	1405.579	-1121.330	0.420	756.009	0.309	20	0.097	K.VCGHYTQVVWR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/3	1405.793	1405.579	152.439	0.456	629.435	0.280	19	0.097	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1405.757	1405.579	126.706	0.512	945.340	0.297	22	0.095	K.VCGHYTQVVWR.K
R4/RRR4-20/3	1405.586	1405.579	4.815	0.473	617.639	0.327	18	0.095	-.VCGHYTQVVWR.-
R4/RRR4-25/3	1384.824	1384.522	218.538	0.405	707.076	0.339	23	0.095	-.RADGVGPVSWDPK.-
R4/RRR4-25/3	1405.065	1405.579	-1080.896	0.497	967.160	0.283	22	0.094	K.VCGHYTQVVWR.K
R4/RRR4-23/3	1405.787	1405.579	148.259	0.547	916.669	0.292	22	0.094	K.VCGHYTQVVWR.K
R4/RRR4-22/3	1405.499	1405.579	-57.644	0.512	731.632	0.279	20	0.093	K.VCGHYTQVVWR.K
R4/RRR4-21/3	1405.774	1405.579	138.985	0.535	656.652	0.264	19	0.093	K.VCGHYTQVVWR.K
R4/RRR4-11/3	1384.226	1384.522	-214.558	0.373	529.401	0.402	20	0.092	-.RADGVGPVSWDPK.-
R4/RRR4-23/3	1405.244	1405.579	-239.448	0.417	547.425	0.287	18	0.092	-.VCGHYTQVVWR.-
R4/RRR4-23/3	1585.798	1585.607	120.698	0.288	688.641	0.345	25	0.091	K.NYHYDTNTCDPGK.V
R4/RRR4-3/3	1405.035	1405.579	-1102.487	0.420	326.218	0.348	16	0.091	-.VCGHYTQVVWR.-
R4/RRR4-23/3	1405.175	1405.579	-288.994	0.389	432.755	0.327	18	0.091	-.VCGHYTQVVWR.-
R4/RRR4-3/3	1548.259	1548.681	-273.042	0.383	676.068	0.297	23	0.090	R.AWSAADAVASWVGEK.K
R4/RRR4-23/3	1584.609	1585.607	-1264.709	0.272	644.584	0.305	21	0.089	K.NYHYDTNTCDPGK.V
R4/RRR4-23/3	1405.256	1405.579	-230.689	0.435	762.325	0.258	19	0.086	-.VCGHYTQVVWR.-
R4/RRR4-23/3	1405.723	1405.579	102.670	0.439	665.341	0.279	18	0.086	-.VCGHYTQVVWR.-
R4/RRR4-23/3	1405.568	1405.579	-8.512	0.454	824.612	0.260	21	0.085	-.VCGHYTQVVWR.-
R4/RRR4-1/3	1548.412	1548.681	-174.451	0.452	611.405	0.331	24	0.083	-.AWSAADAVASWVGEK.-
R4/RRR4-23/3	1406.047	1405.579	333.318	0.484	670.633	0.311	19	0.083	-.VCGHYTQVVWR.-
R4/RRR4-15/3	1405.118	1405.579	-329.263	0.357	501.047	0.329	17	0.083	-.VCGHYTQVVWR.-
R4/RRR4-23/3	1547.351	1548.681	-1510.345	0.308	565.703	0.281	20	0.079	-.AWSAADAVASWVGEK.-
R4/RRR4-23/3	1586.077	1585.607	297.144	0.355	249.352	0.375	18	0.072	-.NYHYDTNTCDPGK.-
R4/RRR4-1/3	1404.837	1405.579	-1243.700	0.451	659.520	0.295	17	0.063	-.VCGHYTQVVWR.-
R4/RRR4-4/2	1487.169	1486.653	-325.989	0.512	1463.055	0.498	22	0.223	K.GLVDSDTLPLNVSR.E
R4/RRR4-4/2	1486.379	1486.653	-184.564	0.512	1477.504	0.485	22	0.222	K.GLVDSDTLPLNVSR.E
R4/RRR4-4/2	1965.306	1966.054	-891.848	0.523	1183.261	0.584	22	0.209	K.ADGSFAISEDTWNEPLGR.G
R4/RRR4-4/2	1486.377	1486.653	-185.718	0.471	1358.381	0.459	21	0.203	K.GLVDSDTLPLNVSR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1554.108	1552.749	231.336	0.591	1389.538	0.407	20	0.194	R.VFISDEFDELLPK.Y
R4/RRR4-4/2	1101.972	1102.223	-228.392	0.566	1093.602	0.476	17	0.190	K.LGIIEDATNR.N
R4/RRR4-4/2	1101.804	1102.223	-381.555	0.508	1198.295	0.396	17	0.181	K.LGIIEDATNR.N
R4/RRR4-4/2	1164.025	1164.245	-189.711	0.500	1045.548	0.443	18	0.179	K.ALDTESVDSVK.I
R4/RRR4-4/2	1101.825	1102.223	-362.102	0.467	1237.563	0.344	17	0.175	K.LGIIEDATNR.N
R4/RRR4-4/2	1578.483	1578.702	-139.045	0.440	1218.951	0.331	17	0.166	K.ETTTEWELLNDVK.A
R4/RRR4-4/2	1166.968	1167.294	-279.567	0.428	963.825	0.393	17	0.166	K.LASLDEYISR.M
R4/RRR4-4/2	1578.244	1578.702	-291.196	0.390	1218.079	0.262	17	0.156	K.ETTTEWELLNDVK.A
R4/RRR4-4/2	1578.088	1578.702	-1025.726	0.348	1070.575	0.257	16	0.147	K.ETTTEWELLNDVK.A
R4/RRR4-4/2	1709.741	1708.936	-114.263	0.465	698.131	0.355	17	0.145	R.RVFISDEFDELLPK.Y
R4/RRR4-4/2	1552.379	1552.749	-239.577	0.261	645.241	0.278	15	0.136	R.VFISDEFDELLPK.Y
R4/RRR4-4/3	1864.937	1864.989	-28.179	0.498	927.600	0.526	31	0.136	R.DKVAQDSESESLKQTAK.L
R4/RRR4-4/3	1701.618	1701.774	-91.864	0.558	1099.005	0.451	25	0.133	K.APHDLYESYYNSNK.S
R4/RRR4-26/2	1369.389	1370.557	-1587.700	0.365	805.526	0.203	14	0.132	K.SAMEEKKGQYAK.F
R4/RRR4-4/3	1864.596	1864.989	-211.386	0.515	689.920	0.548	28	0.125	R.DKVAQDSESESLKQTAK.L
R4/RRR4-4/3	1864.868	1864.989	-65.111	0.482	555.066	0.532	26	0.114	R.DKVAQDSESESLKQTAK.L
R4/RRR4-11/2	1425.243	1424.628	-270.655	0.533	1741.240	0.524	21	0.263	R.IHNAILQTISEGK.F
R4/RRR4-11/2	1424.458	1424.628	-119.613	0.531	1810.378	0.464	22	0.257	R.IHNAILQTISEGK.F
R4/RRR4-11/2	1802.452	1802.018	241.374	0.529	1443.764	0.605	26	0.245	R.ATLFPGDGIGPEIAESVK.Q
R4/RRR4-11/2	1425.038	1424.628	288.546	0.537	1556.080	0.477	20	0.228	R.IHNAILQTISEGK.F
R4/RRR4-11/2	1802.155	1802.018	76.254	0.484	1359.120	0.506	26	0.212	R.ATLFPGDGIGPEIAESVK.Q
R4/RRR4-11/2	1800.718	1802.018	-1281.237	0.386	1429.664	0.464	26	0.208	R.ATLFPGDGIGPEIAESVK.Q
R4/RRR4-11/2	1879.428	1879.302	67.411	0.440	1463.117	0.393	21	0.195	K.NLANPTALMLSAVM*M*LR.H
R4/RRR4-11/2	1242.379	1243.314	-1562.079	0.443	1149.261	0.469	17	0.190	R.HLQFNNQADR.I
R4/RRR4-11/2	1243.075	1243.314	-192.913	0.449	1157.830	0.438	17	0.185	R.HLQFNNQADR.I
R4/RRR4-11/2	1242.982	1243.314	-267.691	0.472	1149.080	0.432	17	0.184	R.HLQFNNQADR.I
R4/RRR4-11/2	1465.260	1465.637	-257.665	0.510	1345.288	0.351	19	0.181	K.TRYDDVNLVTIR.E
R4/RRR4-11/2	1685.426	1684.828	-239.189	0.437	886.915	0.499	17	0.170	R.TESFLTWESLESVR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1199.302	1199.339	-31.302	0.477	928.543	0.441	14	0.169	R.VAEYAFHYAK.T
R4/RRR4-11/2	1878.751	1879.302	-828.249	0.426	999.907	0.437	20	0.167	K.NLANPTALMLSAVM*M*LR.H
R4/RRR4-11/2	1465.178	1465.637	-313.668	0.498	1262.148	0.284	19	0.163	K.TRYDDVNLVTIR.E
R4/RRR4-11/2	1198.799	1199.339	-1288.977	0.391	1138.843	0.305	15	0.160	R.VAEYAFHYAK.T
R4/RRR4-11/2	1199.387	1199.339	40.362	0.425	682.690	0.443	14	0.159	R.VAEYAFHYAK.T
R4/RRR4-11/2	1847.310	1847.921	-874.184	0.458	486.981	0.534	18	0.159	R.ENTEGEYSGLEHQVVR.G
R4/RRR4-11/2	1847.367	1847.921	-843.538	0.465	491.808	0.505	18	0.156	R.ENTEGEYSGLEHQVVR.G
R4/RRR4-11/2	888.920	888.067	-166.042	0.397	656.541	0.409	13	0.152	-.GPM*ATPIGK.-
R4/RRR4-11/2	1878.876	1879.302	-227.505	0.388	708.494	0.415	18	0.150	K.NLANPTALMLSAVM*M*LR.H
R4/RRR4-11/2	1209.411	1208.346	54.302	0.371	878.898	0.151	14	0.128	-.YDDVNLVTIR.-
R4/RRR4-10/2	1826.615	1827.024	-224.522	0.545	1991.670	0.482	22	0.283	K.LAYVALDYEQELEAAK.S
R4/RRR4-10/2	1749.140	1748.915	128.754	0.585	1734.180	0.581	26	0.277	K.SYELPDGQVITIGAER.F
R4/RRR4-11/2	1748.396	1748.915	-871.610	0.535	1809.597	0.527	27	0.272	K.SYELPDGQVITIGAER.F
R4/RRR4-11/2	1748.547	1748.915	-211.369	0.506	1741.695	0.555	26	0.270	K.SYELPDGQVITIGAER.F
R4/RRR4-10/2	1748.395	1748.915	-871.891	0.545	1717.747	0.557	26	0.268	K.SYELPDGQVITIGAER.F
R4/RRR4-9/2	1749.517	1748.915	-228.187	0.584	1520.406	0.577	25	0.248	K.SYELPDGQVITIGAER.F
R4/RRR4-10/2	1748.288	1748.915	-933.573	0.543	1560.649	0.553	25	0.246	K.SYELPDGQVITIGAER.F
R4/RRR4-10/2	1430.041	1430.504	-325.228	0.422	1679.535	0.486	19	0.242	K.GEYDESGPAIVHR.K
R4/RRR4-10/2	1826.298	1827.024	-947.864	0.517	1635.167	0.499	20	0.238	K.LAYVALDYEQELEAAK.S
R4/RRR4-10/3	1748.445	1748.915	-269.755	0.455	1803.577	0.462	29	0.233	K.SYELPDGQVITIGAER.F
R4/RRR4-10/2	1826.442	1827.024	-868.956	0.521	1646.824	0.468	21	0.232	K.LAYVALDYEQELEAAK.S
R4/RRR4-9/2	1747.736	1748.915	-1250.583	0.454	1547.622	0.492	25	0.229	K.SYELPDGQVITIGAER.F
R4/RRR4-2/2	1748.520	1748.915	-226.777	0.514	1498.537	0.511	25	0.229	K.SYELPDGQVITIGAER.F
R4/RRR4-9/2	1748.297	1748.915	-928.385	0.513	1378.358	0.569	24	0.229	K.SYELPDGQVITIGAER.F
R4/RRR4-2/2	1749.806	1748.915	-62.317	0.576	1298.186	0.553	23	0.217	K.SYELPDGQVITIGAER.F
R4/RRR4-14/2	1748.292	1748.915	-931.049	0.509	1375.304	0.503	24	0.214	K.SYELPDGQVITIGAER.F
R4/RRR4-11/2	1748.322	1748.915	-913.665	0.533	1266.332	0.538	23	0.211	K.SYELPDGQVITIGAER.F
R4/RRR4-10/2	1430.136	1430.504	-258.086	0.426	1258.603	0.471	19	0.195	K.GEYDESGPAIVHR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	976.843	977.013	-173.922	0.482	1142.320	0.448	16	0.186	K.AGFAGDDAPR.A
R4/RRR4-9/2	976.787	977.013	-232.343	0.408	1193.660	0.427	16	0.184	K.AGFAGDDAPR.A
R4/RRR4-10/2	977.014	977.013	0.926	0.405	1387.911	0.337	16	0.183	K.AGFAGDDAPR.A
R4/RRR4-9/2	976.545	977.013	-480.648	0.383	1230.149	0.391	16	0.180	K.AGFAGDDAPR.A
R4/RRR4-3/2	977.176	977.013	167.319	0.386	1259.283	0.376	16	0.180	K.AGFAGDDAPR.A
R4/RRR4-10/2	976.312	977.013	-1747.626	0.340	1279.250	0.365	16	0.178	K.AGFAGDDAPR.A
R4/RRR4-10/2	976.870	977.013	-146.468	0.435	1095.296	0.422	15	0.177	K.AGFAGDDAPR.A
R4/RRR4-9/2	976.349	977.013	-1709.688	0.363	1270.686	0.343	16	0.175	K.AGFAGDDAPR.A
R4/RRR4-10/2	1163.585	1164.355	-1525.640	0.344	702.890	0.519	15	0.164	K.EITALAPSSM*K.I
R4/RRR4-10/2	1132.385	1133.193	-1600.822	0.323	863.612	0.414	16	0.158	R.GYSFTTTAER.E
R4/RRR4-9/3	1749.048	1748.915	76.322	0.383	1479.308	0.397	28	0.157	K.SYELPDGQVITIGAER.F
R4/RRR4-10/2	1164.001	1164.355	-304.938	0.362	620.154	0.449	14	0.155	K.EITALAPSSM*K.I
R4/RRR4-9/3	1516.780	1516.687	61.694	0.560	1337.142	0.456	25	0.154	K.IWHHTFYNELR.V
R4/RRR4-9/2	1198.745	1199.430	-1410.170	0.400	677.636	0.370	15	0.152	R.AVFPSIVGRPR.H
R4/RRR4-10/2	1136.414	1137.400	-1753.093	0.384	680.696	0.392	13	0.151	K.IKVVAPPERK.Y
R4/RRR4-10/3	1516.242	1516.687	-294.150	0.524	1279.072	0.464	25	0.150	K.IWHHTFYNELR.V
R4/RRR4-10/2	1163.440	1164.355	-1650.641	0.287	556.415	0.441	14	0.149	K.EITALAPSSM*K.I
R4/RRR4-11/2	1164.016	1164.355	-292.312	0.355	601.013	0.375	14	0.148	K.EITALAPSSM*K.I
R4/RRR4-11/2	1163.784	1164.355	-1354.105	0.315	401.199	0.416	12	0.146	K.EITALAPSSM*K.I
R4/RRR4-9/2	1199.224	1199.430	-172.810	0.393	491.887	0.353	14	0.145	-.AVFPSIVGRPR.-
R4/RRR4-10/2	1199.138	1199.430	-244.090	0.350	696.733	0.293	15	0.144	R.AVFPSIVGRPR.H
R4/RRR4-10/2	1199.337	1199.430	-78.057	0.352	659.947	0.284	15	0.144	R.AVFPSIVGRPR.H
R4/RRR4-9/2	1199.372	1199.430	-48.858	0.340	477.833	0.250	14	0.141	R.AVFPSIVGRPR.H
R4/RRR4-10/2	1136.428	1137.400	-1740.681	0.338	611.664	0.314	12	0.141	K.IKVVAPPERK.Y
R4/RRR4-10/2	1198.536	1199.430	-1584.896	0.289	368.749	0.287	12	0.132	-.AVFPSIVGRPR.-
R4/RRR4-9/3	1516.140	1516.687	-1023.310	0.515	853.731	0.484	20	0.122	K.IWHHTFYNELR.V
R4/RRR4-10/3	1516.682	1516.687	-3.328	0.523	1117.379	0.399	23	0.119	K.IWHHTFYNELR.V
R4/RRR4-10/3	1516.876	1516.687	125.133	0.477	1036.010	0.419	23	0.118	K.IWHHTFYNELR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/3	1145.157	1145.381	-196.964	0.428	1101.707	0.369	21	0.111	R.HTGVMVGMGQK.D
R4/RRR4-9/3	1516.184	1516.687	-994.452	0.494	968.262	0.392	22	0.109	K.IWHHTFYNELR.V
R4/RRR4-9/3	1748.085	1748.915	-1049.815	0.333	1056.327	0.310	25	0.096	K.SYELPDGQVITIGAER.F
R4/RRR4-9/3	1145.401	1145.381	17.293	0.416	903.136	0.276	19	0.086	-.HTGVMVGMGQK.-
R4/RRR4-10/3	1161.566	1161.381	160.138	0.414	734.464	0.237	18	0.083	R.HTGVM*VGMGQK.D
R4/RRR4-10/3	1144.950	1145.381	-377.775	0.352	684.300	0.226	18	0.081	-.HTGVMVGMGQK.-
R4/RRR4-10/3	1161.370	1161.381	-9.040	0.360	992.683	0.170	20	0.077	R.HTGVM*VGMGQK.D
R4/RRR4-10/2	1460.241	1460.531	-198.684	0.433	1446.181	0.514	18	0.221	K.AEYDESGPSIVHR.K
R4/RRR4-10/2	1890.197	1891.089	-1003.655	0.530	1447.314	0.491	21	0.216	K.LSYIALDYDQEMETAK.T
R4/RRR4-10/2	1459.972	1460.531	-1070.720	0.417	1264.781	0.448	17	0.189	K.AEYDESGPSIVHR.K
R4/RRR4-3/2	1553.656	1553.785	-83.661	0.483	2532.688	0.594	23	0.422	K.VHISDLVQGLSGTVK.L
R4/RRR4-3/2	1553.483	1553.785	-195.034	0.462	2546.346	0.557	23	0.411	K.VHISDLVQGLSGTVK.L
R4/RRR4-3/2	1554.380	1553.785	-261.403	0.520	2415.607	0.606	23	0.403	K.VHISDLVQGLSGTVK.L
R4/RRR4-3/2	1343.418	1343.599	-135.396	0.432	2211.787	0.331	17	0.277	R.IIWSNLLQSLR.S
R4/RRR4-2/2	1343.100	1343.599	-372.990	0.466	2058.047	0.344	17	0.257	R.IIWSNLLQSLR.S
R4/RRR4-3/2	1770.825	1771.048	-126.708	0.504	1741.557	0.492	21	0.251	R.VVVLTEENVIASLDLR.S
R4/RRR4-3/2	1352.339	1352.561	-165.104	0.470	1508.504	0.511	20	0.230	K.YVVTLSSGGSILR.A
R4/RRR4-3/2	1352.211	1352.561	-260.011	0.418	1498.133	0.482	19	0.220	K.YVVTLSSGGSILR.A
R4/RRR4-3/2	1957.688	1958.163	-243.262	0.540	1420.803	0.511	20	0.215	K.DGVSVANVEHNLFEWLK.G
R4/RRR4-3/2	1280.953	1281.397	-347.500	0.481	1217.176	0.564	17	0.213	K.FTSDVTNEVIR.E
R4/RRR4-3/2	1958.341	1958.163	91.367	0.540	1350.089	0.533	20	0.213	K.DGVSVANVEHNLFEWLK.G
R4/RRR4-3/2	1343.282	1343.599	-237.039	0.482	1613.124	0.350	16	0.204	R.IIWSNLLQSLR.S
R4/RRR4-3/2	1281.176	1281.397	-173.223	0.493	1161.596	0.517	17	0.199	K.FTSDVTNEVIR.E
R4/RRR4-3/2	1957.443	1958.163	-881.482	0.493	1306.820	0.485	20	0.198	K.DGVSVANVEHNLFEWLK.G
R4/RRR4-3/2	1580.423	1579.735	-197.675	0.429	989.179	0.546	18	0.187	K.ELWSIVFPSDTER.I
R4/RRR4-3/2	1280.531	1281.397	-1461.516	0.398	880.379	0.483	15	0.170	K.FTSDVTNEVIR.E
R4/RRR4-3/2	1352.389	1352.561	-127.889	0.355	684.324	0.525	14	0.160	K.YVVTLSSGGSILR.A
R4/RRR4-3/2	1495.894	1495.772	81.830	0.430	1053.928	0.328	17	0.155	R.VM*HENPSILIIGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1579.447	1579.735	-182.991	0.294	774.860	0.402	17	0.150	K.ELWSIVFPSDTER.I
R4/RRR4-3/2	1078.023	1077.259	-218.701	0.434	995.705	0.254	14	0.148	-.LNLYQLNAK.-
R4/RRR4-3/2	1077.305	1077.259	43.686	0.372	653.863	0.245	13	0.140	K.LNLYQLNAK.T
R4/RRR4-3/3	1409.993	1410.644	-1174.200	0.465	919.487	0.407	22	0.108	K.SSKPLLHVLSSNK.V
R4/RRR4-3/3	1338.590	1338.493	72.376	0.516	906.606	0.352	22	0.100	R.ICQWQVPHNR.V
R4/RRR4-3/3	1410.742	1410.644	69.846	0.419	706.185	0.411	21	0.099	K.SSKPLLHVLSSNK.V
R4/RRR4-3/3	1339.624	1338.493	98.322	0.501	654.673	0.312	19	0.091	R.ICQWQVPHNR.V
R4/RRR4-3/3	1339.284	1338.493	-156.987	0.479	678.344	0.308	19	0.090	R.ICQWQVPHNR.V
R4/RRR4-3/3	1409.804	1410.644	-1309.317	0.413	520.512	0.415	19	0.090	-.SSKPLLHVLSSNK.-
R4/RRR4-3/3	1495.004	1495.772	-1186.348	0.383	1071.478	0.152	22	0.068	-.VM*HENPSILIIGR.-
R4/RRR4-3/3	1495.837	1495.772	43.109	0.409	921.234	0.262	20	0.067	-.VM*HENPSILIIGR.-
R4/RRR4-8/3	1638.832	1638.812	12.348	0.555	1552.639	0.549	30	0.220	R.FRGEDKPPAHLGASR.D
R4/RRR4-8/3	1638.825	1638.812	7.978	0.527	1588.115	0.528	31	0.217	R.FRGEDKPPAHLGASR.D
R4/RRR4-9/3	1638.417	1638.812	-241.763	0.523	1637.009	0.496	32	0.211	R.FRGEDKPPAHLGASR.D
R4/RRR4-9/3	1638.326	1638.812	-297.826	0.577	1315.901	0.566	29	0.191	R.FRGEDKPPAHLGASR.D
R4/RRR4-9/3	1638.398	1638.812	-253.536	0.518	1313.035	0.533	30	0.178	R.FRGEDKPPAHLGASR.D
R4/RRR4-8/3	1638.712	1638.812	-61.171	0.490	1222.369	0.505	28	0.159	R.FRGEDKPPAHLGASR.D
R4/RRR4-6/2	1690.485	1689.801	-187.340	0.562	1968.157	0.593	22	0.317	K.YSNSQAVVYVGCGER.G
R4/RRR4-6/2	1255.576	1256.434	-1484.129	0.429	1159.721	0.502	19	0.195	K.LAADTPLLTGQR.V
R4/RRR4-6/2	1256.157	1256.434	-221.119	0.521	1118.353	0.483	19	0.191	K.LAADTPLLTGQR.V
R4/RRR4-6/2	1255.551	1256.434	-1503.954	0.434	775.089	0.478	16	0.165	K.LAADTPLLTGQR.V
R4/RRR4-6/2	946.497	947.111	-1710.703	0.361	573.013	0.440	14	0.156	K.TVISQALSK.Y
R4/RRR4-6/2	946.926	947.111	-196.096	0.422	651.720	0.369	15	0.155	K.TVISQALSK.Y
R4/RRR4-6/2	947.018	947.111	-98.595	0.359	614.969	0.346	15	0.150	K.TVISQALSK.Y
R4/RRR4-6/2	1170.886	1171.284	-340.744	0.358	740.525	0.310	14	0.144	K.LYDDLTAGFR.N
R4/RRR4-8/3	1823.951	1824.025	-40.761	0.504	2509.340	0.402	34	0.362	R.EILHIQGGQCGNQIGAK.F
R4/RRR4-8/2	1342.972	1343.427	-339.475	0.570	1805.748	0.556	20	0.282	R.INVYYNEASGGR.Y
R4/RRR4-8/2	1624.099	1623.946	94.490	0.506	1743.490	0.591	20	0.280	R.LHFFMVGFAPLTSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1386.272	1385.720	-324.368	0.500	1634.444	0.604	18	0.268	R.MMLTFSVFPSPK.V
R4/RRR4-8/2	1343.057	1343.427	-275.913	0.518	1769.502	0.526	20	0.268	R.INVYYNEASGGR.Y
R4/RRR4-8/2	1343.087	1343.427	-254.029	0.536	1721.090	0.537	20	0.265	R.INVYYNEASGGR.Y
R4/RRR4-8/2	1231.968	1232.391	-343.959	0.512	1836.812	0.463	17	0.260	R.VSEQFTAM*FR.R
R4/RRR4-8/2	1972.809	1974.161	-1195.477	0.516	1616.709	0.509	26	0.241	K.GHYTEGAELIDSVLDVVR.K
R4/RRR4-8/2	1639.554	1639.945	-239.064	0.462	1462.664	0.524	21	0.227	R.LHFFM*VGFAPLTSR.G
R4/RRR4-8/2	1232.023	1232.391	-299.422	0.546	1546.430	0.433	17	0.218	R.VSEQFTAM*FR.R
R4/RRR4-8/2	1974.244	1974.161	42.196	0.566	1291.104	0.558	23	0.214	K.GHYTEGAELIDSVLDVVR.K
R4/RRR4-8/2	1232.017	1232.391	-304.492	0.554	1365.670	0.418	16	0.197	R.VSEQFTAM*FR.R
R4/RRR4-8/2	1698.229	1697.871	211.127	0.514	1151.788	0.505	21	0.196	K.NSSYFVEWIPNNVK.S
R4/RRR4-2/2	1141.307	1140.403	-84.064	0.530	999.950	0.530	17	0.193	K.LAVNLIPFPR.L
R4/RRR4-8/2	1973.244	1974.161	-974.011	0.509	1114.543	0.527	22	0.192	K.GHYTEGAELIDSVLDVVR.K
R4/RRR4-8/2	1216.078	1216.391	-258.209	0.509	1256.516	0.413	17	0.189	R.VSEQFTAMFR.R
R4/RRR4-1/2	1140.032	1140.403	-326.232	0.470	980.857	0.515	17	0.188	K.LAVNLIPFPR.L
R4/RRR4-8/2	1216.049	1216.391	-282.178	0.567	1130.332	0.453	16	0.186	R.VSEQFTAMFR.R
R4/RRR4-7/2	1140.057	1140.403	-304.316	0.508	950.445	0.507	17	0.186	K.LAVNLIPFPR.L
R4/RRR4-8/2	1216.033	1216.391	-295.673	0.455	1164.785	0.434	17	0.185	R.VSEQFTAMFR.R
R4/RRR4-9/2	1140.275	1140.403	-112.487	0.558	1060.970	0.465	17	0.185	K.LAVNLIPFPR.L
R4/RRR4-8/2	1698.241	1697.871	218.047	0.522	1040.537	0.489	20	0.184	K.NSSYFVEWIPNNVK.S
R4/RRR4-8/2	1141.195	1140.403	-182.455	0.581	1076.104	0.455	17	0.184	K.LAVNLIPFPR.L
R4/RRR4-8/2	1140.762	1140.403	316.125	0.547	1054.969	0.452	17	0.182	K.LAVNLIPFPR.L
R4/RRR4-8/3	1824.053	1824.025	15.323	0.498	1578.729	0.426	30	0.181	R.EILHIQGGQCGNQIGAK.F
R4/RRR4-8/2	1747.653	1747.994	-195.401	0.451	856.841	0.535	22	0.180	R.ALTVPELTQQM*WDAK.N
R4/RRR4-9/2	1140.161	1140.403	-212.903	0.527	1063.306	0.432	17	0.179	K.LAVNLIPFPR.L
R4/RRR4-8/3	1823.354	1824.025	-919.218	0.447	1690.792	0.375	31	0.179	R.EILHIQGGQCGNQIGAK.F
R4/RRR4-9/2	1140.237	1140.403	-145.992	0.504	961.957	0.468	16	0.179	K.LAVNLIPFPR.L
R4/RRR4-1/2	1140.426	1140.403	20.977	0.490	893.215	0.469	16	0.176	K.LAVNLIPFPR.L
R4/RRR4-8/2	1697.346	1697.871	-901.648	0.480	1067.990	0.423	20	0.174	K.NSSYFVEWIPNNVK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1141.164	1140.403	-209.283	0.556	860.975	0.464	16	0.173	K.LAVNLIPFPR.L
R4/RRR4-12/2	1141.406	1140.403	3.045	0.500	944.924	0.435	16	0.173	K.LAVNLIPFPR.L
R4/RRR4-8/2	1747.438	1747.994	-892.935	0.465	635.444	0.573	19	0.173	R.ALTVPELTQQM*WDAK.N
R4/RRR4-8/2	1385.497	1385.720	-161.506	0.369	980.409	0.450	15	0.169	R.MMLTFSVFPSPK.V
R4/RRR4-9/2	1697.141	1697.871	-1022.452	0.406	921.589	0.452	19	0.168	K.NSSYFVEWIPNNVK.S
R4/RRR4-8/2	1060.227	1060.251	-23.282	0.432	617.217	0.496	14	0.166	R.YLTASAMFR.G
R4/RRR4-8/2	1732.184	1731.994	109.940	0.437	658.314	0.520	19	0.166	R.ALTVPELTQQMWDAK.N
R4/RRR4-5/2	1140.075	1140.403	-287.772	0.472	658.351	0.492	13	0.166	K.LAVNLIPFPR.L
R4/RRR4-7/2	1140.268	1140.403	-118.608	0.409	753.520	0.453	14	0.164	K.LAVNLIPFPR.L
R4/RRR4-8/2	1747.080	1747.994	-1098.735	0.450	716.291	0.475	20	0.164	R.ALTVPELTQQM*WDAK.N
R4/RRR4-10/2	1140.162	1140.403	-211.400	0.325	649.689	0.451	14	0.158	K.LAVNLIPFPR.L
R4/RRR4-12/2	1141.220	1140.403	-160.565	0.463	576.428	0.430	13	0.157	K.LAVNLIPFPR.L
R4/RRR4-13/2	1141.368	1140.403	-30.638	0.316	565.945	0.426	13	0.153	K.LAVNLIPFPR.L
R4/RRR4-6/2	1141.148	1140.403	-223.985	0.251	729.990	0.410	13	0.152	K.LAVNLIPFPR.L
R4/RRR4-8/2	1075.852	1076.251	-371.592	0.390	387.103	0.315	13	0.145	-.YLTASAM*FR.-
R4/RRR4-8/2	1401.140	1401.719	-1130.464	0.320	764.476	0.340	14	0.145	R.M*MLTFSVFPSPK.V
R4/RRR4-9/2	1733.269	1731.994	158.965	0.256	187.332	0.361	15	0.144	R.ALTVPELTQQMWDAK.N
R4/RRR4-8/2	1059.437	1060.251	-1718.098	0.287	630.740	0.288	14	0.143	R.YLTASAMFR.G
R4/RRR4-8/2	1731.265	1731.994	-1002.087	0.352	286.931	0.433	13	0.142	-.ALTVPELTQQMWDAK.-
R4/RRR4-2/2	1139.876	1140.403	-1343.685	0.230	517.315	0.288	11	0.141	K.LAVNLIPFPR.L
R4/RRR4-1/2	1140.367	1140.403	-31.416	0.267	494.230	0.253	11	0.140	-.LAVNLIPFPR.-
R4/RRR4-8/2	1730.557	1731.994	-1412.775	0.240	572.138	0.303	17	0.139	R.ALTVPELTQQMWDAK.N
R4/RRR4-10/2	1140.071	1140.403	-291.532	0.234	473.691	0.259	11	0.138	-.LAVNLIPFPR.-
R4/RRR4-12/2	1975.788	1974.161	-189.351	0.319	480.063	0.307	16	0.135	K.GHYTEGAELIDSVLDVVR.K
R4/RRR4-9/2	1418.935	1417.719	152.824	0.202	481.400	0.270	12	0.134	R.M*M*LTFSVFPSPK.V
R4/RRR4-8/2	1075.454	1076.251	-1676.295	0.262	249.215	0.389	11	0.129	-.YLTASAM*FR.-
R4/RRR4-8/3	1973.715	1974.161	-226.281	0.476	1232.785	0.343	29	0.116	K.GHYTEGAELIDSVLDVVR.K
R4/RRR4-8/3	1697.853	1697.871	-11.157	0.434	908.723	0.438	23	0.112	K.NSSYFVEWIPNNVK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/3	1640.602	1639.945	-209.815	0.506	1108.045	0.353	29	0.109	R.LHFFM*VGFAPLTSR.G
R4/RRR4-8/3	1639.993	1639.945	29.121	0.423	778.978	0.351	25	0.092	R.LHFFM*VGFAPLTSR.G
R4/RRR4-7/3	1972.976	1974.161	-1110.426	0.415	1207.891	0.241	29	0.091	K.GHYTEGAELIDSVLDVVR.K
R4/RRR4-12/2	1330.022	1330.456	-327.591	0.464	1876.250	0.501	20	0.275	K.FSNACGAICTTK.K
R4/RRR4-12/2	1329.485	1330.456	-1487.177	0.417	1771.398	0.482	20	0.254	K.FSNACGAICTTK.K
R4/RRR4-11/2	1331.078	1330.456	-285.295	0.515	1589.669	0.524	19	0.244	K.FSNACGAICTTK.K
R4/RRR4-11/2	1452.110	1452.588	-330.403	0.500	1632.028	0.502	19	0.241	K.SAGILCSYDPNVR.L
R4/RRR4-11/2	1452.114	1452.588	-327.704	0.458	1598.876	0.480	19	0.232	K.SAGILCSYDPNVR.L
R4/RRR4-11/2	1329.559	1330.456	-1431.105	0.406	1579.638	0.489	19	0.231	K.FSNACGAICTTK.K
R4/RRR4-11/2	1329.568	1330.456	-1424.373	0.440	1535.647	0.506	19	0.231	K.FSNACGAICTTK.K
R4/RRR4-12/2	1329.976	1330.456	-362.585	0.487	1538.285	0.475	19	0.226	K.FSNACGAICTTK.K
R4/RRR4-11/2	1452.095	1452.588	-340.777	0.509	1476.006	0.512	18	0.225	K.SAGILCSYDPNVR.L
R4/RRR4-12/2	1452.219	1452.588	-254.667	0.489	1438.956	0.488	18	0.216	K.SAGILCSYDPNVR.L
R4/RRR4-12/2	1453.433	1452.588	-107.204	0.524	1299.484	0.539	17	0.212	K.SAGILCSYDPNVR.L
R4/RRR4-12/2	1452.161	1452.588	-294.811	0.511	1284.407	0.469	17	0.196	K.SAGILCSYDPNVR.L
R4/RRR4-11/2	1955.601	1953.995	-201.949	0.546	1084.788	0.550	20	0.191	-.VSDDEVAFLTQGDANDEK.-
R4/RRR4-11/2	1905.981	1907.287	-1213.561	0.458	995.570	0.565	24	0.190	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-11/2	1779.577	1779.114	260.989	0.460	766.299	0.626	24	0.187	K.GAIPALPTVAVAQELISK.A
R4/RRR4-11/2	1778.522	1779.114	-897.738	0.449	816.028	0.612	23	0.186	K.GAIPALPTVAVAQELISK.A
R4/RRR4-11/3	1907.343	1907.287	29.739	0.479	1340.269	0.520	31	0.181	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-11/3	1907.403	1907.287	61.320	0.518	1406.205	0.490	30	0.180	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-11/2	1778.436	1779.114	-945.973	0.447	655.075	0.611	23	0.178	K.GAIPALPTVAVAQELISK.A
R4/RRR4-11/2	1906.776	1907.287	-794.461	0.511	800.467	0.563	22	0.177	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-12/2	1906.166	1907.287	-1115.617	0.462	731.094	0.585	20	0.173	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-12/2	1778.615	1779.114	-281.315	0.379	705.557	0.587	22	0.173	K.GAIPALPTVAVAQELISK.A
R4/RRR4-11/2	1907.566	1907.287	147.136	0.469	655.361	0.567	21	0.169	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-12/2	1256.156	1255.404	-198.214	0.474	576.889	0.522	16	0.169	R.LPLWPSEDAAR.A
R4/RRR4-12/2	1907.663	1907.287	197.896	0.451	678.174	0.533	21	0.165	K.KGAIPALPTVAVAQELISK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1255.178	1255.404	-180.616	0.480	584.961	0.465	16	0.163	R.LPLWPSEDAAR.A
R4/RRR4-11/2	1254.596	1255.404	-1445.862	0.407	568.752	0.486	16	0.162	R.LPLWPSEDAAR.A
R4/RRR4-11/2	1254.527	1255.404	-1500.985	0.431	591.338	0.470	16	0.162	R.LPLWPSEDAAR.A
R4/RRR4-11/2	1254.459	1255.404	-1554.941	0.373	718.733	0.444	17	0.161	R.LPLWPSEDAAR.A
R4/RRR4-12/2	1906.863	1907.287	-222.906	0.474	498.033	0.567	18	0.160	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-12/2	1256.312	1255.404	-73.640	0.467	474.741	0.475	14	0.159	R.LPLWPSEDAAR.A
R4/RRR4-10/2	1780.615	1779.114	-280.861	0.410	704.858	0.442	21	0.156	K.GAIPALPTVAVAQELISK.A
R4/RRR4-11/2	987.845	988.160	-319.787	0.369	542.815	0.430	13	0.155	K.LLIVTDGEK.G
R4/RRR4-11/2	987.565	988.160	-1619.664	0.382	505.152	0.403	13	0.154	K.LLIVTDGEK.G
R4/RRR4-11/2	1234.014	1234.254	-194.925	0.459	846.516	0.338	14	0.152	K.DDSIFHNEEK.L
R4/RRR4-11/2	987.923	988.160	-241.064	0.437	583.303	0.363	13	0.152	K.LLIVTDGEK.G
R4/RRR4-11/2	1503.100	1503.599	-332.553	0.393	730.426	0.393	16	0.151	K.DDSIFHNEEKLR.E
R4/RRR4-12/2	988.009	988.160	-153.678	0.370	555.401	0.363	13	0.150	K.LLIVTDGEK.G
R4/RRR4-12/2	988.042	988.160	-120.214	0.371	656.051	0.332	14	0.150	K.LLIVTDGEK.G
R4/RRR4-12/2	987.874	988.160	-290.404	0.331	527.297	0.363	13	0.149	K.LLIVTDGEK.G
R4/RRR4-13/2	1779.106	1779.114	-4.446	0.338	386.828	0.485	16	0.147	K.GAIPALPTVAVAQELISK.A
R4/RRR4-13/2	1254.579	1255.404	-1459.544	0.272	324.073	0.395	12	0.145	R.LPLWPSEDAAR.A
R4/RRR4-11/2	1233.998	1234.254	-208.024	0.407	829.982	0.275	14	0.145	K.DDSIFHNEEK.L
R4/RRR4-11/2	1233.921	1234.254	-270.946	0.391	648.140	0.317	13	0.144	K.DDSIFHNEEK.L
R4/RRR4-13/2	1780.699	1779.114	-233.749	0.305	295.415	0.472	15	0.144	K.GAIPALPTVAVAQELISK.A
R4/RRR4-16/2	1256.420	1255.404	12.706	0.310	337.239	0.308	11	0.142	R.LPLWPSEDAAR.A
R4/RRR4-14/2	1778.207	1779.114	-1075.540	0.223	379.365	0.362	15	0.136	K.GAIPALPTVAVAQELISK.A
R4/RRR4-11/3	1907.408	1907.287	63.630	0.403	1150.887	0.425	29	0.130	K.KGAIPALPTVAVAQELISK.A
R4/RRR4-9/2	1969.673	1969.163	-249.552	0.585	2347.161	0.539	23	0.362	R.TMLELLNQLDGFSSDER.I
R4/RRR4-9/2	1646.230	1645.948	171.684	0.540	2100.738	0.539	23	0.318	K.LAGPQLVQMFIGDGAK.L
R4/RRR4-9/2	1968.408	1969.163	-894.174	0.519	1826.763	0.567	21	0.282	R.TMLELLNQLDGFSSDER.I
R4/RRR4-9/2	1645.255	1645.948	-1031.925	0.507	1686.845	0.557	22	0.261	K.LAGPQLVQMFIGDGAK.L
R4/RRR4-9/2	1793.678	1793.044	-205.095	0.516	1726.355	0.496	22	0.251	K.SPCIIFIDEIDAIGTK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1968.000	1969.163	-1102.340	0.438	1672.784	0.399	21	0.218	R.TMLELLNQLDGFSSDER.I
R4/RRR4-9/3	1680.855	1680.761	56.364	0.485	1752.170	0.401	25	0.199	K.RFDSEVSGDREVQR.T
R4/RRR4-9/2	1661.727	1661.947	-132.626	0.445	1294.677	0.444	20	0.191	K.LAGPQLVQM*FIGDGAK.L
R4/RRR4-9/2	1644.323	1645.948	-2210.766	0.306	1302.240	0.406	19	0.182	K.LAGPQLVQMFIGDGAK.L
R4/RRR4-8/2	1159.271	1159.360	-76.952	0.457	917.712	0.518	15	0.178	K.GVLLYGPPGTGK.T
R4/RRR4-9/2	1158.384	1159.360	-1710.966	0.368	1072.350	0.454	17	0.177	K.GVLLYGPPGTGK.T
R4/RRR4-9/2	1661.278	1661.947	-1007.778	0.442	1164.829	0.420	19	0.176	K.LAGPQLVQM*FIGDGAK.L
R4/RRR4-8/2	1159.069	1159.360	-251.684	0.444	891.893	0.511	15	0.175	K.GVLLYGPPGTGK.T
R4/RRR4-9/2	1159.008	1159.360	-304.411	0.396	891.275	0.488	16	0.172	K.GVLLYGPPGTGK.T
R4/RRR4-9/2	1296.073	1296.448	-290.356	0.383	1407.419	0.273	18	0.171	R.ACAAQTNATFLK.L
R4/RRR4-9/2	1888.631	1888.021	-207.360	0.569	793.028	0.509	21	0.171	K.DSYLILDTLPSEYDSR.V
R4/RRR4-9/2	1196.286	1196.249	31.358	0.512	942.539	0.427	17	0.170	R.STDDFNGAQLK.A
R4/RRR4-9/2	1159.190	1159.360	-147.091	0.421	857.629	0.456	16	0.166	K.GVLLYGPPGTGK.T
R4/RRR4-8/2	1645.539	1645.948	-249.303	0.350	845.664	0.501	18	0.166	K.LAGPQLVQMFIGDGAK.L
R4/RRR4-9/2	1887.254	1888.021	-938.982	0.472	822.425	0.460	20	0.163	K.DSYLILDTLPSEYDSR.V
R4/RRR4-9/3	1968.723	1969.163	-223.932	0.478	1342.105	0.454	29	0.160	R.TMLELLNQLDGFSSDER.I
R4/RRR4-9/2	1660.505	1661.947	-1475.429	0.306	1057.326	0.362	19	0.159	K.LAGPQLVQM*FIGDGAK.L
R4/RRR4-9/2	1195.369	1196.249	-1576.906	0.352	771.985	0.340	16	0.150	R.STDDFNGAQLK.A
R4/RRR4-9/3	1680.377	1680.761	-229.424	0.483	1422.181	0.385	25	0.146	K.RFDSEVSGDREVQR.T
R4/RRR4-8/2	1159.141	1159.360	-189.559	0.338	457.334	0.414	11	0.144	K.GVLLYGPPGTGK.T
R4/RRR4-9/2	1670.762	1669.986	-134.297	0.366	368.392	0.402	15	0.143	R.QTIFLPVIGLVDPEK.L
R4/RRR4-9/2	1669.145	1669.986	-1105.839	0.337	764.073	0.296	19	0.142	R.QTIFLPVIGLVDPEK.L
R4/RRR4-9/2	1668.771	1669.986	-1331.257	0.306	568.345	0.366	17	0.142	R.QTIFLPVIGLVDPEK.L
R4/RRR4-9/2	1195.165	1196.249	-1748.665	0.255	294.785	0.297	13	0.140	-.STDDFNGAQLK.-
R4/RRR4-9/3	1441.110	1440.586	-330.895	0.442	800.668	0.421	19	0.102	R.KIEFPHPSEEAR.A
R4/RRR4-9/3	1680.916	1680.761	92.526	0.442	986.766	0.270	22	0.087	K.RFDSEVSGDREVQR.T
R4/RRR4-7/2	1814.513	1815.103	-878.919	0.592	2808.333	0.588	25	0.479	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-7/2	1815.413	1815.103	171.129	0.598	2632.079	0.566	25	0.430	R.TLKEWIVSSLGPDAVAK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1814.631	1815.103	-260.955	0.599	2422.577	0.585	24	0.392	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-7/2	1516.742	1515.731	7.862	0.519	1551.041	0.546	22	0.245	K.DLDPETTLVVVVSK.T
R4/RRR4-7/2	1372.023	1372.530	-1101.600	0.445	1406.245	0.540	19	0.225	K.TFTTAETM*LNAR.T
R4/RRR4-7/2	1427.875	1426.562	219.461	0.448	1157.928	0.568	16	0.203	K.NAFAFWDWVGGR.Y
R4/RRR4-7/2	1372.046	1372.530	-353.780	0.475	1166.127	0.491	19	0.195	K.TFTTAETM*LNAR.T
R4/RRR4-7/2	1472.381	1472.667	-195.050	0.332	1360.666	0.328	20	0.175	K.EWIVSSLGPDAVAK.H
R4/RRR4-7/2	1372.037	1372.530	-360.297	0.439	872.540	0.470	17	0.170	K.TFTTAETM*LNAR.T
R4/RRR4-7/2	950.887	950.031	-151.372	0.419	459.047	0.479	15	0.158	R.SGSWVGATGK.A
R4/RRR4-7/3	1843.750	1844.139	-211.884	0.445	1475.770	0.397	31	0.157	R.SIKDLDPETTLVVVVSK.T
R4/RRR4-7/2	1316.123	1316.488	-277.839	0.413	961.753	0.348	17	0.155	-.FLANVDPVDVAR.-
R4/RRR4-7/2	1315.656	1316.488	-1396.533	0.351	916.803	0.317	17	0.151	-.FLANVDPVDVAR.-
R4/RRR4-7/2	1051.085	1051.175	-85.455	0.372	874.390	0.289	15	0.147	K.FLEGAASIDK.H
R4/RRR4-7/2	1316.328	1316.488	-121.533	0.462	608.167	0.355	15	0.144	-.FLANVDPVDVAR.-
R4/RRR4-7/2	1051.112	1051.175	-59.594	0.312	840.690	0.198	14	0.137	K.FLEGAASIDK.H
R4/RRR4-1/2	1816.057	1815.103	-25.458	0.337	628.163	0.230	18	0.135	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-11/2	1815.604	1815.103	-275.853	0.408	1045.312	0.200	17	0.134	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-11/2	1815.209	1815.103	58.708	0.422	1047.944	0.189	17	0.132	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-7/3	1703.273	1703.901	-958.559	0.424	1275.450	0.371	30	0.125	K.FAPHIQQLSM*ESNGK.G
R4/RRR4-7/3	1703.168	1703.901	-1020.621	0.450	1140.143	0.415	30	0.125	K.FAPHIQQLSM*ESNGK.G
R4/RRR4-7/3	1703.496	1703.901	-238.331	0.463	1208.615	0.390	30	0.124	K.FAPHIQQLSM*ESNGK.G
R4/RRR4-10/2	1814.070	1815.103	-1123.727	0.329	1013.707	0.071	17	0.124	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-10/2	1814.476	1815.103	-899.586	0.343	1060.368	0.063	17	0.123	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-10/2	1814.465	1815.103	-905.259	0.350	864.761	0.097	16	0.123	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-7/3	1815.017	1815.103	-47.269	0.460	891.994	0.370	29	0.099	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-7/3	1815.348	1815.103	135.348	0.327	906.983	0.282	27	0.084	R.TLKEWIVSSLGPDAVAK.H
R4/RRR4-7/3	1843.631	1844.139	-820.483	0.345	660.825	0.302	25	0.083	R.SIKDLDPETTLVVVVSK.T
R4/RRR4-7/2	1895.346	1896.130	-943.888	0.485	811.032	0.535	23	0.175	R.YLAVEPSTPYNTTTLPK.-
R4/RRR4-10/2	1560.481	1559.788	-197.691	0.541	1903.494	0.507	21	0.278	K.ATAELLFGADNPVLK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1559.408	1559.788	-244.621	0.420	2024.839	0.435	21	0.276	K.ATAELLFGADNPVLK.Q
R4/RRR4-10/2	1700.491	1700.912	-247.942	0.504	1547.421	0.564	21	0.244	R.IGAINVVCSTPEVANR.V
R4/RRR4-10/2	1700.355	1700.912	-918.486	0.501	1414.110	0.566	21	0.229	R.IGAINVVCSTPEVANR.V
R4/RRR4-10/2	972.970	973.192	-228.536	0.495	1305.448	0.461	17	0.202	R.ISLAGLSLAK.C
R4/RRR4-10/2	1390.146	1390.568	-304.704	0.474	1187.328	0.514	22	0.200	R.VATLQSLSGTGSLR.L
R4/RRR4-10/2	1532.436	1532.763	-214.092	0.484	1193.957	0.439	20	0.186	R.TEELQPYVLNVVK.K
R4/RRR4-10/2	1389.642	1390.568	-1389.934	0.350	1261.307	0.419	22	0.185	R.VATLQSLSGTGSLR.L
R4/RRR4-10/2	1389.765	1390.568	-1301.537	0.376	1146.019	0.456	22	0.183	R.VATLQSLSGTGSLR.L
R4/RRR4-10/2	1533.255	1532.763	321.763	0.561	1097.095	0.444	21	0.182	R.TEELQPYVLNVVK.K
R4/RRR4-10/2	972.530	973.192	-1713.947	0.417	1218.446	0.381	16	0.178	R.ISLAGLSLAK.C
R4/RRR4-10/2	1532.606	1532.763	-102.385	0.528	958.645	0.446	20	0.174	R.TEELQPYVLNVVK.K
R4/RRR4-10/2	889.900	890.065	-185.410	0.514	899.583	0.445	13	0.173	R.LAAAFIQR.Y
R4/RRR4-10/2	973.073	973.192	-122.945	0.494	1145.254	0.363	16	0.171	R.ISLAGLSLAK.C
R4/RRR4-10/2	890.040	890.065	-27.872	0.517	876.986	0.439	13	0.171	R.LAAAFIQR.Y
R4/RRR4-10/2	889.946	890.065	-133.259	0.514	906.060	0.429	13	0.171	R.LAAAFIQR.Y
R4/RRR4-10/2	1854.955	1854.988	-18.060	0.545	1131.641	0.653	22	0.169	K.CEYLADAIIDSFHNVS.-
R4/RRR4-10/2	935.963	936.047	-89.818	0.379	696.941	0.390	13	0.156	K.NLGLYAER.I
R4/RRR4-10/2	936.047	936.047	-0.472	0.399	670.103	0.360	13	0.153	K.NLGLYAER.I
R4/RRR4-10/2	936.048	936.047	0.705	0.417	700.249	0.335	12	0.150	K.NLGLYAER.I
R4/RRR4-10/2	1855.248	1854.988	140.528	0.510	975.124	0.612	21	0.138	K.CEYLADAIIDSFHNVS.-
R4/RRR4-9/2	1561.226	1559.788	281.021	0.323	683.463	0.256	17	0.137	K.ATAELLFGADNPVLK.Q
R4/RRR4-1/2	1560.750	1559.788	-24.759	0.332	600.638	0.224	14	0.131	K.ATAELLFGADNPVLK.Q
R4/RRR4-10/3	1697.128	1696.958	100.538	0.439	1392.533	0.313	30	0.123	R.LARPM*YSNPPIHGAR.I
R4/RRR4-10/3	1439.126	1439.554	-298.341	0.407	1137.964	0.351	24	0.109	K.DDSGKDWSFILR.Q
R4/RRR4-10/2	1854.245	1854.988	-942.954	0.425	909.536	0.492	20	0.107	K.CEYLADAIIDSFHNVS.-
R4/RRR4-10/3	1439.681	1439.554	88.300	0.373	1305.877	0.203	26	0.089	K.DDSGKDWSFILR.Q
R4/RRR4-10/3	1439.132	1439.554	-294.256	0.373	736.227	0.255	20	0.080	-.DDSGKDWSFILR.-
R4/RRR4-12/3	1940.856	1940.190	-172.611	0.599	3699.333	0.643	37	1.000	K.VLIAVADNVGSNQLQEIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/3	1941.026	1940.190	-85.170	0.601	3461.323	0.649	37	0.892	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/3	1942.007	1940.190	-94.993	0.596	2966.517	0.623	36	0.661	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/2	1744.221	1743.942	160.705	0.557	2465.865	0.599	32	0.411	K.FAVAAPVAADSGAAAPSAAK.E
R4/RRR4-11/2	1939.623	1940.190	-810.675	0.512	2582.254	0.472	28	0.387	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/2	1743.173	1743.942	-1017.928	0.496	2286.271	0.613	31	0.379	K.FAVAAPVAADSGAAAPSAAK.E
R4/RRR4-12/2	1939.456	1940.190	-896.853	0.522	2296.740	0.543	27	0.356	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/2	1940.614	1940.190	218.890	0.613	2177.164	0.581	26	0.345	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/2	1743.393	1743.942	-891.177	0.571	2031.031	0.648	30	0.344	K.FAVAAPVAADSGAAAPSAAK.E
R4/RRR4-12/2	1939.699	1940.190	-254.228	0.546	2189.677	0.535	25	0.332	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/2	1767.767	1768.131	-206.300	0.534	1924.507	0.502	21	0.279	K.INKGTVEIITPVELIK.K
R4/RRR4-14/2	1940.802	1940.190	-200.524	0.569	1860.993	0.534	25	0.278	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/3	1744.494	1743.942	-257.628	0.472	1687.192	0.447	38	0.209	K.FAVAAPVAADSGAAAPSAAK.E
R4/RRR4-12/2	1411.026	1411.619	-1132.418	0.501	1392.510	0.458	17	0.207	K.KLCQLLDEYTK.V
R4/RRR4-12/3	1541.044	1540.870	113.795	0.340	1739.397	0.422	31	0.200	K.GTVEIITPVELIKK.G
R4/RRR4-12/2	1411.316	1411.619	-215.462	0.491	1162.180	0.489	16	0.193	K.KLCQLLDEYTK.V
R4/RRR4-12/2	1411.381	1411.619	-169.301	0.538	1186.085	0.442	16	0.186	K.KLCQLLDEYTK.V
R4/RRR4-12/2	1412.396	1412.697	-213.737	0.395	1078.047	0.459	18	0.179	K.GTVEIITPVELIK.K
R4/RRR4-12/2	1412.287	1412.697	-290.911	0.379	1161.108	0.395	18	0.174	K.GTVEIITPVELIK.K
R4/RRR4-11/2	1413.397	1412.697	-212.546	0.475	1049.298	0.439	17	0.174	K.GTVEIITPVELIK.K
R4/RRR4-11/2	1411.827	1412.697	-1328.375	0.408	992.595	0.452	16	0.171	K.GTVEIITPVELIK.K
R4/RRR4-12/2	1284.016	1283.446	-336.373	0.544	1259.699	0.324	16	0.170	K.LCQLLDEYTK.V
R4/RRR4-12/2	1284.136	1283.446	-241.950	0.531	1267.596	0.311	16	0.168	K.LCQLLDEYTK.V
R4/RRR4-12/2	1540.493	1540.870	-245.002	0.420	1174.914	0.367	17	0.166	K.GTVEIITPVELIKK.G
R4/RRR4-11/2	1413.278	1412.697	-297.464	0.478	882.448	0.451	16	0.166	K.GTVEIITPVELIK.K
R4/RRR4-11/2	1061.896	1062.199	-286.591	0.420	759.009	0.436	17	0.163	K.VGSSESALLAK.L
R4/RRR4-12/2	1940.430	1940.190	124.011	0.469	899.788	0.435	19	0.160	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-11/2	1062.093	1062.199	-100.247	0.405	822.440	0.375	18	0.159	K.VGSSESALLAK.L
R4/RRR4-12/2	1283.397	1283.446	-38.600	0.516	843.980	0.392	14	0.159	K.LCQLLDEYTK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1063.204	1062.199	4.766	0.447	687.955	0.401	17	0.158	K.VGSSESALLAK.L
R4/RRR4-12/2	1411.819	1412.697	-1334.019	0.389	974.784	0.357	16	0.157	K.GTVEIITPVELIK.K
R4/RRR4-12/2	1062.006	1062.199	-182.802	0.429	721.975	0.349	17	0.153	K.VGSSESALLAK.L
R4/RRR4-12/2	1062.088	1062.199	-104.628	0.371	565.282	0.330	16	0.148	K.VGSSESALLAK.L
R4/RRR4-14/2	1412.033	1412.697	-1181.555	0.351	659.198	0.401	13	0.148	K.GTVEIITPVELIK.K
R4/RRR4-20/2	1061.808	1062.199	-369.637	0.318	615.010	0.297	16	0.145	K.VGSSESALLAK.L
R4/RRR4-11/2	1061.191	1062.199	-1897.783	0.331	715.542	0.214	17	0.141	K.VGSSESALLAK.L
R4/RRR4-11/2	1412.305	1412.697	-277.990	0.337	562.012	0.307	13	0.140	K.GTVEIITPVELIK.K
R4/RRR4-15/2	1411.949	1412.697	-1241.285	0.318	434.797	0.353	11	0.139	K.GTVEIITPVELIK.K
R4/RRR4-15/2	1061.831	1062.199	-347.952	0.235	656.307	0.166	16	0.137	K.VGSSESALLAK.L
R4/RRR4-15/2	1413.723	1412.697	18.481	0.358	731.694	0.204	15	0.135	K.GTVEIITPVELIK.K
R4/RRR4-12/3	1490.365	1490.684	-215.051	0.404	932.334	0.455	28	0.117	K.KGDKVGSSESALLAK.L
R4/RRR4-12/3	1768.119	1768.131	-6.871	0.451	1215.001	0.290	29	0.102	K.INKGTVEIITPVELIK.K
R4/RRR4-12/3	1940.416	1940.190	116.339	0.379	831.571	0.343	23	0.093	K.VLIAVADNVGSNQLQEIR.K
R4/RRR4-12/3	1767.275	1768.131	-1053.173	0.357	741.686	0.227	22	0.067	-.INKGTVEIITPVELIK.-
R4/RRR4-12/3	1817.578	1817.036	-252.557	0.444	1514.137	0.550	33	0.221	K.FAVAAPVAAADSGAAAVAASK.E
R4/RRR4-12/3	1817.069	1817.036	18.481	0.400	1184.747	0.361	27	0.117	K.FAVAAPVAAADSGAAAVAASK.E
R4/RRR4-11/2	1918.726	1919.128	-210.425	0.582	3712.630	0.589	30	0.739	K.VQQVDTTGAGDAFVGALLR.R
R4/RRR4-11/2	1918.626	1919.128	-785.279	0.581	3323.205	0.598	29	0.624	K.VQQVDTTGAGDAFVGALLR.R
R4/RRR4-11/2	1919.512	1919.128	200.757	0.633	3276.349	0.623	29	0.622	K.VQQVDTTGAGDAFVGALLR.R
R4/RRR4-11/3	1918.916	1919.128	-111.099	0.501	2497.063	0.567	37	0.465	K.VQQVDTTGAGDAFVGALLR.R
R4/RRR4-11/2	1579.174	1578.622	-284.435	0.598	2716.054	0.594	26	0.465	R.DNGVDDAGVVFDAGAR.T
R4/RRR4-11/2	1578.014	1578.622	-1022.360	0.529	2227.968	0.585	26	0.360	R.DNGVDDAGVVFDAGAR.T
R4/RRR4-11/2	1578.144	1578.622	-304.171	0.535	2094.558	0.573	23	0.329	R.DNGVDDAGVVFDAGAR.T
R4/RRR4-11/2	1402.252	1401.632	-272.299	0.558	1480.901	0.550	20	0.239	K.ILSIWDQADIVK.V
R4/RRR4-11/2	1317.223	1317.550	-249.536	0.496	1564.966	0.490	19	0.232	K.LLLVTLGDQGCK.Y
R4/RRR4-11/2	991.904	992.197	-296.260	0.487	1703.627	0.418	15	0.232	R.TALAFVTLR.A
R4/RRR4-11/2	1224.652	1225.370	-1406.731	0.506	1618.980	0.449	19	0.229	K.FANACGAITATK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	992.079	992.197	-118.861	0.490	1647.697	0.414	15	0.225	R.TALAFVTLR.A
R4/RRR4-11/2	992.105	992.197	-92.572	0.520	1650.613	0.406	15	0.223	R.TALAFVTLR.A
R4/RRR4-11/2	1402.226	1401.632	-290.815	0.562	1281.446	0.535	19	0.215	K.ILSIWDQADIVK.V
R4/RRR4-11/2	1359.069	1358.480	-303.203	0.528	1376.177	0.492	19	0.214	R.IVQDPSSLQDQK.K
R4/RRR4-11/2	1401.349	1401.632	-202.928	0.535	1301.255	0.497	19	0.208	K.ILSIWDQADIVK.V
R4/RRR4-11/2	1316.572	1317.550	-1506.971	0.395	1381.979	0.473	18	0.206	K.LLLVTLGDQGCK.Y
R4/RRR4-11/2	1358.182	1358.480	-219.834	0.488	1264.882	0.451	19	0.195	R.IVQDPSSLQDQK.K
R4/RRR4-11/2	1224.451	1225.370	-1571.550	0.431	1257.172	0.452	18	0.193	K.FANACGAITATK.K
R4/RRR4-11/2	1316.746	1317.550	-1374.363	0.360	1254.412	0.460	17	0.190	K.LLLVTLGDQGCK.Y
R4/RRR4-11/2	1358.051	1358.480	-316.683	0.489	1110.618	0.468	18	0.186	R.IVQDPSSLQDQK.K
R4/RRR4-11/2	1224.348	1225.370	-1656.685	0.439	1275.794	0.366	18	0.179	K.FANACGAITATK.K
R4/RRR4-11/2	1420.187	1419.565	-266.619	0.476	769.460	0.466	16	0.162	K.EAGALLSYDPNLR.E
R4/RRR4-11/2	1419.945	1419.565	268.284	0.459	839.006	0.397	17	0.157	K.EAGALLSYDPNLR.E
R4/RRR4-11/2	1420.057	1419.565	347.757	0.459	793.629	0.401	16	0.155	K.EAGALLSYDPNLR.E
R4/RRR4-11/3	1513.636	1514.666	-1344.919	0.492	849.768	0.470	26	0.118	R.RIVQDPSSLQDQK.K
R4/RRR4-11/3	1515.168	1514.666	-329.388	0.459	821.224	0.440	25	0.110	R.RIVQDPSSLQDQK.K
R4/RRR4-11/3	1514.009	1514.666	-1097.978	0.356	390.094	0.373	21	0.094	R.RIVQDPSSLQDQK.K
R4/RRR4-11/3	1918.637	1919.128	-256.516	0.303	705.079	0.292	23	0.080	-.VQQVDTTGAGDAFVGALLR.-
R4/RRR4-6/2	1779.349	1779.974	-915.831	0.503	2259.997	0.563	25	0.355	K.SVGPVVDGDAVVTFNFR.A
R4/RRR4-6/2	1780.687	1779.974	-161.623	0.554	2011.673	0.605	24	0.325	K.SVGPVVDGDAVVTFNFR.A
R4/RRR4-6/2	1434.202	1434.578	-262.733	0.531	2217.709	0.487	21	0.324	R.GWDAQVLGEAPYK.F
R4/RRR4-7/2	1780.471	1779.974	280.112	0.567	1959.528	0.587	24	0.310	K.SVGPVVDGDAVVTFNFR.A
R4/RRR4-7/2	1434.054	1434.578	-1065.568	0.439	2226.546	0.394	21	0.297	R.GWDAQVLGEAPYK.F
R4/RRR4-7/2	1780.776	1779.974	-111.493	0.585	1778.620	0.605	23	0.287	K.SVGPVVDGDAVVTFNFR.A
R4/RRR4-6/2	1780.388	1779.974	233.156	0.593	1729.214	0.609	23	0.281	K.SVGPVVDGDAVVTFNFR.A
R4/RRR4-7/2	1780.401	1779.974	240.581	0.579	1752.135	0.591	23	0.279	K.SVGPVVDGDAVVTFNFR.A
R4/RRR4-7/2	1434.121	1434.578	-319.778	0.470	1852.295	0.531	20	0.278	R.GWDAQVLGEAPYK.F
R4/RRR4-6/2	1490.176	1490.598	-284.250	0.453	1760.012	0.529	18	0.265	K.ALEYADFDKFDR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1434.158	1434.578	-293.902	0.407	1887.809	0.451	19	0.261	R.GWDAQVLGEAPYK.F
R4/RRR4-6/2	1490.894	1490.598	198.934	0.473	1727.284	0.519	18	0.258	K.ALEYADFDKFDR.V
R4/RRR4-6/2	1433.722	1434.578	-1298.011	0.368	1908.110	0.410	20	0.253	R.GWDAQVLGEAPYK.F
R4/RRR4-6/2	1490.056	1490.598	-1038.257	0.412	1677.735	0.437	18	0.231	K.ALEYADFDKFDR.V
R4/RRR4-7/2	1433.942	1434.578	-1143.863	0.369	1735.102	0.344	19	0.216	R.GWDAQVLGEAPYK.F
R4/RRR4-7/2	987.913	987.175	-266.349	0.502	1239.697	0.459	17	0.196	K.LVDLALASGK.I
R4/RRR4-7/2	988.096	987.175	-80.308	0.525	1166.858	0.456	17	0.190	K.LVDLALASGK.I
R4/RRR4-6/2	1070.120	1070.307	-175.352	0.496	1549.280	0.295	14	0.187	R.LDQVQLLLK.G
R4/RRR4-6/2	1070.127	1070.307	-169.630	0.536	1504.028	0.315	14	0.186	R.LDQVQLLLK.G
R4/RRR4-6/2	1070.178	1070.307	-121.113	0.506	1387.304	0.346	14	0.184	R.LDQVQLLLK.G
R4/RRR4-7/2	987.044	987.175	-133.609	0.494	1035.501	0.465	17	0.183	K.LVDLALASGK.I
R4/RRR4-7/2	1070.123	1070.307	-172.949	0.516	1455.616	0.315	14	0.182	R.LDQVQLLLK.G
R4/RRR4-7/2	1070.132	1070.307	-164.595	0.507	1495.146	0.298	14	0.182	R.LDQVQLLLK.G
R4/RRR4-6/2	986.434	987.175	-1771.088	0.465	993.900	0.440	17	0.176	K.LVDLALASGK.I
R4/RRR4-6/2	986.604	987.175	-1597.167	0.479	863.503	0.464	16	0.173	K.LVDLALASGK.I
R4/RRR4-6/2	986.971	987.175	-207.926	0.525	865.116	0.442	16	0.170	K.LVDLALASGK.I
R4/RRR4-6/2	1348.461	1349.518	-1529.716	0.405	1008.375	0.402	16	0.166	R.DAILSGKFDQVR.V
R4/RRR4-6/2	1348.577	1349.518	-1443.426	0.436	1019.572	0.386	17	0.165	R.DAILSGKFDQVR.V
R4/RRR4-6/2	1866.494	1866.060	232.895	0.441	478.701	0.563	20	0.164	K.ASDQYLPPFVIVDESGK.S
R4/RRR4-6/2	1865.237	1866.060	-980.261	0.448	595.517	0.512	22	0.164	K.ASDQYLPPFVIVDESGK.S
R4/RRR4-6/2	1349.143	1349.518	-278.480	0.394	1063.530	0.345	17	0.161	R.DAILSGKFDQVR.V
R4/RRR4-7/2	1866.381	1866.060	172.163	0.446	490.445	0.516	20	0.160	K.ASDQYLPPFVIVDESGK.S
R4/RRR4-7/2	1866.270	1866.060	112.866	0.418	490.099	0.514	20	0.159	K.ASDQYLPPFVIVDESGK.S
R4/RRR4-6/2	1349.153	1349.518	-271.309	0.361	810.363	0.390	16	0.155	R.DAILSGKFDQVR.V
R4/RRR4-7/2	1069.466	1070.307	-1727.402	0.419	996.627	0.253	14	0.149	R.LDQVQLLLK.G
R4/RRR4-6/2	1005.993	1006.137	-143.689	0.435	856.654	0.279	16	0.148	-.FQNAVEAVK.-
R4/RRR4-7/2	1865.442	1866.060	-870.413	0.353	403.936	0.446	18	0.148	K.ASDQYLPPFVIVDESGK.S
R4/RRR4-7/2	1005.953	1006.137	-183.494	0.345	841.093	0.271	15	0.146	-.FQNAVEAVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1867.639	1866.060	-226.211	0.341	447.672	0.381	19	0.145	K.ASDQYLPPFVIVDESGK.S
R4/RRR4-7/2	1005.728	1006.137	-407.657	0.393	740.278	0.257	15	0.143	-.FQNAVEAVK.-
R4/RRR4-7/2	1005.713	1006.137	-422.637	0.416	706.497	0.281	15	0.142	-.FQNAVEAVK.-
R4/RRR4-1/2	1435.321	1434.578	-179.273	0.386	671.432	0.290	16	0.142	R.GWDAQVLGEAPYK.F
R4/RRR4-6/3	1482.631	1482.629	1.179	0.425	1144.452	0.349	22	0.110	-.FGHVTFFWNGNR.-
R4/RRR4-6/3	1637.513	1637.861	-213.148	0.435	891.718	0.372	25	0.099	K.LPSHYLVSPPEIER.T
R4/RRR4-6/3	1482.461	1482.629	-113.786	0.385	1096.293	0.255	22	0.088	-.FGHVTFFWNGNR.-
R4/RRR4-6/3	1637.793	1637.861	-41.768	0.418	782.658	0.312	24	0.081	-.LPSHYLVSPPEIER.-
R4/RRR4-3/2	1291.290	1291.478	-145.697	0.527	2154.908	0.542	20	0.331	R.AIADGSLLDFLR.Q
R4/RRR4-4/2	1291.254	1291.478	-174.052	0.477	2126.823	0.517	19	0.317	R.AIADGSLLDFLR.Q
R4/RRR4-4/2	1291.161	1291.478	-246.228	0.466	2040.589	0.475	19	0.291	R.AIADGSLLDFLR.Q
R4/RRR4-3/2	1290.597	1291.478	-1462.166	0.411	1870.349	0.510	19	0.274	R.AIADGSLLDFLR.Q
R4/RRR4-1/2	1291.498	1291.478	15.869	0.509	1737.641	0.478	18	0.248	R.AIADGSLLDFLR.Q
R4/RRR4-3/2	1290.611	1291.478	-1451.050	0.461	1596.156	0.492	18	0.235	R.AIADGSLLDFLR.Q
R4/RRR4-3/2	1886.406	1886.995	-844.904	0.559	1464.487	0.523	23	0.227	K.DITPDDKQELDEALQR.E
R4/RRR4-4/2	1076.581	1077.212	-1520.034	0.392	1426.493	0.508	16	0.218	K.SPAEVFDALK.S
R4/RRR4-4/3	1885.910	1886.995	-1108.650	0.440	1698.082	0.469	30	0.214	K.DITPDDKQELDEALQR.E
R4/RRR4-3/2	1327.925	1328.497	-1187.057	0.458	1380.443	0.496	20	0.213	K.LADLESAPAALTR.L
R4/RRR4-3/2	1887.570	1886.995	-225.574	0.572	1336.220	0.519	22	0.212	K.DITPDDKQELDEALQR.E
R4/RRR4-4/2	1077.080	1077.212	-122.951	0.482	1475.184	0.417	16	0.207	K.SPAEVFDALK.S
R4/RRR4-4/2	1886.487	1886.995	-801.448	0.507	1190.518	0.514	22	0.198	K.DITPDDKQELDEALQR.E
R4/RRR4-3/2	1328.229	1328.497	-202.392	0.499	1344.056	0.440	19	0.198	K.LADLESAPAALTR.L
R4/RRR4-4/2	1328.198	1328.497	-225.811	0.479	1174.193	0.491	18	0.193	K.LADLESAPAALTR.L
R4/RRR4-4/2	1077.087	1077.212	-116.699	0.400	1320.873	0.420	15	0.192	K.SPAEVFDALK.S
R4/RRR4-2/2	1077.827	1077.212	-358.577	0.437	1123.471	0.496	15	0.191	K.SPAEVFDALK.S
R4/RRR4-4/3	1886.558	1886.995	-232.192	0.487	1589.661	0.451	29	0.190	K.DITPDDKQELDEALQR.E
R4/RRR4-4/2	1291.002	1291.478	-369.548	0.424	1224.151	0.434	16	0.185	R.AIADGSLLDFLR.Q
R4/RRR4-1/2	1076.688	1077.212	-1419.812	0.409	1230.715	0.413	15	0.184	K.SPAEVFDALK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1078.028	1077.212	-171.340	0.411	1142.649	0.444	15	0.183	K.SPAEVFDALK.S
R4/RRR4-3/3	1886.114	1886.995	-1000.350	0.507	1483.209	0.441	30	0.170	K.DITPDDKQELDEALQR.E
R4/RRR4-1/2	1291.657	1291.478	138.620	0.351	881.393	0.461	15	0.165	R.AIADGSLLDFLR.Q
R4/RRR4-4/2	1329.516	1328.497	14.402	0.425	989.971	0.367	17	0.160	K.LADLESAPAALTR.L
R4/RRR4-3/2	1207.484	1207.404	66.455	0.396	515.445	0.434	17	0.156	R.QVSTFGLSLVR.L
R4/RRR4-3/2	1208.254	1207.404	-125.107	0.379	370.605	0.429	16	0.154	R.QVSTFGLSLVR.L
R4/RRR4-5/2	1077.968	1077.212	-227.345	0.371	657.066	0.395	14	0.154	K.SPAEVFDALK.S
R4/RRR4-4/2	1207.211	1207.404	-160.814	0.312	457.826	0.465	16	0.152	R.QVSTFGLSLVR.L
R4/RRR4-2/2	1291.832	1291.478	274.702	0.265	592.127	0.406	17	0.149	R.AIADGSLLDFLR.Q
R4/RRR4-2/2	1292.381	1291.478	-75.279	0.207	614.423	0.463	17	0.148	R.AIADGSLLDFLR.Q
R4/RRR4-4/3	1886.543	1886.995	-239.982	0.449	1293.819	0.437	27	0.147	K.DITPDDKQELDEALQR.E
R4/RRR4-4/2	1327.729	1328.497	-1335.052	0.269	874.823	0.252	15	0.140	K.LADLESAPAALTR.L
R4/RRR4-3/3	1886.705	1886.995	-154.301	0.466	1210.148	0.386	28	0.125	K.DITPDDKQELDEALQR.E
R4/RRR4-3/3	1886.845	1886.995	-79.439	0.536	1134.043	0.393	27	0.119	K.DITPDDKQELDEALQR.E
R4/RRR4-4/3	1168.328	1168.373	-38.379	0.419	1042.122	0.318	20	0.098	K.RPLFGPDLPR.T
R4/RRR4-4/3	1168.654	1168.373	241.517	0.422	1017.925	0.289	20	0.092	K.RPLFGPDLPR.T
R4/RRR4-4/3	1168.260	1168.373	-96.546	0.458	880.216	0.276	20	0.088	K.RPLFGPDLPR.T
R4/RRR4-3/3	1168.767	1168.373	337.975	0.330	795.493	0.160	18	0.077	K.RPLFGPDLPR.T
R4/RRR4-4/2	1122.941	1123.284	-306.774	0.506	1907.042	0.485	17	0.276	K.LSEGYLTLAR.D
R4/RRR4-4/2	1349.200	1348.486	-213.312	0.589	1580.337	0.520	17	0.239	R.NLAGEIAQEFQK.R
R4/RRR4-4/2	1123.193	1123.284	-81.168	0.504	1669.942	0.456	17	0.237	K.LSEGYLTLAR.D
R4/RRR4-4/2	1123.087	1123.284	-175.585	0.483	1632.944	0.465	17	0.235	K.LSEGYLTLAR.D
R4/RRR4-4/2	1349.247	1348.486	-177.642	0.545	1391.023	0.516	16	0.217	R.NLAGEIAQEFQK.R
R4/RRR4-4/2	1348.412	1348.486	-55.716	0.529	1492.518	0.452	17	0.213	R.NLAGEIAQEFQK.R
R4/RRR4-3/2	1122.413	1123.284	-1672.205	0.424	1382.496	0.440	17	0.203	K.LSEGYLTLAR.D
R4/RRR4-4/2	1875.631	1876.019	-207.427	0.574	1057.570	0.613	19	0.202	R.LLGSEGDIGSWGHEYVR.N
R4/RRR4-4/2	1370.610	1370.748	-100.819	0.421	1011.692	0.575	17	0.192	R.LLPVALGLLYLGK.Q
R4/RRR4-4/2	1533.433	1532.809	-246.050	0.453	866.043	0.547	18	0.175	R.IGAILGLGIAYAGSQK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1123.275	1123.284	-7.805	0.477	1343.965	0.300	16	0.173	K.LSEGYLTLAR.D
R4/RRR4-1/2	1123.107	1123.284	-158.358	0.408	1553.475	0.197	17	0.171	K.LSEGYLTLAR.D
R4/RRR4-4/2	1371.436	1370.748	-227.619	0.361	648.926	0.556	16	0.164	R.LLPVALGLLYLGK.Q
R4/RRR4-4/2	1370.035	1370.748	-1253.611	0.371	601.872	0.522	17	0.161	R.LLPVALGLLYLGK.Q
R4/RRR4-4/2	899.954	900.098	-160.551	0.431	889.481	0.343	13	0.157	R.IALLLDNK.S
R4/RRR4-4/2	1160.181	1160.293	-96.732	0.382	1141.053	0.275	16	0.157	R.TCLYLTSSSK.Y
R4/RRR4-4/2	900.002	900.098	-106.671	0.450	879.887	0.327	13	0.155	R.IALLLDNK.S
R4/RRR4-1/2	1123.145	1123.284	-124.013	0.376	1241.596	0.217	15	0.154	K.LSEGYLTLAR.D
R4/RRR4-4/2	1278.080	1278.348	-210.238	0.369	503.159	0.440	17	0.154	K.QESVEATAEVSK.T
R4/RRR4-4/2	1450.122	1450.684	-1080.265	0.377	751.826	0.414	18	0.153	R.SATSSM*TSVPKPLK.F
R4/RRR4-1/2	1348.958	1348.486	350.747	0.370	598.897	0.422	15	0.152	R.NLAGEIAQEFQK.R
R4/RRR4-4/2	1278.131	1278.348	-170.379	0.346	330.338	0.421	17	0.151	K.QESVEATAEVSK.T
R4/RRR4-4/2	1278.001	1278.348	-272.235	0.307	488.107	0.414	17	0.149	K.QESVEATAEVSK.T
R4/RRR4-4/2	900.262	900.098	183.314	0.257	832.707	0.186	12	0.137	-.IALLLDNK.-
R4/RRR4-4/2	1160.023	1160.293	-233.534	0.336	628.258	0.247	14	0.137	-.TCLYLTSSSK.-
R4/RRR4-4/2	1160.077	1160.293	-186.873	0.379	595.124	0.130	13	0.121	-.TCLYLTSSSK.-
R4/RRR4-4/3	1232.565	1232.459	86.797	0.369	759.375	0.220	19	0.081	K.FLRPHYGTLK.S
R4/RRR4-4/3	1232.737	1232.459	226.678	0.395	1052.733	0.191	21	0.079	K.FLRPHYGTLK.S
R4/RRR4-4/3	1232.365	1232.459	-76.373	0.431	1106.094	0.171	21	0.078	K.FLRPHYGTLK.S
R4/RRR4-16/2	1435.512	1435.650	-96.346	0.525	2684.500	0.483	23	0.415	K.YIGLLATGLTADAR.S
R4/RRR4-16/2	1434.831	1435.650	-1271.750	0.490	2388.636	0.507	23	0.364	K.YIGLLATGLTADAR.S
R4/RRR4-16/2	1849.517	1850.063	-838.387	0.593	2395.765	0.496	23	0.355	K.ATSAGLKEQEAINFLEK.K
R4/RRR4-16/2	1849.481	1850.063	-857.535	0.571	2149.572	0.529	23	0.323	K.ATSAGLKEQEAINFLEK.K
R4/RRR4-16/2	1849.494	1850.063	-850.512	0.542	1988.595	0.474	23	0.280	K.ATSAGLKEQEAINFLEK.K
R4/RRR4-16/2	1073.071	1073.225	-143.606	0.535	1716.996	0.385	16	0.224	K.ATEIEVGVVR.K
R4/RRR4-16/2	1072.669	1073.225	-1454.694	0.492	1354.651	0.443	16	0.201	K.ATEIEVGVVR.K
R4/RRR4-16/2	1072.972	1073.225	-236.163	0.526	1319.156	0.426	15	0.194	K.ATEIEVGVVR.K
R4/RRR4-16/2	1158.011	1157.304	-253.711	0.457	644.865	0.589	15	0.178	R.HITIFSPEGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	946.442	947.071	-1726.714	0.448	1066.118	0.409	17	0.174	K.SAGVTSIGVR.G
R4/RRR4-16/2	1712.919	1713.999	-1217.748	0.416	945.544	0.409	20	0.162	K.LLDQTSVTHLFPITK.Y
R4/RRR4-16/3	1849.516	1850.063	-838.891	0.450	1341.557	0.458	31	0.159	K.ATSAGLKEQEAINFLEK.K
R4/RRR4-16/2	1157.004	1157.304	-259.858	0.337	453.254	0.458	13	0.152	R.HITIFSPEGR.L
R4/RRR4-16/3	1928.849	1928.090	-125.285	0.466	1301.989	0.447	28	0.152	R.ALTTEEIDQHLTAISER.-
R4/RRR4-16/2	1156.901	1157.304	-349.414	0.297	494.650	0.452	13	0.150	R.HITIFSPEGR.L
R4/RRR4-16/3	1849.953	1850.063	-59.348	0.496	1278.102	0.448	31	0.148	K.ATSAGLKEQEAINFLEK.K
R4/RRR4-15/2	1157.864	1157.304	-380.847	0.266	454.411	0.403	14	0.146	R.HITIFSPEGR.L
R4/RRR4-16/3	1850.855	1850.063	-112.439	0.418	1165.762	0.471	29	0.143	K.ATSAGLKEQEAINFLEK.K
R4/RRR4-16/3	1978.993	1978.235	-122.760	0.488	938.230	0.470	29	0.123	K.ATSAGLKEQEAINFLEKK.M
R4/RRR4-16/3	1928.242	1928.090	79.007	0.335	1008.384	0.447	26	0.120	R.ALTTEEIDQHLTAISER.-
R4/RRR4-16/3	1977.798	1978.235	-221.697	0.450	566.864	0.359	26	0.089	K.ATSAGLKEQEAINFLEKK.M
R4/RRR4-16/3	1220.772	1221.380	-1320.597	0.399	951.996	0.194	18	0.065	-.GKDSVCVVTQK.-
R4/RRR4-16/3	1220.975	1221.380	-332.317	0.428	746.470	0.273	17	0.062	-.GKDSVCVVTQK.-
R4/RRR4-13/2	1594.288	1594.754	-293.488	0.550	2816.257	0.606	26	0.493	R.VADHAGVALAGLTADGR.V
R4/RRR4-13/2	1594.214	1594.754	-969.347	0.562	2732.199	0.578	26	0.461	R.VADHAGVALAGLTADGR.V
R4/RRR4-13/2	1594.166	1594.754	-999.483	0.546	2587.244	0.568	25	0.424	R.VADHAGVALAGLTADGR.V
R4/RRR4-13/2	1717.129	1717.856	-1008.696	0.563	2332.090	0.509	23	0.355	R.FEGYNDYTPEQLIK.D
R4/RRR4-13/2	1712.319	1711.770	-264.320	0.564	2139.068	0.555	24	0.333	R.NQYDTDVTTWSPAGR.L
R4/RRR4-13/2	1711.342	1711.770	-250.877	0.534	1767.397	0.604	22	0.287	R.NQYDTDVTTWSPAGR.L
R4/RRR4-13/2	1444.121	1444.678	-1081.123	0.536	1952.876	0.452	19	0.271	R.LFQVEYAM*EAVK.Q
R4/RRR4-13/2	1443.744	1444.678	-1343.198	0.470	2145.814	0.340	19	0.268	R.LFQVEYAM*EAVK.Q
R4/RRR4-13/2	1711.204	1711.770	-918.029	0.506	1639.969	0.528	21	0.248	R.NQYDTDVTTWSPAGR.L
R4/RRR4-13/2	1378.255	1378.551	-215.300	0.463	1755.083	0.438	19	0.241	K.LTSSNCTVAIVGR.K
R4/RRR4-13/2	1444.013	1444.678	-1156.158	0.540	1745.720	0.439	18	0.239	R.LFQVEYAM*EAVK.Q
R4/RRR4-13/2	1503.002	1503.680	-1119.491	0.442	1645.468	0.429	20	0.225	K.DALSAIKETLQGEK.L
R4/RRR4-13/2	1378.114	1378.551	-317.670	0.468	1632.448	0.428	19	0.224	K.LTSSNCTVAIVGR.K
R4/RRR4-13/2	1502.914	1503.680	-1178.701	0.444	1575.636	0.426	20	0.216	K.DALSAIKETLQGEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1874.195	1874.043	81.620	0.557	1422.815	0.499	20	0.215	R.RFEGYNDYTPEQLIK.D
R4/RRR4-13/2	1873.097	1874.043	-1042.102	0.534	1352.793	0.451	20	0.198	R.RFEGYNDYTPEQLIK.D
R4/RRR4-13/2	1377.633	1378.551	-1395.918	0.382	1441.720	0.384	18	0.193	K.LTSSNCTVAIVGR.K
R4/RRR4-13/2	1874.389	1874.043	185.079	0.554	1046.751	0.496	19	0.182	R.RFEGYNDYTPEQLIK.D
R4/RRR4-13/2	1428.309	1428.678	-258.931	0.400	1063.789	0.388	16	0.167	R.LFQVEYAMEAVK.Q
R4/RRR4-13/2	1428.285	1428.678	-276.337	0.375	1154.997	0.342	17	0.166	R.LFQVEYAMEAVK.Q
R4/RRR4-13/2	1428.097	1428.678	-1110.222	0.327	460.244	0.349	13	0.143	R.LFQVEYAMEAVK.Q
R4/RRR4-13/3	1895.636	1896.112	-251.458	0.495	1115.220	0.454	30	0.134	R.KDDGTVEPFEM*IDVKR.I
R4/RRR4-13/3	1503.769	1503.680	59.418	0.476	794.574	0.520	26	0.125	K.DALSAIKETLQGEK.L
R4/RRR4-13/3	1503.755	1503.680	49.771	0.475	771.484	0.522	25	0.123	K.DALSAIKETLQGEK.L
R4/RRR4-13/3	1503.601	1503.680	-52.825	0.394	747.730	0.443	25	0.105	K.DALSAIKETLQGEK.L
R4/RRR4-13/3	1239.174	1239.410	-191.012	0.449	881.850	0.383	21	0.100	R.SRTHAVLAAANK.A
R4/RRR4-13/3	1594.724	1594.754	-18.981	0.451	853.747	0.368	25	0.096	R.VADHAGVALAGLTADGR.V
R4/RRR4-13/3	1595.682	1594.754	-45.249	0.446	1000.595	0.309	25	0.093	R.VADHAGVALAGLTADGR.V
R4/RRR4-5/2	1596.319	1596.852	-962.930	0.520	2565.318	0.603	24	0.432	R.TGAATNVIFGLALGYK.S
R4/RRR4-1/2	1596.249	1596.852	-1006.846	0.505	2360.905	0.581	23	0.380	R.TGAATNVIFGLALGYK.S
R4/RRR4-5/2	1596.349	1596.852	-944.121	0.528	2253.984	0.619	23	0.373	R.TGAATNVIFGLALGYK.S
R4/RRR4-6/2	1491.246	1490.598	-237.083	0.526	2077.884	0.610	25	0.338	K.TDALDAAGNTTAAIGK.G
R4/RRR4-5/2	1490.127	1490.598	-317.208	0.468	2134.014	0.550	25	0.327	K.TDALDAAGNTTAAIGK.G
R4/RRR4-1/2	1491.258	1490.598	-228.871	0.525	2025.668	0.588	25	0.322	K.TDALDAAGNTTAAIGK.G
R4/RRR4-1/2	1490.758	1490.598	107.541	0.513	2044.934	0.560	24	0.316	K.TDALDAAGNTTAAIGK.G
R4/RRR4-1/2	1597.296	1596.852	279.274	0.565	1931.871	0.607	23	0.313	R.TGAATNVIFGLALGYK.S
R4/RRR4-2/2	1490.424	1490.598	-116.948	0.482	1988.268	0.571	24	0.309	K.TDALDAAGNTTAAIGK.G
R4/RRR4-5/2	1490.235	1490.598	-244.638	0.446	1942.339	0.512	24	0.285	K.TDALDAAGNTTAAIGK.G
R4/RRR4-5/3	1536.752	1536.718	22.291	0.513	1747.661	0.577	35	0.270	R.VKVNPAHAAAAASGGSK.N
R4/RRR4-1/2	1490.054	1490.598	-1039.161	0.399	1897.985	0.467	23	0.265	K.TDALDAAGNTTAAIGK.G
R4/RRR4-6/2	1489.558	1490.598	-1373.966	0.375	1983.703	0.421	23	0.265	K.TDALDAAGNTTAAIGK.G
R4/RRR4-5/2	1400.224	1400.563	-242.964	0.487	1795.639	0.508	22	0.264	K.AADVGADLVGKVER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1490.230	1490.598	-247.761	0.449	1773.552	0.505	23	0.258	K.TDALDAAGNTTAAIGK.G
R4/RRR4-3/2	1490.044	1490.598	-1045.989	0.384	1807.890	0.462	23	0.251	K.TDALDAAGNTTAAIGK.G
R4/RRR4-3/2	1490.161	1490.598	-293.948	0.428	1812.864	0.457	23	0.251	K.TDALDAAGNTTAAIGK.G
R4/RRR4-5/2	1596.238	1596.852	-1013.833	0.487	1525.716	0.596	21	0.249	R.TGAATNVIFGLALGYK.S
R4/RRR4-2/2	1400.211	1400.563	-251.797	0.448	1691.126	0.499	22	0.248	K.AADVGADLVGKVER.N
R4/RRR4-5/2	1400.249	1400.563	-224.509	0.514	1632.180	0.516	22	0.246	K.AADVGADLVGKVER.N
R4/RRR4-1/3	1332.414	1332.447	-24.969	0.526	1635.908	0.584	26	0.245	K.KYIEAGASEHAR.T
R4/RRR4-1/2	1400.310	1400.563	-180.782	0.458	1792.226	0.432	22	0.244	K.AADVGADLVGKVER.N
R4/RRR4-2/2	1490.192	1490.598	-273.237	0.373	1737.638	0.455	22	0.240	K.TDALDAAGNTTAAIGK.G
R4/RRR4-5/2	1400.292	1400.563	-194.075	0.486	1456.958	0.552	22	0.234	K.AADVGADLVGKVER.N
R4/RRR4-6/2	1490.003	1490.598	-1073.380	0.431	1606.884	0.487	23	0.233	K.TDALDAAGNTTAAIGK.G
R4/RRR4-1/2	1270.414	1270.457	-33.887	0.368	1710.613	0.414	18	0.227	K.AAVIGDTIGDPLK.D
R4/RRR4-2/2	1489.364	1490.598	-1504.196	0.321	1741.063	0.377	21	0.222	K.TDALDAAGNTTAAIGK.G
R4/RRR4-1/2	1400.234	1400.563	-235.529	0.463	1470.950	0.445	21	0.210	K.AADVGADLVGKVER.N
R4/RRR4-5/3	1537.025	1536.718	200.323	0.456	1368.011	0.584	33	0.205	R.VKVNPAHAAAAASGGSK.N
R4/RRR4-6/2	1016.003	1016.130	-125.342	0.437	1318.780	0.481	18	0.205	K.AADVGADLVGK.V
R4/RRR4-6/2	1016.097	1016.130	-32.909	0.438	1335.703	0.466	18	0.204	K.AADVGADLVGK.V
R4/RRR4-2/2	1400.366	1400.563	-141.256	0.496	1341.057	0.464	21	0.203	K.AADVGADLVGKVER.N
R4/RRR4-6/2	1399.495	1400.563	-1482.245	0.439	1382.862	0.439	20	0.200	K.AADVGADLVGKVER.N
R4/RRR4-5/2	1015.858	1016.130	-268.905	0.438	1298.400	0.455	17	0.198	K.AADVGADLVGK.V
R4/RRR4-5/3	1536.622	1536.718	-62.685	0.510	1359.430	0.564	33	0.197	R.VKVNPAHAAAAASGGSK.N
R4/RRR4-1/3	1332.395	1332.447	-39.442	0.556	1339.330	0.571	25	0.193	K.KYIEAGASEHAR.T
R4/RRR4-1/2	1400.289	1400.563	-196.174	0.474	1329.657	0.414	21	0.191	K.AADVGADLVGKVER.N
R4/RRR4-1/3	1332.356	1332.447	-68.941	0.585	1193.811	0.613	25	0.189	K.KYIEAGASEHAR.T
R4/RRR4-1/2	1174.340	1173.345	-3.817	0.454	1244.063	0.411	16	0.186	K.FTIFNFGAQK.E
R4/RRR4-5/3	1332.471	1332.447	18.036	0.539	1193.053	0.597	25	0.183	K.KYIEAGASEHAR.T
R4/RRR4-2/2	1015.776	1016.130	-349.685	0.375	1221.292	0.397	17	0.180	K.AADVGADLVGK.V
R4/RRR4-2/3	1331.835	1332.447	-1214.103	0.538	1089.135	0.592	24	0.170	K.KYIEAGASEHAR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1015.891	1016.130	-236.476	0.408	1086.085	0.371	17	0.168	K.AADVGADLVGK.V
R4/RRR4-3/2	1399.907	1400.563	-1186.367	0.426	970.365	0.419	19	0.167	K.AADVGADLVGKVER.N
R4/RRR4-1/2	1015.694	1016.130	-430.719	0.363	1040.140	0.385	17	0.167	K.AADVGADLVGK.V
R4/RRR4-1/2	1015.798	1016.130	-328.705	0.394	1080.853	0.361	17	0.167	K.AADVGADLVGK.V
R4/RRR4-7/2	1173.535	1173.345	162.589	0.417	1115.024	0.348	15	0.166	K.FTIFNFGAQK.E
R4/RRR4-1/2	1596.105	1596.852	-1097.684	0.380	1076.711	0.394	18	0.165	R.TGAATNVIFGLALGYK.S
R4/RRR4-5/2	1173.862	1173.345	-412.162	0.358	814.017	0.452	14	0.164	K.FTIFNFGAQK.E
R4/RRR4-6/2	856.838	857.030	-223.858	0.413	466.690	0.435	11	0.157	K.VVDVLSPK.V
R4/RRR4-2/2	1015.370	1016.130	-1739.305	0.366	1009.181	0.318	17	0.157	K.AADVGADLVGK.V
R4/RRR4-2/2	1259.411	1258.446	-27.863	0.360	866.382	0.398	16	0.157	K.DTSGPSLNILIK.L
R4/RRR4-5/2	856.939	857.030	-105.959	0.429	428.023	0.417	11	0.156	K.VVDVLSPK.V
R4/RRR4-3/2	1174.418	1173.345	62.592	0.329	712.235	0.370	14	0.152	K.FTIFNFGAQK.E
R4/RRR4-3/3	1332.466	1332.447	14.176	0.527	982.171	0.566	24	0.151	K.KYIEAGASEHAR.T
R4/RRR4-6/2	856.945	857.030	-99.672	0.445	467.461	0.394	11	0.151	-.VVDVLSPK.-
R4/RRR4-1/2	856.977	857.030	-61.521	0.370	510.233	0.341	12	0.151	K.VVDVLSPK.V
R4/RRR4-5/3	1332.911	1332.447	348.851	0.531	937.514	0.576	23	0.151	K.KYIEAGASEHAR.T
R4/RRR4-6/2	1172.509	1173.345	-1570.790	0.359	873.605	0.311	14	0.151	K.FTIFNFGAQK.E
R4/RRR4-5/2	856.951	857.030	-91.813	0.378	448.193	0.343	11	0.150	K.VVDVLSPK.V
R4/RRR4-1/2	856.914	857.030	-135.252	0.454	364.876	0.352	10	0.150	K.VVDVLSPK.V
R4/RRR4-2/2	1015.335	1016.130	-1773.370	0.355	788.980	0.313	16	0.149	K.AADVGADLVGK.V
R4/RRR4-2/2	1173.240	1173.345	-89.603	0.345	795.256	0.320	13	0.148	K.FTIFNFGAQK.E
R4/RRR4-1/2	857.084	857.030	64.054	0.352	514.454	0.295	12	0.148	K.VVDVLSPK.V
R4/RRR4-2/2	856.487	857.030	-1806.715	0.300	369.899	0.344	10	0.148	K.VVDVLSPK.V
R4/RRR4-6/2	1173.009	1173.345	-287.208	0.368	908.611	0.260	15	0.147	K.FTIFNFGAQK.E
R4/RRR4-2/2	856.294	857.030	-2033.467	0.365	473.129	0.293	11	0.147	K.VVDVLSPK.V
R4/RRR4-5/3	1332.492	1332.447	33.748	0.495	1163.107	0.487	25	0.145	K.KYIEAGASEHAR.T
R4/RRR4-2/2	856.714	857.030	-369.377	0.288	441.825	0.266	11	0.145	K.VVDVLSPK.V
R4/RRR4-6/2	856.870	857.030	-187.128	0.394	466.946	0.350	11	0.144	-.VVDVLSPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1173.562	1173.345	185.642	0.316	531.609	0.302	12	0.143	K.FTIFNFGAQK.E
R4/RRR4-3/2	856.672	857.030	-418.417	0.239	527.555	0.241	11	0.142	K.VVDVLSPK.V
R4/RRR4-3/2	856.473	857.030	-1822.755	0.321	412.488	0.266	10	0.140	-.VVDVLSPK.-
R4/RRR4-2/2	1172.499	1173.345	-1578.843	0.364	575.817	0.347	12	0.140	-.FTIFNFGAQK.-
R4/RRR4-5/2	1257.568	1258.446	-1498.232	0.293	429.498	0.274	13	0.136	-.DTSGPSLNILIK.-
R4/RRR4-2/3	1537.100	1536.718	249.300	0.499	904.522	0.511	30	0.131	R.VKVNPAHAAAAASGGSK.N
R4/RRR4-4/3	1333.158	1332.447	-217.175	0.410	696.399	0.450	21	0.109	K.KYIEAGASEHAR.T
R4/RRR4-2/3	1331.470	1332.447	-1489.338	0.410	701.114	0.337	21	0.095	K.KYIEAGASEHAR.T
R4/RRR4-3/3	1332.371	1332.447	-57.224	0.396	466.543	0.381	19	0.093	-.KYIEAGASEHAR.-
R4/RRR4-5/2	1597.605	1596.809	-127.955	0.548	1223.499	0.616	21	0.224	K.LGIGGLSAEFTDIFR.R
R4/RRR4-5/2	1173.059	1173.386	-279.785	0.440	1422.107	0.505	19	0.219	K.GILLYGPPGTGK.T
R4/RRR4-5/2	1520.564	1519.724	-105.934	0.469	1572.654	0.421	18	0.214	K.SQFGIIILDDIER.L
R4/RRR4-5/2	1597.447	1596.809	-227.223	0.556	1238.215	0.554	21	0.211	K.LGIGGLSAEFTDIFR.R
R4/RRR4-5/2	1673.400	1673.883	-289.417	0.462	1229.792	0.542	21	0.204	K.GSPLVTCLLEGPTGSGK.S
R4/RRR4-5/2	1596.403	1596.809	-254.598	0.499	1025.547	0.600	19	0.200	K.LGIGGLSAEFTDIFR.R
R4/RRR4-5/2	1674.510	1673.883	-223.420	0.508	1094.378	0.525	20	0.189	K.GSPLVTCLLEGPTGSGK.S
R4/RRR4-5/2	1697.127	1697.871	-1030.829	0.481	1144.857	0.481	20	0.186	R.DGTGVHDSIVNQLLTK.I
R4/RRR4-5/2	1876.480	1877.045	-836.519	0.474	906.065	0.515	21	0.176	K.ESSFLSPDVNLQELAAR.T
R4/RRR4-5/2	1698.436	1697.871	-256.965	0.487	1068.299	0.399	20	0.166	R.DGTGVHDSIVNQLLTK.I
R4/RRR4-6/2	1598.179	1596.809	232.618	0.438	582.888	0.514	17	0.160	K.LGIGGLSAEFTDIFR.R
R4/RRR4-5/2	1876.444	1877.045	-855.979	0.457	847.376	0.414	22	0.159	K.ESSFLSPDVNLQELAAR.T
R4/RRR4-5/2	1674.861	1673.883	-13.422	0.458	949.740	0.414	18	0.159	-.GSPLVTCLLEGPTGSGK.-
R4/RRR4-5/2	1173.190	1173.386	-167.460	0.433	1114.270	0.302	17	0.157	K.GILLYGPPGTGK.T
R4/RRR4-5/2	1266.196	1266.296	-79.447	0.417	1111.865	0.295	15	0.156	R.DLFADAENDQK.T
R4/RRR4-5/2	1055.814	1056.238	-402.930	0.399	641.796	0.414	15	0.155	K.IVNGPEVLSK.F
R4/RRR4-5/2	1876.403	1877.045	-877.400	0.466	803.732	0.407	20	0.154	K.ESSFLSPDVNLQELAAR.T
R4/RRR4-5/2	1056.009	1056.238	-217.347	0.422	450.928	0.374	14	0.150	K.IVNGPEVLSK.F
R4/RRR4-5/2	981.600	981.088	-498.753	0.317	918.928	0.246	15	0.143	K.SAVSYALNR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1598.141	1596.809	208.491	0.270	277.758	0.361	13	0.139	K.LGIGGLSAEFTDIFR.R
R4/RRR4-6/2	1875.999	1877.045	-1094.072	0.209	197.439	0.358	15	0.137	K.ESSFLSPDVNLQELAAR.T
R4/RRR4-5/2	1520.128	1519.724	266.470	0.352	876.220	0.252	13	0.136	K.SQFGIIILDDIER.L
R4/RRR4-5/2	1265.689	1266.296	-1273.286	0.314	682.887	0.188	14	0.131	-.DLFADAENDQK.-
R4/RRR4-5/2	1266.054	1266.296	-191.346	0.328	702.382	0.148	14	0.125	-.DLFADAENDQK.-
R4/RRR4-5/3	1694.907	1694.874	19.452	0.378	1343.589	0.261	26	0.106	R.AHDAVSAGSIALNAIQR.R
R4/RRR4-5/3	1694.568	1694.874	-180.936	0.344	860.395	0.173	26	0.073	R.AHDAVSAGSIALNAIQR.R
R4/RRR4-2/2	1592.846	1593.932	-1313.850	0.433	1683.041	0.526	23	0.253	R.IVLNPISSLADLPLK.N
R4/RRR4-2/2	1549.635	1548.726	-58.674	0.394	1981.154	0.357	21	0.249	K.LGLEFGSNAVITNGR.V
R4/RRR4-2/2	1740.236	1740.935	-979.121	0.470	1382.249	0.601	22	0.234	K.VYSIAAETGLPVDNYK.A
R4/RRR4-2/2	1593.496	1593.932	-274.656	0.516	1300.651	0.591	21	0.225	R.IVLNPISSLADLPLK.N
R4/RRR4-2/2	1593.474	1593.932	-288.336	0.483	1332.543	0.574	21	0.224	R.IVLNPISSLADLPLK.N
R4/RRR4-2/2	1275.095	1275.479	-301.758	0.440	1646.369	0.392	17	0.218	K.VIFVDADQIVR.A
R4/RRR4-2/2	1275.969	1275.479	385.779	0.510	1447.663	0.462	18	0.214	K.VIFVDADQIVR.A
R4/RRR4-1/2	1593.893	1593.932	-25.012	0.489	1137.170	0.542	20	0.199	R.IVLNPISSLADLPLK.N
R4/RRR4-2/2	976.991	977.182	-196.704	0.455	1309.384	0.447	14	0.197	R.GLQFILGTK.R
R4/RRR4-2/2	1123.116	1123.238	-109.082	0.364	1373.648	0.368	16	0.186	R.SADLYELPSK.F
R4/RRR4-2/2	1275.348	1275.479	-102.877	0.496	1329.134	0.377	17	0.185	K.VIFVDADQIVR.A
R4/RRR4-2/3	1886.994	1887.038	-23.665	0.535	1329.798	0.529	29	0.182	K.GVALEDPKTEDLSQEVR.G
R4/RRR4-2/2	1056.175	1056.239	-61.511	0.571	963.058	0.409	14	0.168	R.FGIILYSSR.L
R4/RRR4-2/3	1886.308	1887.038	-919.923	0.477	1208.069	0.524	30	0.164	K.GVALEDPKTEDLSQEVR.G
R4/RRR4-2/2	976.466	977.182	-1762.898	0.362	943.355	0.406	14	0.164	R.GLQFILGTK.R
R4/RRR4-2/2	1360.098	1359.423	-239.329	0.358	870.736	0.415	17	0.159	K.WASSFISGDSSSK.K
R4/RRR4-2/2	1543.200	1543.794	-1035.506	0.380	860.774	0.391	18	0.155	K.VSPGVWYLQLAPGR.S
R4/RRR4-2/2	1402.396	1401.588	-136.861	0.474	618.096	0.414	19	0.155	R.QLAEESLSSIPVK.D
R4/RRR4-2/2	1123.016	1123.238	-198.274	0.374	996.465	0.318	14	0.154	R.SADLYELPSK.F
R4/RRR4-2/2	1359.085	1359.423	-249.327	0.356	899.891	0.360	17	0.154	K.WASSFISGDSSSK.K
R4/RRR4-1/2	1592.663	1593.932	-1429.468	0.246	882.481	0.358	17	0.149	R.IVLNPISSLADLPLK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1592.972	1593.932	-1234.580	0.203	1026.222	0.311	17	0.149	R.IVLNPISSLADLPLK.N
R4/RRR4-2/3	1887.367	1887.038	174.653	0.535	1044.288	0.529	30	0.148	K.GVALEDPKTEDLSQEVR.G
R4/RRR4-2/2	1359.445	1359.423	16.427	0.312	739.390	0.334	16	0.144	K.WASSFISGDSSSK.K
R4/RRR4-3/2	1594.463	1593.932	-295.299	0.358	718.548	0.313	17	0.143	R.IVLNPISSLADLPLK.N
R4/RRR4-2/2	1543.352	1543.794	-287.308	0.347	581.888	0.346	16	0.142	K.VSPGVWYLQLAPGR.S
R4/RRR4-3/2	1594.276	1593.932	216.215	0.299	265.111	0.317	13	0.140	R.IVLNPISSLADLPLK.N
R4/RRR4-10/2	1684.698	1684.961	-156.152	0.567	3090.253	0.591	26	0.559	R.ILVTGGAGFIGSHLVDK.L
R4/RRR4-10/2	1617.855	1617.885	-18.209	0.524	2822.737	0.420	22	0.419	R.SFCYVADMVNGLIK.L
R4/RRR4-10/2	1446.165	1445.753	285.262	0.580	2205.752	0.553	23	0.343	K.TNVIGTLNMLGLAK.R
R4/RRR4-11/2	1204.161	1204.404	-202.096	0.480	2196.426	0.468	18	0.314	R.VVSNFIAQAVR.G
R4/RRR4-10/3	1618.021	1617.885	84.621	0.519	2371.324	0.362	31	0.308	R.SFCYVADMVNGLIK.L
R4/RRR4-10/2	1203.581	1204.404	-1518.539	0.467	2019.218	0.492	18	0.293	R.VVSNFIAQAVR.G
R4/RRR4-11/2	1461.236	1461.753	-1041.090	0.487	2005.774	0.492	23	0.290	K.TNVIGTLNM*LGLAK.R
R4/RRR4-10/2	1444.802	1445.753	-1354.495	0.501	1914.970	0.526	23	0.287	K.TNVIGTLNMLGLAK.R
R4/RRR4-11/2	1204.139	1204.404	-220.605	0.503	2062.354	0.445	19	0.286	R.VVSNFIAQAVR.G
R4/RRR4-11/2	1445.344	1445.753	-284.088	0.529	1921.054	0.512	22	0.283	K.TNVIGTLNMLGLAK.R
R4/RRR4-10/2	1461.361	1461.753	-269.196	0.499	1933.233	0.479	23	0.276	K.TNVIGTLNM*LGLAK.R
R4/RRR4-11/2	1204.123	1204.404	-233.420	0.571	1901.271	0.483	18	0.273	R.VVSNFIAQAVR.G
R4/RRR4-11/2	1461.541	1461.753	-145.432	0.522	1878.678	0.493	23	0.272	K.TNVIGTLNM*LGLAK.R
R4/RRR4-10/2	1635.264	1633.884	233.312	0.601	1978.263	0.438	22	0.269	R.SFCYVADM*VNGLIK.L
R4/RRR4-10/2	1635.293	1633.884	250.753	0.556	1981.881	0.424	22	0.267	R.SFCYVADM*VNGLIK.L
R4/RRR4-10/2	1460.689	1461.753	-1417.082	0.399	1915.259	0.443	22	0.262	K.TNVIGTLNM*LGLAK.R
R4/RRR4-10/2	1460.729	1461.753	-1389.635	0.405	1977.879	0.400	23	0.261	K.TNVIGTLNM*LGLAK.R
R4/RRR4-10/2	1205.064	1204.404	-282.311	0.580	1712.816	0.527	18	0.260	R.VVSNFIAQAVR.G
R4/RRR4-10/2	1633.279	1633.884	-985.838	0.440	1863.055	0.436	21	0.254	R.SFCYVADM*VNGLIK.L
R4/RRR4-11/2	1461.365	1461.753	-266.012	0.486	1748.141	0.464	22	0.247	K.TNVIGTLNM*LGLAK.R
R4/RRR4-12/2	1205.236	1204.404	-139.643	0.503	1689.980	0.463	17	0.239	R.VVSNFIAQAVR.G
R4/RRR4-11/2	1445.406	1445.753	-240.790	0.533	1651.806	0.441	21	0.228	K.TNVIGTLNMLGLAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1445.298	1445.753	-315.695	0.450	1569.928	0.438	21	0.219	K.TNVIGTLNMLGLAK.R
R4/RRR4-10/3	1445.638	1445.753	-79.758	0.510	1916.860	0.387	29	0.218	K.TNVIGTLNMLGLAK.R
R4/RRR4-11/2	1617.376	1617.885	-935.783	0.493	1701.478	0.349	20	0.211	R.SFCYVADMVNGLIK.L
R4/RRR4-11/2	1513.189	1512.693	328.457	0.533	1136.143	0.578	22	0.210	R.GEPLTVQKPGTQTR.S
R4/RRR4-10/2	1203.768	1204.404	-1362.685	0.459	1493.099	0.420	18	0.209	R.VVSNFIAQAVR.G
R4/RRR4-10/3	1445.237	1445.753	-1052.207	0.465	1930.140	0.333	27	0.201	K.TNVIGTLNMLGLAK.R
R4/RRR4-11/2	1512.267	1512.693	-282.851	0.414	1111.549	0.549	22	0.198	R.GEPLTVQKPGTQTR.S
R4/RRR4-11/2	1157.297	1157.344	-40.690	0.481	1310.482	0.428	16	0.195	K.AKEVLGWEPK.I
R4/RRR4-10/2	1512.325	1512.693	-244.303	0.458	928.137	0.587	20	0.192	R.GEPLTVQKPGTQTR.S
R4/RRR4-11/2	1512.391	1512.693	-200.738	0.456	872.848	0.558	20	0.184	R.GEPLTVQKPGTQTR.S
R4/RRR4-10/2	1158.127	1157.344	-188.139	0.411	1272.040	0.391	15	0.183	K.AKEVLGWEPK.I
R4/RRR4-10/2	1512.357	1512.693	-223.087	0.447	890.132	0.541	20	0.182	R.GEPLTVQKPGTQTR.S
R4/RRR4-11/2	1157.179	1157.344	-142.691	0.488	1132.209	0.423	15	0.180	K.AKEVLGWEPK.I
R4/RRR4-10/2	1511.752	1512.693	-1288.112	0.469	802.165	0.550	19	0.178	R.GEPLTVQKPGTQTR.S
R4/RRR4-10/2	1445.406	1445.753	-240.705	0.366	1103.102	0.417	17	0.172	K.TNVIGTLNMLGLAK.R
R4/RRR4-11/2	1157.091	1157.344	-218.676	0.486	1048.807	0.383	14	0.166	K.AKEVLGWEPK.I
R4/RRR4-10/2	1204.177	1204.404	-188.774	0.421	1214.290	0.283	17	0.162	R.VVSNFIAQAVR.G
R4/RRR4-10/2	967.979	968.091	-115.433	0.383	682.222	0.394	12	0.156	R.IFNTYGPR.M
R4/RRR4-11/2	967.840	968.091	-259.665	0.458	646.691	0.384	12	0.156	R.IFNTYGPR.M
R4/RRR4-12/2	967.717	968.091	-387.611	0.404	610.310	0.377	11	0.153	R.IFNTYGPR.M
R4/RRR4-11/2	968.059	968.091	-33.214	0.441	590.051	0.359	11	0.151	R.IFNTYGPR.M
R4/RRR4-10/2	968.547	968.091	472.327	0.436	623.380	0.357	12	0.150	-.IFNTYGPR.-
R4/RRR4-10/2	1596.249	1595.759	307.914	0.470	736.642	0.358	17	0.149	R.DGLVLMEDDFRER.L
R4/RRR4-11/2	967.858	968.091	-241.318	0.428	572.360	0.329	11	0.149	R.IFNTYGPR.M
R4/RRR4-13/2	967.264	968.091	-1893.717	0.287	483.356	0.330	10	0.145	R.IFNTYGPR.M
R4/RRR4-11/2	967.146	968.091	-2017.254	0.354	650.127	0.284	12	0.144	-.IFNTYGPR.-
R4/RRR4-12/2	967.713	968.091	-391.535	0.415	679.883	0.309	12	0.144	-.IFNTYGPR.-
R4/RRR4-10/2	1596.020	1595.759	164.044	0.439	384.482	0.392	16	0.143	-.DGLVLMEDDFRER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	967.365	968.091	-1789.609	0.313	586.192	0.329	11	0.142	-.IFNTYGPR.-
R4/RRR4-12/2	1204.330	1204.404	-60.857	0.312	469.468	0.250	14	0.142	R.VVSNFIAQAVR.G
R4/RRR4-10/3	1445.690	1445.753	-43.677	0.465	1538.873	0.313	26	0.139	-.TNVIGTLNMLGLAK.-
R4/RRR4-11/2	1613.169	1611.759	255.290	0.222	209.558	0.329	13	0.139	R.DGLVLM*EDDFRER.L
R4/RRR4-10/3	1398.217	1398.569	-252.481	0.482	814.961	0.511	24	0.125	R.VAETLM*FDYHR.Q
R4/RRR4-10/3	1382.515	1382.570	-39.252	0.425	929.622	0.465	25	0.119	R.VAETLMFDYHR.Q
R4/RRR4-10/3	1382.589	1382.570	14.282	0.499	757.531	0.492	22	0.119	R.VAETLMFDYHR.Q
R4/RRR4-10/3	1399.030	1398.569	330.911	0.409	488.927	0.551	21	0.118	R.VAETLM*FDYHR.Q
R4/RRR4-11/3	1398.958	1398.569	279.204	0.411	467.506	0.507	21	0.112	R.VAETLM*FDYHR.Q
R4/RRR4-11/3	1398.519	1398.569	-35.747	0.370	670.610	0.484	22	0.111	R.VAETLM*FDYHR.Q
R4/RRR4-10/3	1382.751	1382.570	131.958	0.368	780.718	0.449	23	0.109	R.VAETLMFDYHR.Q
R4/RRR4-10/3	1398.436	1398.569	-94.978	0.351	355.052	0.446	19	0.105	R.VAETLM*FDYHR.Q
R4/RRR4-11/3	1398.134	1398.569	-312.264	0.294	341.102	0.453	17	0.103	R.VAETLM*FDYHR.Q
R4/RRR4-13/1	1046.573	1047.184	-1544.593	0.128	799.641	0.121	13	0.470	K.SAEAVELVTK.E
R4/RRR4-13/2	1699.297	1699.843	-912.502	0.541	1950.514	0.589	24	0.311	K.GNAYAQVAIGTEDVYK.S
R4/RRR4-13/2	1700.414	1699.843	-252.994	0.612	1936.025	0.595	24	0.311	K.GNAYAQVAIGTEDVYK.S
R4/RRR4-13/2	1699.380	1699.843	-273.105	0.547	1917.250	0.573	24	0.301	K.GNAYAQVAIGTEDVYK.S
R4/RRR4-13/2	1046.421	1047.184	-1690.443	0.453	1883.278	0.498	17	0.275	K.SAEAVELVTK.E
R4/RRR4-13/2	1046.993	1047.184	-182.967	0.480	1869.354	0.495	17	0.273	K.SAEAVELVTK.E
R4/RRR4-13/2	1046.976	1047.184	-199.576	0.488	1643.700	0.518	16	0.249	K.SAEAVELVTK.E
R4/RRR4-13/2	1233.134	1233.438	-247.687	0.481	1451.889	0.498	18	0.222	K.VVLVDNADFLK.E
R4/RRR4-13/2	1233.281	1233.438	-128.227	0.471	1438.998	0.488	18	0.219	K.VVLVDNADFLK.E
R4/RRR4-13/2	1233.089	1233.438	-284.136	0.479	1291.101	0.518	18	0.211	K.VVLVDNADFLK.E
R4/RRR4-13/2	1184.812	1184.366	377.535	0.492	1291.891	0.456	15	0.198	K.SPEVVLEWPK.K
R4/RRR4-13/2	1184.261	1184.366	-88.665	0.525	1294.606	0.434	15	0.193	K.SPEVVLEWPK.K
R4/RRR4-13/2	1248.625	1249.396	-1423.261	0.488	1083.045	0.403	17	0.174	K.IASFLDPDGWK.V
R4/RRR4-13/2	1249.179	1249.396	-174.720	0.452	1057.972	0.393	17	0.170	K.IASFLDPDGWK.V
R4/RRR4-13/2	1185.201	1184.366	-139.731	0.447	1066.624	0.384	13	0.166	K.SPEVVLEWPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1504.213	1504.802	-1059.496	0.464	722.073	0.468	18	0.161	K.ILRQPGPLPGLNTK.I
R4/RRR4-13/2	1514.193	1514.766	-1042.056	0.411	431.838	0.514	16	0.159	R.GPTPEPLCQVM*LR.V
R4/RRR4-13/2	1498.318	1498.767	-300.601	0.397	435.144	0.500	16	0.157	R.GPTPEPLCQVMLR.V
R4/RRR4-13/2	1498.460	1498.767	-205.138	0.343	524.265	0.496	17	0.157	R.GPTPEPLCQVMLR.V
R4/RRR4-13/2	1498.042	1498.767	-1154.746	0.380	451.041	0.475	16	0.155	R.GPTPEPLCQVMLR.V
R4/RRR4-13/2	1249.000	1249.396	-318.356	0.361	885.230	0.323	16	0.152	K.IASFLDPDGWK.V
R4/RRR4-13/2	1514.273	1514.766	-326.192	0.344	309.127	0.457	14	0.149	R.GPTPEPLCQVM*LR.V
R4/RRR4-13/2	1514.331	1514.766	-288.098	0.333	422.934	0.412	16	0.149	R.GPTPEPLCQVM*LR.V
R4/RRR4-13/2	1248.617	1249.396	-1429.742	0.342	897.451	0.262	17	0.146	K.IASFLDPDGWK.V
R4/RRR4-14/2	1047.128	1047.184	-53.740	0.323	557.223	0.293	13	0.142	K.SAEAVELVTK.E
R4/RRR4-13/2	1504.236	1504.802	-1044.178	0.352	173.069	0.391	14	0.142	-.ILRQPGPLPGLNTK.-
R4/RRR4-13/2	1604.554	1603.841	-179.212	0.550	1127.638	0.478	21	0.134	K.VVLVDNADFLKELQ.-
R4/RRR4-13/2	1604.049	1603.841	130.324	0.515	1137.106	0.407	21	0.123	-.VVLVDNADFLKELQ.-
R4/RRR4-13/2	1603.351	1603.841	-306.720	0.475	1077.672	0.406	21	0.120	K.VVLVDNADFLKELQ.-
R4/RRR4-13/2	1603.674	1603.841	-104.795	0.364	551.360	0.257	15	0.115	-.VVLVDNADFLKELQ.-
R4/RRR4-13/3	871.963	872.049	-99.374	0.466	470.628	0.438	15	0.108	R.LLHAVYR.V
R4/RRR4-14/3	872.126	872.049	87.852	0.357	405.947	0.386	15	0.102	R.LLHAVYR.V
R4/RRR4-13/2	1603.741	1603.841	-62.420	0.320	830.159	0.272	16	0.099	K.VVLVDNADFLKELQ.-
R4/RRR4-13/3	872.311	872.049	300.793	0.460	583.489	0.333	17	0.099	R.LLHAVYR.V
R4/RRR4-13/3	872.278	872.049	262.906	0.472	587.313	0.320	17	0.099	R.LLHAVYR.V
R4/RRR4-13/2	1604.357	1603.841	-302.865	0.473	855.764	0.316	17	0.099	-.VVLVDNADFLKELQ.-
R4/RRR4-13/3	872.429	872.049	436.426	0.377	512.695	0.309	16	0.097	R.LLHAVYR.V
R4/RRR4-14/3	872.526	872.049	548.040	0.429	597.952	0.319	17	0.097	R.LLHAVYR.V
R4/RRR4-13/2	1602.740	1603.841	-1314.600	0.327	923.678	0.248	19	0.097	K.VVLVDNADFLKELQ.-
R4/RRR4-14/3	871.984	872.049	-75.572	0.384	573.502	0.340	17	0.097	R.LLHAVYR.V
R4/RRR4-13/3	1504.775	1504.802	-17.918	0.451	906.237	0.350	24	0.096	K.ILRQPGPLPGLNTK.I
R4/RRR4-13/3	1515.194	1514.766	283.152	0.431	931.824	0.351	20	0.096	R.GPTPEPLCQVM*LR.V
R4/RRR4-13/3	872.459	872.049	471.459	0.396	676.801	0.323	19	0.094	R.LLHAVYR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1604.279	1603.841	273.632	0.413	811.654	0.205	17	0.094	-.VVLVDNADFLKELQ.-
R4/RRR4-13/3	1504.964	1504.802	107.900	0.444	1041.295	0.298	26	0.094	K.ILRQPGPLPGLNTK.I
R4/RRR4-12/2	1747.045	1748.146	-1206.015	0.479	2389.700	0.547	28	0.375	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-12/2	1747.620	1748.146	-875.780	0.546	2340.392	0.505	26	0.350	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-12/3	1747.573	1748.146	-902.890	0.498	2043.852	0.463	39	0.277	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-12/3	1748.737	1748.146	-234.563	0.512	2104.196	0.431	38	0.275	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-11/2	1349.230	1348.616	-286.720	0.567	1912.790	0.476	20	0.273	K.KLFGVTTLDVVR.A
R4/RRR4-11/2	1348.290	1348.616	-242.333	0.547	1876.089	0.436	20	0.257	K.KLFGVTTLDVVR.A
R4/RRR4-12/2	1348.352	1348.616	-196.375	0.534	1818.372	0.455	20	0.255	K.KLFGVTTLDVVR.A
R4/RRR4-12/2	1747.625	1748.146	-872.976	0.535	1739.133	0.506	25	0.253	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-12/2	1348.418	1348.616	-146.970	0.538	1692.121	0.485	20	0.247	K.KLFGVTTLDVVR.A
R4/RRR4-12/2	1347.675	1348.616	-1444.665	0.480	1745.463	0.409	20	0.234	K.KLFGVTTLDVVR.A
R4/RRR4-11/2	1347.828	1348.616	-1330.223	0.493	1668.778	0.435	20	0.232	K.KLFGVTTLDVVR.A
R4/RRR4-12/2	1279.093	1278.526	-339.199	0.453	1620.162	0.455	20	0.229	K.GVDVVVIPAGVPR.K
R4/RRR4-12/2	1469.321	1469.649	-223.872	0.476	1517.821	0.481	22	0.222	K.AGAGSATLSMAYAAAR.F
R4/RRR4-12/2	1486.118	1485.648	317.028	0.516	1510.862	0.476	22	0.220	K.AGAGSATLSM*AYAAAR.F
R4/RRR4-12/2	1485.861	1485.648	143.876	0.459	1428.564	0.465	21	0.208	K.AGAGSATLSM*AYAAAR.F
R4/RRR4-12/2	1279.000	1278.526	372.325	0.365	1529.326	0.387	20	0.203	K.GVDVVVIPAGVPR.K
R4/RRR4-12/2	1277.591	1278.526	-1518.450	0.335	1566.448	0.353	18	0.199	K.GVDVVVIPAGVPR.K
R4/RRR4-11/2	1277.954	1278.526	-1233.761	0.370	1392.903	0.434	17	0.197	K.GVDVVVIPAGVPR.K
R4/RRR4-12/2	1220.059	1220.443	-315.972	0.543	1310.623	0.396	19	0.189	K.LFGVTTLDVVR.A
R4/RRR4-11/3	1748.291	1748.146	83.078	0.460	1721.118	0.382	35	0.185	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-12/2	1485.244	1485.648	-273.187	0.465	1200.635	0.450	20	0.184	K.AGAGSATLSM*AYAAAR.F
R4/RRR4-11/2	1259.048	1259.391	-273.124	0.493	867.284	0.500	18	0.177	R.IQNAGTEVVEAK.A
R4/RRR4-11/2	1259.110	1259.391	-224.393	0.517	937.755	0.467	18	0.175	R.IQNAGTEVVEAK.A
R4/RRR4-13/2	1220.043	1220.443	-328.621	0.500	1088.452	0.397	18	0.174	K.LFGVTTLDVVR.A
R4/RRR4-11/2	1221.194	1220.443	-204.190	0.529	1121.344	0.374	18	0.172	K.LFGVTTLDVVR.A
R4/RRR4-12/2	1220.119	1220.443	-266.686	0.536	1084.735	0.382	18	0.171	K.LFGVTTLDVVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1258.995	1259.391	-315.731	0.495	876.992	0.436	18	0.168	R.IQNAGTEVVEAK.A
R4/RRR4-12/2	1219.569	1220.443	-1541.299	0.396	1103.920	0.355	18	0.167	K.LFGVTTLDVVR.A
R4/RRR4-11/2	1220.193	1220.443	-205.260	0.524	1080.679	0.353	18	0.166	K.LFGVTTLDVVR.A
R4/RRR4-11/2	1219.639	1220.443	-1483.789	0.456	1168.573	0.314	18	0.165	K.LFGVTTLDVVR.A
R4/RRR4-12/2	1415.041	1415.578	-1089.144	0.441	1028.633	0.370	19	0.163	K.RIQNAGTEVVEAK.A
R4/RRR4-12/2	1102.297	1102.306	-8.620	0.475	973.775	0.308	15	0.153	K.ALEALKSELK.A
R4/RRR4-12/3	1982.616	1983.123	-762.349	0.530	1329.694	0.419	30	0.146	K.TRPSVTFTDEETEQLTK.R
R4/RRR4-12/2	1103.047	1102.306	-235.939	0.270	698.344	0.211	13	0.134	-.ALEALKSELK.-
R4/RRR4-12/3	1416.434	1415.578	-101.283	0.375	547.416	0.525	24	0.107	K.RIQNAGTEVVEAK.A
R4/RRR4-11/3	1747.524	1748.146	-930.765	0.431	877.279	0.410	30	0.107	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-12/3	1982.291	1983.123	-926.738	0.448	1029.235	0.365	27	0.105	K.TRPSVTFTDEETEQLTK.R
R4/RRR4-11/3	1348.521	1348.616	-70.793	0.491	1016.495	0.286	27	0.093	K.KLFGVTTLDVVR.A
R4/RRR4-11/3	1348.760	1348.616	106.915	0.478	1158.145	0.259	28	0.091	-.KLFGVTTLDVVR.-
R4/RRR4-12/3	1348.533	1348.616	-61.668	0.489	930.032	0.314	25	0.083	-.KLFGVTTLDVVR.-
R4/RRR4-12/3	1747.404	1748.146	-999.986	0.321	953.328	0.226	28	0.082	K.VAVLGAAGGIGQPLGLLIK.M
R4/RRR4-12/3	1348.161	1348.616	-338.497	0.435	856.483	0.281	25	0.077	-.KLFGVTTLDVVR.-
R4/RRR4-12/3	1348.654	1348.616	28.078	0.528	989.326	0.263	26	0.076	-.KLFGVTTLDVVR.-
R4/RRR4-11/3	1348.650	1348.616	25.763	0.541	901.216	0.292	25	0.070	-.KLFGVTTLDVVR.-
R4/RRR4-9/2	1885.555	1886.113	-828.838	0.585	3110.543	0.603	25	0.565	R.AVCM*ISNNTAVAEVFSR.I
R4/RRR4-9/2	1794.243	1794.107	75.771	0.598	2964.314	0.619	25	0.534	R.IHFMLSSYAPVISAEK.A
R4/RRR4-9/2	1793.520	1794.107	-887.568	0.577	2906.566	0.631	25	0.525	R.IHFMLSSYAPVISAEK.A
R4/RRR4-9/2	1885.696	1886.113	-221.819	0.610	2536.266	0.621	25	0.432	R.AVCM*ISNNTAVAEVFSR.I
R4/RRR4-9/2	1810.153	1810.107	25.819	0.598	2482.220	0.615	23	0.418	R.IHFM*LSSYAPVISAEK.A
R4/RRR4-9/2	1793.469	1794.107	-916.266	0.568	2476.367	0.602	23	0.412	R.IHFMLSSYAPVISAEK.A
R4/RRR4-9/2	1810.477	1810.107	204.957	0.630	2406.149	0.615	23	0.401	R.IHFM*LSSYAPVISAEK.A
R4/RRR4-9/2	1809.395	1810.107	-948.576	0.602	2307.730	0.625	23	0.385	R.IHFM*LSSYAPVISAEK.A
R4/RRR4-9/2	1532.498	1532.807	-202.419	0.513	2365.048	0.574	22	0.381	R.LISQIISSLTTSLR.F
R4/RRR4-9/2	1869.539	1870.114	-844.995	0.558	2239.841	0.592	23	0.360	R.AVCMISNNTAVAEVFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1885.188	1886.113	-1024.294	0.561	2242.822	0.581	24	0.357	R.AVCM*ISNNTAVAEVFSR.I
R4/RRR4-9/2	1870.038	1870.114	-40.829	0.596	2166.261	0.583	23	0.343	R.AVCMISNNTAVAEVFSR.I
R4/RRR4-9/2	1532.396	1532.807	-269.547	0.485	2078.112	0.567	21	0.325	R.LISQIISSLTTSLR.F
R4/RRR4-9/2	1531.813	1532.807	-1305.691	0.402	2076.299	0.458	21	0.291	R.LISQIISSLTTSLR.F
R4/RRR4-9/2	1716.938	1716.956	-10.384	0.522	1529.487	0.477	23	0.224	R.AIFVDLEPTVIDEVR.T
R4/RRR4-8/2	1001.869	1002.147	-277.731	0.432	1349.820	0.516	16	0.214	K.DVNAAVATIK.T
R4/RRR4-8/2	1001.419	1002.147	-1730.953	0.401	1318.752	0.534	17	0.214	K.DVNAAVATIK.T
R4/RRR4-8/2	1001.398	1002.147	-1751.774	0.405	1293.395	0.521	16	0.209	K.DVNAAVATIK.T
R4/RRR4-9/2	1001.934	1002.147	-213.192	0.470	1297.944	0.503	16	0.208	K.DVNAAVATIK.T
R4/RRR4-8/2	1716.476	1716.956	-280.728	0.472	1549.287	0.386	23	0.206	R.AIFVDLEPTVIDEVR.T
R4/RRR4-9/2	1001.874	1002.147	-272.719	0.417	1162.013	0.557	16	0.205	K.DVNAAVATIK.T
R4/RRR4-9/2	1716.322	1716.956	-955.026	0.509	1310.443	0.466	24	0.201	R.AIFVDLEPTVIDEVR.T
R4/RRR4-9/2	1872.418	1873.093	-897.184	0.505	1078.232	0.557	25	0.198	K.CGINYQPPSVVPGGDLAK.V
R4/RRR4-9/2	1873.359	1873.093	142.438	0.521	1046.419	0.561	25	0.196	K.CGINYQPPSVVPGGDLAK.V
R4/RRR4-8/2	1717.334	1716.956	220.613	0.567	1254.767	0.468	23	0.196	R.AIFVDLEPTVIDEVR.T
R4/RRR4-2/2	1001.574	1002.147	-1575.557	0.368	1244.589	0.478	16	0.195	K.DVNAAVATIK.T
R4/RRR4-1/2	1001.885	1002.147	-261.962	0.447	1190.648	0.484	16	0.195	K.DVNAAVATIK.T
R4/RRR4-9/2	1001.934	1002.147	-213.558	0.475	1037.294	0.542	15	0.194	K.DVNAAVATIK.T
R4/RRR4-1/2	1718.315	1716.956	209.300	0.600	1153.752	0.480	22	0.189	R.AIFVDLEPTVIDEVR.T
R4/RRR4-1/2	1002.012	1002.147	-135.217	0.417	1140.454	0.465	16	0.187	K.DVNAAVATIK.T
R4/RRR4-2/2	1001.742	1002.147	-405.857	0.380	1163.439	0.461	16	0.187	K.DVNAAVATIK.T
R4/RRR4-13/2	1716.545	1716.956	-240.488	0.487	1358.627	0.378	22	0.186	R.AIFVDLEPTVIDEVR.T
R4/RRR4-2/2	1001.782	1002.147	-365.020	0.341	1236.505	0.398	16	0.181	K.DVNAAVATIK.T
R4/RRR4-9/2	1871.989	1873.093	-1127.221	0.440	918.842	0.526	24	0.179	K.CGINYQPPSVVPGGDLAK.V
R4/RRR4-9/2	1716.329	1716.956	-951.170	0.497	1051.616	0.433	21	0.174	R.AIFVDLEPTVIDEVR.T
R4/RRR4-13/2	1716.248	1716.956	-998.299	0.413	1084.290	0.377	21	0.168	R.AIFVDLEPTVIDEVR.T
R4/RRR4-8/2	1716.381	1716.956	-920.468	0.479	942.745	0.382	20	0.160	R.AIFVDLEPTVIDEVR.T
R4/RRR4-1/2	1001.651	1002.147	-496.714	0.275	963.364	0.363	15	0.158	K.DVNAAVATIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/3	1716.504	1716.956	-264.076	0.464	1199.103	0.473	29	0.146	R.AIFVDLEPTVIDEVR.T
R4/RRR4-9/2	1134.209	1133.271	-54.256	0.362	794.320	0.278	13	0.145	K.EIVDLCLDR.V
R4/RRR4-9/2	1133.090	1133.271	-159.772	0.306	814.303	0.246	13	0.142	K.EIVDLCLDR.V
R4/RRR4-7/2	1716.455	1716.956	-877.487	0.321	777.857	0.214	20	0.139	R.AIFVDLEPTVIDEVR.T
R4/RRR4-9/2	1532.363	1532.807	-291.126	0.295	621.924	0.308	13	0.136	R.LISQIISSLTTSLR.F
R4/RRR4-9/2	1133.327	1133.271	50.169	0.304	724.820	0.159	12	0.134	-.EIVDLCLDR.-
R4/RRR4-8/3	1716.570	1716.956	-225.656	0.416	1021.830	0.489	26	0.133	R.AIFVDLEPTVIDEVR.T
R4/RRR4-5/2	1716.567	1716.956	-227.218	0.330	676.695	0.133	15	0.129	R.AIFVDLEPTVIDEVR.T
R4/RRR4-13/2	1132.872	1133.271	-353.151	0.251	521.572	0.221	11	0.122	-.EIVDLCLDR.-
R4/RRR4-13/3	1693.862	1692.855	4.502	0.492	628.160	0.516	27	0.121	R.SLDIERPTYTNLNR.L
R4/RRR4-8/3	1693.200	1692.855	204.443	0.451	512.295	0.499	27	0.115	R.SLDIERPTYTNLNR.L
R4/RRR4-2/3	1692.778	1692.855	-45.366	0.487	454.644	0.481	25	0.113	R.SLDIERPTYTNLNR.L
R4/RRR4-9/3	1532.767	1532.807	-26.218	0.345	862.574	0.461	28	0.112	R.LISQIISSLTTSLR.F
R4/RRR4-13/3	1692.906	1692.855	30.360	0.439	505.032	0.455	25	0.110	R.SLDIERPTYTNLNR.L
R4/RRR4-2/3	1692.172	1692.855	-997.352	0.385	312.669	0.388	21	0.108	R.SLDIERPTYTNLNR.L
R4/RRR4-8/3	1692.570	1692.855	-168.961	0.431	571.595	0.468	28	0.107	-.SLDIERPTYTNLNR.-
R4/RRR4-9/3	1692.964	1692.855	64.856	0.402	592.788	0.421	28	0.106	R.SLDIERPTYTNLNR.L
R4/RRR4-1/3	1693.837	1692.855	-10.244	0.362	395.324	0.378	24	0.105	R.SLDIERPTYTNLNR.L
R4/RRR4-2/3	1693.748	1692.855	-63.484	0.309	350.712	0.330	22	0.105	R.SLDIERPTYTNLNR.L
R4/RRR4-5/3	1692.377	1692.855	-283.142	0.399	400.902	0.366	21	0.104	R.SLDIERPTYTNLNR.L
R4/RRR4-9/3	1692.045	1692.855	-1072.646	0.316	460.360	0.409	25	0.104	R.SLDIERPTYTNLNR.L
R4/RRR4-9/3	1693.047	1692.855	113.775	0.377	485.258	0.393	27	0.104	R.SLDIERPTYTNLNR.L
R4/RRR4-9/3	1810.677	1810.107	-237.776	0.434	1256.295	0.282	27	0.104	R.IHFM*LSSYAPVISAEK.A
R4/RRR4-9/3	1381.597	1381.625	-19.915	0.465	860.285	0.391	22	0.103	R.IDHKFDLMYAK.R
R4/RRR4-9/3	1532.333	1532.807	-310.637	0.379	841.367	0.411	28	0.103	R.LISQIISSLTTSLR.F
R4/RRR4-13/3	1692.664	1692.855	-113.182	0.390	364.617	0.419	23	0.103	-.SLDIERPTYTNLNR.-
R4/RRR4-8/3	1692.571	1692.855	-168.092	0.377	327.096	0.387	22	0.103	-.SLDIERPTYTNLNR.-
R4/RRR4-1/3	1692.938	1692.855	49.452	0.355	496.692	0.376	25	0.102	R.SLDIERPTYTNLNR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/3	1693.087	1692.855	137.528	0.362	447.130	0.346	22	0.102	R.SLDIERPTYTNLNR.L
R4/RRR4-9/3	1382.960	1381.625	243.400	0.445	401.501	0.323	19	0.096	R.IDHKFDLMYAK.R
R4/RRR4-7/3	1693.310	1692.855	269.613	0.341	596.757	0.267	27	0.095	R.SLDIERPTYTNLNR.L
R4/RRR4-9/3	1809.415	1810.107	-937.882	0.370	1426.496	0.174	31	0.092	R.IHFM*LSSYAPVISAEK.A
R4/RRR4-9/3	1532.080	1532.807	-1130.898	0.317	451.476	0.322	21	0.088	R.LISQIISSLTTSLR.F
R4/RRR4-9/3	1382.219	1381.625	-294.326	0.431	645.282	0.230	23	0.087	R.IDHKFDLMYAK.R
R4/RRR4-9/3	1793.376	1794.107	-968.310	0.333	939.908	0.226	29	0.081	R.IHFMLSSYAPVISAEK.A
R4/RRR4-9/3	1716.789	1716.956	-97.899	0.255	495.637	0.324	21	0.079	-.AIFVDLEPTVIDEVR.-
R4/RRR4-9/3	1794.900	1794.107	-116.080	0.345	837.685	0.183	26	0.077	R.IHFMLSSYAPVISAEK.A
R4/RRR4-9/3	1397.563	1397.624	-44.160	0.265	822.199	0.057	21	0.074	-.IDHKFDLM*YAK.-
R4/RRR4-3/2	1252.079	1252.528	-359.719	0.451	1784.944	0.509	20	0.263	R.LILGELQAPAVK.Y
R4/RRR4-2/2	1252.269	1252.528	-207.531	0.392	1596.399	0.501	19	0.236	R.LILGELQAPAVK.Y
R4/RRR4-3/2	1252.143	1252.528	-308.463	0.389	1373.397	0.471	17	0.205	R.LILGELQAPAVK.Y
R4/RRR4-2/2	1121.042	1120.283	-215.660	0.503	1504.308	0.359	15	0.198	R.VTIFDLQQR.L
R4/RRR4-3/2	1497.225	1497.637	-275.879	0.530	1005.120	0.561	20	0.197	R.QGNVGIVEYAYQR.T
R4/RRR4-3/2	1497.166	1497.637	-315.471	0.425	1073.896	0.550	20	0.196	R.QGNVGIVEYAYQR.T
R4/RRR4-2/2	1498.098	1497.637	308.392	0.475	1024.112	0.558	20	0.196	R.QGNVGIVEYAYQR.T
R4/RRR4-2/2	1321.144	1321.501	-271.130	0.423	1082.743	0.507	17	0.189	R.VIGNNIFCLDR.D
R4/RRR4-3/2	1252.322	1252.528	-164.994	0.338	1211.750	0.476	16	0.189	R.LILGELQAPAVK.Y
R4/RRR4-1/2	1251.859	1252.528	-1336.939	0.465	1080.689	0.505	16	0.188	R.LILGELQAPAVK.Y
R4/RRR4-2/2	1321.218	1321.501	-214.586	0.416	937.557	0.557	16	0.186	R.VIGNNIFCLDR.D
R4/RRR4-3/2	1497.079	1497.637	-1044.182	0.371	1036.206	0.500	19	0.182	R.QGNVGIVEYAYQR.T
R4/RRR4-2/2	1322.438	1321.501	-47.830	0.430	1034.515	0.476	17	0.181	R.VIGNNIFCLDR.D
R4/RRR4-1/2	992.158	992.114	44.967	0.449	1136.093	0.417	16	0.178	K.GAGGSAVFVAR.N
R4/RRR4-2/2	1252.183	1252.528	-276.382	0.351	1099.575	0.437	16	0.175	R.LILGELQAPAVK.Y
R4/RRR4-2/2	991.942	992.114	-173.249	0.446	1058.163	0.420	16	0.174	K.GAGGSAVFVAR.N
R4/RRR4-1/2	1252.231	1252.528	-238.239	0.412	1012.853	0.450	15	0.172	R.LILGELQAPAVK.Y
R4/RRR4-3/2	1192.106	1191.402	-248.303	0.469	856.128	0.433	17	0.169	K.TLDVPIYITR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	991.948	992.114	-168.064	0.475	796.412	0.455	16	0.167	K.GAGGSAVFVAR.N
R4/RRR4-3/2	991.893	992.114	-223.126	0.456	868.546	0.426	16	0.165	K.GAGGSAVFVAR.N
R4/RRR4-1/2	1497.087	1497.637	-1038.451	0.419	683.953	0.481	18	0.164	R.QGNVGIVEYAYQR.T
R4/RRR4-3/2	1191.330	1191.402	-59.979	0.435	781.255	0.426	16	0.164	K.TLDVPIYITR.V
R4/RRR4-2/2	1497.172	1497.637	-311.544	0.406	874.594	0.421	18	0.163	R.QGNVGIVEYAYQR.T
R4/RRR4-3/2	991.478	992.114	-1654.456	0.426	748.207	0.449	15	0.160	-.GAGGSAVFVAR.-
R4/RRR4-2/2	1252.336	1252.528	-153.846	0.355	963.101	0.393	14	0.160	R.LILGELQAPAVK.Y
R4/RRR4-2/2	1191.572	1191.402	143.585	0.402	692.013	0.419	16	0.160	K.TLDVPIYITR.V
R4/RRR4-2/2	1191.053	1191.402	-293.548	0.425	741.104	0.396	16	0.159	K.TLDVPIYITR.V
R4/RRR4-2/2	1192.097	1191.402	-256.624	0.448	559.902	0.446	14	0.159	K.TLDVPIYITR.V
R4/RRR4-3/2	1191.198	1191.402	-171.301	0.440	687.675	0.410	15	0.158	K.TLDVPIYITR.V
R4/RRR4-3/2	1120.165	1120.283	-106.090	0.314	858.690	0.328	14	0.151	R.VTIFDLQQR.L
R4/RRR4-2/2	1119.856	1120.283	-382.839	0.364	604.837	0.386	12	0.150	R.VTIFDLQQR.L
R4/RRR4-1/2	772.076	771.928	191.866	0.336	1027.177	0.168	11	0.141	R.LGIEALR.Q
R4/RRR4-2/3	1591.909	1591.750	99.661	0.469	1516.272	0.335	26	0.141	-.AEDRVTIFDLQQR.-
R4/RRR4-2/2	992.094	992.114	-20.315	0.395	409.922	0.409	13	0.141	-.GAGGSAVFVAR.-
R4/RRR4-3/2	1119.415	1120.283	-1673.729	0.301	748.354	0.251	12	0.140	R.VTIFDLQQR.L
R4/RRR4-2/2	1496.511	1497.637	-1424.770	0.325	751.332	0.231	17	0.139	R.QGNVGIVEYAYQR.T
R4/RRR4-2/2	771.766	771.928	-210.063	0.419	849.570	0.183	11	0.139	R.LGIEALR.Q
R4/RRR4-4/2	772.222	771.928	381.615	0.403	851.600	0.177	11	0.139	R.LGIEALR.Q
R4/RRR4-2/2	771.850	771.928	-101.856	0.476	1018.526	0.152	12	0.137	R.LGIEALR.Q
R4/RRR4-2/2	772.023	771.928	122.891	0.497	1006.059	0.164	11	0.136	R.LGIEALR.Q
R4/RRR4-4/2	771.938	771.928	12.830	0.458	992.790	0.112	12	0.133	R.LGIEALR.Q
R4/RRR4-1/2	771.930	771.928	3.155	0.504	1055.552	0.120	12	0.132	R.LGIEALR.Q
R4/RRR4-2/3	1591.602	1591.750	-93.829	0.494	1161.312	0.354	24	0.112	K.AEDRVTIFDLQQR.L
R4/RRR4-3/3	1298.027	1298.434	-314.406	0.467	1389.499	0.261	25	0.107	R.RPGSVSLNQSPR.T
R4/RRR4-1/3	1298.476	1298.434	32.652	0.470	966.909	0.382	21	0.094	-.RPGSVSLNQSPR.-
R4/RRR4-3/3	1298.418	1298.434	-12.609	0.385	667.917	0.305	21	0.090	R.RPGSVSLNQSPR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/3	1298.645	1298.434	163.178	0.369	849.212	0.270	21	0.086	R.RPGSVSLNQSPR.T
R4/RRR4-2/3	1590.751	1591.750	-1260.556	0.445	602.143	0.283	21	0.083	-.AEDRVTIFDLQQR.-
R4/RRR4-1/3	1298.603	1298.434	130.797	0.384	613.856	0.326	20	0.079	-.RPGSVSLNQSPR.-
R4/RRR4-2/3	1298.492	1298.434	45.239	0.342	730.040	0.205	19	0.062	-.RPGSVSLNQSPR.-
R4/RRR4-3/3	1591.641	1591.750	-69.134	0.350	1007.868	0.136	21	0.061	-.AEDRVTIFDLQQR.-
R4/RRR4-7/2	1414.318	1414.577	-183.493	0.497	1879.488	0.553	18	0.289	K.SVTDYITDIVCK.R
R4/RRR4-7/2	1414.179	1414.577	-282.210	0.456	1801.780	0.507	18	0.265	K.SVTDYITDIVCK.R
R4/RRR4-7/2	1413.789	1414.577	-1267.815	0.441	1692.645	0.515	18	0.252	K.SVTDYITDIVCK.R
R4/RRR4-7/2	1653.293	1652.828	282.331	0.498	1574.276	0.534	21	0.244	K.YVELTADYVYPYR.N
R4/RRR4-7/2	1652.302	1652.828	-925.932	0.369	1489.637	0.480	20	0.218	K.YVELTADYVYPYR.N
R4/RRR4-7/2	1652.349	1652.828	-290.734	0.421	1408.117	0.478	20	0.211	K.YVELTADYVYPYR.N
R4/RRR4-6/2	1415.855	1414.577	197.543	0.352	1085.454	0.495	16	0.182	K.SVTDYITDIVCK.R
R4/RRR4-7/2	1406.840	1407.722	-1341.960	0.479	1287.499	0.394	16	0.182	K.MLIAMVETELEK.R
R4/RRR4-7/2	1352.190	1352.520	-244.532	0.472	1356.398	0.327	16	0.177	K.FASLRDEWSLK.N
R4/RRR4-7/2	1236.105	1235.368	-213.712	0.478	906.209	0.369	15	0.159	R.DKIETPEQFK.Q
R4/RRR4-7/2	1234.982	1235.368	-313.245	0.411	942.376	0.325	15	0.155	R.DKIETPEQFK.Q
R4/RRR4-7/2	1600.050	1600.843	-1123.366	0.393	629.559	0.417	19	0.152	K.IYSEMIGNVMTDAR.S
R4/RRR4-7/2	1459.109	1459.576	-320.930	0.293	537.308	0.488	20	0.151	K.EVPTSFGFDTACK.I
R4/RRR4-7/2	1352.347	1352.520	-128.436	0.435	1079.982	0.273	15	0.151	K.FASLRDEWSLK.N
R4/RRR4-7/2	1234.908	1235.368	-373.544	0.458	857.807	0.326	14	0.151	R.DKIETPEQFK.Q
R4/RRR4-7/2	1243.003	1243.435	-348.260	0.355	1094.021	0.251	15	0.150	K.TIQEQLLLER.D
R4/RRR4-7/2	1569.487	1570.763	-1454.320	0.365	828.939	0.356	16	0.148	K.SVTDYITDIVCKR.A
R4/RRR4-7/2	1352.341	1352.520	-132.601	0.439	961.769	0.240	14	0.141	K.FASLRDEWSLK.N
R4/RRR4-7/2	1244.580	1243.435	117.007	0.401	720.242	0.221	13	0.136	K.TIQEQLLLER.D
R4/RRR4-7/3	1414.736	1414.577	113.310	0.298	878.939	0.320	20	0.088	-.SVTDYITDIVCK.-
R4/RRR4-7/3	1415.077	1414.577	-353.854	0.298	756.890	0.316	20	0.086	K.SVTDYITDIVCK.R
R4/RRR4-7/3	1415.296	1414.577	-198.861	0.320	703.713	0.320	20	0.083	-.SVTDYITDIVCK.-
R4/RRR4-9/2	1730.303	1730.933	-945.045	0.469	1795.880	0.421	22	0.243	R.FFYASSACIYPEFK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1557.190	1557.779	-1023.294	0.493	1715.761	0.462	22	0.240	R.ISITGAGGFIGSHIAR.R
R4/RRR4-9/2	1673.681	1672.854	-103.521	0.519	1592.654	0.476	20	0.230	R.SFTFIDECVEGVLR.Y
R4/RRR4-9/2	1558.397	1557.779	-245.723	0.510	1525.255	0.498	21	0.226	R.ISITGAGGFIGSHIAR.R
R4/RRR4-9/2	1558.380	1557.779	-256.961	0.503	1538.948	0.453	21	0.217	R.ISITGAGGFIGSHIAR.R
R4/RRR4-9/2	1456.259	1455.685	-293.309	0.560	1339.686	0.520	20	0.214	K.VVSTQAPVQLGSLR.A
R4/RRR4-9/2	1455.231	1455.685	-312.530	0.461	1323.476	0.500	20	0.207	K.VVSTQAPVQLGSLR.A
R4/RRR4-9/2	1283.102	1283.370	-209.415	0.513	1143.633	0.565	19	0.206	K.TQGVDIAGYGSSK.V
R4/RRR4-9/2	1282.429	1283.370	-1518.069	0.377	1162.349	0.564	18	0.201	K.TQGVDIAGYGSSK.V
R4/RRR4-9/2	1455.270	1455.685	-285.599	0.462	1217.328	0.481	21	0.195	K.VVSTQAPVQLGSLR.A
R4/RRR4-9/2	1282.895	1283.370	-370.834	0.428	1092.251	0.527	19	0.192	K.TQGVDIAGYGSSK.V
R4/RRR4-9/2	1906.278	1906.983	-896.984	0.416	848.592	0.476	24	0.168	K.ESDAWPAEPQDAYGLEK.L
R4/RRR4-9/3	1468.024	1467.654	252.524	0.495	1290.359	0.501	25	0.165	R.FHNIYGPFGTWK.G
R4/RRR4-9/2	1907.210	1906.983	119.302	0.527	682.017	0.492	22	0.164	K.ESDAWPAEPQDAYGLEK.L
R4/RRR4-10/2	1468.307	1467.654	-237.451	0.439	803.856	0.449	16	0.164	R.FHNIYGPFGTWK.G
R4/RRR4-9/2	1468.483	1467.654	-117.028	0.490	803.014	0.435	16	0.162	R.FHNIYGPFGTWK.G
R4/RRR4-9/2	1467.666	1467.654	8.291	0.382	886.437	0.375	17	0.158	R.FHNIYGPFGTWK.G
R4/RRR4-9/2	1468.361	1467.654	-200.254	0.483	781.954	0.392	16	0.156	R.FHNIYGPFGTWK.G
R4/RRR4-9/2	1906.235	1906.983	-919.677	0.395	546.256	0.437	20	0.151	K.ESDAWPAEPQDAYGLEK.L
R4/RRR4-10/2	1468.320	1467.654	-228.694	0.417	680.421	0.361	14	0.147	R.FHNIYGPFGTWK.G
R4/RRR4-9/3	1775.962	1776.029	-37.554	0.502	1001.542	0.537	30	0.146	R.LKSEGHYIIASDWKK.N
R4/RRR4-10/2	1731.603	1730.933	-191.235	0.407	330.241	0.411	15	0.146	R.FFYASSACIYPEFK.Q
R4/RRR4-9/3	1455.819	1455.685	92.451	0.421	1315.440	0.407	25	0.140	K.VVSTQAPVQLGSLR.A
R4/RRR4-10/2	1467.604	1467.654	-34.422	0.345	665.883	0.266	14	0.139	R.FHNIYGPFGTWK.G
R4/RRR4-9/3	1534.282	1534.697	-271.858	0.488	823.370	0.486	24	0.119	K.SEGHYIIASDWKK.N
R4/RRR4-9/3	1467.363	1467.654	-199.189	0.440	931.192	0.374	22	0.102	R.FHNIYGPFGTWK.G
R4/RRR4-9/3	1467.672	1467.654	12.328	0.347	1045.336	0.315	22	0.096	R.FHNIYGPFGTWK.G
R4/RRR4-9/3	1455.262	1455.685	-291.542	0.367	645.529	0.374	23	0.091	K.VVSTQAPVQLGSLR.A
R4/RRR4-7/2	1914.774	1915.178	-211.435	0.493	2835.294	0.542	26	0.471	K.DLGLLVESTTVEQLGIAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1788.360	1789.066	-956.786	0.547	2622.236	0.480	34	0.442	K.ALLQDIAIVTGAEFQAK.D
R4/RRR4-7/2	1637.178	1637.688	-925.212	0.512	2603.121	0.527	26	0.413	K.TNDSAGDGTTTASVLAR.E
R4/RRR4-7/2	1914.724	1915.178	-237.850	0.498	2485.309	0.541	25	0.392	K.DLGLLVESTTVEQLGIAR.K
R4/RRR4-7/2	1790.575	1789.066	-274.581	0.572	2316.248	0.532	24	0.357	K.ALLQDIAIVTGAEFQAK.D
R4/RRR4-7/2	1637.286	1637.688	-246.147	0.526	2238.378	0.504	25	0.333	K.TNDSAGDGTTTASVLAR.E
R4/RRR4-7/2	1638.184	1637.688	303.396	0.572	2188.170	0.525	25	0.330	K.TNDSAGDGTTTASVLAR.E
R4/RRR4-7/2	1481.214	1480.646	-292.665	0.530	1411.259	0.550	20	0.230	R.GYISPQFVTNPEK.S
R4/RRR4-7/3	1789.205	1789.066	78.167	0.466	1538.918	0.507	29	0.206	K.ALLQDIAIVTGAEFQAK.D
R4/RRR4-7/2	1480.221	1480.646	-288.561	0.489	1182.229	0.514	19	0.199	R.GYISPQFVTNPEK.S
R4/RRR4-7/2	1480.172	1480.646	-321.492	0.473	1257.221	0.453	19	0.193	R.GYISPQFVTNPEK.S
R4/RRR4-7/2	1291.034	1291.347	-243.028	0.501	1169.317	0.478	18	0.192	K.VGAATETELEDR.K
R4/RRR4-7/2	1291.085	1291.347	-203.378	0.518	1098.378	0.423	18	0.177	K.VGAATETELEDR.K
R4/RRR4-7/2	1290.533	1291.347	-1410.058	0.465	1131.959	0.398	18	0.175	K.VGAATETELEDR.K
R4/RRR4-7/2	1064.452	1065.161	-1611.084	0.382	1145.071	0.392	14	0.174	K.SLVEFENAR.I
R4/RRR4-7/2	898.949	899.113	-183.135	0.443	868.695	0.458	14	0.170	R.GILNVAAIK.A
R4/RRR4-7/2	1064.461	1065.161	-1602.328	0.362	1106.724	0.307	14	0.159	K.SLVEFENAR.I
R4/RRR4-7/2	1473.196	1473.478	-191.701	0.417	656.414	0.446	16	0.155	R.ELSQTDSAYDSEK.L
R4/RRR4-7/2	1473.042	1473.478	-296.949	0.379	730.370	0.414	17	0.154	R.ELSQTDSAYDSEK.L
R4/RRR4-7/2	1064.457	1065.161	-1605.669	0.312	1100.500	0.250	14	0.151	K.SLVEFENAR.I
R4/RRR4-7/2	898.543	899.113	-1752.948	0.328	589.916	0.322	12	0.143	R.GILNVAAIK.A
R4/RRR4-7/2	857.482	858.018	-1795.907	0.461	959.784	0.204	13	0.142	R.LGADIIQK.A
R4/RRR4-7/2	858.150	858.018	154.573	0.544	1004.661	0.186	13	0.137	R.LGADIIQK.A
R4/RRR4-7/3	1788.882	1789.066	-102.919	0.462	1160.735	0.439	27	0.134	K.ALLQDIAIVTGAEFQAK.D
R4/RRR4-7/2	858.039	858.018	24.884	0.556	1017.843	0.171	13	0.134	R.LGADIIQK.A
R4/RRR4-6/2	1812.759	1813.042	-156.738	0.593	3397.069	0.594	27	0.645	K.IPAEVATEIETAIADLR.S
R4/RRR4-6/2	1812.666	1813.042	-207.945	0.573	3175.855	0.600	27	0.585	K.IPAEVATEIETAIADLR.S
R4/RRR4-6/2	1956.596	1956.213	196.013	0.587	3048.885	0.578	29	0.537	K.GVNPDEAVAM*GAAIQGGILR.G
R4/RRR4-6/2	1956.679	1956.213	238.617	0.591	2715.365	0.560	28	0.447	K.GVNPDEAVAM*GAAIQGGILR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1777.313	1777.956	-927.420	0.552	2032.613	0.566	26	0.319	R.IINEPTAAALSYGTNNK.E
R4/RRR4-6/2	1522.576	1522.728	-99.923	0.503	2086.278	0.503	21	0.308	R.SKFESLVNSLIER.T
R4/RRR4-6/2	1939.635	1940.214	-816.414	0.532	1946.443	0.592	25	0.307	K.GVNPDEAVAMGAAIQGGILR.G
R4/RRR4-6/2	1523.364	1522.728	-239.800	0.585	1835.060	0.529	20	0.276	R.SKFESLVNSLIER.T
R4/RRR4-6/2	1778.144	1777.956	106.066	0.580	1639.345	0.595	24	0.267	R.IINEPTAAALSYGTNNK.E
R4/RRR4-6/2	1939.128	1940.214	-1079.164	0.480	1731.024	0.539	27	0.261	K.GVNPDEAVAMGAAIQGGILR.G
R4/RRR4-6/2	1461.040	1461.515	-326.540	0.504	1510.924	0.642	20	0.261	K.APNGDAWVETTDGK.Q
R4/RRR4-6/2	1523.322	1522.728	-267.134	0.559	1740.370	0.520	20	0.261	R.SKFESLVNSLIER.T
R4/RRR4-6/2	1461.254	1461.515	-179.107	0.505	1481.986	0.641	20	0.258	K.APNGDAWVETTDGK.Q
R4/RRR4-6/2	1355.131	1355.433	-223.582	0.459	1385.016	0.483	18	0.210	R.NNADTTIYSVEK.S
R4/RRR4-6/2	1248.645	1249.438	-1439.907	0.530	1234.229	0.490	18	0.202	K.VQEIVSEIFGK.S
R4/RRR4-6/2	1355.048	1355.433	-284.766	0.426	1077.225	0.443	18	0.178	R.NNADTTIYSVEK.S
R4/RRR4-6/2	1553.246	1553.701	-293.755	0.441	515.418	0.506	17	0.158	R.QAVTNPQNTFFGTK.R
R4/RRR4-7/2	994.135	994.276	-142.297	0.431	1596.573	0.102	14	0.156	K.M*VPYKIVK.A
R4/RRR4-6/2	1552.693	1553.701	-1296.807	0.331	323.774	0.423	14	0.143	R.QAVTNPQNTFFGTK.R
R4/RRR4-10/2	1522.741	1522.728	8.474	0.295	539.728	0.315	13	0.138	R.SKFESLVNSLIER.T
R4/RRR4-1/2	993.405	994.276	-1889.461	0.417	1194.165	0.076	13	0.134	-.M*VPYKIVK.-
R4/RRR4-1/2	993.527	994.276	-1765.872	0.418	1232.972	0.064	14	0.133	K.M*VPYKIVK.A
R4/RRR4-2/2	994.272	994.276	-3.989	0.394	1118.567	0.071	13	0.132	K.M*VPYKIVK.A
R4/RRR4-7/2	994.394	994.276	119.138	0.438	1052.805	0.053	13	0.127	K.M*VPYKIVK.A
R4/RRR4-6/3	1522.479	1522.728	-163.992	0.533	1324.756	0.346	25	0.123	R.SKFESLVNSLIER.T
R4/RRR4-1/2	993.466	994.276	-1827.107	0.379	1064.863	0.015	12	0.123	-.M*VPYKIVK.-
R4/RRR4-6/3	1940.053	1940.214	-83.351	0.369	1148.062	0.396	30	0.121	K.GVNPDEAVAMGAAIQGGILR.G
R4/RRR4-8/2	994.111	994.276	-166.563	0.420	892.592	0.044	12	0.117	-.M*VPYKIVK.-
R4/RRR4-6/3	1522.705	1522.728	-15.255	0.483	924.858	0.312	22	0.092	R.SKFESLVNSLIER.T
R4/RRR4-6/3	1522.397	1522.728	-218.167	0.477	1106.554	0.248	24	0.088	R.SKFESLVNSLIER.T
R4/RRR4-6/3	1938.790	1940.214	-1254.161	0.343	833.174	0.277	26	0.077	-.GVNPDEAVAMGAAIQGGILR.-
R4/RRR4-7/2	1615.078	1615.850	-1100.785	0.539	2638.489	0.539	24	0.426	R.TQNVVACQAVANIVK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1615.336	1615.850	-940.224	0.586	2436.381	0.533	25	0.382	R.TQNVVACQAVANIVK.S
R4/RRR4-7/2	1561.612	1560.863	-160.776	0.419	2434.423	0.394	22	0.334	K.IIQFATEAAITILR.I
R4/RRR4-7/2	1615.212	1615.850	-1017.083	0.559	2057.059	0.530	23	0.311	R.TQNVVACQAVANIVK.S
R4/RRR4-7/2	1557.300	1557.689	-250.928	0.503	1714.245	0.492	20	0.249	K.DSYLLNGYALNTGR.A
R4/RRR4-7/2	1885.529	1886.221	-900.166	0.523	1459.325	0.512	24	0.224	R.EQLAIAEFAESLLIIPK.V
R4/RRR4-7/2	973.878	974.137	-266.542	0.506	1081.950	0.548	16	0.200	K.AGANVVLTTK.G
R4/RRR4-7/2	973.476	974.137	-1710.645	0.405	1108.308	0.536	16	0.196	K.AGANVVLTTK.G
R4/RRR4-7/2	973.744	974.137	-404.890	0.476	1060.964	0.516	16	0.192	K.AGANVVLTTK.G
R4/RRR4-7/2	1222.082	1222.409	-268.462	0.438	1265.235	0.437	16	0.192	R.IACLDFNLQK.T
R4/RRR4-7/2	1196.499	1196.380	99.708	0.352	915.795	0.474	15	0.167	K.YFVEAGAIAVR.R
R4/RRR4-7/2	1562.005	1560.863	91.191	0.373	1343.740	0.256	17	0.161	K.IIQFATEAAITILR.I
R4/RRR4-7/2	1100.479	1101.275	-1636.888	0.452	805.570	0.389	16	0.160	R.IADDDVILVK.G
R4/RRR4-12/2	974.196	974.137	61.192	0.431	659.137	0.419	16	0.159	K.AGANVVLTTK.G
R4/RRR4-7/2	1100.605	1101.275	-1522.007	0.441	723.321	0.370	15	0.154	R.IADDDVILVK.G
R4/RRR4-7/2	1221.976	1222.409	-355.956	0.375	966.051	0.317	15	0.154	R.IACLDFNLQK.T
R4/RRR4-7/2	973.832	973.106	-282.019	0.396	945.208	0.221	16	0.143	-.SSLGPVGLDK.-
R4/RRR4-7/2	973.084	973.106	-22.285	0.314	695.676	0.208	15	0.138	-.SSLGPVGLDK.-
R4/RRR4-7/2	1101.633	1101.275	326.020	0.241	721.903	0.137	14	0.133	R.IADDDVILVK.G
R4/RRR4-7/2	973.043	973.106	-64.438	0.363	492.525	0.244	13	0.115	-.SSLGPVGLDK.-
R4/RRR4-1/3	1270.409	1270.420	-9.321	0.593	1792.090	0.450	28	0.212	R.RPGSVSLNQSPK.T
R4/RRR4-4/3	1270.658	1270.420	187.537	0.518	1757.571	0.428	27	0.199	R.RPGSVSLNQSPK.T
R4/RRR4-3/2	1269.345	1268.527	-143.875	0.463	1303.430	0.431	17	0.192	R.LILGELQAPSVK.Y
R4/RRR4-3/2	1269.364	1268.527	-129.502	0.396	1206.818	0.459	16	0.188	R.LILGELQAPSVK.Y
R4/RRR4-2/3	1270.408	1270.420	-10.189	0.553	1672.162	0.422	26	0.185	R.RPGSVSLNQSPK.T
R4/RRR4-4/3	1270.707	1270.420	226.264	0.541	1604.130	0.446	26	0.184	R.RPGSVSLNQSPK.T
R4/RRR4-2/2	1268.318	1268.527	-165.423	0.444	1161.568	0.447	16	0.183	R.LILGELQAPSVK.Y
R4/RRR4-2/3	1270.128	1270.420	-230.555	0.571	1456.080	0.459	23	0.170	R.RPGSVSLNQSPK.T
R4/RRR4-3/3	1271.627	1270.420	162.938	0.594	1487.281	0.453	26	0.170	R.RPGSVSLNQSPK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1268.163	1268.527	-288.250	0.378	777.382	0.453	15	0.161	R.LILGELQAPSVK.Y
R4/RRR4-1/2	1267.656	1268.527	-1480.416	0.298	901.862	0.377	15	0.155	R.LILGELQAPSVK.Y
R4/RRR4-2/2	1269.071	1268.527	-360.401	0.398	550.945	0.451	14	0.154	R.LILGELQAPSVK.Y
R4/RRR4-1/2	1268.575	1268.527	37.968	0.369	573.088	0.365	13	0.146	R.LILGELQAPSVK.Y
R4/RRR4-2/2	1267.739	1268.527	-1415.033	0.262	626.968	0.368	13	0.144	R.LILGELQAPSVK.Y
R4/RRR4-1/3	1270.473	1270.420	41.418	0.535	1285.181	0.437	25	0.143	R.RPGSVSLNQSPK.T
R4/RRR4-2/3	1270.635	1270.420	169.329	0.534	1427.664	0.371	25	0.138	R.RPGSVSLNQSPK.T
R4/RRR4-4/2	1268.430	1268.527	-77.087	0.288	701.479	0.175	13	0.134	-.LILGELQAPSVK.-
R4/RRR4-1/2	1267.700	1268.527	-1445.983	0.253	561.377	0.304	12	0.132	-.LILGELQAPSVK.-
R4/RRR4-4/3	1270.106	1270.420	-248.633	0.527	1057.394	0.440	23	0.125	R.RPGSVSLNQSPK.T
R4/RRR4-3/3	1269.399	1270.420	-1597.514	0.446	919.870	0.416	21	0.113	R.RPGSVSLNQSPK.T
R4/RRR4-1/3	1269.693	1270.420	-1364.699	0.461	1033.702	0.373	23	0.110	R.RPGSVSLNQSPK.T
R4/RRR4-7/2	1569.007	1569.808	-1151.322	0.450	1768.261	0.439	20	0.244	-.M*HSTNLLLEEPIR.M
R4/RRR4-7/2	1322.096	1321.504	-309.923	0.554	1463.020	0.539	19	0.233	K.LGDLSQTQIFAK.I
R4/RRR4-7/2	1321.155	1321.504	-265.289	0.550	1466.094	0.476	19	0.218	K.LGDLSQTQIFAK.I
R4/RRR4-7/2	1215.001	1215.380	-313.156	0.449	1634.204	0.348	17	0.208	K.IDFLSLSYTR.H
R4/RRR4-7/2	1320.658	1321.504	-1401.719	0.491	1436.261	0.437	19	0.207	K.LGDLSQTQIFAK.I
R4/RRR4-2/2	1322.707	1321.504	153.602	0.506	1129.450	0.512	18	0.195	K.LGDLSQTQIFAK.I
R4/RRR4-1/2	1321.409	1321.504	-72.143	0.421	1178.526	0.495	18	0.194	K.LGDLSQTQIFAK.I
R4/RRR4-7/2	1215.228	1215.380	-125.699	0.453	1335.000	0.374	16	0.186	K.IDFLSLSYTR.H
R4/RRR4-7/2	1321.637	1321.504	100.643	0.441	1106.824	0.445	17	0.180	K.LGDLSQTQIFAK.I
R4/RRR4-7/2	1376.252	1376.623	-269.970	0.464	797.688	0.500	20	0.173	R.GLYPVETISIVGK.I
R4/RRR4-7/3	1868.929	1869.112	-98.577	0.454	1336.379	0.490	26	0.170	K.WGAPNKIDFLSLSYTR.H
R4/RRR4-7/2	1172.114	1172.274	-136.590	0.344	1086.860	0.404	15	0.170	R.WSFTGAFEAR.Q
R4/RRR4-7/2	1214.760	1215.380	-1337.756	0.387	1157.851	0.356	15	0.169	K.IDFLSLSYTR.H
R4/RRR4-7/2	1117.890	1117.346	-409.470	0.381	1062.851	0.356	16	0.164	R.GLFPMLADPR.H
R4/RRR4-7/2	1172.162	1172.274	-95.952	0.305	1228.338	0.304	15	0.163	R.WSFTGAFEAR.Q
R4/RRR4-2/2	1321.985	1321.504	364.757	0.407	691.962	0.491	15	0.163	K.LGDLSQTQIFAK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1321.234	1321.504	-204.853	0.427	710.403	0.436	15	0.158	K.LGDLSQTQIFAK.I
R4/RRR4-7/2	1375.624	1376.623	-1457.412	0.358	865.118	0.352	19	0.153	R.GLYPVETISIVGK.I
R4/RRR4-7/2	1174.195	1174.330	-115.181	0.458	731.981	0.350	14	0.151	-.VFNQDLYFK.-
R4/RRR4-7/3	1321.459	1320.538	-59.582	0.376	1414.580	0.375	23	0.140	K.CNM*AGKPAVVTR.V
R4/RRR4-7/2	1174.055	1174.330	-234.497	0.322	633.008	0.216	13	0.138	-.VFNQDLYFK.-
R4/RRR4-7/2	1173.435	1174.330	-1619.007	0.312	689.720	0.125	13	0.133	K.VFNQDLYFK.R
R4/RRR4-7/2	1117.212	1117.346	-120.179	0.354	518.640	0.281	12	0.131	-.GLFPMLADPR.-
R4/RRR4-3/2	1377.372	1376.623	-182.637	0.109	668.703	0.046	15	0.127	R.GLYPVETISIVGK.I
R4/RRR4-7/3	1304.268	1304.538	-207.904	0.387	1347.517	0.308	23	0.116	K.CNMAGKPAVVTR.V
R4/RRR4-7/3	1868.080	1869.112	-1091.508	0.403	960.781	0.380	24	0.104	K.WGAPNKIDFLSLSYTR.H
R4/RRR4-7/3	1304.045	1304.538	-379.899	0.371	754.594	0.296	19	0.086	K.CNMAGKPAVVTR.V
R4/RRR4-7/3	1304.318	1304.538	-169.175	0.337	734.290	0.247	18	0.082	K.CNMAGKPAVVTR.V
R4/RRR4-15/2	1606.103	1606.584	-300.477	0.554	2607.470	0.569	24	0.428	K.DAAEGQEGEAATEEAK.K
R4/RRR4-15/2	1719.336	1719.920	-923.941	0.526	2616.091	0.500	24	0.405	R.ILDVVYNASNNELVR.T
R4/RRR4-15/2	1719.361	1719.920	-909.829	0.523	2536.328	0.483	24	0.383	R.ILDVVYNASNNELVR.T
R4/RRR4-15/2	1606.076	1606.584	-942.138	0.554	2514.669	0.490	24	0.379	K.DAAEGQEGEAATEEAK.K
R4/RRR4-15/2	1606.096	1606.584	-304.747	0.505	2279.079	0.567	23	0.360	K.DAAEGQEGEAATEEAK.K
R4/RRR4-15/2	1719.418	1719.920	-876.331	0.518	2370.156	0.497	24	0.355	R.ILDVVYNASNNELVR.T
R4/RRR4-15/3	1719.655	1719.920	-154.374	0.602	2273.694	0.495	33	0.347	R.ILDVVYNASNNELVR.T
R4/RRR4-14/2	1656.188	1656.735	-936.845	0.550	2108.984	0.525	24	0.318	R.LDTGNYSWGSEAVTR.K
R4/RRR4-14/2	1657.457	1656.735	-168.173	0.576	2022.372	0.570	23	0.317	R.LDTGNYSWGSEAVTR.K
R4/RRR4-14/2	1606.170	1606.584	-258.767	0.550	2019.784	0.563	22	0.312	K.DAAEGQEGEAATEEAK.K
R4/RRR4-15/2	1656.208	1656.735	-924.561	0.535	1933.757	0.545	23	0.295	R.LDTGNYSWGSEAVTR.K
R4/RRR4-15/3	1720.824	1719.920	-56.117	0.501	2047.137	0.480	29	0.290	R.ILDVVYNASNNELVR.T
R4/RRR4-14/3	1734.425	1734.757	-192.202	0.548	1934.552	0.521	33	0.283	K.KDAAEGQEGEAATEEAK.K
R4/RRR4-14/2	1656.105	1656.735	-987.238	0.535	1849.460	0.536	23	0.280	R.LDTGNYSWGSEAVTR.K
R4/RRR4-15/2	1656.391	1656.735	-207.901	0.539	1819.346	0.531	22	0.273	R.LDTGNYSWGSEAVTR.K
R4/RRR4-15/3	1735.809	1734.757	29.680	0.589	1895.000	0.507	31	0.269	K.KDAAEGQEGEAATEEAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1656.390	1656.735	-208.789	0.518	1742.867	0.522	22	0.261	R.LDTGNYSWGSEAVTR.K
R4/RRR4-15/3	1861.977	1862.930	-1052.344	0.602	1639.366	0.593	36	0.256	K.KDAAEGQEGEAATEEAKK.S
R4/RRR4-15/2	1576.336	1576.650	-199.197	0.536	1459.001	0.579	21	0.241	R.TLDSHIEEQFGSGR.L
R4/RRR4-15/2	1246.038	1246.437	-321.766	0.444	1636.644	0.489	19	0.239	K.SAIVQVDAAPFK.Q
R4/RRR4-14/3	1862.924	1862.930	-3.333	0.609	1519.957	0.596	36	0.235	K.KDAAEGQEGEAATEEAKK.S
R4/RRR4-15/2	1246.079	1246.437	-288.151	0.484	1492.732	0.532	18	0.233	K.SAIVQVDAAPFK.Q
R4/RRR4-15/2	1576.312	1576.650	-214.968	0.523	1310.539	0.550	19	0.216	R.TLDSHIEEQFGSGR.L
R4/RRR4-15/3	1735.676	1734.757	-46.820	0.525	1691.948	0.464	29	0.213	K.KDAAEGQEGEAATEEAK.K
R4/RRR4-15/3	1734.409	1734.757	-201.628	0.564	1666.042	0.456	29	0.205	K.KDAAEGQEGEAATEEAK.K
R4/RRR4-15/3	1863.480	1862.930	-242.163	0.585	1280.882	0.567	34	0.187	K.KDAAEGQEGEAATEEAKK.S
R4/RRR4-19/2	1719.700	1719.920	-128.624	0.464	1202.693	0.395	20	0.176	R.ILDVVYNASNNELVR.T
R4/RRR4-24/2	1607.860	1606.584	171.821	0.394	801.993	0.575	18	0.175	K.DAAEGQEGEAATEEAK.K
R4/RRR4-14/3	1862.676	1862.930	-137.130	0.527	1256.510	0.515	31	0.167	K.KDAAEGQEGEAATEEAKK.S
R4/RRR4-15/3	1720.011	1719.920	52.696	0.530	1429.803	0.444	28	0.165	R.ILDVVYNASNNELVR.T
R4/RRR4-15/2	1245.529	1246.437	-1536.895	0.296	1241.162	0.287	16	0.160	K.SAIVQVDAAPFK.Q
R4/RRR4-15/2	966.207	966.070	142.164	0.419	485.181	0.412	14	0.155	R.ADGYILEGK.E
R4/RRR4-15/2	967.007	966.070	-65.473	0.393	539.573	0.410	14	0.154	R.ADGYILEGK.E
R4/RRR4-13/2	1575.969	1576.650	-1069.446	0.222	645.523	0.155	16	0.131	R.TLDSHIEEQFGSGR.L
R4/RRR4-15/3	1862.944	1862.930	7.708	0.520	785.569	0.530	28	0.127	K.KDAAEGQEGEAATEEAKK.S
R4/RRR4-14/3	1734.125	1734.757	-944.312	0.484	1097.490	0.418	26	0.124	K.KDAAEGQEGEAATEEAK.K
R4/RRR4-5/2	1863.230	1864.066	-988.545	0.563	2723.793	0.546	23	0.445	R.MKEGQSEIYYITGESK.K
R4/RRR4-5/2	1880.222	1880.066	83.192	0.584	1238.795	0.608	25	0.227	R.M*KEGQSEIYYITGESK.K
R4/RRR4-5/2	1879.373	1880.066	-903.430	0.546	999.314	0.575	23	0.197	R.M*KEGQSEIYYITGESK.K
R4/RRR4-5/3	1879.545	1880.066	-811.439	0.493	1302.896	0.488	25	0.165	R.M*KEGQSEIYYITGESK.K
R4/RRR4-5/3	1879.245	1880.066	-971.843	0.524	1279.632	0.478	24	0.159	R.M*KEGQSEIYYITGESK.K
R4/RRR4-5/3	1879.011	1880.066	-1096.680	0.459	1171.602	0.476	24	0.146	R.M*KEGQSEIYYITGESK.K
R4/RRR4-13/2	1939.451	1940.234	-922.108	0.568	4677.540	0.446	30	1.000	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-14/2	1939.758	1940.234	-245.699	0.563	4429.019	0.518	30	0.949	R.SSVQAALQQEIALAAGLLR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1940.051	1940.234	-94.451	0.581	4196.228	0.525	30	0.866	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-14/2	1940.482	1940.234	128.425	0.626	4067.765	0.521	29	0.815	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-13/2	1939.633	1940.234	-827.462	0.569	4045.905	0.466	29	0.780	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-13/2	1940.595	1940.234	186.904	0.627	3792.615	0.505	28	0.714	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-14/3	1865.278	1866.072	-964.690	0.533	3293.957	0.416	39	0.628	R.GLRDAADLVALSGGHTVGR.T
R4/RRR4-14/3	1865.350	1866.072	-925.467	0.558	3235.080	0.431	39	0.616	R.GLRDAADLVALSGGHTVGR.T
R4/RRR4-14/3	1866.013	1866.072	-31.542	0.584	3145.072	0.441	38	0.590	R.GLRDAADLVALSGGHTVGR.T
R4/RRR4-14/2	1539.345	1539.676	-215.438	0.491	1503.688	0.529	23	0.232	R.DAADLVALSGGHTVGR.T
R4/RRR4-13/2	1539.251	1539.676	-276.699	0.481	1367.566	0.561	22	0.224	R.DAADLVALSGGHTVGR.T
R4/RRR4-14/2	1276.533	1277.451	-1507.337	0.432	1573.555	0.453	17	0.223	R.VQDLIDLFASR.G
R4/RRR4-14/2	1745.339	1744.970	212.163	0.543	1283.487	0.578	25	0.220	R.DAVVVSGGPSYAVPLGQK.D
R4/RRR4-14/2	1540.200	1539.676	-309.916	0.510	1316.410	0.549	22	0.217	R.DAADLVALSGGHTVGR.T
R4/RRR4-14/2	1859.310	1859.999	-911.558	0.484	1520.344	0.471	21	0.216	R.GGSNSEQGM*GPNLTLQPR.A
R4/RRR4-14/2	1277.085	1277.451	-287.291	0.521	1374.534	0.496	17	0.214	R.VQDLIDLFASR.G
R4/RRR4-13/2	1276.864	1277.451	-1246.992	0.485	1369.414	0.499	17	0.213	R.VQDLIDLFASR.G
R4/RRR4-14/2	1859.468	1859.999	-826.080	0.503	1425.964	0.505	20	0.213	R.GGSNSEQGM*GPNLTLQPR.A
R4/RRR4-14/2	1277.165	1277.451	-224.960	0.514	1347.056	0.467	17	0.205	R.VQDLIDLFASR.G
R4/RRR4-14/2	1538.691	1539.676	-1293.728	0.464	1235.783	0.530	22	0.205	R.DAADLVALSGGHTVGR.T
R4/RRR4-14/2	1859.409	1859.999	-857.778	0.498	1340.076	0.488	20	0.201	R.GGSNSEQGM*GPNLTLQPR.A
R4/RRR4-13/2	1277.179	1277.451	-213.933	0.521	1341.707	0.446	17	0.200	R.VQDLIDLFASR.G
R4/RRR4-13/2	1744.573	1744.970	-228.132	0.499	1042.552	0.527	23	0.188	R.DAVVVSGGPSYAVPLGQK.D
R4/RRR4-14/2	1744.331	1744.970	-942.359	0.482	1015.379	0.510	23	0.183	R.DAVVVSGGPSYAVPLGQK.D
R4/RRR4-13/2	1538.590	1539.676	-1359.623	0.397	1123.250	0.468	21	0.182	R.DAADLVALSGGHTVGR.T
R4/RRR4-13/2	1744.622	1744.970	-199.984	0.479	946.714	0.535	22	0.182	R.DAVVVSGGPSYAVPLGQK.D
R4/RRR4-12/2	1276.428	1277.451	-1589.857	0.363	1010.840	0.514	15	0.181	R.VQDLIDLFASR.G
R4/RRR4-13/3	1940.097	1940.234	-70.411	0.449	1649.784	0.373	32	0.173	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-14/2	1057.182	1057.226	-41.416	0.447	1217.719	0.313	14	0.167	-.ALQLVEDIR.-
R4/RRR4-14/2	1744.397	1744.970	-904.000	0.410	924.755	0.454	22	0.167	R.DAVVVSGGPSYAVPLGQK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1031.017	1031.188	-166.802	0.339	947.725	0.420	14	0.164	K.AAFFTQFAK.S
R4/RRR4-14/2	1057.079	1057.226	-139.177	0.485	1075.340	0.357	13	0.162	-.ALQLVEDIR.-
R4/RRR4-13/2	1056.994	1057.226	-219.809	0.435	1087.395	0.320	13	0.160	R.ALQLVEDIR.A
R4/RRR4-14/3	1859.622	1859.999	-203.638	0.480	1437.639	0.415	29	0.159	R.GGSNSEQGM*GPNLTLQPR.A
R4/RRR4-13/2	1744.112	1744.970	-1068.064	0.400	876.541	0.415	21	0.158	R.DAVVVSGGPSYAVPLGQK.D
R4/RRR4-14/2	1057.031	1057.226	-185.168	0.462	988.729	0.358	13	0.158	-.ALQLVEDIR.-
R4/RRR4-14/3	1745.572	1744.970	-228.430	0.337	1361.001	0.442	28	0.157	R.DAVVVSGGPSYAVPLGQK.D
R4/RRR4-13/2	1057.027	1057.226	-188.991	0.392	1105.785	0.286	13	0.157	-.ALQLVEDIR.-
R4/RRR4-14/2	1030.437	1031.188	-1704.664	0.299	921.692	0.336	14	0.152	K.AAFFTQFAK.S
R4/RRR4-13/2	1057.060	1057.226	-157.133	0.444	1037.700	0.272	13	0.151	-.ALQLVEDIR.-
R4/RRR4-13/2	1276.257	1277.451	-1724.666	0.297	704.741	0.334	14	0.146	R.VQDLIDLFASR.G
R4/RRR4-14/3	1539.587	1539.676	-57.912	0.438	1091.767	0.478	29	0.137	R.DAADLVALSGGHTVGR.T
R4/RRR4-11/2	1057.058	1057.226	-159.565	0.300	485.845	0.317	11	0.130	-.ALQLVEDIR.-
R4/RRR4-13/3	1539.703	1539.676	17.715	0.418	1140.915	0.433	30	0.129	R.DAADLVALSGGHTVGR.T
R4/RRR4-13/3	1539.276	1539.676	-260.278	0.425	1010.600	0.472	28	0.129	R.DAADLVALSGGHTVGR.T
R4/RRR4-14/3	1745.183	1744.970	122.408	0.373	975.047	0.485	25	0.128	R.DAVVVSGGPSYAVPLGQK.D
R4/RRR4-14/3	1540.807	1539.676	85.603	0.485	948.497	0.472	29	0.125	R.DAADLVALSGGHTVGR.T
R4/RRR4-13/3	1539.872	1539.676	128.035	0.424	766.959	0.478	25	0.114	R.DAADLVALSGGHTVGR.T
R4/RRR4-14/3	1858.974	1859.999	-1092.786	0.407	929.800	0.399	26	0.106	R.GGSNSEQGM*GPNLTLQPR.A
R4/RRR4-14/3	1940.022	1940.234	-109.417	0.357	1095.837	0.338	28	0.105	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-13/3	1939.989	1940.234	-126.648	0.339	930.006	0.381	23	0.104	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-13/3	1859.453	1859.999	-834.324	0.326	1163.246	0.296	29	0.100	R.GGSNSEQGM*GPNLTLQPR.A
R4/RRR4-14/3	1940.144	1940.234	-46.271	0.321	968.776	0.307	25	0.093	R.SSVQAALQQEIALAAGLLR.I
R4/RRR4-16/3	1807.147	1807.001	81.117	0.597	2887.379	0.577	37	0.589	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-17/3	1806.595	1807.001	-225.357	0.565	2985.412	0.511	37	0.577	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-16/3	1806.642	1807.001	-199.429	0.610	2775.615	0.561	36	0.539	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-17/3	1807.149	1807.001	82.235	0.580	2725.625	0.553	37	0.516	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-16/3	1807.084	1807.001	46.159	0.593	2330.225	0.567	35	0.406	K.TPAELSHAANAGLDIAVR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1806.437	1807.001	-868.548	0.544	2266.929	0.651	26	0.388	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-17/3	1806.924	1807.001	-42.568	0.559	2343.812	0.531	36	0.387	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-16/2	1806.514	1807.001	-270.532	0.576	2243.263	0.650	27	0.384	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-16/2	1806.501	1807.001	-833.003	0.559	1972.079	0.657	25	0.335	K.TPAELSHAANAGLDIAVR.M
R4/RRR4-16/2	1506.236	1506.644	-271.465	0.485	1473.464	0.455	21	0.213	R.LAWHSAGTFDVSSK.T
R4/RRR4-16/2	1507.254	1506.644	-259.828	0.494	1288.520	0.521	21	0.210	R.LAWHSAGTFDVSSK.T
R4/RRR4-16/2	1498.008	1498.663	-1108.102	0.498	1207.039	0.509	18	0.201	K.AFFEDYKEAHLK.L
R4/RRR4-16/2	1556.407	1556.831	-272.862	0.502	1018.151	0.542	21	0.193	K.ALLSDPAFRPLVEK.Y
R4/RRR4-16/2	1498.138	1498.663	-1021.214	0.503	1210.240	0.445	19	0.190	K.AFFEDYKEAHLK.L
R4/RRR4-16/2	1498.095	1498.663	-1050.175	0.524	1156.979	0.467	18	0.189	K.AFFEDYKEAHLK.L
R4/RRR4-16/2	1556.337	1556.831	-318.267	0.451	884.732	0.486	20	0.173	K.ALLSDPAFRPLVEK.Y
R4/RRR4-16/2	1008.445	1009.096	-1642.890	0.350	952.023	0.448	14	0.170	R.SGFEGPWTK.N
R4/RRR4-15/2	1099.589	1100.247	-1512.836	0.416	1048.798	0.387	16	0.169	K.EGLLQLPSDK.A
R4/RRR4-15/2	1101.002	1100.247	-223.589	0.518	884.483	0.408	15	0.164	K.EGLLQLPSDK.A
R4/RRR4-16/2	1557.432	1556.831	-256.724	0.522	618.677	0.502	18	0.164	K.ALLSDPAFRPLVEK.Y
R4/RRR4-16/2	1009.090	1009.096	-6.505	0.410	938.146	0.377	14	0.163	R.SGFEGPWTK.N
R4/RRR4-16/2	1010.017	1009.096	-78.505	0.459	1039.591	0.342	14	0.162	R.SGFEGPWTK.N
R4/RRR4-15/2	1101.098	1100.247	-136.170	0.518	918.436	0.382	15	0.162	K.EGLLQLPSDK.A
R4/RRR4-16/2	1100.273	1100.247	23.412	0.498	987.807	0.345	16	0.161	K.EGLLQLPSDK.A
R4/RRR4-16/2	1008.952	1009.096	-143.267	0.455	1025.092	0.330	14	0.160	R.SGFEGPWTK.N
R4/RRR4-16/2	896.514	896.046	522.978	0.292	880.133	0.393	13	0.156	K.TGGPFGTMK.T
R4/RRR4-16/2	1008.432	1009.096	-1655.781	0.318	941.160	0.326	14	0.154	R.SGFEGPWTK.N
R4/RRR4-16/2	1008.457	1009.096	-1630.242	0.347	963.888	0.279	14	0.151	R.SGFEGPWTK.N
R4/RRR4-16/2	1099.527	1100.247	-1569.266	0.337	759.740	0.189	14	0.137	K.EGLLQLPSDK.A
R4/RRR4-17/2	1008.975	1009.096	-120.815	0.363	954.266	0.139	14	0.136	R.SGFEGPWTK.N
R4/RRR4-16/2	911.766	912.046	-307.881	0.298	432.152	0.286	12	0.136	-.TGGPFGTM*K.-
R4/RRR4-16/2	911.463	912.046	-1741.146	0.350	307.628	0.367	10	0.135	-.TGGPFGTM*K.-
R4/RRR4-1/2	1557.287	1556.831	294.076	0.351	619.679	0.236	15	0.134	K.ALLSDPAFRPLVEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	911.524	912.046	-1673.869	0.291	338.908	0.403	11	0.133	-.TGGPFGTM*K.-
R4/RRR4-16/3	1310.464	1310.441	17.030	0.492	762.729	0.460	25	0.113	R.LPDATKGSDHLR.Q
R4/RRR4-15/3	1309.574	1310.441	-1430.283	0.427	463.294	0.488	21	0.107	R.LPDATKGSDHLR.Q
R4/RRR4-15/3	1311.387	1310.441	-41.848	0.433	882.316	0.391	25	0.104	R.LPDATKGSDHLR.Q
R4/RRR4-16/3	1507.620	1506.644	-15.935	0.456	879.774	0.386	26	0.102	R.LAWHSAGTFDVSSK.T
R4/RRR4-15/3	1310.507	1310.441	50.523	0.467	696.525	0.404	25	0.102	R.LPDATKGSDHLR.Q
R4/RRR4-14/3	1310.072	1310.441	-282.544	0.392	523.511	0.341	21	0.094	R.LPDATKGSDHLR.Q
R4/RRR4-16/3	1507.662	1506.644	11.717	0.364	899.568	0.299	27	0.088	R.LAWHSAGTFDVSSK.T
R4/RRR4-16/3	1506.972	1506.644	218.576	0.421	1111.435	0.230	27	0.086	R.LAWHSAGTFDVSSK.T
R4/RRR4-5/2	1324.280	1324.468	-142.160	0.494	2165.423	0.568	21	0.342	K.ILVAGSHADDLGR.Q
R4/RRR4-5/2	1323.637	1324.468	-1387.465	0.472	2078.222	0.588	21	0.332	K.ILVAGSHADDLGR.Q
R4/RRR4-5/2	1718.447	1717.924	-278.860	0.553	2132.068	0.481	23	0.307	R.GVSTVM*VSYSSWNGVK.M
R4/RRR4-5/2	1324.247	1324.468	-167.497	0.467	1668.725	0.537	20	0.255	K.ILVAGSHADDLGR.Q
R4/RRR4-5/2	1058.947	1059.198	-238.365	0.559	1745.766	0.434	17	0.241	R.IGEATALEVR.A
R4/RRR4-5/2	1058.507	1059.198	-1602.318	0.417	1622.170	0.329	17	0.203	R.IGEATALEVR.A
R4/RRR4-5/2	1058.738	1059.198	-436.048	0.445	1403.518	0.406	17	0.198	R.IGEATALEVR.A
R4/RRR4-5/2	1782.455	1782.063	220.521	0.526	1087.634	0.533	21	0.193	R.ATGIPYVFAPCVAVCR.D
R4/RRR4-4/2	1058.985	1059.198	-201.822	0.469	1237.513	0.414	16	0.186	R.IGEATALEVR.A
R4/RRR4-5/2	1455.234	1454.659	-292.674	0.440	881.321	0.504	20	0.175	K.ATIFPHNVGLGATR.D
R4/RRR4-5/2	1781.482	1782.063	-890.267	0.453	944.000	0.492	20	0.174	R.ATGIPYVFAPCVAVCR.D
R4/RRR4-5/2	1277.898	1278.297	-312.689	0.366	1010.250	0.444	16	0.172	R.CYESYSEDPK.V
R4/RRR4-5/2	1781.366	1782.063	-955.483	0.429	945.808	0.470	20	0.170	R.ATGIPYVFAPCVAVCR.D
R4/RRR4-5/3	1454.254	1454.659	-278.904	0.361	1570.789	0.411	29	0.170	K.ATIFPHNVGLGATR.D
R4/RRR4-5/2	1188.250	1188.398	-124.534	0.489	853.432	0.418	16	0.163	K.SSYSPVLPLPK.K
R4/RRR4-5/2	1188.120	1188.398	-234.606	0.425	796.509	0.435	16	0.163	K.SSYSPVLPLPK.K
R4/RRR4-5/2	1454.172	1454.659	-335.575	0.404	746.730	0.452	20	0.161	K.ATIFPHNVGLGATR.D
R4/RRR4-5/2	1187.558	1188.398	-1553.977	0.283	911.530	0.367	16	0.154	K.SSYSPVLPLPK.K
R4/RRR4-5/2	1455.453	1454.659	-141.377	0.378	576.665	0.448	18	0.154	K.ATIFPHNVGLGATR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	851.854	851.927	-86.325	0.283	688.827	0.349	10	0.145	-.IDDAVYR.-
R4/RRR4-5/2	851.970	851.927	50.355	0.289	736.259	0.316	10	0.145	R.IDDAVYR.I
R4/RRR4-5/2	851.823	851.927	-122.262	0.287	805.623	0.282	11	0.144	R.IDDAVYR.I
R4/RRR4-5/3	1454.376	1454.659	-195.033	0.409	1116.137	0.501	27	0.144	K.ATIFPHNVGLGATR.D
R4/RRR4-5/3	1454.381	1454.659	-191.370	0.383	1200.801	0.403	29	0.125	K.ATIFPHNVGLGATR.D
R4/RRR4-5/3	1593.838	1593.835	2.375	0.410	1205.313	0.326	23	0.109	K.M*HANHHLITDFLK.N
R4/RRR4-5/3	1594.085	1593.835	157.678	0.302	953.179	0.105	23	0.069	K.M*HANHHLITDFLK.N
R4/RRR4-13/2	1782.521	1782.884	-203.906	0.538	1752.424	0.514	23	0.260	K.ASEISVSAEEEFNIEK.L
R4/RRR4-13/3	1584.466	1584.823	-226.124	0.528	2012.903	0.445	30	0.255	R.KKIEYSM*QLNASR.I
R4/RRR4-13/2	1782.583	1782.884	-169.144	0.509	1639.688	0.484	22	0.237	K.ASEISVSAEEEFNIEK.L
R4/RRR4-13/2	1782.231	1782.884	-929.738	0.510	1619.591	0.471	22	0.231	K.ASEISVSAEEEFNIEK.L
R4/RRR4-13/3	1584.334	1584.823	-309.605	0.574	1766.075	0.451	29	0.212	R.KKIEYSM*QLNASR.I
R4/RRR4-13/2	1152.550	1153.307	-1528.516	0.531	1036.852	0.508	18	0.191	R.FCSGGVVLASR.D
R4/RRR4-13/2	1152.984	1153.307	-281.259	0.522	965.315	0.499	18	0.184	R.FCSGGVVLASR.D
R4/RRR4-13/2	1192.025	1191.310	-239.795	0.512	1105.690	0.435	17	0.182	K.IVCENTLDAR.L
R4/RRR4-13/2	1152.506	1153.307	-1567.670	0.466	873.710	0.444	17	0.169	R.FCSGGVVLASR.D
R4/RRR4-13/2	1026.813	1027.243	-419.557	0.375	1152.327	0.343	14	0.167	K.ELVVQGLLR.L
R4/RRR4-13/3	1584.723	1584.823	-63.493	0.519	1559.587	0.410	28	0.167	R.KKIEYSM*QLNASR.I
R4/RRR4-13/2	1027.060	1027.243	-178.173	0.438	1086.332	0.351	14	0.166	K.ELVVQGLLR.L
R4/RRR4-13/3	1441.323	1440.651	-227.975	0.562	1650.800	0.353	26	0.159	K.KIEYSMQLNASR.I
R4/RRR4-13/2	1191.335	1191.310	21.006	0.308	875.811	0.281	15	0.145	K.IVCENTLDAR.L
R4/RRR4-13/3	1456.231	1456.650	-288.537	0.550	1344.428	0.419	27	0.144	K.KIEYSM*QLNASR.I
R4/RRR4-13/2	1026.558	1027.243	-1646.462	0.302	797.654	0.190	13	0.137	K.ELVVQGLLR.L
R4/RRR4-13/3	1456.482	1456.650	-115.485	0.556	1149.331	0.442	25	0.133	K.KIEYSM*QLNASR.I
R4/RRR4-13/3	1440.676	1440.651	17.488	0.511	1297.065	0.330	23	0.117	K.KIEYSMQLNASR.I
R4/RRR4-13/3	1619.794	1619.809	-9.125	0.557	817.527	0.433	25	0.110	R.VSHNHHEYKNLLK.E
R4/RRR4-13/3	1568.559	1568.823	-169.361	0.429	1272.215	0.274	24	0.103	R.KKIEYSMQLNASR.I
R4/RRR4-13/3	1456.468	1456.650	-125.069	0.503	929.689	0.360	23	0.101	K.KIEYSM*QLNASR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/3	1620.696	1619.809	-69.556	0.477	813.624	0.379	24	0.101	R.VSHNHHEYKNLLK.E
R4/RRR4-13/3	1619.688	1619.809	-74.891	0.542	748.819	0.381	24	0.100	R.VSHNHHEYKNLLK.E
R4/RRR4-13/3	1568.556	1568.823	-171.001	0.502	1067.327	0.298	24	0.096	R.KKIEYSMQLNASR.I
R4/RRR4-13/3	1619.129	1619.809	-1040.796	0.507	796.046	0.331	23	0.093	R.VSHNHHEYKNLLK.E
R4/RRR4-13/3	1619.186	1619.809	-1005.484	0.463	535.632	0.344	22	0.090	-.VSHNHHEYKNLLK.-
R4/RRR4-13/3	1619.686	1619.809	-76.252	0.451	701.511	0.294	24	0.089	R.VSHNHHEYKNLLK.E
R4/RRR4-13/3	1568.184	1568.823	-1048.843	0.428	811.264	0.255	21	0.082	-.KKIEYSMQLNASR.-
R4/RRR4-13/3	1038.918	1039.297	-365.479	0.510	1065.061	0.205	21	0.081	-.LKEPAVLLR.-
R4/RRR4-13/3	1039.414	1039.297	112.997	0.474	826.462	0.110	17	0.064	-.LKEPAVLLR.-
R4/RRR4-13/3	1039.505	1039.297	200.883	0.483	979.039	0.080	19	0.064	-.LKEPAVLLR.-
R4/RRR4-13/2	1709.544	1708.932	-228.008	0.551	2092.083	0.577	26	0.332	R.GWVPTLLGYSAQGACK.F
R4/RRR4-13/2	1709.440	1708.932	-288.974	0.589	1761.347	0.592	26	0.285	R.GWVPTLLGYSAQGACK.F
R4/RRR4-13/2	1708.404	1708.932	-897.245	0.517	1775.026	0.572	26	0.280	R.GWVPTLLGYSAQGACK.F
R4/RRR4-13/2	1708.590	1708.932	-201.120	0.506	1732.213	0.570	25	0.273	R.GWVPTLLGYSAQGACK.F
R4/RRR4-13/2	1506.046	1505.610	290.911	0.565	1386.142	0.610	20	0.242	K.YYSDIAGPEYAQK.Y
R4/RRR4-13/2	1505.155	1505.610	-302.978	0.516	1285.929	0.541	20	0.215	K.YYSDIAGPEYAQK.Y
R4/RRR4-13/2	1504.551	1505.610	-1372.155	0.347	1213.753	0.496	19	0.193	K.YYSDIAGPEYAQK.Y
R4/RRR4-13/2	1063.064	1063.277	-200.356	0.510	977.899	0.456	15	0.179	K.LGLWGLFTR.G
R4/RRR4-13/2	937.205	938.060	-1984.436	0.451	766.415	0.518	15	0.176	K.SEGALGLYK.G
R4/RRR4-13/2	1085.225	1085.234	-9.207	0.397	833.987	0.502	12	0.173	K.FGFYEFFK.K
R4/RRR4-13/2	1062.994	1063.277	-266.483	0.388	757.000	0.505	14	0.171	K.LGLWGLFTR.G
R4/RRR4-13/2	1062.912	1063.277	-344.142	0.476	850.301	0.449	14	0.170	K.LGLWGLFTR.G
R4/RRR4-1/2	1709.945	1708.932	7.475	0.465	664.389	0.552	19	0.169	R.GWVPTLLGYSAQGACK.F
R4/RRR4-13/2	1213.223	1213.407	-152.448	0.395	1026.540	0.393	14	0.167	K.FGFYEFFKK.C
R4/RRR4-13/2	1063.088	1063.277	-177.779	0.430	745.530	0.472	13	0.167	K.LGLWGLFTR.G
R4/RRR4-13/2	1084.831	1085.234	-373.079	0.392	922.201	0.420	12	0.166	K.FGFYEFFK.K
R4/RRR4-13/2	1062.993	1063.277	-267.751	0.442	659.445	0.439	13	0.161	K.LGLWGLFTR.G
R4/RRR4-13/2	747.789	747.908	-159.820	0.439	756.366	0.464	11	0.161	-.HAVPVPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1063.425	1063.277	139.703	0.431	714.486	0.427	13	0.161	K.LGLWGLFTR.G
R4/RRR4-13/2	1063.175	1063.277	-96.230	0.401	765.757	0.416	13	0.161	K.LGLWGLFTR.G
R4/RRR4-13/2	1212.729	1213.407	-1388.457	0.391	799.823	0.422	13	0.160	K.FGFYEFFKK.C
R4/RRR4-12/2	938.091	938.060	33.789	0.347	764.304	0.409	15	0.158	K.SEGALGLYK.G
R4/RRR4-13/2	1084.377	1085.234	-1717.648	0.245	933.035	0.394	12	0.155	K.FGFYEFFK.K
R4/RRR4-13/2	937.945	938.060	-122.066	0.416	726.996	0.353	15	0.154	K.SEGALGLYK.G
R4/RRR4-13/2	1063.117	1063.277	-150.249	0.364	533.149	0.417	12	0.154	K.LGLWGLFTR.G
R4/RRR4-13/2	1094.008	1094.286	-254.788	0.326	800.937	0.387	16	0.153	K.SITSGFGILAK.E
R4/RRR4-13/2	1063.083	1063.277	-182.962	0.351	754.566	0.348	13	0.152	K.LGLWGLFTR.G
R4/RRR4-13/2	1062.896	1063.277	-358.891	0.375	526.088	0.374	12	0.151	K.LGLWGLFTR.G
R4/RRR4-13/2	1062.985	1063.277	-275.470	0.324	785.610	0.299	13	0.148	K.LGLWGLFTR.G
R4/RRR4-13/2	1093.876	1094.286	-375.814	0.280	835.003	0.342	16	0.148	K.SITSGFGILAK.E
R4/RRR4-13/2	1708.958	1708.932	14.930	0.433	403.010	0.476	15	0.147	-.GWVPTLLGYSAQGACK.-
R4/RRR4-13/2	938.143	938.060	88.863	0.422	530.004	0.329	12	0.147	K.SEGALGLYK.G
R4/RRR4-13/2	1062.874	1063.277	-379.864	0.262	424.138	0.389	11	0.146	K.LGLWGLFTR.G
R4/RRR4-13/3	1708.090	1708.932	-1081.959	0.371	1011.875	0.475	27	0.127	R.GWVPTLLGYSAQGACK.F
R4/RRR4-13/3	1505.541	1505.610	-45.885	0.443	1154.627	0.417	24	0.127	K.YYSDIAGPEYAQK.Y
R4/RRR4-13/3	1213.154	1213.407	-209.642	0.461	639.303	0.480	19	0.112	K.FGFYEFFKK.C
R4/RRR4-13/3	1213.754	1213.407	286.763	0.468	711.117	0.411	19	0.104	K.FGFYEFFKK.C
R4/RRR4-13/3	1213.130	1213.407	-229.629	0.382	500.437	0.383	16	0.099	K.FGFYEFFKK.C
R4/RRR4-13/3	1213.792	1213.407	318.075	0.399	502.831	0.345	17	0.098	K.FGFYEFFKK.C
R4/RRR4-13/3	1212.691	1213.407	-1419.507	0.422	631.934	0.350	19	0.097	K.FGFYEFFKK.C
R4/RRR4-13/3	1505.387	1505.610	-148.368	0.360	860.140	0.341	22	0.093	K.YYSDIAGPEYAQK.Y
R4/RRR4-13/3	1213.135	1213.407	-225.389	0.362	638.444	0.297	18	0.091	K.FGFYEFFKK.C
R4/RRR4-13/3	1505.589	1505.610	-14.046	0.406	744.005	0.325	21	0.089	K.YYSDIAGPEYAQK.Y
R4/RRR4-13/3	1212.727	1213.407	-1390.238	0.271	584.365	0.263	18	0.089	K.FGFYEFFKK.C
R4/RRR4-13/3	1213.679	1213.407	224.588	0.296	663.226	0.272	18	0.088	K.FGFYEFFKK.C
R4/RRR4-22/2	1218.053	1218.386	-274.175	0.511	1650.940	0.426	16	0.227	K.AEIGLWFEPR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1339.221	1339.436	-161.236	0.446	1506.207	0.394	20	0.204	R.NIIHGSDGPETAK.A
R4/RRR4-22/2	1298.772	1299.366	-1230.576	0.360	1344.352	0.413	18	0.192	R.ELVSYTSNEEK.W
R4/RRR4-22/2	1339.153	1339.436	-211.895	0.431	1289.212	0.431	19	0.191	R.NIIHGSDGPETAK.A
R4/RRR4-22/2	1218.041	1218.386	-284.028	0.482	1232.497	0.438	16	0.190	K.AEIGLWFEPR.E
R4/RRR4-22/2	1299.035	1299.366	-255.574	0.392	1135.469	0.414	17	0.177	R.ELVSYTSNEEK.W
R4/RRR4-22/2	1217.562	1218.386	-1502.309	0.365	1258.496	0.360	15	0.176	K.AEIGLWFEPR.E
R4/RRR4-22/2	885.389	886.031	-1860.579	0.381	1152.354	0.403	14	0.176	R.GDLAVVVGR.N
R4/RRR4-22/2	987.608	988.163	-1579.986	0.463	1206.133	0.361	13	0.173	R.GLISEILSR.F
R4/RRR4-22/2	1339.165	1339.436	-203.116	0.448	1104.270	0.396	18	0.171	R.NIIHGSDGPETAK.A
R4/RRR4-22/2	987.979	988.163	-186.708	0.439	1186.850	0.345	14	0.171	R.GLISEILSR.F
R4/RRR4-22/2	1299.015	1299.366	-271.130	0.423	1044.391	0.394	17	0.169	R.ELVSYTSNEEK.W
R4/RRR4-22/2	987.985	988.163	-181.255	0.467	1051.029	0.369	13	0.166	R.GLISEILSR.F
R4/RRR4-22/2	989.000	988.163	-165.842	0.399	1072.389	0.356	12	0.163	R.GLISEILSR.F
R4/RRR4-22/2	885.344	886.031	-1911.565	0.318	920.345	0.362	14	0.156	R.GDLAVVVGR.N
R4/RRR4-22/2	1344.781	1345.572	-1335.605	0.403	581.886	0.453	14	0.153	R.TFIAIKPDGVQR.G
R4/RRR4-22/2	1070.826	1071.252	-399.339	0.399	681.753	0.365	15	0.152	R.KLIGATDPQK.S
R4/RRR4-22/2	1345.544	1345.572	-20.984	0.434	535.583	0.408	14	0.149	R.TFIAIKPDGVQR.G
R4/RRR4-22/2	1070.959	1071.252	-274.562	0.356	568.361	0.338	14	0.146	R.KLIGATDPQK.S
R4/RRR4-22/2	1345.036	1345.572	-1145.193	0.427	556.055	0.368	14	0.146	R.TFIAIKPDGVQR.G
R4/RRR4-22/2	1070.658	1071.252	-1493.334	0.327	580.191	0.296	14	0.143	R.KLIGATDPQK.S
R4/RRR4-22/2	1219.410	1218.386	20.120	0.202	189.489	0.365	10	0.135	-.AEIGLWFEPR.-
R4/RRR4-22/2	987.233	988.163	-1961.326	0.260	774.363	0.266	12	0.134	-.GLISEILSR.-
R4/RRR4-22/2	987.885	988.163	-282.902	0.178	764.373	0.133	12	0.133	R.GLISEILSR.F
R4/RRR4-22/3	1811.629	1812.061	-239.092	0.485	790.786	0.543	30	0.129	R.KLIGATDPQKSEPGTIR.G
R4/RRR4-22/3	1812.039	1812.061	-12.008	0.451	930.034	0.471	32	0.122	R.KLIGATDPQKSEPGTIR.G
R4/RRR4-14/3	1408.067	1407.600	332.448	0.534	2105.425	0.464	28	0.291	R.SHQENVAGVKLPK.F
R4/RRR4-14/2	1239.404	1239.449	-37.006	0.465	1418.365	0.454	16	0.207	R.VNALENVVKPR.L
R4/RRR4-14/2	1080.968	1081.244	-256.163	0.472	903.200	0.412	14	0.166	R.LENTISYIK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	937.466	938.109	-1758.659	0.360	569.833	0.480	13	0.160	R.HVVLQSVR.S
R4/RRR4-14/2	1081.141	1081.244	-95.537	0.460	899.982	0.340	14	0.156	R.LENTISYIK.G
R4/RRR4-14/2	1010.849	1011.111	-259.942	0.388	745.063	0.353	16	0.153	R.ASSFSLAEAK.Y
R4/RRR4-14/2	1761.390	1761.957	-892.429	0.396	329.560	0.459	21	0.153	K.QFAEEQLAEEVALKR.G
R4/RRR4-14/2	937.535	938.109	-1684.352	0.315	554.291	0.415	13	0.152	R.HVVLQSVR.S
R4/RRR4-14/2	938.025	938.109	-89.620	0.343	383.091	0.416	11	0.151	R.HVVLQSVR.S
R4/RRR4-14/2	1080.450	1081.244	-1665.646	0.344	782.933	0.337	14	0.150	R.LENTISYIK.G
R4/RRR4-14/3	1408.252	1407.600	-248.109	0.537	1364.673	0.420	24	0.149	R.SHQENVAGVKLPK.F
R4/RRR4-14/2	1239.652	1239.449	163.695	0.380	662.341	0.384	13	0.148	R.VNALENVVKPR.L
R4/RRR4-14/2	1240.084	1239.449	-295.863	0.305	598.820	0.371	12	0.143	R.VNALENVVKPR.L
R4/RRR4-14/3	1395.786	1395.636	107.655	0.555	1460.778	0.372	26	0.142	R.RVNALENVVKPR.L
R4/RRR4-14/3	1407.024	1407.600	-1123.379	0.514	1202.984	0.454	25	0.142	R.SHQENVAGVKLPK.F
R4/RRR4-14/2	1010.360	1011.111	-1738.114	0.275	467.290	0.263	14	0.141	R.ASSFSLAEAK.Y
R4/RRR4-14/2	1010.707	1011.111	-400.743	0.234	424.004	0.293	13	0.139	R.ASSFSLAEAK.Y
R4/RRR4-15/3	1395.092	1395.636	-1109.906	0.529	1260.624	0.393	25	0.129	R.RVNALENVVKPR.L
R4/RRR4-14/3	1395.162	1395.636	-340.388	0.533	1189.057	0.407	24	0.127	R.RVNALENVVKPR.L
R4/RRR4-15/3	1395.783	1395.636	105.550	0.516	1246.242	0.358	24	0.119	R.RVNALENVVKPR.L
R4/RRR4-15/3	1394.984	1395.636	-1187.667	0.543	1069.434	0.397	23	0.116	R.RVNALENVVKPR.L
R4/RRR4-14/3	1761.413	1761.957	-879.287	0.479	1253.848	0.335	28	0.115	K.QFAEEQLAEEVALKR.G
R4/RRR4-14/3	1655.834	1655.747	52.890	0.411	630.319	0.514	24	0.112	K.GELDELEREDFFR.L
R4/RRR4-14/3	1395.418	1395.636	-156.595	0.504	1063.154	0.365	24	0.108	R.RVNALENVVKPR.L
R4/RRR4-14/3	1761.462	1761.957	-281.698	0.496	1163.154	0.297	26	0.100	K.QFAEEQLAEEVALKR.G
R4/RRR4-14/3	1655.530	1655.747	-131.029	0.405	548.682	0.418	22	0.096	K.GELDELEREDFFR.L
R4/RRR4-14/3	1761.241	1761.957	-976.975	0.381	869.132	0.209	25	0.078	K.QFAEEQLAEEVALKR.G
R4/RRR4-4/2	1762.363	1762.000	206.501	0.589	3015.033	0.601	25	0.539	R.FLVLNAAELAVDGSSVR.F
R4/RRR4-4/2	1762.667	1762.000	-189.462	0.582	2633.078	0.624	24	0.455	R.FLVLNAAELAVDGSSVR.F
R4/RRR4-4/2	1762.204	1762.000	115.918	0.589	2511.739	0.621	24	0.427	R.FLVLNAAELAVDGSSVR.F
R4/RRR4-4/2	1755.308	1754.916	223.792	0.555	2043.963	0.558	23	0.316	R.ETALLYDELLSSASNK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1754.249	1754.916	-953.223	0.522	2004.653	0.494	23	0.290	R.ETALLYDELLSSASNK.Q
R4/RRR4-4/2	1755.414	1754.916	284.180	0.591	1756.944	0.536	22	0.265	R.ETALLYDELLSSASNK.Q
R4/RRR4-4/2	1167.941	1168.348	-350.095	0.372	1711.123	0.313	17	0.208	R.MLQSYLGAER.F
R4/RRR4-4/2	1212.881	1213.324	-366.499	0.467	1427.108	0.407	17	0.201	K.LNVDQTGFYR.V
R4/RRR4-4/2	1213.196	1213.324	-106.028	0.492	1501.921	0.364	17	0.199	K.LNVDQTGFYR.V
R4/RRR4-4/2	1156.327	1156.269	50.230	0.437	1328.826	0.391	17	0.188	K.AAEVSEFFAGK.T
R4/RRR4-8/2	1762.604	1762.000	-225.660	0.424	1280.885	0.443	19	0.187	R.FLVLNAAELAVDGSSVR.F
R4/RRR4-4/2	1188.224	1188.313	-75.489	0.413	1199.942	0.429	18	0.185	K.ISVDATPELSR.D
R4/RRR4-4/2	1156.032	1156.269	-205.638	0.331	1131.319	0.386	15	0.169	K.AAEVSEFFAGK.T
R4/RRR4-4/2	1155.917	1156.269	-305.542	0.263	1067.847	0.336	15	0.156	K.AAEVSEFFAGK.T
R4/RRR4-4/2	1184.119	1184.348	-193.739	0.357	1093.563	0.260	15	0.151	R.M*LQSYLGAER.F
R4/RRR4-4/2	1187.319	1188.313	-1684.221	0.291	871.181	0.330	16	0.148	K.ISVDATPELSR.D
R4/RRR4-4/2	850.725	850.982	-303.400	0.407	878.509	0.270	13	0.147	R.AGYDALLK.I
R4/RRR4-4/2	1167.931	1167.339	-349.993	0.254	253.286	0.587	12	0.142	-.QQGYPVIYAK.-
R4/RRR4-4/3	1451.458	1451.603	-100.358	0.497	1511.586	0.250	27	0.116	-.VKYDDELAAGLEK.-
R4/RRR4-4/3	1451.615	1451.603	7.699	0.462	1387.400	0.120	25	0.080	-.VKYDDELAAGLEK.-
R4/RRR4-4/3	1450.939	1451.603	-1150.388	0.403	1012.022	0.176	22	0.074	-.VKYDDELAAGLEK.-
R4/RRR4-11/3	1650.947	1650.987	-24.193	0.490	2810.664	0.553	35	0.548	K.VLVVANPANTNALILK.E
R4/RRR4-11/3	1789.740	1789.922	-102.117	0.599	2552.990	0.517	39	0.440	R.KQSSALSAASSACDHIR.D
R4/RRR4-11/2	1347.294	1347.648	-263.505	0.494	2694.028	0.355	20	0.369	K.MELVDAAFPLLK.G
R4/RRR4-11/3	1651.458	1650.987	285.973	0.453	2184.518	0.553	36	0.356	K.VLVVANPANTNALILK.E
R4/RRR4-11/2	1348.229	1347.648	-311.725	0.571	2500.495	0.379	20	0.337	K.MELVDAAFPLLK.G
R4/RRR4-11/2	1351.990	1352.451	-341.739	0.537	2187.249	0.488	20	0.320	K.MDATAQELSEEK.T
R4/RRR4-11/2	1651.488	1650.987	-302.895	0.558	2012.052	0.540	26	0.305	K.VLVVANPANTNALILK.E
R4/RRR4-10/2	1650.421	1650.987	-951.616	0.500	1983.864	0.511	26	0.292	K.VLVVANPANTNALILK.E
R4/RRR4-11/2	1351.984	1352.451	-346.269	0.517	2062.569	0.442	20	0.286	K.MDATAQELSEEK.T
R4/RRR4-11/3	1789.754	1789.922	-94.113	0.538	1968.941	0.508	37	0.286	R.KQSSALSAASSACDHIR.D
R4/RRR4-13/2	1650.684	1650.987	-184.366	0.471	2050.141	0.442	24	0.281	K.VLVVANPANTNALILK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1555.163	1555.668	-970.698	0.539	1634.026	0.607	23	0.270	K.SQASALEAHAAPNCK.V
R4/RRR4-11/2	1368.027	1368.450	-309.970	0.518	1853.635	0.472	20	0.264	K.M*DATAQELSEEK.T
R4/RRR4-11/2	1351.958	1352.451	-365.474	0.518	1777.092	0.494	20	0.260	K.MDATAQELSEEK.T
R4/RRR4-11/2	1555.223	1555.668	-287.241	0.528	1580.885	0.594	23	0.260	K.SQASALEAHAAPNCK.V
R4/RRR4-11/2	1555.245	1555.668	-272.909	0.531	1521.873	0.611	22	0.256	K.SQASALEAHAAPNCK.V
R4/RRR4-11/2	1651.416	1650.987	260.706	0.557	1612.750	0.558	24	0.253	K.VLVVANPANTNALILK.E
R4/RRR4-12/2	1650.362	1650.987	-987.780	0.493	1712.838	0.506	24	0.252	K.VLVVANPANTNALILK.E
R4/RRR4-11/2	1367.513	1368.450	-1420.286	0.424	1746.322	0.455	20	0.245	K.M*DATAQELSEEK.T
R4/RRR4-11/2	1651.321	1650.987	202.592	0.541	1575.652	0.527	24	0.241	K.VLVVANPANTNALILK.E
R4/RRR4-10/2	1650.338	1650.987	-1002.113	0.446	1592.442	0.487	24	0.232	K.VLVVANPANTNALILK.E
R4/RRR4-11/2	1368.040	1368.450	-300.391	0.509	1509.433	0.485	19	0.225	K.M*DATAQELSEEK.T
R4/RRR4-2/2	1650.860	1650.987	-77.474	0.492	1351.654	0.511	23	0.212	K.VLVVANPANTNALILK.E
R4/RRR4-10/2	1650.563	1650.987	-257.964	0.488	1375.757	0.499	23	0.212	K.VLVVANPANTNALILK.E
R4/RRR4-12/2	1650.440	1650.987	-940.255	0.481	1395.302	0.478	23	0.209	K.VLVVANPANTNALILK.E
R4/RRR4-5/2	1651.712	1650.987	-167.053	0.498	1284.821	0.496	22	0.202	K.VLVVANPANTNALILK.E
R4/RRR4-11/2	1015.596	1016.174	-1557.842	0.502	1423.630	0.358	15	0.190	K.LNVQVTDVK.N
R4/RRR4-12/2	1649.550	1650.987	-1481.634	0.382	1333.841	0.410	22	0.189	K.VLVVANPANTNALILK.E
R4/RRR4-11/3	1651.734	1650.987	-153.865	0.453	1510.056	0.471	32	0.185	K.VLVVANPANTNALILK.E
R4/RRR4-11/2	1015.877	1016.174	-292.522	0.556	1211.383	0.343	15	0.171	K.LNVQVTDVK.N
R4/RRR4-11/2	1348.474	1347.648	-129.168	0.365	1257.649	0.282	17	0.163	K.MELVDAAFPLLK.G
R4/RRR4-9/2	1015.827	1016.174	-342.195	0.394	1092.846	0.313	14	0.161	K.LNVQVTDVK.N
R4/RRR4-12/2	1015.986	1016.174	-184.635	0.451	1012.028	0.338	13	0.160	K.LNVQVTDVK.N
R4/RRR4-3/2	1652.082	1650.987	57.761	0.393	460.035	0.452	16	0.150	K.VLVVANPANTNALILK.E
R4/RRR4-11/3	1624.530	1624.796	-163.965	0.471	1328.677	0.437	26	0.150	R.KKM*DATAQELSEEK.T
R4/RRR4-2/2	1016.020	1016.174	-151.851	0.392	587.819	0.321	13	0.149	K.LNVQVTDVK.N
R4/RRR4-11/3	1662.689	1661.749	-36.430	0.430	1090.338	0.520	28	0.148	K.QSSALSAASSACDHIR.D
R4/RRR4-9/2	1015.837	1016.174	-332.549	0.414	890.225	0.277	13	0.148	K.LNVQVTDVK.N
R4/RRR4-5/2	1016.893	1016.174	-276.457	0.406	425.059	0.314	12	0.148	K.LNVQVTDVK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1363.210	1363.648	-322.000	0.376	998.607	0.279	15	0.147	-.M*ELVDAAFPLLK.-
R4/RRR4-9/2	1015.657	1016.174	-1498.077	0.388	754.767	0.288	13	0.147	K.LNVQVTDVK.N
R4/RRR4-5/2	1016.641	1016.174	461.002	0.356	414.271	0.242	13	0.146	K.LNVQVTDVK.N
R4/RRR4-11/3	1624.464	1624.796	-204.558	0.476	1302.162	0.431	26	0.145	R.KKM*DATAQELSEEK.T
R4/RRR4-3/2	1017.074	1016.174	-98.124	0.399	639.631	0.269	13	0.145	K.LNVQVTDVK.N
R4/RRR4-11/2	1652.189	1650.987	122.377	0.329	441.539	0.404	15	0.145	K.VLVVANPANTNALILK.E
R4/RRR4-11/3	1661.570	1661.749	-108.373	0.430	1036.987	0.510	26	0.140	K.QSSALSAASSACDHIR.D
R4/RRR4-2/2	1363.662	1363.648	10.850	0.449	718.403	0.231	16	0.137	K.M*ELVDAAFPLLK.G
R4/RRR4-3/2	1015.624	1016.174	-1530.555	0.210	672.781	0.110	13	0.135	K.LNVQVTDVK.N
R4/RRR4-11/3	1625.814	1624.796	11.331	0.468	1034.114	0.420	24	0.118	R.KKM*DATAQELSEEK.T
R4/RRR4-11/3	1624.952	1624.796	96.480	0.481	1059.440	0.363	25	0.108	R.KKM*DATAQELSEEK.T
R4/RRR4-15/2	1419.191	1419.517	-230.140	0.497	2085.272	0.553	19	0.322	K.TVDVEELTVEER.N
R4/RRR4-15/2	1419.096	1419.517	-297.021	0.486	2106.974	0.529	19	0.318	K.TVDVEELTVEER.N
R4/RRR4-14/2	1419.155	1419.517	-255.511	0.505	2002.179	0.548	19	0.307	K.TVDVEELTVEER.N
R4/RRR4-15/2	1418.741	1419.517	-1255.537	0.490	2005.807	0.536	19	0.304	K.TVDVEELTVEER.N
R4/RRR4-14/2	1419.096	1419.517	-297.625	0.475	2046.726	0.508	19	0.302	K.TVDVEELTVEER.N
R4/RRR4-14/2	1419.160	1419.517	-252.145	0.499	1906.436	0.548	18	0.292	K.TVDVEELTVEER.N
R4/RRR4-15/2	1773.559	1774.014	-257.609	0.567	1530.970	0.591	23	0.250	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1773.479	1774.014	-867.981	0.574	1486.274	0.602	22	0.246	K.AAQDIALADLAPTHPIR.L
R4/RRR4-14/2	1773.513	1774.014	-849.187	0.572	1440.442	0.611	22	0.243	K.AAQDIALADLAPTHPIR.L
R4/RRR4-14/2	1773.013	1774.014	-1131.864	0.519	1514.032	0.575	22	0.243	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1774.358	1774.014	194.133	0.562	1464.444	0.595	22	0.242	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1773.322	1774.014	-957.263	0.455	1678.542	0.463	22	0.234	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1374.966	1375.510	-1126.053	0.492	1611.744	0.441	20	0.227	R.IVSSIEQKEEGR.G
R4/RRR4-15/2	1382.900	1383.526	-1179.758	0.497	1707.467	0.365	16	0.219	R.YEEM*VEYM*EK.V
R4/RRR4-15/2	1772.718	1774.014	-1299.195	0.429	1616.169	0.421	23	0.218	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/3	1656.049	1655.831	131.954	0.421	1677.363	0.476	32	0.212	K.LLDSHLVPSSTAAESK.V
R4/RRR4-15/2	1215.869	1216.343	-391.105	0.408	1454.118	0.455	17	0.211	K.EAAESTM*VAYK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/3	1773.699	1774.014	-178.075	0.408	1580.377	0.497	31	0.207	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1376.066	1375.510	-323.481	0.509	1264.217	0.507	19	0.206	R.IVSSIEQKEEGR.G
R4/RRR4-14/2	1773.538	1774.014	-269.279	0.535	1243.968	0.542	21	0.206	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1655.345	1655.831	-294.793	0.494	1252.322	0.521	23	0.206	K.LLDSHLVPSSTAAESK.V
R4/RRR4-15/2	1655.377	1655.831	-274.965	0.467	1271.874	0.505	23	0.204	K.LLDSHLVPSSTAAESK.V
R4/RRR4-15/2	1216.001	1216.343	-282.823	0.397	1318.254	0.440	16	0.194	K.EAAESTM*VAYK.A
R4/RRR4-14/2	1190.925	1190.439	409.832	0.444	1628.175	0.273	16	0.191	K.DSTLIMQLLR.D
R4/RRR4-15/2	1375.128	1375.510	-278.828	0.454	1109.900	0.470	18	0.186	R.IVSSIEQKEEGR.G
R4/RRR4-14/2	1655.445	1655.831	-233.832	0.444	1184.950	0.450	22	0.185	K.LLDSHLVPSSTAAESK.V
R4/RRR4-15/2	1655.408	1655.831	-256.322	0.479	1146.014	0.447	22	0.182	K.LLDSHLVPSSTAAESK.V
R4/RRR4-15/3	1656.738	1655.831	-56.588	0.343	1716.628	0.382	33	0.181	K.LLDSHLVPSSTAAESK.V
R4/RRR4-15/2	1201.036	1200.344	-257.467	0.417	969.940	0.476	15	0.175	K.EAAESTMVAYK.A
R4/RRR4-15/2	1215.843	1216.343	-1237.706	0.445	1014.397	0.425	16	0.172	K.EAAESTM*VAYK.A
R4/RRR4-15/3	1773.165	1774.014	-1045.911	0.376	1346.981	0.477	29	0.166	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1201.139	1200.344	-171.005	0.389	903.353	0.419	16	0.164	K.EAAESTMVAYK.A
R4/RRR4-14/2	1206.220	1206.438	-181.595	0.395	1494.509	0.177	15	0.162	K.DSTLIM*QLLR.D
R4/RRR4-15/3	1655.060	1655.831	-1073.535	0.291	1648.582	0.334	31	0.156	K.LLDSHLVPSSTAAESK.V
R4/RRR4-14/3	1773.590	1774.014	-239.802	0.447	1193.733	0.501	27	0.156	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/2	1206.106	1206.438	-275.919	0.481	1325.018	0.204	15	0.153	K.DSTLIM*QLLR.D
R4/RRR4-15/2	1140.023	1140.271	-218.728	0.494	848.601	0.338	14	0.152	R.GNEEHVTLIK.E
R4/RRR4-15/2	1140.231	1140.271	-35.500	0.498	682.062	0.374	13	0.151	R.GNEEHVTLIK.E
R4/RRR4-14/3	1656.039	1655.831	126.077	0.370	1296.074	0.454	30	0.150	K.LLDSHLVPSSTAAESK.V
R4/RRR4-15/2	1139.507	1140.271	-1553.534	0.468	643.383	0.375	13	0.148	-.GNEEHVTLIK.-
R4/RRR4-1/2	1374.886	1375.510	-1185.071	0.385	445.388	0.394	14	0.148	R.IVSSIEQKEEGR.G
R4/RRR4-14/2	1206.016	1206.438	-350.760	0.496	987.788	0.255	15	0.146	K.DSTLIM*QLLR.D
R4/RRR4-15/2	1375.192	1375.510	-232.162	0.464	649.654	0.295	15	0.141	R.IVSSIEQKEEGR.G
R4/RRR4-14/2	1190.228	1190.439	-177.407	0.405	971.448	0.200	15	0.141	K.DSTLIMQLLR.D
R4/RRR4-14/2	1140.218	1140.271	-46.668	0.449	505.568	0.303	12	0.134	-.GNEEHVTLIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/3	1773.465	1774.014	-876.315	0.318	1223.292	0.403	28	0.130	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/3	1774.236	1774.014	125.372	0.385	1080.804	0.442	29	0.127	K.AAQDIALADLAPTHPIR.L
R4/RRR4-15/3	1656.672	1655.831	-96.499	0.365	1131.209	0.400	27	0.121	K.LLDSHLVPSSTAAESK.V
R4/RRR4-14/3	1655.938	1655.831	64.642	0.286	1191.582	0.296	27	0.103	K.LLDSHLVPSSTAAESK.V
R4/RRR4-8/2	1359.136	1359.471	-246.885	0.460	1428.328	0.450	16	0.208	K.SVYAHWVPEDR.I
R4/RRR4-8/2	1358.601	1359.471	-1380.145	0.434	1232.354	0.410	15	0.182	K.SVYAHWVPEDR.I
R4/RRR4-8/2	1359.143	1359.471	-242.380	0.431	1182.231	0.424	15	0.180	K.SVYAHWVPEDR.I
R4/RRR4-16/2	1159.963	1160.303	-293.499	0.461	1391.315	0.520	19	0.220	K.AVDNSGTVVGIK.C
R4/RRR4-16/2	1784.321	1785.011	-949.989	0.455	1484.896	0.476	20	0.215	R.DGPQLYMIEPSGVSYK.Y
R4/RRR4-15/2	1160.145	1160.303	-136.522	0.471	1241.082	0.497	18	0.201	K.AVDNSGTVVGIK.C
R4/RRR4-15/2	1159.995	1160.303	-266.048	0.469	1171.413	0.524	17	0.199	K.AVDNSGTVVGIK.C
R4/RRR4-16/2	1083.856	1084.248	-362.570	0.468	835.825	0.587	16	0.189	K.VPADLLEQAK.V
R4/RRR4-16/2	1084.131	1084.248	-108.487	0.478	831.082	0.573	16	0.187	K.VPADLLEQAK.V
R4/RRR4-16/2	1085.219	1085.234	-14.284	0.478	1084.274	0.444	14	0.181	R.VFQVEYATK.A
R4/RRR4-15/2	1160.047	1160.303	-220.863	0.377	1075.492	0.474	17	0.181	K.AVDNSGTVVGIK.C
R4/RRR4-16/2	1083.631	1084.248	-1496.359	0.436	694.134	0.563	16	0.177	K.VPADLLEQAK.V
R4/RRR4-16/2	1160.053	1160.303	-215.585	0.448	944.743	0.480	17	0.176	K.AVDNSGTVVGIK.C
R4/RRR4-16/2	1086.146	1085.234	-81.795	0.498	957.297	0.452	14	0.175	R.VFQVEYATK.A
R4/RRR4-16/2	1086.271	1085.234	33.745	0.501	954.194	0.427	14	0.171	R.VFQVEYATK.A
R4/RRR4-16/2	1159.431	1160.303	-1618.920	0.332	856.795	0.463	17	0.165	K.AVDNSGTVVGIK.C
R4/RRR4-16/2	991.900	992.150	-253.305	0.423	549.151	0.486	14	0.160	-.VYGEPISVK.-
R4/RRR4-16/2	1217.978	1218.419	-362.753	0.429	737.126	0.415	16	0.158	K.CKDGIVLGVEK.L
R4/RRR4-16/2	991.985	992.150	-167.379	0.424	566.659	0.429	14	0.155	-.VYGEPISVK.-
R4/RRR4-16/2	1144.683	1145.290	-1407.780	0.396	902.733	0.342	15	0.154	K.IIYGVHDEAK.D
R4/RRR4-16/2	1217.522	1218.419	-1562.998	0.309	876.662	0.358	17	0.153	K.CKDGIVLGVEK.L
R4/RRR4-16/2	1217.966	1218.419	-373.312	0.381	689.434	0.354	16	0.150	K.CKDGIVLGVEK.L
R4/RRR4-15/2	1085.704	1085.234	434.214	0.403	396.586	0.329	11	0.146	R.VFQVEYATK.A
R4/RRR4-16/2	991.251	992.150	-1922.436	0.345	333.756	0.415	11	0.132	-.VYGEPISVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1349.930	1350.435	-1118.210	0.345	881.308	0.517	17	0.112	K.VAAQAALEEM*DAD.-
R4/RRR4-16/2	1350.093	1350.435	-253.823	0.286	738.982	0.317	16	0.072	K.VAAQAALEEM*DAD.-
R4/RRR4-9/2	1808.428	1807.939	270.907	0.614	3016.313	0.648	29	0.561	K.GTVAVGFDADANGDVTAVK.L
R4/RRR4-9/2	1808.261	1807.939	178.306	0.605	2650.363	0.608	28	0.453	K.GTVAVGFDADANGDVTAVK.L
R4/RRR4-9/2	1915.501	1916.121	-848.433	0.557	2624.818	0.611	24	0.447	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/2	1915.514	1916.121	-841.716	0.547	2645.755	0.591	25	0.444	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/2	1915.344	1916.121	-930.581	0.557	2641.518	0.586	24	0.441	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/2	1915.934	1916.121	-98.132	0.573	2529.297	0.602	24	0.422	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/2	1916.654	1916.121	-244.381	0.589	2518.224	0.600	24	0.419	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/2	1807.093	1807.939	-1024.878	0.530	2344.643	0.614	26	0.389	K.GTVAVGFDADANGDVTAVK.L
R4/RRR4-9/2	1915.422	1916.121	-889.570	0.541	2455.722	0.549	24	0.388	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/2	1994.873	1995.225	-176.738	0.585	2372.376	0.568	25	0.378	K.LTDFGVQGAEANNILYLR.D
R4/RRR4-9/2	1994.586	1995.225	-823.939	0.569	2403.192	0.529	25	0.370	K.LTDFGVQGAEANNILYLR.D
R4/RRR4-9/2	1994.571	1995.225	-831.619	0.572	2225.630	0.542	24	0.340	K.LTDFGVQGAEANNILYLR.D
R4/RRR4-9/2	1604.462	1604.808	-215.928	0.490	2234.184	0.476	22	0.323	R.DIDDADKLVAAMQAK.K
R4/RRR4-9/2	1807.460	1807.939	-266.326	0.533	1996.776	0.563	24	0.307	K.GTVAVGFDADANGDVTAVK.L
R4/RRR4-9/2	1604.351	1604.808	-285.771	0.500	2060.953	0.475	22	0.294	R.DIDDADKLVAAMQAK.K
R4/RRR4-9/3	1916.136	1916.121	7.877	0.506	1826.877	0.512	30	0.261	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/2	1315.293	1315.581	-219.463	0.447	1534.223	0.441	17	0.215	K.GIELILSTEIVK.A
R4/RRR4-9/2	1620.021	1620.807	-1105.800	0.465	834.295	0.508	21	0.174	R.DIDDADKLVAAM*QAK.K
R4/RRR4-9/2	1474.489	1474.597	-73.787	0.366	799.608	0.502	20	0.167	R.LPGFHTCVGSGGER.L
R4/RRR4-10/2	1136.965	1137.273	-271.545	0.483	743.349	0.443	16	0.166	K.GYLFPQNAAR.L
R4/RRR4-10/2	1137.036	1137.273	-208.643	0.463	709.340	0.448	16	0.165	K.GYLFPQNAAR.L
R4/RRR4-9/2	1136.871	1137.273	-354.063	0.354	724.577	0.443	16	0.161	K.GYLFPQNAAR.L
R4/RRR4-9/2	1446.683	1447.618	-1341.393	0.430	513.109	0.490	18	0.160	K.ESVAPYERPALSK.G
R4/RRR4-9/2	1446.584	1447.618	-1410.127	0.408	598.523	0.464	18	0.158	K.ESVAPYERPALSK.G
R4/RRR4-9/2	1136.281	1137.273	-1758.255	0.347	768.428	0.399	16	0.157	K.GYLFPQNAAR.L
R4/RRR4-9/2	1474.069	1474.597	-1040.048	0.413	911.199	0.356	20	0.156	R.LPGFHTCVGSGGER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/3	1996.399	1995.225	87.472	0.449	1204.708	0.494	28	0.155	K.LTDFGVQGAEANNILYLR.D
R4/RRR4-9/2	1447.241	1447.618	-261.042	0.418	505.363	0.435	18	0.155	K.ESVAPYERPALSK.G
R4/RRR4-10/2	1136.474	1137.273	-1587.630	0.261	600.323	0.388	15	0.148	K.GYLFPQNAAR.L
R4/RRR4-2/2	1136.983	1137.273	-255.065	0.349	494.476	0.362	12	0.146	K.GYLFPQNAAR.L
R4/RRR4-9/3	1620.625	1620.807	-112.872	0.397	1507.338	0.283	27	0.126	R.DIDDADKLVAAM*QAK.K
R4/RRR4-9/3	1915.406	1916.121	-898.054	0.453	913.792	0.470	26	0.121	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/3	1620.638	1620.807	-104.598	0.406	1375.725	0.294	27	0.116	R.DIDDADKLVAAM*QAK.K
R4/RRR4-9/3	1915.853	1916.121	-140.226	0.433	812.865	0.476	24	0.115	R.LFTSGLAAFYEGYYANK.G
R4/RRR4-9/3	1621.513	1620.807	-182.050	0.462	1298.175	0.315	26	0.114	R.DIDDADKLVAAM*QAK.K
R4/RRR4-9/3	1475.564	1474.597	-22.339	0.439	898.333	0.445	27	0.114	R.LPGFHTCVGSGGER.L
R4/RRR4-9/3	1474.226	1474.597	-252.162	0.408	840.534	0.455	26	0.112	R.LPGFHTCVGSGGER.L
R4/RRR4-9/3	1474.571	1474.597	-17.580	0.432	632.854	0.404	23	0.097	R.LPGFHTCVGSGGER.L
R4/RRR4-4/2	1832.098	1831.958	76.612	0.580	2414.382	0.511	26	0.368	K.TEDLWAALEEGSGEPVK.T
R4/RRR4-4/2	1693.192	1693.893	-1007.451	0.480	2214.148	0.483	22	0.323	R.YGVLDDTYALCM*AGK.Q
R4/RRR4-4/2	1831.372	1831.958	-868.689	0.535	1956.327	0.562	24	0.303	K.TEDLWAALEEGSGEPVK.T
R4/RRR4-4/2	1830.846	1831.958	-1156.966	0.422	1908.822	0.446	23	0.261	K.TEDLWAALEEGSGEPVK.T
R4/RRR4-4/2	1834.797	1834.148	-191.757	0.568	1110.472	0.564	27	0.206	R.FNEVLPVGEGTLVIAFK.G
R4/RRR4-4/2	1582.003	1582.787	-1130.996	0.498	1254.668	0.519	17	0.200	R.GVGAAGHEVAWTWLK.E
R4/RRR4-4/2	1212.061	1212.339	-230.275	0.477	1294.466	0.457	17	0.200	K.LNVNQTGFYR.V
R4/RRR4-4/2	1029.123	1029.172	-48.018	0.466	1375.290	0.415	17	0.198	R.AEANLGNVLK.E
R4/RRR4-4/2	1169.868	1169.223	-304.410	0.533	1110.536	0.494	15	0.191	R.VSYDEELASR.L
R4/RRR4-4/2	1029.209	1029.172	36.092	0.474	1264.863	0.394	17	0.185	R.AEANLGNVLK.E
R4/RRR4-4/2	1211.955	1212.339	-318.489	0.533	1252.507	0.385	17	0.183	K.LNVNQTGFYR.V
R4/RRR4-4/2	1834.785	1834.148	-198.565	0.563	749.431	0.555	23	0.177	R.FNEVLPVGEGTLVIAFK.G
R4/RRR4-4/2	1833.320	1834.148	-999.731	0.517	773.223	0.542	23	0.176	R.FNEVLPVGEGTLVIAFK.G
R4/RRR4-4/2	1168.976	1169.223	-212.683	0.490	1126.721	0.395	15	0.174	R.VSYDEELASR.L
R4/RRR4-4/2	1168.850	1169.223	-320.388	0.478	1046.645	0.380	15	0.167	R.VSYDEELASR.L
R4/RRR4-4/2	1213.091	1212.339	-205.251	0.511	1005.113	0.394	16	0.167	-.LNVNQTGFYR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1582.105	1582.787	-1066.149	0.379	995.905	0.359	20	0.158	R.GVGAAGHEVAWTWLK.E
R4/RRR4-4/2	1212.313	1212.339	-21.977	0.378	889.292	0.375	15	0.155	-.LNVNQTGFYR.-
R4/RRR4-4/2	1105.650	1106.257	-1458.033	0.441	818.533	0.338	14	0.154	R.NQDSIFLLR.G
R4/RRR4-1/2	1169.455	1169.223	198.648	0.392	917.431	0.318	15	0.153	R.VSYDEELASR.L
R4/RRR4-4/2	1168.068	1168.285	-186.538	0.393	823.612	0.366	14	0.150	K.SGEGHLDALLR.G
R4/RRR4-4/2	1106.089	1106.257	-151.939	0.494	789.235	0.306	14	0.149	R.NQDSIFLLR.G
R4/RRR4-4/2	1105.880	1106.257	-341.399	0.438	664.484	0.298	13	0.145	R.NQDSIFLLR.G
R4/RRR4-1/2	1168.849	1169.223	-321.645	0.324	714.341	0.294	13	0.143	R.VSYDEELASR.L
R4/RRR4-4/3	1168.044	1168.285	-206.941	0.497	691.371	0.472	20	0.111	K.SGEGHLDALLR.G
R4/RRR4-4/3	1168.412	1168.285	108.748	0.492	555.004	0.472	19	0.107	K.SGEGHLDALLR.G
R4/RRR4-4/3	1168.199	1168.285	-73.755	0.465	505.666	0.460	19	0.104	K.SGEGHLDALLR.G
R4/RRR4-13/2	1900.461	1900.935	-250.136	0.552	2556.453	0.606	26	0.433	K.SADLFDSEGQSSQSNSIK.Q
R4/RRR4-13/2	1651.282	1649.845	265.398	0.608	2470.371	0.605	24	0.414	K.LLSDLAAAM*EEGDVAK.F
R4/RRR4-13/2	1649.309	1649.845	-933.922	0.550	2253.365	0.572	24	0.358	K.LLSDLAAAM*EEGDVAK.F
R4/RRR4-13/2	1649.265	1649.845	-961.118	0.489	2280.091	0.557	24	0.358	K.LLSDLAAAM*EEGDVAK.F
R4/RRR4-13/2	1900.500	1900.935	-229.515	0.581	2173.213	0.605	26	0.355	K.SADLFDSEGQSSQSNSIK.Q
R4/RRR4-13/3	1491.839	1491.671	113.076	0.553	2312.385	0.450	28	0.336	K.VAEIAAQLEQYQK.A
R4/RRR4-13/3	1490.984	1491.671	-1134.559	0.564	1980.767	0.508	27	0.289	K.VAEIAAQLEQYQK.A
R4/RRR4-13/2	1491.033	1491.671	-1101.955	0.380	1762.124	0.371	19	0.225	K.VAEIAAQLEQYQK.A
R4/RRR4-13/2	1400.250	1400.475	-161.116	0.451	1315.423	0.439	19	0.196	R.YQDIDPTFSGTR.E
R4/RRR4-13/2	1488.898	1488.745	103.481	0.478	1224.588	0.476	19	0.194	R.GILLNAGICQLCR.G
R4/RRR4-13/2	1134.188	1134.267	-69.586	0.532	1368.853	0.403	16	0.194	K.ANEIFEAIAR.Q
R4/RRR4-13/2	1133.999	1134.267	-237.381	0.549	1277.926	0.416	16	0.190	K.ANEIFEAIAR.Q
R4/RRR4-13/2	1134.077	1134.267	-167.730	0.454	1201.585	0.436	15	0.186	K.ANEIFEAIAR.Q
R4/RRR4-13/2	1401.101	1400.475	-267.804	0.524	1079.268	0.460	17	0.181	R.YQDIDPTFSGTR.E
R4/RRR4-13/2	1399.642	1400.475	-1313.608	0.393	1231.098	0.388	18	0.179	R.YQDIDPTFSGTR.E
R4/RRR4-13/2	1307.972	1308.444	-361.848	0.389	909.502	0.376	16	0.157	R.GDVVAITNSM*ER.Y
R4/RRR4-13/2	1307.942	1308.444	-1151.644	0.385	861.262	0.360	16	0.153	R.GDVVAITNSM*ER.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1308.004	1308.444	-337.595	0.381	745.164	0.378	15	0.151	R.GDVVAITNSM*ER.Y
R4/RRR4-13/3	1577.577	1577.741	-104.363	0.527	449.665	0.532	22	0.111	K.FTDAIKEFDSM*TR.L
R4/RRR4-14/2	1651.391	1651.891	-303.580	0.572	2509.681	0.543	24	0.401	R.HLAAQFQEIPLDLR.M
R4/RRR4-14/2	1651.298	1651.891	-967.646	0.535	2033.146	0.526	23	0.307	R.HLAAQFQEIPLDLR.M
R4/RRR4-14/2	1651.143	1651.891	-1061.317	0.569	2050.878	0.494	23	0.300	R.HLAAQFQEIPLDLR.M
R4/RRR4-14/2	1706.421	1706.964	-907.257	0.503	1772.108	0.520	23	0.266	R.IQDNLALVYLSSITR.T
R4/RRR4-14/2	1296.242	1296.411	-131.445	0.498	1825.275	0.442	19	0.252	K.AYISSNLSLGDR.H
R4/RRR4-14/2	1297.119	1296.411	-225.841	0.509	1722.921	0.480	19	0.249	K.AYISSNLSLGDR.H
R4/RRR4-14/2	1296.110	1296.411	-233.102	0.429	1697.132	0.375	19	0.220	K.AYISSNLSLGDR.H
R4/RRR4-14/2	1182.017	1182.372	-300.952	0.465	1286.091	0.403	18	0.188	R.FISDAVASM*PK.L
R4/RRR4-14/2	1181.935	1182.372	-370.275	0.475	1291.502	0.395	18	0.187	R.FISDAVASM*PK.L
R4/RRR4-14/2	1052.158	1052.120	36.701	0.505	957.727	0.447	16	0.177	K.YVDDVVEGR.V
R4/RRR4-14/2	1051.888	1052.120	-220.876	0.436	897.384	0.431	15	0.169	K.YVDDVVEGR.V
R4/RRR4-14/2	1834.037	1834.153	-63.127	0.491	721.685	0.555	19	0.169	R.VIGTLLGSVLPDGTVHVR.N
R4/RRR4-14/2	1799.716	1800.993	-1268.888	0.425	719.009	0.534	20	0.168	R.EVQSPIHLTVDTGFTR.G
R4/RRR4-14/2	1834.072	1834.153	-44.234	0.518	655.998	0.549	19	0.165	R.VIGTLLGSVLPDGTVHVR.N
R4/RRR4-14/2	1051.860	1052.120	-247.537	0.427	845.297	0.403	15	0.163	K.YVDDVVEGR.V
R4/RRR4-14/2	1800.394	1800.993	-890.912	0.398	626.014	0.528	18	0.161	R.EVQSPIHLTVDTGFTR.G
R4/RRR4-14/2	1269.526	1269.511	12.093	0.417	875.680	0.402	14	0.159	K.LYVLIDEIYK.Y
R4/RRR4-14/2	1833.197	1834.153	-1069.726	0.419	680.364	0.500	19	0.159	R.VIGTLLGSVLPDGTVHVR.N
R4/RRR4-14/2	1800.584	1800.993	-228.176	0.407	493.338	0.534	17	0.157	R.EVQSPIHLTVDTGFTR.G
R4/RRR4-14/2	1181.358	1182.372	-1710.113	0.349	1108.808	0.275	17	0.155	R.FISDAVASM*PK.L
R4/RRR4-14/3	1834.035	1834.153	-64.069	0.472	984.974	0.560	34	0.149	R.VIGTLLGSVLPDGTVHVR.N
R4/RRR4-14/3	1834.173	1834.153	11.233	0.420	680.741	0.525	30	0.117	R.VIGTLLGSVLPDGTVHVR.N
R4/RRR4-14/3	1834.144	1834.153	-4.788	0.450	634.691	0.514	29	0.114	R.VIGTLLGSVLPDGTVHVR.N
R4/RRR4-3/2	1602.125	1601.825	187.491	0.541	2568.365	0.443	24	0.378	R.FNAILEELGIEQPK.G
R4/RRR4-3/2	1142.014	1142.331	-277.635	0.427	2043.844	0.512	19	0.303	K.VPIITTVDGAR.A
R4/RRR4-3/2	1142.097	1142.331	-204.824	0.472	1821.409	0.584	19	0.290	K.VPIITTVDGAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1142.108	1142.331	-195.817	0.430	1461.003	0.501	18	0.222	K.VPIITTVDGAR.A
R4/RRR4-3/2	1745.470	1746.041	-902.602	0.514	1151.314	0.593	20	0.208	K.LPLNGTVFLSLNDLTK.R
R4/RRR4-3/2	1656.535	1656.818	-171.371	0.533	1240.308	0.472	18	0.192	R.GLDQLSKDDFYQVK.R
R4/RRR4-3/2	1422.146	1422.608	-326.344	0.357	1338.670	0.344	19	0.177	R.ELGFNIIATSGTAK.V
R4/RRR4-2/2	1142.042	1142.331	-253.828	0.364	946.020	0.475	15	0.172	K.VPIITTVDGAR.A
R4/RRR4-3/2	1777.477	1777.996	-857.350	0.475	790.803	0.497	20	0.167	K.LSVGYTLDQIPNDITK.K
R4/RRR4-3/2	1105.179	1105.309	-117.942	0.295	1178.147	0.333	15	0.163	R.LALEVAPTYK.R
R4/RRR4-3/2	1207.611	1206.419	159.116	0.470	1006.436	0.349	14	0.159	R.LRDYSVAIIR.E
R4/RRR4-3/2	1422.107	1422.608	-1059.195	0.358	574.280	0.434	15	0.147	R.ELGFNIIATSGTAK.V
R4/RRR4-3/2	1207.250	1206.419	-140.627	0.431	920.881	0.247	14	0.143	R.LRDYSVAIIR.E
R4/RRR4-3/2	1560.346	1559.831	-312.113	0.360	880.173	0.287	16	0.142	K.LALPIQQYLEDKK.L
R4/RRR4-3/2	1776.620	1777.996	-1341.412	0.286	566.566	0.397	17	0.141	K.LSVGYTLDQIPNDITK.K
R4/RRR4-24/3	1775.532	1775.858	-183.822	0.551	2761.264	0.470	34	0.465	K.FEANRDVDNPDVIDR.L
R4/RRR4-25/3	1775.277	1775.858	-892.835	0.552	2691.000	0.433	33	0.421	K.FEANRDVDNPDVIDR.L
R4/RRR4-24/3	1774.989	1775.858	-1055.838	0.527	2636.465	0.375	33	0.371	K.FEANRDVDNPDVIDR.L
R4/RRR4-24/3	1775.636	1775.858	-125.269	0.566	2295.619	0.427	32	0.312	K.FEANRDVDNPDVIDR.L
R4/RRR4-24/2	1414.289	1414.542	-179.342	0.514	1726.947	0.573	18	0.285	K.GIEIIYNYGKED.-
R4/RRR4-24/2	1415.104	1414.542	-310.231	0.525	1607.138	0.587	18	0.253	K.GIEIIYNYGKED.-
R4/RRR4-24/2	1415.049	1414.542	-349.439	0.536	1591.277	0.584	18	0.247	K.GIEIIYNYGKED.-
R4/RRR4-25/3	1775.399	1775.858	-259.040	0.496	1819.307	0.387	29	0.201	K.FEANRDVDNPDVIDR.L
R4/RRR4-24/2	1193.873	1194.276	-338.696	0.549	1136.742	0.483	17	0.194	R.LIDDAEAQYR.N
R4/RRR4-24/3	1622.362	1622.763	-247.929	0.413	1608.591	0.452	28	0.188	R.HLFYQDASDLREK.F
R4/RRR4-25/3	1622.435	1622.763	-202.979	0.489	1570.834	0.458	26	0.187	R.HLFYQDASDLREK.F
R4/RRR4-24/2	1193.920	1194.276	-299.509	0.524	1110.973	0.445	17	0.185	R.LIDDAEAQYR.N
R4/RRR4-25/2	1194.052	1194.276	-187.913	0.534	1118.393	0.441	17	0.185	R.LIDDAEAQYR.N
R4/RRR4-25/3	1622.036	1622.763	-1068.105	0.446	1580.431	0.448	27	0.184	R.HLFYQDASDLREK.F
R4/RRR4-24/3	1623.307	1622.763	-281.763	0.490	1472.335	0.492	28	0.183	R.HLFYQDASDLREK.F
R4/RRR4-24/2	1364.462	1365.476	-1480.461	0.405	1252.281	0.394	17	0.182	R.HLFYQDASDLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	1365.187	1365.476	-212.249	0.382	1252.750	0.378	17	0.179	R.HLFYQDASDLR.E
R4/RRR4-24/2	1365.062	1365.476	-303.845	0.351	1181.217	0.406	17	0.177	R.HLFYQDASDLR.E
R4/RRR4-25/2	1193.946	1194.276	-276.942	0.498	1133.704	0.391	17	0.176	R.LIDDAEAQYR.N
R4/RRR4-24/2	1193.383	1194.276	-1590.816	0.417	1089.885	0.392	17	0.173	R.LIDDAEAQYR.N
R4/RRR4-24/2	1157.978	1158.201	-192.922	0.458	1098.673	0.367	16	0.169	R.DVDNPDVIDR.L
R4/RRR4-25/2	1157.395	1158.201	-1564.326	0.314	1024.796	0.418	15	0.168	R.DVDNPDVIDR.L
R4/RRR4-25/2	1193.222	1194.276	-1726.579	0.335	951.670	0.385	16	0.162	R.LIDDAEAQYR.N
R4/RRR4-25/3	1424.505	1424.632	-89.708	0.525	1499.010	0.413	25	0.161	R.ALKDTLNWAVHR.H
R4/RRR4-24/2	1157.980	1158.201	-191.335	0.471	896.878	0.354	15	0.157	R.DVDNPDVIDR.L
R4/RRR4-24/2	1157.740	1158.201	-398.760	0.419	797.588	0.386	14	0.157	R.DVDNPDVIDR.L
R4/RRR4-24/3	1424.502	1424.632	-91.771	0.544	1503.759	0.393	24	0.156	R.ALKDTLNWAVHR.H
R4/RRR4-24/3	1622.624	1622.763	-86.150	0.493	1245.702	0.488	27	0.155	R.HLFYQDASDLREK.F
R4/RRR4-25/2	1157.805	1158.201	-342.373	0.357	868.107	0.315	15	0.151	R.DVDNPDVIDR.L
R4/RRR4-25/3	1424.467	1424.632	-116.657	0.478	1425.998	0.334	24	0.129	R.ALKDTLNWAVHR.H
R4/RRR4-25/3	1424.388	1424.632	-171.976	0.523	1360.645	0.309	23	0.117	R.ALKDTLNWAVHR.H
R4/RRR4-25/3	1622.883	1622.763	74.333	0.460	813.449	0.408	22	0.105	R.HLFYQDASDLREK.F
R4/RRR4-25/3	1775.545	1775.858	-176.373	0.366	925.926	0.302	23	0.092	K.FEANRDVDNPDVIDR.L
R4/RRR4-3/2	1742.163	1742.911	-1006.220	0.535	2362.762	0.554	23	0.374	K.GLKDETYSGDGIALFR.I
R4/RRR4-3/2	1651.369	1650.815	-270.888	0.545	2022.400	0.534	24	0.304	R.ASALAALSSAFNPSSQK.N
R4/RRR4-3/2	1293.099	1293.320	-171.342	0.509	2082.257	0.437	21	0.287	K.DSSQDEAGTAAIK.T
R4/RRR4-3/2	1651.430	1650.815	-233.585	0.507	1892.635	0.504	24	0.275	R.ASALAALSSAFNPSSQK.N
R4/RRR4-3/2	1292.912	1293.320	-316.255	0.434	1855.259	0.374	20	0.238	K.DSSQDEAGTAAIK.T
R4/RRR4-4/2	1651.283	1650.815	284.676	0.483	1592.365	0.448	23	0.222	R.ASALAALSSAFNPSSQK.N
R4/RRR4-3/2	1354.437	1354.486	-36.575	0.421	1354.546	0.505	17	0.211	K.VVEGNEPCFFR.T
R4/RRR4-4/2	1651.713	1650.815	-61.867	0.498	1343.232	0.477	22	0.202	R.ASALAALSSAFNPSSQK.N
R4/RRR4-4/2	1650.283	1650.815	-931.220	0.406	1272.394	0.449	21	0.189	R.ASALAALSSAFNPSSQK.N
R4/RRR4-3/2	1292.408	1293.320	-1483.990	0.306	1412.825	0.324	21	0.180	K.DSSQDEAGTAAIK.T
R4/RRR4-3/2	1873.543	1872.306	126.870	0.438	856.026	0.466	17	0.162	K.EPPQFIALFQPMVILK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1873.820	1872.306	-259.834	0.479	943.985	0.415	18	0.160	K.EPPQFIALFQPMVILK.G
R4/RRR4-3/2	1023.394	1023.211	179.623	0.393	1072.923	0.323	14	0.159	K.ALEAIQHLK.E
R4/RRR4-3/3	1933.181	1932.170	5.876	0.568	891.168	0.593	33	0.152	R.KAASAAVEEFIATQNRPK.T
R4/RRR4-3/3	1862.667	1862.030	-195.304	0.475	1569.826	0.340	30	0.149	R.SSLNHDDVFILDTEKK.I
R4/RRR4-4/2	1292.807	1293.320	-1173.370	0.320	738.306	0.322	18	0.146	K.DSSQDEAGTAAIK.T
R4/RRR4-3/2	1649.931	1650.815	-1144.912	0.311	705.210	0.352	18	0.144	R.ASALAALSSAFNPSSQK.N
R4/RRR4-4/3	1862.025	1862.030	-2.710	0.402	1394.253	0.343	28	0.131	R.SSLNHDDVFILDTEKK.I
R4/RRR4-2/2	1890.013	1888.305	-154.925	0.282	552.461	0.221	14	0.130	K.EPPQFIALFQPM*VILK.G
R4/RRR4-3/3	1743.954	1742.911	24.873	0.449	1267.815	0.372	29	0.126	K.GLKDETYSGDGIALFR.I
R4/RRR4-3/3	1282.789	1282.556	182.328	0.469	1396.456	0.306	23	0.119	R.IQDFKPVPLPK.A
R4/RRR4-3/3	1933.131	1932.170	-20.250	0.497	695.943	0.490	30	0.113	R.KAASAAVEEFIATQNRPK.T
R4/RRR4-3/3	1650.591	1650.815	-135.798	0.327	1058.267	0.363	27	0.105	R.ASALAALSSAFNPSSQK.N
R4/RRR4-3/3	1650.974	1650.815	96.726	0.384	946.216	0.379	26	0.102	R.ASALAALSSAFNPSSQK.N
R4/RRR4-3/3	1932.096	1932.170	-38.479	0.482	639.274	0.402	29	0.097	R.KAASAAVEEFIATQNRPK.T
R4/RRR4-3/3	1283.037	1282.556	375.819	0.434	1127.978	0.279	22	0.095	R.IQDFKPVPLPK.A
R4/RRR4-3/3	1282.871	1282.556	246.451	0.425	1112.432	0.267	22	0.092	R.IQDFKPVPLPK.A
R4/RRR4-4/3	1861.542	1862.030	-263.167	0.289	1229.288	0.195	25	0.086	R.SSLNHDDVFILDTEKK.I
R4/RRR4-13/2	1566.242	1565.732	-313.813	0.544	1981.942	0.553	23	0.306	R.LAIAGM*GTDENSLTR.I
R4/RRR4-13/2	1565.518	1565.732	-137.129	0.501	1761.739	0.567	22	0.276	R.LAIAGM*GTDENSLTR.I
R4/RRR4-13/2	1564.551	1565.732	-1397.850	0.400	1733.372	0.441	22	0.238	R.LAIAGM*GTDENSLTR.I
R4/RRR4-13/2	1369.049	1369.416	-269.155	0.475	1672.524	0.453	19	0.236	R.SITDEISGDFER.A
R4/RRR4-13/2	1369.147	1369.416	-197.059	0.440	1669.508	0.402	19	0.223	R.SITDEISGDFER.A
R4/RRR4-13/2	1030.625	1031.225	-1557.400	0.408	1366.469	0.492	15	0.210	R.VLVEIACAR.G
R4/RRR4-13/2	958.826	959.127	-314.844	0.523	1248.193	0.509	15	0.208	R.GPAQLFAVR.Q
R4/RRR4-13/2	959.026	959.127	-105.276	0.545	1129.271	0.531	14	0.201	R.GPAQLFAVR.Q
R4/RRR4-13/2	1030.462	1031.225	-1716.030	0.437	1304.006	0.441	15	0.196	R.VLVEIACAR.G
R4/RRR4-13/2	1383.268	1384.605	-1694.981	0.342	1243.718	0.489	16	0.192	R.AVILWTLDPAER.D
R4/RRR4-13/2	1057.943	1058.171	-215.793	0.507	1318.003	0.392	16	0.188	R.DAVLANEVAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1057.857	1058.171	-297.523	0.454	1389.949	0.358	16	0.187	R.DAVLANEVAR.K
R4/RRR4-13/2	1368.413	1369.416	-1468.223	0.346	1417.715	0.347	19	0.186	R.SITDEISGDFER.A
R4/RRR4-13/2	1057.751	1058.171	-397.562	0.416	1196.845	0.384	16	0.177	R.DAVLANEVAR.K
R4/RRR4-13/2	1349.858	1350.418	-1158.608	0.499	1209.817	0.378	17	0.177	R.YNDEYGHPINK.D
R4/RRR4-13/2	1146.265	1145.419	-134.650	0.377	711.615	0.499	17	0.165	K.LLVPLISAYR.Y
R4/RRR4-13/2	1384.177	1384.605	-310.087	0.247	535.997	0.316	12	0.135	R.AVILWTLDPAER.D
R4/RRR4-14/2	1819.471	1820.040	-864.681	0.541	2121.621	0.575	23	0.333	K.SAQDIALADLPTTHPIR.L
R4/RRR4-14/2	1819.518	1820.040	-839.088	0.556	1982.616	0.569	24	0.308	K.SAQDIALADLPTTHPIR.L
R4/RRR4-14/2	1819.524	1820.040	-835.586	0.549	1911.796	0.576	24	0.299	K.SAQDIALADLPTTHPIR.L
R4/RRR4-14/2	1337.354	1337.504	-112.206	0.577	1709.292	0.581	20	0.276	R.KEAAENTLVAYK.S
R4/RRR4-15/2	1820.330	1820.040	159.837	0.565	1791.288	0.561	23	0.276	K.SAQDIALADLPTTHPIR.L
R4/RRR4-14/2	1337.210	1337.504	-219.894	0.542	1757.766	0.555	20	0.275	R.KEAAENTLVAYK.S
R4/RRR4-15/2	1819.496	1820.040	-850.874	0.525	1766.126	0.568	23	0.275	K.SAQDIALADLPTTHPIR.L
R4/RRR4-15/2	1819.303	1820.040	-957.565	0.492	1753.944	0.528	23	0.262	K.SAQDIALADLPTTHPIR.L
R4/RRR4-14/2	1337.077	1337.504	-320.277	0.516	1490.177	0.506	19	0.228	R.KEAAENTLVAYK.S
R4/RRR4-14/2	1051.951	1052.163	-202.008	0.444	1305.312	0.595	16	0.226	R.GNEAYVASIK.E
R4/RRR4-15/2	1419.247	1419.563	-223.143	0.499	1517.035	0.468	20	0.222	R.IISSIEQKEESR.G
R4/RRR4-14/2	1640.159	1639.832	200.164	0.511	1346.501	0.545	24	0.220	K.LLDSHLVPSATAAESK.V
R4/RRR4-14/2	1419.490	1419.563	-51.287	0.537	1346.565	0.524	19	0.217	R.IISSIEQKEESR.G
R4/RRR4-15/2	1418.755	1419.563	-1278.134	0.470	1423.100	0.486	19	0.216	R.IISSIEQKEESR.G
R4/RRR4-14/2	1419.098	1419.563	-328.426	0.449	1354.981	0.490	19	0.210	R.IISSIEQKEESR.G
R4/RRR4-13/2	1419.094	1419.563	-331.274	0.477	1411.080	0.460	19	0.209	R.IISSIEQKEESR.G
R4/RRR4-14/2	1419.189	1419.563	-264.563	0.471	1348.584	0.476	19	0.207	R.IISSIEQKEESR.G
R4/RRR4-13/2	1419.066	1419.563	-351.211	0.480	1402.972	0.450	19	0.206	R.IISSIEQKEESR.G
R4/RRR4-14/2	1318.529	1319.400	-1423.669	0.356	1584.012	0.372	18	0.206	K.TADVGELTVEER.N
R4/RRR4-15/2	1639.358	1639.832	-289.826	0.469	1270.332	0.506	23	0.204	K.LLDSHLVPSATAAESK.V
R4/RRR4-14/2	1639.423	1639.832	-249.934	0.463	1262.535	0.505	23	0.203	K.LLDSHLVPSATAAESK.V
R4/RRR4-15/2	1319.120	1319.400	-213.443	0.474	1456.213	0.413	18	0.203	K.TADVGELTVEER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1319.155	1319.400	-186.706	0.496	1405.632	0.430	18	0.202	K.TADVGELTVEER.N
R4/RRR4-15/2	1420.109	1419.563	-320.519	0.483	1268.664	0.478	19	0.200	R.IISSIEQKEESR.G
R4/RRR4-15/2	1318.487	1319.400	-1455.659	0.351	1501.617	0.381	18	0.199	K.TADVGELTVEER.N
R4/RRR4-15/2	1319.099	1319.400	-228.854	0.465	1357.124	0.436	18	0.198	K.TADVGELTVEER.N
R4/RRR4-15/2	1639.634	1639.832	-121.240	0.481	1199.752	0.495	23	0.196	K.LLDSHLVPSATAAESK.V
R4/RRR4-15/2	1052.081	1052.163	-78.159	0.388	1059.065	0.561	15	0.195	R.GNEAYVASIK.E
R4/RRR4-14/2	1319.051	1319.400	-265.434	0.489	1419.422	0.391	18	0.195	K.TADVGELTVEER.N
R4/RRR4-15/2	1639.354	1639.832	-292.291	0.455	1158.593	0.509	22	0.194	K.LLDSHLVPSATAAESK.V
R4/RRR4-14/2	1419.083	1419.563	-339.214	0.450	1192.654	0.458	18	0.189	R.IISSIEQKEESR.G
R4/RRR4-14/2	1051.492	1052.163	-1593.213	0.396	970.916	0.553	15	0.188	R.GNEAYVASIK.E
R4/RRR4-14/2	1052.031	1052.163	-125.995	0.479	964.927	0.528	15	0.187	R.GNEAYVASIK.E
R4/RRR4-14/2	1639.303	1639.832	-935.664	0.488	1062.236	0.478	22	0.182	K.LLDSHLVPSATAAESK.V
R4/RRR4-15/2	1051.967	1052.163	-186.641	0.499	805.345	0.524	14	0.177	R.GNEAYVASIK.E
R4/RRR4-13/2	1418.994	1419.563	-1109.320	0.443	1166.781	0.378	18	0.174	R.IISSIEQKEESR.G
R4/RRR4-15/2	1051.554	1052.163	-1534.553	0.399	661.443	0.537	14	0.169	R.GNEAYVASIK.E
R4/RRR4-14/2	1209.099	1209.331	-192.562	0.364	905.926	0.438	16	0.166	K.EAAENTLVAYK.S
R4/RRR4-15/2	1210.190	1209.331	-116.712	0.435	836.347	0.451	15	0.166	K.EAAENTLVAYK.S
R4/RRR4-14/2	1208.949	1209.331	-317.053	0.392	771.827	0.454	15	0.162	K.EAAENTLVAYK.S
R4/RRR4-15/2	1210.212	1209.331	-98.702	0.385	859.452	0.375	16	0.157	K.EAAENTLVAYK.S
R4/RRR4-15/3	1820.893	1820.040	-80.871	0.416	1443.091	0.405	31	0.154	K.SAQDIALADLPTTHPIR.L
R4/RRR4-14/2	1419.290	1419.563	-193.202	0.385	648.541	0.367	16	0.151	R.IISSIEQKEESR.G
R4/RRR4-14/2	1420.075	1419.563	-345.012	0.455	453.720	0.389	15	0.151	R.IISSIEQKEESR.G
R4/RRR4-14/2	1208.445	1209.331	-1565.112	0.287	620.152	0.397	14	0.148	K.EAAENTLVAYK.S
R4/RRR4-14/2	1641.004	1639.832	105.454	0.395	482.714	0.388	15	0.143	K.LLDSHLVPSATAAESK.V
R4/RRR4-14/3	1640.141	1639.832	189.109	0.343	1412.125	0.359	32	0.134	K.LLDSHLVPSATAAESK.V
R4/RRR4-14/3	1337.667	1337.504	122.493	0.496	994.611	0.485	26	0.131	R.KEAAENTLVAYK.S
R4/RRR4-15/3	1338.807	1337.504	227.147	0.500	985.569	0.475	26	0.128	R.KEAAENTLVAYK.S
R4/RRR4-15/3	1639.685	1639.832	-89.733	0.368	1273.842	0.374	30	0.126	K.LLDSHLVPSATAAESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/3	1639.336	1639.832	-303.282	0.367	1013.718	0.349	27	0.102	K.LLDSHLVPSATAAESK.V
R4/RRR4-14/3	1819.601	1820.040	-241.678	0.339	876.577	0.326	27	0.093	K.SAQDIALADLPTTHPIR.L
R4/RRR4-15/3	1821.488	1820.040	246.641	0.280	655.994	0.321	27	0.088	K.SAQDIALADLPTTHPIR.L
R4/RRR4-15/3	1820.689	1820.040	-193.149	0.307	758.952	0.280	30	0.085	K.SAQDIALADLPTTHPIR.L
R4/RRR4-15/3	1337.166	1337.504	-253.516	0.436	355.097	0.368	18	0.084	-.KEAAENTLVAYK.-
R4/RRR4-14/3	1639.268	1639.832	-956.942	0.305	719.723	0.270	25	0.083	K.LLDSHLVPSATAAESK.V
R4/RRR4-14/3	1818.374	1820.040	-2022.024	0.297	791.001	0.167	29	0.078	K.SAQDIALADLPTTHPIR.L
R4/RRR4-17/3	1829.303	1828.957	189.533	0.578	2037.042	0.493	36	0.291	K.AAVGHPDTLGDCPFSQR.V
R4/RRR4-17/3	1828.399	1828.957	-854.841	0.535	1661.511	0.477	33	0.212	K.AAVGHPDTLGDCPFSQR.V
R4/RRR4-17/3	1498.733	1498.753	-13.048	0.560	1661.120	0.433	29	0.190	K.LYHLQVALEHFK.G
R4/RRR4-17/2	1828.224	1828.957	-951.018	0.527	1034.686	0.529	22	0.188	K.AAVGHPDTLGDCPFSQR.V
R4/RRR4-17/3	1828.684	1828.957	-149.555	0.567	1395.869	0.512	32	0.184	K.AAVGHPDTLGDCPFSQR.V
R4/RRR4-17/2	1893.658	1894.114	-241.271	0.527	787.240	0.611	20	0.183	K.YPTPSLVTPPEYASVGSK.I
R4/RRR4-17/2	1893.502	1894.114	-854.023	0.528	735.274	0.586	18	0.173	K.YPTPSLVTPPEYASVGSK.I
R4/RRR4-17/2	1828.396	1828.957	-856.375	0.499	701.368	0.537	20	0.168	K.AAVGHPDTLGDCPFSQR.V
R4/RRR4-17/2	1892.711	1894.114	-1273.237	0.446	711.928	0.544	19	0.166	K.YPTPSLVTPPEYASVGSK.I
R4/RRR4-17/2	1616.367	1616.885	-941.972	0.486	1121.247	0.368	17	0.166	K.LIDVQNKPDWFLK.I
R4/RRR4-17/2	1616.626	1616.885	-160.758	0.502	1111.513	0.361	17	0.163	K.LIDVQNKPDWFLK.I
R4/RRR4-17/3	1122.928	1122.301	-333.066	0.536	1490.754	0.421	21	0.163	K.EHLIAGWAPK.V
R4/RRR4-17/2	990.711	990.095	-388.069	0.367	813.429	0.463	13	0.163	K.VPVFNGGDGK.W
R4/RRR4-17/2	1828.214	1828.957	-956.247	0.495	664.890	0.510	19	0.162	K.AAVGHPDTLGDCPFSQR.V
R4/RRR4-17/2	1265.212	1264.488	-218.860	0.430	974.763	0.323	16	0.156	K.IFSCFTTFLK.S
R4/RRR4-17/2	1121.799	1122.301	-1343.290	0.344	433.543	0.517	14	0.156	K.EHLIAGWAPK.V
R4/RRR4-17/3	1392.040	1392.630	-1146.114	0.452	1446.540	0.410	26	0.155	K.AAKEHLIAGWAPK.V
R4/RRR4-17/3	1393.219	1392.630	-295.956	0.461	1457.199	0.405	26	0.155	K.AAKEHLIAGWAPK.V
R4/RRR4-17/2	990.936	990.095	-160.761	0.365	608.176	0.442	12	0.153	K.VPVFNGGDGK.W
R4/RRR4-17/2	1264.075	1264.488	-327.150	0.362	988.117	0.240	16	0.146	K.IFSCFTTFLK.S
R4/RRR4-17/2	1616.483	1616.885	-249.163	0.472	991.152	0.287	16	0.146	K.LIDVQNKPDWFLK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/3	1498.543	1498.753	-140.753	0.519	1325.842	0.426	27	0.145	K.LYHLQVALEHFK.G
R4/RRR4-17/2	1122.305	1122.301	3.752	0.390	228.259	0.408	11	0.142	-.EHLIAGWAPK.-
R4/RRR4-17/2	989.305	990.095	-1814.213	0.253	262.274	0.308	12	0.141	-.VPVFNGGDGK.-
R4/RRR4-17/2	989.985	990.095	-111.321	0.319	469.481	0.270	12	0.140	K.VPVFNGGDGK.W
R4/RRR4-17/3	1498.170	1498.753	-1059.488	0.480	1317.088	0.406	26	0.138	K.LYHLQVALEHFK.G
R4/RRR4-17/3	1122.505	1122.301	182.566	0.516	1441.294	0.307	21	0.123	K.EHLIAGWAPK.V
R4/RRR4-17/3	1122.050	1122.301	-224.590	0.414	1244.212	0.309	20	0.108	-.EHLIAGWAPK.-
R4/RRR4-17/3	1393.587	1392.630	-31.253	0.328	492.246	0.320	17	0.053	-.AAKEHLIAGWAPK.-
R4/RRR4-11/2	1497.078	1497.546	-313.772	0.518	1938.599	0.567	22	0.304	R.SALDEVTDTGAFDR.S
R4/RRR4-11/2	1740.273	1739.942	190.970	0.629	2051.802	0.498	23	0.300	R.LYEALDKCEEILSR.Q
R4/RRR4-11/2	1739.423	1739.942	-875.402	0.599	1952.262	0.526	22	0.293	R.LYEALDKCEEILSR.Q
R4/RRR4-11/2	1497.170	1497.546	-251.601	0.534	1845.627	0.557	22	0.287	R.SALDEVTDTGAFDR.S
R4/RRR4-11/3	1887.971	1888.159	-99.982	0.545	1992.637	0.496	35	0.284	K.GLDHAIGFTSVKPIFER.T
R4/RRR4-11/2	1739.341	1739.942	-923.241	0.596	1841.642	0.529	22	0.278	R.LYEALDKCEEILSR.Q
R4/RRR4-11/3	1888.547	1888.159	206.181	0.568	1825.691	0.546	32	0.275	K.GLDHAIGFTSVKPIFER.T
R4/RRR4-11/2	1540.152	1539.666	316.824	0.575	1670.993	0.496	21	0.247	R.YICGNQLTEADVR.L
R4/RRR4-11/2	1496.707	1497.546	-1232.017	0.410	1675.524	0.474	21	0.239	R.SALDEVTDTGAFDR.S
R4/RRR4-11/2	1361.024	1361.484	-338.571	0.450	1688.345	0.454	19	0.237	K.TVVNNESSEIIR.M
R4/RRR4-11/2	1361.149	1361.484	-246.700	0.442	1672.209	0.460	19	0.237	K.TVVNNESSEIIR.M
R4/RRR4-11/2	1540.202	1539.666	-301.966	0.578	1520.164	0.488	20	0.226	R.YICGNQLTEADVR.L
R4/RRR4-11/2	1540.229	1539.666	-284.154	0.603	1491.579	0.500	20	0.226	R.YICGNQLTEADVR.L
R4/RRR4-11/2	1362.096	1361.484	-285.450	0.487	1350.565	0.524	18	0.216	K.TVVNNESSEIIR.M
R4/RRR4-11/3	1888.884	1888.159	-145.858	0.526	1689.746	0.429	32	0.198	K.GLDHAIGFTSVKPIFER.T
R4/RRR4-11/2	1362.003	1361.484	-353.879	0.479	1013.207	0.486	18	0.183	K.TVVNNESSEIIR.M
R4/RRR4-11/2	1362.051	1361.484	-318.720	0.488	991.784	0.431	18	0.173	K.TVVNNESSEIIR.M
R4/RRR4-11/2	1326.097	1326.501	-305.505	0.466	1239.329	0.338	17	0.171	R.M*LNTEFNEIAK.N
R4/RRR4-11/3	1256.542	1255.403	111.498	0.478	1380.051	0.486	22	0.169	R.FDEVYAVHFK.C
R4/RRR4-11/2	1336.003	1336.432	-322.551	0.443	1201.278	0.331	18	0.169	K.KQEPYDEAVTR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1336.117	1336.432	-236.660	0.489	1160.629	0.342	18	0.169	K.KQEPYDEAVTR.L
R4/RRR4-11/3	1255.007	1255.403	-316.648	0.425	1568.738	0.416	24	0.167	R.FDEVYAVHFK.C
R4/RRR4-11/2	1336.146	1336.432	-214.755	0.450	1049.876	0.327	17	0.160	K.KQEPYDEAVTR.L
R4/RRR4-11/3	1255.645	1255.403	193.534	0.473	1428.195	0.412	24	0.150	R.FDEVYAVHFK.C
R4/RRR4-11/2	1362.782	1361.484	219.791	0.261	471.749	0.259	14	0.139	K.TVVNNESSEIIR.M
R4/RRR4-11/3	1497.424	1497.546	-81.865	0.406	701.245	0.473	23	0.106	R.SALDEVTDTGAFDR.S
R4/RRR4-12/3	1337.086	1336.432	-259.849	0.430	1194.571	0.288	22	0.100	K.KQEPYDEAVTR.L
R4/RRR4-11/3	1336.032	1336.432	-300.972	0.433	815.738	0.334	20	0.092	K.KQEPYDEAVTR.L
R4/RRR4-12/3	1336.962	1336.432	-352.733	0.359	1176.399	0.220	21	0.086	K.KQEPYDEAVTR.L
R4/RRR4-12/3	1982.194	1983.123	-975.611	0.499	1517.308	0.375	31	0.159	-.TRPSVTFTNEETEELTK.-
R4/RRR4-16/1	994.489	995.065	-1589.292	0.207	826.138	0.256	13	0.681	K.LSELGFAEE.-
R4/RRR4-15/1	994.437	995.065	-1641.640	0.194	544.387	0.343	11	0.565	K.LSELGFAEE.-
R4/RRR4-16/1	994.445	995.065	-1633.870	0.179	489.253	0.279	10	0.548	K.LSELGFAEE.-
R4/RRR4-16/3	1820.843	1820.945	-55.725	0.524	2656.475	0.500	36	0.461	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/3	1820.409	1820.945	-846.016	0.593	2264.805	0.530	36	0.365	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-16/2	1820.389	1820.945	-857.317	0.577	2214.630	0.588	26	0.355	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/3	1821.737	1820.945	-114.303	0.575	2013.514	0.568	33	0.326	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-16/2	1820.378	1820.945	-863.376	0.569	2061.101	0.575	27	0.324	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/2	1820.432	1820.945	-833.219	0.561	1947.560	0.588	26	0.309	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-16/3	1820.853	1820.945	-50.681	0.498	1992.167	0.521	33	0.298	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/2	1820.403	1820.945	-849.105	0.570	1903.453	0.558	27	0.294	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/2	1821.289	1820.945	189.736	0.582	1711.784	0.585	26	0.273	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/2	1534.179	1534.657	-312.728	0.462	1495.132	0.535	21	0.233	R.LAWHSAGTFDVSSR.T
R4/RRR4-15/2	1534.319	1534.657	-221.250	0.466	1547.365	0.506	21	0.233	R.LAWHSAGTFDVSSR.T
R4/RRR4-16/3	1534.805	1534.657	96.428	0.440	1793.585	0.459	29	0.224	R.LAWHSAGTFDVSSR.T
R4/RRR4-15/3	1820.259	1820.945	-929.021	0.548	1621.424	0.515	30	0.222	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/2	1533.998	1534.657	-1085.218	0.442	1408.858	0.529	21	0.222	R.LAWHSAGTFDVSSR.T
R4/RRR4-15/2	1310.173	1310.398	-172.287	0.486	1537.582	0.445	20	0.219	R.LPDATQGSDHLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1310.185	1310.398	-162.940	0.487	1520.498	0.420	20	0.212	R.LPDATQGSDHLR.Q
R4/RRR4-15/2	1309.931	1310.398	-357.946	0.481	1516.643	0.418	20	0.211	R.LPDATQGSDHLR.Q
R4/RRR4-16/2	1309.881	1310.398	-1161.627	0.473	1364.383	0.427	20	0.199	R.LPDATQGSDHLR.Q
R4/RRR4-16/2	1309.610	1310.398	-1369.604	0.484	1335.455	0.429	20	0.197	R.LPDATQGSDHLR.Q
R4/RRR4-15/2	1310.316	1310.398	-62.849	0.470	1329.218	0.429	19	0.196	R.LPDATQGSDHLR.Q
R4/RRR4-15/2	1600.169	1600.751	-991.755	0.455	761.068	0.527	23	0.175	K.SYPTVSDEYLAAVGK.A
R4/RRR4-16/3	1821.109	1820.945	90.715	0.516	1275.926	0.523	28	0.174	K.NPGEQSHAANAGLDIAVR.L
R4/RRR4-15/2	1601.184	1600.751	271.485	0.447	452.134	0.583	20	0.168	K.SYPTVSDEYLAAVGK.A
R4/RRR4-15/2	1601.226	1600.751	297.552	0.403	660.873	0.517	23	0.168	K.SYPTVSDEYLAAVGK.A
R4/RRR4-15/3	1534.932	1534.657	179.577	0.474	1543.699	0.401	27	0.164	R.LAWHSAGTFDVSSR.T
R4/RRR4-15/2	1575.178	1574.870	196.664	0.526	601.474	0.424	19	0.156	K.ALM*ADPAFRPLVEK.Y
R4/RRR4-15/2	1558.615	1558.870	-164.149	0.466	768.898	0.354	19	0.151	K.ALMADPAFRPLVEK.Y
R4/RRR4-16/3	1534.388	1534.657	-175.966	0.489	1245.281	0.462	26	0.148	R.LAWHSAGTFDVSSR.T
R4/RRR4-15/2	1574.370	1574.870	-318.063	0.423	470.174	0.396	17	0.147	-.ALM*ADPAFRPLVEK.-
R4/RRR4-15/2	1558.097	1558.870	-1141.277	0.392	738.812	0.309	19	0.146	K.ALMADPAFRPLVEK.Y
R4/RRR4-16/2	1599.450	1600.751	-1442.922	0.300	322.693	0.399	17	0.145	K.SYPTVSDEYLAAVGK.A
R4/RRR4-15/2	1574.356	1574.870	-964.329	0.404	469.957	0.352	17	0.144	-.ALM*ADPAFRPLVEK.-
R4/RRR4-15/2	1557.956	1558.870	-1232.071	0.373	737.937	0.280	19	0.143	K.ALMADPAFRPLVEK.Y
R4/RRR4-16/2	1599.580	1600.751	-1360.980	0.294	161.591	0.449	13	0.138	-.SYPTVSDEYLAAVGK.-
R4/RRR4-15/3	1534.685	1534.657	18.053	0.477	1097.798	0.463	25	0.134	R.LAWHSAGTFDVSSR.T
R4/RRR4-16/3	1535.408	1534.657	-163.210	0.502	1164.340	0.440	26	0.134	R.LAWHSAGTFDVSSR.T
R4/RRR4-15/3	1533.634	1534.657	-1323.550	0.455	1039.096	0.425	23	0.121	R.LAWHSAGTFDVSSR.T
R4/RRR4-15/3	1310.453	1310.398	41.883	0.448	708.703	0.460	24	0.106	-.LPDATQGSDHLR.-
R4/RRR4-16/3	1310.561	1310.398	124.699	0.501	568.887	0.452	22	0.106	R.LPDATQGSDHLR.Q
R4/RRR4-17/3	1310.553	1310.398	118.674	0.346	582.857	0.452	23	0.102	R.LPDATQGSDHLR.Q
R4/RRR4-16/3	1310.478	1310.398	61.362	0.434	597.781	0.418	22	0.097	-.LPDATQGSDHLR.-
R4/RRR4-15/3	1310.778	1310.398	290.290	0.327	571.863	0.276	20	0.088	R.LPDATQGSDHLR.Q
R4/RRR4-2/2	1762.570	1762.040	-267.204	0.591	2645.417	0.486	24	0.403	K.LVENYAELLASQGLLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1761.656	1762.040	-218.831	0.493	2141.191	0.418	22	0.287	K.LVENYAELLASQGLLK.T
R4/RRR4-2/2	1762.547	1762.040	-280.336	0.575	2022.301	0.481	22	0.286	K.LVENYAELLASQGLLK.T
R4/RRR4-3/2	1761.476	1762.040	-890.787	0.495	2027.774	0.442	22	0.277	K.LVENYAELLASQGLLK.T
R4/RRR4-2/2	1939.515	1939.115	206.830	0.527	1597.381	0.557	21	0.246	K.SVGSSAQAEISYLTWNPK.F
R4/RRR4-3/2	1761.369	1762.040	-951.733	0.391	1793.808	0.359	20	0.223	K.LVENYAELLASQGLLK.T
R4/RRR4-2/2	1318.135	1318.416	-213.323	0.444	1390.428	0.436	20	0.201	K.LNSGDISPNVSSK.L
R4/RRR4-2/2	1792.641	1790.989	-194.627	0.536	1197.262	0.488	19	0.189	R.LASGAEQGELCIWDLK.N
R4/RRR4-2/2	1318.192	1318.416	-170.124	0.472	985.386	0.436	18	0.171	K.LNSGDISPNVSSK.L
R4/RRR4-2/2	1318.016	1318.416	-303.822	0.456	1029.635	0.412	18	0.169	K.LNSGDISPNVSSK.L
R4/RRR4-2/2	1499.466	1498.793	-218.881	0.462	758.683	0.424	20	0.160	K.VSAELKPVIATLTR.L
R4/RRR4-2/2	1160.425	1159.315	95.528	0.346	948.759	0.335	15	0.153	K.GAVNLCLAANR.M
R4/RRR4-2/2	1498.402	1498.793	-261.526	0.390	571.636	0.405	18	0.150	K.VSAELKPVIATLTR.L
R4/RRR4-2/2	1160.394	1159.315	68.519	0.292	827.687	0.296	15	0.144	K.GAVNLCLAANR.M
R4/RRR4-2/2	1498.462	1498.793	-221.642	0.340	656.978	0.248	19	0.139	K.VSAELKPVIATLTR.L
R4/RRR4-2/2	1160.401	1159.315	74.849	0.323	517.341	0.199	13	0.127	-.GAVNLCLAANR.-
R4/RRR4-2/3	1499.616	1498.793	-118.077	0.415	1087.065	0.410	25	0.119	K.VSAELKPVIATLTR.L
R4/RRR4-2/3	1494.187	1494.592	-271.328	0.463	746.717	0.499	22	0.119	R.NQKPLTSFSDSNR.T
R4/RRR4-2/3	1498.803	1498.793	7.007	0.395	1080.478	0.402	24	0.117	K.VSAELKPVIATLTR.L
R4/RRR4-2/3	1330.781	1330.514	201.053	0.393	799.848	0.452	19	0.107	-.SIQHALVVGDYK.-
R4/RRR4-2/3	1494.561	1494.592	-20.335	0.431	575.098	0.437	22	0.103	R.NQKPLTSFSDSNR.T
R4/RRR4-2/3	1418.163	1418.663	-353.602	0.365	1158.538	0.308	25	0.101	R.KIPGVVAASSFDVK.I
R4/RRR4-3/3	1494.599	1494.592	5.225	0.441	760.045	0.387	22	0.100	R.NQKPLTSFSDSNR.T
R4/RRR4-2/3	1493.668	1494.592	-1291.502	0.429	528.817	0.392	20	0.098	R.NQKPLTSFSDSNR.T
R4/RRR4-7/3	1493.963	1494.592	-1093.328	0.349	660.880	0.390	20	0.097	R.NQKPLTSFSDSNR.T
R4/RRR4-3/3	1494.435	1494.592	-105.255	0.393	787.110	0.354	21	0.096	R.NQKPLTSFSDSNR.T
R4/RRR4-2/3	1761.976	1762.040	-36.184	0.351	1328.864	0.222	26	0.095	K.LVENYAELLASQGLLK.T
R4/RRR4-1/3	1500.234	1498.793	294.886	0.399	742.269	0.358	21	0.093	K.VSAELKPVIATLTR.L
R4/RRR4-2/3	1498.504	1498.793	-193.252	0.365	777.675	0.325	20	0.090	K.VSAELKPVIATLTR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/3	1330.458	1330.514	-42.398	0.364	727.935	0.343	18	0.088	K.SIQHALVVGDYK.G
R4/RRR4-9/2	1650.247	1650.767	-923.746	0.533	3000.901	0.558	26	0.522	K.SVIGETGSDVTTDQLK.E
R4/RRR4-9/2	1553.341	1553.781	-283.805	0.538	1629.374	0.470	21	0.236	K.YLTEDPLFQLVSK.L
R4/RRR4-9/2	1553.362	1553.781	-270.402	0.529	1664.286	0.452	21	0.235	K.YLTEDPLFQLVSK.L
R4/RRR4-9/2	1139.200	1139.328	-113.238	0.436	1078.164	0.486	17	0.187	R.LPAVASYVYR.R
R4/RRR4-9/2	1345.685	1345.529	116.496	0.397	1339.001	0.329	18	0.176	R.SIGIGSQLIWDR.A
R4/RRR4-9/2	1345.080	1345.529	-334.483	0.354	1229.989	0.377	17	0.175	R.SIGIGSQLIWDR.A
R4/RRR4-9/2	1571.527	1571.882	-226.764	0.391	483.562	0.576	17	0.163	K.LYEVVPPILTELGK.V
R4/RRR4-9/2	1345.345	1345.529	-137.022	0.367	1209.269	0.284	18	0.161	R.SIGIGSQLIWDR.A
R4/RRR4-9/2	1139.198	1139.328	-114.850	0.352	852.034	0.399	15	0.158	R.LPAVASYVYR.R
R4/RRR4-9/2	1571.297	1571.882	-1012.004	0.330	552.618	0.509	19	0.157	K.LYEVVPPILTELGK.V
R4/RRR4-9/2	1571.370	1571.882	-965.362	0.323	481.528	0.538	17	0.156	K.LYEVVPPILTELGK.V
R4/RRR4-9/2	1095.324	1094.332	-7.781	0.436	510.938	0.428	14	0.155	R.ALGLPLERPK.S
R4/RRR4-9/2	1584.530	1584.713	-116.029	0.403	723.910	0.410	19	0.155	K.SQLQELIPEQQDR.L
R4/RRR4-9/2	1095.247	1094.332	-77.650	0.415	438.146	0.426	13	0.153	R.ALGLPLERPK.S
R4/RRR4-9/2	1094.092	1094.332	-219.853	0.334	605.539	0.414	15	0.152	R.ALGLPLERPK.S
R4/RRR4-9/2	1139.278	1139.328	-44.235	0.457	814.691	0.310	15	0.149	R.LPAVASYVYR.R
R4/RRR4-9/2	1571.659	1571.882	-142.454	0.360	305.386	0.461	14	0.142	-.LYEVVPPILTELGK.-
R4/RRR4-9/2	1138.101	1138.347	-216.946	0.142	186.418	0.624	15	0.131	K.VVPGFGHGVLR.K
R4/RRR4-6/2	1787.413	1787.905	-276.300	0.541	3942.229	0.543	29	0.795	K.GGYVVTEAGFGSDIGTEK.F
R4/RRR4-6/2	1784.321	1783.010	175.071	0.480	1731.309	0.488	24	0.250	K.STTTVGLCQALGAFLDK.K
R4/RRR4-6/2	1345.176	1345.483	-228.604	0.530	1250.231	0.468	18	0.198	R.LDIDPESITWR.R
R4/RRR4-6/2	1345.246	1345.483	-176.441	0.517	1034.236	0.460	17	0.180	R.LDIDPESITWR.R
R4/RRR4-6/2	1263.475	1263.468	5.561	0.398	1094.783	0.439	17	0.176	K.SYGVNVVVAINK.F
R4/RRR4-6/2	1344.832	1345.483	-1231.311	0.500	1039.839	0.426	17	0.175	R.LDIDPESITWR.R
R4/RRR4-6/2	1119.197	1119.201	-3.458	0.336	1295.328	0.349	14	0.174	R.ACESQADPLK.F
R4/RRR4-6/2	1113.735	1114.322	-1429.310	0.339	542.140	0.513	16	0.159	K.GAPSGFVLPIR.D
R4/RRR4-6/2	1485.972	1486.587	-1090.026	0.397	690.948	0.439	17	0.156	K.FASDTEAEM*DVVR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1782.610	1783.010	-224.844	0.403	783.637	0.405	18	0.150	K.STTTVGLCQALGAFLDK.K
R4/RRR4-6/2	1486.078	1486.587	-1018.105	0.331	612.631	0.429	16	0.149	K.FASDTEAEM*DVVR.N
R4/RRR4-6/2	1099.038	1099.266	-207.390	0.397	1000.436	0.288	14	0.147	K.GAVDLGLAVQR.A
R4/RRR4-6/2	1113.978	1114.322	-310.121	0.357	614.802	0.324	16	0.146	K.GAPSGFVLPIR.D
R4/RRR4-6/2	1113.452	1114.322	-1684.673	0.298	430.152	0.420	13	0.145	K.GAPSGFVLPIR.D
R4/RRR4-12/2	1317.221	1317.560	-258.367	0.415	1050.014	0.553	16	0.191	R.GLVVVHPYFTGK.E
R4/RRR4-12/2	1739.157	1738.839	183.560	0.479	1167.092	0.455	22	0.184	R.GDGADPWLLDHADLSR.L
R4/RRR4-12/2	1156.194	1156.316	-106.067	0.471	1017.137	0.448	16	0.175	R.AGAIGVSVYYR.L
R4/RRR4-12/2	1317.346	1317.560	-162.891	0.418	850.851	0.529	16	0.175	R.GLVVVHPYFTGK.E
R4/RRR4-12/2	1479.589	1480.603	-1365.431	0.198	1243.536	0.414	18	0.173	R.FVFPETSGLDDPR.V
R4/RRR4-12/2	1389.011	1389.495	-349.555	0.369	1215.250	0.358	19	0.170	K.EAVGAEAAFGPDVR.E
R4/RRR4-12/2	1133.858	1134.224	-323.581	0.379	904.197	0.416	16	0.164	R.VNPFVDDATR.A
R4/RRR4-12/2	1330.203	1330.466	-198.410	0.432	721.408	0.415	19	0.156	R.CGGGGALPDGVTLR.G
R4/RRR4-12/2	1500.143	1500.591	-299.827	0.423	490.704	0.484	14	0.151	K.ANGYGGEVELFESK.G
R4/RRR4-12/2	1330.196	1330.466	-203.842	0.417	636.080	0.398	18	0.151	R.CGGGGALPDGVTLR.G
R4/RRR4-12/2	1330.777	1330.466	234.370	0.383	998.807	0.299	19	0.151	R.CGGGGALPDGVTLR.G
R4/RRR4-12/2	1500.598	1500.591	4.438	0.426	583.322	0.406	17	0.150	K.ANGYGGEVELFESK.G
R4/RRR4-12/2	1479.470	1480.603	-1446.478	0.166	1022.838	0.347	17	0.149	R.FVFPETSGLDDPR.V
R4/RRR4-12/2	1389.085	1389.495	-296.299	0.400	851.857	0.338	16	0.147	-.EAVGAEAAFGPDVR.-
R4/RRR4-12/2	1500.019	1500.591	-1051.113	0.404	628.807	0.368	17	0.147	K.ANGYGGEVELFESK.G
R4/RRR4-12/2	1389.025	1389.495	-339.944	0.339	802.533	0.308	16	0.143	K.EAVGAEAAFGPDVR.E
R4/RRR4-13/2	1134.312	1134.224	77.866	0.232	792.005	0.298	14	0.141	R.VNPFVDDATR.A
R4/RRR4-13/2	1480.196	1480.603	-275.662	0.183	293.857	0.434	14	0.137	R.FVFPETSGLDDPR.V
R4/RRR4-13/2	1480.145	1480.603	-310.413	0.150	236.603	0.419	13	0.134	R.FVFPETSGLDDPR.V
R4/RRR4-22/1	955.396	956.120	-1809.451	0.284	924.182	0.374	11	0.638	K.ALVAYYQK.Y
R4/RRR4-22/1	955.470	956.120	-1731.977	0.285	811.451	0.223	11	0.505	K.ALVAYYQK.Y
R4/RRR4-22/1	955.562	956.120	-1634.943	0.296	637.458	0.261	10	0.474	K.ALVAYYQK.Y
R4/RRR4-22/2	951.954	952.090	-143.035	0.493	991.622	0.463	13	0.180	K.TSQIYAIR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1086.985	1087.297	-287.748	0.493	915.439	0.491	16	0.180	K.AFEPILLAGR.S
R4/RRR4-22/2	1087.006	1087.297	-268.369	0.486	850.566	0.502	16	0.178	K.AFEPILLAGR.S
R4/RRR4-22/2	951.951	952.090	-146.251	0.487	942.603	0.460	13	0.177	K.TSQIYAIR.Q
R4/RRR4-22/2	1086.973	1087.297	-298.564	0.406	818.588	0.499	16	0.173	K.AFEPILLAGR.S
R4/RRR4-22/2	1088.087	1087.297	-193.611	0.397	885.213	0.453	16	0.170	K.AFEPILLAGR.S
R4/RRR4-21/2	951.803	952.090	-301.795	0.414	917.531	0.427	13	0.169	K.TSQIYAIR.Q
R4/RRR4-21/2	884.741	885.043	-343.007	0.370	1011.583	0.412	12	0.169	R.TLLVADPR.R
R4/RRR4-22/2	884.511	885.043	-1737.568	0.384	1010.390	0.406	12	0.169	R.TLLVADPR.R
R4/RRR4-20/2	951.991	952.090	-104.189	0.442	977.814	0.390	13	0.168	K.TSQIYAIR.Q
R4/RRR4-21/2	1087.121	1087.297	-161.798	0.375	808.590	0.465	15	0.167	K.AFEPILLAGR.S
R4/RRR4-22/2	885.035	885.043	-9.077	0.413	828.897	0.455	11	0.166	R.TLLVADPR.R
R4/RRR4-21/2	884.916	885.043	-143.840	0.403	1008.974	0.388	12	0.166	-.TLLVADPR.-
R4/RRR4-22/2	884.948	885.043	-108.139	0.393	818.140	0.453	11	0.165	R.TLLVADPR.R
R4/RRR4-22/2	951.489	952.090	-1687.509	0.405	916.534	0.395	13	0.165	K.TSQIYAIR.Q
R4/RRR4-22/2	1308.935	1309.490	-1191.557	0.426	908.875	0.414	17	0.164	K.TAVAVSYCKPGR.G
R4/RRR4-22/2	1309.044	1309.490	-341.446	0.428	775.893	0.451	16	0.162	K.TAVAVSYCKPGR.G
R4/RRR4-21/2	1087.300	1087.297	3.084	0.343	725.538	0.465	14	0.161	K.AFEPILLAGR.S
R4/RRR4-22/2	955.914	956.120	-215.450	0.406	814.679	0.395	13	0.161	K.ALVAYYQK.Y
R4/RRR4-21/2	951.940	952.090	-157.700	0.373	939.928	0.328	13	0.157	K.TSQIYAIR.Q
R4/RRR4-22/2	1309.102	1309.490	-297.286	0.382	758.303	0.418	16	0.157	K.TAVAVSYCKPGR.G
R4/RRR4-21/2	951.402	952.090	-1778.647	0.361	803.250	0.336	13	0.154	K.TSQIYAIR.Q
R4/RRR4-22/2	1087.354	1087.297	53.304	0.320	536.691	0.423	13	0.151	K.AFEPILLAGR.S
R4/RRR4-19/2	955.995	956.120	-131.032	0.296	826.475	0.323	13	0.150	K.ALVAYYQK.Y
R4/RRR4-22/2	955.581	956.120	-1614.680	0.327	802.460	0.313	13	0.149	K.ALVAYYQK.Y
R4/RRR4-19/2	955.654	956.120	-488.913	0.278	669.322	0.332	12	0.146	K.ALVAYYQK.Y
R4/RRR4-22/2	955.336	956.120	-1872.698	0.313	603.946	0.267	12	0.142	-.ALVAYYQK.-
R4/RRR4-21/2	1309.025	1309.490	-356.416	0.322	519.313	0.305	14	0.141	K.TAVAVSYCKPGR.G
R4/RRR4-19/2	951.545	952.090	-1628.092	0.284	617.136	0.188	13	0.140	K.TSQIYAIR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	951.664	952.090	-448.892	0.285	720.834	0.221	13	0.140	-.TSQIYAIR.-
R4/RRR4-20/2	884.663	885.043	-430.921	0.221	535.867	0.300	10	0.140	R.TLLVADPR.R
R4/RRR4-22/2	1086.332	1087.297	-1814.078	0.256	223.998	0.369	10	0.125	-.AFEPILLAGR.-
R4/RRR4-22/3	1041.814	1041.229	-399.778	0.335	918.431	0.337	20	0.093	R.TLLVADPRR.C
R4/RRR4-22/3	1328.652	1328.628	18.318	0.441	1152.925	0.234	22	0.088	R.LKAFEPILLAGR.S
R4/RRR4-22/3	1328.257	1328.628	-279.643	0.427	1265.513	0.185	21	0.086	-.LKAFEPILLAGR.-
R4/RRR4-22/3	1328.375	1328.628	-191.135	0.456	1209.265	0.198	23	0.084	R.LKAFEPILLAGR.S
R4/RRR4-22/3	1041.326	1041.229	93.037	0.286	807.088	0.300	19	0.084	R.TLLVADPRR.C
R4/RRR4-22/3	1041.369	1041.229	134.213	0.275	776.321	0.280	18	0.082	R.TLLVADPRR.C
R4/RRR4-9/3	1769.644	1769.891	-140.223	0.575	2744.928	0.502	32	0.488	R.HYAHVDCPGHADYVK.N
R4/RRR4-10/3	1769.407	1769.891	-274.240	0.590	2633.338	0.513	32	0.460	R.HYAHVDCPGHADYVK.N
R4/RRR4-10/3	1769.669	1769.891	-125.899	0.597	2505.138	0.494	32	0.408	R.HYAHVDCPGHADYVK.N
R4/RRR4-10/2	1693.344	1692.898	264.301	0.591	2440.354	0.592	25	0.404	K.ILDHGEAGDNVGLLLR.G
R4/RRR4-10/2	1692.198	1692.898	-1007.567	0.516	2437.174	0.551	25	0.388	K.ILDHGEAGDNVGLLLR.G
R4/RRR4-10/3	1769.687	1769.891	-115.728	0.561	1857.473	0.521	27	0.269	R.HYAHVDCPGHADYVK.N
R4/RRR4-10/2	1755.361	1756.016	-945.283	0.492	1196.388	0.531	21	0.202	K.SFLM*PIEDVFSIQGR.G
R4/RRR4-10/2	1756.346	1756.016	188.329	0.491	1066.248	0.541	20	0.193	K.SFLM*PIEDVFSIQGR.G
R4/RRR4-10/2	1755.537	1756.016	-273.562	0.479	936.566	0.551	19	0.184	K.SFLM*PIEDVFSIQGR.G
R4/RRR4-10/2	1649.448	1649.847	-242.467	0.469	1040.362	0.442	19	0.173	K.LM*DAVDEYIPDPVR.Q
R4/RRR4-10/2	1739.287	1740.016	-997.183	0.499	723.317	0.520	19	0.169	K.SFLMPIEDVFSIQGR.G
R4/RRR4-10/2	1157.059	1157.344	-246.936	0.446	1025.266	0.380	16	0.167	K.FPGDEIPIIR.G
R4/RRR4-10/2	1561.346	1561.676	-211.931	0.417	947.174	0.418	19	0.160	R.GSALSALQGTNDEIGK.N
R4/RRR4-10/2	1739.623	1740.016	-226.811	0.446	705.490	0.453	19	0.159	K.SFLMPIEDVFSIQGR.G
R4/RRR4-10/2	1156.785	1157.344	-1351.244	0.408	878.992	0.366	16	0.158	K.FPGDEIPIIR.G
R4/RRR4-10/2	1156.596	1157.344	-1515.547	0.399	952.865	0.329	16	0.156	K.FPGDEIPIIR.G
R4/RRR4-17/2	1728.175	1726.949	131.237	0.387	885.911	0.392	20	0.154	K.TGEDVEILGLTPSGPLK.T
R4/RRR4-10/2	1726.710	1726.949	-139.022	0.315	416.326	0.349	15	0.136	K.TGEDVEILGLTPSGPLK.T
R4/RRR4-10/3	1797.373	1797.011	201.722	0.417	612.626	0.542	30	0.117	R.TKPHVNVGTIGHVDHGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/3	1797.088	1797.011	42.941	0.406	661.847	0.515	30	0.114	R.TKPHVNVGTIGHVDHGK.T
R4/RRR4-10/3	1796.361	1797.011	-921.581	0.379	484.458	0.422	27	0.096	R.TKPHVNVGTIGHVDHGK.T
R4/RRR4-6/3	1719.929	1720.875	-1134.380	0.458	2491.823	0.417	36	0.364	R.RVHVAGPAGSAAADRER.I
R4/RRR4-6/2	1586.229	1586.683	-286.720	0.439	1841.440	0.477	24	0.262	R.VDVSPETLEPTGGER.R
R4/RRR4-6/2	1308.840	1309.407	-1201.092	0.447	1811.201	0.468	20	0.257	R.LEFDAGELTTGR.D
R4/RRR4-6/3	1434.841	1435.574	-1211.251	0.502	1827.471	0.459	31	0.238	R.RVHVAGPAGSAAADR.E
R4/RRR4-6/2	1352.056	1352.479	-313.560	0.439	1529.681	0.522	17	0.234	R.VAEDGWWSVFR.V
R4/RRR4-6/2	1587.393	1586.683	-183.232	0.490	1610.418	0.477	23	0.233	R.VDVSPETLEPTGGER.R
R4/RRR4-5/2	1352.418	1352.479	-44.597	0.417	1683.933	0.443	17	0.233	R.VAEDGWWSVFR.V
R4/RRR4-6/2	1587.275	1586.683	-257.374	0.512	1591.658	0.475	23	0.231	R.VDVSPETLEPTGGER.R
R4/RRR4-5/2	1353.347	1352.479	-97.400	0.401	1516.637	0.499	15	0.225	R.VAEDGWWSVFR.V
R4/RRR4-6/2	1352.160	1352.479	-236.116	0.420	1520.411	0.467	17	0.220	R.VAEDGWWSVFR.V
R4/RRR4-6/3	1720.842	1720.875	-18.906	0.448	1792.766	0.440	35	0.218	R.RVHVAGPAGSAAADRER.I
R4/RRR4-6/2	1162.412	1163.348	-1670.804	0.416	1544.636	0.423	17	0.215	R.VLETEVAVFR.A
R4/RRR4-6/2	1163.209	1163.348	-120.163	0.533	1360.645	0.449	17	0.205	R.VLETEVAVFR.A
R4/RRR4-5/2	1586.309	1586.683	-236.382	0.425	1372.117	0.462	22	0.204	R.VDVSPETLEPTGGER.R
R4/RRR4-5/2	1353.262	1352.479	-160.739	0.403	1010.688	0.487	14	0.178	R.VAEDGWWSVFR.V
R4/RRR4-6/2	1352.354	1352.479	-92.492	0.425	1044.292	0.470	14	0.178	R.VAEDGWWSVFR.V
R4/RRR4-6/2	1352.113	1352.479	-271.440	0.414	831.398	0.546	13	0.175	R.VAEDGWWSVFR.V
R4/RRR4-5/2	1309.194	1309.407	-163.250	0.368	996.331	0.395	16	0.162	R.LEFDAGELTTGR.D
R4/RRR4-5/2	1586.060	1586.683	-1025.896	0.354	1025.549	0.380	19	0.162	R.VDVSPETLEPTGGER.R
R4/RRR4-6/2	1564.318	1564.688	-237.279	0.378	864.026	0.398	20	0.155	R.VHVAGPAGSAAADRER.I
R4/RRR4-6/2	856.498	857.033	-1796.898	0.337	552.132	0.447	11	0.154	K.TPGVTILR.S
R4/RRR4-5/2	856.308	857.033	-2020.923	0.285	673.068	0.427	12	0.153	K.TPGVTILR.S
R4/RRR4-5/2	856.929	857.033	-121.605	0.277	698.958	0.397	12	0.151	K.TPGVTILR.S
R4/RRR4-6/2	856.886	857.033	-172.479	0.387	667.691	0.338	12	0.150	K.TPGVTILR.S
R4/RRR4-6/2	1564.471	1564.688	-139.508	0.398	401.038	0.483	16	0.149	R.VHVAGPAGSAAADRER.I
R4/RRR4-5/2	1353.146	1352.479	-246.259	0.298	673.447	0.320	12	0.142	-.VAEDGWWSVFR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	856.486	857.033	-1811.649	0.230	577.881	0.274	11	0.139	-.TPGVTILR.-
R4/RRR4-6/3	1720.903	1720.875	16.633	0.415	1096.726	0.415	29	0.121	R.RVHVAGPAGSAAADRER.I
R4/RRR4-20/3	1639.100	1639.905	-1104.494	0.501	3146.431	0.449	35	0.590	K.IKHTGPGLLSM*ANAGR.D
R4/RRR4-20/3	1639.193	1639.905	-1047.403	0.459	2951.270	0.376	34	0.474	K.IKHTGPGLLSM*ANAGR.D
R4/RRR4-20/3	1639.587	1639.905	-194.585	0.522	2087.218	0.491	30	0.305	K.IKHTGPGLLSM*ANAGR.D
R4/RRR4-20/2	1566.309	1566.739	-275.827	0.504	1787.654	0.511	21	0.264	K.VYFDVEIDGKPAGR.V
R4/RRR4-21/2	1567.091	1566.739	225.044	0.544	1654.092	0.564	21	0.261	K.VYFDVEIDGKPAGR.V
R4/RRR4-20/2	1566.288	1566.739	-288.885	0.468	1545.152	0.499	20	0.230	K.VYFDVEIDGKPAGR.V
R4/RRR4-20/2	1924.415	1925.198	-929.121	0.534	977.985	0.582	25	0.196	R.IIPSFMIQGGDFTLGDGR.G
R4/RRR4-21/2	1941.610	1941.197	213.149	0.510	759.351	0.593	25	0.184	R.IIPSFM*IQGGDFTLGDGR.G
R4/RRR4-21/2	1941.029	1941.197	-86.661	0.533	686.559	0.583	26	0.181	R.IIPSFM*IQGGDFTLGDGR.G
R4/RRR4-20/2	1940.737	1941.197	-237.642	0.525	621.631	0.582	26	0.178	R.IIPSFM*IQGGDFTLGDGR.G
R4/RRR4-21/2	1940.487	1941.197	-883.711	0.478	574.485	0.585	24	0.173	R.IIPSFM*IQGGDFTLGDGR.G
R4/RRR4-21/2	1926.554	1925.198	185.406	0.470	700.264	0.539	23	0.171	R.IIPSFMIQGGDFTLGDGR.G
R4/RRR4-20/2	1940.548	1941.197	-852.262	0.511	531.136	0.551	25	0.170	R.IIPSFM*IQGGDFTLGDGR.G
R4/RRR4-20/2	1940.013	1941.197	-1129.429	0.475	585.743	0.549	24	0.169	R.IIPSFM*IQGGDFTLGDGR.G
R4/RRR4-21/2	1398.299	1398.574	-197.211	0.362	427.833	0.550	20	0.158	K.HTGPGLLSM*ANAGR.D
R4/RRR4-20/3	1942.408	1941.197	108.986	0.443	974.793	0.578	30	0.154	R.IIPSFM*IQGGDFTLGDGR.G
R4/RRR4-20/2	867.014	867.091	-89.604	0.377	781.405	0.317	13	0.151	R.VVM*GLFGK.T
R4/RRR4-20/2	867.071	867.091	-23.090	0.378	697.242	0.329	13	0.151	R.VVM*GLFGK.T
R4/RRR4-21/2	866.919	867.091	-199.210	0.352	673.852	0.352	12	0.151	R.VVM*GLFGK.T
R4/RRR4-20/2	867.067	867.091	-28.174	0.337	611.575	0.346	13	0.150	R.VVM*GLFGK.T
R4/RRR4-21/2	866.945	867.091	-169.405	0.306	625.797	0.343	13	0.149	R.VVM*GLFGK.T
R4/RRR4-21/2	866.827	867.091	-305.873	0.347	527.846	0.325	12	0.148	R.VVM*GLFGK.T
R4/RRR4-20/2	1013.761	1014.115	-349.958	0.365	830.063	0.306	13	0.146	K.ADLTEVTHK.V
R4/RRR4-20/2	851.044	851.092	-55.908	0.211	346.113	0.397	11	0.143	R.VVMGLFGK.T
R4/RRR4-20/3	1229.220	1229.365	-118.004	0.486	1278.831	0.305	22	0.109	-.SKADLTEVTHK.-
R4/RRR4-20/3	1228.984	1229.365	-310.650	0.487	1001.094	0.358	21	0.104	K.SKADLTEVTHK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/3	1230.570	1229.365	166.833	0.438	1071.504	0.280	22	0.093	K.SKADLTEVTHK.V
R4/RRR4-21/3	1229.332	1229.365	-27.311	0.475	1099.206	0.277	21	0.092	-.SKADLTEVTHK.-
R4/RRR4-20/3	1229.668	1229.365	246.759	0.531	938.506	0.320	20	0.092	-.SKADLTEVTHK.-
R4/RRR4-20/3	1640.755	1639.905	-91.729	0.355	696.098	0.307	25	0.087	K.IKHTGPGLLSM*ANAGR.D
R4/RRR4-21/3	1943.013	1941.197	-95.244	0.347	468.766	0.332	23	0.085	-.IIPSFM*IQGGDFTLGDGR.-
R4/RRR4-20/3	1940.847	1941.197	-180.829	0.229	764.806	0.033	24	0.070	-.IIPSFM*IQGGDFTLGDGR.-
R4/RRR4-10/2	1260.034	1260.378	-273.493	0.563	1909.189	0.568	18	0.301	K.HGEIDYEAVVK.L
R4/RRR4-10/2	1260.100	1260.378	-221.399	0.577	1693.937	0.594	17	0.276	K.HGEIDYEAVVK.L
R4/RRR4-10/2	1277.241	1277.451	-165.321	0.512	1664.207	0.520	19	0.252	R.AIASNIDANFLK.I
R4/RRR4-10/2	1260.116	1260.378	-208.085	0.525	1481.182	0.588	18	0.248	K.HGEIDYEAVVK.L
R4/RRR4-10/2	1277.284	1277.451	-131.095	0.414	1456.966	0.504	18	0.221	R.AIASNIDANFLK.I
R4/RRR4-10/2	1276.913	1277.451	-1208.591	0.381	1508.600	0.397	18	0.204	R.AIASNIDANFLK.I
R4/RRR4-10/2	1953.580	1953.203	193.355	0.508	1125.670	0.556	22	0.199	R.TLM*ELLNQLDGFDELGK.V
R4/RRR4-9/2	1277.016	1277.451	-342.244	0.426	1321.395	0.417	17	0.190	R.AIASNIDANFLK.I
R4/RRR4-10/2	1722.369	1722.964	-928.997	0.483	1096.711	0.477	18	0.179	-.IVSSAIIDKYIGESAR.-
R4/RRR4-10/2	1819.636	1818.127	-270.808	0.519	594.058	0.460	19	0.157	R.ESIELPLM*NPELFLR.V
R4/RRR4-10/2	1818.791	1818.127	-185.575	0.497	623.149	0.441	19	0.156	R.ESIELPLM*NPELFLR.V
R4/RRR4-10/3	1723.791	1722.964	-100.626	0.476	1386.241	0.428	28	0.155	K.IVSSAIIDKYIGESAR.L
R4/RRR4-10/2	1817.244	1818.127	-1039.305	0.382	570.622	0.341	18	0.143	R.ESIELPLM*NPELFLR.V
R4/RRR4-10/3	1723.141	1722.964	103.262	0.419	1165.994	0.460	31	0.138	K.IVSSAIIDKYIGESAR.L
R4/RRR4-10/3	1652.705	1652.751	-27.982	0.402	1160.207	0.411	23	0.126	R.RFSEGTSADREIQR.T
R4/RRR4-10/3	1408.614	1408.628	-10.189	0.487	923.698	0.407	25	0.109	R.KIEIPLPNEQAR.M
R4/RRR4-10/3	1652.732	1652.751	-11.203	0.473	853.449	0.397	22	0.103	R.RFSEGTSADREIQR.T
R4/RRR4-10/3	1652.269	1652.751	-292.423	0.466	947.375	0.349	23	0.098	R.RFSEGTSADREIQR.T
R4/RRR4-10/3	1408.284	1408.628	-244.799	0.404	742.045	0.317	23	0.089	R.KIEIPLPNEQAR.M
R4/RRR4-9/3	1722.654	1722.964	-180.509	0.228	670.116	0.291	22	0.081	K.IVSSAIIDKYIGESAR.L
R4/RRR4-10/3	1408.306	1408.628	-229.407	0.339	903.244	0.231	24	0.081	R.KIEIPLPNEQAR.M
R4/RRR4-8/2	1157.080	1157.302	-192.119	0.502	2230.053	0.518	20	0.338	R.DPAAATSGVVIR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1157.081	1157.302	-191.484	0.518	2079.995	0.504	20	0.308	R.DPAAATSGVVIR.R
R4/RRR4-8/2	1242.960	1242.447	-392.598	0.538	1659.064	0.538	19	0.257	R.NLVVVSSPDLAK.E
R4/RRR4-8/2	1713.229	1711.882	203.061	0.468	1360.312	0.583	20	0.229	K.GQDMVFTVYGDHWR.K
R4/RRR4-8/2	1242.368	1242.447	-63.823	0.482	1187.678	0.575	17	0.210	R.NLVVVSSPDLAK.E
R4/RRR4-8/2	1164.058	1164.290	-200.223	0.432	1115.266	0.444	17	0.181	K.LAGYDIPAESK.I
R4/RRR4-8/2	1163.534	1164.290	-1513.560	0.439	1053.580	0.468	16	0.180	K.LAGYDIPAESK.I
R4/RRR4-8/2	1103.345	1103.342	2.041	0.468	1182.723	0.306	16	0.166	R.RFGDILLLR.M
R4/RRR4-8/2	1163.377	1164.290	-1649.317	0.355	1019.549	0.382	16	0.163	K.LAGYDIPAESK.I
R4/RRR4-8/2	1711.578	1711.882	-178.236	0.329	986.085	0.392	18	0.160	K.GQDMVFTVYGDHWR.K
R4/RRR4-8/2	1102.965	1103.342	-342.967	0.419	1117.965	0.291	16	0.160	R.RFGDILLLR.M
R4/RRR4-8/2	1103.144	1103.342	-180.646	0.480	1158.009	0.278	16	0.160	R.RFGDILLLR.M
R4/RRR4-8/3	1890.866	1892.018	-1141.519	0.528	1430.228	0.420	34	0.160	R.FLEEEKAVEAHGNDFR.F
R4/RRR4-8/2	1319.465	1320.435	-1497.357	0.405	911.090	0.329	14	0.152	K.LFEDHFVQER.M
R4/RRR4-8/2	947.037	947.156	-126.195	0.545	1090.304	0.214	13	0.143	R.FGDILLLR.M
R4/RRR4-8/2	1712.135	1711.882	148.485	0.362	643.304	0.275	14	0.135	K.GQDMVFTVYGDHWR.K
R4/RRR4-1/2	1320.505	1320.435	53.535	0.271	659.405	0.185	12	0.133	-.LFEDHFVQER.-
R4/RRR4-16/2	1097.278	1097.295	-15.243	0.570	1699.588	0.494	17	0.252	K.APLLAAWAQR.F
R4/RRR4-16/2	1008.004	1008.107	-102.165	0.516	1940.018	0.347	16	0.243	R.FGELDVAEK.V
R4/RRR4-16/2	1097.258	1097.295	-33.766	0.575	1513.037	0.515	17	0.235	K.APLLAAWAQR.F
R4/RRR4-16/2	1007.843	1008.107	-262.783	0.474	1890.284	0.323	16	0.231	R.FGELDVAEK.V
R4/RRR4-16/2	1096.883	1097.295	-376.235	0.569	1492.425	0.475	17	0.223	K.APLLAAWAQR.F
R4/RRR4-16/2	1844.424	1845.091	-906.686	0.544	1315.021	0.508	23	0.209	K.VFDEEKAPLLAAWAQR.F
R4/RRR4-16/2	1845.416	1845.091	176.971	0.559	1202.807	0.523	22	0.201	K.VFDEEKAPLLAAWAQR.F
R4/RRR4-16/2	1844.625	1845.091	-253.526	0.555	1130.538	0.499	21	0.189	K.VFDEEKAPLLAAWAQR.F
R4/RRR4-16/2	1456.440	1456.709	-185.920	0.505	1014.793	0.504	21	0.186	K.QLLAAVETLEGALK.D
R4/RRR4-15/2	1008.338	1008.107	230.085	0.364	1512.975	0.233	15	0.174	R.FGELDVAEK.V
R4/RRR4-16/2	1457.555	1456.709	-106.565	0.528	838.960	0.491	20	0.173	K.QLLAAVETLEGALK.D
R4/RRR4-16/2	1389.301	1388.590	-209.182	0.389	410.101	0.524	17	0.158	K.VLPDVDGVVEFAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1456.310	1456.709	-274.802	0.465	665.493	0.437	19	0.158	K.QLLAAVETLEGALK.D
R4/RRR4-15/2	1008.239	1008.107	131.745	0.376	1236.952	0.245	14	0.158	R.FGELDVAEK.V
R4/RRR4-16/2	1947.537	1947.213	166.812	0.484	408.162	0.547	18	0.155	K.QLLAAVETLEGALKDCSK.G
R4/RRR4-16/2	1388.209	1388.590	-275.671	0.358	369.113	0.465	18	0.154	K.VLPDVDGVVEFAK.M
R4/RRR4-16/2	1388.248	1388.590	-247.529	0.343	356.234	0.441	17	0.150	K.VLPDVDGVVEFAK.M
R4/RRR4-16/3	1844.679	1845.091	-224.122	0.458	1312.283	0.361	28	0.127	K.VFDEEKAPLLAAWAQR.F
R4/RRR4-16/2	1635.857	1634.904	-28.711	0.398	999.360	0.490	21	0.112	K.MMLAEAAAAAAAAAAASKN.-
R4/RRR4-16/3	1844.324	1845.091	-960.780	0.424	1294.821	0.276	25	0.106	K.VFDEEKAPLLAAWAQR.F
R4/RRR4-16/2	1635.140	1634.904	144.994	0.290	765.546	0.322	20	0.078	K.MMLAEAAAAAAAAAAASKN.-
R4/RRR4-16/2	1634.957	1634.904	32.830	0.320	862.160	0.311	20	0.077	K.MMLAEAAAAAAAAAAASKN.-
R4/RRR4-15/3	1845.293	1845.091	109.663	0.305	782.458	0.131	21	0.074	-.VFDEEKAPLLAAWAQR.-
R4/RRR4-16/3	1844.400	1845.091	-919.218	0.327	783.014	0.127	23	0.073	-.VFDEEKAPLLAAWAQR.-
R4/RRR4-7/2	1158.162	1158.327	-142.359	0.475	1777.350	0.459	18	0.251	K.ALEDALAVLDK.I
R4/RRR4-7/2	1158.293	1158.327	-29.450	0.452	1765.423	0.422	17	0.239	K.ALEDALAVLDK.I
R4/RRR4-7/2	1707.276	1705.937	199.108	0.467	1421.250	0.402	20	0.194	K.WPYEAAALAFEAIPR.T
R4/RRR4-7/2	1359.082	1359.551	-345.811	0.445	1398.312	0.359	18	0.186	R.TLAQNCGLNVIR.I
R4/RRR4-7/2	1120.935	1121.250	-281.521	0.440	1243.875	0.403	16	0.184	R.NLQDAM*SVAR.N
R4/RRR4-7/2	1120.980	1121.250	-241.534	0.429	1252.320	0.394	16	0.183	R.NLQDAM*SVAR.N
R4/RRR4-7/2	1120.933	1121.250	-283.925	0.408	1243.645	0.349	16	0.174	R.NLQDAM*SVAR.N
R4/RRR4-6/2	1707.433	1705.937	291.521	0.467	678.232	0.575	15	0.168	K.WPYEAAALAFEAIPR.T
R4/RRR4-7/2	1363.262	1363.618	-261.316	0.412	1229.118	0.318	16	0.166	R.IILLDCPVEYK.K
R4/RRR4-7/2	960.061	960.107	-47.965	0.437	953.083	0.354	15	0.161	R.IDDIVSGIK.K
R4/RRR4-7/2	960.082	960.107	-26.157	0.445	937.298	0.347	15	0.160	R.IDDIVSGIK.K
R4/RRR4-7/2	960.076	960.107	-32.534	0.480	793.443	0.369	14	0.157	R.IDDIVSGIK.K
R4/RRR4-7/2	763.663	763.904	-317.307	0.414	834.212	0.277	11	0.146	R.AGLFEVK.K
R4/RRR4-7/2	1317.130	1317.431	-229.289	0.395	1012.774	0.220	17	0.141	R.GASKDVLNEVER.N
R4/RRR4-7/3	1318.401	1317.431	-22.309	0.391	1002.542	0.318	21	0.094	R.GASKDVLNEVER.N
R4/RRR4-8/2	1850.388	1851.159	-959.741	0.490	2032.058	0.501	24	0.295	K.AVGEEMGIGFLGIGFQPK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1531.033	1530.662	243.060	0.490	1861.663	0.545	23	0.285	R.EVDAVISSGVTPAER.L
R4/RRR4-8/2	1867.129	1867.158	-15.514	0.477	1754.781	0.548	23	0.266	K.AVGEEM*GIGFLGIGFQPK.W
R4/RRR4-8/2	1930.836	1931.267	-223.753	0.573	1242.838	0.650	27	0.234	R.AGLALQPIATAIFANSPFK.E
R4/RRR4-8/2	1272.615	1271.553	48.527	0.487	1612.863	0.457	17	0.229	K.WALSDIPIMPK.G
R4/RRR4-8/2	1530.203	1530.662	-300.899	0.371	1541.679	0.482	21	0.222	R.EVDAVISSGVTPAER.L
R4/RRR4-8/2	1930.895	1931.267	-192.993	0.553	1150.156	0.616	26	0.216	R.AGLALQPIATAIFANSPFK.E
R4/RRR4-8/2	1259.211	1259.431	-175.662	0.555	1591.347	0.405	17	0.214	R.DLAEEILQLSK.N
R4/RRR4-8/2	1259.162	1259.431	-214.563	0.571	1572.622	0.393	17	0.209	R.DLAEEILQLSK.N
R4/RRR4-8/2	1930.353	1931.267	-994.574	0.522	1125.775	0.594	26	0.209	R.AGLALQPIATAIFANSPFK.E
R4/RRR4-8/2	1867.260	1868.058	-966.036	0.525	1115.916	0.577	21	0.204	R.SGM*LPFVFDDSFGFER.Y
R4/RRR4-8/2	1849.835	1851.159	-1259.925	0.388	1122.683	0.482	22	0.182	K.AVGEEMGIGFLGIGFQPK.W
R4/RRR4-8/2	1259.297	1259.431	-106.619	0.399	1522.330	0.276	17	0.182	R.DLAEEILQLSK.N
R4/RRR4-8/2	1271.271	1271.553	-222.921	0.324	739.507	0.465	13	0.157	K.WALSDIPIMPK.G
R4/RRR4-8/2	1286.441	1287.553	-1646.592	0.382	786.798	0.416	13	0.156	K.WALSDIPIM*PK.G
R4/RRR4-8/2	994.073	994.166	-93.990	0.517	743.908	0.378	13	0.155	-.LLNLYETK.-
R4/RRR4-8/2	993.969	994.166	-199.441	0.541	601.940	0.380	13	0.153	-.LLNLYETK.-
R4/RRR4-8/2	993.905	994.166	-263.388	0.477	593.263	0.347	13	0.150	-.LLNLYETK.-
R4/RRR4-8/2	1287.376	1287.553	-137.879	0.359	791.636	0.341	14	0.149	K.WALSDIPIM*PK.G
R4/RRR4-8/2	1310.038	1310.477	-335.392	0.218	1245.967	0.419	16	0.147	R.SVDPVFQELLY.-
R4/RRR4-8/2	1287.217	1287.553	-261.739	0.394	378.390	0.348	10	0.138	-.WALSDIPIM*PK.-
R4/RRR4-8/2	1853.842	1852.059	-117.468	0.329	359.703	0.367	13	0.136	R.SGMLPFVFDDSFGFER.Y
R4/RRR4-8/2	1309.940	1310.477	-1176.436	0.162	627.592	0.234	13	0.068	R.SVDPVFQELLY.-
R4/RRR4-21/3	1841.421	1842.027	-874.960	0.506	1924.248	0.473	28	0.256	K.ERLEFLDVDKCECK.S
R4/RRR4-22/3	1841.264	1842.027	-960.415	0.519	1873.985	0.487	28	0.252	K.ERLEFLDVDKCECK.S
R4/RRR4-22/3	1841.706	1842.027	-175.156	0.528	1703.955	0.528	28	0.238	K.ERLEFLDVDKCECK.S
R4/RRR4-21/2	1017.925	1018.146	-217.841	0.470	1641.920	0.471	19	0.237	K.STLVEGGGIGK.A
R4/RRR4-21/2	1017.896	1018.146	-246.836	0.441	1658.618	0.429	19	0.229	K.STLVEGGGIGK.A
R4/RRR4-22/2	1017.907	1018.146	-235.647	0.440	1481.541	0.447	18	0.213	K.STLVEGGGIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1017.409	1018.146	-1712.713	0.404	1436.803	0.454	18	0.209	K.STLVEGGGIGK.A
R4/RRR4-22/2	1018.003	1018.146	-141.212	0.444	1510.935	0.409	18	0.208	K.STLVEGGGIGK.A
R4/RRR4-22/2	1556.164	1556.726	-1007.053	0.478	1368.866	0.452	18	0.203	R.LEFLDVDKCECK.S
R4/RRR4-22/3	1841.847	1842.027	-98.065	0.516	1465.968	0.497	26	0.188	K.ERLEFLDVDKCECK.S
R4/RRR4-21/2	1071.208	1071.209	-1.098	0.377	1355.120	0.376	16	0.186	K.AIETATSHIK.V
R4/RRR4-21/3	1841.586	1842.027	-240.488	0.515	1455.912	0.474	25	0.179	K.ERLEFLDVDKCECK.S
R4/RRR4-22/2	1441.336	1441.695	-249.540	0.430	779.697	0.552	20	0.179	K.LLPGVEVKDEITK.A
R4/RRR4-22/2	1442.392	1441.695	-210.565	0.476	776.119	0.534	20	0.178	K.LLPGVEVKDEITK.A
R4/RRR4-22/2	1093.514	1094.286	-1624.920	0.453	1006.703	0.428	16	0.174	K.AKESLTGIFK.T
R4/RRR4-21/2	1093.961	1094.286	-297.776	0.483	895.279	0.457	16	0.173	K.AKESLTGIFK.T
R4/RRR4-22/2	1093.985	1094.286	-275.722	0.432	1027.244	0.414	16	0.173	K.AKESLTGIFK.T
R4/RRR4-21/2	1440.771	1441.695	-1338.994	0.391	788.054	0.516	20	0.172	K.LLPGVEVKDEITK.A
R4/RRR4-21/2	1441.233	1441.695	-321.683	0.392	763.987	0.516	20	0.171	K.LLPGVEVKDEITK.A
R4/RRR4-22/2	1356.061	1356.575	-1120.157	0.468	1129.053	0.380	17	0.171	R.AAVM*DWHTLAPK.I
R4/RRR4-21/2	1356.280	1356.575	-218.051	0.454	1073.980	0.393	17	0.170	R.AAVM*DWHTLAPK.I
R4/RRR4-21/2	1441.366	1441.695	-228.893	0.405	767.078	0.492	20	0.169	K.LLPGVEVKDEITK.A
R4/RRR4-22/2	1093.938	1094.286	-319.160	0.519	903.338	0.408	16	0.167	K.AKESLTGIFK.T
R4/RRR4-21/2	1356.125	1356.575	-332.646	0.408	1101.617	0.362	17	0.166	R.AAVM*DWHTLAPK.I
R4/RRR4-21/3	1841.696	1842.027	-180.342	0.491	1398.787	0.454	25	0.164	K.ERLEFLDVDKCECK.S
R4/RRR4-22/2	1017.372	1018.146	-1748.999	0.304	1091.294	0.355	17	0.163	K.STLVEGGGIGK.A
R4/RRR4-22/2	1441.396	1441.695	-207.822	0.386	681.106	0.477	19	0.163	K.LLPGVEVKDEITK.A
R4/RRR4-22/2	1355.988	1356.575	-1173.851	0.392	1041.200	0.336	17	0.159	R.AAVM*DWHTLAPK.I
R4/RRR4-21/2	1094.143	1094.286	-130.546	0.405	795.325	0.397	15	0.159	K.AKESLTGIFK.T
R4/RRR4-21/2	1070.965	1071.209	-228.946	0.383	922.918	0.357	14	0.156	K.AIETATSHIK.V
R4/RRR4-21/2	1094.079	1094.286	-189.529	0.290	693.239	0.382	13	0.149	K.AKESLTGIFK.T
R4/RRR4-22/2	1356.060	1356.575	-1120.971	0.415	997.690	0.270	16	0.148	R.AAVM*DWHTLAPK.I
R4/RRR4-21/2	1340.085	1340.576	-367.616	0.313	681.278	0.312	14	0.142	R.AAVMDWHTLAPK.I
R4/RRR4-11/2	1653.399	1652.751	-213.461	0.599	3178.303	0.567	27	1.000	K.AAAVVAGNGATNGATNGVH.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1654.236	1652.751	294.234	0.659	3016.152	0.599	27	0.889	K.AAAVVAGNGATNGATNGVH.-
R4/RRR4-11/2	1654.230	1652.751	290.683	0.601	3006.853	0.553	27	0.870	K.AAAVVAGNGATNGATNGVH.-
R4/RRR4-11/2	1654.359	1652.751	-237.612	0.437	2816.247	0.464	27	0.740	K.AAAVVAGNGATNGATNGVH.-
R4/RRR4-11/2	1654.245	1652.751	299.710	0.482	2704.705	0.504	27	0.683	K.AAAVVAGNGATNGATNGVH.-
R4/RRR4-11/2	1169.320	1169.442	-104.981	0.557	1919.726	0.490	19	0.280	R.ALVDVLAALKR.A
R4/RRR4-11/2	1169.259	1169.442	-157.343	0.546	1745.129	0.501	18	0.258	R.ALVDVLAALKR.A
R4/RRR4-11/2	1168.550	1169.442	-1624.519	0.517	1706.680	0.498	18	0.252	R.ALVDVLAALKR.A
R4/RRR4-11/2	1012.966	1013.256	-287.562	0.530	1233.180	0.496	17	0.204	R.ALVDVLAALK.R
R4/RRR4-11/2	1012.657	1013.256	-1583.401	0.455	1269.206	0.490	17	0.203	R.ALVDVLAALK.R
R4/RRR4-11/2	1012.806	1013.256	-445.729	0.466	1252.765	0.490	17	0.202	R.ALVDVLAALK.R
R4/RRR4-10/2	1151.185	1150.310	-108.336	0.423	1058.579	0.535	17	0.193	K.SPLTTVYAAAR.A
R4/RRR4-11/2	1298.111	1298.396	-220.043	0.406	1381.192	0.377	15	0.188	R.SDEELM*EICR.R
R4/RRR4-12/2	1150.229	1150.310	-70.106	0.375	1152.210	0.453	16	0.183	K.SPLTTVYAAAR.A
R4/RRR4-10/2	1151.267	1150.310	-37.181	0.428	1014.135	0.482	16	0.181	K.SPLTTVYAAAR.A
R4/RRR4-12/2	1150.346	1150.310	32.078	0.397	833.434	0.447	15	0.165	K.SPLTTVYAAAR.A
R4/RRR4-10/2	1150.258	1150.310	-45.197	0.358	719.184	0.368	16	0.153	K.SPLTTVYAAAR.A
R4/RRR4-11/2	1150.148	1150.310	-141.115	0.288	675.561	0.412	16	0.152	K.SPLTTVYAAAR.A
R4/RRR4-11/2	1150.782	1150.310	411.893	0.266	593.896	0.317	16	0.145	K.SPLTTVYAAAR.A
R4/RRR4-11/2	1151.071	1150.310	-208.013	0.288	397.509	0.292	14	0.144	K.SPLTTVYAAAR.A
R4/RRR4-11/2	1151.352	1150.310	36.729	0.260	555.355	0.343	13	0.143	K.SPLTTVYAAAR.A
R4/RRR4-11/3	1477.136	1476.789	235.052	0.490	1200.406	0.354	24	0.115	R.QELMEMGFHLIK.S
R4/RRR4-11/3	1523.813	1523.718	62.534	0.402	1044.663	0.394	22	0.113	R.EVVGDRDFFIVAR.T
R4/RRR4-11/3	1523.569	1523.718	-98.019	0.415	974.644	0.368	23	0.103	R.EVVGDRDFFIVAR.T
R4/RRR4-11/3	1523.959	1523.718	158.817	0.402	951.254	0.372	23	0.102	R.EVVGDRDFFIVAR.T
R4/RRR4-11/3	1476.769	1476.789	-13.988	0.376	1145.751	0.235	24	0.087	R.QELMEMGFHLIK.S
R4/RRR4-11/3	1477.829	1476.789	26.742	0.421	775.256	0.203	22	0.080	R.QELMEMGFHLIK.S
R4/RRR4-7/2	1104.943	1105.224	-254.815	0.436	621.823	0.549	17	0.170	K.VVGVDTSGSGVK.L
R4/RRR4-7/2	1104.370	1105.224	-1683.560	0.319	689.866	0.539	17	0.164	K.VVGVDTSGSGVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1104.815	1105.224	-371.428	0.356	557.515	0.459	16	0.154	K.VVGVDTSGSGVK.L
R4/RRR4-7/2	1474.102	1474.730	-1107.385	0.434	2171.885	0.524	22	0.326	R.LGANSLLDIVVFGR.A
R4/RRR4-7/2	1474.663	1474.730	-45.134	0.564	1991.347	0.582	21	0.314	R.LGANSLLDIVVFGR.A
R4/RRR4-6/2	1474.083	1474.730	-1120.689	0.480	2080.716	0.522	21	0.310	R.LGANSLLDIVVFGR.A
R4/RRR4-7/2	1474.604	1474.730	-85.738	0.516	1860.966	0.559	22	0.288	R.LGANSLLDIVVFGR.A
R4/RRR4-6/2	1475.496	1474.730	-158.708	0.534	1763.216	0.589	20	0.281	R.LGANSLLDIVVFGR.A
R4/RRR4-7/2	1295.224	1295.427	-157.260	0.436	1770.630	0.507	20	0.260	R.ATNTILATGGYGR.A
R4/RRR4-6/2	1474.445	1474.730	-193.864	0.449	1721.777	0.501	21	0.252	R.LGANSLLDIVVFGR.A
R4/RRR4-6/2	1295.316	1295.427	-85.506	0.399	1582.245	0.507	19	0.235	R.ATNTILATGGYGR.A
R4/RRR4-6/2	1474.023	1474.730	-1161.602	0.464	1586.368	0.503	19	0.234	R.LGANSLLDIVVFGR.A
R4/RRR4-6/2	1295.176	1295.427	-194.512	0.451	1486.958	0.524	20	0.230	R.ATNTILATGGYGR.A
R4/RRR4-7/2	1294.653	1295.427	-1374.457	0.389	1440.244	0.518	20	0.221	R.ATNTILATGGYGR.A
R4/RRR4-7/2	1295.145	1295.427	-218.055	0.442	1405.883	0.515	20	0.219	R.ATNTILATGGYGR.A
R4/RRR4-7/2	1609.408	1608.819	-256.573	0.493	1181.668	0.544	21	0.205	K.AVIELENYGLPFSR.T
R4/RRR4-7/2	1608.504	1608.819	-196.736	0.430	1214.065	0.527	21	0.203	K.AVIELENYGLPFSR.T
R4/RRR4-1/2	1474.628	1474.730	-69.131	0.458	1167.070	0.515	19	0.196	R.LGANSLLDIVVFGR.A
R4/RRR4-6/2	1474.208	1474.730	-1035.299	0.430	1206.784	0.500	18	0.195	R.LGANSLLDIVVFGR.A
R4/RRR4-7/2	1165.972	1166.336	-312.571	0.454	1283.934	0.426	17	0.193	R.VM*QNNAAVFR.T
R4/RRR4-7/2	1166.088	1166.336	-212.792	0.552	1220.198	0.441	17	0.191	R.VM*QNNAAVFR.T
R4/RRR4-6/2	1165.880	1166.336	-392.198	0.418	1290.068	0.410	17	0.189	R.VM*QNNAAVFR.T
R4/RRR4-6/2	1474.562	1474.730	-114.303	0.389	1178.479	0.455	17	0.183	R.LGANSLLDIVVFGR.A
R4/RRR4-7/2	1126.978	1127.231	-225.715	0.466	1038.818	0.467	18	0.182	R.AFGGQSLDFGK.G
R4/RRR4-6/2	1128.304	1127.231	64.825	0.453	954.781	0.503	17	0.182	R.AFGGQSLDFGK.G
R4/RRR4-6/2	1608.326	1608.819	-307.446	0.356	1101.692	0.470	20	0.181	K.AVIELENYGLPFSR.T
R4/RRR4-7/2	1165.964	1166.336	-319.924	0.506	1255.529	0.369	17	0.180	R.VM*QNNAAVFR.T
R4/RRR4-6/2	1608.397	1608.819	-263.662	0.427	985.784	0.477	20	0.177	K.AVIELENYGLPFSR.T
R4/RRR4-7/2	1126.258	1127.231	-1757.269	0.366	1124.729	0.417	18	0.177	R.AFGGQSLDFGK.G
R4/RRR4-6/2	1294.754	1295.427	-1295.483	0.313	1284.955	0.360	19	0.176	R.ATNTILATGGYGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1116.113	1116.338	-201.913	0.389	1272.773	0.345	15	0.176	K.TIAWLDKLR.N
R4/RRR4-6/2	1127.010	1127.231	-196.593	0.398	947.509	0.479	17	0.176	R.AFGGQSLDFGK.G
R4/RRR4-7/2	1127.173	1127.231	-51.879	0.407	1069.246	0.411	18	0.174	R.AFGGQSLDFGK.G
R4/RRR4-7/2	1608.248	1608.819	-980.073	0.343	1015.692	0.452	20	0.172	K.AVIELENYGLPFSR.T
R4/RRR4-6/2	1165.934	1166.336	-345.765	0.397	863.203	0.455	15	0.168	R.VM*QNNAAVFR.T
R4/RRR4-7/2	1116.162	1116.338	-157.807	0.375	975.590	0.399	13	0.163	-.TIAWLDKLR.-
R4/RRR4-6/2	1608.029	1608.819	-1116.727	0.302	922.007	0.417	19	0.161	K.AVIELENYGLPFSR.T
R4/RRR4-7/3	1790.437	1790.992	-870.846	0.454	1006.017	0.534	30	0.144	R.AAIGLSEHGFNTACITK.L
R4/RRR4-4/2	1609.839	1608.819	12.046	0.338	453.594	0.318	14	0.140	K.AVIELENYGLPFSR.T
R4/RRR4-7/3	1791.800	1790.992	-107.296	0.416	781.784	0.513	27	0.121	R.AAIGLSEHGFNTACITK.L
R4/RRR4-6/3	1518.994	1518.658	222.166	0.520	938.159	0.447	25	0.119	K.HSLGYWENEKVR.L
R4/RRR4-7/3	1790.471	1790.992	-851.751	0.372	618.235	0.516	23	0.111	R.AAIGLSEHGFNTACITK.L
R4/RRR4-7/3	1519.457	1518.658	-132.933	0.552	663.776	0.466	22	0.110	K.HSLGYWENEKVR.L
R4/RRR4-7/3	1519.947	1518.658	190.813	0.560	728.014	0.428	23	0.106	K.HSLGYWENEKVR.L
R4/RRR4-7/3	1519.118	1518.658	303.874	0.566	598.830	0.392	21	0.099	K.HSLGYWENEKVR.L
R4/RRR4-6/3	1518.570	1518.658	-58.109	0.564	715.980	0.365	21	0.096	K.HSLGYWENEKVR.L
R4/RRR4-7/2	1218.073	1218.336	-215.971	0.486	2031.649	0.471	20	0.290	R.ALIAEGSCGSPR.S
R4/RRR4-7/2	999.971	1000.174	-203.999	0.488	1860.775	0.493	17	0.272	K.AAGEVLALQK.R
R4/RRR4-7/2	999.953	1000.174	-221.634	0.530	1896.845	0.472	17	0.272	K.AAGEVLALQK.R
R4/RRR4-7/2	1217.351	1218.336	-1635.431	0.370	2023.709	0.381	20	0.262	R.ALIAEGSCGSPR.S
R4/RRR4-7/2	999.570	1000.174	-1609.276	0.473	1747.513	0.417	16	0.236	K.AAGEVLALQK.R
R4/RRR4-7/2	1217.258	1218.336	-1711.898	0.396	1681.580	0.424	20	0.229	R.ALIAEGSCGSPR.S
R4/RRR4-7/2	1264.213	1264.453	-189.687	0.537	1351.771	0.550	20	0.225	R.ILAFSQDVVSGK.I
R4/RRR4-7/2	1193.145	1193.334	-158.913	0.541	1282.664	0.568	17	0.222	R.VNQGLTVYGNK.G
R4/RRR4-7/2	1817.511	1816.951	-242.892	0.554	1174.410	0.635	20	0.219	K.QGVAVTQENSLLDNTAR.I
R4/RRR4-7/2	1264.151	1264.453	-239.285	0.465	1185.177	0.573	19	0.211	R.ILAFSQDVVSGK.I
R4/RRR4-7/2	1816.364	1816.951	-876.473	0.500	1072.411	0.643	20	0.210	K.QGVAVTQENSLLDNTAR.I
R4/RRR4-7/2	1816.503	1816.951	-247.138	0.480	1090.991	0.634	20	0.209	K.QGVAVTQENSLLDNTAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1263.764	1264.453	-1339.749	0.503	1384.058	0.457	20	0.207	R.ILAFSQDVVSGK.I
R4/RRR4-7/2	1162.027	1162.364	-290.660	0.463	1010.779	0.506	16	0.185	R.AVGALVALYER.A
R4/RRR4-7/2	1192.351	1193.334	-1668.488	0.401	909.537	0.534	17	0.181	R.VNQGLTVYGNK.G
R4/RRR4-7/2	1266.269	1266.429	-126.531	0.383	788.308	0.451	14	0.163	R.YVEWLYQHK.Q
R4/RRR4-7/2	1187.294	1187.330	-30.381	0.397	692.278	0.426	15	0.156	R.DPGLAPNSFLR.T
R4/RRR4-7/2	1162.261	1162.364	-88.553	0.417	745.059	0.416	13	0.154	R.AVGALVALYER.A
R4/RRR4-7/2	1266.557	1266.429	101.540	0.377	591.740	0.361	13	0.149	R.YVEWLYQHK.Q
R4/RRR4-7/2	1187.187	1187.330	-120.521	0.367	635.980	0.352	15	0.148	R.DPGLAPNSFLR.T
R4/RRR4-7/2	1162.429	1162.364	56.497	0.353	745.059	0.347	13	0.146	-.AVGALVALYER.-
R4/RRR4-7/2	1187.375	1187.330	38.399	0.311	604.473	0.370	14	0.146	R.DPGLAPNSFLR.T
R4/RRR4-6/2	1805.363	1805.925	-867.776	0.535	1845.040	0.640	23	0.309	R.SLGYAYVNYSSPADAAR.A
R4/RRR4-6/2	1953.501	1954.081	-811.184	0.570	1882.764	0.599	22	0.301	K.NLSENTTEDDLKEIFGK.F
R4/RRR4-6/2	1953.334	1954.081	-897.126	0.560	1543.143	0.554	22	0.241	K.NLSENTTEDDLKEIFGK.F
R4/RRR4-6/2	1018.203	1018.213	-10.234	0.489	1148.484	0.382	15	0.175	K.VAEAMEVLR.N
R4/RRR4-6/2	1315.100	1315.415	-240.070	0.416	740.454	0.480	14	0.164	R.FDDKEWYVGR.A
R4/RRR4-6/2	1182.286	1182.418	-112.114	0.429	772.412	0.380	17	0.157	K.FGTITSAVVMR.E
R4/RRR4-6/3	1549.893	1549.863	19.458	0.463	1393.498	0.394	25	0.149	-.M*VGSKPLYVALAQR.-
R4/RRR4-6/2	1183.302	1182.418	-98.153	0.255	605.234	0.331	16	0.142	K.FGTITSAVVMR.E
R4/RRR4-6/2	1183.299	1182.418	-101.464	0.206	603.394	0.315	13	0.136	K.FGTITSAVVMR.E
R4/RRR4-6/3	1831.583	1831.172	224.800	0.408	1259.965	0.398	26	0.132	R.ALEM*LNFTPINGKPIR.I
R4/RRR4-6/3	1830.955	1831.172	-119.271	0.420	1144.014	0.422	27	0.127	R.ALEM*LNFTPINGKPIR.I
R4/RRR4-6/3	1442.889	1443.588	-1181.075	0.484	887.373	0.480	23	0.122	K.KFDDKEWYVGR.A
R4/RRR4-6/3	1442.991	1443.588	-1109.973	0.480	669.333	0.541	20	0.121	K.KFDDKEWYVGR.A
R4/RRR4-6/3	1830.733	1831.172	-240.870	0.388	996.033	0.390	26	0.108	R.ALEM*LNFTPINGKPIR.I
R4/RRR4-19/2	1576.465	1576.776	-197.395	0.541	1592.438	0.478	21	0.232	K.SNGQILAINEIFEK.N
R4/RRR4-19/3	1274.769	1274.574	153.653	0.500	2525.940	0.157	25	0.227	R.VRFPCIQIIK.T
R4/RRR4-19/3	1273.991	1274.574	-1245.922	0.507	2487.863	0.168	25	0.224	R.VRFPCIQIIK.T
R4/RRR4-19/3	1274.632	1274.574	45.750	0.552	2443.392	0.176	25	0.218	R.VRFPCIQIIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-19/2	1576.393	1576.776	-243.617	0.534	1500.278	0.443	21	0.213	K.SNGQILAINEIFEK.N
R4/RRR4-19/2	1575.757	1576.776	-1284.741	0.384	1661.311	0.319	21	0.203	K.SNGQILAINEIFEK.N
R4/RRR4-19/2	1134.159	1134.272	-99.923	0.380	1192.450	0.426	15	0.184	R.FHQYQVVGR.G
R4/RRR4-19/2	1134.014	1134.272	-228.201	0.426	971.191	0.410	14	0.169	R.FHQYQVVGR.G
R4/RRR4-19/2	1134.061	1134.272	-186.410	0.421	930.759	0.355	15	0.161	R.FHQYQVVGR.G
R4/RRR4-19/2	1264.000	1264.479	-380.080	0.433	1321.715	0.230	16	0.160	R.M*KLWATNEVR.A
R4/RRR4-19/2	1192.084	1192.303	-184.629	0.322	382.462	0.578	15	0.158	R.GLPTPTDEHPK.I
R4/RRR4-19/2	1274.039	1274.574	-1208.145	0.382	1150.403	0.260	15	0.155	R.VRFPCIQIIK.T
R4/RRR4-18/2	1133.994	1134.272	-246.236	0.336	743.156	0.326	13	0.149	R.FHQYQVVGR.G
R4/RRR4-19/2	1264.241	1264.479	-189.125	0.462	1074.708	0.233	15	0.147	R.M*KLWATNEVR.A
R4/RRR4-19/2	1273.923	1274.574	-1299.656	0.390	1144.878	0.197	15	0.146	R.VRFPCIQIIK.T
R4/RRR4-18/2	1133.973	1134.272	-264.596	0.375	714.522	0.278	13	0.145	R.FHQYQVVGR.G
R4/RRR4-19/2	1134.336	1134.272	56.709	0.358	669.686	0.283	13	0.145	R.FHQYQVVGR.G
R4/RRR4-19/2	1192.058	1192.303	-206.407	0.254	322.887	0.441	14	0.145	R.GLPTPTDEHPK.I
R4/RRR4-19/2	1191.366	1192.303	-1630.712	0.224	231.209	0.559	12	0.143	R.GLPTPTDEHPK.I
R4/RRR4-12/2	1134.237	1134.272	-30.507	0.276	192.806	0.289	10	0.142	-.FHQYQVVGR.-
R4/RRR4-20/2	1135.170	1134.272	-90.235	0.367	266.928	0.282	11	0.142	-.FHQYQVVGR.-
R4/RRR4-19/2	1264.121	1264.479	-284.351	0.437	1027.032	0.197	15	0.141	R.M*KLWATNEVR.A
R4/RRR4-19/2	1274.083	1274.574	-386.083	0.413	903.002	0.206	14	0.138	R.VRFPCIQIIK.T
R4/RRR4-19/3	1478.595	1478.614	-13.264	0.418	705.450	0.492	20	0.112	R.TGYHNM*YKEYR.D
R4/RRR4-19/3	1238.282	1238.460	-143.837	0.444	805.384	0.457	20	0.111	K.SDIKFPLVYR.K
R4/RRR4-19/3	1478.496	1478.614	-79.969	0.437	605.682	0.491	21	0.110	R.TGYHNM*YKEYR.D
R4/RRR4-19/3	1478.771	1478.614	106.337	0.370	359.892	0.415	15	0.091	-.TGYHNM*YKEYR.-
R4/RRR4-19/3	1238.439	1238.460	-16.581	0.340	709.448	0.366	18	0.091	K.SDIKFPLVYR.K
R4/RRR4-15/2	1688.194	1687.833	214.485	0.528	3134.392	0.600	27	0.571	K.VVTAAAAGGGGELTVEER.N
R4/RRR4-15/2	1688.225	1687.833	232.540	0.549	2932.703	0.571	26	0.505	K.VVTAAAAGGGGELTVEER.N
R4/RRR4-15/2	1687.403	1687.833	-255.670	0.475	2937.208	0.500	26	0.477	K.VVTAAAAGGGGELTVEER.N
R4/RRR4-15/2	1954.757	1955.136	-194.529	0.561	2693.980	0.606	27	0.461	K.DAADATLAAYQAAQDIAM*K.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1687.186	1687.833	-979.283	0.434	2928.942	0.444	26	0.453	K.VVTAAAAGGGGELTVEER.N
R4/RRR4-15/2	1772.461	1773.021	-882.571	0.590	2360.890	0.528	23	0.361	R.ARVEAELSNICAGILR.L
R4/RRR4-15/2	1954.654	1955.136	-247.406	0.546	2207.960	0.585	25	0.351	K.DAADATLAAYQAAQDIAM*K.E
R4/RRR4-15/2	1545.231	1545.757	-990.011	0.517	2422.235	0.429	23	0.343	R.VEAELSNICAGILR.L
R4/RRR4-15/2	1772.672	1773.021	-197.303	0.566	2201.691	0.484	23	0.318	R.ARVEAELSNICAGILR.L
R4/RRR4-14/2	1545.535	1545.757	-143.594	0.521	2199.376	0.402	22	0.294	R.VEAELSNICAGILR.L
R4/RRR4-15/2	1545.274	1545.757	-312.939	0.550	2020.955	0.444	22	0.279	R.VEAELSNICAGILR.L
R4/RRR4-15/2	1772.623	1773.021	-225.213	0.533	1678.494	0.504	21	0.245	R.ARVEAELSNICAGILR.L
R4/RRR4-14/2	1772.487	1773.021	-867.914	0.458	1493.680	0.479	23	0.220	R.ARVEAELSNICAGILR.L
R4/RRR4-15/2	1938.482	1939.136	-856.060	0.437	1125.906	0.562	21	0.196	K.DAADATLAAYQAAQDIAMK.E
R4/RRR4-15/2	1938.416	1939.136	-890.008	0.440	1165.837	0.494	21	0.187	K.DAADATLAAYQAAQDIAMK.E
R4/RRR4-14/2	1772.347	1773.021	-947.219	0.452	1201.990	0.444	21	0.184	R.ARVEAELSNICAGILR.L
R4/RRR4-15/2	1939.289	1939.136	78.754	0.485	819.717	0.562	21	0.176	K.DAADATLAAYQAAQDIAMK.E
R4/RRR4-15/2	1025.870	1026.212	-333.772	0.347	415.028	0.615	16	0.166	R.LVPAAAAVDAK.V
R4/RRR4-14/2	1025.917	1026.212	-287.929	0.325	328.534	0.566	15	0.158	R.LVPAAAAVDAK.V
R4/RRR4-15/2	1025.864	1026.212	-339.503	0.325	284.217	0.530	14	0.155	R.LVPAAAAVDAK.V
R4/RRR4-15/2	1025.688	1026.212	-1489.573	0.280	400.605	0.533	16	0.154	R.LVPAAAAVDAK.V
R4/RRR4-14/2	1025.911	1026.212	-293.540	0.257	416.325	0.452	15	0.148	R.LVPAAAAVDAK.V
R4/RRR4-14/2	1025.748	1026.212	-452.817	0.239	319.684	0.473	15	0.147	R.LVPAAAAVDAK.V
R4/RRR4-15/3	1688.448	1687.833	-228.798	0.498	986.416	0.491	29	0.132	K.VVTAAAAGGGGELTVEER.N
R4/RRR4-15/3	1773.676	1773.021	-195.162	0.500	1322.293	0.339	30	0.122	R.ARVEAELSNICAGILR.L
R4/RRR4-15/3	1954.869	1955.136	-136.684	0.438	976.473	0.427	30	0.116	K.DAADATLAAYQAAQDIAM*K.E
R4/RRR4-15/3	1687.687	1687.833	-86.963	0.362	901.868	0.331	24	0.091	K.VVTAAAAGGGGELTVEER.N
R4/RRR4-14/3	1772.924	1773.021	-54.952	0.360	1267.197	0.212	25	0.090	R.ARVEAELSNICAGILR.L
R4/RRR4-15/3	1954.105	1955.136	-1042.400	0.262	685.733	0.292	23	0.082	K.DAADATLAAYQAAQDIAM*K.E
R4/RRR4-15/3	1937.692	1939.136	-1265.139	0.370	836.515	0.263	25	0.082	K.DAADATLAAYQAAQDIAMK.E
R4/RRR4-25/3	1456.319	1456.668	-240.256	0.382	1734.487	0.413	27	1.000	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/2	1536.270	1536.798	-997.540	0.558	2060.034	0.558	23	0.321	K.KLLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	1536.356	1536.798	-288.377	0.545	2026.428	0.548	23	0.312	K.KLLGVTIYSSDAIR.S
R4/RRR4-24/2	1536.421	1536.798	-246.209	0.530	1975.630	0.561	23	0.308	K.KLLGVTIYSSDAIR.S
R4/RRR4-25/2	1537.450	1536.798	-227.091	0.586	1843.469	0.598	22	0.298	K.KLLGVTIYSSDAIR.S
R4/RRR4-25/2	1409.219	1408.625	-289.024	0.581	1701.146	0.607	21	0.280	K.LLGVTIYSSDAIR.S
R4/RRR4-25/2	1409.192	1408.625	-307.971	0.614	1716.847	0.581	21	0.274	K.LLGVTIYSSDAIR.S
R4/RRR4-24/2	1536.364	1536.798	-283.435	0.527	1810.609	0.525	22	0.272	K.KLLGVTIYSSDAIR.S
R4/RRR4-24/2	1537.300	1536.798	-325.075	0.587	1776.866	0.530	22	0.268	K.KLLGVTIYSSDAIR.S
R4/RRR4-24/2	1838.189	1838.014	95.541	0.513	1662.592	0.601	26	0.268	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1457.395	1456.668	-187.983	0.525	1547.861	0.654	21	0.262	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/2	1839.299	1838.014	155.393	0.567	1565.816	0.587	25	0.250	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1408.593	1408.625	-22.653	0.564	1610.018	0.540	21	0.250	K.LLGVTIYSSDAIR.S
R4/RRR4-22/2	1457.198	1456.668	-323.283	0.476	1570.037	0.591	21	0.249	R.SGTLIDAIGIYVHP.-
R4/RRR4-22/2	1457.197	1456.668	-324.376	0.494	1601.849	0.575	21	0.249	R.SGTLIDAIGIYVHP.-
R4/RRR4-23/2	1409.238	1408.625	-275.641	0.516	1593.987	0.543	21	0.248	K.LLGVTIYSSDAIR.S
R4/RRR4-25/2	1837.786	1838.014	-124.423	0.531	1486.548	0.613	25	0.248	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-18/2	1457.359	1456.668	-213.023	0.460	1519.712	0.612	20	0.246	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/2	1457.073	1456.668	278.757	0.497	1653.040	0.530	21	0.245	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/2	1837.624	1838.014	-212.649	0.497	1610.576	0.535	26	0.244	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-23/2	1408.313	1408.625	-222.007	0.511	1612.178	0.512	21	0.243	K.LLGVTIYSSDAIR.S
R4/RRR4-24/2	1838.270	1838.014	140.161	0.509	1522.422	0.575	25	0.243	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1837.684	1838.014	-179.863	0.529	1615.010	0.524	26	0.241	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-19/2	1408.126	1408.625	-355.679	0.490	1616.738	0.498	21	0.240	K.LLGVTIYSSDAIR.S
R4/RRR4-24/2	1408.387	1408.625	-169.574	0.535	1598.350	0.506	21	0.240	K.LLGVTIYSSDAIR.S
R4/RRR4-24/2	1457.028	1456.668	247.674	0.457	1606.004	0.533	21	0.239	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/2	1837.707	1838.014	-167.202	0.514	1508.272	0.561	25	0.238	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1838.246	1838.014	126.842	0.539	1412.339	0.602	25	0.237	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1736.188	1735.876	180.136	0.517	1451.615	0.562	26	0.235	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1456.183	1456.668	-333.935	0.443	1608.080	0.513	21	0.235	R.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	1837.637	1838.014	-205.652	0.541	1443.467	0.579	25	0.235	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1838.171	1838.014	85.684	0.546	1499.202	0.548	25	0.233	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1837.582	1838.014	-235.441	0.469	1445.322	0.563	26	0.231	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1992.635	1993.210	-792.918	0.508	1324.803	0.624	22	0.231	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-25/2	1838.629	1838.014	-209.603	0.522	1547.629	0.515	25	0.231	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1837.571	1838.014	-241.439	0.518	1446.672	0.559	25	0.230	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-22/2	1456.790	1456.668	83.826	0.494	1568.010	0.544	21	0.230	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/2	1839.401	1838.014	211.231	0.542	1474.337	0.546	25	0.230	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1837.594	1838.014	-229.110	0.548	1412.535	0.564	25	0.228	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1838.314	1838.014	164.002	0.534	1347.067	0.589	24	0.226	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1408.250	1408.625	-267.227	0.515	1575.070	0.458	21	0.225	K.LLGVTIYSSDAIR.S
R4/RRR4-25/2	1839.110	1838.014	52.619	0.507	1429.903	0.545	25	0.225	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1837.681	1838.014	-181.662	0.530	1306.522	0.587	24	0.221	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1837.939	1838.014	-40.876	0.549	1341.433	0.570	24	0.221	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1837.563	1838.014	-246.105	0.510	1267.039	0.587	25	0.218	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1838.549	1838.014	-253.165	0.548	1351.379	0.542	25	0.216	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1837.385	1838.014	-888.902	0.474	1322.351	0.551	25	0.216	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1456.383	1456.668	-196.268	0.458	1599.773	0.462	21	0.214	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/2	1837.615	1838.014	-217.448	0.513	1322.118	0.546	24	0.214	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1994.593	1993.210	192.586	0.515	1061.572	0.642	22	0.210	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-23/2	1736.248	1735.876	214.543	0.520	1152.745	0.581	24	0.209	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/2	1837.604	1838.014	-223.512	0.532	1209.190	0.572	23	0.208	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1837.207	1838.014	-986.220	0.532	1251.004	0.544	24	0.207	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1838.448	1838.014	237.181	0.508	1140.837	0.592	23	0.206	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1992.776	1993.210	-218.457	0.491	1054.115	0.623	22	0.205	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1838.346	1838.014	181.582	0.530	1219.175	0.543	24	0.204	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1993.724	1993.210	-244.944	0.546	1008.025	0.631	21	0.203	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1992.471	1993.210	-875.448	0.508	962.003	0.642	22	0.202	K.EFSIPLQDSGHVVGFFGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1735.265	1735.876	-931.477	0.473	1130.447	0.556	24	0.201	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-23/2	1735.471	1735.876	-234.267	0.521	1069.701	0.578	23	0.201	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/3	1736.508	1735.876	-212.842	0.479	1441.905	0.538	31	0.200	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1991.757	1993.210	-1235.248	0.454	1070.579	0.593	22	0.200	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1736.183	1735.876	176.822	0.488	1123.212	0.546	24	0.199	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/2	1992.641	1993.210	-790.089	0.495	957.749	0.623	23	0.199	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1737.258	1735.876	220.056	0.495	1188.041	0.514	25	0.199	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-23/2	1993.163	1993.210	-23.810	0.492	995.065	0.612	22	0.199	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-25/2	1838.585	1838.014	-234.048	0.449	1341.188	0.463	24	0.199	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-21/2	1735.398	1735.876	-276.467	0.453	1125.066	0.549	23	0.198	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1992.443	1993.210	-889.717	0.516	997.392	0.608	21	0.197	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1838.493	1838.014	261.349	0.535	1144.555	0.547	23	0.197	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1735.724	1735.876	-88.288	0.475	1153.085	0.524	24	0.197	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1735.752	1735.876	-71.992	0.422	1186.678	0.505	24	0.195	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1991.725	1993.210	-1251.620	0.445	1009.934	0.587	22	0.194	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-25/2	1837.606	1838.014	-222.379	0.530	1017.028	0.577	23	0.194	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/2	1736.239	1735.876	209.537	0.465	1060.785	0.546	23	0.194	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/2	1837.843	1838.014	-92.842	0.495	1006.101	0.590	21	0.193	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-1/2	1735.220	1735.876	-957.467	0.421	1109.137	0.530	23	0.193	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-23/2	1991.985	1993.210	-1120.352	0.495	1012.455	0.573	22	0.193	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-25/2	1993.485	1993.210	138.092	0.517	906.188	0.618	21	0.193	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1735.367	1735.876	-872.227	0.483	1070.827	0.531	23	0.192	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-23/2	1456.282	1456.668	-265.727	0.399	1417.863	0.488	20	0.191	R.SGTLIDAIGIYVHP.-
R4/RRR4-21/2	1456.931	1456.668	180.881	0.445	1426.743	0.497	20	0.191	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/2	1993.826	1993.210	-193.288	0.528	892.079	0.608	21	0.190	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1456.260	1456.668	-280.949	0.438	1427.307	0.491	20	0.190	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/2	1407.549	1408.625	-1479.418	0.394	1375.385	0.382	20	0.189	K.LLGVTIYSSDAIR.S
R4/RRR4-24/2	1992.446	1993.210	-888.241	0.501	866.613	0.610	21	0.189	K.EFSIPLQDSGHVVGFFGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1737.240	1735.876	210.121	0.462	1050.596	0.516	23	0.188	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/2	1839.383	1838.014	201.715	0.566	953.721	0.572	22	0.187	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-23/2	1736.522	1735.876	-204.583	0.561	938.956	0.557	22	0.187	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1837.370	1838.014	-897.172	0.443	1130.309	0.493	23	0.187	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1735.309	1735.876	-905.771	0.459	973.212	0.546	22	0.187	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1455.545	1456.668	-1463.188	0.331	1480.537	0.402	20	0.186	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/2	1992.144	1993.210	-1040.304	0.445	926.360	0.571	21	0.185	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-1/2	1992.844	1993.210	-184.475	0.488	850.355	0.590	21	0.184	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-23/2	1736.192	1735.876	182.252	0.442	1034.573	0.504	23	0.184	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1736.252	1735.876	216.869	0.470	907.641	0.551	22	0.184	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1838.178	1838.014	89.613	0.524	985.881	0.538	22	0.184	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1456.288	1456.668	-261.438	0.426	1438.999	0.457	20	0.184	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/2	1735.703	1735.876	-100.069	0.432	1089.390	0.479	23	0.183	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/2	1736.345	1735.876	270.801	0.468	1016.872	0.500	23	0.183	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/2	1737.290	1735.876	238.728	0.534	987.108	0.508	22	0.181	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1735.332	1735.876	-892.706	0.446	976.054	0.510	22	0.181	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1992.992	1993.210	-109.758	0.482	741.930	0.606	20	0.180	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-2/2	1735.337	1735.876	-889.670	0.453	863.557	0.548	21	0.179	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-23/2	1991.625	1993.210	-1805.702	0.437	828.694	0.576	20	0.179	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-21/2	1735.421	1735.876	-263.059	0.449	924.161	0.511	22	0.178	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/2	1839.337	1838.014	176.292	0.484	836.988	0.555	21	0.177	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-23/2	1995.141	1993.210	-35.017	0.520	683.425	0.588	21	0.176	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-23/2	1408.181	1408.625	-316.365	0.397	1106.099	0.420	18	0.175	K.LLGVTIYSSDAIR.S
R4/RRR4-22/2	1992.963	1993.210	-124.504	0.451	743.553	0.566	19	0.172	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1994.747	1993.210	-233.157	0.493	774.247	0.544	20	0.172	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-24/2	1838.263	1838.014	136.165	0.450	982.543	0.473	21	0.172	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-24/3	1736.693	1735.876	-105.906	0.466	1378.287	0.482	31	0.171	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1456.228	1456.668	-303.320	0.403	1405.314	0.417	19	0.169	R.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-19/2	1735.447	1735.876	-248.381	0.441	831.417	0.476	21	0.167	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1455.748	1456.668	-1322.780	0.315	1455.961	0.342	19	0.167	R.SGTLIDAIGIYVHP.-
R4/RRR4-15/2	1456.310	1456.668	-246.722	0.382	1347.370	0.436	19	0.166	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/2	1839.516	1838.014	-271.136	0.474	965.046	0.429	21	0.164	K.IGPWGGNGGSAQDISVPPK.K
R4/RRR4-25/2	1455.766	1456.668	-1310.568	0.328	1343.825	0.388	19	0.159	R.SGTLIDAIGIYVHP.-
R4/RRR4-19/2	1735.343	1735.876	-886.421	0.417	661.765	0.473	19	0.159	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1991.771	1993.210	-1228.601	0.363	688.222	0.447	19	0.155	K.EFSIPLQDSGHVVGFFGR.S
R4/RRR4-20/2	1735.135	1735.876	-1006.555	0.421	648.325	0.430	19	0.154	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-20/2	1456.081	1456.668	-1093.426	0.349	1149.048	0.477	18	0.154	R.SGTLIDAIGIYVHP.-
R4/RRR4-22/2	1736.505	1735.876	-214.597	0.408	698.865	0.414	19	0.154	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/2	1837.910	1838.014	-56.465	0.420	640.513	0.448	18	0.151	-.IGPWGGNGGSAQDISVPPK.-
R4/RRR4-18/2	1456.297	1456.668	-255.804	0.395	1148.487	0.464	18	0.148	R.SGTLIDAIGIYVHP.-
R4/RRR4-22/2	1736.643	1735.876	-134.631	0.373	583.883	0.378	18	0.147	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-25/3	1966.586	1966.187	203.851	0.407	1180.605	0.473	38	0.147	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-22/2	1408.121	1408.625	-1071.020	0.277	421.609	0.451	13	0.146	K.LLGVTIYSSDAIR.S
R4/RRR4-25/3	1966.286	1966.187	50.610	0.458	1259.779	0.450	41	0.146	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/2	1407.600	1408.625	-1442.918	0.315	607.343	0.335	13	0.142	K.LLGVTIYSSDAIR.S
R4/RRR4-23/2	1456.190	1456.668	-328.972	0.410	971.673	0.499	17	0.141	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/3	1967.110	1966.187	-38.790	0.483	1094.995	0.480	39	0.140	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-17/2	1455.882	1456.668	-1230.234	0.300	542.197	0.393	14	0.140	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/3	1967.023	1966.187	-83.421	0.461	1061.227	0.474	36	0.138	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-15/2	1455.410	1456.668	-1556.282	0.270	899.142	0.455	16	0.137	R.SGTLIDAIGIYVHP.-
R4/RRR4-19/2	1456.447	1456.668	-152.125	0.283	586.128	0.383	14	0.136	R.SGTLIDAIGIYVHP.-
R4/RRR4-21/2	1456.123	1456.668	-1063.965	0.357	847.394	0.457	17	0.134	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/3	1966.707	1966.187	-244.705	0.441	982.358	0.483	37	0.133	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.066	1966.187	-61.292	0.448	970.779	0.485	37	0.133	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.326	1966.187	71.064	0.427	981.542	0.471	35	0.132	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-1/2	1455.807	1456.668	-1282.526	0.304	526.926	0.290	14	0.131	-.SGTLIDAIGIYVHP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/3	1966.138	1966.187	-24.767	0.422	944.256	0.480	36	0.131	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-23/2	1455.924	1456.668	-1201.354	0.296	749.605	0.419	15	0.130	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/2	1456.317	1456.668	-241.592	0.440	930.253	0.459	16	0.130	R.SGTLIDAIGIYVHP.-
R4/RRR4-25/3	1966.503	1966.187	161.274	0.469	885.049	0.491	35	0.130	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-9/2	1456.353	1456.668	-216.785	0.365	799.409	0.432	16	0.129	R.SGTLIDAIGIYVHP.-
R4/RRR4-21/2	1455.759	1456.668	-1315.032	0.279	994.538	0.384	17	0.129	R.SGTLIDAIGIYVHP.-
R4/RRR4-10/2	1456.455	1456.668	-146.492	0.375	829.254	0.420	15	0.127	-.SGTLIDAIGIYVHP.-
R4/RRR4-24/2	1456.078	1456.668	-1095.446	0.310	657.447	0.348	14	0.127	R.SGTLIDAIGIYVHP.-
R4/RRR4-14/2	1456.266	1456.668	-276.912	0.328	897.501	0.401	16	0.126	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/3	1965.360	1966.187	-931.980	0.430	906.095	0.467	36	0.126	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.502	1966.187	160.807	0.423	962.326	0.447	37	0.124	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1967.040	1966.187	-74.831	0.383	1078.594	0.400	35	0.123	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1967.449	1966.187	133.628	0.447	1071.262	0.408	37	0.122	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.395	1966.187	106.365	0.414	742.727	0.487	34	0.122	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.063	1966.187	-62.880	0.422	854.804	0.448	36	0.119	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.840	1966.187	-176.898	0.407	973.699	0.414	35	0.119	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1537.332	1536.798	-304.012	0.421	1145.038	0.392	27	0.119	K.KLLGVTIYSSDAIR.S
R4/RRR4-25/3	1536.959	1536.798	104.976	0.466	1076.596	0.410	26	0.119	K.KLLGVTIYSSDAIR.S
R4/RRR4-15/2	1455.997	1456.668	-1151.512	0.315	890.144	0.344	16	0.119	R.SGTLIDAIGIYVHP.-
R4/RRR4-24/3	1966.123	1966.187	-32.614	0.368	1094.446	0.362	32	0.117	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.995	1966.187	-97.428	0.425	839.688	0.440	35	0.117	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.915	1966.187	-138.609	0.432	986.790	0.406	37	0.117	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.539	1966.187	179.855	0.441	1066.204	0.380	37	0.116	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1967.025	1966.187	-82.581	0.442	708.073	0.453	32	0.116	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.283	1966.187	49.022	0.343	506.226	0.470	28	0.115	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.497	1966.187	158.566	0.438	773.063	0.431	35	0.114	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.478	1966.187	148.761	0.414	606.212	0.451	32	0.113	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.236	1966.187	25.299	0.416	851.082	0.407	34	0.112	K.IGPWGGNGGSAQDISVPPKK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/3	1966.280	1966.187	47.435	0.388	698.990	0.432	33	0.112	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1967.542	1966.187	181.412	0.427	761.196	0.412	33	0.111	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.346	1966.187	81.524	0.333	579.074	0.420	28	0.110	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.997	1966.187	-96.401	0.373	546.108	0.421	31	0.110	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.407	1966.187	112.529	0.372	814.067	0.393	33	0.110	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.468	1966.187	143.532	0.371	772.467	0.397	33	0.109	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.226	1966.187	20.255	0.406	740.150	0.395	33	0.108	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1967.065	1966.187	-61.946	0.409	631.060	0.397	31	0.107	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.703	1966.187	-246.573	0.396	800.539	0.375	34	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-23/3	1966.388	1966.187	103.003	0.323	504.598	0.363	27	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1737.019	1735.876	82.419	0.439	822.321	0.400	26	0.103	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/3	1967.221	1966.187	17.693	0.409	691.714	0.353	31	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1966.400	1966.187	109.073	0.240	532.768	0.317	27	0.102	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1736.939	1735.876	36.216	0.404	588.782	0.444	23	0.102	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/3	1965.931	1966.187	-130.146	0.316	590.413	0.288	30	0.100	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-24/3	1966.765	1966.187	-214.817	0.348	586.638	0.287	28	0.100	K.IGPWGGNGGSAQDISVPPKK.L
R4/RRR4-25/3	1736.270	1735.876	227.507	0.445	607.581	0.414	23	0.099	K.IVTSANNTYEAGVPNGK.E
R4/RRR4-24/3	1537.619	1536.798	-116.433	0.390	883.853	0.320	28	0.091	K.KLLGVTIYSSDAIR.S
R4/RRR4-11/2	1818.396	1818.927	-844.656	0.601	3077.939	0.682	27	0.594	R.HETADINTFSWGVANR.G
R4/RRR4-11/2	1818.282	1818.927	-907.601	0.611	3040.061	0.682	28	0.584	R.HETADINTFSWGVANR.G
R4/RRR4-10/2	1818.399	1818.927	-842.971	0.618	2903.461	0.723	28	0.567	R.HETADINTFSWGVANR.G
R4/RRR4-11/2	1818.622	1818.927	-168.081	0.624	2873.552	0.689	28	0.544	R.HETADINTFSWGVANR.G
R4/RRR4-10/2	1819.640	1818.927	-158.567	0.666	2712.381	0.693	28	0.505	R.HETADINTFSWGVANR.G
R4/RRR4-11/3	1627.616	1627.700	-51.545	0.517	2636.157	0.509	33	0.449	R.HKEHISAYGEGNER.R
R4/RRR4-10/2	1818.376	1818.927	-855.910	0.629	2410.873	0.718	26	0.445	R.HETADINTFSWGVANR.G
R4/RRR4-10/2	1810.594	1811.095	-831.208	0.562	2365.718	0.535	24	0.367	K.IIAEYIWIGGSGM*DLR.S
R4/RRR4-10/2	1811.108	1811.095	7.374	0.570	2228.853	0.541	25	0.344	K.IIAEYIWIGGSGM*DLR.S
R4/RRR4-11/3	1627.463	1627.700	-146.003	0.524	2234.302	0.513	32	0.341	R.HKEHISAYGEGNER.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/3	1628.024	1627.700	199.918	0.511	2090.239	0.502	30	0.303	R.HKEHISAYGEGNER.R
R4/RRR4-10/2	1810.169	1811.095	-1066.716	0.491	2092.078	0.482	24	0.301	K.IIAEYIWIGGSGM*DLR.S
R4/RRR4-11/3	1628.501	1627.700	-122.603	0.515	1845.766	0.550	29	0.275	R.HKEHISAYGEGNER.R
R4/RRR4-10/3	1627.579	1627.700	-74.453	0.536	1847.236	0.521	29	0.262	R.HKEHISAYGEGNER.R
R4/RRR4-10/3	1627.239	1627.700	-283.716	0.519	1904.713	0.478	29	0.253	R.HKEHISAYGEGNER.R
R4/RRR4-11/3	1818.351	1818.927	-869.261	0.516	1504.436	0.475	29	0.186	R.HETADINTFSWGVANR.G
R4/RRR4-10/2	1440.260	1440.667	-283.050	0.409	1144.615	0.381	19	0.171	R.TLSGPVTDPSKLPK.W
R4/RRR4-10/3	1399.811	1399.555	183.321	0.523	1736.459	0.331	26	0.164	K.SM*RNDGGYEIIK.S
R4/RRR4-10/2	1441.171	1440.667	-345.229	0.408	1075.779	0.354	18	0.162	-.TLSGPVTDPSKLPK.-
R4/RRR4-11/2	1441.247	1440.667	-292.541	0.430	870.629	0.377	18	0.155	-.TLSGPVTDPSKLPK.-
R4/RRR4-10/2	1440.306	1440.667	-251.589	0.420	768.243	0.398	17	0.153	-.TLSGPVTDPSKLPK.-
R4/RRR4-11/2	1441.242	1440.667	-295.685	0.442	755.004	0.380	16	0.149	-.TLSGPVTDPSKLPK.-
R4/RRR4-11/2	1440.589	1440.667	-53.936	0.420	819.899	0.346	17	0.149	-.TLSGPVTDPSKLPK.-
R4/RRR4-10/3	1818.469	1818.927	-252.500	0.471	1464.385	0.367	28	0.145	R.HETADINTFSWGVANR.G
R4/RRR4-10/3	1818.951	1818.927	12.909	0.509	1262.526	0.437	26	0.144	R.HETADINTFSWGVANR.G
R4/RRR4-10/3	1362.363	1362.387	-17.724	0.470	1591.984	0.280	27	0.132	K.EHISAYGEGNER.R
R4/RRR4-11/3	1783.498	1783.886	-218.081	0.431	840.205	0.508	28	0.123	R.HKEHISAYGEGNERR.L
R4/RRR4-10/3	1810.256	1811.095	-1018.685	0.464	1109.215	0.383	25	0.115	K.IIAEYIWIGGSGM*DLR.S
R4/RRR4-10/3	1399.294	1399.555	-186.993	0.526	701.607	0.428	22	0.105	K.SM*RNDGGYEIIK.S
R4/RRR4-10/3	1819.173	1818.927	135.770	0.507	849.693	0.411	22	0.104	-.HETADINTFSWGVANR.-
R4/RRR4-10/3	1399.910	1399.555	254.151	0.491	1143.293	0.302	24	0.100	K.SM*RNDGGYEIIK.S
R4/RRR4-11/3	1399.445	1399.555	-78.836	0.449	848.202	0.350	21	0.096	K.SM*RNDGGYEIIK.S
R4/RRR4-11/3	1818.218	1818.927	-942.757	0.344	640.306	0.274	23	0.085	R.HETADINTFSWGVANR.G
R4/RRR4-11/3	1362.570	1362.387	134.856	0.395	829.193	0.156	21	0.063	-.EHISAYGEGNER.-
R4/RRR4-6/2	1281.114	1281.437	-252.938	0.326	819.873	0.363	16	0.150	R.EIAEAYLGSSIK.N
R4/RRR4-6/2	1281.117	1281.437	-250.548	0.287	445.397	0.315	13	0.137	-.EIAEAYLGSSIK.-
R4/RRR4-4/2	1479.593	1478.672	-53.259	0.488	1859.132	0.564	21	0.290	R.EVIAIASNALDSFK.N
R4/RRR4-3/2	1937.370	1936.194	91.282	0.552	1980.329	0.470	25	0.279	R.IVLEADGYQPYLISPEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1936.428	1936.194	121.170	0.573	1564.018	0.553	22	0.243	R.IVLEADGYQPYLISPEK.G
R4/RRR4-3/2	1935.573	1936.194	-840.078	0.536	1570.976	0.524	22	0.237	R.IVLEADGYQPYLISPEK.G
R4/RRR4-4/2	1935.623	1936.194	-813.995	0.462	1522.517	0.463	22	0.217	R.IVLEADGYQPYLISPEK.G
R4/RRR4-3/2	1643.259	1643.608	-212.990	0.522	1226.860	0.569	23	0.212	R.SAFDSASNGPSSGSESR.S
R4/RRR4-4/2	1936.996	1936.194	-102.628	0.498	1495.433	0.442	22	0.209	R.IVLEADGYQPYLISPEK.G
R4/RRR4-4/2	1782.339	1782.035	171.556	0.443	1179.420	0.579	23	0.207	R.VLLDIVNASANATPGLGR.Y
R4/RRR4-4/2	1782.889	1782.035	-82.038	0.453	1093.032	0.567	23	0.198	R.VLLDIVNASANATPGLGR.Y
R4/RRR4-3/2	1140.133	1140.358	-197.982	0.428	903.469	0.468	15	0.169	R.LPNLLSGLQGK.S
R4/RRR4-3/2	931.721	932.093	-400.615	0.359	990.592	0.384	13	0.163	R.AVALELCR.E
R4/RRR4-3/2	1781.489	1782.035	-869.989	0.338	824.507	0.418	19	0.154	R.VLLDIVNASANATPGLGR.Y
R4/RRR4-3/2	1781.365	1782.035	-940.225	0.285	818.337	0.351	19	0.146	R.VLLDIVNASANATPGLGR.Y
R4/RRR4-5/2	1783.788	1782.035	-138.898	0.281	191.535	0.396	14	0.140	R.VLLDIVNASANATPGLGR.Y
R4/RRR4-1/2	1643.606	1643.608	-1.461	0.357	496.703	0.352	15	0.136	R.SAFDSASNGPSSGSESR.S
R4/RRR4-3/3	1116.387	1116.255	118.915	0.530	1625.192	0.274	22	0.131	R.HFDLSNVKR.I
R4/RRR4-3/3	1116.674	1116.255	376.767	0.571	1585.862	0.274	22	0.127	R.HFDLSNVKR.I
R4/RRR4-5/2	1783.402	1782.035	206.399	0.281	160.465	0.402	13	0.124	-.VLLDIVNASANATPGLGR.-
R4/RRR4-3/3	1116.586	1116.255	297.025	0.576	1611.582	0.244	22	0.121	R.HFDLSNVKR.I
R4/RRR4-3/3	1212.808	1212.295	-402.774	0.446	1067.254	0.357	21	0.106	R.RPADPEEELR.W
R4/RRR4-3/3	1212.484	1212.295	156.699	0.423	852.157	0.418	19	0.106	R.RPADPEEELR.W
R4/RRR4-17/2	1605.366	1604.746	-237.466	0.582	1981.020	0.650	24	0.336	K.WLAANVSAEVAESTR.I
R4/RRR4-16/2	1604.746	1604.746	0.106	0.528	1972.802	0.626	24	0.326	K.WLAANVSAEVAESTR.I
R4/RRR4-18/2	1605.904	1604.746	98.991	0.517	1971.817	0.565	22	0.306	K.WLAANVSAEVAESTR.I
R4/RRR4-16/2	1340.091	1340.501	-306.400	0.517	1839.466	0.574	22	0.291	R.IIYGGSVTGANCK.E
R4/RRR4-16/2	1604.255	1604.746	-307.005	0.562	1760.478	0.566	23	0.276	K.WLAANVSAEVAESTR.I
R4/RRR4-16/2	1341.073	1340.501	-320.236	0.513	1661.133	0.586	22	0.269	R.IIYGGSVTGANCK.E
R4/RRR4-17/2	1340.007	1340.501	-369.648	0.480	1794.602	0.517	22	0.268	R.IIYGGSVTGANCK.E
R4/RRR4-16/2	1604.419	1604.746	-204.487	0.521	1621.042	0.610	22	0.268	K.WLAANVSAEVAESTR.I
R4/RRR4-16/2	1341.131	1340.501	-276.401	0.528	1616.295	0.597	22	0.267	R.IIYGGSVTGANCK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1375.072	1375.547	-346.509	0.516	1793.918	0.482	19	0.258	K.VIACVGETLEQR.E
R4/RRR4-17/2	1374.905	1375.547	-1197.700	0.497	1870.110	0.444	19	0.258	K.VIACVGETLEQR.E
R4/RRR4-16/2	1376.126	1375.547	-307.007	0.551	1820.654	0.468	19	0.258	K.VIACVGETLEQR.E
R4/RRR4-17/2	1339.688	1340.501	-1357.316	0.449	1702.926	0.523	22	0.256	R.IIYGGSVTGANCK.E
R4/RRR4-16/2	1375.096	1375.547	-328.696	0.504	1820.935	0.453	20	0.255	K.VIACVGETLEQR.E
R4/RRR4-17/2	1604.006	1604.746	-1087.850	0.523	1504.690	0.596	22	0.250	K.WLAANVSAEVAESTR.I
R4/RRR4-17/2	1375.059	1375.547	-355.862	0.522	1665.475	0.475	19	0.240	K.VIACVGETLEQR.E
R4/RRR4-17/2	1603.820	1604.746	-1204.319	0.469	1589.534	0.516	22	0.239	K.WLAANVSAEVAESTR.I
R4/RRR4-17/2	1374.537	1375.547	-1466.759	0.416	1729.573	0.442	19	0.239	K.VIACVGETLEQR.E
R4/RRR4-17/2	1340.112	1340.501	-290.955	0.460	1515.559	0.515	21	0.232	R.IIYGGSVTGANCK.E
R4/RRR4-16/2	1395.139	1395.497	-257.364	0.443	1305.897	0.559	19	0.217	R.SLLGESNEFVGDK.V
R4/RRR4-17/2	1396.120	1395.497	-270.601	0.468	1095.400	0.602	18	0.207	R.SLLGESNEFVGDK.V
R4/RRR4-17/2	1395.151	1395.497	-248.498	0.414	1251.416	0.531	19	0.206	R.SLLGESNEFVGDK.V
R4/RRR4-16/2	1636.326	1636.748	-258.413	0.464	1199.029	0.532	21	0.202	K.VATPDQAQEVHDGLR.K
R4/RRR4-16/2	1394.992	1395.497	-1082.241	0.417	1247.363	0.509	19	0.202	R.SLLGESNEFVGDK.V
R4/RRR4-16/2	1424.037	1424.560	-1072.376	0.437	1383.308	0.450	19	0.201	R.ESGSTMDVVAAQTK.A
R4/RRR4-16/2	1764.407	1764.921	-860.578	0.466	1152.409	0.499	20	0.190	K.VATPDQAQEVHDGLRK.W
R4/RRR4-17/2	1395.059	1395.497	-314.513	0.373	1260.028	0.443	19	0.189	R.SLLGESNEFVGDK.V
R4/RRR4-16/2	1764.314	1764.921	-913.712	0.444	1182.983	0.483	19	0.188	K.VATPDQAQEVHDGLRK.W
R4/RRR4-16/2	1424.344	1424.560	-152.116	0.425	1171.638	0.448	18	0.183	R.ESGSTMDVVAAQTK.A
R4/RRR4-16/2	1636.186	1636.748	-957.726	0.487	1003.910	0.494	20	0.180	K.VATPDQAQEVHDGLR.K
R4/RRR4-16/2	1424.100	1424.560	-323.747	0.440	1153.512	0.399	18	0.173	R.ESGSTMDVVAAQTK.A
R4/RRR4-16/2	1440.022	1440.559	-1071.070	0.381	1050.087	0.442	18	0.173	R.ESGSTM*DVVAAQTK.A
R4/RRR4-16/2	1440.035	1440.559	-1061.878	0.418	1082.318	0.423	18	0.173	R.ESGSTM*DVVAAQTK.A
R4/RRR4-16/2	1764.439	1764.921	-273.929	0.445	1001.379	0.464	19	0.172	K.VATPDQAQEVHDGLRK.W
R4/RRR4-17/2	1424.078	1424.560	-339.400	0.426	1169.995	0.380	18	0.171	R.ESGSTMDVVAAQTK.A
R4/RRR4-16/2	1440.049	1440.559	-1052.260	0.441	1016.864	0.411	18	0.167	R.ESGSTM*DVVAAQTK.A
R4/RRR4-16/2	1394.574	1395.497	-1382.648	0.286	997.412	0.445	18	0.167	R.SLLGESNEFVGDK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1440.121	1440.559	-305.237	0.417	1052.841	0.392	18	0.167	R.ESGSTM*DVVAAQTK.A
R4/RRR4-17/2	1440.015	1440.559	-1075.411	0.384	920.930	0.428	17	0.164	R.ESGSTM*DVVAAQTK.A
R4/RRR4-17/2	1439.709	1440.559	-1288.841	0.372	980.679	0.353	18	0.158	R.ESGSTM*DVVAAQTK.A
R4/RRR4-17/2	1440.134	1440.559	-295.882	0.423	835.823	0.379	17	0.154	R.ESGSTM*DVVAAQTK.A
R4/RRR4-16/3	1604.736	1604.746	-6.159	0.428	864.268	0.506	24	0.125	K.WLAANVSAEVAESTR.I
R4/RRR4-16/3	1375.088	1375.547	-334.762	0.410	1277.881	0.315	25	0.112	K.VIACVGETLEQR.E
R4/RRR4-16/3	1604.581	1604.746	-102.875	0.252	648.743	0.319	21	0.084	K.WLAANVSAEVAESTR.I
R4/RRR4-16/3	1604.496	1604.746	-156.106	0.282	618.878	0.298	21	0.083	K.WLAANVSAEVAESTR.I
R4/RRR4-13/2	1901.518	1902.181	-877.273	0.595	2917.733	0.594	26	0.513	K.NPINYTQIAVLADDILK.N
R4/RRR4-13/1	821.440	821.984	-1885.497	0.174	756.349	0.188	10	0.493	-.YVILGEK.-
R4/RRR4-13/1	821.444	821.984	-1879.599	0.178	788.141	0.144	10	0.489	-.YVILGEK.-
R4/RRR4-13/2	1612.268	1612.674	-252.473	0.555	2744.280	0.566	25	0.460	K.VGDLDSYEIEGGETK.S
R4/RRR4-13/2	1901.572	1902.181	-848.402	0.537	2608.640	0.603	25	0.443	K.NPINYTQIAVLADDILK.N
R4/RRR4-13/2	1902.519	1902.181	178.224	0.618	2595.285	0.585	25	0.432	K.NPINYTQIAVLADDILK.N
R4/RRR4-13/2	1612.265	1612.674	-253.992	0.552	2563.341	0.545	24	0.411	K.VGDLDSYEIEGGETK.S
R4/RRR4-12/2	1612.076	1612.674	-994.303	0.497	2174.141	0.566	23	0.342	K.VGDLDSYEIEGGETK.S
R4/RRR4-13/2	1612.275	1612.674	-248.143	0.571	2062.222	0.591	23	0.331	K.VGDLDSYEIEGGETK.S
R4/RRR4-13/3	1901.750	1902.181	-227.311	0.452	1858.172	0.412	31	0.224	K.NPINYTQIAVLADDILK.N
R4/RRR4-13/2	1753.436	1753.910	-271.048	0.528	1365.009	0.492	22	0.211	R.DSKDNIEM*TVSELQK.N
R4/RRR4-13/2	1193.117	1193.326	-175.952	0.507	1199.349	0.499	19	0.200	K.GLCGGINSTSVK.V
R4/RRR4-13/2	1192.480	1193.326	-1553.108	0.411	1071.132	0.471	19	0.182	K.GLCGGINSTSVK.V
R4/RRR4-13/2	1192.945	1193.326	-320.691	0.478	971.490	0.488	19	0.181	K.GLCGGINSTSVK.V
R4/RRR4-13/3	1901.704	1902.181	-251.267	0.472	1757.310	0.338	32	0.176	K.NPINYTQIAVLADDILK.N
R4/RRR4-13/2	1059.788	1060.226	-414.763	0.394	880.648	0.506	16	0.174	K.NVIVAITSDK.G
R4/RRR4-13/2	1754.513	1753.910	-227.337	0.503	953.668	0.472	19	0.172	R.DSKDNIEM*TVSELQK.N
R4/RRR4-13/3	1784.026	1783.988	21.560	0.383	1271.982	0.340	26	0.118	R.NAGEM*LDRLTLTYNR.T
R4/RRR4-10/3	1644.137	1643.995	86.702	0.504	2075.743	0.523	35	0.302	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1644.301	1643.995	186.769	0.504	1918.917	0.523	35	0.268	K.TLLLGEKPVTVFGIR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/3	1644.224	1643.995	139.865	0.486	1853.964	0.510	33	0.252	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1643.676	1643.995	-194.620	0.473	1805.906	0.507	33	0.242	K.TLLLGEKPVTVFGIR.N
R4/RRR4-1/3	1644.660	1643.995	-203.809	0.435	1546.413	0.513	31	0.202	K.TLLLGEKPVTVFGIR.N
R4/RRR4-10/3	1644.519	1643.995	-290.376	0.486	1395.251	0.553	30	0.196	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/2	1644.588	1643.995	-247.809	0.470	1123.807	0.499	20	0.189	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1644.197	1643.995	123.336	0.456	1442.109	0.518	32	0.188	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1644.166	1643.995	104.349	0.460	1604.157	0.448	32	0.186	K.TLLLGEKPVTVFGIR.N
R4/RRR4-10/2	1643.519	1643.995	-290.433	0.470	852.193	0.516	21	0.177	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/2	1643.500	1643.995	-301.760	0.477	848.338	0.501	21	0.174	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1644.963	1643.995	-19.443	0.548	1124.699	0.573	29	0.169	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/2	1643.968	1643.995	-16.058	0.494	559.535	0.515	17	0.161	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1644.936	1643.995	-35.856	0.466	1369.059	0.448	30	0.157	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1643.541	1643.995	-277.103	0.428	1067.685	0.519	28	0.147	K.TLLLGEKPVTVFGIR.N
R4/RRR4-24/2	1644.550	1643.995	-271.341	0.306	292.460	0.405	12	0.141	K.TLLLGEKPVTVFGIR.N
R4/RRR4-2/2	1643.193	1643.995	-1099.535	0.337	298.033	0.344	12	0.139	K.TLLLGEKPVTVFGIR.N
R4/RRR4-1/2	1643.438	1643.995	-949.923	0.335	307.999	0.340	12	0.139	K.TLLLGEKPVTVFGIR.N
R4/RRR4-23/2	1645.144	1643.995	91.197	0.357	319.868	0.326	12	0.137	-.TLLLGEKPVTVFGIR.-
R4/RRR4-12/3	1643.415	1643.995	-964.100	0.382	900.390	0.499	24	0.131	K.TLLLGEKPVTVFGIR.N
R4/RRR4-23/2	1645.537	1643.995	-278.767	0.333	239.213	0.367	10	0.127	-.TLLLGEKPVTVFGIR.-
R4/RRR4-3/3	1643.543	1643.995	-275.314	0.417	1044.355	0.426	28	0.123	K.TLLLGEKPVTVFGIR.N
R4/RRR4-2/3	1644.293	1643.995	182.191	0.382	808.207	0.471	23	0.120	K.TLLLGEKPVTVFGIR.N
R4/RRR4-9/3	1644.483	1643.995	298.093	0.399	877.808	0.457	26	0.120	K.TLLLGEKPVTVFGIR.N
R4/RRR4-12/3	1642.997	1643.995	-1219.316	0.348	1069.644	0.388	27	0.116	K.TLLLGEKPVTVFGIR.N
R4/RRR4-11/3	1643.942	1643.995	-31.930	0.319	692.015	0.328	24	0.097	K.TLLLGEKPVTVFGIR.N
R4/RRR4-17/2	1384.421	1384.476	-39.498	0.509	1547.818	0.564	20	0.248	K.GPGLYYVDSEGAR.L
R4/RRR4-17/2	1226.033	1226.449	-340.397	0.512	1512.319	0.541	17	0.240	K.LLANILYSYR.G
R4/RRR4-17/2	1226.057	1226.449	-321.018	0.513	1493.859	0.531	17	0.236	K.LLANILYSYR.G
R4/RRR4-17/2	1226.148	1226.449	-246.003	0.462	1512.001	0.524	17	0.235	K.LLANILYSYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1227.171	1226.449	-227.340	0.464	1420.384	0.528	17	0.226	K.LLANILYSYR.G
R4/RRR4-17/2	1226.232	1226.449	-177.790	0.562	1359.789	0.533	17	0.223	K.LLANILYSYR.G
R4/RRR4-17/2	1334.301	1333.429	-96.130	0.537	1324.245	0.523	18	0.215	K.LSGDDVGELHYK.Y
R4/RRR4-17/2	1332.982	1333.429	-335.957	0.507	1508.391	0.437	18	0.213	K.LSGDDVGELHYK.Y
R4/RRR4-17/2	1333.087	1333.429	-257.037	0.465	1434.234	0.460	18	0.211	K.LSGDDVGELHYK.Y
R4/RRR4-17/2	1225.930	1226.449	-1242.872	0.419	1320.781	0.481	16	0.204	K.LLANILYSYR.G
R4/RRR4-17/2	1495.230	1494.695	-312.010	0.505	859.242	0.530	20	0.182	R.YVM*PVEEAAELAR.R
R4/RRR4-17/2	1373.098	1373.518	-306.842	0.482	947.679	0.493	19	0.179	R.ASM*GGYISSQTVR.K
R4/RRR4-17/2	1494.095	1494.695	-1074.189	0.464	872.173	0.510	20	0.179	R.YVM*PVEEAAELAR.R
R4/RRR4-17/2	1478.227	1478.696	-317.856	0.397	908.294	0.497	20	0.176	R.YVMPVEEAAELAR.R
R4/RRR4-17/2	1372.545	1373.518	-1441.819	0.418	961.161	0.469	19	0.174	R.ASM*GGYISSQTVR.K
R4/RRR4-17/2	1478.196	1478.696	-339.150	0.399	942.216	0.465	20	0.173	R.YVMPVEEAAELAR.R
R4/RRR4-17/2	1478.138	1478.696	-1056.650	0.394	961.150	0.455	20	0.173	R.YVMPVEEAAELAR.R
R4/RRR4-17/2	1494.117	1494.695	-1059.341	0.467	873.910	0.442	20	0.169	R.YVM*PVEEAAELAR.R
R4/RRR4-17/2	1372.547	1373.518	-1440.032	0.405	855.679	0.442	19	0.165	R.ASM*GGYISSQTVR.K
R4/RRR4-17/2	969.962	970.107	-149.405	0.431	774.830	0.421	13	0.163	R.AIYQATFR.D
R4/RRR4-17/2	969.865	970.107	-249.781	0.435	771.212	0.373	13	0.157	R.AIYQATFR.D
R4/RRR4-17/2	969.280	970.107	-1889.905	0.269	831.683	0.297	13	0.145	R.AIYQATFR.D
R4/RRR4-17/2	887.894	888.004	-123.569	0.407	946.890	0.257	13	0.145	K.GVIVAADSR.A
R4/RRR4-18/3	1333.195	1333.429	-175.658	0.463	617.051	0.496	23	0.112	K.LSGDDVGELHYK.Y
R4/RRR4-17/3	1333.503	1333.429	56.171	0.394	478.687	0.401	23	0.098	K.LSGDDVGELHYK.Y
R4/RRR4-18/3	1333.691	1333.429	197.172	0.413	363.867	0.368	19	0.097	K.LSGDDVGELHYK.Y
R4/RRR4-17/3	1333.111	1333.429	-238.628	0.393	402.661	0.363	21	0.097	K.LSGDDVGELHYK.Y
R4/RRR4-15/2	1263.052	1263.420	-292.227	0.480	1705.546	0.542	19	0.262	K.SLITISGEVDTK.A
R4/RRR4-15/2	966.264	966.203	63.912	0.516	1768.853	0.439	15	0.261	K.VGLSLVLKH.-
R4/RRR4-15/2	966.014	966.203	-196.150	0.446	1651.047	0.508	15	0.258	K.VGLSLVLKH.-
R4/RRR4-15/3	1839.446	1837.934	-265.829	0.583	1637.752	0.571	35	0.247	K.HHSNTAVGAELSHSFSR.N
R4/RRR4-15/2	1263.261	1263.420	-125.960	0.504	1475.511	0.547	18	0.235	K.SLITISGEVDTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1263.199	1263.420	-175.301	0.550	1489.359	0.524	19	0.233	K.SLITISGEVDTK.A
R4/RRR4-15/2	1997.596	1998.217	-814.117	0.504	1279.691	0.576	24	0.217	K.FTLTTCTPEGVTITAAGTR.K
R4/RRR4-15/3	1837.924	1837.934	-5.078	0.528	1508.466	0.520	33	0.204	K.HHSNTAVGAELSHSFSR.N
R4/RRR4-15/3	1837.552	1837.934	-208.267	0.537	1492.207	0.521	34	0.202	K.HHSNTAVGAELSHSFSR.N
R4/RRR4-15/2	1997.595	1998.217	-814.546	0.490	968.338	0.578	22	0.189	K.FTLTTCTPEGVTITAAGTR.K
R4/RRR4-15/3	1621.574	1621.816	-149.969	0.508	1731.744	0.366	28	0.179	R.KNESVFGELQTQLK.N
R4/RRR4-15/2	1997.042	1998.217	-1092.195	0.442	835.518	0.523	20	0.169	K.FTLTTCTPEGVTITAAGTR.K
R4/RRR4-15/2	1227.292	1227.435	-117.480	0.421	790.236	0.419	16	0.160	K.SILSLVVPDQR.S
R4/RRR4-15/3	1621.810	1621.816	-3.867	0.463	1657.780	0.336	26	0.160	R.KNESVFGELQTQLK.N
R4/RRR4-15/2	1227.305	1227.435	-106.705	0.358	860.583	0.403	15	0.158	K.SILSLVVPDQR.S
R4/RRR4-15/2	1226.618	1227.435	-1486.327	0.369	759.466	0.391	15	0.154	K.SILSLVVPDQR.S
R4/RRR4-15/2	1493.065	1493.644	-1060.355	0.363	992.167	0.323	16	0.151	K.NESVFGELQTQLK.N
R4/RRR4-15/3	1621.751	1621.816	-40.445	0.495	1473.453	0.345	26	0.139	R.KNESVFGELQTQLK.N
R4/RRR4-15/2	1492.624	1493.644	-1356.788	0.301	626.017	0.277	14	0.135	K.NESVFGELQTQLK.N
R4/RRR4-15/3	1226.985	1227.435	-368.384	0.299	1112.408	0.227	21	0.082	K.SILSLVVPDQR.S
R4/RRR4-9/2	1572.419	1571.806	-246.335	0.458	1604.886	0.536	20	0.243	R.ISITGAGGFIASHIAR.R
R4/RRR4-9/2	1572.327	1571.806	-304.985	0.451	980.986	0.469	17	0.169	R.ISITGAGGFIASHIAR.R
R4/RRR4-10/2	1572.008	1571.806	129.242	0.302	311.552	0.432	16	0.143	R.ISITGAGGFIASHIAR.R
R4/RRR4-15/2	1667.669	1668.820	-1293.960	0.367	2210.464	0.211	22	0.245	R.NDFDTCVDLLSQLK.V
R4/RRR4-15/2	1191.652	1192.390	-1462.229	0.446	1580.754	0.476	17	0.231	K.LVEVTQLFSR.F
R4/RRR4-15/2	1193.206	1192.390	-154.082	0.579	1465.668	0.459	17	0.216	K.LVEVTQLFSR.F
R4/RRR4-15/2	1192.212	1192.390	-149.281	0.531	1427.429	0.472	17	0.216	K.LVEVTQLFSR.F
R4/RRR4-15/2	1373.109	1373.579	-343.349	0.429	1471.565	0.469	18	0.215	R.DIYEHAVVLSVK.I
R4/RRR4-15/2	1373.333	1373.579	-179.341	0.462	1340.513	0.472	18	0.204	R.DIYEHAVVLSVK.I
R4/RRR4-15/2	1833.349	1833.078	148.217	0.565	1034.027	0.572	23	0.199	K.EIPSLQVINQTLSYAR.E
R4/RRR4-15/2	1832.468	1833.078	-881.332	0.501	1079.109	0.536	23	0.195	K.EIPSLQVINQTLSYAR.E
R4/RRR4-15/2	1122.420	1123.155	-1549.803	0.477	820.860	0.334	15	0.155	K.IEDQDAFER.D
R4/RRR4-15/2	1122.236	1123.155	-1715.018	0.404	882.878	0.284	15	0.150	K.IEDQDAFER.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1122.931	1123.155	-199.924	0.500	798.408	0.297	15	0.149	K.IEDQDAFER.D
R4/RRR4-15/2	1831.508	1833.078	-1955.407	0.282	631.186	0.263	19	0.137	K.EIPSLQVINQTLSYAR.E
R4/RRR4-15/3	1365.975	1365.466	-360.076	0.427	959.652	0.423	23	0.113	K.TVRDELAGCSEK.G
R4/RRR4-15/3	1897.420	1898.046	-859.510	0.300	1026.214	0.291	26	0.088	K.HAVELEQSFM*EGAYNR.V
R4/RRR4-2/2	1472.387	1471.596	-142.495	0.493	2165.608	0.512	19	0.322	K.TALSNFEAALDYR.N
R4/RRR4-3/2	1472.595	1471.596	-1.215	0.496	1828.286	0.528	18	0.273	K.TALSNFEAALDYR.N
R4/RRR4-2/2	1471.115	1471.596	-328.548	0.382	1931.490	0.474	18	0.272	K.TALSNFEAALDYR.N
R4/RRR4-2/2	1263.480	1264.370	-1499.651	0.327	1751.461	0.259	19	0.200	R.ADQSLFEAGVAR.E
R4/RRR4-2/2	1263.488	1264.370	-1493.634	0.357	1572.285	0.329	18	0.196	R.ADQSLFEAGVAR.E
R4/RRR4-2/2	1470.751	1471.596	-1258.255	0.293	1438.251	0.336	18	0.183	K.TALSNFEAALDYR.N
R4/RRR4-2/2	1264.027	1264.370	-271.467	0.430	1424.212	0.321	18	0.182	R.ADQSLFEAGVAR.E
R4/RRR4-2/2	1385.019	1384.562	330.741	0.478	1149.694	0.409	15	0.176	K.YIDNLTNIYVR.F
R4/RRR4-3/2	1384.661	1384.562	71.657	0.424	1135.586	0.414	15	0.176	K.YIDNLTNIYVR.F
R4/RRR4-2/2	1174.064	1174.417	-301.967	0.423	1408.275	0.280	16	0.174	R.LYLINSPVVR.A
R4/RRR4-3/2	1383.477	1384.562	-1511.265	0.363	598.723	0.440	14	0.153	K.YIDNLTNIYVR.F
R4/RRR4-2/2	1313.309	1312.458	-113.422	0.337	611.522	0.449	14	0.152	K.HVFLSAGDFYR.A
R4/RRR4-2/2	1260.095	1260.379	-225.870	0.408	791.358	0.323	16	0.148	K.EADRDIINSVK.D
R4/RRR4-2/2	862.593	862.993	-464.372	0.269	963.594	0.278	12	0.146	R.GPEYGVLK.R
R4/RRR4-2/2	1095.731	1096.347	-1479.626	0.269	852.062	0.285	13	0.142	R.M*M*TIIDLAR.N
R4/RRR4-2/2	1312.469	1312.458	8.526	0.271	381.258	0.434	12	0.140	-.HVFLSAGDFYR.-
R4/RRR4-2/2	1174.197	1174.417	-188.484	0.333	866.508	0.201	14	0.138	-.LYLINSPVVR.-
R4/RRR4-2/2	862.282	862.993	-1990.379	0.252	596.040	0.268	10	0.125	-.GPEYGVLK.-
R4/RRR4-3/2	1174.172	1174.417	-209.760	0.359	396.482	0.271	11	0.119	-.LYLINSPVVR.-
R4/RRR4-15/2	1401.156	1401.636	-343.204	0.400	1171.263	0.451	18	0.185	R.TIKDEGVIALWR.G
R4/RRR4-15/2	1400.456	1401.636	-1561.311	0.385	1039.894	0.431	18	0.173	R.TIKDEGVIALWR.G
R4/RRR4-15/2	1401.364	1401.636	-194.101	0.401	1044.484	0.415	18	0.171	R.TIKDEGVIALWR.G
R4/RRR4-15/2	895.854	895.976	-136.754	0.263	695.316	0.386	12	0.148	K.GIADCFGR.T
R4/RRR4-15/2	895.444	895.976	-1716.490	0.259	678.287	0.295	12	0.142	K.GIADCFGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	895.580	895.976	-443.714	0.171	799.858	0.200	12	0.134	K.GIADCFGR.T
R4/RRR4-15/3	1401.751	1401.636	82.348	0.487	1388.739	0.312	24	0.120	R.TIKDEGVIALWR.G
R4/RRR4-15/3	1401.312	1401.636	-231.907	0.385	964.350	0.190	21	0.075	-.TIKDEGVIALWR.-
R4/RRR4-15/3	1401.286	1401.636	-250.391	0.336	794.426	0.241	22	0.072	-.TIKDEGVIALWR.-
R4/RRR4-11/2	1441.807	1442.643	-1277.231	0.492	1557.722	0.568	20	0.248	R.VPTANVSVVDLTAR.I
R4/RRR4-11/2	1443.213	1442.643	-298.590	0.537	1372.553	0.588	20	0.233	R.VPTANVSVVDLTAR.I
R4/RRR4-11/2	1121.237	1121.351	-102.494	0.504	1307.916	0.531	16	0.216	R.VLDLLSYVAK.V
R4/RRR4-11/2	1441.850	1442.643	-1247.217	0.498	1171.364	0.595	20	0.214	R.VPTANVSVVDLTAR.I
R4/RRR4-11/2	1276.863	1277.538	-1315.553	0.467	1422.057	0.446	17	0.207	R.RVLDLLSYVAK.V
R4/RRR4-11/2	1121.049	1121.351	-270.923	0.446	1236.052	0.471	16	0.196	R.VLDLLSYVAK.V
R4/RRR4-11/2	1386.230	1386.536	-221.657	0.472	907.834	0.491	22	0.176	R.GAAQNIIPSSTGAAK.A
R4/RRR4-11/2	1178.133	1178.320	-159.275	0.425	1133.490	0.407	16	0.175	K.AGISLNDNFVK.L
R4/RRR4-11/2	1121.092	1121.351	-232.251	0.420	900.814	0.476	15	0.173	R.VLDLLSYVAK.V
R4/RRR4-11/2	1177.286	1178.320	-1732.790	0.338	1310.853	0.319	17	0.172	K.AGISLNDNFVK.L
R4/RRR4-11/2	1387.225	1386.536	-225.294	0.476	835.630	0.453	21	0.166	R.GAAQNIIPSSTGAAK.A
R4/RRR4-11/2	1441.681	1442.643	-1364.731	0.447	1042.379	0.379	18	0.163	R.VPTANVSVVDLTAR.I
R4/RRR4-11/2	1675.730	1675.781	-30.732	0.451	634.583	0.460	16	0.157	K.LVSWYDNEWGYSR.R
R4/RRR4-11/2	819.803	819.931	-156.534	0.461	714.025	0.374	12	0.153	-.VGINGFGR.-
R4/RRR4-11/2	820.083	819.931	185.859	0.372	820.201	0.302	13	0.150	K.VGINGFGR.I
R4/RRR4-11/2	1177.465	1178.320	-1580.192	0.291	1084.836	0.257	15	0.149	K.AGISLNDNFVK.L
R4/RRR4-11/2	1676.548	1675.781	-139.530	0.467	358.946	0.419	14	0.148	K.LVSWYDNEWGYSR.R
R4/RRR4-11/2	1676.203	1675.781	252.176	0.461	399.566	0.416	14	0.147	K.LVSWYDNEWGYSR.R
R4/RRR4-11/2	1385.675	1386.536	-1347.083	0.292	883.960	0.290	20	0.145	R.GAAQNIIPSSTGAAK.A
R4/RRR4-11/2	819.936	819.931	5.359	0.365	839.256	0.210	13	0.141	K.VGINGFGR.I
R4/RRR4-10/2	1121.443	1121.351	82.144	0.345	616.000	0.271	12	0.140	R.VLDLLSYVAK.V
R4/RRR4-7/2	1663.459	1663.805	-208.711	0.564	3352.828	0.510	26	0.591	K.ATDSESTEVILDAALK.S
R4/RRR4-7/2	1663.265	1663.805	-928.957	0.548	2566.963	0.480	23	0.386	K.ATDSESTEVILDAALK.S
R4/RRR4-7/2	1662.674	1663.805	-1285.623	0.395	2460.020	0.388	24	0.336	K.ATDSESTEVILDAALK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1761.412	1761.914	-855.090	0.551	1872.410	0.477	23	0.266	K.VENQEGVVNFDEILR.E
R4/RRR4-8/2	1761.488	1761.914	-242.206	0.556	1736.956	0.491	22	0.251	K.VENQEGVVNFDEILR.E
R4/RRR4-7/2	1761.497	1761.914	-237.479	0.540	1705.208	0.430	23	0.232	K.VENQEGVVNFDEILR.E
R4/RRR4-8/2	1761.426	1761.914	-277.804	0.553	1566.074	0.454	21	0.220	K.VENQEGVVNFDEILR.E
R4/RRR4-8/2	1762.476	1761.914	-248.948	0.595	1459.638	0.495	21	0.218	K.VENQEGVVNFDEILR.E
R4/RRR4-2/2	1763.167	1761.914	144.187	0.525	1422.655	0.416	21	0.198	K.VENQEGVVNFDEILR.E
R4/RRR4-8/2	1155.771	1155.369	348.779	0.439	735.133	0.613	19	0.185	R.GLVPLLAEGSAK.A
R4/RRR4-7/2	956.163	956.208	-47.072	0.520	1287.264	0.389	14	0.185	K.AALIVVLTR.G
R4/RRR4-7/2	1188.077	1187.285	-175.977	0.456	1054.053	0.472	17	0.183	K.ILAGLENDDAR.V
R4/RRR4-7/2	1155.746	1155.369	326.964	0.420	926.594	0.521	19	0.182	R.GLVPLLAEGSAK.A
R4/RRR4-7/2	956.181	956.208	-28.121	0.431	1132.118	0.428	14	0.180	K.AALIVVLTR.G
R4/RRR4-8/2	1186.898	1187.285	-327.173	0.459	1086.906	0.440	17	0.180	K.ILAGLENDDAR.V
R4/RRR4-8/2	1187.222	1187.285	-53.174	0.426	1231.092	0.361	17	0.176	K.ILAGLENDDAR.V
R4/RRR4-7/2	1813.528	1814.097	-867.514	0.502	766.387	0.545	23	0.175	R.SAPLPMSPLESLASSAVR.T
R4/RRR4-7/2	1187.418	1187.285	112.226	0.472	1054.198	0.420	17	0.175	K.ILAGLENDDAR.V
R4/RRR4-7/2	1186.983	1187.285	-254.945	0.436	1126.041	0.387	17	0.173	K.ILAGLENDDAR.V
R4/RRR4-8/2	1186.537	1187.285	-1477.614	0.396	1098.931	0.379	17	0.170	K.ILAGLENDDAR.V
R4/RRR4-7/2	956.058	956.208	-156.572	0.419	1053.372	0.365	13	0.165	K.AALIVVLTR.G
R4/RRR4-8/2	1813.052	1814.097	-1131.449	0.317	664.833	0.551	21	0.162	R.SAPLPMSPLESLASSAVR.T
R4/RRR4-7/2	1830.507	1830.096	224.791	0.525	393.848	0.544	20	0.161	R.SAPLPM*SPLESLASSAVR.T
R4/RRR4-8/2	1155.051	1155.369	-276.621	0.212	767.858	0.481	18	0.153	R.GLVPLLAEGSAK.A
R4/RRR4-8/2	1829.335	1830.096	-965.675	0.359	343.457	0.544	18	0.153	R.SAPLPM*SPLESLASSAVR.T
R4/RRR4-8/2	1204.269	1204.376	-88.959	0.416	923.960	0.319	16	0.151	R.GDLGM*EIPVEK.I
R4/RRR4-7/2	1829.473	1830.096	-889.843	0.390	290.832	0.460	19	0.151	R.SAPLPM*SPLESLASSAVR.T
R4/RRR4-7/2	1829.422	1830.096	-918.178	0.355	355.427	0.452	19	0.149	R.SAPLPM*SPLESLASSAVR.T
R4/RRR4-3/2	1762.896	1761.914	-10.043	0.447	500.527	0.387	16	0.146	K.VENQEGVVNFDEILR.E
R4/RRR4-8/2	1828.626	1830.096	-1355.128	0.299	316.450	0.364	18	0.143	R.SAPLPM*SPLESLASSAVR.T
R4/RRR4-8/2	1154.704	1155.369	-1446.352	0.181	399.299	0.434	14	0.139	R.GLVPLLAEGSAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1154.918	1155.369	-391.783	0.191	505.964	0.357	15	0.138	R.GLVPLLAEGSAK.A
R4/RRR4-4/2	1427.246	1426.728	-338.904	0.587	2429.980	0.583	19	0.398	R.LPLLDLNIYVPR.D
R4/RRR4-4/2	1426.531	1426.728	-138.665	0.533	2124.049	0.561	19	0.333	R.LPLLDLNIYVPR.D
R4/RRR4-4/2	1426.223	1426.728	-1058.800	0.533	2011.660	0.524	19	0.303	R.LPLLDLNIYVPR.D
R4/RRR4-4/2	1402.267	1402.576	-220.869	0.501	1527.877	0.426	19	0.214	R.VFFANDTYLPSK.M
R4/RRR4-4/2	1155.991	1156.273	-244.410	0.420	1078.879	0.463	15	0.181	K.LDGNFIYASR.T
R4/RRR4-3/2	1162.166	1161.353	-161.148	0.368	914.514	0.513	14	0.175	K.MSDFLGYSLK.A
R4/RRR4-4/2	1155.474	1156.273	-1561.736	0.353	1097.429	0.391	15	0.169	K.LDGNFIYASR.T
R4/RRR4-4/2	1402.165	1402.576	-293.622	0.445	1122.848	0.343	17	0.164	R.VFFANDTYLPSK.M
R4/RRR4-4/2	1240.306	1240.474	-136.089	0.336	874.748	0.382	18	0.157	K.SLLPVAGDQVLK.L
R4/RRR4-4/2	1239.966	1240.474	-1219.521	0.387	389.722	0.428	13	0.147	K.SLLPVAGDQVLK.L
R4/RRR4-4/2	1401.697	1402.576	-1344.001	0.335	723.174	0.335	14	0.144	R.VFFANDTYLPSK.M
R4/RRR4-4/3	1827.741	1827.117	-206.304	0.412	1006.551	0.519	26	0.139	R.LPLLDLNIYVPRDER.F
R4/RRR4-3/2	1161.440	1161.353	75.731	0.257	632.137	0.239	12	0.133	-.MSDFLGYSLK.-
R4/RRR4-4/2	1239.551	1240.474	-1555.764	0.208	521.518	0.207	13	0.131	-.SLLPVAGDQVLK.-
R4/RRR4-4/3	1782.473	1782.079	221.713	0.503	920.237	0.390	29	0.105	K.LVRPVLGGSQELPYPR.R
R4/RRR4-4/3	1782.723	1782.079	-200.525	0.490	849.058	0.393	29	0.102	K.LVRPVLGGSQELPYPR.R
R4/RRR4-12/2	1767.430	1767.022	231.609	0.555	1990.763	0.549	24	0.305	R.VLDTHVEGGNLFIVPR.F
R4/RRR4-12/2	1766.646	1767.022	-213.154	0.495	1810.434	0.552	23	0.278	R.VLDTHVEGGNLFIVPR.F
R4/RRR4-12/2	1766.372	1767.022	-936.630	0.497	1881.789	0.511	23	0.277	R.VLDTHVEGGNLFIVPR.F
R4/RRR4-12/2	1735.322	1734.932	225.664	0.577	1496.866	0.572	26	0.243	K.LSLNAGGLALPSFSDSGK.V
R4/RRR4-12/2	1204.881	1205.299	-348.101	0.471	1595.863	0.468	18	0.231	R.AWDLAESDAVK.L
R4/RRR4-12/2	1204.442	1205.299	-1545.916	0.396	1640.214	0.415	17	0.222	R.AWDLAESDAVK.L
R4/RRR4-12/2	1413.832	1414.739	-1353.216	0.389	1468.499	0.464	20	0.213	R.VVVLNTANLPM*VK.E
R4/RRR4-12/2	1205.083	1205.299	-179.589	0.510	1462.715	0.449	17	0.212	R.AWDLAESDAVK.L
R4/RRR4-12/2	1735.452	1734.932	-277.235	0.504	1060.086	0.596	23	0.202	K.LSLNAGGLALPSFSDSGK.V
R4/RRR4-12/2	1186.134	1186.383	-210.845	0.454	1179.314	0.496	20	0.197	K.LVSSQPASGIVK.I
R4/RRR4-12/2	1734.189	1734.932	-1007.881	0.455	988.074	0.568	23	0.190	K.LSLNAGGLALPSFSDSGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1414.171	1414.739	-1112.551	0.426	1032.402	0.534	18	0.188	R.VVVLNTANLPM*VK.E
R4/RRR4-12/2	1186.033	1186.383	-296.236	0.456	1001.855	0.449	19	0.176	K.LVSSQPASGIVK.I
R4/RRR4-12/2	1185.587	1186.383	-1519.693	0.416	979.958	0.434	19	0.172	K.LVSSQPASGIVK.I
R4/RRR4-12/2	1233.083	1232.402	-259.612	0.526	965.639	0.423	17	0.168	K.GTCGIVLPEASK.E
R4/RRR4-12/2	1489.983	1489.690	197.658	0.404	951.124	0.419	18	0.162	K.GTCGIVLPEASKEK.V
R4/RRR4-12/3	1767.012	1767.022	-5.732	0.521	1195.668	0.368	30	0.119	-.VLDTHVEGGNLFIVPR.-
R4/RRR4-8/2	1495.056	1494.716	227.862	0.576	2959.134	0.495	22	0.481	K.VADFFDAAVNLALK.V
R4/RRR4-8/2	1494.169	1494.716	-1038.758	0.474	2722.369	0.478	22	0.421	K.VADFFDAAVNLALK.V
R4/RRR4-8/2	1494.184	1494.716	-1028.423	0.494	2595.150	0.491	21	0.398	K.VADFFDAAVNLALK.V
R4/RRR4-8/2	1092.076	1092.273	-180.908	0.551	1960.964	0.569	19	0.310	K.LIVAGASAYAR.L
R4/RRR4-8/2	1092.053	1092.273	-202.550	0.576	1744.802	0.574	19	0.280	K.LIVAGASAYAR.L
R4/RRR4-8/2	1208.108	1208.392	-236.299	0.540	1817.789	0.528	18	0.276	K.VLENVHIAANK.N
R4/RRR4-8/2	1092.011	1092.273	-240.903	0.549	1733.356	0.562	19	0.274	K.LIVAGASAYAR.L
R4/RRR4-8/2	1208.328	1208.392	-53.461	0.580	1751.068	0.515	18	0.263	K.VLENVHIAANK.N
R4/RRR4-8/2	1586.333	1586.796	-292.366	0.384	1002.332	0.497	24	0.179	K.NTVPGDVSAM*VPGGIR.M
R4/RRR4-8/2	999.862	1000.046	-184.734	0.409	744.505	0.463	13	0.164	K.YSEGYPGAR.Y
R4/RRR4-8/2	999.869	1000.046	-177.508	0.316	909.019	0.407	13	0.160	K.YSEGYPGAR.Y
R4/RRR4-8/2	1586.326	1586.796	-296.844	0.335	815.145	0.397	22	0.154	K.NTVPGDVSAM*VPGGIR.M
R4/RRR4-8/2	999.853	1000.046	-194.288	0.307	648.914	0.350	12	0.146	K.YSEGYPGAR.Y
R4/RRR4-8/3	1260.207	1260.381	-138.031	0.496	1383.584	0.390	22	0.142	K.LRHDVEEYAK.Q
R4/RRR4-8/2	1662.509	1661.946	-263.696	0.270	794.790	0.321	17	0.141	-.ISAVSIFFETMPYR.-
R4/RRR4-8/3	1260.306	1260.381	-59.330	0.503	1315.047	0.344	22	0.122	K.LRHDVEEYAK.Q
R4/RRR4-7/2	1554.233	1554.729	-319.801	0.479	2871.897	0.567	22	0.490	R.LAIGDLATQYFADR.D
R4/RRR4-7/2	1554.603	1554.729	-81.168	0.518	2265.563	0.588	21	0.366	R.LAIGDLATQYFADR.D
R4/RRR4-7/2	1403.011	1403.521	-1079.284	0.508	2053.365	0.496	19	0.301	K.TFSYAGFEQQPK.T
R4/RRR4-7/2	1496.104	1496.543	-294.045	0.503	1935.867	0.527	23	0.290	K.SESAQGDAAASAM*AGR.G
R4/RRR4-7/2	1554.861	1554.729	85.547	0.517	1868.638	0.473	20	0.264	R.LAIGDLATQYFADR.D
R4/RRR4-7/2	1968.577	1969.224	-838.992	0.570	1401.871	0.581	25	0.234	R.FNIFSGCPSGQTATIVLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1091.393	1091.328	59.389	0.358	1225.777	0.312	14	0.164	R.LLDIIHPAAK.I
R4/RRR4-7/2	1175.221	1175.318	-82.367	0.332	1027.202	0.371	15	0.160	K.SQFFVNSFAK.A
R4/RRR4-7/3	1288.309	1288.516	-160.585	0.347	1109.628	0.143	23	0.073	K.SLEEKKELLAK.C
R4/RRR4-6/1	1441.842	1442.640	-1250.399	0.252	670.778	0.373	17	0.522	K.LAQLPGTSIEGVEK.G
R4/RRR4-6/1	1441.877	1442.640	-1226.083	0.234	706.662	0.355	17	0.521	K.LAQLPGTSIEGVEK.G
R4/RRR4-6/2	1884.448	1885.107	-883.010	0.586	2661.708	0.595	26	0.452	K.IYQEYGITAENVIATAK.S
R4/RRR4-6/2	1884.587	1885.107	-808.752	0.562	2476.919	0.591	26	0.410	K.IYQEYGITAENVIATAK.S
R4/RRR4-6/2	1403.042	1403.608	-1119.664	0.523	2504.219	0.574	24	0.409	K.AIGIDKFGASAPAGK.I
R4/RRR4-6/2	1884.430	1885.107	-892.440	0.562	2383.250	0.593	26	0.391	K.IYQEYGITAENVIATAK.S
R4/RRR4-6/2	1403.367	1403.608	-172.362	0.532	2389.878	0.542	24	0.374	K.AIGIDKFGASAPAGK.I
R4/RRR4-6/2	1403.304	1403.608	-217.215	0.504	2317.463	0.520	23	0.352	K.AIGIDKFGASAPAGK.I
R4/RRR4-6/2	1376.200	1376.540	-247.561	0.497	1932.888	0.426	19	0.261	R.VSLEAGSTLGWQK.Y
R4/RRR4-6/2	1377.141	1376.540	-290.778	0.530	1754.291	0.485	19	0.252	R.VSLEAGSTLGWQK.Y
R4/RRR4-6/2	1376.235	1376.540	-222.377	0.502	1740.576	0.404	18	0.229	R.VSLEAGSTLGWQK.Y
R4/RRR4-1/2	1442.266	1442.640	-259.651	0.465	822.211	0.517	22	0.178	K.LAQLPGTSIEGVEK.G
R4/RRR4-6/2	1443.391	1442.640	-172.672	0.497	650.195	0.543	20	0.173	K.LAQLPGTSIEGVEK.G
R4/RRR4-6/2	1443.184	1442.640	-316.836	0.471	719.281	0.515	21	0.173	K.LAQLPGTSIEGVEK.G
R4/RRR4-6/2	1443.262	1442.640	-262.186	0.479	578.217	0.553	19	0.171	K.LAQLPGTSIEGVEK.G
R4/RRR4-5/2	1442.291	1442.640	-242.668	0.448	645.325	0.517	20	0.169	K.LAQLPGTSIEGVEK.G
R4/RRR4-1/2	1442.382	1442.640	-179.499	0.445	610.272	0.502	20	0.166	K.LAQLPGTSIEGVEK.G
R4/RRR4-5/2	1442.144	1442.640	-344.742	0.447	555.983	0.519	19	0.165	K.LAQLPGTSIEGVEK.G
R4/RRR4-5/2	1441.833	1442.640	-1256.657	0.420	632.711	0.485	20	0.164	K.LAQLPGTSIEGVEK.G
R4/RRR4-5/2	1376.126	1376.540	-301.847	0.330	1235.526	0.284	19	0.162	R.VSLEAGSTLGWQK.Y
R4/RRR4-2/2	1442.403	1442.640	-164.726	0.429	351.300	0.517	16	0.158	K.LAQLPGTSIEGVEK.G
R4/RRR4-6/2	1172.233	1172.314	-68.581	0.450	437.617	0.459	15	0.157	K.ESVLPEAVTAR.V
R4/RRR4-6/2	998.661	999.193	-1537.793	0.550	423.648	0.378	14	0.155	K.RPSVLALSR.Q
R4/RRR4-1/2	1443.106	1442.640	324.131	0.420	406.586	0.445	17	0.154	K.LAQLPGTSIEGVEK.G
R4/RRR4-2/2	1442.001	1442.640	-1139.594	0.397	366.728	0.455	16	0.153	K.LAQLPGTSIEGVEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	998.631	999.193	-1568.737	0.458	510.564	0.310	14	0.149	K.RPSVLALSR.Q
R4/RRR4-6/2	1171.948	1172.314	-312.959	0.295	390.489	0.400	14	0.146	K.ESVLPEAVTAR.V
R4/RRR4-5/2	1403.959	1403.608	250.147	0.369	440.838	0.407	15	0.145	K.AIGIDKFGASAPAGK.I
R4/RRR4-6/2	998.580	999.193	-1619.577	0.413	454.717	0.249	13	0.144	K.RPSVLALSR.Q
R4/RRR4-5/2	1403.648	1403.608	28.208	0.348	476.698	0.350	16	0.143	K.AIGIDKFGASAPAGK.I
R4/RRR4-5/2	1403.440	1403.608	-120.270	0.348	512.555	0.349	15	0.138	-.AIGIDKFGASAPAGK.-
R4/RRR4-3/2	999.035	999.193	-157.864	0.413	236.293	0.298	12	0.134	-.RPSVLALSR.-
R4/RRR4-6/2	1172.128	1172.314	-158.420	0.286	388.848	0.280	13	0.134	-.ESVLPEAVTAR.-
R4/RRR4-6/3	1615.963	1616.734	-1098.892	0.323	738.905	0.435	26	0.101	K.M*FGDFQKDTPEER.N
R4/RRR4-6/3	1616.476	1616.734	-159.938	0.388	721.311	0.401	25	0.098	K.M*FGDFQKDTPEER.N
R4/RRR4-6/3	1616.902	1616.734	104.529	0.367	831.594	0.368	26	0.096	K.M*FGDFQKDTPEER.N
R4/RRR4-10/2	1535.146	1533.665	314.667	0.600	2573.332	0.455	24	0.381	K.VLGAFLEGGSPDENK.A
R4/RRR4-10/2	1985.663	1985.143	-242.609	0.592	1162.614	0.538	20	0.194	K.LSDFGTQGADSNNILYLR.E
R4/RRR4-10/2	1984.538	1985.143	-811.145	0.568	1174.779	0.520	20	0.192	K.LSDFGTQGADSNNILYLR.E
R4/RRR4-10/2	1984.086	1985.143	-1040.024	0.523	1183.125	0.470	20	0.183	K.LSDFGTQGADSNNILYLR.E
R4/RRR4-10/2	1587.153	1586.769	242.720	0.481	1130.414	0.419	24	0.179	R.EVDDADKLVAAIQAK.K
R4/RRR4-10/2	1586.490	1586.769	-176.468	0.465	1123.180	0.391	23	0.173	R.EVDDADKLVAAIQAK.K
R4/RRR4-10/2	1587.056	1586.769	181.325	0.480	980.446	0.414	23	0.169	R.EVDDADKLVAAIQAK.K
R4/RRR4-10/2	1431.295	1431.619	-226.825	0.424	635.692	0.424	18	0.156	K.EAVAPYERPALSK.G
R4/RRR4-10/2	1431.320	1431.619	-209.029	0.465	512.399	0.440	17	0.155	K.EAVAPYERPALSK.G
R4/RRR4-10/2	1431.204	1431.619	-290.231	0.419	573.810	0.384	18	0.151	K.EAVAPYERPALSK.G
R4/RRR4-10/3	1471.910	1472.624	-1168.436	0.385	787.938	0.467	26	0.111	R.LPGFHVCVGSGGER.L
R4/RRR4-10/3	1472.905	1472.624	191.379	0.439	742.544	0.401	25	0.100	R.LPGFHVCVGSGGER.L
R4/RRR4-10/3	1472.804	1472.624	122.684	0.453	688.037	0.372	24	0.095	R.LPGFHVCVGSGGER.L
R4/RRR4-24/2	1805.333	1806.035	-945.443	0.498	1888.751	0.502	26	0.277	R.VCCLSIIDPGDSDIIK.T
R4/RRR4-24/2	1805.430	1806.035	-891.682	0.518	1777.842	0.471	25	0.253	R.VCCLSIIDPGDSDIIK.T
R4/RRR4-24/2	1805.383	1806.035	-917.815	0.506	1554.623	0.497	24	0.232	R.VCCLSIIDPGDSDIIK.T
R4/RRR4-24/2	1334.133	1334.520	-291.076	0.489	1828.772	0.320	17	0.221	K.SEIEYYAM*LAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	1334.113	1334.520	-306.223	0.524	1782.862	0.339	17	0.219	K.SEIEYYAM*LAK.T
R4/RRR4-24/2	1462.525	1462.693	-114.877	0.550	1313.714	0.487	19	0.207	R.KSEIEYYAM*LAK.T
R4/RRR4-24/2	1318.221	1318.521	-227.613	0.500	1568.917	0.360	17	0.202	K.SEIEYYAMLAK.T
R4/RRR4-24/2	1462.337	1462.693	-243.747	0.558	980.792	0.515	20	0.189	R.KSEIEYYAM*LAK.T
R4/RRR4-24/2	1462.518	1462.693	-119.733	0.508	999.627	0.484	20	0.184	R.KSEIEYYAM*LAK.T
R4/RRR4-24/2	1524.350	1524.827	-313.941	0.478	1017.994	0.471	17	0.177	K.LVIISNNCPPLRK.S
R4/RRR4-24/2	1333.950	1334.520	-1180.053	0.373	1614.583	0.205	17	0.177	K.SEIEYYAM*LAK.T
R4/RRR4-23/2	1805.429	1806.035	-892.225	0.397	1059.861	0.411	21	0.169	R.VCCLSIIDPGDSDIIK.T
R4/RRR4-24/2	1523.845	1524.827	-1304.726	0.439	1071.483	0.403	17	0.169	-.LVIISNNCPPLRK.-
R4/RRR4-24/2	1524.582	1524.827	-160.987	0.513	946.232	0.443	17	0.168	K.LVIISNNCPPLRK.S
R4/RRR4-24/3	1463.128	1462.693	298.338	0.452	1474.481	0.435	23	0.168	R.KSEIEYYAM*LAK.T
R4/RRR4-24/2	1395.583	1396.654	-1488.681	0.248	1233.924	0.262	17	0.156	K.LVIISNNCPPLR.K
R4/RRR4-24/2	1446.837	1446.693	99.381	0.437	774.305	0.341	14	0.146	R.KSEIEYYAMLAK.T
R4/RRR4-24/2	1395.424	1396.654	-1602.914	0.202	652.528	0.119	14	0.129	K.LVIISNNCPPLR.K
R4/RRR4-24/3	1634.691	1634.880	-116.009	0.456	968.170	0.415	25	0.113	K.STDNINNKLQLVM*K.S
R4/RRR4-24/3	1634.602	1634.880	-170.845	0.440	769.701	0.463	25	0.112	K.STDNINNKLQLVM*K.S
R4/RRR4-24/3	1462.785	1462.693	62.999	0.368	950.944	0.351	22	0.097	R.KSEIEYYAM*LAK.T
R4/RRR4-23/3	1634.558	1634.880	-197.478	0.393	639.816	0.384	23	0.096	K.STDNINNKLQLVM*K.S
R4/RRR4-24/3	1635.478	1634.880	-246.814	0.362	572.553	0.390	23	0.096	K.STDNINNKLQLVM*K.S
R4/RRR4-24/3	1619.780	1618.881	-62.679	0.331	519.920	0.377	24	0.094	K.STDNINNKLQLVMK.S
R4/RRR4-6/2	1726.806	1726.956	-86.900	0.567	2989.921	0.421	25	0.455	R.LDQLQLLLNGASANGAK.K
R4/RRR4-6/2	1726.613	1726.956	-199.162	0.572	2975.326	0.414	26	0.450	R.LDQLQLLLNGASANGAK.K
R4/RRR4-6/2	1726.484	1726.956	-274.065	0.536	2653.511	0.386	25	0.369	R.LDQLQLLLNGASANGAK.K
R4/RRR4-6/2	1133.820	1134.219	-352.640	0.499	2361.089	0.438	20	0.336	K.GIDACIASGGGR.M
R4/RRR4-6/2	1134.012	1134.219	-182.639	0.447	2131.678	0.438	20	0.296	K.GIDACIASGGGR.M
R4/RRR4-6/2	974.983	975.121	-142.231	0.500	770.801	0.580	16	0.186	K.LVDTALASGK.I
R4/RRR4-6/2	974.951	975.121	-175.515	0.450	734.205	0.576	16	0.181	K.LVDTALASGK.I
R4/RRR4-6/2	974.578	975.121	-1588.798	0.382	779.566	0.522	16	0.172	K.LVDTALASGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1726.191	1726.956	-1025.397	0.406	1260.340	0.385	27	0.129	R.LDQLQLLLNGASANGAK.K
R4/RRR4-12/2	1809.702	1810.238	-851.081	0.487	1843.849	0.475	25	0.259	K.VAILGASGGIGQPLALLMK.M
R4/RRR4-12/2	1457.153	1457.635	-331.212	0.523	1594.277	0.586	23	0.258	K.AGAGSATLSM*AYAAAK.F
R4/RRR4-12/2	1809.355	1810.238	-1043.626	0.448	1636.202	0.477	25	0.233	K.VAILGASGGIGQPLALLMK.M
R4/RRR4-12/2	1456.616	1457.635	-1390.181	0.461	1429.647	0.555	22	0.229	K.AGAGSATLSM*AYAAAK.F
R4/RRR4-12/2	1503.006	1502.697	206.373	0.458	1541.460	0.447	21	0.218	R.ANTFVAEVLGLDPR.D
R4/RRR4-12/2	1185.582	1186.427	-1560.285	0.441	1438.223	0.449	19	0.210	R.LLGVTTLDVVR.A
R4/RRR4-12/2	1186.256	1186.427	-143.941	0.540	1315.147	0.480	19	0.208	R.LLGVTTLDVVR.A
R4/RRR4-12/3	1826.804	1826.237	-238.028	0.496	1460.419	0.520	32	0.200	K.VAILGASGGIGQPLALLM*K.M
R4/RRR4-12/2	1457.091	1457.635	-1062.438	0.493	1150.858	0.550	19	0.198	K.AGAGSATLSM*AYAAAK.F
R4/RRR4-12/2	1502.143	1502.697	-1037.482	0.292	1397.126	0.330	19	0.177	R.ANTFVAEVLGLDPR.D
R4/RRR4-12/2	1245.177	1245.365	-151.388	0.470	787.306	0.418	19	0.163	R.IQNGGTEVVEAK.A
R4/RRR4-12/2	1244.958	1245.365	-327.355	0.455	749.045	0.432	18	0.163	R.IQNGGTEVVEAK.A
R4/RRR4-12/2	1825.706	1826.237	-841.325	0.319	1009.185	0.424	20	0.162	K.VAILGASGGIGQPLALLM*K.M
R4/RRR4-12/2	1246.047	1245.365	-255.831	0.453	568.946	0.465	18	0.162	R.IQNGGTEVVEAK.A
R4/RRR4-12/2	1245.934	1245.365	-346.163	0.498	499.178	0.453	18	0.161	R.IQNGGTEVVEAK.A
R4/RRR4-12/2	1245.083	1245.365	-226.429	0.446	619.097	0.386	17	0.153	R.IQNGGTEVVEAK.A
R4/RRR4-12/2	1245.573	1245.365	168.225	0.409	445.382	0.396	17	0.153	R.IQNGGTEVVEAK.A
R4/RRR4-12/2	1348.542	1347.502	29.634	0.517	1068.968	0.300	16	0.151	R.DDLFNINAGIVR.T
R4/RRR4-12/2	1809.272	1810.238	-1089.691	0.387	705.103	0.424	18	0.149	K.VAILGASGGIGQPLALLMK.M
R4/RRR4-12/3	1977.953	1977.198	-124.093	0.419	1530.408	0.336	28	0.146	R.CGIEEILSLGPLNEFER.A
R4/RRR4-12/3	1503.094	1502.697	264.756	0.479	1375.906	0.396	30	0.142	R.ANTFVAEVLGLDPR.D
R4/RRR4-12/2	1824.866	1826.237	-1303.113	0.236	714.021	0.344	18	0.139	K.VAILGASGGIGQPLALLM*K.M
R4/RRR4-12/3	1502.702	1502.697	3.404	0.496	1112.839	0.407	28	0.121	R.ANTFVAEVLGLDPR.D
R4/RRR4-12/3	1502.615	1502.697	-54.896	0.515	990.907	0.407	27	0.113	R.ANTFVAEVLGLDPR.D
R4/RRR4-12/3	1825.496	1826.237	-956.723	0.257	1058.738	0.179	27	0.075	K.VAILGASGGIGQPLALLM*K.M
R4/RRR4-10/2	1199.162	1198.397	-197.017	0.587	1991.245	0.525	18	0.301	K.AQELGLQVIAR.I
R4/RRR4-10/2	1199.211	1198.397	-155.557	0.585	1908.347	0.497	18	0.280	K.AQELGLQVIAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1638.334	1638.910	-964.989	0.498	1721.773	0.585	24	0.273	R.TPMGGFLGALSSLSATK.L
R4/RRR4-10/2	1638.451	1638.910	-280.944	0.505	1498.095	0.624	23	0.254	R.TPMGGFLGALSSLSATK.L
R4/RRR4-10/2	1654.483	1654.910	-258.781	0.484	1615.761	0.561	23	0.252	R.TPM*GGFLGALSSLSATK.L
R4/RRR4-10/2	1538.977	1539.543	-1020.209	0.439	1719.196	0.468	20	0.244	R.EDQDAYAIQSNER.G
R4/RRR4-10/2	1942.413	1942.207	106.866	0.532	1480.447	0.571	24	0.239	R.NSGAFAWEIVPIEVPVGR.G
R4/RRR4-10/2	1088.987	1089.185	-181.533	0.485	1448.397	0.566	19	0.239	K.ALANAGLESSR.V
R4/RRR4-10/2	1941.900	1942.207	-158.104	0.514	1426.385	0.592	24	0.237	R.NSGAFAWEIVPIEVPVGR.G
R4/RRR4-10/2	1539.241	1539.543	-196.680	0.474	1555.204	0.453	19	0.221	R.EDQDAYAIQSNER.G
R4/RRR4-10/2	1540.070	1539.543	-307.636	0.537	1396.058	0.507	19	0.217	R.EDQDAYAIQSNER.G
R4/RRR4-10/2	1638.729	1638.910	-110.772	0.503	1132.159	0.566	21	0.201	R.TPMGGFLGALSSLSATK.L
R4/RRR4-10/2	1088.851	1089.185	-307.383	0.379	1366.911	0.418	17	0.194	K.ALANAGLESSR.V
R4/RRR4-10/2	1941.485	1942.207	-889.421	0.511	1031.375	0.560	22	0.192	R.NSGAFAWEIVPIEVPVGR.G
R4/RRR4-10/3	1941.409	1942.207	-928.469	0.362	1658.756	0.393	33	0.182	R.NSGAFAWEIVPIEVPVGR.G
R4/RRR4-10/2	1656.520	1654.910	-236.216	0.440	985.807	0.521	20	0.180	R.TPM*GGFLGALSSLSATK.L
R4/RRR4-10/3	1959.679	1960.180	-768.460	0.487	1196.708	0.477	32	0.149	K.INVHGGAVSLGHPLGCSGAR.I
R4/RRR4-9/2	1639.821	1638.910	-54.700	0.317	424.132	0.415	19	0.146	R.TPMGGFLGALSSLSATK.L
R4/RRR4-10/2	1097.158	1097.419	-238.433	0.310	832.793	0.205	14	0.136	-.ILVTLLGVLR.-
R4/RRR4-10/3	1960.026	1960.180	-78.941	0.466	922.856	0.427	31	0.111	K.INVHGGAVSLGHPLGCSGAR.I
R4/RRR4-21/2	1992.468	1993.113	-828.011	0.627	2736.950	0.676	29	0.504	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-21/2	1992.607	1993.113	-757.844	0.614	2337.358	0.690	28	0.419	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-22/3	1992.893	1993.113	-110.323	0.521	2356.909	0.555	38	0.402	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-22/3	1992.520	1993.113	-801.665	0.506	2146.456	0.613	36	0.383	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-23/3	1992.785	1993.113	-164.611	0.493	2027.859	0.580	35	0.335	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-20/3	1992.579	1993.113	-771.871	0.492	1776.393	0.593	35	0.284	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-20/3	1992.914	1993.113	-99.816	0.523	1837.470	0.533	36	0.266	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-22/3	1992.909	1993.113	-102.397	0.462	1673.469	0.580	33	0.259	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-23/3	1992.488	1993.113	-817.624	0.477	1702.517	0.563	35	0.255	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-22/3	1993.100	1993.113	-6.279	0.515	1718.743	0.553	34	0.255	K.SHSTETKLEATGDASCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/3	1993.778	1993.113	-168.060	0.527	1629.737	0.580	34	0.250	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-21/2	1222.000	1222.321	-263.270	0.470	1628.576	0.508	20	0.244	K.LEATGDASCVAK.L
R4/RRR4-21/2	1221.935	1222.321	-317.191	0.469	1568.735	0.495	20	0.234	K.LEATGDASCVAK.L
R4/RRR4-21/2	1222.084	1222.321	-194.423	0.487	1503.672	0.513	20	0.231	K.LEATGDASCVAK.L
R4/RRR4-22/2	1221.493	1222.321	-1500.982	0.448	1488.971	0.491	20	0.224	K.LEATGDASCVAK.L
R4/RRR4-20/3	1992.820	1993.113	-147.467	0.486	1466.087	0.572	33	0.218	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-22/2	1222.075	1222.321	-201.939	0.460	1429.344	0.473	20	0.214	K.LEATGDASCVAK.L
R4/RRR4-22/2	1221.971	1222.321	-287.523	0.441	1398.466	0.487	19	0.213	K.LEATGDASCVAK.L
R4/RRR4-22/3	1993.126	1993.113	6.713	0.466	1422.690	0.553	33	0.204	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-22/3	1992.761	1993.113	-176.778	0.489	1239.747	0.552	31	0.179	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-23/2	1221.974	1222.329	-291.530	0.423	732.673	0.531	18	0.173	K.LNPSADAGSVYK.T
R4/RRR4-22/2	1221.986	1222.329	-281.508	0.375	938.427	0.439	20	0.170	K.LNPSADAGSVYK.T
R4/RRR4-22/2	1222.012	1222.329	-260.462	0.342	956.523	0.427	20	0.168	K.LNPSADAGSVYK.T
R4/RRR4-22/2	1221.921	1222.329	-335.030	0.324	840.195	0.434	19	0.162	K.LNPSADAGSVYK.T
R4/RRR4-23/2	1221.893	1222.329	-358.485	0.348	715.097	0.461	18	0.161	K.LNPSADAGSVYK.T
R4/RRR4-22/2	994.954	995.151	-198.936	0.358	774.019	0.420	13	0.160	K.LTVEYELK.D
R4/RRR4-22/2	1160.981	1161.201	-189.891	0.372	1187.185	0.271	17	0.158	K.DGASLSPEQEK.M
R4/RRR4-21/2	1168.059	1168.361	-259.809	0.476	810.671	0.351	14	0.153	K.VCLDVHSLPK.V
R4/RRR4-23/2	1221.492	1222.329	-1508.601	0.267	515.413	0.456	16	0.149	K.LNPSADAGSVYK.T
R4/RRR4-22/2	1168.243	1168.361	-102.038	0.513	694.372	0.359	14	0.149	-.VCLDVHSLPK.-
R4/RRR4-22/2	1168.143	1168.361	-187.260	0.422	846.725	0.292	14	0.147	K.VCLDVHSLPK.V
R4/RRR4-22/2	995.053	995.151	-98.757	0.332	695.678	0.306	13	0.147	K.LTVEYELK.D
R4/RRR4-22/2	1160.879	1161.201	-278.819	0.386	984.617	0.254	16	0.147	-.DGASLSPEQEK.-
R4/RRR4-22/2	994.904	995.151	-249.402	0.299	634.374	0.298	12	0.144	K.LTVEYELK.D
R4/RRR4-21/3	1992.740	1993.113	-187.747	0.435	901.122	0.532	30	0.138	K.SHSTETKLEATGDASCVAK.L
R4/RRR4-21/2	1167.545	1168.361	-1560.165	0.404	815.680	0.227	14	0.138	-.VCLDVHSLPK.-
R4/RRR4-21/2	1168.013	1168.361	-299.233	0.390	678.490	0.208	14	0.137	-.VCLDVHSLPK.-
R4/RRR4-22/2	1167.499	1168.361	-1599.657	0.311	723.887	0.100	14	0.133	K.VCLDVHSLPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1928.449	1929.081	-849.086	0.589	1902.241	0.675	25	0.329	R.VPASQGEQLGQIATSNATR.R
R4/RRR4-9/2	1598.433	1598.730	-186.179	0.477	2160.287	0.449	22	0.303	R.SSICYIDGDEGILR.Y
R4/RRR4-9/2	1117.891	1118.311	-376.503	0.534	1972.129	0.520	19	0.297	K.APTIAAAAYLR.L
R4/RRR4-9/2	1599.313	1598.730	-261.408	0.477	2073.763	0.433	22	0.285	R.SSICYIDGDEGILR.Y
R4/RRR4-9/2	1117.455	1118.311	-1665.160	0.447	1859.543	0.524	18	0.279	K.APTIAAAAYLR.L
R4/RRR4-9/2	1118.188	1118.311	-110.438	0.531	1874.544	0.487	18	0.272	K.APTIAAAAYLR.L
R4/RRR4-9/2	1480.263	1479.662	-270.107	0.505	1673.181	0.560	21	0.264	K.IYDPGYLNTAPVR.S
R4/RRR4-9/2	1598.158	1598.730	-986.644	0.398	2155.048	0.301	22	0.260	R.SSICYIDGDEGILR.Y
R4/RRR4-9/2	1479.318	1479.662	-233.284	0.471	1452.784	0.529	20	0.228	K.IYDPGYLNTAPVR.S
R4/RRR4-9/2	1956.580	1957.326	-895.325	0.587	1166.708	0.623	23	0.220	R.AM*GFPTEFFPVLFAIPR.M
R4/RRR4-9/2	1479.197	1479.662	-315.330	0.485	1296.022	0.541	19	0.214	K.IYDPGYLNTAPVR.S
R4/RRR4-9/2	914.832	915.029	-216.627	0.476	1071.420	0.417	15	0.174	R.GGALAVVDGR.T
R4/RRR4-9/2	914.402	915.029	-1784.941	0.402	825.653	0.403	14	0.158	R.GGALAVVDGR.T
R4/RRR4-9/2	1100.828	1100.321	-449.183	0.329	580.666	0.360	12	0.147	R.MAGWLAHWK.E
R4/RRR4-9/2	1100.597	1100.321	251.681	0.331	730.758	0.288	13	0.143	-.MAGWLAHWK.-
R4/RRR4-9/3	1929.886	1929.081	-101.553	0.480	1005.325	0.509	28	0.138	R.VPASQGEQLGQIATSNATR.R
R4/RRR4-9/2	1100.536	1100.321	196.180	0.236	527.044	0.280	11	0.137	R.MAGWLAHWK.E
R4/RRR4-26/2	1768.841	1769.955	-1198.194	0.510	1815.836	0.458	24	0.255	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/2	1769.161	1769.955	-1016.657	0.537	1742.322	0.439	23	0.239	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/2	1768.621	1769.955	-1323.506	0.472	1624.126	0.470	22	0.233	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/2	1384.286	1384.537	-181.969	0.540	1643.670	0.430	19	0.226	K.M*QGVESFDVDIK.E
R4/RRR4-26/2	1383.935	1384.537	-1161.465	0.447	1531.125	0.367	19	0.201	K.M*QGVESFDVDIK.E
R4/RRR4-27/2	1430.169	1429.601	-302.597	0.497	919.407	0.563	21	0.190	K.GNVTPDAVLQTVSK.T
R4/RRR4-26/2	1429.220	1429.601	-267.075	0.456	982.838	0.538	21	0.188	K.GNVTPDAVLQTVSK.T
R4/RRR4-27/2	1429.064	1429.601	-1078.456	0.499	815.428	0.575	20	0.185	K.GNVTPDAVLQTVSK.T
R4/RRR4-26/2	1370.046	1370.542	-363.056	0.370	1334.842	0.383	18	0.184	R.VGM*SCEGCVGAVK.R
R4/RRR4-26/2	1369.952	1370.542	-1164.577	0.374	1422.890	0.335	19	0.183	R.VGM*SCEGCVGAVK.R
R4/RRR4-26/2	1429.118	1429.601	-338.974	0.476	911.792	0.521	21	0.182	K.GNVTPDAVLQTVSK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/2	1429.043	1429.601	-1093.723	0.475	827.912	0.520	20	0.177	K.GNVTPDAVLQTVSK.T
R4/RRR4-27/2	1429.289	1429.601	-218.577	0.463	687.605	0.549	19	0.173	K.GNVTPDAVLQTVSK.T
R4/RRR4-27/2	1428.598	1429.601	-1406.197	0.320	977.866	0.426	21	0.167	K.GNVTPDAVLQTVSK.T
R4/RRR4-26/2	1370.045	1370.542	-363.861	0.376	1147.952	0.355	17	0.165	R.VGM*SCEGCVGAVK.R
R4/RRR4-25/2	1429.166	1429.601	-305.380	0.338	895.156	0.458	18	0.165	K.GNVTPDAVLQTVSK.T
R4/RRR4-27/2	1384.194	1384.537	-248.498	0.404	1084.977	0.323	18	0.160	K.M*QGVESFDVDIK.E
R4/RRR4-26/3	1525.703	1526.729	-1331.477	0.418	1243.342	0.483	27	0.153	R.VGM*SCEGCVGAVKR.V
R4/RRR4-27/2	1383.477	1384.537	-1493.544	0.368	831.528	0.282	18	0.146	K.M*QGVESFDVDIK.E
R4/RRR4-27/3	1769.308	1769.955	-933.194	0.481	1248.109	0.453	29	0.146	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/2	1836.984	1837.921	-1057.723	0.329	1225.160	0.477	22	0.145	K.TSFWDAEPAPVEATAASS.-
R4/RRR4-25/2	1428.473	1429.601	-1494.089	0.224	608.040	0.364	17	0.143	K.GNVTPDAVLQTVSK.T
R4/RRR4-26/3	1769.262	1769.955	-959.689	0.457	1236.777	0.409	29	0.132	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/3	1769.337	1769.955	-917.194	0.456	1008.498	0.472	27	0.130	K.M*QGVESFDVDIKEQK.V
R4/RRR4-25/3	1769.537	1769.955	-236.733	0.467	1203.270	0.408	29	0.129	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/3	1527.565	1526.729	-107.505	0.429	1040.001	0.460	26	0.127	R.VGM*SCEGCVGAVKR.V
R4/RRR4-25/3	1769.193	1769.955	-998.757	0.445	1067.231	0.429	28	0.124	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/2	1837.092	1837.921	-998.211	0.338	936.226	0.514	20	0.115	K.TSFWDAEPAPVEATAASS.-
R4/RRR4-26/3	1526.353	1526.729	-246.522	0.470	842.222	0.447	24	0.112	R.VGM*SCEGCVGAVKR.V
R4/RRR4-26/2	1837.206	1837.921	-935.905	0.279	1098.151	0.389	22	0.110	K.TSFWDAEPAPVEATAASS.-
R4/RRR4-25/3	1769.882	1769.955	-41.398	0.440	844.841	0.386	26	0.104	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/3	1754.226	1753.955	154.721	0.376	394.556	0.399	23	0.102	K.MQGVESFDVDIKEQK.V
R4/RRR4-27/3	1770.655	1769.955	-169.925	0.458	748.052	0.391	25	0.102	K.M*QGVESFDVDIKEQK.V
R4/RRR4-26/3	1753.961	1753.955	3.231	0.391	293.702	0.428	21	0.091	-.MQGVESFDVDIKEQK.-
R4/RRR4-26/3	1754.100	1753.955	83.012	0.363	319.100	0.367	20	0.068	-.MQGVESFDVDIKEQK.-
R4/RRR4-13/2	1893.942	1894.969	-1073.558	0.552	2659.140	0.554	27	0.435	K.TEGKETEEDSSAAGLLEK.L
R4/RRR4-13/2	1895.355	1894.969	204.349	0.611	2423.830	0.584	27	0.396	K.TEGKETEEDSSAAGLLEK.L
R4/RRR4-13/2	1894.306	1894.969	-880.354	0.594	2197.029	0.570	27	0.347	K.TEGKETEEDSSAAGLLEK.L
R4/RRR4-13/2	1607.945	1608.814	-1165.974	0.512	2184.040	0.433	23	0.302	K.FKDLVEEISESLAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1608.510	1608.814	-189.809	0.570	2017.058	0.497	22	0.295	K.FKDLVEEISESLAK.T
R4/RRR4-13/2	1607.678	1608.814	-1332.877	0.505	1969.116	0.445	22	0.272	K.FKDLVEEISESLAK.T
R4/RRR4-13/2	1332.889	1333.467	-1187.045	0.515	1899.200	0.427	19	0.259	K.DLVEEISESLAK.T
R4/RRR4-13/2	1315.282	1315.495	-162.402	0.545	1625.300	0.478	20	0.238	K.ICANHLVASTTK.M
R4/RRR4-13/2	1315.032	1315.495	-352.926	0.500	1334.779	0.471	19	0.205	K.ICANHLVASTTK.M
R4/RRR4-13/2	1479.121	1479.526	-274.372	0.341	1326.137	0.328	18	0.171	K.ETEEDSSAAGLLEK.L
R4/RRR4-13/3	1765.988	1765.898	51.636	0.464	943.911	0.445	29	0.117	K.KSEEVATKEESTEAVK.E
R4/RRR4-13/3	1766.142	1765.898	138.564	0.465	779.580	0.482	28	0.115	K.KSEEVATKEESTEAVK.E
R4/RRR4-13/3	1608.563	1608.814	-156.834	0.521	963.702	0.335	25	0.097	K.FKDLVEEISESLAK.T
R4/RRR4-13/3	1608.440	1608.814	-233.747	0.525	958.305	0.308	25	0.088	-.FKDLVEEISESLAK.-
R4/RRR4-11/2	1811.727	1812.096	-203.998	0.529	1974.448	0.555	24	0.305	R.DKPYCGLLVGLVSAYR.Y
R4/RRR4-11/2	1991.202	1991.298	-47.999	0.545	1627.953	0.618	26	0.268	R.AFSGLGGLGVDEPAMVSALAK.W
R4/RRR4-11/2	1578.270	1578.665	-251.162	0.495	1599.458	0.556	21	0.253	R.HIEEDLGHEETLR.E
R4/RRR4-11/2	1812.720	1812.096	-207.668	0.527	1613.417	0.539	22	0.248	R.DKPYCGLLVGLVSAYR.Y
R4/RRR4-11/2	1990.514	1991.298	-898.945	0.515	1344.564	0.603	24	0.227	R.AFSGLGGLGVDEPAMVSALAK.W
R4/RRR4-11/2	1577.527	1578.665	-1359.904	0.527	1401.527	0.541	20	0.227	R.HIEEDLGHEETLR.E
R4/RRR4-11/2	959.741	960.067	-340.505	0.483	1633.978	0.322	15	0.202	R.TAEELLGAR.K
R4/RRR4-11/2	959.425	960.067	-1716.429	0.415	1649.182	0.308	15	0.201	R.TAEELLGAR.K
R4/RRR4-11/2	959.904	960.067	-169.657	0.473	1502.873	0.352	15	0.196	R.TAEELLGAR.K
R4/RRR4-11/2	1174.019	1173.338	-272.569	0.546	1389.544	0.386	18	0.192	R.EAALCLATPAR.Y
R4/RRR4-11/2	1172.687	1173.338	-1412.166	0.479	1389.399	0.368	18	0.189	R.EAALCLATPAR.Y
R4/RRR4-12/3	1578.227	1578.665	-278.602	0.504	1303.535	0.562	26	0.186	R.HIEEDLGHEETLR.E
R4/RRR4-12/3	1579.941	1578.665	174.888	0.489	1399.248	0.526	27	0.186	R.HIEEDLGHEETLR.E
R4/RRR4-11/2	1172.404	1173.338	-1654.999	0.331	1550.161	0.202	19	0.172	R.EAALCLATPAR.Y
R4/RRR4-11/2	1186.087	1186.385	-251.628	0.473	409.137	0.532	13	0.163	R.SKPHLVETFK.H
R4/RRR4-11/3	1578.839	1578.665	110.489	0.518	1239.018	0.512	25	0.162	R.HIEEDLGHEETLR.E
R4/RRR4-11/2	1186.094	1186.385	-246.259	0.420	635.504	0.440	16	0.160	R.SKPHLVETFK.H
R4/RRR4-11/2	1058.855	1059.155	-284.292	0.495	837.104	0.366	15	0.159	K.LVENDDVVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1058.891	1059.155	-250.750	0.453	675.298	0.396	15	0.159	K.LVENDDVVR.I
R4/RRR4-12/2	1059.011	1059.155	-136.495	0.459	680.918	0.391	15	0.158	K.LVENDDVVR.I
R4/RRR4-11/2	1058.821	1059.155	-316.679	0.506	713.726	0.375	15	0.158	K.LVENDDVVR.I
R4/RRR4-11/2	1185.606	1186.385	-1504.694	0.406	567.233	0.418	15	0.155	R.SKPHLVETFK.H
R4/RRR4-11/3	1578.910	1578.665	155.383	0.486	1197.458	0.496	25	0.153	R.HIEEDLGHEETLR.E
R4/RRR4-12/2	1991.235	1991.298	-31.765	0.374	793.466	0.407	18	0.146	R.AFSGLGGLGVDEPAMVSALAK.W
R4/RRR4-12/3	1578.843	1578.665	112.816	0.510	999.575	0.523	23	0.142	R.HIEEDLGHEETLR.E
R4/RRR4-11/3	1578.995	1578.665	209.459	0.490	1045.885	0.501	25	0.139	R.HIEEDLGHEETLR.E
R4/RRR4-11/3	1811.908	1812.096	-104.179	0.322	1302.751	0.350	24	0.124	R.DKPYCGLLVGLVSAYR.Y
R4/RRR4-13/3	1578.419	1578.665	-156.280	0.428	886.352	0.480	23	0.122	R.HIEEDLGHEETLR.E
R4/RRR4-11/3	1812.001	1812.096	-52.584	0.384	967.180	0.346	24	0.097	R.DKPYCGLLVGLVSAYR.Y
R4/RRR4-8/2	1444.848	1444.573	191.037	0.517	2433.221	0.406	20	0.336	K.AESLDDAIQIVNR.N
R4/RRR4-8/2	1967.002	1968.071	-1055.344	0.524	2002.858	0.628	24	0.330	R.ADEHVDVTNPATQEVVSR.I
R4/RRR4-8/2	1967.641	1968.071	-219.195	0.542	1887.915	0.627	24	0.311	R.ADEHVDVTNPATQEVVSR.I
R4/RRR4-8/2	1444.154	1444.573	-290.511	0.500	2332.918	0.362	20	0.304	K.AESLDDAIQIVNR.N
R4/RRR4-8/2	1444.156	1444.573	-289.239	0.476	2128.001	0.372	19	0.274	K.AESLDDAIQIVNR.N
R4/RRR4-8/2	1589.122	1588.703	264.377	0.493	1361.743	0.551	23	0.222	K.YGNGASIFTTSGVSAR.K
R4/RRR4-8/3	1968.754	1968.071	-161.738	0.505	1581.464	0.517	31	0.217	R.ADEHVDVTNPATQEVVSR.I
R4/RRR4-8/3	1968.000	1968.071	-36.160	0.485	1525.212	0.519	29	0.210	R.ADEHVDVTNPATQEVVSR.I
R4/RRR4-8/2	1205.045	1204.312	-222.675	0.612	1225.767	0.506	18	0.204	K.LAENITTEQGK.T
R4/RRR4-8/2	1162.526	1163.305	-1535.095	0.393	1525.097	0.382	17	0.204	R.IPLTTADEFR.A
R4/RRR4-8/2	1162.925	1163.305	-328.022	0.429	1433.047	0.412	16	0.201	R.IPLTTADEFR.A
R4/RRR4-8/2	1203.852	1204.312	-383.181	0.572	1233.068	0.481	18	0.200	K.LAENITTEQGK.T
R4/RRR4-8/2	1205.053	1204.312	-215.663	0.551	1206.687	0.477	18	0.197	K.LAENITTEQGK.T
R4/RRR4-8/2	1163.146	1163.305	-137.328	0.467	1301.966	0.411	16	0.190	R.IPLTTADEFR.A
R4/RRR4-8/3	1967.942	1968.071	-66.118	0.426	1361.863	0.472	29	0.168	R.ADEHVDVTNPATQEVVSR.I
R4/RRR4-8/2	1220.384	1220.400	-13.204	0.434	739.406	0.476	17	0.167	R.LLIGGEFVESR.A
R4/RRR4-8/2	1221.002	1220.400	-326.859	0.296	322.435	0.263	15	0.144	R.LLIGGEFVESR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1220.634	1220.400	192.827	0.268	259.071	0.302	13	0.143	R.LLIGGEFVESR.A
R4/RRR4-12/2	1102.067	1102.183	-105.943	0.309	898.757	0.129	15	0.131	-.LIQSGADNGAR.-
R4/RRR4-14/2	1969.474	1970.261	-910.413	0.556	4468.031	0.544	30	0.979	K.SAELIGQAIANNPAFLALR.Q
R4/RRR4-13/2	1970.237	1970.261	-12.280	0.617	3870.942	0.563	30	0.772	K.SAELIGQAIANNPAFLALR.Q
R4/RRR4-13/2	1969.518	1970.261	-887.578	0.575	3623.906	0.533	29	0.678	K.SAELIGQAIANNPAFLALR.Q
R4/RRR4-14/2	1969.500	1970.261	-896.787	0.580	3530.800	0.554	30	0.661	K.SAELIGQAIANNPAFLALR.Q
R4/RRR4-14/2	1969.638	1970.261	-826.481	0.583	3368.049	0.556	29	0.614	K.SAELIGQAIANNPAFLALR.Q
R4/RRR4-13/2	1969.322	1970.261	-987.763	0.559	2703.453	0.520	27	0.428	K.SAELIGQAIANNPAFLALR.Q
R4/RRR4-13/2	1942.484	1942.158	168.002	0.552	1603.826	0.644	27	0.277	R.NFNIALDDVSITSLSFGK.E
R4/RRR4-13/3	1663.357	1662.872	292.318	0.407	2219.769	0.270	30	0.230	K.AVVAQYNASQLITQR.E
R4/RRR4-13/2	1662.326	1662.872	-932.649	0.490	1591.433	0.467	23	0.229	K.AVVAQYNASQLITQR.E
R4/RRR4-14/2	1662.295	1662.872	-951.301	0.483	1722.377	0.392	23	0.226	K.AVVAQYNASQLITQR.E
R4/RRR4-14/2	1662.438	1662.872	-261.940	0.490	1488.555	0.424	21	0.206	K.AVVAQYNASQLITQR.E
R4/RRR4-13/2	1662.294	1662.872	-952.112	0.466	1520.849	0.404	22	0.206	K.AVVAQYNASQLITQR.E
R4/RRR4-14/2	1374.348	1374.485	-100.545	0.519	1235.502	0.515	20	0.205	R.ARPNLVESTSGSR.D
R4/RRR4-14/2	1662.398	1662.872	-285.809	0.493	1415.181	0.426	21	0.200	K.AVVAQYNASQLITQR.E
R4/RRR4-14/2	1374.170	1374.485	-230.107	0.491	1240.365	0.485	20	0.199	R.ARPNLVESTSGSR.D
R4/RRR4-13/2	1374.303	1374.485	-133.422	0.522	1247.000	0.471	20	0.197	R.ARPNLVESTSGSR.D
R4/RRR4-13/2	1662.435	1662.872	-263.413	0.503	1375.237	0.429	21	0.197	K.AVVAQYNASQLITQR.E
R4/RRR4-13/2	1374.081	1374.485	-295.257	0.539	1050.042	0.520	19	0.191	R.ARPNLVESTSGSR.D
R4/RRR4-13/2	1374.146	1374.485	-248.109	0.500	1195.586	0.448	19	0.187	R.ARPNLVESTSGSR.D
R4/RRR4-14/2	1373.662	1374.485	-1331.500	0.497	1140.731	0.469	19	0.187	R.ARPNLVESTSGSR.D
R4/RRR4-15/2	1972.033	1970.261	-116.326	0.450	1029.713	0.429	18	0.163	K.SAELIGQAIANNPAFLALR.Q
R4/RRR4-14/2	1206.027	1206.459	-359.546	0.389	361.553	0.552	15	0.159	R.VPVPPAGAGTLVK.L
R4/RRR4-14/2	1079.898	1080.133	-218.208	0.401	629.566	0.408	15	0.158	R.TLGENFNER.V
R4/RRR4-13/2	1206.179	1206.459	-233.022	0.302	572.859	0.509	16	0.155	R.VPVPPAGAGTLVK.L
R4/RRR4-13/2	1079.645	1080.133	-452.950	0.387	613.866	0.387	15	0.155	R.TLGENFNER.V
R4/RRR4-13/3	1662.691	1662.872	-108.853	0.381	1696.297	0.303	28	0.155	K.AVVAQYNASQLITQR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1079.433	1080.133	-1579.990	0.382	487.477	0.420	13	0.154	R.TLGENFNER.V
R4/RRR4-13/2	1079.978	1080.133	-144.389	0.468	602.096	0.346	15	0.153	R.TLGENFNER.V
R4/RRR4-14/2	1205.677	1206.459	-1482.997	0.355	461.251	0.467	16	0.151	-.VPVPPAGAGTLVK.-
R4/RRR4-14/2	1207.013	1206.459	-371.019	0.282	340.341	0.515	14	0.149	R.VPVPPAGAGTLVK.L
R4/RRR4-13/2	1206.296	1206.459	-135.866	0.308	307.385	0.483	14	0.146	-.VPVPPAGAGTLVK.-
R4/RRR4-14/2	1079.376	1080.133	-1633.160	0.237	524.242	0.311	14	0.142	R.TLGENFNER.V
R4/RRR4-14/2	1205.982	1206.459	-397.022	0.239	271.693	0.333	12	0.093	-.VPVPPAGAGTLVK.-
R4/RRR4-8/2	1499.574	1499.803	-153.139	0.492	1544.462	0.526	21	0.237	R.LGPNYLMLPANAPK.C
R4/RRR4-8/2	1971.781	1970.240	-233.389	0.571	1385.980	0.565	22	0.226	R.EGNFDLVGNNMPVFFIR.D
R4/RRR4-8/2	1969.488	1970.240	-892.378	0.504	1347.774	0.488	22	0.205	R.EGNFDLVGNNMPVFFIR.D
R4/RRR4-8/2	1515.093	1515.802	-1131.467	0.452	1093.786	0.485	19	0.185	R.LGPNYLM*LPANAPK.C
R4/RRR4-8/2	1516.264	1515.802	305.767	0.503	1171.664	0.445	19	0.183	R.LGPNYLM*LPANAPK.C
R4/RRR4-8/2	1151.081	1151.384	-264.173	0.460	912.397	0.522	17	0.183	R.APGVQTPIIVR.F
R4/RRR4-8/2	1515.559	1515.802	-160.956	0.441	1098.748	0.467	18	0.181	R.LGPNYLM*LPANAPK.C
R4/RRR4-8/2	1152.279	1151.384	-91.020	0.413	841.885	0.498	17	0.173	R.APGVQTPIIVR.F
R4/RRR4-8/2	1969.489	1970.240	-891.881	0.500	1027.152	0.471	19	0.173	R.EGNFDLVGNNMPVFFIR.D
R4/RRR4-7/2	1151.286	1151.384	-85.356	0.337	1024.923	0.438	16	0.171	R.APGVQTPIIVR.F
R4/RRR4-7/2	1151.288	1151.384	-83.229	0.420	778.869	0.477	15	0.166	R.APGVQTPIIVR.F
R4/RRR4-8/2	1680.139	1680.796	-989.366	0.394	953.375	0.392	18	0.159	K.DLTDSIAAGNYPEWK.L
R4/RRR4-8/2	1621.417	1621.861	-274.608	0.354	705.034	0.437	17	0.152	K.TWPEDIIPLQPVGR.M
R4/RRR4-8/2	1680.590	1680.796	-122.802	0.375	805.338	0.304	17	0.142	K.DLTDSIAAGNYPEWK.L
R4/RRR4-8/2	1679.757	1680.796	-1217.298	0.282	777.483	0.294	16	0.139	K.DLTDSIAAGNYPEWK.L
R4/RRR4-8/2	1972.144	1970.240	-48.959	0.420	365.987	0.339	13	0.134	R.EGNFDLVGNNMPVFFIR.D
R4/RRR4-8/3	1144.908	1144.351	-388.537	0.440	860.838	0.378	19	0.101	R.HAEKVPIPPR.V
R4/RRR4-8/3	1144.053	1144.351	-261.313	0.389	472.877	0.340	17	0.093	R.HAEKVPIPPR.V
R4/RRR4-8/3	1144.205	1144.351	-128.056	0.351	650.633	0.288	18	0.087	R.HAEKVPIPPR.V
R4/RRR4-8/3	1143.556	1144.351	-1575.186	0.335	776.159	0.253	19	0.083	R.HAEKVPIPPR.V
R4/RRR4-5/2	1650.463	1650.881	-254.197	0.504	2690.613	0.473	25	0.414	R.FASEVAGVQDLGMLGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1690.067	1690.899	-1086.994	0.489	2128.162	0.527	22	0.322	K.TIVENFYM*TDAITR.A
R4/RRR4-5/2	1690.182	1690.899	-1019.044	0.515	2087.438	0.511	22	0.310	K.TIVENFYM*TDAITR.A
R4/RRR4-5/2	1690.217	1690.899	-998.306	0.527	2112.950	0.494	21	0.308	K.TIVENFYM*TDAITR.A
R4/RRR4-5/2	1934.312	1934.140	89.274	0.538	1435.724	0.598	26	0.241	R.ALSEVAGAQLPYDSLSGVR.D
R4/RRR4-5/2	1933.823	1934.140	-164.210	0.522	1498.187	0.540	26	0.234	R.ALSEVAGAQLPYDSLSGVR.D
R4/RRR4-5/2	1934.093	1934.140	-24.284	0.549	1322.424	0.592	25	0.226	R.ALSEVAGAQLPYDSLSGVR.D
R4/RRR4-5/2	1648.456	1648.754	-181.273	0.443	1617.870	0.431	23	0.222	K.GTETIDVTDAVGSNIR.V
R4/RRR4-5/2	1648.165	1648.754	-966.959	0.454	1597.400	0.396	22	0.211	K.GTETIDVTDAVGSNIR.V
R4/RRR4-5/2	1269.423	1269.516	-73.458	0.412	1342.231	0.458	17	0.200	R.SVVDKNLGPLVK.T
R4/RRR4-5/2	1363.108	1363.541	-318.922	0.409	1065.598	0.390	19	0.169	R.ANVILPSSAFSEK.E
R4/RRR4-5/2	1363.248	1363.541	-215.245	0.404	1068.769	0.378	19	0.167	R.ANVILPSSAFSEK.E
R4/RRR4-5/2	1363.094	1363.541	-329.165	0.310	1173.094	0.312	20	0.162	R.ANVILPSSAFSEK.E
R4/RRR4-5/2	1269.046	1269.340	-231.802	0.400	887.096	0.409	16	0.161	R.GSGEEIGTYVEK.L
R4/RRR4-5/2	1269.171	1269.516	-272.586	0.417	845.342	0.390	15	0.155	R.SVVDKNLGPLVK.T
R4/RRR4-5/2	1269.219	1269.340	-95.753	0.417	747.971	0.404	16	0.155	R.GSGEEIGTYVEK.L
R4/RRR4-5/2	1269.561	1269.516	35.913	0.401	914.986	0.356	15	0.154	R.SVVDKNLGPLVK.T
R4/RRR4-5/2	1269.188	1269.340	-120.259	0.459	667.609	0.387	15	0.150	R.GSGEEIGTYVEK.L
R4/RRR4-5/2	1362.634	1363.541	-1403.466	0.304	850.607	0.262	17	0.142	R.ANVILPSSAFSEK.E
R4/RRR4-16/2	1363.198	1363.587	-286.477	0.480	2141.898	0.476	19	0.308	K.TDLLLAANPVHAK.V
R4/RRR4-16/3	1491.691	1491.760	-46.680	0.580	1956.724	0.447	30	0.249	R.KTDLLLAANPVHAK.V
R4/RRR4-16/3	1491.782	1491.760	14.755	0.540	1668.703	0.448	27	0.200	R.KTDLLLAANPVHAK.V
R4/RRR4-16/3	1491.216	1491.760	-1038.648	0.538	1621.537	0.446	27	0.192	R.KTDLLLAANPVHAK.V
R4/RRR4-16/2	1447.570	1446.630	-41.665	0.443	914.839	0.489	19	0.176	R.GLPYDLVAVDLDR.K
R4/RRR4-16/2	1389.397	1389.582	-133.206	0.510	893.420	0.486	19	0.175	K.LLGSTNPSPFVTR.V
R4/RRR4-16/2	1447.329	1446.630	-208.578	0.403	628.103	0.580	16	0.169	R.GLPYDLVAVDLDR.K
R4/RRR4-16/2	1389.063	1389.582	-1096.379	0.448	687.848	0.520	17	0.167	K.LLGSTNPSPFVTR.V
R4/RRR4-16/2	884.437	885.086	-1870.542	0.448	830.751	0.350	13	0.156	R.VELALALR.G
R4/RRR4-16/2	884.627	885.086	-521.248	0.495	795.911	0.342	13	0.155	R.VELALALR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	833.960	834.044	-100.657	0.489	607.167	0.358	11	0.154	K.VPVLIHR.G
R4/RRR4-16/2	833.428	834.044	-1945.435	0.349	643.667	0.392	11	0.153	K.VPVLIHR.G
R4/RRR4-16/2	885.043	885.086	-49.541	0.528	800.471	0.328	13	0.153	R.VELALALR.G
R4/RRR4-16/2	833.885	834.044	-191.258	0.421	538.000	0.353	11	0.152	K.VPVLIHR.G
R4/RRR4-16/2	1389.247	1389.582	-241.622	0.332	728.732	0.387	16	0.149	K.LLGSTNPSPFVTR.V
R4/RRR4-16/2	1446.151	1446.630	-332.526	0.235	367.513	0.351	15	0.139	R.GLPYDLVAVDLDR.K
R4/RRR4-16/2	1364.345	1363.587	-178.099	0.289	647.715	0.259	14	0.134	K.TDLLLAANPVHAK.V
R4/RRR4-15/3	1492.080	1491.760	214.891	0.416	678.804	0.352	21	0.092	R.KTDLLLAANPVHAK.V
R4/RRR4-3/2	1761.820	1760.968	-83.853	0.593	2493.046	0.617	23	0.420	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-3/2	1761.688	1760.968	-159.057	0.566	2352.018	0.593	22	0.381	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-4/2	1761.300	1760.968	189.316	0.536	2257.193	0.569	23	0.356	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-4/2	1760.318	1760.968	-939.712	0.557	2008.429	0.604	22	0.322	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-3/3	1760.606	1760.968	-205.895	0.447	1785.003	0.494	30	0.247	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-3/2	1760.300	1760.968	-950.155	0.474	1488.502	0.586	19	0.240	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-1/2	1760.744	1760.968	-127.156	0.489	1465.972	0.501	22	0.221	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-1/2	1760.944	1760.968	-13.392	0.489	1128.670	0.566	21	0.202	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-3/2	1176.401	1176.262	117.856	0.390	1397.993	0.399	16	0.194	K.AGEFFYSAQR.S
R4/RRR4-3/2	1726.891	1726.951	-35.139	0.507	1244.517	0.415	21	0.185	R.TYNELVEYNIVLQK.A
R4/RRR4-3/2	971.093	971.176	-85.308	0.429	751.713	0.499	16	0.172	K.LGSLSGLVPK.E
R4/RRR4-4/2	970.946	971.176	-237.776	0.375	898.007	0.450	17	0.170	K.LGSLSGLVPK.E
R4/RRR4-3/2	970.642	971.176	-1584.896	0.393	697.888	0.479	15	0.165	K.LGSLSGLVPK.E
R4/RRR4-3/2	1727.724	1726.951	-131.783	0.530	979.697	0.393	21	0.165	R.TYNELVEYNIVLQK.A
R4/RRR4-4/2	971.102	971.176	-76.229	0.433	815.735	0.413	16	0.163	K.LGSLSGLVPK.E
R4/RRR4-4/2	970.936	971.176	-247.740	0.368	703.251	0.424	15	0.158	K.LGSLSGLVPK.E
R4/RRR4-3/2	970.518	971.176	-1713.020	0.329	743.040	0.419	16	0.158	K.LGSLSGLVPK.E
R4/RRR4-1/2	970.947	971.176	-236.010	0.379	823.517	0.367	16	0.157	K.LGSLSGLVPK.E
R4/RRR4-4/3	1930.987	1931.146	-82.410	0.445	1310.721	0.450	30	0.153	K.VRPAYSFGVDPVWHGSR.S
R4/RRR4-5/2	1696.482	1695.854	-219.804	0.405	890.198	0.354	17	0.150	K.NISSEFEQWNTLVK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/2	1761.747	1760.968	-125.415	0.374	445.022	0.431	18	0.150	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-4/2	1761.669	1760.968	-170.179	0.337	500.341	0.340	16	0.141	K.FTSAFQEIVDAYGIAK.Y
R4/RRR4-3/3	1930.799	1931.146	-179.915	0.411	800.156	0.347	25	0.091	K.VRPAYSFGVDPVWHGSR.S
R4/RRR4-4/2	1614.367	1614.776	-254.268	0.323	873.362	0.319	20	0.077	K.FVPFAFASIIEEED.-
R4/RRR4-13/2	1745.444	1746.001	-894.338	0.454	2263.629	0.419	23	0.310	K.GVDVILDNIGGLYLQR.N
R4/RRR4-13/2	1745.249	1746.001	-1006.615	0.406	1718.799	0.363	21	0.216	K.GVDVILDNIGGLYLQR.N
R4/RRR4-13/2	1058.972	1059.159	-176.388	0.374	1312.481	0.452	16	0.195	R.NLNSLAVDGR.L
R4/RRR4-13/2	1067.087	1067.174	-81.764	0.444	1104.813	0.440	15	0.180	K.VFVTAGSEEK.L
R4/RRR4-13/2	1066.718	1067.174	-428.998	0.356	999.039	0.402	16	0.166	K.VFVTAGSEEK.L
R4/RRR4-13/2	942.293	943.126	-1950.593	0.319	1034.402	0.348	14	0.158	R.LTIQAAGLR.N
R4/RRR4-13/2	1100.324	1099.312	11.171	0.457	879.098	0.349	16	0.157	R.RLTIQAAGLR.N
R4/RRR4-13/2	1066.370	1067.174	-1696.708	0.339	883.892	0.366	15	0.156	K.VFVTAGSEEK.L
R4/RRR4-13/2	1099.018	1099.312	-268.666	0.474	705.216	0.355	16	0.154	R.RLTIQAAGLR.N
R4/RRR4-13/2	988.016	988.160	-146.489	0.344	829.218	0.332	14	0.151	K.ALIVSEVEK.N
R4/RRR4-13/2	988.048	988.160	-113.646	0.388	658.350	0.364	12	0.149	K.ALIVSEVEK.N
R4/RRR4-13/2	1098.449	1099.312	-1701.218	0.460	433.574	0.392	13	0.148	-.RLTIQAAGLR.-
R4/RRR4-13/2	987.269	988.160	-1921.260	0.260	678.782	0.273	11	0.138	-.ALIVSEVEK.-
R4/RRR4-13/3	1745.363	1746.001	-941.178	0.357	1111.475	0.294	27	0.095	K.GVDVILDNIGGLYLQR.N
R4/RRR4-6/2	1318.047	1318.372	-247.894	0.462	1715.556	0.314	16	0.206	R.GDLTQEEIQER.Q
R4/RRR4-6/2	1096.802	1097.157	-325.025	0.412	1108.394	0.492	15	0.188	R.YSEALADAEK.T
R4/RRR4-6/2	1096.915	1097.157	-221.074	0.427	1254.974	0.417	15	0.186	R.YSEALADAEK.T
R4/RRR4-6/2	1318.048	1318.372	-246.593	0.449	1403.804	0.309	15	0.178	-.GDLTQEEIQER.-
R4/RRR4-6/2	1096.511	1097.157	-1506.028	0.352	1060.972	0.424	16	0.172	R.YSEALADAEK.T
R4/RRR4-6/2	1310.960	1311.469	-1154.881	0.445	881.603	0.447	17	0.169	R.QVLVDLQENPR.A
R4/RRR4-6/2	1311.247	1311.469	-170.091	0.441	809.246	0.467	17	0.169	R.QVLVDLQENPR.A
R4/RRR4-6/2	1312.176	1311.469	-224.556	0.489	724.957	0.445	17	0.164	R.QVLVDLQENPR.A
R4/RRR4-6/2	1186.519	1187.370	-1564.212	0.322	993.008	0.306	14	0.150	K.TVELKPDWAK.G
R4/RRR4-6/3	1610.915	1609.807	67.019	0.470	1199.797	0.445	25	0.140	K.KKDFETAIQHYTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1659.488	1659.740	-152.224	0.486	1095.832	0.368	23	0.110	-.ANRGDLTQEEIQER.-
R4/RRR4-6/3	1887.387	1886.098	153.730	0.326	955.356	0.412	24	0.109	R.LGAAHLGLGDAASAVAAYEK.G
R4/RRR4-6/3	1658.822	1659.740	-1159.819	0.464	979.607	0.388	23	0.107	-.ANRGDLTQEEIQER.-
R4/RRR4-6/3	1659.568	1659.740	-103.856	0.480	1150.710	0.322	25	0.103	-.ANRGDLTQEEIQER.-
R4/RRR4-6/3	1887.580	1886.098	256.264	0.207	765.029	0.343	26	0.084	R.LGAAHLGLGDAASAVAAYEK.G
R4/RRR4-3/2	1497.263	1497.725	-309.154	0.498	2293.024	0.455	20	0.326	R.SALLQGQALQALQR.F
R4/RRR4-3/2	1513.720	1512.798	-52.058	0.487	1210.897	0.411	18	0.182	K.MDIFNTFIELLR.Q
R4/RRR4-3/3	1600.616	1600.786	-106.610	0.483	1374.793	0.437	26	0.158	K.CECLDILGDVLHR.F
R4/RRR4-3/2	948.253	949.129	-1983.588	0.362	859.897	0.383	13	0.157	K.IEALVFTR.L
R4/RRR4-1/2	1497.306	1497.725	-280.525	0.311	1029.908	0.353	17	0.155	R.SALLQGQALQALQR.F
R4/RRR4-3/2	1396.302	1396.651	-250.836	0.282	880.890	0.384	14	0.149	R.ELPACLPILVDR.M
R4/RRR4-3/2	1057.054	1057.229	-165.473	0.352	842.920	0.305	15	0.148	K.SIQNVGLAVR.Y
R4/RRR4-3/2	1056.967	1057.229	-248.542	0.292	985.043	0.145	15	0.136	K.SIQNVGLAVR.Y
R4/RRR4-3/3	1102.689	1102.271	379.991	0.498	327.850	0.535	15	0.114	R.VLRPNFEAR.T
R4/RRR4-1/3	1102.320	1102.271	44.321	0.463	359.840	0.541	15	0.114	R.VLRPNFEAR.T
R4/RRR4-3/3	1102.420	1102.271	134.860	0.497	395.726	0.520	16	0.113	R.VLRPNFEAR.T
R4/RRR4-1/3	1102.456	1102.271	168.339	0.462	313.578	0.449	15	0.100	-.VLRPNFEAR.-
R4/RRR4-3/3	1101.943	1102.271	-298.743	0.462	301.053	0.456	14	0.100	-.VLRPNFEAR.-
R4/RRR4-16/2	1549.243	1549.750	-976.068	0.531	2468.693	0.465	25	0.366	K.KEDIDGFLVGGASLK.G
R4/RRR4-16/2	1751.184	1751.956	-1014.740	0.547	2097.882	0.515	25	0.312	R.IIYGGSVNAANCAELAK.K
R4/RRR4-16/2	1450.237	1450.619	-263.965	0.567	1941.599	0.584	22	0.309	K.GPDFATIINSVTSK.K
R4/RRR4-16/2	1751.222	1751.956	-992.694	0.535	2062.786	0.504	25	0.303	R.IIYGGSVNAANCAELAK.K
R4/RRR4-16/2	1450.382	1450.619	-163.482	0.575	1837.737	0.610	22	0.302	K.GPDFATIINSVTSK.K
R4/RRR4-16/2	1450.184	1450.619	-300.701	0.526	1845.856	0.553	22	0.285	K.GPDFATIINSVTSK.K
R4/RRR4-16/2	1751.300	1751.956	-948.256	0.564	1737.031	0.471	24	0.245	R.IIYGGSVNAANCAELAK.K
R4/RRR4-16/2	1230.115	1230.353	-194.249	0.453	1392.341	0.490	20	0.214	K.TNVSPEVASGIR.I
R4/RRR4-16/2	1229.672	1230.353	-1370.919	0.448	1403.847	0.436	20	0.204	K.TNVSPEVASGIR.I
R4/RRR4-16/2	1229.568	1230.353	-1456.074	0.398	1121.995	0.408	19	0.175	K.TNVSPEVASGIR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1606.341	1606.765	-264.532	0.487	888.751	0.499	21	0.175	K.VATPEQAQEVHAAVR.D
R4/RRR4-17/2	1449.731	1450.619	-1305.974	0.270	384.010	0.329	12	0.135	-.GPDFATIINSVTSK.-
R4/RRR4-16/3	1578.360	1578.792	-274.428	0.381	683.243	0.539	25	0.119	K.GPDFATIINSVTSKK.V
R4/RRR4-16/3	1578.293	1578.792	-316.912	0.338	714.111	0.471	23	0.107	K.GPDFATIINSVTSKK.V
R4/RRR4-16/3	1578.824	1578.792	20.301	0.312	445.125	0.416	20	0.093	K.GPDFATIINSVTSKK.V
R4/RRR4-16/2	1628.522	1628.852	-203.264	0.540	2478.138	0.574	24	0.403	R.GELLVGIIGTLDTGNR.Y
R4/RRR4-16/2	1627.455	1628.852	-1477.299	0.398	2229.828	0.539	24	0.340	R.GELLVGIIGTLDTGNR.Y
R4/RRR4-16/2	1628.435	1628.852	-257.034	0.516	2085.313	0.590	24	0.333	R.GELLVGIIGTLDTGNR.Y
R4/RRR4-16/2	1699.198	1698.866	196.235	0.520	1832.377	0.588	24	0.293	R.VDFAPGGTNPPHVHPR.A
R4/RRR4-16/2	1698.387	1698.866	-282.636	0.444	1635.153	0.523	23	0.246	R.VDFAPGGTNPPHVHPR.A
R4/RRR4-16/2	1698.292	1698.866	-929.334	0.504	1244.134	0.595	22	0.220	R.VDFAPGGTNPPHVHPR.A
R4/RRR4-15/2	1629.205	1628.852	217.216	0.401	1284.454	0.471	20	0.194	R.GELLVGIIGTLDTGNR.Y
R4/RRR4-16/2	1278.142	1278.508	-286.766	0.490	1326.849	0.393	16	0.187	R.GLMHFQFNVGK.T
R4/RRR4-17/2	957.904	958.137	-244.656	0.499	1330.112	0.368	15	0.185	R.ATEVGIVLR.G
R4/RRR4-16/2	1278.204	1278.508	-238.091	0.513	1272.006	0.352	16	0.175	R.GLMHFQFNVGK.T
R4/RRR4-16/2	1277.981	1278.508	-1197.904	0.476	1238.661	0.345	16	0.172	R.GLMHFQFNVGK.T
R4/RRR4-15/2	989.455	990.138	-1706.346	0.452	825.941	0.422	14	0.166	R.AGETFVIPR.G
R4/RRR4-12/2	990.001	990.138	-138.218	0.430	978.610	0.335	14	0.160	R.AGETFVIPR.G
R4/RRR4-16/2	989.950	990.138	-190.542	0.429	815.470	0.374	14	0.159	R.AGETFVIPR.G
R4/RRR4-19/2	958.021	958.137	-121.298	0.371	1091.935	0.321	13	0.159	R.ATEVGIVLR.G
R4/RRR4-16/2	1294.107	1294.507	-310.186	0.464	749.127	0.406	16	0.159	R.GLM*HFQFNVGK.T
R4/RRR4-19/2	990.158	990.138	20.080	0.474	803.858	0.373	14	0.159	R.AGETFVIPR.G
R4/RRR4-16/2	1294.112	1294.507	-305.833	0.482	799.315	0.387	16	0.158	R.GLM*HFQFNVGK.T
R4/RRR4-17/2	989.964	990.138	-176.440	0.474	781.244	0.369	14	0.158	R.AGETFVIPR.G
R4/RRR4-18/2	989.465	990.138	-1696.182	0.392	847.999	0.347	14	0.157	R.AGETFVIPR.G
R4/RRR4-16/2	989.974	990.138	-166.049	0.455	808.755	0.349	14	0.156	R.AGETFVIPR.G
R4/RRR4-19/2	989.876	990.138	-265.512	0.412	927.119	0.319	14	0.156	R.AGETFVIPR.G
R4/RRR4-15/2	989.850	990.138	-291.989	0.431	796.608	0.347	14	0.156	R.AGETFVIPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	989.921	990.138	-220.108	0.430	790.399	0.347	14	0.156	R.AGETFVIPR.G
R4/RRR4-16/2	1294.153	1294.507	-274.224	0.454	734.311	0.382	16	0.156	R.GLM*HFQFNVGK.T
R4/RRR4-1/2	991.067	990.138	-71.729	0.470	869.019	0.331	14	0.155	R.AGETFVIPR.G
R4/RRR4-16/2	989.898	990.138	-242.747	0.433	807.431	0.339	14	0.155	R.AGETFVIPR.G
R4/RRR4-14/2	990.278	990.138	141.614	0.441	777.853	0.342	14	0.155	R.AGETFVIPR.G
R4/RRR4-18/2	990.097	990.138	-41.749	0.506	827.142	0.342	14	0.155	R.AGETFVIPR.G
R4/RRR4-17/2	989.443	990.138	-1717.874	0.365	837.733	0.332	14	0.155	R.AGETFVIPR.G
R4/RRR4-16/2	990.114	990.138	-24.560	0.447	768.290	0.337	14	0.154	R.AGETFVIPR.G
R4/RRR4-15/2	989.923	990.138	-217.386	0.487	719.136	0.359	13	0.154	R.AGETFVIPR.G
R4/RRR4-17/2	989.976	990.138	-163.575	0.487	810.062	0.331	14	0.154	R.AGETFVIPR.G
R4/RRR4-14/2	990.096	990.138	-41.873	0.495	765.725	0.328	14	0.152	R.AGETFVIPR.G
R4/RRR4-16/2	1628.930	1628.852	47.758	0.306	621.083	0.486	16	0.151	R.GELLVGIIGTLDTGNR.Y
R4/RRR4-19/2	989.738	990.138	-405.089	0.389	714.701	0.284	13	0.147	R.AGETFVIPR.G
R4/RRR4-13/2	989.858	990.138	-283.328	0.365	932.633	0.239	14	0.147	R.AGETFVIPR.G
R4/RRR4-14/2	990.014	990.138	-124.984	0.396	769.685	0.262	14	0.147	R.AGETFVIPR.G
R4/RRR4-25/2	989.863	990.138	-278.874	0.356	818.458	0.241	14	0.146	R.AGETFVIPR.G
R4/RRR4-16/2	989.632	990.138	-1526.400	0.372	778.914	0.236	14	0.145	R.AGETFVIPR.G
R4/RRR4-25/2	989.336	990.138	-1826.222	0.372	818.666	0.220	14	0.144	R.AGETFVIPR.G
R4/RRR4-25/2	989.829	990.138	-312.899	0.343	845.978	0.212	14	0.144	R.AGETFVIPR.G
R4/RRR4-13/2	990.091	990.138	-47.438	0.363	689.863	0.200	14	0.142	R.AGETFVIPR.G
R4/RRR4-18/2	989.693	990.138	-451.128	0.284	813.621	0.204	13	0.142	R.AGETFVIPR.G
R4/RRR4-13/2	990.046	990.138	-93.073	0.410	671.583	0.211	13	0.141	R.AGETFVIPR.G
R4/RRR4-24/2	989.765	990.138	-377.740	0.305	661.509	0.149	13	0.139	R.AGETFVIPR.G
R4/RRR4-5/2	990.307	990.138	171.283	0.182	765.336	0.059	14	0.135	R.AGETFVIPR.G
R4/RRR4-16/2	989.997	990.138	-142.424	0.344	969.371	0.022	14	0.129	R.AGETFVIPR.G
R4/RRR4-16/3	1413.810	1413.688	86.668	0.531	973.844	0.319	25	0.088	-.ALRVDTGVVELLK.-
R4/RRR4-16/3	1413.505	1413.688	-129.645	0.508	977.627	0.304	25	0.085	-.ALRVDTGVVELLK.-
R4/RRR4-16/3	1414.070	1413.688	271.207	0.487	1093.708	0.217	26	0.082	-.ALRVDTGVVELLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1258.723	1259.434	-1363.888	0.426	2005.642	0.550	20	0.307	R.VNLVQVLGSDSK.V
R4/RRR4-6/2	1259.104	1259.434	-263.388	0.531	1928.590	0.579	19	0.306	R.VNLVQVLGSDSK.V
R4/RRR4-6/2	1258.594	1259.434	-1466.561	0.479	1826.805	0.555	18	0.282	R.VNLVQVLGSDSK.V
R4/RRR4-6/2	1987.485	1987.110	189.332	0.606	1895.176	0.484	21	0.268	K.DCFNQIESLSFLENNR.V
R4/RRR4-6/3	1453.656	1453.667	-7.852	0.430	1825.811	0.409	28	0.211	K.APKPPAQAVDPFSK.F
R4/RRR4-6/2	1299.438	1299.626	-145.726	0.394	1096.815	0.490	19	0.186	R.VFVPLVLSLPSK.V
R4/RRR4-6/2	1127.968	1128.258	-257.646	0.409	972.480	0.529	17	0.184	R.ALSYLSSTSAK.Q
R4/RRR4-6/2	1206.519	1207.446	-1601.402	0.379	1160.800	0.454	18	0.183	K.FFLGIGLPGSAK.D
R4/RRR4-6/2	1400.196	1400.520	-231.863	0.433	1169.541	0.391	18	0.173	K.DTSVSLSANHLQK.L
R4/RRR4-6/2	1128.209	1128.258	-42.933	0.389	914.263	0.400	16	0.161	R.ALSYLSSTSAK.Q
R4/RRR4-6/2	1299.015	1299.626	-1244.108	0.290	800.713	0.368	16	0.149	R.VFVPLVLSLPSK.V
R4/RRR4-6/2	1299.254	1299.626	-287.100	0.309	704.847	0.365	16	0.147	R.VFVPLVLSLPSK.V
R4/RRR4-6/3	1453.901	1453.667	161.290	0.475	1383.895	0.387	25	0.142	K.APKPPAQAVDPFSK.F
R4/RRR4-6/3	1453.491	1453.667	-121.824	0.363	995.316	0.289	21	0.091	K.APKPPAQAVDPFSK.F
R4/RRR4-6/3	1986.483	1987.110	-821.298	0.407	996.466	0.267	23	0.084	-.DCFNQIESLSFLENNR.-
R4/RRR4-4/3	1454.088	1453.667	290.477	0.284	961.636	0.206	21	0.079	K.APKPPAQAVDPFSK.F
R4/RRR4-3/2	1548.133	1548.762	-1055.458	0.357	2244.736	0.467	21	0.320	R.EVVEIATNALDVFK.S
R4/RRR4-3/2	1157.952	1158.290	-292.529	0.472	1266.455	0.359	15	0.176	K.SQIVQNELAR.L
R4/RRR4-3/3	1142.594	1143.280	-1480.500	0.494	1303.347	0.334	20	0.117	R.HFDINNVKR.I
R4/RRR4-3/3	1143.224	1143.280	-49.235	0.498	1248.539	0.298	19	0.105	R.HFDINNVKR.I
R4/RRR4-3/3	1143.423	1143.280	125.366	0.531	1069.354	0.337	19	0.103	R.HFDINNVKR.I
R4/RRR4-3/3	1142.834	1143.280	-391.384	0.432	1373.372	0.251	21	0.102	R.HFDINNVKR.I
R4/RRR4-4/3	1143.029	1143.280	-220.522	0.446	748.979	0.252	17	0.086	R.HFDINNVKR.I
R4/RRR4-17/2	1698.739	1699.882	-1265.464	0.362	2306.095	0.488	23	0.337	K.AITEIFAEAGFSDVTK.N
R4/RRR4-17/2	1699.042	1699.882	-1086.380	0.394	1811.902	0.520	25	0.268	K.AITEIFAEAGFSDVTK.N
R4/RRR4-17/2	1190.264	1190.334	-58.902	0.570	1899.931	0.436	18	0.260	K.NFLAVLADNGR.L
R4/RRR4-17/2	1699.062	1699.882	-1074.405	0.310	1549.116	0.402	24	0.206	K.AITEIFAEAGFSDVTK.N
R4/RRR4-17/2	1196.216	1195.435	-183.786	0.469	654.324	0.544	14	0.172	K.KSPLFSQFIK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1196.536	1195.435	84.970	0.453	634.457	0.478	14	0.162	K.KSPLFSQFIK.D
R4/RRR4-17/2	1189.399	1190.334	-1631.350	0.376	919.133	0.392	17	0.162	K.NFLAVLADNGR.L
R4/RRR4-17/2	1066.609	1067.262	-1554.332	0.361	647.360	0.470	12	0.157	K.SPLFSQFIK.D
R4/RRR4-17/2	1185.969	1186.430	-390.298	0.398	391.093	0.414	14	0.155	R.AKQM*EM*FLR.Q
R4/RRR4-17/2	1491.287	1491.737	-303.229	0.464	719.140	0.386	19	0.155	R.FVDLTM*AHKGEVK.V
R4/RRR4-17/2	1491.165	1491.737	-1057.662	0.446	752.436	0.356	19	0.152	R.FVDLTM*AHKGEVK.V
R4/RRR4-17/2	1491.194	1491.737	-1038.018	0.425	760.980	0.355	19	0.152	R.FVDLTM*AHKGEVK.V
R4/RRR4-17/2	1185.871	1186.430	-1319.029	0.330	279.146	0.328	12	0.147	R.AKQM*EM*FLR.Q
R4/RRR4-17/2	1068.072	1067.262	-178.783	0.418	588.849	0.371	12	0.147	-.SPLFSQFIK.-
R4/RRR4-17/2	1186.121	1186.430	-261.321	0.376	314.567	0.278	11	0.144	R.AKQM*EM*FLR.Q
R4/RRR4-16/2	1700.942	1699.882	35.011	0.367	460.743	0.372	15	0.140	K.AITEIFAEAGFSDVTK.N
R4/RRR4-17/2	1190.146	1190.334	-158.491	0.230	590.548	0.296	14	0.137	-.NFLAVLADNGR.-
R4/RRR4-1/2	1632.393	1630.910	297.271	0.564	1960.177	0.441	22	0.267	R.LDQPIILTGFSALNK.L
R4/RRR4-1/2	1017.896	1018.148	-248.640	0.426	1296.826	0.439	15	0.193	R.GGAWVVVDSK.I
R4/RRR4-1/2	1858.140	1857.998	76.197	0.399	1277.689	0.466	20	0.192	R.TNVDYTVDLLNAAEYR.E
R4/RRR4-1/2	1631.779	1630.910	-80.331	0.478	1285.882	0.437	20	0.190	R.LDQPIILTGFSALNK.L
R4/RRR4-1/2	1631.203	1630.910	180.246	0.360	993.856	0.348	19	0.156	R.LDQPIILTGFSALNK.L
R4/RRR4-1/2	1656.570	1656.861	-176.320	0.417	816.396	0.427	17	0.155	R.FSGLNNTVYSELALK.A
R4/RRR4-1/2	1730.938	1730.065	-73.465	0.392	613.886	0.484	17	0.149	K.GIIFLGPPSAAMAALGDK.I
R4/RRR4-2/2	1631.117	1630.910	127.186	0.357	777.859	0.310	18	0.144	R.LDQPIILTGFSALNK.L
R4/RRR4-1/2	1631.295	1630.933	222.722	0.361	688.098	0.362	15	0.140	R.SPGINDIGIVAWIM*K.L
R4/RRR4-2/2	1631.906	1630.910	-1.996	0.333	478.132	0.290	15	0.137	R.LDQPIILTGFSALNK.L
R4/RRR4-1/2	1017.432	1018.148	-1692.098	0.234	684.060	0.261	13	0.136	R.GGAWVVVDSK.I
R4/RRR4-3/2	1858.111	1857.998	60.779	0.339	335.439	0.337	14	0.136	R.TNVDYTVDLLNAAEYR.E
R4/RRR4-1/3	1956.549	1957.175	-833.331	0.412	989.731	0.414	27	0.114	R.LSSSVIAHELKLESGETR.W
R4/RRR4-1/3	1957.085	1957.175	-45.839	0.394	819.363	0.407	25	0.102	R.LSSSVIAHELKLESGETR.W
R4/RRR4-1/3	1957.478	1957.175	155.512	0.400	1098.099	0.298	27	0.097	R.LSSSVIAHELKLESGETR.W
R4/RRR4-6/2	1663.395	1662.822	-257.594	0.520	1131.953	0.493	20	0.189	K.TDEFVIHSPTLTSSK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1662.203	1662.822	-977.134	0.500	1082.466	0.510	20	0.188	K.TDEFVIHSPTLTSSK.W
R4/RRR4-6/2	1892.880	1893.087	-109.677	0.449	1085.835	0.518	22	0.186	R.SLEDHSPLPGVTLGDIGGK.F
R4/RRR4-6/2	1129.042	1129.249	-183.985	0.476	769.346	0.582	18	0.185	R.QGALANEQLGK.L
R4/RRR4-6/2	1662.524	1662.822	-180.033	0.488	1024.502	0.450	19	0.173	K.TDEFVIHSPTLTSSK.W
R4/RRR4-6/2	1187.337	1188.313	-1668.934	0.399	1148.290	0.343	16	0.168	R.LTEEEANLLR.L
R4/RRR4-6/2	1865.523	1865.036	261.697	0.520	768.902	0.510	19	0.165	K.QFGPQTGGPETQVLNYK.T
R4/RRR4-6/2	1129.035	1129.249	-189.517	0.385	594.678	0.521	17	0.164	R.QGALANEQLGK.L
R4/RRR4-6/2	1187.573	1188.313	-1469.417	0.454	1065.607	0.332	16	0.162	R.LTEEEANLLR.L
R4/RRR4-6/3	1893.214	1893.087	66.985	0.484	1209.304	0.491	31	0.154	R.SLEDHSPLPGVTLGDIGGK.F
R4/RRR4-6/3	1992.855	1993.209	-178.275	0.455	1225.948	0.476	30	0.152	R.KQFGPQTGGPETQVLNYK.T
R4/RRR4-6/2	1187.550	1188.313	-1488.622	0.425	893.893	0.298	16	0.151	R.LTEEEANLLR.L
R4/RRR4-6/2	1892.529	1893.087	-825.996	0.434	536.434	0.489	17	0.150	R.SLEDHSPLPGVTLGDIGGK.F
R4/RRR4-5/2	1188.134	1188.313	-151.339	0.419	732.091	0.314	15	0.149	R.LTEEEANLLR.L
R4/RRR4-6/2	1368.790	1369.635	-1352.072	0.306	880.935	0.279	17	0.143	R.LFPLLASAYAFR.F
R4/RRR4-6/2	1893.264	1893.087	93.343	0.369	336.261	0.347	18	0.139	R.SLEDHSPLPGVTLGDIGGK.F
R4/RRR4-6/3	1894.017	1893.087	-37.023	0.486	995.511	0.406	26	0.112	R.SLEDHSPLPGVTLGDIGGK.F
R4/RRR4-6/3	1894.521	1893.087	229.378	0.324	902.283	0.264	25	0.083	R.SLEDHSPLPGVTLGDIGGK.F
R4/RRR4-3/2	1174.957	1175.274	-270.580	0.500	2452.719	0.524	21	0.382	R.LAGEEASGITAR.H
R4/RRR4-3/2	1174.531	1175.274	-1488.548	0.468	2251.063	0.493	21	0.333	R.LAGEEASGITAR.H
R4/RRR4-3/2	1175.040	1175.274	-199.602	0.461	2222.720	0.497	21	0.329	R.LAGEEASGITAR.H
R4/RRR4-3/2	1790.218	1790.864	-921.965	0.502	1403.173	0.553	24	0.227	K.SSAPVDESNAQDIVTEK.V
R4/RRR4-3/2	1606.894	1606.802	57.404	0.414	1854.915	0.235	21	0.203	K.IDDIYAVELIGGATR.V
R4/RRR4-3/2	1632.306	1632.750	-272.776	0.380	700.158	0.430	20	0.156	K.FVEYSVSGLTDASEK.Y
R4/RRR4-3/2	1632.153	1632.750	-980.946	0.363	629.481	0.461	19	0.155	K.FVEYSVSGLTDASEK.Y
R4/RRR4-3/2	1156.317	1156.274	36.783	0.328	875.049	0.373	17	0.153	K.SPALAALADGNR.L
R4/RRR4-3/2	1632.335	1632.750	-254.544	0.330	621.087	0.371	21	0.148	K.FVEYSVSGLTDASEK.Y
R4/RRR4-3/2	977.911	978.167	-262.062	0.439	911.809	0.186	13	0.139	R.LYLAELQK.I
R4/RRR4-3/2	977.933	978.167	-239.520	0.431	907.016	0.169	13	0.137	R.LYLAELQK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1389.704	1389.537	120.637	0.510	1086.611	0.393	23	0.116	K.KRVDEVVSEAEK.V
R4/RRR4-3/3	1388.853	1389.537	-1215.831	0.429	947.215	0.354	22	0.099	K.KRVDEVVSEAEK.V
R4/RRR4-4/2	1729.519	1729.912	-227.782	0.467	1694.070	0.431	20	0.228	R.ISEAFSGSSLISDFIR.S
R4/RRR4-4/2	1729.407	1729.912	-872.472	0.481	1649.013	0.420	20	0.220	R.ISEAFSGSSLISDFIR.S
R4/RRR4-4/2	1228.281	1228.336	-44.319	0.516	1562.632	0.425	17	0.218	K.LNIDETGFYR.V
R4/RRR4-4/2	1228.075	1228.336	-213.016	0.471	1545.002	0.357	17	0.201	K.LNIDETGFYR.V
R4/RRR4-4/2	1228.909	1228.336	-348.169	0.474	1303.842	0.415	16	0.191	K.LNIDETGFYR.V
R4/RRR4-4/2	1027.445	1027.243	197.505	0.425	1139.487	0.477	16	0.189	R.VLGGVIIEAR.E
R4/RRR4-4/2	1027.068	1027.243	-170.543	0.425	1277.560	0.393	17	0.185	R.VLGGVIIEAR.E
R4/RRR4-4/2	1429.150	1429.598	-314.379	0.388	1263.030	0.420	20	0.185	K.ISIDATPDLAGDIK.Q
R4/RRR4-4/2	1429.206	1429.598	-274.788	0.393	1039.966	0.406	19	0.167	K.ISIDATPDLAGDIK.Q
R4/RRR4-11/2	1228.772	1228.336	356.057	0.389	1096.120	0.358	14	0.165	K.LNIDETGFYR.V
R4/RRR4-4/2	1300.400	1299.414	-10.414	0.397	870.070	0.362	14	0.153	K.EAEISQFFATR.T
R4/RRR4-4/2	996.219	996.182	37.410	0.349	665.529	0.401	13	0.152	R.SIVTLFTSK.E
R4/RRR4-4/2	995.954	996.182	-230.084	0.350	596.775	0.410	13	0.152	R.SIVTLFTSK.E
R4/RRR4-4/2	1027.120	1027.243	-119.753	0.232	632.387	0.317	12	0.138	R.VLGGVIIEAR.E
R4/RRR4-4/2	1299.105	1299.414	-238.408	0.275	847.262	0.228	15	0.138	K.EAEISQFFATR.T
R4/RRR4-5/2	1597.681	1596.812	-82.122	0.479	788.078	0.566	19	0.177	R.VLGSVGEPINPTAWR.W
R4/RRR4-5/2	1242.547	1242.364	147.449	0.296	703.166	0.387	13	0.148	R.WFYDVIGDAR.C
R4/RRR4-5/2	1242.695	1242.364	266.746	0.314	435.631	0.413	13	0.148	R.WFYDVIGDAR.C
R4/RRR4-5/2	1242.908	1242.364	-367.692	0.129	456.571	0.328	14	0.132	R.WFYDVIGDAR.C
R4/RRR4-2/2	1648.107	1648.802	-1031.328	0.499	2786.231	0.491	24	0.441	K.YLAAEQGGGQTIVANR.V
R4/RRR4-2/2	1624.178	1623.746	266.737	0.553	2151.973	0.575	22	0.341	R.LAGESNTELLDFASR.F
R4/RRR4-2/2	1623.570	1623.746	-109.016	0.561	2123.177	0.571	22	0.334	R.LAGESNTELLDFASR.F
R4/RRR4-2/2	1623.293	1623.746	-279.797	0.550	2037.773	0.567	22	0.319	R.LAGESNTELLDFASR.F
R4/RRR4-2/2	1268.413	1268.403	7.760	0.453	1622.648	0.376	17	0.212	R.FAQAQLDVYGR.A
R4/RRR4-2/2	1267.456	1268.403	-1540.833	0.412	1461.556	0.407	18	0.203	R.FAQAQLDVYGR.A
R4/RRR4-2/2	1262.777	1263.340	-1241.317	0.435	1235.132	0.494	15	0.199	K.YYQDAYNAVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1263.028	1263.340	-247.835	0.413	1197.945	0.460	15	0.189	K.YYQDAYNAVR.K
R4/RRR4-2/2	1178.118	1178.323	-174.243	0.514	1149.722	0.418	18	0.181	K.FISSNGLNAVR.I
R4/RRR4-2/2	1107.902	1108.229	-296.682	0.392	980.229	0.330	14	0.157	R.INETTFNLR.V
R4/RRR4-8/2	1268.085	1268.403	-251.578	0.363	589.747	0.381	14	0.149	R.FAQAQLDVYGR.A
R4/RRR4-2/2	1178.096	1178.323	-193.472	0.458	553.738	0.366	14	0.147	K.FISSNGLNAVR.I
R4/RRR4-7/2	1268.012	1268.403	-309.044	0.301	686.881	0.340	15	0.146	R.FAQAQLDVYGR.A
R4/RRR4-2/2	1292.207	1292.378	-132.708	0.372	738.374	0.322	14	0.145	K.YYEDAYNVVR.K
R4/RRR4-2/2	1107.963	1108.229	-241.634	0.440	689.511	0.293	13	0.145	R.INETTFNLR.V
R4/RRR4-15/2	1564.992	1565.532	-987.290	0.533	2622.789	0.551	23	0.427	K.DAEGQDAEATTEEAK.K
R4/RRR4-15/2	1565.014	1565.532	-973.116	0.508	2527.063	0.546	23	0.404	K.DAEGQDAEATTEEAK.K
R4/RRR4-15/2	1560.225	1560.650	-273.215	0.513	1631.987	0.602	22	0.269	R.TLDAHIEEQFGSGR.L
R4/RRR4-15/2	1560.251	1560.650	-256.574	0.461	1231.286	0.547	20	0.208	R.TLDAHIEEQFGSGR.L
R4/RRR4-15/2	1560.292	1560.650	-230.201	0.476	1123.285	0.591	19	0.207	R.TLDAHIEEQFGSGR.L
R4/RRR4-14/3	1560.662	1560.650	7.867	0.439	1470.759	0.498	27	0.188	R.TLDAHIEEQFGSGR.L
R4/RRR4-15/3	1560.101	1560.650	-995.966	0.425	1399.175	0.454	30	0.161	R.TLDAHIEEQFGSGR.L
R4/RRR4-14/3	1559.981	1560.650	-1072.919	0.402	1210.244	0.489	28	0.150	R.TLDAHIEEQFGSGR.L
R4/RRR4-14/3	1560.093	1560.650	-1000.915	0.362	1281.766	0.428	27	0.140	R.TLDAHIEEQFGSGR.L
R4/RRR4-15/3	1559.713	1560.650	-1245.724	0.276	508.973	0.320	20	0.087	-.TLDAHIEEQFGSGR.-
R4/RRR4-3/2	1476.382	1476.703	-218.074	0.494	2285.083	0.512	20	0.344	R.VLQQASQIFQSVK.I
R4/RRR4-3/2	1476.236	1476.703	-316.792	0.520	2272.968	0.510	21	0.341	R.VLQQASQIFQSVK.I
R4/RRR4-3/3	1661.220	1661.754	-926.681	0.560	2183.781	0.499	28	0.333	K.YGASHLELENEKDR.N
R4/RRR4-3/2	1476.301	1476.703	-272.823	0.529	2113.488	0.524	20	0.318	R.VLQQASQIFQSVK.I
R4/RRR4-3/2	1564.716	1564.767	-32.521	0.474	2126.968	0.490	20	0.309	K.IATELSLWQEAFR.S
R4/RRR4-3/3	1661.589	1661.754	-99.677	0.599	1981.225	0.473	30	0.271	K.YGASHLELENEKDR.N
R4/RRR4-3/2	1565.507	1564.767	-166.398	0.510	1452.427	0.518	19	0.225	K.IATELSLWQEAFR.S
R4/RRR4-3/3	1969.293	1970.007	-873.200	0.437	1311.202	0.531	34	0.181	R.GGDGGSSAGGQRPAVAPEQDR.W
R4/RRR4-3/2	1566.084	1564.767	203.142	0.435	955.388	0.478	15	0.171	K.IATELSLWQEAFR.S
R4/RRR4-1/2	1476.018	1476.703	-1144.519	0.354	1144.359	0.357	18	0.167	R.VLQQASQIFQSVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1969.533	1970.007	-241.495	0.430	1237.934	0.508	32	0.164	R.GGDGGSSAGGQRPAVAPEQDR.W
R4/RRR4-2/2	1476.094	1476.703	-1093.117	0.370	1013.395	0.396	17	0.164	R.VLQQASQIFQSVK.I
R4/RRR4-3/2	1509.494	1509.732	-158.621	0.423	299.089	0.504	18	0.155	K.QAALQALHDLITSK.R
R4/RRR4-3/2	1330.033	1330.509	-358.980	0.448	753.191	0.346	18	0.154	K.EKIEAEELLQK.Q
R4/RRR4-3/2	1330.132	1330.509	-284.670	0.468	628.466	0.342	18	0.152	K.EKIEAEELLQK.Q
R4/RRR4-3/2	1330.254	1330.509	-192.420	0.450	643.955	0.336	17	0.150	K.EKIEAEELLQK.Q
R4/RRR4-2/2	1475.890	1476.703	-1231.891	0.342	885.807	0.335	15	0.149	R.VLQQASQIFQSVK.I
R4/RRR4-5/2	1566.090	1564.767	207.363	0.377	767.365	0.381	13	0.148	K.IATELSLWQEAFR.S
R4/RRR4-3/3	1266.692	1266.433	204.943	0.462	1048.571	0.490	24	0.136	K.VNHLSGAVHFGK.M
R4/RRR4-4/2	1566.324	1564.767	-283.485	0.234	648.848	0.205	16	0.135	K.IATELSLWQEAFR.S
R4/RRR4-3/3	1969.904	1970.007	-52.844	0.419	1043.704	0.474	31	0.134	R.GGDGGSSAGGQRPAVAPEQDR.W
R4/RRR4-3/3	1265.811	1266.433	-1285.603	0.414	888.603	0.433	21	0.110	K.VNHLSGAVHFGK.M
R4/RRR4-3/3	1970.461	1970.007	230.977	0.347	691.688	0.466	27	0.109	R.GGDGGSSAGGQRPAVAPEQDR.W
R4/RRR4-3/3	1970.308	1970.007	152.977	0.302	479.723	0.342	23	0.091	R.GGDGGSSAGGQRPAVAPEQDR.W
R4/RRR4-3/3	1970.167	1970.007	81.490	0.287	596.823	0.277	24	0.085	-.GGDGGSSAGGQRPAVAPEQDR.-
R4/RRR4-13/2	1564.404	1564.680	-176.924	0.481	2128.611	0.476	21	0.307	K.SADWSHFLTGSLDK.S
R4/RRR4-13/2	1261.000	1261.407	-323.870	0.423	1656.699	0.469	19	0.236	R.TIITAGEDATIR.I
R4/RRR4-12/2	1261.129	1261.407	-221.510	0.459	1390.196	0.540	19	0.224	R.TIITAGEDATIR.I
R4/RRR4-12/2	1683.439	1683.851	-245.945	0.484	1194.589	0.567	20	0.206	K.GHFGPINALAFNPDGR.S
R4/RRR4-13/2	1260.864	1261.407	-1227.761	0.351	1443.268	0.426	18	0.202	R.TIITAGEDATIR.I
R4/RRR4-12/2	1351.859	1351.481	280.799	0.444	1254.817	0.413	17	0.186	R.IWDTETGQCLK.E
R4/RRR4-13/2	1261.845	1261.279	-345.679	0.472	964.749	0.527	16	0.184	R.SFSSGGEDGYVR.L
R4/RRR4-12/2	1260.669	1261.407	-1382.469	0.356	1250.609	0.414	18	0.184	R.TIITAGEDATIR.I
R4/RRR4-13/2	1262.126	1261.279	-122.193	0.515	916.033	0.496	17	0.178	R.SFSSGGEDGYVR.L
R4/RRR4-13/2	1261.071	1261.279	-165.985	0.468	991.148	0.481	16	0.178	R.SFSSGGEDGYVR.L
R4/RRR4-12/2	1260.416	1261.407	-1584.409	0.342	1128.248	0.371	18	0.169	R.TIITAGEDATIR.I
R4/RRR4-12/2	1260.516	1261.279	-1403.035	0.375	900.666	0.426	17	0.164	R.SFSSGGEDGYVR.L
R4/RRR4-12/2	1085.587	1086.264	-1549.153	0.333	1159.036	0.328	16	0.164	K.ILQEEIGGVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1260.961	1261.279	-253.387	0.383	778.238	0.440	15	0.159	R.SFSSGGEDGYVR.L
R4/RRR4-12/2	1260.496	1261.279	-1419.279	0.357	795.350	0.387	16	0.155	R.SFSSGGEDGYVR.L
R4/RRR4-13/2	1086.121	1086.264	-131.961	0.362	1065.420	0.281	16	0.154	K.ILQEEIGGVK.G
R4/RRR4-12/2	1085.816	1086.264	-413.447	0.281	901.244	0.276	14	0.145	K.ILQEEIGGVK.G
R4/RRR4-13/2	1260.933	1261.407	-376.807	0.222	801.005	0.271	17	0.141	R.TIITAGEDATIR.I
R4/RRR4-15/2	1262.048	1261.407	-285.184	0.118	151.905	0.276	14	0.141	R.TIITAGEDATIR.I
R4/RRR4-12/2	1204.035	1204.404	-306.958	0.567	1817.959	0.434	18	0.249	R.VVSNFVAQALR.K
R4/RRR4-12/2	1204.144	1204.404	-215.825	0.582	1725.156	0.453	18	0.242	R.VVSNFVAQALR.K
R4/RRR4-12/2	1204.024	1204.404	-315.808	0.518	1795.163	0.407	18	0.239	R.VVSNFVAQALR.K
R4/RRR4-12/2	1447.565	1447.726	-111.860	0.486	1494.151	0.443	21	0.213	K.TNVVGTLNM*LGLAK.R
R4/RRR4-12/2	1228.271	1228.337	-53.690	0.449	1419.995	0.456	18	0.210	K.VVQDTIDPNAR.I
R4/RRR4-10/2	1204.299	1204.404	-87.088	0.458	1660.496	0.325	18	0.205	R.VVSNFVAQALR.K
R4/RRR4-12/2	1432.308	1431.727	-293.255	0.386	893.106	0.504	17	0.170	K.TNVVGTLNMLGLAK.R
R4/RRR4-12/2	1227.288	1228.337	-1674.563	0.333	1137.637	0.375	18	0.169	K.VVQDTIDPNAR.I
R4/RRR4-12/2	1206.880	1207.358	-397.538	0.455	637.602	0.483	16	0.163	R.KEPLTVYGDGK.Q
R4/RRR4-12/2	1333.085	1332.577	-369.546	0.349	939.635	0.327	16	0.152	R.VVSNFVAQALRK.E
R4/RRR4-12/2	1332.692	1332.577	87.130	0.366	757.288	0.357	14	0.147	R.VVSNFVAQALRK.E
R4/RRR4-12/2	1333.251	1332.577	-244.607	0.283	558.667	0.155	13	0.125	-.VVSNFVAQALRK.-
R4/RRR4-14/2	1145.905	1146.276	-324.453	0.464	1451.782	0.407	20	0.203	R.LSGVTADGQGIK.V
R4/RRR4-14/2	1108.002	1108.293	-263.352	0.436	1339.251	0.429	16	0.197	K.M*EGLLWGASK.L
R4/RRR4-14/2	1145.858	1146.276	-365.924	0.464	1233.762	0.419	19	0.186	R.LSGVTADGQGIK.V
R4/RRR4-14/2	1151.159	1151.338	-155.137	0.540	1077.327	0.444	15	0.182	K.KLDEYLLTR.S
R4/RRR4-14/2	1107.980	1108.293	-283.580	0.430	1131.038	0.418	15	0.178	K.M*EGLLWGASK.L
R4/RRR4-14/2	1151.098	1151.338	-208.647	0.497	1095.551	0.404	15	0.176	K.KLDEYLLTR.S
R4/RRR4-13/2	1151.093	1151.338	-213.115	0.522	1067.057	0.411	15	0.176	K.KLDEYLLTR.S
R4/RRR4-14/2	1272.729	1272.480	196.286	0.456	830.370	0.486	16	0.174	R.WFTHIDALLR.L
R4/RRR4-13/2	1150.528	1151.338	-1577.068	0.476	1065.573	0.378	15	0.170	K.KLDEYLLTR.S
R4/RRR4-14/2	1272.336	1272.480	-112.936	0.449	833.674	0.458	16	0.170	R.WFTHIDALLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1151.241	1151.338	-84.189	0.482	1055.230	0.355	15	0.166	K.KLDEYLLTR.S
R4/RRR4-13/2	1745.289	1745.866	-906.203	0.467	554.686	0.551	22	0.166	K.VESTAVPSASTPDVADAK.A
R4/RRR4-13/2	1109.169	1108.293	-111.736	0.426	1073.826	0.359	14	0.164	K.M*EGLLWGASK.L
R4/RRR4-14/2	1746.259	1745.866	225.513	0.493	441.574	0.559	20	0.163	K.VESTAVPSASTPDVADAK.A
R4/RRR4-14/2	1145.404	1146.276	-1639.388	0.321	1239.573	0.282	19	0.162	R.LSGVTADGQGIK.V
R4/RRR4-14/2	1745.386	1745.866	-275.867	0.442	528.536	0.536	21	0.162	K.VESTAVPSASTPDVADAK.A
R4/RRR4-14/2	1745.288	1745.866	-906.976	0.403	490.984	0.557	21	0.162	K.VESTAVPSASTPDVADAK.A
R4/RRR4-14/2	1272.498	1272.480	14.663	0.384	712.066	0.444	15	0.160	R.WFTHIDALLR.L
R4/RRR4-13/2	1745.133	1745.866	-996.228	0.408	475.811	0.512	21	0.158	K.VESTAVPSASTPDVADAK.A
R4/RRR4-14/2	1107.469	1108.293	-1651.610	0.299	890.748	0.393	14	0.157	K.M*EGLLWGASK.L
R4/RRR4-13/2	1109.240	1108.293	-47.709	0.356	970.972	0.342	14	0.157	K.M*EGLLWGASK.L
R4/RRR4-14/2	1449.316	1449.701	-266.041	0.454	641.498	0.441	18	0.157	R.NVKM*EGLLWGASK.L
R4/RRR4-13/2	1745.303	1745.866	-898.480	0.408	450.103	0.518	20	0.157	K.VESTAVPSASTPDVADAK.A
R4/RRR4-14/2	1272.020	1272.480	-362.646	0.395	653.154	0.443	14	0.156	-.WFTHIDALLR.-
R4/RRR4-13/2	1151.068	1151.338	-234.499	0.443	936.260	0.317	14	0.155	K.KLDEYLLTR.S
R4/RRR4-13/2	1108.797	1108.293	-448.894	0.364	941.637	0.273	14	0.148	K.M*EGLLWGASK.L
R4/RRR4-14/2	1151.738	1151.338	349.150	0.348	675.932	0.228	13	0.141	K.KLDEYLLTR.S
R4/RRR4-14/3	1272.184	1272.480	-233.358	0.357	1204.028	0.406	21	0.125	R.WFTHIDALLR.L
R4/RRR4-14/3	1272.185	1272.480	-232.059	0.335	816.583	0.386	18	0.098	-.WFTHIDALLR.-
R4/RRR4-14/3	1272.438	1272.480	-32.689	0.325	753.691	0.357	18	0.094	R.WFTHIDALLR.L
R4/RRR4-14/3	1272.129	1272.480	-276.101	0.312	727.387	0.362	17	0.094	R.WFTHIDALLR.L
R4/RRR4-14/3	1272.344	1272.480	-107.172	0.286	664.295	0.368	17	0.093	R.WFTHIDALLR.L
R4/RRR4-14/3	1272.576	1272.480	75.697	0.320	746.333	0.341	18	0.092	R.WFTHIDALLR.L
R4/RRR4-16/2	1558.224	1557.814	264.119	0.568	1719.229	0.578	24	0.277	K.KLPSILVDETSVQK.I
R4/RRR4-16/2	1557.341	1557.814	-304.461	0.562	1532.388	0.519	23	0.237	K.KLPSILVDETSVQK.I
R4/RRR4-16/2	1557.480	1557.814	-215.052	0.517	1316.789	0.581	21	0.226	K.KLPSILVDETSVQK.I
R4/RRR4-16/2	1977.628	1977.164	234.914	0.615	1342.125	0.544	24	0.217	K.EGYEGQISANNIEIGIIR.S
R4/RRR4-16/2	1976.460	1977.164	-864.699	0.542	1208.183	0.563	23	0.208	K.EGYEGQISANNIEIGIIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1073.028	1073.225	-184.233	0.478	972.948	0.585	16	0.196	K.AANGVVIATEK.K
R4/RRR4-16/2	1072.505	1073.225	-1608.347	0.393	900.772	0.562	17	0.184	K.AANGVVIATEK.K
R4/RRR4-16/2	1073.843	1073.225	-356.601	0.317	1137.108	0.413	16	0.173	K.AANGVVIATEK.K
R4/RRR4-16/2	1072.459	1073.225	-1651.913	0.370	795.055	0.540	16	0.173	K.AANGVVIATEK.K
R4/RRR4-16/2	1073.779	1073.225	-416.485	0.318	987.268	0.437	16	0.168	K.AANGVVIATEK.K
R4/RRR4-16/2	1976.466	1977.164	-861.785	0.511	798.760	0.485	18	0.160	K.EGYEGQISANNIEIGIIR.S
R4/RRR4-16/2	1157.135	1156.357	-192.745	0.299	561.801	0.451	15	0.152	K.ETIPVTQLVR.E
R4/RRR4-16/2	1156.131	1156.357	-196.513	0.333	527.858	0.419	15	0.152	K.ETIPVTQLVR.E
R4/RRR4-16/2	1155.599	1156.357	-1526.073	0.319	454.451	0.458	14	0.152	K.ETIPVTQLVR.E
R4/RRR4-16/2	1719.253	1718.926	190.884	0.552	902.843	0.505	20	0.106	K.VLSPAEIKDFLEEVE.-
R4/RRR4-16/2	1718.304	1718.926	-946.585	0.471	710.302	0.471	18	0.095	K.VLSPAEIKDFLEEVE.-
R4/RRR4-16/3	1561.249	1560.863	248.463	0.454	982.165	0.287	26	0.091	R.LYKETIPVTQLVR.E
R4/RRR4-16/3	1560.660	1560.863	-129.894	0.445	983.459	0.271	26	0.088	R.LYKETIPVTQLVR.E
R4/RRR4-16/2	1718.334	1718.926	-929.255	0.430	622.520	0.418	16	0.087	K.VLSPAEIKDFLEEVE.-
R4/RRR4-16/3	1560.737	1560.863	-80.466	0.424	852.179	0.217	26	0.081	R.LYKETIPVTQLVR.E
R4/RRR4-3/2	1711.605	1710.897	-171.008	0.567	2086.069	0.518	20	0.310	R.IAICVFDDIAEQCR.E
R4/RRR4-3/2	1710.723	1710.897	-101.888	0.521	2046.839	0.482	20	0.293	R.IAICVFDDIAEQCR.E
R4/RRR4-3/2	1487.151	1486.653	336.184	0.400	1514.675	0.405	21	0.205	R.LASSLSSPATPADLR.A
R4/RRR4-3/2	1487.129	1486.653	321.369	0.446	1338.911	0.417	22	0.192	R.LASSLSSPATPADLR.A
R4/RRR4-3/2	1158.511	1158.397	99.274	0.428	1381.081	0.381	17	0.190	R.AAVAAM*PELLR.S
R4/RRR4-3/2	1487.304	1486.653	-235.324	0.425	1321.760	0.404	22	0.188	R.LASSLSSPATPADLR.A
R4/RRR4-3/2	1687.744	1687.920	-104.146	0.503	1132.663	0.513	18	0.188	R.AVSDEIKNVIIASATR.K
R4/RRR4-3/2	998.272	998.245	27.889	0.515	925.366	0.479	14	0.178	K.LLVLLQNGK.Q
R4/RRR4-3/2	1237.027	1236.402	-304.611	0.500	968.586	0.460	16	0.175	K.LNNVITHPEAK.H
R4/RRR4-3/2	998.199	998.245	-45.703	0.494	941.665	0.404	14	0.167	K.LLVLLQNGK.Q
R4/RRR4-3/2	1158.020	1158.397	-326.350	0.360	1142.356	0.290	16	0.157	R.AAVAAM*PELLR.S
R4/RRR4-3/2	1235.724	1236.402	-1362.124	0.408	817.603	0.388	15	0.156	K.LNNVITHPEAK.H
R4/RRR4-3/2	1236.323	1236.402	-64.333	0.472	747.631	0.381	15	0.154	K.LNNVITHPEAK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	997.581	998.245	-1672.194	0.296	758.469	0.407	12	0.152	K.LLVLLQNGK.Q
R4/RRR4-3/2	1641.219	1641.806	-969.933	0.349	680.741	0.379	17	0.144	R.SDADILGPHSQYLPK.I
R4/RRR4-1/2	1710.742	1710.897	-90.650	0.368	678.109	0.261	14	0.134	R.IAICVFDDIAEQCR.E
R4/RRR4-18/2	1059.212	1058.254	-39.256	0.481	1217.750	0.440	18	0.190	K.VIILGDSGVGK.T
R4/RRR4-18/2	1037.028	1037.191	-157.452	0.441	939.605	0.504	16	0.181	K.ATIGADFLTK.E
R4/RRR4-18/2	1057.443	1058.254	-1716.937	0.350	1124.712	0.452	18	0.181	K.VIILGDSGVGK.T
R4/RRR4-18/2	1036.393	1037.191	-1740.351	0.349	954.565	0.512	16	0.178	K.ATIGADFLTK.E
R4/RRR4-19/2	1036.543	1037.191	-1594.811	0.322	1108.168	0.417	17	0.174	K.ATIGADFLTK.E
R4/RRR4-19/2	1188.805	1188.359	375.546	0.393	1024.612	0.396	17	0.170	R.FQSLGVAFYR.G
R4/RRR4-19/2	1037.225	1037.191	32.390	0.402	688.599	0.505	14	0.166	K.ATIGADFLTK.E
R4/RRR4-18/2	1036.809	1037.191	-370.047	0.319	855.298	0.471	15	0.166	K.ATIGADFLTK.E
R4/RRR4-18/2	1187.529	1188.359	-1545.766	0.394	905.968	0.415	15	0.165	R.FQSLGVAFYR.G
R4/RRR4-19/2	1227.815	1227.348	381.664	0.385	400.216	0.542	16	0.163	K.GNIPYFETSAK.D
R4/RRR4-18/2	1187.750	1188.359	-1359.415	0.425	935.083	0.370	16	0.162	R.FQSLGVAFYR.G
R4/RRR4-18/2	1227.069	1227.348	-227.958	0.427	376.157	0.515	15	0.162	K.GNIPYFETSAK.D
R4/RRR4-18/2	1226.816	1227.348	-1252.254	0.431	413.423	0.489	16	0.161	K.GNIPYFETSAK.D
R4/RRR4-19/2	1037.650	1037.191	443.232	0.342	756.690	0.459	14	0.161	K.ATIGADFLTK.E
R4/RRR4-18/2	1615.138	1613.746	243.366	0.484	780.716	0.467	16	0.160	K.EGFNVEAAFECIAR.N
R4/RRR4-19/2	1188.057	1188.359	-255.436	0.384	909.240	0.357	16	0.159	R.FQSLGVAFYR.G
R4/RRR4-19/2	1187.976	1188.359	-323.990	0.456	709.589	0.406	14	0.157	R.FQSLGVAFYR.G
R4/RRR4-18/2	1187.241	1188.359	-1789.624	0.349	829.321	0.364	15	0.155	R.FQSLGVAFYR.G
R4/RRR4-18/2	1678.548	1678.870	-192.028	0.347	682.394	0.377	17	0.149	R.LFTLQIWDTAGQER.F
R4/RRR4-19/2	1226.506	1227.348	-1506.228	0.309	471.258	0.345	17	0.148	K.GNIPYFETSAK.D
R4/RRR4-19/2	1679.959	1678.870	53.158	0.431	463.552	0.391	16	0.148	R.LFTLQIWDTAGQER.F
R4/RRR4-19/2	1227.086	1227.348	-213.986	0.234	409.188	0.395	16	0.145	K.GNIPYFETSAK.D
R4/RRR4-18/2	1678.966	1678.870	57.711	0.382	468.404	0.353	15	0.143	R.LFTLQIWDTAGQER.F
R4/RRR4-18/2	1677.875	1678.870	-1192.394	0.416	477.099	0.341	15	0.142	R.LFTLQIWDTAGQER.F
R4/RRR4-18/2	1226.815	1227.348	-1253.254	0.240	421.592	0.251	16	0.142	K.GNIPYFETSAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1057.914	1058.254	-321.579	0.306	499.253	0.292	12	0.139	K.VIILGDSGVGK.T
R4/RRR4-19/2	1678.122	1678.870	-1044.911	0.295	741.470	0.212	16	0.135	R.LFTLQIWDTAGQER.F
R4/RRR4-18/2	1058.015	1058.254	-226.077	0.202	588.565	0.211	13	0.134	K.VIILGDSGVGK.T
R4/RRR4-19/2	1677.911	1678.870	-1170.696	0.359	838.580	0.172	17	0.133	R.LFTLQIWDTAGQER.F
R4/RRR4-14/3	1928.922	1929.100	-92.538	0.567	2765.251	0.560	32	0.553	K.YAHKDEEYDSM*LGVVR.E
R4/RRR4-14/2	1354.207	1354.536	-243.173	0.530	1930.728	0.575	22	0.305	R.IPSGEVWVGNPAK.F
R4/RRR4-15/2	1354.157	1354.536	-280.795	0.513	1910.702	0.566	21	0.299	R.IPSGEVWVGNPAK.F
R4/RRR4-15/2	1354.295	1354.536	-178.065	0.487	1748.684	0.501	21	0.257	R.IPSGEVWVGNPAK.F
R4/RRR4-15/2	1354.328	1354.536	-153.742	0.504	1685.271	0.524	20	0.255	R.IPSGEVWVGNPAK.F
R4/RRR4-14/2	1353.791	1354.536	-1292.530	0.497	1596.791	0.560	20	0.252	R.IPSGEVWVGNPAK.F
R4/RRR4-14/2	1354.250	1354.536	-211.341	0.510	1514.586	0.509	20	0.230	R.IPSGEVWVGNPAK.F
R4/RRR4-15/2	1002.097	1002.150	-53.284	0.512	891.799	0.439	17	0.172	R.LGSTIQGGLR.V
R4/RRR4-14/2	1002.020	1002.150	-130.145	0.477	843.388	0.387	17	0.162	R.LGSTIQGGLR.V
R4/RRR4-15/2	1816.172	1816.131	22.678	0.470	330.396	0.510	20	0.160	R.EIPPELILPDNILPNK.A
R4/RRR4-15/2	1002.019	1002.150	-131.123	0.513	647.088	0.420	15	0.159	R.LGSTIQGGLR.V
R4/RRR4-14/2	1125.162	1124.223	-54.366	0.485	492.582	0.424	13	0.157	K.TFDEIELEK.M
R4/RRR4-14/2	1123.950	1124.223	-242.990	0.486	552.153	0.401	14	0.157	K.TFDEIELEK.M
R4/RRR4-14/2	1001.491	1002.150	-1662.061	0.442	609.308	0.411	15	0.157	R.LGSTIQGGLR.V
R4/RRR4-15/2	1123.926	1124.223	-265.000	0.381	553.645	0.404	14	0.155	K.TFDEIELEK.M
R4/RRR4-14/2	1816.628	1816.131	274.268	0.430	207.090	0.502	16	0.154	R.EIPPELILPDNILPNK.A
R4/RRR4-14/2	1123.934	1124.223	-257.699	0.417	587.612	0.345	14	0.151	K.TFDEIELEK.M
R4/RRR4-15/2	1815.223	1816.131	-1054.012	0.379	319.626	0.490	16	0.151	R.EIPPELILPDNILPNK.A
R4/RRR4-14/2	1816.396	1816.131	146.433	0.344	387.859	0.447	19	0.151	R.EIPPELILPDNILPNK.A
R4/RRR4-15/2	1815.561	1816.131	-867.217	0.360	345.231	0.472	17	0.151	R.EIPPELILPDNILPNK.A
R4/RRR4-15/2	1123.895	1124.223	-292.569	0.348	549.111	0.359	14	0.151	K.TFDEIELEK.M
R4/RRR4-15/2	1815.521	1816.131	-889.154	0.348	252.780	0.436	17	0.149	R.EIPPELILPDNILPNK.A
R4/RRR4-14/2	1815.679	1816.131	-249.813	0.290	420.278	0.401	19	0.146	R.EIPPELILPDNILPNK.A
R4/RRR4-14/2	1814.928	1816.131	-1217.236	0.245	318.019	0.419	19	0.145	R.EIPPELILPDNILPNK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1123.366	1124.223	-1657.271	0.311	463.316	0.311	13	0.144	-.TFDEIELEK.-
R4/RRR4-14/3	1102.495	1102.290	186.269	0.325	1725.575	0.219	24	0.128	K.HSM*VGAGSLVK.Q
R4/RRR4-14/3	1102.420	1102.290	118.562	0.402	1233.419	0.242	22	0.093	K.HSM*VGAGSLVK.Q
R4/RRR4-15/3	1101.876	1102.290	-376.736	0.364	1129.943	0.229	22	0.086	K.HSM*VGAGSLVK.Q
R4/RRR4-11/2	1577.435	1577.807	-236.393	0.564	2926.987	0.603	25	0.520	R.IAVLGASGYTGAEIVR.L
R4/RRR4-11/2	1577.060	1577.807	-1110.940	0.480	2778.507	0.537	25	0.457	R.IAVLGASGYTGAEIVR.L
R4/RRR4-11/2	1993.573	1993.205	184.885	0.603	1449.789	0.614	21	0.243	K.EANLYTEIAEGIHAYGIK.G
R4/RRR4-11/2	1298.170	1298.597	-329.687	0.327	1291.073	0.514	16	0.200	R.AIIISVIDNLVK.G
R4/RRR4-11/2	973.119	973.149	-30.399	0.503	1294.615	0.445	15	0.198	K.VSNIIIDAK.S
R4/RRR4-11/2	972.661	973.149	-503.211	0.438	1213.538	0.424	15	0.186	K.VSNIIIDAK.S
R4/RRR4-11/2	1992.996	1993.205	-105.396	0.538	759.071	0.627	19	0.182	K.EANLYTEIAEGIHAYGIK.G
R4/RRR4-11/2	973.013	973.149	-139.373	0.453	975.922	0.471	14	0.178	K.VSNIIIDAK.S
R4/RRR4-11/2	1298.124	1298.597	-365.163	0.364	981.389	0.483	15	0.173	R.AIIISVIDNLVK.G
R4/RRR4-11/2	1035.982	1036.163	-175.221	0.446	1029.434	0.409	15	0.172	K.IVDLSADFR.L
R4/RRR4-11/2	1297.495	1298.597	-1625.097	0.264	893.995	0.314	15	0.145	R.AIIISVIDNLVK.G
R4/RRR4-11/2	1189.100	1189.253	-129.388	0.281	769.716	0.284	14	0.140	K.STYEGEEFVK.L
R4/RRR4-12/2	1308.070	1308.457	-296.866	0.432	2449.059	0.396	20	0.335	K.VSCADITTLATR.D
R4/RRR4-13/2	1308.099	1308.457	-274.302	0.456	2199.507	0.451	19	0.309	K.VSCADITTLATR.D
R4/RRR4-17/2	1308.208	1308.457	-190.889	0.449	2159.178	0.396	19	0.286	K.VSCADITTLATR.D
R4/RRR4-11/2	1308.098	1308.457	-275.706	0.422	2138.875	0.391	20	0.282	K.VSCADITTLATR.D
R4/RRR4-13/2	1307.919	1308.457	-1179.283	0.431	1975.697	0.427	20	0.268	K.VSCADITTLATR.D
R4/RRR4-12/2	1308.115	1308.457	-262.411	0.461	1978.088	0.427	19	0.268	K.VSCADITTLATR.D
R4/RRR4-12/2	1308.126	1308.457	-253.798	0.444	2068.592	0.375	19	0.266	K.VSCADITTLATR.D
R4/RRR4-12/2	1735.317	1734.933	221.855	0.534	1567.520	0.590	25	0.255	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-17/2	1307.671	1308.457	-1370.090	0.385	1942.169	0.342	19	0.241	K.VSCADITTLATR.D
R4/RRR4-12/2	1735.434	1734.933	-288.596	0.575	1429.220	0.597	24	0.240	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-11/2	1307.993	1308.457	-355.668	0.380	1939.432	0.325	19	0.236	K.VSCADITTLATR.D
R4/RRR4-14/2	1308.470	1308.457	9.581	0.384	1896.265	0.342	19	0.235	K.VSCADITTLATR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1308.196	1308.457	-200.531	0.381	1795.787	0.378	18	0.231	K.VSCADITTLATR.D
R4/RRR4-13/2	1735.340	1734.933	235.116	0.551	1395.862	0.570	24	0.229	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-11/2	1735.343	1734.933	236.809	0.531	1283.232	0.577	23	0.219	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-14/2	985.044	985.163	-120.580	0.508	1427.849	0.460	17	0.212	R.DIGIAAGLVR.I
R4/RRR4-14/2	1735.465	1734.933	-270.460	0.543	1139.466	0.609	22	0.212	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-12/2	1734.398	1734.933	-887.751	0.517	1279.630	0.545	23	0.212	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-17/2	984.287	985.163	-1911.283	0.486	1446.753	0.435	17	0.208	R.DIGIAAGLVR.I
R4/RRR4-14/2	1734.361	1734.933	-909.090	0.494	1241.753	0.529	23	0.205	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-11/3	1734.830	1734.933	-59.687	0.426	1389.376	0.558	28	0.203	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-14/2	984.430	985.163	-1765.738	0.480	1308.967	0.469	16	0.202	R.DIGIAAGLVR.I
R4/RRR4-11/2	984.598	985.163	-1594.080	0.459	1415.370	0.420	17	0.202	R.DIGIAAGLVR.I
R4/RRR4-17/2	1734.285	1734.933	-953.395	0.433	1150.052	0.556	22	0.201	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-12/2	984.518	985.163	-1675.417	0.492	1279.492	0.465	16	0.199	R.DIGIAAGLVR.I
R4/RRR4-12/2	985.073	985.163	-91.741	0.494	1370.951	0.420	17	0.199	R.DIGIAAGLVR.I
R4/RRR4-13/2	985.015	985.163	-150.789	0.493	1361.792	0.423	17	0.198	R.DIGIAAGLVR.I
R4/RRR4-13/2	1734.402	1734.933	-885.490	0.481	1284.786	0.478	23	0.198	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-14/2	984.422	985.163	-1773.089	0.491	1262.309	0.465	16	0.198	R.DIGIAAGLVR.I
R4/RRR4-13/2	984.343	985.163	-1854.206	0.446	1249.303	0.459	16	0.195	R.DIGIAAGLVR.I
R4/RRR4-11/2	985.032	985.163	-133.384	0.506	1385.101	0.388	17	0.193	R.DIGIAAGLVR.I
R4/RRR4-12/2	984.528	985.163	-1664.953	0.410	1271.038	0.436	16	0.192	R.DIGIAAGLVR.I
R4/RRR4-17/2	1734.294	1734.933	-948.095	0.487	1033.675	0.550	21	0.191	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-11/2	1734.317	1734.933	-934.951	0.459	1090.181	0.522	22	0.190	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-17/2	985.219	985.163	57.525	0.524	1284.152	0.389	16	0.184	R.DIGIAAGLVR.I
R4/RRR4-11/2	985.021	985.163	-144.573	0.525	1184.379	0.422	16	0.184	R.DIGIAAGLVR.I
R4/RRR4-11/2	1733.752	1734.933	-1261.871	0.314	1096.301	0.490	23	0.182	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-1/2	1572.278	1571.714	-278.129	0.541	919.066	0.499	22	0.181	K.DVPVNSVTQELDVR.T
R4/RRR4-12/2	1571.907	1571.714	123.097	0.500	796.297	0.523	22	0.178	K.DVPVNSVTQELDVR.T
R4/RRR4-13/2	1734.417	1734.933	-876.658	0.459	1066.380	0.463	21	0.178	R.DAIVASGGPYFDVPLGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	986.017	985.163	-148.276	0.524	1144.119	0.394	16	0.176	R.DIGIAAGLVR.I
R4/RRR4-11/2	1571.808	1571.714	60.010	0.505	776.704	0.500	22	0.174	K.DVPVNSVTQELDVR.T
R4/RRR4-14/2	1572.037	1571.714	205.878	0.474	758.106	0.495	22	0.172	K.DVPVNSVTQELDVR.T
R4/RRR4-12/2	1571.193	1571.714	-971.393	0.457	827.827	0.473	22	0.172	K.DVPVNSVTQELDVR.T
R4/RRR4-14/2	1734.086	1734.933	-1068.521	0.380	1160.494	0.382	22	0.171	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-12/2	1571.204	1571.714	-963.983	0.413	812.536	0.458	22	0.168	K.DVPVNSVTQELDVR.T
R4/RRR4-14/2	1572.294	1571.714	-268.392	0.480	672.034	0.486	21	0.167	K.DVPVNSVTQELDVR.T
R4/RRR4-11/2	1571.192	1571.714	-971.549	0.427	793.787	0.447	22	0.166	K.DVPVNSVTQELDVR.T
R4/RRR4-14/2	1571.172	1571.714	-984.888	0.385	758.928	0.424	22	0.161	K.DVPVNSVTQELDVR.T
R4/RRR4-1/2	1734.342	1734.933	-920.183	0.398	901.538	0.387	20	0.157	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-11/2	1307.307	1308.457	-1649.893	0.302	1192.528	0.262	17	0.157	K.VSCADITTLATR.D
R4/RRR4-12/2	1572.133	1571.714	267.234	0.395	256.118	0.465	18	0.157	K.DVPVNSVTQELDVR.T
R4/RRR4-12/2	1137.593	1138.307	-1510.835	0.349	968.412	0.286	13	0.150	R.WHVAEALRR.D
R4/RRR4-12/2	1138.064	1138.307	-214.371	0.354	722.422	0.346	13	0.149	R.WHVAEALRR.D
R4/RRR4-12/2	1137.946	1138.307	-318.330	0.365	476.818	0.386	11	0.147	R.WHVAEALRR.D
R4/RRR4-9/2	1734.245	1734.933	-976.149	0.338	707.139	0.374	17	0.147	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-13/2	1307.430	1308.457	-1554.873	0.279	974.641	0.257	16	0.147	K.VSCADITTLATR.D
R4/RRR4-2/2	1571.165	1571.714	-988.944	0.383	735.859	0.285	21	0.147	K.DVPVNSVTQELDVR.T
R4/RRR4-3/2	985.421	985.163	263.392	0.304	437.413	0.257	15	0.146	R.DIGIAAGLVR.I
R4/RRR4-9/2	1734.502	1734.933	-249.434	0.307	579.932	0.392	17	0.146	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-2/2	1734.110	1734.933	-1054.809	0.357	664.800	0.355	17	0.145	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-17/2	1733.473	1734.933	-1423.394	0.273	854.548	0.278	19	0.144	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-9/2	1733.671	1734.933	-1308.752	0.251	527.950	0.380	17	0.143	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-3/2	985.332	985.163	172.831	0.176	355.502	0.274	15	0.143	R.DIGIAAGLVR.I
R4/RRR4-12/2	1562.094	1562.856	-1130.870	0.304	722.504	0.301	16	0.139	R.FDGSKPIM*DPVLVK.K
R4/RRR4-13/2	1733.698	1734.933	-1293.125	0.256	637.882	0.242	18	0.138	R.DAIVASGGPYFDVPLGR.R
R4/RRR4-12/2	1562.491	1562.856	-233.990	0.193	665.450	0.131	15	0.127	R.FDGSKPIM*DPVLVK.K
R4/RRR4-12/2	1645.398	1645.838	-268.001	0.580	3173.561	0.528	25	0.551	K.IKDEEGNPAFALVNK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1645.427	1645.838	-250.808	0.615	2464.314	0.541	23	0.388	K.IKDEEGNPAFALVNK.A
R4/RRR4-12/2	1645.222	1645.838	-985.210	0.600	2313.171	0.537	23	0.358	K.IKDEEGNPAFALVNK.A
R4/RRR4-12/2	1722.505	1722.922	-243.352	0.572	1928.122	0.498	23	0.281	K.IRDEEGYPAFALVNK.V
R4/RRR4-12/2	1845.411	1845.993	-859.758	0.556	1397.576	0.654	28	0.254	K.ILPWGDEAYAGGSANAPR.G
R4/RRR4-12/2	1723.444	1722.922	-278.527	0.591	1686.918	0.512	22	0.251	K.IRDEEGYPAFALVNK.V
R4/RRR4-12/2	1845.395	1845.993	-868.258	0.557	1313.996	0.663	27	0.246	K.ILPWGDEAYAGGSANAPR.G
R4/RRR4-12/2	1723.365	1722.922	257.637	0.594	1698.790	0.466	22	0.239	K.IRDEEGYPAFALVNK.V
R4/RRR4-12/2	1845.250	1845.993	-947.352	0.532	1189.933	0.651	26	0.228	K.ILPWGDEAYAGGSANAPR.G
R4/RRR4-12/2	1080.883	1081.161	-258.335	0.470	1420.342	0.467	17	0.213	K.ADEGFSVTVR.G
R4/RRR4-12/2	1080.531	1081.161	-1512.776	0.443	1578.877	0.393	17	0.212	K.ADEGFSVTVR.G
R4/RRR4-12/2	1080.431	1081.161	-1605.614	0.398	1466.754	0.392	16	0.200	K.ADEGFSVTVR.G
R4/RRR4-12/2	1163.310	1164.252	-1674.251	0.383	1054.864	0.363	16	0.164	R.LNFDAFHGDK.D
R4/RRR4-12/2	1229.062	1229.362	-244.324	0.444	880.729	0.376	18	0.159	R.GGSVCLAPTNPR.D
R4/RRR4-12/2	1228.938	1229.362	-346.268	0.445	686.380	0.404	16	0.154	R.GGSVCLAPTNPR.D
R4/RRR4-12/2	1228.486	1229.362	-1531.906	0.380	693.383	0.384	16	0.151	R.GGSVCLAPTNPR.D
R4/RRR4-14/2	1407.159	1407.463	-216.098	0.468	2066.989	0.367	19	0.264	K.TVDSEELTVEER.N
R4/RRR4-13/2	1407.109	1407.463	-251.955	0.438	1829.653	0.414	19	0.245	K.TVDSEELTVEER.N
R4/RRR4-14/2	1407.012	1407.463	-321.153	0.470	1868.855	0.393	19	0.245	K.TVDSEELTVEER.N
R4/RRR4-13/2	1407.063	1407.463	-285.204	0.430	1788.743	0.402	19	0.237	K.TVDSEELTVEER.N
R4/RRR4-13/2	1406.796	1407.463	-1188.216	0.399	1723.111	0.331	18	0.212	K.TVDSEELTVEER.N
R4/RRR4-14/2	1229.073	1229.342	-219.641	0.497	1277.981	0.471	17	0.200	K.DAAENTM*VAYK.A
R4/RRR4-14/2	1813.539	1814.078	-851.239	0.525	1208.081	0.501	21	0.194	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/2	1406.646	1407.463	-1295.579	0.402	1517.133	0.343	18	0.194	K.TVDSEELTVEER.N
R4/RRR4-14/2	1682.309	1681.869	262.542	0.480	956.095	0.545	22	0.186	K.LLDSHLVPSSTAPESK.V
R4/RRR4-14/2	1813.633	1814.078	-246.314	0.548	1015.084	0.510	22	0.183	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/2	1813.474	1814.078	-887.525	0.551	912.592	0.502	21	0.174	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/2	1228.375	1229.342	-1606.225	0.331	1172.071	0.385	17	0.173	K.DAAENTM*VAYK.A
R4/RRR4-14/2	1228.904	1229.342	-357.560	0.422	1131.416	0.383	17	0.172	K.DAAENTM*VAYK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1681.472	1681.869	-236.475	0.471	650.934	0.560	19	0.170	K.LLDSHLVPSSTAPESK.V
R4/RRR4-14/3	1813.598	1814.078	-265.432	0.360	1508.198	0.428	32	0.169	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/2	1681.411	1681.869	-272.820	0.431	744.295	0.520	20	0.168	K.LLDSHLVPSSTAPESK.V
R4/RRR4-14/2	1813.744	1814.078	-185.005	0.449	691.340	0.455	18	0.155	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/2	1813.094	1814.078	-1097.726	0.324	608.796	0.468	18	0.151	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/2	1813.321	1814.078	-972.000	0.360	675.328	0.329	19	0.143	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/3	1813.517	1814.078	-863.476	0.397	1329.380	0.409	34	0.140	K.AAQDIALAELPPTHPIR.L
R4/RRR4-16/2	1682.376	1681.869	-293.477	0.328	314.615	0.376	13	0.138	K.LLDSHLVPSSTAPESK.V
R4/RRR4-14/3	1813.529	1814.078	-856.888	0.365	1085.266	0.463	31	0.132	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/3	1990.881	1991.106	-113.694	0.372	989.010	0.490	30	0.130	R.IISSIEQKEESRGNEDR.V
R4/RRR4-14/3	1813.945	1814.078	-73.722	0.336	1144.135	0.410	30	0.125	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/3	1813.587	1814.078	-271.813	0.395	1095.446	0.422	29	0.124	K.AAQDIALAELPPTHPIR.L
R4/RRR4-14/3	1991.022	1991.106	-42.660	0.388	816.596	0.475	28	0.115	R.IISSIEQKEESRGNEDR.V
R4/RRR4-14/3	1990.832	1991.106	-138.327	0.382	771.540	0.479	28	0.113	R.IISSIEQKEESRGNEDR.V
R4/RRR4-14/3	1813.654	1814.078	-234.842	0.321	1180.367	0.344	32	0.111	K.AAQDIALAELPPTHPIR.L
R4/RRR4-13/3	1814.296	1814.078	120.647	0.312	844.809	0.353	28	0.097	K.AAQDIALAELPPTHPIR.L
R4/RRR4-13/3	1991.318	1991.106	106.387	0.312	514.363	0.387	25	0.092	R.IISSIEQKEESRGNEDR.V
R4/RRR4-9/2	1783.520	1784.047	-859.045	0.575	1674.849	0.535	21	0.253	R.LINSDEVQSVVKPINK.E
R4/RRR4-9/2	1783.732	1784.047	-177.066	0.590	1684.982	0.500	22	0.245	R.LINSDEVQSVVKPINK.E
R4/RRR4-9/2	1783.400	1784.047	-926.451	0.550	1469.730	0.449	20	0.206	R.LINSDEVQSVVKPINK.E
R4/RRR4-10/3	1794.835	1795.160	-181.299	0.385	866.649	0.387	28	0.099	R.IAVASALAATAVPSLVLAR.G
R4/RRR4-9/3	1794.658	1795.160	-839.462	0.335	984.721	0.230	27	0.080	-.IAVASALAATAVPSLVLAR.-
R4/RRR4-2/2	1665.330	1664.798	-282.218	0.599	1608.328	0.558	24	0.254	K.FTPSAVAIDLNSGESR.E
R4/RRR4-2/2	1664.065	1664.798	-1044.614	0.484	1734.706	0.478	24	0.248	K.FTPSAVAIDLNSGESR.E
R4/RRR4-2/2	1664.442	1664.798	-214.767	0.507	1713.995	0.472	24	0.244	K.FTPSAVAIDLNSGESR.E
R4/RRR4-2/2	1154.282	1155.288	-1742.821	0.316	1637.735	0.405	19	0.216	K.FQVTGFSVGGR.V
R4/RRR4-2/2	1154.549	1155.288	-1510.811	0.375	1493.646	0.325	18	0.189	K.FQVTGFSVGGR.V
R4/RRR4-2/3	1794.551	1795.057	-841.467	0.438	1286.568	0.549	32	0.182	K.AM*VTLTHGPENVKPQR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1172.093	1172.272	-153.097	0.464	1084.456	0.414	16	0.176	R.AVTDNLGYYR.L
R4/RRR4-2/2	1171.579	1172.272	-1449.870	0.392	1130.123	0.381	16	0.172	R.AVTDNLGYYR.L
R4/RRR4-2/2	1587.420	1587.797	-238.222	0.329	939.578	0.381	17	0.157	K.EQCNQNILLSLVR.L
R4/RRR4-2/2	1588.263	1587.797	294.739	0.397	1027.955	0.324	18	0.156	K.EQCNQNILLSLVR.L
R4/RRR4-2/2	1171.365	1172.272	-1632.634	0.350	805.627	0.373	15	0.155	R.AVTDNLGYYR.L
R4/RRR4-2/2	1317.132	1317.389	-195.917	0.414	511.769	0.445	14	0.152	R.ASHPNYEIETR.G
R4/RRR4-2/2	1587.502	1587.797	-186.305	0.347	1069.886	0.278	18	0.152	K.EQCNQNILLSLVR.L
R4/RRR4-2/2	798.919	798.997	-97.256	0.343	817.717	0.259	11	0.145	K.LGQILVR.I
R4/RRR4-2/2	798.818	798.997	-224.024	0.338	982.354	0.209	11	0.143	K.LGQILVR.I
R4/RRR4-2/2	798.591	798.997	-509.868	0.426	860.211	0.195	11	0.139	K.LGQILVR.I
R4/RRR4-3/2	1172.753	1172.272	411.172	0.196	673.167	0.229	13	0.135	R.AVTDNLGYYR.L
R4/RRR4-15/2	1238.114	1237.387	-221.177	0.538	1699.767	0.574	20	0.272	K.TLASDGLAGLYR.G
R4/RRR4-14/2	1237.054	1237.387	-270.458	0.507	1462.254	0.568	19	0.239	K.TLASDGLAGLYR.G
R4/RRR4-15/2	1237.437	1237.387	40.507	0.466	1569.350	0.511	19	0.237	K.TLASDGLAGLYR.G
R4/RRR4-14/2	1237.329	1237.387	-47.261	0.496	1487.346	0.525	19	0.232	K.TLASDGLAGLYR.G
R4/RRR4-14/2	1237.060	1237.387	-265.112	0.425	1381.578	0.535	18	0.220	K.TLASDGLAGLYR.G
R4/RRR4-14/2	1361.244	1361.590	-255.188	0.514	1432.292	0.398	17	0.198	K.LLVQNQEEM*LK.A
R4/RRR4-14/2	1360.913	1361.590	-1235.794	0.529	1309.694	0.405	17	0.189	K.LLVQNQEEM*LK.A
R4/RRR4-14/2	1322.198	1322.537	-257.487	0.370	808.425	0.522	16	0.168	R.GFGPSVAGIVVYR.G
R4/RRR4-14/2	1475.486	1475.675	-128.172	0.429	666.431	0.482	18	0.164	R.YFPTQALNFAFR.D
R4/RRR4-14/2	1475.456	1475.675	-148.506	0.445	604.752	0.480	17	0.162	R.YFPTQALNFAFR.D
R4/RRR4-14/2	1322.123	1322.537	-313.898	0.362	598.741	0.551	15	0.161	R.GFGPSVAGIVVYR.G
R4/RRR4-14/2	1322.194	1322.537	-260.358	0.279	571.577	0.504	14	0.150	R.GFGPSVAGIVVYR.G
R4/RRR4-14/2	1474.970	1475.675	-1159.112	0.320	612.626	0.383	18	0.149	R.YFPTQALNFAFR.D
R4/RRR4-17/2	1240.774	1241.401	-1315.162	0.429	1723.302	0.539	18	0.262	K.AFM*DATGGLWR.T
R4/RRR4-17/2	1699.570	1699.889	-188.356	0.499	1631.722	0.570	20	0.257	R.VATELELQQAFHQGK.Y
R4/RRR4-17/2	1240.637	1241.401	-1426.431	0.466	1722.064	0.470	18	0.245	K.AFM*DATGGLWR.T
R4/RRR4-17/2	1698.733	1699.889	-1273.036	0.471	1483.258	0.564	20	0.237	R.VATELELQQAFHQGK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1874.636	1875.067	-230.461	0.517	1449.960	0.544	24	0.229	K.LAEEIEKGASSVEGVEVK.L
R4/RRR4-17/2	1240.997	1241.401	-326.354	0.387	1688.576	0.389	18	0.222	K.AFM*DATGGLWR.T
R4/RRR4-17/2	1241.018	1241.401	-309.873	0.442	1612.247	0.415	18	0.220	K.AFM*DATGGLWR.T
R4/RRR4-17/2	1241.141	1241.401	-210.503	0.354	1677.680	0.374	17	0.216	K.AFM*DATGGLWR.T
R4/RRR4-17/2	1699.567	1699.889	-190.229	0.512	1264.856	0.572	18	0.214	R.VATELELQQAFHQGK.Y
R4/RRR4-17/2	1874.538	1875.067	-818.183	0.522	1338.021	0.508	23	0.208	K.LAEEIEKGASSVEGVEVK.L
R4/RRR4-17/2	1240.761	1241.401	-1325.438	0.447	1335.525	0.467	19	0.204	K.AFM*DATGGLWR.T
R4/RRR4-17/2	1240.658	1241.401	-1408.938	0.355	1434.507	0.431	18	0.203	K.AFM*DATGGLWR.T
R4/RRR4-17/2	1744.319	1744.966	-947.208	0.491	1067.492	0.547	24	0.198	K.LWQVPETLSDDVLTK.M
R4/RRR4-18/2	1744.487	1744.966	-275.588	0.458	1105.095	0.537	24	0.198	K.LWQVPETLSDDVLTK.M
R4/RRR4-17/2	1745.365	1744.966	229.346	0.577	834.325	0.622	22	0.196	K.LWQVPETLSDDVLTK.M
R4/RRR4-17/2	1744.518	1744.966	-258.038	0.491	1069.773	0.532	24	0.195	K.LWQVPETLSDDVLTK.M
R4/RRR4-17/2	1473.116	1473.486	-252.219	0.420	976.231	0.574	22	0.190	K.GGSPYGSGTFAGDGSR.V
R4/RRR4-18/2	1744.450	1744.966	-871.968	0.458	1086.066	0.494	24	0.189	K.LWQVPETLSDDVLTK.M
R4/RRR4-18/2	1473.030	1473.486	-310.500	0.478	1045.189	0.517	22	0.188	K.GGSPYGSGTFAGDGSR.V
R4/RRR4-18/2	1474.030	1473.486	-310.040	0.398	886.313	0.606	21	0.187	K.GGSPYGSGTFAGDGSR.V
R4/RRR4-17/2	1744.139	1744.966	-1051.060	0.489	890.123	0.561	22	0.187	K.LWQVPETLSDDVLTK.M
R4/RRR4-17/2	1224.953	1225.402	-367.285	0.373	1116.500	0.455	17	0.182	K.AFMDATGGLWR.T
R4/RRR4-17/2	1745.469	1744.966	-285.745	0.478	893.767	0.522	22	0.181	K.LWQVPETLSDDVLTK.M
R4/RRR4-17/2	1473.081	1473.486	-275.913	0.371	862.020	0.581	21	0.181	K.GGSPYGSGTFAGDGSR.V
R4/RRR4-18/2	1473.138	1473.486	-236.756	0.443	842.208	0.515	20	0.173	K.GGSPYGSGTFAGDGSR.V
R4/RRR4-17/2	1062.872	1063.276	-380.891	0.468	1014.788	0.413	14	0.172	R.FGM*M*AAQFK.A
R4/RRR4-17/2	1225.131	1225.402	-221.922	0.385	1021.340	0.415	16	0.170	K.AFMDATGGLWR.T
R4/RRR4-17/2	1472.545	1473.486	-1321.909	0.306	998.513	0.458	22	0.170	K.GGSPYGSGTFAGDGSR.V
R4/RRR4-17/2	1062.924	1063.276	-331.802	0.470	1081.351	0.373	14	0.169	R.FGM*M*AAQFK.A
R4/RRR4-18/2	1224.876	1225.402	-1249.340	0.351	1028.356	0.408	16	0.169	K.AFMDATGGLWR.T
R4/RRR4-17/2	1063.083	1063.276	-182.145	0.501	970.036	0.395	14	0.167	R.FGM*M*AAQFK.A
R4/RRR4-17/2	1240.826	1241.401	-1273.467	0.371	1203.772	0.280	17	0.162	K.AFM*DATGGLWR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1032.006	1031.277	-263.096	0.306	1027.567	0.359	13	0.160	R.FGMMAAQFK.A
R4/RRR4-17/2	1225.114	1225.402	-235.317	0.345	681.039	0.415	14	0.154	K.AFMDATGGLWR.T
R4/RRR4-17/2	1030.536	1031.277	-1694.759	0.294	924.642	0.318	13	0.151	R.FGMMAAQFK.A
R4/RRR4-18/2	1225.155	1225.402	-201.631	0.302	370.254	0.324	12	0.144	K.AFMDATGGLWR.T
R4/RRR4-18/2	1225.916	1225.402	-397.358	0.345	543.379	0.285	13	0.143	K.AFMDATGGLWR.T
R4/RRR4-17/2	1744.961	1744.966	-3.130	0.245	308.150	0.356	11	0.136	K.LWQVPETLSDDVLTK.M
R4/RRR4-12/2	1603.435	1603.887	-282.727	0.532	2144.529	0.580	23	0.343	K.HIVQDLKPEIPVSK.N
R4/RRR4-12/3	1941.086	1940.104	-9.570	0.524	2058.990	0.534	33	0.328	R.FSPNTFQPTIVSGSWDR.T
R4/RRR4-12/2	1603.393	1603.887	-309.155	0.508	1837.226	0.603	22	0.298	K.HIVQDLKPEIPVSK.N
R4/RRR4-12/2	1455.977	1456.618	-1130.757	0.421	2096.296	0.386	19	0.275	R.YWLCAATQDSIK.I
R4/RRR4-12/2	1603.394	1603.887	-308.850	0.531	1621.637	0.561	20	0.255	K.HIVQDLKPEIPVSK.N
R4/RRR4-12/2	1248.654	1249.398	-1400.871	0.448	1655.987	0.476	19	0.240	R.LWDLSTGVTTR.R
R4/RRR4-12/2	1249.120	1249.398	-223.247	0.551	1648.173	0.472	19	0.240	R.LWDLSTGVTTR.R
R4/RRR4-12/2	1248.904	1249.398	-396.514	0.531	1476.460	0.525	18	0.232	R.LWDLSTGVTTR.R
R4/RRR4-12/2	1939.548	1940.104	-804.710	0.476	1268.401	0.571	24	0.217	R.FSPNTFQPTIVSGSWDR.T
R4/RRR4-12/2	1939.526	1940.104	-816.461	0.464	1221.829	0.572	24	0.212	R.FSPNTFQPTIVSGSWDR.T
R4/RRR4-12/2	1573.422	1573.775	-224.856	0.491	1145.409	0.454	20	0.184	K.DGVTLLWDLAEGKR.L
R4/RRR4-12/2	1939.350	1940.104	-907.193	0.445	1093.191	0.476	23	0.182	R.FSPNTFQPTIVSGSWDR.T
R4/RRR4-12/2	1573.238	1573.775	-979.858	0.444	1132.623	0.429	18	0.176	K.DGVTLLWDLAEGKR.L
R4/RRR4-12/2	1574.054	1573.775	177.923	0.524	929.179	0.469	18	0.171	K.DGVTLLWDLAEGKR.L
R4/RRR4-12/2	1121.997	1121.262	-236.319	0.493	791.021	0.428	14	0.165	K.LWNTLGECK.Y
R4/RRR4-12/2	1122.027	1121.262	-209.579	0.456	648.681	0.396	13	0.155	K.LWNTLGECK.Y
R4/RRR4-12/2	1121.931	1121.262	-295.373	0.456	654.859	0.390	13	0.155	K.LWNTLGECK.Y
R4/RRR4-12/3	1573.659	1573.775	-74.008	0.366	944.705	0.339	27	0.096	K.DGVTLLWDLAEGKR.L
R4/RRR4-12/3	1573.763	1573.775	-7.719	0.391	585.204	0.379	23	0.093	K.DGVTLLWDLAEGKR.L
R4/RRR4-12/3	1574.034	1573.775	165.315	0.408	694.800	0.346	25	0.091	K.DGVTLLWDLAEGKR.L
R4/RRR4-11/2	1557.203	1557.767	-1007.875	0.405	1846.682	0.595	22	0.293	R.VPTPNVSVVDLTCR.I
R4/RRR4-11/2	1556.770	1557.767	-1287.041	0.405	1745.242	0.595	22	0.278	R.VPTPNVSVVDLTCR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1290.000	1290.402	-312.413	0.465	1788.280	0.440	20	0.248	K.VVDDSTLEINGK.K
R4/RRR4-11/2	1557.187	1557.767	-1017.635	0.424	1417.755	0.637	19	0.244	R.VPTPNVSVVDLTCR.I
R4/RRR4-11/2	1789.032	1789.884	-1038.304	0.470	1050.365	0.537	18	0.189	K.LVSWYDNEWGYSNR.V
R4/RRR4-11/2	1051.877	1052.121	-232.751	0.448	1115.065	0.445	14	0.182	K.YDSTHGPFK.G
R4/RRR4-11/2	1508.707	1508.854	-98.083	0.459	1239.149	0.405	18	0.179	R.VLDLIAHMALVNAK.-
R4/RRR4-11/2	1051.874	1052.121	-235.429	0.316	1036.313	0.384	13	0.163	K.YDSTHGPFK.G
R4/RRR4-11/2	1051.847	1052.121	-261.276	0.363	775.044	0.416	13	0.158	K.YDSTHGPFK.G
R4/RRR4-11/2	1509.616	1508.854	-158.446	0.310	442.640	0.375	14	0.139	R.VLDLIAHMALVNAK.-
R4/RRR4-10/2	1423.260	1423.620	-253.483	0.498	2153.477	0.587	21	0.344	R.GGDLVSAFAELMGR.Q
R4/RRR4-10/2	1423.120	1423.620	-352.189	0.473	2188.009	0.565	21	0.343	R.GGDLVSAFAELMGR.Q
R4/RRR4-10/2	1423.404	1423.620	-151.872	0.495	2075.727	0.594	21	0.332	R.GGDLVSAFAELMGR.Q
R4/RRR4-10/2	1439.696	1439.619	53.295	0.513	2075.032	0.560	21	0.322	R.GGDLVSAFAELM*GR.Q
R4/RRR4-10/2	1438.669	1439.619	-1359.905	0.348	1518.846	0.462	19	0.215	R.GGDLVSAFAELM*GR.Q
R4/RRR4-10/3	1595.564	1595.678	-71.419	0.462	1797.357	0.403	29	0.202	R.YHGHSMSDPGSTYR.T
R4/RRR4-10/3	1595.683	1595.678	3.052	0.456	1707.127	0.434	32	0.196	R.YHGHSMSDPGSTYR.T
R4/RRR4-10/2	1438.480	1439.619	-1491.671	0.374	1093.214	0.460	17	0.177	R.GGDLVSAFAELM*GR.Q
R4/RRR4-10/3	1423.650	1423.620	21.224	0.480	1562.676	0.411	26	0.175	R.GGDLVSAFAELMGR.Q
R4/RRR4-10/2	1269.551	1270.376	-1441.270	0.422	1021.689	0.379	17	0.164	K.GFGVESFGADRK.E
R4/RRR4-10/2	1958.784	1958.178	-201.746	0.498	680.668	0.519	19	0.164	K.ESPMPDTSELFTNVYVK.G
R4/RRR4-10/2	1974.318	1974.178	71.302	0.447	386.087	0.564	17	0.158	K.ESPM*PDTSELFTNVYVK.G
R4/RRR4-10/2	1269.443	1270.376	-1526.846	0.380	1024.239	0.328	17	0.157	K.GFGVESFGADRK.E
R4/RRR4-10/2	1973.032	1974.178	-1090.880	0.400	468.186	0.531	18	0.155	K.ESPM*PDTSELFTNVYVK.G
R4/RRR4-10/2	1269.420	1270.376	-1545.586	0.380	1012.091	0.320	17	0.155	K.GFGVESFGADRK.E
R4/RRR4-10/2	1004.835	1005.152	-316.634	0.379	912.127	0.320	14	0.153	K.RGDYVPGLK.V
R4/RRR4-10/2	1004.402	1005.152	-1747.875	0.397	760.512	0.349	13	0.152	K.RGDYVPGLK.V
R4/RRR4-10/2	1004.435	1005.152	-1714.540	0.404	917.195	0.278	14	0.149	K.RGDYVPGLK.V
R4/RRR4-10/3	1595.508	1595.678	-107.105	0.455	1284.414	0.383	27	0.129	R.YHGHSMSDPGSTYR.T
R4/RRR4-10/3	1929.073	1930.174	-1092.793	0.410	1175.867	0.405	23	0.126	K.EHAIANGPIVLEMDTYR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/3	1611.696	1611.677	11.769	0.405	840.763	0.399	25	0.103	R.YHGHSM*SDPGSTYR.T
R4/RRR4-10/3	1611.826	1611.677	92.211	0.355	753.465	0.292	26	0.087	R.YHGHSM*SDPGSTYR.T
R4/RRR4-7/2	1696.283	1695.849	256.481	0.544	2411.422	0.473	23	0.354	K.LGYADLVEEVSVGESK.I
R4/RRR4-7/2	1696.133	1695.849	167.716	0.513	2182.436	0.470	23	0.312	K.LGYADLVEEVSVGESK.I
R4/RRR4-7/2	1289.953	1289.417	-361.306	0.495	1114.956	0.501	19	0.193	K.LGGTVDDTELIR.G
R4/RRR4-7/2	1330.992	1331.414	-318.522	0.451	1346.685	0.372	17	0.183	R.GSNQLVIDEAER.S
R4/RRR4-7/2	1289.033	1289.417	-298.875	0.435	1125.672	0.401	18	0.174	K.LGGTVDDTELIR.G
R4/RRR4-7/2	1327.484	1327.597	-85.279	0.401	1096.484	0.341	17	0.161	K.IAVIQFQVSPPK.T
R4/RRR4-7/2	931.000	931.069	-74.318	0.500	1059.370	0.324	13	0.161	K.IDDIVTVR.-
R4/RRR4-7/2	1289.046	1289.417	-288.614	0.447	984.193	0.343	18	0.158	K.LGGTVDDTELIR.G
R4/RRR4-7/2	931.030	931.069	-41.176	0.473	1076.549	0.283	13	0.156	K.IDDIVTVR.-
R4/RRR4-7/2	931.000	931.069	-74.187	0.463	1036.758	0.275	13	0.153	K.IDDIVTVR.-
R4/RRR4-7/2	1203.063	1203.407	-287.259	0.384	865.368	0.187	14	0.133	-.ASGCNVLLIQK.-
R4/RRR4-20/1	1343.688	1344.496	-1349.666	0.085	723.250	0.368	17	0.516	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/3	1254.654	1254.544	87.855	0.499	2638.599	0.435	31	0.408	K.VSVVPSAAALVIK.A
R4/RRR4-20/3	1344.460	1344.496	-27.249	0.487	2550.124	0.410	33	0.373	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/2	1344.089	1344.496	-303.940	0.440	2226.383	0.466	23	0.317	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/2	1344.173	1344.496	-241.254	0.465	2044.870	0.509	23	0.301	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/3	1254.821	1254.544	221.469	0.478	1754.045	0.477	28	0.225	K.VSVVPSAAALVIK.A
R4/RRR4-20/3	1639.970	1639.792	109.059	0.538	1914.748	0.387	29	0.217	K.HSGNISLDDVIEIAR.I
R4/RRR4-20/2	1639.670	1639.792	-74.344	0.585	1112.228	0.598	22	0.211	K.HSGNISLDDVIEIAR.I
R4/RRR4-21/2	1639.396	1639.792	-242.021	0.565	1017.069	0.617	22	0.207	K.HSGNISLDDVIEIAR.I
R4/RRR4-21/2	1640.349	1639.792	-271.065	0.582	961.332	0.631	22	0.206	K.HSGNISLDDVIEIAR.I
R4/RRR4-21/2	1639.301	1639.792	-300.068	0.555	1039.589	0.597	22	0.205	K.HSGNISLDDVIEIAR.I
R4/RRR4-20/2	1638.930	1639.792	-1139.673	0.561	1088.005	0.575	22	0.204	K.HSGNISLDDVIEIAR.I
R4/RRR4-20/2	1640.385	1639.792	-248.518	0.603	948.700	0.624	22	0.204	K.HSGNISLDDVIEIAR.I
R4/RRR4-20/3	1343.858	1344.496	-1222.966	0.428	1635.060	0.445	30	0.194	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/2	1254.339	1254.544	-164.240	0.452	1022.590	0.515	22	0.189	K.VSVVPSAAALVIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1254.269	1254.544	-220.086	0.514	779.495	0.527	21	0.179	K.VSVVPSAAALVIK.A
R4/RRR4-21/2	1254.313	1254.544	-184.352	0.459	937.595	0.483	21	0.179	K.VSVVPSAAALVIK.A
R4/RRR4-20/2	1695.502	1695.880	-223.975	0.409	1154.724	0.441	19	0.176	K.EILGTCVSVGCTVDGK.D
R4/RRR4-21/2	1255.018	1254.544	378.464	0.489	827.699	0.493	21	0.176	K.VSVVPSAAALVIK.A
R4/RRR4-20/2	1343.619	1344.496	-1401.002	0.341	1189.183	0.399	19	0.174	R.VTGGEVGAASSLAPK.I
R4/RRR4-21/2	1254.537	1254.544	-5.818	0.440	902.689	0.453	22	0.173	K.VSVVPSAAALVIK.A
R4/RRR4-20/2	1253.605	1254.544	-1551.509	0.384	919.761	0.461	22	0.173	K.VSVVPSAAALVIK.A
R4/RRR4-20/2	1344.129	1344.496	-273.689	0.335	1097.508	0.393	20	0.168	R.VTGGEVGAASSLAPK.I
R4/RRR4-21/2	1343.613	1344.496	-1405.565	0.312	1366.126	0.270	19	0.167	R.VTGGEVGAASSLAPK.I
R4/RRR4-21/2	1343.897	1344.496	-1193.265	0.294	1306.699	0.288	19	0.165	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/3	1254.475	1254.544	-55.458	0.430	1456.238	0.430	25	0.163	K.VSVVPSAAALVIK.A
R4/RRR4-20/2	1254.339	1254.544	-163.557	0.334	844.939	0.424	21	0.162	K.VSVVPSAAALVIK.A
R4/RRR4-20/2	881.941	882.082	-160.707	0.375	372.208	0.510	13	0.161	K.IGPLGLSPK.K
R4/RRR4-21/2	881.827	882.082	-290.824	0.361	328.628	0.503	12	0.159	K.IGPLGLSPK.K
R4/RRR4-21/2	881.670	882.082	-468.628	0.371	333.578	0.480	12	0.158	K.IGPLGLSPK.K
R4/RRR4-20/2	881.889	882.082	-220.276	0.376	338.673	0.437	12	0.156	K.IGPLGLSPK.K
R4/RRR4-20/2	1344.104	1344.496	-292.642	0.328	958.367	0.345	19	0.155	R.VTGGEVGAASSLAPK.I
R4/RRR4-21/2	881.873	882.082	-238.607	0.385	285.080	0.435	11	0.155	K.IGPLGLSPK.K
R4/RRR4-20/2	881.849	882.082	-265.826	0.352	327.707	0.429	12	0.154	K.IGPLGLSPK.K
R4/RRR4-20/2	881.669	882.082	-470.017	0.374	290.082	0.426	11	0.154	K.IGPLGLSPK.K
R4/RRR4-20/2	881.991	882.082	-104.198	0.399	289.723	0.456	11	0.152	-.IGPLGLSPK.-
R4/RRR4-18/2	1254.330	1254.544	-171.172	0.395	450.640	0.431	15	0.149	-.VSVVPSAAALVIK.-
R4/RRR4-19/2	881.812	882.082	-308.046	0.263	287.779	0.382	11	0.148	K.IGPLGLSPK.K
R4/RRR4-19/2	881.946	882.082	-155.153	0.262	257.792	0.424	10	0.147	K.IGPLGLSPK.K
R4/RRR4-20/2	882.181	882.082	112.473	0.268	398.660	0.368	12	0.147	K.IGPLGLSPK.K
R4/RRR4-22/2	1254.412	1254.544	-105.180	0.289	354.283	0.417	14	0.146	K.VSVVPSAAALVIK.A
R4/RRR4-19/2	1343.925	1344.496	-1172.742	0.276	634.113	0.279	17	0.140	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/2	882.417	882.082	379.817	0.286	256.638	0.401	10	0.139	-.IGPLGLSPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/3	1639.679	1639.792	-69.012	0.537	1362.060	0.384	26	0.138	K.HSGNISLDDVIEIAR.I
R4/RRR4-20/2	1640.649	1639.792	-87.284	0.371	386.136	0.275	17	0.137	-.HSGNISLDDVIEIAR.-
R4/RRR4-20/3	1639.563	1639.792	-139.923	0.405	1528.939	0.311	26	0.137	K.HSGNISLDDVIEIAR.I
R4/RRR4-19/2	1343.932	1344.496	-1167.544	0.214	584.254	0.181	18	0.136	R.VTGGEVGAASSLAPK.I
R4/RRR4-20/2	1254.195	1254.544	-278.769	0.273	375.522	0.290	14	0.135	-.VSVVPSAAALVIK.-
R4/RRR4-19/2	1343.869	1344.496	-1214.336	0.166	652.827	0.098	19	0.133	R.VTGGEVGAASSLAPK.I
R4/RRR4-21/3	1639.518	1639.792	-167.259	0.417	929.697	0.358	23	0.100	K.HSGNISLDDVIEIAR.I
R4/RRR4-20/3	1343.997	1344.496	-372.569	0.362	912.573	0.345	31	0.095	R.VTGGEVGAASSLAPK.I
R4/RRR4-21/3	1639.850	1639.792	35.822	0.423	755.215	0.378	22	0.093	-.HSGNISLDDVIEIAR.-
R4/RRR4-20/2	1731.128	1731.793	-964.822	0.277	949.094	0.248	21	0.073	K.DLQEEISDGEVEIPSA.-
R4/RRR4-7/3	1981.716	1981.204	-247.053	0.567	2978.007	0.621	39	0.670	K.QIGVIGWGSQGPAQAQNLR.D
R4/RRR4-7/2	1788.408	1789.021	-904.482	0.535	3220.244	0.579	26	0.589	R.FDYILTQQAFVTVDK.N
R4/RRR4-7/2	1789.084	1789.021	35.134	0.572	3185.457	0.589	26	0.584	R.FDYILTQQAFVTVDK.N
R4/RRR4-7/3	1981.057	1981.204	-74.672	0.505	2492.226	0.520	35	0.436	K.QIGVIGWGSQGPAQAQNLR.D
R4/RRR4-7/2	1980.615	1981.204	-804.901	0.542	2069.407	0.629	25	0.342	K.QIGVIGWGSQGPAQAQNLR.D
R4/RRR4-7/2	1980.650	1981.204	-787.145	0.551	1981.271	0.641	25	0.330	K.QIGVIGWGSQGPAQAQNLR.D
R4/RRR4-7/2	1980.526	1981.204	-849.756	0.513	1915.966	0.631	26	0.316	K.QIGVIGWGSQGPAQAQNLR.D
R4/RRR4-7/2	1698.581	1698.920	-200.143	0.467	1041.987	0.470	19	0.176	K.GMLEVYNSLTEEGKK.E
R4/RRR4-7/2	1662.350	1662.849	-301.305	0.454	618.994	0.525	20	0.166	K.EGLPAFPM*GNIDQTR.M
R4/RRR4-7/2	1360.148	1359.512	-268.486	0.427	799.842	0.453	16	0.163	K.VSLAGHDEYIVR.G
R4/RRR4-7/2	1662.537	1662.849	-188.300	0.354	684.543	0.509	20	0.162	K.EGLPAFPM*GNIDQTR.M
R4/RRR4-7/2	1662.182	1662.849	-1005.599	0.338	532.402	0.455	18	0.151	K.EGLPAFPM*GNIDQTR.M
R4/RRR4-7/2	1359.325	1359.512	-138.225	0.405	631.076	0.372	15	0.147	K.VSLAGHDEYIVR.G
R4/RRR4-7/2	1646.218	1646.849	-994.283	0.310	439.544	0.418	16	0.144	K.EGLPAFPMGNIDQTR.M
R4/RRR4-7/3	1616.595	1616.800	-126.952	0.399	1038.984	0.444	25	0.123	K.EKVSLAGHDEYIVR.G
R4/RRR4-7/3	1616.982	1616.800	113.183	0.370	817.587	0.434	24	0.106	K.EKVSLAGHDEYIVR.G
R4/RRR4-7/3	1616.637	1616.800	-101.048	0.350	787.450	0.435	23	0.104	K.EKVSLAGHDEYIVR.G
R4/RRR4-5/2	1214.094	1213.406	-257.622	0.412	784.070	0.414	15	0.159	K.AVDEIEPALKK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1212.505	1213.406	-1572.292	0.346	553.138	0.450	13	0.150	-.AVDEIEPALKK.-
R4/RRR4-1/2	1212.908	1213.406	-411.613	0.344	300.470	0.410	11	0.140	-.AVDEIEPALKK.-
R4/RRR4-1/2	1213.352	1213.406	-43.855	0.325	446.178	0.312	12	0.139	-.AVDEIEPALKK.-
R4/RRR4-10/2	1480.254	1480.711	-309.862	0.462	1819.938	0.424	22	0.246	R.ASIYNAM*PLAGVEK.L
R4/RRR4-10/2	1284.193	1283.502	-241.844	0.506	1085.150	0.589	18	0.205	K.NVGPSGVTIAIVR.K
R4/RRR4-10/2	1480.190	1480.711	-1031.000	0.474	1318.098	0.423	20	0.191	R.ASIYNAM*PLAGVEK.L
R4/RRR4-10/2	1283.051	1283.502	-352.467	0.507	1114.172	0.500	19	0.191	K.NVGPSGVTIAIVR.K
R4/RRR4-10/2	1282.779	1283.502	-1347.474	0.352	1139.074	0.515	19	0.190	K.NVGPSGVTIAIVR.K
R4/RRR4-10/2	1949.460	1949.109	180.527	0.560	826.298	0.589	23	0.187	K.YTSLPPFDAIEQNPEAR.F
R4/RRR4-10/2	1068.180	1068.250	-65.519	0.476	1082.723	0.441	16	0.181	R.FGLIYAGAQK.N
R4/RRR4-10/2	1480.236	1480.711	-321.942	0.461	1123.516	0.438	18	0.177	R.ASIYNAM*PLAGVEK.L
R4/RRR4-10/2	1948.373	1949.109	-894.069	0.479	615.685	0.589	21	0.173	K.YTSLPPFDAIEQNPEAR.F
R4/RRR4-10/2	1068.058	1068.250	-180.849	0.509	951.846	0.437	15	0.172	R.FGLIYAGAQK.N
R4/RRR4-10/2	1948.339	1949.109	-911.303	0.460	652.000	0.565	22	0.171	K.YTSLPPFDAIEQNPEAR.F
R4/RRR4-10/2	1067.515	1068.250	-1630.661	0.432	1020.731	0.383	15	0.166	R.FGLIYAGAQK.N
R4/RRR4-10/2	1110.939	1111.232	-264.351	0.399	920.259	0.419	17	0.165	K.FSAASVAWSGK.D
R4/RRR4-10/2	1237.147	1237.494	-281.294	0.441	869.359	0.383	17	0.160	R.SLM*NVPFTLAK.G
R4/RRR4-10/2	1237.085	1237.494	-331.586	0.493	661.972	0.421	16	0.156	-.SLM*NVPFTLAK.-
R4/RRR4-10/2	1237.215	1237.494	-225.662	0.447	646.132	0.386	15	0.150	-.SLM*NVPFTLAK.-
R4/RRR4-10/2	1110.925	1111.232	-276.698	0.293	548.025	0.474	13	0.147	-.FSAASVAWSGK.-
R4/RRR4-10/2	1221.244	1221.494	-205.685	0.325	613.038	0.300	14	0.142	R.SLMNVPFTLAK.G
R4/RRR4-2/2	1826.558	1827.071	-830.760	0.525	2343.015	0.567	24	0.374	K.FAALQQSIQSYLDTIK.G
R4/RRR4-2/2	1828.077	1827.071	3.576	0.595	2177.726	0.583	22	0.346	K.FAALQQSIQSYLDTIK.G
R4/RRR4-2/2	1292.057	1292.335	-215.734	0.484	1901.584	0.383	19	0.246	R.SLDSSDSPLSQR.A
R4/RRR4-2/2	1293.008	1292.335	-253.830	0.495	1503.446	0.462	19	0.219	R.SLDSSDSPLSQR.A
R4/RRR4-2/2	1057.353	1057.229	117.462	0.418	1316.902	0.431	17	0.195	K.VLLNAVASNR.F
R4/RRR4-2/2	1292.022	1292.335	-242.842	0.448	1415.592	0.374	18	0.191	R.SLDSSDSPLSQR.A
R4/RRR4-1/2	1827.720	1827.071	-192.499	0.483	795.284	0.536	19	0.172	K.FAALQQSIQSYLDTIK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1305.312	1305.540	-174.523	0.417	998.411	0.323	16	0.154	K.GSSLQCLVSILK.S
R4/RRR4-1/2	1667.957	1666.943	8.397	0.426	759.326	0.392	16	0.149	R.VLEGTQAELVLQPLR.L
R4/RRR4-1/2	1668.073	1666.943	77.686	0.396	820.318	0.286	16	0.139	R.VLEGTQAELVLQPLR.L
R4/RRR4-2/2	1668.093	1666.943	89.796	0.387	613.922	0.328	14	0.137	-.VLEGTQAELVLQPLR.-
R4/RRR4-1/2	1667.951	1666.943	4.800	0.365	819.412	0.247	16	0.136	R.VLEGTQAELVLQPLR.L
R4/RRR4-1/2	1600.188	1600.799	-1009.953	0.410	1056.016	0.200	18	0.136	K.VSGGIDLDTVNIIQR.D
R4/RRR4-2/2	1304.705	1305.540	-1409.944	0.241	727.134	0.282	13	0.135	K.GSSLQCLVSILK.S
R4/RRR4-2/3	1941.406	1941.991	-818.483	0.360	938.110	0.409	24	0.107	K.DASDLQPSTGEAASADIHR.V
R4/RRR4-2/3	1942.173	1941.991	94.201	0.341	467.409	0.332	21	0.055	-.DASDLQPSTGEAASADIHR.-
R4/RRR4-10/2	1695.413	1694.909	-293.315	0.587	2203.422	0.557	22	0.345	R.IVTFNSDWQLLTEK.E
R4/RRR4-10/2	1928.611	1929.246	-850.348	0.500	1791.358	0.560	26	0.278	K.TAPINIGLAAFELIDEIK.A
R4/RRR4-10/2	1694.276	1694.909	-966.803	0.512	1721.732	0.512	20	0.255	R.IVTFNSDWQLLTEK.E
R4/RRR4-9/2	1694.409	1694.909	-295.945	0.504	1769.753	0.478	20	0.252	R.IVTFNSDWQLLTEK.E
R4/RRR4-10/2	1742.179	1742.950	-1019.774	0.418	1418.794	0.379	20	0.187	R.DEDPAAVAATIPSFLPK.L
R4/RRR4-10/2	1693.719	1694.909	-1296.901	0.390	1317.039	0.386	18	0.182	R.IVTFNSDWQLLTEK.E
R4/RRR4-9/2	1607.480	1607.786	-191.454	0.460	1117.691	0.442	21	0.181	R.DLPDSTFTISELIR.N
R4/RRR4-9/2	1607.593	1607.786	-120.458	0.454	1073.278	0.402	21	0.172	R.DLPDSTFTISELIR.N
R4/RRR4-10/2	1607.493	1607.786	-182.921	0.472	938.437	0.431	20	0.168	R.DLPDSTFTISELIR.N
R4/RRR4-10/2	1607.399	1607.786	-241.964	0.481	1006.998	0.402	21	0.168	R.DLPDSTFTISELIR.N
R4/RRR4-10/2	1116.777	1117.231	-407.795	0.385	667.592	0.463	16	0.162	K.SCPGVENVVR.Y
R4/RRR4-10/2	1455.195	1455.683	-336.349	0.372	605.648	0.469	18	0.158	R.LTAPPEQILPGYR.S
R4/RRR4-10/2	1607.165	1607.786	-1011.663	0.340	950.729	0.309	21	0.152	R.DLPDSTFTISELIR.N
R4/RRR4-9/2	1456.114	1455.683	297.019	0.391	379.580	0.457	15	0.151	R.LTAPPEQILPGYR.S
R4/RRR4-10/2	1117.849	1117.231	-343.111	0.311	517.748	0.437	15	0.151	K.SCPGVENVVR.Y
R4/RRR4-10/2	1455.196	1455.683	-335.507	0.329	395.140	0.433	16	0.149	R.LTAPPEQILPGYR.S
R4/RRR4-10/2	1455.253	1455.683	-296.288	0.366	322.469	0.407	14	0.146	R.LTAPPEQILPGYR.S
R4/RRR4-12/2	1608.759	1607.786	-17.170	0.419	545.968	0.362	16	0.145	R.DLPDSTFTISELIR.N
R4/RRR4-10/2	1116.291	1117.231	-1743.125	0.189	310.682	0.323	13	0.132	-.SCPGVENVVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1291.117	1290.530	-321.152	0.571	1499.665	0.544	18	0.240	K.IPISLIYDDIK.S
R4/RRR4-10/2	1524.452	1524.699	-162.687	0.474	1606.562	0.450	19	0.226	R.FSFEETTATLHLK.L
R4/RRR4-10/2	1308.187	1307.650	-354.866	0.475	1416.634	0.470	19	0.212	R.VVLLIDVPIIGR.I
R4/RRR4-10/2	1308.017	1307.650	281.412	0.477	1080.621	0.487	17	0.186	R.VVLLIDVPIIGR.I
R4/RRR4-11/2	1307.081	1307.650	-1204.020	0.486	868.815	0.492	16	0.173	R.VVLLIDVPIIGR.I
R4/RRR4-10/2	1936.342	1937.228	-977.145	0.462	394.585	0.551	16	0.155	K.STYNDIKPGSIIPYLVR.V
R4/RRR4-10/2	1937.654	1937.228	220.551	0.464	362.963	0.535	15	0.151	K.STYNDIKPGSIIPYLVR.V
R4/RRR4-10/2	1291.248	1290.530	-218.903	0.453	879.768	0.324	15	0.149	-.IPISLIYDDIK.-
R4/RRR4-10/2	1307.068	1307.650	-1213.680	0.364	520.903	0.357	14	0.145	R.VVLLIDVPIIGR.I
R4/RRR4-10/2	1787.522	1787.003	-269.844	0.419	678.340	0.332	18	0.141	-.SGEIPIPYKPDVDVEK.-
R4/RRR4-10/2	1786.406	1787.003	-896.655	0.383	608.249	0.381	17	0.141	-.SGEIPIPYKPDVDVEK.-
R4/RRR4-10/3	1937.057	1937.228	-88.536	0.403	951.039	0.377	25	0.103	K.STYNDIKPGSIIPYLVR.V
R4/RRR4-10/3	1936.925	1937.228	-156.811	0.372	836.734	0.344	25	0.092	K.STYNDIKPGSIIPYLVR.V
R4/RRR4-10/3	1937.891	1937.228	-174.297	0.334	827.401	0.276	25	0.083	K.STYNDIKPGSIIPYLVR.V
R4/RRR4-10/3	1753.793	1754.046	-145.013	0.228	998.357	0.197	25	0.072	K.QGITTM*QVPFSFRPK.D
R4/RRR4-6/2	1852.036	1852.034	1.282	0.554	1507.009	0.507	25	0.228	K.ANFLSADDFEPSLIPSK.T
R4/RRR4-6/2	1851.352	1852.034	-911.163	0.535	1387.920	0.536	24	0.221	K.ANFLSADDFEPSLIPSK.T
R4/RRR4-6/2	1653.296	1653.865	-952.110	0.472	1325.707	0.531	20	0.214	K.GKWHAPLIDNPNYK.G
R4/RRR4-5/2	1851.547	1852.034	-263.489	0.509	1398.362	0.490	24	0.212	K.ANFLSADDFEPSLIPSK.T
R4/RRR4-6/2	1333.765	1334.632	-1404.469	0.408	1260.603	0.548	20	0.210	K.KPAAPVKPVAEVK.K
R4/RRR4-6/2	1334.353	1334.632	-209.813	0.450	1068.727	0.546	21	0.197	K.KPAAPVKPVAEVK.K
R4/RRR4-6/2	1851.447	1852.034	-859.468	0.465	1241.001	0.469	23	0.193	K.ANFLSADDFEPSLIPSK.T
R4/RRR4-5/2	1851.534	1852.034	-270.698	0.476	1010.998	0.475	21	0.176	K.ANFLSADDFEPSLIPSK.T
R4/RRR4-6/2	1334.281	1334.632	-263.780	0.376	851.930	0.434	20	0.164	K.KPAAPVKPVAEVK.K
R4/RRR4-6/2	1468.203	1468.641	-299.012	0.469	861.385	0.424	16	0.162	K.WHAPLIDNPNYK.G
R4/RRR4-6/2	1468.055	1468.641	-1083.507	0.436	952.042	0.372	17	0.160	K.WHAPLIDNPNYK.G
R4/RRR4-1/2	1851.918	1852.034	-62.517	0.448	838.636	0.413	19	0.156	K.ANFLSADDFEPSLIPSK.T
R4/RRR4-6/2	1026.217	1026.253	-35.150	0.485	757.898	0.332	13	0.152	K.KIFDVLYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1306.329	1306.531	-155.267	0.346	649.404	0.416	15	0.152	K.LADIPFLEPYK.T
R4/RRR4-5/2	1334.014	1334.632	-1216.883	0.395	493.318	0.386	17	0.149	K.KPAAPVKPVAEVK.K
R4/RRR4-6/2	1467.472	1468.641	-1482.417	0.289	804.931	0.302	15	0.143	K.WHAPLIDNPNYK.G
R4/RRR4-1/2	1851.163	1852.034	-1013.376	0.391	521.001	0.343	16	0.140	K.ANFLSADDFEPSLIPSK.T
R4/RRR4-6/2	1305.625	1306.531	-1464.279	0.221	479.992	0.306	15	0.137	K.LADIPFLEPYK.T
R4/RRR4-6/3	1334.697	1334.632	48.828	0.377	1077.118	0.405	25	0.117	K.KPAAPVKPVAEVK.K
R4/RRR4-6/3	1468.358	1468.641	-193.009	0.492	1538.132	0.198	25	0.107	K.WHAPLIDNPNYK.G
R4/RRR4-6/3	1335.577	1334.632	-41.181	0.332	651.966	0.383	20	0.095	K.KPAAPVKPVAEVK.K
R4/RRR4-6/3	1334.528	1334.632	-78.738	0.328	607.531	0.373	21	0.093	K.KPAAPVKPVAEVK.K
R4/RRR4-1/3	1335.655	1334.632	17.259	0.316	502.396	0.326	20	0.090	K.KPAAPVKPVAEVK.K
R4/RRR4-6/3	1334.009	1334.632	-1220.522	0.348	466.227	0.355	18	0.089	-.KPAAPVKPVAEVK.-
R4/RRR4-8/2	1854.383	1854.950	-847.147	0.573	2018.237	0.649	24	0.343	K.HLTSTYSSDETKEDIK.L
R4/RRR4-8/2	1854.426	1854.950	-824.217	0.580	1899.883	0.643	24	0.321	K.HLTSTYSSDETKEDIK.L
R4/RRR4-8/2	1660.435	1659.861	-257.537	0.547	1601.216	0.503	22	0.238	K.ELQGVVFDDVPEALK.H
R4/RRR4-8/2	1659.380	1659.861	-291.199	0.438	1574.696	0.477	22	0.228	K.ELQGVVFDDVPEALK.H
R4/RRR4-8/2	1659.516	1659.861	-208.764	0.476	1513.029	0.443	21	0.213	K.ELQGVVFDDVPEALK.H
R4/RRR4-8/2	1340.267	1340.509	-181.025	0.432	1215.812	0.447	17	0.188	R.LLFGNTAYGDLR.Q
R4/RRR4-8/2	1340.232	1340.509	-207.340	0.459	1165.491	0.446	17	0.184	R.LLFGNTAYGDLR.Q
R4/RRR4-8/2	1340.331	1340.509	-133.332	0.395	845.816	0.442	15	0.162	R.LLFGNTAYGDLR.Q
R4/RRR4-8/2	989.957	990.130	-175.019	0.423	1123.110	0.303	13	0.161	R.ELVAELCR.H
R4/RRR4-8/2	1031.363	1032.132	-1720.110	0.331	1108.335	0.282	15	0.156	K.VYIYSSGSR.E
R4/RRR4-8/3	1854.323	1854.950	-879.998	0.561	1142.126	0.524	36	0.153	K.HLTSTYSSDETKEDIK.L
R4/RRR4-8/2	1031.545	1032.132	-1542.598	0.376	1204.297	0.219	15	0.153	K.VYIYSSGSR.E
R4/RRR4-8/2	989.945	990.130	-187.513	0.378	834.636	0.309	12	0.150	R.ELVAELCR.H
R4/RRR4-8/2	1032.182	1032.132	48.561	0.282	947.982	0.295	14	0.149	K.VYIYSSGSR.E
R4/RRR4-7/3	1854.067	1854.950	-1018.400	0.497	1112.817	0.502	34	0.145	K.HLTSTYSSDETKEDIK.L
R4/RRR4-8/2	1341.056	1340.509	-338.865	0.310	256.982	0.274	12	0.141	R.LLFGNTAYGDLR.Q
R4/RRR4-8/2	989.738	990.130	-396.615	0.354	685.846	0.218	11	0.138	-.ELVAELCR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/3	1854.599	1854.950	-189.420	0.556	858.566	0.526	31	0.133	K.HLTSTYSSDETKEDIK.L
R4/RRR4-1/3	1854.920	1854.950	-15.823	0.502	790.313	0.495	31	0.123	K.HLTSTYSSDETKEDIK.L
R4/RRR4-2/3	1854.977	1854.950	14.869	0.541	721.815	0.505	31	0.122	K.HLTSTYSSDETKEDIK.L
R4/RRR4-8/3	1854.606	1854.950	-185.854	0.521	775.595	0.475	30	0.118	K.HLTSTYSSDETKEDIK.L
R4/RRR4-15/3	1854.902	1854.950	-25.724	0.545	667.896	0.493	28	0.118	K.HLTSTYSSDETKEDIK.L
R4/RRR4-7/3	1854.417	1854.950	-828.850	0.510	844.604	0.454	31	0.117	K.HLTSTYSSDETKEDIK.L
R4/RRR4-2/3	1854.198	1854.950	-947.310	0.534	865.059	0.440	32	0.115	K.HLTSTYSSDETKEDIK.L
R4/RRR4-7/3	1854.700	1854.950	-135.245	0.479	769.062	0.453	32	0.114	K.HLTSTYSSDETKEDIK.L
R4/RRR4-16/3	1854.634	1854.950	-170.700	0.492	656.621	0.470	29	0.114	K.HLTSTYSSDETKEDIK.L
R4/RRR4-16/3	1854.664	1854.950	-154.656	0.505	640.171	0.471	29	0.114	K.HLTSTYSSDETKEDIK.L
R4/RRR4-8/3	1855.016	1854.950	35.858	0.484	726.262	0.457	30	0.114	K.HLTSTYSSDETKEDIK.L
R4/RRR4-1/3	1854.462	1854.950	-263.610	0.529	559.834	0.458	26	0.110	K.HLTSTYSSDETKEDIK.L
R4/RRR4-15/3	1855.022	1854.950	38.828	0.513	550.445	0.442	27	0.109	K.HLTSTYSSDETKEDIK.L
R4/RRR4-1/3	1854.638	1854.950	-168.521	0.444	403.391	0.330	24	0.102	K.HLTSTYSSDETKEDIK.L
R4/RRR4-2/3	1854.139	1854.950	-979.433	0.443	610.625	0.329	28	0.098	K.HLTSTYSSDETKEDIK.L
R4/RRR4-8/3	1983.234	1983.123	56.259	0.391	961.913	0.329	30	0.095	R.KHLTSTYSSDETKEDIK.L
R4/RRR4-8/3	1982.854	1983.123	-135.642	0.391	811.918	0.334	29	0.091	R.KHLTSTYSSDETKEDIK.L
R4/RRR4-8/3	1982.281	1983.123	-932.024	0.387	624.602	0.351	28	0.090	R.KHLTSTYSSDETKEDIK.L
R4/RRR4-11/2	1215.755	1216.373	-1334.848	0.475	1557.694	0.418	18	0.215	K.IRDSASQLIGR.T
R4/RRR4-12/2	1186.995	1187.368	-315.284	0.478	1591.476	0.384	18	0.211	K.VLEVKGEDAVK.M
R4/RRR4-12/2	1187.076	1187.368	-246.467	0.540	1419.151	0.446	17	0.207	K.VLEVKGEDAVK.M
R4/RRR4-12/2	1216.078	1216.373	-243.308	0.473	1459.383	0.364	18	0.194	K.IRDSASQLIGR.T
R4/RRR4-12/2	1215.652	1216.373	-1419.866	0.476	1375.266	0.402	17	0.194	K.IRDSASQLIGR.T
R4/RRR4-12/2	1297.276	1297.569	-226.380	0.417	1176.131	0.477	19	0.191	K.LIVTVLPSLGER.Y
R4/RRR4-11/2	1298.079	1297.569	-378.192	0.547	980.852	0.531	18	0.189	K.LIVTVLPSLGER.Y
R4/RRR4-11/2	1186.833	1187.368	-1297.536	0.418	1338.674	0.376	16	0.185	K.VLEVKGEDAVK.M
R4/RRR4-11/2	1216.170	1216.373	-167.583	0.466	1361.777	0.354	18	0.184	K.IRDSASQLIGR.T
R4/RRR4-12/2	1187.083	1187.368	-241.206	0.490	1139.968	0.420	16	0.179	K.VLEVKGEDAVK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1297.311	1297.569	-199.571	0.441	897.271	0.502	18	0.177	K.LIVTVLPSLGER.Y
R4/RRR4-12/2	1298.014	1297.569	343.855	0.493	808.672	0.511	17	0.175	K.LIVTVLPSLGER.Y
R4/RRR4-11/2	1215.961	1216.373	-339.290	0.498	1024.466	0.430	16	0.174	K.IRDSASQLIGR.T
R4/RRR4-12/2	1215.660	1216.373	-1413.411	0.439	1221.007	0.342	18	0.173	K.IRDSASQLIGR.T
R4/RRR4-11/2	1297.387	1297.569	-140.294	0.439	968.862	0.395	18	0.166	K.LIVTVLPSLGER.Y
R4/RRR4-11/2	1296.781	1297.569	-1382.587	0.437	906.581	0.412	16	0.163	K.LIVTVLPSLGER.Y
R4/RRR4-11/2	1294.285	1295.508	-1723.157	0.340	1162.290	0.305	16	0.161	K.LEFLQPSFSVK.D
R4/RRR4-11/2	1327.869	1328.495	-1228.415	0.305	930.549	0.337	16	0.150	R.YLSSALFEELR.A
R4/RRR4-12/2	1295.465	1295.508	-33.893	0.454	750.254	0.353	14	0.149	K.LEFLQPSFSVK.D
R4/RRR4-11/2	1296.115	1295.508	-304.043	0.441	757.110	0.301	14	0.144	K.LEFLQPSFSVK.D
R4/RRR4-11/2	1296.225	1295.508	-219.385	0.270	701.845	0.206	14	0.136	-.LEFLQPSFSVK.-
R4/RRR4-11/3	1618.760	1619.822	-1278.085	0.492	1243.767	0.368	31	0.121	K.DRPAISM*LEDAEKK.G
R4/RRR4-12/3	1619.308	1619.822	-938.086	0.521	604.643	0.346	25	0.093	K.DRPAISM*LEDAEKK.G
R4/RRR4-11/3	1618.731	1619.822	-1296.034	0.423	626.533	0.320	26	0.090	K.DRPAISM*LEDAEKK.G
R4/RRR4-2/2	1312.453	1312.597	-110.230	0.428	1776.177	0.399	19	0.235	R.LVLGSAMGLCYK.Q
R4/RRR4-2/2	1504.518	1504.648	-86.560	0.532	1653.779	0.360	20	0.210	R.M*LLENNPNESQAK.R
R4/RRR4-2/2	1721.435	1721.958	-887.222	0.377	1137.448	0.511	19	0.189	R.GPPALVFTFPQM*EDR.L
R4/RRR4-3/2	1394.452	1393.697	-176.010	0.388	556.082	0.537	19	0.162	R.ALATAPIIPVAVEK.G
R4/RRR4-2/2	1473.383	1473.606	-151.956	0.379	348.023	0.548	14	0.154	R.QQELAAYFTNCK.L
R4/RRR4-3/2	1189.936	1190.248	-262.647	0.371	897.097	0.272	17	0.148	K.GWSESASPNVR.G
R4/RRR4-2/2	1707.104	1705.958	85.305	0.417	540.299	0.403	16	0.146	R.GPPALVFTFPQMEDR.L
R4/RRR4-2/2	1189.811	1190.248	-367.945	0.383	798.881	0.262	16	0.144	K.GWSESASPNVR.G
R4/RRR4-2/2	1705.310	1705.958	-969.306	0.384	449.600	0.375	14	0.141	R.GPPALVFTFPQMEDR.L
R4/RRR4-3/2	1189.951	1190.248	-250.193	0.443	712.059	0.275	15	0.141	-.GWSESASPNVR.-
R4/RRR4-3/2	1705.683	1705.958	-162.270	0.334	328.353	0.374	12	0.138	R.GPPALVFTFPQMEDR.L
R4/RRR4-2/2	1313.670	1312.597	55.771	0.346	679.766	0.277	14	0.138	R.LVLGSAMGLCYK.Q
R4/RRR4-3/2	1393.188	1393.697	-1086.191	0.265	276.637	0.381	13	0.138	R.ALATAPIIPVAVEK.G
R4/RRR4-2/2	1189.347	1190.248	-1603.112	0.273	773.870	0.176	16	0.136	K.GWSESASPNVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1123.004	1122.296	-261.075	0.487	1560.332	0.495	17	0.233	K.ALIAAEYSGVK.V
R4/RRR4-8/2	1122.930	1122.296	-326.620	0.392	1651.434	0.420	17	0.224	K.ALIAAEYSGVK.V
R4/RRR4-8/2	1337.353	1336.434	-60.846	0.536	1228.695	0.560	17	0.215	K.SFTSEFPHVER.Y
R4/RRR4-8/2	1122.091	1122.296	-183.161	0.431	1538.746	0.424	16	0.212	K.ALIAAEYSGVK.V
R4/RRR4-8/2	1886.823	1887.209	-205.353	0.332	1442.479	0.387	22	0.189	R.LGIAPYVAVSEEAAIAALK.R
R4/RRR4-8/2	1218.279	1218.490	-173.725	0.379	1247.877	0.412	16	0.183	K.MLVIGSEPPFK.V
R4/RRR4-8/2	1336.028	1336.434	-305.133	0.478	960.565	0.493	16	0.180	K.SFTSEFPHVER.Y
R4/RRR4-8/2	1336.138	1336.434	-222.453	0.459	933.661	0.480	16	0.176	K.SFTSEFPHVER.Y
R4/RRR4-8/2	1094.070	1094.286	-198.148	0.375	749.046	0.539	15	0.172	K.NPLDLLPPSK.M
R4/RRR4-8/2	1093.859	1094.286	-391.378	0.325	628.214	0.490	14	0.159	K.NPLDLLPPSK.M
R4/RRR4-8/2	1218.130	1218.490	-296.772	0.330	1148.232	0.291	15	0.158	-.MLVIGSEPPFK.-
R4/RRR4-8/2	1093.520	1094.286	-1619.761	0.300	615.961	0.433	13	0.151	K.NPLDLLPPSK.M
R4/RRR4-9/2	776.508	776.906	-514.277	0.475	922.532	0.225	11	0.143	K.VGGFLQR.M
R4/RRR4-9/2	776.816	776.906	-116.415	0.418	897.562	0.215	11	0.142	K.VGGFLQR.M
R4/RRR4-8/2	1094.397	1094.286	101.962	0.241	530.950	0.340	12	0.141	K.NPLDLLPPSK.M
R4/RRR4-9/2	1094.934	1094.286	-322.112	0.200	556.432	0.344	13	0.139	K.NPLDLLPPSK.M
R4/RRR4-8/2	776.376	776.906	-1977.214	0.436	840.006	0.238	11	0.138	-.VGGFLQR.-
R4/RRR4-7/2	1385.277	1385.595	-230.206	0.522	1515.960	0.517	20	0.231	K.SQGATILTGGVRPK.H
R4/RRR4-7/2	1462.234	1462.626	-269.167	0.496	1402.359	0.561	20	0.231	K.SPIVVFDDVDVEK.A
R4/RRR4-7/2	1462.416	1462.626	-143.886	0.510	1421.102	0.551	20	0.231	K.SPIVVFDDVDVEK.A
R4/RRR4-7/2	1306.032	1306.446	-317.859	0.463	1280.901	0.567	19	0.219	R.LGPVVSEGQYEK.I
R4/RRR4-7/2	1306.012	1306.446	-333.239	0.484	1293.120	0.549	19	0.217	R.LGPVVSEGQYEK.I
R4/RRR4-7/2	1385.325	1385.595	-195.465	0.503	1357.874	0.503	19	0.211	K.SQGATILTGGVRPK.H
R4/RRR4-6/2	1307.398	1306.446	-36.861	0.459	1156.314	0.573	18	0.208	R.LGPVVSEGQYEK.I
R4/RRR4-7/2	1494.042	1494.628	-1064.988	0.409	1577.809	0.374	20	0.205	R.ELGEGGIDNYLSVK.Q
R4/RRR4-7/2	1305.544	1306.446	-1461.086	0.403	1234.994	0.521	19	0.203	R.LGPVVSEGQYEK.I
R4/RRR4-7/2	1494.326	1494.628	-202.755	0.459	1130.784	0.473	18	0.184	R.ELGEGGIDNYLSVK.Q
R4/RRR4-7/2	1162.259	1162.226	28.379	0.427	1215.638	0.361	16	0.175	K.VSDPLEEGCR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1162.992	1162.226	-201.775	0.433	916.503	0.379	16	0.162	K.VSDPLEEGCR.L
R4/RRR4-7/2	1858.230	1859.971	-2019.466	0.294	1092.220	0.368	17	0.158	K.QVTEYASDEPWGWYK.S
R4/RRR4-7/2	1161.840	1162.226	-332.754	0.408	831.181	0.372	15	0.157	K.VSDPLEEGCR.L
R4/RRR4-7/2	1161.125	1162.226	-1814.376	0.258	742.558	0.263	14	0.140	K.VSDPLEEGCR.L
R4/RRR4-10/3	1492.170	1491.714	306.736	0.562	3251.059	0.376	30	0.559	K.KVSPEVIAEYTVR.T
R4/RRR4-10/3	1492.750	1491.714	24.465	0.578	2685.277	0.419	28	0.409	K.KVSPEVIAEYTVR.T
R4/RRR4-16/3	1491.553	1491.714	-107.962	0.537	2547.852	0.426	27	0.377	K.KVSPEVIAEYTVR.T
R4/RRR4-11/3	1491.761	1491.714	31.540	0.559	2565.612	0.385	27	0.357	K.KVSPEVIAEYTVR.T
R4/RRR4-11/3	1492.881	1491.714	112.054	0.568	2453.183	0.421	27	0.348	K.KVSPEVIAEYTVR.T
R4/RRR4-11/3	1490.800	1491.714	-1287.745	0.505	2251.605	0.382	27	0.280	K.KVSPEVIAEYTVR.T
R4/RRR4-10/2	1491.399	1491.714	-211.855	0.581	1717.098	0.577	21	0.275	K.KVSPEVIAEYTVR.T
R4/RRR4-10/2	1569.296	1569.698	-257.436	0.534	1817.719	0.521	24	0.271	K.GDAVLGEGASESLHVK.D
R4/RRR4-10/2	1492.289	1491.714	-285.488	0.546	1724.372	0.562	21	0.271	K.KVSPEVIAEYTVR.T
R4/RRR4-11/2	1492.292	1491.714	-283.437	0.560	1745.744	0.538	21	0.267	K.KVSPEVIAEYTVR.T
R4/RRR4-10/2	1569.187	1569.698	-966.237	0.519	1750.396	0.507	24	0.258	K.GDAVLGEGASESLHVK.D
R4/RRR4-11/2	1491.239	1491.714	-319.106	0.591	1545.451	0.561	20	0.247	K.KVSPEVIAEYTVR.T
R4/RRR4-10/2	1569.278	1569.698	-268.986	0.501	1661.092	0.482	23	0.240	K.GDAVLGEGASESLHVK.D
R4/RRR4-11/2	1490.660	1491.714	-1381.738	0.458	1528.149	0.451	20	0.218	K.KVSPEVIAEYTVR.T
R4/RRR4-10/2	1492.311	1491.714	-270.634	0.556	1278.539	0.551	19	0.216	K.KVSPEVIAEYTVR.T
R4/RRR4-12/3	1491.900	1491.714	125.463	0.428	1975.711	0.343	28	0.206	K.KVSPEVIAEYTVR.T
R4/RRR4-10/2	1364.076	1363.541	-342.122	0.503	778.715	0.496	18	0.173	K.VSPEVIAEYTVR.T
R4/RRR4-10/2	1363.160	1363.541	-280.108	0.460	754.898	0.496	18	0.171	K.VSPEVIAEYTVR.T
R4/RRR4-10/3	1312.578	1312.501	58.979	0.528	1535.808	0.420	24	0.169	K.KPWSLSFSFGR.A
R4/RRR4-10/2	1155.940	1155.240	-260.097	0.471	418.447	0.549	15	0.164	K.ANSEATLGTYK.G
R4/RRR4-10/2	1312.293	1312.501	-158.853	0.394	732.473	0.436	18	0.162	K.KPWSLSFSFGR.A
R4/RRR4-10/2	1363.101	1363.541	-324.133	0.477	742.330	0.431	17	0.161	K.VSPEVIAEYTVR.T
R4/RRR4-11/2	1362.578	1363.541	-1444.768	0.278	824.547	0.388	18	0.153	K.VSPEVIAEYTVR.T
R4/RRR4-10/2	1312.514	1312.501	10.111	0.356	626.066	0.357	15	0.148	K.KPWSLSFSFGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1363.135	1363.541	-298.526	0.276	746.998	0.308	17	0.144	K.VSPEVIAEYTVR.T
R4/RRR4-10/2	1311.644	1312.501	-1419.941	0.237	637.096	0.341	17	0.143	K.KPWSLSFSFGR.A
R4/RRR4-11/2	1311.864	1312.501	-1251.522	0.226	445.810	0.421	14	0.143	K.KPWSLSFSFGR.A
R4/RRR4-10/3	1312.063	1312.501	-334.325	0.477	1334.832	0.410	22	0.142	K.KPWSLSFSFGR.A
R4/RRR4-10/3	1312.610	1312.501	83.742	0.459	1378.369	0.337	22	0.126	K.KPWSLSFSFGR.A
R4/RRR4-9/2	1254.866	1255.316	-360.188	0.395	1548.431	0.465	17	0.222	K.SIESSDLNFSR.Y
R4/RRR4-9/2	1254.525	1255.316	-1432.280	0.416	1502.446	0.430	17	0.211	K.SIESSDLNFSR.Y
R4/RRR4-9/2	1688.762	1688.818	-33.612	0.470	1460.482	0.391	19	0.198	K.FLQSLEFFEENER.K
R4/RRR4-9/2	1255.100	1255.316	-172.530	0.438	1370.421	0.410	17	0.195	K.SIESSDLNFSR.Y
R4/RRR4-9/2	1639.511	1639.960	-274.266	0.401	667.754	0.506	20	0.163	K.LSGLPPETVFQPLLK.D
R4/RRR4-10/2	1559.046	1557.749	190.499	0.446	947.220	0.360	16	0.154	K.M*EDNLLEFFPSAK.R
R4/RRR4-9/2	1639.486	1639.960	-290.027	0.408	554.299	0.446	19	0.154	K.LSGLPPETVFQPLLK.D
R4/RRR4-9/2	1639.683	1639.960	-169.026	0.423	497.924	0.462	18	0.154	K.LSGLPPETVFQPLLK.D
R4/RRR4-10/2	1558.474	1557.749	-177.572	0.461	983.477	0.337	16	0.152	K.M*EDNLLEFFPSAK.R
R4/RRR4-9/2	975.133	975.123	9.905	0.462	769.040	0.289	13	0.146	-.FPDIEVVR.-
R4/RRR4-10/2	974.616	975.123	-1551.111	0.395	836.088	0.229	13	0.142	-.FPDIEVVR.-
R4/RRR4-9/2	975.110	975.123	-13.072	0.384	682.233	0.263	13	0.135	-.FPDIEVVR.-
R4/RRR4-9/2	975.103	975.123	-20.355	0.416	786.557	0.213	13	0.135	-.FPDIEVVR.-
R4/RRR4-9/3	1406.429	1406.526	-69.271	0.500	1330.658	0.365	24	0.131	K.RTSEALSEHFTK.E
R4/RRR4-10/2	1172.996	1173.385	-332.512	0.490	1521.096	0.549	20	0.242	K.VIAISDVTGAVK.N
R4/RRR4-10/2	1173.784	1173.385	341.445	0.524	1336.870	0.550	20	0.224	K.VIAISDVTGAVK.N
R4/RRR4-10/2	1556.786	1556.788	-0.992	0.471	1504.194	0.490	20	0.222	R.GVLFATEALLAEHGK.G
R4/RRR4-10/2	1173.098	1173.385	-245.125	0.480	1316.629	0.514	20	0.213	K.VIAISDVTGAVK.N
R4/RRR4-10/2	1081.430	1082.259	-1696.319	0.432	1485.054	0.437	17	0.212	R.M*GAFTLGVNR.V
R4/RRR4-10/2	1162.127	1162.320	-166.842	0.500	1289.383	0.499	19	0.207	K.TAVANIPYGGAK.G
R4/RRR4-10/2	1747.264	1747.879	-927.112	0.503	1467.417	0.438	23	0.206	K.GGIGCSPGDLSISELER.L
R4/RRR4-10/2	1081.885	1082.259	-346.850	0.449	1298.743	0.448	17	0.198	R.M*GAFTLGVNR.V
R4/RRR4-10/2	1556.503	1556.788	-183.486	0.471	1309.553	0.467	19	0.197	R.GVLFATEALLAEHGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1747.344	1747.879	-880.823	0.514	1260.452	0.419	23	0.184	K.GGIGCSPGDLSISELER.L
R4/RRR4-10/2	1161.925	1162.320	-341.370	0.470	1199.666	0.420	18	0.183	K.TAVANIPYGGAK.G
R4/RRR4-10/2	1301.304	1301.387	-63.378	0.438	1241.021	0.399	18	0.182	K.DDGTLASYVGFR.V
R4/RRR4-10/2	1161.869	1162.320	-389.334	0.413	1191.932	0.370	18	0.173	K.TAVANIPYGGAK.G
R4/RRR4-10/2	1301.086	1301.387	-231.834	0.389	752.264	0.474	14	0.160	K.DDGTLASYVGFR.V
R4/RRR4-10/2	1301.126	1301.387	-200.774	0.385	877.125	0.396	15	0.157	K.DDGTLASYVGFR.V
R4/RRR4-4/2	1610.682	1610.835	-95.218	0.511	3225.790	0.560	23	0.580	R.NGILEAYSGILQGFK.S
R4/RRR4-4/2	1610.484	1610.835	-218.807	0.523	2901.331	0.568	23	0.499	R.NGILEAYSGILQGFK.S
R4/RRR4-4/2	1338.016	1337.452	-326.641	0.550	1751.825	0.515	19	0.262	R.VVCEATQSTDVK.I
R4/RRR4-4/2	1336.972	1337.452	-360.322	0.477	1777.284	0.456	19	0.249	R.VVCEATQSTDVK.I
R4/RRR4-4/2	1513.331	1513.764	-286.859	0.460	1427.277	0.591	21	0.237	K.GLLLQTLSSPVASAR.S
R4/RRR4-4/2	1366.309	1366.502	-141.192	0.478	1549.248	0.425	17	0.214	R.TAAYETLNEVVR.C
R4/RRR4-4/2	1336.557	1337.452	-1422.513	0.416	1530.563	0.405	19	0.208	R.VVCEATQSTDVK.I
R4/RRR4-4/2	1513.326	1513.764	-290.258	0.397	1329.261	0.453	21	0.196	K.GLLLQTLSSPVASAR.S
R4/RRR4-4/2	1513.450	1513.764	-208.526	0.406	1210.891	0.447	21	0.186	K.GLLLQTLSSPVASAR.S
R4/RRR4-4/2	1365.441	1366.502	-1513.383	0.371	1166.739	0.409	17	0.176	R.TAAYETLNEVVR.C
R4/RRR4-4/2	1020.961	1021.109	-144.700	0.432	954.015	0.360	15	0.162	K.DTTAWTLGR.I
R4/RRR4-4/2	954.842	955.133	-305.579	0.351	761.227	0.340	13	0.147	-.VAGIEIPQK.-
R4/RRR4-4/2	1365.466	1366.502	-1495.692	0.333	1091.376	0.205	17	0.144	R.TAAYETLNEVVR.C
R4/RRR4-4/2	1020.728	1021.109	-374.438	0.305	627.464	0.207	14	0.138	K.DTTAWTLGR.I
R4/RRR4-24/2	1369.908	1369.592	231.697	0.508	1665.305	0.525	19	0.253	R.LVVIVDVVDQNR.A
R4/RRR4-23/2	1368.591	1369.592	-1466.064	0.452	1791.090	0.379	18	0.231	R.LVVIVDVVDQNR.A
R4/RRR4-23/2	1355.163	1355.524	-267.124	0.416	1159.545	0.546	17	0.200	R.VALVNYGKDYGR.L
R4/RRR4-23/2	1356.292	1355.524	-171.213	0.471	1221.035	0.500	17	0.199	R.VALVNYGKDYGR.L
R4/RRR4-24/2	1369.132	1369.592	-336.834	0.369	1167.116	0.457	17	0.184	R.LVVIVDVVDQNR.A
R4/RRR4-23/2	863.965	864.024	-68.251	0.420	616.688	0.495	13	0.167	R.VALVNYGK.D
R4/RRR4-23/2	863.904	864.024	-139.402	0.356	594.004	0.500	12	0.162	R.VALVNYGK.D
R4/RRR4-24/2	863.380	864.024	-1909.709	0.314	510.715	0.496	12	0.157	R.VALVNYGK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1356.485	1355.524	-28.487	0.406	785.133	0.420	14	0.155	R.VALVNYGKDYGR.L
R4/RRR4-23/2	863.519	864.024	-1748.474	0.321	434.920	0.484	11	0.155	R.VALVNYGK.D
R4/RRR4-23/2	1102.857	1103.275	-379.989	0.403	722.838	0.384	14	0.154	R.ALVDAPDM*VR.C
R4/RRR4-23/2	1086.891	1087.275	-354.573	0.324	874.211	0.359	14	0.154	R.ALVDAPDMVR.C
R4/RRR4-24/2	863.547	864.024	-553.608	0.293	624.873	0.432	13	0.154	R.VALVNYGK.D
R4/RRR4-24/2	1102.784	1103.275	-446.185	0.383	878.805	0.341	14	0.154	R.ALVDAPDM*VR.C
R4/RRR4-24/2	864.125	864.024	117.373	0.332	513.110	0.419	12	0.153	R.VALVNYGK.D
R4/RRR4-23/2	1087.027	1087.275	-228.716	0.371	832.173	0.354	14	0.153	R.ALVDAPDMVR.C
R4/RRR4-23/2	1259.108	1259.517	-326.010	0.470	771.672	0.341	17	0.152	R.LSLTDIKIDIK.R
R4/RRR4-23/2	1259.265	1259.517	-201.323	0.487	856.405	0.296	18	0.150	R.LSLTDIKIDIK.R
R4/RRR4-23/2	1102.679	1103.275	-1451.543	0.365	724.216	0.343	14	0.150	R.ALVDAPDM*VR.C
R4/RRR4-24/2	863.556	864.024	-543.536	0.291	547.219	0.381	12	0.149	R.VALVNYGK.D
R4/RRR4-23/2	1258.665	1259.517	-1475.817	0.438	916.431	0.266	18	0.148	R.LSLTDIKIDIK.R
R4/RRR4-23/2	1369.907	1369.592	230.982	0.351	414.796	0.333	14	0.144	R.LVVIVDVVDQNR.A
R4/RRR4-23/3	1369.809	1369.592	158.857	0.439	1482.418	0.361	24	0.144	R.LVVIVDVVDQNR.A
R4/RRR4-24/2	1369.260	1369.592	-243.003	0.258	622.924	0.272	14	0.138	R.LVVIVDVVDQNR.A
R4/RRR4-23/2	1369.128	1369.592	-340.144	0.219	444.444	0.310	12	0.137	R.LVVIVDVVDQNR.A
R4/RRR4-23/3	1369.782	1369.592	139.151	0.508	1254.915	0.414	24	0.135	R.LVVIVDVVDQNR.A
R4/RRR4-23/3	1369.771	1369.592	130.840	0.318	815.900	0.345	19	0.090	-.LVVIVDVVDQNR.-
R4/RRR4-24/1	445.046	445.449	-908.207	-2.446	2.172	0.000	2	0.836	R.GGGASP.-
R4/RRR4-12/1	445.035	445.449	-932.439	-2.321	2.330	0.000	2	0.810	R.GGGASP.-
R4/RRR4-3/1	445.042	445.449	-917.294	-1.730	7.940	0.000	3	0.793	R.GGGASP.-
R4/RRR4-27/1	445.030	445.449	-944.693	-1.214	6.667	0.000	3	0.766	R.GGGASP.-
R4/RRR4-19/1	445.047	445.449	-906.141	-1.822	2.279	0.000	2	0.738	R.GGGASP.-
R4/RRR4-19/1	445.026	445.449	-953.781	-1.222	7.010	0.296	3	0.724	R.GGGASP.-
R4/RRR4-4/1	445.007	445.449	-995.365	-1.498	2.032	0.000	2	0.714	R.GGGASP.-
R4/RRR4-22/1	445.030	445.449	-944.005	-0.976	2.959	0.000	2	0.712	R.GGGASP.-
R4/RRR4-3/1	445.020	445.449	-966.862	-1.407	1.899	0.000	2	0.710	R.GGGASP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/1	445.043	445.449	-914.265	-1.169	2.645	0.000	2	0.707	R.GGGASP.-
R4/RRR4-10/1	445.039	445.449	-924.728	-1.307	3.176	0.000	2	0.707	R.GGGASP.-
R4/RRR4-14/1	445.038	445.449	-925.004	-0.690	5.622	0.913	3	0.614	R.GGGASP.-
R4/RRR4-12/2	1841.475	1840.028	243.506	0.594	4119.923	0.584	29	0.875	R.AFIAGVADDNGYGWAIAK.A
R4/RRR4-12/2	1839.452	1840.028	-859.282	0.571	3834.638	0.557	29	0.761	R.AFIAGVADDNGYGWAIAK.A
R4/RRR4-12/2	1839.626	1840.028	-219.406	0.557	3405.503	0.511	28	0.605	R.AFIAGVADDNGYGWAIAK.A
R4/RRR4-12/2	1839.211	1840.028	-990.937	0.543	3181.829	0.521	27	0.548	R.AFIAGVADDNGYGWAIAK.A
R4/RRR4-12/2	1558.219	1556.808	264.749	0.531	892.823	0.494	18	0.175	K.MIEYSYVNAPLQK.E
R4/RRR4-12/3	1441.649	1441.661	-8.851	0.477	1703.754	0.364	28	0.175	K.IRVNTISAGPLGSR.A
R4/RRR4-12/3	1441.580	1441.661	-56.371	0.462	1721.047	0.338	27	0.169	K.IRVNTISAGPLGSR.A
R4/RRR4-12/2	1172.163	1172.317	-131.571	0.461	522.198	0.523	16	0.164	R.VNTISAGPLGSR.A
R4/RRR4-12/2	1172.034	1172.317	-241.691	0.482	641.888	0.467	16	0.161	R.VNTISAGPLGSR.A
R4/RRR4-12/2	1112.982	1113.205	-200.391	0.418	661.638	0.397	16	0.156	R.YAGSSNWTVK.E
R4/RRR4-12/2	1112.370	1113.205	-1654.171	0.367	734.161	0.365	16	0.153	R.YAGSSNWTVK.E
R4/RRR4-12/2	1112.504	1113.205	-1533.022	0.376	500.831	0.413	14	0.152	R.YAGSSNWTVK.E
R4/RRR4-12/2	1171.692	1172.317	-1390.585	0.444	539.991	0.378	17	0.151	R.VNTISAGPLGSR.A
R4/RRR4-12/2	1441.438	1441.661	-155.153	0.394	679.751	0.371	16	0.146	K.IRVNTISAGPLGSR.A
R4/RRR4-12/2	1441.249	1441.661	-286.679	0.305	414.729	0.372	16	0.141	K.IRVNTISAGPLGSR.A
R4/RRR4-12/3	1441.385	1441.661	-192.076	0.400	969.421	0.273	23	0.087	K.IRVNTISAGPLGSR.A
R4/RRR4-6/2	1514.254	1514.615	-238.655	0.433	1611.763	0.491	20	0.236	K.EIAQGYCDSFAPR.D
R4/RRR4-6/2	1221.936	1221.346	-336.729	0.443	1376.961	0.453	17	0.205	R.HFEVDLSAFR.N
R4/RRR4-6/2	1210.953	1211.348	-327.751	0.373	1300.301	0.397	16	0.186	K.GEFVEYIPTR.E
R4/RRR4-6/2	1210.970	1211.348	-313.693	0.409	1207.606	0.425	16	0.185	K.GEFVEYIPTR.E
R4/RRR4-6/2	1338.380	1339.521	-1604.818	0.400	1111.360	0.406	16	0.173	K.KGEFVEYIPTR.E
R4/RRR4-6/2	1222.202	1221.346	-118.470	0.370	957.184	0.463	15	0.172	R.HFEVDLSAFR.N
R4/RRR4-4/2	1221.907	1221.346	-360.284	0.395	941.733	0.445	13	0.168	R.HFEVDLSAFR.N
R4/RRR4-6/2	1373.089	1373.604	-1106.845	0.411	742.964	0.437	19	0.162	K.VEPLVNM*GQITR.A
R4/RRR4-2/2	1340.747	1339.521	168.794	0.497	347.454	0.498	15	0.161	K.KGEFVEYIPTR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1373.243	1373.604	-263.636	0.403	607.758	0.444	18	0.158	K.VEPLVNM*GQITR.A
R4/RRR4-6/2	1373.873	1373.604	196.154	0.433	515.577	0.449	17	0.157	K.VEPLVNM*GQITR.A
R4/RRR4-6/2	1211.103	1211.348	-203.364	0.321	1005.902	0.332	14	0.155	K.GEFVEYIPTR.E
R4/RRR4-6/2	1339.176	1339.521	-258.519	0.328	801.523	0.352	14	0.149	K.KGEFVEYIPTR.E
R4/RRR4-6/2	1217.913	1218.535	-1336.381	0.398	796.023	0.301	13	0.143	-.FLLGWLM*PPK.-
R4/RRR4-7/2	1525.188	1525.555	-241.199	0.465	1436.460	0.549	23	0.231	K.YVSGSYDSGEGFEK.L
R4/RRR4-7/2	1348.011	1347.502	-365.091	0.454	1229.969	0.511	16	0.201	R.DNIDNIQIVFR.E
R4/RRR4-7/2	1197.366	1197.453	-72.357	0.413	1433.639	0.335	16	0.186	K.ELVQNLLVLR.F
R4/RRR4-7/2	1289.328	1289.421	-71.944	0.393	1525.598	0.279	15	0.180	R.GGYFDQYGIIR.D
R4/RRR4-7/2	1197.325	1197.453	-106.922	0.471	1513.654	0.257	16	0.177	K.ELVQNLLVLR.F
R4/RRR4-7/2	1196.612	1197.453	-1542.321	0.326	1337.502	0.234	15	0.161	K.ELVQNLLVLR.F
R4/RRR4-1/2	1197.667	1197.453	179.759	0.398	458.561	0.283	12	0.141	K.ELVQNLLVLR.F
R4/RRR4-7/2	1347.312	1347.502	-141.456	0.287	485.243	0.382	11	0.139	R.DNIDNIQIVFR.E
R4/RRR4-7/3	1954.963	1955.202	-122.609	0.323	821.143	0.450	25	0.107	K.AAWQIFTPLLHDIDEGK.V
R4/RRR4-7/3	1254.575	1253.383	153.540	0.503	979.575	0.365	21	0.105	K.LNKEISEYEK.S
R4/RRR4-7/3	1954.568	1955.202	-838.372	0.261	815.538	0.257	25	0.078	K.AAWQIFTPLLHDIDEGK.V
R4/RRR4-7/2	1319.068	1319.487	-318.524	0.350	1570.159	0.419	20	0.213	R.SVTVTNDGATILK.S
R4/RRR4-7/2	1512.540	1512.775	-156.116	0.348	1588.735	0.403	20	0.210	R.SDLMNIAMTTLSSK.I
R4/RRR4-7/2	1319.782	1319.487	224.633	0.421	1332.313	0.450	19	0.198	R.SVTVTNDGATILK.S
R4/RRR4-7/2	1319.122	1319.487	-277.393	0.371	1239.832	0.380	19	0.177	R.SVTVTNDGATILK.S
R4/RRR4-7/3	1489.361	1488.625	-178.203	0.446	1109.180	0.531	22	0.155	R.VLKDDAVEEKGER.A
R4/RRR4-7/3	1313.049	1313.356	-234.441	0.481	916.694	0.429	24	0.113	R.GASEHVLDEAER.S
R4/RRR4-7/3	1399.551	1400.604	-1471.522	0.472	884.652	0.430	21	0.111	K.IIGHGINCFVNR.Q
R4/RRR4-7/3	1132.557	1132.254	268.188	0.445	1103.634	0.354	21	0.109	K.KSHAIDAFSR.A
R4/RRR4-7/3	1400.783	1400.604	127.768	0.540	697.254	0.466	20	0.106	-.IIGHGINCFVNR.-
R4/RRR4-7/3	1400.629	1400.604	17.639	0.477	854.326	0.391	22	0.103	K.IIGHGINCFVNR.Q
R4/RRR4-7/3	1312.931	1313.356	-324.266	0.437	608.315	0.339	20	0.090	R.GASEHVLDEAER.S
R4/RRR4-7/3	1313.196	1313.356	-122.112	0.441	464.716	0.387	19	0.080	-.GASEHVLDEAER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1513.744	1514.706	-1300.167	0.517	1654.485	0.447	22	0.232	R.KLAEDNNVPLSSVK.G
R4/RRR4-9/2	1514.373	1514.706	-220.203	0.567	1458.034	0.536	20	0.230	R.KLAEDNNVPLSSVK.G
R4/RRR4-9/2	1514.255	1514.706	-298.812	0.546	1499.791	0.508	21	0.229	R.KLAEDNNVPLSSVK.G
R4/RRR4-9/2	1232.861	1233.438	-1283.256	0.472	1601.410	0.445	20	0.226	R.VIDGAIGAEFLK.A
R4/RRR4-9/2	1987.457	1987.203	128.531	0.527	1172.500	0.535	23	0.198	K.EALAAPGLSYTDVPNAQIR.K
R4/RRR4-9/2	1233.144	1233.438	-239.146	0.497	1256.879	0.470	18	0.197	R.VIDGAIGAEFLK.A
R4/RRR4-9/2	1986.506	1987.203	-856.690	0.458	1152.631	0.495	23	0.188	K.EALAAPGLSYTDVPNAQIR.K
R4/RRR4-8/2	1015.177	1015.229	-51.150	0.447	1116.560	0.328	15	0.165	K.ISINDLVIK.A
R4/RRR4-9/2	1143.198	1143.402	-178.708	0.387	753.574	0.398	14	0.155	K.KISINDLVIK.A
R4/RRR4-9/2	1014.610	1015.229	-1599.781	0.449	900.089	0.309	15	0.154	K.ISINDLVIK.A
R4/RRR4-9/2	1143.086	1143.402	-277.053	0.401	835.744	0.350	14	0.152	K.KISINDLVIK.A
R4/RRR4-9/2	1015.259	1015.229	30.015	0.437	888.327	0.259	15	0.147	K.ISINDLVIK.A
R4/RRR4-9/2	1014.963	1015.229	-262.145	0.454	771.494	0.239	14	0.142	K.ISINDLVIK.A
R4/RRR4-9/3	1713.381	1713.917	-899.113	0.429	1135.105	0.372	29	0.114	K.LRGELNPLQESSGGKK.I
R4/RRR4-9/3	1143.564	1143.402	142.053	0.497	1383.599	0.256	22	0.106	K.KISINDLVIK.A
R4/RRR4-9/3	1143.311	1143.402	-79.912	0.408	763.469	0.167	18	0.061	-.KISINDLVIK.-
R4/RRR4-9/3	1143.213	1143.402	-165.705	0.375	633.608	0.208	18	0.057	-.KISINDLVIK.-
R4/RRR4-8/2	1705.691	1705.914	-131.188	0.548	1758.300	0.536	21	0.265	R.DNGMHALIIYDDLSK.Q
R4/RRR4-8/2	1312.294	1312.580	-218.751	0.409	1509.189	0.346	18	0.194	K.AILSTINPELLK.S
R4/RRR4-8/2	1704.495	1705.914	-1423.242	0.455	1195.431	0.494	18	0.191	R.DNGMHALIIYDDLSK.Q
R4/RRR4-8/2	1721.285	1721.913	-948.739	0.521	1097.380	0.505	22	0.191	R.DNGM*HALIIYDDLSK.Q
R4/RRR4-8/3	1439.341	1439.689	-242.367	0.446	1921.973	0.293	29	0.179	R.GIRPAINVGLSVSR.V
R4/RRR4-8/3	1439.832	1439.689	100.068	0.484	1826.659	0.309	29	0.170	R.GIRPAINVGLSVSR.V
R4/RRR4-7/2	1312.247	1312.580	-254.494	0.332	1403.883	0.262	17	0.170	K.AILSTINPELLK.S
R4/RRR4-8/2	1301.130	1301.514	-296.096	0.362	1291.091	0.300	18	0.169	K.TAIAIDTILNQK.Q
R4/RRR4-7/2	1312.405	1312.580	-134.304	0.356	1324.848	0.263	17	0.165	K.AILSTINPELLK.S
R4/RRR4-8/2	1721.093	1721.913	-1060.960	0.468	579.107	0.516	19	0.164	R.DNGM*HALIIYDDLSK.Q
R4/RRR4-16/2	1301.417	1301.514	-74.756	0.383	1155.081	0.328	15	0.162	K.TAIAIDTILNQK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1439.420	1439.689	-187.353	0.489	613.570	0.493	18	0.162	R.GIRPAINVGLSVSR.V
R4/RRR4-8/2	1312.070	1312.580	-1154.931	0.404	1122.011	0.314	16	0.159	K.AILSTINPELLK.S
R4/RRR4-8/2	1438.939	1439.689	-1219.875	0.427	663.196	0.467	18	0.159	R.GIRPAINVGLSVSR.V
R4/RRR4-8/2	1721.047	1721.913	-1087.595	0.462	586.032	0.443	19	0.156	R.DNGM*HALIIYDDLSK.Q
R4/RRR4-8/2	1312.187	1312.580	-300.879	0.337	1092.333	0.296	16	0.155	K.AILSTINPELLK.S
R4/RRR4-8/2	1077.105	1077.298	-180.580	0.506	928.039	0.298	14	0.151	R.KIELDAFLK.Q
R4/RRR4-8/2	1438.893	1439.689	-1251.482	0.396	453.542	0.453	16	0.151	R.GIRPAINVGLSVSR.V
R4/RRR4-8/2	1076.628	1077.298	-1556.016	0.449	886.082	0.282	14	0.149	R.KIELDAFLK.Q
R4/RRR4-7/2	1311.747	1312.580	-1401.628	0.285	970.221	0.267	16	0.147	K.AILSTINPELLK.S
R4/RRR4-8/2	1077.137	1077.298	-150.112	0.453	764.699	0.281	13	0.145	R.KIELDAFLK.Q
R4/RRR4-7/2	1302.260	1301.514	-195.710	0.352	675.817	0.300	15	0.144	K.TAIAIDTILNQK.Q
R4/RRR4-17/2	1302.476	1301.514	-29.292	0.317	835.377	0.172	16	0.137	K.TAIAIDTILNQK.Q
R4/RRR4-1/2	1300.924	1301.514	-1226.282	0.335	643.980	0.240	14	0.136	-.TAIAIDTILNQK.-
R4/RRR4-7/2	1301.740	1301.514	173.570	0.339	929.319	0.155	16	0.136	K.TAIAIDTILNQK.Q
R4/RRR4-17/2	1302.773	1301.514	198.808	0.403	984.067	0.148	17	0.135	K.TAIAIDTILNQK.Q
R4/RRR4-6/2	1312.361	1312.580	-167.335	0.271	580.319	0.191	12	0.133	K.AILSTINPELLK.S
R4/RRR4-1/2	1301.189	1301.514	-251.199	0.381	666.235	0.202	13	0.133	-.TAIAIDTILNQK.-
R4/RRR4-8/2	1704.264	1705.914	-2148.171	0.287	896.716	0.123	17	0.130	R.DNGMHALIIYDDLSK.Q
R4/RRR4-2/2	1301.241	1301.514	-210.918	0.321	658.374	0.080	13	0.129	-.TAIAIDTILNQK.-
R4/RRR4-7/3	1439.773	1439.689	58.998	0.431	1385.637	0.293	25	0.117	R.GIRPAINVGLSVSR.V
R4/RRR4-8/3	1077.527	1077.298	212.685	0.494	1343.213	0.313	23	0.115	R.KIELDAFLK.Q
R4/RRR4-8/3	1077.302	1077.298	3.044	0.486	1227.388	0.318	22	0.108	R.KIELDAFLK.Q
R4/RRR4-8/3	1354.728	1355.589	-1377.685	0.427	1067.663	0.352	25	0.105	R.KSVHEPMQTGLK.A
R4/RRR4-7/3	1439.521	1439.689	-116.797	0.449	1287.989	0.261	24	0.102	R.GIRPAINVGLSVSR.V
R4/RRR4-1/3	1440.177	1439.689	339.913	0.391	1423.245	0.209	24	0.101	R.GIRPAINVGLSVSR.V
R4/RRR4-8/3	1077.088	1077.298	-195.771	0.442	1109.948	0.300	21	0.098	R.KIELDAFLK.Q
R4/RRR4-8/3	1438.900	1439.689	-1246.848	0.409	1209.255	0.242	25	0.094	R.GIRPAINVGLSVSR.V
R4/RRR4-7/3	1439.806	1439.689	81.957	0.428	1175.399	0.225	22	0.089	R.GIRPAINVGLSVSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/3	1356.028	1355.589	324.620	0.425	707.653	0.297	22	0.087	R.KSVHEPMQTGLK.A
R4/RRR4-8/3	1355.539	1355.589	-36.601	0.368	798.379	0.260	22	0.081	-.KSVHEPMQTGLK.-
R4/RRR4-14/2	1797.643	1798.032	-217.243	0.612	2771.988	0.588	26	0.473	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1798.608	1798.032	-236.935	0.622	2657.465	0.590	26	0.447	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1797.645	1798.032	-216.425	0.608	2631.678	0.576	26	0.436	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1738.498	1738.962	-267.453	0.561	2510.911	0.592	22	0.416	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/2	1738.298	1738.962	-960.280	0.584	2484.958	0.595	22	0.411	K.SPFQEYTDLLAKPTK.A
R4/RRR4-14/2	1738.431	1738.962	-883.156	0.579	2375.754	0.573	22	0.381	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/2	1797.494	1798.032	-858.565	0.608	2194.145	0.590	25	0.353	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1738.539	1738.962	-243.643	0.557	2085.717	0.579	21	0.328	K.SPFQEYTDLLAKPTK.A
R4/RRR4-14/2	1738.300	1738.962	-958.729	0.570	2125.971	0.543	21	0.324	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/2	1670.745	1669.860	-68.857	0.543	2012.538	0.569	21	0.311	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1670.301	1669.860	265.089	0.577	1947.263	0.575	22	0.303	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1670.469	1669.860	-234.295	0.560	1927.517	0.569	22	0.299	K.VLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1797.861	1798.032	-95.519	0.590	1901.798	0.562	23	0.293	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1669.577	1669.860	-169.519	0.516	1822.174	0.581	21	0.286	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1670.036	1669.860	105.820	0.537	1889.922	0.547	21	0.285	K.VLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1738.575	1738.962	-223.426	0.568	1792.500	0.550	21	0.274	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/2	1796.850	1798.032	-1218.104	0.529	1734.287	0.574	23	0.273	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1670.794	1669.860	-39.543	0.478	1608.544	0.545	19	0.245	K.VLQFAGIEDVFTSSR.G
R4/RRR4-11/2	1670.579	1669.860	-168.685	0.413	1639.098	0.513	21	0.242	K.VLQFAGIEDVFTSSR.G
R4/RRR4-10/2	1670.369	1669.860	-294.414	0.461	1453.907	0.520	19	0.222	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/3	1797.960	1798.032	-40.329	0.493	1574.374	0.472	30	0.196	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1670.247	1669.860	232.843	0.410	1410.111	0.391	20	0.192	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1404.232	1403.565	-237.823	0.507	1036.090	0.510	16	0.188	K.TYGFLTPDFWR.E
R4/RRR4-14/2	1670.145	1669.860	171.645	0.449	1006.333	0.525	18	0.184	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1669.232	1669.860	-977.787	0.432	1109.795	0.489	17	0.183	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1404.220	1403.565	-246.632	0.515	947.167	0.503	16	0.182	K.TYGFLTPDFWR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1404.206	1403.565	-256.836	0.509	893.302	0.506	15	0.178	K.TYGFLTPDFWR.E
R4/RRR4-14/3	1798.748	1798.032	-158.783	0.493	1529.704	0.441	31	0.177	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1404.336	1403.565	-163.699	0.396	733.906	0.545	13	0.170	K.TYGFLTPDFWR.E
R4/RRR4-13/2	1404.182	1403.565	-273.930	0.483	729.132	0.510	14	0.170	K.TYGFLTPDFWR.E
R4/RRR4-13/2	1403.367	1403.565	-141.913	0.457	849.356	0.463	15	0.169	K.TYGFLTPDFWR.E
R4/RRR4-13/2	1402.692	1403.565	-1339.819	0.527	761.064	0.493	14	0.168	K.TYGFLTPDFWR.E
R4/RRR4-14/2	1403.231	1403.565	-239.127	0.397	743.453	0.495	13	0.165	K.TYGFLTPDFWR.E
R4/RRR4-13/2	1798.980	1798.032	-29.307	0.478	635.614	0.564	15	0.165	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1402.968	1403.565	-1141.889	0.483	694.282	0.479	14	0.164	K.TYGFLTPDFWR.E
R4/RRR4-13/2	1403.197	1403.565	-263.216	0.405	805.629	0.445	14	0.163	K.TYGFLTPDFWR.E
R4/RRR4-14/2	1669.297	1669.860	-938.729	0.422	896.681	0.412	17	0.160	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/2	1136.969	1137.307	-298.250	0.414	643.159	0.423	14	0.157	K.IGQPHTVPCK.V
R4/RRR4-14/2	1136.938	1137.307	-326.042	0.347	773.086	0.402	15	0.157	K.IGQPHTVPCK.V
R4/RRR4-17/2	1669.330	1669.860	-918.907	0.374	862.830	0.393	17	0.156	K.VLQFAGIEDVFTSSR.G
R4/RRR4-15/2	1403.190	1403.565	-268.190	0.384	726.608	0.418	13	0.156	K.TYGFLTPDFWR.E
R4/RRR4-14/2	1670.453	1669.860	-244.045	0.386	408.427	0.467	13	0.149	K.VLQFAGIEDVFTSSR.G
R4/RRR4-2/2	1669.904	1669.860	26.644	0.333	379.212	0.435	15	0.149	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/3	1738.834	1738.962	-73.632	0.492	1212.142	0.470	26	0.148	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/2	1138.037	1137.307	-238.368	0.370	570.905	0.381	13	0.148	-.IGQPHTVPCK.-
R4/RRR4-14/2	1402.567	1403.565	-1429.241	0.274	632.016	0.369	13	0.147	K.TYGFLTPDFWR.E
R4/RRR4-2/2	1669.991	1669.860	78.623	0.295	539.131	0.389	16	0.147	K.VLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1403.378	1403.565	-133.799	0.420	554.652	0.424	11	0.145	-.TYGFLTPDFWR.-
R4/RRR4-15/2	1402.327	1403.565	-1600.786	0.262	653.758	0.338	13	0.145	K.TYGFLTPDFWR.E
R4/RRR4-15/2	1670.989	1669.860	77.697	0.461	714.592	0.344	16	0.144	K.VLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1670.434	1669.860	-255.849	0.286	409.928	0.385	14	0.144	K.VLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1403.066	1403.565	-357.310	0.299	482.666	0.362	11	0.144	K.TYGFLTPDFWR.E
R4/RRR4-13/2	1798.839	1798.032	-107.651	0.391	308.438	0.428	13	0.143	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-13/2	1138.080	1137.307	-200.490	0.308	506.509	0.309	13	0.143	K.IGQPHTVPCK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1670.774	1669.860	-51.195	0.306	527.386	0.328	15	0.142	K.VLQFAGIEDVFTSSR.G
R4/RRR4-2/2	1670.872	1669.860	7.136	0.308	334.778	0.399	13	0.142	-.VLQFAGIEDVFTSSR.-
R4/RRR4-13/2	1137.085	1137.307	-195.928	0.292	474.520	0.256	12	0.136	-.IGQPHTVPCK.-
R4/RRR4-15/2	1670.683	1669.860	-105.869	0.399	642.737	0.253	15	0.135	-.VLQFAGIEDVFTSSR.-
R4/RRR4-15/2	1670.434	1669.860	-255.335	0.415	741.350	0.187	16	0.131	K.VLQFAGIEDVFTSSR.G
R4/RRR4-14/3	1739.409	1738.962	257.822	0.507	912.186	0.493	26	0.128	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/3	1797.886	1798.032	-81.701	0.428	1201.870	0.384	28	0.123	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-13/3	1739.056	1738.962	54.477	0.458	866.646	0.470	24	0.120	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/3	1798.059	1798.032	14.523	0.485	1077.326	0.404	26	0.118	K.KVLQFAGIEDVFTSSR.G
R4/RRR4-14/3	1738.993	1738.962	17.833	0.483	856.073	0.432	26	0.111	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/3	1739.108	1738.962	84.572	0.460	642.674	0.474	22	0.110	K.SPFQEYTDLLAKPTK.A
R4/RRR4-12/3	1739.498	1738.962	-267.483	0.405	760.279	0.431	22	0.107	K.SPFQEYTDLLAKPTK.A
R4/RRR4-13/3	1739.027	1738.962	37.370	0.317	553.777	0.319	21	0.091	K.SPFQEYTDLLAKPTK.A
R4/RRR4-7/2	1496.090	1496.689	-1071.878	0.375	1316.955	0.381	20	0.183	R.GYISPQFVTNLEK.S
R4/RRR4-7/2	1555.703	1554.856	-98.976	0.504	922.862	0.498	20	0.180	K.EILPILEKTTQLR.A
R4/RRR4-7/2	1556.617	1556.829	-136.751	0.451	1108.608	0.462	20	0.180	K.LGLLSVTSGANPVSLK.K
R4/RRR4-7/2	1556.330	1556.829	-321.651	0.452	1112.732	0.446	20	0.177	K.LGLLSVTSGANPVSLK.K
R4/RRR4-7/2	1555.714	1554.856	-91.892	0.485	933.473	0.458	20	0.174	K.EILPILEKTTQLR.A
R4/RRR4-7/2	1496.311	1496.689	-253.546	0.392	1090.805	0.399	19	0.170	R.GYISPQFVTNLEK.S
R4/RRR4-7/2	1556.156	1556.829	-1078.420	0.362	1000.326	0.368	19	0.157	K.LGLLSVTSGANPVSLK.K
R4/RRR4-6/2	1577.310	1577.721	-260.863	0.528	1985.504	0.464	26	0.280	K.FAGAISDGGDIVLEGR.V
R4/RRR4-6/2	1577.312	1577.721	-259.853	0.520	1895.497	0.478	26	0.272	K.FAGAISDGGDIVLEGR.V
R4/RRR4-6/2	1577.041	1577.721	-1068.020	0.556	1781.817	0.523	25	0.268	K.FAGAISDGGDIVLEGR.V
R4/RRR4-6/2	1548.430	1548.722	-189.345	0.481	1693.984	0.473	22	0.242	R.AIGAELVSFDEAIGR.A
R4/RRR4-6/2	1548.218	1548.722	-974.262	0.495	1564.791	0.511	23	0.237	R.AIGAELVSFDEAIGR.A
R4/RRR4-6/2	1549.133	1548.722	265.906	0.534	1520.329	0.515	22	0.232	R.AIGAELVSFDEAIGR.A
R4/RRR4-6/2	1132.125	1132.337	-187.918	0.504	1232.902	0.389	16	0.181	K.VAQFDALIVR.S
R4/RRR4-6/2	1132.241	1132.337	-85.494	0.418	1217.480	0.355	16	0.174	K.VAQFDALIVR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1131.947	1132.337	-345.652	0.315	777.732	0.135	13	0.131	-.VAQFDALIVR.-
R4/RRR4-6/3	1920.172	1921.101	-1007.283	0.356	915.633	0.360	27	0.095	R.VSHESPAAEAPLESIQVR.L
R4/RRR4-19/3	1633.513	1632.831	-195.531	0.612	2935.835	0.444	35	0.499	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1633.008	1632.831	108.520	0.552	2756.482	0.506	22	0.434	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1633.214	1632.831	235.125	0.572	2738.363	0.508	22	0.431	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1632.376	1632.831	-279.815	0.506	2701.152	0.500	22	0.421	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1632.301	1632.831	-939.903	0.529	2735.667	0.450	22	0.408	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1420.406	1420.639	-164.260	0.488	2467.703	0.502	21	0.374	R.VNQAIYLLTTGAR.E
R4/RRR4-18/2	1632.437	1632.831	-242.153	0.499	2620.224	0.408	22	0.370	K.TIAECLADELINAAK.G
R4/RRR4-19/3	1632.801	1632.831	-18.201	0.583	2518.876	0.404	33	0.354	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1420.453	1420.639	-131.587	0.499	2221.482	0.568	20	0.349	R.VNQAIYLLTTGAR.E
R4/RRR4-19/2	1420.243	1420.639	-279.712	0.503	2177.116	0.562	21	0.340	R.VNQAIYLLTTGAR.E
R4/RRR4-19/2	1632.297	1632.831	-942.605	0.497	2432.042	0.421	22	0.338	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1420.309	1420.639	-232.804	0.533	2144.900	0.557	20	0.332	R.VNQAIYLLTTGAR.E
R4/RRR4-19/3	1632.183	1632.831	-1013.043	0.564	2317.148	0.430	31	0.320	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1420.190	1420.639	-316.879	0.506	2017.994	0.547	20	0.308	R.VNQAIYLLTTGAR.E
R4/RRR4-18/3	1633.431	1632.831	-245.687	0.540	2368.449	0.365	32	0.297	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1631.693	1632.831	-1314.085	0.348	2473.469	0.235	22	0.291	K.TIAECLADELINAAK.G
R4/RRR4-18/2	1631.832	1632.831	-1228.438	0.390	2265.788	0.326	22	0.283	K.TIAECLADELINAAK.G
R4/RRR4-18/2	1419.743	1420.639	-1339.337	0.366	1982.628	0.485	21	0.282	R.VNQAIYLLTTGAR.E
R4/RRR4-19/2	1420.922	1420.639	200.027	0.508	1786.741	0.552	20	0.275	R.VNQAIYLLTTGAR.E
R4/RRR4-18/2	1632.148	1632.831	-1034.511	0.429	2070.063	0.397	21	0.271	K.TIAECLADELINAAK.G
R4/RRR4-19/2	1419.816	1420.639	-1287.872	0.395	1590.472	0.486	19	0.231	R.VNQAIYLLTTGAR.E
R4/RRR4-18/3	1632.729	1632.831	-62.520	0.554	1811.087	0.420	29	0.212	K.TIAECLADELINAAK.G
R4/RRR4-20/2	1420.181	1420.639	-323.434	0.379	1383.238	0.492	18	0.209	R.VNQAIYLLTTGAR.E
R4/RRR4-18/2	1419.501	1420.639	-1510.778	0.469	1156.987	0.489	17	0.190	R.VNQAIYLLTTGAR.E
R4/RRR4-19/2	1577.386	1576.825	-279.479	0.591	516.912	0.625	20	0.182	R.RVNQAIYLLTTGAR.E
R4/RRR4-19/2	1577.507	1576.825	-202.387	0.607	580.731	0.572	20	0.176	R.RVNQAIYLLTTGAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-19/2	1223.813	1224.354	-1262.831	0.389	725.992	0.565	17	0.175	K.HATYLPHTAGR.Y
R4/RRR4-20/2	1420.327	1420.639	-220.043	0.408	916.633	0.469	18	0.172	R.VNQAIYLLTTGAR.E
R4/RRR4-19/2	1223.643	1224.354	-1401.788	0.330	701.468	0.575	18	0.171	K.HATYLPHTAGR.Y
R4/RRR4-19/2	1223.468	1224.354	-1545.593	0.363	718.465	0.541	18	0.171	K.HATYLPHTAGR.Y
R4/RRR4-19/2	1576.415	1576.825	-261.244	0.576	484.745	0.574	18	0.171	R.RVNQAIYLLTTGAR.E
R4/RRR4-19/2	1224.049	1224.354	-249.926	0.382	601.473	0.567	17	0.170	K.HATYLPHTAGR.Y
R4/RRR4-19/2	1577.196	1576.825	235.713	0.561	399.910	0.555	17	0.165	R.RVNQAIYLLTTGAR.E
R4/RRR4-19/2	1576.396	1576.825	-273.286	0.558	368.490	0.571	16	0.165	R.RVNQAIYLLTTGAR.E
R4/RRR4-19/2	1576.264	1576.825	-993.668	0.555	439.620	0.533	18	0.165	R.RVNQAIYLLTTGAR.E
R4/RRR4-19/2	1223.941	1224.354	-337.978	0.331	518.137	0.550	16	0.162	K.HATYLPHTAGR.Y
R4/RRR4-19/2	1421.365	1420.639	-193.523	0.347	643.120	0.444	15	0.154	R.VNQAIYLLTTGAR.E
R4/RRR4-20/2	1419.693	1420.639	-1374.657	0.405	482.404	0.463	14	0.154	R.VNQAIYLLTTGAR.E
R4/RRR4-19/2	1224.131	1224.354	-182.696	0.303	464.130	0.484	15	0.153	K.HATYLPHTAGR.Y
R4/RRR4-19/2	1100.807	1101.275	-426.724	0.429	880.630	0.299	14	0.151	R.KAQCPLVER.L
R4/RRR4-19/2	1100.924	1101.275	-319.804	0.451	800.629	0.301	14	0.149	R.KAQCPLVER.L
R4/RRR4-19/2	1100.926	1101.275	-318.246	0.386	815.062	0.260	14	0.145	R.KAQCPLVER.L
R4/RRR4-19/2	1421.198	1420.639	-310.882	0.231	350.847	0.387	13	0.142	R.VNQAIYLLTTGAR.E
R4/RRR4-18/2	1419.831	1420.639	-1276.993	0.329	281.603	0.394	11	0.129	-.VNQAIYLLTTGAR.-
R4/RRR4-18/3	1224.369	1224.354	12.478	0.541	638.022	0.546	21	0.128	K.HATYLPHTAGR.Y
R4/RRR4-20/3	1223.939	1224.354	-339.390	0.520	523.696	0.558	20	0.128	K.HATYLPHTAGR.Y
R4/RRR4-23/3	1224.037	1224.354	-259.542	0.519	612.601	0.543	20	0.127	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.548	1224.354	159.004	0.517	683.722	0.514	22	0.124	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.518	1224.354	134.711	0.539	603.469	0.524	21	0.124	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.563	1224.354	171.900	0.428	402.518	0.546	18	0.124	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1633.130	1632.831	183.774	0.408	1387.254	0.322	29	0.123	K.TIAECLADELINAAK.G
R4/RRR4-20/3	1224.586	1224.354	190.344	0.513	556.133	0.522	21	0.122	K.HATYLPHTAGR.Y
R4/RRR4-20/3	1224.289	1224.354	-52.475	0.541	486.554	0.524	20	0.122	K.HATYLPHTAGR.Y
R4/RRR4-6/3	1224.989	1224.354	-298.220	0.367	221.361	0.490	15	0.120	K.HATYLPHTAGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/3	1224.558	1224.354	167.851	0.542	585.278	0.501	21	0.120	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.384	1224.354	24.928	0.545	613.278	0.497	22	0.120	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.577	1224.354	182.996	0.530	559.675	0.501	22	0.119	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.448	1224.354	77.423	0.537	623.091	0.494	22	0.119	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.448	1224.354	77.723	0.521	547.489	0.499	21	0.119	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.523	1224.354	139.060	0.503	617.717	0.492	21	0.119	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.520	1224.354	136.361	0.558	500.291	0.498	20	0.118	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1225.289	1224.354	-53.082	0.540	399.418	0.486	18	0.117	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.630	1224.354	226.179	0.445	354.608	0.470	17	0.116	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.684	1224.354	271.007	0.512	346.457	0.474	16	0.116	K.HATYLPHTAGR.Y
R4/RRR4-18/2	1632.042	1632.831	-1099.395	0.339	732.510	0.055	14	0.116	-.TIAECLADELINAAK.-
R4/RRR4-17/3	1224.757	1224.354	330.222	0.499	498.047	0.479	20	0.116	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.310	1224.354	-35.974	0.495	655.489	0.466	22	0.115	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.415	1224.354	50.426	0.492	569.319	0.471	20	0.115	K.HATYLPHTAGR.Y
R4/RRR4-23/3	1224.517	1224.354	134.261	0.516	569.804	0.462	21	0.114	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.695	1224.354	279.553	0.563	452.355	0.457	20	0.114	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.082	1224.354	-222.774	0.420	436.432	0.447	19	0.113	K.HATYLPHTAGR.Y
R4/RRR4-17/3	1224.505	1224.354	124.214	0.469	546.663	0.450	20	0.113	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.441	1224.354	71.274	0.553	552.342	0.449	21	0.113	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.551	1224.354	161.703	0.530	566.039	0.448	20	0.112	K.HATYLPHTAGR.Y
R4/RRR4-23/3	1224.236	1224.354	-95.982	0.437	482.375	0.440	19	0.112	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.116	1224.354	-194.262	0.382	411.285	0.430	19	0.112	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.192	1224.354	-132.291	0.446	539.817	0.437	20	0.111	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1224.464	1224.354	90.621	0.460	499.281	0.433	20	0.111	K.HATYLPHTAGR.Y
R4/RRR4-20/3	1224.243	1224.354	-90.281	0.303	348.380	0.396	17	0.111	K.HATYLPHTAGR.Y
R4/RRR4-15/3	1224.945	1224.354	-334.514	0.401	353.983	0.324	18	0.110	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.912	1224.354	-361.661	0.484	557.000	0.427	20	0.110	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1223.889	1224.354	-380.520	0.485	645.842	0.422	21	0.110	K.HATYLPHTAGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/3	1224.504	1224.354	123.614	0.409	586.289	0.425	21	0.109	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1224.699	1224.354	282.551	0.355	389.030	0.335	18	0.109	K.HATYLPHTAGR.Y
R4/RRR4-19/3	1223.707	1224.354	-1349.848	0.471	541.600	0.406	20	0.108	K.HATYLPHTAGR.Y
R4/RRR4-21/3	1224.071	1224.354	-231.178	0.382	412.904	0.361	18	0.108	K.HATYLPHTAGR.Y
R4/RRR4-17/3	1224.297	1224.354	-46.025	0.488	532.857	0.401	21	0.108	K.HATYLPHTAGR.Y
R4/RRR4-24/3	1224.651	1224.354	243.571	0.486	454.719	0.380	19	0.108	K.HATYLPHTAGR.Y
R4/RRR4-18/3	1225.160	1224.354	-158.769	0.372	245.872	0.430	14	0.107	-.HATYLPHTAGR.-
R4/RRR4-16/3	1223.447	1224.354	-1562.994	0.458	471.222	0.296	18	0.104	K.HATYLPHTAGR.Y
R4/RRR4-21/3	1224.046	1224.354	-251.588	0.403	467.075	0.438	18	0.103	-.HATYLPHTAGR.-
R4/RRR4-18/3	1224.823	1224.354	384.784	0.325	244.236	0.360	14	0.098	-.HATYLPHTAGR.-
R4/RRR4-7/2	1422.282	1422.565	-199.941	0.456	1811.594	0.448	24	0.253	R.YGTAGLLSPNTEAK.I
R4/RRR4-7/2	1366.960	1367.536	-1156.115	0.462	1298.233	0.645	24	0.238	R.HSGVVALIDAATGR.R
R4/RRR4-7/2	1367.339	1367.536	-144.847	0.435	1298.608	0.641	23	0.235	R.HSGVVALIDAATGR.R
R4/RRR4-7/2	1367.404	1367.536	-96.936	0.487	1163.289	0.677	22	0.231	R.HSGVVALIDAATGR.R
R4/RRR4-7/2	1422.213	1422.565	-248.419	0.479	1492.575	0.472	23	0.221	R.YGTAGLLSPNTEAK.I
R4/RRR4-7/2	1421.597	1422.565	-1389.008	0.403	1513.522	0.437	23	0.213	R.YGTAGLLSPNTEAK.I
R4/RRR4-7/2	1732.261	1732.873	-933.304	0.524	1300.606	0.470	21	0.197	K.NAEATQSTLTPDGWLK.T
R4/RRR4-7/2	1784.795	1784.989	-108.772	0.332	1186.302	0.422	22	0.176	R.IVATIEEISATTPDPAR.R
R4/RRR4-7/2	1733.222	1732.873	202.131	0.567	964.374	0.475	20	0.172	K.NAEATQSTLTPDGWLK.T
R4/RRR4-7/2	1784.770	1784.989	-122.974	0.383	847.172	0.455	21	0.161	R.IVATIEEISATTPDPAR.R
R4/RRR4-7/2	1066.442	1066.234	194.990	0.380	681.820	0.416	12	0.156	R.ITFTELWR.A
R4/RRR4-7/2	1066.220	1066.234	-13.505	0.256	690.401	0.268	12	0.139	R.ITFTELWR.A
R4/RRR4-7/3	1562.317	1562.799	-309.064	0.368	888.670	0.520	32	0.127	R.AVAGAASALAAHPVSLR.K
R4/RRR4-7/3	1562.404	1562.799	-253.330	0.273	742.969	0.194	28	0.075	R.AVAGAASALAAHPVSLR.K
R4/RRR4-6/2	1530.229	1530.784	-1019.000	0.515	1594.858	0.525	19	0.243	K.CPFDAIEIINLPK.D
R4/RRR4-6/2	1215.061	1215.297	-194.539	0.365	1066.219	0.289	15	0.153	R.GSELQNYFTR.I
R4/RRR4-6/3	1522.800	1522.816	-10.390	0.441	777.802	0.518	24	0.121	K.AIIKPQYVDHIPK.A
R4/RRR4-6/3	1522.919	1522.816	67.515	0.401	1016.291	0.426	28	0.116	K.AIIKPQYVDHIPK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1143.594	1143.274	280.695	0.531	1028.535	0.389	21	0.113	R.FRDESLTFK.I
R4/RRR4-6/3	1756.591	1756.899	-175.976	0.368	923.261	0.425	28	0.110	K.AVQGNVGQVLDQKDER.G
R4/RRR4-6/3	1143.533	1143.274	227.390	0.498	1103.119	0.338	22	0.106	R.FRDESLTFK.I
R4/RRR4-6/3	1756.622	1756.899	-158.095	0.361	672.087	0.472	24	0.106	K.AVQGNVGQVLDQKDER.G
R4/RRR4-6/3	1756.052	1756.899	-1054.884	0.335	609.456	0.443	22	0.099	K.AVQGNVGQVLDQKDER.G
R4/RRR4-6/3	1956.121	1955.204	-42.420	0.389	1231.659	0.255	24	0.095	R.FKNPPDWQEILTYFR.G
R4/RRR4-12/1	431.993	432.410	-967.958	-2.366	4.431	0.000	2	0.681	R.QGGGGG.-
R4/RRR4-24/1	432.001	432.410	-949.944	-1.206	18.514	0.000	4	0.643	R.QGGGGG.-
R4/RRR4-5/1	431.992	432.410	-970.228	-1.095	32.421	0.692	4	0.609	R.QGGGGG.-
R4/RRR4-21/1	432.009	432.410	-930.653	-0.930	5.056	0.000	2	0.572	R.QGGGGG.-
R4/RRR4-5/2	1687.387	1687.870	-287.164	0.483	2497.164	0.426	25	0.355	R.VVDSLDDLSLDIPSAK.S
R4/RRR4-5/2	1688.521	1687.870	-207.354	0.553	2472.186	0.418	24	0.345	R.VVDSLDDLSLDIPSAK.S
R4/RRR4-5/2	1686.774	1687.870	-1246.567	0.419	2411.706	0.348	24	0.314	R.VVDSLDDLSLDIPSAK.S
R4/RRR4-5/2	1686.576	1687.870	-1363.954	0.373	2253.215	0.326	23	0.281	R.VVDSLDDLSLDIPSAK.S
R4/RRR4-5/2	1756.409	1755.946	264.222	0.585	1168.139	0.646	21	0.224	K.SVAPIIEEYFSTGDVK.L
R4/RRR4-5/2	1755.301	1755.946	-940.236	0.484	1309.250	0.580	22	0.222	K.SVAPIIEEYFSTGDVK.L
R4/RRR4-6/2	1687.528	1687.870	-202.977	0.372	1749.685	0.265	20	0.198	R.VVDSLDDLSLDIPSAK.S
R4/RRR4-5/2	1882.288	1883.132	-983.090	0.440	541.668	0.565	19	0.161	R.AVIDDVLAPLNLDEISGK.L
R4/RRR4-5/2	1038.134	1038.179	-43.474	0.428	761.666	0.407	14	0.159	K.SQFQTLVSK.A
R4/RRR4-5/2	1754.647	1754.923	-157.672	0.436	813.257	0.389	20	0.152	R.VRDGLDDLALDIPDAR.E
R4/RRR4-5/2	1037.865	1038.179	-303.372	0.358	605.753	0.352	13	0.148	K.SQFQTLVSK.A
R4/RRR4-5/2	1882.279	1883.132	-987.517	0.348	378.263	0.444	16	0.140	-.AVIDDVLAPLNLDEISGK.-
R4/RRR4-5/3	1850.677	1851.009	-180.129	0.430	953.328	0.440	28	0.116	K.LAASDLKELGYDDFHR.Y
R4/RRR4-5/3	1850.660	1851.009	-189.260	0.417	803.230	0.347	28	0.092	K.LAASDLKELGYDDFHR.Y
R4/RRR4-19/2	1429.272	1429.604	-233.228	0.494	1374.667	0.547	17	0.223	R.DNFFFAGIDKVR.F
R4/RRR4-20/2	1174.058	1174.286	-195.076	0.419	1251.997	0.452	15	0.192	R.DNFFFAGIDK.V
R4/RRR4-19/2	1429.081	1429.604	-1069.019	0.456	1177.103	0.457	17	0.187	R.DNFFFAGIDKVR.F
R4/RRR4-19/2	1429.190	1429.604	-290.725	0.461	917.853	0.522	15	0.178	R.DNFFFAGIDKVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1174.003	1174.286	-241.807	0.313	1155.551	0.420	14	0.175	R.DNFFFAGIDK.V
R4/RRR4-19/2	1173.948	1174.286	-289.586	0.383	1097.022	0.404	14	0.172	R.DNFFFAGIDK.V
R4/RRR4-19/2	893.770	894.007	-266.047	0.334	1145.433	0.321	14	0.162	K.GGEYAVGIK.N
R4/RRR4-19/2	1174.020	1174.286	-227.516	0.313	1012.260	0.360	14	0.159	R.DNFFFAGIDK.V
R4/RRR4-20/2	1006.986	1007.210	-222.822	0.458	926.810	0.291	13	0.153	R.FPFLLVDR.V
R4/RRR4-20/2	1007.266	1007.210	55.354	0.434	595.900	0.313	11	0.148	R.FPFLLVDR.V
R4/RRR4-19/2	1007.219	1007.210	9.043	0.466	620.918	0.304	11	0.146	R.FPFLLVDR.V
R4/RRR4-20/2	1173.204	1174.286	-1780.459	0.212	681.108	0.401	14	0.145	R.DNFFFAGIDK.V
R4/RRR4-19/2	1006.783	1007.210	-424.985	0.437	627.010	0.333	11	0.144	-.FPFLLVDR.-
R4/RRR4-19/2	1007.235	1007.210	24.723	0.449	629.956	0.267	11	0.143	R.FPFLLVDR.V
R4/RRR4-20/2	1007.142	1007.210	-67.423	0.422	626.967	0.274	11	0.142	-.FPFLLVDR.-
R4/RRR4-19/2	1007.204	1007.210	-6.152	0.400	645.708	0.225	11	0.141	R.FPFLLVDR.V
R4/RRR4-19/2	1007.084	1007.210	-125.175	0.381	625.280	0.215	11	0.139	-.FPFLLVDR.-
R4/RRR4-19/2	893.976	894.007	-34.802	0.301	610.661	0.307	12	0.138	-.GGEYAVGIK.-
R4/RRR4-20/2	1006.983	1007.210	-225.619	0.405	613.667	0.209	11	0.138	-.FPFLLVDR.-
R4/RRR4-20/2	1006.523	1007.210	-1680.816	0.434	594.418	0.290	11	0.137	-.FPFLLVDR.-
R4/RRR4-20/2	1006.909	1007.210	-299.809	0.412	631.488	0.223	11	0.136	-.FPFLLVDR.-
R4/RRR4-19/3	1633.432	1633.983	-952.799	0.475	1179.283	0.441	26	0.136	R.FRKPVIAGDTLIM*R.M
R4/RRR4-19/2	1006.961	1007.210	-247.875	0.383	637.801	0.191	11	0.135	-.FPFLLVDR.-
R4/RRR4-19/2	1006.514	1007.210	-1690.076	0.385	642.316	0.204	11	0.131	-.FPFLLVDR.-
R4/RRR4-19/3	1635.447	1633.983	284.085	0.497	862.615	0.474	24	0.120	R.FRKPVIAGDTLIM*R.M
R4/RRR4-19/3	1634.109	1633.983	76.998	0.466	1005.573	0.377	25	0.108	R.FRKPVIAGDTLIM*R.M
R4/RRR4-20/3	1634.309	1633.983	200.151	0.462	799.473	0.315	24	0.083	-.FRKPVIAGDTLIM*R.-
R4/RRR4-20/3	1632.840	1633.983	-1316.328	0.346	703.712	0.247	19	0.074	-.FRKPVIAGDTLIM*R.-
R4/RRR4-12/3	1959.754	1959.187	-221.895	0.519	2473.268	0.578	36	0.463	R.DADVVISTLGALQIADQTK.L
R4/RRR4-12/3	1958.617	1959.187	-804.321	0.434	2630.504	0.483	37	0.450	R.DADVVISTLGALQIADQTK.L
R4/RRR4-12/3	1958.347	1959.187	-942.664	0.428	2693.738	0.439	35	0.445	R.DADVVISTLGALQIADQTK.L
R4/RRR4-12/2	1959.648	1959.187	235.819	0.529	1783.049	0.536	26	0.268	R.DADVVISTLGALQIADQTK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1205.149	1205.432	-235.253	0.519	1676.799	0.568	20	0.267	R.ILVVGGTGYIGR.H
R4/RRR4-12/2	1959.715	1959.187	-241.885	0.526	1672.468	0.551	25	0.256	R.DADVVISTLGALQIADQTK.L
R4/RRR4-12/2	1204.666	1205.432	-1469.809	0.514	1652.806	0.529	19	0.253	R.ILVVGGTGYIGR.H
R4/RRR4-12/2	1958.489	1959.187	-869.883	0.398	1533.039	0.462	25	0.217	R.DADVVISTLGALQIADQTK.L
R4/RRR4-12/2	1205.301	1205.432	-108.246	0.373	1083.042	0.503	18	0.186	R.ILVVGGTGYIGR.H
R4/RRR4-12/2	852.835	853.004	-198.709	0.402	764.675	0.404	14	0.160	R.HVVLASAR.L
R4/RRR4-12/2	962.403	963.116	-1784.332	0.378	741.768	0.339	12	0.151	K.AQLLQSFR.D
R4/RRR4-12/2	962.806	963.116	-322.571	0.456	858.016	0.295	13	0.151	K.AQLLQSFR.D
R4/RRR4-12/2	1960.315	1959.187	65.043	0.405	767.355	0.422	18	0.151	R.DADVVISTLGALQIADQTK.L
R4/RRR4-12/2	962.986	963.116	-134.849	0.452	727.044	0.324	12	0.150	K.AQLLQSFR.D
R4/RRR4-12/2	853.166	853.004	190.563	0.239	401.906	0.347	10	0.140	R.HVVLASAR.L
R4/RRR4-12/2	1960.781	1959.187	-207.660	0.326	454.370	0.411	14	0.138	R.DADVVISTLGALQIADQTK.L
R4/RRR4-12/3	1065.506	1065.251	239.963	0.539	991.665	0.367	20	0.105	R.LGHPTTALVR.D
R4/RRR4-12/3	1065.638	1065.251	363.847	0.514	979.498	0.347	20	0.099	-.LGHPTTALVR.-
R4/RRR4-12/3	1065.180	1065.251	-66.693	0.494	958.172	0.334	20	0.098	R.LGHPTTALVR.D
R4/RRR4-2/2	1843.327	1843.924	-868.900	0.577	2497.805	0.533	24	0.391	R.LPQDLSDEIEEDPTGGK.I
R4/RRR4-2/2	1843.388	1843.924	-835.396	0.558	2343.930	0.549	24	0.366	R.LPQDLSDEIEEDPTGGK.I
R4/RRR4-2/2	1843.449	1843.924	-258.071	0.572	2117.886	0.555	23	0.326	R.LPQDLSDEIEEDPTGGK.I
R4/RRR4-2/2	1875.493	1876.097	-857.588	0.551	1262.575	0.597	24	0.225	K.TQVEEVPLALCQFQGR.L
R4/RRR4-2/2	1356.069	1356.509	-325.453	0.469	1082.254	0.411	19	0.175	R.FLAVGSYDNTIR.I
R4/RRR4-2/2	984.997	985.206	-212.880	0.505	989.099	0.370	16	0.164	R.LLAGVGSVLR.L
R4/RRR4-2/2	985.176	985.206	-30.400	0.505	1007.492	0.358	16	0.163	R.LLAGVGSVLR.L
R4/RRR4-2/2	1356.009	1356.509	-369.168	0.427	916.028	0.392	17	0.161	R.FLAVGSYDNTIR.I
R4/RRR4-2/2	1461.313	1461.645	-227.612	0.371	1128.840	0.278	19	0.155	R.LGETFNETAIPLR.Y
R4/RRR4-2/2	985.272	985.206	67.152	0.497	944.603	0.311	16	0.154	R.LLAGVGSVLR.L
R4/RRR4-2/2	1355.532	1356.509	-1462.484	0.293	690.994	0.322	16	0.143	R.FLAVGSYDNTIR.I
R4/RRR4-2/2	1461.159	1461.645	-333.049	0.346	866.499	0.115	17	0.129	R.LGETFNETAIPLR.Y
R4/RRR4-2/3	1427.341	1427.741	-281.247	0.376	1058.899	0.159	22	0.071	-.ILRPGLAISEMAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1292.203	1292.509	-237.786	0.479	1759.950	0.490	19	0.256	K.FSGKDVVLVATR.R
R4/RRR4-18/2	1291.932	1292.509	-1224.582	0.513	1466.727	0.523	19	0.229	K.FSGKDVVLVATR.R
R4/RRR4-18/2	1292.205	1292.509	-235.701	0.502	1445.135	0.526	18	0.227	K.FSGKDVVLVATR.R
R4/RRR4-18/2	1292.349	1292.509	-124.167	0.502	1453.620	0.472	19	0.216	K.FSGKDVVLVATR.R
R4/RRR4-18/2	1837.526	1837.967	-240.846	0.569	1172.463	0.596	20	0.214	R.NNTEYKLDTFSSVYR.R
R4/RRR4-18/2	1292.246	1292.509	-204.522	0.523	1352.007	0.507	18	0.213	K.FSGKDVVLVATR.R
R4/RRR4-18/2	1837.183	1837.967	-974.237	0.522	1248.880	0.563	20	0.213	R.NNTEYKLDTFSSVYR.R
R4/RRR4-18/2	1837.584	1837.967	-209.389	0.554	1128.109	0.597	20	0.210	R.NNTEYKLDTFSSVYR.R
R4/RRR4-18/2	1292.326	1292.509	-142.454	0.487	1347.366	0.490	18	0.209	K.FSGKDVVLVATR.R
R4/RRR4-18/2	872.755	873.032	-318.257	0.423	1091.209	0.378	13	0.171	K.DVVLVATR.R
R4/RRR4-18/2	1068.059	1068.297	-223.034	0.377	736.703	0.399	13	0.155	K.AVIIHVPYR.L
R4/RRR4-18/2	1068.208	1068.297	-83.512	0.425	898.638	0.328	14	0.155	K.AVIIHVPYR.L
R4/RRR4-18/2	872.778	873.032	-292.577	0.321	1060.686	0.275	13	0.154	K.DVVLVATR.R
R4/RRR4-18/2	872.475	873.032	-1790.447	0.384	814.716	0.334	12	0.153	K.DVVLVATR.R
R4/RRR4-18/2	872.408	873.032	-1866.930	0.358	972.710	0.259	12	0.149	K.DVVLVATR.R
R4/RRR4-18/2	872.584	873.032	-515.181	0.385	954.894	0.254	12	0.148	K.DVVLVATR.R
R4/RRR4-18/2	872.469	873.032	-1797.335	0.322	1059.879	0.218	12	0.147	K.DVVLVATR.R
R4/RRR4-18/2	1067.793	1068.297	-1412.032	0.378	625.541	0.311	12	0.145	K.AVIIHVPYR.L
R4/RRR4-18/2	1421.759	1420.682	54.459	0.370	1057.507	0.211	19	0.142	K.KFSGKDVVLVATR.R
R4/RRR4-18/3	1838.562	1837.967	-220.939	0.487	834.087	0.508	28	0.124	R.NNTEYKLDTFSSVYR.R
R4/RRR4-18/3	1420.812	1420.682	91.627	0.413	1543.720	0.257	25	0.121	K.KFSGKDVVLVATR.R
R4/RRR4-18/3	1292.414	1292.509	-73.961	0.378	1392.064	0.209	23	0.099	-.FSGKDVVLVATR.-
R4/RRR4-18/3	1837.379	1837.967	-866.989	0.390	451.314	0.401	24	0.093	R.NNTEYKLDTFSSVYR.R
R4/RRR4-18/3	1420.396	1420.682	-201.983	0.391	990.175	0.277	24	0.090	K.KFSGKDVVLVATR.R
R4/RRR4-18/3	1292.318	1292.509	-148.718	0.386	1240.383	0.162	22	0.082	-.FSGKDVVLVATR.-
R4/RRR4-18/3	1420.494	1420.682	-132.411	0.367	868.408	0.225	23	0.082	K.KFSGKDVVLVATR.R
R4/RRR4-18/3	1420.827	1420.682	102.096	0.431	794.014	0.224	22	0.082	K.KFSGKDVVLVATR.R
R4/RRR4-18/3	1421.068	1420.682	272.542	0.346	1082.542	0.199	24	0.081	K.KFSGKDVVLVATR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/3	1292.532	1292.509	17.551	0.371	1038.886	0.187	20	0.074	-.FSGKDVVLVATR.-
R4/RRR4-18/3	1292.396	1292.509	-87.604	0.367	1185.295	0.098	22	0.071	-.FSGKDVVLVATR.-
R4/RRR4-18/3	1292.877	1292.509	285.739	0.406	1063.356	0.115	20	0.068	-.FSGKDVVLVATR.-
R4/RRR4-7/2	1628.379	1629.877	-1538.643	0.354	1393.113	0.422	22	0.195	R.SLAIGQCDVALVVGAR.L
R4/RRR4-7/2	1492.004	1492.662	-1114.778	0.367	596.297	0.632	20	0.170	K.GVVPDTHPLSATAAR.S
R4/RRR4-7/2	1703.360	1704.024	-979.652	0.387	633.937	0.507	20	0.160	K.LVDTTGIPFLPTPM*GK.G
R4/RRR4-7/2	1629.716	1629.877	-98.613	0.404	832.068	0.341	18	0.146	-.SLAIGQCDVALVVGAR.-
R4/RRR4-7/2	1703.276	1704.024	-1029.155	0.315	337.131	0.467	15	0.141	-.LVDTTGIPFLPTPM*GK.-
R4/RRR4-7/3	1121.327	1121.315	11.332	0.466	1266.418	0.429	24	0.140	R.KPHVGIVGDAK.R
R4/RRR4-7/2	957.459	958.094	-1712.856	0.244	814.577	0.211	14	0.137	K.ATTIADIPR.L
R4/RRR4-7/2	957.855	958.094	-250.740	0.302	881.785	0.165	15	0.137	K.ATTIADIPR.L
R4/RRR4-7/3	1971.196	1971.246	-25.418	0.451	1558.235	0.279	27	0.132	R.KPAVINVIIDPYAGAESGR.M
R4/RRR4-7/3	1121.489	1121.315	156.421	0.447	1125.823	0.445	24	0.130	R.KPHVGIVGDAK.R
R4/RRR4-7/3	1971.992	1971.246	-129.373	0.397	1395.159	0.279	28	0.116	R.KPAVINVIIDPYAGAESGR.M
R4/RRR4-7/3	1970.627	1971.246	-824.054	0.354	813.611	0.213	24	0.076	R.KPAVINVIIDPYAGAESGR.M
R4/RRR4-17/2	1663.129	1663.767	-988.001	0.514	2540.370	0.575	25	0.416	K.DLASAGADVGSATDWVK.N
R4/RRR4-17/2	1663.390	1663.767	-227.342	0.542	2432.719	0.567	25	0.391	K.DLASAGADVGSATDWVK.N
R4/RRR4-17/2	1663.935	1663.767	101.205	0.553	2370.631	0.594	25	0.388	K.DLASAGADVGSATDWVK.N
R4/RRR4-16/2	1248.036	1248.478	-355.591	0.538	2464.427	0.502	19	0.375	K.LLNANSITM*VR.I
R4/RRR4-16/2	1247.852	1248.478	-1306.895	0.498	2203.303	0.495	19	0.325	K.LLNANSITM*VR.I
R4/RRR4-17/2	1248.059	1248.478	-337.141	0.513	1844.472	0.491	19	0.268	K.LLNANSITM*VR.I
R4/RRR4-16/2	1662.166	1663.767	-2172.744	0.316	2318.091	0.232	26	0.266	K.DLASAGADVGSATDWVK.N
R4/RRR4-16/2	1247.987	1248.478	-394.553	0.535	1603.591	0.497	19	0.240	K.LLNANSITM*VR.I
R4/RRR4-17/2	1247.517	1248.478	-1576.750	0.489	1555.766	0.470	18	0.227	K.LLNANSITM*VR.I
R4/RRR4-17/2	1247.616	1248.478	-1496.938	0.466	1606.829	0.442	18	0.226	K.LLNANSITM*VR.I
R4/RRR4-17/2	1533.888	1534.736	-1208.380	0.438	1404.086	0.518	23	0.220	R.IYDTDPTVLNALAK.T
R4/RRR4-17/2	1534.249	1534.736	-318.140	0.497	1343.673	0.513	23	0.215	R.IYDTDPTVLNALAK.T
R4/RRR4-17/2	1533.956	1534.736	-1163.788	0.425	1274.596	0.486	22	0.201	R.IYDTDPTVLNALAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1233.131	1232.479	-282.737	0.452	1091.373	0.477	17	0.186	K.LLNANSITMVR.I
R4/RRR4-17/2	1232.189	1232.479	-236.152	0.467	1087.332	0.469	17	0.185	K.LLNANSITMVR.I
R4/RRR4-16/2	1397.260	1397.556	-212.196	0.469	934.505	0.372	17	0.158	R.DASNLIDPPEVVK.L
R4/RRR4-17/2	963.985	964.229	-253.715	0.461	783.832	0.391	12	0.157	-.VM*VM*LPNK.-
R4/RRR4-17/2	1398.032	1397.556	341.587	0.465	1072.414	0.310	18	0.156	R.DASNLIDPPEVVK.L
R4/RRR4-16/2	1398.205	1397.556	-251.283	0.469	813.612	0.405	16	0.155	-.DASNLIDPPEVVK.-
R4/RRR4-17/2	964.045	964.229	-190.959	0.499	722.299	0.345	13	0.154	K.VM*VM*LPNK.D
R4/RRR4-17/2	963.910	964.229	-331.344	0.455	714.974	0.330	13	0.152	K.VM*VM*LPNK.D
R4/RRR4-17/2	1231.391	1232.479	-1700.702	0.263	805.840	0.355	15	0.149	K.LLNANSITMVR.I
R4/RRR4-16/2	1397.184	1397.556	-266.539	0.436	847.751	0.328	16	0.148	R.DASNLIDPPEVVK.L
R4/RRR4-17/3	1534.281	1534.736	-297.195	0.415	1036.018	0.369	26	0.106	R.IYDTDPTVLNALAK.T
R4/RRR4-5/2	1790.295	1789.966	184.335	0.556	1665.317	0.514	22	0.245	R.ASSGDLDNTNIISQILK.L
R4/RRR4-5/2	1181.217	1181.365	-125.898	0.457	1632.696	0.476	16	0.237	K.SPLEVFVSFR.G
R4/RRR4-5/2	1181.322	1181.365	-36.546	0.475	1398.946	0.451	16	0.207	K.SPLEVFVSFR.G
R4/RRR4-5/2	1789.464	1789.966	-841.480	0.518	1323.663	0.479	20	0.198	R.ASSGDLDNTNIISQILK.L
R4/RRR4-5/2	1124.085	1124.226	-125.652	0.494	1360.090	0.422	16	0.198	K.FSENVLDATK.K
R4/RRR4-5/2	1789.171	1789.966	-1005.855	0.504	1348.673	0.449	19	0.193	R.ASSGDLDNTNIISQILK.L
R4/RRR4-5/2	1239.328	1239.427	-79.449	0.442	1512.029	0.339	17	0.193	K.VM*DGLFSLANR.L
R4/RRR4-5/2	1124.035	1124.226	-170.318	0.488	1249.466	0.415	16	0.187	K.FSENVLDATK.K
R4/RRR4-5/2	1123.312	1124.226	-1709.015	0.379	1211.351	0.416	16	0.182	K.FSENVLDATK.K
R4/RRR4-5/2	1116.384	1117.232	-1659.849	0.400	785.224	0.409	16	0.160	R.LEGELADLEK.G
R4/RRR4-5/2	1116.310	1117.232	-1726.864	0.347	859.239	0.401	16	0.159	R.LEGELADLEK.G
R4/RRR4-5/2	1238.968	1239.427	-371.390	0.383	953.147	0.301	16	0.151	K.VM*DGLFSLANR.L
R4/RRR4-5/2	1181.878	1181.365	-413.510	0.340	602.331	0.444	11	0.150	K.SPLEVFVSFR.G
R4/RRR4-5/2	1299.189	1299.455	-205.502	0.394	1007.804	0.283	17	0.149	R.AAVEDVQPDKVK.F
R4/RRR4-5/3	1299.486	1299.455	23.628	0.336	1138.385	0.253	27	0.088	R.AAVEDVQPDKVK.F
R4/RRR4-5/3	1298.866	1299.455	-1227.340	0.303	622.428	0.323	23	0.085	R.AAVEDVQPDKVK.F
R4/RRR4-11/2	1319.134	1319.488	-269.594	0.529	2090.058	0.418	19	0.282	R.DDLFNINAGIVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1319.134	1319.488	-269.594	0.506	2006.745	0.407	19	0.267	R.DDLFNINAGIVK.G
R4/RRR4-12/2	1319.072	1319.488	-316.481	0.474	2064.895	0.361	19	0.263	R.DDLFNINAGIVK.G
R4/RRR4-11/2	1318.635	1319.488	-1409.627	0.443	1976.724	0.358	19	0.250	R.DDLFNINAGIVK.G
R4/RRR4-12/2	1319.037	1319.488	-343.501	0.337	1991.109	0.291	18	0.235	R.DDLFNINAGIVK.G
R4/RRR4-12/2	1234.020	1234.295	-223.796	0.516	896.672	0.493	18	0.178	R.TQDGGTEVVEAK.A
R4/RRR4-11/2	1234.022	1234.295	-221.911	0.487	988.594	0.450	18	0.175	R.TQDGGTEVVEAK.A
R4/RRR4-12/2	1234.023	1234.295	-221.514	0.486	901.205	0.463	18	0.173	R.TQDGGTEVVEAK.A
R4/RRR4-12/2	1233.476	1234.295	-1479.452	0.459	919.780	0.423	18	0.168	R.TQDGGTEVVEAK.A
R4/RRR4-11/2	1390.117	1390.482	-263.226	0.427	1055.105	0.354	17	0.161	K.RTQDGGTEVVEAK.A
R4/RRR4-11/2	1235.045	1234.295	-203.486	0.363	799.366	0.412	17	0.159	R.TQDGGTEVVEAK.A
R4/RRR4-11/2	1234.711	1234.295	337.586	0.447	611.651	0.457	15	0.158	R.TQDGGTEVVEAK.A
R4/RRR4-11/2	1234.401	1234.295	85.835	0.412	589.196	0.390	15	0.151	R.TQDGGTEVVEAK.A
R4/RRR4-11/2	1390.146	1390.482	-242.523	0.429	871.107	0.343	16	0.150	K.RTQDGGTEVVEAK.A
R4/RRR4-11/2	1235.070	1234.295	-183.061	0.349	580.650	0.337	15	0.144	-.TQDGGTEVVEAK.-
R4/RRR4-25/2	1391.873	1390.482	282.227	0.197	139.667	0.289	14	0.138	-.RTQDGGTEVVEAK.-
R4/RRR4-11/2	1390.341	1390.482	-101.149	0.353	608.786	0.174	13	0.119	-.RTQDGGTEVVEAK.-
R4/RRR4-7/2	1372.106	1372.553	-326.824	0.561	3648.597	0.552	25	0.700	R.NVNSALAASGIGGIK.V
R4/RRR4-7/2	1372.187	1372.553	-267.112	0.556	3528.162	0.550	25	0.662	R.NVNSALAASGIGGIK.V
R4/RRR4-7/2	1371.557	1372.553	-1459.144	0.472	3465.753	0.510	24	0.624	R.NVNSALAASGIGGIK.V
R4/RRR4-7/2	1799.386	1797.989	221.032	0.540	1107.584	0.538	22	0.197	R.EISLNYATFQPGTTVR.D
R4/RRR4-7/2	1756.325	1755.949	214.739	0.561	1105.716	0.545	21	0.197	R.DISLNYATFQPGTTVK.D
R4/RRR4-7/2	1611.332	1611.845	-941.768	0.404	1497.575	0.347	21	0.193	R.SEVVQM*YVSLGINR.M
R4/RRR4-7/2	1611.437	1611.845	-253.711	0.494	1348.831	0.415	20	0.192	R.SEVVQM*YVSLGINR.M
R4/RRR4-13/2	1756.425	1755.949	271.539	0.522	1043.027	0.539	20	0.190	R.DISLNYATFQPGTTVK.D
R4/RRR4-7/2	1756.378	1755.949	244.778	0.509	1001.920	0.550	20	0.189	R.DISLNYATFQPGTTVK.D
R4/RRR4-7/2	1799.369	1797.989	211.372	0.555	857.877	0.578	20	0.185	R.EISLNYATFQPGTTVR.D
R4/RRR4-14/2	1755.547	1755.949	-229.635	0.453	1030.974	0.520	20	0.185	R.DISLNYATFQPGTTVK.D
R4/RRR4-13/2	1755.366	1755.949	-904.838	0.490	1048.273	0.486	20	0.180	R.DISLNYATFQPGTTVK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1755.468	1755.949	-274.911	0.484	899.311	0.546	19	0.180	R.DISLNYATFQPGTTVK.D
R4/RRR4-7/2	1799.536	1797.989	-252.530	0.556	849.261	0.551	20	0.180	R.EISLNYATFQPGTTVR.D
R4/RRR4-7/2	1074.411	1075.201	-1671.247	0.448	977.993	0.428	14	0.172	R.HFGLFNPDK.T
R4/RRR4-13/2	1755.355	1755.949	-910.702	0.483	786.591	0.531	18	0.171	R.DISLNYATFQPGTTVK.D
R4/RRR4-13/2	1075.380	1075.201	167.068	0.360	833.520	0.465	14	0.167	R.HFGLFNPDK.T
R4/RRR4-13/2	1074.943	1075.201	-240.741	0.387	972.967	0.382	14	0.164	R.HFGLFNPDK.T
R4/RRR4-7/2	1074.646	1075.201	-1451.791	0.458	862.977	0.393	14	0.163	R.HFGLFNPDK.T
R4/RRR4-7/2	1075.858	1075.201	-320.085	0.461	861.101	0.392	14	0.162	R.HFGLFNPDK.T
R4/RRR4-12/2	1074.286	1075.201	-1788.261	0.405	725.796	0.292	13	0.146	R.HFGLFNPDK.T
R4/RRR4-7/3	1372.859	1372.553	224.010	0.257	1000.038	0.229	27	0.077	R.NVNSALAASGIGGIK.V
R4/RRR4-17/2	1776.823	1775.896	-41.180	0.556	2914.632	0.501	25	0.472	R.TEDDIALANSVDVGSLR.H
R4/RRR4-18/2	1775.493	1775.896	-227.676	0.532	2602.072	0.436	25	0.378	R.TEDDIALANSVDVGSLR.H
R4/RRR4-18/2	1712.359	1712.926	-917.839	0.580	2372.602	0.547	27	0.372	R.NQDTGLAELPATVAALK.N
R4/RRR4-18/2	1712.524	1712.926	-235.619	0.569	2110.053	0.575	26	0.333	R.NQDTGLAELPATVAALK.N
R4/RRR4-17/2	1712.531	1712.926	-231.114	0.566	2067.435	0.543	26	0.315	R.NQDTGLAELPATVAALK.N
R4/RRR4-17/2	1712.149	1712.926	-1041.021	0.561	1990.967	0.518	25	0.295	R.NQDTGLAELPATVAALK.N
R4/RRR4-17/2	1713.604	1712.926	-188.599	0.631	1835.724	0.530	25	0.273	R.NQDTGLAELPATVAALK.N
R4/RRR4-18/2	1711.766	1712.926	-1265.704	0.423	1769.748	0.542	24	0.267	R.NQDTGLAELPATVAALK.N
R4/RRR4-17/2	1187.651	1188.359	-1443.136	0.441	1729.418	0.357	17	0.219	R.AFAYFVLSGGR.F
R4/RRR4-18/2	1775.416	1775.896	-270.787	0.499	1599.176	0.431	22	0.217	R.TEDDIALANSVDVGSLR.H
R4/RRR4-17/2	1188.058	1188.359	-254.405	0.471	1424.299	0.338	16	0.184	R.AFAYFVLSGGR.F
R4/RRR4-17/2	1188.211	1188.359	-124.951	0.462	1218.645	0.390	15	0.177	R.AFAYFVLSGGR.F
R4/RRR4-18/2	1323.871	1324.380	-1143.248	0.429	812.675	0.513	15	0.174	K.VVYDEYNHER.H
R4/RRR4-18/2	1323.944	1324.380	-330.760	0.400	739.792	0.493	15	0.167	K.VVYDEYNHER.H
R4/RRR4-18/2	985.956	986.168	-215.370	0.350	803.554	0.275	16	0.147	K.FVLSM*SASK.D
R4/RRR4-18/2	1187.588	1188.359	-1495.791	0.357	845.682	0.274	14	0.144	R.AFAYFVLSGGR.F
R4/RRR4-18/2	1187.912	1188.359	-378.222	0.379	696.586	0.297	14	0.143	R.AFAYFVLSGGR.F
R4/RRR4-18/2	986.014	986.168	-156.375	0.394	506.458	0.327	14	0.143	-.FVLSM*SASK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	985.799	986.168	-375.126	0.342	534.195	0.183	14	0.138	-.FVLSM*SASK.-
R4/RRR4-23/1	1558.691	1559.526	-1180.934	0.258	677.626	0.254	14	0.564	R.YFNIAENEGEEED.-
R4/RRR4-23/1	1560.693	1559.526	107.241	0.525	703.148	0.522	14	0.550	R.YFNIAENEGEEED.-
R4/RRR4-23/1	1558.801	1559.526	-1110.317	0.172	406.482	0.060	11	0.550	-.YFNIAENEGEEED.-
R4/RRR4-23/1	1558.674	1559.526	-1191.944	0.277	455.594	0.243	12	0.538	R.YFNIAENEGEEED.-
R4/RRR4-23/2	1560.272	1559.526	-163.504	0.514	1596.240	0.493	19	0.216	R.YFNIAENEGEEED.-
R4/RRR4-23/2	1112.033	1112.215	-164.008	0.453	1192.380	0.440	18	0.188	K.VTVTSDGAFSK.R
R4/RRR4-23/2	1190.003	1190.289	-240.614	0.425	1174.741	0.384	18	0.175	K.AGNLGDSVTVTR.D
R4/RRR4-23/2	1268.145	1268.401	-202.906	0.386	1076.307	0.427	17	0.173	K.VTVTSDGAFSKR.Y
R4/RRR4-23/2	1267.510	1268.401	-1496.429	0.358	1035.889	0.443	17	0.172	K.VTVTSDGAFSKR.Y
R4/RRR4-23/2	1268.119	1268.401	-223.185	0.397	976.929	0.439	16	0.169	K.VTVTSDGAFSKR.Y
R4/RRR4-23/2	1558.420	1559.526	-1355.836	0.342	1437.640	0.393	18	0.165	R.YFNIAENEGEEED.-
R4/RRR4-23/2	1111.512	1112.215	-1536.703	0.342	972.339	0.394	17	0.163	K.VTVTSDGAFSK.R
R4/RRR4-23/2	1190.076	1190.289	-179.796	0.413	808.712	0.429	17	0.161	K.AGNLGDSVTVTR.D
R4/RRR4-23/2	1189.907	1190.289	-321.715	0.427	917.806	0.370	18	0.159	K.AGNLGDSVTVTR.D
R4/RRR4-23/2	1111.493	1112.215	-1553.804	0.328	992.800	0.309	17	0.153	K.VTVTSDGAFSK.R
R4/RRR4-23/2	1049.557	1050.252	-1619.227	0.394	856.472	0.324	14	0.152	K.IM*EIASLEK.F
R4/RRR4-23/2	1050.090	1050.252	-154.773	0.495	708.981	0.294	13	0.143	-.IM*EIASLEK.-
R4/RRR4-23/2	1049.427	1050.252	-1744.031	0.354	907.681	0.166	14	0.137	K.IM*EIASLEK.F
R4/RRR4-23/2	1559.005	1559.526	-978.673	0.324	1270.854	0.368	17	0.128	R.YFNIAENEGEEED.-
R4/RRR4-5/2	1081.166	1081.241	-69.488	0.391	841.351	0.425	14	0.160	-.ACNFASGLIK.-
R4/RRR4-5/2	1208.557	1209.374	-1507.525	0.336	830.375	0.414	15	0.154	R.GEVVVGGYSITK.G
R4/RRR4-5/2	1035.201	1036.077	-1817.813	0.335	959.329	0.315	14	0.153	R.EFVESPDGR.K
R4/RRR4-5/2	1608.081	1608.771	-1054.257	0.433	890.677	0.348	20	0.152	R.FVLCGGAPLSSDTQR.F
R4/RRR4-5/2	1608.312	1608.771	-286.438	0.405	857.706	0.354	20	0.152	R.FVLCGGAPLSSDTQR.F
R4/RRR4-5/2	1080.990	1081.241	-232.485	0.334	755.234	0.358	14	0.149	R.ACNFASGLIK.L
R4/RRR4-5/2	1035.781	1036.077	-286.724	0.316	567.836	0.375	11	0.145	R.EFVESPDGR.K
R4/RRR4-5/2	864.811	864.969	-182.861	0.261	843.015	0.256	12	0.139	R.AAIFADTR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1035.972	1036.077	-101.239	0.296	573.785	0.277	11	0.134	-.EFVESPDGR.-
R4/RRR4-5/3	1075.265	1075.283	-16.536	0.486	1137.006	0.307	21	0.101	R.LEKFEIPAK.I
R4/RRR4-5/3	1075.379	1075.283	89.692	0.437	852.891	0.284	19	0.088	R.LEKFEIPAK.I
R4/RRR4-5/3	1075.206	1075.283	-71.366	0.502	676.461	0.320	17	0.064	-.LEKFEIPAK.-
R4/RRR4-3/2	1177.731	1178.403	-1424.103	0.461	1757.615	0.507	17	0.259	K.LPTAILSTYAK.A
R4/RRR4-3/2	1614.506	1614.827	-199.341	0.529	1315.820	0.555	19	0.218	R.IVSLLSESYNPHVR.Y
R4/RRR4-3/2	1178.260	1178.403	-121.953	0.463	1583.581	0.416	18	0.217	K.LPTAILSTYAK.A
R4/RRR4-3/2	1909.419	1910.163	-915.771	0.485	1079.783	0.538	23	0.193	K.KAPEPEPTFQILTNPAR.V
R4/RRR4-3/2	1909.080	1910.163	-1094.547	0.507	953.301	0.576	22	0.191	K.KAPEPEPTFQILTNPAR.V
R4/RRR4-3/2	1230.035	1229.413	-308.433	0.449	1061.237	0.499	18	0.186	K.FSATAGLGVIHR.G
R4/RRR4-3/2	1177.587	1178.403	-1546.757	0.405	1201.279	0.361	17	0.173	K.LPTAILSTYAK.A
R4/RRR4-3/2	1228.937	1229.413	-388.311	0.430	856.476	0.477	16	0.168	K.FSATAGLGVIHR.G
R4/RRR4-2/2	1178.442	1178.403	33.184	0.329	1119.198	0.376	17	0.168	K.LPTAILSTYAK.A
R4/RRR4-3/2	1909.708	1910.163	-238.795	0.451	744.670	0.478	20	0.161	K.KAPEPEPTFQILTNPAR.V
R4/RRR4-3/3	1614.648	1614.827	-111.068	0.432	697.037	0.586	28	0.131	R.IVSLLSESYNPHVR.Y
R4/RRR4-3/3	1614.832	1614.827	3.130	0.481	713.157	0.559	27	0.128	R.IVSLLSESYNPHVR.Y
R4/RRR4-3/2	1350.288	1349.583	-218.490	0.234	858.173	0.066	15	0.125	R.YGGMYALALAYR.G
R4/RRR4-3/3	1614.495	1614.827	-206.518	0.414	576.085	0.538	26	0.116	R.IVSLLSESYNPHVR.Y
R4/RRR4-3/3	1229.643	1229.413	187.669	0.433	555.078	0.538	22	0.115	K.FSATAGLGVIHR.G
R4/RRR4-3/3	1909.844	1910.163	-167.433	0.424	1346.673	0.288	28	0.113	K.KAPEPEPTFQILTNPAR.V
R4/RRR4-3/3	1229.688	1229.413	223.954	0.408	471.266	0.542	22	0.112	K.FSATAGLGVIHR.G
R4/RRR4-3/3	1909.611	1910.163	-815.024	0.420	1421.097	0.226	31	0.105	-.KAPEPEPTFQILTNPAR.-
R4/RRR4-3/3	1717.508	1717.841	-194.808	0.408	1103.372	0.339	26	0.105	K.AGEM*LAYAHDTQHEK.I
R4/RRR4-3/3	1910.317	1910.163	81.031	0.470	1372.956	0.247	30	0.105	-.KAPEPEPTFQILTNPAR.-
R4/RRR4-3/3	1717.710	1717.841	-76.961	0.429	599.453	0.445	20	0.100	K.AGEM*LAYAHDTQHEK.I
R4/RRR4-2/3	1614.825	1614.827	-1.533	0.372	417.503	0.453	21	0.100	R.IVSLLSESYNPHVR.Y
R4/RRR4-3/3	1229.383	1229.413	-24.273	0.370	389.116	0.454	19	0.099	K.FSATAGLGVIHR.G
R4/RRR4-1/3	1909.714	1910.163	-235.628	0.338	536.658	0.363	24	0.092	K.KAPEPEPTFQILTNPAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1717.551	1717.841	-169.781	0.402	498.706	0.381	20	0.088	-.AGEM*LAYAHDTQHEK.-
R4/RRR4-2/3	1911.625	1910.163	242.633	0.298	710.158	0.156	23	0.074	-.KAPEPEPTFQILTNPAR.-
R4/RRR4-2/2	1766.365	1767.020	-939.822	0.571	3245.841	0.600	29	0.603	K.VAIIGSGPAGLAAADQLNK.M
R4/RRR4-2/2	1766.401	1767.020	-919.009	0.551	3162.504	0.601	29	0.580	K.VAIIGSGPAGLAAADQLNK.M
R4/RRR4-2/2	1766.617	1767.020	-228.820	0.505	2434.990	0.562	26	0.389	K.VAIIGSGPAGLAAADQLNK.M
R4/RRR4-1/2	1171.266	1170.341	-63.725	0.394	1703.642	0.426	16	0.230	R.VGLLVESAEPR.E
R4/RRR4-2/3	1844.868	1844.926	-31.804	0.534	1274.916	0.555	34	0.184	K.GHADHVLISGHDGGTGASR.W
R4/RRR4-2/3	1844.791	1844.926	-73.319	0.554	1161.862	0.594	35	0.182	K.GHADHVLISGHDGGTGASR.W
R4/RRR4-2/2	1432.266	1432.607	-238.725	0.453	1142.670	0.426	17	0.179	R.VFIETPIQNTNR.A
R4/RRR4-2/3	1845.171	1844.926	133.226	0.548	1211.391	0.563	34	0.178	K.GHADHVLISGHDGGTGASR.W
R4/RRR4-2/2	1432.089	1432.607	-1063.183	0.427	1108.430	0.430	18	0.178	R.VFIETPIQNTNR.A
R4/RRR4-2/3	1680.146	1680.867	-1027.393	0.419	1366.192	0.506	32	0.177	K.M*AQGAKPGEGGELPGHK.V
R4/RRR4-2/2	1530.705	1529.716	-7.008	0.463	1288.506	0.371	17	0.177	R.DALCLHELAFPSR.A
R4/RRR4-2/2	1432.259	1432.607	-243.599	0.441	1178.394	0.382	18	0.175	R.VFIETPIQNTNR.A
R4/RRR4-2/3	1680.702	1680.867	-98.964	0.430	899.784	0.467	29	0.119	K.M*AQGAKPGEGGELPGHK.V
R4/RRR4-2/3	1664.482	1664.868	-232.424	0.375	386.898	0.362	21	0.059	-.MAQGAKPGEGGELPGHK.-
R4/RRR4-11/2	1720.328	1720.910	-922.270	0.528	2387.966	0.456	22	0.343	K.NLSLGTEAFWLGQQR.K
R4/RRR4-11/2	1720.357	1720.910	-905.459	0.538	2282.286	0.416	21	0.310	K.NLSLGTEAFWLGQQR.K
R4/RRR4-11/2	1516.318	1516.679	-238.654	0.506	1331.971	0.522	19	0.212	K.IDTNGVVSALLEER.L
R4/RRR4-11/2	1516.465	1516.679	-141.422	0.396	1272.719	0.390	20	0.181	K.IDTNGVVSALLEER.L
R4/RRR4-11/2	1515.499	1516.679	-1442.547	0.372	1168.916	0.387	18	0.171	K.IDTNGVVSALLEER.L
R4/RRR4-11/2	792.946	792.906	51.169	0.424	866.167	0.293	13	0.150	K.SGVGFVAR.Y
R4/RRR4-11/2	792.986	792.906	101.037	0.397	869.638	0.265	13	0.147	K.SGVGFVAR.Y
R4/RRR4-11/2	1719.569	1720.910	-1365.624	0.315	1073.571	0.275	16	0.147	K.NLSLGTEAFWLGQQR.K
R4/RRR4-11/2	792.981	792.906	94.862	0.405	873.662	0.251	13	0.146	K.SGVGFVAR.Y
R4/RRR4-11/3	1702.678	1701.903	-132.399	0.439	1022.469	0.346	24	0.099	-.GKIDTNGVVSALLEER.-
R4/RRR4-11/3	921.171	921.079	100.520	0.382	1231.037	0.244	19	0.093	R.KSGVGFVAR.Y
R4/RRR4-11/3	920.888	921.079	-207.771	0.333	1128.520	0.095	17	0.069	R.KSGVGFVAR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1624.133	1624.726	-983.529	0.489	2154.420	0.512	22	0.321	K.GCVFTYDAVGSYER.T
R4/RRR4-17/2	1624.318	1624.726	-251.881	0.484	2068.689	0.508	22	0.306	K.GCVFTYDAVGSYER.T
R4/RRR4-17/2	1688.149	1687.870	165.825	0.494	1383.642	0.556	24	0.226	R.DAVTPLSETEAVDLVK.D
R4/RRR4-16/2	1687.181	1687.870	-1003.814	0.477	1358.514	0.566	24	0.226	R.DAVTPLSETEAVDLVK.D
R4/RRR4-16/2	1721.183	1720.988	113.417	0.572	1685.906	0.415	21	0.224	R.DIYTGDKLEIVVINK.A
R4/RRR4-16/2	1687.277	1687.870	-947.012	0.447	1376.973	0.517	24	0.216	R.DAVTPLSETEAVDLVK.D
R4/RRR4-16/2	1688.264	1687.870	234.347	0.517	1275.368	0.551	24	0.215	R.DAVTPLSETEAVDLVK.D
R4/RRR4-16/2	1624.184	1624.726	-951.912	0.418	1341.199	0.505	20	0.209	K.GCVFTYDAVGSYER.T
R4/RRR4-17/2	1686.598	1687.870	-1351.087	0.293	1409.272	0.470	24	0.204	R.DAVTPLSETEAVDLVK.D
R4/RRR4-17/2	1687.288	1687.870	-940.330	0.434	1227.834	0.496	23	0.198	R.DAVTPLSETEAVDLVK.D
R4/RRR4-17/2	1050.981	1051.264	-269.995	0.501	949.890	0.449	15	0.174	K.SPSPLLLPAR.D
R4/RRR4-17/2	1050.659	1051.264	-1532.131	0.442	972.365	0.446	15	0.173	K.SPSPLLLPAR.D
R4/RRR4-17/2	995.920	996.056	-136.782	0.333	988.116	0.425	14	0.168	K.DVFASATER.D
R4/RRR4-16/2	1623.519	1624.726	-1363.310	0.262	951.378	0.460	19	0.164	K.GCVFTYDAVGSYER.T
R4/RRR4-17/2	1051.207	1051.264	-54.347	0.379	816.216	0.440	13	0.161	K.SPSPLLLPAR.D
R4/RRR4-17/2	995.900	996.056	-156.701	0.327	816.587	0.386	14	0.156	K.DVFASATER.D
R4/RRR4-17/2	995.831	996.056	-226.547	0.273	857.182	0.363	14	0.153	K.DVFASATER.D
R4/RRR4-16/2	1050.502	1051.264	-1682.244	0.362	721.265	0.387	13	0.152	K.SPSPLLLPAR.D
R4/RRR4-16/2	995.826	996.056	-231.589	0.256	865.951	0.303	13	0.147	K.DVFASATER.D
R4/RRR4-16/2	995.169	996.056	-1901.763	0.236	567.078	0.384	11	0.143	K.DVFASATER.D
R4/RRR4-16/2	995.548	996.056	-1519.297	0.247	811.241	0.198	14	0.139	K.DVFASATER.D
R4/RRR4-16/2	1293.657	1294.482	-1414.697	0.509	1580.539	0.525	18	0.242	K.SDLLLASNPVHK.S
R4/RRR4-16/2	1294.111	1294.482	-287.295	0.514	1573.905	0.479	18	0.230	K.SDLLLASNPVHK.S
R4/RRR4-16/2	1294.194	1294.482	-223.324	0.514	1525.117	0.483	19	0.227	K.SDLLLASNPVHK.S
R4/RRR4-16/2	1458.409	1458.775	-251.908	0.456	1334.784	0.526	18	0.213	K.VRPAWLAILFGSK.T
R4/RRR4-16/2	1458.416	1458.775	-246.869	0.474	1029.518	0.546	17	0.190	K.VRPAWLAILFGSK.T
R4/RRR4-16/2	1363.300	1362.601	-221.793	0.528	1162.746	0.456	19	0.188	K.LLGVWSSPYAIR.V
R4/RRR4-16/2	1363.213	1362.601	-285.216	0.497	1034.733	0.456	18	0.179	K.LLGVWSSPYAIR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1458.236	1458.775	-1058.981	0.473	854.019	0.522	16	0.173	-.VRPAWLAILFGSK.-
R4/RRR4-16/2	1362.651	1362.601	36.964	0.464	775.061	0.487	16	0.169	K.LLGVWSSPYAIR.V
R4/RRR4-16/2	1657.174	1656.771	243.694	0.530	631.069	0.507	20	0.168	K.SLPYEYVEENLGDK.S
R4/RRR4-16/2	1362.223	1362.601	-278.413	0.418	822.800	0.429	16	0.162	K.LLGVWSSPYAIR.V
R4/RRR4-16/2	1657.212	1656.771	266.592	0.514	611.364	0.432	20	0.158	K.SLPYEYVEENLGDK.S
R4/RRR4-16/2	1656.148	1656.771	-983.220	0.452	608.415	0.426	20	0.156	K.SLPYEYVEENLGDK.S
R4/RRR4-16/2	1363.556	1362.601	-33.278	0.410	582.070	0.407	15	0.153	K.LLGVWSSPYAIR.V
R4/RRR4-18/2	1361.398	1362.601	-1623.191	0.348	427.915	0.421	13	0.149	K.LLGVWSSPYAIR.V
R4/RRR4-17/2	1363.508	1362.601	-68.120	0.346	462.029	0.375	13	0.146	K.LLGVWSSPYAIR.V
R4/RRR4-16/2	1362.310	1362.601	-213.955	0.424	621.001	0.350	15	0.146	-.LLGVWSSPYAIR.-
R4/RRR4-18/2	1362.091	1362.601	-1111.798	0.405	416.062	0.397	12	0.144	-.LLGVWSSPYAIR.-
R4/RRR4-16/2	1362.306	1362.601	-217.281	0.292	507.336	0.370	12	0.143	K.LLGVWSSPYAIR.V
R4/RRR4-18/2	1362.318	1362.601	-208.742	0.271	541.351	0.320	14	0.143	K.LLGVWSSPYAIR.V
R4/RRR4-6/2	1363.827	1362.601	166.387	0.306	489.243	0.253	13	0.138	-.LLGVWSSPYAIR.-
R4/RRR4-16/2	940.713	941.196	-515.225	0.490	885.910	0.198	12	0.134	-.VRVVLNLK.-
R4/RRR4-16/2	941.199	941.196	3.433	0.472	994.116	0.136	13	0.133	-.VRVVLNLK.-
R4/RRR4-16/2	940.531	941.196	-1775.708	0.435	914.690	0.109	12	0.129	R.VRVVLNLK.S
R4/RRR4-5/2	1330.187	1329.569	-288.432	0.428	1038.110	0.447	16	0.174	R.ALVEGPFLDVLR.S
R4/RRR4-5/2	1329.100	1329.569	-353.981	0.356	1118.612	0.358	17	0.165	R.ALVEGPFLDVLR.S
R4/RRR4-5/2	1501.184	1501.664	-320.662	0.448	817.039	0.444	17	0.161	K.LPADTPYSQFAYK.F
R4/RRR4-5/2	1180.287	1179.348	-51.204	0.454	695.296	0.453	16	0.161	K.NITGLVEAYAK.N
R4/RRR4-5/2	987.188	987.175	12.389	0.364	1282.533	0.215	14	0.155	R.NELVALLSK.Y
R4/RRR4-5/2	1378.864	1379.504	-1192.485	0.388	704.721	0.436	16	0.153	R.SSSIGNGVQFLNR.H
R4/RRR4-5/2	1329.155	1329.569	-312.606	0.367	505.303	0.428	13	0.147	R.ALVEGPFLDVLR.S
R4/RRR4-5/3	1447.443	1447.573	-90.274	0.544	1316.106	0.323	28	0.120	K.SKDREEIAEIEK.M
R4/RRR4-14/2	1779.520	1777.978	-258.525	0.568	2231.610	0.590	23	0.361	K.NVLTNFWGM*SFTTDK.L
R4/RRR4-14/2	1197.920	1198.305	-322.323	0.545	1686.253	0.463	16	0.240	R.TCYAQASQIR.Q
R4/RRR4-14/2	1197.321	1198.305	-1661.767	0.477	1502.870	0.437	17	0.215	R.TCYAQASQIR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1198.069	1198.305	-196.890	0.560	1437.622	0.455	17	0.213	R.TCYAQASQIR.Q
R4/RRR4-14/2	1580.448	1579.824	-239.118	0.508	1121.453	0.554	22	0.204	K.ATSSIFPLQNVFVR.K
R4/RRR4-13/2	1197.916	1198.305	-325.390	0.537	1260.792	0.428	16	0.191	R.TCYAQASQIR.Q
R4/RRR4-14/2	1579.394	1579.824	-273.154	0.425	986.727	0.467	21	0.177	K.ATSSIFPLQNVFVR.K
R4/RRR4-14/2	1777.397	1777.978	-892.372	0.437	891.425	0.483	18	0.169	K.NVLTNFWGM*SFTTDK.L
R4/RRR4-13/2	890.909	890.021	-126.106	0.442	774.431	0.412	13	0.163	K.APSVFNVR.N
R4/RRR4-14/2	889.932	890.021	-100.655	0.350	730.265	0.440	13	0.161	K.APSVFNVR.N
R4/RRR4-14/2	889.565	890.021	-514.982	0.325	749.818	0.449	13	0.160	K.APSVFNVR.N
R4/RRR4-14/2	889.988	890.021	-38.054	0.467	569.493	0.434	11	0.158	K.APSVFNVR.N
R4/RRR4-13/2	889.768	890.021	-285.477	0.333	688.274	0.434	12	0.157	K.APSVFNVR.N
R4/RRR4-13/2	985.780	986.182	-409.324	0.368	612.064	0.417	13	0.157	R.LFCIGFTK.R
R4/RRR4-13/2	985.668	986.182	-1541.607	0.337	647.506	0.420	13	0.156	R.LFCIGFTK.R
R4/RRR4-14/2	985.940	986.182	-247.075	0.375	580.794	0.444	13	0.156	-.LFCIGFTK.-
R4/RRR4-13/2	889.856	890.021	-187.071	0.368	570.629	0.434	11	0.155	K.APSVFNVR.N
R4/RRR4-14/2	986.005	986.182	-180.501	0.425	567.715	0.377	13	0.155	R.LFCIGFTK.R
R4/RRR4-13/2	1579.205	1579.824	-1028.800	0.366	711.556	0.402	18	0.154	K.ATSSIFPLQNVFVR.K
R4/RRR4-13/2	1579.997	1579.824	109.758	0.379	749.443	0.356	18	0.150	K.ATSSIFPLQNVFVR.K
R4/RRR4-14/2	986.098	986.182	-85.996	0.448	631.678	0.344	13	0.150	-.LFCIGFTK.-
R4/RRR4-13/2	985.845	986.182	-343.474	0.324	519.789	0.354	12	0.149	R.LFCIGFTK.R
R4/RRR4-13/2	1779.226	1777.978	139.455	0.405	392.550	0.456	15	0.148	K.NVLTNFWGM*SFTTDK.L
R4/RRR4-14/2	1578.658	1579.824	-1376.069	0.268	828.152	0.320	19	0.147	K.ATSSIFPLQNVFVR.K
R4/RRR4-16/2	1579.221	1579.824	-1018.478	0.365	541.316	0.360	16	0.146	K.ATSSIFPLQNVFVR.K
R4/RRR4-12/2	1579.686	1579.824	-87.785	0.318	658.940	0.335	17	0.145	K.ATSSIFPLQNVFVR.K
R4/RRR4-11/2	1579.523	1579.824	-191.121	0.314	634.688	0.298	17	0.143	K.ATSSIFPLQNVFVR.K
R4/RRR4-14/2	1578.898	1579.824	-1223.949	0.249	619.218	0.306	17	0.141	K.ATSSIFPLQNVFVR.K
R4/RRR4-14/2	1578.726	1579.824	-1332.812	0.233	718.128	0.270	18	0.140	K.ATSSIFPLQNVFVR.K
R4/RRR4-22/2	1749.079	1748.918	92.008	0.598	2321.405	0.565	25	0.369	K.ATDDKAGQEALLNVFR.A
R4/RRR4-22/2	1748.358	1748.918	-894.949	0.547	2214.872	0.585	24	0.356	K.ATDDKAGQEALLNVFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1721.479	1721.929	-262.345	0.526	2350.033	0.468	25	0.342	R.AAEACEQFGGVLVTLR.M
R4/RRR4-22/2	1749.469	1748.918	-257.657	0.537	2155.472	0.536	24	0.329	K.ATDDKAGQEALLNVFR.A
R4/RRR4-22/2	1721.293	1721.929	-953.477	0.529	2094.829	0.501	23	0.307	R.AAEACEQFGGVLVTLR.M
R4/RRR4-22/2	1721.273	1721.929	-965.083	0.516	2149.040	0.465	24	0.305	R.AAEACEQFGGVLVTLR.M
R4/RRR4-22/2	1766.616	1767.017	-227.434	0.509	1890.111	0.544	25	0.289	K.ITLIGTSGISGSYVELR.-
R4/RRR4-22/2	1218.812	1218.387	350.026	0.505	1838.983	0.465	18	0.261	K.AGQEALLNVFR.A
R4/RRR4-22/2	1219.056	1218.387	-272.442	0.502	1514.907	0.483	17	0.225	K.AGQEALLNVFR.A
R4/RRR4-22/2	1219.599	1218.387	173.916	0.527	1331.898	0.495	16	0.209	K.AGQEALLNVFR.A
R4/RRR4-22/2	1618.101	1617.740	224.003	0.570	1262.110	0.489	20	0.202	K.YLESFGPEENYLR.K
R4/RRR4-22/2	1617.113	1617.740	-1009.225	0.503	1241.473	0.449	20	0.192	K.YLESFGPEENYLR.K
R4/RRR4-22/2	1617.028	1617.740	-1061.826	0.510	1189.696	0.452	20	0.189	K.YLESFGPEENYLR.K
R4/RRR4-22/2	1617.953	1617.740	132.307	0.405	318.035	0.379	12	0.142	K.YLESFGPEENYLR.K
R4/RRR4-10/2	1461.171	1460.527	-244.393	0.528	1915.095	0.564	20	0.298	K.AISTSNAYDDQFK.Q
R4/RRR4-10/2	1317.573	1318.416	-1402.307	0.404	2069.768	0.451	21	0.287	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1318.407	1318.416	-6.464	0.485	1750.244	0.596	21	0.282	R.LANDTQGTVEAAK.W
R4/RRR4-9/2	1461.082	1460.527	-305.329	0.542	1688.632	0.547	20	0.261	K.AISTSNAYDDQFK.Q
R4/RRR4-9/2	1460.878	1460.527	241.071	0.514	1697.173	0.539	20	0.260	K.AISTSNAYDDQFK.Q
R4/RRR4-10/2	1460.085	1460.527	-304.028	0.509	1561.707	0.581	20	0.254	K.AISTSNAYDDQFK.Q
R4/RRR4-10/2	1318.259	1318.416	-119.311	0.413	1640.308	0.493	20	0.239	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1318.794	1318.416	287.747	0.449	1533.633	0.539	20	0.238	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1318.201	1318.416	-163.342	0.513	1650.515	0.467	21	0.236	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1318.759	1318.416	261.201	0.518	1456.127	0.543	20	0.232	R.LANDTQGTVEAAK.W
R4/RRR4-9/2	1317.431	1318.416	-1511.100	0.348	1684.187	0.422	21	0.227	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1318.348	1318.416	-51.322	0.458	1373.728	0.565	20	0.227	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1319.267	1318.416	-112.724	0.476	1444.167	0.523	20	0.225	R.LANDTQGTVEAAK.W
R4/RRR4-12/2	1318.155	1318.416	-198.180	0.444	1403.208	0.510	21	0.218	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1318.008	1318.416	-310.141	0.454	1450.837	0.487	20	0.218	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1286.145	1286.493	-271.559	0.490	1322.834	0.532	19	0.217	K.IPATAECVPSIK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1317.543	1318.416	-1425.571	0.377	1575.221	0.416	21	0.215	R.LANDTQGTVEAAK.W
R4/RRR4-9/2	1317.560	1318.416	-1412.171	0.418	1468.565	0.453	20	0.212	R.LANDTQGTVEAAK.W
R4/RRR4-12/2	1318.089	1318.416	-248.257	0.454	1300.876	0.501	20	0.207	R.LANDTQGTVEAAK.W
R4/RRR4-1/2	1318.074	1318.416	-259.964	0.437	1319.330	0.473	19	0.202	R.LANDTQGTVEAAK.W
R4/RRR4-10/2	1459.606	1460.527	-1320.374	0.347	1334.074	0.470	20	0.200	K.AISTSNAYDDQFK.Q
R4/RRR4-10/2	1287.144	1286.493	-271.728	0.542	1147.714	0.501	19	0.196	K.IPATAECVPSIK.E
R4/RRR4-10/2	1286.163	1286.493	-257.085	0.487	1123.359	0.505	19	0.194	K.IPATAECVPSIK.E
R4/RRR4-1/2	1318.117	1318.416	-226.888	0.458	1296.279	0.437	20	0.194	R.LANDTQGTVEAAK.W
R4/RRR4-9/2	1460.141	1460.527	-265.444	0.394	1231.115	0.468	18	0.191	K.AISTSNAYDDQFK.Q
R4/RRR4-9/2	1179.019	1178.320	-255.940	0.485	807.332	0.439	16	0.165	R.GVTSNPSIFQK.A
R4/RRR4-10/2	1425.485	1424.580	-66.446	0.409	1044.311	0.371	17	0.163	K.DAESAYWELVIK.D
R4/RRR4-9/2	1177.595	1178.320	-1468.767	0.401	849.812	0.411	16	0.162	R.GVTSNPSIFQK.A
R4/RRR4-10/2	1177.495	1178.320	-1554.781	0.361	868.889	0.392	17	0.160	R.GVTSNPSIFQK.A
R4/RRR4-10/2	1178.020	1178.320	-254.910	0.463	667.851	0.392	15	0.154	R.GVTSNPSIFQK.A
R4/RRR4-10/2	1178.150	1178.320	-144.412	0.435	819.677	0.349	16	0.154	R.GVTSNPSIFQK.A
R4/RRR4-9/2	1177.347	1178.320	-1680.495	0.322	695.851	0.401	15	0.152	R.GVTSNPSIFQK.A
R4/RRR4-18/1	401.365	401.396	-77.254	-2.202	17.607	0.000	3	0.934	R.GPGGGG.-
R4/RRR4-30/1	401.065	401.396	-827.381	-1.217	47.716	0.371	4	0.838	R.GPGGGG.-
R4/RRR4-22/1	401.377	401.396	-47.663	-1.336	19.542	0.000	3	0.838	R.GPGGGG.-
R4/RRR4-10/1	401.287	401.396	-271.318	-1.270	50.014	0.810	4	0.821	R.GPGGGG.-
R4/RRR4-15/1	401.176	401.396	-551.105	-2.373	1.668	0.000	1	0.811	R.GPGGGG.-
R4/RRR4-30/1	401.223	401.396	-432.638	-1.614	17.000	0.000	2	0.780	R.GPGGGG.-
R4/RRR4-25/1	401.199	401.396	-492.937	-1.512	13.029	0.000	2	0.777	R.GPGGGG.-
R4/RRR4-27/1	401.189	401.396	-517.669	-0.467	27.778	0.789	4	0.738	R.GPGGGG.-
R4/RRR4-22/1	401.134	401.396	-654.480	-0.846	1.757	0.000	1	0.727	R.GPGGGG.-
R4/RRR4-16/1	401.237	401.396	-397.531	-1.070	34.916	0.636	3	0.722	R.GPGGGG.-
R4/RRR4-8/1	401.107	401.396	-722.442	-0.983	34.851	0.599	3	0.717	R.GPGGGG.-
R4/RRR4-5/1	401.200	401.396	-490.494	-1.378	21.187	0.369	2	0.713	R.GPGGGG.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-27/1	401.188	401.396	-519.501	-1.366	21.501	0.369	2	0.711	R.GPGGGG.-
R4/RRR4-21/1	401.554	401.396	394.626	-1.351	12.551	0.450	2	0.706	R.GPGGGG.-
R4/RRR4-25/1	401.185	401.396	-528.356	-1.051	35.143	0.820	3	0.704	R.GPGGGG.-
R4/RRR4-2/1	401.189	401.396	-516.753	-1.433	21.840	0.665	2	0.698	R.GPGGGG.-
R4/RRR4-8/1	401.215	401.396	-453.093	-1.177	20.998	0.379	2	0.694	R.GPGGGG.-
R4/RRR4-17/1	401.207	401.396	-471.564	-1.187	21.204	0.384	2	0.694	R.GPGGGG.-
R4/RRR4-21/1	401.219	401.396	-442.102	-1.462	10.000	0.000	1	0.678	-.GPGGGG.-
R4/RRR4-30/1	401.261	401.396	-338.465	-0.995	21.208	0.600	2	0.649	R.GPGGGG.-
R4/RRR4-25/1	401.276	401.396	-299.855	-1.041	21.581	0.643	2	0.647	R.GPGGGG.-
R4/RRR4-19/1	401.281	401.396	-287.952	-0.371	24.796	0.914	3	0.633	R.GPGGGG.-
R4/RRR4-22/1	401.241	401.396	-388.220	-0.962	4.540	0.840	2	0.625	R.GPGGGG.-
R4/RRR4-20/1	401.261	401.396	-338.312	-1.035	21.448	0.614	2	0.620	-.GPGGGG.-
R4/RRR4-4/2	1010.545	1011.116	-1559.087	0.398	1000.564	0.399	13	0.166	K.FGDFANALR.I
R4/RRR4-4/2	1011.022	1011.116	-92.777	0.442	812.040	0.407	13	0.160	K.FGDFANALR.I
R4/RRR4-4/2	1010.292	1011.116	-1810.581	0.279	383.107	0.305	12	0.143	K.FGDFANALR.I
R4/RRR4-18/3	1538.339	1538.759	-273.675	0.478	1847.007	0.465	30	0.227	R.M*NTKPSHGPIHFR.A
R4/RRR4-18/2	1431.304	1431.702	-278.491	0.481	1499.668	0.584	20	0.226	K.LGSQIDILAPIKY.-
R4/RRR4-18/2	1431.338	1431.702	-254.704	0.425	1404.733	0.566	19	0.203	K.LGSQIDILAPIKY.-
R4/RRR4-18/3	1539.775	1538.759	10.054	0.425	1747.331	0.416	28	0.195	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/3	1538.388	1538.759	-241.672	0.533	1624.362	0.469	30	0.192	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/3	1538.157	1538.759	-1044.469	0.463	1521.848	0.501	28	0.192	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/2	1431.303	1431.702	-279.176	0.471	1401.599	0.540	20	0.191	K.LGSQIDILAPIKY.-
R4/RRR4-18/3	1538.609	1538.759	-97.804	0.474	1575.458	0.421	27	0.172	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/3	1538.657	1538.759	-66.648	0.453	1505.515	0.449	29	0.170	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/2	1426.790	1427.594	-1267.954	0.477	993.547	0.390	16	0.162	R.CEEM*CISGGLVR.Q
R4/RRR4-18/3	1539.762	1538.759	1.944	0.515	1299.104	0.479	26	0.158	R.M*NTKPSHGPIHFR.A
R4/RRR4-18/3	1538.352	1538.759	-265.435	0.456	1348.344	0.452	27	0.155	R.M*NTKPSHGPIHFR.A
R4/RRR4-18/3	1538.872	1538.759	73.352	0.479	1388.526	0.431	27	0.153	R.M*NTKPSHGPIHFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/3	1538.831	1538.759	46.859	0.511	1285.583	0.458	26	0.150	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/2	886.958	887.016	-65.654	0.391	785.947	0.333	12	0.149	R.GEAALANLK.A
R4/RRR4-17/2	886.659	887.016	-403.576	0.393	814.437	0.318	12	0.148	R.GEAALANLK.A
R4/RRR4-18/2	1431.196	1431.702	-1054.864	0.404	1102.331	0.544	18	0.147	K.LGSQIDILAPIKY.-
R4/RRR4-17/2	886.397	887.016	-1832.357	0.357	802.813	0.306	12	0.146	R.GEAALANLK.A
R4/RRR4-17/3	1538.660	1538.759	-64.738	0.481	1310.837	0.432	26	0.145	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/3	1537.347	1538.759	-1573.879	0.423	1363.721	0.391	24	0.142	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/3	1522.557	1522.760	-133.306	0.422	1362.444	0.390	26	0.139	R.MNTKPSHGPIHFR.A
R4/RRR4-17/3	1524.026	1522.760	175.520	0.445	1249.395	0.409	25	0.134	R.MNTKPSHGPIHFR.A
R4/RRR4-17/3	1538.477	1538.759	-184.120	0.475	1256.795	0.387	27	0.128	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/2	1431.208	1431.702	-346.007	0.354	775.915	0.557	15	0.125	K.LGSQIDILAPIKY.-
R4/RRR4-17/3	1538.255	1538.759	-980.528	0.437	916.684	0.412	24	0.114	R.M*NTKPSHGPIHFR.A
R4/RRR4-18/3	1522.833	1522.760	48.343	0.436	1172.281	0.334	25	0.111	R.MNTKPSHGPIHFR.A
R4/RRR4-15/3	1538.468	1538.759	-189.493	0.273	557.872	0.464	21	0.110	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/3	1090.832	1091.279	-411.109	0.430	723.861	0.496	16	0.109	-.YCLLGHLSK.-
R4/RRR4-17/3	1538.812	1538.759	34.328	0.434	782.685	0.406	23	0.109	R.M*NTKPSHGPIHFR.A
R4/RRR4-18/3	1538.677	1538.759	-53.398	0.348	405.414	0.313	21	0.105	R.M*NTKPSHGPIHFR.A
R4/RRR4-17/3	1522.676	1522.760	-55.138	0.454	785.573	0.370	21	0.104	R.MNTKPSHGPIHFR.A
R4/RRR4-17/3	1090.904	1091.279	-344.920	0.357	751.806	0.435	18	0.103	K.YCLLGHLSK.E
R4/RRR4-17/3	1091.090	1091.279	-173.425	0.391	682.934	0.433	17	0.102	K.YCLLGHLSK.E
R4/RRR4-18/3	1522.450	1522.760	-204.246	0.397	1078.010	0.292	25	0.099	R.MNTKPSHGPIHFR.A
R4/RRR4-18/3	1538.301	1538.759	-298.992	0.315	640.827	0.246	23	0.094	R.M*NTKPSHGPIHFR.A
R4/RRR4-18/3	1523.445	1522.760	-207.046	0.397	791.822	0.199	24	0.082	-.MNTKPSHGPIHFR.-
R4/RRR4-22/2	1965.486	1965.195	148.095	0.589	1959.189	0.660	28	0.336	R.IWVFSGDTDAVLPVTSTR.Y
R4/RRR4-22/2	1964.589	1965.195	-819.942	0.506	1729.774	0.605	27	0.281	R.IWVFSGDTDAVLPVTSTR.Y
R4/RRR4-22/2	1964.274	1965.195	-981.264	0.565	1560.081	0.574	26	0.251	R.IWVFSGDTDAVLPVTSTR.Y
R4/RRR4-21/2	1964.122	1965.195	-1058.637	0.505	1411.860	0.557	25	0.228	R.IWVFSGDTDAVLPVTSTR.Y
R4/RRR4-22/2	1536.163	1536.713	-1012.115	0.578	1282.178	0.548	22	0.219	K.HSTVYFNLAEVQK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1537.086	1536.713	243.058	0.632	1108.371	0.566	22	0.209	K.HSTVYFNLAEVQK.A
R4/RRR4-22/2	1536.332	1536.713	-249.093	0.575	1072.067	0.553	21	0.202	K.HSTVYFNLAEVQK.A
R4/RRR4-22/3	1298.325	1298.479	-118.749	0.528	1528.838	0.469	26	0.182	R.GAGHEVPLHRPK.Q
R4/RRR4-22/2	905.943	906.064	-133.947	0.444	1146.904	0.385	13	0.176	K.GLNFVTVR.G
R4/RRR4-25/2	906.054	906.064	-11.636	0.429	1138.615	0.380	12	0.173	K.GLNFVTVR.G
R4/RRR4-21/2	1964.196	1965.195	-1020.822	0.470	866.872	0.526	20	0.173	R.IWVFSGDTDAVLPVTSTR.Y
R4/RRR4-22/2	905.811	906.064	-280.353	0.462	1123.450	0.377	12	0.172	K.GLNFVTVR.G
R4/RRR4-22/2	905.995	906.064	-76.504	0.409	937.403	0.376	12	0.162	K.GLNFVTVR.G
R4/RRR4-21/2	905.964	906.064	-110.428	0.361	1049.529	0.334	12	0.161	K.GLNFVTVR.G
R4/RRR4-22/3	1299.726	1298.479	190.926	0.500	1513.224	0.394	26	0.155	R.GAGHEVPLHRPK.Q
R4/RRR4-24/2	905.990	906.064	-81.910	0.368	869.935	0.333	12	0.154	K.GLNFVTVR.G
R4/RRR4-22/2	1091.488	1092.316	-1680.098	0.291	624.788	0.421	14	0.150	K.ALHVSPIINK.S
R4/RRR4-22/2	1091.497	1092.316	-1671.558	0.298	658.561	0.397	14	0.149	K.ALHVSPIINK.S
R4/RRR4-22/2	1092.100	1092.316	-198.617	0.331	444.530	0.422	12	0.148	K.ALHVSPIINK.S
R4/RRR4-22/3	1298.823	1298.479	265.483	0.498	1202.468	0.405	24	0.127	R.GAGHEVPLHRPK.Q
R4/RRR4-21/3	1298.199	1298.479	-215.949	0.485	1026.768	0.419	22	0.115	-.GAGHEVPLHRPK.-
R4/RRR4-24/3	1298.542	1298.479	48.867	0.463	1028.985	0.407	22	0.115	-.GAGHEVPLHRPK.-
R4/RRR4-21/3	1298.164	1298.479	-243.543	0.389	600.070	0.433	19	0.103	R.GAGHEVPLHRPK.Q
R4/RRR4-25/3	1298.093	1298.479	-298.450	0.453	843.564	0.386	21	0.103	R.GAGHEVPLHRPK.Q
R4/RRR4-24/3	1297.976	1298.479	-1161.350	0.433	861.358	0.381	20	0.099	-.GAGHEVPLHRPK.-
R4/RRR4-19/2	1610.350	1610.741	-243.422	0.549	1519.921	0.497	20	0.226	K.DGTNVEEAFQCIVK.N
R4/RRR4-18/2	1610.158	1610.741	-985.678	0.493	1492.431	0.492	20	0.223	K.DGTNVEEAFQCIVK.N
R4/RRR4-18/2	1610.123	1610.741	-1007.751	0.495	1435.773	0.515	20	0.222	K.DGTNVEEAFQCIVK.N
R4/RRR4-19/2	1610.041	1610.741	-1058.829	0.507	1382.711	0.513	20	0.216	K.DGTNVEEAFQCIVK.N
R4/RRR4-19/2	1609.775	1610.741	-1225.039	0.407	1428.320	0.470	20	0.210	K.DGTNVEEAFQCIVK.N
R4/RRR4-18/2	1610.077	1610.741	-1036.373	0.469	1107.049	0.447	18	0.178	K.DGTNVEEAFQCIVK.N
R4/RRR4-13/2	1116.172	1115.393	-198.392	0.570	2045.789	0.476	17	0.294	K.LLLAYVGIPR.Y
R4/RRR4-14/2	1115.251	1115.393	-128.075	0.492	1819.648	0.328	17	0.223	K.LLLAYVGIPR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1190.156	1190.286	-109.212	0.403	1568.730	0.395	18	0.211	R.EALSGDTIDLR.A
R4/RRR4-13/2	1074.194	1074.255	-57.060	0.439	1476.297	0.504	16	0.200	R.TFLLSLVGSH.-
R4/RRR4-13/2	1189.334	1190.286	-1645.645	0.337	1518.310	0.350	17	0.195	R.EALSGDTIDLR.A
R4/RRR4-13/2	1189.545	1190.286	-1467.392	0.358	1509.655	0.282	18	0.183	R.EALSGDTIDLR.A
R4/RRR4-14/2	1021.173	1021.152	20.969	0.439	1034.108	0.373	13	0.167	R.ALIQQEYR.T
R4/RRR4-13/2	1436.216	1436.554	-236.193	0.465	1192.309	0.336	17	0.166	K.FGTYLEHDIGQR.T
R4/RRR4-13/2	1020.305	1021.152	-1815.492	0.347	950.561	0.385	13	0.162	R.ALIQQEYR.T
R4/RRR4-14/2	1190.050	1190.286	-198.525	0.404	1061.526	0.306	16	0.157	R.EALSGDTIDLR.A
R4/RRR4-13/2	1020.530	1021.152	-1593.981	0.368	936.862	0.328	13	0.156	R.ALIQQEYR.T
R4/RRR4-13/2	1115.129	1115.393	-237.226	0.428	931.393	0.346	14	0.156	K.LLLAYVGIPR.Y
R4/RRR4-13/2	1020.576	1021.152	-1548.440	0.309	929.101	0.264	13	0.147	R.ALIQQEYR.T
R4/RRR4-14/2	1190.032	1190.286	-213.961	0.318	738.355	0.280	15	0.143	R.EALSGDTIDLR.A
R4/RRR4-14/2	1190.204	1190.286	-68.883	0.280	651.367	0.169	16	0.137	R.EALSGDTIDLR.A
R4/RRR4-13/2	1073.438	1074.255	-1697.399	0.363	1235.731	0.410	16	0.134	R.TFLLSLVGSH.-
R4/RRR4-14/2	1074.059	1074.255	-183.030	0.296	784.542	0.476	13	0.109	R.TFLLSLVGSH.-
R4/RRR4-14/2	1074.120	1074.255	-125.912	0.175	558.525	0.285	13	0.092	R.TFLLSLVGSH.-
R4/RRR4-16/2	1389.231	1389.573	-247.442	0.504	1944.852	0.424	19	0.263	K.VIACIGETLEQR.E
R4/RRR4-16/2	1452.085	1452.613	-1055.907	0.503	1554.106	0.477	20	0.226	R.EAGTTM*EVVAAQTK.A
R4/RRR4-16/2	1389.158	1389.573	-300.073	0.512	1475.966	0.446	19	0.213	K.VIACIGETLEQR.E
R4/RRR4-16/2	1602.397	1602.773	-235.690	0.529	1157.388	0.584	22	0.212	K.WLATNVSPAVAESTR.I
R4/RRR4-16/2	1389.123	1389.573	-325.465	0.493	1504.356	0.417	19	0.209	K.VIACIGETLEQR.E
R4/RRR4-16/2	1353.031	1353.500	-347.177	0.475	1116.758	0.583	20	0.207	R.IIYGGSVNGANCK.E
R4/RRR4-16/2	1452.060	1452.613	-1072.535	0.472	1348.875	0.485	19	0.206	R.EAGTTM*EVVAAQTK.A
R4/RRR4-16/2	1451.889	1452.613	-1191.229	0.460	1373.386	0.473	19	0.205	R.EAGTTM*EVVAAQTK.A
R4/RRR4-16/2	1602.298	1602.773	-297.599	0.493	1148.159	0.559	22	0.205	K.WLATNVSPAVAESTR.I
R4/RRR4-16/2	1050.078	1050.233	-148.150	0.458	1259.950	0.448	16	0.194	K.VAYALSQGIK.V
R4/RRR4-16/2	1603.085	1602.773	195.322	0.551	931.297	0.587	20	0.193	K.WLATNVSPAVAESTR.I
R4/RRR4-16/2	1050.028	1050.233	-195.498	0.459	1224.586	0.402	16	0.183	K.VAYALSQGIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1049.404	1050.233	-1747.824	0.388	1282.125	0.378	16	0.182	K.VAYALSQGIK.V
R4/RRR4-16/2	1389.038	1389.573	-1108.739	0.451	1163.108	0.385	18	0.175	K.VIACIGETLEQR.E
R4/RRR4-16/2	1388.601	1389.573	-1424.923	0.334	1205.956	0.353	18	0.170	K.VIACIGETLEQR.E
R4/RRR4-20/2	1674.335	1674.919	-949.140	0.512	917.236	0.503	21	0.178	R.SYLNLPSEVVPNTLK.K
R4/RRR4-20/2	1674.270	1674.919	-987.862	0.435	955.466	0.419	21	0.166	R.SYLNLPSEVVPNTLK.K
R4/RRR4-20/2	1264.006	1264.371	-289.585	0.405	445.776	0.527	15	0.161	K.GGAPAEFQPSFR.G
R4/RRR4-21/2	1263.573	1264.371	-1427.450	0.428	452.457	0.508	15	0.160	K.GGAPAEFQPSFR.G
R4/RRR4-20/2	1264.117	1264.371	-202.003	0.385	426.599	0.530	15	0.160	K.GGAPAEFQPSFR.G
R4/RRR4-20/2	1264.102	1264.371	-213.240	0.384	455.237	0.520	15	0.160	K.GGAPAEFQPSFR.G
R4/RRR4-20/2	1265.386	1264.371	11.939	0.420	380.891	0.496	15	0.158	K.GGAPAEFQPSFR.G
R4/RRR4-20/2	1264.992	1264.371	-300.587	0.406	425.540	0.472	16	0.158	K.GGAPAEFQPSFR.G
R4/RRR4-21/2	1264.076	1264.371	-234.360	0.421	423.577	0.462	15	0.156	K.GGAPAEFQPSFR.G
R4/RRR4-20/2	1802.364	1803.092	-961.742	0.474	577.504	0.439	19	0.153	R.SYLNLPSEVVPNTLKK.S
R4/RRR4-20/2	1341.211	1340.551	-254.293	0.374	808.253	0.326	13	0.145	K.YLFHEGVLYAK.K
R4/RRR4-20/2	1264.328	1264.371	-34.050	0.337	384.908	0.369	14	0.145	-.GGAPAEFQPSFR.-
R4/RRR4-21/2	1263.299	1264.371	-1644.855	0.234	444.179	0.392	15	0.144	K.GGAPAEFQPSFR.G
R4/RRR4-20/2	1675.723	1674.919	-117.314	0.493	545.354	0.385	16	0.144	R.SYLNLPSEVVPNTLK.K
R4/RRR4-20/2	1802.512	1803.092	-879.337	0.476	378.205	0.375	16	0.141	R.SYLNLPSEVVPNTLKK.S
R4/RRR4-20/2	1803.536	1803.092	246.999	0.466	373.988	0.350	17	0.141	R.SYLNLPSEVVPNTLKK.S
R4/RRR4-20/2	1341.544	1340.551	-4.710	0.259	844.160	0.203	14	0.135	K.YLFHEGVLYAK.K
R4/RRR4-21/3	1284.371	1284.409	-29.668	0.428	1123.384	0.268	21	0.093	R.GPPRFEGDRPR.F
R4/RRR4-20/3	1284.112	1284.409	-231.905	0.375	496.945	0.361	16	0.091	R.GPPRFEGDRPR.F
R4/RRR4-20/3	1283.840	1284.409	-1225.922	0.375	633.383	0.326	17	0.088	R.GPPRFEGDRPR.F
R4/RRR4-15/2	1294.968	1295.430	-358.111	0.516	1471.529	0.690	23	0.272	R.HSGLAVAGLAADGR.Q
R4/RRR4-15/2	1042.034	1041.182	-141.656	0.464	1025.690	0.375	14	0.166	R.VFQVEYAGK.A
R4/RRR4-10/2	1847.508	1848.090	-858.583	0.554	1726.294	0.535	23	0.263	R.YFKGEDFPVQNYIVK.E
R4/RRR4-10/2	1847.497	1848.090	-864.818	0.532	1452.737	0.582	22	0.241	R.YFKGEDFPVQNYIVK.E
R4/RRR4-10/2	1848.215	1848.090	67.795	0.555	1442.449	0.550	22	0.232	R.YFKGEDFPVQNYIVK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1340.196	1340.481	-213.735	0.499	1528.164	0.423	18	0.214	K.YEEDLDAM*LPK.C
R4/RRR4-10/2	1083.528	1084.297	-1637.523	0.536	1340.816	0.447	17	0.202	K.KGVIIVNNAR.G
R4/RRR4-10/2	1084.149	1084.297	-137.735	0.577	1367.137	0.400	17	0.194	K.KGVIIVNNAR.G
R4/RRR4-10/2	1084.043	1084.297	-235.897	0.503	1140.529	0.410	16	0.179	K.KGVIIVNNAR.G
R4/RRR4-10/2	1409.778	1409.568	148.892	0.348	757.174	0.355	18	0.149	K.GEDFPVQNYIVK.E
R4/RRR4-8/2	1084.537	1084.297	221.766	0.241	169.605	0.170	12	0.143	-.KGVIIVNNAR.-
R4/RRR4-10/2	1325.556	1324.482	55.733	0.297	242.121	0.290	11	0.138	-.YEEDLDAMLPK.-
R4/RRR4-10/3	1847.931	1848.090	-86.015	0.488	1159.848	0.451	29	0.136	R.YFKGEDFPVQNYIVK.E
R4/RRR4-10/3	1848.003	1848.090	-47.055	0.470	923.943	0.514	27	0.132	R.YFKGEDFPVQNYIVK.E
R4/RRR4-10/3	1085.537	1085.276	241.794	0.449	1711.448	0.143	23	0.103	R.LKIDPELEK.E
R4/RRR4-10/3	1085.232	1085.276	-40.245	0.482	1645.325	0.163	22	0.103	R.LKIDPELEK.E
R4/RRR4-10/3	1085.523	1085.276	228.432	0.481	1602.130	0.141	22	0.095	R.LKIDPELEK.E
R4/RRR4-10/3	1849.426	1848.090	182.340	0.396	730.147	0.336	23	0.089	R.YFKGEDFPVQNYIVK.E
R4/RRR4-4/2	1698.479	1698.943	-273.538	0.448	1096.711	0.489	18	0.184	R.LIWSTQFENFLATK.W
R4/RRR4-4/2	1374.223	1374.524	-219.585	0.352	1006.479	0.390	15	0.162	R.DWLSAYWTGFK.S
R4/RRR4-4/2	983.981	984.178	-200.719	0.461	960.063	0.363	14	0.162	R.LNVLGNVVR.K
R4/RRR4-4/2	1467.183	1466.583	-273.517	0.432	810.152	0.431	17	0.162	K.YHLGTSYDRPTR.G
R4/RRR4-3/2	983.925	984.178	-257.971	0.414	820.516	0.397	13	0.160	R.LNVLGNVVR.K
R4/RRR4-4/2	1215.994	1216.278	-234.665	0.544	777.544	0.375	15	0.159	K.VYYELDEER.K
R4/RRR4-3/2	983.542	984.178	-1667.867	0.366	863.218	0.372	13	0.157	R.LNVLGNVVR.K
R4/RRR4-4/2	1216.059	1216.278	-180.989	0.500	766.078	0.366	15	0.157	K.VYYELDEER.K
R4/RRR4-2/2	984.308	984.178	132.584	0.395	927.105	0.339	13	0.156	R.LNVLGNVVR.K
R4/RRR4-4/2	985.099	984.178	-79.931	0.508	866.789	0.342	13	0.154	R.LNVLGNVVR.K
R4/RRR4-3/2	984.076	984.178	-103.529	0.405	854.211	0.335	13	0.153	R.LNVLGNVVR.K
R4/RRR4-4/2	984.140	984.178	-38.705	0.441	915.873	0.291	14	0.151	R.LNVLGNVVR.K
R4/RRR4-4/2	1466.664	1466.583	55.546	0.379	559.610	0.330	15	0.144	K.YHLGTSYDRPTR.G
R4/RRR4-3/2	1374.324	1374.524	-146.249	0.358	949.515	0.234	15	0.142	R.DWLSAYWTGFK.S
R4/RRR4-4/2	1466.291	1466.583	-199.534	0.349	439.671	0.286	13	0.137	-.YHLGTSYDRPTR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1698.172	1698.943	-1045.696	0.291	566.506	0.275	15	0.135	R.LIWSTQFENFLATK.W
R4/RRR4-4/3	1709.049	1708.964	49.654	0.361	1072.706	0.439	27	0.123	R.AADLGVENIVIGM*PHR.G
R4/RRR4-17/2	1406.058	1406.551	-351.996	0.552	2520.675	0.529	25	0.397	K.AM*AQVSQAGSGGLGR.V
R4/RRR4-17/2	1406.213	1406.551	-241.206	0.568	2497.435	0.526	25	0.391	K.AM*AQVSQAGSGGLGR.V
R4/RRR4-16/2	1532.108	1531.776	216.917	0.586	2130.484	0.617	23	0.351	K.AVASINSVLTDLVTK.G
R4/RRR4-17/2	1406.156	1406.551	-281.965	0.559	2311.355	0.506	25	0.348	K.AM*AQVSQAGSGGLGR.V
R4/RRR4-17/2	1531.438	1531.776	-221.347	0.506	2101.274	0.609	23	0.343	K.AVASINSVLTDLVTK.G
R4/RRR4-16/2	1532.268	1531.776	322.050	0.542	1882.747	0.565	22	0.293	K.AVASINSVLTDLVTK.G
R4/RRR4-17/2	1531.431	1531.776	-226.065	0.530	1748.898	0.623	22	0.290	K.AVASINSVLTDLVTK.G
R4/RRR4-17/2	1531.346	1531.776	-282.125	0.516	1853.019	0.539	22	0.281	K.AVASINSVLTDLVTK.G
R4/RRR4-17/2	1879.598	1880.077	-255.778	0.545	1544.837	0.614	26	0.261	R.DLSPLTCAQCLSTAVSR.F
R4/RRR4-17/2	1489.966	1490.547	-1064.451	0.532	1873.832	0.442	19	0.259	R.FDQYCGAQQGCR.I
R4/RRR4-17/2	1241.008	1241.333	-262.690	0.463	1496.287	0.569	20	0.240	K.GSTGVGFATSTAGK.G
R4/RRR4-17/2	1489.979	1490.547	-1055.320	0.515	1650.044	0.392	18	0.217	R.FDQYCGAQQGCR.I
R4/RRR4-17/2	1241.001	1241.333	-268.118	0.468	1157.810	0.556	20	0.204	K.GSTGVGFATSTAGK.G
R4/RRR4-17/2	1879.292	1880.077	-952.538	0.553	1123.430	0.561	23	0.202	R.DLSPLTCAQCLSTAVSR.F
R4/RRR4-17/2	1240.747	1241.333	-1281.514	0.416	1019.796	0.511	19	0.183	K.GSTGVGFATSTAGK.G
R4/RRR4-17/2	1878.618	1880.077	-1312.769	0.424	925.355	0.475	21	0.170	R.DLSPLTCAQCLSTAVSR.F
R4/RRR4-16/3	1643.743	1643.829	-52.194	0.493	1787.567	0.553	32	0.267	R.SPAAEALGPTHVLHSR.Y
R4/RRR4-16/2	1141.097	1141.303	-180.969	0.473	1403.601	0.578	19	0.234	R.VPSPVTAGSAVR.L
R4/RRR4-16/2	1030.914	1031.145	-225.132	0.408	1331.120	0.566	20	0.221	K.VAAATAAAGEAK.G
R4/RRR4-16/2	1140.899	1141.303	-354.530	0.410	1156.735	0.590	18	0.208	R.VPSPVTAGSAVR.L
R4/RRR4-15/2	1031.206	1031.145	59.056	0.347	1384.311	0.482	20	0.207	K.VAAATAAAGEAK.G
R4/RRR4-16/2	1030.788	1031.145	-347.146	0.309	1238.860	0.528	20	0.198	K.VAAATAAAGEAK.G
R4/RRR4-16/2	1211.036	1211.308	-225.617	0.503	1441.815	0.378	19	0.196	R.VSFGENFSPAR.A
R4/RRR4-15/2	1211.247	1211.308	-50.401	0.470	1412.223	0.357	18	0.189	R.VSFGENFSPAR.A
R4/RRR4-15/2	1210.869	1211.308	-364.277	0.425	1404.244	0.359	18	0.189	R.VSFGENFSPAR.A
R4/RRR4-16/2	1211.080	1211.308	-189.113	0.490	1283.532	0.326	19	0.174	R.VSFGENFSPAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1211.018	1211.308	-240.280	0.466	1120.912	0.370	17	0.170	R.VSFGENFSPAR.A
R4/RRR4-15/2	1140.477	1141.303	-1605.460	0.388	795.974	0.498	16	0.167	R.VPSPVTAGSAVR.L
R4/RRR4-16/3	1643.540	1643.829	-176.012	0.482	1076.825	0.550	28	0.157	R.SPAAEALGPTHVLHSR.Y
R4/RRR4-15/2	1210.872	1211.308	-361.444	0.402	950.399	0.337	16	0.156	R.VSFGENFSPAR.A
R4/RRR4-16/3	1643.416	1643.829	-252.017	0.412	1054.898	0.532	27	0.149	R.SPAAEALGPTHVLHSR.Y
R4/RRR4-15/3	1643.756	1643.829	-44.373	0.361	558.098	0.443	28	0.101	R.SPAAEALGPTHVLHSR.Y
R4/RRR4-16/3	1454.693	1454.694	-0.481	0.366	999.399	0.342	27	0.098	K.VKEGVEVPQLVEK.V
R4/RRR4-15/3	1644.014	1643.829	113.147	0.177	351.953	0.361	26	0.090	R.SPAAEALGPTHVLHSR.Y
R4/RRR4-16/3	1454.673	1454.694	-13.864	0.329	672.253	0.252	22	0.082	K.VKEGVEVPQLVEK.V
R4/RRR4-15/3	1454.443	1454.694	-172.842	0.293	782.418	0.176	24	0.076	K.VKEGVEVPQLVEK.V
R4/RRR4-8/2	1817.337	1816.986	193.854	0.563	2352.144	0.527	23	0.361	K.VSAATGYIDYEKLEEK.A
R4/RRR4-8/2	1930.234	1931.043	-939.704	0.580	2177.124	0.604	24	0.356	R.YYGGNDVIDEIENLCR.D
R4/RRR4-8/2	1931.503	1931.043	238.749	0.593	2171.527	0.588	23	0.348	R.YYGGNDVIDEIENLCR.D
R4/RRR4-8/2	1931.489	1931.043	231.524	0.630	2088.855	0.609	23	0.340	R.YYGGNDVIDEIENLCR.D
R4/RRR4-8/2	1619.254	1619.839	-982.031	0.436	1943.428	0.438	22	0.267	K.ISATSIYFESLPYK.V
R4/RRR4-8/2	1619.432	1619.839	-251.809	0.457	1875.266	0.396	21	0.246	K.ISATSIYFESLPYK.V
R4/RRR4-8/2	1207.060	1207.398	-280.932	0.465	1521.354	0.499	18	0.230	K.LIICGGSAYPR.D
R4/RRR4-8/2	1206.541	1207.398	-1543.735	0.486	1517.511	0.484	19	0.227	K.LIICGGSAYPR.D
R4/RRR4-8/2	1619.399	1619.839	-272.228	0.435	1650.003	0.430	20	0.225	K.ISATSIYFESLPYK.V
R4/RRR4-8/2	1207.213	1207.398	-153.613	0.457	1479.851	0.425	18	0.209	K.LIICGGSAYPR.D
R4/RRR4-8/3	1930.735	1931.043	-159.787	0.479	1661.930	0.442	28	0.204	R.YYGGNDVIDEIENLCR.D
R4/RRR4-8/2	1817.405	1816.986	231.371	0.518	1346.230	0.484	19	0.202	K.VSAATGYIDYEKLEEK.A
R4/RRR4-8/2	1316.885	1317.426	-1174.044	0.428	1111.940	0.504	19	0.190	K.VSAATGYIDYEK.L
R4/RRR4-10/2	1855.511	1856.027	-819.446	0.555	2701.109	0.621	27	0.474	R.TLGATHTVNAAKEDAVEK.I
R4/RRR4-10/2	1736.315	1736.813	-288.027	0.571	2163.845	0.545	21	0.333	K.GQEDLCESFFAYNR.A
R4/RRR4-10/2	1736.353	1736.813	-265.738	0.568	1929.197	0.536	20	0.291	K.GQEDLCESFFAYNR.A
R4/RRR4-10/2	1663.311	1663.850	-927.827	0.356	1904.337	0.336	21	0.232	K.AFGASEVIAVDVLDEK.L
R4/RRR4-10/2	1737.658	1736.813	-89.458	0.565	1308.493	0.562	19	0.219	K.GQEDLCESFFAYNR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1663.762	1663.850	-53.177	0.347	1639.377	0.306	21	0.195	K.AFGASEVIAVDVLDEK.L
R4/RRR4-10/2	1049.996	1050.190	-184.893	0.437	1032.518	0.409	15	0.171	K.LAESGAFNLK.N
R4/RRR4-10/2	1049.950	1050.190	-229.213	0.449	895.273	0.404	15	0.164	K.LAESGAFNLK.N
R4/RRR4-10/2	1050.015	1050.190	-167.049	0.450	712.544	0.438	14	0.160	K.LAESGAFNLK.N
R4/RRR4-10/3	1855.959	1856.027	-36.858	0.498	926.438	0.594	34	0.154	R.TLGATHTVNAAKEDAVEK.I
R4/RRR4-10/2	1058.054	1058.210	-148.306	0.358	714.221	0.357	17	0.149	R.GVDVAVEALGK.A
R4/RRR4-10/3	1854.970	1856.027	-1112.423	0.486	706.188	0.560	30	0.128	R.TLGATHTVNAAKEDAVEK.I
R4/RRR4-10/3	1856.687	1856.027	-183.568	0.484	700.219	0.546	31	0.124	R.TLGATHTVNAAKEDAVEK.I
R4/RRR4-2/2	1911.855	1911.144	-151.751	0.593	1576.749	0.576	26	0.255	R.YEAVGVDPSTTLLEFLR.T
R4/RRR4-2/2	1910.417	1911.144	-906.961	0.539	1413.791	0.588	25	0.238	R.YEAVGVDPSTTLLEFLR.T
R4/RRR4-2/2	1911.510	1911.144	191.797	0.579	1424.297	0.558	25	0.232	R.YEAVGVDPSTTLLEFLR.T
R4/RRR4-2/3	1388.142	1388.547	-292.452	0.470	1519.611	0.534	27	0.210	R.CSSRPAPPPGFSK.L
R4/RRR4-2/2	1267.183	1267.543	-284.511	0.425	993.990	0.565	19	0.192	K.LVSAPVILEAVR.L
R4/RRR4-2/2	1267.425	1267.543	-93.377	0.434	1013.769	0.492	19	0.183	K.LVSAPVILEAVR.L
R4/RRR4-2/2	1731.473	1731.974	-869.664	0.468	1038.967	0.456	21	0.176	K.YINISQIPELSAINR.S
R4/RRR4-2/2	1311.952	1312.411	-350.862	0.425	750.078	0.481	16	0.164	K.HSNVDSSDLPIK.S
R4/RRR4-2/2	1312.149	1312.411	-200.020	0.463	500.243	0.537	15	0.163	K.HSNVDSSDLPIK.S
R4/RRR4-2/3	1388.202	1388.547	-249.708	0.442	696.013	0.437	20	0.102	R.CSSRPAPPPGFSK.L
R4/RRR4-2/3	1464.223	1464.709	-332.411	0.320	1104.432	0.194	24	0.077	K.TM*HVAAACAVAAFK.L
R4/RRR4-3/2	1307.125	1307.481	-273.288	0.396	1229.744	0.407	16	0.179	R.AALSLAYQNLSR.V
R4/RRR4-3/2	1354.146	1354.405	-191.285	0.433	817.789	0.480	20	0.172	R.QAIEEFSSDATR.F
R4/RRR4-3/2	1196.173	1196.380	-173.455	0.433	1185.957	0.345	15	0.170	K.LGFYDLQLAR.D
R4/RRR4-3/2	1354.077	1354.405	-242.382	0.490	684.162	0.465	20	0.167	R.QAIEEFSSDATR.F
R4/RRR4-3/2	1196.120	1196.380	-217.888	0.440	1077.403	0.367	15	0.167	K.LGFYDLQLAR.D
R4/RRR4-3/2	1452.301	1452.640	-233.661	0.348	892.217	0.443	17	0.161	K.AGWPIAGTPDPTLR.I
R4/RRR4-3/2	1195.917	1196.380	-387.873	0.386	1173.669	0.287	15	0.160	K.LGFYDLQLAR.D
R4/RRR4-3/2	1354.043	1354.405	-267.707	0.393	803.428	0.384	20	0.158	R.QAIEEFSSDATR.F
R4/RRR4-3/2	1618.221	1618.813	-986.820	0.427	753.373	0.367	19	0.150	R.ASGEGVQPQEYVLIK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1618.255	1618.813	-965.463	0.445	770.358	0.341	19	0.147	R.ASGEGVQPQEYVLIK.M
R4/RRR4-3/2	1619.569	1618.813	-150.638	0.488	652.277	0.377	18	0.147	R.ASGEGVQPQEYVLIK.M
R4/RRR4-3/3	1881.916	1882.025	-58.243	0.480	1095.484	0.504	31	0.146	R.QVGLEHAEVLSASNEAAR.A
R4/RRR4-3/2	1451.737	1452.640	-1314.121	0.262	616.066	0.390	16	0.142	K.AGWPIAGTPDPTLR.I
R4/RRR4-1/2	1196.309	1196.380	-59.013	0.350	596.292	0.280	12	0.140	K.LGFYDLQLAR.D
R4/RRR4-3/3	1881.380	1882.025	-877.055	0.385	380.246	0.411	24	0.092	R.QVGLEHAEVLSASNEAAR.A
R4/RRR4-11/2	1823.493	1824.159	-916.489	0.579	1982.490	0.639	26	0.332	K.TQKPVVAFIAGLTAPPGR.R
R4/RRR4-11/2	1824.345	1824.159	101.903	0.578	1449.239	0.645	24	0.254	K.TQKPVVAFIAGLTAPPGR.R
R4/RRR4-11/2	1823.651	1824.159	-829.398	0.519	1443.249	0.598	24	0.241	K.TQKPVVAFIAGLTAPPGR.R
R4/RRR4-11/3	1954.256	1955.204	-999.739	0.468	1826.485	0.459	34	0.236	K.KGGTEHLGLPVFNSVAEAK.A
R4/RRR4-11/2	1187.043	1187.325	-238.429	0.470	1307.335	0.508	20	0.210	R.EAGVTVVESPAK.I
R4/RRR4-11/2	1187.078	1187.325	-208.305	0.435	1167.165	0.517	19	0.198	R.EAGVTVVESPAK.I
R4/RRR4-11/2	1186.692	1187.325	-1380.540	0.419	1164.020	0.522	19	0.198	R.EAGVTVVESPAK.I
R4/RRR4-10/2	1186.538	1187.325	-1510.116	0.357	1156.422	0.433	19	0.180	R.EAGVTVVESPAK.I
R4/RRR4-10/2	1186.890	1187.325	-367.922	0.367	993.550	0.454	17	0.172	R.EAGVTVVESPAK.I
R4/RRR4-11/2	1085.008	1085.263	-235.348	0.331	639.004	0.560	15	0.162	R.MGHAGAIVSGGK.G
R4/RRR4-10/3	1955.119	1955.204	-43.193	0.356	1584.054	0.350	29	0.159	K.KGGTEHLGLPVFNSVAEAK.A
R4/RRR4-11/2	1084.749	1085.263	-1399.328	0.234	824.829	0.424	16	0.150	R.MGHAGAIVSGGK.G
R4/RRR4-11/3	1954.349	1955.204	-952.048	0.447	1209.280	0.463	30	0.146	K.KGGTEHLGLPVFNSVAEAK.A
R4/RRR4-11/3	1456.173	1455.753	288.924	0.457	1041.321	0.501	26	0.139	K.IGIM*PGYIHKPGR.V
R4/RRR4-10/3	1955.205	1955.204	0.769	0.299	737.675	0.303	25	0.086	K.KGGTEHLGLPVFNSVAEAK.A
R4/RRR4-8/2	1644.529	1644.762	-142.246	0.512	1824.722	0.418	24	0.244	R.LDSDNPVADAESIVAK.A
R4/RRR4-8/2	962.351	963.112	-1835.892	0.450	1420.541	0.335	13	0.186	R.IGDLELFR.A
R4/RRR4-8/2	962.952	963.112	-166.577	0.522	1337.413	0.358	13	0.183	R.IGDLELFR.A
R4/RRR4-8/2	963.020	963.112	-96.003	0.546	1300.465	0.359	13	0.181	R.IGDLELFR.A
R4/RRR4-8/2	1643.642	1644.762	-1293.954	0.386	1480.460	0.276	22	0.176	R.LDSDNPVADAESIVAK.A
R4/RRR4-8/2	1001.891	1002.062	-171.223	0.378	700.507	0.435	15	0.160	K.FASTFSADR.T
R4/RRR4-8/2	1001.153	1002.062	-1912.470	0.378	369.102	0.378	13	0.151	K.FASTFSADR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1001.129	1002.062	-1936.486	0.275	539.906	0.316	14	0.143	K.FASTFSADR.T
R4/RRR4-8/2	959.357	959.165	200.929	0.337	834.605	0.236	13	0.141	R.ISLADIAKK.L
R4/RRR4-8/3	1424.129	1424.497	-259.055	0.478	1192.454	0.441	23	0.136	R.FEAHSNQQFCR.Y
R4/RRR4-8/2	959.666	959.165	-522.018	0.316	534.592	0.243	11	0.105	-.ISLADIAKK.-
R4/RRR4-8/3	1424.063	1424.497	-305.237	0.446	633.885	0.409	19	0.099	R.FEAHSNQQFCR.Y
R4/RRR4-8/3	1423.671	1424.497	-1286.028	0.398	785.333	0.362	20	0.095	R.FEAHSNQQFCR.Y
R4/RRR4-11/2	1569.415	1569.657	-154.359	0.551	2232.532	0.517	25	0.338	K.NFGDEALIGEGSFGR.V
R4/RRR4-11/2	1570.049	1569.657	250.355	0.586	1742.318	0.522	25	0.264	K.NFGDEALIGEGSFGR.V
R4/RRR4-11/2	1570.313	1569.657	-219.688	0.618	1744.428	0.478	24	0.250	K.NFGDEALIGEGSFGR.V
R4/RRR4-11/2	996.046	996.189	-143.280	0.369	646.117	0.447	15	0.159	K.ALQPLLNAR.A
R4/RRR4-11/2	1367.102	1367.538	-320.050	0.382	540.559	0.503	17	0.158	K.GAQPGPVLSWAQR.V
R4/RRR4-6/2	1180.923	1181.372	-381.497	0.388	1130.327	0.271	16	0.156	R.VYFGVLRNGR.S
R4/RRR4-6/2	1180.972	1181.372	-339.389	0.392	1019.213	0.303	16	0.156	R.VYFGVLRNGR.S
R4/RRR4-6/2	1180.967	1181.372	-343.330	0.372	940.654	0.284	15	0.149	R.VYFGVLRNGR.S
R4/RRR4-11/2	1344.375	1344.501	-93.861	0.314	862.237	0.275	16	0.141	R.GQQSLVTWATPR.L
R4/RRR4-11/2	1366.598	1367.538	-1423.495	0.338	460.910	0.318	16	0.141	K.GAQPGPVLSWAQR.V
R4/RRR4-10/2	995.908	996.189	-283.082	0.244	438.261	0.300	11	0.119	-.ALQPLLNAR.-
R4/RRR4-17/1	1072.641	1072.280	337.755	0.288	802.577	0.419	14	0.638	K.LLLIGDSGVGK.S
R4/RRR4-17/2	1638.722	1638.849	-77.375	0.556	2215.316	0.570	22	0.351	K.TNLNVEQVFFSIAR.D
R4/RRR4-17/2	1638.343	1638.849	-921.864	0.574	2182.448	0.576	22	0.347	K.TNLNVEQVFFSIAR.D
R4/RRR4-16/2	1639.186	1638.849	206.407	0.541	1771.138	0.530	22	0.268	K.TNLNVEQVFFSIAR.D
R4/RRR4-16/2	1638.729	1638.849	-73.565	0.507	1569.783	0.529	22	0.242	K.TNLNVEQVFFSIAR.D
R4/RRR4-17/2	1637.637	1638.849	-1354.697	0.390	1692.715	0.457	21	0.236	K.TNLNVEQVFFSIAR.D
R4/RRR4-17/2	1165.105	1165.278	-148.446	0.444	1617.964	0.416	17	0.220	K.GQALADEYGIK.F
R4/RRR4-17/2	1164.434	1165.278	-1588.623	0.369	1640.142	0.407	17	0.219	K.GQALADEYGIK.F
R4/RRR4-17/2	1164.909	1165.278	-317.268	0.438	1583.804	0.422	17	0.218	K.GQALADEYGIK.F
R4/RRR4-17/2	1558.418	1558.764	-222.307	0.513	1296.573	0.435	19	0.193	R.IKLQIWDTAGQER.F
R4/RRR4-17/2	1071.947	1072.280	-311.544	0.379	1259.950	0.453	18	0.193	K.LLLIGDSGVGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1072.034	1072.280	-230.545	0.417	1441.618	0.358	18	0.192	K.LLLIGDSGVGK.S
R4/RRR4-17/2	1558.189	1558.764	-1013.602	0.505	1260.446	0.402	19	0.183	R.IKLQIWDTAGQER.F
R4/RRR4-17/2	1072.112	1072.280	-157.782	0.449	1190.848	0.405	18	0.181	K.LLLIGDSGVGK.S
R4/RRR4-17/3	1558.918	1558.764	99.492	0.478	1528.965	0.434	27	0.175	R.IKLQIWDTAGQER.F
R4/RRR4-17/2	1000.999	1001.114	-115.356	0.463	796.994	0.330	13	0.153	R.ADYDYLIK.L
R4/RRR4-17/2	1000.878	1001.114	-236.965	0.412	647.399	0.326	13	0.150	R.ADYDYLIK.L
R4/RRR4-17/2	1072.220	1072.280	-56.708	0.400	784.482	0.334	15	0.150	K.LLLIGDSGVGK.S
R4/RRR4-9/2	1638.837	1638.849	-7.292	0.387	502.608	0.379	16	0.146	K.TNLNVEQVFFSIAR.D
R4/RRR4-17/2	1000.836	1001.114	-278.446	0.380	720.084	0.255	13	0.144	R.ADYDYLIK.L
R4/RRR4-16/2	1072.630	1072.280	327.187	0.364	690.981	0.274	14	0.141	K.LLLIGDSGVGK.S
R4/RRR4-17/3	1639.124	1638.849	168.349	0.466	1162.092	0.424	25	0.130	K.TNLNVEQVFFSIAR.D
R4/RRR4-17/3	1559.181	1558.764	268.267	0.433	957.115	0.434	25	0.115	R.IKLQIWDTAGQER.F
R4/RRR4-17/3	1638.477	1638.849	-227.818	0.330	659.958	0.312	22	0.078	-.TNLNVEQVFFSIAR.-
R4/RRR4-24/2	1964.321	1964.232	45.286	0.482	1320.574	0.485	22	0.199	K.ANNM*VFVSGVLGLNPETGK.F
R4/RRR4-25/2	1405.295	1404.596	-215.078	0.459	1127.206	0.480	20	0.189	R.STYQVAALPLNAR.I
R4/RRR4-25/2	1287.012	1287.489	-372.026	0.482	784.660	0.569	18	0.181	K.APAALGPYSQAIK.A
R4/RRR4-24/2	1287.173	1287.489	-246.515	0.430	923.167	0.493	17	0.175	K.APAALGPYSQAIK.A
R4/RRR4-25/2	1404.273	1404.596	-231.016	0.398	1051.362	0.433	19	0.174	R.STYQVAALPLNAR.I
R4/RRR4-25/2	1287.009	1287.489	-374.500	0.507	707.158	0.536	17	0.172	K.APAALGPYSQAIK.A
R4/RRR4-24/2	1403.684	1404.596	-1366.260	0.384	930.057	0.475	18	0.172	R.STYQVAALPLNAR.I
R4/RRR4-24/2	1287.180	1287.489	-241.187	0.473	612.384	0.574	16	0.172	K.APAALGPYSQAIK.A
R4/RRR4-24/2	1404.118	1404.596	-341.608	0.483	917.096	0.440	18	0.168	R.STYQVAALPLNAR.I
R4/RRR4-24/2	1055.996	1056.151	-147.900	0.475	720.069	0.495	16	0.168	K.ASGASYSSVVK.T
R4/RRR4-25/2	1287.027	1287.489	-360.511	0.376	687.648	0.538	16	0.166	K.APAALGPYSQAIK.A
R4/RRR4-25/2	1403.864	1404.596	-1237.357	0.355	1025.593	0.381	19	0.164	R.STYQVAALPLNAR.I
R4/RRR4-24/2	1287.026	1287.489	-360.891	0.430	696.682	0.463	17	0.161	K.APAALGPYSQAIK.A
R4/RRR4-24/2	1540.501	1540.807	-199.276	0.518	674.390	0.418	19	0.158	K.TTIM*LADLQDFKK.V
R4/RRR4-25/2	1540.867	1540.807	39.388	0.365	741.332	0.370	17	0.150	K.TTIM*LADLQDFKK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	1540.285	1540.807	-990.701	0.433	799.103	0.323	18	0.148	K.TTIM*LADLQDFKK.V
R4/RRR4-25/2	1963.791	1964.232	-225.599	0.419	649.751	0.417	18	0.147	K.ANNM*VFVSGVLGLNPETGK.F
R4/RRR4-24/2	1964.453	1964.232	112.845	0.413	466.627	0.442	18	0.146	K.ANNM*VFVSGVLGLNPETGK.F
R4/RRR4-25/2	1965.458	1964.232	115.403	0.348	238.887	0.421	18	0.143	-.ANNM*VFVSGVLGLNPETGK.-
R4/RRR4-24/2	1964.250	1964.232	9.135	0.294	497.666	0.368	19	0.140	K.ANNM*VFVSGVLGLNPETGK.F
R4/RRR4-24/3	1963.573	1964.232	-847.456	0.361	930.964	0.332	27	0.091	K.ANNM*VFVSGVLGLNPETGK.F
R4/RRR4-13/3	1899.183	1900.082	-1002.588	0.492	1720.499	0.556	36	0.257	K.AHAAENAKPVEKTEFEK.L
R4/RRR4-13/2	1097.986	1098.304	-291.158	0.370	1513.456	0.475	19	0.220	K.HGM*VAAGALVR.Q
R4/RRR4-13/2	1293.210	1293.491	-217.530	0.511	1385.167	0.457	18	0.208	R.KLTDDEIAFIK.E
R4/RRR4-13/2	1293.172	1293.491	-247.549	0.527	1231.807	0.518	18	0.207	R.KLTDDEIAFIK.E
R4/RRR4-13/2	1098.116	1098.304	-172.491	0.362	1256.900	0.455	19	0.192	K.HGM*VAAGALVR.Q
R4/RRR4-13/2	1098.052	1098.304	-230.594	0.448	1053.236	0.488	18	0.186	K.HGM*VAAGALVR.Q
R4/RRR4-13/3	1899.549	1900.082	-809.125	0.462	1239.847	0.577	34	0.184	K.AHAAENAKPVEKTEFEK.L
R4/RRR4-13/2	1385.193	1385.543	-253.555	0.444	763.357	0.324	20	0.150	R.IPCGEVWGGNPAK.F
R4/RRR4-13/2	1384.441	1385.543	-1522.859	0.356	769.972	0.271	20	0.145	R.IPCGEVWGGNPAK.F
R4/RRR4-13/2	1384.535	1385.543	-1455.018	0.384	753.084	0.267	19	0.143	R.IPCGEVWGGNPAK.F
R4/RRR4-13/2	1386.908	1385.543	263.904	0.307	568.467	0.289	15	0.139	R.IPCGEVWGGNPAK.F
R4/RRR4-13/3	1098.179	1098.304	-114.908	0.477	1825.506	0.170	22	0.126	K.HGM*VAAGALVR.Q
R4/RRR4-13/3	1098.149	1098.304	-142.339	0.425	1532.190	0.239	22	0.115	K.HGM*VAAGALVR.Q
R4/RRR4-13/3	1799.767	1800.846	-1158.309	0.462	706.909	0.479	27	0.109	K.SAHQDEEHDSM*IGATR.E
R4/RRR4-13/3	1098.396	1098.304	83.500	0.426	1347.147	0.157	21	0.084	K.HGM*VAAGALVR.Q
R4/RRR4-7/2	1346.341	1346.600	-192.667	0.541	2606.578	0.399	20	0.368	R.KFDLGALVDLVR.K
R4/RRR4-7/2	1346.255	1346.600	-257.160	0.567	2525.149	0.376	20	0.343	R.KFDLGALVDLVR.K
R4/RRR4-7/2	1201.107	1201.312	-170.704	0.415	1127.609	0.496	20	0.191	K.IVDPDTGASLGR.N
R4/RRR4-7/2	1075.183	1075.198	-14.304	0.447	1480.385	0.327	17	0.189	R.VTAEDLASIR.M
R4/RRR4-7/2	1220.273	1219.404	-107.621	0.543	941.597	0.537	16	0.187	R.VIVTEACAVEK.V
R4/RRR4-6/2	1201.318	1201.312	5.238	0.407	1103.987	0.477	20	0.186	K.IVDPDTGASLGR.N
R4/RRR4-7/2	1218.819	1219.404	-1303.767	0.496	907.825	0.482	15	0.174	R.VIVTEACAVEK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1219.005	1219.404	-327.696	0.490	975.660	0.446	16	0.173	R.VIVTEACAVEK.V
R4/RRR4-7/2	1201.148	1201.312	-136.958	0.404	965.015	0.446	19	0.172	K.IVDPDTGASLGR.N
R4/RRR4-7/2	1200.382	1201.312	-1612.446	0.291	973.649	0.431	19	0.165	K.IVDPDTGASLGR.N
R4/RRR4-7/2	1075.223	1075.198	23.274	0.346	1027.891	0.174	16	0.140	R.VTAEDLASIR.M
R4/RRR4-7/2	1474.688	1474.773	-57.421	0.304	769.065	0.316	15	0.140	R.KFDLGALVDLVRK.H
R4/RRR4-7/3	1346.266	1346.600	-248.619	0.371	1029.240	0.174	23	0.074	-.KFDLGALVDLVR.-
R4/RRR4-3/3	1821.947	1821.066	-65.435	0.545	1749.199	0.513	32	0.245	R.QAVALLQDNYPEFIAK.K
R4/RRR4-3/2	1820.952	1821.066	-62.707	0.472	1296.355	0.574	20	0.217	R.QAVALLQDNYPEFIAK.K
R4/RRR4-3/2	1821.278	1821.066	116.663	0.471	1204.799	0.578	21	0.211	R.QAVALLQDNYPEFIAK.K
R4/RRR4-3/3	1821.973	1821.066	-51.423	0.535	1413.955	0.529	30	0.194	R.QAVALLQDNYPEFIAK.K
R4/RRR4-3/2	1171.013	1170.384	-318.019	0.536	1173.344	0.461	17	0.190	K.IVLTINNPASK.K
R4/RRR4-9/2	1820.325	1821.066	-959.517	0.498	946.245	0.574	18	0.186	R.QAVALLQDNYPEFIAK.K
R4/RRR4-3/2	1170.599	1170.384	184.229	0.481	1080.080	0.452	16	0.180	K.IVLTINNPASK.K
R4/RRR4-3/2	1821.250	1821.066	101.538	0.515	1027.831	0.504	17	0.178	R.QAVALLQDNYPEFIAK.K
R4/RRR4-3/2	1169.770	1170.384	-1383.449	0.432	896.602	0.468	16	0.171	K.IVLTINNPASK.K
R4/RRR4-3/2	1142.902	1143.362	-403.700	0.417	939.043	0.342	14	0.156	K.M*M*SPFLTQR.T
R4/RRR4-3/2	1722.219	1722.024	113.633	0.510	603.977	0.416	18	0.152	K.VFINVPWWYLAANK.M
R4/RRR4-3/2	1721.313	1722.024	-997.211	0.375	373.221	0.315	15	0.140	K.VFINVPWWYLAANK.M
R4/RRR4-3/3	1256.762	1256.497	211.823	0.440	979.673	0.363	20	0.105	R.KVPANEEPIMK.G
R4/RRR4-3/3	1272.461	1272.496	-28.089	0.456	1230.340	0.276	23	0.100	R.KVPANEEPIM*K.G
R4/RRR4-3/3	1272.710	1272.496	167.879	0.508	1319.688	0.252	24	0.099	R.KVPANEEPIM*K.G
R4/RRR4-3/3	1256.384	1256.497	-90.115	0.445	1099.144	0.283	22	0.095	R.KVPANEEPIMK.G
R4/RRR4-3/3	1271.678	1272.496	-1434.364	0.373	845.867	0.280	21	0.089	R.KVPANEEPIM*K.G
R4/RRR4-3/3	1272.694	1272.496	155.615	0.460	698.245	0.326	20	0.087	-.KVPANEEPIM*K.-
R4/RRR4-7/3	1272.796	1272.496	235.685	0.336	709.455	0.239	20	0.081	-.KVPANEEPIM*K.-
R4/RRR4-9/3	1272.314	1272.496	-144.147	0.417	690.853	0.279	19	0.081	-.KVPANEEPIM*K.-
R4/RRR4-3/3	1272.537	1272.496	31.807	0.453	723.599	0.214	20	0.076	-.KVPANEEPIM*K.-
R4/RRR4-8/2	1536.609	1536.756	-96.461	0.505	998.802	0.540	21	0.191	K.AALAPYFELTNAVR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1535.812	1536.756	-1269.845	0.377	932.530	0.443	20	0.167	K.AALAPYFELTNAVR.V
R4/RRR4-8/2	948.768	949.086	-335.603	0.464	1226.813	0.290	13	0.164	R.VGDLELFR.A
R4/RRR4-8/2	1536.287	1536.756	-306.242	0.427	717.945	0.466	18	0.161	K.AALAPYFELTNAVR.V
R4/RRR4-5/2	1767.761	1766.974	-120.348	0.569	3202.737	0.543	26	0.567	K.HVLAVLDDLSADELGAK.I
R4/RRR4-5/2	1391.188	1390.615	-307.732	0.524	1897.405	0.569	20	0.297	K.LPFAAAQIGQAFR.N
R4/RRR4-5/2	1389.749	1390.615	-1346.129	0.464	1558.184	0.551	19	0.244	K.LPFAAAQIGQAFR.N
R4/RRR4-5/2	1117.064	1116.290	-203.057	0.480	1504.858	0.514	18	0.232	R.VGIDEVASVVK.Q
R4/RRR4-5/2	1116.495	1116.290	184.274	0.417	1393.563	0.462	16	0.206	R.VGIDEVASVVK.Q
R4/RRR4-6/2	976.859	977.144	-292.488	0.494	1066.721	0.562	13	0.202	K.ANVLAFWR.Q
R4/RRR4-6/2	1606.350	1606.847	-310.340	0.422	1020.596	0.427	20	0.169	R.VFTPSVIEPSFGIGR.I
R4/RRR4-5/2	1607.329	1606.847	300.841	0.421	678.798	0.452	17	0.154	R.VFTPSVIEPSFGIGR.I
R4/RRR4-6/2	1116.382	1116.290	83.175	0.372	929.618	0.257	17	0.147	R.VGIDEVASVVK.Q
R4/RRR4-5/2	1389.919	1390.615	-1223.169	0.229	795.187	0.395	15	0.147	K.LPFAAAQIGQAFR.N
R4/RRR4-1/2	1390.037	1390.615	-1138.243	0.334	482.354	0.369	15	0.144	K.LPFAAAQIGQAFR.N
R4/RRR4-5/2	1115.630	1116.290	-1492.400	0.166	679.437	0.195	15	0.133	R.VGIDEVASVVK.Q
R4/RRR4-14/1	467.042	467.454	-886.078	-2.000	53.887	0.000	4	1.000	R.GYGGGG.G
R4/RRR4-24/1	467.480	467.454	55.524	-1.155	7.865	0.000	4	0.962	R.GYGGGG.G
R4/RRR4-14/1	467.894	467.454	941.902	-2.441	24.607	0.000	2	0.925	R.GYGGGG.G
R4/RRR4-22/1	467.828	467.454	799.926	-2.194	21.382	0.000	2	0.878	R.GYGGGG.G
R4/RRR4-28/1	467.792	467.454	724.084	-0.805	23.814	0.000	3	0.874	R.GYGGGG.G
R4/RRR4-4/1	467.916	467.454	989.350	-0.990	39.139	0.000	3	0.852	R.GYGGGG.G
R4/RRR4-24/1	467.760	467.454	654.770	-0.929	42.071	0.007	3	0.849	R.GYGGGG.G
R4/RRR4-27/1	467.428	467.454	-57.102	-1.829	1.688	0.000	2	0.840	R.GYGGGG.G
R4/RRR4-27/1	467.426	467.454	-60.508	-1.487	4.340	0.595	3	0.828	R.GYGGGG.G
R4/RRR4-20/1	467.275	467.454	-384.256	-1.344	4.369	0.405	3	0.824	R.GYGGGG.G
R4/RRR4-18/1	467.432	467.454	-48.065	-0.873	1.974	0.000	2	0.820	R.GYGGGG.G
R4/RRR4-29/1	467.446	467.454	-18.335	-1.546	2.236	0.000	2	0.817	R.GYGGGG.G
R4/RRR4-29/1	467.287	467.454	-358.437	-1.077	1.763	0.000	2	0.811	R.GYGGGG.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/1	467.444	467.454	-21.740	-1.238	2.170	0.000	2	0.809	R.GYGGGG.G
R4/RRR4-18/1	467.849	467.454	846.471	-0.854	21.677	0.000	2	0.801	R.GYGGGG.G
R4/RRR4-29/1	467.857	467.454	863.598	-1.058	15.788	0.000	2	0.798	R.GYGGGG.G
R4/RRR4-29/1	467.906	467.454	968.829	-0.913	22.871	0.000	2	0.797	R.GYGGGG.G
R4/RRR4-19/1	467.794	467.454	728.791	-1.320	19.994	0.000	2	0.794	R.GYGGGG.G
R4/RRR4-30/1	467.835	467.454	816.008	-0.978	22.878	0.000	2	0.794	R.GYGGGG.G
R4/RRR4-29/1	467.906	467.454	966.999	-0.923	9.932	0.000	2	0.788	-.GYGGGG.-
R4/RRR4-24/1	467.455	467.454	0.786	-1.687	1.584	0.447	2	0.783	R.GYGGGG.G
R4/RRR4-27/1	467.602	467.454	315.647	-1.719	14.370	0.000	2	0.777	-.GYGGGG.-
R4/RRR4-18/1	467.784	467.454	706.168	-1.738	21.247	0.000	2	0.773	-.GYGGGG.-
R4/RRR4-30/1	467.482	467.454	59.715	-1.520	1.715	0.064	2	0.768	-.GYGGGG.-
R4/RRR4-18/1	467.880	467.454	912.360	-1.266	59.727	0.521	3	0.768	R.GYGGGG.G
R4/RRR4-16/1	467.905	467.454	964.908	-1.146	44.268	0.488	3	0.766	R.GYGGGG.G
R4/RRR4-19/1	467.482	467.454	60.107	-1.615	2.205	0.606	2	0.763	R.GYGGGG.G
R4/RRR4-28/1	467.441	467.454	-28.943	-1.872	1.829	0.618	2	0.760	-.GYGGGG.-
R4/RRR4-8/1	467.870	467.454	890.006	-1.350	21.275	0.000	2	0.760	-.GYGGGG.-
R4/RRR4-9/1	467.666	467.454	452.789	-0.728	76.827	0.724	4	0.757	R.GYGGGG.G
R4/RRR4-16/1	467.872	467.454	894.058	-0.435	71.274	0.738	4	0.738	R.GYGGGG.G
R4/RRR4-26/1	467.788	467.454	715.845	-0.605	68.068	0.856	4	0.734	R.GYGGGG.G
R4/RRR4-28/1	467.829	467.454	803.325	-1.076	44.274	0.773	3	0.729	R.GYGGGG.G
R4/RRR4-13/1	467.826	467.454	796.657	-1.058	25.679	0.302	2	0.723	R.GYGGGG.G
R4/RRR4-15/1	467.087	467.454	-789.923	-0.533	63.851	0.935	4	0.720	R.GYGGGG.G
R4/RRR4-27/1	467.262	467.454	-413.876	-1.305	4.067	0.050	2	0.708	-.GYGGGG.-
R4/RRR4-19/1	467.309	467.454	-312.570	-1.414	15.995	0.192	2	0.697	-.GYGGGG.-
R4/RRR4-10/1	467.835	467.454	816.269	-1.344	23.568	0.371	2	0.694	-.GYGGGG.-
R4/RRR4-14/1	467.342	467.454	-241.943	-0.766	34.674	0.890	3	0.683	R.GYGGGG.G
R4/RRR4-5/1	467.880	467.454	911.575	-0.311	45.386	0.777	3	0.666	R.GYGGGG.G
R4/RRR4-27/1	467.798	467.454	735.591	-0.715	47.340	0.944	3	0.663	R.GYGGGG.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/1	467.832	467.454	809.078	-1.334	14.310	0.715	2	0.661	-.GYGGGG.-
R4/RRR4-28/1	467.432	467.454	-47.803	-0.590	31.640	0.775	3	0.659	-.GYGGGG.-
R4/RRR4-3/1	467.373	467.454	-175.125	-0.496	39.653	0.918	3	0.651	R.GYGGGG.G
R4/RRR4-6/1	467.717	467.454	563.470	-0.795	39.228	0.876	3	0.649	-.GYGGGG.-
R4/RRR4-16/1	467.501	467.454	98.997	-0.450	53.253	0.968	3	0.630	R.GYGGGG.G
R4/RRR4-29/1	467.889	467.454	931.706	-0.358	29.355	0.937	3	0.623	-.GYGGGG.-
R4/RRR4-18/1	467.538	467.454	178.599	-0.335	38.509	0.906	3	0.621	-.GYGGGG.-
R4/RRR4-22/1	467.114	467.454	-730.901	-0.975	23.270	0.765	2	0.611	-.GYGGGG.-
R4/RRR4-23/1	467.752	467.454	637.898	-1.542	10.000	0.472	1	0.598	-.GYGGGG.-
R4/RRR4-2/1	467.710	467.454	548.557	-0.937	17.171	0.940	2	0.589	-.GYGGGG.-
R4/RRR4-13/1	467.798	467.454	735.722	-0.474	18.948	0.909	2	0.585	R.GYGGGG.G
R4/RRR4-25/1	467.785	467.454	708.914	-0.712	19.160	0.903	2	0.574	-.GYGGGG.-
R4/RRR4-21/1	467.299	467.454	-334.586	-0.863	1.894	0.870	2	0.572	-.GYGGGG.-
R4/RRR4-2/1	467.883	467.454	918.634	-0.778	9.280	0.823	2	0.570	-.GYGGGG.-
R4/RRR4-4/1	467.818	467.454	780.443	-0.739	22.499	0.786	2	0.565	-.GYGGGG.-
R4/RRR4-10/1	467.520	467.454	139.716	-0.670	30.584	0.810	2	0.552	-.GYGGGG.-
R4/RRR4-21/2	1925.416	1924.960	237.341	0.603	2316.745	0.661	25	0.399	R.SLNDGDVVEFSVGSGNDGR.T
R4/RRR4-20/2	1924.261	1924.960	-885.420	0.498	2062.350	0.649	25	0.345	R.SLNDGDVVEFSVGSGNDGR.T
R4/RRR4-21/2	1925.285	1924.960	169.439	0.576	1991.016	0.679	24	0.343	R.SLNDGDVVEFSVGSGNDGR.T
R4/RRR4-20/2	1924.260	1924.960	-886.184	0.519	1889.618	0.638	24	0.312	R.SLNDGDVVEFSVGSGNDGR.T
R4/RRR4-20/2	1923.713	1924.960	-1171.633	0.496	1842.094	0.620	24	0.299	R.SLNDGDVVEFSVGSGNDGR.T
R4/RRR4-10/2	1545.557	1545.760	-131.947	0.531	2153.194	0.556	20	0.336	K.TYVVQDGDIIFFK.F
R4/RRR4-10/3	1708.516	1707.874	-210.453	0.536	1950.054	0.534	33	0.296	R.GAHAGEGLGNAFLSHIR.A
R4/RRR4-10/2	1544.439	1545.760	-1507.477	0.371	1872.562	0.487	20	0.267	K.TYVVQDGDIIFFK.F
R4/RRR4-10/3	1708.594	1707.874	-164.438	0.557	1568.723	0.532	32	0.220	R.GAHAGEGLGNAFLSHIR.A
R4/RRR4-10/3	1707.753	1707.874	-71.137	0.531	1442.903	0.561	31	0.211	R.GAHAGEGLGNAFLSHIR.A
R4/RRR4-10/3	1948.242	1948.206	18.337	0.598	1430.635	0.533	33	0.196	R.LKDIEFVQNKIDDLEK.S
R4/RRR4-10/2	1066.646	1067.307	-1561.970	0.404	1059.704	0.532	17	0.191	K.IGIVGLPNVGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1067.046	1067.307	-245.162	0.484	1062.219	0.493	18	0.189	K.IGIVGLPNVGK.S
R4/RRR4-10/3	1948.758	1948.206	-230.498	0.592	1291.765	0.559	33	0.186	R.LKDIEFVQNKIDDLEK.S
R4/RRR4-10/2	1066.692	1067.307	-1518.170	0.397	953.907	0.509	17	0.180	K.IGIVGLPNVGK.S
R4/RRR4-10/2	1057.608	1057.224	364.134	0.216	502.241	0.462	13	0.141	K.STFFNIVTK.L
R4/RRR4-9/2	1544.918	1545.760	-1195.948	0.240	392.348	0.268	11	0.119	-.TYVVQDGDIIFFK.-
R4/RRR4-10/3	1947.434	1948.206	-912.582	0.428	635.685	0.330	26	0.089	R.LKDIEFVQNKIDDLEK.S
R4/RRR4-8/2	1532.674	1531.821	-96.149	0.554	2239.041	0.600	24	0.366	K.ALGVDILTGFGAIVGK.Q
R4/RRR4-8/2	1532.013	1531.821	125.583	0.558	2194.663	0.606	24	0.360	K.ALGVDILTGFGAIVGK.Q
R4/RRR4-8/2	1414.241	1413.605	-257.870	0.548	2055.633	0.567	20	0.322	K.GLGLENINVVTQR.G
R4/RRR4-8/2	1413.456	1413.605	-105.818	0.530	1925.019	0.461	20	0.270	K.GLGLENINVVTQR.G
R4/RRR4-8/2	1413.289	1413.605	-223.737	0.554	1747.132	0.501	19	0.256	K.GLGLENINVVTQR.G
R4/RRR4-8/3	1426.375	1426.640	-186.844	0.509	2126.044	0.375	26	0.255	K.DGKPVQIELIDAK.T
R4/RRR4-8/3	1426.618	1426.640	-15.467	0.502	1795.694	0.377	25	0.195	K.DGKPVQIELIDAK.T
R4/RRR4-8/2	1351.981	1352.477	-368.185	0.471	944.405	0.478	18	0.176	R.NIDYHTGVFASK.I
R4/RRR4-8/2	1426.436	1426.640	-143.910	0.442	714.123	0.491	18	0.165	K.DGKPVQIELIDAK.T
R4/RRR4-8/2	1378.582	1379.500	-1395.490	0.393	811.086	0.472	16	0.163	K.SLGLQVSSPGYDR.Q
R4/RRR4-8/2	1426.157	1426.640	-339.763	0.389	730.528	0.483	18	0.163	K.DGKPVQIELIDAK.T
R4/RRR4-8/3	1426.552	1426.640	-61.943	0.506	1417.426	0.394	22	0.148	K.DGKPVQIELIDAK.T
R4/RRR4-8/2	1378.440	1379.500	-1499.023	0.284	710.997	0.399	16	0.148	K.SLGLQVSSPGYDR.Q
R4/RRR4-8/2	1378.449	1379.500	-1492.796	0.260	741.881	0.332	16	0.142	K.SLGLQVSSPGYDR.Q
R4/RRR4-11/2	1579.476	1578.858	-242.599	0.504	1277.054	0.586	22	0.219	R.VSAPAVTMSFAGGAALK.L
R4/RRR4-11/2	1377.115	1376.530	-301.986	0.438	1353.752	0.506	18	0.212	R.ASAYSILDTCFK.G
R4/RRR4-11/2	1578.397	1578.858	-293.185	0.434	1320.669	0.535	22	0.211	R.VSAPAVTMSFAGGAALK.L
R4/RRR4-11/2	1579.130	1578.858	172.621	0.488	1253.218	0.544	21	0.207	R.VSAPAVTMSFAGGAALK.L
R4/RRR4-11/2	1594.453	1594.858	-254.803	0.493	1087.798	0.566	24	0.200	R.VSAPAVTM*SFAGGAALK.L
R4/RRR4-11/2	1165.673	1166.349	-1442.090	0.473	1209.290	0.497	18	0.200	R.LPTSVYSALSK.A
R4/RRR4-11/2	1166.134	1166.349	-184.433	0.439	1035.155	0.541	18	0.193	R.LPTSVYSALSK.A
R4/RRR4-11/2	1166.010	1166.349	-291.452	0.437	900.193	0.503	17	0.178	R.LPTSVYSALSK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	857.905	858.021	-135.382	0.405	1062.992	0.309	15	0.159	R.SAGLIGLAR.N
R4/RRR4-11/2	857.450	858.021	-1837.527	0.386	1039.423	0.310	15	0.158	R.SAGLIGLAR.N
R4/RRR4-11/2	857.800	858.021	-258.434	0.460	971.997	0.333	14	0.158	R.SAGLIGLAR.N
R4/RRR4-11/2	1376.150	1376.530	-277.019	0.360	847.848	0.388	15	0.154	R.ASAYSILDTCFK.G
R4/RRR4-11/2	974.045	974.095	-51.236	0.283	277.123	0.462	13	0.150	R.QSGPVFNPK.S
R4/RRR4-11/2	973.987	974.095	-111.578	0.178	217.690	0.368	12	0.137	-.QSGPVFNPK.-
R4/RRR4-11/2	974.194	974.095	101.473	0.187	317.202	0.386	14	0.137	-.QSGPVFNPK.-
R4/RRR4-11/2	1375.183	1376.530	-1711.979	0.194	421.326	0.307	12	0.134	R.ASAYSILDTCFK.G
R4/RRR4-8/2	1727.742	1726.953	-122.285	0.618	2412.739	0.607	26	0.403	R.LNLEAAGVEVDNIGAIK.V
R4/RRR4-8/2	1727.434	1726.953	279.357	0.619	2253.552	0.583	26	0.362	R.LNLEAAGVEVDNIGAIK.V
R4/RRR4-8/2	1726.374	1726.953	-917.125	0.487	2327.036	0.524	24	0.355	R.LNLEAAGVEVDNIGAIK.V
R4/RRR4-8/2	1858.382	1859.065	-908.243	0.475	2206.067	0.472	24	0.317	K.ELAITSDEALSLEELPK.R
R4/RRR4-8/3	1629.903	1629.799	63.985	0.412	2018.166	0.457	29	0.274	R.TSVPNIWAVGDVTNR.M
R4/RRR4-8/2	1629.168	1629.799	-1004.012	0.493	1076.093	0.504	21	0.188	R.TSVPNIWAVGDVTNR.M
R4/RRR4-8/2	1045.939	1046.160	-211.597	0.342	1273.668	0.419	17	0.186	R.TVVASNLEGR.G
R4/RRR4-8/2	1045.935	1046.160	-215.227	0.356	1055.692	0.411	16	0.171	R.TVVASNLEGR.G
R4/RRR4-8/2	1041.795	1042.213	-401.653	0.355	904.573	0.332	15	0.154	K.ILVYGSSFR.G
R4/RRR4-8/2	1045.742	1046.160	-400.488	0.324	826.219	0.371	15	0.154	R.TVVASNLEGR.G
R4/RRR4-8/2	1042.017	1042.213	-188.541	0.384	738.257	0.372	13	0.152	K.ILVYGSSFR.G
R4/RRR4-7/2	1628.512	1629.799	-1408.300	0.250	699.897	0.251	15	0.132	R.TSVPNIWAVGDVTNR.M
R4/RRR4-8/3	1629.577	1629.799	-136.272	0.399	1121.444	0.392	24	0.118	R.TSVPNIWAVGDVTNR.M
R4/RRR4-8/2	1594.046	1594.702	-1041.495	0.545	2051.942	0.525	23	0.310	R.IEEELGDAAVYAGEK.F
R4/RRR4-8/2	1791.252	1791.983	-969.280	0.470	665.479	0.529	23	0.167	R.GAVPSGASTGIYEALELR.D
R4/RRR4-8/2	1791.447	1791.983	-859.959	0.495	676.621	0.509	23	0.165	R.GAVPSGASTGIYEALELR.D
R4/RRR4-7/2	1133.016	1133.320	-269.898	0.518	1768.631	0.507	20	0.262	K.ALVSAGLSSSIK.V
R4/RRR4-7/2	1133.056	1133.320	-234.445	0.470	1785.677	0.468	20	0.254	K.ALVSAGLSSSIK.V
R4/RRR4-7/2	1783.353	1783.963	-905.467	0.520	1683.457	0.513	25	0.252	R.DISLNYATFQPGTTVR.D
R4/RRR4-14/2	1133.026	1133.320	-261.035	0.433	1698.915	0.503	19	0.250	K.ALVSAGLSSSIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1132.994	1133.320	-289.247	0.461	1606.167	0.509	19	0.241	K.ALVSAGLSSSIK.V
R4/RRR4-13/2	1132.726	1133.320	-1411.615	0.401	1551.060	0.478	18	0.225	K.ALVSAGLSSSIK.V
R4/RRR4-14/2	1783.437	1783.963	-858.261	0.520	1392.917	0.538	23	0.223	R.DISLNYATFQPGTTVR.D
R4/RRR4-14/2	1133.251	1133.320	-61.325	0.496	1423.106	0.519	18	0.223	K.ALVSAGLSSSIK.V
R4/RRR4-7/2	1563.323	1562.751	-274.396	0.547	1502.329	0.442	20	0.213	R.DNVEAYWPSVIIR.Y
R4/RRR4-13/2	1133.150	1133.320	-150.795	0.416	1328.339	0.518	17	0.210	K.ALVSAGLSSSIK.V
R4/RRR4-7/2	1562.310	1562.751	-283.195	0.467	1496.650	0.393	20	0.203	R.DNVEAYWPSVIIR.Y
R4/RRR4-7/2	1562.339	1562.751	-264.460	0.460	1488.663	0.348	20	0.193	R.DNVEAYWPSVIIR.Y
R4/RRR4-14/2	1783.236	1783.963	-971.440	0.444	1097.994	0.450	21	0.178	R.DISLNYATFQPGTTVR.D
R4/RRR4-7/2	1568.449	1567.767	-203.243	0.472	894.889	0.500	19	0.177	R.IYYPDKEALDALR.G
R4/RRR4-7/2	1568.247	1567.767	306.698	0.426	744.168	0.486	18	0.166	R.IYYPDKEALDALR.G
R4/RRR4-7/2	1568.208	1567.767	281.800	0.450	719.886	0.487	17	0.165	R.IYYPDKEALDALR.G
R4/RRR4-14/2	916.002	916.097	-104.139	0.416	743.622	0.403	13	0.160	R.SEVVQLLK.S
R4/RRR4-7/2	915.496	916.097	-1754.657	0.414	743.735	0.376	13	0.158	R.SEVVQLLK.S
R4/RRR4-7/2	916.046	916.097	-56.017	0.450	707.838	0.372	13	0.157	R.SEVVQLLK.S
R4/RRR4-14/2	915.716	916.097	-417.845	0.373	795.154	0.361	13	0.156	R.SEVVQLLK.S
R4/RRR4-13/2	915.939	916.097	-172.854	0.418	776.607	0.375	13	0.156	-.SEVVQLLK.-
R4/RRR4-7/2	915.939	916.097	-173.122	0.410	729.030	0.342	13	0.154	R.SEVVQLLK.S
R4/RRR4-13/2	1562.349	1562.751	-257.875	0.370	810.491	0.299	17	0.145	R.DNVEAYWPSVIIR.Y
R4/RRR4-13/2	915.373	916.097	-1889.049	0.308	685.374	0.229	12	0.142	R.SEVVQLLK.S
R4/RRR4-13/2	1566.634	1567.767	-1365.843	0.299	667.832	0.246	17	0.139	R.IYYPDKEALDALR.G
R4/RRR4-13/2	915.422	916.097	-1835.851	0.290	562.165	0.166	10	0.135	-.SEVVQLLK.-
R4/RRR4-7/3	1567.587	1567.767	-115.222	0.433	836.749	0.464	29	0.116	R.IYYPDKEALDALR.G
R4/RRR4-13/3	1568.782	1567.767	9.621	0.495	621.360	0.473	22	0.111	R.IYYPDKEALDALR.G
R4/RRR4-13/3	1567.928	1567.767	103.137	0.405	445.054	0.434	21	0.105	R.IYYPDKEALDALR.G
R4/RRR4-13/3	1567.863	1567.767	61.206	0.347	484.095	0.436	23	0.103	R.IYYPDKEALDALR.G
R4/RRR4-7/3	1567.726	1567.767	-26.649	0.357	468.984	0.416	23	0.102	R.IYYPDKEALDALR.G
R4/RRR4-14/3	1567.485	1567.767	-180.491	0.327	488.246	0.412	22	0.101	R.IYYPDKEALDALR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/3	1567.675	1567.767	-59.100	0.300	390.591	0.389	20	0.100	R.IYYPDKEALDALR.G
R4/RRR4-7/3	1568.104	1567.767	215.560	0.394	581.239	0.379	26	0.099	R.IYYPDKEALDALR.G
R4/RRR4-13/3	1566.946	1567.767	-1165.587	0.289	438.447	0.373	22	0.098	R.IYYPDKEALDALR.G
R4/RRR4-14/3	1568.199	1567.767	275.977	0.384	523.931	0.343	23	0.097	R.IYYPDKEALDALR.G
R4/RRR4-6/2	1786.301	1786.919	-908.360	0.522	1458.033	0.531	24	0.228	-.AVFASGSPFDPVEYDGK.-
R4/RRR4-6/2	1787.043	1786.919	69.499	0.586	1356.835	0.579	23	0.228	R.AVFASGSPFDPVEYDGK.I
R4/RRR4-6/2	1786.504	1786.919	-232.784	0.552	1411.321	0.520	23	0.219	-.AVFASGSPFDPVEYDGK.-
R4/RRR4-6/2	979.956	980.100	-146.819	0.566	1538.832	0.418	15	0.214	K.AYELGLASR.L
R4/RRR4-1/2	1788.523	1786.919	-221.705	0.512	1185.214	0.598	21	0.212	R.AVFASGSPFDPVEYDGK.I
R4/RRR4-6/2	1165.713	1166.355	-1412.737	0.489	1299.495	0.502	19	0.208	K.ISAHIAANVAAK.A
R4/RRR4-6/2	979.273	980.100	-1871.559	0.457	1481.628	0.376	15	0.199	K.AYELGLASR.L
R4/RRR4-3/2	980.466	980.100	374.988	0.438	1399.374	0.413	14	0.198	K.AYELGLASR.L
R4/RRR4-6/2	979.983	980.100	-119.579	0.511	1433.608	0.356	15	0.191	K.AYELGLASR.L
R4/RRR4-6/2	1166.154	1166.355	-172.880	0.430	1118.761	0.468	18	0.185	K.ISAHIAANVAAK.A
R4/RRR4-6/2	1314.691	1315.584	-1444.029	0.413	678.910	0.589	19	0.176	K.TIKPTVLIGTSGK.G
R4/RRR4-6/2	1315.272	1315.584	-238.270	0.434	670.949	0.551	20	0.173	K.TIKPTVLIGTSGK.G
R4/RRR4-6/2	1315.240	1315.584	-262.666	0.378	656.651	0.567	19	0.170	K.TIKPTVLIGTSGK.G
R4/RRR4-6/3	1294.664	1294.528	105.425	0.470	1312.389	0.404	26	0.138	R.KISAHIAANVAAK.A
R4/RRR4-6/3	1294.526	1294.528	-2.102	0.446	1124.738	0.355	24	0.110	R.KISAHIAANVAAK.A
R4/RRR4-6/3	1294.488	1294.528	-31.612	0.487	779.176	0.403	21	0.101	R.KISAHIAANVAAK.A
R4/RRR4-9/2	1306.278	1306.406	-98.192	0.458	1306.811	0.451	18	0.197	K.LGVSYNQPDGQK.L
R4/RRR4-9/3	1892.003	1892.191	-99.704	0.425	1511.049	0.484	35	0.190	R.IEELVGVPVHYIGVGPGR.D
R4/RRR4-9/2	1305.899	1306.406	-1157.763	0.387	1024.673	0.466	17	0.176	K.LGVSYNQPDGQK.L
R4/RRR4-9/2	1305.646	1306.406	-1352.382	0.354	980.843	0.422	18	0.167	K.LGVSYNQPDGQK.L
R4/RRR4-9/2	1171.219	1170.381	-138.158	0.396	719.651	0.473	14	0.159	-.LDVLSGLPEVK.-
R4/RRR4-9/3	1891.395	1892.191	-952.017	0.400	1186.148	0.520	32	0.159	R.IEELVGVPVHYIGVGPGR.D
R4/RRR4-9/2	1171.330	1170.381	-43.234	0.467	779.563	0.423	14	0.158	K.LDVLSGLPEVK.L
R4/RRR4-9/2	1235.207	1235.371	-133.380	0.414	682.519	0.428	16	0.156	R.SYSELPLAAQR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1736.670	1736.906	-136.109	0.467	460.318	0.497	17	0.154	K.YEVLPGWQSDISSVR.S
R4/RRR4-9/3	1892.012	1892.191	-94.947	0.393	1074.082	0.438	31	0.125	R.IEELVGVPVHYIGVGPGR.D
R4/RRR4-3/2	1262.347	1261.514	-132.064	0.486	1519.739	0.490	18	0.226	R.ALLDEMAVVATK.E
R4/RRR4-4/2	1079.970	1080.261	-270.571	0.406	912.307	0.399	13	0.161	R.LSAAWQLYK.S
R4/RRR4-3/2	1277.040	1277.513	-371.363	0.310	926.906	0.383	15	0.155	R.ALLDEM*AVVATK.E
R4/RRR4-3/2	1261.332	1261.514	-144.692	0.255	896.656	0.270	16	0.142	R.ALLDEMAVVATK.E
R4/RRR4-10/2	1799.505	1800.002	-277.164	0.548	2032.927	0.463	22	0.285	R.LDSYLEFQSANSALLK.G
R4/RRR4-10/2	1524.179	1523.668	-322.090	0.547	1520.719	0.438	17	0.213	K.INDDEVEYWIVK.A
R4/RRR4-10/2	1414.647	1415.578	-1368.828	0.384	1309.326	0.329	21	0.174	R.GNIASAINTIQANK.V
R4/RRR4-10/2	1452.170	1452.593	-292.533	0.390	949.277	0.399	15	0.157	K.NIDSFISDWGIGK.V
R4/RRR4-10/2	877.032	877.023	10.943	0.341	884.464	0.245	13	0.143	R.DLFLAAAR.I
R4/RRR4-10/2	1414.450	1415.578	-1508.382	0.341	379.341	0.353	15	0.141	R.GNIASAINTIQANK.V
R4/RRR4-12/2	1346.258	1346.619	-268.326	0.392	979.873	0.295	18	0.152	R.KLPDGSLM*EIVK.V
R4/RRR4-12/2	1346.250	1346.619	-274.512	0.370	722.137	0.370	16	0.150	R.KLPDGSLM*EIVK.V
R4/RRR4-12/2	1346.169	1346.619	-335.285	0.416	782.001	0.328	16	0.148	R.KLPDGSLM*EIVK.V
R4/RRR4-12/2	1211.896	1212.358	-382.025	0.114	152.122	0.544	16	0.130	R.AIPGYGGGM*SSAK.A
R4/RRR4-12/2	1211.806	1212.358	-1284.713	0.038	246.153	0.531	19	0.118	R.AIPGYGGGM*SSAK.A
R4/RRR4-12/2	1211.348	1212.358	-1664.634	-0.084	210.888	0.469	18	0.099	R.AIPGYGGGM*SSAK.A
R4/RRR4-8/2	1951.606	1952.155	-796.036	0.568	1066.353	0.620	23	0.207	K.VPVLETPDGPVSESNAIAR.Y
R4/RRR4-8/2	1952.546	1952.155	201.060	0.587	959.617	0.620	23	0.198	K.VPVLETPDGPVSESNAIAR.Y
R4/RRR4-8/2	1951.418	1952.155	-892.548	0.520	795.143	0.629	21	0.186	K.VPVLETPDGPVSESNAIAR.Y
R4/RRR4-9/2	1951.833	1952.155	-165.329	0.469	555.681	0.545	18	0.159	K.VPVLETPDGPVSESNAIAR.Y
R4/RRR4-9/2	1951.834	1952.155	-164.702	0.405	503.082	0.468	18	0.149	K.VPVLETPDGPVSESNAIAR.Y
R4/RRR4-9/2	1951.778	1952.155	-193.500	0.271	303.866	0.356	15	0.137	K.VPVLETPDGPVSESNAIAR.Y
R4/RRR4-7/2	1917.009	1917.115	-55.860	0.576	1634.875	0.592	25	0.265	K.NLPATAQVASQQGQYLAR.C
R4/RRR4-7/2	1478.447	1478.629	-123.195	0.386	1400.522	0.395	18	0.193	K.EIQDVLDDIYVR.Y
R4/RRR4-7/2	1059.891	1060.226	-316.936	0.392	960.140	0.469	16	0.174	K.ALSLVDSQVK.N
R4/RRR4-7/2	1478.370	1478.629	-175.792	0.346	1207.197	0.328	18	0.166	K.EIQDVLDDIYVR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1966.349	1966.135	109.170	0.468	1107.886	0.432	27	0.127	K.GDAEKESVELNIEEFKK.A
R4/RRR4-7/3	1502.270	1502.632	-242.064	0.414	1019.313	0.352	25	0.102	K.M*KDAEENPEGPIR.I
R4/RRR4-7/3	1501.910	1502.632	-1150.343	0.405	624.192	0.275	20	0.084	K.M*KDAEENPEGPIR.I
R4/RRR4-7/3	1502.625	1502.632	-4.651	0.454	736.060	0.273	21	0.084	K.M*KDAEENPEGPIR.I
R4/RRR4-8/2	1135.835	1136.323	-430.596	0.312	1268.295	0.402	16	0.180	K.ALIAAEYTGVK.V
R4/RRR4-8/2	1135.965	1136.323	-315.543	0.322	999.923	0.371	14	0.157	K.ALIAAEYTGVK.V
R4/RRR4-9/2	1207.172	1206.480	-255.774	0.298	867.521	0.297	15	0.143	K.M*LVIGSTPPFK.V
R4/RRR4-12/2	1419.176	1419.606	-303.992	0.490	1847.809	0.531	19	0.277	R.AFQLYSSGIFTGK.C
R4/RRR4-12/2	1419.552	1419.606	-38.003	0.469	1807.391	0.526	19	0.269	R.AFQLYSSGIFTGK.C
R4/RRR4-11/2	1420.025	1419.606	295.687	0.500	1814.856	0.520	19	0.269	R.AFQLYSSGIFTGK.C
R4/RRR4-12/2	1539.323	1539.719	-257.835	0.479	1463.059	0.531	23	0.227	K.AVANQPVSVAIEAGGR.A
R4/RRR4-11/2	1419.228	1419.606	-266.971	0.440	1527.598	0.476	19	0.223	R.AFQLYSSGIFTGK.C
R4/RRR4-12/2	1539.299	1539.719	-273.111	0.478	1370.657	0.522	22	0.215	K.AVANQPVSVAIEAGGR.A
R4/RRR4-15/2	1540.317	1539.719	-261.564	0.552	1112.454	0.624	22	0.214	K.AVANQPVSVAIEAGGR.A
R4/RRR4-13/2	1539.350	1539.719	-240.491	0.545	1161.373	0.593	22	0.212	K.AVANQPVSVAIEAGGR.A
R4/RRR4-13/2	1539.135	1539.719	-1031.957	0.518	1127.555	0.597	22	0.209	K.AVANQPVSVAIEAGGR.A
R4/RRR4-23/2	1539.145	1539.719	-1025.507	0.523	1107.179	0.598	23	0.209	K.AVANQPVSVAIEAGGR.A
R4/RRR4-11/2	1539.264	1539.719	-295.946	0.493	1117.974	0.592	23	0.208	K.AVANQPVSVAIEAGGR.A
R4/RRR4-14/2	1539.295	1539.719	-275.895	0.559	1025.462	0.628	21	0.207	K.AVANQPVSVAIEAGGR.A
R4/RRR4-11/2	1540.230	1539.719	-318.336	0.534	1152.516	0.565	22	0.205	K.AVANQPVSVAIEAGGR.A
R4/RRR4-24/2	1539.305	1539.719	-269.212	0.523	1108.845	0.578	22	0.204	K.AVANQPVSVAIEAGGR.A
R4/RRR4-16/2	1539.285	1539.719	-282.658	0.525	1015.981	0.609	23	0.204	K.AVANQPVSVAIEAGGR.A
R4/RRR4-13/2	1539.333	1539.719	-250.993	0.566	1074.289	0.580	23	0.203	K.AVANQPVSVAIEAGGR.A
R4/RRR4-13/2	1419.657	1419.606	36.170	0.415	1381.141	0.467	16	0.203	R.AFQLYSSGIFTGK.C
R4/RRR4-11/2	1539.303	1539.719	-271.122	0.544	1097.106	0.571	22	0.202	K.AVANQPVSVAIEAGGR.A
R4/RRR4-24/2	1539.291	1539.719	-278.680	0.531	1156.921	0.537	23	0.201	K.AVANQPVSVAIEAGGR.A
R4/RRR4-10/2	1539.388	1539.719	-215.670	0.507	1033.120	0.593	21	0.200	K.AVANQPVSVAIEAGGR.A
R4/RRR4-11/2	1419.106	1419.606	-353.185	0.410	1230.927	0.502	17	0.197	R.AFQLYSSGIFTGK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1539.351	1539.719	-239.696	0.469	1071.807	0.533	22	0.192	K.AVANQPVSVAIEAGGR.A
R4/RRR4-24/2	1539.314	1539.719	-263.643	0.515	1119.169	0.514	21	0.191	K.AVANQPVSVAIEAGGR.A
R4/RRR4-14/2	1539.427	1539.719	-190.134	0.544	962.249	0.554	22	0.189	K.AVANQPVSVAIEAGGR.A
R4/RRR4-17/2	1540.055	1539.719	218.978	0.488	984.804	0.548	21	0.188	K.AVANQPVSVAIEAGGR.A
R4/RRR4-23/2	1539.310	1539.719	-266.348	0.506	937.193	0.552	22	0.187	K.AVANQPVSVAIEAGGR.A
R4/RRR4-23/2	1539.272	1539.719	-291.251	0.525	915.121	0.555	22	0.187	K.AVANQPVSVAIEAGGR.A
R4/RRR4-13/2	1540.127	1539.719	266.189	0.448	897.087	0.553	19	0.181	K.AVANQPVSVAIEAGGR.A
R4/RRR4-10/2	1419.505	1419.606	-71.470	0.415	885.696	0.553	15	0.179	R.AFQLYSSGIFTGK.C
R4/RRR4-12/2	1538.667	1539.719	-1337.115	0.372	985.199	0.502	21	0.179	K.AVANQPVSVAIEAGGR.A
R4/RRR4-17/2	1539.272	1539.719	-290.933	0.484	792.068	0.530	20	0.174	K.AVANQPVSVAIEAGGR.A
R4/RRR4-10/2	1538.749	1539.719	-1283.813	0.394	805.316	0.517	20	0.171	K.AVANQPVSVAIEAGGR.A
R4/RRR4-14/2	1538.627	1539.719	-1363.808	0.423	824.186	0.499	20	0.170	K.AVANQPVSVAIEAGGR.A
R4/RRR4-13/2	1540.297	1539.719	-274.603	0.463	769.251	0.527	18	0.170	K.AVANQPVSVAIEAGGR.A
R4/RRR4-13/2	1333.993	1334.536	-1160.272	0.434	1187.181	0.342	17	0.168	K.CGIAVEPSYPLK.K
R4/RRR4-10/2	1538.565	1539.719	-1403.891	0.367	853.926	0.446	20	0.164	K.AVANQPVSVAIEAGGR.A
R4/RRR4-14/2	1419.283	1419.606	-228.659	0.356	828.379	0.421	15	0.158	R.AFQLYSSGIFTGK.C
R4/RRR4-13/2	1334.315	1334.536	-166.600	0.409	1003.320	0.347	16	0.157	K.CGIAVEPSYPLK.K
R4/RRR4-13/2	1040.971	1041.099	-122.512	0.323	792.836	0.241	14	0.143	K.SWGESGYVR.M
R4/RRR4-12/2	1040.920	1041.099	-171.684	0.349	855.879	0.206	15	0.142	K.SWGESGYVR.M
R4/RRR4-13/2	1419.516	1419.606	-63.707	0.377	585.300	0.283	15	0.141	R.AFQLYSSGIFTGK.C
R4/RRR4-13/2	1420.180	1419.606	-300.760	0.324	502.570	0.294	14	0.141	R.AFQLYSSGIFTGK.C
R4/RRR4-13/2	1040.962	1041.099	-131.452	0.323	764.636	0.217	14	0.141	K.SWGESGYVR.M
R4/RRR4-13/2	1419.163	1419.606	-312.881	0.274	711.985	0.276	15	0.141	R.AFQLYSSGIFTGK.C
R4/RRR4-12/2	1418.553	1419.606	-1451.628	0.323	865.954	0.223	15	0.139	R.AFQLYSSGIFTGK.C
R4/RRR4-11/2	1041.015	1041.099	-80.519	0.358	658.359	0.190	13	0.138	K.SWGESGYVR.M
R4/RRR4-13/2	1333.971	1334.536	-1177.180	0.365	691.765	0.287	13	0.138	K.CGIAVEPSYPLK.K
R4/RRR4-14/2	1040.814	1041.099	-273.809	0.198	651.846	0.075	13	0.133	K.SWGESGYVR.M
R4/RRR4-12/3	1462.150	1462.709	-1069.302	0.447	949.465	0.371	24	0.104	K.CGIAVEPSYPLKK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/3	1463.177	1462.709	320.345	0.464	1019.968	0.358	25	0.104	-.CGIAVEPSYPLKK.-
R4/RRR4-13/3	1462.644	1462.709	-44.803	0.462	850.575	0.320	24	0.094	K.CGIAVEPSYPLKK.G
R4/RRR4-11/3	1462.703	1462.709	-3.994	0.430	849.954	0.319	23	0.091	-.CGIAVEPSYPLKK.-
R4/RRR4-12/3	1462.624	1462.709	-58.113	0.450	781.933	0.296	23	0.090	K.CGIAVEPSYPLKK.G
R4/RRR4-11/3	1462.714	1462.709	3.413	0.389	794.762	0.291	24	0.085	-.CGIAVEPSYPLKK.-
R4/RRR4-13/3	1462.435	1462.709	-187.846	0.430	711.399	0.278	22	0.082	-.CGIAVEPSYPLKK.-
R4/RRR4-12/3	1462.732	1462.709	15.341	0.373	676.622	0.219	21	0.080	-.CGIAVEPSYPLKK.-
R4/RRR4-18/2	1677.243	1675.904	202.746	0.461	916.083	0.547	22	0.184	K.ALADEIGIPFLETSAK.D
R4/RRR4-17/2	1675.324	1675.904	-945.802	0.461	705.467	0.534	19	0.168	K.ALADEIGIPFLETSAK.D
R4/RRR4-18/2	1677.403	1675.904	298.565	0.485	716.234	0.513	20	0.167	K.ALADEIGIPFLETSAK.D
R4/RRR4-17/2	1130.944	1131.348	-358.952	0.466	817.045	0.441	14	0.164	K.AFM*TM*AGEIK.N
R4/RRR4-17/2	1130.946	1131.348	-356.353	0.368	889.841	0.369	15	0.157	K.AFM*TM*AGEIK.N
R4/RRR4-17/3	1905.671	1906.178	-793.264	0.360	1330.107	0.453	34	0.155	R.M*ASQPATNASKPATVQMR.G
R4/RRR4-18/2	1677.325	1675.904	251.643	0.457	648.120	0.381	19	0.148	K.ALADEIGIPFLETSAK.D
R4/RRR4-17/2	1675.137	1675.904	-1058.102	0.250	486.096	0.289	14	0.134	K.ALADEIGIPFLETSAK.D
R4/RRR4-17/3	1922.376	1922.177	103.758	0.390	1173.702	0.400	35	0.125	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-17/3	1921.998	1922.177	-93.445	0.403	1048.109	0.413	33	0.119	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-17/3	1979.981	1980.127	-73.631	0.410	933.036	0.454	25	0.118	K.QWLNEIDRYASENVNK.L
R4/RRR4-17/3	1980.029	1980.127	-49.791	0.446	824.416	0.458	24	0.112	K.QWLNEIDRYASENVNK.L
R4/RRR4-18/3	1921.353	1922.177	-952.350	0.394	819.555	0.439	30	0.112	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-17/3	1923.014	1922.177	-85.310	0.425	876.603	0.421	31	0.112	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-17/3	1923.249	1922.177	37.312	0.435	831.935	0.430	30	0.111	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-18/3	1921.351	1922.177	-953.116	0.388	843.369	0.400	31	0.106	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-17/3	1921.928	1922.177	-129.856	0.400	703.050	0.408	29	0.104	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-17/3	1923.093	1922.177	-44.051	0.377	707.495	0.407	28	0.104	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-18/3	1922.531	1922.177	184.757	0.335	676.332	0.318	28	0.093	R.M*ASQPATNASKPATVQM*R.G
R4/RRR4-17/3	1905.741	1906.178	-229.828	0.322	633.144	0.288	25	0.091	R.M*ASQPATNASKPATVQMR.G
R4/RRR4-17/3	1979.449	1980.127	-850.071	0.373	503.916	0.373	21	0.088	-.QWLNEIDRYASENVNK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1245.099	1245.368	-216.790	0.566	1772.450	0.495	20	0.260	K.SINDIAASQGIR.I
R4/RRR4-11/2	1244.784	1245.368	-1276.277	0.547	1645.915	0.477	19	0.239	K.SINDIAASQGIR.I
R4/RRR4-11/2	1610.508	1610.883	-233.591	0.488	1814.795	0.388	23	0.236	R.VLNISGVQLIGINNR.S
R4/RRR4-12/2	1245.014	1245.368	-285.349	0.484	1647.896	0.414	19	0.223	K.SINDIAASQGIR.I
R4/RRR4-11/2	1245.011	1245.368	-287.513	0.547	1555.670	0.455	19	0.223	K.SINDIAASQGIR.I
R4/RRR4-11/2	1441.455	1441.565	-77.177	0.478	1516.902	0.349	19	0.194	R.SLETFVVDTSNTK.M
R4/RRR4-11/2	1610.233	1610.883	-1028.137	0.410	1440.233	0.353	21	0.188	R.VLNISGVQLIGINNR.S
R4/RRR4-11/3	1775.536	1776.073	-868.501	0.521	1614.162	0.431	34	0.186	K.KPLKEVIEAAGQAPPAR.D
R4/RRR4-11/3	1775.324	1776.073	-988.398	0.489	1516.401	0.433	34	0.172	K.KPLKEVIEAAGQAPPAR.D
R4/RRR4-11/2	1346.502	1346.515	-10.331	0.367	814.396	0.522	15	0.169	R.DFYGALASAFKR.N
R4/RRR4-11/2	1345.530	1346.515	-1480.272	0.379	894.905	0.464	15	0.166	R.DFYGALASAFKR.N
R4/RRR4-11/2	1346.202	1346.515	-233.614	0.298	702.517	0.542	14	0.160	R.DFYGALASAFKR.N
R4/RRR4-12/2	1610.392	1610.883	-306.063	0.412	1040.637	0.348	19	0.158	R.VLNISGVQLIGINNR.S
R4/RRR4-12/2	1610.240	1610.883	-1023.722	0.368	1078.281	0.247	19	0.147	R.VLNISGVQLIGINNR.S
R4/RRR4-11/2	1609.891	1610.883	-1241.302	0.334	1057.972	0.243	19	0.146	R.VLNISGVQLIGINNR.S
R4/RRR4-11/3	1775.460	1776.073	-911.569	0.477	1213.817	0.423	30	0.135	K.KPLKEVIEAAGQAPPAR.D
R4/RRR4-7/2	1607.058	1607.833	-1107.802	0.490	2504.384	0.507	23	0.385	R.SPPIEEVINTGVVPR.F
R4/RRR4-7/2	1606.761	1607.833	-1293.556	0.388	2290.315	0.440	22	0.321	R.SPPIEEVINTGVVPR.F
R4/RRR4-8/2	1602.625	1601.903	-174.386	0.561	2118.863	0.504	21	0.312	R.IVTVCLEGLENILK.V
R4/RRR4-7/2	1602.474	1601.903	-268.609	0.586	2005.125	0.491	21	0.289	R.IVTVCLEGLENILK.V
R4/RRR4-7/2	1601.393	1601.903	-945.734	0.530	2007.197	0.479	21	0.287	R.IVTVCLEGLENILK.V
R4/RRR4-7/2	1344.907	1344.624	211.151	0.511	1676.141	0.640	20	0.285	K.VVVESGAVPIFVK.L
R4/RRR4-7/2	1344.303	1344.624	-239.227	0.467	1633.015	0.576	20	0.260	K.VVVESGAVPIFVK.L
R4/RRR4-7/2	1601.733	1601.903	-106.757	0.518	1872.212	0.452	21	0.260	R.IVTVCLEGLENILK.V
R4/RRR4-7/2	1344.471	1344.624	-114.435	0.373	1120.285	0.481	17	0.183	K.VVVESGAVPIFVK.L
R4/RRR4-7/2	1975.611	1976.416	-916.428	0.423	722.033	0.443	19	0.151	R.LVELLM*HPSASVLIPALR.T
R4/RRR4-7/3	1976.441	1976.416	13.046	0.430	1393.245	0.345	31	0.132	R.LVELLM*HPSASVLIPALR.T
R4/RRR4-7/3	1957.941	1958.078	-70.020	0.355	702.879	0.507	31	0.112	K.EAAWAISNATSGGTHDQIK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/3	1958.646	1958.078	-221.365	0.328	616.515	0.347	28	0.086	K.EAAWAISNATSGGTHDQIK.Y
R4/RRR4-8/2	1123.490	1124.318	-1632.677	0.506	1698.799	0.523	17	0.258	R.LPANLIQAQR.D
R4/RRR4-8/2	1124.003	1124.318	-281.866	0.579	1578.663	0.543	17	0.250	R.LPANLIQAQR.D
R4/RRR4-8/2	1123.499	1124.318	-1624.709	0.586	1484.149	0.551	17	0.241	R.LPANLIQAQR.D
R4/RRR4-8/2	1257.157	1257.423	-212.763	0.433	1306.384	0.304	17	0.170	K.GWNLNLAELAR.I
R4/RRR4-8/2	1257.136	1257.423	-229.323	0.475	1160.305	0.339	17	0.167	K.GWNLNLAELAR.I
R4/RRR4-8/2	1965.678	1965.112	-221.593	0.428	812.115	0.507	17	0.161	R.VGGLSNSEIADVFAEWNR.G
R4/RRR4-8/2	1256.458	1257.423	-1569.034	0.437	1077.646	0.326	16	0.160	K.GWNLNLAELAR.I
R4/RRR4-8/2	1209.507	1209.292	177.999	0.422	914.629	0.328	16	0.155	R.DLFGAHTYER.I
R4/RRR4-8/2	1209.345	1209.292	43.675	0.387	683.342	0.365	15	0.152	R.DLFGAHTYER.I
R4/RRR4-8/2	1209.849	1209.292	-367.518	0.382	814.751	0.308	15	0.149	R.DLFGAHTYER.I
R4/RRR4-9/2	1792.480	1792.023	255.490	0.556	1595.668	0.527	26	0.245	K.TEAIFPATLETISNVGK.V
R4/RRR4-9/2	1492.473	1491.706	-156.247	0.545	1326.389	0.534	20	0.218	K.ELAITNLTNCLTK.E
R4/RRR4-9/2	1793.431	1792.023	227.978	0.545	1384.269	0.502	25	0.215	K.TEAIFPATLETISNVGK.V
R4/RRR4-9/2	1373.156	1373.494	-247.307	0.506	1197.148	0.503	20	0.199	R.VLQDPSSSAEALR.T
R4/RRR4-9/2	1373.214	1373.494	-204.589	0.494	1185.968	0.487	20	0.195	R.VLQDPSSSAEALR.T
R4/RRR4-9/2	1446.235	1446.665	-298.135	0.471	837.834	0.595	19	0.188	K.IPGTSELQISLCK.E
R4/RRR4-9/2	1323.144	1323.437	-222.139	0.520	1093.156	0.489	16	0.188	K.SQLEEDPIVHR.H
R4/RRR4-9/2	1372.855	1373.494	-1197.526	0.405	1294.561	0.410	20	0.188	R.VLQDPSSSAEALR.T
R4/RRR4-9/2	1323.156	1323.437	-213.254	0.479	1066.978	0.499	16	0.187	K.SQLEEDPIVHR.H
R4/RRR4-9/2	1491.527	1491.706	-120.063	0.465	1010.117	0.515	18	0.185	K.ELAITNLTNCLTK.E
R4/RRR4-9/2	1446.053	1446.665	-1118.027	0.466	814.675	0.540	19	0.179	K.IPGTSELQISLCK.E
R4/RRR4-9/2	1446.171	1446.665	-342.850	0.440	709.922	0.568	18	0.175	K.IPGTSELQISLCK.E
R4/RRR4-13/3	1679.163	1679.898	-1036.105	0.500	1129.889	0.494	29	0.145	K.TPFQEYTDLLARPK.G
R4/RRR4-13/3	1678.558	1679.898	-1398.086	0.390	675.794	0.455	26	0.105	K.TPFQEYTDLLARPK.G
R4/RRR4-13/3	1679.514	1679.898	-228.849	0.388	583.225	0.389	26	0.095	K.TPFQEYTDLLARPK.G
R4/RRR4-4/2	1869.446	1870.006	-836.981	0.429	695.526	0.467	20	0.158	K.TYEPSEEPFDISLVSR.E
R4/RRR4-4/2	1187.387	1187.416	-24.192	0.348	631.059	0.436	14	0.151	K.FGALVDALKPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1394.541	1395.540	-1437.466	0.358	1543.484	0.358	19	0.198	K.EGDYVTLVQSGVK.S
R4/RRR4-7/2	1396.177	1395.540	-260.944	0.483	1478.798	0.356	19	0.192	K.EGDYVTLVQSGVK.S
R4/RRR4-7/2	1394.671	1395.540	-1344.013	0.393	1406.303	0.339	20	0.184	K.EGDYVTLVQSGVK.S
R4/RRR4-7/2	1143.714	1144.303	-1394.200	0.438	1286.746	0.384	16	0.182	R.AEVSDIAIAVR.E
R4/RRR4-7/2	1031.690	1032.200	-1467.854	0.358	1440.152	0.299	16	0.179	K.LAEAGMNVAR.L
R4/RRR4-7/2	1263.629	1264.496	-1481.938	0.409	790.152	0.433	14	0.155	R.AISSLLSAQFVK.E
R4/RRR4-7/2	1495.328	1495.854	-1023.706	0.309	844.250	0.393	15	0.149	R.LALYQGVVPIYMK.F
R4/RRR4-7/2	1394.768	1395.540	-1274.571	0.271	687.589	0.240	15	0.136	K.EGDYVTLVQSGVK.S
R4/RRR4-6/2	1202.367	1202.419	-43.951	0.537	1924.251	0.471	20	0.275	R.LLAVEGCAALGK.L
R4/RRR4-6/2	1284.228	1284.442	-167.091	0.488	1660.056	0.453	18	0.235	K.FAATVEQNYLK.T
R4/RRR4-6/2	1201.846	1202.419	-1312.909	0.469	1587.942	0.458	18	0.226	R.LLAVEGCAALGK.L
R4/RRR4-7/2	1203.160	1202.419	-216.104	0.399	1504.204	0.424	18	0.209	R.LLAVEGCAALGK.L
R4/RRR4-6/2	1284.223	1284.442	-171.096	0.487	1491.375	0.400	18	0.205	K.FAATVEQNYLK.T
R4/RRR4-6/2	1534.360	1533.749	-254.599	0.336	1561.837	0.376	20	0.203	K.ESDIVDWFVPVVK.R
R4/RRR4-6/2	1285.131	1284.442	-243.096	0.544	1300.692	0.466	18	0.202	K.FAATVEQNYLK.T
R4/RRR4-6/3	1766.823	1766.115	-166.018	0.528	1509.328	0.504	31	0.199	K.VLQALIPILDQSVVEK.N
R4/RRR4-6/2	1766.302	1766.115	106.430	0.520	1110.277	0.529	25	0.198	K.VLQALIPILDQSVVEK.N
R4/RRR4-6/2	1766.511	1766.115	224.799	0.524	912.191	0.518	23	0.181	K.VLQALIPILDQSVVEK.N
R4/RRR4-6/2	1766.397	1766.115	160.351	0.520	803.847	0.537	22	0.177	K.VLQALIPILDQSVVEK.N
R4/RRR4-6/2	1189.815	1190.335	-1281.421	0.503	805.197	0.398	13	0.158	K.INNPHYLYR.M
R4/RRR4-6/3	1766.196	1766.115	46.084	0.402	742.274	0.324	24	0.086	K.VLQALIPILDQSVVEK.N
R4/RRR4-8/2	1259.910	1260.404	-393.287	0.455	1583.290	0.471	19	0.229	R.AFATGGYAAM*QR.V
R4/RRR4-8/2	1259.816	1260.404	-1264.298	0.469	1397.320	0.453	19	0.207	R.AFATGGYAAM*QR.V
R4/RRR4-8/2	1259.945	1260.404	-365.484	0.472	1267.031	0.494	18	0.202	R.AFATGGYAAM*QR.V
R4/RRR4-8/2	1404.428	1404.596	-119.924	0.441	881.034	0.407	16	0.159	K.TRPFDSILAEVR.A
R4/RRR4-8/2	1451.070	1451.696	-1123.780	0.415	521.712	0.468	15	0.154	K.LIEILNPSNKPGR.I
R4/RRR4-8/2	1450.750	1451.696	-1345.228	0.355	439.282	0.387	13	0.142	K.LIEILNPSNKPGR.I
R4/RRR4-8/2	1451.204	1451.696	-339.889	0.211	187.645	0.404	13	0.139	K.LIEILNPSNKPGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1528.563	1529.669	-1381.838	0.291	1016.246	0.170	18	0.135	R.AFVLQGGDCAESFK.E
R4/RRR4-8/3	976.217	976.244	-27.526	0.437	894.300	0.326	16	0.092	-.VKLPHLIR.-
R4/RRR4-8/3	976.121	976.244	-125.836	0.347	855.599	0.302	16	0.088	R.VKLPHLIR.A
R4/RRR4-8/3	976.525	976.244	288.534	0.457	719.132	0.311	15	0.086	-.VKLPHLIR.-
R4/RRR4-8/3	1404.887	1404.596	207.878	0.413	1159.453	0.192	21	0.076	-.TRPFDSILAEVR.-
R4/RRR4-8/3	1404.499	1404.596	-69.149	0.364	1156.289	0.151	21	0.069	-.TRPFDSILAEVR.-
R4/RRR4-2/2	1505.610	1505.742	-88.038	0.474	1783.284	0.483	20	0.255	K.IAGIQGGFFELQPK.E
R4/RRR4-6/2	1336.161	1335.534	-279.903	0.537	1246.039	0.505	19	0.204	R.INTLLQGYSGIR.F
R4/RRR4-1/2	1336.070	1335.534	-348.102	0.494	1245.907	0.472	19	0.198	R.INTLLQGYSGIR.F
R4/RRR4-1/2	1335.406	1335.534	-95.867	0.513	1205.134	0.476	18	0.194	R.INTLLQGYSGIR.F
R4/RRR4-18/2	1336.346	1335.534	-140.968	0.509	1208.572	0.457	19	0.192	R.INTLLQGYSGIR.F
R4/RRR4-5/2	1336.164	1335.534	-277.428	0.537	1274.159	0.429	19	0.191	R.INTLLQGYSGIR.F
R4/RRR4-1/2	1336.163	1335.534	-278.437	0.537	1089.362	0.497	18	0.190	R.INTLLQGYSGIR.F
R4/RRR4-6/2	1335.315	1335.534	-164.642	0.507	1177.264	0.437	18	0.185	R.INTLLQGYSGIR.F
R4/RRR4-6/2	1335.321	1335.534	-159.873	0.530	983.032	0.459	17	0.175	R.INTLLQGYSGIR.F
R4/RRR4-3/2	1505.463	1505.742	-185.884	0.423	1157.670	0.401	17	0.173	K.IAGIQGGFFELQPK.E
R4/RRR4-2/2	1335.227	1335.534	-230.674	0.456	864.532	0.464	18	0.171	R.INTLLQGYSGIR.F
R4/RRR4-2/2	1335.164	1335.534	-277.636	0.410	864.455	0.462	18	0.170	R.INTLLQGYSGIR.F
R4/RRR4-18/2	1335.099	1335.534	-327.171	0.480	911.080	0.429	17	0.167	R.INTLLQGYSGIR.F
R4/RRR4-1/2	1505.575	1505.742	-111.786	0.392	887.076	0.419	17	0.160	K.IAGIQGGFFELQPK.E
R4/RRR4-1/2	1335.887	1335.534	265.185	0.329	746.496	0.358	16	0.151	R.INTLLQGYSGIR.F
R4/RRR4-5/2	1505.087	1505.742	-1103.053	0.378	509.195	0.423	15	0.148	K.IAGIQGGFFELQPK.E
R4/RRR4-7/2	1506.990	1505.742	165.123	0.366	312.597	0.454	16	0.148	-.IAGIQGGFFELQPK.-
R4/RRR4-1/2	1482.142	1481.759	259.173	0.385	740.194	0.365	15	0.145	K.LLNANVTPCLPLR.G
R4/RRR4-7/2	1506.976	1505.742	155.862	0.344	328.060	0.330	16	0.145	K.IAGIQGGFFELQPK.E
R4/RRR4-7/2	1159.660	1160.296	-1415.572	0.374	1217.794	0.252	16	0.157	R.VDEIVTCAPR.R
R4/RRR4-4/2	1496.109	1495.616	330.570	0.519	837.260	0.434	16	0.160	K.VSTILNDEFQNSK.E
R4/RRR4-4/2	1494.987	1495.616	-1093.143	0.403	889.549	0.383	17	0.156	K.VSTILNDEFQNSK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1746.412	1746.858	-255.838	0.435	1186.721	0.271	26	0.096	R.FGHNEIDEPSFTQPK.M
R4/RRR4-4/3	1746.505	1746.858	-202.510	0.358	859.396	0.222	24	0.079	R.FGHNEIDEPSFTQPK.M
R4/RRR4-3/3	1746.714	1746.858	-82.833	0.333	713.346	0.166	20	0.074	-.FGHNEIDEPSFTQPK.-
R4/RRR4-3/3	1981.924	1982.146	-112.323	0.541	1891.889	0.571	38	0.301	K.RPDGGVDGVITDFPATAHR.Y
R4/RRR4-3/3	1981.458	1982.146	-854.430	0.502	1665.311	0.451	38	0.202	K.RPDGGVDGVITDFPATAHR.Y
R4/RRR4-3/2	1118.031	1118.351	-286.657	0.525	1264.290	0.456	18	0.197	K.LGFGVVDAVIK.A
R4/RRR4-3/2	1118.245	1118.351	-94.885	0.563	1247.447	0.433	18	0.191	K.LGFGVVDAVIK.A
R4/RRR4-3/2	1118.132	1118.351	-196.512	0.545	1246.276	0.427	18	0.190	K.LGFGVVDAVIK.A
R4/RRR4-3/2	1201.445	1201.395	41.720	0.401	874.801	0.392	18	0.160	K.TLSGDSPLVIAK.G
R4/RRR4-3/2	1086.180	1086.219	-36.253	0.380	767.656	0.402	13	0.156	R.LSDFLDFTK.G
R4/RRR4-3/2	1201.324	1201.395	-59.175	0.362	553.573	0.412	15	0.149	K.TLSGDSPLVIAK.G
R4/RRR4-3/2	1077.147	1077.215	-63.837	0.293	624.891	0.394	13	0.145	K.TYNVNGAPLK.G
R4/RRR4-4/2	1086.901	1086.219	-293.966	0.312	564.031	0.334	11	0.142	R.LSDFLDFTK.G
R4/RRR4-3/3	1981.251	1982.146	-959.174	0.425	1165.281	0.465	33	0.141	K.RPDGGVDGVITDFPATAHR.Y
R4/RRR4-3/2	1201.089	1201.395	-255.723	0.243	500.802	0.256	15	0.137	K.TLSGDSPLVIAK.G
R4/RRR4-6/2	1677.722	1678.891	-1296.933	0.531	2402.582	0.468	23	0.350	K.NQVAM*NPINTVFDAK.R
R4/RRR4-6/2	1679.426	1678.891	-278.026	0.584	1977.785	0.608	22	0.321	K.NQVAM*NPINTVFDAK.R
R4/RRR4-6/2	1678.388	1678.891	-898.555	0.542	2029.411	0.544	22	0.309	K.NQVAM*NPINTVFDAK.R
R4/RRR4-6/2	1662.147	1662.892	-1052.817	0.545	1766.846	0.534	22	0.267	K.NQVAMNPINTVFDAK.R
R4/RRR4-6/2	1662.301	1662.892	-959.841	0.521	1513.986	0.545	21	0.237	K.NQVAMNPINTVFDAK.R
R4/RRR4-6/2	1229.047	1229.325	-226.993	0.526	1689.043	0.422	19	0.232	R.VEIIANDQGNR.I
R4/RRR4-6/2	1228.961	1229.325	-297.345	0.496	1654.506	0.376	18	0.216	R.VEIIANDQGNR.I
R4/RRR4-6/2	1661.702	1662.892	-1321.889	0.374	1549.853	0.414	20	0.209	K.NQVAMNPINTVFDAK.R
R4/RRR4-6/2	1835.428	1835.078	191.569	0.550	1233.301	0.473	23	0.194	K.NQVAM*NPINTVFDAKR.L
R4/RRR4-6/2	1834.489	1835.078	-868.588	0.531	970.139	0.541	22	0.187	K.NQVAM*NPINTVFDAKR.L
R4/RRR4-6/2	1833.948	1835.078	-1164.930	0.499	523.618	0.539	20	0.165	K.NQVAM*NPINTVFDAKR.L
R4/RRR4-6/2	1475.011	1474.554	311.060	0.369	537.072	0.522	19	0.161	R.TTPSYVGFTDTER.L
R4/RRR4-6/2	1474.188	1474.554	-248.796	0.254	556.620	0.492	19	0.150	R.TTPSYVGFTDTER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1474.057	1474.554	-338.109	0.262	549.653	0.458	19	0.149	R.TTPSYVGFTDTER.L
R4/RRR4-4/2	1554.362	1555.664	-1484.934	0.285	1609.578	0.076	18	0.153	R.CWEDVFDAISNAK.H
R4/RRR4-10/3	1316.381	1315.498	-88.891	0.240	1104.055	0.073	22	0.064	K.QGGDKDLLLDLK.A
R4/RRR4-5/2	1233.104	1232.369	-215.324	0.562	1673.109	0.492	18	0.245	R.NELSGALTGLTR.V
R4/RRR4-5/2	1232.151	1232.369	-177.433	0.432	1456.078	0.481	17	0.216	R.NELSGALTGLTR.V
R4/RRR4-5/2	1246.579	1247.468	-1519.983	0.334	840.159	0.387	18	0.157	K.IDIGVFDALKR.K
R4/RRR4-5/2	969.874	969.120	-254.450	0.462	861.737	0.344	14	0.156	R.LNIGGEPIR.I
R4/RRR4-5/2	1247.237	1247.468	-185.692	0.421	668.755	0.392	16	0.154	K.IDIGVFDALKR.K
R4/RRR4-5/2	969.067	969.120	-55.163	0.429	709.706	0.301	13	0.146	R.LNIGGEPIR.I
R4/RRR4-6/2	1247.067	1247.468	-323.169	0.296	426.009	0.336	15	0.144	K.IDIGVFDALKR.K
R4/RRR4-5/2	970.060	969.120	-61.796	0.429	599.514	0.300	12	0.144	R.LNIGGEPIR.I
R4/RRR4-5/2	1084.955	1085.234	-257.930	0.341	811.450	0.259	14	0.142	R.FKEEVAAYK.-
R4/RRR4-18/2	968.578	968.132	461.251	0.379	608.602	0.285	11	0.142	-.HLLEEAKK.-
R4/RRR4-18/2	968.923	968.132	-216.222	0.336	606.324	0.198	11	0.138	K.HLLEEAKK.R
R4/RRR4-18/2	967.870	968.132	-271.485	0.357	721.286	0.284	11	0.134	-.HLLEEAKK.-
R4/RRR4-2/2	1521.076	1520.624	297.857	0.560	2404.305	0.555	23	0.380	R.VEQGSLTGETASVNK.T
R4/RRR4-1/2	1520.268	1520.624	-235.054	0.526	2072.994	0.527	22	0.310	R.VEQGSLTGETASVNK.T
R4/RRR4-3/2	1520.306	1520.624	-209.679	0.487	1791.580	0.458	22	0.250	R.VEQGSLTGETASVNK.T
R4/RRR4-2/2	1520.214	1520.624	-270.499	0.519	1618.479	0.462	23	0.230	R.VEQGSLTGETASVNK.T
R4/RRR4-1/2	1520.105	1520.624	-1002.348	0.464	1518.568	0.459	22	0.218	R.VEQGSLTGETASVNK.T
R4/RRR4-2/2	1520.143	1520.624	-317.629	0.460	1246.072	0.372	20	0.175	R.VEQGSLTGETASVNK.T
R4/RRR4-3/2	1519.384	1520.624	-1478.586	0.384	1218.173	0.305	20	0.163	R.VEQGSLTGETASVNK.T
R4/RRR4-3/2	895.654	896.028	-418.661	0.318	917.416	0.405	12	0.160	R.HAAPSVWK.L
R4/RRR4-3/2	895.363	896.028	-1864.740	0.386	609.622	0.460	10	0.156	R.HAAPSVWK.L
R4/RRR4-2/2	1130.080	1130.363	-251.206	0.434	661.280	0.375	14	0.150	R.VLQLISSTLR.V
R4/RRR4-1/2	1978.670	1978.232	222.105	0.423	907.206	0.357	20	0.149	R.SGYIQLLDGSVVLLDEGAK.A
R4/RRR4-3/2	1519.696	1520.624	-1272.274	0.374	895.389	0.281	21	0.147	R.VEQGSLTGETASVNK.T
R4/RRR4-3/2	1000.989	1001.119	-130.647	0.439	1058.800	0.240	13	0.147	K.GAVENLLER.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1000.575	1001.119	-1547.578	0.377	732.407	0.259	12	0.141	K.GAVENLLER.S
R4/RRR4-3/2	1978.795	1978.232	-221.671	0.387	609.916	0.362	19	0.141	R.SGYIQLLDGSVVLLDEGAK.A
R4/RRR4-1/2	1000.993	1001.119	-126.487	0.397	1046.544	0.183	13	0.141	K.GAVENLLER.S
R4/RRR4-3/2	1001.031	1001.119	-87.955	0.411	1004.427	0.195	13	0.141	K.GAVENLLER.S
R4/RRR4-4/2	1979.133	1978.232	-50.395	0.218	658.736	0.170	19	0.129	R.SGYIQLLDGSVVLLDEGAK.A
R4/RRR4-24/2	1798.278	1798.924	-918.105	0.549	2579.225	0.596	24	0.432	K.CANGGLDLDWDTVFSK.I
R4/RRR4-25/2	1800.418	1798.924	274.901	0.627	2574.303	0.557	24	0.414	K.CANGGLDLDWDTVFSK.I
R4/RRR4-25/2	1798.331	1798.924	-888.666	0.565	2270.388	0.625	24	0.379	K.CANGGLDLDWDTVFSK.I
R4/RRR4-25/2	1798.301	1798.924	-905.294	0.555	2280.908	0.609	23	0.374	K.CANGGLDLDWDTVFSK.I
R4/RRR4-24/2	1798.314	1798.924	-898.275	0.536	2146.618	0.585	23	0.341	K.CANGGLDLDWDTVFSK.I
R4/RRR4-25/2	1797.610	1798.924	-1291.353	0.485	2069.000	0.566	24	0.322	K.CANGGLDLDWDTVFSK.I
R4/RRR4-24/2	1798.284	1798.924	-915.039	0.534	1932.115	0.576	23	0.303	K.CANGGLDLDWDTVFSK.I
R4/RRR4-25/2	1626.344	1626.790	-274.905	0.485	1913.478	0.509	22	0.280	K.YGWTAFCGPVGPTGR.D
R4/RRR4-24/2	1799.149	1798.924	125.107	0.503	1602.836	0.580	21	0.255	K.CANGGLDLDWDTVFSK.I
R4/RRR4-25/2	1626.354	1626.790	-268.956	0.482	1557.870	0.499	20	0.230	K.YGWTAFCGPVGPTGR.D
R4/RRR4-25/2	1625.753	1626.790	-1256.755	0.411	1717.762	0.402	22	0.227	K.YGWTAFCGPVGPTGR.D
R4/RRR4-25/3	1843.114	1842.041	40.175	0.562	1421.104	0.594	29	0.221	R.SKYGWTAFCGPVGPTGR.D
R4/RRR4-25/3	1841.999	1842.041	-22.780	0.571	1369.731	0.579	28	0.207	R.SKYGWTAFCGPVGPTGR.D
R4/RRR4-25/3	1841.931	1842.041	-59.474	0.542	1397.703	0.560	28	0.204	R.SKYGWTAFCGPVGPTGR.D
R4/RRR4-25/3	1842.667	1842.041	-203.105	0.559	1447.489	0.538	29	0.203	R.SKYGWTAFCGPVGPTGR.D
R4/RRR4-25/2	1626.240	1626.790	-955.828	0.478	1208.622	0.529	19	0.201	K.YGWTAFCGPVGPTGR.D
R4/RRR4-25/2	1626.327	1626.790	-285.749	0.475	1317.496	0.478	19	0.200	K.YGWTAFCGPVGPTGR.D
R4/RRR4-24/2	1626.239	1626.790	-956.582	0.456	1178.644	0.490	19	0.191	K.YGWTAFCGPVGPTGR.D
R4/RRR4-24/2	1626.239	1626.790	-956.808	0.454	1197.288	0.390	19	0.174	K.YGWTAFCGPVGPTGR.D
R4/RRR4-24/2	1136.906	1137.185	-246.036	0.524	924.162	0.410	17	0.169	K.IDTDGQGFQR.G
R4/RRR4-25/2	1136.497	1137.185	-1489.454	0.461	894.797	0.409	17	0.167	K.IDTDGQGFQR.G
R4/RRR4-25/2	1136.480	1137.185	-1504.775	0.453	862.808	0.414	17	0.167	K.IDTDGQGFQR.G
R4/RRR4-25/2	1136.931	1137.185	-223.631	0.510	850.241	0.402	17	0.165	K.IDTDGQGFQR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	1136.464	1137.185	-1518.478	0.494	798.555	0.405	17	0.164	K.IDTDGQGFQR.G
R4/RRR4-24/2	1136.883	1137.185	-265.857	0.540	734.780	0.428	16	0.164	K.IDTDGQGFQR.G
R4/RRR4-25/2	1136.907	1137.185	-244.851	0.507	872.943	0.387	17	0.164	K.IDTDGQGFQR.G
R4/RRR4-25/2	1137.109	1137.185	-66.608	0.398	757.780	0.394	17	0.160	K.IDTDGQGFQR.G
R4/RRR4-23/2	1137.125	1137.185	-52.179	0.503	746.176	0.386	16	0.159	K.IDTDGQGFQR.G
R4/RRR4-25/2	1138.140	1137.185	-39.008	0.434	480.541	0.387	14	0.154	K.IDTDGQGFQR.G
R4/RRR4-25/2	1138.250	1137.185	57.590	0.490	546.034	0.360	15	0.153	K.IDTDGQGFQR.G
R4/RRR4-26/2	1137.204	1137.185	17.053	0.335	453.312	0.352	14	0.150	K.IDTDGQGFQR.G
R4/RRR4-29/2	1137.388	1137.185	179.490	0.298	677.964	0.303	16	0.147	K.IDTDGQGFQR.G
R4/RRR4-29/2	1137.784	1137.185	-353.348	0.298	590.786	0.303	16	0.147	K.IDTDGQGFQR.G
R4/RRR4-29/2	1137.401	1137.185	190.790	0.312	533.409	0.299	15	0.147	K.IDTDGQGFQR.G
R4/RRR4-24/2	1625.648	1626.790	-1321.381	0.284	562.955	0.402	16	0.145	K.YGWTAFCGPVGPTGR.D
R4/RRR4-25/2	1137.006	1137.185	-157.929	0.275	628.550	0.284	15	0.145	K.IDTDGQGFQR.G
R4/RRR4-25/2	1626.116	1626.790	-1032.550	0.339	741.726	0.311	16	0.142	K.YGWTAFCGPVGPTGR.D
R4/RRR4-25/2	1625.702	1626.790	-1288.275	0.312	545.089	0.379	14	0.142	K.YGWTAFCGPVGPTGR.D
R4/RRR4-2/2	1064.130	1064.257	-119.385	0.410	951.249	0.409	14	0.166	-.FEILEAITK.-
R4/RRR4-6/2	1063.693	1064.257	-1474.567	0.398	832.454	0.352	14	0.155	-.FEILEAITK.-
R4/RRR4-6/2	1063.681	1064.257	-1485.749	0.423	874.919	0.353	14	0.154	-.FEILEAITK.-
R4/RRR4-1/2	1064.165	1064.257	-86.591	0.459	874.896	0.334	14	0.151	-.FEILEAITK.-
R4/RRR4-6/2	1064.134	1064.257	-115.703	0.439	820.754	0.345	14	0.151	-.FEILEAITK.-
R4/RRR4-1/2	1065.130	1064.257	-119.388	0.532	919.083	0.312	14	0.150	-.FEILEAITK.-
R4/RRR4-18/2	1064.087	1064.257	-160.237	0.413	910.335	0.309	14	0.150	-.FEILEAITK.-
R4/RRR4-1/2	1063.642	1064.257	-1522.524	0.390	833.530	0.328	14	0.149	-.FEILEAITK.-
R4/RRR4-5/2	1064.125	1064.257	-123.873	0.376	812.887	0.328	14	0.149	-.FEILEAITK.-
R4/RRR4-18/2	1064.304	1064.257	44.565	0.347	823.981	0.298	14	0.144	-.FEILEAITK.-
R4/RRR4-18/2	1063.926	1064.257	-311.937	0.328	710.693	0.338	13	0.143	-.FEILEAITK.-
R4/RRR4-5/2	1063.515	1064.257	-1642.204	0.270	626.841	0.271	13	0.140	-.FEILEAITK.-
R4/RRR4-5/2	1064.142	1064.257	-108.223	0.322	670.811	0.246	13	0.139	-.FEILEAITK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1063.946	1064.257	-292.828	0.261	743.696	0.267	14	0.138	-.FEILEAITK.-
R4/RRR4-3/2	1617.364	1616.883	298.444	0.512	2008.671	0.531	21	0.301	K.SQPDLAILAVNTFVK.D
R4/RRR4-3/2	1617.698	1616.883	-114.559	0.577	1854.850	0.587	20	0.293	K.SQPDLAILAVNTFVK.D
R4/RRR4-3/2	1617.678	1616.883	-127.048	0.504	1530.291	0.581	19	0.246	K.SQPDLAILAVNTFVK.D
R4/RRR4-5/2	1617.769	1616.883	-70.809	0.439	1342.145	0.568	18	0.219	K.SQPDLAILAVNTFVK.D
R4/RRR4-3/2	1450.403	1450.576	-119.668	0.293	1216.018	0.258	16	0.153	K.LYDINAELVEDR.G
R4/RRR4-3/2	1011.785	1012.140	-352.396	0.421	940.597	0.301	13	0.152	-.YNDPIYVK.-
R4/RRR4-3/2	1011.946	1012.140	-192.510	0.490	892.894	0.315	13	0.152	-.YNDPIYVK.-
R4/RRR4-3/2	1012.069	1012.140	-70.543	0.419	699.911	0.266	12	0.144	K.YNDPIYVK.M
R4/RRR4-3/2	981.792	982.114	-329.178	0.200	807.945	0.242	13	0.135	R.TSFLEAWK.S
R4/RRR4-3/3	1510.345	1510.757	-273.735	0.406	962.241	0.354	24	0.099	-.LQHANCAVVLSAVK.-
R4/RRR4-3/3	1510.656	1510.757	-67.369	0.460	703.121	0.385	24	0.094	-.LQHANCAVVLSAVK.-
R4/RRR4-3/3	1510.047	1510.757	-1135.764	0.422	821.086	0.252	25	0.083	R.LQHANCAVVLSAVK.I
R4/RRR4-15/2	1936.468	1937.097	-843.799	0.630	2978.267	0.592	25	0.529	K.IEDLSSQLQTQAAEQFK.A
R4/RRR4-15/2	1520.691	1520.840	-97.954	0.515	2094.842	0.454	20	0.292	K.NILFVISKPDVFK.S
R4/RRR4-15/2	1528.341	1528.645	-199.044	0.532	1605.989	0.576	20	0.257	K.SPNSDTYVIFGEAK.I
R4/RRR4-15/2	1520.237	1520.840	-1057.752	0.519	1834.463	0.397	20	0.239	K.NILFVISKPDVFK.S
R4/RRR4-15/2	1527.955	1528.645	-1109.382	0.526	1471.458	0.541	20	0.232	K.SPNSDTYVIFGEAK.I
R4/RRR4-15/2	1528.272	1528.645	-244.959	0.526	1430.371	0.539	20	0.227	K.SPNSDTYVIFGEAK.I
R4/RRR4-15/2	1519.741	1520.840	-1385.187	0.401	1535.891	0.304	19	0.188	K.NILFVISKPDVFK.S
R4/RRR4-16/2	1519.572	1520.840	-1496.693	0.458	1002.203	0.436	16	0.170	K.NILFVISKPDVFK.S
R4/RRR4-15/2	1043.905	1044.184	-267.721	0.414	810.213	0.482	15	0.169	K.APDLSNVISK.A
R4/RRR4-15/2	1044.088	1044.184	-92.243	0.457	830.357	0.460	15	0.169	K.APDLSNVISK.A
R4/RRR4-15/2	1043.542	1044.184	-1578.131	0.361	730.260	0.446	14	0.159	K.APDLSNVISK.A
R4/RRR4-16/2	1521.230	1520.840	257.262	0.450	561.433	0.366	18	0.148	-.NILFVISKPDVFK.-
R4/RRR4-17/2	1522.150	1520.840	204.260	0.344	492.521	0.393	14	0.146	K.NILFVISKPDVFK.S
R4/RRR4-17/2	1521.966	1520.840	82.730	0.258	366.493	0.378	15	0.144	K.NILFVISKPDVFK.S
R4/RRR4-17/2	1521.628	1520.840	-139.493	0.335	287.893	0.303	13	0.143	K.NILFVISKPDVFK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1519.886	1520.840	-1289.515	0.265	764.844	0.228	17	0.139	K.NILFVISKPDVFK.S
R4/RRR4-3/2	1200.243	1200.453	-175.213	0.485	1972.834	0.361	19	0.251	K.LLDSIVALLSR.T
R4/RRR4-3/2	1542.237	1542.718	-312.682	0.522	1715.402	0.465	22	0.244	R.FGPIIEQNVDPANK.G
R4/RRR4-3/2	1542.240	1542.718	-310.458	0.525	1619.958	0.497	22	0.240	R.FGPIIEQNVDPANK.G
R4/RRR4-3/2	1543.082	1542.718	236.718	0.569	1645.256	0.455	22	0.232	R.FGPIIEQNVDPANK.G
R4/RRR4-3/2	1200.368	1200.453	-71.462	0.559	1648.194	0.422	18	0.226	K.LLDSIVALLSR.T
R4/RRR4-3/2	1200.101	1200.453	-294.497	0.482	1702.937	0.353	19	0.216	K.LLDSIVALLSR.T
R4/RRR4-3/2	1875.658	1876.193	-820.632	0.578	1232.044	0.591	22	0.215	R.VLGIANIAGQIVHEITAR.L
R4/RRR4-3/2	1776.671	1777.015	-194.309	0.426	1410.109	0.369	20	0.184	K.QFLVTSLATLSAQSPGR.F
R4/RRR4-3/2	1102.992	1103.210	-197.877	0.355	1074.919	0.476	16	0.180	R.TSGYSVSFVR.L
R4/RRR4-3/2	1103.145	1103.210	-58.892	0.254	256.991	0.335	10	0.098	-.TSGYSVSFVR.-
R4/RRR4-5/2	1761.719	1761.997	-158.360	0.506	1311.588	0.487	22	0.201	K.LSFSQDSPPISIISAAK.V
R4/RRR4-5/2	1761.311	1761.997	-959.828	0.448	1129.222	0.357	21	0.163	K.LSFSQDSPPISIISAAK.V
R4/RRR4-5/2	1761.414	1761.997	-901.175	0.451	1157.834	0.357	19	0.162	K.LSFSQDSPPISIISAAK.V
R4/RRR4-5/2	1454.237	1453.621	-264.922	0.392	850.828	0.382	17	0.153	R.IWLDYADASAISK.G
R4/RRR4-5/2	1017.024	1017.206	-179.751	0.387	937.088	0.266	13	0.147	R.FPTVQGIVR.R
R4/RRR4-5/2	1017.112	1017.206	-92.583	0.425	972.947	0.216	13	0.142	-.FPTVQGIVR.-
R4/RRR4-5/2	1016.386	1017.206	-1796.473	0.345	814.153	0.232	13	0.141	R.FPTVQGIVR.R
R4/RRR4-5/2	944.714	944.067	-375.211	0.424	897.063	0.204	12	0.137	-.GEVIQLER.-
R4/RRR4-5/2	943.910	944.067	-167.602	0.361	832.715	0.210	12	0.133	-.GEVIQLER.-
R4/RRR4-5/3	1840.134	1839.981	83.123	0.438	984.294	0.474	32	0.126	K.VNDSKDPSAPEVDLPGAK.F
R4/RRR4-5/3	1839.106	1839.981	-1023.023	0.411	977.586	0.431	31	0.115	K.VNDSKDPSAPEVDLPGAK.F
R4/RRR4-23/2	1319.989	1320.493	-1142.676	0.512	1734.691	0.488	17	0.252	K.SEIEYYAM*LGK.V
R4/RRR4-23/2	1319.865	1320.493	-1237.311	0.391	1194.188	0.432	16	0.182	K.SEIEYYAM*LGK.V
R4/RRR4-23/2	1522.246	1522.854	-1059.412	0.463	969.923	0.434	16	0.166	K.LIILANNCPPLRK.S
R4/RRR4-24/2	1396.056	1394.681	269.629	0.335	122.751	0.509	11	0.140	-.LIILANNCPPLR.-
R4/RRR4-24/2	1395.886	1394.681	147.303	0.218	151.793	0.433	13	0.138	-.LIILANNCPPLR.-
R4/RRR4-23/3	1394.725	1394.681	31.891	0.363	1079.850	0.350	26	0.103	K.LIILANNCPPLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1672.333	1672.857	-913.963	0.605	2023.106	0.587	22	0.324	R.AKDVALVYNECYAR.L
R4/RRR4-16/2	1672.307	1672.857	-929.865	0.588	1862.748	0.583	21	0.296	R.AKDVALVYNECYAR.L
R4/RRR4-16/2	1672.587	1672.857	-161.674	0.627	1785.934	0.578	21	0.283	R.AKDVALVYNECYAR.L
R4/RRR4-16/2	1445.939	1446.534	-1106.091	0.491	1832.259	0.486	18	0.264	R.AACYDCGTSVWR.D
R4/RRR4-16/3	1671.749	1672.857	-1264.663	0.534	1866.077	0.478	28	0.250	-.AKDVALVYNECYAR.-
R4/RRR4-16/2	1447.024	1446.534	339.837	0.522	1647.457	0.519	18	0.249	R.AACYDCGTSVWR.D
R4/RRR4-16/2	1446.003	1446.534	-1062.098	0.445	1723.065	0.430	18	0.235	R.AACYDCGTSVWR.D
R4/RRR4-16/3	1672.503	1672.857	-212.312	0.582	1748.020	0.474	28	0.222	R.AKDVALVYNECYAR.L
R4/RRR4-16/2	1473.273	1473.606	-226.845	0.502	1325.664	0.503	19	0.211	K.DVALVYNECYAR.L
R4/RRR4-15/2	1446.280	1446.534	-176.052	0.415	1518.434	0.398	17	0.204	R.AACYDCGTSVWR.D
R4/RRR4-16/2	1473.126	1473.606	-326.936	0.444	1334.700	0.466	19	0.203	K.DVALVYNECYAR.L
R4/RRR4-16/3	1673.623	1672.857	-140.221	0.569	1729.372	0.417	28	0.195	R.AKDVALVYNECYAR.L
R4/RRR4-16/2	1473.070	1473.606	-1045.407	0.428	1315.430	0.395	19	0.188	K.DVALVYNECYAR.L
R4/RRR4-16/2	1267.085	1267.367	-223.464	0.519	1299.894	0.387	18	0.186	R.LSDKDDFLADK.V
R4/RRR4-16/2	1267.036	1267.367	-261.739	0.498	1309.407	0.382	18	0.186	R.LSDKDDFLADK.V
R4/RRR4-15/2	1267.119	1267.367	-196.016	0.457	1382.109	0.346	18	0.185	R.LSDKDDFLADK.V
R4/RRR4-15/3	1672.225	1672.857	-978.864	0.500	1435.834	0.454	27	0.168	R.AKDVALVYNECYAR.L
R4/RRR4-16/2	1267.176	1267.367	-151.368	0.472	1044.884	0.338	17	0.161	R.LSDKDDFLADK.V
R4/RRR4-18/2	1475.005	1473.606	271.218	0.341	171.939	0.503	15	0.156	K.DVALVYNECYAR.L
R4/RRR4-15/2	1475.002	1473.606	269.475	0.483	696.626	0.391	15	0.152	K.DVALVYNECYAR.L
R4/RRR4-17/2	1473.039	1473.606	-1066.625	0.322	1112.948	0.213	17	0.147	K.DVALVYNECYAR.L
R4/RRR4-18/2	1474.709	1473.606	70.437	0.258	144.456	0.447	14	0.146	-.DVALVYNECYAR.-
R4/RRR4-18/2	1474.537	1473.606	-46.633	0.296	157.611	0.395	12	0.142	-.DVALVYNECYAR.-
R4/RRR4-14/2	1472.846	1473.606	-1198.525	0.257	728.563	0.238	15	0.139	K.DVALVYNECYAR.L
R4/RRR4-15/3	1672.464	1672.857	-235.817	0.462	1151.689	0.400	25	0.123	R.AKDVALVYNECYAR.L
R4/RRR4-17/3	1672.645	1672.857	-127.200	0.385	967.228	0.348	22	0.101	R.AKDVALVYNECYAR.L
R4/RRR4-3/2	1162.472	1163.351	-1621.637	0.476	1349.287	0.451	17	0.203	K.VNLVQSLFSR.V
R4/RRR4-3/2	1011.835	1012.183	-345.057	0.434	1164.369	0.463	15	0.189	R.LSDFLAFAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1012.003	1012.183	-178.284	0.530	1006.524	0.479	15	0.184	R.LSDFLAFAK.G
R4/RRR4-3/2	1163.108	1163.351	-210.282	0.447	1037.550	0.432	15	0.175	K.VNLVQSLFSR.V
R4/RRR4-3/2	1212.107	1212.421	-259.358	0.454	866.435	0.479	18	0.173	K.TLSGNPPTIIAK.G
R4/RRR4-3/2	1211.880	1212.421	-1275.164	0.426	728.971	0.508	17	0.168	K.TLSGNPPTIIAK.G
R4/RRR4-3/2	1211.861	1212.421	-1291.148	0.376	512.740	0.504	14	0.156	K.TLSGNPPTIIAK.G
R4/RRR4-3/2	1162.660	1163.351	-1459.307	0.325	831.563	0.363	14	0.152	K.VNLVQSLFSR.V
R4/RRR4-3/3	1698.671	1698.861	-111.917	0.432	903.568	0.505	28	0.128	K.GAGVDGIITDFPATAHR.Y
R4/RRR4-3/3	1699.717	1698.861	-85.195	0.472	923.679	0.486	29	0.126	K.GAGVDGIITDFPATAHR.Y
R4/RRR4-3/3	1699.215	1698.861	209.123	0.362	758.154	0.379	25	0.095	K.GAGVDGIITDFPATAHR.Y
R4/RRR4-2/2	1517.051	1517.584	-1013.002	0.531	2806.688	0.576	27	0.482	K.NVANAGGDSVGDTLAR.Q
R4/RRR4-3/2	1513.547	1512.776	-152.211	0.560	1704.268	0.586	22	0.274	R.LPLITISDSGNLLR.D
R4/RRR4-2/2	1512.297	1512.776	-318.144	0.543	1630.552	0.600	22	0.268	R.LPLITISDSGNLLR.D
R4/RRR4-3/2	1513.602	1512.776	-115.723	0.557	1524.532	0.581	21	0.249	R.LPLITISDSGNLLR.D
R4/RRR4-1/2	1512.699	1512.776	-51.527	0.477	1515.823	0.543	21	0.237	R.LPLITISDSGNLLR.D
R4/RRR4-2/2	1512.115	1512.776	-1102.056	0.507	1396.781	0.577	20	0.232	R.LPLITISDSGNLLR.D
R4/RRR4-3/2	1512.301	1512.776	-315.066	0.543	1391.651	0.561	20	0.228	R.LPLITISDSGNLLR.D
R4/RRR4-2/2	1513.263	1512.776	322.858	0.567	1310.644	0.587	20	0.226	R.LPLITISDSGNLLR.D
R4/RRR4-1/2	1512.251	1512.776	-1011.521	0.522	1365.922	0.529	20	0.218	R.LPLITISDSGNLLR.D
R4/RRR4-3/2	1641.599	1640.905	-186.878	0.473	1173.772	0.498	18	0.191	R.FSTALSILKDEFLR.S
R4/RRR4-2/2	1628.498	1627.909	-253.340	0.361	724.127	0.423	18	0.151	-.ILTLQGGEAVYPLPR.-
R4/RRR4-2/2	1627.558	1627.909	-216.550	0.317	490.194	0.320	15	0.136	K.ILTLQGGEAVYPLPR.I
R4/RRR4-2/3	1902.653	1903.001	-183.123	0.385	814.065	0.425	28	0.105	K.AIAAASGDNARPASSESAQK.N
R4/RRR4-3/3	1902.998	1903.001	-1.558	0.403	619.032	0.439	27	0.099	K.AIAAASGDNARPASSESAQK.N
R4/RRR4-1/3	1903.986	1903.001	-7.667	0.448	740.672	0.398	26	0.097	K.AIAAASGDNARPASSESAQK.N
R4/RRR4-18/2	1464.114	1464.562	-306.955	0.548	1405.094	0.422	21	0.201	K.FDSDGNLIDAQIR.E
R4/RRR4-18/2	1630.550	1630.999	-276.148	0.484	1095.864	0.535	21	0.196	R.IKQVLLSLQAFTLR.L
R4/RRR4-19/2	1464.163	1464.562	-273.496	0.548	1241.580	0.456	20	0.193	K.FDSDGNLIDAQIR.E
R4/RRR4-18/2	1465.178	1464.562	-263.278	0.626	1335.875	0.426	21	0.193	K.FDSDGNLIDAQIR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1631.738	1630.999	-160.319	0.464	1210.593	0.454	19	0.188	R.IKQVLLSLQAFTLR.L
R4/RRR4-19/2	1464.043	1464.562	-1041.066	0.515	1286.858	0.379	20	0.182	K.FDSDGNLIDAQIR.E
R4/RRR4-18/2	1631.393	1630.999	242.292	0.470	939.206	0.506	19	0.178	R.IKQVLLSLQAFTLR.L
R4/RRR4-19/2	1464.339	1464.562	-152.894	0.541	1160.523	0.400	20	0.177	K.FDSDGNLIDAQIR.E
R4/RRR4-18/2	1390.368	1389.668	-216.595	0.523	908.621	0.473	19	0.176	K.QVLLSLQAFTLR.L
R4/RRR4-18/2	1390.129	1389.668	332.960	0.491	809.373	0.481	18	0.171	K.QVLLSLQAFTLR.L
R4/RRR4-19/2	932.365	933.003	-1762.766	0.398	918.407	0.380	13	0.163	K.NALDWASR.G
R4/RRR4-18/2	933.066	933.003	67.892	0.378	818.337	0.351	13	0.155	K.NALDWASR.G
R4/RRR4-18/2	932.369	933.003	-1758.293	0.359	870.055	0.339	13	0.155	K.NALDWASR.G
R4/RRR4-18/2	932.500	933.003	-1616.373	0.387	920.628	0.312	13	0.154	K.NALDWASR.G
R4/RRR4-19/2	932.485	933.003	-1632.812	0.358	889.498	0.327	13	0.154	K.NALDWASR.G
R4/RRR4-18/2	1463.522	1464.562	-1398.157	0.424	1017.537	0.297	19	0.154	K.FDSDGNLIDAQIR.E
R4/RRR4-19/2	932.266	933.003	-1868.937	0.342	890.155	0.302	13	0.151	K.NALDWASR.G
R4/RRR4-18/2	1388.527	1389.668	-1546.330	0.349	330.648	0.291	14	0.140	-.QVLLSLQAFTLR.-
R4/RRR4-15/2	1817.460	1818.019	-860.383	0.577	2732.902	0.681	27	0.502	K.ALAVGADVSLDTATGNLTK.Y
R4/RRR4-15/2	1817.380	1818.019	-904.615	0.559	2578.912	0.682	27	0.466	K.ALAVGADVSLDTATGNLTK.Y
R4/RRR4-15/2	1817.326	1818.019	-934.151	0.537	2481.681	0.657	26	0.433	K.ALAVGADVSLDTATGNLTK.Y
R4/RRR4-15/2	1590.495	1590.845	-220.903	0.623	1672.046	0.539	22	0.257	K.KADLIFGEIQSQIK.N
R4/RRR4-15/2	1591.178	1590.845	209.865	0.636	1649.337	0.504	22	0.244	K.KADLIFGEIQSQIK.N
R4/RRR4-15/2	1590.311	1590.845	-968.030	0.589	1632.388	0.498	22	0.242	K.KADLIFGEIQSQIK.N
R4/RRR4-15/2	1461.698	1462.673	-1354.669	0.415	1785.780	0.373	19	0.228	K.ADLIFGEIQSQIK.N
R4/RRR4-15/2	1462.396	1462.673	-189.433	0.529	1637.183	0.445	19	0.228	K.ADLIFGEIQSQIK.N
R4/RRR4-15/2	1463.572	1462.673	-68.816	0.553	1526.702	0.481	19	0.224	K.ADLIFGEIQSQIK.N
R4/RRR4-15/2	1461.780	1462.673	-1298.895	0.403	1617.106	0.412	18	0.217	K.ADLIFGEIQSQIK.N
R4/RRR4-15/2	1462.403	1462.673	-184.660	0.475	1464.148	0.443	19	0.209	K.ADLIFGEIQSQIK.N
R4/RRR4-19/2	1819.059	1818.019	22.103	0.476	796.850	0.568	20	0.174	K.ALAVGADVSLDTATGNLTK.Y
R4/RRR4-15/2	1435.777	1436.643	-1303.828	0.477	925.632	0.415	15	0.162	K.ASALLQHEWRPK.S
R4/RRR4-15/2	1589.929	1590.845	-1209.065	0.377	325.741	0.373	13	0.140	-.KADLIFGEIQSQIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1435.986	1436.643	-1157.924	0.438	613.449	0.255	13	0.132	-.ASALLQHEWRPK.-
R4/RRR4-24/3	1721.532	1721.810	-161.744	0.577	2175.183	0.553	30	0.348	K.HGYIGEFEFVDDHR.S
R4/RRR4-24/3	1722.587	1721.810	-129.696	0.631	2265.834	0.505	30	0.342	K.HGYIGEFEFVDDHR.S
R4/RRR4-24/3	1722.495	1721.810	-183.440	0.553	2202.932	0.482	29	0.318	K.HGYIGEFEFVDDHR.S
R4/RRR4-24/3	1721.673	1721.810	-79.593	0.613	1936.080	0.509	28	0.272	K.HGYIGEFEFVDDHR.S
R4/RRR4-23/3	1722.574	1721.810	-137.480	0.525	1871.928	0.517	28	0.264	K.HGYIGEFEFVDDHR.S
R4/RRR4-23/3	1722.122	1721.810	181.600	0.537	1821.317	0.526	27	0.259	K.HGYIGEFEFVDDHR.S
R4/RRR4-24/3	1638.110	1637.818	179.029	0.518	1747.852	0.495	31	0.228	R.FDVGVKEIESWTAR.L
R4/RRR4-24/3	1721.020	1721.810	-1042.955	0.559	1572.606	0.505	27	0.205	K.HGYIGEFEFVDDHR.S
R4/RRR4-24/2	1637.412	1637.818	-248.371	0.568	1191.770	0.506	23	0.201	R.FDVGVKEIESWTAR.L
R4/RRR4-24/3	1637.369	1637.818	-274.707	0.536	1615.449	0.464	30	0.194	R.FDVGVKEIESWTAR.L
R4/RRR4-24/2	1637.290	1637.818	-935.693	0.516	834.833	0.527	20	0.178	R.FDVGVKEIESWTAR.L
R4/RRR4-23/2	1637.917	1637.818	60.727	0.502	821.322	0.483	19	0.170	R.FDVGVKEIESWTAR.L
R4/RRR4-24/2	1636.808	1637.818	-1231.511	0.465	765.257	0.483	20	0.168	R.FDVGVKEIESWTAR.L
R4/RRR4-23/3	1721.298	1721.810	-880.929	0.454	1463.075	0.428	25	0.164	K.HGYIGEFEFVDDHR.S
R4/RRR4-24/2	788.454	788.909	-578.771	0.362	654.045	0.430	11	0.158	K.CGVISPR.F
R4/RRR4-23/2	959.020	959.122	-107.128	0.356	882.088	0.350	15	0.157	R.VSVLNDALK.T
R4/RRR4-23/2	958.935	959.122	-195.619	0.407	764.347	0.370	14	0.157	R.VSVLNDALK.T
R4/RRR4-24/2	958.959	959.122	-170.207	0.395	866.867	0.327	15	0.155	R.VSVLNDALK.T
R4/RRR4-24/2	788.402	788.909	-1917.471	0.364	564.404	0.402	10	0.153	K.CGVISPR.F
R4/RRR4-23/2	958.960	959.122	-168.930	0.405	951.183	0.292	15	0.152	-.VSVLNDALK.-
R4/RRR4-24/2	958.948	959.122	-181.572	0.412	915.488	0.284	15	0.152	R.VSVLNDALK.T
R4/RRR4-24/3	1637.271	1637.818	-947.565	0.415	1439.942	0.409	30	0.151	R.FDVGVKEIESWTAR.L
R4/RRR4-24/2	958.950	959.122	-179.912	0.385	864.979	0.284	15	0.151	R.VSVLNDALK.T
R4/RRR4-24/2	788.387	788.909	-1935.987	0.323	571.803	0.383	10	0.148	-.CGVISPR.-
R4/RRR4-24/2	959.012	959.122	-114.917	0.309	634.145	0.302	13	0.146	R.VSVLNDALK.T
R4/RRR4-24/2	959.143	959.122	21.942	0.302	664.645	0.255	13	0.143	R.VSVLNDALK.T
R4/RRR4-24/2	959.792	959.122	-344.824	0.319	711.367	0.229	14	0.143	R.VSVLNDALK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/2	958.907	959.122	-224.481	0.281	669.353	0.243	13	0.142	R.VSVLNDALK.T
R4/RRR4-24/2	958.293	959.122	-1914.448	0.254	551.343	0.218	12	0.140	R.VSVLNDALK.T
R4/RRR4-24/2	788.907	788.909	-2.345	0.312	568.145	0.245	10	0.140	-.CGVISPR.-
R4/RRR4-24/2	958.285	959.122	-1922.641	0.178	513.230	0.232	11	0.135	-.VSVLNDALK.-
R4/RRR4-23/3	1637.991	1637.818	106.387	0.447	1146.408	0.440	26	0.133	R.FDVGVKEIESWTAR.L
R4/RRR4-23/3	1637.901	1637.818	50.890	0.365	865.764	0.388	25	0.103	R.FDVGVKEIESWTAR.L
R4/RRR4-24/3	1638.001	1637.818	111.993	0.383	906.098	0.331	24	0.097	R.FDVGVKEIESWTAR.L
R4/RRR4-24/3	1639.400	1637.818	-255.285	0.347	621.506	0.355	24	0.095	R.FDVGVKEIESWTAR.L
R4/RRR4-24/3	1638.700	1637.818	-71.781	0.375	680.763	0.341	23	0.094	R.FDVGVKEIESWTAR.L
R4/RRR4-24/3	1721.854	1721.810	25.476	0.325	635.630	0.268	21	0.090	K.HGYIGEFEFVDDHR.S
R4/RRR4-24/3	1722.810	1721.810	0.162	0.369	859.495	0.252	23	0.087	K.HGYIGEFEFVDDHR.S
R4/RRR4-16/2	1616.464	1616.797	-206.523	0.539	2207.409	0.564	23	0.348	K.FPTLVTHQESLESK.V
R4/RRR4-15/2	1616.542	1616.797	-158.191	0.547	2229.921	0.549	23	0.347	K.FPTLVTHQESLESK.V
R4/RRR4-15/2	1616.415	1616.797	-236.752	0.522	2288.581	0.515	23	0.347	K.FPTLVTHQESLESK.V
R4/RRR4-15/2	1616.319	1616.797	-296.684	0.548	1966.360	0.505	22	0.289	K.FPTLVTHQESLESK.V
R4/RRR4-16/2	1616.211	1616.797	-984.107	0.519	1793.118	0.500	21	0.262	K.FPTLVTHQESLESK.V
R4/RRR4-16/2	1247.932	1248.325	-316.175	0.540	1099.031	0.419	17	0.177	R.EAISQITNESR.E
R4/RRR4-15/3	1491.668	1491.759	-61.332	0.525	1671.650	0.387	27	0.175	K.KYHAFLASEAIIK.Q
R4/RRR4-16/3	1491.463	1491.759	-199.008	0.491	1614.075	0.399	28	0.170	K.KYHAFLASEAIIK.Q
R4/RRR4-16/3	1491.236	1491.759	-1024.225	0.531	1659.451	0.380	28	0.170	K.KYHAFLASEAIIK.Q
R4/RRR4-16/3	1616.442	1616.797	-219.903	0.435	1436.587	0.458	27	0.169	K.FPTLVTHQESLESK.V
R4/RRR4-15/2	1247.636	1248.325	-1358.442	0.463	949.623	0.411	17	0.168	R.EAISQITNESR.E
R4/RRR4-15/2	1247.923	1248.325	-323.732	0.456	987.855	0.388	17	0.166	R.EAISQITNESR.E
R4/RRR4-15/2	1247.657	1248.325	-1341.541	0.439	1026.302	0.354	17	0.163	R.EAISQITNESR.E
R4/RRR4-15/3	1872.998	1873.099	-54.434	0.526	1029.910	0.577	29	0.161	K.AGKFPTLVTHQESLESK.V
R4/RRR4-15/3	1873.071	1873.099	-15.212	0.486	1023.542	0.564	30	0.156	K.AGKFPTLVTHQESLESK.V
R4/RRR4-16/3	1873.082	1873.099	-9.427	0.483	852.277	0.566	28	0.141	K.AGKFPTLVTHQESLESK.V
R4/RRR4-15/3	1872.325	1873.099	-950.727	0.488	864.372	0.557	29	0.140	K.AGKFPTLVTHQESLESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/3	1872.802	1873.099	-159.271	0.504	870.113	0.549	28	0.139	K.AGKFPTLVTHQESLESK.V
R4/RRR4-15/3	1616.648	1616.797	-92.413	0.435	1277.810	0.394	27	0.132	K.FPTLVTHQESLESK.V
R4/RRR4-16/3	1872.495	1873.099	-859.623	0.430	827.244	0.494	28	0.123	K.AGKFPTLVTHQESLESK.V
R4/RRR4-16/3	1615.746	1616.797	-1272.693	0.414	994.624	0.442	24	0.121	K.FPTLVTHQESLESK.V
R4/RRR4-16/3	1491.826	1491.759	45.162	0.512	1225.220	0.368	25	0.120	K.KYHAFLASEAIIK.Q
R4/RRR4-16/3	1616.151	1616.797	-1021.008	0.366	1154.405	0.381	26	0.118	K.FPTLVTHQESLESK.V
R4/RRR4-12/3	1871.647	1873.099	-1314.329	0.399	647.430	0.480	23	0.112	K.AGKFPTLVTHQESLESK.V
R4/RRR4-15/3	1491.739	1491.759	-13.068	0.469	1106.898	0.337	23	0.106	K.KYHAFLASEAIIK.Q
R4/RRR4-15/3	1491.562	1491.759	-132.136	0.470	1205.209	0.308	25	0.103	-.KYHAFLASEAIIK.-
R4/RRR4-15/3	1616.903	1616.797	65.711	0.418	762.812	0.399	22	0.101	K.FPTLVTHQESLESK.V
R4/RRR4-15/3	1616.407	1616.797	-241.609	0.325	945.406	0.358	25	0.100	K.FPTLVTHQESLESK.V
R4/RRR4-12/3	1871.856	1873.099	-1202.333	0.409	607.569	0.350	23	0.094	K.AGKFPTLVTHQESLESK.V
R4/RRR4-20/1	998.358	999.102	-1752.067	0.234	628.872	0.329	11	0.576	R.LNAYIQGGY.-
R4/RRR4-21/1	998.330	999.102	-1779.464	0.249	598.916	0.286	11	0.572	R.LNAYIQGGY.-
R4/RRR4-21/1	998.346	999.102	-1763.861	0.229	470.990	0.280	10	0.561	R.LNAYIQGGY.-
R4/RRR4-21/1	998.306	999.102	-1804.343	0.267	396.080	0.292	9	0.556	R.LNAYIQGGY.-
R4/RRR4-21/2	1324.104	1324.593	-370.413	0.448	1515.454	0.337	17	0.193	R.VLQAM*QLM*TEK.R
R4/RRR4-21/2	1324.067	1324.593	-1156.049	0.423	1482.388	0.323	17	0.187	R.VLQAM*QLM*TEK.R
R4/RRR4-21/2	1324.239	1324.593	-268.025	0.477	1386.515	0.338	17	0.182	R.VLQAM*QLM*TEK.R
R4/RRR4-20/2	945.808	946.083	-291.928	0.443	936.891	0.417	15	0.170	K.SIAGIVTER.D
R4/RRR4-20/2	945.921	946.083	-172.035	0.450	931.145	0.378	15	0.164	K.SIAGIVTER.D
R4/RRR4-21/2	945.858	946.083	-239.099	0.475	956.908	0.365	15	0.163	K.SIAGIVTER.D
R4/RRR4-20/2	945.910	946.083	-183.557	0.438	1000.080	0.343	15	0.162	K.SIAGIVTER.D
R4/RRR4-21/2	945.489	946.083	-1691.614	0.410	997.627	0.327	15	0.159	K.SIAGIVTER.D
R4/RRR4-21/2	1480.218	1480.780	-1058.133	0.409	348.627	0.443	17	0.155	R.VLQAM*QLM*TEKR.I
R4/RRR4-21/2	1480.208	1480.780	-1064.840	0.324	314.675	0.441	17	0.151	R.VLQAM*QLM*TEKR.I
R4/RRR4-21/2	1480.240	1480.780	-1043.312	0.323	297.676	0.368	17	0.148	R.VLQAM*QLM*TEKR.I
R4/RRR4-21/2	998.957	999.102	-145.191	0.333	765.723	0.631	13	0.139	R.LNAYIQGGY.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1000.089	999.102	-12.317	0.392	883.434	0.553	14	0.128	R.LNAYIQGGY.-
R4/RRR4-21/2	998.441	999.102	-1668.057	0.250	842.112	0.402	13	0.096	R.LNAYIQGGY.-
R4/RRR4-4/2	1823.367	1824.025	-912.187	0.549	1249.179	0.538	22	0.208	R.LLSSGNVYTQEEILTR.I
R4/RRR4-4/2	1823.447	1824.025	-867.965	0.539	1132.916	0.559	22	0.203	R.LLSSGNVYTQEEILTR.I
R4/RRR4-4/2	1343.989	1344.495	-1123.766	0.457	917.322	0.478	16	0.172	K.VFANAETTISYK.I
R4/RRR4-4/2	1279.024	1279.491	-365.822	0.490	667.320	0.437	15	0.159	K.LSEVNPM*LGFR.G
R4/RRR4-4/2	1287.136	1287.361	-175.465	0.359	740.028	0.444	18	0.157	K.ANADTPADALTAR.N
R4/RRR4-4/2	1279.037	1279.491	-355.959	0.427	810.776	0.374	16	0.156	K.LSEVNPM*LGFR.G
R4/RRR4-4/2	1286.984	1287.361	-293.928	0.372	721.176	0.422	18	0.155	K.ANADTPADALTAR.N
R4/RRR4-4/2	1278.624	1279.491	-1463.976	0.316	530.320	0.307	13	0.140	K.LSEVNPM*LGFR.G
R4/RRR4-4/2	1650.237	1650.813	-958.029	0.283	814.881	0.156	14	0.126	K.GILQNDPFEVFDQK.G
R4/RRR4-15/2	1147.084	1147.261	-154.727	0.461	1491.625	0.510	18	0.229	K.EAISQVVGESK.E
R4/RRR4-15/2	1147.077	1147.261	-160.492	0.477	1228.803	0.506	17	0.202	K.EAISQVVGESK.E
R4/RRR4-16/2	1147.096	1147.261	-144.479	0.494	1194.233	0.470	16	0.192	K.EAISQVVGESK.E
R4/RRR4-16/2	1146.865	1147.261	-346.173	0.359	1162.389	0.405	16	0.176	K.EAISQVVGESK.E
R4/RRR4-16/2	1146.445	1147.261	-1588.666	0.278	817.466	0.392	15	0.153	K.EAISQVVGESK.E
R4/RRR4-17/2	1610.469	1610.752	-176.273	0.531	2562.236	0.543	22	0.412	R.FALENQAVNEATFR.C
R4/RRR4-17/2	1609.575	1610.752	-1356.788	0.357	2038.027	0.488	21	0.291	R.FALENQAVNEATFR.C
R4/RRR4-17/2	1210.572	1211.393	-1508.961	0.310	551.954	0.505	17	0.156	R.VPIVPSDGAISR.T
R4/RRR4-17/2	1210.678	1211.393	-1420.642	0.305	620.753	0.438	16	0.151	R.VPIVPSDGAISR.T
R4/RRR4-17/2	1211.081	1211.393	-258.566	0.269	625.992	0.440	17	0.150	R.VPIVPSDGAISR.T
R4/RRR4-17/3	1502.564	1502.695	-87.492	0.367	898.992	0.379	23	0.098	R.TRETTLPVNELTK.S
R4/RRR4-17/3	1229.042	1229.324	-229.844	0.415	1029.184	0.208	21	0.080	K.FHGVAENPTEK.I
R4/RRR4-17/3	1229.295	1229.324	-23.029	0.374	1262.772	0.149	23	0.079	K.FHGVAENPTEK.I
R4/RRR4-3/2	1565.014	1565.711	-1087.806	0.496	1633.718	0.443	19	0.229	K.IENINDQYWTLR.A
R4/RRR4-3/2	1217.549	1218.296	-1439.073	0.349	1595.611	0.252	18	0.184	R.EGETAAEILER.I
R4/RRR4-3/2	1217.930	1218.296	-301.647	0.335	1485.329	0.250	16	0.174	R.EGETAAEILER.I
R4/RRR4-3/3	1736.935	1736.908	15.528	0.497	1302.155	0.510	30	0.170	R.YPDVPSFLEYVHNR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1174.129	1175.231	-1795.636	0.411	936.448	0.391	16	0.161	K.SPVSDGETQVR.Y
R4/RRR4-3/2	1217.597	1218.296	-1399.296	0.235	1262.445	0.193	16	0.150	R.EGETAAEILER.I
R4/RRR4-3/2	1639.604	1640.767	-1322.978	0.273	1151.807	0.246	18	0.147	R.SSQLEDGDIICFQK.S
R4/RRR4-2/3	1736.197	1736.908	-988.141	0.321	367.366	0.388	16	0.063	-.YPDVPSFLEYVHNR.-
R4/RRR4-22/2	1004.625	1005.192	-1564.922	0.371	1395.120	0.358	16	0.187	-.FALLADNLK.-
R4/RRR4-22/2	1005.094	1005.192	-98.624	0.471	1352.917	0.353	16	0.183	-.FALLADNLK.-
R4/RRR4-21/2	1005.040	1005.192	-151.743	0.465	1305.895	0.341	16	0.179	R.FALLADNLK.V
R4/RRR4-22/2	1185.543	1186.339	-1519.233	0.452	964.050	0.468	18	0.178	K.FLADGLGTYTK.A
R4/RRR4-22/2	1187.108	1186.339	-195.201	0.523	958.901	0.459	18	0.178	K.FLADGLGTYTK.A
R4/RRR4-22/2	1004.525	1005.192	-1664.902	0.411	1304.496	0.278	16	0.168	R.FALLADNLK.V
R4/RRR4-22/2	1186.226	1186.339	-95.640	0.439	918.117	0.407	18	0.167	K.FLADGLGTYTK.A
R4/RRR4-21/2	1186.215	1186.339	-104.311	0.411	1013.887	0.363	18	0.164	K.FLADGLGTYTK.A
R4/RRR4-21/2	1187.080	1186.339	-218.619	0.429	908.949	0.400	17	0.164	K.FLADGLGTYTK.A
R4/RRR4-21/2	1186.188	1186.339	-127.744	0.389	966.069	0.371	18	0.163	K.FLADGLGTYTK.A
R4/RRR4-22/2	1160.715	1161.379	-1437.808	0.416	1407.342	0.184	16	0.158	R.RFALLADNLK.V
R4/RRR4-22/2	1160.625	1161.379	-1515.138	0.374	1403.694	0.178	16	0.157	R.RFALLADNLK.V
R4/RRR4-21/2	1188.134	1188.353	-184.624	0.429	716.452	0.387	14	0.150	K.ALGLELDLSEK.G
R4/RRR4-21/2	1161.434	1161.379	47.585	0.346	1361.811	0.117	16	0.147	R.RFALLADNLK.V
R4/RRR4-21/2	1161.098	1161.379	-242.175	0.413	1013.662	0.149	14	0.135	-.RFALLADNLK.-
R4/RRR4-21/2	1161.979	1161.379	-345.359	0.351	844.356	0.103	13	0.127	-.RFALLADNLK.-
R4/RRR4-23/3	1892.153	1892.096	30.042	0.499	2553.596	0.454	33	0.407	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1892.347	1892.096	132.856	0.592	2350.693	0.643	24	0.401	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1891.499	1892.096	-847.095	0.556	2368.341	0.603	24	0.390	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1892.623	1892.096	-251.042	0.599	2209.490	0.630	24	0.369	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1468.332	1467.693	-245.952	0.551	1772.372	0.506	20	0.262	R.IFYILWSPDNAK.V
R4/RRR4-23/3	1891.934	1892.096	-86.150	0.410	2171.549	0.350	31	0.258	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1966.223	1965.999	114.227	0.541	1431.730	0.639	24	0.251	R.TTSYEDFTSSLPEGDCR.F
R4/RRR4-23/2	1966.279	1965.999	142.618	0.569	1224.545	0.687	25	0.242	R.TTSYEDFTSSLPEGDCR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1468.049	1467.693	243.897	0.562	1520.615	0.496	19	0.229	R.IFYILWSPDNAK.V
R4/RRR4-23/2	1467.365	1467.693	-223.753	0.457	1446.402	0.468	18	0.213	R.IFYILWSPDNAK.V
R4/RRR4-23/2	1467.330	1467.693	-247.456	0.423	1420.577	0.461	18	0.209	R.IFYILWSPDNAK.V
R4/RRR4-23/2	1467.384	1467.693	-210.567	0.426	1476.702	0.418	18	0.206	R.IFYILWSPDNAK.V
R4/RRR4-23/2	1467.160	1467.693	-1047.449	0.411	1490.214	0.387	18	0.200	R.IFYILWSPDNAK.V
R4/RRR4-24/2	1966.483	1965.999	246.518	0.522	1117.987	0.555	23	0.200	R.TTSYEDFTSSLPEGDCR.F
R4/RRR4-23/2	1468.523	1467.693	-116.107	0.547	1345.047	0.433	18	0.196	R.IFYILWSPDNAK.V
R4/RRR4-23/2	1965.209	1965.999	-913.760	0.514	896.971	0.586	22	0.189	R.TTSYEDFTSSLPEGDCR.F
R4/RRR4-23/2	1892.013	1892.096	-44.109	0.441	410.193	0.549	20	0.163	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1891.557	1892.096	-816.258	0.448	533.011	0.519	19	0.161	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1070.990	1071.190	-186.527	0.383	877.058	0.341	15	0.156	K.MLYASSNER.F
R4/RRR4-23/2	1892.134	1892.096	19.826	0.341	297.908	0.502	19	0.154	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1070.817	1071.190	-348.690	0.349	742.051	0.350	14	0.151	K.MLYASSNER.F
R4/RRR4-23/2	1070.925	1071.190	-247.475	0.457	698.805	0.302	14	0.148	K.MLYASSNER.F
R4/RRR4-24/2	1467.116	1467.693	-1077.774	0.330	912.962	0.278	16	0.147	R.IFYILWSPDNAK.V
R4/RRR4-23/2	1892.629	1892.096	-247.548	0.199	203.511	0.455	19	0.143	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1891.934	1892.096	-85.981	0.199	185.785	0.386	17	0.142	R.FAIYDFDFLTAEDVPK.S
R4/RRR4-23/2	1376.418	1376.528	-80.557	0.483	1594.024	0.452	18	0.226	K.CCDSIVQLPQR.I
R4/RRR4-22/2	1377.134	1376.528	-287.401	0.538	1558.959	0.453	18	0.222	K.CCDSIVQLPQR.I
R4/RRR4-19/2	1376.264	1376.528	-192.303	0.485	1553.326	0.435	18	0.218	K.CCDSIVQLPQR.I
R4/RRR4-20/2	1377.215	1376.528	-227.909	0.480	1457.103	0.471	17	0.215	K.CCDSIVQLPQR.I
R4/RRR4-18/2	1376.088	1376.528	-320.985	0.500	1521.858	0.436	18	0.215	K.CCDSIVQLPQR.I
R4/RRR4-23/2	1377.095	1376.528	-315.593	0.514	1484.586	0.446	18	0.213	K.CCDSIVQLPQR.I
R4/RRR4-23/2	1377.093	1376.528	-316.661	0.549	1381.416	0.473	17	0.208	K.CCDSIVQLPQR.I
R4/RRR4-22/2	1376.963	1376.528	316.760	0.531	1371.693	0.461	17	0.205	K.CCDSIVQLPQR.I
R4/RRR4-21/2	1376.206	1376.528	-234.926	0.515	1442.419	0.427	17	0.204	K.CCDSIVQLPQR.I
R4/RRR4-19/2	1376.068	1376.528	-335.136	0.453	1480.425	0.402	17	0.203	K.CCDSIVQLPQR.I
R4/RRR4-22/2	1377.148	1376.528	-276.818	0.501	1377.705	0.447	17	0.203	K.CCDSIVQLPQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1376.122	1376.528	-295.887	0.461	1485.701	0.398	17	0.202	K.CCDSIVQLPQR.I
R4/RRR4-19/2	1375.671	1376.528	-1354.031	0.418	1427.245	0.418	17	0.201	K.CCDSIVQLPQR.I
R4/RRR4-1/2	1375.967	1376.528	-1138.136	0.443	1437.984	0.408	17	0.200	K.CCDSIVQLPQR.I
R4/RRR4-18/2	1376.841	1376.528	227.862	0.489	1540.712	0.358	18	0.199	K.CCDSIVQLPQR.I
R4/RRR4-18/2	1375.956	1376.528	-1145.887	0.482	1401.696	0.413	17	0.198	K.CCDSIVQLPQR.I
R4/RRR4-18/2	1376.597	1376.528	50.020	0.487	1592.998	0.311	18	0.194	K.CCDSIVQLPQR.I
R4/RRR4-18/2	1754.242	1754.855	-922.168	0.517	1094.557	0.505	24	0.193	R.CDDELEPGKCTAACK.S
R4/RRR4-18/2	1376.993	1376.528	338.537	0.482	1371.406	0.394	17	0.191	K.CCDSIVQLPQR.I
R4/RRR4-1/2	1376.161	1376.528	-267.319	0.412	1473.643	0.342	17	0.190	K.CCDSIVQLPQR.I
R4/RRR4-26/2	1375.564	1376.528	-1432.375	0.421	1460.448	0.341	17	0.189	K.CCDSIVQLPQR.I
R4/RRR4-18/2	1377.096	1376.528	-314.882	0.472	1524.814	0.312	18	0.188	K.CCDSIVQLPQR.I
R4/RRR4-21/2	1375.547	1376.528	-1444.498	0.380	1334.911	0.369	17	0.184	K.CCDSIVQLPQR.I
R4/RRR4-2/2	1375.900	1376.528	-1187.224	0.453	1138.478	0.418	16	0.178	K.CCDSIVQLPQR.I
R4/RRR4-26/2	1376.031	1376.528	-362.106	0.468	1132.974	0.388	16	0.173	K.CCDSIVQLPQR.I
R4/RRR4-17/2	1755.093	1754.855	135.712	0.554	776.341	0.497	21	0.171	R.CDDELEPGKCTAACK.S
R4/RRR4-17/2	1376.378	1376.528	-109.559	0.367	1381.366	0.258	17	0.169	K.CCDSIVQLPQR.I
R4/RRR4-26/2	1376.112	1376.528	-303.007	0.455	1236.527	0.320	17	0.169	K.CCDSIVQLPQR.I
R4/RRR4-22/2	1754.150	1754.855	-975.124	0.481	781.828	0.479	21	0.168	R.CDDELEPGKCTAACK.S
R4/RRR4-22/2	1754.245	1754.855	-920.771	0.507	736.466	0.476	21	0.167	R.CDDELEPGKCTAACK.S
R4/RRR4-17/2	1278.044	1277.359	-247.127	0.364	837.216	0.423	16	0.162	K.ECVEAPGDFPR.G
R4/RRR4-18/2	1754.110	1754.855	-998.040	0.513	658.256	0.454	20	0.160	R.CDDELEPGKCTAACK.S
R4/RRR4-18/2	1062.886	1063.091	-193.248	0.411	968.188	0.343	14	0.160	R.CDDELEPGK.C
R4/RRR4-16/2	1278.266	1277.359	-72.758	0.321	678.714	0.452	15	0.158	K.ECVEAPGDFPR.G
R4/RRR4-22/2	1062.799	1063.091	-275.288	0.462	946.008	0.331	14	0.158	R.CDDELEPGK.C
R4/RRR4-18/2	1754.125	1754.855	-989.516	0.501	545.145	0.457	19	0.157	R.CDDELEPGKCTAACK.S
R4/RRR4-17/2	1754.177	1754.855	-959.614	0.489	564.226	0.447	19	0.156	R.CDDELEPGKCTAACK.S
R4/RRR4-17/2	1063.002	1063.091	-84.036	0.390	945.320	0.305	14	0.155	R.CDDELEPGK.C
R4/RRR4-14/2	1375.910	1376.528	-1179.384	0.377	989.708	0.307	15	0.155	K.CCDSIVQLPQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1062.762	1063.091	-310.666	0.398	972.453	0.301	14	0.154	-.CDDELEPGK.-
R4/RRR4-21/2	1062.922	1063.091	-159.491	0.428	963.167	0.294	14	0.154	R.CDDELEPGK.C
R4/RRR4-22/2	1754.122	1754.855	-990.774	0.467	458.037	0.444	17	0.152	R.CDDELEPGKCTAACK.S
R4/RRR4-1/2	1376.144	1376.528	-279.867	0.358	1180.572	0.222	16	0.152	K.CCDSIVQLPQR.I
R4/RRR4-1/2	1063.190	1063.091	93.094	0.288	928.982	0.295	14	0.151	R.CDDELEPGK.C
R4/RRR4-17/2	1754.309	1754.855	-884.027	0.513	548.601	0.412	18	0.151	R.CDDELEPGKCTAACK.S
R4/RRR4-19/2	1062.661	1063.091	-406.325	0.350	865.084	0.286	14	0.150	R.CDDELEPGK.C
R4/RRR4-18/2	1062.688	1063.091	-380.622	0.415	962.033	0.261	14	0.150	R.CDDELEPGK.C
R4/RRR4-17/2	1277.627	1277.359	210.674	0.308	675.457	0.354	15	0.149	K.ECVEAPGDFPR.G
R4/RRR4-17/2	1376.189	1376.528	-246.940	0.380	904.533	0.283	15	0.149	K.CCDSIVQLPQR.I
R4/RRR4-23/2	1062.894	1063.091	-186.220	0.412	936.273	0.254	14	0.148	R.CDDELEPGK.C
R4/RRR4-17/2	1062.359	1063.091	-1635.579	0.287	971.254	0.247	14	0.148	R.CDDELEPGK.C
R4/RRR4-2/2	1376.463	1376.528	-47.287	0.368	807.427	0.283	15	0.147	K.CCDSIVQLPQR.I
R4/RRR4-27/2	1276.909	1277.359	-353.299	0.202	833.472	0.341	16	0.147	K.ECVEAPGDFPR.G
R4/RRR4-21/2	1062.327	1063.091	-1665.594	0.299	952.207	0.224	14	0.146	R.CDDELEPGK.C
R4/RRR4-17/2	1375.483	1376.528	-1491.119	0.277	862.856	0.266	14	0.146	K.CCDSIVQLPQR.I
R4/RRR4-18/2	1062.401	1063.091	-1595.639	0.232	989.484	0.226	14	0.145	R.CDDELEPGK.C
R4/RRR4-17/2	1062.560	1063.091	-1445.374	0.327	1039.710	0.180	14	0.144	R.CDDELEPGK.C
R4/RRR4-17/2	1062.296	1063.091	-1694.571	0.292	1050.106	0.165	14	0.143	-.CDDELEPGK.-
R4/RRR4-1/2	1277.120	1277.359	-187.483	0.275	587.129	0.285	14	0.143	K.ECVEAPGDFPR.G
R4/RRR4-18/2	1277.020	1277.359	-265.541	0.210	876.273	0.247	16	0.142	K.ECVEAPGDFPR.G
R4/RRR4-26/2	1062.604	1063.091	-459.465	0.256	958.982	0.182	14	0.142	R.CDDELEPGK.C
R4/RRR4-17/2	1062.347	1063.091	-1646.661	0.323	1028.703	0.161	14	0.142	-.CDDELEPGK.-
R4/RRR4-26/2	1062.268	1063.091	-1721.587	0.318	935.098	0.181	14	0.142	R.CDDELEPGK.C
R4/RRR4-27/2	1277.016	1277.359	-268.898	0.188	770.718	0.288	16	0.142	K.ECVEAPGDFPR.G
R4/RRR4-18/2	1062.815	1063.091	-260.768	0.325	968.306	0.168	14	0.141	-.CDDELEPGK.-
R4/RRR4-17/2	1062.836	1063.091	-241.064	0.335	990.405	0.152	14	0.140	R.CDDELEPGK.C
R4/RRR4-21/2	1277.237	1277.359	-95.536	0.268	694.570	0.202	15	0.139	K.ECVEAPGDFPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/2	1277.004	1277.359	-278.296	0.225	593.523	0.222	14	0.139	K.ECVEAPGDFPR.G
R4/RRR4-18/2	1277.017	1277.359	-268.418	0.214	672.216	0.235	14	0.139	K.ECVEAPGDFPR.G
R4/RRR4-27/2	1276.402	1277.359	-1537.323	0.195	615.248	0.247	14	0.139	K.ECVEAPGDFPR.G
R4/RRR4-22/2	1276.456	1277.359	-1494.574	0.179	824.170	0.221	15	0.139	K.ECVEAPGDFPR.G
R4/RRR4-21/2	1062.466	1063.091	-1533.889	0.310	991.574	0.127	14	0.138	R.CDDELEPGK.C
R4/RRR4-1/2	1276.935	1277.359	-332.869	0.188	688.350	0.164	15	0.136	K.ECVEAPGDFPR.G
R4/RRR4-21/2	1277.124	1277.359	-184.031	0.239	691.903	0.116	15	0.136	K.ECVEAPGDFPR.G
R4/RRR4-18/2	1062.334	1063.091	-1659.013	0.264	940.087	0.081	14	0.135	-.CDDELEPGK.-
R4/RRR4-18/3	1755.955	1754.855	57.125	0.458	844.189	0.497	27	0.127	R.CDDELEPGKCTAACK.S
R4/RRR4-18/3	1755.193	1754.855	193.106	0.503	808.816	0.501	27	0.126	R.CDDELEPGKCTAACK.S
R4/RRR4-17/3	1754.555	1754.855	-171.505	0.434	984.093	0.421	28	0.119	R.CDDELEPGKCTAACK.S
R4/RRR4-22/3	1754.101	1754.855	-1003.323	0.451	761.537	0.449	26	0.115	R.CDDELEPGKCTAACK.S
R4/RRR4-15/3	1754.159	1754.855	-970.101	0.410	748.903	0.447	25	0.114	R.CDDELEPGKCTAACK.S
R4/RRR4-17/3	1754.738	1754.855	-67.034	0.435	890.729	0.421	29	0.114	R.CDDELEPGKCTAACK.S
R4/RRR4-18/3	1753.940	1754.855	-1095.036	0.452	724.305	0.446	27	0.113	R.CDDELEPGKCTAACK.S
R4/RRR4-17/3	1755.244	1754.855	221.874	0.422	765.961	0.434	25	0.113	R.CDDELEPGKCTAACK.S
R4/RRR4-22/3	1754.667	1754.855	-107.857	0.503	762.691	0.432	27	0.111	R.CDDELEPGKCTAACK.S
R4/RRR4-18/3	1754.977	1754.855	69.541	0.419	834.543	0.392	27	0.108	R.CDDELEPGKCTAACK.S
R4/RRR4-16/3	1754.635	1754.855	-125.966	0.428	817.735	0.377	26	0.105	R.CDDELEPGKCTAACK.S
R4/RRR4-21/3	1754.571	1754.855	-162.502	0.369	801.031	0.380	26	0.105	R.CDDELEPGKCTAACK.S
R4/RRR4-22/3	1754.539	1754.855	-180.718	0.381	660.406	0.387	24	0.104	R.CDDELEPGKCTAACK.S
R4/RRR4-18/3	1754.062	1754.855	-1025.228	0.370	554.991	0.409	23	0.103	-.CDDELEPGKCTAACK.-
R4/RRR4-19/3	1754.673	1754.855	-103.984	0.364	779.438	0.366	26	0.103	R.CDDELEPGKCTAACK.S
R4/RRR4-20/3	1754.493	1754.855	-206.892	0.323	421.126	0.395	21	0.103	-.CDDELEPGKCTAACK.-
R4/RRR4-1/3	1754.776	1754.855	-45.054	0.368	548.393	0.341	22	0.101	R.CDDELEPGKCTAACK.S
R4/RRR4-21/3	1754.412	1754.855	-253.275	0.384	542.339	0.376	23	0.100	-.CDDELEPGKCTAACK.-
R4/RRR4-4/3	1753.488	1754.855	-1353.913	0.393	1029.585	0.315	26	0.100	-.CDDELEPGKCTAACK.-
R4/RRR4-21/3	1754.117	1754.855	-993.681	0.386	678.451	0.317	25	0.097	R.CDDELEPGKCTAACK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/3	1754.230	1754.855	-929.231	0.371	639.214	0.304	25	0.097	R.CDDELEPGKCTAACK.S
R4/RRR4-15/3	1754.183	1754.855	-956.163	0.318	599.549	0.274	22	0.097	R.CDDELEPGKCTAACK.S
R4/RRR4-22/3	1754.029	1754.855	-1044.513	0.273	820.942	0.298	27	0.095	R.CDDELEPGKCTAACK.S
R4/RRR4-18/3	1375.916	1376.528	-1174.983	0.437	1006.586	0.257	21	0.087	K.CCDSIVQLPQR.I
R4/RRR4-18/3	1375.855	1376.528	-1219.887	0.395	771.023	0.209	19	0.076	-.CCDSIVQLPQR.-
R4/RRR4-22/3	1376.970	1376.528	322.039	0.381	749.511	0.215	18	0.070	-.CCDSIVQLPQR.-
R4/RRR4-22/3	1376.434	1376.528	-68.379	0.387	761.852	0.177	18	0.063	-.CCDSIVQLPQR.-
R4/RRR4-14/2	1695.307	1695.895	-939.637	0.467	991.273	0.598	22	0.197	K.LLESHLVPSSTAPESK.V
R4/RRR4-14/2	1695.467	1695.895	-253.443	0.486	763.454	0.571	20	0.177	K.LLESHLVPSSTAPESK.V
R4/RRR4-14/2	1695.315	1695.895	-935.228	0.465	844.598	0.514	20	0.172	K.LLESHLVPSSTAPESK.V
R4/RRR4-13/2	1898.411	1898.214	104.120	0.600	1633.147	0.625	28	0.273	K.VM*VGLPTTGGVTPVPGAAEK.A
R4/RRR4-13/2	1882.413	1882.214	105.654	0.559	1549.689	0.587	27	0.251	K.VMVGLPTTGGVTPVPGAAEK.A
R4/RRR4-13/2	1898.049	1898.214	-87.058	0.582	1480.566	0.588	28	0.244	K.VM*VGLPTTGGVTPVPGAAEK.A
R4/RRR4-13/2	1595.259	1594.853	255.566	0.554	1575.995	0.477	18	0.227	K.FASFETIVEM*IYK.H
R4/RRR4-13/2	1897.529	1898.214	-890.537	0.520	1377.334	0.561	27	0.225	K.VM*VGLPTTGGVTPVPGAAEK.A
R4/RRR4-13/2	1882.482	1882.214	142.398	0.532	1191.410	0.532	25	0.199	K.VMVGLPTTGGVTPVPGAAEK.A
R4/RRR4-13/2	1881.657	1882.214	-830.248	0.481	1074.973	0.538	24	0.190	K.VMVGLPTTGGVTPVPGAAEK.A
R4/RRR4-13/2	1594.768	1594.853	-53.217	0.498	1066.313	0.432	19	0.176	K.FASFETIVEM*IYK.H
R4/RRR4-13/2	1594.446	1594.853	-255.644	0.500	883.672	0.436	17	0.165	K.FASFETIVEM*IYK.H
R4/RRR4-4/2	1578.395	1578.853	-291.556	0.331	933.963	0.442	15	0.164	K.FASFETIVEMIYK.H
R4/RRR4-13/2	1594.369	1594.853	-304.190	0.419	932.251	0.405	17	0.163	K.FASFETIVEM*IYK.H
R4/RRR4-12/2	1579.946	1578.853	59.081	0.327	921.926	0.357	17	0.155	K.FASFETIVEMIYK.H
R4/RRR4-13/2	1594.124	1594.853	-1087.646	0.397	660.442	0.366	16	0.149	K.FASFETIVEM*IYK.H
R4/RRR4-13/2	1594.586	1594.853	-167.936	0.260	190.262	0.225	13	0.146	K.FASFETIVEM*IYK.H
R4/RRR4-1/2	1897.418	1898.214	-949.439	0.420	438.452	0.422	19	0.145	K.VM*VGLPTTGGVTPVPGAAEK.A
R4/RRR4-1/2	1579.414	1578.853	-278.888	0.323	617.474	0.364	14	0.145	K.FASFETIVEMIYK.H
R4/RRR4-13/2	1593.756	1594.853	-1319.595	0.291	694.505	0.295	16	0.143	K.FASFETIVEM*IYK.H
R4/RRR4-14/2	1686.515	1686.932	-247.892	0.456	2834.059	0.447	26	0.433	R.LISEATAAAGTGLIELR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1686.584	1686.932	-206.721	0.459	2873.501	0.424	26	0.433	R.LISEATAAAGTGLIELR.R
R4/RRR4-14/2	1220.150	1220.470	-262.565	0.544	2405.867	0.561	21	0.385	R.MLLGLNAAGFGR.-
R4/RRR4-14/2	1686.486	1686.932	-265.320	0.464	2557.677	0.427	26	0.367	R.LISEATAAAGTGLIELR.R
R4/RRR4-14/2	1220.066	1220.470	-332.127	0.483	1937.739	0.568	19	0.302	R.MLLGLNAAGFGR.-
R4/RRR4-14/2	1237.025	1236.469	-359.701	0.546	1752.437	0.543	20	0.270	R.M*LLGLNAAGFGR.-
R4/RRR4-14/2	1235.659	1236.469	-1469.069	0.524	1654.506	0.546	20	0.258	R.M*LLGLNAAGFGR.-
R4/RRR4-14/2	1235.840	1236.469	-1321.931	0.479	1534.031	0.550	19	0.242	R.M*LLGLNAAGFGR.-
R4/RRR4-15/2	1236.001	1236.469	-380.108	0.436	1420.453	0.542	18	0.226	R.M*LLGLNAAGFGR.-
R4/RRR4-14/2	1417.051	1417.509	-324.234	0.449	1293.546	0.535	21	0.212	R.SPNVAYVPAGDNGR.M
R4/RRR4-14/2	1218.665	1219.437	-1457.885	0.439	1562.588	0.339	16	0.198	K.DLQM*VNLTLR.L
R4/RRR4-14/2	1417.000	1417.509	-1067.765	0.486	1011.940	0.570	20	0.196	R.SPNVAYVPAGDNGR.M
R4/RRR4-14/2	1417.152	1417.509	-252.589	0.521	984.555	0.550	20	0.191	R.SPNVAYVPAGDNGR.M
R4/RRR4-14/2	1418.077	1417.509	-305.350	0.494	918.054	0.572	19	0.189	R.SPNVAYVPAGDNGR.M
R4/RRR4-14/2	1418.007	1417.509	352.318	0.447	921.960	0.579	19	0.189	R.SPNVAYVPAGDNGR.M
R4/RRR4-15/2	1235.370	1236.469	-1704.401	0.450	1006.039	0.511	16	0.183	R.M*LLGLNAAGFGR.-
R4/RRR4-14/2	1219.007	1219.437	-354.048	0.395	1447.901	0.288	16	0.179	K.DLQM*VNLTLR.L
R4/RRR4-14/2	1219.113	1219.437	-266.040	0.522	1503.046	0.260	16	0.175	K.DLQM*VNLTLR.L
R4/RRR4-15/2	1236.160	1236.469	-250.408	0.442	819.979	0.364	15	0.153	R.M*LLGLNAAGFGR.-
R4/RRR4-15/2	1685.920	1686.932	-1196.726	0.314	1152.389	0.275	18	0.151	R.LISEATAAAGTGLIELR.R
R4/RRR4-18/2	1438.484	1438.614	-90.870	0.515	1558.176	0.468	21	0.225	R.AITVDKAQPQGPGR.D
R4/RRR4-18/2	1438.165	1438.614	-313.174	0.480	1340.873	0.426	20	0.194	R.AITVDKAQPQGPGR.D
R4/RRR4-18/2	1275.232	1275.434	-158.477	0.467	1226.193	0.376	16	0.176	R.GFGFVTFDEKK.A
R4/RRR4-18/2	1275.238	1275.434	-153.868	0.415	1170.628	0.340	16	0.167	R.GFGFVTFDEKK.A
R4/RRR4-18/2	879.556	879.980	-483.675	0.469	1324.903	0.213	14	0.158	K.FGNLTEAK.V
R4/RRR4-18/2	879.815	879.980	-188.092	0.471	1069.829	0.275	14	0.156	K.FGNLTEAK.V
R4/RRR4-18/2	1147.497	1147.261	205.864	0.363	722.918	0.370	13	0.150	R.GFGFVTFDEK.K
R4/RRR4-18/2	879.420	879.980	-1779.788	0.456	942.837	0.259	14	0.150	K.FGNLTEAK.V
R4/RRR4-17/2	879.985	879.980	5.202	0.438	564.168	0.248	13	0.145	K.FGNLTEAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1147.112	1147.261	-130.495	0.310	481.258	0.281	14	0.142	R.GFGFVTFDEK.K
R4/RRR4-18/2	1147.030	1147.261	-201.915	0.260	573.412	0.285	15	0.141	R.GFGFVTFDEK.K
R4/RRR4-18/2	1438.810	1438.614	136.527	0.355	523.995	0.360	13	0.138	-.AITVDKAQPQGPGR.-
R4/RRR4-8/3	1756.810	1756.896	-49.114	0.535	2627.178	0.501	34	0.443	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-14/3	1756.506	1756.896	-222.478	0.598	2423.907	0.544	34	0.409	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-13/3	1757.335	1756.896	251.047	0.601	2340.396	0.507	32	0.366	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-13/3	1757.064	1756.896	96.286	0.564	2180.669	0.559	32	0.356	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-14/3	1756.925	1756.896	16.954	0.594	2036.866	0.533	32	0.306	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-14/3	1756.431	1756.896	-265.357	0.591	1949.921	0.565	31	0.304	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-12/3	1757.243	1756.896	198.385	0.568	2031.044	0.513	33	0.294	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-14/2	1609.232	1609.716	-302.023	0.555	1958.683	0.491	23	0.284	R.ISQEVSGDALGEEFK.G
R4/RRR4-14/2	1609.097	1609.716	-1009.155	0.524	1912.924	0.478	23	0.273	R.ISQEVSGDALGEEFK.G
R4/RRR4-20/3	1757.030	1756.896	76.532	0.571	1952.245	0.484	29	0.267	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-14/2	1373.210	1373.537	-239.540	0.533	1417.504	0.353	18	0.188	K.KLEIDDDQKLR.A
R4/RRR4-14/2	1373.238	1373.537	-218.583	0.539	1345.241	0.359	18	0.183	K.KLEIDDDQKLR.A
R4/RRR4-14/2	1373.371	1373.537	-121.299	0.529	1347.471	0.344	18	0.181	K.KLEIDDDQKLR.A
R4/RRR4-14/2	1350.957	1351.484	-1133.558	0.522	1232.502	0.385	19	0.180	K.FNIANPTTGCQK.K
R4/RRR4-14/2	1350.637	1351.484	-1371.514	0.465	1156.703	0.342	19	0.168	K.FNIANPTTGCQK.K
R4/RRR4-20/3	1757.101	1756.896	116.979	0.524	1353.446	0.480	27	0.168	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-21/3	1757.170	1756.896	156.796	0.481	1499.061	0.415	30	0.163	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-14/2	1350.938	1351.484	-1147.622	0.498	1067.421	0.329	18	0.159	K.FNIANPTTGCQK.K
R4/RRR4-21/3	1757.020	1756.896	70.993	0.493	1132.575	0.442	26	0.134	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-13/3	1373.720	1373.537	133.137	0.460	1127.049	0.385	23	0.117	K.KLEIDDDQKLR.A
R4/RRR4-13/3	1373.581	1373.537	32.070	0.432	1123.344	0.380	23	0.116	K.KLEIDDDQKLR.A
R4/RRR4-14/3	1372.756	1373.537	-1301.931	0.426	1026.308	0.404	23	0.115	K.KLEIDDDQKLR.A
R4/RRR4-11/3	1756.528	1756.896	-210.137	0.449	728.228	0.443	25	0.110	K.KGDNDLPGLTDTEKPR.M
R4/RRR4-13/3	1373.810	1373.537	199.168	0.483	979.772	0.375	22	0.108	K.KLEIDDDQKLR.A
R4/RRR4-14/3	1373.737	1373.537	145.435	0.472	1030.964	0.349	23	0.105	K.KLEIDDDQKLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-19/3	1373.177	1373.537	-263.630	0.418	845.300	0.371	21	0.102	K.KLEIDDDQKLR.A
R4/RRR4-12/3	1373.427	1373.537	-80.653	0.403	781.713	0.369	21	0.101	K.KLEIDDDQKLR.A
R4/RRR4-14/3	1373.844	1373.537	223.894	0.461	681.534	0.328	20	0.096	K.KLEIDDDQKLR.A
R4/RRR4-12/3	1372.203	1373.537	-1706.517	0.378	727.075	0.332	20	0.096	K.KLEIDDDQKLR.A
R4/RRR4-19/3	1373.004	1373.537	-1120.449	0.342	584.977	0.304	16	0.095	K.KLEIDDDQKLR.A
R4/RRR4-19/3	1372.614	1373.537	-1405.760	0.338	609.592	0.305	18	0.095	K.KLEIDDDQKLR.A
R4/RRR4-15/3	1373.908	1373.537	270.535	0.460	865.469	0.279	21	0.091	K.KLEIDDDQKLR.A
R4/RRR4-15/3	1373.686	1373.537	108.541	0.435	868.883	0.265	20	0.090	K.KLEIDDDQKLR.A
R4/RRR4-15/3	1373.147	1373.537	-284.901	0.350	717.231	0.279	18	0.089	-.KLEIDDDQKLR.-
R4/RRR4-14/3	1373.953	1373.537	303.275	0.336	806.221	0.192	20	0.085	K.KLEIDDDQKLR.A
R4/RRR4-1/2	1686.309	1686.844	-912.850	0.529	2720.198	0.434	23	0.403	R.YYDLSSQEIGELIR.F
R4/RRR4-1/2	1687.892	1686.844	28.826	0.524	2353.495	0.455	21	0.337	R.YYDLSSQEIGELIR.F
R4/RRR4-1/2	1398.400	1398.632	-166.057	0.438	1278.044	0.497	17	0.202	R.DSVLLQLPHFTK.E
R4/RRR4-1/2	1257.048	1257.377	-262.650	0.444	1071.642	0.438	14	0.173	K.TGYFQVTDLGR.I
R4/RRR4-1/2	979.708	980.143	-445.416	0.277	842.860	0.378	13	0.151	R.LSAYGITVR.E
R4/RRR4-2/2	1398.195	1398.632	-312.932	0.311	610.832	0.393	15	0.147	R.DSVLLQLPHFTK.E
R4/RRR4-1/2	979.927	980.143	-221.166	0.350	594.738	0.359	12	0.145	-.LSAYGITVR.-
R4/RRR4-1/2	1288.043	1287.572	366.574	0.271	632.849	0.410	13	0.141	-.VVYIAPIEALAK.-
R4/RRR4-1/2	1397.768	1398.632	-1337.356	0.254	470.542	0.275	14	0.137	R.DSVLLQLPHFTK.E
R4/RRR4-2/2	1686.697	1686.844	-87.152	0.322	886.468	0.178	17	0.134	R.YYDLSSQEIGELIR.F
R4/RRR4-16/2	1398.180	1397.561	-273.355	0.537	1612.419	0.500	19	0.240	K.LYGSTLSWNVTR.C
R4/RRR4-16/2	1397.802	1397.561	173.029	0.499	1553.187	0.491	19	0.231	K.LYGSTLSWNVTR.C
R4/RRR4-15/2	1397.367	1397.561	-138.930	0.400	1501.776	0.421	18	0.208	K.LYGSTLSWNVTR.C
R4/RRR4-16/2	1397.168	1397.561	-282.141	0.505	1385.129	0.450	18	0.204	K.LYGSTLSWNVTR.C
R4/RRR4-16/2	1108.364	1107.285	71.404	0.516	1224.764	0.431	15	0.190	K.KVLEVYEAR.L
R4/RRR4-16/2	1677.643	1677.908	-158.706	0.488	1359.485	0.393	19	0.188	K.AWWTDLMARPSSQK.V
R4/RRR4-16/2	1106.992	1107.285	-265.293	0.490	1194.754	0.385	15	0.179	K.KVLEVYEAR.L
R4/RRR4-16/2	1107.041	1107.285	-220.710	0.492	1239.383	0.361	15	0.178	K.KVLEVYEAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1397.462	1397.561	-71.108	0.386	1207.992	0.374	18	0.175	K.LYGSTLSWNVTR.C
R4/RRR4-16/2	1677.303	1677.908	-960.235	0.488	1398.604	0.319	18	0.175	K.AWWTDLMARPSSQK.V
R4/RRR4-16/2	1677.792	1677.908	-69.808	0.505	1397.990	0.301	19	0.172	K.AWWTDLMARPSSQK.V
R4/RRR4-15/2	978.425	979.112	-1728.772	0.455	788.505	0.464	13	0.170	K.VLEVYEAR.L
R4/RRR4-2/2	1397.006	1397.561	-1116.175	0.414	1218.135	0.339	17	0.170	K.LYGSTLSWNVTR.C
R4/RRR4-16/2	978.825	979.112	-293.714	0.443	920.618	0.431	13	0.169	-.VLEVYEAR.-
R4/RRR4-16/2	978.859	979.112	-258.556	0.455	753.169	0.439	13	0.166	K.VLEVYEAR.L
R4/RRR4-15/2	978.825	979.112	-293.964	0.486	864.966	0.397	13	0.165	K.VLEVYEAR.L
R4/RRR4-18/2	1397.280	1397.561	-201.678	0.406	784.321	0.474	15	0.165	K.LYGSTLSWNVTR.C
R4/RRR4-15/2	978.890	979.112	-226.778	0.457	744.995	0.421	13	0.164	K.VLEVYEAR.L
R4/RRR4-15/2	1397.740	1397.561	128.800	0.391	1101.342	0.324	16	0.160	K.LYGSTLSWNVTR.C
R4/RRR4-16/2	978.833	979.112	-286.081	0.464	867.161	0.361	13	0.160	K.VLEVYEAR.L
R4/RRR4-16/2	1693.316	1693.908	-943.056	0.459	533.198	0.459	19	0.158	K.AWWTDLM*ARPSSQK.V
R4/RRR4-16/2	1396.274	1397.561	-1642.274	0.307	942.464	0.386	15	0.158	-.LYGSTLSWNVTR.-
R4/RRR4-16/2	978.491	979.112	-1661.462	0.425	761.123	0.354	13	0.156	K.VLEVYEAR.L
R4/RRR4-2/2	978.947	979.112	-169.233	0.361	718.216	0.358	13	0.154	K.VLEVYEAR.L
R4/RRR4-16/2	978.490	979.112	-1661.964	0.411	752.634	0.331	13	0.153	K.VLEVYEAR.L
R4/RRR4-16/2	978.441	979.112	-1713.103	0.373	774.598	0.329	13	0.153	K.VLEVYEAR.L
R4/RRR4-16/2	1693.302	1693.908	-951.380	0.418	643.055	0.373	20	0.152	K.AWWTDLM*ARPSSQK.V
R4/RRR4-16/2	1693.534	1693.908	-221.127	0.465	531.735	0.387	18	0.150	K.AWWTDLM*ARPSSQK.V
R4/RRR4-14/2	1533.250	1533.580	-215.735	0.550	2430.556	0.577	24	0.394	R.AAGGASGGEELTVEER.N
R4/RRR4-14/2	1532.936	1533.580	-1075.346	0.458	2418.700	0.546	23	0.380	R.AAGGASGGEELTVEER.N
R4/RRR4-15/2	1534.700	1533.580	78.454	0.544	2261.199	0.620	23	0.376	R.AAGGASGGEELTVEER.N
R4/RRR4-14/2	1534.084	1533.580	-324.001	0.568	2242.935	0.571	23	0.355	R.AAGGASGGEELTVEER.N
R4/RRR4-14/2	1389.180	1389.537	-257.763	0.512	1348.701	0.516	19	0.216	R.IISSIEQKEEGR.G
R4/RRR4-14/2	1389.155	1389.537	-275.483	0.461	1177.221	0.517	19	0.200	R.IISSIEQKEEGR.G
R4/RRR4-14/2	1389.105	1389.537	-312.072	0.434	867.919	0.523	17	0.177	R.IISSIEQKEEGR.G
R4/RRR4-15/2	1389.574	1389.537	26.908	0.335	307.030	0.410	16	0.150	R.IISSIEQKEEGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1634.240	1634.812	-965.010	0.519	2307.230	0.409	22	0.313	K.VLNFAIDDSILEER.I
R4/RRR4-15/2	1633.530	1634.812	-1401.351	0.391	2556.356	0.242	22	0.307	K.VLNFAIDDSILEER.I
R4/RRR4-14/2	1634.456	1634.812	-218.332	0.582	2201.263	0.429	22	0.301	K.VLNFAIDDSILEER.I
R4/RRR4-14/2	1633.719	1634.812	-1284.726	0.453	2225.721	0.370	22	0.289	K.VLNFAIDDSILEER.I
R4/RRR4-15/2	1633.882	1634.812	-1184.633	0.355	1995.338	0.207	20	0.215	K.VLNFAIDDSILEER.I
R4/RRR4-14/2	1021.458	1022.181	-1692.620	0.420	1257.739	0.469	14	0.197	K.GFILDGFPR.T
R4/RRR4-15/2	1022.054	1022.181	-125.558	0.482	1193.852	0.484	14	0.196	K.GFILDGFPR.T
R4/RRR4-14/2	1021.582	1022.181	-1570.527	0.437	1240.074	0.456	14	0.193	K.GFILDGFPR.T
R4/RRR4-14/2	1022.030	1022.181	-148.682	0.484	1163.431	0.467	14	0.190	K.GFILDGFPR.T
R4/RRR4-15/2	1022.072	1022.181	-107.227	0.455	1225.588	0.435	14	0.189	K.GFILDGFPR.T
R4/RRR4-15/2	1021.892	1022.181	-284.211	0.442	1110.281	0.478	14	0.188	K.GFILDGFPR.T
R4/RRR4-14/2	1344.102	1343.463	-269.596	0.382	213.813	0.465	13	0.153	K.QTEPVIDYYSK.K
R4/RRR4-14/2	1038.016	1038.266	-240.931	0.410	804.811	0.340	15	0.150	R.LILVGPPGSGK.G
R4/RRR4-14/2	1343.231	1343.463	-173.607	0.267	223.552	0.370	13	0.144	K.QTEPVIDYYSK.K
R4/RRR4-15/2	1039.216	1038.266	-47.670	0.438	675.157	0.316	14	0.144	R.LILVGPPGSGK.G
R4/RRR4-14/2	1037.335	1038.266	-1866.833	0.312	654.940	0.266	14	0.139	R.LILVGPPGSGK.G
R4/RRR4-14/2	1344.552	1343.463	65.873	0.296	180.079	0.343	12	0.137	-.QTEPVIDYYSK.-
R4/RRR4-1/2	1634.573	1634.812	-146.933	0.277	576.372	0.182	14	0.132	K.VLNFAIDDSILEER.I
R4/RRR4-5/3	1950.666	1951.255	-817.014	0.547	1945.195	0.567	33	0.309	K.SKLDAQPELFIHIVPDK.A
R4/RRR4-5/2	1611.323	1610.812	-304.799	0.515	1729.152	0.573	23	0.272	K.ASNTLSIIDSGVGM*TK.S
R4/RRR4-5/3	1950.676	1951.255	-811.643	0.548	1708.112	0.523	32	0.239	K.SKLDAQPELFIHIVPDK.A
R4/RRR4-5/2	1610.355	1610.812	-284.986	0.455	1488.242	0.551	22	0.234	K.ASNTLSIIDSGVGM*TK.S
R4/RRR4-4/2	1610.179	1610.812	-1017.122	0.447	1423.661	0.556	22	0.228	K.ASNTLSIIDSGVGM*TK.S
R4/RRR4-5/3	1950.621	1951.255	-840.006	0.542	1639.980	0.510	32	0.221	K.SKLDAQPELFIHIVPDK.A
R4/RRR4-5/2	1594.150	1594.813	-1046.497	0.375	1518.273	0.489	21	0.221	K.ASNTLSIIDSGVGMTK.S
R4/RRR4-5/2	1610.305	1610.812	-938.576	0.477	1341.923	0.559	21	0.220	K.ASNTLSIIDSGVGM*TK.S
R4/RRR4-4/2	1735.650	1736.004	-204.827	0.513	1308.104	0.529	23	0.214	K.LDAQPELFIHIVPDK.A
R4/RRR4-5/2	1593.616	1594.813	-1382.438	0.353	1481.018	0.451	22	0.209	K.ASNTLSIIDSGVGMTK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1610.150	1610.812	-1035.161	0.411	1322.181	0.505	21	0.205	K.ASNTLSIIDSGVGM*TK.S
R4/RRR4-5/2	1735.456	1736.004	-894.688	0.569	1131.692	0.568	21	0.205	K.LDAQPELFIHIVPDK.A
R4/RRR4-4/2	1735.338	1736.004	-963.188	0.496	1039.606	0.574	21	0.198	K.LDAQPELFIHIVPDK.A
R4/RRR4-5/2	1735.348	1736.004	-957.396	0.532	1053.215	0.525	20	0.189	K.LDAQPELFIHIVPDK.A
R4/RRR4-5/2	1734.690	1736.004	-1338.122	0.487	1032.033	0.529	20	0.188	K.LDAQPELFIHIVPDK.A
R4/RRR4-4/2	1736.601	1736.004	-232.775	0.546	997.223	0.531	20	0.187	K.LDAQPELFIHIVPDK.A
R4/RRR4-5/2	1594.003	1594.813	-1138.689	0.351	1052.793	0.418	18	0.167	K.ASNTLSIIDSGVGMTK.S
R4/RRR4-4/3	1950.743	1951.255	-777.252	0.393	1163.045	0.492	30	0.148	K.SKLDAQPELFIHIVPDK.A
R4/RRR4-4/3	1950.097	1951.255	-1109.956	0.312	594.197	0.390	22	0.093	-.SKLDAQPELFIHIVPDK.-
R4/RRR4-16/2	1664.174	1662.849	196.098	0.435	957.135	0.563	16	0.184	R.FWGQYIDDMFSPR.I
R4/RRR4-16/2	1307.682	1308.509	-1401.117	0.452	940.393	0.471	18	0.175	K.SELLLASNPVHK.K
R4/RRR4-16/2	1308.111	1308.509	-304.812	0.424	915.478	0.492	17	0.175	K.SELLLASNPVHK.K
R4/RRR4-16/2	1308.246	1308.509	-201.459	0.468	945.850	0.461	17	0.173	K.SELLLASNPVHK.K
R4/RRR4-16/2	1351.598	1350.614	-11.650	0.279	765.984	0.433	14	0.152	R.VLGSWASPFVMR.V
R4/RRR4-16/2	1349.858	1350.614	-1304.277	0.296	573.817	0.482	13	0.151	R.VLGSWASPFVMR.V
R4/RRR4-16/2	1366.334	1366.613	-205.289	0.353	366.342	0.377	12	0.143	R.VLGSWASPFVM*R.V
R4/RRR4-15/2	1308.216	1308.509	-224.113	0.260	375.178	0.308	16	0.143	K.SELLLASNPVHK.K
R4/RRR4-16/2	1365.977	1366.613	-1201.164	0.294	376.991	0.386	11	0.141	R.VLGSWASPFVM*R.V
R4/RRR4-15/2	1308.099	1308.509	-314.362	0.183	568.700	0.391	15	0.139	K.SELLLASNPVHK.K
R4/RRR4-16/2	1365.585	1366.613	-1489.583	0.251	490.481	0.304	14	0.139	R.VLGSWASPFVM*R.V
R4/RRR4-16/3	1436.695	1436.682	9.228	0.504	859.089	0.386	22	0.101	K.KSELLLASNPVHK.K
R4/RRR4-16/3	1436.415	1436.682	-186.391	0.426	758.529	0.336	21	0.089	K.KSELLLASNPVHK.K
R4/RRR4-14/2	1986.601	1987.198	-806.050	0.534	2199.200	0.578	26	0.348	K.GDVSDEAVAALDKIEAALAK.F
R4/RRR4-14/2	1987.603	1987.198	204.413	0.582	2184.635	0.556	26	0.337	K.GDVSDEAVAALDKIEAALAK.F
R4/RRR4-14/2	1986.620	1987.198	-796.428	0.559	2146.035	0.535	25	0.323	K.GDVSDEAVAALDKIEAALAK.F
R4/RRR4-14/2	1101.169	1101.322	-139.497	0.317	895.543	0.319	14	0.151	R.FQIFFSAIK.N
R4/RRR4-14/3	1985.967	1987.198	-1126.498	0.431	1383.506	0.413	37	0.150	K.GDVSDEAVAALDKIEAALAK.F
R4/RRR4-14/2	1101.168	1101.322	-140.387	0.265	577.209	0.323	13	0.142	R.FQIFFSAIK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1101.177	1101.322	-131.936	0.269	706.921	0.265	13	0.140	R.FQIFFSAIK.N
R4/RRR4-14/3	1986.394	1987.198	-910.647	0.383	1304.285	0.376	39	0.129	K.GDVSDEAVAALDKIEAALAK.F
R4/RRR4-14/3	1823.342	1823.039	166.717	0.495	760.810	0.505	26	0.120	K.FIEEVNKIHAYTETK.Q
R4/RRR4-14/3	1823.209	1823.039	93.699	0.405	508.271	0.449	22	0.099	K.FIEEVNKIHAYTETK.Q
R4/RRR4-14/3	1822.803	1823.039	-129.551	0.420	653.707	0.405	25	0.097	K.FIEEVNKIHAYTETK.Q
R4/RRR4-14/3	1355.979	1356.509	-1131.175	0.461	504.611	0.369	18	0.094	K.QDPQFLLEHTK.K
R4/RRR4-14/3	1356.492	1356.509	-12.385	0.388	957.872	0.297	23	0.090	K.QDPQFLLEHTK.K
R4/RRR4-14/3	1356.567	1356.509	42.851	0.335	791.644	0.265	22	0.083	K.QDPQFLLEHTK.K
R4/RRR4-3/3	1908.375	1909.022	-865.840	0.496	2671.540	0.531	35	0.491	K.TQEKDADAM*QVDNAVEK.K
R4/RRR4-3/3	1908.707	1909.022	-165.564	0.504	2593.818	0.497	34	0.445	K.TQEKDADAM*QVDNAVEK.K
R4/RRR4-3/3	1908.846	1909.022	-92.623	0.520	2496.247	0.500	36	0.414	K.TQEKDADAM*QVDNAVEK.K
R4/RRR4-3/2	1402.288	1402.645	-255.703	0.410	1205.531	0.430	18	0.180	K.MGAILASGILDAGGR.N
R4/RRR4-3/2	1402.037	1402.645	-1150.769	0.332	908.435	0.435	16	0.158	K.MGAILASGILDAGGR.N
R4/RRR4-3/2	1908.924	1909.022	-51.948	0.468	876.539	0.404	19	0.154	K.TQEKDADAM*QVDNAVEK.K
R4/RRR4-3/2	1402.284	1402.645	-258.759	0.303	451.878	0.338	11	0.127	-.MGAILASGILDAGGR.-
R4/RRR4-6/2	1375.281	1375.492	-154.070	0.470	1383.565	0.431	16	0.199	K.NSLENYAYNMR.N
R4/RRR4-6/2	1391.079	1391.492	-297.859	0.483	1357.520	0.395	17	0.191	K.NSLENYAYNM*R.N
R4/RRR4-6/2	1391.185	1391.492	-221.269	0.506	1188.876	0.453	17	0.189	K.NSLENYAYNM*R.N
R4/RRR4-6/2	1390.283	1391.492	-1593.127	0.303	1130.687	0.196	17	0.146	K.NSLENYAYNM*R.N
R4/RRR4-16/2	1669.368	1669.904	-923.067	0.577	1318.089	0.570	22	0.226	R.RVEPYVAYGYPNLK.S
R4/RRR4-16/2	1668.905	1669.904	-1201.811	0.565	1272.385	0.553	21	0.216	R.RVEPYVAYGYPNLK.S
R4/RRR4-16/2	1670.353	1669.904	269.405	0.587	1174.115	0.476	21	0.191	R.RVEPYVAYGYPNLK.S
R4/RRR4-15/2	1669.220	1669.904	-1012.195	0.505	954.552	0.475	19	0.175	R.RVEPYVAYGYPNLK.S
R4/RRR4-16/2	1267.011	1266.429	-330.548	0.381	968.147	0.403	15	0.166	K.EANNFLWPFK.L
R4/RRR4-16/2	1266.101	1266.429	-259.805	0.360	930.021	0.370	15	0.159	K.EANNFLWPFK.L
R4/RRR4-16/2	1512.636	1513.718	-1380.361	0.264	1033.738	0.343	21	0.156	R.VEPYVAYGYPNLK.S
R4/RRR4-15/2	1513.010	1513.718	-1131.993	0.256	887.706	0.352	19	0.150	R.VEPYVAYGYPNLK.S
R4/RRR4-16/2	1335.152	1335.622	-352.835	0.443	1002.337	0.292	15	0.149	R.LRQIFNGVFLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1267.092	1266.429	-266.752	0.295	600.021	0.326	11	0.140	-.EANNFLWPFK.-
R4/RRR4-16/2	1266.119	1266.429	-245.683	0.234	758.500	0.255	13	0.139	K.EANNFLWPFK.L
R4/RRR4-16/2	1512.415	1513.718	-1527.171	0.181	913.097	0.237	20	0.138	R.VEPYVAYGYPNLK.S
R4/RRR4-15/2	1266.280	1266.429	-118.021	0.283	666.133	0.244	11	0.136	K.EANNFLWPFK.L
R4/RRR4-16/3	1670.461	1669.904	-266.077	0.408	1005.691	0.389	24	0.108	R.RVEPYVAYGYPNLK.S
R4/RRR4-15/3	1669.731	1669.904	-104.471	0.348	950.746	0.370	22	0.100	R.RVEPYVAYGYPNLK.S
R4/RRR4-6/2	1506.171	1506.598	-284.158	0.549	2575.361	0.612	24	0.440	R.TKNEAALEAATDSGK.Q
R4/RRR4-6/2	1506.160	1506.598	-291.314	0.547	2599.714	0.597	24	0.440	R.TKNEAALEAATDSGK.Q
R4/RRR4-6/2	1505.600	1506.598	-1330.620	0.467	2479.336	0.537	24	0.390	R.TKNEAALEAATDSGK.Q
R4/RRR4-6/2	1498.244	1497.679	-291.300	0.526	2102.148	0.593	22	0.340	R.SFASVSAAQFPWAK.M
R4/RRR4-6/2	1099.163	1099.306	-129.838	0.480	1393.493	0.435	14	0.203	R.DLVLQLLER.I
R4/RRR4-6/2	1098.677	1099.306	-1486.900	0.498	1366.690	0.397	14	0.193	R.DLVLQLLER.I
R4/RRR4-6/2	912.749	913.100	-384.863	0.391	826.324	0.398	12	0.156	R.GILLNGAVR.K
R4/RRR4-6/2	1099.199	1099.306	-97.643	0.407	835.486	0.338	12	0.151	R.DLVLQLLER.I
R4/RRR4-6/3	1507.850	1506.598	167.862	0.452	1124.151	0.404	25	0.121	R.TKNEAALEAATDSGK.Q
R4/RRR4-6/3	1506.257	1506.598	-226.601	0.469	947.569	0.384	24	0.105	R.TKNEAALEAATDSGK.Q
R4/RRR4-6/3	1506.000	1506.598	-1064.102	0.398	644.558	0.288	23	0.085	R.TKNEAALEAATDSGK.Q
R4/RRR4-21/2	1381.212	1381.475	-191.260	0.523	1539.911	0.514	21	0.236	R.WVGAAVDFSEGSR.A
R4/RRR4-21/3	1981.919	1982.204	-144.230	0.479	1928.614	0.405	29	0.235	K.YGAKPDAETLDM*LNTVAR.Q
R4/RRR4-21/2	1380.882	1381.475	-1157.050	0.481	1499.335	0.499	21	0.227	R.WVGAAVDFSEGSR.A
R4/RRR4-21/2	1382.016	1381.475	-333.428	0.541	1428.621	0.523	21	0.226	R.WVGAAVDFSEGSR.A
R4/RRR4-21/3	1981.588	1982.204	-817.980	0.430	1784.834	0.379	29	0.198	K.YGAKPDAETLDM*LNTVAR.Q
R4/RRR4-22/2	958.739	959.084	-360.272	0.454	742.619	0.332	13	0.153	R.WAADNLLR.A
R4/RRR4-21/2	958.832	959.084	-262.935	0.497	694.287	0.338	13	0.153	R.WAADNLLR.A
R4/RRR4-21/2	958.215	959.084	-1956.387	0.398	651.495	0.337	12	0.151	R.WAADNLLR.A
R4/RRR4-22/2	958.934	959.084	-156.422	0.444	673.130	0.301	13	0.149	R.WAADNLLR.A
R4/RRR4-22/2	958.417	959.084	-1744.679	0.375	535.042	0.326	11	0.147	R.WAADNLLR.A
R4/RRR4-21/2	958.522	959.084	-1633.996	0.405	725.995	0.256	13	0.145	R.WAADNLLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/3	1076.222	1076.314	-85.349	0.487	986.168	0.290	18	0.092	R.QKEVVVVFK.V
R4/RRR4-21/3	1981.548	1982.204	-838.665	0.385	790.589	0.299	24	0.083	-.YGAKPDAETLDM*LNTVAR.-
R4/RRR4-22/3	1982.049	1982.204	-78.433	0.439	732.625	0.249	23	0.080	K.YGAKPDAETLDM*LNTVAR.Q
R4/RRR4-21/3	1076.387	1076.314	68.224	0.377	770.231	0.172	18	0.078	R.QKEVVVVFK.V
R4/RRR4-15/2	1395.221	1394.579	-257.437	0.483	2417.534	0.566	20	0.387	R.SVQMEGLTWGASK.L
R4/RRR4-15/2	1879.537	1880.095	-831.706	0.558	1682.812	0.656	33	0.289	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-15/2	1880.489	1880.095	210.067	0.591	1403.148	0.687	32	0.260	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-14/2	1410.108	1410.578	-334.604	0.504	1670.593	0.462	20	0.237	R.SVQM*EGLTWGASK.L
R4/RRR4-14/2	1410.096	1410.578	-342.769	0.503	1800.994	0.394	20	0.235	R.SVQM*EGLTWGASK.L
R4/RRR4-14/2	1880.615	1880.095	-255.966	0.573	1182.149	0.667	30	0.229	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-14/2	1879.450	1880.095	-877.802	0.550	1131.631	0.685	29	0.227	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-15/2	1409.938	1410.578	-1166.381	0.481	1608.133	0.449	20	0.227	R.SVQM*EGLTWGASK.L
R4/RRR4-14/2	1880.477	1880.095	203.492	0.579	1081.064	0.677	28	0.220	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-14/2	1511.284	1511.659	-248.522	0.478	1445.370	0.498	21	0.220	K.TYVSGNAISKDDIK.V
R4/RRR4-15/2	1410.589	1410.578	7.755	0.490	1620.608	0.395	20	0.215	R.SVQM*EGLTWGASK.L
R4/RRR4-15/2	1879.552	1880.095	-823.491	0.541	1039.423	0.672	28	0.215	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-15/2	1510.486	1511.659	-1442.633	0.414	1347.438	0.507	21	0.210	K.TYVSGNAISKDDIK.V
R4/RRR4-15/2	1510.624	1511.659	-1350.752	0.462	1243.691	0.541	20	0.208	K.TYVSGNAISKDDIK.V
R4/RRR4-14/2	1511.216	1511.659	-294.228	0.474	1268.991	0.523	20	0.207	K.TYVSGNAISKDDIK.V
R4/RRR4-15/3	1880.214	1880.095	63.574	0.490	1242.887	0.612	37	0.201	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-14/2	1511.164	1511.659	-328.591	0.508	1156.216	0.532	20	0.200	K.TYVSGNAISKDDIK.V
R4/RRR4-15/2	1511.168	1511.659	-325.754	0.499	1043.138	0.527	19	0.189	K.TYVSGNAISKDDIK.V
R4/RRR4-15/2	1409.430	1410.578	-1528.700	0.359	1547.783	0.278	20	0.184	R.SVQM*EGLTWGASK.L
R4/RRR4-15/3	1880.099	1880.095	2.330	0.433	1111.544	0.561	34	0.166	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-14/3	1880.113	1880.095	9.363	0.427	991.074	0.591	33	0.162	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-15/2	1323.585	1324.467	-1425.538	0.357	995.739	0.273	16	0.148	R.WYDTVAAALASR.F
R4/RRR4-15/3	1880.911	1880.095	-98.274	0.419	939.864	0.556	33	0.146	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-15/2	1323.437	1324.467	-1538.010	0.317	870.572	0.204	16	0.137	R.WYDTVAAALASR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1324.142	1324.467	-245.643	0.299	708.095	0.169	15	0.130	-.WYDTVAAALASR.-
R4/RRR4-14/3	1879.897	1880.095	-105.817	0.363	827.635	0.457	32	0.114	K.AVGVNLPGGGAASSAAAAAPAAK.D
R4/RRR4-14/3	1879.833	1880.095	-139.722	0.258	640.509	0.204	28	0.081	-.AVGVNLPGGGAASSAAAAAPAAK.-
R4/RRR4-21/2	1965.659	1965.230	218.654	0.581	1813.343	0.575	24	0.283	R.IAECLVGDETGIIVFTAR.N
R4/RRR4-21/2	1964.521	1965.230	-872.759	0.526	1653.387	0.615	24	0.272	R.IAECLVGDETGIIVFTAR.N
R4/RRR4-21/2	1963.913	1965.230	-1183.124	0.515	1574.762	0.557	23	0.245	R.IAECLVGDETGIIVFTAR.N
R4/RRR4-21/2	1130.103	1129.377	-242.858	0.474	821.171	0.438	14	0.163	R.LAVDKWGIVK.A
R4/RRR4-21/2	1135.935	1136.237	-266.618	0.339	756.802	0.442	16	0.158	K.AAESPADFTVK.E
R4/RRR4-21/2	1135.801	1136.237	-384.687	0.250	651.165	0.256	15	0.138	K.AAESPADFTVK.E
R4/RRR4-21/2	1135.446	1136.237	-1581.302	0.187	640.829	0.210	15	0.134	K.AAESPADFTVK.E
R4/RRR4-21/3	1799.014	1799.070	-31.287	0.443	984.224	0.430	24	0.117	K.VDQLRPGTHGHNLLLK.V
R4/RRR4-21/3	1963.625	1965.230	-1841.433	0.313	1093.375	0.368	27	0.109	R.IAECLVGDETGIIVFTAR.N
R4/RRR4-21/3	1798.721	1799.070	-194.453	0.446	910.935	0.382	23	0.102	K.VDQLRPGTHGHNLLLK.V
R4/RRR4-21/3	1799.003	1799.070	-37.311	0.433	740.879	0.327	23	0.088	K.VDQLRPGTHGHNLLLK.V
R4/RRR4-21/3	1965.075	1965.230	-79.049	0.281	781.893	0.254	22	0.077	R.IAECLVGDETGIIVFTAR.N
R4/RRR4-24/2	1079.642	1080.176	-1425.681	0.491	1716.610	0.569	19	0.272	R.LAGSSAAAFER.C
R4/RRR4-24/2	1079.541	1080.176	-1519.609	0.501	1695.174	0.552	19	0.265	R.LAGSSAAAFER.C
R4/RRR4-25/2	1079.734	1080.176	-411.127	0.493	1621.511	0.555	19	0.256	R.LAGSSAAAFER.C
R4/RRR4-25/2	1079.935	1080.176	-224.096	0.502	1680.265	0.516	19	0.254	R.LAGSSAAAFER.C
R4/RRR4-24/2	1472.905	1473.569	-1133.306	0.386	1524.408	0.511	21	0.228	R.TSDAVSLAFGDAYR.N
R4/RRR4-24/2	1734.075	1734.963	-1092.110	0.487	1195.679	0.465	19	0.187	R.VGGPCGYGVCYLYLR.R
R4/RRR4-25/2	1734.971	1734.963	4.403	0.541	1159.885	0.467	19	0.184	R.VGGPCGYGVCYLYLR.R
R4/RRR4-24/2	1735.243	1734.963	161.466	0.529	1102.574	0.435	19	0.175	R.VGGPCGYGVCYLYLR.R
R4/RRR4-25/2	1733.547	1734.963	-1397.766	0.461	1027.581	0.447	18	0.172	R.VGGPCGYGVCYLYLR.R
R4/RRR4-25/2	1734.182	1734.963	-1030.054	0.487	1085.457	0.414	19	0.171	R.VGGPCGYGVCYLYLR.R
R4/RRR4-25/2	1199.172	1199.374	-169.039	0.408	862.876	0.346	14	0.156	R.TCWYTVQIK.T
R4/RRR4-24/2	1198.681	1199.374	-1416.986	0.333	873.740	0.288	14	0.149	R.TCWYTVQIK.T
R4/RRR4-24/2	1198.495	1199.374	-1572.691	0.300	785.592	0.290	13	0.145	R.TCWYTVQIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	1198.398	1199.374	-1654.041	0.291	910.754	0.224	14	0.143	R.TCWYTVQIK.T
R4/RRR4-25/2	1198.953	1199.374	-352.579	0.226	622.826	0.192	12	0.136	R.TCWYTVQIK.T
R4/RRR4-19/2	1214.744	1214.437	253.834	0.414	1822.292	0.446	18	0.251	R.GSDVIIVLVGNK.T
R4/RRR4-19/2	1466.222	1465.633	-281.128	0.459	1677.631	0.489	21	0.243	R.DSSVAVIVFDVASR.Q
R4/RRR4-18/2	1466.103	1465.633	321.218	0.469	1552.890	0.531	20	0.238	R.DSSVAVIVFDVASR.Q
R4/RRR4-19/2	1466.120	1465.633	332.989	0.513	1538.812	0.511	20	0.232	R.DSSVAVIVFDVASR.Q
R4/RRR4-18/2	1465.128	1465.633	-1030.266	0.339	1698.305	0.426	19	0.228	R.DSSVAVIVFDVASR.Q
R4/RRR4-18/2	1465.085	1465.633	-1059.713	0.363	1603.580	0.392	19	0.211	R.DSSVAVIVFDVASR.Q
R4/RRR4-19/2	1465.194	1465.633	-301.046	0.386	1499.145	0.410	20	0.205	R.DSSVAVIVFDVASR.Q
R4/RRR4-22/2	1465.317	1465.633	-216.211	0.362	1391.423	0.401	19	0.192	R.DSSVAVIVFDVASR.Q
R4/RRR4-18/2	1316.561	1317.432	-1425.425	0.343	1127.528	0.351	17	0.167	-.LQLWDTAGQER.-
R4/RRR4-17/2	1317.165	1317.432	-203.813	0.434	827.057	0.408	15	0.161	R.LQLWDTAGQER.F
R4/RRR4-18/2	1328.336	1327.529	-145.490	0.406	794.246	0.436	16	0.160	K.DLGVM*FIETSAK.A
R4/RRR4-17/2	1317.097	1317.432	-255.509	0.385	892.729	0.372	15	0.157	-.LQLWDTAGQER.-
R4/RRR4-19/2	1317.199	1317.432	-177.409	0.440	761.865	0.394	15	0.157	R.LQLWDTAGQER.F
R4/RRR4-17/2	1317.189	1317.432	-185.033	0.441	836.245	0.356	15	0.153	-.LQLWDTAGQER.-
R4/RRR4-18/2	1317.048	1317.432	-292.611	0.399	803.527	0.343	15	0.152	R.LQLWDTAGQER.F
R4/RRR4-18/2	1316.342	1317.432	-1592.899	0.278	885.417	0.296	15	0.148	R.LQLWDTAGQER.F
R4/RRR4-19/2	1317.297	1317.432	-103.133	0.384	873.587	0.286	15	0.148	R.LQLWDTAGQER.F
R4/RRR4-18/2	1316.446	1317.432	-1513.626	0.283	883.432	0.281	15	0.147	R.LQLWDTAGQER.F
R4/RRR4-18/2	1316.415	1317.432	-1537.379	0.306	694.283	0.315	14	0.146	R.LQLWDTAGQER.F
R4/RRR4-18/2	1316.367	1317.432	-1573.988	0.294	898.423	0.238	15	0.144	R.LQLWDTAGQER.F
R4/RRR4-18/2	1311.121	1311.530	-312.797	0.308	469.478	0.399	14	0.144	K.DLGVMFIETSAK.A
R4/RRR4-19/2	1317.179	1317.432	-192.749	0.342	584.455	0.309	13	0.143	-.LQLWDTAGQER.-
R4/RRR4-19/2	1316.918	1317.432	-1153.282	0.308	775.155	0.215	15	0.140	R.LQLWDTAGQER.F
R4/RRR4-19/2	1213.698	1214.437	-1436.880	0.201	840.621	0.251	16	0.136	R.GSDVIIVLVGNK.T
R4/RRR4-19/2	1317.418	1317.432	-10.651	0.360	847.418	0.174	15	0.135	-.LQLWDTAGQER.-
R4/RRR4-2/2	1797.524	1798.029	-839.751	0.497	1830.081	0.550	23	0.280	K.ATLSPALETALDYYLR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1797.671	1798.029	-199.735	0.509	1562.884	0.543	21	0.241	K.ATLSPALETALDYYLR.V
R4/RRR4-2/2	1261.931	1262.354	-335.856	0.348	1141.846	0.439	18	0.177	R.EPAAFSGAVGEAR.A
R4/RRR4-2/2	1450.537	1451.560	-1399.194	0.346	1012.168	0.315	16	0.151	K.EAFTEDELEVLR.D
R4/RRR4-2/2	1109.013	1109.218	-185.100	0.348	765.985	0.369	16	0.150	K.NAVTSVAFSGR.A
R4/RRR4-2/2	1261.998	1262.354	-282.673	0.314	671.482	0.432	14	0.148	R.EPAAFSGAVGEAR.A
R4/RRR4-2/2	1480.324	1479.662	-228.824	0.316	783.761	0.346	16	0.146	K.NIITSSFQAPSWK.V
R4/RRR4-2/2	1479.220	1479.662	-299.599	0.292	660.474	0.251	15	0.135	K.NIITSSFQAPSWK.V
R4/RRR4-14/3	1770.345	1770.922	-893.801	0.588	2090.014	0.564	32	0.339	K.KGENDLPGLTDTEKPR.M
R4/RRR4-14/3	1770.764	1770.922	-89.867	0.566	2069.267	0.527	31	0.315	K.KGENDLPGLTDTEKPR.M
R4/RRR4-14/3	1770.716	1770.922	-116.732	0.601	1706.109	0.572	30	0.260	K.KGENDLPGLTDTEKPR.M
R4/RRR4-13/3	1770.649	1770.922	-155.010	0.559	1698.486	0.518	29	0.235	K.KGENDLPGLTDTEKPR.M
R4/RRR4-13/3	1769.915	1770.922	-1137.761	0.506	1667.945	0.462	30	0.206	K.KGENDLPGLTDTEKPR.M
R4/RRR4-13/3	1770.455	1770.922	-264.777	0.548	1329.140	0.503	27	0.172	K.KGENDLPGLTDTEKPR.M
R4/RRR4-17/2	1471.218	1471.598	-258.869	0.508	1546.600	0.627	27	0.264	K.KPVASDEGGAGAAGGVK.E
R4/RRR4-17/2	1274.472	1275.352	-1479.512	0.403	1490.265	0.438	18	0.211	K.AQIWDTAGQER.F
R4/RRR4-17/2	1275.036	1275.352	-248.766	0.514	1344.129	0.487	17	0.209	K.AQIWDTAGQER.F
R4/RRR4-16/2	1274.939	1275.352	-325.515	0.491	1347.971	0.474	17	0.206	K.AQIWDTAGQER.F
R4/RRR4-16/2	1081.924	1081.204	-259.897	0.461	1335.444	0.462	17	0.204	K.STIGVEFATR.S
R4/RRR4-16/2	1275.073	1275.352	-220.144	0.495	1281.071	0.479	17	0.202	K.AQIWDTAGQER.F
R4/RRR4-17/2	1274.505	1275.352	-1454.113	0.389	1352.709	0.421	17	0.195	K.AQIWDTAGQER.F
R4/RRR4-17/2	1080.344	1081.204	-1727.348	0.393	1171.027	0.488	16	0.192	K.STIGVEFATR.S
R4/RRR4-17/2	1080.544	1081.204	-1540.632	0.429	1124.024	0.495	16	0.191	K.STIGVEFATR.S
R4/RRR4-16/2	1274.814	1275.352	-1210.292	0.408	1305.705	0.414	17	0.190	K.AQIWDTAGQER.F
R4/RRR4-18/2	1275.054	1275.352	-235.031	0.419	1258.284	0.431	17	0.190	K.AQIWDTAGQER.F
R4/RRR4-17/2	1080.604	1081.204	-1485.255	0.402	1183.374	0.452	16	0.187	K.STIGVEFATR.S
R4/RRR4-17/3	1471.518	1471.598	-54.600	0.486	1584.603	0.415	32	0.177	K.KPVASDEGGAGAAGGVK.E
R4/RRR4-17/3	1472.411	1471.598	-127.451	0.518	1436.301	0.449	33	0.167	K.KPVASDEGGAGAAGGVK.E
R4/RRR4-18/2	1058.440	1058.254	177.146	0.367	949.303	0.437	16	0.166	K.IVLIGDSGVGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1081.239	1081.204	32.656	0.372	969.364	0.399	15	0.165	K.STIGVEFATR.S
R4/RRR4-17/3	1471.627	1471.598	20.032	0.482	1277.221	0.386	31	0.130	K.KPVASDEGGAGAAGGVK.E
R4/RRR4-12/2	1859.648	1859.933	-153.773	0.540	1753.213	0.583	21	0.276	R.DAGVNFFDNAEVYANGR.A
R4/RRR4-12/2	1858.629	1859.933	-1243.556	0.438	1641.677	0.513	21	0.241	R.DAGVNFFDNAEVYANGR.A
R4/RRR4-12/2	1218.951	1219.330	-312.342	0.382	1029.525	0.287	16	0.152	K.LFWGGQGPNDK.G
R4/RRR4-12/2	1047.258	1047.188	67.504	0.374	1154.227	0.249	12	0.151	R.SLVDDTLRK.V
R4/RRR4-12/2	918.420	919.015	-1741.738	0.299	621.128	0.422	13	0.151	R.SLVDDTLR.K
R4/RRR4-12/2	1046.897	1047.188	-278.534	0.360	825.887	0.335	12	0.149	R.SLVDDTLRK.V
R4/RRR4-12/2	919.085	919.015	77.250	0.264	585.962	0.352	13	0.144	R.SLVDDTLR.K
R4/RRR4-12/2	1219.226	1219.330	-86.022	0.379	873.422	0.236	16	0.142	K.LFWGGQGPNDK.G
R4/RRR4-12/2	1219.173	1219.330	-129.611	0.366	812.522	0.197	15	0.136	K.LFWGGQGPNDK.G
R4/RRR4-18/2	1312.696	1313.502	-1379.846	0.434	1637.642	0.491	19	0.240	K.FM*EVISGTGDIK.A
R4/RRR4-18/2	1313.041	1313.502	-352.000	0.471	1738.131	0.432	19	0.238	K.FM*EVISGTGDIK.A
R4/RRR4-18/2	1312.947	1313.502	-1187.760	0.462	1588.412	0.422	19	0.219	K.FM*EVISGTGDIK.A
R4/RRR4-18/2	1673.525	1673.805	-168.095	0.469	1292.601	0.493	23	0.204	K.ENHDFLASVGLDDLK.A
R4/RRR4-18/2	1296.384	1297.503	-1639.144	0.338	1312.166	0.447	18	0.193	K.FMEVISGTGDIK.A
R4/RRR4-18/2	1673.231	1673.805	-943.473	0.470	1133.673	0.469	23	0.187	K.ENHDFLASVGLDDLK.A
R4/RRR4-18/2	1673.311	1673.805	-296.091	0.490	1044.001	0.483	22	0.183	K.ENHDFLASVGLDDLK.A
R4/RRR4-18/2	1257.548	1257.484	51.746	0.440	723.648	0.464	14	0.162	R.AM*DFLVELFR.N
R4/RRR4-18/2	1552.209	1552.708	-322.505	0.377	932.464	0.419	17	0.161	K.GSSSCTNGLLWLTR.A
R4/RRR4-18/2	1297.015	1297.503	-377.369	0.282	794.370	0.363	16	0.149	K.FMEVISGTGDIK.A
R4/RRR4-18/2	1552.445	1552.708	-170.006	0.316	826.868	0.342	16	0.145	K.GSSSCTNGLLWLTR.A
R4/RRR4-17/2	1675.463	1673.805	-204.804	0.375	275.919	0.312	14	0.140	K.ENHDFLASVGLDDLK.A
R4/RRR4-17/2	1673.766	1673.805	-23.453	0.307	361.072	0.320	14	0.139	K.ENHDFLASVGLDDLK.A
R4/RRR4-7/2	1471.284	1471.678	-268.510	0.381	3060.539	0.357	21	0.453	K.ESIVDVEGVVSLPK.E
R4/RRR4-6/2	1531.486	1531.652	-108.456	0.562	2374.675	0.497	25	0.356	R.VWTEVGGLDEAAAGR.S
R4/RRR4-6/2	1531.106	1531.652	-1012.499	0.533	2221.167	0.491	25	0.327	R.VWTEVGGLDEAAAGR.S
R4/RRR4-6/2	1531.240	1531.652	-269.671	0.560	2094.445	0.502	25	0.309	R.VWTEVGGLDEAAAGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1531.127	1531.652	-998.651	0.472	1844.945	0.499	25	0.270	R.VWTEVGGLDEAAAGR.S
R4/RRR4-7/2	1049.968	1050.235	-254.514	0.385	956.469	0.348	13	0.158	R.VFEVGPVFR.A
R4/RRR4-6/2	1018.022	1018.151	-127.679	0.411	599.322	0.409	13	0.156	R.TPANQAIFR.I
R4/RRR4-7/2	1018.032	1018.151	-117.094	0.467	669.493	0.371	13	0.153	R.TPANQAIFR.I
R4/RRR4-7/2	1017.837	1018.151	-309.943	0.444	624.482	0.365	13	0.152	R.TPANQAIFR.I
R4/RRR4-7/2	1017.547	1018.151	-1581.508	0.372	614.142	0.363	13	0.151	R.TPANQAIFR.I
R4/RRR4-8/2	1049.962	1050.235	-260.695	0.446	798.919	0.301	13	0.148	R.VFEVGPVFR.A
R4/RRR4-6/2	1050.047	1050.235	-179.753	0.236	384.587	0.363	12	0.143	R.VFEVGPVFR.A
R4/RRR4-6/2	1049.966	1050.235	-256.730	0.201	265.806	0.385	12	0.137	-.VFEVGPVFR.-
R4/RRR4-7/2	1049.947	1050.235	-274.693	0.235	458.472	0.256	10	0.131	-.VFEVGPVFR.-
R4/RRR4-5/2	1018.014	1018.151	-135.257	0.340	707.673	0.128	13	0.130	-.TPANQAIFR.-
R4/RRR4-16/2	1318.127	1318.542	-315.779	0.460	1109.777	0.533	16	0.196	K.FAFILYDTLSK.S
R4/RRR4-16/2	1318.055	1318.542	-370.602	0.444	922.720	0.476	16	0.174	K.FAFILYDTLSK.S
R4/RRR4-16/2	1023.426	1024.199	-1737.398	0.463	576.447	0.561	15	0.173	R.GPLPASQVVR.D
R4/RRR4-16/2	1023.857	1024.199	-334.668	0.437	525.372	0.573	15	0.171	R.GPLPASQVVR.D
R4/RRR4-16/2	1023.528	1024.199	-1637.580	0.389	400.118	0.557	13	0.161	R.GPLPASQVVR.D
R4/RRR4-16/3	1295.144	1295.473	-255.076	0.445	1319.073	0.441	23	0.150	R.DRGPLPASQVVR.D
R4/RRR4-16/2	1190.942	1191.234	-245.976	0.481	890.722	0.509	16	0.109	R.VGSAADWSNHF.-
R4/RRR4-16/3	1295.176	1295.473	-229.972	0.373	892.256	0.397	23	0.102	R.DRGPLPASQVVR.D
R4/RRR4-16/2	1190.902	1191.234	-279.500	0.509	810.802	0.491	16	0.101	R.VGSAADWSNHF.-
R4/RRR4-5/2	1624.406	1623.811	-250.032	0.387	931.065	0.452	17	0.163	K.ANGTLTIQDSGIGM*TK.A
R4/RRR4-5/2	1292.010	1292.375	-283.119	0.409	948.847	0.350	17	0.157	R.EIISNSSDALDK.I
R4/RRR4-5/2	1624.368	1623.811	-273.253	0.390	824.062	0.439	17	0.156	K.ANGTLTIQDSGIGM*TK.A
R4/RRR4-5/2	1624.361	1623.811	-277.927	0.388	668.622	0.469	16	0.153	K.ANGTLTIQDSGIGM*TK.A
R4/RRR4-5/2	1291.910	1292.375	-360.569	0.356	799.261	0.363	16	0.152	R.EIISNSSDALDK.I
R4/RRR4-5/2	1292.068	1292.375	-238.285	0.411	712.422	0.367	15	0.150	R.EIISNSSDALDK.I
R4/RRR4-5/2	1561.180	1561.719	-988.917	0.461	861.393	0.315	20	0.150	R.EIISNSSDALDKIR.Y
R4/RRR4-5/2	1561.356	1561.719	-233.416	0.456	750.732	0.329	20	0.149	R.EIISNSSDALDKIR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1561.408	1561.719	-199.769	0.437	849.856	0.296	21	0.148	R.EIISNSSDALDKIR.Y
R4/RRR4-4/2	1562.345	1561.719	-240.400	0.499	703.685	0.317	20	0.146	R.EIISNSSDALDKIR.Y
R4/RRR4-4/2	1291.972	1292.375	-312.410	0.339	827.760	0.298	16	0.146	R.EIISNSSDALDK.I
R4/RRR4-5/2	1561.271	1561.719	-288.010	0.443	866.263	0.266	21	0.145	R.EIISNSSDALDKIR.Y
R4/RRR4-4/2	1291.380	1292.375	-1549.548	0.326	562.733	0.321	14	0.142	R.EIISNSSDALDK.I
R4/RRR4-26/2	1351.105	1350.542	-324.292	0.444	1234.206	0.618	19	0.222	K.ETVASAPVVVYSK.S
R4/RRR4-26/2	1350.028	1350.542	-1125.088	0.351	1376.967	0.527	19	0.214	K.ETVASAPVVVYSK.S
R4/RRR4-26/2	1154.216	1154.340	-107.840	0.499	951.029	0.421	15	0.169	K.LFEQLGATFK.A
R4/RRR4-25/2	1542.589	1541.814	-146.646	0.456	719.777	0.500	19	0.164	K.LVPLLTEAGAIASSAK.T
R4/RRR4-26/2	1154.228	1154.340	-97.231	0.425	733.679	0.407	14	0.156	K.LFEQLGATFK.A
R4/RRR4-26/2	1349.507	1350.542	-1512.472	0.285	776.888	0.455	15	0.154	-.ETVASAPVVVYSK.-
R4/RRR4-25/2	1541.583	1541.814	-150.713	0.357	762.780	0.372	19	0.150	K.LVPLLTEAGAIASSAK.T
R4/RRR4-26/2	1542.101	1541.814	186.294	0.371	819.787	0.331	20	0.148	K.LVPLLTEAGAIASSAK.T
R4/RRR4-25/2	1541.351	1541.814	-301.185	0.331	623.519	0.401	18	0.148	K.LVPLLTEAGAIASSAK.T
R4/RRR4-26/2	1541.357	1541.814	-297.450	0.331	651.088	0.391	18	0.147	K.LVPLLTEAGAIASSAK.T
R4/RRR4-26/2	1541.186	1541.814	-1059.819	0.216	491.835	0.281	18	0.137	K.LVPLLTEAGAIASSAK.T
R4/RRR4-26/3	1742.277	1742.862	-912.451	0.439	1100.275	0.264	25	0.089	K.HIGGCDDTLVLNNEGK.L
R4/RRR4-17/2	1773.488	1772.978	-277.295	0.544	1599.448	0.577	25	0.257	R.NQDVSLTELPATVSAVK.N
R4/RRR4-17/2	1772.341	1772.978	-926.291	0.532	1493.019	0.566	24	0.240	R.NQDVSLTELPATVSAVK.N
R4/RRR4-17/2	1772.301	1772.978	-948.971	0.521	1337.463	0.554	23	0.220	R.NQDVSLTELPATVSAVK.N
R4/RRR4-17/2	1339.317	1338.407	-67.065	0.477	728.486	0.515	15	0.173	K.IVYDEYNHER.Y
R4/RRR4-17/2	1337.995	1338.407	-308.894	0.421	834.474	0.408	15	0.161	K.IVYDEYNHER.Y
R4/RRR4-17/2	1337.405	1338.407	-1501.532	0.401	627.708	0.366	13	0.149	K.IVYDEYNHER.Y
R4/RRR4-15/2	1950.594	1951.208	-830.345	0.566	2083.282	0.594	29	0.335	K.TAFIPFITAGDPDLATTAK.A
R4/RRR4-15/2	1952.308	1951.208	51.011	0.595	1931.431	0.617	28	0.317	K.TAFIPFITAGDPDLATTAK.A
R4/RRR4-15/2	1950.497	1951.208	-880.353	0.537	1983.944	0.531	28	0.298	K.TAFIPFITAGDPDLATTAK.A
R4/RRR4-16/2	1951.573	1951.208	187.233	0.529	1844.785	0.519	28	0.274	K.TAFIPFITAGDPDLATTAK.A
R4/RRR4-15/3	1921.719	1922.086	-191.309	0.477	1478.272	0.560	34	0.216	R.AEAAAVGEDERVISGTFAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1329.202	1329.438	-178.294	0.398	992.580	0.431	21	0.171	R.QLGEAASPEEGLK.R
R4/RRR4-15/2	1044.014	1044.227	-204.247	0.451	797.762	0.382	14	0.157	K.VQSLLQDIK.Q
R4/RRR4-15/3	1921.087	1922.086	-1043.577	0.374	1180.791	0.481	30	0.147	R.AEAAAVGEDERVISGTFAK.L
R4/RRR4-15/2	1328.565	1329.438	-1414.205	0.277	631.062	0.340	18	0.143	R.QLGEAASPEEGLK.R
R4/RRR4-15/2	1328.632	1329.438	-1363.727	0.279	571.406	0.290	16	0.138	-.QLGEAASPEEGLK.-
R4/RRR4-15/3	1921.526	1922.086	-814.144	0.363	636.802	0.486	25	0.107	R.AEAAAVGEDERVISGTFAK.L
R4/RRR4-25/2	1366.148	1366.552	-296.344	0.438	1516.128	0.342	18	0.194	K.LQAFWNHPAGPK.T
R4/RRR4-25/2	954.821	955.154	-349.535	0.404	1014.186	0.506	13	0.185	R.YSM*VITPK.N
R4/RRR4-25/2	954.765	955.154	-408.032	0.415	957.161	0.499	13	0.181	R.YSM*VITPK.N
R4/RRR4-25/2	954.320	955.154	-1927.517	0.351	951.286	0.464	13	0.172	R.YSM*VITPK.N
R4/RRR4-25/2	1367.158	1366.552	-288.692	0.349	961.021	0.438	16	0.166	K.LQAFWNHPAGPK.T
R4/RRR4-25/2	1366.134	1366.552	-306.205	0.380	1055.127	0.306	16	0.155	K.LQAFWNHPAGPK.T
R4/RRR4-25/2	1365.434	1366.552	-1555.087	0.317	782.153	0.204	15	0.136	K.LQAFWNHPAGPK.T
R4/RRR4-25/2	1690.157	1689.715	262.409	0.455	989.332	0.561	21	0.131	K.DYFSDQKDDVASLEG.-
R4/RRR4-25/3	1844.360	1844.103	139.824	0.367	759.421	0.459	25	0.109	K.WGISIANVADFAKPPEK.I
R4/RRR4-25/3	1843.758	1844.103	-187.445	0.394	852.491	0.403	26	0.104	K.WGISIANVADFAKPPEK.I
R4/RRR4-25/3	1844.160	1844.103	30.891	0.431	770.696	0.415	25	0.103	K.WGISIANVADFAKPPEK.I
R4/RRR4-25/2	1688.995	1689.715	-1021.149	0.325	495.796	0.440	16	0.098	K.DYFSDQKDDVASLEG.-
R4/RRR4-25/2	1688.490	1689.715	-1321.583	0.218	640.633	0.314	18	0.081	K.DYFSDQKDDVASLEG.-
R4/RRR4-25/3	1843.578	1844.103	-829.639	0.267	657.251	0.254	23	0.081	-.WGISIANVADFAKPPEK.-
R4/RRR4-25/2	1618.155	1618.637	-298.693	0.355	945.978	0.466	20	0.109	K.DYFSDEKDAAASLEG.-
R4/RRR4-25/2	1618.042	1618.637	-988.366	0.306	891.641	0.416	20	0.097	K.DYFSDEKDAAASLEG.-
R4/RRR4-25/2	1618.038	1618.637	-991.396	0.317	812.999	0.443	19	0.097	K.DYFSDEKDAAASLEG.-
R4/RRR4-11/2	1614.402	1614.744	-212.323	0.516	1551.390	0.362	20	0.198	K.TWQGRPENVEAAQK.A
R4/RRR4-12/2	1614.419	1614.744	-201.779	0.513	1392.480	0.411	19	0.194	K.TWQGRPENVEAAQK.A
R4/RRR4-11/2	1614.286	1614.744	-284.771	0.507	1315.989	0.414	19	0.188	K.TWQGRPENVEAAQK.A
R4/RRR4-12/2	1614.233	1614.744	-938.970	0.464	1296.166	0.375	19	0.180	K.TWQGRPENVEAAQK.A
R4/RRR4-11/2	1614.321	1614.744	-263.149	0.478	1261.383	0.375	18	0.176	K.TWQGRPENVEAAQK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1615.234	1614.744	304.144	0.517	1141.092	0.378	18	0.167	K.TWQGRPENVEAAQK.A
R4/RRR4-11/2	929.843	930.044	-217.014	0.437	649.912	0.410	14	0.159	K.ANSLAQLGR.Y
R4/RRR4-11/2	929.907	930.044	-147.480	0.437	746.203	0.369	15	0.157	K.ANSLAQLGR.Y
R4/RRR4-12/2	929.872	930.044	-186.065	0.464	769.688	0.359	15	0.157	K.ANSLAQLGR.Y
R4/RRR4-11/2	1500.292	1499.771	-320.281	0.322	685.011	0.458	21	0.157	R.TVVSIPCGPSALAVK.E
R4/RRR4-11/2	929.410	930.044	-1763.561	0.431	586.329	0.332	14	0.151	K.ANSLAQLGR.Y
R4/RRR4-12/2	929.418	930.044	-1754.984	0.431	547.434	0.330	14	0.150	K.ANSLAQLGR.Y
R4/RRR4-12/2	929.286	930.044	-1897.394	0.396	690.032	0.312	15	0.150	K.ANSLAQLGR.Y
R4/RRR4-12/2	1500.455	1499.771	-211.393	0.342	692.180	0.362	21	0.150	R.TVVSIPCGPSALAVK.E
R4/RRR4-11/2	1499.532	1499.771	-160.084	0.274	681.585	0.302	20	0.142	R.TVVSIPCGPSALAVK.E
R4/RRR4-11/3	1129.213	1129.295	-73.103	0.468	1575.113	0.306	22	0.139	R.AKANSLAQLGR.Y
R4/RRR4-11/2	1499.285	1499.771	-324.906	0.221	608.376	0.278	20	0.138	R.TVVSIPCGPSALAVK.E
R4/RRR4-12/2	1499.238	1499.771	-1025.609	0.218	492.751	0.301	18	0.138	R.TVVSIPCGPSALAVK.E
R4/RRR4-11/3	1129.393	1129.295	86.920	0.472	1539.204	0.214	22	0.110	R.AKANSLAQLGR.Y
R4/RRR4-10/3	1505.858	1504.756	67.955	0.607	3358.503	0.493	32	0.681	K.KVSPQLIAEYTVR.A
R4/RRR4-11/3	1506.089	1504.756	221.591	0.611	2820.073	0.464	30	0.471	K.KVSPQLIAEYTVR.A
R4/RRR4-10/3	1504.445	1504.756	-206.975	0.576	2783.963	0.435	30	0.442	K.KVSPQLIAEYTVR.A
R4/RRR4-10/3	1504.503	1504.756	-168.515	0.593	2629.639	0.456	30	0.409	K.KVSPQLIAEYTVR.A
R4/RRR4-11/3	1504.631	1504.756	-83.059	0.577	2585.624	0.439	28	0.391	K.KVSPQLIAEYTVR.A
R4/RRR4-11/3	1504.594	1504.756	-107.840	0.563	2557.744	0.422	29	0.371	K.KVSPQLIAEYTVR.A
R4/RRR4-10/2	1504.414	1504.756	-228.009	0.485	1809.616	0.496	21	0.264	K.KVSPQLIAEYTVR.A
R4/RRR4-11/2	1504.247	1504.756	-1006.323	0.485	1608.800	0.505	20	0.240	K.KVSPQLIAEYTVR.A
R4/RRR4-10/2	1504.325	1504.756	-287.599	0.476	1693.682	0.461	21	0.240	K.KVSPQLIAEYTVR.A
R4/RRR4-10/2	1505.212	1504.756	303.680	0.569	1610.425	0.498	20	0.239	K.KVSPQLIAEYTVR.A
R4/RRR4-1/2	1505.935	1504.756	119.465	0.439	1292.764	0.438	18	0.192	K.KVSPQLIAEYTVR.A
R4/RRR4-11/2	1377.151	1376.583	-314.514	0.451	813.282	0.518	17	0.175	K.VSPQLIAEYTVR.A
R4/RRR4-10/2	1377.344	1376.583	-174.018	0.519	589.513	0.522	17	0.169	K.VSPQLIAEYTVR.A
R4/RRR4-11/2	1377.301	1376.583	-205.582	0.496	601.751	0.499	17	0.166	K.VSPQLIAEYTVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1376.255	1376.583	-238.743	0.448	567.723	0.515	17	0.166	K.VSPQLIAEYTVR.A
R4/RRR4-11/2	1376.118	1376.583	-338.772	0.422	714.470	0.475	18	0.166	K.VSPQLIAEYTVR.A
R4/RRR4-10/2	1295.698	1296.501	-1395.554	0.401	751.130	0.457	18	0.165	K.KPWALSFSFGR.A
R4/RRR4-10/3	1296.205	1296.501	-228.892	0.548	1463.078	0.428	24	0.164	K.KPWALSFSFGR.A
R4/RRR4-10/2	1296.144	1296.501	-276.076	0.380	691.766	0.442	18	0.160	K.KPWALSFSFGR.A
R4/RRR4-10/3	1296.497	1296.501	-3.397	0.525	1441.611	0.417	25	0.156	K.KPWALSFSFGR.A
R4/RRR4-1/2	1377.293	1376.583	-211.006	0.358	372.387	0.435	14	0.150	K.VSPQLIAEYTVR.A
R4/RRR4-10/2	1375.584	1376.583	-1457.543	0.268	633.959	0.407	18	0.150	K.VSPQLIAEYTVR.A
R4/RRR4-10/2	1296.061	1296.501	-340.710	0.241	476.449	0.412	15	0.143	K.KPWALSFSFGR.A
R4/RRR4-9/3	1505.527	1504.756	-152.339	0.438	1319.231	0.411	30	0.137	K.KVSPQLIAEYTVR.A
R4/RRR4-1/3	1504.664	1504.756	-61.209	0.386	1172.049	0.342	25	0.111	K.KVSPQLIAEYTVR.A
R4/RRR4-1/3	1505.140	1504.756	255.692	0.403	1090.192	0.258	24	0.092	K.KVSPQLIAEYTVR.A
R4/RRR4-10/2	1424.209	1424.542	-234.144	0.490	2060.598	0.518	18	0.309	K.YAFEYAYLNNR.K
R4/RRR4-10/2	1425.053	1424.542	-343.721	0.474	1791.374	0.545	17	0.275	K.YAFEYAYLNNR.K
R4/RRR4-10/2	1281.272	1281.433	-126.100	0.567	1383.554	0.583	18	0.237	K.LADGLFLESCR.E
R4/RRR4-10/2	1280.954	1281.433	-375.792	0.512	1283.315	0.553	18	0.219	K.LADGLFLESCR.E
R4/RRR4-10/2	1280.525	1281.433	-1494.701	0.349	1157.183	0.539	16	0.195	K.LADGLFLESCR.E
R4/RRR4-10/2	1806.230	1807.127	-1053.566	0.356	653.518	0.403	21	0.145	R.AVTLIPGDGIGPLVTGAVR.Q
R4/RRR4-10/3	1859.796	1860.105	-167.099	0.425	706.801	0.478	24	0.110	R.HLQFPSFADRLETAVK.R
R4/RRR4-10/3	1861.059	1860.105	-24.915	0.366	725.941	0.425	24	0.101	R.HLQFPSFADRLETAVK.R
R4/RRR4-10/3	1860.194	1860.105	47.474	0.416	447.748	0.459	21	0.099	R.HLQFPSFADRLETAVK.R
R4/RRR4-16/1	1015.564	1016.174	-1589.585	0.270	824.179	0.483	15	0.659	K.LVLVGDGGTGK.T
R4/RRR4-16/1	1015.601	1016.174	-1553.240	0.329	727.683	0.382	15	0.559	K.LVLVGDGGTGK.T
R4/RRR4-16/1	1015.547	1016.174	-1606.008	0.265	536.661	0.497	14	0.547	K.LVLVGDGGTGK.T
R4/RRR4-17/2	1537.156	1537.655	-325.743	0.519	1499.189	0.400	20	0.204	K.IQFDVWDTAGQEK.F
R4/RRR4-16/2	1516.243	1516.752	-998.199	0.526	1247.033	0.439	20	0.191	R.VCENIPIVLCGNK.V
R4/RRR4-16/2	1516.019	1516.752	-1146.626	0.478	1158.438	0.399	21	0.178	R.VCENIPIVLCGNK.V
R4/RRR4-16/2	1516.286	1516.752	-308.344	0.537	969.272	0.448	20	0.174	R.VCENIPIVLCGNK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1215.281	1215.337	-45.902	0.372	974.458	0.342	15	0.156	K.NLQYYDISAK.S
R4/RRR4-17/2	1016.848	1016.174	-320.900	0.351	888.084	0.351	16	0.155	K.LVLVGDGGTGK.T
R4/RRR4-16/2	1015.868	1016.174	-301.323	0.334	908.554	0.247	17	0.146	K.LVLVGDGGTGK.T
R4/RRR4-18/2	1015.665	1016.174	-1490.109	0.294	751.208	0.271	15	0.143	K.LVLVGDGGTGK.T
R4/RRR4-17/2	1016.147	1016.174	-26.642	0.347	576.810	0.265	14	0.141	K.LVLVGDGGTGK.T
R4/RRR4-17/2	1017.039	1016.174	-132.437	0.385	850.215	0.211	17	0.141	K.LVLVGDGGTGK.T
R4/RRR4-16/2	1015.922	1016.174	-248.159	0.336	652.226	0.233	14	0.139	K.LVLVGDGGTGK.T
R4/RRR4-17/2	1015.977	1016.174	-193.916	0.357	696.506	0.221	14	0.138	K.LVLVGDGGTGK.T
R4/RRR4-14/2	1913.652	1912.269	200.732	0.518	1700.175	0.559	23	0.261	R.AFGMIAGGSGITPMFQVAR.A
R4/RRR4-13/2	1914.075	1912.269	-101.554	0.483	1252.804	0.549	23	0.207	R.AFGMIAGGSGITPMFQVAR.A
R4/RRR4-13/2	1228.123	1228.377	-207.524	0.427	941.232	0.399	15	0.163	R.AILENPNDITK.V
R4/RRR4-13/2	1227.633	1228.377	-1424.558	0.435	995.777	0.319	15	0.154	R.AILENPNDITK.V
R4/RRR4-14/2	1227.209	1228.377	-1772.245	0.311	678.150	0.373	16	0.149	R.AILENPNDITK.V
R4/RRR4-13/2	1227.515	1228.377	-1521.447	0.309	928.054	0.226	15	0.141	R.AILENPNDITK.V
R4/RRR4-14/3	1544.526	1544.780	-164.783	0.457	1584.220	0.226	26	0.118	K.AHLPAPAEDIQILR.C
R4/RRR4-13/3	1436.745	1436.615	90.111	0.426	947.387	0.405	24	0.108	K.AM*AAHLDELGYTK.E
R4/RRR4-13/3	1544.087	1544.780	-1099.505	0.410	1376.064	0.207	26	0.096	K.AHLPAPAEDIQILR.C
R4/RRR4-13/3	1436.208	1436.615	-284.401	0.328	641.308	0.244	22	0.080	K.AM*AAHLDELGYTK.E
R4/RRR4-10/2	1113.600	1114.314	-1543.277	0.386	1321.358	0.391	16	0.187	K.APLLIGCDVR.S
R4/RRR4-10/2	1114.159	1114.314	-139.080	0.372	1228.922	0.353	16	0.173	K.APLLIGCDVR.S
R4/RRR4-10/2	1286.762	1287.445	-1311.713	0.452	804.230	0.515	15	0.172	K.TFASWGVDYLK.Y
R4/RRR4-10/2	1113.543	1114.314	-1594.814	0.418	1022.069	0.419	14	0.170	K.APLLIGCDVR.S
R4/RRR4-10/2	1160.149	1160.349	-172.825	0.390	998.096	0.353	15	0.160	R.SHFSIWALAK.A
R4/RRR4-10/2	1159.952	1160.349	-343.429	0.393	861.924	0.391	15	0.160	R.SHFSIWALAK.A
R4/RRR4-10/2	1159.422	1160.349	-1666.981	0.351	498.631	0.393	13	0.148	R.SHFSIWALAK.A
R4/RRR4-10/2	1287.056	1287.445	-302.569	0.270	443.252	0.388	11	0.139	K.TFASWGVDYLK.Y
R4/RRR4-10/3	1501.322	1501.601	-186.392	0.379	1000.159	0.356	26	0.101	-.M*PGSLDHEEQDVK.T
R4/RRR4-10/3	1500.661	1501.601	-1297.015	0.385	629.467	0.317	21	0.087	-.M*PGSLDHEEQDVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/3	1501.213	1501.601	-259.319	0.309	857.459	0.271	21	0.083	-.M*PGSLDHEEQDVK.T
R4/RRR4-12/2	1499.344	1499.693	-233.353	0.512	1336.815	0.468	20	0.204	R.SIGISNYDIFLTR.D
R4/RRR4-12/2	1499.236	1499.693	-305.725	0.526	1137.046	0.471	19	0.187	R.SIGISNYDIFLTR.D
R4/RRR4-12/2	1500.333	1499.693	-240.298	0.572	1022.045	0.470	18	0.178	R.SIGISNYDIFLTR.D
R4/RRR4-12/2	898.039	898.085	-51.278	0.572	1088.542	0.368	13	0.169	K.TPAQLVLR.W
R4/RRR4-12/2	898.012	898.085	-81.138	0.507	1180.793	0.331	13	0.168	K.TPAQLVLR.W
R4/RRR4-12/2	897.546	898.085	-1719.358	0.513	1206.255	0.316	13	0.167	K.TPAQLVLR.W
R4/RRR4-12/2	1123.060	1123.284	-199.792	0.425	840.855	0.399	14	0.161	K.REDLFITTK.L
R4/RRR4-12/2	1122.288	1123.284	-1783.777	0.361	551.121	0.330	11	0.143	K.REDLFITTK.L
R4/RRR4-13/2	898.140	898.085	61.194	0.398	670.379	0.232	12	0.141	K.TPAQLVLR.W
R4/RRR4-12/3	1652.733	1652.786	-31.797	0.460	658.660	0.495	26	0.112	K.LWNSDHGHVVEACK.D
R4/RRR4-12/3	1652.633	1652.786	-92.809	0.342	372.752	0.449	21	0.095	K.LWNSDHGHVVEACK.D
R4/RRR4-14/2	1455.369	1454.561	-132.047	0.611	1626.218	0.629	21	0.277	R.DLVGVAYTEEETK.A
R4/RRR4-13/2	1454.315	1454.561	-169.691	0.552	1666.165	0.580	21	0.268	R.DLVGVAYTEEETK.A
R4/RRR4-13/2	1454.069	1454.561	-339.472	0.509	1643.834	0.567	21	0.261	R.DLVGVAYTEEETK.A
R4/RRR4-14/2	1454.002	1454.561	-1075.622	0.498	1645.318	0.561	21	0.260	R.DLVGVAYTEEETK.A
R4/RRR4-13/2	1453.591	1454.561	-1359.108	0.421	1758.916	0.467	21	0.249	R.DLVGVAYTEEETK.A
R4/RRR4-14/2	1453.926	1454.561	-1128.142	0.478	1645.966	0.518	21	0.248	R.DLVGVAYTEEETK.A
R4/RRR4-13/2	1665.647	1664.883	-142.281	0.519	784.767	0.579	23	0.185	R.FANGGAYPPDLSLITK.A
R4/RRR4-14/2	1665.897	1664.883	8.554	0.495	720.742	0.527	22	0.173	R.FANGGAYPPDLSLITK.A
R4/RRR4-14/2	1665.436	1664.883	-269.188	0.498	644.234	0.523	22	0.169	R.FANGGAYPPDLSLITK.A
R4/RRR4-14/2	1666.020	1664.883	82.632	0.482	721.190	0.519	20	0.169	R.FANGGAYPPDLSLITK.A
R4/RRR4-13/2	1664.562	1664.883	-193.420	0.390	775.833	0.500	22	0.168	R.FANGGAYPPDLSLITK.A
R4/RRR4-14/2	1665.654	1664.883	-137.796	0.477	641.255	0.478	22	0.164	R.FANGGAYPPDLSLITK.A
R4/RRR4-13/3	1889.501	1890.049	-821.495	0.486	1387.477	0.456	31	0.162	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-13/2	1664.431	1664.883	-272.366	0.353	664.078	0.473	20	0.159	R.FANGGAYPPDLSLITK.A
R4/RRR4-14/2	1664.175	1664.883	-1029.463	0.400	547.304	0.464	21	0.158	R.FANGGAYPPDLSLITK.A
R4/RRR4-13/2	1665.582	1664.883	-181.246	0.496	543.119	0.471	19	0.157	R.FANGGAYPPDLSLITK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1664.427	1664.883	-274.794	0.438	571.256	0.466	19	0.157	R.FANGGAYPPDLSLITK.A
R4/RRR4-13/2	1663.946	1664.883	-1167.276	0.349	645.741	0.445	21	0.156	R.FANGGAYPPDLSLITK.A
R4/RRR4-14/2	1890.378	1890.049	174.576	0.497	536.993	0.456	18	0.151	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-14/3	1890.713	1890.049	-178.225	0.481	1310.554	0.408	30	0.139	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-13/3	1889.955	1890.049	-49.703	0.494	1147.750	0.417	29	0.127	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-13/3	1889.618	1890.049	-228.447	0.485	1218.111	0.378	29	0.123	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-15/2	1666.440	1664.883	-266.454	0.215	117.201	0.426	14	0.117	-.FANGGAYPPDLSLITK.-
R4/RRR4-14/3	1978.724	1979.247	-771.907	0.421	1195.149	0.358	27	0.117	R.EGLHYNPYFPGGAIAM*PK.M
R4/RRR4-14/3	1891.114	1890.049	34.882	0.461	1076.355	0.387	26	0.115	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-14/3	1889.770	1890.049	-147.669	0.472	1142.321	0.366	29	0.114	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-14/3	1889.192	1890.049	-985.726	0.383	732.845	0.342	26	0.094	K.LSDRFPQPYPNEQAAR.F
R4/RRR4-13/3	1979.812	1979.247	-220.466	0.341	635.270	0.372	23	0.085	-.EGLHYNPYFPGGAIAM*PK.-
R4/RRR4-14/3	1978.799	1979.247	-226.952	0.325	728.787	0.296	23	0.083	-.EGLHYNPYFPGGAIAM*PK.-
R4/RRR4-9/2	1148.113	1148.249	-118.650	0.496	2037.812	0.446	19	0.286	K.ISGLESGISER.S
R4/RRR4-9/2	1490.762	1489.696	44.136	0.551	1756.926	0.573	20	0.277	K.IASLQSEITSLQAK.G
R4/RRR4-9/3	1392.883	1391.510	269.047	0.457	1684.024	0.408	28	0.190	R.DKISGLESGISER.S
R4/RRR4-9/2	1491.130	1489.696	291.604	0.443	991.095	0.542	17	0.184	K.IASLQSEITSLQAK.G
R4/RRR4-9/3	1187.715	1187.328	326.502	0.433	2185.070	0.137	26	0.164	R.AKEEAEAVALR.A
R4/RRR4-9/3	1187.383	1187.328	46.173	0.421	2006.099	0.150	25	0.143	R.AKEEAEAVALR.A
R4/RRR4-18/2	1763.364	1764.013	-937.603	0.506	1622.849	0.537	23	0.247	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-17/2	1213.003	1213.323	-263.910	0.518	1419.423	0.551	19	0.229	R.AGGVDDAPLVGNK.A
R4/RRR4-18/2	1212.475	1213.323	-1528.505	0.492	1442.739	0.511	19	0.222	R.AGGVDDAPLVGNK.A
R4/RRR4-18/2	1213.017	1213.323	-252.602	0.538	1336.029	0.513	19	0.213	R.AGGVDDAPLVGNK.A
R4/RRR4-18/2	1762.744	1764.013	-1291.126	0.463	1308.766	0.480	21	0.199	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-18/2	1764.493	1764.013	272.796	0.542	1141.042	0.546	21	0.198	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-18/2	1213.113	1213.323	-173.051	0.520	1012.173	0.524	17	0.186	R.AGGVDDAPLVGNK.A
R4/RRR4-18/2	1765.051	1764.013	21.947	0.548	882.677	0.584	20	0.186	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-18/2	1487.393	1486.740	-234.569	0.483	866.792	0.498	22	0.177	K.SFGVLIPDQGIALR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1762.548	1764.013	-1402.901	0.468	951.080	0.518	19	0.177	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-18/2	1486.390	1486.740	-236.292	0.435	888.466	0.428	22	0.167	K.SFGVLIPDQGIALR.G
R4/RRR4-17/2	1214.171	1213.323	-125.304	0.433	699.176	0.449	19	0.162	R.AGGVDDAPLVGNK.A
R4/RRR4-18/2	1485.659	1486.740	-1405.344	0.355	623.040	0.413	19	0.153	K.SFGVLIPDQGIALR.G
R4/RRR4-17/2	1487.435	1486.740	-205.670	0.426	635.949	0.373	18	0.150	K.SFGVLIPDQGIALR.G
R4/RRR4-18/3	1763.286	1764.013	-982.126	0.415	1224.865	0.467	30	0.148	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-19/2	1487.912	1486.740	115.811	0.414	582.162	0.255	15	0.134	-.SFGVLIPDQGIALR.-
R4/RRR4-19/2	1487.344	1486.740	-267.175	0.355	540.472	0.215	16	0.133	-.SFGVLIPDQGIALR.-
R4/RRR4-18/3	1763.520	1764.013	-280.363	0.358	1176.405	0.360	26	0.115	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-18/3	1763.301	1764.013	-973.785	0.372	1004.842	0.386	27	0.108	K.SGGLGDLKYPLISDVTK.S
R4/RRR4-18/3	1723.602	1722.927	-189.502	0.319	846.670	0.377	26	0.093	K.EGVIQHSTINNLAIGR.S
R4/RRR4-20/2	1361.077	1360.541	-341.436	0.466	1596.952	0.501	17	0.237	K.FVAYTSAWTWK.K
R4/RRR4-12/2	1134.059	1134.350	-257.450	0.377	1552.898	0.502	18	0.230	K.VAVEFIATVGK.Q
R4/RRR4-12/2	1359.844	1360.541	-1251.392	0.483	1376.368	0.498	18	0.215	K.FVAYTSAWTWK.K
R4/RRR4-21/2	1360.806	1360.541	195.368	0.553	1357.997	0.501	18	0.214	K.FVAYTSAWTWK.K
R4/RRR4-20/2	1359.207	1360.541	-1722.193	0.286	1637.568	0.265	18	0.190	K.FVAYTSAWTWK.K
R4/RRR4-12/2	1360.490	1360.541	-37.583	0.378	917.886	0.542	15	0.181	K.FVAYTSAWTWK.K
R4/RRR4-20/2	1360.138	1360.541	-297.113	0.413	870.916	0.489	17	0.174	K.FVAYTSAWTWK.K
R4/RRR4-20/2	1291.065	1291.481	-323.346	0.417	1043.412	0.414	16	0.170	R.GVNVIYALTGQR.R
R4/RRR4-13/2	1591.880	1590.846	21.412	0.498	793.500	0.475	19	0.170	K.EVFWLPVDSAWLK.I
R4/RRR4-20/2	1360.358	1360.541	-134.880	0.441	836.225	0.448	14	0.165	K.FVAYTSAWTWK.K
R4/RRR4-21/2	1291.124	1291.481	-277.529	0.331	999.867	0.404	16	0.164	R.GVNVIYALTGQR.R
R4/RRR4-12/2	1291.289	1291.481	-149.490	0.397	1071.396	0.343	16	0.161	R.GVNVIYALTGQR.R
R4/RRR4-21/2	1291.131	1291.481	-271.837	0.297	1027.561	0.364	16	0.160	R.GVNVIYALTGQR.R
R4/RRR4-12/2	1291.190	1291.481	-226.214	0.369	1029.417	0.330	16	0.157	R.GVNVIYALTGQR.R
R4/RRR4-21/2	1290.941	1291.481	-1196.310	0.316	1053.487	0.325	16	0.157	R.GVNVIYALTGQR.R
R4/RRR4-13/2	1592.097	1590.846	158.065	0.487	619.944	0.430	17	0.156	K.EVFWLPVDSAWLK.I
R4/RRR4-21/2	1361.048	1360.541	-362.674	0.385	652.645	0.384	14	0.152	K.FVAYTSAWTWK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1590.978	1590.846	83.528	0.441	707.171	0.349	18	0.151	K.EVFWLPVDSAWLK.I
R4/RRR4-12/2	1591.359	1590.846	-306.723	0.383	553.310	0.379	16	0.149	K.EVFWLPVDSAWLK.I
R4/RRR4-20/2	1291.096	1291.481	-299.631	0.328	989.536	0.262	16	0.148	R.GVNVIYALTGQR.R
R4/RRR4-21/2	1589.389	1590.846	-1550.119	0.354	611.303	0.362	16	0.148	K.EVFWLPVDSAWLK.I
R4/RRR4-21/2	1361.603	1360.541	45.805	0.350	390.169	0.394	11	0.146	K.FVAYTSAWTWK.K
R4/RRR4-21/2	1590.454	1590.846	-247.006	0.413	513.176	0.351	15	0.145	K.EVFWLPVDSAWLK.I
R4/RRR4-13/2	1290.966	1291.481	-1176.940	0.281	466.180	0.379	14	0.145	R.GVNVIYALTGQR.R
R4/RRR4-20/2	1290.924	1291.481	-1209.794	0.364	462.247	0.298	14	0.143	R.GVNVIYALTGQR.R
R4/RRR4-13/2	1590.371	1590.846	-299.292	0.359	480.040	0.304	15	0.143	K.EVFWLPVDSAWLK.I
R4/RRR4-12/2	1359.715	1360.541	-1346.959	0.228	624.306	0.286	14	0.141	K.FVAYTSAWTWK.K
R4/RRR4-21/2	1359.289	1360.541	-1661.379	0.262	293.093	0.317	11	0.138	-.FVAYTSAWTWK.-
R4/RRR4-12/2	1589.666	1590.846	-1375.013	0.210	626.103	0.220	17	0.137	K.EVFWLPVDSAWLK.I
R4/RRR4-14/2	1592.046	1590.846	126.231	0.283	170.748	0.334	12	0.124	-.EVFWLPVDSAWLK.-
R4/RRR4-15/2	1875.067	1874.127	-32.493	0.498	1633.305	0.610	24	0.268	K.QLVNDGVVAISEVTGFPK.L
R4/RRR4-16/2	1595.042	1594.746	186.021	0.566	1192.748	0.621	23	0.226	K.LAEAPYLDSVDWSK.W
R4/RRR4-16/2	1594.269	1594.746	-300.480	0.501	1036.903	0.551	22	0.197	K.LAEAPYLDSVDWSK.W
R4/RRR4-16/2	1863.956	1863.098	-76.171	0.550	928.872	0.550	17	0.177	K.EVLIFDAEEDLAVSLAK.Y
R4/RRR4-15/2	1348.507	1349.601	-1556.902	0.370	1494.347	0.260	19	0.175	R.GAFTVVLSGGSLIK.N
R4/RRR4-16/2	1350.069	1349.601	347.828	0.479	1312.113	0.339	19	0.174	R.GAFTVVLSGGSLIK.N
R4/RRR4-16/2	1593.477	1594.746	-1428.583	0.357	954.903	0.399	20	0.162	K.LAEAPYLDSVDWSK.W
R4/RRR4-15/2	1349.067	1349.601	-1140.047	0.389	929.080	0.328	17	0.150	R.GAFTVVLSGGSLIK.N
R4/RRR4-15/2	1348.612	1349.601	-1478.613	0.322	841.441	0.357	15	0.147	R.GAFTVVLSGGSLIK.N
R4/RRR4-7/2	945.841	945.055	-227.906	0.458	881.542	0.360	14	0.158	R.LDAANTLAR.A
R4/RRR4-7/2	944.825	945.055	-244.998	0.397	850.798	0.377	14	0.158	R.LDAANTLAR.A
R4/RRR4-7/3	1762.034	1761.914	68.394	0.405	771.521	0.471	27	0.111	R.TGVEQGPQIDGEQFKK.I
R4/RRR4-7/3	1761.892	1761.914	-12.281	0.461	692.259	0.466	26	0.108	R.TGVEQGPQIDGEQFKK.I
R4/RRR4-7/3	1761.815	1761.914	-56.375	0.378	534.895	0.434	23	0.097	R.TGVEQGPQIDGEQFKK.I
R4/RRR4-10/2	1275.002	1275.434	-339.615	0.458	1476.437	0.432	19	0.209	K.EIVGSIQSQVSK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1274.531	1275.434	-1497.216	0.382	1391.241	0.455	19	0.204	K.EIVGSIQSQVSK.I
R4/RRR4-10/2	1447.715	1448.430	-1188.038	0.439	1681.328	0.267	17	0.192	R.DFEYSSEAQESR.K
R4/RRR4-10/2	1949.082	1949.189	-55.129	0.516	844.135	0.561	20	0.180	R.SILEELCGNVHSIYWK.S
R4/RRR4-10/2	1776.553	1776.068	273.425	0.500	744.725	0.522	24	0.173	R.YGLPPSFLSAVLAPSQK.G
R4/RRR4-10/2	1776.380	1776.068	175.647	0.457	478.659	0.529	21	0.162	R.YGLPPSFLSAVLAPSQK.G
R4/RRR4-10/2	1776.413	1776.068	194.253	0.508	617.752	0.486	22	0.162	R.YGLPPSFLSAVLAPSQK.G
R4/RRR4-10/2	1775.934	1776.068	-75.809	0.426	588.166	0.508	20	0.160	R.YGLPPSFLSAVLAPSQK.G
R4/RRR4-10/2	1947.596	1949.189	-1850.735	0.419	537.130	0.443	18	0.150	R.SILEELCGNVHSIYWK.S
R4/RRR4-10/2	1775.364	1776.068	-962.989	0.355	529.127	0.369	19	0.144	R.YGLPPSFLSAVLAPSQK.G
R4/RRR4-9/2	1295.231	1295.420	-146.577	0.455	1628.668	0.431	18	0.224	K.ADIEDYLASVAK.G
R4/RRR4-8/2	1295.334	1295.420	-67.073	0.394	923.636	0.491	15	0.172	K.ADIEDYLASVAK.G
R4/RRR4-8/2	1295.448	1295.420	21.680	0.350	982.575	0.426	16	0.166	K.ADIEDYLASVAK.G
R4/RRR4-8/2	1017.125	1017.158	-33.056	0.378	789.191	0.428	16	0.161	K.GLATIADEVK.Q
R4/RRR4-9/2	1294.987	1295.420	-335.225	0.338	961.205	0.373	15	0.157	K.ADIEDYLASVAK.G
R4/RRR4-9/2	1294.488	1295.420	-1497.306	0.354	926.811	0.368	15	0.156	K.ADIEDYLASVAK.G
R4/RRR4-8/2	1016.947	1017.158	-207.998	0.336	451.021	0.421	13	0.148	K.GLATIADEVK.Q
R4/RRR4-9/2	1419.136	1418.534	-281.052	0.553	1436.445	0.603	19	0.245	R.GPLLDEDGPSYVR.V
R4/RRR4-9/2	1418.113	1418.534	-297.659	0.520	1427.154	0.589	19	0.239	R.GPLLDEDGPSYVR.V
R4/RRR4-9/2	1418.157	1418.534	-266.223	0.517	1419.546	0.572	19	0.235	R.GPLLDEDGPSYVR.V
R4/RRR4-9/2	1895.586	1896.007	-222.682	0.516	1651.179	0.429	20	0.223	R.ENINNFEENDFQILR.V
R4/RRR4-9/2	1895.273	1896.007	-917.244	0.538	1337.757	0.449	19	0.195	R.ENINNFEENDFQILR.V
R4/RRR4-9/2	1047.519	1048.217	-1625.905	0.343	987.219	0.386	15	0.162	R.ALFVQADGVK.L
R4/RRR4-9/2	1047.485	1048.217	-1658.335	0.359	817.244	0.375	14	0.154	R.ALFVQADGVK.L
R4/RRR4-9/2	1033.236	1033.161	72.923	0.418	751.259	0.317	14	0.148	K.LTSTQDVLR.G
R4/RRR4-9/2	1047.494	1048.217	-1650.374	0.260	732.086	0.299	14	0.142	R.ALFVQADGVK.L
R4/RRR4-7/2	1966.035	1966.330	-150.170	0.500	1318.761	0.545	22	0.213	R.YFELSGLPM*LVLIGPDGK.T
R4/RRR4-7/2	927.870	928.108	-257.524	0.395	640.769	0.555	14	0.172	K.VPVSELVGK.T
R4/RRR4-6/2	928.280	928.108	185.893	0.355	735.096	0.464	14	0.163	K.VPVSELVGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1587.310	1587.719	-258.062	0.413	821.033	0.462	18	0.162	K.DNQTIHSLFGTPTR.D
R4/RRR4-6/2	1762.618	1763.050	-245.663	0.430	672.667	0.498	20	0.162	-.MPWLAVPFSDSEALAK.L
R4/RRR4-7/2	928.098	928.108	-10.898	0.353	566.097	0.491	13	0.160	K.VPVSELVGK.T
R4/RRR4-7/2	927.978	928.108	-140.200	0.361	564.628	0.480	13	0.160	K.VPVSELVGK.T
R4/RRR4-6/2	927.415	928.108	-1830.393	0.326	534.293	0.471	13	0.156	K.VPVSELVGK.T
R4/RRR4-6/2	1763.213	1763.050	92.868	0.435	574.527	0.436	19	0.152	-.MPWLAVPFSDSEALAK.L
R4/RRR4-1/2	928.207	928.108	107.159	0.209	569.517	0.417	13	0.143	-.VPVSELVGK.-
R4/RRR4-7/2	1764.240	1763.050	108.220	0.367	318.320	0.328	14	0.137	-.MPWLAVPFSDSEALAK.L
R4/RRR4-5/2	928.152	928.108	47.409	0.162	353.842	0.313	11	0.137	-.VPVSELVGK.-
R4/RRR4-2/2	928.049	928.108	-63.538	0.131	556.031	0.198	12	0.134	-.VPVSELVGK.-
R4/RRR4-8/2	1518.051	1518.781	-1142.590	0.329	1463.533	0.472	20	0.209	R.LISQVISSLTTSLR.F
R4/RRR4-8/2	1539.760	1538.597	106.742	0.478	1002.407	0.556	19	0.190	R.DAFNTFFSETSSGK.H
R4/RRR4-8/2	1689.468	1688.943	-281.592	0.527	1163.027	0.472	21	0.188	R.ALFVDLEPTVIDEVK.T
R4/RRR4-8/2	1688.464	1688.943	-284.515	0.505	1375.769	0.385	21	0.188	R.ALFVDLEPTVIDEVK.T
R4/RRR4-8/2	1687.729	1688.943	-1315.432	0.358	668.567	0.331	17	0.142	R.ALFVDLEPTVIDEVK.T
R4/RRR4-23/3	1774.729	1774.911	-102.843	0.522	2921.729	0.423	33	0.498	R.HGTHAEFTTCLWTGR.V
R4/RRR4-23/2	1115.897	1116.296	-359.291	0.507	1278.960	0.469	17	0.202	R.KVTIQNLSGR.D
R4/RRR4-23/2	988.063	988.123	-61.538	0.474	1068.406	0.476	14	0.185	K.VTIQNLSGR.D
R4/RRR4-23/2	1115.504	1116.296	-1611.547	0.453	1035.004	0.480	16	0.183	R.KVTIQNLSGR.D
R4/RRR4-23/2	1115.484	1116.296	-1629.577	0.467	896.207	0.491	16	0.178	R.KVTIQNLSGR.D
R4/RRR4-23/2	988.043	988.123	-81.242	0.418	978.665	0.481	13	0.177	K.VTIQNLSGR.D
R4/RRR4-23/2	987.944	988.123	-182.378	0.414	954.195	0.403	13	0.165	K.VTIQNLSGR.D
R4/RRR4-23/3	1774.365	1774.911	-873.904	0.378	1314.507	0.366	26	0.128	R.HGTHAEFTTCLWTGR.V
R4/RRR4-23/3	1115.234	1116.296	-1854.795	0.449	1132.491	0.304	20	0.100	R.KVTIQNLSGR.D
R4/RRR4-26/3	1116.007	1116.296	-260.475	0.372	603.243	0.413	17	0.095	R.KVTIQNLSGR.D
R4/RRR4-4/2	1675.672	1675.862	-114.029	0.441	2408.341	0.622	23	0.403	K.AAVAVLGDLADTLGSSSK.D
R4/RRR4-4/2	1498.181	1496.732	300.202	0.520	1584.640	0.484	21	0.232	R.GIFEAYSGILQGIK.G
R4/RRR4-4/2	1497.385	1496.732	-232.268	0.496	1696.430	0.416	22	0.229	R.GIFEAYSGILQGIK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1336.280	1336.476	-147.114	0.469	1295.530	0.372	17	0.180	R.ASAYEALNEIVR.V
R4/RRR4-4/2	1496.276	1496.732	-306.085	0.347	1335.781	0.364	19	0.180	R.GIFEAYSGILQGIK.G
R4/RRR4-4/2	1336.203	1336.476	-204.849	0.433	1090.644	0.396	15	0.168	R.ASAYEALNEIVR.V
R4/RRR4-1/2	1337.421	1336.476	-41.343	0.392	330.956	0.300	12	0.137	-.ASAYEALNEIVR.-
R4/RRR4-4/3	1675.256	1675.862	-962.074	0.226	1002.593	0.164	23	0.068	K.AAVAVLGDLADTLGSSSK.D
R4/RRR4-8/2	1274.192	1274.448	-200.886	0.449	866.401	0.586	14	0.184	K.HALVVYDDLTK.Q
R4/RRR4-8/2	1053.381	1053.237	137.199	0.373	914.781	0.475	14	0.169	R.GLLDSVPVPR.I
R4/RRR4-8/2	1740.701	1741.879	-1255.356	0.373	713.341	0.462	19	0.155	R.EVAAFAQFGSDLDAATK.Q
R4/RRR4-8/2	1740.876	1741.879	-1154.024	0.362	521.059	0.422	16	0.143	R.EVAAFAQFGSDLDAATK.Q
R4/RRR4-11/2	1424.800	1425.558	-1237.393	0.425	1101.507	0.515	19	0.191	K.LSSTSVTVEDCVK.E
R4/RRR4-11/2	1424.973	1425.558	-1115.406	0.456	884.189	0.523	16	0.175	K.LSSTSVTVEDCVK.E
R4/RRR4-11/2	1058.876	1059.243	-348.229	0.464	513.010	0.579	16	0.174	K.LGPQNAIFAK.A
R4/RRR4-11/2	1933.782	1935.169	-1238.028	0.438	768.758	0.552	19	0.172	K.TPATPFFFNTLYDPFR.K
R4/RRR4-11/2	1058.538	1059.243	-1615.689	0.373	452.599	0.581	15	0.165	K.LGPQNAIFAK.A
R4/RRR4-11/2	1060.049	1059.243	-183.948	0.445	412.765	0.464	15	0.160	K.LGPQNAIFAK.A
R4/RRR4-11/2	1540.348	1540.848	-977.052	0.395	965.324	0.352	17	0.156	K.VM*DVVLPFFESLK.L
R4/RRR4-11/2	1934.441	1935.169	-895.887	0.425	571.031	0.476	17	0.153	K.TPATPFFFNTLYDPFR.K
R4/RRR4-11/2	1540.032	1540.848	-1182.766	0.379	816.370	0.285	16	0.142	K.VM*DVVLPFFESLK.L
R4/RRR4-11/2	1539.979	1540.848	-1217.312	0.270	671.716	0.285	14	0.136	-.VM*DVVLPFFESLK.-
R4/RRR4-14/2	1093.092	1093.218	-115.438	0.418	995.623	0.509	17	0.185	R.NINASFASLR.Q
R4/RRR4-13/2	1345.998	1346.496	-370.872	0.479	1026.509	0.489	20	0.184	R.DM*TALSGAHTIGR.A
R4/RRR4-13/2	1345.850	1346.496	-1226.518	0.473	959.579	0.521	19	0.184	R.DM*TALSGAHTIGR.A
R4/RRR4-13/2	991.540	992.150	-1628.853	0.437	1371.026	0.336	14	0.181	R.GFEVIDAIK.T
R4/RRR4-13/2	1346.012	1346.496	-360.044	0.457	825.368	0.545	18	0.179	R.DM*TALSGAHTIGR.A
R4/RRR4-14/2	991.982	992.150	-170.095	0.416	1379.103	0.318	14	0.179	-.GFEVIDAIK.-
R4/RRR4-14/2	1093.330	1093.218	102.398	0.438	845.062	0.497	16	0.175	R.NINASFASLR.Q
R4/RRR4-14/2	1347.042	1346.496	-337.591	0.436	869.506	0.481	19	0.172	R.DM*TALSGAHTIGR.A
R4/RRR4-14/2	992.092	992.150	-59.375	0.412	1347.716	0.273	14	0.169	-.GFEVIDAIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1093.180	1093.218	-35.348	0.395	890.958	0.437	16	0.167	R.NINASFASLR.Q
R4/RRR4-14/2	1549.188	1549.732	-999.530	0.473	753.434	0.462	23	0.167	K.M*GNLLPSSGTATEVR.L
R4/RRR4-13/2	991.849	992.150	-304.423	0.379	1318.668	0.254	14	0.165	-.GFEVIDAIK.-
R4/RRR4-13/2	1533.216	1533.733	-992.020	0.445	663.213	0.483	22	0.165	K.MGNLLPSSGTATEVR.L
R4/RRR4-13/2	991.888	992.150	-265.158	0.413	1230.032	0.296	14	0.164	-.GFEVIDAIK.-
R4/RRR4-14/2	1549.320	1549.732	-266.559	0.473	707.559	0.460	22	0.164	K.M*GNLLPSSGTATEVR.L
R4/RRR4-14/2	991.429	992.150	-1741.664	0.353	1263.540	0.253	14	0.162	-.GFEVIDAIK.-
R4/RRR4-14/2	1548.886	1549.732	-1195.528	0.432	665.308	0.462	21	0.161	K.M*GNLLPSSGTATEVR.L
R4/RRR4-13/2	1533.379	1533.733	-231.447	0.418	396.906	0.432	18	0.152	K.MGNLLPSSGTATEVR.L
R4/RRR4-13/2	1533.216	1533.733	-992.020	0.435	449.362	0.369	19	0.148	K.MGNLLPSSGTATEVR.L
R4/RRR4-8/2	1356.568	1355.560	5.721	0.634	1458.553	0.533	17	0.230	R.TFLDQLVEVYK.Q
R4/RRR4-8/2	1355.190	1355.560	-274.076	0.507	1392.892	0.537	17	0.225	R.TFLDQLVEVYK.Q
R4/RRR4-7/2	1355.274	1355.560	-211.814	0.508	1464.173	0.492	16	0.221	R.TFLDQLVEVYK.Q
R4/RRR4-8/2	1354.625	1355.560	-1432.914	0.456	1016.432	0.494	15	0.182	R.TFLDQLVEVYK.Q
R4/RRR4-8/2	888.927	889.077	-168.327	0.481	1067.411	0.357	12	0.168	K.RPDIIFK.W
R4/RRR4-8/2	1149.531	1150.349	-1586.424	0.372	734.800	0.489	15	0.164	R.IPLVSFTGSTK.V
R4/RRR4-8/2	1150.120	1150.349	-200.308	0.392	732.957	0.457	15	0.161	R.IPLVSFTGSTK.V
R4/RRR4-7/2	1354.909	1355.560	-1222.424	0.332	845.265	0.371	14	0.153	R.TFLDQLVEVYK.Q
R4/RRR4-8/2	1150.149	1150.349	-174.754	0.329	723.005	0.400	15	0.153	R.IPLVSFTGSTK.V
R4/RRR4-8/2	888.545	889.077	-1728.507	0.380	776.157	0.339	11	0.152	K.RPDIIFK.W
R4/RRR4-8/2	888.296	889.077	-2010.033	0.283	495.933	0.298	11	0.144	K.RPDIIFK.W
R4/RRR4-7/2	1150.474	1150.349	108.380	0.275	309.978	0.349	11	0.132	-.IPLVSFTGSTK.-
R4/RRR4-8/3	1609.535	1609.854	-198.444	0.404	1045.059	0.315	25	0.096	R.KEHQFLAELGLAPR.N
R4/RRR4-11/3	1752.951	1752.910	23.278	0.473	1880.238	0.300	30	0.184	-.VNTLHDGVALAQETQR.-
R4/RRR4-11/2	1099.061	1099.266	-187.110	0.418	1427.942	0.290	16	0.177	K.VLQDVLAGQR.G
R4/RRR4-11/2	1448.359	1448.603	-168.529	0.469	1178.087	0.375	16	0.168	R.SGEAINTLESWIK.I
R4/RRR4-11/2	1525.483	1525.820	-221.248	0.360	1068.933	0.410	18	0.166	K.TVFNILGPLLNPAR.V
R4/RRR4-11/3	1752.887	1752.910	-12.972	0.537	1494.344	0.372	27	0.152	-.VNTLHDGVALAQETQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/3	1752.477	1752.910	-247.721	0.493	1102.083	0.240	25	0.085	-.VNTLHDGVALAQETQR.-
R4/RRR4-5/2	1457.461	1458.513	-1411.868	0.459	2137.492	0.530	23	0.325	R.VYGSSSNDVSSVTR.Q
R4/RRR4-5/2	1458.201	1458.513	-214.663	0.504	1827.930	0.543	22	0.280	R.VYGSSSNDVSSVTR.Q
R4/RRR4-5/2	1350.786	1349.519	198.267	0.483	1636.903	0.513	16	0.245	R.GLAYIQDNLWR.L
R4/RRR4-5/2	1348.832	1349.519	-1254.528	0.425	1330.422	0.375	15	0.183	R.GLAYIQDNLWR.L
R4/RRR4-5/2	1349.619	1349.519	73.790	0.327	523.829	0.341	12	0.138	-.GLAYIQDNLWR.-
R4/RRR4-5/3	1668.095	1666.821	165.022	0.496	1163.910	0.442	27	0.136	R.NNLQAHGVTEQSVLR.A
R4/RRR4-5/3	1366.462	1366.591	-94.728	0.355	1021.780	0.386	28	0.106	-.TAILAEAIASHLR.-
R4/RRR4-5/3	1366.541	1366.591	-36.933	0.361	613.701	0.394	22	0.093	R.TAILAEAIASHLR.Q
R4/RRR4-6/2	1613.244	1612.810	270.063	0.509	1109.840	0.550	19	0.201	K.VLEPLFSYWNSTR.Q
R4/RRR4-7/2	1613.341	1612.810	-291.085	0.489	955.216	0.540	18	0.186	K.VLEPLFSYWNSTR.Q
R4/RRR4-7/2	1612.408	1612.810	-249.793	0.411	1189.208	0.433	19	0.183	K.VLEPLFSYWNSTR.Q
R4/RRR4-7/2	1613.251	1612.810	274.236	0.436	1113.906	0.417	19	0.176	K.VLEPLFSYWNSTR.Q
R4/RRR4-6/2	1170.988	1171.374	-330.154	0.382	750.157	0.536	16	0.171	R.NVLAPAAPYVR.K
R4/RRR4-6/3	1338.913	1338.538	281.172	0.567	1349.959	0.485	25	0.167	K.VGIKDHESVVVR.I
R4/RRR4-6/2	1171.163	1171.374	-180.818	0.376	490.400	0.454	14	0.154	R.NVLAPAAPYVR.K
R4/RRR4-6/2	1611.434	1612.810	-1478.538	0.236	1023.810	0.302	17	0.150	K.VLEPLFSYWNSTR.Q
R4/RRR4-7/2	1171.152	1171.374	-189.601	0.304	584.948	0.409	14	0.148	R.NVLAPAAPYVR.K
R4/RRR4-6/3	1243.746	1244.385	-1321.405	0.472	955.632	0.570	21	0.148	R.THRVETTFPR.L
R4/RRR4-7/3	1245.012	1244.385	-300.603	0.503	1032.508	0.543	22	0.148	R.THRVETTFPR.L
R4/RRR4-6/3	1338.488	1338.538	-37.341	0.569	1229.921	0.460	24	0.146	K.VGIKDHESVVVR.I
R4/RRR4-6/2	1171.083	1171.374	-248.683	0.333	587.536	0.320	14	0.143	R.NVLAPAAPYVR.K
R4/RRR4-6/2	1612.320	1612.810	-304.482	0.269	869.807	0.231	16	0.139	K.VLEPLFSYWNSTR.Q
R4/RRR4-6/3	1338.890	1338.538	263.620	0.586	1066.779	0.481	23	0.137	K.VGIKDHESVVVR.I
R4/RRR4-6/3	1244.526	1244.385	113.558	0.528	767.783	0.568	19	0.135	R.THRVETTFPR.L
R4/RRR4-7/3	1244.780	1244.385	318.910	0.526	738.727	0.558	19	0.132	R.THRVETTFPR.L
R4/RRR4-6/3	1244.350	1244.385	-27.818	0.521	787.898	0.505	20	0.123	R.THRVETTFPR.L
R4/RRR4-5/3	1245.256	1244.385	-103.653	0.446	543.471	0.374	17	0.098	R.THRVETTFPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1243.986	1244.385	-321.027	0.443	649.384	0.369	18	0.097	R.THRVETTFPR.L
R4/RRR4-8/2	1067.106	1066.269	-153.359	0.394	637.837	0.468	14	0.161	R.LVFQVCTAK.M
R4/RRR4-8/2	1067.193	1066.269	-71.660	0.239	304.267	0.306	10	0.130	-.LVFQVCTAK.-
R4/RRR4-8/3	1295.169	1295.475	-236.543	0.464	777.665	0.502	24	0.120	K.AVAHHTTAAFIR.V
R4/RRR4-8/3	1420.342	1421.670	-1644.153	0.441	1016.979	0.430	24	0.118	R.ELLKPSASVALHR.H
R4/RRR4-8/3	1421.338	1421.670	-234.281	0.438	1042.562	0.417	26	0.117	R.ELLKPSASVALHR.H
R4/RRR4-8/3	1295.014	1295.475	-356.832	0.463	555.465	0.512	22	0.113	K.AVAHHTTAAFIR.V
R4/RRR4-9/3	1295.600	1295.475	96.867	0.442	453.321	0.479	21	0.107	K.AVAHHTTAAFIR.V
R4/RRR4-9/3	1295.873	1295.475	308.510	0.408	587.072	0.468	22	0.106	K.AVAHHTTAAFIR.V
R4/RRR4-8/3	1295.143	1295.475	-257.251	0.417	506.263	0.445	21	0.099	-.AVAHHTTAAFIR.-
R4/RRR4-6/2	1642.388	1642.792	-246.948	0.524	1699.005	0.563	23	0.265	K.LAGLSAGGGEEPQQLSK.N
R4/RRR4-6/2	1498.303	1497.717	-276.825	0.589	1689.505	0.506	22	0.254	K.FLANITVADYIEK.Y
R4/RRR4-6/2	1642.338	1642.792	-277.596	0.515	1465.599	0.521	21	0.223	K.LAGLSAGGGEEPQQLSK.N
R4/RRR4-6/2	1375.224	1375.550	-237.765	0.478	1259.453	0.434	19	0.191	K.LLFYDLYGGGEK.V
R4/RRR4-6/2	1374.870	1375.550	-1226.139	0.469	1032.229	0.446	18	0.177	K.LLFYDLYGGGEK.V
R4/RRR4-6/2	1374.307	1375.550	-1636.987	0.356	894.262	0.447	14	0.162	K.LLFYDLYGGGEK.V
R4/RRR4-6/2	1324.541	1325.403	-1410.460	0.327	1021.375	0.231	15	0.142	R.TSELEDNEFIK.F
R4/RRR4-7/2	1675.360	1675.864	-900.472	0.519	1400.690	0.517	22	0.218	K.GGILKDDADWSTLGVK.D
R4/RRR4-7/2	1225.089	1225.333	-199.843	0.506	1447.148	0.389	17	0.197	K.SALLSYSDNVR.G
R4/RRR4-7/2	1224.928	1225.333	-331.709	0.411	1398.677	0.342	17	0.184	K.SALLSYSDNVR.G
R4/RRR4-7/2	1148.941	1149.322	-332.547	0.364	809.399	0.377	15	0.155	K.ELFGIDLVSR.V
R4/RRR4-7/2	1149.234	1149.322	-76.559	0.299	811.532	0.373	15	0.151	K.ELFGIDLVSR.V
R4/RRR4-7/3	1503.473	1503.547	-49.490	0.562	1321.702	0.418	25	0.143	R.VHCAESGEESLER.E
R4/RRR4-7/3	1503.293	1503.547	-169.710	0.534	1319.228	0.397	25	0.137	R.VHCAESGEESLER.E
R4/RRR4-7/3	1502.939	1503.547	-1072.949	0.473	1159.459	0.354	25	0.112	R.VHCAESGEESLER.E
R4/RRR4-7/2	1108.479	1109.214	-1570.510	0.424	1764.552	0.337	17	0.220	R.IAEGYELASR.I
R4/RRR4-6/2	1108.375	1109.214	-1664.221	0.394	1566.056	0.350	17	0.201	R.IAEGYELASR.I
R4/RRR4-6/2	1108.360	1109.214	-1677.941	0.392	1301.540	0.406	15	0.187	R.IAEGYELASR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1057.241	1057.226	14.637	0.367	1128.681	0.324	15	0.162	K.AVLAVADLER.K
R4/RRR4-7/2	1369.471	1369.635	-120.393	0.411	538.345	0.440	18	0.157	K.QQQILLATQVVK.M
R4/RRR4-6/2	1369.627	1369.635	-6.133	0.311	596.354	0.384	19	0.149	K.QQQILLATQVVK.M
R4/RRR4-6/2	1058.065	1057.226	-152.702	0.393	993.670	0.282	14	0.148	-.AVLAVADLER.-
R4/RRR4-6/2	1369.188	1369.635	-327.610	0.283	342.351	0.444	14	0.145	K.QQQILLATQVVK.M
R4/RRR4-6/2	977.839	978.081	-248.057	0.438	1051.850	0.174	14	0.141	R.FQELSPEK.L
R4/RRR4-7/2	978.220	978.081	143.297	0.320	1036.863	0.106	14	0.135	R.FQELSPEK.L
R4/RRR4-7/2	1503.074	1503.597	-1015.905	0.445	1607.174	0.541	22	0.247	R.ASQPTDTTTSPLAGR.L
R4/RRR4-7/2	1504.188	1503.597	-272.649	0.445	1454.188	0.495	22	0.219	R.ASQPTDTTTSPLAGR.L
R4/RRR4-7/2	1088.994	1089.313	-293.063	0.361	1889.345	0.248	18	0.212	R.LFVVIGAGGAGK.A
R4/RRR4-7/2	1503.142	1503.597	-303.465	0.422	1429.793	0.462	22	0.209	R.ASQPTDTTTSPLAGR.L
R4/RRR4-7/2	1332.230	1332.525	-222.279	0.406	892.831	0.481	20	0.173	K.IATTATEIVDVAK.M
R4/RRR4-7/2	1332.146	1332.525	-285.434	0.415	896.910	0.460	20	0.170	K.IATTATEIVDVAK.M
R4/RRR4-7/2	1942.005	1941.189	-95.049	0.462	1028.232	0.425	22	0.167	R.EAAECGATVVSGLEMFIR.Q
R4/RRR4-7/2	1332.234	1332.525	-219.061	0.390	661.169	0.490	18	0.162	K.IATTATEIVDVAK.M
R4/RRR4-7/2	1089.122	1089.313	-175.553	0.246	781.813	0.091	15	0.128	R.LFVVIGAGGAGK.A
R4/RRR4-5/2	1772.534	1771.950	-235.655	0.532	2015.366	0.527	23	0.302	R.LYLDQYGGSGDVWIGK.V
R4/RRR4-5/2	1771.118	1771.950	-1037.815	0.403	1538.844	0.424	21	0.210	R.LYLDQYGGSGDVWIGK.V
R4/RRR4-5/2	1118.088	1118.263	-156.550	0.383	911.351	0.386	14	0.159	R.VLQGCSAINR.L
R4/RRR4-5/2	1617.161	1617.778	-1002.911	0.401	646.579	0.393	18	0.151	K.DLDLDIPYDEPALK.A
R4/RRR4-5/2	1617.348	1617.778	-266.593	0.374	575.574	0.395	18	0.149	K.DLDLDIPYDEPALK.A
R4/RRR4-5/2	1617.275	1617.778	-932.056	0.364	667.381	0.370	19	0.149	K.DLDLDIPYDEPALK.A
R4/RRR4-5/2	1032.694	1033.120	-413.374	0.296	730.242	0.401	13	0.148	K.FPGDDGVLGR.A
R4/RRR4-5/2	1118.033	1118.263	-205.837	0.359	805.176	0.294	15	0.147	R.VLQGCSAINR.L
R4/RRR4-5/2	1117.392	1118.263	-1679.500	0.177	656.141	0.055	13	0.130	R.VLQGCSAINR.L
R4/RRR4-8/2	1355.117	1354.620	367.223	0.469	897.861	0.471	18	0.170	K.IGPALATGNTVVLK.T
R4/RRR4-8/2	1355.102	1354.620	356.204	0.438	842.658	0.471	17	0.165	K.IGPALATGNTVVLK.T
R4/RRR4-8/2	1556.546	1556.789	-156.737	0.474	744.648	0.487	17	0.165	K.GYFIQPTIFTNVR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1663.432	1663.898	-281.215	0.387	723.481	0.530	18	0.161	K.EAGFPAGVLNVISGFGK.I
R4/RRR4-8/2	1820.399	1821.131	-954.029	0.405	824.106	0.466	20	0.160	K.TAEQTPLSGLVMAQFVK.E
R4/RRR4-8/2	1354.319	1354.620	-223.264	0.407	663.716	0.425	16	0.152	K.IGPALATGNTVVLK.T
R4/RRR4-7/2	1970.461	1970.255	104.661	0.465	836.705	0.468	22	0.164	K.ALQLPEYPNAAELEAVLK.T
R4/RRR4-8/2	1969.412	1970.255	-938.542	0.409	460.816	0.452	19	0.148	K.ALQLPEYPNAAELEAVLK.T
R4/RRR4-4/2	1579.215	1579.672	-289.972	0.547	1897.173	0.483	24	0.273	K.VM*ANADTPEDATTAR.Q
R4/RRR4-4/2	1579.226	1579.672	-283.225	0.541	1896.977	0.482	24	0.273	K.VM*ANADTPEDATTAR.Q
R4/RRR4-4/2	1579.062	1579.672	-1022.807	0.532	1524.629	0.464	22	0.220	K.VM*ANADTPEDATTAR.Q
R4/RRR4-4/2	971.043	971.048	-5.120	0.439	1275.273	0.352	13	0.178	R.SDFEGIFR.A
R4/RRR4-4/2	971.055	971.048	7.236	0.429	1046.213	0.313	13	0.159	R.SDFEGIFR.A
R4/RRR4-4/2	970.396	971.048	-1708.190	0.306	1059.253	0.235	13	0.148	R.SDFEGIFR.A
R4/RRR4-4/3	1975.796	1976.215	-212.348	0.257	1104.537	0.135	27	0.071	K.VGICGEHGGEPLSVAFFAK.A
R4/RRR4-3/3	1976.234	1976.215	9.992	0.329	589.194	0.225	21	0.066	-.VGICGEHGGEPLSVAFFAK.-
R4/RRR4-7/2	1198.395	1199.296	-1590.599	0.449	849.544	0.551	16	0.181	R.GPPEADELSKR.M
R4/RRR4-7/3	1701.013	1701.950	-1141.704	0.451	1252.567	0.445	26	0.145	R.VNNERWEGVPFILK.A
R4/RRR4-6/2	1047.154	1047.188	-31.874	0.468	1648.657	0.365	16	0.213	K.SSVLESIVGR.D
R4/RRR4-6/3	1506.202	1506.729	-1016.405	0.453	1027.495	0.550	27	0.151	R.GPAEASVDAVHLVLK.E
R4/RRR4-6/3	1506.499	1506.729	-152.810	0.465	691.917	0.589	24	0.133	R.GPAEASVDAVHLVLK.E
R4/RRR4-6/2	1047.181	1047.188	-6.502	0.267	909.987	0.093	14	0.130	K.SSVLESIVGR.D
R4/RRR4-6/3	1506.969	1506.729	160.201	0.510	867.502	0.476	26	0.120	R.GPAEASVDAVHLVLK.E
R4/RRR4-6/3	1706.019	1705.809	123.281	0.401	417.442	0.522	23	0.107	K.TEGGQEYAEFLHAPR.K
R4/RRR4-6/3	1705.735	1705.809	-43.694	0.310	604.771	0.503	28	0.106	K.TEGGQEYAEFLHAPR.K
R4/RRR4-6/3	1705.974	1705.809	96.909	0.314	455.863	0.448	25	0.096	K.TEGGQEYAEFLHAPR.K
R4/RRR4-6/3	1675.063	1675.911	-1106.545	0.346	1041.691	0.249	24	0.083	K.SSVLESIVGRDFLPR.G
R4/RRR4-4/2	1712.101	1710.825	161.646	0.572	1702.512	0.605	22	0.279	R.SIQSFDPLASSSWER.V
R4/RRR4-4/2	1712.528	1710.825	-174.348	0.529	1404.669	0.527	21	0.222	R.SIQSFDPLASSSWER.V
R4/RRR4-4/2	1859.043	1860.061	-1088.903	0.523	1018.754	0.659	23	0.213	R.GVVPASGFSFSSQQFWK.V
R4/RRR4-4/2	1860.167	1860.061	57.223	0.569	735.613	0.609	22	0.185	R.GVVPASGFSFSSQQFWK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1859.863	1860.061	-106.555	0.562	723.760	0.590	22	0.181	R.GVVPASGFSFSSQQFWK.V
R4/RRR4-4/2	1751.256	1752.004	-1000.995	0.496	835.570	0.510	19	0.170	K.EFQNGFLPAVLSLSTK.F
R4/RRR4-4/2	1752.574	1752.004	-245.744	0.489	857.542	0.467	20	0.166	K.EFQNGFLPAVLSLSTK.F
R4/RRR4-4/3	1619.890	1620.875	-1228.811	0.317	1146.731	0.198	24	0.080	K.VIKENKDLDLPAHK.V
R4/RRR4-5/2	1241.105	1241.459	-286.346	0.443	1586.987	0.477	19	0.231	K.SPGLDDILVALK.T
R4/RRR4-5/2	1240.806	1241.459	-1336.021	0.486	1369.371	0.521	19	0.219	K.SPGLDDILVALK.T
R4/RRR4-5/2	1241.162	1241.459	-239.772	0.447	1492.246	0.447	19	0.214	K.SPGLDDILVALK.T
R4/RRR4-5/2	885.411	885.043	416.283	0.381	658.429	0.482	12	0.163	K.VITDAIPR.N
R4/RRR4-5/2	885.478	885.043	492.992	0.432	704.071	0.399	13	0.159	K.VITDAIPR.N
R4/RRR4-5/2	1589.151	1589.774	-1024.826	0.418	367.453	0.503	18	0.157	K.VIPIFNENDAISTR.K
R4/RRR4-5/2	1589.197	1589.774	-995.443	0.376	278.876	0.457	17	0.152	K.VIPIFNENDAISTR.K
R4/RRR4-5/2	1588.689	1589.774	-1316.594	0.323	267.538	0.480	17	0.150	K.VIPIFNENDAISTR.K
R4/RRR4-5/2	885.225	885.043	205.723	0.342	494.109	0.237	12	0.140	-.VITDAIPR.-
R4/RRR4-5/3	1884.114	1884.120	-3.426	0.348	983.258	0.270	24	0.083	K.ILLDVADALEANEDLIR.S
R4/RRR4-11/2	1708.512	1708.940	-251.365	0.574	3111.447	0.637	27	0.585	R.HVVIVDDLVQSGGTLR.E
R4/RRR4-11/2	1709.062	1708.940	71.453	0.594	3076.117	0.602	27	0.560	R.HVVIVDDLVQSGGTLR.E
R4/RRR4-11/2	1608.289	1608.731	-275.631	0.510	2971.683	0.472	24	0.475	R.VEEEGDVATAFTLAR.I
R4/RRR4-11/2	1608.197	1608.731	-957.264	0.499	2662.858	0.482	25	0.410	R.VEEEGDVATAFTLAR.I
R4/RRR4-11/2	1607.673	1608.731	-1284.063	0.374	2683.903	0.324	25	0.358	R.VEEEGDVATAFTLAR.I
R4/RRR4-11/2	1421.133	1421.767	-1153.020	0.468	668.326	0.476	14	0.159	K.LLLNFPM*VVCAK.V
R4/RRR4-11/2	1421.112	1421.767	-1168.115	0.312	561.418	0.226	14	0.135	K.LLLNFPM*VVCAK.V
R4/RRR4-5/2	1520.238	1520.712	-313.099	0.387	2003.550	0.352	20	0.252	R.TLFDLQEVSAQIR.E
R4/RRR4-6/2	1819.562	1820.101	-848.590	0.474	1541.769	0.527	22	0.233	K.SAIGIGTLLM*DGLGDTIR.V
R4/RRR4-5/2	1520.196	1520.712	-1000.355	0.400	1838.694	0.359	19	0.231	R.TLFDLQEVSAQIR.E
R4/RRR4-6/2	1520.267	1520.712	-294.006	0.413	1686.425	0.362	19	0.214	R.TLFDLQEVSAQIR.E
R4/RRR4-5/2	1520.093	1520.712	-1068.081	0.357	1635.204	0.347	18	0.205	R.TLFDLQEVSAQIR.E
R4/RRR4-6/2	1821.054	1820.101	-26.163	0.466	890.267	0.580	20	0.182	K.SAIGIGTLLM*DGLGDTIR.V
R4/RRR4-6/2	1519.413	1520.712	-1517.963	0.317	1580.045	0.239	20	0.180	R.TLFDLQEVSAQIR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1645.122	1644.958	100.204	0.398	1539.855	0.245	20	0.174	R.GIAMEGATDALIQLIK.D
R4/RRR4-6/2	1519.928	1520.712	-1177.348	0.342	1317.423	0.283	17	0.166	R.TLFDLQEVSAQIR.E
R4/RRR4-6/2	1819.401	1820.101	-937.225	0.366	658.032	0.487	17	0.152	K.SAIGIGTLLM*DGLGDTIR.V
R4/RRR4-6/2	1662.299	1660.958	205.975	0.479	1068.661	0.325	18	0.152	R.GIAM*EGATDALIQLIK.D
R4/RRR4-5/2	862.069	862.008	71.424	0.363	715.369	0.342	11	0.148	-.APELLYR.-
R4/RRR4-5/2	861.388	862.008	-1886.765	0.252	610.732	0.280	11	0.138	-.APELLYR.-
R4/RRR4-6/2	1660.448	1660.958	-912.092	0.354	926.974	0.199	18	0.134	R.GIAM*EGATDALIQLIK.D
R4/RRR4-4/2	1650.352	1650.773	-255.697	0.465	919.372	0.460	16	0.165	K.YLVTYSSHEPSNPR.D
R4/RRR4-4/2	1075.194	1075.286	-85.475	0.429	812.814	0.424	13	0.162	R.VVLNIFDVR.T
R4/RRR4-4/2	1220.920	1221.343	-347.840	0.455	876.526	0.403	15	0.162	K.STYTGFELFR.I
R4/RRR4-4/2	1075.171	1075.286	-107.113	0.395	734.773	0.366	13	0.153	R.VVLNIFDVR.T
R4/RRR4-4/2	1303.983	1304.439	-350.095	0.336	878.649	0.362	16	0.151	K.QANALFWSPGGR.F
R4/RRR4-4/2	1074.944	1075.286	-319.105	0.372	739.090	0.314	13	0.147	R.VVLNIFDVR.T
R4/RRR4-3/2	1248.878	1249.441	-1255.230	0.450	1474.601	0.505	18	0.224	R.AALNLAYQGLSK.V
R4/RRR4-3/2	1248.798	1249.441	-1319.725	0.413	1044.076	0.408	16	0.168	R.AALNLAYQGLSK.V
R4/RRR4-3/2	1423.818	1424.586	-1245.901	0.294	1165.308	0.173	19	0.141	K.AGWPVAGSPDPTLR.I
R4/RRR4-24/3	1900.213	1901.012	-949.550	0.514	2634.333	0.407	37	0.407	R.RASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-23/2	1745.244	1744.825	240.680	0.550	1809.171	0.576	24	0.280	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-24/3	1900.559	1901.012	-238.906	0.544	2108.771	0.411	40	0.270	R.RASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-23/2	1744.202	1744.825	-933.560	0.494	1531.553	0.583	24	0.245	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-24/2	1744.270	1744.825	-894.496	0.488	1450.708	0.568	24	0.232	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-23/2	1744.172	1744.825	-950.704	0.501	1420.971	0.568	24	0.228	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-24/2	1744.351	1744.825	-272.849	0.508	1258.283	0.565	23	0.210	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-24/2	1744.179	1744.825	-946.418	0.539	1059.367	0.583	22	0.196	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-24/2	1168.422	1169.268	-1584.772	0.368	621.908	0.406	15	0.155	R.FYTDEAPGLR.L
R4/RRR4-23/3	1901.350	1901.012	178.663	0.458	1563.904	0.346	32	0.154	R.RASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-23/2	1168.869	1169.268	-342.694	0.408	530.000	0.397	14	0.153	R.FYTDEAPGLR.L
R4/RRR4-24/2	1170.321	1169.268	45.131	0.367	356.366	0.316	13	0.147	R.FYTDEAPGLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	1168.298	1169.268	-1691.206	0.288	415.413	0.368	14	0.147	R.FYTDEAPGLR.L
R4/RRR4-24/2	1168.411	1169.268	-1594.218	0.263	419.634	0.327	14	0.142	-.FYTDEAPGLR.-
R4/RRR4-24/3	1744.787	1744.825	-22.061	0.535	728.364	0.525	31	0.123	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-24/3	1744.449	1744.825	-216.201	0.493	636.962	0.445	30	0.104	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-24/3	1744.919	1744.825	53.932	0.487	575.958	0.454	28	0.104	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-23/3	1745.006	1744.825	103.605	0.357	450.601	0.365	29	0.094	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-23/3	1744.299	1744.825	-877.572	0.327	486.603	0.337	28	0.091	R.ASTAGGSGGFSGGGGSNM*LR.F
R4/RRR4-15/2	1868.620	1868.124	265.916	0.594	2779.981	0.644	29	0.499	R.LQAQSALAEAAAASGVALPK.G
R4/RRR4-15/2	1866.923	1868.124	-1182.614	0.396	2744.438	0.527	30	0.442	R.LQAQSALAEAAAASGVALPK.G
R4/RRR4-15/2	1867.627	1868.124	-267.317	0.540	2226.313	0.606	28	0.363	R.LQAQSALAEAAAASGVALPK.G
R4/RRR4-15/3	1867.412	1868.124	-919.725	0.501	2175.431	0.520	36	0.348	R.LQAQSALAEAAAASGVALPK.G
R4/RRR4-15/3	1867.750	1868.124	-200.836	0.457	2186.150	0.485	36	0.332	R.LQAQSALAEAAAASGVALPK.G
R4/RRR4-15/2	1480.145	1480.565	-284.522	0.496	954.957	0.515	21	0.184	K.QYLAGGQDTSNLGR.G
R4/RRR4-15/2	1480.236	1480.565	-223.048	0.437	1043.927	0.471	22	0.181	K.QYLAGGQDTSNLGR.G
R4/RRR4-15/2	1481.797	1480.565	156.776	0.415	278.124	0.518	17	0.157	K.QYLAGGQDTSNLGR.G
R4/RRR4-15/2	1479.660	1480.565	-1290.977	0.372	646.397	0.416	19	0.153	K.QYLAGGQDTSNLGR.G
R4/RRR4-15/2	1066.972	1067.174	-190.098	0.305	777.544	0.327	13	0.146	K.SVIQVDDYK.K
R4/RRR4-15/2	1066.479	1067.174	-1594.014	0.130	886.836	0.238	13	0.133	K.SVIQVDDYK.K
R4/RRR4-17/2	1759.358	1759.979	-924.497	0.559	2545.800	0.554	25	0.413	K.IAELKEALESVTAEQK.Y
R4/RRR4-17/2	1204.827	1205.297	-391.509	0.470	1104.628	0.467	17	0.185	K.EALESVTAEQK.Y
R4/RRR4-17/2	1181.138	1180.292	-130.778	0.464	923.217	0.352	15	0.157	K.DEHLDPINVK.I
R4/RRR4-17/2	1179.460	1180.292	-1558.418	0.378	798.254	0.354	14	0.151	K.DEHLDPINVK.I
R4/RRR4-17/3	1760.012	1759.979	18.454	0.489	825.852	0.516	28	0.125	K.IAELKEALESVTAEQK.Y
R4/RRR4-17/3	1759.343	1759.979	-932.864	0.411	819.281	0.441	24	0.107	K.IAELKEALESVTAEQK.Y
R4/RRR4-17/3	1180.392	1180.292	84.824	0.484	1062.795	0.327	21	0.101	K.DEHLDPINVK.I
R4/RRR4-17/3	1180.487	1180.292	165.250	0.477	989.859	0.331	21	0.098	K.DEHLDPINVK.I
R4/RRR4-17/3	1180.360	1180.292	57.598	0.437	909.282	0.276	19	0.088	K.DEHLDPINVK.I
R4/RRR4-18/3	1180.520	1180.292	193.093	0.399	548.091	0.290	17	0.086	-.DEHLDPINVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1567.362	1567.727	-233.459	0.537	2886.597	0.557	23	0.490	K.LQLNDFTGAVFEGR.L
R4/RRR4-18/2	1568.713	1567.727	-9.414	0.528	2148.331	0.537	22	0.329	K.LQLNDFTGAVFEGR.L
R4/RRR4-18/2	1567.302	1567.727	-272.293	0.494	1982.581	0.538	21	0.301	K.LQLNDFTGAVFEGR.L
R4/RRR4-18/2	1132.136	1132.209	-65.495	0.411	1169.154	0.399	18	0.176	K.NSDVAAAVAGTR.W
R4/RRR4-18/2	1887.779	1887.060	-149.378	0.435	670.798	0.437	18	0.151	R.LYSPDDFAQLESM*PTR.V
R4/RRR4-18/2	1131.369	1132.209	-1631.479	0.220	544.510	0.335	15	0.137	K.NSDVAAAVAGTR.W
R4/RRR4-22/2	1495.011	1494.625	259.071	0.572	2361.963	0.610	21	0.395	R.TYCAEIAHNVSTK.K
R4/RRR4-22/2	1494.226	1494.625	-267.747	0.545	2037.535	0.597	20	0.329	R.TYCAEIAHNVSTK.K
R4/RRR4-22/2	1494.106	1494.625	-1019.462	0.530	1815.427	0.548	19	0.278	R.TYCAEIAHNVSTK.K
R4/RRR4-22/2	1172.000	1172.357	-304.901	0.513	1678.273	0.492	17	0.246	R.AAQLDIVVTNK.L
R4/RRR4-21/2	1172.181	1172.357	-149.952	0.446	1734.306	0.437	16	0.238	R.AAQLDIVVTNK.L
R4/RRR4-22/2	1173.351	1172.357	-5.072	0.517	1669.221	0.456	17	0.236	R.AAQLDIVVTNK.L
R4/RRR4-22/2	1172.033	1172.357	-276.583	0.488	1661.964	0.463	16	0.235	R.AAQLDIVVTNK.L
R4/RRR4-21/2	1171.788	1172.357	-1343.035	0.436	1513.668	0.412	16	0.208	R.AAQLDIVVTNK.L
R4/RRR4-26/2	1172.051	1172.357	-261.954	0.345	1340.768	0.436	16	0.194	R.AAQLDIVVTNK.L
R4/RRR4-22/2	1223.242	1223.442	-163.911	0.438	919.306	0.401	14	0.165	R.YLCLKPSWR.R
R4/RRR4-22/2	1223.310	1223.442	-107.854	0.398	955.731	0.304	14	0.153	R.YLCLKPSWR.R
R4/RRR4-22/2	1223.280	1223.442	-133.179	0.393	717.763	0.294	12	0.144	R.YLCLKPSWR.R
R4/RRR4-27/3	1671.210	1671.814	-962.678	0.439	2318.025	0.394	31	0.315	R.VTSGEQQVVSGM*NYR.L
R4/RRR4-27/2	1671.670	1671.814	-86.540	0.568	1119.882	0.542	21	0.199	R.VTSGEQQVVSGM*NYR.L
R4/RRR4-27/2	1671.284	1671.814	-918.416	0.480	1191.525	0.459	21	0.188	R.VTSGEQQVVSGM*NYR.L
R4/RRR4-27/2	1043.036	1043.116	-76.606	0.377	863.576	0.541	17	0.180	R.HASLSSDGLR.F
R4/RRR4-26/2	1042.328	1043.116	-1720.339	0.385	702.520	0.545	16	0.173	R.HASLSSDGLR.F
R4/RRR4-27/2	1042.397	1043.116	-1653.744	0.360	680.544	0.567	16	0.172	R.HASLSSDGLR.F
R4/RRR4-27/2	1042.717	1043.116	-384.155	0.357	726.327	0.540	15	0.170	R.HASLSSDGLR.F
R4/RRR4-26/2	1042.799	1043.116	-304.402	0.362	666.519	0.527	15	0.167	R.HASLSSDGLR.F
R4/RRR4-27/2	1043.002	1043.116	-109.713	0.422	529.864	0.500	14	0.163	R.HASLSSDGLR.F
R4/RRR4-26/2	1042.322	1043.116	-1726.222	0.282	434.751	0.517	14	0.154	R.HASLSSDGLR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-27/3	1827.866	1828.001	-74.002	0.434	1492.579	0.287	28	0.127	R.RVTSGEQQVVSGM*NYR.L
R4/RRR4-4/2	1177.299	1177.332	-27.519	0.394	1437.084	0.420	15	0.202	K.SFEVTELPVR.S
R4/RRR4-4/2	1195.942	1196.338	-332.787	0.475	1280.601	0.468	15	0.199	K.HNEIQTVNIK.T
R4/RRR4-2/2	1178.380	1177.332	40.874	0.357	1190.032	0.414	15	0.179	-.SFEVTELPVR.-
R4/RRR4-4/2	1177.341	1177.332	7.944	0.387	1092.232	0.441	14	0.177	K.SFEVTELPVR.S
R4/RRR4-4/2	1176.982	1177.332	-297.993	0.316	1217.607	0.330	14	0.167	K.SFEVTELPVR.S
R4/RRR4-1/2	1322.088	1322.449	-274.178	0.364	882.057	0.390	15	0.157	R.LENTLNYGLER.V
R4/RRR4-3/2	1196.017	1196.338	-269.706	0.375	770.635	0.387	16	0.156	K.HNEIQTVNIK.T
R4/RRR4-1/2	1321.955	1322.449	-374.973	0.356	709.087	0.351	15	0.148	R.LENTLNYGLER.V
R4/RRR4-4/2	1557.631	1557.799	-108.050	0.395	902.233	0.241	18	0.140	R.QMYLLGYLANQSR.V
R4/RRR4-3/2	1519.066	1518.819	162.763	0.520	1753.291	0.528	20	0.266	R.LLEVELYPTLLSK.A
R4/RRR4-3/2	1335.911	1336.691	-1336.316	0.326	883.176	0.457	17	0.163	R.ALALVVPSVVVLR.T
R4/RRR4-6/2	1336.582	1336.691	-81.858	0.423	670.127	0.447	15	0.154	-.ALALVVPSVVVLR.-
R4/RRR4-1/2	1431.278	1431.702	-297.059	0.357	1273.053	0.209	18	0.151	R.GIPIYAISQVLEK.I
R4/RRR4-6/2	1412.311	1412.572	-185.574	0.324	661.683	0.353	15	0.141	K.SSSASAFFLPLER.V
R4/RRR4-2/2	1336.462	1336.691	-171.738	0.306	413.393	0.440	12	0.128	-.ALALVVPSVVVLR.-
R4/RRR4-3/2	1336.703	1336.691	8.646	0.300	400.377	0.309	12	0.126	-.ALALVVPSVVVLR.-
R4/RRR4-4/2	1221.103	1221.388	-234.185	0.561	1693.469	0.416	17	0.228	R.AVAYLLTNAER.V
R4/RRR4-4/2	1202.261	1202.388	-105.974	0.467	1432.827	0.513	19	0.224	R.HALSAISAIYR.L
R4/RRR4-4/2	1220.631	1221.388	-1443.966	0.445	1622.650	0.399	17	0.217	R.AVAYLLTNAER.V
R4/RRR4-4/2	1220.787	1221.388	-1315.606	0.450	1556.340	0.355	17	0.201	R.AVAYLLTNAER.V
R4/RRR4-4/2	1201.422	1202.388	-1640.910	0.406	1171.977	0.404	18	0.179	R.HALSAISAIYR.L
R4/RRR4-4/2	1168.883	1169.354	-404.910	0.400	950.748	0.386	15	0.163	R.LIDTFYQIR.A
R4/RRR4-3/2	1203.178	1202.388	-174.887	0.356	713.363	0.450	15	0.159	R.HALSAISAIYR.L
R4/RRR4-3/2	1202.641	1202.388	211.593	0.294	759.040	0.478	14	0.158	R.HALSAISAIYR.L
R4/RRR4-4/2	1818.476	1819.009	-845.292	0.461	542.087	0.460	18	0.152	K.LVDRPQNYTLAPESSK.Q
R4/RRR4-4/2	1201.308	1202.388	-1736.360	0.306	637.832	0.373	14	0.147	R.HALSAISAIYR.L
R4/RRR4-4/2	1819.274	1819.009	146.336	0.435	377.858	0.367	15	0.139	K.LVDRPQNYTLAPESSK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/3	1819.108	1819.009	54.806	0.418	717.716	0.476	22	0.106	K.LVDRPQNYTLAPESSK.Q
R4/RRR4-14/2	1879.817	1879.019	-108.029	0.633	2534.516	0.582	24	0.420	R.AWDVLNEIFNEDGSLR.Q
R4/RRR4-14/2	1293.526	1294.485	-1518.865	0.498	1400.940	0.575	19	0.234	K.VIQDHVATVVGR.W
R4/RRR4-14/2	1293.576	1294.485	-1480.094	0.494	1424.966	0.536	19	0.228	K.VIQDHVATVVGR.W
R4/RRR4-14/2	1294.180	1294.485	-236.193	0.512	1358.837	0.509	19	0.216	K.VIQDHVATVVGR.W
R4/RRR4-14/2	935.085	935.059	27.351	0.477	474.459	0.403	13	0.157	R.VLGEDFVR.I
R4/RRR4-14/2	934.519	935.059	-1653.038	0.401	473.725	0.399	13	0.154	R.VLGEDFVR.I
R4/RRR4-11/2	1494.653	1494.781	-85.898	0.552	3098.452	0.491	24	0.514	K.MVGYALQAAEILSK.E
R4/RRR4-11/2	1494.362	1494.781	-281.242	0.518	2608.867	0.536	23	0.418	K.MVGYALQAAEILSK.E
R4/RRR4-11/2	1494.376	1494.781	-272.063	0.532	2674.195	0.497	23	0.417	K.MVGYALQAAEILSK.E
R4/RRR4-11/2	1510.185	1510.781	-1059.915	0.451	2341.015	0.521	24	0.358	K.M*VGYALQAAEILSK.E
R4/RRR4-11/2	1202.070	1201.355	-237.587	0.529	1947.751	0.381	19	0.253	K.EGISAEVINLR.S
R4/RRR4-11/2	1200.719	1201.355	-1366.553	0.497	1619.439	0.337	18	0.203	K.EGISAEVINLR.S
R4/RRR4-11/2	1704.238	1704.929	-995.335	0.444	861.537	0.417	21	0.160	R.IAGADVPM*PYAANLER.M
R4/RRR4-11/2	1704.257	1704.929	-983.973	0.426	776.525	0.406	20	0.155	R.IAGADVPM*PYAANLER.M
R4/RRR4-11/2	1704.399	1704.929	-900.274	0.376	773.300	0.373	20	0.150	R.IAGADVPM*PYAANLER.M
R4/RRR4-17/2	1551.297	1551.685	-250.557	0.504	2710.639	0.466	21	0.412	K.LQIWDTAGQESFR.S
R4/RRR4-18/2	1550.836	1551.685	-1195.885	0.457	2541.055	0.512	21	0.394	K.LQIWDTAGQESFR.S
R4/RRR4-17/2	1551.266	1551.685	-271.004	0.484	2576.944	0.486	21	0.392	K.LQIWDTAGQESFR.S
R4/RRR4-18/2	1550.534	1551.685	-1391.396	0.429	2458.639	0.502	21	0.373	K.LQIWDTAGQESFR.S
R4/RRR4-18/2	1551.100	1551.685	-1025.023	0.508	2376.585	0.538	21	0.370	K.LQIWDTAGQESFR.S
R4/RRR4-17/2	1551.750	1551.685	42.165	0.476	2146.990	0.457	21	0.303	K.LQIWDTAGQESFR.S
R4/RRR4-17/2	1358.248	1358.435	-137.884	0.432	1130.185	0.471	16	0.185	R.AVSYEEGEQFAK.E
R4/RRR4-18/2	1320.179	1320.519	-258.715	0.441	1325.444	0.350	16	0.177	-.GAAGALLVYDITR.-
R4/RRR4-18/2	1358.242	1358.435	-142.391	0.426	1118.381	0.427	16	0.176	R.AVSYEEGEQFAK.E
R4/RRR4-18/2	1358.094	1358.435	-251.492	0.403	1060.758	0.441	16	0.175	R.AVSYEEGEQFAK.E
R4/RRR4-17/2	1358.144	1358.435	-214.792	0.426	933.126	0.456	15	0.169	R.AVSYEEGEQFAK.E
R4/RRR4-18/2	1359.097	1358.435	-249.145	0.466	749.784	0.516	14	0.168	R.AVSYEEGEQFAK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1320.920	1320.519	303.875	0.343	923.734	0.441	16	0.163	R.GAAGALLVYDITR.R
R4/RRR4-17/2	1357.733	1358.435	-1257.576	0.306	656.043	0.360	14	0.145	R.AVSYEEGEQFAK.E
R4/RRR4-17/2	1319.901	1320.519	-1229.801	0.380	744.872	0.349	14	0.145	R.GAAGALLVYDITR.R
R4/RRR4-18/2	1320.102	1320.519	-316.976	0.349	667.397	0.325	14	0.141	R.GAAGALLVYDITR.R
R4/RRR4-17/2	1201.609	1202.383	-1480.885	0.449	2038.202	0.353	18	0.258	K.INIKDDVSAVK.K
R4/RRR4-17/2	1201.814	1202.383	-1309.174	0.436	1692.280	0.361	18	0.217	K.INIKDDVSAVK.K
R4/RRR4-17/2	1201.976	1202.383	-339.163	0.414	1653.081	0.336	18	0.207	K.INIKDDVSAVK.K
R4/RRR4-17/2	1197.118	1197.323	-171.579	0.520	1128.822	0.544	18	0.204	R.HLVAVQTDEGK.A
R4/RRR4-17/2	1196.990	1197.323	-279.204	0.501	1089.404	0.444	18	0.182	R.HLVAVQTDEGK.A
R4/RRR4-17/2	1197.000	1197.323	-270.405	0.469	1014.091	0.442	17	0.176	R.HLVAVQTDEGK.A
R4/RRR4-17/3	1771.949	1771.955	-3.159	0.446	615.213	0.515	27	0.111	R.HLVAVQTDEGKAFAER.E
R4/RRR4-21/2	1500.572	1499.734	-108.487	0.616	1686.469	0.618	20	0.282	K.APLLDVTQFGYFK.V
R4/RRR4-21/2	1500.461	1499.734	-182.914	0.600	1716.755	0.602	20	0.281	K.APLLDVTQFGYFK.V
R4/RRR4-21/2	1498.678	1499.734	-1376.061	0.455	1809.058	0.564	20	0.281	K.APLLDVTQFGYFK.V
R4/RRR4-21/2	1586.020	1585.829	120.535	0.540	1099.098	0.454	18	0.180	R.ILFDKYHPGYFGK.V
R4/RRR4-21/3	969.404	969.077	338.269	0.492	769.144	0.501	16	0.120	K.YHPGYFGK.V
R4/RRR4-21/3	969.318	969.077	249.060	0.468	728.945	0.445	17	0.108	K.YHPGYFGK.V
R4/RRR4-21/3	968.925	969.077	-157.034	0.423	580.705	0.377	15	0.096	K.YHPGYFGK.V
R4/RRR4-22/2	1495.183	1495.659	-319.574	0.533	1960.805	0.615	22	0.322	K.ITLISDFGEISGSR.G
R4/RRR4-22/2	1495.291	1495.659	-247.414	0.508	1850.961	0.593	22	0.297	K.ITLISDFGEISGSR.G
R4/RRR4-22/2	1495.337	1495.659	-216.538	0.514	1599.737	0.624	22	0.270	K.ITLISDFGEISGSR.G
R4/RRR4-22/2	1623.347	1623.832	-299.850	0.458	1519.648	0.522	22	0.232	R.KITLISDFGEISGSR.G
R4/RRR4-22/2	1623.332	1623.832	-926.994	0.429	1538.655	0.497	21	0.227	R.KITLISDFGEISGSR.G
R4/RRR4-22/3	1623.507	1623.832	-201.261	0.388	1722.787	0.393	27	0.191	R.KITLISDFGEISGSR.G
R4/RRR4-22/3	1624.593	1623.832	-147.693	0.481	1423.141	0.504	27	0.186	R.KITLISDFGEISGSR.G
R4/RRR4-22/3	1495.499	1495.659	-107.554	0.393	1477.948	0.415	27	0.161	K.ITLISDFGEISGSR.G
R4/RRR4-22/2	1520.790	1519.837	-30.964	0.428	1075.593	0.535	22	0.147	K.IMLTHVLHGQGSII.-
R4/RRR4-22/3	1623.756	1623.832	-47.181	0.416	1321.675	0.393	27	0.137	R.KITLISDFGEISGSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1519.188	1519.837	-1088.866	0.392	1129.328	0.458	21	0.134	K.IMLTHVLHGQGSII.-
R4/RRR4-22/3	1495.649	1495.659	-6.731	0.420	1266.022	0.380	24	0.129	-.ITLISDFGEISGSR.-
R4/RRR4-22/2	1535.418	1535.837	-273.638	0.396	1023.716	0.406	20	0.113	K.IM*LTHVLHGQGSII.-
R4/RRR4-22/2	1535.226	1535.837	-1052.445	0.405	1278.924	0.264	21	0.109	K.IM*LTHVLHGQGSII.-
R4/RRR4-22/2	1536.704	1535.837	-86.332	0.412	817.956	0.416	20	0.108	K.IM*LTHVLHGQGSII.-
R4/RRR4-22/3	1495.718	1495.659	39.315	0.377	1104.308	0.328	24	0.103	-.ITLISDFGEISGSR.-
R4/RRR4-22/2	1518.641	1519.837	-1450.770	0.207	765.364	0.197	18	0.090	K.IMLTHVLHGQGSII.-
R4/RRR4-14/2	1617.214	1617.743	-948.444	0.502	2745.032	0.503	25	0.434	R.ELTAEVQQSGVTGAAR.V
R4/RRR4-14/2	1617.300	1617.743	-275.004	0.532	2753.144	0.465	24	0.420	R.ELTAEVQQSGVTGAAR.V
R4/RRR4-13/2	1617.225	1617.743	-941.624	0.529	2570.034	0.492	24	0.392	R.ELTAEVQQSGVTGAAR.V
R4/RRR4-13/2	1617.171	1617.743	-974.816	0.499	2301.869	0.456	23	0.327	R.ELTAEVQQSGVTGAAR.V
R4/RRR4-13/2	1363.216	1363.455	-175.462	0.463	1392.343	0.491	19	0.212	K.VFGESSPEAQPSK.S
R4/RRR4-14/2	1363.040	1363.455	-305.194	0.455	1072.205	0.461	17	0.178	K.VFGESSPEAQPSK.S
R4/RRR4-13/2	917.708	918.075	-400.728	0.372	1105.136	0.375	14	0.168	K.GIVGPVYGR.F
R4/RRR4-10/2	1870.525	1871.037	-810.905	0.493	2976.432	0.482	24	0.480	K.LAYVALDYEQELDTAR.S
R4/RRR4-10/2	1870.711	1871.037	-174.920	0.550	2256.574	0.541	23	0.348	K.LAYVALDYEQELDTAR.S
R4/RRR4-10/2	1870.497	1871.037	-826.103	0.526	1832.299	0.543	24	0.280	K.LAYVALDYEQELDTAR.S
R4/RRR4-3/2	1561.256	1560.692	-279.857	0.455	1186.188	0.470	20	0.190	R.TYINPYATFADAGR.K
R4/RRR4-4/2	1560.602	1560.692	-57.791	0.404	1006.642	0.465	18	0.173	R.TYINPYATFADAGR.K
R4/RRR4-3/2	1587.653	1587.888	-148.422	0.454	802.470	0.459	19	0.163	K.LLVFQSTLPSLGVGR.L
R4/RRR4-3/3	1581.378	1581.799	-266.549	0.487	1433.241	0.424	30	0.159	R.LTTHAIPASQSLVSR.W
R4/RRR4-3/2	1331.269	1331.500	-174.063	0.380	648.657	0.445	18	0.158	R.QADTGAIVSLLSR.I
R4/RRR4-3/2	1331.062	1331.500	-330.647	0.404	513.695	0.464	17	0.157	R.QADTGAIVSLLSR.I
R4/RRR4-3/2	1587.294	1587.888	-1007.281	0.389	837.463	0.395	19	0.155	K.LLVFQSTLPSLGVGR.L
R4/RRR4-2/2	1589.297	1587.888	257.877	0.410	874.828	0.377	19	0.155	K.LLVFQSTLPSLGVGR.L
R4/RRR4-3/2	1331.283	1331.500	-163.485	0.391	542.126	0.439	17	0.154	R.QADTGAIVSLLSR.I
R4/RRR4-2/2	1331.442	1331.500	-43.828	0.427	437.832	0.409	16	0.151	R.QADTGAIVSLLSR.I
R4/RRR4-3/2	1581.231	1581.799	-994.340	0.339	700.463	0.377	20	0.147	R.LTTHAIPASQSLVSR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1332.320	1331.500	-136.064	0.266	361.878	0.459	13	0.144	R.QADTGAIVSLLSR.I
R4/RRR4-2/2	1331.368	1331.500	-99.560	0.301	398.893	0.352	14	0.142	R.QADTGAIVSLLSR.I
R4/RRR4-5/3	1581.411	1581.799	-245.988	0.287	958.101	0.217	25	0.077	R.LTTHAIPASQSLVSR.W
R4/RRR4-17/2	1744.544	1744.968	-243.506	0.631	1772.292	0.609	26	0.292	K.KLSVETTANQDPLVTK.G
R4/RRR4-17/2	1744.506	1744.968	-265.619	0.593	1643.510	0.590	25	0.268	K.KLSVETTANQDPLVTK.G
R4/RRR4-17/2	1744.521	1744.968	-256.704	0.573	1482.633	0.594	24	0.248	K.KLSVETTANQDPLVTK.G
R4/RRR4-17/2	1616.329	1616.795	-289.335	0.460	1635.826	0.529	20	0.246	K.LSVETTANQDPLVTK.G
R4/RRR4-17/2	1616.315	1616.795	-297.745	0.475	1528.824	0.533	19	0.234	K.LSVETTANQDPLVTK.G
R4/RRR4-17/2	1616.395	1616.795	-248.041	0.479	1244.923	0.528	18	0.202	K.LSVETTANQDPLVTK.G
R4/RRR4-17/3	1505.677	1505.702	-16.810	0.567	1479.938	0.414	27	0.159	K.NVRPDYLSNIWK.V
R4/RRR4-17/2	1505.530	1505.702	-115.124	0.434	791.731	0.370	15	0.151	K.NVRPDYLSNIWK.V
R4/RRR4-17/2	1505.247	1505.702	-303.122	0.425	814.889	0.355	15	0.150	K.NVRPDYLSNIWK.V
R4/RRR4-17/3	1505.949	1505.702	163.927	0.572	871.577	0.389	25	0.105	K.NVRPDYLSNIWK.V
R4/RRR4-17/3	1505.214	1505.702	-325.384	0.498	654.239	0.345	23	0.078	-.NVRPDYLSNIWK.-
R4/RRR4-24/3	1717.510	1717.776	-155.600	0.559	1996.484	0.477	30	0.281	K.HGYIGEFEELDDHR.S
R4/RRR4-24/2	898.942	899.073	-146.635	0.430	652.839	0.403	12	0.156	K.IVVQLNGR.L
R4/RRR4-24/2	960.940	961.095	-161.510	0.307	575.517	0.351	12	0.144	R.TSVLNDALK.S
R4/RRR4-24/2	960.448	961.095	-1720.019	0.270	751.780	0.311	13	0.143	R.TSVLNDALK.S
R4/RRR4-24/2	898.494	899.073	-1762.854	0.327	871.550	0.220	13	0.141	K.IVVQLNGR.L
R4/RRR4-25/2	1032.114	1032.173	-57.132	0.462	1399.101	0.506	17	0.219	K.AVQASELVSK.H
R4/RRR4-25/2	1032.088	1032.173	-82.164	0.464	1375.055	0.429	16	0.200	K.AVQASELVSK.H
R4/RRR4-24/2	1032.301	1032.173	123.989	0.431	1235.386	0.491	16	0.199	K.AVQASELVSK.H
R4/RRR4-24/2	1032.294	1032.173	117.229	0.468	1204.504	0.503	15	0.199	K.AVQASELVSK.H
R4/RRR4-25/2	1031.414	1032.173	-1710.766	0.357	1034.235	0.471	15	0.178	K.AVQASELVSK.H
R4/RRR4-24/2	1032.903	1032.173	-261.800	0.450	946.083	0.379	14	0.161	K.AVQASELVSK.H
R4/RRR4-25/2	1504.878	1504.716	107.915	0.342	535.397	0.499	14	0.150	K.NKQHVVQPPTVEK.C
R4/RRR4-25/3	1247.775	1247.424	282.722	0.497	919.645	0.449	22	0.117	R.SKAVQASELVSK.H
R4/RRR4-25/3	1247.504	1247.424	64.607	0.475	872.761	0.401	22	0.105	R.SKAVQASELVSK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/3	1247.121	1247.424	-243.006	0.359	1006.684	0.326	23	0.096	R.SKAVQASELVSK.H
R4/RRR4-17/3	1403.558	1403.520	26.849	0.579	2525.914	0.423	31	0.369	K.IKSEGEAEAAAAQK.S
R4/RRR4-17/3	1403.688	1403.520	119.610	0.557	2258.923	0.371	29	0.278	K.IKSEGEAEAAAAQK.S
R4/RRR4-17/3	1403.589	1403.520	48.830	0.561	2254.782	0.357	30	0.269	K.IKSEGEAEAAAAQK.S
R4/RRR4-16/3	1403.650	1403.520	92.660	0.574	2168.876	0.389	30	0.266	K.IKSEGEAEAAAAQK.S
R4/RRR4-9/2	1886.337	1887.141	-959.625	0.462	2432.743	0.532	25	0.378	R.AVCMISNSTSVVEVFSR.I
R4/RRR4-9/2	1886.103	1887.141	-1083.732	0.440	1908.242	0.509	23	0.278	R.AVCMISNSTSVVEVFSR.I
R4/RRR4-9/2	1600.312	1599.804	-308.373	0.569	1492.687	0.577	19	0.245	R.TIQFVDWCPTGFK.C
R4/RRR4-9/2	1599.431	1599.804	-233.984	0.486	1434.688	0.559	19	0.232	R.TIQFVDWCPTGFK.C
R4/RRR4-9/2	1598.821	1599.804	-1244.230	0.334	1219.482	0.456	17	0.185	R.TIQFVDWCPTGFK.C
R4/RRR4-9/2	1886.079	1887.141	-1096.729	0.371	1246.715	0.382	19	0.173	R.AVCMISNSTSVVEVFSR.I
R4/RRR4-25/2	1311.110	1311.573	-353.702	0.460	963.413	0.476	17	0.176	K.TVTAMDVVYALK.R
R4/RRR4-25/2	1328.247	1327.555	-232.347	0.379	1255.989	0.346	18	0.172	K.ETIQGITKPAIR.R
R4/RRR4-24/2	1468.072	1467.759	213.535	0.446	825.790	0.453	16	0.164	K.TVTAMDVVYALKR.Q
R4/RRR4-24/2	1311.230	1311.573	-262.348	0.429	654.490	0.498	15	0.163	K.TVTAMDVVYALK.R
R4/RRR4-25/2	1467.543	1467.759	-147.554	0.350	922.737	0.424	16	0.162	K.TVTAMDVVYALKR.Q
R4/RRR4-25/2	1467.282	1467.759	-326.319	0.347	885.136	0.412	16	0.159	K.TVTAMDVVYALKR.Q
R4/RRR4-24/2	1483.052	1483.758	-1154.103	0.413	481.305	0.502	16	0.159	K.TVTAM*DVVYALKR.Q
R4/RRR4-24/2	1484.333	1483.758	-287.501	0.402	452.512	0.485	16	0.157	K.TVTAM*DVVYALKR.Q
R4/RRR4-25/2	1468.332	1467.759	-291.981	0.367	749.767	0.438	15	0.157	K.TVTAMDVVYALKR.Q
R4/RRR4-25/2	1483.369	1483.758	-263.256	0.414	446.663	0.453	15	0.153	K.TVTAM*DVVYALKR.Q
R4/RRR4-25/2	1483.244	1483.758	-1024.026	0.390	346.082	0.478	14	0.153	K.TVTAM*DVVYALKR.Q
R4/RRR4-25/2	1483.440	1483.758	-215.042	0.387	385.188	0.458	14	0.151	K.TVTAM*DVVYALKR.Q
R4/RRR4-24/2	1311.015	1311.573	-1191.909	0.347	583.314	0.395	14	0.147	K.TVTAMDVVYALK.R
R4/RRR4-25/2	1327.069	1327.572	-1135.808	0.297	674.256	0.344	15	0.144	K.TVTAM*DVVYALK.R
R4/RRR4-11/2	1743.407	1743.895	-280.816	0.595	2426.557	0.606	24	0.407	K.AYYAVEEVKENATQK.S
R4/RRR4-11/2	1743.420	1743.895	-273.580	0.592	1902.123	0.609	22	0.310	K.AYYAVEEVKENATQK.S
R4/RRR4-11/2	1087.960	1088.283	-297.618	0.492	1701.812	0.581	19	0.274	R.VVGVLLGTSSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1087.535	1088.283	-1612.239	0.521	1625.528	0.544	18	0.254	R.VVGVLLGTSSR.G
R4/RRR4-11/2	1088.162	1088.283	-111.910	0.434	1520.101	0.584	18	0.248	R.VVGVLLGTSSR.G
R4/RRR4-11/3	1974.476	1974.338	70.026	0.508	971.015	0.555	32	0.149	K.VVVHPLVLLSIVDHYNR.V
R4/RRR4-16/2	1662.448	1662.908	-277.699	0.580	2391.886	0.516	23	0.367	K.LQQVLNVYDEILSK.N
R4/RRR4-16/2	1661.513	1662.908	-1445.986	0.416	2261.855	0.437	21	0.316	K.LQQVLNVYDEILSK.N
R4/RRR4-16/2	1663.350	1662.908	265.976	0.633	1903.901	0.498	21	0.275	K.LQQVLNVYDEILSK.N
R4/RRR4-16/2	1342.950	1343.460	-1127.553	0.409	1640.938	0.377	17	0.214	R.YVCTQFPEGNK.T
R4/RRR4-16/2	1342.870	1343.460	-1187.431	0.471	1572.836	0.325	17	0.196	R.YVCTQFPEGNK.T
R4/RRR4-16/2	1274.948	1275.439	-386.110	0.450	960.288	0.434	16	0.170	K.LRDPNGQVTFK.H
R4/RRR4-16/2	1274.990	1275.439	-353.063	0.420	1046.164	0.370	16	0.165	K.LRDPNGQVTFK.H
R4/RRR4-16/2	1274.925	1275.439	-1191.076	0.417	668.467	0.420	14	0.154	K.LRDPNGQVTFK.H
R4/RRR4-16/3	1275.486	1275.439	36.984	0.448	926.204	0.404	25	0.108	K.LRDPNGQVTFK.H
R4/RRR4-16/3	1275.618	1275.439	140.929	0.383	744.168	0.418	22	0.101	K.LRDPNGQVTFK.H
R4/RRR4-16/3	1275.224	1275.439	-169.098	0.394	573.359	0.387	21	0.095	K.LRDPNGQVTFK.H
R4/RRR4-16/2	1519.290	1518.782	-324.899	0.493	2294.105	0.525	21	0.349	K.ASILLLQDAAAYLR.K
R4/RRR4-16/2	1518.530	1518.782	-166.547	0.402	2314.612	0.449	21	0.328	K.ASILLLQDAAAYLR.K
R4/RRR4-16/2	1518.322	1518.782	-303.898	0.309	2315.017	0.316	20	0.288	K.ASILLLQDAAAYLR.K
R4/RRR4-16/2	1518.346	1518.782	-288.411	0.335	1482.694	0.381	17	0.194	K.ASILLLQDAAAYLR.K
R4/RRR4-16/2	1146.762	1147.288	-1334.185	0.385	1275.448	0.413	17	0.186	K.ALAAEM*GPNTR.V
R4/RRR4-16/2	1517.990	1518.782	-1184.094	0.293	1593.307	0.273	18	0.185	K.ASILLLQDAAAYLR.K
R4/RRR4-16/2	1147.047	1147.288	-210.302	0.422	1043.776	0.485	17	0.183	K.ALAAEM*GPNTR.V
R4/RRR4-16/2	1146.985	1147.288	-264.754	0.457	1139.771	0.436	16	0.181	K.ALAAEM*GPNTR.V
R4/RRR4-16/2	1101.746	1102.180	-395.244	0.495	1112.445	0.391	17	0.175	K.NVDEAVEGLR.A
R4/RRR4-11/2	1306.148	1306.490	-262.338	0.491	2649.014	0.415	21	0.382	K.AFGAELVLTDAAK.G
R4/RRR4-11/2	1306.256	1306.490	-179.646	0.519	2400.566	0.467	21	0.351	K.AFGAELVLTDAAK.G
R4/RRR4-11/2	1115.028	1115.310	-253.389	0.416	1045.158	0.403	16	0.169	K.IQGIGAGFVPR.N
R4/RRR4-11/2	1307.957	1308.572	-1238.271	0.387	890.691	0.415	15	0.160	K.TPM*VYLNNIVK.G
R4/RRR4-12/2	1114.486	1115.310	-1642.023	0.375	750.679	0.365	14	0.149	-.IQGIGAGFVPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1305.958	1306.490	-1175.898	0.337	890.076	0.320	15	0.147	K.AFGAELVLTDAAK.G
R4/RRR4-12/2	1306.379	1306.490	-84.782	0.344	881.257	0.253	19	0.144	K.AFGAELVLTDAAK.G
R4/RRR4-11/2	1114.516	1115.310	-1614.184	0.288	716.328	0.290	14	0.141	K.IQGIGAGFVPR.N
R4/RRR4-11/2	1651.018	1651.932	-1162.623	0.481	2662.891	0.560	25	0.438	R.VPQVGSIAINDGVILR.N
R4/RRR4-11/2	1651.274	1651.932	-1007.032	0.499	2216.651	0.545	23	0.342	R.VPQVGSIAINDGVILR.N
R4/RRR4-11/2	1650.975	1651.932	-1188.906	0.475	2105.062	0.578	24	0.333	R.VPQVGSIAINDGVILR.N
R4/RRR4-11/2	1922.384	1922.258	65.625	0.557	1183.357	0.642	24	0.224	K.LIANIEAQPSIAVQNVLK.S
R4/RRR4-11/2	1106.928	1107.281	-320.392	0.500	1301.344	0.555	16	0.220	K.YGAVEDILVK.M
R4/RRR4-11/2	1922.717	1922.258	239.330	0.539	1087.867	0.580	22	0.200	K.LIANIEAQPSIAVQNVLK.S
R4/RRR4-11/2	1107.085	1107.281	-178.013	0.415	1304.701	0.462	16	0.199	K.YGAVEDILVK.M
R4/RRR4-11/2	1923.046	1922.258	-110.885	0.602	939.014	0.617	22	0.197	K.LIANIEAQPSIAVQNVLK.S
R4/RRR4-11/2	1921.985	1922.258	-142.607	0.551	880.014	0.614	22	0.192	K.LIANIEAQPSIAVQNVLK.S
R4/RRR4-11/2	1107.101	1107.281	-163.522	0.447	1071.841	0.511	15	0.190	K.YGAVEDILVK.M
R4/RRR4-11/2	1922.802	1922.258	-237.996	0.594	964.037	0.546	23	0.186	K.LIANIEAQPSIAVQNVLK.S
R4/RRR4-11/2	1923.381	1922.258	63.809	0.564	969.149	0.531	23	0.183	K.LIANIEAQPSIAVQNVLK.S
R4/RRR4-12/3	1558.941	1558.824	75.609	0.481	2065.805	0.475	29	0.286	K.FGM*LADKIYEVAGK.L
R4/RRR4-6/3	1558.325	1558.824	-321.294	0.437	1886.593	0.382	28	0.210	K.FGM*LADKIYEVAGK.L
R4/RRR4-6/2	1072.832	1072.199	-343.242	0.381	555.279	0.551	16	0.166	K.IPGHFGSTAGK.H
R4/RRR4-12/3	1558.614	1558.824	-134.941	0.440	1579.974	0.390	27	0.166	K.FGM*LADKIYEVAGK.L
R4/RRR4-12/2	1024.990	1025.227	-231.928	0.457	740.707	0.421	16	0.161	R.LGIEPAIGVR.A
R4/RRR4-6/2	1071.984	1072.199	-200.974	0.341	492.738	0.446	15	0.153	K.IPGHFGSTAGK.H
R4/RRR4-6/2	1072.150	1072.199	-45.863	0.349	566.362	0.378	16	0.150	K.IPGHFGSTAGK.H
R4/RRR4-6/3	1558.743	1558.824	-51.983	0.519	1312.490	0.442	25	0.150	K.FGM*LADKIYEVAGK.L
R4/RRR4-12/2	1073.266	1072.199	62.788	0.270	314.471	0.339	13	0.141	-.IPGHFGSTAGK.-
R4/RRR4-6/3	1542.087	1542.824	-1129.672	0.365	1168.459	0.302	24	0.103	K.FGMLADKIYEVAGK.L
R4/RRR4-10/3	1558.871	1558.824	30.725	0.328	1035.724	0.294	23	0.094	K.FGM*LADKIYEVAGK.L
R4/RRR4-16/2	1532.092	1532.672	-1033.744	0.473	1056.072	0.521	18	0.187	R.ATEGPIVADKNCEK.I
R4/RRR4-16/2	1532.000	1532.672	-1094.065	0.452	1051.784	0.504	19	0.184	R.ATEGPIVADKNCEK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1000.952	1001.116	-163.861	0.426	546.229	0.469	15	0.161	R.ATEGPIVADK.N
R4/RRR4-16/2	973.461	974.220	-1812.361	0.386	647.649	0.440	15	0.160	R.VVTSLTLLK.S
R4/RRR4-16/2	1000.995	1001.116	-121.044	0.349	661.727	0.446	16	0.158	R.ATEGPIVADK.N
R4/RRR4-16/2	1000.653	1001.116	-463.684	0.326	605.669	0.449	15	0.155	R.ATEGPIVADK.N
R4/RRR4-16/2	973.852	974.220	-378.254	0.377	662.674	0.367	15	0.153	R.VVTSLTLLK.S
R4/RRR4-16/2	974.014	974.220	-212.138	0.378	669.291	0.303	15	0.148	R.VVTSLTLLK.S
R4/RRR4-1/2	1714.932	1714.987	-31.957	0.403	1490.947	0.398	20	0.200	K.VQLVQFGILSPDEIR.Q
R4/RRR4-1/2	1715.253	1714.987	155.853	0.436	1228.540	0.319	19	0.164	K.VQLVQFGILSPDEIR.Q
R4/RRR4-2/2	964.918	965.130	-220.799	0.408	622.686	0.381	12	0.154	R.IPFGFIDR.T
R4/RRR4-2/2	1565.839	1565.708	83.618	0.456	1391.676	0.171	18	0.149	K.EAFEWVIGEIESR.F
R4/RRR4-2/2	964.883	965.130	-257.099	0.312	471.507	0.371	12	0.148	R.IPFGFIDR.T
R4/RRR4-2/3	1575.023	1575.831	-1151.215	0.349	1412.199	0.403	29	0.147	K.TPSLSVYLKPEVNK.K
R4/RRR4-2/2	964.953	965.130	-183.741	0.264	478.989	0.343	12	0.144	R.IPFGFIDR.T
R4/RRR4-1/2	1715.457	1714.987	275.312	0.367	703.327	0.270	15	0.135	-.VQLVQFGILSPDEIR.-
R4/RRR4-10/2	1344.417	1344.539	-91.399	0.548	1815.648	0.543	21	0.280	R.LVDIGTVTAQQAK.D
R4/RRR4-10/2	1345.416	1344.539	-91.695	0.580	1636.064	0.613	21	0.275	R.LVDIGTVTAQQAK.D
R4/RRR4-10/2	1115.274	1114.314	-35.417	0.485	1051.136	0.351	15	0.164	-.LLNCEVPLR.-
R4/RRR4-10/2	1169.200	1168.350	-128.448	0.393	836.399	0.371	15	0.156	K.DWGFSGVMLR.-
R4/RRR4-10/2	1168.380	1168.350	25.400	0.360	748.532	0.322	13	0.146	K.DWGFSGVMLR.-
R4/RRR4-10/2	1184.281	1184.349	-57.748	0.228	693.662	0.136	13	0.132	K.DWGFSGVM*LR.-
R4/RRR4-3/2	1637.347	1637.902	-952.560	0.419	573.360	0.488	19	0.158	R.IPGTELLPGDIVSIGR.S
R4/RRR4-3/2	1637.284	1637.902	-991.108	0.440	550.198	0.492	17	0.156	R.IPGTELLPGDIVSIGR.S
R4/RRR4-3/2	1637.693	1637.902	-127.963	0.415	471.822	0.491	17	0.154	R.IPGTELLPGDIVSIGR.S
R4/RRR4-3/2	1512.455	1512.690	-155.801	0.364	844.739	0.396	14	0.152	R.NIFEYPQPTFQK.L
R4/RRR4-2/2	1637.759	1637.902	-87.438	0.431	521.897	0.421	18	0.149	R.IPGTELLPGDIVSIGR.S
R4/RRR4-2/2	1637.425	1637.902	-292.486	0.410	502.679	0.410	17	0.147	R.IPGTELLPGDIVSIGR.S
R4/RRR4-3/2	1277.334	1276.460	-99.075	0.327	859.718	0.316	14	0.144	R.APDGGCIAFVLR.T
R4/RRR4-3/2	1346.079	1346.597	-1131.208	0.408	916.905	0.260	14	0.140	R.TDAVIQVIPYVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1346.302	1346.597	-219.410	0.315	490.151	0.335	12	0.137	-.TDAVIQVIPYVK.-
R4/RRR4-3/2	1275.247	1276.460	-1740.817	0.165	712.105	0.108	14	0.127	R.APDGGCIAFVLR.T
R4/RRR4-7/3	1170.243	1170.303	-51.289	0.468	1363.451	0.501	20	0.175	K.FGAAVVSPEHR.Y
R4/RRR4-7/3	1170.403	1170.303	85.705	0.437	1379.958	0.495	21	0.174	K.FGAAVVSPEHR.Y
R4/RRR4-7/3	1170.400	1170.303	83.823	0.509	1294.553	0.500	20	0.166	K.FGAAVVSPEHR.Y
R4/RRR4-8/3	1170.215	1170.303	-75.302	0.425	1451.101	0.431	21	0.162	K.FGAAVVSPEHR.Y
R4/RRR4-8/2	1481.066	1481.590	-1031.497	0.385	775.363	0.304	18	0.144	K.SSPFESLTTENLR.F
R4/RRR4-7/3	1299.757	1298.475	216.921	0.515	999.405	0.387	22	0.109	K.KFGAAVVSPEHR.Y
R4/RRR4-8/3	1299.041	1298.475	-335.320	0.529	1232.417	0.296	24	0.104	K.KFGAAVVSPEHR.Y
R4/RRR4-7/3	1299.143	1298.475	-256.836	0.536	1007.433	0.352	22	0.102	K.KFGAAVVSPEHR.Y
R4/RRR4-16/2	1479.775	1479.660	77.642	0.455	2223.381	0.457	19	0.315	R.STNEALLVIEAYR.T
R4/RRR4-16/2	1479.388	1479.660	-184.443	0.358	1938.717	0.451	18	0.266	R.STNEALLVIEAYR.T
R4/RRR4-15/2	1548.032	1546.705	211.759	0.397	1315.531	0.418	18	0.187	K.DLSGSFAFVVFDNK.S
R4/RRR4-16/2	1479.030	1479.660	-1105.268	0.300	1517.227	0.285	17	0.181	R.STNEALLVIEAYR.T
R4/RRR4-15/2	1030.602	1031.188	-1543.772	0.469	1131.073	0.378	15	0.174	R.LDNLSSLIR.Q
R4/RRR4-15/2	1030.986	1031.188	-197.090	0.555	1121.439	0.355	15	0.169	R.LDNLSSLIR.Q
R4/RRR4-15/2	1031.025	1031.188	-158.844	0.528	1101.595	0.342	15	0.166	R.LDNLSSLIR.Q
R4/RRR4-16/2	1030.570	1031.188	-1574.590	0.443	1165.535	0.300	15	0.163	R.LDNLSSLIR.Q
R4/RRR4-15/2	1479.024	1479.660	-1109.495	0.310	1108.487	0.246	15	0.147	R.STNEALLVIEAYR.T
R4/RRR4-15/2	1548.109	1546.705	262.049	0.371	462.845	0.319	12	0.131	-.DLSGSFAFVVFDNK.-
R4/RRR4-16/2	1031.029	1031.188	-154.568	0.359	722.202	0.184	12	0.124	-.LDNLSSLIR.-
R4/RRR4-18/2	1590.234	1590.716	-304.014	0.490	1474.648	0.490	24	0.222	R.EYVAEGSAPALPETR.R
R4/RRR4-19/2	1590.263	1590.716	-285.993	0.432	1458.834	0.486	23	0.218	R.EYVAEGSAPALPETR.R
R4/RRR4-22/2	1591.104	1590.716	244.579	0.560	1306.373	0.547	23	0.218	R.EYVAEGSAPALPETR.R
R4/RRR4-18/2	1591.278	1590.716	-276.270	0.516	1279.155	0.517	23	0.208	R.EYVAEGSAPALPETR.R
R4/RRR4-19/2	1590.228	1590.716	-308.096	0.478	1291.008	0.512	23	0.208	R.EYVAEGSAPALPETR.R
R4/RRR4-20/2	1590.311	1590.716	-255.420	0.491	1257.943	0.505	22	0.203	R.EYVAEGSAPALPETR.R
R4/RRR4-18/3	1543.041	1542.890	97.858	0.506	1582.654	0.487	28	0.199	R.LLELGVKPVFLTGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1590.300	1590.716	-262.504	0.480	1143.263	0.504	22	0.194	R.EYVAEGSAPALPETR.R
R4/RRR4-22/2	1590.176	1590.716	-971.192	0.440	1268.532	0.449	23	0.193	R.EYVAEGSAPALPETR.R
R4/RRR4-19/2	1590.118	1590.716	-1008.264	0.443	1174.972	0.454	22	0.187	R.EYVAEGSAPALPETR.R
R4/RRR4-18/2	1541.842	1542.890	-1332.218	0.427	1144.462	0.432	20	0.180	R.LLELGVKPVFLTGR.T
R4/RRR4-22/2	1542.572	1542.890	-206.970	0.457	1119.579	0.437	20	0.180	R.LLELGVKPVFLTGR.T
R4/RRR4-18/2	1590.237	1590.716	-302.166	0.454	1130.851	0.432	21	0.179	R.EYVAEGSAPALPETR.R
R4/RRR4-19/3	1542.068	1542.890	-1185.623	0.473	1373.243	0.507	26	0.178	R.LLELGVKPVFLTGR.T
R4/RRR4-20/2	1590.223	1590.716	-311.177	0.406	1086.194	0.441	22	0.178	R.EYVAEGSAPALPETR.R
R4/RRR4-17/2	1590.281	1590.716	-274.441	0.477	1007.469	0.461	21	0.177	R.EYVAEGSAPALPETR.R
R4/RRR4-17/2	1590.206	1590.716	-952.310	0.453	875.602	0.472	20	0.170	R.EYVAEGSAPALPETR.R
R4/RRR4-18/2	1542.195	1542.890	-1102.870	0.463	996.296	0.419	19	0.169	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1542.105	1542.890	-1161.299	0.433	1391.212	0.465	26	0.167	R.LLELGVKPVFLTGR.T
R4/RRR4-17/2	1590.003	1590.716	-1080.566	0.420	953.176	0.415	21	0.167	R.EYVAEGSAPALPETR.R
R4/RRR4-22/2	1541.653	1542.890	-1455.878	0.386	1026.066	0.394	19	0.166	R.LLELGVKPVFLTGR.T
R4/RRR4-18/2	1542.584	1542.890	-199.190	0.438	992.861	0.390	18	0.163	R.LLELGVKPVFLTGR.T
R4/RRR4-18/2	1541.543	1542.890	-1527.305	0.343	1170.401	0.301	20	0.161	R.LLELGVKPVFLTGR.T
R4/RRR4-22/2	1589.656	1590.716	-1300.081	0.315	1184.260	0.286	22	0.160	R.EYVAEGSAPALPETR.R
R4/RRR4-19/2	1541.405	1542.890	-1617.359	0.384	930.726	0.377	18	0.159	R.LLELGVKPVFLTGR.T
R4/RRR4-19/2	1541.552	1542.890	-1521.498	0.385	896.411	0.381	18	0.158	R.LLELGVKPVFLTGR.T
R4/RRR4-19/2	1541.364	1542.890	-2294.655	0.382	857.885	0.387	18	0.157	R.LLELGVKPVFLTGR.T
R4/RRR4-19/2	1541.512	1542.890	-1547.510	0.403	812.722	0.387	17	0.155	R.LLELGVKPVFLTGR.T
R4/RRR4-19/2	1541.464	1542.890	-1578.615	0.359	775.765	0.376	17	0.152	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1541.629	1542.890	-1471.158	0.433	1249.662	0.466	25	0.152	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1542.120	1542.890	-1151.522	0.371	1467.434	0.387	27	0.151	R.LLELGVKPVFLTGR.T
R4/RRR4-19/2	1541.624	1542.890	-1474.410	0.371	816.212	0.342	17	0.150	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1542.148	1542.890	-1133.519	0.418	1386.448	0.415	27	0.150	R.LLELGVKPVFLTGR.T
R4/RRR4-18/2	1541.424	1542.890	-1605.186	0.336	768.924	0.354	17	0.150	R.LLELGVKPVFLTGR.T
R4/RRR4-18/2	1541.493	1542.890	-1559.602	0.366	635.913	0.298	15	0.141	R.LLELGVKPVFLTGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/3	1541.921	1542.890	-1281.260	0.438	1137.132	0.465	25	0.140	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1541.912	1542.890	-1287.223	0.450	1095.143	0.468	25	0.137	R.LLELGVKPVFLTGR.T
R4/RRR4-22/3	1542.126	1542.890	-1147.826	0.432	1273.926	0.384	26	0.131	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1541.532	1542.890	-1534.752	0.370	1213.490	0.380	25	0.126	R.LLELGVKPVFLTGR.T
R4/RRR4-18/3	1542.041	1542.890	-1202.912	0.418	1302.321	0.353	26	0.125	R.LLELGVKPVFLTGR.T
R4/RRR4-22/3	1542.236	1542.890	-1075.817	0.487	1070.021	0.422	25	0.124	R.LLELGVKPVFLTGR.T
R4/RRR4-17/3	1541.566	1542.890	-1512.200	0.371	1132.261	0.374	25	0.118	R.LLELGVKPVFLTGR.T
R4/RRR4-18/3	1541.738	1542.890	-1399.938	0.291	1075.775	0.358	24	0.112	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1541.866	1542.890	-1316.920	0.367	798.938	0.384	22	0.105	R.LLELGVKPVFLTGR.T
R4/RRR4-20/3	1541.988	1542.890	-1237.494	0.295	879.945	0.365	23	0.104	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1746.439	1746.902	-266.350	0.342	750.848	0.441	25	0.104	R.EYVAEGSAPALPETRR.L
R4/RRR4-19/3	1747.898	1746.902	-2.747	0.360	455.225	0.474	20	0.099	R.EYVAEGSAPALPETRR.L
R4/RRR4-18/3	1541.774	1542.890	-1376.677	0.318	788.614	0.326	22	0.098	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1541.479	1542.890	-1568.878	0.308	565.551	0.299	21	0.097	R.LLELGVKPVFLTGR.T
R4/RRR4-19/3	1746.990	1746.902	50.060	0.319	557.928	0.370	22	0.089	R.EYVAEGSAPALPETRR.L
R4/RRR4-23/2	1867.361	1867.118	130.369	0.563	1915.750	0.593	26	0.306	K.DM*PVLQDGPPPGGFAPVR.Y
R4/RRR4-23/2	1866.623	1867.118	-266.152	0.502	1830.824	0.562	24	0.282	K.DM*PVLQDGPPPGGFAPVR.Y
R4/RRR4-23/2	1867.858	1867.118	-139.794	0.573	1661.713	0.528	25	0.250	K.DM*PVLQDGPPPGGFAPVR.Y
R4/RRR4-23/2	1944.595	1945.205	-830.702	0.516	995.176	0.548	23	0.189	R.TALVPVLQAEEDERFVK.E
R4/RRR4-23/2	1571.323	1570.726	-257.727	0.514	776.107	0.585	22	0.186	R.TALVPVLQAEEDER.F
R4/RRR4-23/2	1571.219	1570.726	314.378	0.477	838.229	0.541	22	0.182	R.TALVPVLQAEEDER.F
R4/RRR4-23/3	1867.115	1867.118	-1.723	0.340	1236.825	0.367	27	0.121	K.DM*PVLQDGPPPGGFAPVR.Y
R4/RRR4-12/2	1038.586	1039.254	-1610.536	0.449	952.685	0.466	17	0.178	R.LGVEPVIGVR.A
R4/RRR4-6/2	1038.660	1039.254	-1538.632	0.428	981.761	0.431	17	0.173	R.LGVEPVIGVR.A
R4/RRR4-6/2	1038.957	1039.254	-286.555	0.474	870.269	0.456	17	0.173	R.LGVEPVIGVR.A
R4/RRR4-12/2	1038.520	1039.254	-1674.656	0.415	902.378	0.452	17	0.172	R.LGVEPVIGVR.A
R4/RRR4-12/2	1038.564	1039.254	-1631.554	0.419	726.822	0.455	15	0.164	R.LGVEPVIGVR.A
R4/RRR4-6/2	1038.635	1039.254	-1562.835	0.355	709.599	0.450	15	0.160	R.LGVEPVIGVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1917.368	1918.049	-879.280	0.568	1759.627	0.634	26	0.298	K.FWEVVCDEHGIDPTGR.Y
R4/RRR4-8/2	1918.335	1918.049	149.374	0.584	1685.007	0.633	26	0.287	K.FWEVVCDEHGIDPTGR.Y
R4/RRR4-8/2	1431.900	1432.514	-1130.532	0.522	1804.298	0.568	19	0.284	R.VNVYYNEASCGR.F
R4/RRR4-8/2	1431.452	1432.514	-1444.706	0.447	1738.163	0.520	19	0.260	R.VNVYYNEASCGR.F
R4/RRR4-8/2	1431.493	1432.514	-1415.584	0.465	1744.219	0.509	19	0.259	R.VNVYYNEASCGR.F
R4/RRR4-8/2	1917.739	1918.049	-162.203	0.613	1351.793	0.620	24	0.240	K.FWEVVCDEHGIDPTGR.Y
R4/RRR4-8/2	1253.008	1253.344	-268.676	0.489	994.198	0.503	17	0.185	R.YAGTSDLQLER.V
R4/RRR4-8/2	1253.325	1253.344	-14.713	0.454	961.112	0.458	18	0.176	R.YAGTSDLQLER.V
R4/RRR4-8/2	1253.116	1253.344	-182.378	0.479	937.849	0.438	17	0.171	R.YAGTSDLQLER.V
R4/RRR4-8/3	1919.773	1918.049	-144.309	0.410	721.078	0.528	26	0.120	K.FWEVVCDEHGIDPTGR.Y
R4/RRR4-8/3	1919.535	1918.049	254.199	0.383	569.272	0.448	22	0.099	K.FWEVVCDEHGIDPTGR.Y
R4/RRR4-2/3	1916.783	1918.049	-1185.617	0.373	674.943	0.414	23	0.097	K.FWEVVCDEHGIDPTGR.Y
R4/RRR4-19/2	1761.372	1761.995	-924.135	0.483	2382.358	0.487	25	0.354	R.CGAVSGLSTVVNAVSLAR.L
R4/RRR4-19/2	1184.032	1184.411	-320.830	0.444	1734.991	0.483	17	0.250	R.AALDVVELVVR.E
R4/RRR4-19/2	1288.033	1288.474	-343.689	0.479	831.807	0.467	15	0.167	R.VQVDYTQPIPK.D
R4/RRR4-19/2	1184.184	1184.411	-192.168	0.392	844.134	0.353	16	0.154	R.AALDVVELVVR.E
R4/RRR4-19/2	1184.072	1184.411	-286.593	0.231	699.901	0.367	15	0.143	R.AALDVVELVVR.E
R4/RRR4-6/2	1003.079	1003.135	-55.490	0.430	774.545	0.341	13	0.151	R.VAVTNTLER.R
R4/RRR4-6/2	1002.450	1003.135	-1686.180	0.354	672.954	0.352	12	0.147	R.VAVTNTLER.R
R4/RRR4-25/2	1220.570	1220.400	139.572	0.466	1937.586	0.412	17	0.260	K.SDFVVQIGVQK.V
R4/RRR4-25/2	1486.896	1487.596	-1146.769	0.329	1685.896	0.387	21	0.218	K.ATLDITADYGYGAR.G
R4/RRR4-25/2	1167.489	1167.274	184.787	0.492	1068.252	0.450	14	0.179	K.GWDEGVTQM*K.V
R4/RRR4-25/2	1167.806	1167.274	-401.965	0.503	1065.544	0.443	14	0.177	K.GWDEGVTQM*K.V
R4/RRR4-25/2	1167.787	1167.274	-418.642	0.407	604.952	0.360	12	0.146	K.GWDEGVTQM*K.V
R4/RRR4-21/2	1421.056	1421.619	-1102.885	0.458	1673.278	0.576	18	0.265	K.CHFVAIDIFNGK.K
R4/RRR4-21/2	1421.154	1421.619	-328.209	0.499	1442.423	0.645	18	0.254	K.CHFVAIDIFNGK.K
R4/RRR4-21/2	1422.106	1421.619	343.640	0.484	1207.208	0.583	17	0.214	K.CHFVAIDIFNGK.K
R4/RRR4-21/2	1420.666	1421.619	-1378.369	0.445	1329.734	0.514	18	0.211	K.CHFVAIDIFNGK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1300.322	1300.483	-124.253	0.494	1428.844	0.444	20	0.209	R.LPTDDSLLGQIK.T
R4/RRR4-21/2	1300.240	1300.483	-188.010	0.452	1323.409	0.449	20	0.200	R.LPTDDSLLGQIK.T
R4/RRR4-21/2	1422.129	1421.619	-345.375	0.477	992.681	0.475	17	0.178	K.CHFVAIDIFNGK.K
R4/RRR4-21/2	1299.830	1300.483	-1275.542	0.473	1205.129	0.355	19	0.173	R.LPTDDSLLGQIK.T
R4/RRR4-21/2	1136.010	1135.255	-216.052	0.296	237.409	0.539	13	0.155	K.TYPQQAGTIR.K
R4/RRR4-21/2	1134.934	1135.255	-283.250	0.321	308.113	0.387	15	0.153	K.TYPQQAGTIR.K
R4/RRR4-21/2	1135.926	1135.255	-290.332	0.254	234.992	0.555	14	0.153	K.TYPQQAGTIR.K
R4/RRR4-21/2	1135.325	1135.255	61.512	0.252	276.131	0.348	14	0.148	K.TYPQQAGTIR.K
R4/RRR4-21/2	1134.951	1135.255	-268.898	0.242	319.783	0.368	16	0.148	K.TYPQQAGTIR.K
R4/RRR4-20/2	1134.927	1135.255	-290.157	0.278	223.088	0.416	13	0.148	-.TYPQQAGTIR.-
R4/RRR4-21/2	1301.390	1300.483	-72.030	0.308	596.705	0.391	14	0.146	R.LPTDDSLLGQIK.T
R4/RRR4-21/2	1134.909	1135.255	-306.128	0.255	301.623	0.380	15	0.146	-.TYPQQAGTIR.-
R4/RRR4-21/2	1134.806	1135.255	-397.001	0.251	271.463	0.345	14	0.145	-.TYPQQAGTIR.-
R4/RRR4-20/2	1134.895	1135.255	-318.107	0.202	326.417	0.352	16	0.145	K.TYPQQAGTIR.K
R4/RRR4-21/2	1134.572	1135.255	-1487.772	0.210	258.709	0.451	14	0.143	-.TYPQQAGTIR.-
R4/RRR4-21/2	1134.900	1135.255	-313.574	0.245	208.792	0.443	14	0.143	-.TYPQQAGTIR.-
R4/RRR4-20/2	1134.565	1135.255	-1494.473	0.188	206.807	0.452	14	0.142	-.TYPQQAGTIR.-
R4/RRR4-23/2	1135.069	1135.255	-164.779	0.219	198.752	0.307	13	0.134	-.TYPQQAGTIR.-
R4/RRR4-21/2	1301.193	1300.483	-224.099	0.307	269.054	0.392	11	0.126	-.LPTDDSLLGQIK.-
R4/RRR4-21/3	1422.615	1421.619	-2.902	0.371	1156.828	0.214	25	0.084	K.CHFVAIDIFNGK.K
R4/RRR4-21/3	1422.354	1421.619	-186.512	0.323	902.518	0.212	20	0.077	K.CHFVAIDIFNGK.K
R4/RRR4-2/2	1515.885	1515.734	100.104	0.485	1020.274	0.433	20	0.172	K.QALEDSTLVGLLQK.I
R4/RRR4-2/2	1202.379	1203.289	-1593.271	0.461	724.206	0.390	14	0.155	R.DSNYIGLQHR.F
R4/RRR4-2/2	1202.062	1201.307	-204.282	0.314	776.233	0.364	16	0.150	K.YLFEVTDDAK.T
R4/RRR4-2/2	1202.782	1203.289	-1256.918	0.376	781.436	0.293	14	0.145	R.DSNYIGLQHR.F
R4/RRR4-2/2	1305.273	1305.545	-208.390	0.182	882.888	0.164	15	0.129	K.VGSYLLDTVIPK.F
R4/RRR4-12/2	1610.307	1610.905	-995.520	0.514	1094.047	0.472	20	0.184	R.M*PNLHFIPVNLGNK.E
R4/RRR4-12/2	1146.239	1146.321	-71.311	0.481	1188.300	0.312	17	0.166	R.FPDIASVQLR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1145.745	1146.321	-1379.760	0.475	995.079	0.363	16	0.164	R.FPDIASVQLR.M
R4/RRR4-12/2	1145.723	1146.321	-1398.808	0.416	1003.911	0.347	16	0.161	R.FPDIASVQLR.M
R4/RRR4-12/3	1757.280	1758.015	-990.360	0.446	1114.685	0.394	28	0.118	K.EVLNRFPDIASVQLR.M
R4/RRR4-2/2	1359.346	1358.523	-130.477	0.458	614.967	0.512	19	0.165	K.QESLADAVQGIVK.F
R4/RRR4-2/3	1509.810	1509.736	49.490	0.499	1066.208	0.522	28	0.148	R.LSGLVTNLITAGHGR.E
R4/RRR4-3/2	1877.698	1876.230	250.024	0.383	698.843	0.340	15	0.136	R.LASFQYAPSIPPFIVPK.Q
R4/RRR4-2/3	1509.965	1509.736	152.139	0.369	930.392	0.451	28	0.115	R.LSGLVTNLITAGHGR.E
R4/RRR4-2/3	1581.021	1581.747	-1095.232	0.398	1364.283	0.295	27	0.114	K.LACHSVASWCHPR.A
R4/RRR4-21/2	1071.576	1072.240	-1557.983	0.436	1667.912	0.461	19	0.237	R.VLVVDGGGSLR.C
R4/RRR4-21/2	1073.030	1072.240	-197.012	0.524	1544.155	0.441	19	0.220	R.VLVVDGGGSLR.C
R4/RRR4-22/2	1072.118	1072.240	-114.270	0.311	1160.781	0.415	16	0.174	R.VLVVDGGGSLR.C
R4/RRR4-21/2	1329.363	1329.616	-190.983	0.345	1432.156	0.266	18	0.172	R.RQVFAGPIVTLK.V
R4/RRR4-21/2	1277.656	1278.484	-1435.194	0.355	666.426	0.424	17	0.155	R.ALQPVFQVYGR.R
R4/RRR4-21/2	1329.859	1329.616	183.342	0.349	1144.215	0.273	16	0.153	R.RQVFAGPIVTLK.V
R4/RRR4-21/2	1278.123	1278.484	-283.609	0.349	584.536	0.364	15	0.147	R.ALQPVFQVYGR.R
R4/RRR4-21/3	1329.532	1329.616	-63.516	0.406	1204.865	0.268	22	0.097	R.RQVFAGPIVTLK.V
R4/RRR4-21/3	1329.834	1329.616	164.507	0.378	650.287	0.403	19	0.094	R.RQVFAGPIVTLK.V
R4/RRR4-12/2	1753.235	1752.092	81.804	0.616	2071.251	0.551	28	0.318	K.AVVAGASGGIGQPLSLLLK.L
R4/RRR4-12/2	1751.527	1752.092	-895.846	0.504	2024.562	0.501	27	0.295	K.AVVAGASGGIGQPLSLLLK.L
R4/RRR4-12/2	1751.563	1752.092	-875.137	0.521	1964.725	0.523	27	0.292	K.AVVAGASGGIGQPLSLLLK.L
R4/RRR4-12/2	1135.628	1136.280	-1458.788	0.342	571.428	0.464	15	0.152	R.AETFVAEIAGK.S
R4/RRR4-14/2	1609.230	1609.850	-1010.213	0.406	898.648	0.442	19	0.166	K.STSSIFPLQNVFIR.K
R4/RRR4-14/2	1610.231	1609.850	237.188	0.461	697.653	0.469	18	0.162	K.STSSIFPLQNVFIR.K
R4/RRR4-14/2	1609.448	1609.850	-251.089	0.416	718.266	0.446	18	0.159	K.STSSIFPLQNVFIR.K
R4/RRR4-14/2	1609.076	1609.850	-1106.260	0.355	782.205	0.406	18	0.155	K.STSSIFPLQNVFIR.K
R4/RRR4-14/2	1609.686	1609.850	-102.502	0.446	713.017	0.361	17	0.148	K.STSSIFPLQNVFIR.K
R4/RRR4-13/2	1610.567	1609.850	-176.415	0.340	335.291	0.394	13	0.143	K.STSSIFPLQNVFIR.K
R4/RRR4-12/2	1657.135	1657.850	-1038.048	0.512	2220.213	0.665	32	0.384	K.GLPLGSGLGSSAASAAAAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1658.470	1657.850	-230.305	0.608	1886.096	0.692	31	0.335	K.GLPLGSGLGSSAASAAAAAK.A
R4/RRR4-12/2	1656.914	1657.850	-1171.861	0.451	1720.470	0.618	30	0.282	K.GLPLGSGLGSSAASAAAAAK.A
R4/RRR4-12/2	1163.059	1162.364	-262.189	0.532	1856.875	0.429	18	0.253	K.AVDALFGSLLR.Q
R4/RRR4-12/2	1162.219	1162.364	-124.585	0.457	1701.772	0.405	18	0.228	K.AVDALFGSLLR.Q
R4/RRR4-12/2	1417.534	1417.544	-7.222	0.495	689.559	0.484	17	0.163	R.QDDLVLAGLESEK.A
R4/RRR4-14/2	1619.197	1618.813	238.370	0.554	2326.984	0.422	22	0.320	K.VLNFAIDDAILEER.I
R4/RRR4-14/2	1618.415	1618.813	-246.294	0.533	2345.469	0.392	22	0.315	K.VLNFAIDDAILEER.I
R4/RRR4-15/2	1618.536	1618.813	-171.612	0.536	2375.803	0.363	22	0.310	K.VLNFAIDDAILEER.I
R4/RRR4-15/2	1618.587	1618.813	-139.912	0.576	2238.764	0.382	21	0.291	K.VLNFAIDDAILEER.I
R4/RRR4-15/2	1612.203	1611.778	264.389	0.563	1765.803	0.552	23	0.273	K.TPGLDDVTGEPLIQR.K
R4/RRR4-15/2	1612.321	1611.778	-284.738	0.550	1753.362	0.557	23	0.273	K.TPGLDDVTGEPLIQR.K
R4/RRR4-15/2	1618.141	1618.813	-1036.429	0.493	2175.781	0.300	22	0.260	K.VLNFAIDDAILEER.I
R4/RRR4-14/2	1611.344	1611.778	-270.170	0.511	1677.095	0.505	23	0.249	K.TPGLDDVTGEPLIQR.K
R4/RRR4-14/2	1611.134	1611.778	-1023.648	0.533	1502.714	0.490	22	0.224	K.TPGLDDVTGEPLIQR.K
R4/RRR4-15/2	1611.290	1611.778	-303.917	0.513	1256.780	0.494	20	0.199	K.TPGLDDVTGEPLIQR.K
R4/RRR4-13/2	1610.647	1610.883	-147.367	0.523	2340.698	0.544	24	0.366	K.IAIVGFGNFGQFLAR.T
R4/RRR4-13/2	1610.360	1610.883	-948.908	0.531	2025.638	0.544	23	0.310	K.IAIVGFGNFGQFLAR.T
R4/RRR4-13/2	1610.185	1610.883	-1057.974	0.438	2011.997	0.457	22	0.281	K.IAIVGFGNFGQFLAR.T
R4/RRR4-13/2	1209.898	1210.363	-385.415	0.540	1429.402	0.446	16	0.209	R.AEAFLNIFER.E
R4/RRR4-13/2	1397.239	1396.528	-207.468	0.385	944.136	0.379	15	0.157	-.DGWDGLPFVFDK.-
R4/RRR4-13/2	1210.003	1210.363	-298.664	0.400	784.408	0.396	13	0.154	R.AEAFLNIFER.E
R4/RRR4-13/2	1611.498	1610.883	-240.057	0.325	418.037	0.422	14	0.143	K.IAIVGFGNFGQFLAR.T
R4/RRR4-13/2	1396.175	1396.528	-253.928	0.455	825.833	0.253	15	0.138	R.DGWDGLPFVFDK.V
R4/RRR4-17/2	1501.563	1501.750	-125.050	0.589	2112.318	0.586	24	0.339	K.AVASINSVLTDLVAK.G
R4/RRR4-17/2	1501.453	1501.750	-198.613	0.493	1833.268	0.548	23	0.281	K.AVASINSVLTDLVAK.G
R4/RRR4-17/2	1501.326	1501.750	-283.689	0.498	1694.827	0.584	22	0.271	K.AVASINSVLTDLVAK.G
R4/RRR4-17/2	1379.232	1379.540	-224.113	0.481	1575.080	0.461	18	0.226	K.ANNVIYGLAQCR.G
R4/RRR4-17/2	1379.074	1379.540	-339.467	0.399	1098.422	0.280	16	0.152	K.ANNVIYGLAQCR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1348.158	1348.405	-183.961	0.405	919.730	0.353	18	0.151	K.ATSQASQAGSGGLGR.T
R4/RRR4-22/2	1737.313	1737.720	-235.006	0.597	2138.026	0.604	24	0.348	K.DATDDFEDVGHSTTAR.A
R4/RRR4-21/2	1737.488	1737.720	-133.861	0.594	1874.955	0.588	23	0.298	K.DATDDFEDVGHSTTAR.A
R4/RRR4-22/2	1737.163	1737.720	-898.954	0.562	1908.120	0.557	23	0.294	K.DATDDFEDVGHSTTAR.A
R4/RRR4-22/2	1888.388	1888.025	192.979	0.568	1765.789	0.590	28	0.284	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/2	1887.557	1888.025	-248.343	0.546	1781.686	0.580	28	0.283	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/2	1887.370	1888.025	-879.243	0.583	1463.831	0.651	26	0.260	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-21/2	1887.455	1888.025	-833.925	0.536	1479.199	0.622	26	0.253	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/2	1737.056	1737.720	-960.755	0.539	1584.646	0.537	22	0.243	K.DATDDFEDVGHSTTAR.A
R4/RRR4-22/3	1888.728	1888.025	-157.604	0.513	1706.654	0.497	35	0.226	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/3	1888.139	1888.025	60.551	0.518	1610.918	0.430	32	0.186	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/3	1887.796	1888.025	-121.361	0.468	1486.595	0.445	31	0.174	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/3	1644.466	1643.819	-215.448	0.525	1231.094	0.481	25	0.154	K.HNSKDDCWLIIGGK.V
R4/RRR4-21/3	1887.842	1888.025	-96.746	0.465	1422.721	0.409	32	0.153	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-21/3	1888.437	1888.025	219.160	0.492	1352.521	0.434	32	0.153	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/3	1737.102	1737.720	-933.883	0.366	1077.530	0.539	29	0.152	K.DATDDFEDVGHSTTAR.A
R4/RRR4-21/3	1887.654	1888.025	-196.675	0.488	1189.870	0.457	31	0.142	K.FLEDHPGGDDVLLSSTGK.D
R4/RRR4-22/3	1643.290	1643.819	-933.328	0.499	1093.921	0.422	23	0.123	K.HNSKDDCWLIIGGK.V
R4/RRR4-20/3	1737.842	1737.720	70.402	0.380	611.092	0.528	24	0.119	K.DATDDFEDVGHSTTAR.A
R4/RRR4-22/3	1737.000	1737.720	-992.830	0.281	910.004	0.445	27	0.116	K.DATDDFEDVGHSTTAR.A
R4/RRR4-21/3	1737.257	1737.720	-267.017	0.286	924.005	0.446	29	0.116	K.DATDDFEDVGHSTTAR.A
R4/RRR4-22/3	1737.636	1737.720	-48.599	0.296	737.527	0.488	26	0.115	K.DATDDFEDVGHSTTAR.A
R4/RRR4-23/3	1737.690	1737.720	-17.313	0.347	713.740	0.464	25	0.112	K.DATDDFEDVGHSTTAR.A
R4/RRR4-21/3	1738.717	1737.720	-1.494	0.364	633.260	0.472	25	0.111	K.DATDDFEDVGHSTTAR.A
R4/RRR4-23/3	1737.551	1737.720	-97.328	0.289	766.096	0.430	27	0.107	K.DATDDFEDVGHSTTAR.A
R4/RRR4-20/3	1737.128	1737.720	-918.962	0.281	714.040	0.434	26	0.106	K.DATDDFEDVGHSTTAR.A
R4/RRR4-21/3	1737.376	1737.720	-198.606	0.316	474.578	0.445	22	0.104	K.DATDDFEDVGHSTTAR.A
R4/RRR4-23/3	1737.356	1737.720	-209.708	0.251	614.001	0.336	24	0.092	-.DATDDFEDVGHSTTAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1325.403	1324.591	-142.501	0.547	1746.389	0.615	22	0.290	K.VVDAPEILAVIGK.V
R4/RRR4-10/2	1532.104	1532.592	-319.545	0.523	1922.687	0.475	22	0.274	K.IADAEENLGESEVR.E
R4/RRR4-10/2	1532.151	1532.592	-288.369	0.548	1819.614	0.504	22	0.268	K.IADAEENLGESEVR.E
R4/RRR4-10/2	1531.435	1532.592	-1412.746	0.403	1869.270	0.382	22	0.242	K.IADAEENLGESEVR.E
R4/RRR4-10/2	1324.315	1324.591	-209.369	0.483	1489.226	0.556	21	0.239	K.VVDAPEILAVIGK.V
R4/RRR4-10/2	1324.242	1324.591	-264.486	0.459	1390.990	0.539	20	0.223	K.VVDAPEILAVIGK.V
R4/RRR4-11/2	1532.374	1532.592	-142.590	0.478	1417.687	0.493	21	0.216	K.IADAEENLGESEVR.E
R4/RRR4-1/2	1325.208	1324.591	-290.070	0.399	1053.746	0.476	18	0.180	K.VVDAPEILAVIGK.V
R4/RRR4-10/2	1353.390	1352.391	-0.508	0.302	723.237	0.396	14	0.149	K.NLFEEGGDWER.K
R4/RRR4-10/2	1353.503	1352.391	83.710	0.323	309.362	0.363	12	0.140	-.NLFEEGGDWER.-
R4/RRR4-14/2	1631.538	1631.894	-219.323	0.501	1973.092	0.488	24	0.284	R.LPFDDASVGSVLAVIK.K
R4/RRR4-14/2	1622.477	1621.773	-183.119	0.529	1825.353	0.535	21	0.277	K.VENLGDQFITEISR.V
R4/RRR4-13/2	1631.733	1631.894	-99.016	0.490	1915.807	0.463	23	0.268	R.LPFDDASVGSVLAVIK.K
R4/RRR4-14/2	1631.438	1631.894	-280.351	0.535	1585.060	0.458	23	0.224	R.LPFDDASVGSVLAVIK.K
R4/RRR4-13/2	1750.797	1749.946	-85.360	0.400	705.850	0.441	16	0.152	K.KVENLGDQFITEISR.V
R4/RRR4-18/2	1750.494	1749.946	-258.905	0.424	500.266	0.393	15	0.142	K.KVENLGDQFITEISR.V
R4/RRR4-16/2	1631.878	1631.894	-10.100	0.336	1007.414	0.219	18	0.139	R.LPFDDASVGSVLAVIK.K
R4/RRR4-14/2	1654.758	1654.926	-101.856	0.571	1944.791	0.558	23	0.301	K.IASLDTHIALACAGLK.A
R4/RRR4-14/2	1101.914	1102.263	-317.850	0.514	1926.417	0.496	18	0.281	R.ALLEVVESGGK.N
R4/RRR4-14/2	1102.025	1102.263	-216.382	0.520	1901.959	0.462	18	0.268	R.ALLEVVESGGK.N
R4/RRR4-14/2	1102.085	1102.263	-161.934	0.530	1710.721	0.491	17	0.250	R.ALLEVVESGGK.N
R4/RRR4-13/2	1101.881	1102.263	-347.527	0.376	1326.800	0.418	15	0.190	R.ALLEVVESGGK.N
R4/RRR4-14/2	920.430	921.075	-1793.205	0.348	762.766	0.405	13	0.157	R.YIAGLQQK.Y
R4/RRR4-14/2	920.946	921.075	-140.473	0.389	759.112	0.363	13	0.155	R.YIAGLQQK.Y
R4/RRR4-14/2	920.437	921.075	-1785.209	0.271	785.429	0.326	13	0.147	R.YIAGLQQK.Y
R4/RRR4-13/2	1101.891	1102.263	-339.080	0.275	594.403	0.257	13	0.136	-.ALLEVVESGGK.-
R4/RRR4-14/3	1655.171	1654.926	148.409	0.442	566.783	0.517	26	0.110	K.IASLDTHIALACAGLK.A
R4/RRR4-14/3	1654.408	1654.926	-920.469	0.396	359.984	0.334	21	0.089	K.IASLDTHIALACAGLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1470.301	1469.712	-280.265	0.534	2159.399	0.543	21	0.332	K.SGLVALNLDLAQVR.Q
R4/RRR4-9/2	1468.854	1469.712	-1268.549	0.412	2300.512	0.406	21	0.313	K.SGLVALNLDLAQVR.Q
R4/RRR4-9/2	1468.893	1469.712	-1241.592	0.384	2168.785	0.361	21	0.278	K.SGLVALNLDLAQVR.Q
R4/RRR4-9/2	1432.424	1432.653	-160.232	0.542	1618.416	0.457	20	0.231	K.WGNIQFPLPFGR.V
R4/RRR4-9/2	1432.251	1432.653	-281.299	0.507	1579.928	0.468	20	0.229	K.WGNIQFPLPFGR.V
R4/RRR4-9/2	1432.510	1432.653	-99.881	0.566	1488.195	0.465	19	0.218	K.WGNIQFPLPFGR.V
R4/RRR4-9/2	1432.733	1432.653	55.837	0.482	1439.058	0.444	19	0.209	K.WGNIQFPLPFGR.V
R4/RRR4-9/2	1432.494	1432.653	-111.335	0.506	1242.943	0.470	17	0.195	K.WGNIQFPLPFGR.V
R4/RRR4-9/2	1432.363	1432.653	-202.893	0.520	1065.530	0.459	17	0.179	-.WGNIQFPLPFGR.-
R4/RRR4-9/2	1067.374	1067.131	228.543	0.407	644.988	0.457	13	0.157	R.GELDDTAAFK.N
R4/RRR4-1/2	1432.773	1432.653	83.693	0.377	416.541	0.330	12	0.140	-.WGNIQFPLPFGR.-
R4/RRR4-9/2	1066.355	1067.131	-1670.554	0.227	597.500	0.266	13	0.136	R.GELDDTAAFK.N
R4/RRR4-2/2	1390.030	1390.563	-1106.363	0.370	1301.546	0.443	21	0.194	K.VGESPEEIAAFLK.S
R4/RRR4-2/2	1293.363	1292.547	-143.192	0.460	1026.651	0.410	16	0.170	R.LVEAFVPFLEK.L
R4/RRR4-2/3	1849.675	1849.848	-94.109	0.559	1071.783	0.590	34	0.169	K.TEDESRPLEDGTGEASR.S
R4/RRR4-2/2	1293.361	1292.547	-144.801	0.430	708.950	0.488	12	0.159	R.LVEAFVPFLEK.L
R4/RRR4-2/3	1849.833	1849.848	-8.520	0.586	815.727	0.603	32	0.148	K.TEDESRPLEDGTGEASR.S
R4/RRR4-2/2	1390.342	1390.563	-159.887	0.320	847.151	0.278	18	0.144	K.VGESPEEIAAFLK.S
R4/RRR4-1/2	1204.382	1203.416	-28.018	0.290	1030.422	0.198	15	0.139	K.ILLENAGAVFR.T
R4/RRR4-1/2	1390.299	1390.563	-190.978	0.322	336.936	0.306	13	0.136	-.VGESPEEIAAFLK.-
R4/RRR4-1/2	1390.113	1390.563	-324.528	0.334	445.844	0.286	13	0.132	-.VGESPEEIAAFLK.-
R4/RRR4-2/3	1849.239	1849.848	-872.883	0.539	826.245	0.510	31	0.125	K.TEDESRPLEDGTGEASR.S
R4/RRR4-1/2	1791.391	1790.906	271.502	0.578	1870.925	0.650	24	0.317	R.LSSDDGYLESLTSAGFK.V
R4/RRR4-1/2	1453.261	1452.638	-259.793	0.443	1047.353	0.554	19	0.193	R.AIISGTSSIYNLGR.K
R4/RRR4-1/2	1544.272	1544.732	-299.030	0.429	1698.717	0.136	20	0.166	R.SNQEELGSVLNLLK.Y
R4/RRR4-1/2	1453.137	1452.638	344.558	0.427	844.570	0.474	17	0.166	R.AIISGTSSIYNLGR.K
R4/RRR4-1/2	1452.447	1452.638	-131.976	0.346	642.797	0.382	15	0.145	R.AIISGTSSIYNLGR.K
R4/RRR4-1/2	1789.594	1790.906	-1295.426	0.304	280.890	0.361	13	0.131	-.LSSDDGYLESLTSAGFK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-1/3	1907.522	1906.975	-238.305	0.422	953.870	0.392	24	0.105	K.HGICSNCHENAYQCR.Q
R4/RRR4-1/2	1117.459	1118.219	-1580.021	0.376	1140.198	0.346	16	0.167	R.ELSEIAEQAK.R
R4/RRR4-1/2	1117.935	1118.219	-254.811	0.422	913.068	0.404	16	0.165	R.ELSEIAEQAK.R
R4/RRR4-2/2	1274.081	1274.406	-255.583	0.446	527.710	0.443	16	0.158	R.ELSEIAEQAKR.R
R4/RRR4-2/2	1274.050	1274.406	-280.383	0.413	475.699	0.451	15	0.156	R.ELSEIAEQAKR.R
R4/RRR4-2/2	1061.172	1061.133	37.082	0.329	1056.435	0.300	15	0.156	R.EAQWATAQR.T
R4/RRR4-1/2	1274.236	1274.406	-134.003	0.456	594.617	0.387	16	0.154	R.ELSEIAEQAKR.R
R4/RRR4-2/2	1274.388	1274.406	-14.182	0.404	479.142	0.384	15	0.151	R.ELSEIAEQAKR.R
R4/RRR4-2/2	1118.124	1118.219	-85.916	0.478	711.530	0.335	14	0.149	R.ELSEIAEQAK.R
R4/RRR4-2/2	1117.974	1118.219	-219.976	0.455	763.015	0.320	14	0.148	R.ELSEIAEQAK.R
R4/RRR4-1/2	1061.080	1061.133	-50.149	0.288	640.238	0.258	12	0.139	R.EAQWATAQR.T
R4/RRR4-1/2	1061.067	1061.133	-62.727	0.242	809.271	0.087	14	0.131	R.EAQWATAQR.T
R4/RRR4-15/2	1214.837	1215.342	-1242.329	0.551	1754.102	0.402	18	0.231	R.SLEGLQANVQR.L
R4/RRR4-20/2	1215.021	1215.342	-265.084	0.569	1780.158	0.389	18	0.230	R.SLEGLQANVQR.L
R4/RRR4-20/2	1214.954	1215.342	-319.819	0.583	1743.822	0.400	18	0.228	R.SLEGLQANVQR.L
R4/RRR4-20/2	1214.616	1215.342	-1425.311	0.496	1720.991	0.396	18	0.227	R.SLEGLQANVQR.L
R4/RRR4-15/2	1215.063	1215.342	-230.412	0.550	1729.908	0.394	18	0.227	R.SLEGLQANVQR.L
R4/RRR4-19/2	1215.095	1215.342	-203.603	0.530	1703.653	0.391	18	0.223	R.SLEGLQANVQR.L
R4/RRR4-19/2	1216.476	1215.342	110.753	0.523	1588.204	0.381	17	0.208	R.SLEGLQANVQR.L
R4/RRR4-15/2	1214.532	1215.342	-1494.161	0.523	1551.147	0.389	17	0.206	R.SLEGLQANVQR.L
R4/RRR4-19/2	1214.289	1215.342	-1695.717	0.455	1584.215	0.242	18	0.180	R.SLEGLQANVQR.L
R4/RRR4-15/2	974.439	975.085	-1694.129	0.405	655.966	0.376	11	0.154	K.HWQNYVK.T
R4/RRR4-9/2	1216.155	1215.342	-153.792	0.367	952.227	0.305	16	0.153	R.SLEGLQANVQR.L
R4/RRR4-15/2	974.415	975.085	-1718.672	0.405	660.585	0.371	10	0.153	K.HWQNYVK.T
R4/RRR4-15/2	974.930	975.085	-159.381	0.426	597.956	0.327	10	0.148	K.HWQNYVK.T
R4/RRR4-9/2	1215.753	1215.342	339.124	0.343	618.914	0.231	14	0.126	-.SLEGLQANVQR.-
R4/RRR4-15/3	1456.954	1457.659	-1174.295	0.533	842.600	0.485	27	0.122	K.KYAPTIGISVDHR.R
R4/RRR4-15/3	1457.285	1457.659	-257.782	0.528	805.711	0.454	24	0.113	K.KYAPTIGISVDHR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/3	1458.148	1457.659	335.850	0.467	915.628	0.409	24	0.109	K.KYAPTIGISVDHR.R
R4/RRR4-18/3	1458.061	1457.659	276.544	0.364	605.399	0.288	22	0.087	K.KYAPTIGISVDHR.R
R4/RRR4-18/2	1630.806	1629.749	35.015	0.597	1763.774	0.548	20	0.274	R.VNIYYDELDSELR.F
R4/RRR4-18/2	1063.114	1063.232	-110.862	0.428	1100.195	0.426	15	0.178	R.LSLYNPSLR.V
R4/RRR4-18/3	1620.309	1619.762	-280.698	0.471	1066.374	0.423	27	0.122	R.LGHATGATPAEFYQR.R
R4/RRR4-10/2	1194.120	1194.366	-206.051	0.445	1046.894	0.418	16	0.174	R.HQDVDIVVIR.E
R4/RRR4-10/2	1194.119	1194.366	-206.769	0.463	822.375	0.451	15	0.167	R.HQDVDIVVIR.E
R4/RRR4-23/2	1621.062	1620.911	93.005	0.523	1460.526	0.530	20	0.227	K.SGKFDAILCIGAVIR.G
R4/RRR4-23/2	1307.999	1307.502	380.997	0.456	1095.244	0.477	18	0.186	R.LM*GSLTNTQGLR.F
R4/RRR4-23/2	1307.120	1307.502	-293.444	0.418	1108.801	0.463	18	0.183	R.LM*GSLTNTQGLR.F
R4/RRR4-23/2	1306.660	1307.502	-1414.034	0.414	940.703	0.464	18	0.173	R.LM*GSLTNTQGLR.F
R4/RRR4-23/2	747.389	747.908	-2038.582	0.370	826.612	0.376	11	0.157	R.FGVVVAR.F
R4/RRR4-23/2	747.794	747.908	-153.597	0.423	774.869	0.360	11	0.156	R.FGVVVAR.F
R4/RRR4-23/2	747.793	747.908	-154.252	0.411	797.071	0.340	11	0.154	R.FGVVVAR.F
R4/RRR4-23/3	1621.030	1620.911	73.134	0.504	1405.049	0.362	27	0.139	K.SGKFDAILCIGAVIR.G
R4/RRR4-23/2	1308.403	1307.502	-76.244	0.249	533.359	0.294	14	0.138	R.LM*GSLTNTQGLR.F
R4/RRR4-23/2	1390.516	1391.468	-1408.344	0.427	1263.617	0.442	18	0.190	K.AGEVVNWSSENAK.W
R4/RRR4-23/2	1390.590	1391.468	-1354.825	0.420	1380.603	0.350	18	0.182	K.AGEVVNWSSENAK.W
R4/RRR4-23/2	949.137	950.031	-2000.704	0.387	1133.560	0.329	14	0.163	R.GDFAIDVGR.N
R4/RRR4-23/2	912.091	912.112	-22.365	0.382	766.434	0.378	13	0.154	R.GLVGPIISR.F
R4/RRR4-23/2	911.509	912.112	-1763.204	0.259	963.597	0.291	14	0.147	R.GLVGPIISR.F
R4/RRR4-23/2	1391.095	1391.468	-268.850	0.427	846.151	0.283	17	0.144	K.AGEVVNWSSENAK.W
R4/RRR4-11/2	1492.155	1492.742	-1066.417	0.464	2162.677	0.433	21	0.299	K.LQFLSLLDNTVTK.Q
R4/RRR4-11/2	1491.871	1492.742	-1257.677	0.389	1998.267	0.364	20	0.254	K.LQFLSLLDNTVTK.Q
R4/RRR4-11/2	1501.375	1501.667	-195.116	0.475	1635.486	0.494	20	0.239	K.AAIVNSQTLEEVAR.L
R4/RRR4-11/2	1501.156	1501.667	-1009.944	0.468	1645.586	0.458	20	0.232	K.AAIVNSQTLEEVAR.L
R4/RRR4-11/2	1595.113	1595.862	-1099.825	0.433	1571.016	0.466	20	0.223	R.LTNLAEIDPLASLPK.L
R4/RRR4-11/2	1500.649	1501.667	-1349.043	0.383	1217.511	0.384	20	0.176	K.AAIVNSQTLEEVAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1595.514	1595.862	-218.827	0.381	846.617	0.367	16	0.148	R.LTNLAEIDPLASLPK.L
R4/RRR4-9/2	1585.384	1585.824	-278.532	0.493	2557.665	0.364	21	0.346	R.FELTFYALNPELK.V
R4/RRR4-9/2	1585.351	1585.824	-299.390	0.443	2128.434	0.368	21	0.275	R.FELTFYALNPELK.V
R4/RRR4-8/2	1041.827	1042.170	-329.953	0.399	920.771	0.453	13	0.169	K.YAELVYAGR.W
R4/RRR4-8/2	1041.404	1042.170	-1700.704	0.390	898.819	0.415	12	0.162	K.YAELVYAGR.W
R4/RRR4-9/2	1005.286	1005.196	90.357	0.280	766.352	0.300	12	0.140	K.HNVPIPVTK.K
R4/RRR4-12/2	1280.143	1279.421	-217.359	0.559	1048.855	0.579	20	0.206	R.LVGDVDFAEVSK.V
R4/RRR4-12/2	1278.603	1279.421	-1426.375	0.424	1059.511	0.519	20	0.191	R.LVGDVDFAEVSK.V
R4/RRR4-12/2	1466.354	1466.834	-328.112	0.347	1232.574	0.467	21	0.190	R.SNIVGLPVSLLLLK.A
R4/RRR4-12/2	1466.325	1466.834	-1031.763	0.386	1049.869	0.545	20	0.190	R.SNIVGLPVSLLLLK.A
R4/RRR4-12/2	1278.623	1279.421	-1410.169	0.398	900.879	0.536	19	0.181	R.LVGDVDFAEVSK.V
R4/RRR4-12/2	1468.290	1466.834	311.650	0.472	812.988	0.495	18	0.169	R.SNIVGLPVSLLLLK.A
R4/RRR4-12/2	1012.678	1013.130	-447.297	0.388	655.728	0.382	14	0.154	R.TPNPESIVR.E
R4/RRR4-12/2	1013.175	1013.130	45.122	0.370	684.501	0.360	14	0.152	R.TPNPESIVR.E
R4/RRR4-12/2	1012.470	1013.130	-1643.976	0.376	548.270	0.349	13	0.149	R.TPNPESIVR.E
R4/RRR4-12/2	1013.080	1013.130	-49.020	0.371	463.199	0.256	12	0.142	R.TPNPESIVR.E
R4/RRR4-12/2	1466.812	1466.834	-14.909	0.383	513.937	0.325	14	0.139	R.SNIVGLPVSLLLLK.A
R4/RRR4-18/2	1878.428	1878.113	168.256	0.655	3496.752	0.591	26	0.667	R.IVNAGGECLTFDQLALR.A
R4/RRR4-18/2	1876.805	1878.113	-1233.339	0.551	2966.472	0.605	25	0.528	R.IVNAGGECLTFDQLALR.A
R4/RRR4-18/2	1878.500	1878.113	206.639	0.636	2976.492	0.592	26	0.523	R.IVNAGGECLTFDQLALR.A
R4/RRR4-19/2	1877.567	1878.113	-825.405	0.577	2768.694	0.622	26	0.487	R.IVNAGGECLTFDQLALR.A
R4/RRR4-19/2	1876.670	1878.113	-1305.520	0.535	2834.476	0.575	26	0.483	R.IVNAGGECLTFDQLALR.A
R4/RRR4-19/2	1877.573	1878.113	-822.468	0.598	2724.762	0.577	25	0.456	R.IVNAGGECLTFDQLALR.A
R4/RRR4-18/2	1183.119	1182.398	-236.633	0.488	1862.727	0.521	19	0.278	R.APLGQNTVLLR.G
R4/RRR4-18/3	1879.151	1878.113	20.314	0.578	1605.201	0.545	32	0.233	R.IVNAGGECLTFDQLALR.A
R4/RRR4-17/2	1183.246	1182.398	-129.200	0.479	1495.345	0.527	18	0.233	R.APLGQNTVLLR.G
R4/RRR4-18/2	1181.566	1182.398	-1554.915	0.470	1460.568	0.516	19	0.227	R.APLGQNTVLLR.G
R4/RRR4-19/2	1182.153	1182.398	-207.412	0.509	1403.524	0.521	19	0.223	R.APLGQNTVLLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1182.161	1182.398	-200.678	0.500	1523.666	0.464	19	0.222	R.APLGQNTVLLR.G
R4/RRR4-18/2	1182.752	1182.398	300.244	0.462	1433.674	0.491	18	0.218	R.APLGQNTVLLR.G
R4/RRR4-18/2	1181.735	1182.398	-1411.611	0.502	1376.957	0.504	18	0.216	R.APLGQNTVLLR.G
R4/RRR4-18/2	1183.107	1182.398	-246.880	0.445	1406.545	0.481	19	0.214	R.APLGQNTVLLR.G
R4/RRR4-19/2	1182.152	1182.398	-209.069	0.448	1400.009	0.466	18	0.209	R.APLGQNTVLLR.G
R4/RRR4-19/2	1182.280	1182.398	-100.205	0.497	1303.848	0.479	18	0.204	R.APLGQNTVLLR.G
R4/RRR4-20/2	1183.278	1182.398	-102.087	0.430	1248.702	0.482	18	0.199	R.APLGQNTVLLR.G
R4/RRR4-19/2	1183.270	1182.398	-108.296	0.491	1308.762	0.447	18	0.198	R.APLGQNTVLLR.G
R4/RRR4-20/2	1183.366	1182.398	-26.964	0.442	1298.073	0.452	18	0.198	R.APLGQNTVLLR.G
R4/RRR4-20/2	1183.039	1182.398	-304.333	0.422	1216.059	0.432	18	0.187	R.APLGQNTVLLR.G
R4/RRR4-20/2	1181.617	1182.398	-1511.639	0.428	842.966	0.520	17	0.178	R.APLGQNTVLLR.G
R4/RRR4-17/2	1181.557	1182.398	-1563.010	0.374	988.976	0.470	17	0.177	R.APLGQNTVLLR.G
R4/RRR4-17/2	1183.375	1182.398	-19.514	0.402	982.257	0.440	17	0.173	R.APLGQNTVLLR.G
R4/RRR4-20/2	1181.471	1182.398	-1635.768	0.409	989.255	0.435	17	0.173	R.APLGQNTVLLR.G
R4/RRR4-17/2	1181.319	1182.398	-1765.534	0.295	799.997	0.420	15	0.158	R.APLGQNTVLLR.G
R4/RRR4-18/2	1181.813	1182.398	-1344.798	0.143	675.994	0.417	14	0.143	R.APLGQNTVLLR.G
R4/RRR4-18/2	1181.717	1182.398	-1426.344	0.176	549.733	0.406	12	0.142	R.APLGQNTVLLR.G
R4/RRR4-18/3	1877.908	1878.113	-109.417	0.457	1127.059	0.376	28	0.115	R.IVNAGGECLTFDQLALR.A
R4/RRR4-13/3	1561.524	1561.786	-168.086	0.522	1603.196	0.474	29	0.197	K.RGEEVLKAEEMAAK.Y
R4/RRR4-13/2	1263.511	1262.437	58.663	0.482	1203.676	0.467	16	0.191	K.LSAILSWENTK.K
R4/RRR4-13/3	1561.408	1561.786	-242.905	0.507	1525.070	0.449	29	0.176	K.RGEEVLKAEEMAAK.Y
R4/RRR4-13/3	1562.921	1561.786	86.429	0.535	1467.391	0.442	28	0.166	K.RGEEVLKAEEMAAK.Y
R4/RRR4-13/2	865.904	866.033	-149.614	0.433	1287.761	0.383	13	0.131	K.KLIGCFGA.-
R4/RRR4-13/3	1577.750	1577.785	-22.403	0.393	1300.020	0.338	32	0.116	K.RGEEVLKAEEM*AAK.Y
R4/RRR4-13/2	865.972	866.033	-71.274	0.457	1236.071	0.352	13	0.115	K.KLIGCFGA.-
R4/RRR4-13/3	1577.177	1577.785	-1023.181	0.390	1042.311	0.390	30	0.111	K.RGEEVLKAEEM*AAK.Y
R4/RRR4-13/3	1577.753	1577.785	-20.773	0.396	953.783	0.356	29	0.101	K.RGEEVLKAEEM*AAK.Y
R4/RRR4-13/2	865.856	866.033	-205.902	0.416	1145.245	0.326	13	0.101	K.KLIGCFGA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/3	1577.156	1577.785	-1036.236	0.400	972.329	0.298	29	0.093	K.RGEEVLKAEEM*AAK.Y
R4/RRR4-24/3	1578.118	1577.785	211.169	0.392	994.926	0.256	28	0.088	K.RGEEVLKAEEM*AAK.Y
R4/RRR4-11/2	1558.295	1558.671	-241.810	0.514	1360.261	0.562	21	0.226	R.GCSANVFLDNAAYR.Q
R4/RRR4-11/2	1558.152	1558.671	-977.795	0.538	1379.175	0.547	21	0.225	R.GCSANVFLDNAAYR.Q
R4/RRR4-11/2	1558.107	1558.671	-1006.583	0.523	1166.095	0.553	20	0.205	R.GCSANVFLDNAAYR.Q
R4/RRR4-11/2	1314.069	1314.477	-311.070	0.263	368.704	0.545	15	0.150	R.QHAFWVPVSSR.Y
R4/RRR4-11/3	1713.868	1714.857	-1163.859	0.402	1176.263	0.490	24	0.149	R.RGCSANVFLDNAAYR.Q
R4/RRR4-11/2	1314.234	1314.477	-185.076	0.263	241.509	0.596	13	0.149	R.QHAFWVPVSSR.Y
R4/RRR4-11/2	1314.250	1314.477	-173.056	0.228	404.787	0.535	16	0.147	R.QHAFWVPVSSR.Y
R4/RRR4-17/2	1732.209	1733.002	-1038.296	0.450	2021.475	0.472	22	0.286	K.ILFEQILVTEGNSLR.D
R4/RRR4-17/2	1731.751	1733.002	-1303.628	0.383	1782.622	0.362	21	0.225	K.ILFEQILVTEGNSLR.D
R4/RRR4-17/2	1563.557	1562.733	-112.359	0.487	648.352	0.641	21	0.185	K.QQAPGPAM*EVGSFAR.A
R4/RRR4-17/2	1364.155	1364.526	-272.274	0.367	1017.451	0.482	17	0.176	R.IAASFDELEAVAK.Q
R4/RRR4-17/2	1564.047	1562.733	201.352	0.430	444.950	0.595	19	0.167	K.QQAPGPAM*EVGSFAR.A
R4/RRR4-17/2	1731.689	1733.002	-1339.451	0.295	1169.019	0.276	18	0.154	K.ILFEQILVTEGNSLR.D
R4/RRR4-17/2	1562.793	1562.733	38.557	0.322	358.955	0.524	18	0.152	K.QQAPGPAM*EVGSFAR.A
R4/RRR4-18/2	1733.069	1733.002	38.672	0.374	441.624	0.392	13	0.140	K.ILFEQILVTEGNSLR.D
R4/RRR4-17/2	1364.264	1364.526	-192.200	0.209	760.830	0.319	16	0.139	R.IAASFDELEAVAK.Q
R4/RRR4-17/2	1364.131	1364.526	-290.051	0.228	370.284	0.395	13	0.138	R.IAASFDELEAVAK.Q
R4/RRR4-19/2	1422.099	1422.567	-329.885	0.443	1308.125	0.547	18	0.214	R.GPTESIYQGGVWK.V
R4/RRR4-19/2	948.240	949.086	-1952.758	0.378	1083.072	0.392	15	0.171	K.SPSIGFVNK.I
R4/RRR4-19/2	1449.900	1450.663	-1219.772	0.369	1181.221	0.357	18	0.169	K.VRVELPDAYPYK.S
R4/RRR4-19/2	948.435	949.086	-1745.548	0.332	973.837	0.307	14	0.152	K.SPSIGFVNK.I
R4/RRR4-16/3	1974.750	1975.066	-160.193	0.494	1597.649	0.584	33	0.247	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-16/3	1974.622	1975.066	-225.123	0.492	1532.583	0.578	33	0.233	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-14/2	1975.618	1975.066	-227.048	0.567	1250.394	0.617	21	0.220	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-14/2	1017.028	1017.188	-158.322	0.428	1460.044	0.454	17	0.212	R.AMIGQVAGGGR.T
R4/RRR4-14/2	1975.388	1975.066	163.902	0.529	1243.731	0.581	21	0.211	R.ASGDYAIVISHNPDNGTSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1974.439	1975.066	-826.456	0.500	963.820	0.614	19	0.191	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-15/2	1254.176	1254.504	-262.080	0.414	1183.167	0.448	18	0.186	R.ATLSIGNVLPIR.S
R4/RRR4-14/2	1033.002	1033.188	-180.521	0.439	1107.102	0.434	17	0.180	R.AM*IGQVAGGGR.T
R4/RRR4-13/2	1254.238	1254.504	-212.574	0.355	1268.227	0.324	19	0.172	R.ATLSIGNVLPIR.S
R4/RRR4-16/3	1974.135	1975.066	-980.803	0.473	1146.503	0.563	31	0.170	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-16/2	1254.280	1254.504	-179.378	0.351	1093.644	0.380	17	0.168	R.ATLSIGNVLPIR.S
R4/RRR4-14/2	1032.400	1033.188	-1736.580	0.360	937.071	0.423	15	0.164	R.AM*IGQVAGGGR.T
R4/RRR4-15/2	1255.315	1254.504	-151.043	0.442	957.735	0.379	17	0.162	R.ATLSIGNVLPIR.S
R4/RRR4-14/2	1032.993	1033.188	-188.938	0.404	827.711	0.416	15	0.160	R.AM*IGQVAGGGR.T
R4/RRR4-13/2	1255.235	1254.504	-214.747	0.360	942.985	0.355	17	0.158	R.ATLSIGNVLPIR.S
R4/RRR4-16/2	1254.199	1254.504	-244.308	0.306	992.635	0.335	17	0.157	R.ATLSIGNVLPIR.S
R4/RRR4-13/2	1255.445	1254.504	-47.456	0.307	982.573	0.327	18	0.156	R.ATLSIGNVLPIR.S
R4/RRR4-15/2	1255.548	1254.504	35.046	0.407	916.518	0.329	17	0.154	R.ATLSIGNVLPIR.S
R4/RRR4-17/3	1975.232	1975.066	84.752	0.498	1098.413	0.502	31	0.147	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-16/2	1254.253	1254.504	-200.663	0.249	902.631	0.276	16	0.146	R.ATLSIGNVLPIR.S
R4/RRR4-2/2	1255.261	1254.504	-193.869	0.249	544.484	0.348	13	0.142	R.ATLSIGNVLPIR.S
R4/RRR4-1/2	1254.408	1254.504	-76.582	0.222	605.429	0.306	14	0.141	R.ATLSIGNVLPIR.S
R4/RRR4-14/3	1974.872	1975.066	-98.527	0.436	931.313	0.532	29	0.140	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-13/2	1253.760	1254.504	-1395.459	0.232	648.170	0.205	14	0.137	-.ATLSIGNVLPIR.-
R4/RRR4-17/2	1254.260	1254.504	-194.805	0.246	776.009	0.148	15	0.135	R.ATLSIGNVLPIR.S
R4/RRR4-13/3	1974.627	1975.066	-222.704	0.445	933.162	0.505	28	0.133	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-14/3	1975.512	1975.066	226.606	0.331	1035.350	0.432	26	0.124	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-17/3	1974.051	1975.066	-1023.455	0.323	538.613	0.428	25	0.101	R.ASGDYAIVISHNPDNGTSR.I
R4/RRR4-12/2	1465.232	1465.634	-274.967	0.511	1524.684	0.481	19	0.226	R.FPYYGNYVNLSK.L
R4/RRR4-12/2	1465.161	1465.634	-323.448	0.495	1353.583	0.496	18	0.211	R.FPYYGNYVNLSK.L
R4/RRR4-12/2	1465.445	1465.634	-128.884	0.545	1169.765	0.473	17	0.190	R.FPYYGNYVNLSK.L
R4/RRR4-12/2	1020.986	1021.192	-202.258	0.517	622.144	0.369	13	0.156	K.LEYDLLVR.Y
R4/RRR4-13/2	1021.054	1021.192	-135.094	0.511	641.070	0.341	13	0.153	K.LEYDLLVR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1020.901	1021.192	-286.106	0.468	609.335	0.341	13	0.153	K.LEYDLLVR.Y
R4/RRR4-12/2	980.572	981.174	-1638.332	0.383	820.004	0.345	15	0.153	K.IAGLHAAISK.L
R4/RRR4-11/2	1020.806	1021.192	-379.087	0.470	613.029	0.340	13	0.153	K.LEYDLLVR.Y
R4/RRR4-12/2	980.383	981.174	-1832.723	0.350	794.802	0.367	14	0.152	K.IAGLHAAISK.L
R4/RRR4-12/2	980.659	981.174	-1549.168	0.409	834.203	0.333	14	0.151	K.IAGLHAAISK.L
R4/RRR4-12/2	1020.457	1021.192	-1704.657	0.432	660.226	0.291	13	0.148	K.LEYDLLVR.Y
R4/RRR4-11/2	1020.668	1021.192	-1497.860	0.408	621.666	0.252	13	0.145	K.LEYDLLVR.Y
R4/RRR4-16/2	1465.998	1465.634	249.165	0.326	472.415	0.324	14	0.142	R.FPYYGNYVNLSK.L
R4/RRR4-18/2	1770.304	1769.934	209.309	0.548	1489.597	0.515	23	0.228	K.DGATDPTFLYFSHGLK.E
R4/RRR4-18/2	1769.435	1769.934	-283.120	0.514	1391.479	0.501	23	0.214	K.DGATDPTFLYFSHGLK.E
R4/RRR4-18/2	1503.196	1502.650	-303.454	0.535	1248.806	0.559	19	0.214	R.EIENGILWEVDGK.W
R4/RRR4-18/2	1768.904	1769.934	-1151.451	0.500	1260.558	0.515	22	0.204	K.DGATDPTFLYFSHGLK.E
R4/RRR4-18/2	1503.317	1502.650	-222.230	0.567	967.902	0.593	17	0.196	R.EIENGILWEVDGK.W
R4/RRR4-18/2	1503.433	1502.650	-144.928	0.525	956.737	0.597	16	0.194	R.EIENGILWEVDGK.W
R4/RRR4-18/2	1502.193	1502.650	-305.694	0.427	961.761	0.541	17	0.184	R.EIENGILWEVDGK.W
R4/RRR4-18/2	1502.171	1502.650	-320.207	0.440	874.483	0.478	17	0.170	R.EIENGILWEVDGK.W
R4/RRR4-19/2	1065.041	1064.217	-165.727	0.432	963.712	0.408	15	0.169	K.VVDIVDTFR.L
R4/RRR4-18/2	1064.224	1064.217	7.293	0.496	1018.612	0.378	15	0.168	K.VVDIVDTFR.L
R4/RRR4-18/2	1064.000	1064.217	-204.323	0.446	1024.600	0.324	15	0.160	K.VVDIVDTFR.L
R4/RRR4-18/2	1064.087	1064.217	-122.267	0.493	815.773	0.373	14	0.159	K.VVDIVDTFR.L
R4/RRR4-19/2	1063.613	1064.217	-1512.435	0.371	919.419	0.350	14	0.158	K.VVDIVDTFR.L
R4/RRR4-18/2	1502.483	1502.650	-112.016	0.292	728.898	0.388	15	0.148	R.EIENGILWEVDGK.W
R4/RRR4-19/2	1063.833	1064.217	-361.568	0.295	609.009	0.382	12	0.148	K.VVDIVDTFR.L
R4/RRR4-16/2	1288.996	1289.467	-366.894	0.455	1455.652	0.560	19	0.235	R.VVGGWASPFVNR.V
R4/RRR4-16/2	1288.987	1289.467	-373.165	0.451	1322.406	0.583	18	0.225	R.VVGGWASPFVNR.V
R4/RRR4-16/2	1112.877	1113.251	-337.382	0.453	1322.230	0.505	17	0.211	K.VPNLAAWADR.F
R4/RRR4-16/2	1157.997	1158.327	-285.222	0.510	1282.883	0.502	17	0.207	K.IAGVELLDEAK.V
R4/RRR4-16/2	1113.174	1113.251	-69.580	0.507	1242.307	0.478	17	0.200	K.VPNLAAWADR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1112.518	1113.251	-1561.946	0.478	1245.042	0.478	17	0.200	K.VPNLAAWADR.F
R4/RRR4-16/2	1158.017	1158.327	-268.300	0.496	1190.661	0.486	17	0.196	K.IAGVELLDEAK.V
R4/RRR4-16/2	1288.629	1289.467	-1430.859	0.362	1223.060	0.501	18	0.195	R.VVGGWASPFVNR.V
R4/RRR4-16/2	1157.479	1158.327	-1601.236	0.384	1300.850	0.404	17	0.187	K.IAGVELLDEAK.V
R4/RRR4-11/2	1933.700	1933.152	-234.376	0.566	1579.519	0.633	23	0.266	R.SFLQAVSTVTEEAPSPLR.V
R4/RRR4-11/2	1933.137	1933.152	-7.449	0.510	1641.294	0.564	23	0.256	R.SFLQAVSTVTEEAPSPLR.V
R4/RRR4-11/2	1589.624	1589.856	-146.389	0.490	2009.359	0.334	21	0.248	K.LSWVDIFEEIPIK.V
R4/RRR4-11/2	1933.869	1933.152	-146.732	0.540	1491.313	0.586	23	0.243	R.SFLQAVSTVTEEAPSPLR.V
R4/RRR4-11/2	1589.323	1589.856	-967.708	0.440	1639.521	0.290	19	0.194	K.LSWVDIFEEIPIK.V
R4/RRR4-11/2	929.793	930.084	-313.877	0.453	1207.614	0.328	14	0.168	R.SNQGVLALK.A
R4/RRR4-20/2	1935.489	1935.169	165.699	0.626	1798.766	0.587	29	0.289	R.IWVFSGDADSVVPLTATR.Y
R4/RRR4-20/2	1934.066	1935.169	-1090.915	0.502	1768.226	0.556	29	0.275	R.IWVFSGDADSVVPLTATR.Y
R4/RRR4-20/2	1934.620	1935.169	-803.089	0.542	1616.493	0.544	28	0.251	R.IWVFSGDADSVVPLTATR.Y
R4/RRR4-21/2	1935.085	1935.169	-43.886	0.565	1020.717	0.531	23	0.187	R.IWVFSGDADSVVPLTATR.Y
R4/RRR4-20/2	1154.155	1154.297	-122.909	0.358	728.256	0.414	13	0.156	K.YYNLPEVQK.A
R4/RRR4-20/2	1154.175	1154.297	-105.722	0.419	699.089	0.357	13	0.152	K.YYNLPEVQK.A
R4/RRR4-20/2	1154.089	1154.297	-180.735	0.380	700.986	0.344	13	0.150	K.YYNLPEVQK.A
R4/RRR4-21/2	1155.424	1154.297	110.565	0.319	582.848	0.250	11	0.134	-.YYNLPEVQK.-
R4/RRR4-21/3	1326.916	1326.492	320.116	0.421	749.684	0.449	21	0.108	R.GAGHEVPLHRPR.Q
R4/RRR4-19/3	1326.703	1326.492	159.589	0.366	601.547	0.434	19	0.101	R.GAGHEVPLHRPR.Q
R4/RRR4-21/3	1326.751	1326.492	195.712	0.385	691.900	0.394	21	0.098	R.GAGHEVPLHRPR.Q
R4/RRR4-21/3	1326.433	1326.492	-44.881	0.363	547.896	0.370	19	0.094	R.GAGHEVPLHRPR.Q
R4/RRR4-20/3	1326.246	1326.492	-186.411	0.424	800.678	0.326	21	0.092	R.GAGHEVPLHRPR.Q
R4/RRR4-15/2	1427.187	1427.542	-249.183	0.530	2053.620	0.500	20	0.370	K.NLKDEPVAAEQNV.-
R4/RRR4-15/2	1885.716	1886.138	-224.757	0.535	931.472	0.565	22	0.186	K.SGATVLPDLVAAQEWLSK.N
R4/RRR4-15/2	1885.615	1886.138	-810.325	0.506	936.531	0.551	22	0.183	K.SGATVLPDLVAAQEWLSK.N
R4/RRR4-15/2	1481.534	1481.499	23.750	0.438	867.340	0.408	15	0.158	K.AGYEYDEETFEK.I
R4/RRR4-16/2	1481.231	1481.499	-181.404	0.426	818.508	0.394	15	0.155	K.AGYEYDEETFEK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1427.320	1427.542	-156.002	0.562	1084.564	0.548	19	0.134	K.NLKDEPVAAEQNV.-
R4/RRR4-16/2	1428.382	1427.542	-112.684	0.605	934.962	0.571	19	0.125	K.NLKDEPVAAEQNV.-
R4/RRR4-9/2	1311.037	1311.380	-262.667	0.566	1480.612	0.484	19	0.223	K.AGNEQFVTETSK.W
R4/RRR4-8/2	1299.811	1299.499	240.989	0.306	785.734	0.440	16	0.156	K.VPDVYGVFQFK.V
R4/RRR4-9/2	1420.806	1421.624	-1283.270	0.375	769.792	0.376	17	0.151	R.VLISGSLDLFSNR.F
R4/RRR4-8/2	1420.850	1421.624	-1252.036	0.274	776.221	0.429	14	0.149	R.VLISGSLDLFSNR.F
R4/RRR4-8/2	1299.332	1299.499	-128.776	0.298	257.921	0.392	10	0.133	-.VPDVYGVFQFK.-
R4/RRR4-9/2	1404.275	1404.550	-196.576	0.484	1253.418	0.486	20	0.200	R.TLAIDFAPDADVR.L
R4/RRR4-9/2	1404.979	1404.550	305.999	0.524	1171.625	0.469	19	0.190	R.TLAIDFAPDADVR.L
R4/RRR4-8/2	822.903	822.932	-34.609	0.353	1209.938	0.425	13	0.183	R.LGFAASTR.H
R4/RRR4-8/2	822.878	822.932	-65.856	0.316	946.626	0.365	12	0.157	R.LGFAASTR.H
R4/RRR4-9/2	1287.300	1287.488	-145.863	0.345	1015.008	0.338	16	0.155	K.DASLVEIVTAIR.E
R4/RRR4-8/2	822.722	822.932	-255.613	0.323	875.240	0.380	11	0.155	R.LGFAASTR.H
R4/RRR4-9/2	1286.461	1287.488	-1579.836	0.263	1110.595	0.249	17	0.148	K.DASLVEIVTAIR.E
R4/RRR4-9/2	1388.961	1389.487	-1101.837	0.471	2202.043	0.429	21	0.304	R.VVLDCATADPDGR.K
R4/RRR4-9/2	1389.018	1389.487	-338.623	0.454	1890.765	0.490	20	0.273	R.VVLDCATADPDGR.K
R4/RRR4-9/2	1388.604	1389.487	-1360.024	0.401	1999.743	0.368	20	0.256	R.VVLDCATADPDGR.K
R4/RRR4-9/2	1441.648	1441.698	-35.042	0.502	1519.410	0.488	18	0.223	K.SGLVALNLDIAQVK.E
R4/RRR4-9/2	1441.114	1441.698	-1102.233	0.474	1625.062	0.366	18	0.206	K.SGLVALNLDIAQVK.E
R4/RRR4-9/2	1978.588	1978.192	200.456	0.628	3943.746	0.570	30	0.799	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-9/2	1977.590	1978.192	-812.694	0.573	3657.473	0.578	30	0.712	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-9/2	1977.676	1978.192	-769.199	0.582	3316.003	0.546	28	0.592	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-8/2	1977.897	1978.192	-150.027	0.516	2975.043	0.493	27	0.480	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-6/2	1979.644	1978.192	229.046	0.495	2654.516	0.541	26	0.425	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-9/2	1979.954	1978.192	-120.622	0.472	1126.479	0.537	22	0.192	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-9/3	1977.929	1978.192	-133.628	0.447	1425.901	0.465	31	0.176	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-7/2	1978.177	1978.192	-7.713	0.341	389.629	0.365	17	0.140	R.SNFGALLDTVELQLASGGGK.S
R4/RRR4-8/2	1978.686	1978.192	250.196	0.243	629.430	0.184	17	0.130	R.SNFGALLDTVELQLASGGGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/3	1888.432	1888.964	-813.953	0.521	1973.905	0.523	32	0.293	R.TIGHTVTSPDDTAEQCR.S
R4/RRR4-15/3	1888.560	1888.964	-214.928	0.567	2009.328	0.491	34	0.282	R.TIGHTVTSPDDTAEQCR.S
R4/RRR4-16/3	1888.748	1888.964	-114.850	0.567	1829.053	0.549	32	0.274	R.TIGHTVTSPDDTAEQCR.S
R4/RRR4-16/3	1889.222	1888.964	136.666	0.554	1438.992	0.568	30	0.212	R.TIGHTVTSPDDTAEQCR.S
R4/RRR4-15/3	1888.691	1888.964	-145.192	0.535	1286.431	0.540	28	0.180	R.TIGHTVTSPDDTAEQCR.S
R4/RRR4-15/3	1888.886	1888.964	-41.726	0.548	1291.087	0.521	29	0.174	R.TIGHTVTSPDDTAEQCR.S
R4/RRR4-16/2	1831.785	1831.063	-151.901	0.457	851.946	0.520	21	0.170	K.NAGVLALFDVDGTLTAPR.K
R4/RRR4-16/2	1402.233	1402.405	-122.731	0.418	410.141	0.335	15	0.146	K.GGNDYEIFESDR.T
R4/RRR4-15/2	1402.015	1402.405	-278.720	0.430	809.211	0.274	17	0.144	K.GGNDYEIFESDR.T
R4/RRR4-15/2	1402.098	1402.405	-219.061	0.405	582.637	0.283	16	0.143	K.GGNDYEIFESDR.T
R4/RRR4-16/2	1402.144	1402.405	-186.134	0.441	671.298	0.249	16	0.139	K.GGNDYEIFESDR.T
R4/RRR4-15/2	1402.008	1402.405	-283.961	0.380	687.014	0.142	16	0.132	K.GGNDYEIFESDR.T
R4/RRR4-14/2	1347.382	1346.517	-100.376	0.501	1290.413	0.620	20	0.232	R.TLTGIQIWGSGGR.G
R4/RRR4-14/2	1044.014	1043.202	-180.557	0.572	1510.427	0.386	16	0.203	R.GLVAQAQSLR.S
R4/RRR4-14/2	1346.604	1346.517	64.590	0.407	915.226	0.592	17	0.188	R.TLTGIQIWGSGGR.G
R4/RRR4-14/2	1073.187	1073.228	-38.973	0.437	1248.753	0.329	18	0.171	R.SLATAAQAAIR.A
R4/RRR4-14/2	1346.489	1346.517	-20.969	0.327	755.605	0.448	15	0.155	R.TLTGIQIWGSGGR.G
R4/RRR4-13/2	1347.257	1346.517	-193.263	0.251	822.076	0.428	16	0.153	R.TLTGIQIWGSGGR.G
R4/RRR4-13/2	1347.634	1346.517	87.254	0.196	408.779	0.431	16	0.140	R.TLTGIQIWGSGGR.G
R4/RRR4-17/2	956.943	957.149	-216.114	0.521	1291.954	0.448	15	0.198	R.AAVLLLDNK.K
R4/RRR4-17/2	956.870	957.149	-293.032	0.560	1256.403	0.442	15	0.194	R.AAVLLLDNK.K
R4/RRR4-17/2	1197.012	1197.323	-261.094	0.460	1061.176	0.482	17	0.185	R.RDDADLPPVAK.R
R4/RRR4-17/2	956.546	957.149	-1681.532	0.509	1120.546	0.442	15	0.185	R.AAVLLLDNK.K
R4/RRR4-17/2	1197.175	1197.323	-123.913	0.454	894.315	0.504	16	0.177	R.RDDADLPPVAK.R
R4/RRR4-17/2	1196.929	1197.323	-329.852	0.471	791.062	0.451	15	0.164	R.RDDADLPPVAK.R
R4/RRR4-17/2	1348.101	1348.533	-321.018	0.426	947.179	0.369	16	0.160	K.SREPVVQLYTR.D
R4/RRR4-17/2	1349.209	1348.533	-240.716	0.468	816.333	0.336	15	0.150	K.SREPVVQLYTR.D
R4/RRR4-17/2	1347.715	1348.533	-1352.956	0.431	606.822	0.374	14	0.149	K.SREPVVQLYTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1347.179	1347.414	-174.370	0.507	2000.236	0.593	20	0.321	K.APVTSAEVSQDSR.F
R4/RRR4-12/2	1347.031	1347.414	-285.098	0.514	1870.984	0.534	20	0.283	K.APVTSAEVSQDSR.F
R4/RRR4-12/2	1346.311	1347.414	-1566.809	0.456	1747.052	0.512	20	0.259	K.APVTSAEVSQDSR.F
R4/RRR4-12/2	1800.918	1801.849	-1075.302	0.396	654.299	0.487	24	0.159	R.FAPGGESYASGSEDGTIR.I
R4/RRR4-12/3	1949.516	1949.144	191.192	0.482	523.701	0.536	28	0.111	R.ACAFSEDTHLLLTGGVEK.I
R4/RRR4-9/2	1791.466	1791.940	-265.149	0.511	1636.708	0.567	25	0.260	K.SYELPDGQVITIGNER.-
R4/RRR4-10/2	1791.563	1791.940	-210.804	0.525	1491.517	0.567	24	0.241	K.SYELPDGQVITIGNER.-
R4/RRR4-9/2	1791.346	1791.940	-892.542	0.503	1532.612	0.548	24	0.241	K.SYELPDGQVITIGNER.-
R4/RRR4-10/2	1791.220	1791.940	-963.145	0.498	1509.298	0.556	24	0.240	K.SYELPDGQVITIGNER.-
R4/RRR4-10/2	1791.175	1791.940	-988.393	0.503	1510.208	0.551	24	0.239	K.SYELPDGQVITIGNER.-
R4/RRR4-9/2	1791.634	1791.940	-171.160	0.513	1423.598	0.555	23	0.230	K.SYELPDGQVITIGNER.-
R4/RRR4-9/2	1954.547	1955.244	-870.573	0.527	1235.111	0.632	24	0.226	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-10/2	1954.496	1955.244	-896.718	0.477	1256.268	0.601	24	0.221	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-10/2	1954.509	1955.244	-890.197	0.493	749.917	0.627	20	0.183	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-10/2	1954.706	1955.244	-789.137	0.529	764.909	0.592	20	0.179	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-9/2	1954.621	1955.244	-832.580	0.484	975.904	0.494	22	0.176	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-9/2	1954.683	1955.244	-800.734	0.498	762.473	0.573	20	0.175	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-9/3	1955.749	1955.244	-253.651	0.450	941.876	0.403	30	0.112	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-9/3	1955.014	1955.244	-117.690	0.397	839.487	0.426	29	0.111	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-11/3	1955.479	1955.244	120.984	0.440	752.491	0.413	27	0.106	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-10/3	1954.535	1955.244	-876.504	0.376	870.743	0.379	29	0.104	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-9/3	1954.425	1955.244	-933.123	0.387	632.036	0.413	25	0.103	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-11/3	1955.686	1955.244	226.806	0.413	521.740	0.379	24	0.099	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-10/3	1954.526	1955.244	-881.489	0.398	598.563	0.378	24	0.099	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-1/3	1955.331	1955.244	44.914	0.350	567.035	0.376	23	0.098	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-11/3	1954.741	1955.244	-771.090	0.410	687.469	0.354	26	0.097	R.VAPEEHPVLLTEAPINPK.S
R4/RRR4-9/3	1955.861	1955.244	-196.358	0.395	638.123	0.373	25	0.096	-.VAPEEHPVLLTEAPINPK.-
R4/RRR4-10/3	1954.866	1955.244	-193.796	0.341	607.178	0.334	27	0.095	R.VAPEEHPVLLTEAPINPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	1348.498	1349.602	-1565.175	0.394	1092.878	0.387	16	0.166	K.VGLVYQFNIAPK.K
R4/RRR4-25/2	1091.864	1092.252	-356.603	0.467	1068.968	0.339	14	0.163	K.SAQLLEQM*R.L
R4/RRR4-25/2	1091.758	1092.252	-453.532	0.431	1216.578	0.254	15	0.158	K.SAQLLEQM*R.L
R4/RRR4-25/3	1387.824	1387.588	170.915	0.411	915.465	0.523	24	0.132	R.LHM*ATDAGKDIAK.K
R4/RRR4-25/3	1387.344	1387.588	-175.858	0.448	1051.789	0.434	24	0.122	R.LHM*ATDAGKDIAK.K
R4/RRR4-25/3	1387.173	1387.588	-299.404	0.347	894.790	0.337	24	0.093	R.LHM*ATDAGKDIAK.K
R4/RRR4-20/2	1424.200	1423.726	334.194	0.461	916.364	0.585	22	0.192	K.QSLAGIPLLVLGNK.I
R4/RRR4-20/2	1423.488	1423.726	-167.431	0.481	1190.178	0.418	24	0.184	K.QSLAGIPLLVLGNK.I
R4/RRR4-20/2	1440.399	1440.710	-216.381	0.393	993.742	0.469	19	0.174	K.QALVDQLGLELIK.D
R4/RRR4-20/2	1055.998	1056.195	-186.277	0.410	1010.219	0.431	14	0.173	K.SELHDLLTK.Q
R4/RRR4-20/2	1422.844	1423.726	-1326.436	0.378	626.503	0.531	20	0.165	K.QSLAGIPLLVLGNK.I
R4/RRR4-20/2	1056.059	1056.195	-128.761	0.324	938.843	0.331	14	0.154	K.SELHDLLTK.Q
R4/RRR4-20/2	1055.756	1056.195	-416.521	0.300	858.790	0.339	13	0.150	K.SELHDLLTK.Q
R4/RRR4-4/2	1571.135	1571.718	-1010.315	0.418	2189.630	0.500	21	0.321	R.GLEGLTVQQAIDGNR.L
R4/RRR4-4/2	1572.223	1571.718	-315.207	0.513	1904.062	0.557	20	0.291	R.GLEGLTVQQAIDGNR.L
R4/RRR4-4/2	1570.924	1571.718	-1145.208	0.425	1955.752	0.487	20	0.279	R.GLEGLTVQQAIDGNR.L
R4/RRR4-4/2	1571.249	1571.718	-299.272	0.431	1863.115	0.504	20	0.270	R.GLEGLTVQQAIDGNR.L
R4/RRR4-2/2	1571.178	1571.718	-982.858	0.447	1881.174	0.464	21	0.263	R.GLEGLTVQQAIDGNR.L
R4/RRR4-4/2	1650.221	1649.744	290.053	0.513	1529.110	0.552	21	0.241	R.YGDQTSTITAAHVER.G
R4/RRR4-5/3	1649.287	1649.744	-277.845	0.531	1264.420	0.673	26	0.226	R.YGDQTSTITAAHVER.G
R4/RRR4-4/2	1650.222	1649.744	290.573	0.507	1524.745	0.494	19	0.224	R.YGDQTSTITAAHVER.G
R4/RRR4-7/3	1650.131	1649.744	235.154	0.478	1382.230	0.608	28	0.217	R.YGDQTSTITAAHVER.G
R4/RRR4-4/3	1648.695	1649.744	-1246.441	0.503	1273.617	0.640	26	0.215	R.YGDQTSTITAAHVER.G
R4/RRR4-4/2	1649.254	1649.744	-297.515	0.495	1281.346	0.556	19	0.213	R.YGDQTSTITAAHVER.G
R4/RRR4-4/2	1382.748	1383.685	-1405.365	0.421	1481.595	0.441	19	0.210	R.EILAGVNPMVIAR.L
R4/RRR4-5/3	1649.217	1649.744	-928.452	0.506	1193.420	0.643	26	0.204	R.YGDQTSTITAAHVER.G
R4/RRR4-6/3	1649.119	1649.744	-988.087	0.460	1255.179	0.616	26	0.203	R.YGDQTSTITAAHVER.G
R4/RRR4-5/3	1649.766	1649.744	13.676	0.508	1244.938	0.603	26	0.196	R.YGDQTSTITAAHVER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1649.711	1649.744	-20.055	0.503	1161.110	0.634	27	0.195	R.YGDQTSTITAAHVER.G
R4/RRR4-4/2	1383.243	1383.685	-320.918	0.489	1266.057	0.425	19	0.188	R.EILAGVNPMVIAR.L
R4/RRR4-4/2	1399.174	1399.685	-1083.253	0.470	1051.537	0.511	18	0.187	R.EILAGVNPM*VIAR.L
R4/RRR4-4/3	1648.763	1649.744	-1204.619	0.525	1236.475	0.580	26	0.187	R.YGDQTSTITAAHVER.G
R4/RRR4-2/3	1649.782	1649.744	23.472	0.513	1097.269	0.627	24	0.187	R.YGDQTSTITAAHVER.G
R4/RRR4-4/3	1649.895	1649.744	91.928	0.510	1047.089	0.642	25	0.185	R.YGDQTSTITAAHVER.G
R4/RRR4-6/3	1649.817	1649.744	44.400	0.493	1086.264	0.613	26	0.179	R.YGDQTSTITAAHVER.G
R4/RRR4-7/3	1649.880	1649.744	82.690	0.458	1027.032	0.631	25	0.178	R.YGDQTSTITAAHVER.G
R4/RRR4-4/2	1383.351	1383.685	-242.475	0.497	1162.770	0.410	18	0.177	R.EILAGVNPMVIAR.L
R4/RRR4-1/3	1649.071	1649.744	-1017.295	0.486	1058.287	0.598	25	0.172	R.YGDQTSTITAAHVER.G
R4/RRR4-2/3	1649.113	1649.744	-991.877	0.435	1131.078	0.561	26	0.167	R.YGDQTSTITAAHVER.G
R4/RRR4-4/2	1383.212	1383.685	-343.142	0.387	1097.329	0.354	18	0.164	R.EILAGVNPMVIAR.L
R4/RRR4-2/3	1649.633	1649.744	-67.371	0.493	916.841	0.613	24	0.162	R.YGDQTSTITAAHVER.G
R4/RRR4-1/2	1570.439	1571.718	-1455.153	0.326	978.444	0.418	16	0.161	R.GLEGLTVQQAIDGNR.L
R4/RRR4-4/2	1399.746	1399.685	43.635	0.432	853.911	0.400	16	0.158	R.EILAGVNPM*VIAR.L
R4/RRR4-4/2	1398.649	1399.685	-1459.903	0.291	886.728	0.326	17	0.150	R.EILAGVNPM*VIAR.L
R4/RRR4-4/2	1572.295	1571.718	-269.560	0.394	735.687	0.304	17	0.142	R.GLEGLTVQQAIDGNR.L
R4/RRR4-5/2	1400.782	1399.685	69.388	0.342	457.589	0.321	13	0.141	R.EILAGVNPM*VIAR.L
R4/RRR4-7/3	1650.530	1649.744	-130.017	0.347	461.105	0.500	20	0.114	R.YGDQTSTITAAHVER.G
R4/RRR4-16/2	1406.002	1405.487	-345.940	0.506	1449.984	0.539	18	0.232	R.FYCWDTAGQEK.F
R4/RRR4-16/2	1404.388	1405.487	-1498.701	0.429	1555.371	0.474	18	0.227	R.FYCWDTAGQEK.F
R4/RRR4-16/2	1405.042	1405.487	-317.420	0.437	1506.919	0.430	18	0.212	R.FYCWDTAGQEK.F
R4/RRR4-16/3	1763.397	1762.988	232.583	0.559	1476.001	0.555	30	0.209	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/2	1762.285	1762.988	-969.163	0.548	1193.161	0.545	19	0.205	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/3	1762.910	1762.988	-44.777	0.516	1328.937	0.569	27	0.194	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/2	1762.229	1762.988	-1001.362	0.519	1059.959	0.490	18	0.183	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/2	1763.312	1762.988	184.101	0.501	933.553	0.510	17	0.177	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/3	1762.608	1762.988	-216.498	0.515	1174.663	0.565	27	0.172	K.SNYNFEKPFLYLAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1762.712	1762.988	-157.020	0.458	811.516	0.494	16	0.167	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/3	1762.588	1762.988	-227.545	0.507	1127.693	0.564	26	0.167	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/2	1761.985	1762.988	-1140.477	0.502	682.524	0.482	15	0.159	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/2	1763.455	1762.988	265.527	0.479	712.336	0.440	16	0.156	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/3	1762.379	1762.988	-915.903	0.491	1028.573	0.524	26	0.144	K.SNYNFEKPFLYLAR.K
R4/RRR4-16/3	1762.743	1762.988	-139.591	0.537	851.690	0.558	24	0.139	K.SNYNFEKPFLYLAR.K
R4/RRR4-9/2	1423.105	1423.550	-313.821	0.512	2210.297	0.529	23	0.338	K.FIASEGDTVTPGTK.V
R4/RRR4-9/2	1795.371	1795.885	-846.350	0.521	1869.605	0.630	24	0.308	K.SAAPAETHVAPSEDSTPK.E
R4/RRR4-9/2	1423.172	1423.550	-266.748	0.477	1988.060	0.450	22	0.276	K.FIASEGDTVTPGTK.V
R4/RRR4-9/2	1795.371	1795.885	-845.941	0.486	1618.192	0.638	23	0.271	K.SAAPAETHVAPSEDSTPK.E
R4/RRR4-9/2	1795.449	1795.885	-244.035	0.534	1518.790	0.675	22	0.268	K.SAAPAETHVAPSEDSTPK.E
R4/RRR4-9/2	1424.231	1423.550	-224.770	0.523	1706.643	0.518	20	0.255	K.FIASEGDTVTPGTK.V
R4/RRR4-9/2	1398.922	1399.466	-1106.607	0.472	1369.240	0.401	17	0.191	R.DADNM*NFADIEK.G
R4/RRR4-9/2	1399.131	1399.466	-240.278	0.489	1338.446	0.408	17	0.190	R.DADNM*NFADIEK.G
R4/RRR4-9/2	1398.573	1399.466	-1357.434	0.405	1330.019	0.296	17	0.169	R.DADNM*NFADIEK.G
R4/RRR4-20/2	1215.953	1216.282	-271.527	0.499	691.009	0.544	15	0.174	R.AQGSYTFADQK.T
R4/RRR4-20/2	1216.120	1216.282	-133.158	0.492	667.506	0.501	15	0.167	R.AQGSYTFADQK.T
R4/RRR4-19/2	1216.045	1216.282	-195.590	0.504	663.381	0.497	15	0.167	R.AQGSYTFADQK.T
R4/RRR4-20/2	1215.997	1216.282	-235.168	0.478	690.459	0.476	15	0.164	R.AQGSYTFADQK.T
R4/RRR4-20/3	1760.596	1761.017	-239.764	0.448	1133.440	0.545	30	0.160	K.VYFHDVVGGTKPTAIR.V
R4/RRR4-19/2	887.516	888.004	-551.694	0.340	1184.937	0.207	13	0.151	R.NEVLSAVR.E
R4/RRR4-19/2	887.841	888.004	-183.703	0.376	1127.780	0.218	13	0.150	R.NEVLSAVR.E
R4/RRR4-19/2	887.824	888.004	-202.737	0.373	1149.119	0.190	13	0.148	-.NEVLSAVR.-
R4/RRR4-20/3	1760.502	1761.017	-862.912	0.450	965.801	0.539	29	0.142	K.VYFHDVVGGTKPTAIR.V
R4/RRR4-19/3	1760.972	1761.017	-25.706	0.433	1056.300	0.503	29	0.141	K.VYFHDVVGGTKPTAIR.V
R4/RRR4-20/2	888.062	888.004	65.748	0.385	1160.183	0.111	13	0.138	R.NEVLSAVR.E
R4/RRR4-20/2	887.750	888.004	-286.470	0.361	993.416	0.127	12	0.135	R.NEVLSAVR.E
R4/RRR4-19/3	1760.791	1761.017	-128.551	0.482	886.268	0.534	28	0.135	K.VYFHDVVGGTKPTAIR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/3	1761.144	1761.017	72.113	0.458	869.824	0.535	28	0.134	K.VYFHDVVGGTKPTAIR.V
R4/RRR4-19/3	1760.802	1761.017	-122.500	0.448	757.904	0.540	28	0.127	K.VYFHDVVGGTKPTAIR.V
R4/RRR4-17/2	1455.358	1455.595	-163.765	0.514	2259.655	0.506	22	0.338	K.GVISLDTSGSSYLR.A
R4/RRR4-17/2	1455.344	1455.595	-173.105	0.514	1872.114	0.501	21	0.274	K.GVISLDTSGSSYLR.A
R4/RRR4-17/2	1455.155	1455.595	-303.460	0.449	1652.711	0.453	20	0.231	K.GVISLDTSGSSYLR.A
R4/RRR4-17/2	1003.170	1003.180	-9.472	0.470	1199.690	0.305	14	0.164	K.AIQAFSPLR.I
R4/RRR4-17/3	1769.688	1769.936	-140.600	0.335	1114.181	0.343	28	0.104	R.ILNPQYLSQSSDTFR.D
R4/RRR4-12/2	1358.895	1359.421	-1126.576	0.458	1759.609	0.499	23	0.258	K.AEEPSASGDPLASK.S
R4/RRR4-13/2	1264.316	1264.326	-7.903	0.536	1736.105	0.489	20	0.253	K.FGDAVQEDVGAR.L
R4/RRR4-12/2	1263.533	1264.326	-1423.328	0.548	1680.926	0.504	20	0.250	K.FGDAVQEDVGAR.L
R4/RRR4-12/2	1263.530	1264.326	-1426.045	0.555	1426.783	0.517	20	0.225	K.FGDAVQEDVGAR.L
R4/RRR4-12/2	1264.029	1264.326	-236.209	0.576	1487.661	0.483	20	0.223	K.FGDAVQEDVGAR.L
R4/RRR4-13/2	1263.995	1264.326	-262.853	0.538	1550.176	0.440	20	0.219	K.FGDAVQEDVGAR.L
R4/RRR4-12/2	1358.953	1359.421	-345.754	0.460	1377.878	0.520	21	0.217	K.AEEPSASGDPLASK.S
R4/RRR4-12/2	1359.046	1359.421	-277.262	0.475	1255.397	0.568	20	0.215	K.AEEPSASGDPLASK.S
R4/RRR4-13/2	1263.433	1264.326	-1503.099	0.434	1130.685	0.350	17	0.166	K.FGDAVQEDVGAR.L
R4/RRR4-12/2	1411.387	1411.587	-142.495	0.420	618.180	0.417	16	0.154	K.LNGYGYDNLILR.V
R4/RRR4-13/2	1411.918	1411.587	235.122	0.416	386.717	0.411	13	0.145	-.LNGYGYDNLILR.-
R4/RRR4-12/2	1410.840	1411.587	-1242.087	0.300	356.855	0.326	13	0.141	K.LNGYGYDNLILR.V
R4/RRR4-18/2	1264.280	1264.326	-36.956	0.302	830.539	0.219	16	0.135	-.FGDAVQEDVGAR.-
R4/RRR4-14/2	1617.263	1617.742	-297.041	0.452	2158.623	0.375	23	0.281	R.ELDGAELGTVAWAER.N
R4/RRR4-14/2	1498.780	1497.679	67.999	0.544	1326.859	0.604	21	0.235	K.IDWSGAPFVVSYR.G
R4/RRR4-14/2	1497.397	1497.679	-188.603	0.326	1303.114	0.311	18	0.169	K.IDWSGAPFVVSYR.G
R4/RRR4-14/2	1497.105	1497.679	-1054.550	0.350	940.004	0.434	19	0.166	K.IDWSGAPFVVSYR.G
R4/RRR4-14/3	1845.299	1846.032	-941.959	0.470	985.026	0.518	32	0.138	R.VVSDDGKTQQVALTLDR.S
R4/RRR4-14/3	1846.212	1846.032	97.771	0.508	624.599	0.539	28	0.119	R.VVSDDGKTQQVALTLDR.S
R4/RRR4-14/3	1845.208	1846.032	-991.572	0.381	531.379	0.401	25	0.094	R.VVSDDGKTQQVALTLDR.S
R4/RRR4-12/2	1358.648	1359.509	-1374.331	0.431	1624.308	0.494	19	0.260	R.IGEVISGEGVHYV.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1199.489	1200.327	-1536.580	0.376	1495.118	0.283	17	0.181	K.SGLSLNDQLPR.N
R4/RRR4-12/2	1200.128	1200.327	-166.558	0.410	1318.065	0.332	16	0.175	K.SGLSLNDQLPR.N
R4/RRR4-12/2	1201.027	1200.327	-250.741	0.490	1347.617	0.311	16	0.172	K.SGLSLNDQLPR.N
R4/RRR4-12/2	1533.421	1533.797	-245.972	0.344	841.792	0.425	18	0.157	K.IFTAAWEVPPVFR.W
R4/RRR4-8/2	1706.638	1706.840	-118.632	0.544	1784.773	0.549	21	0.274	R.TGFDLQHVQDGLYGR.H
R4/RRR4-8/2	1712.906	1712.969	-37.141	0.533	1494.264	0.555	24	0.239	K.QTLDLGSTGLLPLEVR.F
R4/RRR4-8/2	1712.528	1712.969	-258.139	0.510	1404.335	0.551	24	0.228	K.QTLDLGSTGLLPLEVR.F
R4/RRR4-7/2	1712.634	1712.969	-196.356	0.462	1186.774	0.517	22	0.198	K.QTLDLGSTGLLPLEVR.F
R4/RRR4-8/2	1713.879	1712.969	-52.479	0.502	910.021	0.511	19	0.175	K.QTLDLGSTGLLPLEVR.F
R4/RRR4-7/2	1712.766	1712.969	-118.708	0.476	928.416	0.473	20	0.171	K.QTLDLGSTGLLPLEVR.F
R4/RRR4-8/2	1201.302	1200.369	-55.405	0.488	950.559	0.391	16	0.166	R.IYVTNSLFSR.W
R4/RRR4-7/2	1712.384	1712.969	-928.551	0.412	784.241	0.493	18	0.164	K.QTLDLGSTGLLPLEVR.F
R4/RRR4-8/2	1200.391	1200.369	18.603	0.276	1122.565	0.215	16	0.147	R.IYVTNSLFSR.W
R4/RRR4-2/2	1712.829	1712.969	-82.105	0.283	570.424	0.250	15	0.134	K.QTLDLGSTGLLPLEVR.F
R4/RRR4-7/3	1706.507	1706.840	-195.992	0.406	902.185	0.530	25	0.133	R.TGFDLQHVQDGLYGR.H
R4/RRR4-7/3	1707.078	1706.840	139.736	0.394	850.828	0.509	25	0.124	R.TGFDLQHVQDGLYGR.H
R4/RRR4-4/3	1708.447	1706.840	-230.456	0.375	311.193	0.340	21	0.083	-.TGFDLQHVQDGLYGR.-
R4/RRR4-17/2	1522.259	1522.773	-997.391	0.477	1854.170	0.433	19	0.251	K.FVNDLHALISPPAK.G
R4/RRR4-17/2	1521.789	1522.773	-1307.695	0.432	1662.672	0.402	20	0.220	K.FVNDLHALISPPAK.G
R4/RRR4-17/2	1559.187	1558.677	-315.172	0.501	1094.170	0.525	23	0.195	K.FVSNGQPGPAQNVDK.S
R4/RRR4-17/2	1558.637	1558.677	-25.892	0.441	1118.324	0.521	22	0.194	K.FVSNGQPGPAQNVDK.S
R4/RRR4-17/2	1559.337	1558.677	-219.114	0.526	987.675	0.528	22	0.188	K.FVSNGQPGPAQNVDK.S
R4/RRR4-17/2	1558.262	1558.677	-267.037	0.566	929.883	0.498	23	0.181	K.FVSNGQPGPAQNVDK.S
R4/RRR4-17/2	1558.294	1558.677	-246.682	0.542	918.751	0.484	23	0.178	K.FVSNGQPGPAQNVDK.S
R4/RRR4-17/2	1558.183	1558.677	-318.361	0.527	776.399	0.501	22	0.173	K.FVSNGQPGPAQNVDK.S
R4/RRR4-17/3	1705.553	1705.917	-214.081	0.477	856.040	0.496	27	0.123	K.HQELLKNEQYQM*K.L
R4/RRR4-17/3	1522.577	1522.773	-129.323	0.480	587.266	0.513	25	0.113	K.FVNDLHALISPPAK.G
R4/RRR4-17/3	1522.424	1522.773	-229.945	0.409	800.989	0.469	29	0.113	K.FVNDLHALISPPAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/3	1705.541	1705.917	-220.974	0.442	551.400	0.479	22	0.106	K.HQELLKNEQYQM*K.L
R4/RRR4-17/3	1705.111	1705.917	-1062.376	0.505	469.961	0.478	21	0.105	K.HQELLKNEQYQM*K.L
R4/RRR4-17/3	1522.337	1522.773	-287.020	0.423	507.041	0.445	24	0.101	K.FVNDLHALISPPAK.G
R4/RRR4-21/2	1215.778	1216.366	-1310.250	0.467	1638.320	0.339	16	0.206	R.LLEELERGEK.G
R4/RRR4-21/2	1216.234	1216.366	-109.186	0.523	1647.711	0.304	16	0.197	R.LLEELERGEK.G
R4/RRR4-22/2	1090.997	1091.247	-229.455	0.402	1625.062	0.272	15	0.191	K.FGVLANWQR.E
R4/RRR4-22/3	1806.509	1806.930	-233.622	0.563	1436.750	0.508	29	0.189	R.INM*SCVNHETGAVDSR.K
R4/RRR4-22/2	1090.988	1091.247	-237.874	0.497	1563.927	0.284	15	0.187	K.FGVLANWQR.E
R4/RRR4-21/2	1216.270	1216.366	-79.487	0.487	1588.634	0.262	16	0.184	R.LLEELERGEK.G
R4/RRR4-22/2	1216.070	1216.366	-244.115	0.524	1547.892	0.283	16	0.183	R.LLEELERGEK.G
R4/RRR4-22/2	1216.197	1216.366	-139.894	0.498	1448.979	0.302	15	0.179	R.LLEELERGEK.G
R4/RRR4-22/2	1215.524	1216.366	-1520.541	0.489	1488.663	0.239	15	0.170	R.LLEELERGEK.G
R4/RRR4-22/3	1806.701	1806.930	-126.964	0.530	1520.079	0.404	30	0.163	R.INM*SCVNHETGAVDSR.K
R4/RRR4-21/3	1806.383	1806.930	-859.044	0.510	1297.269	0.482	27	0.162	R.INM*SCVNHETGAVDSR.K
R4/RRR4-22/3	1806.550	1806.930	-210.946	0.470	1235.599	0.462	27	0.148	R.INM*SCVNHETGAVDSR.K
R4/RRR4-3/2	1380.206	1379.690	-352.051	0.595	2043.835	0.464	19	0.286	R.VTIDLLEMVFAK.G
R4/RRR4-3/2	1394.793	1395.690	-1363.698	0.478	1810.052	0.423	18	0.243	R.VTIDLLEM*VFAK.G
R4/RRR4-3/2	1395.303	1395.690	-277.568	0.469	1549.212	0.431	17	0.215	R.VTIDLLEM*VFAK.G
R4/RRR4-3/2	1379.114	1379.690	-1146.192	0.484	1526.944	0.334	17	0.191	R.VTIDLLEMVFAK.G
R4/RRR4-3/2	1394.783	1395.690	-1371.257	0.375	1452.846	0.357	17	0.190	R.VTIDLLEM*VFAK.G
R4/RRR4-4/2	1379.947	1379.690	186.979	0.453	1297.391	0.322	17	0.171	R.VTIDLLEMVFAK.G
R4/RRR4-1/2	1396.162	1395.690	339.625	0.409	844.018	0.375	14	0.153	R.VTIDLLEM*VFAK.G
R4/RRR4-4/2	1380.154	1379.690	336.875	0.437	750.666	0.379	15	0.153	R.VTIDLLEMVFAK.G
R4/RRR4-4/2	1380.974	1379.690	206.345	0.460	638.380	0.367	16	0.151	R.VTIDLLEMVFAK.G
R4/RRR4-3/2	1380.943	1379.690	183.387	0.271	159.470	0.390	14	0.146	-.VTIDLLEMVFAK.-
R4/RRR4-17/2	1874.611	1874.126	259.971	0.532	1301.178	0.522	23	0.208	K.LAEEIKKGASSVEGVEVK.I
R4/RRR4-17/2	1014.742	1015.299	-1539.184	0.392	1512.761	0.402	15	0.206	R.FGMMAAQMK.A
R4/RRR4-17/2	1729.281	1728.967	182.343	0.561	1086.452	0.563	24	0.204	K.IWQVPETLSEEVLGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1728.354	1728.967	-935.768	0.493	983.113	0.545	23	0.191	K.IWQVPETLSEEVLGK.M
R4/RRR4-17/2	1728.583	1728.967	-222.805	0.493	1071.421	0.504	24	0.191	K.IWQVPETLSEEVLGK.M
R4/RRR4-17/2	1046.928	1047.298	-354.804	0.432	1053.198	0.468	14	0.182	R.FGM*M*AAQMK.A
R4/RRR4-17/2	1728.647	1728.967	-185.683	0.499	946.901	0.495	23	0.181	K.IWQVPETLSEEVLGK.M
R4/RRR4-17/2	1046.969	1047.298	-314.796	0.456	1245.654	0.362	16	0.179	R.FGM*M*AAQMK.A
R4/RRR4-17/2	1728.617	1728.967	-202.756	0.472	931.687	0.465	23	0.175	K.IWQVPETLSEEVLGK.M
R4/RRR4-17/2	1046.771	1047.298	-1463.109	0.421	958.691	0.434	15	0.172	R.FGM*M*AAQMK.A
R4/RRR4-17/2	1729.319	1728.967	204.287	0.534	799.840	0.488	21	0.171	K.IWQVPETLSEEVLGK.M
R4/RRR4-14/2	1858.999	1859.285	-154.617	0.531	1170.201	0.603	22	0.211	R.LPLVGPLLTPPVSVASVAK.V
R4/RRR4-14/2	1858.626	1859.285	-895.344	0.523	1112.321	0.564	23	0.199	R.LPLVGPLLTPPVSVASVAK.V
R4/RRR4-14/2	1586.308	1586.772	-293.266	0.473	1010.474	0.551	20	0.188	K.INGTANINAISVAAEK.G
R4/RRR4-14/2	1586.232	1586.772	-973.607	0.465	968.851	0.564	20	0.187	K.INGTANINAISVAAEK.G
R4/RRR4-14/2	1858.416	1859.285	-1008.960	0.490	739.830	0.578	19	0.172	R.LPLVGPLLTPPVSVASVAK.V
R4/RRR4-14/2	961.744	962.080	-349.471	0.415	686.976	0.456	14	0.163	R.ATEAELLSK.F
R4/RRR4-14/2	961.819	962.080	-272.175	0.377	721.125	0.371	14	0.154	R.ATEAELLSK.F
R4/RRR4-14/2	961.366	962.080	-1787.977	0.361	590.774	0.390	14	0.144	-.ATEAELLSK.-
R4/RRR4-21/2	1343.294	1343.485	-142.863	0.489	1099.204	0.475	20	0.188	K.EAFELVSGEM*SK.T
R4/RRR4-22/2	1685.721	1685.902	-107.684	0.494	818.551	0.566	25	0.185	R.LDPGVTASHAFVLETK.V
R4/RRR4-21/2	1342.997	1343.485	-364.612	0.466	1179.328	0.420	19	0.183	K.EAFELVSGEM*SK.T
R4/RRR4-22/2	1686.312	1685.902	243.840	0.496	698.361	0.542	25	0.176	R.LDPGVTASHAFVLETK.V
R4/RRR4-22/2	1686.395	1685.902	293.270	0.460	617.705	0.542	24	0.171	R.LDPGVTASHAFVLETK.V
R4/RRR4-22/2	1327.097	1327.486	-293.624	0.457	1040.272	0.404	18	0.171	K.EAFELVSGEMSK.T
R4/RRR4-22/2	1240.345	1239.405	-48.232	0.472	809.041	0.465	16	0.169	R.FQGSPAVITYR.V
R4/RRR4-22/2	1239.037	1239.405	-297.694	0.356	976.788	0.375	18	0.163	R.FQGSPAVITYR.V
R4/RRR4-22/2	1240.113	1239.405	-236.223	0.449	755.548	0.422	16	0.161	R.FQGSPAVITYR.V
R4/RRR4-21/2	1686.499	1685.902	-239.473	0.418	508.909	0.512	20	0.159	R.LDPGVTASHAFVLETK.V
R4/RRR4-22/2	1328.388	1327.486	-73.884	0.357	778.452	0.439	14	0.157	K.EAFELVSGEMSK.T
R4/RRR4-21/2	1238.989	1239.405	-336.245	0.403	592.236	0.403	14	0.152	R.FQGSPAVITYR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1238.255	1239.405	-1741.604	0.301	696.423	0.363	15	0.148	R.FQGSPAVITYR.V
R4/RRR4-21/2	1342.943	1343.485	-1151.608	0.308	661.670	0.343	15	0.145	K.EAFELVSGEM*SK.T
R4/RRR4-23/2	1240.632	1239.405	183.797	0.303	218.331	0.398	11	0.111	-.FQGSPAVITYR.-
R4/RRR4-13/2	1604.389	1603.839	-281.567	0.542	1091.903	0.471	18	0.181	K.LNSSLSQVLVNCLR.Y
R4/RRR4-13/2	1295.045	1295.379	-258.536	0.390	1176.189	0.369	18	0.171	K.GSVSTESAVTQTK.F
R4/RRR4-13/2	1295.143	1295.379	-182.700	0.418	897.772	0.424	16	0.162	K.GSVSTESAVTQTK.F
R4/RRR4-13/2	1294.814	1295.379	-1212.306	0.329	1035.643	0.340	17	0.157	K.GSVSTESAVTQTK.F
R4/RRR4-14/2	1295.019	1295.379	-278.396	0.377	770.485	0.378	16	0.151	K.GSVSTESAVTQTK.F
R4/RRR4-13/3	1173.482	1173.385	83.394	0.509	1335.523	0.328	25	0.120	K.ALKDLGLDVTK.G
R4/RRR4-13/3	1173.072	1173.385	-266.956	0.554	969.782	0.364	22	0.104	K.ALKDLGLDVTK.G
R4/RRR4-11/2	1328.878	1329.486	-1214.031	0.457	1248.814	0.515	19	0.205	K.IPATWQGIEASR.L
R4/RRR4-11/2	1328.905	1329.486	-1193.460	0.422	986.904	0.425	18	0.170	K.IPATWQGIEASR.L
R4/RRR4-11/2	977.910	978.127	-222.749	0.435	1092.320	0.346	13	0.166	R.RVEELFGK.I
R4/RRR4-11/2	977.993	978.127	-137.725	0.457	1113.887	0.313	14	0.163	R.RVEELFGK.I
R4/RRR4-11/2	977.557	978.127	-1610.947	0.452	1185.936	0.288	14	0.163	R.RVEELFGK.I
R4/RRR4-11/3	1101.106	1101.278	-157.086	0.490	1755.685	0.302	25	0.162	K.KGEDAGLALVK.K
R4/RRR4-11/2	1328.618	1329.486	-1410.462	0.376	549.219	0.311	15	0.142	K.IPATWQGIEASR.L
R4/RRR4-3/3	1281.630	1281.443	146.334	0.523	1507.295	0.516	24	0.200	K.HVVDDGLELRK.A
R4/RRR4-3/2	1911.580	1912.302	-903.591	0.491	1057.371	0.497	24	0.185	K.GLLPELLPLLYDQTVVK.Q
R4/RRR4-3/2	1911.851	1912.302	-236.286	0.494	859.244	0.498	22	0.172	K.GLLPELLPLLYDQTVVK.Q
R4/RRR4-3/3	1282.363	1281.443	-62.893	0.503	1286.780	0.497	22	0.163	K.HVVDDGLELRK.A
R4/RRR4-3/2	1911.541	1912.302	-923.850	0.486	758.051	0.475	21	0.163	K.GLLPELLPLLYDQTVVK.Q
R4/RRR4-3/3	1281.751	1281.443	241.174	0.570	1113.434	0.501	22	0.146	K.HVVDDGLELRK.A
R4/RRR4-3/3	1678.232	1678.935	-1017.848	0.372	838.253	0.489	29	0.116	K.IM*ASPPLADKYNSVR.S
R4/RRR4-10/2	1594.470	1594.836	-229.951	0.539	1619.389	0.514	22	0.243	R.LPGYLGEYLALTGAR.L
R4/RRR4-10/2	1594.558	1594.836	-175.038	0.543	1531.644	0.538	22	0.239	R.LPGYLGEYLALTGAR.L
R4/RRR4-10/2	1295.034	1295.424	-301.934	0.467	1669.770	0.447	19	0.234	R.SVVTGDVYEGIR.A
R4/RRR4-10/2	1296.319	1295.424	-80.906	0.451	1477.504	0.517	19	0.228	R.SVVTGDVYEGIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1593.854	1594.836	-1246.878	0.474	1504.252	0.475	22	0.220	R.LPGYLGEYLALTGAR.L
R4/RRR4-10/2	1413.382	1412.561	-126.528	0.369	553.085	0.509	14	0.154	K.CFSAETVEDIIK.A
R4/RRR4-17/2	1778.268	1779.029	-993.088	0.545	1141.514	0.522	24	0.200	K.IWQVPETLHEEVLGK.M
R4/RRR4-17/2	1777.871	1779.029	-1217.403	0.511	988.231	0.482	23	0.181	K.IWQVPETLHEEVLGK.M
R4/RRR4-17/2	1778.415	1779.029	-910.598	0.482	862.190	0.513	21	0.176	K.IWQVPETLHEEVLGK.M
R4/RRR4-17/3	1857.100	1857.039	32.915	0.445	806.708	0.472	26	0.115	R.WPTEM*ELEHAFHQGK.Y
R4/RRR4-17/3	1856.772	1857.039	-144.328	0.388	665.674	0.491	22	0.109	R.WPTEM*ELEHAFHQGK.Y
R4/RRR4-17/3	1840.501	1841.039	-838.144	0.320	714.742	0.226	23	0.079	R.WPTEMELEHAFHQGK.Y
R4/RRR4-15/2	1057.021	1057.139	-112.427	0.461	1334.326	0.487	17	0.209	R.APIGEEVEGR.R
R4/RRR4-15/2	1056.337	1057.139	-1711.201	0.429	1193.480	0.466	17	0.192	R.APIGEEVEGR.R
R4/RRR4-14/2	1057.000	1057.139	-131.890	0.463	1091.154	0.501	17	0.192	R.APIGEEVEGR.R
R4/RRR4-14/2	1057.005	1057.139	-127.140	0.465	1053.857	0.501	17	0.190	R.APIGEEVEGR.R
R4/RRR4-15/2	1057.000	1057.139	-132.701	0.485	1206.263	0.431	16	0.187	R.APIGEEVEGR.R
R4/RRR4-15/2	1045.905	1046.200	-282.193	0.380	972.210	0.412	16	0.167	R.SQGELTGILK.E
R4/RRR4-15/2	1260.000	1260.384	-306.054	0.312	599.982	0.390	15	0.149	K.ATVSHNSQLFR.F
R4/RRR4-14/2	1260.226	1260.384	-125.874	0.394	321.657	0.404	12	0.148	K.ATVSHNSQLFR.F
R4/RRR4-15/2	1260.055	1260.384	-262.315	0.351	541.095	0.373	14	0.148	K.ATVSHNSQLFR.F
R4/RRR4-14/2	1260.406	1260.384	17.426	0.347	875.870	0.264	15	0.144	K.ATVSHNSQLFR.F
R4/RRR4-15/2	1045.882	1046.200	-305.144	0.267	621.323	0.349	14	0.143	R.SQGELTGILK.E
R4/RRR4-15/2	1260.177	1260.384	-165.228	0.359	485.579	0.297	13	0.142	K.ATVSHNSQLFR.F
R4/RRR4-14/2	1314.858	1315.536	-1279.773	0.415	1120.848	0.443	16	0.180	R.YVTVGAYCLLR.S
R4/RRR4-15/2	1381.880	1382.549	-1211.501	0.396	1114.291	0.407	17	0.171	R.IPTGELWAGNPAR.F
R4/RRR4-15/2	1381.648	1382.549	-1380.075	0.375	979.407	0.410	15	0.161	R.IPTGELWAGNPAR.F
R4/RRR4-15/2	1314.412	1315.536	-1620.947	0.280	865.643	0.417	15	0.156	R.YVTVGAYCLLR.S
R4/RRR4-14/3	1461.239	1461.706	-320.855	0.483	1656.774	0.299	24	0.147	R.KLTNEEIM*EIPK.L
R4/RRR4-15/2	1314.569	1315.536	-1501.258	0.310	545.510	0.380	14	0.146	R.YVTVGAYCLLR.S
R4/RRR4-15/3	1461.757	1461.706	34.442	0.467	1029.779	0.324	22	0.098	R.KLTNEEIM*EIPK.L
R4/RRR4-16/2	1859.431	1859.111	172.674	0.570	868.618	0.572	22	0.187	K.VFVESSLPVIEYYNAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1074.945	1075.155	-196.092	0.562	1031.954	0.387	15	0.170	R.VDDNIETIR.K
R4/RRR4-16/2	1859.245	1859.111	72.266	0.545	598.090	0.541	18	0.164	K.VFVESSLPVIEYYNAK.D
R4/RRR4-16/2	1074.450	1075.155	-1591.534	0.394	970.581	0.351	15	0.160	R.VDDNIETIR.K
R4/RRR4-16/2	1074.315	1075.155	-1717.097	0.419	1027.229	0.328	15	0.160	R.VDDNIETIR.K
R4/RRR4-16/3	1799.994	1800.088	-52.561	0.430	1299.244	0.463	29	0.155	K.KIDAAKPIPEVFEDVK.A
R4/RRR4-16/3	1799.997	1800.088	-50.724	0.414	1057.550	0.380	30	0.110	K.KIDAAKPIPEVFEDVK.A
R4/RRR4-16/3	1800.474	1800.088	215.009	0.422	614.184	0.449	25	0.102	K.KIDAAKPIPEVFEDVK.A
R4/RRR4-9/3	1305.043	1305.594	-1192.072	0.530	1780.414	0.541	25	0.262	R.HVVLITNVKPGK.L
R4/RRR4-9/3	1305.628	1305.594	25.674	0.533	1435.644	0.466	23	0.174	R.HVVLITNVKPGK.L
R4/RRR4-9/2	1833.273	1835.050	-2066.459	0.347	895.116	0.502	17	0.163	R.ISFAGFDGKPEDVLNPK.K
R4/RRR4-9/2	1237.967	1238.374	-329.698	0.233	1151.911	0.293	16	0.153	K.FFSPEELVNR.H
R4/RRR4-9/2	1299.181	1298.471	-223.315	0.528	1775.216	0.552	22	0.277	R.LLAGESGIGPIDR.F
R4/RRR4-9/2	1118.042	1117.278	-211.421	0.482	1705.712	0.553	19	0.265	K.ALESAGLALGSK.S
R4/RRR4-9/2	1297.661	1298.471	-1398.633	0.390	1687.970	0.556	21	0.260	R.LLAGESGIGPIDR.F
R4/RRR4-9/2	1118.312	1117.278	31.026	0.436	1583.118	0.568	19	0.251	K.ALESAGLALGSK.S
R4/RRR4-9/2	1297.979	1298.471	-380.013	0.455	1569.440	0.535	21	0.243	R.LLAGESGIGPIDR.F
R4/RRR4-9/2	1118.296	1117.278	16.356	0.413	1197.191	0.590	19	0.213	K.ALESAGLALGSK.S
R4/RRR4-9/2	1055.027	1055.125	-93.375	0.449	785.146	0.281	13	0.145	R.FDASNFPTR.F
R4/RRR4-9/2	1055.091	1055.125	-32.447	0.453	979.687	0.212	14	0.142	-.FDASNFPTR.-
R4/RRR4-9/2	1055.045	1055.125	-76.547	0.443	657.038	0.250	13	0.139	-.FDASNFPTR.-
R4/RRR4-8/3	1851.516	1852.072	-842.978	0.525	1533.751	0.495	31	0.200	R.LTLADALVYACNQGVDK.I
R4/RRR4-8/2	1190.795	1191.271	-400.440	0.367	1107.091	0.513	17	0.187	K.EVAAASEISGEK.F
R4/RRR4-8/2	1273.059	1272.388	-259.347	0.466	1002.729	0.470	18	0.179	K.GLTFDSGGYNIK.T
R4/RRR4-8/2	1190.894	1191.271	-317.131	0.387	864.390	0.477	16	0.167	K.EVAAASEISGEK.F
R4/RRR4-8/2	1272.073	1272.388	-248.768	0.411	1029.176	0.369	18	0.163	K.GLTFDSGGYNIK.T
R4/RRR4-8/3	1851.573	1852.072	-270.303	0.452	1342.578	0.427	29	0.150	R.LTLADALVYACNQGVDK.I
R4/RRR4-8/3	1850.654	1852.072	-1310.681	0.362	1283.812	0.307	25	0.112	R.LTLADALVYACNQGVDK.I
R4/RRR4-5/2	1580.338	1580.764	-270.357	0.442	1388.507	0.554	20	0.224	K.LTEVSVSDKLEGFR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1925.721	1926.267	-805.339	0.412	1030.005	0.439	20	0.168	K.LDQDQVLM*LQSPIALPK.A
R4/RRR4-5/2	1580.294	1580.764	-298.334	0.393	1062.017	0.395	18	0.166	K.LTEVSVSDKLEGFR.A
R4/RRR4-5/2	1012.512	1013.130	-1602.795	0.398	447.555	0.490	12	0.158	K.NPVELDGLR.K
R4/RRR4-5/2	1012.905	1013.130	-222.366	0.415	659.986	0.404	13	0.155	K.NPVELDGLR.K
R4/RRR4-5/2	1012.348	1013.130	-1765.602	0.272	276.628	0.308	10	0.142	K.NPVELDGLR.K
R4/RRR4-14/2	1348.121	1347.366	-182.422	0.532	1168.652	0.455	18	0.190	K.YEDQIDSYGEK.G
R4/RRR4-14/2	1346.962	1347.366	-300.474	0.496	1274.984	0.400	18	0.187	K.YEDQIDSYGEK.G
R4/RRR4-14/2	1515.251	1515.784	-1014.367	0.456	756.247	0.560	20	0.176	K.VLGGGKPADVFLWR.N
R4/RRR4-14/2	1346.269	1347.366	-1562.401	0.327	1194.340	0.298	18	0.162	K.YEDQIDSYGEK.G
R4/RRR4-14/2	941.793	942.050	-273.542	0.312	320.157	0.468	11	0.151	K.QYAVFDAK.V
R4/RRR4-14/2	942.053	942.050	3.495	0.265	372.134	0.461	12	0.148	K.QYAVFDAK.V
R4/RRR4-14/2	941.476	942.050	-1676.325	0.306	204.640	0.428	9	0.145	-.QYAVFDAK.-
R4/RRR4-16/2	1419.385	1419.648	-185.771	0.460	1415.354	0.496	17	0.214	K.GANEVLLVIEAYK.T
R4/RRR4-16/2	1419.009	1419.648	-1157.972	0.369	1096.972	0.469	17	0.179	K.GANEVLLVIEAYK.T
R4/RRR4-16/2	1418.243	1419.648	-1700.748	0.326	1331.465	0.356	16	0.176	K.GANEVLLVIEAYK.T
R4/RRR4-16/3	1851.077	1851.084	-3.686	0.422	1223.116	0.526	33	0.164	K.VTAVPAKEEEICGATFK.V
R4/RRR4-16/2	1141.532	1141.299	204.365	0.493	1181.123	0.515	18	0.146	K.VEGSTILTALH.-
R4/RRR4-16/3	1851.842	1851.084	-131.057	0.464	994.956	0.482	32	0.130	K.VTAVPAKEEEICGATFK.V
R4/RRR4-16/2	1141.115	1141.299	-162.404	0.476	1037.702	0.514	17	0.127	K.VEGSTILTALH.-
R4/RRR4-16/2	1141.201	1141.299	-86.861	0.494	1098.113	0.473	18	0.124	K.VEGSTILTALH.-
R4/RRR4-15/2	1413.174	1412.610	-309.875	0.520	1315.780	0.548	21	0.220	K.VVEVVESSPPEIK.A
R4/RRR4-20/2	1413.052	1412.610	313.349	0.503	1218.407	0.530	20	0.206	K.VVEVVESSPPEIK.A
R4/RRR4-15/2	1659.334	1659.948	-975.503	0.431	1152.775	0.521	23	0.196	K.SGTTPLSPAIVFILDK.V
R4/RRR4-19/2	1413.096	1412.610	344.704	0.483	1078.500	0.532	19	0.194	K.VVEVVESSPPEIK.A
R4/RRR4-20/2	1413.195	1412.610	-295.056	0.520	989.582	0.557	18	0.192	K.VVEVVESSPPEIK.A
R4/RRR4-15/2	1412.244	1412.610	-259.925	0.465	1045.135	0.529	19	0.191	K.VVEVVESSPPEIK.A
R4/RRR4-19/2	1412.250	1412.610	-256.240	0.403	1134.705	0.448	19	0.182	K.VVEVVESSPPEIK.A
R4/RRR4-15/2	1659.471	1659.948	-287.936	0.422	1009.661	0.467	22	0.177	K.SGTTPLSPAIVFILDK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1412.253	1412.610	-254.072	0.440	1052.340	0.425	18	0.173	K.VVEVVESSPPEIK.A
R4/RRR4-15/3	1782.413	1782.844	-242.290	0.440	1309.522	0.493	32	0.165	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-15/2	1659.012	1659.948	-1170.379	0.332	820.738	0.458	20	0.162	K.SGTTPLSPAIVFILDK.V
R4/RRR4-15/2	1659.591	1659.948	-215.763	0.373	840.692	0.445	19	0.161	K.SGTTPLSPAIVFILDK.V
R4/RRR4-15/2	1782.389	1782.844	-255.921	0.299	637.150	0.541	25	0.161	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-15/2	1660.513	1659.948	-262.539	0.410	750.957	0.456	19	0.160	K.SGTTPLSPAIVFILDK.V
R4/RRR4-20/2	1782.273	1782.844	-883.964	0.271	721.492	0.504	26	0.159	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-15/2	1781.688	1782.844	-1213.283	0.274	717.508	0.506	25	0.159	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-20/2	1782.191	1782.844	-929.896	0.243	787.565	0.486	26	0.158	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-15/2	1658.710	1659.948	-1353.135	0.261	1019.725	0.355	21	0.157	K.SGTTPLSPAIVFILDK.V
R4/RRR4-15/2	1660.078	1659.948	78.871	0.415	625.431	0.467	18	0.157	K.SGTTPLSPAIVFILDK.V
R4/RRR4-21/2	1659.533	1659.948	-250.815	0.339	703.694	0.454	19	0.156	K.SGTTPLSPAIVFILDK.V
R4/RRR4-21/2	1412.214	1412.610	-281.736	0.339	701.423	0.412	19	0.156	K.VVEVVESSPPEIK.A
R4/RRR4-12/2	1660.139	1659.948	115.301	0.371	510.557	0.456	15	0.149	K.SGTTPLSPAIVFILDK.V
R4/RRR4-9/2	1660.139	1659.948	115.449	0.317	910.021	0.310	18	0.147	K.SGTTPLSPAIVFILDK.V
R4/RRR4-21/2	1412.059	1412.610	-1102.022	0.264	427.764	0.330	17	0.144	K.VVEVVESSPPEIK.A
R4/RRR4-12/2	1659.898	1659.948	-30.287	0.288	419.104	0.428	15	0.144	K.SGTTPLSPAIVFILDK.V
R4/RRR4-15/2	1782.228	1782.844	-909.268	0.193	691.046	0.339	25	0.141	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-20/3	1783.295	1782.844	254.120	0.327	650.199	0.445	23	0.100	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-15/3	1781.902	1782.844	-1092.694	0.325	722.690	0.366	26	0.091	K.AEPEPEPEAPAAETTSR.E
R4/RRR4-25/3	1365.692	1365.565	93.173	0.550	3434.526	0.317	33	0.565	R.HHVIGQYVVGQK.G
R4/RRR4-25/3	1365.354	1365.565	-154.842	0.539	2869.083	0.398	30	0.441	R.HHVIGQYVVGQK.G
R4/RRR4-24/3	1365.612	1365.565	34.812	0.537	2699.294	0.446	31	0.418	R.HHVIGQYVVGQK.G
R4/RRR4-25/3	1365.220	1365.565	-253.194	0.559	2465.843	0.466	29	0.369	R.HHVIGQYVVGQK.G
R4/RRR4-24/3	1365.731	1365.565	121.544	0.534	2458.053	0.408	29	0.334	R.HHVIGQYVVGQK.G
R4/RRR4-24/3	1365.587	1365.565	16.388	0.537	2271.936	0.392	27	0.285	R.HHVIGQYVVGQK.G
R4/RRR4-24/2	1270.084	1270.374	-228.817	0.406	843.534	0.580	20	0.186	K.VPPNSASLEEAR.H
R4/RRR4-25/2	1270.013	1270.374	-285.323	0.431	609.821	0.597	18	0.177	K.VPPNSASLEEAR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	1270.040	1270.374	-263.626	0.423	632.488	0.574	18	0.175	K.VPPNSASLEEAR.H
R4/RRR4-24/2	1270.071	1270.374	-239.423	0.406	617.477	0.575	19	0.174	K.VPPNSASLEEAR.H
R4/RRR4-25/2	1269.926	1270.374	-353.989	0.373	680.905	0.551	19	0.172	K.VPPNSASLEEAR.H
R4/RRR4-24/2	1269.973	1270.374	-316.472	0.396	626.298	0.558	18	0.171	K.VPPNSASLEEAR.H
R4/RRR4-25/2	1270.109	1270.374	-208.954	0.354	563.108	0.607	17	0.170	K.VPPNSASLEEAR.H
R4/RRR4-25/2	1270.033	1270.374	-269.605	0.395	535.197	0.541	17	0.166	K.VPPNSASLEEAR.H
R4/RRR4-24/2	1270.038	1270.374	-265.748	0.344	409.978	0.561	15	0.160	K.VPPNSASLEEAR.H
R4/RRR4-25/3	1366.100	1365.565	-341.670	0.418	872.122	0.325	22	0.094	R.HHVIGQYVVGQK.G
R4/RRR4-10/2	1000.208	1000.219	-11.030	0.431	562.350	0.430	13	0.154	-.FSLAPLVPR.-
R4/RRR4-10/2	1000.211	1000.219	-8.215	0.445	586.017	0.367	13	0.145	-.FSLAPLVPR.-
R4/RRR4-17/2	1950.732	1951.227	-254.674	0.524	1051.415	0.593	22	0.199	R.VCPSVTMGLEPGEAFTVR.N
R4/RRR4-17/2	1966.762	1967.226	-236.696	0.542	805.694	0.618	21	0.186	R.VCPSVTM*GLEPGEAFTVR.N
R4/RRR4-17/2	1777.750	1777.874	-69.671	0.494	1203.835	0.432	20	0.183	K.DGAPDSFHFVEDWVR.T
R4/RRR4-17/2	1777.584	1777.874	-163.627	0.517	906.570	0.480	18	0.170	K.DGAPDSFHFVEDWVR.T
R4/RRR4-17/2	1777.228	1777.874	-928.704	0.441	1016.003	0.385	18	0.161	K.DGAPDSFHFVEDWVR.T
R4/RRR4-17/2	1244.450	1245.365	-1543.344	0.351	910.808	0.387	15	0.158	K.EAVNQSLENLK.T
R4/RRR4-17/2	1245.012	1245.365	-284.267	0.366	892.838	0.366	16	0.156	K.EAVNQSLENLK.T
R4/RRR4-17/2	1244.542	1245.365	-1468.461	0.220	750.973	0.213	16	0.136	K.EAVNQSLENLK.T
R4/RRR4-9/2	1935.482	1936.174	-877.108	0.462	1771.157	0.515	26	0.262	K.GVYAYDFGDTAGLTPLM*K.M
R4/RRR4-8/2	1553.640	1552.749	-70.895	0.527	994.639	0.471	21	0.181	R.FIDIPEEVAEVYK.L
R4/RRR4-8/2	1553.395	1552.749	-228.859	0.427	721.959	0.433	19	0.161	R.FIDIPEEVAEVYK.L
R4/RRR4-9/2	1257.906	1258.440	-1223.349	0.370	624.308	0.508	17	0.160	K.AVEPAACPTLTK.G
R4/RRR4-7/2	1553.872	1552.749	79.456	0.438	738.333	0.432	17	0.159	R.FIDIPEEVAEVYK.L
R4/RRR4-1/2	1553.670	1552.749	-51.114	0.447	613.955	0.376	17	0.151	R.FIDIPEEVAEVYK.L
R4/RRR4-9/2	1552.243	1552.749	-973.155	0.388	795.523	0.317	20	0.151	R.FIDIPEEVAEVYK.L
R4/RRR4-8/2	1554.002	1552.749	163.279	0.469	471.699	0.373	16	0.148	R.FIDIPEEVAEVYK.L
R4/RRR4-9/2	1552.122	1552.749	-1051.484	0.298	600.985	0.256	18	0.142	R.FIDIPEEVAEVYK.L
R4/RRR4-9/2	1552.245	1552.749	-971.892	0.252	591.247	0.210	17	0.138	R.FIDIPEEVAEVYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1553.193	1552.749	286.180	0.366	455.197	0.302	14	0.132	-.FIDIPEEVAEVYK.-
R4/RRR4-9/3	1552.893	1552.749	92.585	0.415	1252.734	0.354	24	0.120	R.FIDIPEEVAEVYK.L
R4/RRR4-11/2	899.946	900.058	-124.364	0.443	1414.253	0.352	15	0.189	K.LGDLLAAAR.V
R4/RRR4-11/2	1108.992	1109.257	-239.643	0.444	866.951	0.443	14	0.168	K.REDLFITSK.L
R4/RRR4-11/2	1010.059	1010.126	-66.865	0.379	709.185	0.423	15	0.158	R.AIGVSNFSSK.K
R4/RRR4-11/2	1108.163	1109.257	-1895.787	0.425	593.167	0.429	14	0.158	K.REDLFITSK.L
R4/RRR4-11/2	900.955	900.058	-113.896	0.494	710.371	0.369	15	0.156	K.LGDLLAAAR.V
R4/RRR4-12/2	1010.021	1010.126	-104.203	0.410	589.429	0.364	15	0.152	R.AIGVSNFSSK.K
R4/RRR4-11/2	1009.904	1010.126	-220.238	0.351	466.564	0.431	12	0.150	R.AIGVSNFSSK.K
R4/RRR4-11/2	1009.509	1010.126	-1606.471	0.302	554.208	0.326	14	0.144	R.AIGVSNFSSK.K
R4/RRR4-3/2	1721.283	1720.822	268.974	0.495	1324.205	0.497	24	0.207	R.TLSFAIADGSQPGNEGR.E
R4/RRR4-3/2	1720.257	1720.822	-912.201	0.440	1274.524	0.476	23	0.196	R.TLSFAIADGSQPGNEGR.E
R4/RRR4-3/2	1719.707	1720.822	-1233.374	0.284	1131.186	0.409	22	0.169	R.TLSFAIADGSQPGNEGR.E
R4/RRR4-3/2	1242.094	1242.298	-164.461	0.368	946.309	0.393	17	0.162	R.EGFDAAM*EEAR.Q
R4/RRR4-3/2	1242.022	1242.298	-222.730	0.407	772.440	0.411	16	0.158	R.EGFDAAM*EEAR.Q
R4/RRR4-3/2	1267.907	1268.444	-1215.919	0.366	723.557	0.372	18	0.152	R.EADGTLRPLPAK.H
R4/RRR4-3/2	1268.166	1268.444	-220.377	0.364	629.370	0.361	17	0.149	R.EADGTLRPLPAK.H
R4/RRR4-3/2	1267.980	1268.444	-367.471	0.347	594.195	0.328	17	0.146	R.EADGTLRPLPAK.H
R4/RRR4-14/2	1125.211	1125.383	-153.056	0.483	1400.437	0.422	15	0.200	K.IAIDLLEPIK.R
R4/RRR4-14/2	1125.257	1125.383	-112.138	0.448	1291.135	0.414	15	0.189	K.IAIDLLEPIK.R
R4/RRR4-16/2	1126.427	1125.383	39.172	0.411	1205.759	0.444	14	0.186	K.IAIDLLEPIK.R
R4/RRR4-14/3	1591.196	1591.706	-951.688	0.484	1112.145	0.518	29	0.150	R.LAWHDAGTYDVNTK.T
R4/RRR4-14/2	1124.552	1125.383	-1633.422	0.265	596.907	0.356	12	0.143	K.IAIDLLEPIK.R
R4/RRR4-16/2	1125.842	1125.383	408.512	0.269	560.702	0.287	12	0.140	K.IAIDLLEPIK.R
R4/RRR4-16/2	1125.282	1125.383	-89.939	0.228	724.310	0.204	12	0.135	K.IAIDLLEPIK.R
R4/RRR4-14/3	1943.195	1944.203	-1036.222	0.401	950.268	0.402	30	0.106	R.M*GLSDKDIVALSGGHTLGR.A
R4/RRR4-14/3	1591.716	1591.706	6.214	0.395	650.379	0.456	23	0.104	R.LAWHDAGTYDVNTK.T
R4/RRR4-14/3	1591.728	1591.706	13.713	0.283	490.086	0.329	22	0.087	R.LAWHDAGTYDVNTK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1685.523	1685.852	-195.955	0.513	2004.490	0.558	22	0.311	K.EANAFQGLLFADTCK.N
R4/RRR4-5/2	1500.215	1500.699	-323.804	0.490	1537.648	0.512	19	0.233	K.TM*SLVTGVLDYER.F
R4/RRR4-5/2	1210.120	1209.420	-248.958	0.498	1165.318	0.531	20	0.204	K.VPGATDLGLIPR.K
R4/RRR4-5/2	1209.082	1209.420	-280.563	0.464	1130.189	0.545	20	0.202	K.VPGATDLGLIPR.K
R4/RRR4-5/2	1210.183	1209.420	-196.942	0.469	1166.298	0.519	20	0.201	K.VPGATDLGLIPR.K
R4/RRR4-2/2	1210.005	1209.420	-344.299	0.386	796.033	0.511	16	0.169	K.VPGATDLGLIPR.K
R4/RRR4-2/2	1210.529	1209.420	90.562	0.367	430.691	0.365	13	0.142	-.VPGATDLGLIPR.-
R4/RRR4-17/2	1290.789	1291.438	-1281.061	0.410	938.026	0.373	15	0.160	R.LNEQVQEFKR.L
R4/RRR4-17/2	1769.779	1770.965	-1238.881	0.460	592.032	0.535	18	0.159	R.VGDLGQLTPTDQVLASR.H
R4/RRR4-17/2	885.082	885.086	-4.304	0.328	1032.913	0.247	13	0.147	R.LALLAIDR.A
R4/RRR4-17/2	1291.262	1291.438	-136.787	0.342	321.077	0.295	13	0.144	R.LNEQVQEFKR.L
R4/RRR4-23/2	1786.450	1786.963	-849.822	0.418	609.245	0.561	20	0.165	K.EAALAAVPNDNPTIFDK.I
R4/RRR4-23/2	1788.454	1786.963	275.028	0.533	558.616	0.525	18	0.159	K.EAALAAVPNDNPTIFDK.I
R4/RRR4-23/2	1656.284	1656.950	-1009.308	0.432	994.401	0.289	19	0.148	R.DINPQAPTHIVIIPK.V
R4/RRR4-23/2	1656.596	1656.950	-214.232	0.472	953.122	0.282	19	0.144	R.DINPQAPTHIVIIPK.V
R4/RRR4-23/2	1655.936	1656.950	-1220.243	0.412	648.470	0.357	16	0.143	R.DINPQAPTHIVIIPK.V
R4/RRR4-23/3	1465.225	1464.605	-260.229	0.518	1138.646	0.446	30	0.133	K.VVAKQEGLEDGYR.I
R4/RRR4-23/3	1465.541	1464.605	-44.380	0.506	881.703	0.490	28	0.125	K.VVAKQEGLEDGYR.I
R4/RRR4-11/1	963.567	964.183	-1682.861	0.235	776.756	0.332	12	0.524	R.TALAFVTLK.S
R4/RRR4-12/1	963.526	964.183	-1724.865	0.265	724.727	0.345	12	0.519	R.TALAFVTLK.S
R4/RRR4-11/1	963.594	964.183	-1654.415	0.254	735.971	0.321	12	0.511	R.TALAFVTLK.S
R4/RRR4-11/1	963.561	964.183	-1688.716	0.219	625.426	0.369	11	0.491	R.TALAFVTLK.S
R4/RRR4-12/1	963.530	964.183	-1721.110	0.240	628.260	0.344	11	0.486	R.TALAFVTLK.S
R4/RRR4-12/1	963.544	964.183	-1706.154	0.192	691.234	0.262	12	0.480	R.TALAFVTLK.S
R4/RRR4-11/2	1689.913	1689.761	90.013	0.443	1213.857	0.531	19	0.201	K.NGVNAEGCLFDEHAR.T
R4/RRR4-11/2	1690.196	1689.761	257.840	0.467	1162.152	0.506	19	0.192	K.NGVNAEGCLFDEHAR.T
R4/RRR4-11/2	1690.231	1689.761	278.841	0.496	1148.045	0.506	19	0.191	K.NGVNAEGCLFDEHAR.T
R4/RRR4-11/2	963.625	964.183	-1621.658	0.432	1009.547	0.438	15	0.176	R.TALAFVTLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	963.995	964.183	-195.736	0.434	968.030	0.449	15	0.175	R.TALAFVTLK.S
R4/RRR4-12/2	963.697	964.183	-506.685	0.382	1049.975	0.420	15	0.174	R.TALAFVTLK.S
R4/RRR4-11/2	1795.073	1794.037	19.875	0.478	1397.051	0.297	21	0.172	K.IFHYGSISLITEPCR.-
R4/RRR4-12/2	964.074	964.183	-113.805	0.468	975.033	0.412	15	0.171	R.TALAFVTLK.S
R4/RRR4-11/2	963.654	964.183	-1592.006	0.394	966.918	0.403	15	0.168	R.TALAFVTLK.S
R4/RRR4-12/2	963.292	964.183	-1969.335	0.340	1068.161	0.375	15	0.167	R.TALAFVTLK.S
R4/RRR4-12/2	963.647	964.183	-1598.751	0.159	248.295	0.305	12	0.139	-.TALAFVTLK.-
R4/RRR4-12/3	1690.711	1689.761	-29.743	0.451	899.218	0.359	28	0.101	K.NGVNAEGCLFDEHAR.T
R4/RRR4-12/3	1690.460	1689.761	-178.478	0.409	696.155	0.393	26	0.100	K.NGVNAEGCLFDEHAR.T
R4/RRR4-12/3	1688.573	1689.761	-1299.919	0.352	506.949	0.376	25	0.097	K.NGVNAEGCLFDEHAR.T
R4/RRR4-11/3	1689.018	1689.761	-1035.134	0.324	633.882	0.371	27	0.096	K.NGVNAEGCLFDEHAR.T
R4/RRR4-11/3	1690.598	1689.761	-96.989	0.438	571.278	0.354	22	0.095	K.NGVNAEGCLFDEHAR.T
R4/RRR4-11/3	1689.543	1689.761	-129.406	0.310	496.984	0.344	24	0.094	K.NGVNAEGCLFDEHAR.T
R4/RRR4-12/3	1689.792	1689.761	18.316	0.344	390.439	0.359	23	0.094	-.NGVNAEGCLFDEHAR.-
R4/RRR4-12/3	1690.744	1689.761	-10.408	0.440	708.222	0.330	24	0.093	K.NGVNAEGCLFDEHAR.T
R4/RRR4-12/3	1793.241	1794.037	-1004.570	0.386	1029.113	0.270	26	0.087	-.IFHYGSISLITEPCR.-
R4/RRR4-13/2	1216.263	1217.442	-1796.750	0.428	1569.362	0.415	17	0.215	R.EALFVLAQLGR.K
R4/RRR4-13/2	1217.069	1217.442	-307.997	0.467	1023.236	0.478	14	0.178	R.EALFVLAQLGR.K
R4/RRR4-12/2	1290.495	1290.493	1.555	0.474	1213.369	0.380	15	0.175	R.YQILAGVIEQR.M
R4/RRR4-13/2	1290.267	1290.493	-176.178	0.440	1283.640	0.350	15	0.175	R.YQILAGVIEQR.M
R4/RRR4-13/2	1290.160	1290.493	-259.420	0.450	1093.678	0.386	15	0.169	R.YQILAGVIEQR.M
R4/RRR4-13/2	1290.300	1290.493	-150.459	0.377	1044.794	0.394	15	0.166	R.YQILAGVIEQR.M
R4/RRR4-12/2	1217.206	1217.442	-194.297	0.404	937.550	0.417	15	0.165	R.EALFVLAQLGR.K
R4/RRR4-13/2	1120.036	1119.335	-267.888	0.495	586.780	0.444	16	0.163	R.LLADDLFLAK.L
R4/RRR4-13/2	1216.758	1217.442	-1388.186	0.384	1154.121	0.325	14	0.161	-.EALFVLAQLGR.-
R4/RRR4-12/2	1119.172	1119.335	-146.552	0.513	640.026	0.396	16	0.158	R.LLADDLFLAK.L
R4/RRR4-13/2	1119.172	1119.335	-146.115	0.495	647.990	0.385	16	0.157	R.LLADDLFLAK.L
R4/RRR4-12/2	1118.819	1119.335	-1359.233	0.379	600.540	0.371	16	0.153	R.LLADDLFLAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1118.681	1119.335	-1482.967	0.346	587.503	0.353	16	0.151	R.LLADDLFLAK.L
R4/RRR4-13/2	1118.863	1119.335	-423.668	0.398	557.293	0.313	15	0.148	R.LLADDLFLAK.L
R4/RRR4-13/2	1119.236	1119.335	-88.784	0.237	689.175	0.267	14	0.140	R.LLADDLFLAK.L
R4/RRR4-8/2	1323.212	1322.491	-211.117	0.439	795.794	0.503	16	0.172	K.WYNAEEVILGK.K
R4/RRR4-8/2	1322.547	1322.491	42.529	0.418	845.671	0.466	15	0.167	K.WYNAEEVILGK.K
R4/RRR4-8/2	1070.077	1070.223	-136.800	0.439	925.427	0.408	15	0.165	K.VYAYGAAQVK.K
R4/RRR4-8/2	1070.920	1070.223	-283.718	0.346	689.314	0.383	14	0.150	K.VYAYGAAQVK.K
R4/RRR4-8/2	1321.698	1322.491	-1360.227	0.433	593.609	0.409	14	0.150	-.WYNAEEVILGK.-
R4/RRR4-9/3	1933.190	1932.162	14.395	0.374	962.403	0.421	29	0.113	K.TLTETNKNLDEIVELAK.K
R4/RRR4-9/3	1932.820	1932.162	-177.256	0.322	1183.032	0.335	30	0.109	K.TLTETNKNLDEIVELAK.K
R4/RRR4-8/3	1933.519	1932.162	185.270	0.344	1041.243	0.267	25	0.091	-.TLTETNKNLDEIVELAK.-
R4/RRR4-8/3	1931.275	1932.162	-979.810	0.421	733.260	0.328	24	0.086	-.TLTETNKNLDEIVELAK.-
R4/RRR4-9/3	1932.576	1932.162	214.851	0.248	982.786	0.219	28	0.081	K.TLTETNKNLDEIVELAK.K
R4/RRR4-11/2	1558.692	1558.868	-113.481	0.499	1618.292	0.507	21	0.240	K.GAALNAVQIAEM*LLK.-
R4/RRR4-10/2	1558.277	1558.868	-1024.629	0.469	1497.695	0.540	20	0.233	K.GAALNAVQIAEM*LLK.-
R4/RRR4-10/2	1160.043	1160.260	-187.618	0.509	1493.674	0.495	17	0.226	R.AAEGVTIIDDR.A
R4/RRR4-11/2	1558.196	1558.868	-1076.621	0.466	1489.467	0.484	20	0.219	K.GAALNAVQIAEM*LLK.-
R4/RRR4-10/2	1559.201	1558.868	213.692	0.527	1457.149	0.492	20	0.217	K.GAALNAVQIAEM*LLK.-
R4/RRR4-11/2	1558.300	1558.868	-1009.764	0.427	1323.528	0.464	19	0.197	K.GAALNAVQIAEM*LLK.-
R4/RRR4-10/2	1161.300	1160.260	34.517	0.535	1131.275	0.464	17	0.188	R.AAEGVTIIDDR.A
R4/RRR4-10/2	1159.679	1160.260	-1367.088	0.391	1218.913	0.361	17	0.174	R.AAEGVTIIDDR.A
R4/RRR4-11/3	1997.920	1998.189	-134.773	0.369	1445.177	0.445	32	0.170	R.AHAPAAVASGAVVVDNSSAFR.M
R4/RRR4-10/2	1558.732	1558.868	-87.714	0.368	973.023	0.292	18	0.148	K.GAALNAVQIAEM*LLK.-
R4/RRR4-11/3	1997.676	1998.189	-759.697	0.409	1218.549	0.437	28	0.141	R.AHAPAAVASGAVVVDNSSAFR.M
R4/RRR4-12/2	1314.144	1313.522	-288.413	0.455	1668.736	0.432	20	0.229	K.VLDVGCGIGGPLR.E
R4/RRR4-12/2	1313.438	1313.522	-64.098	0.410	1423.663	0.340	18	0.184	K.VLDVGCGIGGPLR.E
R4/RRR4-12/2	1239.962	1240.381	-339.437	0.406	920.357	0.529	19	0.180	R.VAGVSGTCDFVK.A
R4/RRR4-12/2	1489.852	1490.643	-1205.718	0.346	1001.158	0.409	19	0.163	K.ALEYVGLAPQGSER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1313.348	1313.522	-132.622	0.307	479.519	0.282	17	0.141	K.VLDVGCGIGGPLR.E
R4/RRR4-6/2	1467.039	1466.835	139.491	0.526	1645.973	0.555	21	0.258	K.LIFVDPALLPVLR.D
R4/RRR4-6/2	1466.402	1466.835	-296.791	0.434	1619.483	0.522	20	0.244	K.LIFVDPALLPVLR.D
R4/RRR4-6/2	1307.391	1307.434	-33.115	0.483	1616.870	0.472	19	0.234	R.VDAAEVFDTIAR.R
R4/RRR4-6/2	1466.075	1466.835	-1204.394	0.411	1490.328	0.537	20	0.232	K.LIFVDPALLPVLR.D
R4/RRR4-7/2	1466.439	1466.835	-271.067	0.430	1358.742	0.528	20	0.217	K.LIFVDPALLPVLR.D
R4/RRR4-7/2	1306.542	1307.434	-1452.943	0.388	1611.212	0.397	18	0.214	R.VDAAEVFDTIAR.R
R4/RRR4-7/2	1466.549	1466.835	-195.742	0.380	1415.928	0.465	20	0.208	K.LIFVDPALLPVLR.D
R4/RRR4-7/2	1274.127	1274.492	-287.862	0.433	1282.392	0.438	18	0.191	R.LASALVSSLGISR.G
R4/RRR4-6/2	1307.581	1307.434	112.680	0.517	1052.289	0.526	16	0.190	R.VDAAEVFDTIAR.R
R4/RRR4-6/2	1274.371	1274.492	-95.078	0.458	1115.280	0.444	16	0.177	R.LASALVSSLGISR.G
R4/RRR4-5/2	1466.359	1466.835	-326.023	0.354	676.980	0.474	13	0.155	K.LIFVDPALLPVLR.D
R4/RRR4-20/2	1466.403	1466.835	-295.872	0.252	151.230	0.325	11	0.144	K.LIFVDPALLPVLR.D
R4/RRR4-2/2	1466.039	1466.835	-1228.726	0.302	456.365	0.307	14	0.142	K.LIFVDPALLPVLR.D
R4/RRR4-2/2	1466.561	1466.835	-187.893	0.341	563.985	0.273	15	0.141	K.LIFVDPALLPVLR.D
R4/RRR4-6/2	1274.255	1274.492	-186.559	0.320	411.462	0.290	14	0.138	-.LASALVSSLGISR.-
R4/RRR4-5/2	1466.336	1466.835	-341.726	0.216	546.243	0.306	13	0.138	K.LIFVDPALLPVLR.D
R4/RRR4-6/2	1273.410	1274.492	-1639.872	0.297	585.895	0.235	15	0.136	R.LASALVSSLGISR.G
R4/RRR4-15/2	1466.299	1466.835	-1051.070	0.186	743.659	0.197	13	0.133	K.LIFVDPALLPVLR.D
R4/RRR4-7/2	1306.626	1307.434	-1388.193	0.218	806.183	0.173	14	0.133	R.VDAAEVFDTIAR.R
R4/RRR4-7/2	1026.455	1026.215	235.030	0.463	1402.221	0.463	19	0.209	K.IGGIGTVPVGR.V
R4/RRR4-3/2	1026.044	1026.215	-167.252	0.492	1335.472	0.475	19	0.206	K.IGGIGTVPVGR.V
R4/RRR4-4/2	1026.027	1026.215	-183.723	0.478	1379.576	0.455	19	0.206	K.IGGIGTVPVGR.V
R4/RRR4-9/2	1026.080	1026.215	-131.568	0.437	1231.674	0.506	19	0.202	K.IGGIGTVPVGR.V
R4/RRR4-1/2	1026.141	1026.215	-72.260	0.470	1342.879	0.451	19	0.202	K.IGGIGTVPVGR.V
R4/RRR4-4/2	1026.022	1026.215	-188.378	0.466	1261.846	0.474	18	0.199	K.IGGIGTVPVGR.V
R4/RRR4-9/2	1025.673	1026.215	-1507.740	0.456	1264.495	0.463	19	0.198	K.IGGIGTVPVGR.V
R4/RRR4-14/2	1026.123	1026.215	-89.682	0.486	1194.321	0.483	18	0.196	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1026.026	1026.215	-185.036	0.411	1235.242	0.460	19	0.194	K.IGGIGTVPVGR.V
R4/RRR4-8/2	1026.066	1026.215	-145.293	0.457	1243.050	0.437	19	0.191	K.IGGIGTVPVGR.V
R4/RRR4-13/2	1025.993	1026.215	-217.023	0.478	1085.817	0.478	18	0.187	K.IGGIGTVPVGR.V
R4/RRR4-16/2	1026.115	1026.215	-97.677	0.401	1234.871	0.418	18	0.186	K.IGGIGTVPVGR.V
R4/RRR4-9/2	1026.014	1026.215	-196.732	0.429	1077.134	0.477	18	0.186	K.IGGIGTVPVGR.V
R4/RRR4-8/2	1026.051	1026.215	-160.450	0.467	1044.125	0.474	18	0.184	K.IGGIGTVPVGR.V
R4/RRR4-2/2	1025.919	1026.215	-289.361	0.458	1057.540	0.469	17	0.183	K.IGGIGTVPVGR.V
R4/RRR4-5/2	1025.989	1026.215	-220.723	0.433	1105.239	0.442	18	0.182	K.IGGIGTVPVGR.V
R4/RRR4-10/2	1026.043	1026.215	-168.088	0.507	1084.454	0.444	18	0.182	K.IGGIGTVPVGR.V
R4/RRR4-1/2	1026.062	1026.215	-149.350	0.438	1028.892	0.469	17	0.181	K.IGGIGTVPVGR.V
R4/RRR4-11/2	1026.080	1026.215	-131.688	0.418	1104.923	0.437	18	0.181	K.IGGIGTVPVGR.V
R4/RRR4-6/2	1025.994	1026.215	-215.710	0.462	925.258	0.491	17	0.179	K.IGGIGTVPVGR.V
R4/RRR4-7/2	1026.097	1026.215	-115.338	0.489	944.600	0.480	17	0.179	K.IGGIGTVPVGR.V
R4/RRR4-3/2	1025.992	1026.215	-217.501	0.483	1051.520	0.439	18	0.179	K.IGGIGTVPVGR.V
R4/RRR4-13/2	1026.175	1026.215	-38.730	0.454	943.341	0.474	17	0.177	K.IGGIGTVPVGR.V
R4/RRR4-1/2	1026.130	1026.215	-82.880	0.433	923.675	0.474	17	0.176	K.IGGIGTVPVGR.V
R4/RRR4-2/2	1025.903	1026.215	-305.358	0.448	1088.691	0.409	18	0.176	K.IGGIGTVPVGR.V
R4/RRR4-6/2	1025.930	1026.215	-278.378	0.445	788.853	0.515	16	0.175	K.IGGIGTVPVGR.V
R4/RRR4-6/2	1026.278	1026.215	61.248	0.471	828.970	0.492	16	0.174	K.IGGIGTVPVGR.V
R4/RRR4-4/2	1026.002	1026.215	-208.071	0.498	909.117	0.457	17	0.174	K.IGGIGTVPVGR.V
R4/RRR4-2/2	1025.519	1026.215	-1658.397	0.463	962.069	0.437	17	0.173	K.IGGIGTVPVGR.V
R4/RRR4-3/2	1025.637	1026.215	-1543.487	0.416	962.904	0.440	17	0.173	K.IGGIGTVPVGR.V
R4/RRR4-14/2	1025.901	1026.215	-307.149	0.450	877.943	0.470	16	0.173	K.IGGIGTVPVGR.V
R4/RRR4-10/2	1025.616	1026.215	-1563.334	0.389	934.121	0.451	17	0.172	K.IGGIGTVPVGR.V
R4/RRR4-15/2	1025.990	1026.215	-219.530	0.429	966.879	0.425	18	0.172	K.IGGIGTVPVGR.V
R4/RRR4-14/2	1025.947	1026.215	-262.024	0.462	916.282	0.443	17	0.172	K.IGGIGTVPVGR.V
R4/RRR4-11/2	1025.636	1026.215	-1544.324	0.431	877.943	0.465	16	0.172	K.IGGIGTVPVGR.V
R4/RRR4-5/2	1025.585	1026.215	-1594.183	0.407	906.660	0.451	17	0.172	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1026.054	1026.215	-156.750	0.470	896.674	0.442	17	0.171	K.IGGIGTVPVGR.V
R4/RRR4-15/2	1025.922	1026.215	-286.018	0.325	915.024	0.446	17	0.168	K.IGGIGTVPVGR.V
R4/RRR4-11/2	1026.071	1026.215	-140.877	0.456	695.134	0.484	15	0.167	K.IGGIGTVPVGR.V
R4/RRR4-12/2	1025.536	1026.215	-1641.655	0.423	785.791	0.447	16	0.166	K.IGGIGTVPVGR.V
R4/RRR4-8/2	1260.901	1261.411	-1201.119	0.423	782.107	0.478	15	0.166	K.ANISPNAPWYK.G
R4/RRR4-8/2	1026.049	1026.215	-162.359	0.338	871.764	0.444	15	0.165	K.IGGIGTVPVGR.V
R4/RRR4-12/2	1025.617	1026.215	-1562.497	0.387	876.541	0.400	16	0.163	K.IGGIGTVPVGR.V
R4/RRR4-9/2	1026.545	1026.215	322.435	0.338	643.157	0.488	15	0.162	K.IGGIGTVPVGR.V
R4/RRR4-5/2	1025.576	1026.215	-1603.031	0.435	659.458	0.453	15	0.162	K.IGGIGTVPVGR.V
R4/RRR4-12/2	1026.115	1026.215	-97.319	0.458	714.726	0.423	15	0.160	K.IGGIGTVPVGR.V
R4/RRR4-15/2	1026.044	1026.215	-167.133	0.405	593.140	0.430	14	0.157	K.IGGIGTVPVGR.V
R4/RRR4-8/2	1751.207	1752.026	-1041.784	0.419	832.312	0.418	20	0.157	K.AGMVVTFAPSNVTTEVK.S
R4/RRR4-9/2	1026.351	1026.215	132.581	0.303	452.834	0.381	13	0.149	K.IGGIGTVPVGR.V
R4/RRR4-8/2	1751.327	1752.026	-972.850	0.482	565.616	0.448	17	0.149	K.AGMVVTFAPSNVTTEVK.S
R4/RRR4-8/2	1751.501	1752.026	-873.001	0.478	710.274	0.396	18	0.147	K.AGMVVTFAPSNVTTEVK.S
R4/RRR4-9/2	1026.468	1026.215	247.671	0.246	435.054	0.268	14	0.145	K.IGGIGTVPVGR.V
R4/RRR4-10/2	1025.445	1026.215	-1731.470	0.215	580.589	0.292	13	0.143	K.IGGIGTVPVGR.V
R4/RRR4-8/2	1262.381	1261.411	-23.724	0.398	617.184	0.344	13	0.142	-.ANISPNAPWYK.-
R4/RRR4-13/2	1025.419	1026.215	-1756.468	0.101	596.752	0.132	14	0.137	K.IGGIGTVPVGR.V
R4/RRR4-2/2	1025.706	1026.215	-1475.223	0.304	658.657	0.197	13	0.136	-.IGGIGTVPVGR.-
R4/RRR4-15/2	1206.114	1206.330	-179.842	0.418	1288.684	0.483	18	0.199	K.GGAFVEAPVSGSK.K
R4/RRR4-15/2	1205.951	1206.330	-315.506	0.467	1132.335	0.463	19	0.185	K.GGAFVEAPVSGSK.K
R4/RRR4-14/2	1828.755	1827.067	-171.435	0.468	1050.166	0.529	18	0.183	R.SLGLGDLDFSAVYEVLK.G
R4/RRR4-15/2	1239.282	1240.390	-1705.581	0.356	1361.084	0.317	17	0.175	K.SFFLGEIGNGAK.M
R4/RRR4-15/2	1239.632	1240.390	-1422.128	0.359	901.531	0.414	15	0.160	K.SFFLGEIGNGAK.M
R4/RRR4-15/2	1205.511	1206.330	-1513.569	0.380	913.982	0.391	17	0.158	K.GGAFVEAPVSGSK.K
R4/RRR4-15/2	1241.147	1240.390	-195.876	0.348	753.111	0.379	15	0.151	K.SFFLGEIGNGAK.M
R4/RRR4-15/2	1239.774	1240.390	-1307.309	0.378	798.279	0.347	15	0.149	K.SFFLGEIGNGAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1240.986	1240.390	-326.134	0.335	1050.362	0.226	16	0.145	K.SFFLGEIGNGAK.M
R4/RRR4-13/2	1828.196	1827.067	70.748	0.356	210.237	0.404	12	0.123	-.SLGLGDLDFSAVYEVLK.-
R4/RRR4-14/2	1070.947	1071.249	-282.682	0.476	911.821	0.443	16	0.172	K.IVAISLDDPK.A
R4/RRR4-14/2	1364.011	1364.439	-314.940	0.417	638.887	0.519	16	0.165	K.VIEETNESWEK.L
R4/RRR4-14/2	1070.977	1071.249	-255.123	0.410	922.829	0.401	16	0.165	K.IVAISLDDPK.A
R4/RRR4-14/2	1070.444	1071.249	-1691.510	0.398	919.651	0.409	15	0.164	K.IVAISLDDPK.A
R4/RRR4-14/3	1515.286	1515.737	-298.537	0.417	1005.487	0.404	25	0.112	R.AGDGVFHFVVEIPK.E
R4/RRR4-14/3	1515.334	1515.737	-267.137	0.380	1015.557	0.359	26	0.103	R.AGDGVFHFVVEIPK.E
R4/RRR4-14/3	1515.369	1515.737	-243.740	0.404	993.174	0.355	25	0.101	R.AGDGVFHFVVEIPK.E
R4/RRR4-15/2	1481.610	1480.688	-52.856	0.495	896.453	0.495	21	0.178	R.EIEEALLEHLGVK.R
R4/RRR4-15/2	1642.723	1641.871	-90.826	0.290	644.369	0.381	15	0.142	R.VYEVATFYTMFNR.T
R4/RRR4-14/3	1692.865	1692.896	-18.603	0.434	913.200	0.337	23	0.093	K.KVNEILSHYPSNYK.Q
R4/RRR4-7/2	1101.385	1101.315	63.741	0.378	1072.186	0.372	15	0.166	K.NISVIAVCPK.G
R4/RRR4-7/2	1100.887	1101.315	-390.326	0.355	830.562	0.358	13	0.151	K.NISVIAVCPK.G
R4/RRR4-7/2	1101.442	1101.315	115.650	0.280	920.797	0.275	13	0.144	K.NISVIAVCPK.G
R4/RRR4-7/2	1168.001	1168.368	-315.275	0.425	1199.924	0.666	20	0.228	R.AALPVGTVSGAPK.V
R4/RRR4-7/2	1502.542	1502.732	-126.516	0.501	1685.493	0.417	20	0.226	R.GCVLVASSPEILTR.V
R4/RRR4-6/2	1168.034	1168.368	-286.440	0.403	1252.347	0.618	21	0.223	R.AALPVGTVSGAPK.V
R4/RRR4-6/2	1502.515	1502.732	-144.690	0.455	1665.196	0.409	20	0.222	R.GCVLVASSPEILTR.V
R4/RRR4-7/2	1169.176	1168.368	-164.370	0.435	1182.432	0.624	20	0.219	R.AALPVGTVSGAPK.V
R4/RRR4-7/2	1502.203	1502.732	-1020.488	0.345	1591.490	0.407	20	0.212	R.GCVLVASSPEILTR.V
R4/RRR4-7/2	1167.970	1168.368	-342.015	0.394	1016.281	0.608	20	0.199	R.AALPVGTVSGAPK.V
R4/RRR4-6/2	1320.035	1320.347	-237.225	0.408	553.741	0.524	17	0.162	R.HATTEDAFQDGK.S
R4/RRR4-6/2	1167.873	1168.368	-425.179	0.202	551.490	0.456	17	0.144	R.AALPVGTVSGAPK.V
R4/RRR4-6/2	1167.772	1168.368	-1371.244	0.125	388.598	0.335	14	0.133	R.AALPVGTVSGAPK.V
R4/RRR4-9/2	1665.474	1665.871	-239.114	0.492	1603.802	0.532	22	0.244	K.GFAIGNGLTDPAIQYK.A
R4/RRR4-9/2	1729.215	1729.822	-932.541	0.547	1474.007	0.578	21	0.240	K.EAFVSSSEEPFTVDGK.E
R4/RRR4-9/2	1665.600	1665.871	-163.014	0.516	1376.140	0.506	21	0.212	K.GFAIGNGLTDPAIQYK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1665.197	1665.871	-1008.538	0.526	988.841	0.543	19	0.185	K.GFAIGNGLTDPAIQYK.A
R4/RRR4-9/2	1696.443	1696.923	-283.971	0.483	770.424	0.493	20	0.168	R.NLEVGIPELLENDIK.V
R4/RRR4-9/2	1696.175	1696.923	-1033.717	0.485	682.634	0.458	19	0.159	R.NLEVGIPELLENDIK.V
R4/RRR4-9/2	1696.438	1696.923	-286.642	0.478	693.173	0.435	18	0.155	R.NLEVGIPELLENDIK.V
R4/RRR4-16/2	1641.110	1641.889	-1087.726	0.432	1156.122	0.512	23	0.196	R.TQYPYVTGSSIIALK.Y
R4/RRR4-16/2	1787.913	1788.082	-94.887	0.481	1168.432	0.503	23	0.195	R.NKFDPLWNSLVIGGVK.K
R4/RRR4-16/3	1787.328	1788.082	-984.431	0.477	1684.565	0.416	27	0.195	R.NKFDPLWNSLVIGGVK.K
R4/RRR4-16/2	1641.032	1641.889	-1135.229	0.403	1085.509	0.499	23	0.187	R.TQYPYVTGSSIIALK.Y
R4/RRR4-17/2	1641.128	1641.889	-1076.448	0.438	926.430	0.560	21	0.186	R.TQYPYVTGSSIIALK.Y
R4/RRR4-16/2	1642.234	1641.889	210.423	0.463	845.767	0.510	21	0.175	R.TQYPYVTGSSIIALK.Y
R4/RRR4-17/2	1788.345	1788.082	147.360	0.448	838.085	0.408	20	0.158	R.NKFDPLWNSLVIGGVK.K
R4/RRR4-16/2	1655.466	1654.885	-253.724	0.486	1088.694	0.313	21	0.157	K.ITTEGATIYPPYSLK.T
R4/RRR4-16/2	1787.222	1788.082	-1044.151	0.313	765.378	0.367	19	0.148	R.NKFDPLWNSLVIGGVK.K
R4/RRR4-17/2	1654.092	1654.885	-1087.331	0.308	769.233	0.359	18	0.148	K.ITTEGATIYPPYSLK.T
R4/RRR4-17/2	1654.390	1654.885	-299.996	0.411	786.068	0.337	18	0.147	K.ITTEGATIYPPYSLK.T
R4/RRR4-17/2	1654.238	1654.885	-998.344	0.316	637.825	0.339	17	0.143	K.ITTEGATIYPPYSLK.T
R4/RRR4-17/2	1788.348	1788.082	149.072	0.420	516.549	0.366	16	0.142	R.NKFDPLWNSLVIGGVK.K
R4/RRR4-16/2	1654.426	1654.885	-278.232	0.415	705.783	0.285	18	0.140	K.ITTEGATIYPPYSLK.T
R4/RRR4-16/2	1654.460	1654.885	-257.727	0.429	763.594	0.272	18	0.139	K.ITTEGATIYPPYSLK.T
R4/RRR4-17/2	1786.296	1788.082	-2125.807	0.262	455.444	0.312	15	0.136	R.NKFDPLWNSLVIGGVK.K
R4/RRR4-16/3	1787.841	1788.082	-135.509	0.424	1388.221	0.282	27	0.114	R.NKFDPLWNSLVIGGVK.K
R4/RRR4-17/3	1787.511	1788.082	-881.587	0.312	780.116	0.214	23	0.072	-.NKFDPLWNSLVIGGVK.-
R4/RRR4-4/2	1732.517	1731.934	-241.310	0.588	1982.031	0.526	22	0.296	K.LNSELLNNLGNFINR.V
R4/RRR4-4/2	1732.070	1731.934	78.774	0.570	1809.853	0.508	22	0.266	K.LNSELLNNLGNFINR.V
R4/RRR4-4/2	1732.660	1731.934	-158.754	0.563	1726.878	0.511	22	0.255	K.LNSELLNNLGNFINR.V
R4/RRR4-6/2	1733.229	1731.934	170.484	0.392	734.809	0.432	18	0.155	K.LNSELLNNLGNFINR.V
R4/RRR4-4/2	1253.180	1253.470	-231.610	0.324	755.756	0.344	14	0.147	K.LLNPTELIDPK.C
R4/RRR4-4/2	1253.034	1253.470	-348.696	0.283	797.513	0.324	14	0.145	K.LLNPTELIDPK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1252.491	1253.470	-1584.855	0.263	413.576	0.288	12	0.130	-.LLNPTELIDPK.-
R4/RRR4-4/3	1300.119	1300.450	-255.230	0.404	910.751	0.368	22	0.099	K.RPWDFVSAGHK.I
R4/RRR4-6/2	1106.118	1106.300	-164.664	0.473	1838.295	0.523	17	0.276	K.TALLQSFLGR.Q
R4/RRR4-6/2	1888.818	1889.099	-149.065	0.564	1512.567	0.572	22	0.242	R.APDQTLELTGQAIDFLR.G
R4/RRR4-6/2	1105.986	1106.300	-284.243	0.475	1446.416	0.589	16	0.242	K.TALLQSFLGR.Q
R4/RRR4-6/2	1888.611	1889.099	-258.901	0.542	1515.355	0.517	21	0.228	R.APDQTLELTGQAIDFLR.G
R4/RRR4-6/2	1105.920	1106.300	-344.708	0.527	1305.962	0.493	16	0.208	K.TALLQSFLGR.Q
R4/RRR4-6/2	1888.060	1889.099	-1083.257	0.481	1169.349	0.537	19	0.196	R.APDQTLELTGQAIDFLR.G
R4/RRR4-6/2	1332.047	1332.533	-366.342	0.427	962.090	0.389	15	0.162	K.GRLETTWTVLR.K
R4/RRR4-6/2	1332.256	1332.533	-208.949	0.490	859.433	0.409	15	0.161	K.GRLETTWTVLR.K
R4/RRR4-6/2	1331.347	1332.533	-1646.954	0.346	498.389	0.331	15	0.145	K.GRLETTWTVLR.K
R4/RRR4-8/2	1589.164	1589.821	-1045.696	0.573	2826.279	0.653	24	0.515	K.THINIVVIGHVDSGK.S
R4/RRR4-8/2	1589.296	1589.821	-962.254	0.596	2839.764	0.615	24	0.502	K.THINIVVIGHVDSGK.S
R4/RRR4-8/3	1589.208	1589.821	-1017.979	0.537	2577.212	0.581	34	0.473	K.THINIVVIGHVDSGK.S
R4/RRR4-8/3	1588.697	1589.821	-1341.065	0.500	2340.154	0.605	33	0.420	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1589.757	1589.821	-40.027	0.520	2331.115	0.502	32	0.358	K.THINIVVIGHVDSGK.S
R4/RRR4-8/3	1589.233	1589.821	-1001.900	0.538	2179.038	0.562	31	0.354	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1590.697	1589.821	-77.795	0.564	2224.489	0.538	33	0.348	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1591.081	1589.821	164.160	0.534	2186.910	0.527	30	0.338	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1589.186	1589.821	-1031.630	0.516	1894.029	0.575	29	0.297	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1589.638	1589.821	-115.126	0.578	1961.628	0.548	33	0.291	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1589.695	1589.821	-79.655	0.500	1751.384	0.578	29	0.269	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1588.887	1589.821	-1220.925	0.438	1572.394	0.534	27	0.220	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1589.611	1589.821	-132.689	0.526	1456.454	0.560	29	0.208	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1589.772	1589.821	-30.553	0.508	1489.575	0.534	29	0.204	K.THINIVVIGHVDSGK.S
R4/RRR4-8/3	1590.126	1589.821	192.594	0.432	1371.902	0.531	27	0.188	K.THINIVVIGHVDSGK.S
R4/RRR4-8/2	1121.088	1121.268	-161.155	0.465	908.675	0.507	14	0.179	K.STTTGHLIYK.L
R4/RRR4-1/2	1120.603	1121.268	-1490.476	0.389	915.644	0.506	14	0.177	K.STTTGHLIYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1120.995	1121.268	-244.285	0.421	891.557	0.502	14	0.176	K.STTTGHLIYK.L
R4/RRR4-1/2	1120.504	1121.268	-1578.787	0.389	850.890	0.487	15	0.172	K.STTTGHLIYK.L
R4/RRR4-9/3	1589.274	1589.821	-976.220	0.509	1166.916	0.563	28	0.171	K.THINIVVIGHVDSGK.S
R4/RRR4-5/2	1121.172	1121.268	-86.229	0.408	780.483	0.499	13	0.169	K.STTTGHLIYK.L
R4/RRR4-8/2	1121.045	1121.268	-199.277	0.377	786.569	0.474	14	0.167	K.STTTGHLIYK.L
R4/RRR4-3/2	1120.971	1121.268	-265.917	0.386	816.304	0.464	13	0.166	K.STTTGHLIYK.L
R4/RRR4-3/2	1120.692	1121.268	-1411.042	0.424	684.176	0.495	13	0.166	K.STTTGHLIYK.L
R4/RRR4-2/2	1121.079	1121.268	-169.456	0.367	837.065	0.438	14	0.164	K.STTTGHLIYK.L
R4/RRR4-2/2	1122.128	1121.268	-125.435	0.408	738.266	0.460	13	0.163	K.STTTGHLIYK.L
R4/RRR4-6/2	1121.054	1121.268	-191.958	0.377	654.649	0.480	13	0.162	K.STTTGHLIYK.L
R4/RRR4-16/2	1120.960	1121.268	-275.859	0.371	718.132	0.454	13	0.161	K.STTTGHLIYK.L
R4/RRR4-1/2	1120.583	1121.268	-1508.749	0.353	881.894	0.396	14	0.161	K.STTTGHLIYK.L
R4/RRR4-5/2	1120.538	1121.268	-1548.254	0.382	822.927	0.403	14	0.160	K.STTTGHLIYK.L
R4/RRR4-3/2	1121.054	1121.268	-191.412	0.380	685.771	0.449	13	0.160	K.STTTGHLIYK.L
R4/RRR4-5/2	1120.845	1121.268	-378.678	0.331	769.170	0.402	14	0.157	K.STTTGHLIYK.L
R4/RRR4-15/2	1120.731	1121.268	-1375.815	0.368	665.504	0.401	13	0.154	K.STTTGHLIYK.L
R4/RRR4-9/3	1589.188	1589.821	-1030.704	0.466	1170.368	0.490	26	0.151	K.THINIVVIGHVDSGK.S
R4/RRR4-8/2	1120.816	1121.268	-404.250	0.308	653.968	0.343	13	0.148	K.STTTGHLIYK.L
R4/RRR4-8/2	1590.305	1589.821	305.601	0.318	419.599	0.515	14	0.148	K.THINIVVIGHVDSGK.S
R4/RRR4-9/2	1590.934	1589.821	71.679	0.312	547.108	0.382	16	0.143	K.THINIVVIGHVDSGK.S
R4/RRR4-7/3	1589.410	1589.821	-259.001	0.291	1019.899	0.396	24	0.117	K.THINIVVIGHVDSGK.S
R4/RRR4-2/3	1589.207	1589.821	-1018.442	0.314	812.749	0.238	22	0.090	K.THINIVVIGHVDSGK.S
R4/RRR4-9/3	1590.532	1589.821	-182.302	0.271	746.014	0.225	24	0.089	K.THINIVVIGHVDSGK.S
R4/RRR4-9/2	1093.022	1093.215	-177.279	0.464	1724.098	0.451	18	0.242	K.IGYDNAAAVAK.K
R4/RRR4-9/2	1092.957	1093.215	-236.997	0.466	1582.033	0.493	17	0.234	K.IGYDNAAAVAK.K
R4/RRR4-9/2	1092.427	1093.215	-1641.107	0.383	1583.201	0.456	17	0.224	K.IGYDNAAAVAK.K
R4/RRR4-9/2	1453.248	1453.643	-272.328	0.482	1335.836	0.488	17	0.204	K.VNM*EYGLDPTIGK.A
R4/RRR4-9/2	1452.553	1453.643	-1443.339	0.349	1433.165	0.438	18	0.201	K.VNM*EYGLDPTIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1166.060	1166.306	-211.640	0.392	831.111	0.427	18	0.163	R.LLGDASVSFEK.N
R4/RRR4-9/2	1166.308	1166.306	2.140	0.367	593.671	0.322	15	0.144	R.LLGDASVSFEK.N
R4/RRR4-9/2	1160.979	1161.204	-194.954	0.461	1187.984	0.358	16	0.170	R.GDAVDELTNAR.C
R4/RRR4-10/2	957.969	958.182	-223.295	0.368	263.184	0.457	12	0.155	K.GLPIVGVFR.S
R4/RRR4-9/2	958.843	958.182	-354.231	0.351	293.960	0.451	13	0.155	K.GLPIVGVFR.S
R4/RRR4-9/2	949.963	950.074	-117.171	0.492	628.082	0.386	12	0.155	K.VELFSQAR.D
R4/RRR4-9/2	957.966	958.182	-225.980	0.336	226.623	0.475	12	0.155	K.GLPIVGVFR.S
R4/RRR4-9/2	949.724	950.074	-369.493	0.447	592.000	0.322	12	0.148	K.VELFSQAR.D
R4/RRR4-9/2	957.594	958.182	-1663.453	0.256	189.015	0.483	11	0.141	-.GLPIVGVFR.-
R4/RRR4-10/2	957.833	958.182	-365.982	0.286	144.700	0.319	10	0.122	-.GLPIVGVFR.-
R4/RRR4-3/2	1490.914	1490.689	150.972	0.466	2338.028	0.437	24	0.330	K.AVSVFNASAVGAGLAR.S
R4/RRR4-1/2	1102.960	1102.227	-242.285	0.329	1005.981	0.128	15	0.134	-.RATELADVAR.-
R4/RRR4-3/3	1804.263	1803.949	174.622	0.341	1048.198	0.282	29	0.089	R.AELASQLSEKEEEIAR.L
R4/RRR4-4/2	1289.247	1289.441	-150.371	0.191	1016.255	0.140	15	0.131	-.M*NVIGEPIDER.G
R4/RRR4-13/2	950.079	950.117	-39.899	0.457	657.362	0.381	14	0.156	K.YLSGLGIAR.Q
R4/RRR4-14/2	950.018	950.117	-104.599	0.382	635.147	0.362	14	0.152	K.YLSGLGIAR.Q
R4/RRR4-13/2	949.956	950.117	-169.307	0.415	640.047	0.312	14	0.148	K.YLSGLGIAR.Q
R4/RRR4-13/2	949.917	950.117	-210.817	0.383	670.285	0.298	14	0.147	K.YLSGLGIAR.Q
R4/RRR4-13/2	1438.624	1439.641	-1406.270	0.340	754.424	0.355	14	0.144	R.SQIQAYVFDVIR.A
R4/RRR4-13/2	1330.075	1329.398	-243.995	0.372	1079.320	0.428	18	0.113	R.DGLLQGQATTTSH.-
R4/RRR4-13/2	1329.519	1329.398	91.298	0.251	896.580	0.224	16	0.073	R.DGLLQGQATTTSH.-
R4/RRR4-13/2	1329.483	1329.398	63.672	0.224	946.200	0.145	18	0.069	R.DGLLQGQATTTSH.-
R4/RRR4-8/2	1447.167	1447.533	-253.780	0.594	1495.456	0.525	24	0.234	R.EVEAIGGNVSASASR.E
R4/RRR4-8/2	1447.088	1447.533	-308.790	0.532	1388.609	0.503	23	0.216	R.EVEAIGGNVSASASR.E
R4/RRR4-8/2	1719.647	1721.011	-1378.947	0.266	1106.163	0.331	20	0.155	K.AYVPEMVEVLIDSVR.N
R4/RRR4-8/2	1509.736	1509.688	32.146	0.429	520.361	0.476	17	0.154	K.QSSGGLFSWLLGEK.S
R4/RRR4-5/2	1650.408	1650.856	-272.455	0.502	1268.365	0.458	20	0.194	R.QFLTLNALNEFDPK.I
R4/RRR4-5/2	1651.338	1650.856	292.675	0.549	1387.234	0.377	22	0.189	R.QFLTLNALNEFDPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1649.656	1650.856	-1337.702	0.410	1338.145	0.382	20	0.185	R.QFLTLNALNEFDPK.I
R4/RRR4-6/2	1652.402	1650.856	-275.534	0.560	813.485	0.462	17	0.163	R.QFLTLNALNEFDPK.I
R4/RRR4-5/2	1117.080	1117.235	-138.935	0.415	431.224	0.429	15	0.156	K.VTTTDDPVIR.R
R4/RRR4-5/2	1116.990	1117.235	-219.841	0.250	280.601	0.218	13	0.143	K.VTTTDDPVIR.R
R4/RRR4-6/2	1650.109	1650.856	-1062.056	0.348	882.511	0.258	18	0.143	R.QFLTLNALNEFDPK.I
R4/RRR4-5/2	1116.382	1117.235	-1664.568	0.273	250.369	0.324	13	0.137	-.VTTTDDPVIR.-
R4/RRR4-5/3	1340.431	1340.512	-60.945	0.499	1153.540	0.227	23	0.088	R.SIHSWDIVVQR.V
R4/RRR4-4/2	1393.559	1394.683	-1528.358	0.506	2093.844	0.522	20	0.317	K.FFALQVLESVIK.Y
R4/RRR4-4/2	1357.033	1356.505	-349.221	0.435	869.416	0.437	15	0.164	K.LLSEEIFDFSR.G
R4/RRR4-4/2	1218.522	1219.404	-1549.054	0.398	819.073	0.253	14	0.140	R.DLLNLCEITK.G
R4/RRR4-4/2	1356.239	1356.505	-196.677	0.270	688.247	0.304	13	0.139	K.LLSEEIFDFSR.G
R4/RRR4-17/2	1667.411	1667.847	-262.040	0.501	2063.576	0.499	21	0.302	K.TNQNVEQVFFTIAR.D
R4/RRR4-17/2	1667.356	1667.847	-295.093	0.541	1938.947	0.488	21	0.279	K.TNQNVEQVFFTIAR.D
R4/RRR4-17/2	1666.605	1667.847	-1349.443	0.364	1927.531	0.321	19	0.232	K.TNQNVEQVFFTIAR.D
R4/RRR4-17/2	1868.504	1869.109	-861.517	0.345	679.138	0.430	19	0.147	R.LTETVAAAAEPPTIQISR.Q
R4/RRR4-8/3	1705.308	1704.907	235.946	0.527	1551.068	0.465	27	0.192	K.LTPHSYIGEAEFLAR.N
R4/RRR4-8/2	1459.192	1459.629	-300.355	0.406	1080.230	0.317	21	0.160	R.QFIEGLDLPEAAR.S
R4/RRR4-8/2	1459.198	1459.629	-296.326	0.359	534.336	0.241	17	0.138	R.QFIEGLDLPEAAR.S
R4/RRR4-8/3	1569.809	1569.828	-12.301	0.522	1189.204	0.408	25	0.130	R.DLKPFFSEFGLIR.Y
R4/RRR4-8/3	1704.981	1704.907	43.179	0.401	733.774	0.414	21	0.098	K.LTPHSYIGEAEFLAR.N
R4/RRR4-10/2	1355.655	1356.467	-1340.426	0.486	1555.295	0.501	19	0.232	K.TLEAEAAHGTVTR.H
R4/RRR4-10/2	1356.025	1356.467	-326.637	0.489	1471.182	0.536	20	0.232	K.TLEAEAAHGTVTR.H
R4/RRR4-9/2	1355.691	1356.467	-1313.838	0.468	1367.843	0.503	20	0.214	K.TLEAEAAHGTVTR.H
R4/RRR4-10/2	1356.060	1356.467	-300.625	0.502	1191.672	0.523	18	0.201	K.TLEAEAAHGTVTR.H
R4/RRR4-9/2	1355.618	1356.467	-1368.100	0.497	1158.607	0.529	18	0.199	K.TLEAEAAHGTVTR.H
R4/RRR4-10/2	1773.976	1775.079	-1188.534	0.498	1395.349	0.355	20	0.182	R.NILNGTVFREPILCK.N
R4/RRR4-10/2	1775.515	1775.079	246.346	0.513	1098.988	0.455	22	0.182	R.NILNGTVFREPILCK.N
R4/RRR4-10/2	1774.509	1775.079	-887.073	0.541	1061.279	0.449	18	0.173	R.NILNGTVFREPILCK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1776.739	1775.079	-191.545	0.531	690.991	0.516	19	0.168	R.NILNGTVFREPILCK.N
R4/RRR4-10/2	1776.093	1775.079	8.230	0.535	1093.839	0.372	19	0.163	R.NILNGTVFREPILCK.N
R4/RRR4-10/2	1775.377	1775.079	168.643	0.488	734.721	0.427	19	0.157	R.NILNGTVFREPILCK.N
R4/RRR4-17/3	1981.833	1981.147	-158.879	0.618	2840.866	0.631	38	0.618	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-16/3	1981.068	1981.147	-39.969	0.576	2454.930	0.618	35	0.482	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-16/3	1981.420	1981.147	138.185	0.588	2462.520	0.615	35	0.482	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-17/2	1980.734	1981.147	-208.783	0.545	1936.758	0.606	24	0.311	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-17/2	1981.349	1981.147	102.479	0.592	1853.589	0.580	23	0.289	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-17/2	1980.595	1981.147	-785.869	0.528	1905.917	0.548	24	0.289	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-16/2	1981.083	1981.147	-32.113	0.532	1837.161	0.571	23	0.284	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-16/2	1981.481	1981.147	169.515	0.597	1802.910	0.580	23	0.281	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-16/2	1980.451	1981.147	-858.567	0.550	1791.892	0.552	23	0.272	K.DLSVIATEVGEEGQEYLK.L
R4/RRR4-16/3	1245.349	1245.408	-47.459	0.497	1445.517	0.327	22	0.131	-.AREVLLEASEK.-
R4/RRR4-16/3	1245.900	1245.408	396.553	0.418	1063.729	0.262	20	0.088	-.AREVLLEASEK.-
R4/RRR4-12/2	1945.633	1946.197	-805.969	0.575	2940.370	0.579	30	0.512	R.GINSLVDVGGGYGAVAAAVVR.A
R4/RRR4-12/2	1944.963	1946.197	-1151.971	0.451	2227.242	0.525	27	0.335	R.GINSLVDVGGGYGAVAAAVVR.A
R4/RRR4-12/2	1126.234	1127.187	-1738.825	0.427	980.167	0.494	16	0.181	R.DGEATYTLTR.V
R4/RRR4-12/2	1126.384	1127.187	-1604.894	0.419	839.348	0.488	15	0.172	R.DGEATYTLTR.V
R4/RRR4-12/2	1126.402	1127.187	-1589.217	0.349	808.117	0.357	15	0.153	R.DGEATYTLTR.V
R4/RRR4-8/2	1021.995	1022.137	-139.223	0.486	1445.522	0.330	15	0.187	K.SAEGEFLLR.V
R4/RRR4-8/2	1021.963	1022.137	-170.256	0.452	1420.448	0.325	15	0.184	K.SAEGEFLLR.V
R4/RRR4-8/2	1399.113	1399.660	-1108.719	0.250	742.335	0.337	14	0.141	K.VLWLIENVDAVK.N
R4/RRR4-8/3	1578.506	1578.662	-99.494	0.517	944.640	0.505	29	0.133	K.VFGQHVTDCSNASR.T
R4/RRR4-8/2	1399.339	1399.660	-229.993	0.164	434.011	0.279	12	0.130	-.VLWLIENVDAVK.-
R4/RRR4-8/3	1578.236	1578.662	-271.036	0.452	598.206	0.510	25	0.112	K.VFGQHVTDCSNASR.T
R4/RRR4-9/2	1958.465	1959.060	-816.505	0.490	1113.556	0.582	22	0.203	R.AEYDSVTDQEALDAFKR.V
R4/RRR4-13/2	1254.621	1254.504	93.723	0.439	931.562	0.476	15	0.170	K.INNAVAQVLLAK.R
R4/RRR4-9/3	1983.369	1984.197	-924.537	0.475	1215.026	0.473	33	0.150	R.IIAETGAGQHGVATATVCAR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/3	1983.529	1984.197	-843.168	0.413	962.787	0.403	29	0.108	R.IIAETGAGQHGVATATVCAR.F
R4/RRR4-4/2	1994.268	1993.204	32.379	0.465	1857.721	0.460	24	0.257	R.FLGVTDSSLLADGGELEIR.I
R4/RRR4-4/2	1485.363	1485.625	-176.365	0.464	1125.834	0.434	20	0.180	R.GVVDSNDLPLNVSR.E
R4/RRR4-4/2	1657.455	1657.804	-211.166	0.397	1274.220	0.297	19	0.164	R.VFISDDFDGELFPR.Y
R4/RRR4-4/2	1485.216	1485.625	-275.884	0.402	1004.852	0.385	18	0.163	R.GVVDSNDLPLNVSR.E
R4/RRR4-5/2	1486.153	1485.625	-318.303	0.416	842.624	0.374	17	0.154	R.GVVDSNDLPLNVSR.E
R4/RRR4-5/2	1486.781	1485.625	105.687	0.322	698.373	0.347	17	0.147	R.GVVDSNDLPLNVSR.E
R4/RRR4-1/2	1486.632	1485.625	5.138	0.361	615.063	0.337	17	0.146	R.GVVDSNDLPLNVSR.E
R4/RRR4-5/2	1486.842	1485.625	146.609	0.327	374.979	0.388	14	0.145	R.GVVDSNDLPLNVSR.E
R4/RRR4-1/2	1486.612	1485.625	-8.204	0.298	400.933	0.365	14	0.143	R.GVVDSNDLPLNVSR.E
R4/RRR4-2/2	1486.411	1485.625	-143.952	0.292	513.485	0.350	15	0.143	R.GVVDSNDLPLNVSR.E
R4/RRR4-2/2	1486.431	1485.625	-130.771	0.246	441.062	0.320	15	0.140	R.GVVDSNDLPLNVSR.E
R4/RRR4-4/2	1484.594	1485.625	-1371.714	0.312	800.640	0.230	17	0.139	R.GVVDSNDLPLNVSR.E
R4/RRR4-2/2	1322.307	1322.449	-108.020	0.474	1766.181	0.457	17	0.246	K.GVADFLQEVTSR.K
R4/RRR4-2/2	1449.518	1450.622	-1455.672	0.483	1226.037	0.515	18	0.201	R.KGVADFLQEVTSR.K
R4/RRR4-2/2	1450.297	1450.622	-224.782	0.486	1154.098	0.536	17	0.198	R.KGVADFLQEVTSR.K
R4/RRR4-1/2	1321.199	1322.449	-1708.443	0.434	1334.772	0.404	18	0.190	K.GVADFLQEVTSR.K
R4/RRR4-2/2	1321.538	1322.449	-1450.353	0.418	1365.722	0.329	17	0.178	K.GVADFLQEVTSR.K
R4/RRR4-1/2	1321.607	1322.449	-1398.027	0.390	1013.790	0.396	17	0.166	K.GVADFLQEVTSR.K
R4/RRR4-1/2	1697.816	1696.797	11.422	0.450	437.155	0.597	18	0.161	K.STSHPASLTTSTYGASK.L
R4/RRR4-2/2	1321.742	1322.449	-1295.061	0.265	857.122	0.076	16	0.130	K.GVADFLQEVTSR.K
R4/RRR4-9/2	1168.357	1168.368	-9.810	0.522	1536.147	0.360	16	0.200	K.AEEIVLQPIR.E
R4/RRR4-9/2	1168.125	1168.368	-208.750	0.415	1546.100	0.332	16	0.196	K.AEEIVLQPIR.E
R4/RRR4-9/2	1186.129	1186.340	-178.743	0.474	1250.251	0.437	17	0.189	R.EISGAVQLPGSK.S
R4/RRR4-9/2	1186.054	1186.340	-241.621	0.429	1296.662	0.382	17	0.182	R.EISGAVQLPGSK.S
R4/RRR4-9/2	1168.083	1168.368	-244.500	0.436	1296.055	0.329	15	0.174	K.AEEIVLQPIR.E
R4/RRR4-9/2	1706.214	1706.922	-1003.739	0.433	648.460	0.508	21	0.165	K.TFPNYFDVLSTFVR.-
R4/RRR4-9/2	1185.677	1186.340	-1407.021	0.370	1022.894	0.341	15	0.156	R.EISGAVQLPGSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1191.979	1192.346	-309.035	0.493	1556.771	0.449	18	0.223	K.VGGIEVDSLFR.T
R4/RRR4-8/2	1818.555	1818.148	224.155	0.487	1345.027	0.544	24	0.217	R.TSIPGIFAIGDVAAFPLK.M
R4/RRR4-8/2	1192.128	1192.346	-184.109	0.502	1537.205	0.434	18	0.217	K.VGGIEVDSLFR.T
R4/RRR4-8/2	1192.056	1192.346	-244.102	0.473	1331.008	0.482	18	0.207	K.VGGIEVDSLFR.T
R4/RRR4-8/2	1817.364	1818.148	-984.929	0.434	826.828	0.488	22	0.166	R.TSIPGIFAIGDVAAFPLK.M
R4/RRR4-8/2	1817.574	1818.148	-868.749	0.419	755.564	0.500	22	0.165	R.TSIPGIFAIGDVAAFPLK.M
R4/RRR4-8/2	1192.251	1192.346	-80.574	0.354	571.504	0.266	15	0.142	K.VGGIEVDSLFR.T
R4/RRR4-8/3	1296.465	1296.503	-29.108	0.387	978.857	0.371	25	0.103	K.IGGNLPGVHYIR.-
R4/RRR4-8/3	1296.982	1296.503	370.362	0.303	787.576	0.361	24	0.091	K.IGGNLPGVHYIR.-
R4/RRR4-8/3	1296.922	1296.503	324.639	0.372	995.999	0.261	25	0.086	K.IGGNLPGVHYIR.-
R4/RRR4-9/2	1118.032	1117.235	-181.526	0.483	833.368	0.485	17	0.175	K.VVTDEGLVER.A
R4/RRR4-9/2	1207.875	1208.300	-352.205	0.313	1489.319	0.197	17	0.165	K.VDFGDIDGLEK.I
R4/RRR4-9/2	1116.751	1117.235	-434.227	0.362	824.932	0.406	17	0.160	K.VVTDEGLVER.A
R4/RRR4-9/3	1421.870	1421.670	141.287	0.399	1008.068	0.337	27	0.098	R.GVLAKPTHDTIIR.L
R4/RRR4-9/3	1421.166	1421.670	-1061.802	0.379	722.997	0.233	23	0.080	R.GVLAKPTHDTIIR.L
R4/RRR4-7/2	1762.271	1761.957	178.929	0.584	3046.546	0.534	25	0.517	K.YGLAADNVVDAVLVDAR.G
R4/RRR4-7/2	1761.512	1761.957	-253.394	0.555	2666.717	0.530	24	0.425	K.YGLAADNVVDAVLVDAR.G
R4/RRR4-7/2	1761.424	1761.957	-872.809	0.549	2587.789	0.493	26	0.396	K.YGLAADNVVDAVLVDAR.G
R4/RRR4-7/2	1729.500	1728.972	-273.587	0.518	1003.077	0.515	22	0.187	R.WQAVAPSLPDDLFIR.V
R4/RRR4-7/2	1728.559	1728.972	-239.312	0.475	898.450	0.504	21	0.177	R.WQAVAPSLPDDLFIR.V
R4/RRR4-8/2	1728.298	1728.972	-971.645	0.460	996.620	0.461	22	0.177	R.WQAVAPSLPDDLFIR.V
R4/RRR4-7/2	1728.370	1728.972	-929.384	0.477	841.541	0.490	21	0.172	R.WQAVAPSLPDDLFIR.V
R4/RRR4-6/2	1729.555	1728.972	-241.935	0.466	687.356	0.476	19	0.162	R.WQAVAPSLPDDLFIR.V
R4/RRR4-8/2	1729.831	1728.972	-81.793	0.420	646.464	0.475	18	0.159	R.WQAVAPSLPDDLFIR.V
R4/RRR4-4/2	1762.407	1761.957	256.028	0.402	319.707	0.289	16	0.137	K.YGLAADNVVDAVLVDAR.G
R4/RRR4-5/2	1559.309	1558.759	-289.472	0.510	1913.796	0.499	22	0.278	K.TFGSSADIFAGIFPK.N
R4/RRR4-6/2	1559.476	1558.759	-182.037	0.462	1138.692	0.462	17	0.180	K.TFGSSADIFAGIFPK.N
R4/RRR4-5/2	1557.968	1558.759	-1152.767	0.312	1398.784	0.346	18	0.180	K.TFGSSADIFAGIFPK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1191.154	1191.363	-176.242	0.367	801.570	0.552	14	0.173	K.HAENVPWPLK.T
R4/RRR4-5/2	1190.997	1191.363	-308.468	0.335	835.834	0.554	13	0.172	K.HAENVPWPLK.T
R4/RRR4-4/2	1560.207	1558.759	287.954	0.355	499.511	0.349	15	0.140	K.TFGSSADIFAGIFPK.N
R4/RRR4-5/3	1365.071	1364.574	365.566	0.455	1090.792	0.401	25	0.116	R.FIKEEFGQIPR.I
R4/RRR4-5/3	1364.530	1364.574	-32.142	0.509	1036.514	0.404	22	0.115	R.FIKEEFGQIPR.I
R4/RRR4-6/3	1365.211	1364.574	-266.648	0.489	1144.770	0.352	22	0.111	R.FIKEEFGQIPR.I
R4/RRR4-5/3	1364.102	1364.574	-347.062	0.392	837.025	0.411	20	0.105	R.FIKEEFGQIPR.I
R4/RRR4-6/3	1365.745	1364.574	125.443	0.389	811.643	0.272	22	0.087	R.FIKEEFGQIPR.I
R4/RRR4-5/2	1488.240	1488.622	-257.471	0.496	1542.738	0.560	23	0.246	K.IDSPSGVDVTVSPSK.L
R4/RRR4-6/2	1338.306	1337.421	-85.595	0.465	1559.586	0.469	21	0.226	R.NVGSNANAVYEAK.I
R4/RRR4-6/2	1338.088	1337.421	-249.488	0.475	1474.899	0.500	20	0.224	R.NVGSNANAVYEAK.I
R4/RRR4-5/2	1337.092	1337.421	-246.560	0.494	1464.255	0.491	21	0.222	R.NVGSNANAVYEAK.I
R4/RRR4-5/2	1336.694	1337.421	-1295.322	0.417	1226.651	0.570	20	0.212	R.NVGSNANAVYEAK.I
R4/RRR4-5/2	1488.239	1488.622	-257.965	0.444	1296.686	0.532	20	0.209	K.IDSPSGVDVTVSPSK.L
R4/RRR4-5/2	1488.144	1488.622	-322.402	0.425	1333.691	0.517	20	0.209	K.IDSPSGVDVTVSPSK.L
R4/RRR4-5/2	1337.107	1337.421	-235.020	0.542	1262.932	0.522	20	0.209	R.NVGSNANAVYEAK.I
R4/RRR4-5/2	1394.084	1394.512	-307.795	0.412	1248.629	0.450	20	0.191	K.DLATGTESTPFVR.G
R4/RRR4-6/2	1336.607	1337.421	-1360.811	0.393	1017.042	0.493	18	0.180	R.NVGSNANAVYEAK.I
R4/RRR4-5/2	1395.333	1394.512	-128.515	0.321	991.009	0.400	18	0.161	K.DLATGTESTPFVR.G
R4/RRR4-8/2	1333.901	1334.460	-1171.733	0.455	1185.177	0.474	18	0.191	K.LLVSDSFPGNER.N
R4/RRR4-8/2	1723.409	1724.038	-948.115	0.375	568.379	0.463	16	0.150	R.IAWEEPFGPVLPVIR.I
R4/RRR4-8/2	1723.209	1724.038	-1064.536	0.337	784.061	0.361	18	0.147	R.IAWEEPFGPVLPVIR.I
R4/RRR4-8/2	1334.176	1334.460	-212.961	0.331	662.052	0.321	15	0.142	K.LLVSDSFPGNER.N
R4/RRR4-8/3	1243.115	1243.395	-225.962	0.485	1136.099	0.438	23	0.131	R.GPDHFPFQGLK.D
R4/RRR4-8/3	1243.585	1243.395	153.518	0.484	997.621	0.424	21	0.115	-.GPDHFPFQGLK.-
R4/RRR4-9/2	1488.163	1488.670	-1016.129	0.353	1660.921	0.306	21	0.200	R.SNVIVEYPGTVPGR.A
R4/RRR4-9/2	1488.092	1488.670	-1063.569	0.284	1116.234	0.405	17	0.166	R.SNVIVEYPGTVPGR.A
R4/RRR4-9/2	1983.376	1984.152	-898.414	0.498	715.250	0.475	18	0.154	R.ELQDEGFDVQTAGYGLLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/3	1872.767	1873.056	-154.730	0.481	1258.642	0.406	27	0.135	K.KLQEYVHDINENIEK.L
R4/RRR4-9/2	1556.214	1556.743	-985.149	0.372	1373.466	0.335	19	0.175	R.NDAGLAAAELALAVEK.H
R4/RRR4-9/2	1311.036	1311.466	-328.974	0.457	972.905	0.433	18	0.170	K.IINQDPPALSDK.S
R4/RRR4-9/2	1294.674	1294.439	182.461	0.349	626.611	0.376	13	0.143	-.VLYSDKDVQAR.-
R4/RRR4-8/2	1755.541	1754.918	-215.199	0.590	2826.286	0.594	24	0.492	K.IPFSSFDILTDDEVR.Q
R4/RRR4-8/2	1754.548	1754.918	-211.553	0.591	2322.638	0.586	22	0.377	K.IPFSSFDILTDDEVR.Q
R4/RRR4-8/2	1635.903	1635.950	-28.935	0.452	504.196	0.447	17	0.149	R.LESLVNSSPVMAFIK.G
R4/RRR4-6/2	1001.085	1001.162	-77.004	0.532	1283.705	0.446	17	0.198	R.IGAATALEVR.A
R4/RRR4-6/2	1397.295	1396.486	-137.711	0.402	1395.422	0.415	18	0.197	K.GFTISDWEGIDR.I
R4/RRR4-6/2	1231.123	1231.464	-278.027	0.450	1231.370	0.456	19	0.193	R.ITVGTTILDAVK.A
R4/RRR4-6/2	1232.135	1231.464	-267.861	0.513	895.340	0.526	18	0.183	R.ITVGTTILDAVK.A
R4/RRR4-6/2	1231.006	1231.464	-373.137	0.281	645.260	0.492	16	0.154	R.ITVGTTILDAVK.A
R4/RRR4-5/2	1397.791	1396.486	218.666	0.305	497.995	0.221	13	0.132	-.GFTISDWEGIDR.-
R4/RRR4-8/2	1945.943	1945.335	-201.819	0.585	2573.192	0.636	24	0.445	R.LPAPVTTSAVELVALPLPR.V
R4/RRR4-8/2	1944.800	1945.335	-791.393	0.517	2004.012	0.595	22	0.317	R.LPAPVTTSAVELVALPLPR.V
R4/RRR4-8/3	1224.483	1224.354	105.768	0.463	858.463	0.371	22	0.100	R.GHHVSFVSTPR.N
R4/RRR4-8/3	1224.368	1224.354	11.578	0.455	675.378	0.380	19	0.092	-.GHHVSFVSTPR.-
R4/RRR4-14/2	1705.782	1705.894	-65.577	0.575	2826.689	0.508	25	0.457	R.YVFTGASWVTNAFNK.V
R4/RRR4-13/2	1706.601	1705.894	-171.940	0.481	650.938	0.345	16	0.140	R.YVFTGASWVTNAFNK.V
R4/RRR4-14/3	1567.999	1567.684	201.675	0.411	711.862	0.521	25	0.117	K.AFDEKHGFTSTAGAK.V
R4/RRR4-14/3	1567.994	1567.684	198.396	0.355	771.901	0.487	25	0.112	K.AFDEKHGFTSTAGAK.V
R4/RRR4-5/2	1593.113	1593.763	-1038.724	0.336	1593.118	0.375	20	0.204	R.ESYLNASAIVDAALR.T
R4/RRR4-5/2	1656.310	1656.864	-941.137	0.403	744.844	0.415	21	0.155	K.IIEEAPAPNVTAQFR.S
R4/RRR4-5/2	1528.176	1526.761	272.037	0.418	832.276	0.279	18	0.139	K.AEGLTFIGPPPSAIR.D
R4/RRR4-4/2	1193.186	1193.334	-124.840	0.508	1527.518	0.383	18	0.205	R.AVAYLLSNADR.V
R4/RRR4-3/2	1427.263	1427.549	-200.444	0.471	1103.554	0.492	17	0.188	R.NPVYQNAGNFFR.L
R4/RRR4-3/2	1427.247	1427.549	-211.856	0.419	1107.281	0.426	17	0.176	R.NPVYQNAGNFFR.L
R4/RRR4-3/2	1295.965	1296.500	-1187.421	0.451	1165.156	0.417	15	0.175	R.SAGLAIYAQVFR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1042.143	1042.209	-63.631	0.354	828.518	0.412	13	0.159	R.LSDFLTFAK.D
R4/RRR4-3/2	1041.885	1042.209	-312.190	0.391	1070.016	0.246	15	0.151	R.LSDFLTFAK.D
R4/RRR4-3/2	1041.939	1042.209	-260.353	0.273	698.942	0.242	11	0.137	R.LSDFLTFAK.D
R4/RRR4-5/2	1039.826	1039.124	-287.021	0.384	739.760	0.480	14	0.165	K.ANITESFTR.Q
R4/RRR4-5/2	1039.171	1039.124	45.289	0.373	757.520	0.455	14	0.162	K.ANITESFTR.Q
R4/RRR4-5/2	1786.217	1787.010	-1006.490	0.500	896.107	0.419	20	0.160	K.LGNFVEGNTQIPIIDR.E
R4/RRR4-5/2	1165.342	1165.391	-42.300	0.417	623.065	0.404	14	0.152	R.MAFLQANITR.D
R4/RRR4-5/2	1459.875	1458.599	189.155	0.492	1131.590	0.456	15	0.183	K.YNVESWLDYLR.S
R4/RRR4-5/2	1459.484	1458.599	-78.992	0.385	1236.617	0.403	17	0.182	K.YNVESWLDYLR.S
R4/RRR4-5/2	1459.645	1458.599	31.656	0.342	833.854	0.374	15	0.153	K.YNVESWLDYLR.S
R4/RRR4-5/2	1176.895	1177.249	-301.761	0.351	763.083	0.336	15	0.148	R.SLATDAEWQR.S
R4/RRR4-5/2	1358.153	1358.520	-270.864	0.394	874.192	0.258	16	0.141	K.VSLSENEPILEK.M
R4/RRR4-14/2	1857.373	1858.206	-989.883	0.490	3342.727	0.490	26	0.578	R.GCIVSQDLSVLNLVIVK.Q
R4/RRR4-14/2	1858.610	1858.206	218.073	0.618	2959.512	0.565	26	0.508	R.GCIVSQDLSVLNLVIVK.Q
R4/RRR4-14/2	1857.795	1858.206	-221.808	0.543	2688.838	0.469	25	0.407	R.GCIVSQDLSVLNLVIVK.Q
R4/RRR4-13/2	1860.054	1858.206	-81.662	0.506	1091.731	0.436	19	0.171	R.GCIVSQDLSVLNLVIVK.Q
R4/RRR4-6/2	1859.955	1858.206	-135.448	0.380	497.971	0.316	16	0.137	R.GCIVSQDLSVLNLVIVK.Q
R4/RRR4-14/3	1859.530	1858.206	174.831	0.455	1242.434	0.398	29	0.131	R.GCIVSQDLSVLNLVIVK.Q
R4/RRR4-1/2	1860.958	1861.044	-46.226	0.401	1063.638	0.456	19	0.172	R.LDIDFAEVYANSALYR.S
R4/RRR4-8/2	1503.473	1503.768	-196.473	0.482	2358.301	0.386	20	0.317	K.TVFIQELINNIAK.A
R4/RRR4-8/2	1503.491	1503.768	-184.500	0.478	2261.199	0.356	20	0.291	K.TVFIQELINNIAK.A
R4/RRR4-8/2	1774.473	1774.992	-859.008	0.428	1095.044	0.478	19	0.178	R.GISELGIYPAVDPLDSK.S
R4/RRR4-8/2	1774.106	1774.992	-1066.570	0.346	656.818	0.395	15	0.141	R.GISELGIYPAVDPLDSK.S
R4/RRR4-15/3	1948.734	1949.071	-173.421	0.489	2886.807	0.472	31	0.521	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-16/3	1948.979	1949.071	-47.318	0.523	2462.985	0.494	30	0.403	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-15/2	1910.295	1910.068	119.174	0.575	2352.009	0.595	25	0.382	R.ASGSCDFAGAATIVTQQPK.I
R4/RRR4-14/2	1909.434	1910.068	-858.246	0.542	2360.586	0.559	25	0.371	R.ASGSCDFAGAATIVTQQPK.I
R4/RRR4-15/2	1909.591	1910.068	-250.735	0.537	2306.705	0.585	25	0.370	R.ASGSCDFAGAATIVTQQPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1909.660	1910.068	-214.309	0.558	2266.584	0.583	25	0.361	R.ASGSCDFAGAATIVTQQPK.I
R4/RRR4-15/3	1948.935	1949.071	-70.218	0.512	2194.283	0.484	29	0.328	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-14/3	1948.991	1949.071	-41.570	0.515	2090.485	0.513	29	0.318	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-14/3	1948.867	1949.071	-105.370	0.492	2092.007	0.511	30	0.316	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-14/2	1909.074	1910.068	-1047.924	0.501	2094.845	0.538	25	0.316	R.ASGSCDFAGAATIVTQQPK.I
R4/RRR4-16/3	1949.075	1949.071	1.776	0.528	1977.877	0.499	30	0.283	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-16/3	1949.584	1949.071	-250.811	0.535	2007.427	0.422	29	0.253	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-14/3	1948.802	1949.071	-138.452	0.497	1433.804	0.523	25	0.197	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-15/3	1948.152	1949.071	-987.914	0.352	1368.028	0.355	27	0.134	K.VAHATYAFNDYYQTAGR.A
R4/RRR4-15/3	1910.951	1910.068	-61.458	0.463	959.497	0.416	29	0.111	R.ASGSCDFAGAATIVTQQPK.I
R4/RRR4-14/3	1909.618	1910.068	-236.313	0.285	693.393	0.232	23	0.069	-.ASGSCDFAGAATIVTQQPK.-
R4/RRR4-3/2	1315.467	1315.458	6.924	0.446	1162.378	0.394	15	0.176	R.FTWTIENFTR.I
R4/RRR4-3/2	1315.609	1315.458	115.064	0.431	629.883	0.411	12	0.152	R.FTWTIENFTR.I
R4/RRR4-3/2	1314.886	1315.458	-1198.921	0.269	841.930	0.283	13	0.142	R.FTWTIENFTR.I
R4/RRR4-3/2	1189.022	1188.313	-245.755	0.311	850.067	0.276	14	0.142	-.VELSSPSAELR.-
R4/RRR4-3/2	1188.909	1188.313	-340.522	0.309	681.587	0.269	13	0.138	-.VELSSPSAELR.-
R4/RRR4-3/2	1188.268	1188.313	-37.775	0.288	632.673	0.240	12	0.135	-.VELSSPSAELR.-
R4/RRR4-25/3	1934.689	1934.877	-97.536	0.505	2807.750	0.497	39	0.522	R.GGGGYGGGGGYGNQGGYGDGNR.G
R4/RRR4-25/3	1934.478	1934.877	-207.010	0.533	2781.741	0.479	40	0.498	R.GGGGYGGGGGYGNQGGYGDGNR.G
R4/RRR4-25/3	1936.032	1934.877	80.270	0.539	2235.562	0.555	37	0.384	R.GGGGYGGGGGYGNQGGYGDGNR.G
R4/RRR4-25/3	1542.622	1542.675	-34.640	0.425	494.303	0.599	24	0.122	K.SAM*DAM*DGKELEGR.S
R4/RRR4-25/3	1543.652	1542.675	-14.669	0.354	481.553	0.533	24	0.108	K.SAM*DAM*DGKELEGR.S
R4/RRR4-25/3	1542.061	1542.675	-1049.875	0.322	337.971	0.521	21	0.103	K.SAM*DAM*DGKELEGR.S
R4/RRR4-22/2	1832.194	1832.006	103.271	0.550	2492.260	0.603	29	0.415	K.GGTDSVIGVTLLGADGSGVR.I
R4/RRR4-23/2	1831.444	1832.006	-855.084	0.530	2542.850	0.567	29	0.413	K.GGTDSVIGVTLLGADGSGVR.I
R4/RRR4-22/2	1831.497	1832.006	-826.113	0.510	2530.892	0.568	29	0.411	K.GGTDSVIGVTLLGADGSGVR.I
R4/RRR4-22/2	1831.403	1832.006	-877.432	0.488	2545.377	0.557	29	0.409	K.GGTDSVIGVTLLGADGSGVR.I
R4/RRR4-23/2	1831.491	1832.006	-829.525	0.518	2506.174	0.578	29	0.409	K.GGTDSVIGVTLLGADGSGVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	978.546	979.072	-1564.025	0.431	1080.644	0.559	14	0.199	R.GNLDIFSGR.G
R4/RRR4-24/2	978.849	979.072	-228.789	0.461	1145.293	0.507	14	0.196	R.GNLDIFSGR.G
R4/RRR4-27/2	978.887	979.072	-189.381	0.469	1068.020	0.507	14	0.191	R.GNLDIFSGR.G
R4/RRR4-23/2	978.827	979.072	-251.310	0.472	1047.513	0.504	14	0.189	R.GNLDIFSGR.G
R4/RRR4-27/2	978.808	979.072	-270.328	0.447	1071.520	0.481	14	0.186	R.GNLDIFSGR.G
R4/RRR4-23/2	978.479	979.072	-1633.204	0.397	1029.276	0.495	14	0.184	R.GNLDIFSGR.G
R4/RRR4-22/2	978.912	979.072	-164.111	0.447	886.135	0.527	13	0.181	R.GNLDIFSGR.G
R4/RRR4-24/2	979.041	979.072	-31.653	0.484	912.729	0.486	13	0.177	R.GNLDIFSGR.G
R4/RRR4-21/2	978.882	979.072	-194.635	0.415	950.242	0.481	13	0.177	R.GNLDIFSGR.G
R4/RRR4-27/2	978.205	979.072	-1913.653	0.409	895.109	0.492	13	0.175	R.GNLDIFSGR.G
R4/RRR4-21/2	1832.222	1832.006	118.505	0.354	355.863	0.546	21	0.154	K.GGTDSVIGVTLLGADGSGVR.I
R4/RRR4-2/2	1326.942	1327.555	-1219.216	0.498	1528.802	0.495	19	0.230	R.VGQIIAQLLSER.L
R4/RRR4-2/2	1877.323	1878.071	-933.971	0.469	1133.701	0.463	21	0.180	K.AQSDVSSAVTTIQEIISK.E
R4/RRR4-2/2	1481.018	1481.634	-1094.856	0.324	790.520	0.370	20	0.149	R.ALDLPVYFGDAGSR.E
R4/RRR4-2/2	1327.048	1327.555	-1139.035	0.300	857.473	0.372	14	0.149	R.VGQIIAQLLSER.L
R4/RRR4-6/2	1879.535	1878.071	247.695	0.376	528.574	0.384	18	0.141	K.AQSDVSSAVTTIQEIISK.E
R4/RRR4-1/2	1130.461	1130.318	126.328	0.353	1302.223	0.304	15	0.170	K.FVLNDPSLPK.S
R4/RRR4-8/2	1257.042	1257.455	-329.955	0.366	825.164	0.386	14	0.151	K.AAIDVVCNPLGK.S
R4/RRR4-1/2	1257.194	1257.455	-208.471	0.323	744.590	0.323	14	0.142	K.AAIDVVCNPLGK.S
R4/RRR4-1/2	1708.304	1709.111	-1061.282	0.261	962.044	0.300	18	0.141	R.LLAALGPSFLGPVAILR.V
R4/RRR4-8/2	1130.126	1130.318	-170.916	0.241	845.138	0.101	13	0.131	-.FVLNDPSLPK.-
R4/RRR4-8/2	1130.116	1130.318	-179.260	0.241	665.620	0.116	12	0.131	-.FVLNDPSLPK.-
R4/RRR4-26/2	1632.079	1631.683	242.940	0.580	1940.749	0.603	26	0.315	K.GSPAADEEQSTAAAAVR.F
R4/RRR4-26/2	1631.424	1631.683	-159.675	0.541	1967.932	0.570	25	0.308	K.GSPAADEEQSTAAAAVR.F
R4/RRR4-26/2	1631.206	1631.683	-293.526	0.530	1482.397	0.598	24	0.247	K.GSPAADEEQSTAAAAVR.F
R4/RRR4-26/3	1631.298	1631.683	-237.039	0.455	1013.848	0.452	29	0.124	K.GSPAADEEQSTAAAAVR.F
R4/RRR4-26/3	1760.458	1759.856	-226.951	0.439	866.506	0.427	31	0.109	R.KGSPAADEEQSTAAAAVR.F
R4/RRR4-26/3	1759.741	1759.856	-65.765	0.456	661.000	0.425	28	0.100	R.KGSPAADEEQSTAAAAVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/3	1759.831	1759.856	-14.313	0.423	562.254	0.427	26	0.097	R.KGSPAADEEQSTAAAAVR.F
R4/RRR4-2/2	1825.156	1825.076	43.524	0.600	2291.284	0.612	25	0.379	R.LTQM*NTDLFGGVDAVVK.Y
R4/RRR4-3/2	1824.302	1825.076	-975.719	0.441	1453.301	0.491	21	0.215	R.LTQM*NTDLFGGVDAVVK.Y
R4/RRR4-3/2	1824.829	1825.076	-136.215	0.435	981.093	0.485	19	0.172	R.LTQM*NTDLFGGVDAVVK.Y
R4/RRR4-2/2	929.605	930.086	-518.483	0.363	901.970	0.188	13	0.138	R.VWDIGALR.K
R4/RRR4-8/2	1085.883	1086.227	-317.807	0.313	932.587	0.312	16	0.149	R.NLAASVQNIR.A
R4/RRR4-8/3	1499.350	1499.653	-202.452	0.486	532.517	0.541	22	0.116	R.HTSKPEAEYPALR.F
R4/RRR4-8/3	1499.564	1499.653	-59.499	0.444	432.292	0.498	22	0.107	R.HTSKPEAEYPALR.F
R4/RRR4-8/3	1499.507	1499.653	-97.346	0.426	405.526	0.467	20	0.102	R.HTSKPEAEYPALR.F
R4/RRR4-8/3	1780.125	1779.976	84.171	0.406	995.188	0.322	26	0.093	K.VDLSHAALDALVDAAAAR.L
R4/RRR4-4/2	1295.691	1295.639	40.103	0.401	1025.406	0.541	18	0.188	K.NVILQLLALVAK.Q
R4/RRR4-4/2	1392.200	1392.625	-306.277	0.431	1287.862	0.400	16	0.183	R.SVEQLGYITLLR.Q
R4/RRR4-4/2	1525.146	1525.642	-326.783	0.356	1212.010	0.387	19	0.174	R.SSPESSVLTDVFTR.L
R4/RRR4-4/2	1525.144	1525.642	-327.907	0.369	852.568	0.423	18	0.158	R.SSPESSVLTDVFTR.L
R4/RRR4-19/2	1258.250	1258.490	-190.586	0.487	2081.369	0.535	19	0.316	R.SIVGATLEVIQK.K
R4/RRR4-19/2	1259.262	1258.490	-181.294	0.597	1942.446	0.534	19	0.294	R.SIVGATLEVIQK.K
R4/RRR4-19/2	1257.587	1258.490	-1517.681	0.442	1896.748	0.508	19	0.279	R.SIVGATLEVIQK.K
R4/RRR4-19/2	1385.876	1386.662	-1292.555	0.427	1049.088	0.513	17	0.184	R.SIVGATLEVIQKK.R
R4/RRR4-18/2	1258.091	1258.490	-317.320	0.435	633.323	0.435	14	0.154	R.SIVGATLEVIQK.K
R4/RRR4-20/2	1687.450	1687.985	-911.886	0.523	2274.764	0.671	24	0.399	R.HVVFGQVIEGM*DIVK.M
R4/RRR4-20/2	1688.253	1687.985	159.634	0.548	2023.012	0.624	24	0.337	R.HVVFGQVIEGM*DIVK.M
R4/RRR4-20/2	1994.633	1994.193	221.187	0.609	1450.070	0.617	27	0.250	R.VVIGLYGDDVPQTAENFR.A
R4/RRR4-20/2	1993.269	1994.193	-968.587	0.582	1180.349	0.654	26	0.229	R.VVIGLYGDDVPQTAENFR.A
R4/RRR4-20/2	1993.453	1994.193	-875.877	0.569	1208.838	0.630	26	0.226	R.VVIGLYGDDVPQTAENFR.A
R4/RRR4-20/3	1687.680	1687.985	-181.074	0.337	1157.060	0.156	24	0.074	R.HVVFGQVIEGM*DIVK.M
R4/RRR4-13/2	1129.697	1130.320	-1440.435	0.478	2266.655	0.581	22	0.364	K.VAVITGGASGIGK.A
R4/RRR4-14/2	1130.079	1130.320	-214.044	0.500	2305.120	0.527	22	0.353	K.VAVITGGASGIGK.A
R4/RRR4-15/2	1131.219	1130.320	-89.251	0.542	2110.912	0.600	22	0.343	K.VAVITGGASGIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1129.490	1130.320	-1625.088	0.403	2313.533	0.484	22	0.339	K.VAVITGGASGIGK.A
R4/RRR4-13/2	1129.950	1130.320	-327.950	0.483	2177.092	0.535	22	0.333	K.VAVITGGASGIGK.A
R4/RRR4-15/2	1328.246	1328.497	-189.669	0.510	2029.836	0.535	19	0.307	K.VIIADVQDELGR.S
R4/RRR4-15/2	1130.166	1130.320	-136.460	0.533	1908.105	0.573	21	0.300	K.VAVITGGASGIGK.A
R4/RRR4-15/2	1328.373	1328.497	-93.240	0.536	1930.944	0.551	19	0.297	K.VIIADVQDELGR.S
R4/RRR4-15/2	1328.516	1328.497	14.321	0.464	1810.307	0.541	19	0.275	K.VIIADVQDELGR.S
R4/RRR4-15/2	1329.466	1328.497	-23.540	0.407	744.755	0.378	14	0.150	-.VIIADVQDELGR.-
R4/RRR4-15/2	1328.161	1328.497	-253.473	0.360	737.853	0.345	14	0.147	K.VIIADVQDELGR.S
R4/RRR4-15/2	1328.216	1328.497	-211.981	0.350	756.007	0.365	14	0.147	-.VIIADVQDELGR.-
R4/RRR4-15/2	1328.239	1328.497	-194.463	0.367	666.729	0.332	13	0.138	-.VIIADVQDELGR.-
R4/RRR4-16/2	1329.281	1328.497	-162.902	0.185	585.965	0.184	14	0.135	K.VIIADVQDELGR.S
R4/RRR4-22/2	1522.026	1522.638	-1062.703	0.517	2132.260	0.615	21	0.353	R.TYCAEIAHNVSTR.K
R4/RRR4-3/2	1481.018	1479.750	181.659	0.523	665.374	0.491	17	0.164	R.AQVQIPLEVVNLR.A
R4/RRR4-2/2	1479.111	1479.750	-1111.085	0.392	809.631	0.446	18	0.162	R.AQVQIPLEVVNLR.A
R4/RRR4-2/2	1578.223	1578.750	-970.324	0.305	884.224	0.355	18	0.148	R.ALQYFPTIEDPGAR.R
R4/RRR4-3/2	1479.133	1479.750	-1096.003	0.311	454.393	0.270	14	0.137	R.AQVQIPLEVVNLR.A
R4/RRR4-2/2	1113.663	1114.233	-1413.791	0.315	940.693	0.123	13	0.131	R.AVEYFELSR.K
R4/RRR4-4/2	1356.362	1356.550	-138.888	0.503	2388.938	0.528	19	0.370	R.LLVLEAADQLDR.H
R4/RRR4-4/2	1356.298	1356.550	-186.558	0.496	2304.491	0.521	19	0.352	R.LLVLEAADQLDR.H
R4/RRR4-4/2	1356.193	1356.550	-264.033	0.459	2063.260	0.502	19	0.303	R.LLVLEAADQLDR.H
R4/RRR4-4/2	1240.037	1240.434	-320.953	0.441	1602.280	0.565	20	0.254	R.VPATNILLGEGR.G
R4/RRR4-4/2	1239.979	1240.434	-368.462	0.484	1394.569	0.634	20	0.247	R.VPATNILLGEGR.G
R4/RRR4-4/2	1241.109	1240.434	-262.570	0.490	1330.083	0.583	19	0.228	R.VPATNILLGEGR.G
R4/RRR4-14/2	1630.643	1629.842	-121.984	0.544	2292.640	0.620	24	0.384	K.WGTIDVLVNNAGITR.D
R4/RRR4-14/2	1313.584	1312.540	33.218	0.555	2360.777	0.557	22	0.376	K.LEAPVVIVTGASR.G
R4/RRR4-14/2	1629.458	1629.842	-236.209	0.489	2053.860	0.468	23	0.291	K.WGTIDVLVNNAGITR.D
R4/RRR4-14/2	1629.573	1629.842	-165.717	0.492	1905.455	0.525	22	0.285	K.WGTIDVLVNNAGITR.D
R4/RRR4-14/2	1312.344	1312.540	-149.984	0.467	1754.800	0.483	21	0.254	K.LEAPVVIVTGASR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1312.523	1312.540	-13.023	0.351	888.117	0.463	16	0.164	K.LEAPVVIVTGASR.G
R4/RRR4-3/2	1137.237	1137.228	8.224	0.361	1163.362	0.393	16	0.174	K.NIFVASSNER.L
R4/RRR4-3/2	1020.887	1021.152	-260.025	0.334	708.537	0.434	14	0.155	R.ALGSTPGVYR.V
R4/RRR4-3/2	1020.969	1021.152	-179.536	0.372	454.376	0.413	11	0.146	R.ALGSTPGVYR.V
R4/RRR4-3/3	1787.059	1787.048	6.014	0.381	1462.059	0.321	26	0.132	K.LIDKYDLYGQVAYPK.H
R4/RRR4-3/3	1786.796	1787.048	-141.378	0.331	663.886	0.349	19	0.086	K.LIDKYDLYGQVAYPK.H
R4/RRR4-13/2	1209.710	1210.365	-1371.882	0.545	1878.629	0.687	22	0.331	K.APSAAVAQPAAAGK.V
R4/RRR4-13/2	1209.682	1210.365	-1395.699	0.500	1584.251	0.637	21	0.270	K.APSAAVAQPAAAGK.V
R4/RRR4-13/2	1210.122	1210.365	-201.303	0.516	1332.820	0.661	20	0.245	K.APSAAVAQPAAAGK.V
R4/RRR4-13/2	987.612	988.123	-1535.101	0.349	1175.979	0.316	14	0.164	K.SQLQGVSLR.V
R4/RRR4-13/2	988.030	988.123	-94.874	0.423	836.800	0.376	13	0.157	K.SQLQGVSLR.V
R4/RRR4-13/2	1209.310	1210.365	-1704.216	0.327	394.550	0.389	13	0.137	-.APSAAVAQPAAAGK.-
R4/RRR4-20/2	750.221	749.798	566.043	0.188	845.852	0.185	12	0.131	R.QAFGGGGR.F
R4/RRR4-20/3	1124.828	1124.237	-364.668	0.367	1434.668	0.264	24	0.111	R.QAFGGGGRFAR.L
R4/RRR4-20/3	1124.495	1124.237	229.933	0.279	1116.055	0.080	23	0.068	-.QAFGGGGRFAR.-
R4/RRR4-6/2	1507.351	1507.670	-212.538	0.507	3050.580	0.523	24	0.520	K.IFEVGDVVTLDGSR.D
R4/RRR4-23/2	1464.451	1464.562	-76.467	0.490	2432.232	0.459	23	0.355	R.FEALDANGDGVLSR.A
R4/RRR4-24/2	1464.113	1464.562	-307.791	0.503	2281.390	0.470	22	0.330	R.FEALDANGDGVLSR.A
R4/RRR4-23/2	1464.101	1464.562	-316.156	0.461	2341.833	0.427	22	0.327	R.FEALDANGDGVLSR.A
R4/RRR4-24/2	1183.826	1184.240	-350.672	0.298	903.487	0.211	15	0.137	R.GFVADDDAFAR.S
R4/RRR4-11/2	1543.132	1543.651	-987.550	0.498	2374.461	0.464	24	0.345	K.ITGCYVVGSAGSDEK.V
R4/RRR4-11/2	1543.172	1543.651	-311.620	0.530	2148.161	0.531	24	0.327	K.ITGCYVVGSAGSDEK.V
R4/RRR4-11/2	1542.924	1543.651	-1122.743	0.496	1921.326	0.480	24	0.276	K.ITGCYVVGSAGSDEK.V
R4/RRR4-11/3	1352.452	1352.475	-17.537	0.454	1137.873	0.429	26	0.126	K.FGFDDAFNYKK.E
R4/RRR4-11/3	1352.048	1352.475	-316.786	0.469	940.750	0.482	24	0.125	K.FGFDDAFNYKK.E
R4/RRR4-11/3	1352.851	1352.475	278.276	0.473	1006.190	0.403	25	0.112	K.FGFDDAFNYKK.E
R4/RRR4-11/3	1352.484	1352.475	6.770	0.438	876.338	0.360	24	0.099	K.FGFDDAFNYKK.E
R4/RRR4-16/2	1582.479	1582.734	-161.519	0.482	2405.812	0.473	21	0.354	R.SNVGELLEYSLETK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1582.396	1582.734	-214.451	0.477	2336.250	0.384	20	0.311	R.SNVGELLEYSLETK.K
R4/RRR4-16/2	1581.333	1582.734	-1522.942	0.311	1118.083	0.223	18	0.146	R.SNVGELLEYSLETK.K
R4/RRR4-16/3	1489.778	1490.622	-1241.459	0.471	1103.449	0.505	29	0.145	K.HGGIDSM*SADDLKK.L
R4/RRR4-16/3	1490.948	1490.622	219.731	0.503	1042.631	0.459	28	0.129	K.HGGIDSM*SADDLKK.L
R4/RRR4-21/2	1908.610	1910.072	-1293.808	0.507	2330.896	0.496	23	0.348	R.YALYDFDFVTGENVQK.S
R4/RRR4-21/2	1412.216	1412.617	-284.596	0.467	1279.170	0.298	17	0.165	K.IFFIAWSPSTSR.I
R4/RRR4-21/2	1413.063	1412.617	316.466	0.411	1007.298	0.327	16	0.155	K.IFFIAWSPSTSR.I
R4/RRR4-21/2	1411.898	1412.617	-1221.385	0.321	663.809	0.325	14	0.142	K.IFFIAWSPSTSR.I
R4/RRR4-2/2	1502.273	1502.649	-251.072	0.443	1054.404	0.507	18	0.183	R.NPIDSSTIDLLEGK.L
R4/RRR4-2/3	1648.320	1648.845	-927.917	0.449	1675.935	0.385	29	0.182	R.KHHEEVQGLSVVASK.A
R4/RRR4-2/2	1376.684	1377.606	-1400.438	0.235	1217.675	0.168	17	0.142	K.VCLTTGLGSLLSR.W
R4/RRR4-3/2	1489.345	1489.698	-237.468	0.497	2603.137	0.495	22	0.403	K.AFVQQAEVILADGK.L
R4/RRR4-3/2	1657.563	1657.933	-223.931	0.565	1608.605	0.525	22	0.245	K.KLVQENISSALDIVK.S
R4/RRR4-12/2	1577.167	1576.843	206.140	0.559	2048.079	0.582	24	0.326	R.MFYGPGGPYALFAGK.D
R4/RRR4-12/2	1592.265	1592.842	-993.115	0.510	1615.391	0.626	22	0.271	R.M*FYGPGGPYALFAGK.D
R4/RRR4-12/2	1591.761	1592.842	-1311.104	0.445	1625.681	0.616	22	0.268	R.M*FYGPGGPYALFAGK.D
R4/RRR4-12/2	1577.395	1576.843	-284.678	0.542	1594.818	0.584	22	0.258	R.MFYGPGGPYALFAGK.D
R4/RRR4-12/2	1592.216	1592.842	-1024.520	0.469	1594.980	0.543	23	0.247	R.M*FYGPGGPYALFAGK.D
R4/RRR4-12/2	1166.326	1167.254	-1658.269	0.381	1174.516	0.389	15	0.175	K.GQIYDVTQSR.M
R4/RRR4-12/2	1166.202	1167.254	-1764.903	0.344	1069.264	0.383	15	0.166	K.GQIYDVTQSR.M
R4/RRR4-12/2	1576.408	1576.843	-276.468	0.460	769.498	0.482	18	0.164	R.MFYGPGGPYALFAGK.D
R4/RRR4-12/2	1166.377	1167.254	-1614.108	0.360	1001.302	0.387	15	0.164	K.GQIYDVTQSR.M
R4/RRR4-9/3	1754.832	1755.873	-1166.553	0.539	2341.672	0.576	32	0.419	R.TAVHQGIGHQTYAESR.G
R4/RRR4-9/3	1756.593	1755.873	-159.492	0.566	2281.114	0.556	33	0.388	R.TAVHQGIGHQTYAESR.G
R4/RRR4-9/3	1755.582	1755.873	-166.034	0.512	1881.398	0.532	30	0.280	R.TAVHQGIGHQTYAESR.G
R4/RRR4-9/3	1774.998	1774.094	-54.336	0.416	1402.299	0.513	31	0.184	R.APEYLALNDKVISLVK.G
R4/RRR4-9/3	1775.521	1774.094	241.304	0.406	813.855	0.611	27	0.146	R.APEYLALNDKVISLVK.G
R4/RRR4-9/3	1773.859	1774.094	-133.126	0.464	826.306	0.597	26	0.145	R.APEYLALNDKVISLVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1572.308	1572.786	-305.183	0.537	2488.976	0.454	22	0.362	K.M*FVLDEADEMLSR.G
R4/RRR4-9/2	1572.339	1572.786	-285.086	0.528	2361.059	0.482	21	0.347	K.M*FVLDEADEMLSR.G
R4/RRR4-9/2	1573.006	1572.786	140.019	0.546	2202.688	0.487	21	0.320	K.M*FVLDEADEMLSR.G
R4/RRR4-9/2	1587.744	1588.785	-1289.352	0.461	2189.284	0.475	22	0.315	K.M*FVLDEADEM*LSR.G
R4/RRR4-9/2	1588.244	1588.785	-973.420	0.509	1869.726	0.502	21	0.274	K.M*FVLDEADEM*LSR.G
R4/RRR4-9/2	1588.359	1588.785	-269.036	0.504	1861.117	0.495	21	0.270	K.M*FVLDEADEM*LSR.G
R4/RRR4-9/2	1084.897	1085.322	-392.919	0.392	1115.689	0.391	15	0.171	R.VLIATDLLAR.G
R4/RRR4-9/2	1572.107	1572.786	-1071.099	0.366	1145.239	0.291	19	0.159	K.MFVLDEADEM*LSR.G
R4/RRR4-9/2	1572.389	1572.786	-253.152	0.409	715.694	0.392	18	0.155	K.MFVLDEADEM*LSR.G
R4/RRR4-9/2	1571.890	1572.786	-1210.049	0.255	491.289	0.271	16	0.141	K.MFVLDEADEM*LSR.G
R4/RRR4-10/2	1557.919	1556.786	85.536	0.430	268.410	0.337	13	0.138	-.MFVLDEADEMLSR.-
R4/RRR4-6/3	1660.974	1660.893	48.967	0.542	2346.119	0.432	34	0.333	R.IINEPTAAAIAYGIDK.K
R4/RRR4-6/3	1661.992	1660.893	59.839	0.599	2524.137	0.338	36	0.322	R.IINEPTAAAIAYGIDK.K
R4/RRR4-6/2	1660.355	1660.893	-928.741	0.549	1821.929	0.583	26	0.290	R.IINEPTAAAIAYGIDK.K
R4/RRR4-5/2	1662.285	1660.893	236.610	0.573	1753.213	0.602	26	0.286	R.IINEPTAAAIAYGIDK.K
R4/RRR4-6/2	1661.398	1660.893	-298.435	0.578	1582.263	0.611	25	0.265	R.IINEPTAAAIAYGIDK.K
R4/RRR4-5/2	1789.483	1789.066	233.955	0.569	1558.703	0.587	26	0.255	R.IINEPTAAAIAYGIDKK.A
R4/RRR4-6/2	1660.099	1660.893	-1083.839	0.512	1555.180	0.558	24	0.246	R.IINEPTAAAIAYGIDK.K
R4/RRR4-6/2	1659.749	1660.893	-1295.413	0.435	1570.610	0.506	25	0.235	R.IINEPTAAAIAYGIDK.K
R4/RRR4-6/2	1788.463	1789.066	-898.978	0.552	1442.558	0.558	25	0.234	R.IINEPTAAAIAYGIDKK.A
R4/RRR4-5/2	1788.545	1789.066	-852.729	0.535	1358.469	0.556	24	0.223	R.IINEPTAAAIAYGIDKK.A
R4/RRR4-6/2	1788.530	1789.066	-861.019	0.520	1320.686	0.534	25	0.215	R.IINEPTAAAIAYGIDKK.A
R4/RRR4-6/2	1788.519	1789.066	-867.528	0.533	1162.728	0.598	23	0.213	R.IINEPTAAAIAYGIDKK.A
R4/RRR4-1/2	1660.250	1660.893	-992.074	0.415	1112.305	0.566	23	0.200	R.IINEPTAAAIAYGIDK.K
R4/RRR4-1/2	1660.218	1660.893	-1011.710	0.404	959.270	0.516	22	0.180	R.IINEPTAAAIAYGIDK.K
R4/RRR4-5/3	1659.952	1660.893	-1172.601	0.281	1477.507	0.132	28	0.089	R.IINEPTAAAIAYGIDK.K
R4/RRR4-24/2	1199.190	1199.425	-196.910	0.544	2205.313	0.482	19	0.319	R.VDIGQVLLSVR.C
R4/RRR4-17/2	1199.682	1199.425	214.871	0.525	2191.689	0.475	19	0.315	R.VDIGQVLLSVR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1200.268	1199.425	-131.244	0.578	2094.155	0.493	19	0.304	R.VDIGQVLLSVR.C
R4/RRR4-17/2	1200.304	1199.425	-101.659	0.577	2088.986	0.490	19	0.302	R.VDIGQVLLSVR.C
R4/RRR4-25/2	1199.446	1199.425	17.189	0.527	2055.309	0.503	19	0.302	R.VDIGQVLLSVR.C
R4/RRR4-1/2	1200.127	1199.425	-248.990	0.521	1967.852	0.527	19	0.295	R.VDIGQVLLSVR.C
R4/RRR4-18/2	1200.396	1199.425	-24.745	0.530	2065.113	0.459	19	0.290	R.VDIGQVLLSVR.C
R4/RRR4-24/2	1199.256	1199.425	-141.871	0.550	2089.796	0.431	19	0.285	R.VDIGQVLLSVR.C
R4/RRR4-24/2	1199.294	1199.425	-109.912	0.478	1929.839	0.486	18	0.277	R.VDIGQVLLSVR.C
R4/RRR4-25/2	1199.257	1199.425	-140.952	0.465	1142.440	0.491	17	0.193	R.VDIGQVLLSVR.C
R4/RRR4-18/2	1199.183	1199.425	-203.037	0.448	1231.608	0.445	17	0.190	R.VDIGQVLLSVR.C
R4/RRR4-14/2	1198.900	1199.425	-1276.205	0.417	1379.378	0.380	16	0.189	R.VDIGQVLLSVR.C
R4/RRR4-25/2	1198.872	1199.425	-1299.724	0.448	1233.098	0.395	16	0.181	R.VDIGQVLLSVR.C
R4/RRR4-15/2	1199.203	1199.425	-186.085	0.332	1227.556	0.357	17	0.174	R.VDIGQVLLSVR.C
R4/RRR4-4/2	1199.055	1199.425	-309.356	0.437	944.899	0.421	15	0.167	R.VDIGQVLLSVR.C
R4/RRR4-15/2	1199.323	1199.425	-85.204	0.387	1049.877	0.320	16	0.159	R.VDIGQVLLSVR.C
R4/RRR4-15/2	1198.971	1199.425	-379.941	0.359	750.664	0.400	15	0.157	R.VDIGQVLLSVR.C
R4/RRR4-13/2	1199.377	1199.425	-40.181	0.391	704.497	0.387	13	0.152	R.VDIGQVLLSVR.C
R4/RRR4-13/2	1199.168	1199.425	-215.292	0.276	462.053	0.314	13	0.144	R.VDIGQVLLSVR.C
R4/RRR4-16/3	1567.277	1567.726	-286.993	0.459	1108.483	0.418	29	0.123	R.CKPNNAVHASEALR.R
R4/RRR4-16/3	1567.631	1567.726	-60.820	0.460	775.490	0.460	25	0.113	R.CKPNNAVHASEALR.R
R4/RRR4-17/3	1567.737	1567.726	7.597	0.421	853.629	0.411	26	0.107	R.CKPNNAVHASEALR.R
R4/RRR4-16/3	1567.062	1567.726	-1064.907	0.445	818.041	0.416	25	0.107	R.CKPNNAVHASEALR.R
R4/RRR4-25/3	1567.677	1567.726	-30.945	0.409	960.317	0.376	26	0.106	R.CKPNNAVHASEALR.R
R4/RRR4-25/3	1567.491	1567.726	-150.340	0.362	645.998	0.327	23	0.093	R.CKPNNAVHASEALR.R
R4/RRR4-26/3	1567.594	1567.726	-84.253	0.295	711.553	0.238	22	0.085	R.CKPNNAVHASEALR.R
R4/RRR4-25/3	1566.861	1567.726	-1193.508	0.314	821.833	0.241	25	0.085	R.CKPNNAVHASEALR.R
R4/RRR4-12/2	1488.166	1488.629	-311.702	0.560	1980.042	0.564	24	0.310	R.TKGEAGTGNVVEAVR.H
R4/RRR4-13/2	1489.212	1488.629	-280.488	0.551	1836.476	0.557	24	0.286	R.TKGEAGTGNVVEAVR.H
R4/RRR4-13/2	1489.085	1488.629	307.463	0.586	1683.743	0.571	23	0.268	R.TKGEAGTGNVVEAVR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	994.823	995.144	-324.190	0.434	549.901	0.488	12	0.162	K.VPFVCGCR.N
R4/RRR4-13/3	1488.328	1488.629	-202.471	0.490	1099.222	0.333	27	0.101	-.TKGEAGTGNVVEAVR.-
R4/RRR4-12/3	1488.060	1488.629	-1057.225	0.484	726.464	0.369	23	0.089	-.TKGEAGTGNVVEAVR.-
R4/RRR4-13/3	1488.864	1488.629	158.777	0.526	954.096	0.309	27	0.086	-.TKGEAGTGNVVEAVR.-
R4/RRR4-13/3	1488.169	1488.629	-309.489	0.483	637.324	0.346	23	0.066	-.TKGEAGTGNVVEAVR.-
R4/RRR4-18/3	1501.762	1501.669	62.025	0.566	2221.732	0.495	31	0.334	K.SLSHVAVNFSQPSK.N
R4/RRR4-18/2	1298.674	1299.585	-1475.887	0.432	2008.727	0.486	19	0.290	R.TLINNLIIGVTK.G
R4/RRR4-18/3	1501.877	1501.669	139.059	0.572	1824.329	0.526	28	0.263	K.SLSHVAVNFSQPSK.N
R4/RRR4-18/2	1299.070	1299.585	-1169.126	0.497	1775.713	0.488	19	0.258	R.TLINNLIIGVTK.G
R4/RRR4-18/2	1299.169	1299.585	-321.329	0.487	1660.834	0.458	18	0.235	R.TLINNLIIGVTK.G
R4/RRR4-18/3	1501.304	1501.669	-243.659	0.546	1792.171	0.427	26	0.215	K.SLSHVAVNFSQPSK.N
R4/RRR4-9/3	1797.102	1797.946	-1029.493	0.516	2405.198	0.470	35	0.372	K.YFRPAEVDSLQGDATK.A
R4/RRR4-9/3	1798.350	1797.946	225.339	0.564	1914.698	0.474	35	0.257	K.YFRPAEVDSLQGDATK.A
R4/RRR4-9/2	1047.649	1048.220	-1504.746	0.371	1388.358	0.245	16	0.166	K.VFLGNLSAAR.D
R4/RRR4-20/2	1316.943	1316.443	-380.677	0.477	2072.527	0.524	22	0.310	R.ATGGEVGASSALAPK.I
R4/RRR4-20/2	1316.016	1316.443	-324.937	0.409	2006.424	0.399	22	0.264	R.ATGGEVGASSALAPK.I
R4/RRR4-20/2	1316.412	1316.443	-23.681	0.401	1755.673	0.381	22	0.226	R.ATGGEVGASSALAPK.I
R4/RRR4-20/2	1662.234	1662.860	-981.462	0.475	2274.438	0.451	24	0.321	K.AITSGVLAGCSDAIAQK.I
R4/RRR4-20/2	1662.991	1662.860	78.880	0.553	2026.503	0.517	23	0.299	K.AITSGVLAGCSDAIAQK.I
R4/RRR4-20/2	1662.282	1662.860	-952.192	0.474	1847.968	0.453	22	0.254	K.AITSGVLAGCSDAIAQK.I
R4/RRR4-20/2	983.991	984.135	-146.155	0.454	463.302	0.453	14	0.160	K.ISGVPNLQR.R
R4/RRR4-20/2	984.054	984.135	-82.193	0.426	464.981	0.392	14	0.154	K.ISGVPNLQR.R
R4/RRR4-20/2	983.866	984.135	-273.853	0.383	392.980	0.358	13	0.150	K.ISGVPNLQR.R
R4/RRR4-11/3	1987.194	1987.161	16.468	0.511	1637.873	0.498	31	0.217	R.TPNVFDNKYYVDLQNR.Q
R4/RRR4-11/3	1987.276	1987.161	58.239	0.515	1407.326	0.568	27	0.209	R.TPNVFDNKYYVDLQNR.Q
R4/RRR4-11/3	1986.342	1987.161	-918.499	0.417	1361.567	0.461	26	0.163	R.TPNVFDNKYYVDLQNR.Q
R4/RRR4-11/2	934.843	935.016	-185.534	0.322	870.457	0.303	12	0.145	-.TPNVFDNK.-
R4/RRR4-22/2	1648.675	1647.917	-147.119	0.476	1502.146	0.442	21	0.213	R.SGKM*ELPEWVDIVK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1647.373	1647.917	-940.255	0.507	1097.813	0.538	20	0.197	R.SGKM*ELPEWVDIVK.T
R4/RRR4-22/2	1647.106	1647.917	-1102.976	0.495	1126.493	0.508	20	0.193	R.SGKM*ELPEWVDIVK.T
R4/RRR4-22/2	1647.551	1647.917	-222.723	0.487	1168.127	0.490	20	0.193	R.SGKM*ELPEWVDIVK.T
R4/RRR4-22/2	1375.231	1375.615	-280.006	0.473	843.032	0.431	18	0.168	K.M*ELPEWVDIVK.T
R4/RRR4-22/2	1375.173	1375.615	-322.576	0.425	719.185	0.390	17	0.157	K.M*ELPEWVDIVK.T
R4/RRR4-22/2	1374.992	1375.615	-1183.864	0.434	727.887	0.363	17	0.155	K.M*ELPEWVDIVK.T
R4/RRR4-22/2	1359.171	1359.616	-327.953	0.431	877.916	0.321	18	0.154	K.MELPEWVDIVK.T
R4/RRR4-22/2	1359.324	1359.616	-215.326	0.447	875.972	0.288	18	0.150	K.MELPEWVDIVK.T
R4/RRR4-22/2	1358.553	1359.616	-1522.769	0.341	805.518	0.268	17	0.145	K.MELPEWVDIVK.T
R4/RRR4-22/2	1648.038	1647.917	73.175	0.372	373.992	0.338	12	0.137	-.SGKM*ELPEWVDIVK.-
R4/RRR4-22/3	1647.472	1647.917	-270.974	0.364	915.602	0.171	24	0.074	R.SGKM*ELPEWVDIVK.T
R4/RRR4-22/3	1647.601	1647.917	-192.591	0.366	1212.009	0.104	27	0.071	R.SGKM*ELPEWVDIVK.T
R4/RRR4-20/2	1793.048	1793.055	-4.026	0.636	2860.466	0.575	23	0.484	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-21/2	1791.881	1793.055	-1216.996	0.562	2813.872	0.576	23	0.475	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-21/2	1792.142	1793.055	-1070.481	0.556	2782.223	0.529	23	0.449	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-22/2	1794.303	1793.055	138.590	0.594	2700.765	0.569	23	0.446	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-20/2	1793.792	1793.055	-146.952	0.649	2618.754	0.569	22	0.425	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-21/2	1793.528	1793.055	264.942	0.608	2609.963	0.565	22	0.423	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-20/2	1793.301	1793.055	137.712	0.608	2590.370	0.571	22	0.421	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-22/2	1794.656	1793.055	-223.018	0.637	2401.741	0.589	22	0.388	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-15/2	1794.008	1793.055	-26.273	0.604	2070.134	0.604	21	0.332	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-21/2	1794.253	1793.055	110.753	0.567	2115.115	0.547	21	0.321	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-22/2	1792.709	1793.055	-193.346	0.586	1937.389	0.556	22	0.296	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-15/2	1794.735	1793.055	-178.460	0.576	1798.428	0.549	21	0.273	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-15/2	1792.123	1793.055	-1081.081	0.508	1642.368	0.530	21	0.248	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-23/2	1794.581	1793.055	-264.645	0.521	1229.311	0.461	18	0.187	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-24/2	1792.213	1793.055	-1030.952	0.496	797.679	0.536	17	0.173	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-2/2	1794.441	1793.055	215.954	0.436	756.015	0.496	16	0.164	K.AM*SIM*NSFINDIFEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1794.671	1793.055	-214.488	0.260	464.308	0.310	16	0.142	K.AM*SIM*NSFINDIFEK.L
R4/RRR4-23/3	1901.792	1902.051	-136.595	0.461	1124.773	0.419	31	0.126	K.FLEDHPGGDDVLLSSTAK.D
R4/RRR4-23/3	1901.375	1902.051	-884.365	0.439	997.926	0.417	30	0.116	K.FLEDHPGGDDVLLSSTAK.D
R4/RRR4-22/3	1902.696	1902.051	-187.044	0.465	864.361	0.377	28	0.101	K.FLEDHPGGDDVLLSSTAK.D
R4/RRR4-22/3	1901.819	1902.051	-122.398	0.427	1048.621	0.318	30	0.099	K.FLEDHPGGDDVLLSSTAK.D
R4/RRR4-22/3	1901.421	1902.051	-860.100	0.397	745.125	0.337	26	0.092	K.FLEDHPGGDDVLLSSTAK.D
R4/RRR4-23/3	1901.664	1902.051	-204.401	0.394	761.160	0.320	25	0.090	K.FLEDHPGGDDVLLSSTAK.D
R4/RRR4-16/3	1534.079	1534.721	-1073.577	0.512	2127.361	0.535	31	0.339	K.AAAVGANSQAAQSM*LK.Q
R4/RRR4-16/3	1534.515	1534.721	-134.561	0.513	1642.307	0.476	27	0.211	K.AAAVGANSQAAQSM*LK.Q
R4/RRR4-16/3	1534.676	1534.721	-29.117	0.377	1445.377	0.513	28	0.192	K.AAAVGANSQAAQSM*LK.Q
R4/RRR4-16/2	1009.054	1008.110	-55.283	0.361	721.097	0.364	13	0.151	R.TTIFSPEGR.L
R4/RRR4-16/2	1007.780	1008.110	-328.830	0.298	744.752	0.270	14	0.143	R.TTIFSPEGR.L
R4/RRR4-16/2	1007.853	1008.110	-255.552	0.306	660.660	0.278	12	0.141	R.TTIFSPEGR.L
R4/RRR4-21/3	1814.747	1815.018	-149.725	0.463	1692.086	0.517	34	0.233	K.IGSLVDVQTSKDPEGLR.I
R4/RRR4-21/3	1814.949	1815.018	-38.298	0.425	1768.702	0.430	34	0.211	K.IGSLVDVQTSKDPEGLR.I
R4/RRR4-21/2	1146.849	1147.304	-397.529	0.451	1068.451	0.461	18	0.183	K.IGSLVDVQTSK.D
R4/RRR4-21/2	1146.916	1147.304	-338.898	0.388	1129.434	0.351	18	0.167	K.IGSLVDVQTSK.D
R4/RRR4-21/3	1814.577	1815.018	-243.865	0.394	1242.405	0.476	31	0.151	K.IGSLVDVQTSKDPEGLR.I
R4/RRR4-21/2	1146.200	1147.304	-1840.885	0.290	887.908	0.316	17	0.149	K.IGSLVDVQTSK.D
R4/RRR4-6/2	1317.086	1316.486	-304.222	0.555	2286.595	0.535	19	0.353	K.SIQVIVVTDGER.I
R4/RRR4-6/2	1315.679	1316.486	-1377.711	0.451	2273.609	0.475	19	0.331	K.SIQVIVVTDGER.I
R4/RRR4-6/2	1315.608	1316.486	-1431.576	0.391	1999.035	0.405	18	0.265	K.SIQVIVVTDGER.I
R4/RRR4-6/2	1785.716	1786.123	-228.910	0.422	762.746	0.540	20	0.169	R.ILGLGDLGCQGMGIPVGK.L
R4/RRR4-6/2	1785.560	1786.123	-878.291	0.437	832.017	0.513	20	0.169	R.ILGLGDLGCQGMGIPVGK.L
R4/RRR4-6/2	1801.446	1802.123	-933.599	0.453	790.231	0.495	21	0.166	R.ILGLGDLGCQGM*GIPVGK.L
R4/RRR4-6/2	1801.387	1802.123	-966.526	0.395	752.859	0.509	20	0.164	R.ILGLGDLGCQGM*GIPVGK.L
R4/RRR4-6/2	1802.730	1802.123	-218.241	0.502	644.856	0.516	20	0.163	R.ILGLGDLGCQGM*GIPVGK.L
R4/RRR4-1/2	1787.185	1786.123	34.623	0.288	490.167	0.313	16	0.137	R.ILGLGDLGCQGMGIPVGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1784.924	1786.123	-1235.846	0.263	523.988	0.228	16	0.133	R.ILGLGDLGCQGMGIPVGK.L
R4/RRR4-6/3	1802.043	1802.123	-44.499	0.399	910.507	0.438	28	0.111	R.ILGLGDLGCQGM*GIPVGK.L
R4/RRR4-16/2	1830.290	1831.000	-937.057	0.503	2011.732	0.601	25	0.323	R.GLYM*GSGGGANAVNPGYTK.G
R4/RRR4-16/2	1299.991	1300.400	-315.569	0.262	569.639	0.459	18	0.150	R.QPIGTAAQGAEEK.D
R4/RRR4-2/2	1300.119	1300.400	-216.562	0.288	407.074	0.423	16	0.147	R.QPIGTAAQGAEEK.D
R4/RRR4-16/2	1299.644	1300.400	-1355.519	0.230	443.187	0.460	17	0.145	R.QPIGTAAQGAEEK.D
R4/RRR4-16/2	1300.091	1300.400	-238.321	0.222	341.446	0.471	14	0.142	R.QPIGTAAQGAEEK.D
R4/RRR4-1/2	1299.969	1300.400	-332.339	0.274	262.287	0.438	12	0.140	-.QPIGTAAQGAEEK.-
R4/RRR4-13/3	1846.120	1845.008	60.769	0.576	2116.062	0.573	35	0.346	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/3	1844.591	1845.008	-226.888	0.557	2087.832	0.538	36	0.319	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-14/3	1844.987	1845.008	-11.329	0.587	1930.430	0.511	35	0.270	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-14/3	1844.954	1845.008	-29.048	0.568	1948.910	0.461	33	0.253	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/2	1151.406	1152.279	-1632.012	0.387	1549.243	0.420	17	0.213	R.AALYLASDEAK.Y
R4/RRR4-13/2	1152.350	1152.279	61.560	0.532	1540.725	0.421	17	0.213	R.AALYLASDEAK.Y
R4/RRR4-14/2	1151.945	1152.279	-291.078	0.509	1432.008	0.458	17	0.211	R.AALYLASDEAK.Y
R4/RRR4-14/2	1151.464	1152.279	-1581.210	0.380	1625.877	0.371	17	0.210	R.AALYLASDEAK.Y
R4/RRR4-13/2	1151.510	1152.279	-1541.168	0.380	1590.436	0.356	17	0.204	R.AALYLASDEAK.Y
R4/RRR4-14/2	1151.920	1152.279	-312.980	0.487	1449.007	0.417	17	0.203	R.AALYLASDEAK.Y
R4/RRR4-14/3	1844.977	1845.008	-16.506	0.514	1526.478	0.456	31	0.182	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/2	1845.649	1845.008	-194.941	0.508	908.633	0.511	21	0.175	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/3	1845.182	1845.008	94.475	0.523	1390.727	0.484	31	0.173	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/3	1845.486	1845.008	259.655	0.541	742.367	0.487	33	0.119	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/3	1845.488	1845.008	260.948	0.498	591.446	0.506	30	0.117	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/3	1845.642	1845.008	-198.930	0.454	981.833	0.409	29	0.115	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-14/3	1845.906	1845.008	-55.432	0.466	567.640	0.489	29	0.114	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/3	1845.250	1845.008	131.595	0.503	541.776	0.434	28	0.106	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-13/3	1845.693	1845.008	-171.063	0.435	768.782	0.394	25	0.104	K.YVNGHNLVVDGGFTSHK.G
R4/RRR4-14/3	1845.303	1845.008	160.653	0.467	638.448	0.411	29	0.104	K.YVNGHNLVVDGGFTSHK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1365.861	1366.608	-1283.259	0.312	568.492	0.495	16	0.152	R.IAAPYDLVM*QTK.Q
R4/RRR4-13/2	1772.411	1772.962	-877.416	0.538	1774.741	0.640	27	0.298	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-13/2	1772.270	1772.962	-957.278	0.513	1790.351	0.591	27	0.286	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-13/2	1771.463	1772.962	-1414.848	0.450	1312.969	0.537	24	0.211	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-13/3	1773.242	1772.962	158.688	0.431	1039.848	0.604	34	0.169	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-12/3	1772.599	1772.962	-205.228	0.382	819.446	0.573	30	0.140	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-12/3	1773.852	1772.962	-62.136	0.421	793.181	0.543	31	0.132	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-13/3	1772.255	1772.962	-965.930	0.359	870.298	0.514	32	0.129	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-12/3	1773.076	1772.962	64.446	0.429	756.211	0.525	31	0.126	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-14/3	1772.878	1772.962	-47.529	0.430	692.265	0.539	30	0.125	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-14/3	1772.327	1772.962	-925.374	0.335	675.863	0.518	28	0.119	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-13/3	1773.827	1772.962	-76.218	0.331	710.039	0.467	31	0.111	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-14/3	1772.330	1772.962	-923.196	0.366	607.123	0.464	29	0.109	R.GM*GDAADLVALSGGHTVGK.-
R4/RRR4-13/3	1757.974	1756.962	6.775	0.266	248.159	0.394	24	0.103	R.GMGDAADLVALSGGHTVGK.-
R4/RRR4-10/2	1506.219	1506.601	-254.398	0.498	2074.301	0.598	24	0.335	K.LASLSQGAAGESSTAR.E
R4/RRR4-10/2	1357.304	1356.553	-183.894	0.454	1517.679	0.533	19	0.233	R.GVAIGVGQSEILGR.I
R4/RRR4-10/2	1355.945	1356.553	-1189.977	0.341	265.557	0.431	12	0.127	-.GVAIGVGQSEILGR.-
R4/RRR4-15/2	1908.333	1909.040	-897.622	0.520	2015.513	0.634	24	0.333	R.ASGSCDFAGAASIVNQQPK.I
R4/RRR4-15/2	1908.465	1909.040	-828.081	0.557	1996.918	0.625	23	0.326	R.ASGSCDFAGAASIVNQQPK.I
R4/RRR4-15/3	1962.822	1963.098	-141.268	0.487	1604.568	0.487	30	0.207	K.VAHATYAFNDFYQTTGR.A
R4/RRR4-15/3	1962.714	1963.098	-196.203	0.466	1344.144	0.538	30	0.187	K.VAHATYAFNDFYQTTGR.A
R4/RRR4-15/3	1962.886	1963.098	-108.142	0.551	1422.406	0.482	28	0.178	K.VAHATYAFNDFYQTTGR.A
R4/RRR4-20/3	1962.898	1963.098	-101.966	0.474	771.551	0.471	25	0.114	K.VAHATYAFNDFYQTTGR.A
R4/RRR4-19/3	1961.917	1963.098	-1115.095	0.386	584.574	0.419	22	0.098	K.VAHATYAFNDFYQTTGR.A
R4/RRR4-10/2	1885.468	1885.236	123.081	0.629	1913.502	0.602	28	0.311	R.QAIPFLESLVVADVAALK.D
R4/RRR4-10/3	1884.700	1885.236	-817.806	0.530	2060.536	0.453	33	0.282	R.QAIPFLESLVVADVAALK.D
R4/RRR4-10/2	1885.621	1885.236	204.430	0.591	1855.484	0.530	28	0.280	R.QAIPFLESLVVADVAALK.D
R4/RRR4-10/3	1884.772	1885.236	-247.028	0.522	1736.692	0.416	31	0.203	R.QAIPFLESLVVADVAALK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1397.006	1397.473	-335.372	0.421	917.693	0.414	18	0.162	K.DGTGTLTVFTNDR.G
R4/RRR4-10/3	1885.122	1885.236	-60.904	0.444	1202.193	0.404	28	0.129	R.QAIPFLESLVVADVAALK.D
R4/RRR4-9/2	1828.779	1829.048	-147.531	0.562	1888.826	0.571	25	0.297	R.GIYAYGFEKPSAIQQR.A
R4/RRR4-9/2	1829.429	1829.048	208.702	0.555	1629.834	0.597	24	0.267	R.GIYAYGFEKPSAIQQR.A
R4/RRR4-9/3	1828.489	1829.048	-855.050	0.432	1719.719	0.523	30	0.243	R.GIYAYGFEKPSAIQQR.A
R4/RRR4-9/2	1828.420	1829.048	-893.261	0.595	1285.669	0.574	24	0.222	R.GIYAYGFEKPSAIQQR.A
R4/RRR4-9/3	1828.520	1829.048	-838.413	0.463	1308.872	0.555	29	0.187	R.GIYAYGFEKPSAIQQR.A
R4/RRR4-8/3	1830.195	1829.048	80.330	0.416	1304.310	0.535	26	0.181	R.GIYAYGFEKPSAIQQR.A
R4/RRR4-9/2	926.003	926.138	-146.912	0.278	682.560	0.392	14	0.148	R.AVLPIISGR.-
R4/RRR4-9/2	926.089	926.138	-53.559	0.217	631.161	0.361	13	0.141	R.AVLPIISGR.-
R4/RRR4-14/2	1422.175	1421.622	-315.662	0.553	1707.777	0.616	22	0.284	K.LPGLFIWSADSSK.V
R4/RRR4-14/2	1420.844	1421.622	-1255.488	0.496	1783.512	0.553	22	0.276	K.LPGLFIWSADSSK.V
R4/RRR4-14/2	1422.285	1421.622	-237.559	0.535	1704.771	0.582	21	0.273	K.LPGLFIWSADSSK.V
R4/RRR4-15/2	1422.178	1421.622	-312.993	0.508	1731.034	0.548	21	0.267	K.LPGLFIWSADSSK.V
R4/RRR4-15/2	1421.332	1421.622	-204.812	0.473	1625.995	0.588	20	0.262	K.LPGLFIWSADSSK.V
R4/RRR4-14/2	1421.335	1421.622	-202.572	0.519	1575.364	0.584	21	0.257	K.LPGLFIWSADSSK.V
R4/RRR4-14/2	1421.398	1421.622	-158.202	0.515	1401.847	0.602	20	0.240	K.LPGLFIWSADSSK.V
R4/RRR4-15/2	1420.944	1421.622	-1184.744	0.455	1361.172	0.596	20	0.232	K.LPGLFIWSADSSK.V
R4/RRR4-15/2	1337.806	1338.404	-1197.966	0.407	1408.748	0.499	17	0.215	K.VSSYGFEYETR.G
R4/RRR4-14/2	1420.589	1421.622	-1435.327	0.440	1217.449	0.547	19	0.207	K.LPGLFIWSADSSK.V
R4/RRR4-14/2	1337.941	1338.404	-346.700	0.451	1170.751	0.506	17	0.197	K.VSSYGFEYETR.G
R4/RRR4-15/2	1338.117	1338.404	-215.170	0.466	958.894	0.515	16	0.183	K.VSSYGFEYETR.G
R4/RRR4-15/2	1421.257	1421.622	-257.890	0.454	857.420	0.547	15	0.177	K.LPGLFIWSADSSK.V
R4/RRR4-14/2	1337.198	1338.404	-1654.123	0.259	887.827	0.346	16	0.151	K.VSSYGFEYETR.G
R4/RRR4-15/2	1337.243	1338.404	-1620.649	0.182	656.135	0.297	14	0.137	K.VSSYGFEYETR.G
R4/RRR4-12/2	1700.340	1700.782	-260.998	0.520	2148.395	0.518	25	0.321	R.ASGYDVESSASSDAILK.A
R4/RRR4-12/2	1700.371	1700.782	-242.991	0.521	2016.792	0.515	24	0.298	R.ASGYDVESSASSDAILK.A
R4/RRR4-13/2	1700.412	1700.782	-218.792	0.491	1712.746	0.467	24	0.242	R.ASGYDVESSASSDAILK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1624.789	1624.819	-18.131	0.480	1108.023	0.409	20	0.171	K.VYQGQLVGPSTFEAK.L
R4/RRR4-16/2	1588.304	1588.742	-276.402	0.416	2919.033	0.424	25	0.445	K.ALADAVTEGLSAAEAAK.Q
R4/RRR4-11/2	1326.605	1325.538	50.982	0.516	1713.451	0.582	19	0.274	R.YSGNFLVNLLGK.W
R4/RRR4-11/2	1325.213	1325.538	-245.999	0.563	1575.783	0.564	19	0.252	R.YSGNFLVNLLGK.W
R4/RRR4-11/2	1326.336	1325.538	-152.648	0.576	1415.518	0.584	18	0.237	R.YSGNFLVNLLGK.W
R4/RRR4-11/2	1324.586	1325.538	-1477.796	0.429	1504.791	0.454	19	0.216	R.YSGNFLVNLLGK.W
R4/RRR4-10/2	1325.214	1325.538	-245.075	0.458	1223.138	0.552	17	0.209	R.YSGNFLVNLLGK.W
R4/RRR4-11/2	1325.178	1325.538	-271.967	0.453	1111.320	0.541	16	0.196	R.YSGNFLVNLLGK.W
R4/RRR4-10/2	1325.064	1325.538	-358.200	0.485	1085.610	0.508	18	0.191	R.YSGNFLVNLLGK.W
R4/RRR4-11/2	1325.589	1325.538	38.921	0.482	928.328	0.528	17	0.184	R.YSGNFLVNLLGK.W
R4/RRR4-10/2	1325.479	1325.538	-44.579	0.482	856.905	0.543	16	0.181	R.YSGNFLVNLLGK.W
R4/RRR4-1/2	1325.072	1325.538	-352.470	0.487	921.056	0.504	17	0.179	R.YSGNFLVNLLGK.W
R4/RRR4-11/2	1165.023	1165.278	-219.500	0.456	1150.780	0.361	17	0.170	K.TWIEVSGSSAK.D
R4/RRR4-11/2	1165.025	1165.278	-217.502	0.386	873.669	0.403	16	0.160	K.TWIEVSGSSAK.D
R4/RRR4-22/2	1472.052	1472.624	-1071.582	0.530	2022.159	0.482	20	0.291	R.AFVVHELEDDLGK.G
R4/RRR4-22/2	1472.299	1472.624	-221.922	0.503	2020.544	0.466	20	0.286	R.AFVVHELEDDLGK.G
R4/RRR4-22/2	1472.473	1472.624	-102.908	0.505	1853.212	0.435	20	0.253	R.AFVVHELEDDLGK.G
R4/RRR4-23/2	1324.073	1324.511	-331.837	0.330	447.846	0.541	15	0.155	K.QIPLSGPNSVVGR.A
R4/RRR4-22/2	1325.010	1324.511	377.507	0.309	444.316	0.466	15	0.149	K.QIPLSGPNSVVGR.A
R4/RRR4-23/2	1324.169	1324.511	-259.507	0.284	466.766	0.453	16	0.148	K.QIPLSGPNSVVGR.A
R4/RRR4-22/2	1324.201	1324.511	-234.722	0.325	462.568	0.404	15	0.146	K.QIPLSGPNSVVGR.A
R4/RRR4-23/2	1323.925	1324.511	-1201.926	0.277	416.195	0.388	15	0.144	K.QIPLSGPNSVVGR.A
R4/RRR4-16/2	1294.973	1295.467	-382.597	0.447	1256.150	0.589	17	0.218	R.VNQSFVIATSTK.L
R4/RRR4-16/2	1295.174	1295.467	-226.653	0.498	1241.718	0.548	17	0.210	R.VNQSFVIATSTK.L
R4/RRR4-16/2	1294.728	1295.467	-1346.953	0.388	1187.675	0.541	16	0.199	R.VNQSFVIATSTK.L
R4/RRR4-16/2	1451.101	1451.653	-1072.879	0.472	1033.457	0.428	18	0.171	K.RVNQSFVIATSTK.L
R4/RRR4-22/2	1256.996	1256.479	-384.708	0.568	2096.432	0.339	18	0.259	R.ALDWAIANLLR.R
R4/RRR4-22/2	1256.106	1256.479	-297.596	0.487	2047.086	0.343	18	0.256	R.ALDWAIANLLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1244.418	1245.385	-1585.097	0.404	1413.292	0.525	19	0.221	R.IGVAM*DYSASSK.R
R4/RRR4-22/2	1245.073	1245.385	-251.111	0.480	1219.123	0.559	18	0.211	R.IGVAM*DYSASSK.R
R4/RRR4-22/2	1244.799	1245.385	-1278.029	0.439	1291.631	0.522	18	0.209	R.IGVAM*DYSASSK.R
R4/RRR4-12/2	1662.202	1662.786	-955.774	0.524	2280.363	0.382	21	0.302	R.SEQIFQEAIQQQGR.G
R4/RRR4-11/3	1661.674	1661.796	-73.662	0.517	956.686	0.452	28	0.122	K.TKVDELEKDNLSNR.Q
R4/RRR4-27/2	1122.480	1123.284	-1612.331	0.484	1060.592	0.480	16	0.186	R.VCGNPHGLIR.K
R4/RRR4-27/2	1122.483	1123.284	-1609.272	0.479	1045.971	0.453	16	0.181	R.VCGNPHGLIR.K
R4/RRR4-28/2	1122.415	1123.284	-1670.347	0.449	1076.535	0.440	16	0.180	R.VCGNPHGLIR.K
R4/RRR4-28/2	1123.023	1123.284	-232.724	0.457	1064.216	0.441	16	0.179	R.VCGNPHGLIR.K
R4/RRR4-28/2	1122.970	1123.284	-280.708	0.426	1107.866	0.419	16	0.178	R.VCGNPHGLIR.K
R4/RRR4-27/2	1122.399	1123.284	-1684.771	0.439	1033.929	0.444	16	0.178	R.VCGNPHGLIR.K
R4/RRR4-27/2	1122.952	1123.284	-296.522	0.484	1040.897	0.437	16	0.178	R.VCGNPHGLIR.K
R4/RRR4-27/2	1122.653	1123.284	-1456.780	0.478	1015.413	0.434	16	0.176	R.VCGNPHGLIR.K
R4/RRR4-28/2	1122.463	1123.284	-1627.408	0.418	939.233	0.436	16	0.171	R.VCGNPHGLIR.K
R4/RRR4-28/2	1122.998	1123.284	-255.734	0.426	920.570	0.434	15	0.169	R.VCGNPHGLIR.K
R4/RRR4-28/2	1122.810	1123.284	-423.269	0.462	896.901	0.418	15	0.167	R.VCGNPHGLIR.K
R4/RRR4-28/2	975.881	976.120	-245.781	0.353	1180.058	0.291	11	0.162	K.YGLM*CCR.Q
R4/RRR4-27/2	1123.167	1123.284	-104.716	0.444	1046.066	0.320	16	0.160	R.VCGNPHGLIR.K
R4/RRR4-27/2	975.502	976.120	-1663.904	0.377	1043.622	0.303	11	0.158	K.YGLM*CCR.Q
R4/RRR4-27/2	975.811	976.120	-317.694	0.396	940.788	0.322	11	0.156	K.YGLM*CCR.Q
R4/RRR4-28/2	975.778	976.120	-351.583	0.385	950.703	0.314	11	0.156	K.YGLM*CCR.Q
R4/RRR4-27/2	975.247	976.120	-1926.475	0.410	946.624	0.288	11	0.153	K.YGLM*CCR.Q
R4/RRR4-27/2	975.662	976.120	-470.967	0.349	1083.187	0.242	11	0.151	K.YGLM*CCR.Q
R4/RRR4-28/2	975.769	976.120	-360.621	0.387	945.568	0.215	11	0.144	K.YGLM*CCR.Q
R4/RRR4-27/2	959.462	960.120	-1733.973	0.242	661.258	0.276	9	0.141	K.YGLMCCR.Q
R4/RRR4-9/2	1174.145	1174.329	-157.314	0.441	1263.525	0.331	16	0.173	K.RDELTLEGLK.Q
R4/RRR4-9/2	1173.663	1174.329	-1424.554	0.434	1272.551	0.324	16	0.172	K.RDELTLEGLK.Q
R4/RRR4-9/2	1173.533	1174.329	-1535.093	0.458	1290.142	0.296	16	0.169	K.RDELTLEGLK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1018.768	1018.143	-369.269	0.412	885.703	0.311	14	0.150	-.DELTLEGLK.-
R4/RRR4-8/2	1951.610	1952.120	-775.959	0.571	1990.461	0.589	23	0.317	K.GLHSSLNHLANEFDQIR.S
R4/RRR4-8/2	1425.786	1426.561	-1248.646	0.444	1233.264	0.459	18	0.191	R.SSGGFWTWLTGAR.S
R4/RRR4-8/2	1426.178	1426.561	-269.276	0.449	1031.999	0.502	17	0.183	R.SSGGFWTWLTGAR.S
R4/RRR4-8/2	1427.258	1426.561	-212.798	0.433	1154.398	0.439	17	0.180	R.SSGGFWTWLTGAR.S
R4/RRR4-8/2	1427.104	1426.561	-321.007	0.353	735.283	0.402	16	0.153	R.SSGGFWTWLTGAR.S
R4/RRR4-8/2	1426.126	1426.561	-305.344	0.381	674.158	0.367	15	0.147	R.SSGGFWTWLTGAR.S
R4/RRR4-8/2	1425.704	1426.561	-1306.084	0.322	400.754	0.360	12	0.140	R.SSGGFWTWLTGAR.S
R4/RRR4-13/2	1827.253	1828.059	-991.325	0.488	1893.886	0.512	25	0.279	R.ELGDFPLPIALVENSGR.C
R4/RRR4-13/2	1827.770	1828.059	-158.264	0.454	1263.430	0.555	21	0.209	R.ELGDFPLPIALVENSGR.C
R4/RRR4-13/2	1827.403	1828.059	-908.766	0.479	1201.660	0.548	21	0.203	R.ELGDFPLPIALVENSGR.C
R4/RRR4-13/2	1149.064	1149.237	-151.051	0.327	878.027	0.291	16	0.146	K.SSTVNSIVGER.V
R4/RRR4-13/2	1148.954	1149.237	-246.866	0.371	746.068	0.321	15	0.146	K.SSTVNSIVGER.V
R4/RRR4-14/2	1597.730	1598.786	-1290.982	0.456	1843.735	0.546	23	0.281	R.RLDADDGVAAVVLAGR.G
R4/RRR4-14/2	1131.779	1132.286	-1335.339	0.329	1209.712	0.224	15	0.152	K.AIEVCEAIAR.N
R4/RRR4-14/2	1131.653	1132.286	-1446.926	0.220	566.727	0.214	13	0.134	-.AIEVCEAIAR.-
R4/RRR4-22/2	1077.945	1078.207	-243.365	0.389	637.054	0.553	16	0.169	K.GHAVGDIPGVR.F
R4/RRR4-22/2	1078.120	1078.207	-80.927	0.396	478.487	0.548	14	0.162	K.GHAVGDIPGVR.F
R4/RRR4-22/2	1077.539	1078.207	-1551.974	0.334	501.099	0.473	15	0.154	K.GHAVGDIPGVR.F
R4/RRR4-21/2	1077.993	1078.207	-199.172	0.362	384.161	0.462	14	0.150	-.GHAVGDIPGVR.-
R4/RRR4-22/3	1206.352	1206.380	-22.757	0.431	1182.101	0.393	26	0.122	R.KGHAVGDIPGVR.F
R4/RRR4-19/3	1206.567	1206.380	156.097	0.487	849.225	0.464	22	0.120	R.KGHAVGDIPGVR.F
R4/RRR4-23/3	1206.403	1206.380	19.261	0.487	958.747	0.432	24	0.118	R.KGHAVGDIPGVR.F
R4/RRR4-21/3	1206.639	1206.380	215.904	0.460	1147.176	0.380	25	0.118	R.KGHAVGDIPGVR.F
R4/RRR4-23/3	1205.954	1206.380	-353.995	0.440	945.840	0.415	24	0.114	R.KGHAVGDIPGVR.F
R4/RRR4-22/3	1206.203	1206.380	-146.546	0.471	986.180	0.403	24	0.114	R.KGHAVGDIPGVR.F
R4/RRR4-21/3	1206.143	1206.380	-196.801	0.464	1070.106	0.371	26	0.111	R.KGHAVGDIPGVR.F
R4/RRR4-21/3	1205.991	1206.380	-322.918	0.435	984.372	0.372	23	0.109	R.KGHAVGDIPGVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/3	1206.640	1206.380	216.817	0.443	1085.336	0.352	25	0.109	R.KGHAVGDIPGVR.F
R4/RRR4-28/3	1206.373	1206.380	-5.249	0.429	977.036	0.367	24	0.107	R.KGHAVGDIPGVR.F
R4/RRR4-18/3	1206.640	1206.380	216.512	0.453	833.533	0.376	23	0.104	R.KGHAVGDIPGVR.F
R4/RRR4-27/3	1206.681	1206.380	250.445	0.432	652.120	0.374	22	0.103	R.KGHAVGDIPGVR.F
R4/RRR4-26/3	1206.214	1206.380	-137.561	0.442	696.543	0.366	22	0.102	R.KGHAVGDIPGVR.F
R4/RRR4-19/3	1207.421	1206.380	34.252	0.453	990.047	0.314	25	0.099	R.KGHAVGDIPGVR.F
R4/RRR4-28/3	1206.363	1206.380	-13.622	0.409	733.508	0.360	21	0.098	-.KGHAVGDIPGVR.-
R4/RRR4-20/3	1206.889	1206.380	-407.945	0.452	676.468	0.311	21	0.097	R.KGHAVGDIPGVR.F
R4/RRR4-28/3	1206.566	1206.380	155.032	0.436	730.368	0.353	22	0.094	-.KGHAVGDIPGVR.-
R4/RRR4-20/3	1206.744	1206.380	303.090	0.400	729.178	0.343	21	0.093	-.KGHAVGDIPGVR.-
R4/RRR4-20/3	1207.094	1206.380	-237.624	0.384	934.882	0.259	22	0.092	R.KGHAVGDIPGVR.F
R4/RRR4-1/3	1205.404	1206.380	-1643.626	0.390	761.605	0.284	21	0.091	-.KGHAVGDIPGVR.-
R4/RRR4-24/3	1205.874	1206.380	-1252.641	0.395	964.109	0.226	23	0.088	R.KGHAVGDIPGVR.F
R4/RRR4-27/3	1206.377	1206.380	-2.357	0.349	499.266	0.303	18	0.081	-.KGHAVGDIPGVR.-
R4/RRR4-17/3	1206.432	1206.380	43.921	0.334	691.747	0.221	21	0.068	-.KGHAVGDIPGVR.-
R4/RRR4-28/2	1304.026	1304.437	-316.095	0.523	2620.595	0.563	23	0.430	K.NVAAGAAGGPYISR.A
R4/RRR4-27/2	1304.173	1304.437	-203.309	0.519	2341.361	0.577	23	0.378	K.NVAAGAAGGPYISR.A
R4/RRR4-27/2	1303.624	1304.437	-1394.865	0.432	2079.359	0.501	23	0.305	K.NVAAGAAGGPYISR.A
R4/RRR4-27/2	1304.091	1304.437	-266.413	0.541	1850.619	0.541	22	0.282	K.NVAAGAAGGPYISR.A
R4/RRR4-28/2	1303.158	1304.437	-1754.267	0.446	1575.929	0.520	21	0.238	K.NVAAGAAGGPYISR.A
R4/RRR4-10/2	1205.349	1204.357	-6.766	0.440	1602.130	0.519	18	0.243	R.YVDIGIPANNK.G
R4/RRR4-16/2	1204.093	1204.357	-219.699	0.371	1378.616	0.540	17	0.218	R.YVDIGIPANNK.G
R4/RRR4-16/2	1205.158	1204.357	-165.965	0.440	1431.681	0.461	17	0.211	R.YVDIGIPANNK.G
R4/RRR4-10/2	1203.306	1204.357	-1709.973	0.393	1226.366	0.405	18	0.183	R.YVDIGIPANNK.G
R4/RRR4-16/2	1204.198	1204.357	-132.849	0.342	1087.582	0.468	16	0.179	R.YVDIGIPANNK.G
R4/RRR4-10/2	1203.393	1204.357	-1637.511	0.371	1087.993	0.415	17	0.174	R.YVDIGIPANNK.G
R4/RRR4-10/2	1464.276	1464.730	-311.018	0.375	735.490	0.451	19	0.162	K.QSIGCLFWLLAR.M
R4/RRR4-10/2	1464.276	1464.730	-311.269	0.337	684.169	0.404	18	0.154	K.QSIGCLFWLLAR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1463.780	1464.730	-1336.098	0.318	497.423	0.402	16	0.148	K.QSIGCLFWLLAR.M
R4/RRR4-10/2	1464.650	1464.730	-54.973	0.322	479.810	0.270	14	0.139	K.QSIGCLFWLLAR.M
R4/RRR4-8/3	1970.017	1968.415	-202.498	0.412	1366.774	0.379	31	0.139	R.LVELLLHPSPSVLIPALR.T
R4/RRR4-17/2	1174.080	1174.374	-251.594	0.517	1635.898	0.518	17	0.249	K.LSELGILSWR.L
R4/RRR4-17/2	1704.185	1704.776	-936.251	0.558	1709.093	0.484	21	0.247	R.LNADDWENDENLKK.I
R4/RRR4-17/2	1705.328	1704.776	-263.321	0.561	1535.284	0.491	21	0.228	R.LNADDWENDENLKK.I
R4/RRR4-17/2	1174.111	1174.374	-224.996	0.497	1315.173	0.514	16	0.213	K.LSELGILSWR.L
R4/RRR4-17/2	1174.064	1174.374	-264.946	0.417	1112.968	0.501	14	0.189	K.LSELGILSWR.L
R4/RRR4-17/2	1173.849	1174.374	-1303.231	0.367	961.259	0.535	14	0.182	K.LSELGILSWR.L
R4/RRR4-17/2	1173.428	1174.374	-1663.779	0.454	936.281	0.469	14	0.174	K.LSELGILSWR.L
R4/RRR4-10/2	1085.323	1085.234	81.606	0.492	1036.045	0.508	15	0.188	K.YGVSGYPTLK.F
R4/RRR4-11/2	1085.949	1085.234	-263.218	0.443	764.642	0.542	15	0.177	K.YGVSGYPTLK.F
R4/RRR4-11/2	1085.092	1085.234	-131.635	0.438	587.069	0.509	13	0.164	K.YGVSGYPTLK.F
R4/RRR4-10/2	1084.893	1085.234	-315.727	0.459	603.414	0.491	13	0.163	K.YGVSGYPTLK.F
R4/RRR4-10/2	1085.091	1085.234	-132.763	0.353	721.036	0.437	14	0.158	K.YGVSGYPTLK.F
R4/RRR4-10/2	971.039	971.134	-98.110	0.446	491.800	0.436	11	0.156	K.HLAPIYEK.L
R4/RRR4-11/2	1085.021	1085.234	-197.543	0.328	551.961	0.501	12	0.156	K.YGVSGYPTLK.F
R4/RRR4-10/2	970.922	971.134	-219.055	0.367	593.883	0.339	12	0.148	K.HLAPIYEK.L
R4/RRR4-10/2	970.406	971.134	-1786.713	0.342	605.370	0.342	12	0.148	K.HLAPIYEK.L
R4/RRR4-11/3	1826.132	1826.237	-57.860	0.423	2701.919	0.489	36	0.474	K.VAILGAAGGIGQPLSLLM*K.L
R4/RRR4-11/3	1825.734	1826.237	-825.828	0.483	2552.517	0.516	39	0.438	K.VAILGAAGGIGQPLSLLM*K.L
R4/RRR4-12/2	1825.727	1826.237	-829.579	0.552	2687.169	0.540	27	0.431	K.VAILGAAGGIGQPLSLLM*K.L
R4/RRR4-11/2	1826.608	1826.237	203.611	0.602	2549.111	0.585	27	0.417	K.VAILGAAGGIGQPLSLLM*K.L
R4/RRR4-11/2	1809.614	1810.238	-899.973	0.545	2467.452	0.556	26	0.390	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/3	1810.241	1810.238	1.980	0.427	2324.443	0.534	37	0.387	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/2	1826.457	1826.237	120.571	0.611	2289.625	0.616	26	0.376	K.VAILGAAGGIGQPLSLLM*K.L
R4/RRR4-11/3	1825.639	1826.237	-878.182	0.425	2305.070	0.463	34	0.346	K.VAILGAAGGIGQPLSLLM*K.L
R4/RRR4-11/2	1824.833	1826.237	-1321.118	0.413	2306.201	0.435	26	0.320	K.VAILGAAGGIGQPLSLLM*K.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1810.364	1810.238	70.160	0.620	1970.246	0.579	25	0.305	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/3	1809.746	1810.238	-272.627	0.440	1923.273	0.504	35	0.274	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-12/3	1810.586	1810.238	193.081	0.405	1527.384	0.504	30	0.205	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/2	1810.519	1810.238	155.835	0.471	1409.079	0.415	21	0.192	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-12/3	1810.090	1810.238	-82.030	0.367	1634.956	0.420	33	0.188	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-12/2	1810.765	1810.238	-261.715	0.433	1299.291	0.363	20	0.173	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-12/2	1809.073	1810.238	-1200.331	0.375	996.712	0.371	19	0.156	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/2	1809.465	1810.238	-982.665	0.340	982.644	0.342	19	0.152	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/2	1809.044	1810.238	-1216.526	0.349	1112.049	0.273	20	0.150	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/2	1809.503	1810.238	-961.601	0.352	1032.500	0.247	20	0.143	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-12/2	1809.107	1810.238	-1181.020	0.296	1066.278	0.233	19	0.143	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-11/2	1808.853	1810.238	-1322.247	0.283	854.757	0.271	18	0.140	K.VAILGAAGGIGQPLSLLMK.L
R4/RRR4-14/2	1537.519	1536.841	-209.721	0.556	2543.258	0.593	23	0.426	R.ALALQENPGLVILGK.Q
R4/RRR4-14/2	1537.523	1536.841	-207.730	0.549	2179.512	0.583	22	0.349	R.ALALQENPGLVILGK.Q
R4/RRR4-9/2	1929.114	1929.161	-24.537	0.572	1818.107	0.557	24	0.283	R.FQIGPEQIETLYQYAK.F
R4/RRR4-9/3	1625.433	1624.868	-268.514	0.467	1138.980	0.384	26	0.117	R.YLNAIQTNAPHLLR.Y
R4/RRR4-9/3	1624.979	1624.868	68.247	0.417	710.160	0.391	26	0.095	-.YLNAIQTNAPHLLR.-
R4/RRR4-10/3	1624.914	1624.868	28.126	0.299	631.490	0.292	21	0.083	R.YLNAIQTNAPHLLR.Y
R4/RRR4-24/3	1674.751	1675.740	-1190.714	0.540	1763.558	0.359	28	0.183	K.HGYVGEYEVVDDHR.A
R4/RRR4-23/3	1674.517	1675.740	-1331.596	0.454	1773.340	0.290	28	0.160	K.HGYVGEYEVVDDHR.A
R4/RRR4-25/2	1259.835	1260.466	-1297.862	0.466	1673.095	0.510	19	0.250	R.FTTFALSGFIR.A
R4/RRR4-25/2	1260.295	1260.466	-135.874	0.435	1388.978	0.572	18	0.230	R.FTTFALSGFIR.A
R4/RRR4-25/2	1260.101	1260.466	-290.191	0.499	1453.622	0.522	18	0.228	R.FTTFALSGFIR.A
R4/RRR4-25/2	1260.277	1260.466	-150.060	0.529	1376.431	0.536	17	0.223	R.FTTFALSGFIR.A
R4/RRR4-25/2	1674.347	1674.796	-269.071	0.506	1322.759	0.475	19	0.200	R.AQGDADSALDRLWQK.R
R4/RRR4-25/2	1674.363	1674.796	-259.709	0.510	1019.522	0.486	18	0.177	R.AQGDADSALDRLWQK.R
R4/RRR4-25/2	1260.277	1260.466	-149.768	0.398	976.494	0.466	16	0.175	R.FTTFALSGFIR.A
R4/RRR4-25/2	1675.542	1674.796	-152.401	0.502	1003.659	0.468	18	0.173	R.AQGDADSALDRLWQK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/2	1259.987	1260.466	-380.977	0.448	603.723	0.542	16	0.171	R.FTTFALSGFIR.A
R4/RRR4-25/2	1259.444	1260.466	-1609.838	0.364	849.822	0.478	16	0.169	R.FTTFALSGFIR.A
R4/RRR4-26/2	1259.599	1260.466	-1486.484	0.361	550.433	0.489	15	0.159	R.FTTFALSGFIR.A
R4/RRR4-26/2	1259.920	1260.466	-1230.333	0.260	297.219	0.423	14	0.148	R.FTTFALSGFIR.A
R4/RRR4-26/2	1674.359	1674.796	-262.049	0.354	869.569	0.266	17	0.141	R.AQGDADSALDRLWQK.R
R4/RRR4-26/2	1674.476	1674.796	-191.910	0.357	501.285	0.294	14	0.136	R.AQGDADSALDRLWQK.R
R4/RRR4-7/2	1239.607	1240.388	-1440.528	0.522	1803.896	0.560	19	0.283	K.YGVTESTLLTR.N
R4/RRR4-7/2	1239.973	1240.388	-335.879	0.541	1469.595	0.591	19	0.249	K.YGVTESTLLTR.N
R4/RRR4-7/2	1868.688	1869.154	-249.802	0.574	1444.499	0.550	26	0.233	R.LPIYVVQPQDGLDAIAR.N
R4/RRR4-7/2	1239.941	1240.388	-361.265	0.561	1142.810	0.552	17	0.206	K.YGVTESTLLTR.N
R4/RRR4-7/2	1868.499	1869.154	-888.516	0.519	1042.143	0.513	23	0.186	R.LPIYVVQPQDGLDAIAR.N
R4/RRR4-6/2	1869.311	1869.154	84.125	0.519	1071.990	0.461	23	0.179	R.LPIYVVQPQDGLDAIAR.N
R4/RRR4-11/2	1240.784	1240.388	320.245	0.123	483.722	0.275	13	0.131	K.YGVTESTLLTR.N
R4/RRR4-7/3	1868.391	1869.154	-946.438	0.347	1116.692	0.183	27	0.076	R.LPIYVVQPQDGLDAIAR.N
R4/RRR4-12/2	944.057	944.071	-14.734	0.479	1565.280	0.391	15	0.211	R.SAVQAALQR.E
R4/RRR4-12/2	943.938	944.071	-141.072	0.479	1344.345	0.423	14	0.196	R.SAVQAALQR.E
R4/RRR4-12/2	943.257	944.071	-1928.936	0.394	1425.529	0.355	14	0.189	R.SAVQAALQR.E
R4/RRR4-14/2	1026.883	1027.243	-351.447	0.399	1278.852	0.387	16	0.183	R.EIALAAGLIR.I
R4/RRR4-14/2	1026.936	1027.243	-299.447	0.417	1141.287	0.381	15	0.172	R.EIALAAGLIR.I
R4/RRR4-14/2	1026.565	1027.243	-1639.175	0.373	970.822	0.401	14	0.164	R.EIALAAGLIR.I
R4/RRR4-13/2	1027.143	1027.243	-97.341	0.308	976.791	0.159	14	0.137	R.EIALAAGLIR.I
R4/RRR4-20/2	1368.842	1369.546	-1248.264	0.497	1550.356	0.511	20	0.237	K.HLLDETISDVVK.S
R4/RRR4-20/2	1369.113	1369.546	-317.076	0.513	1524.790	0.512	20	0.234	K.HLLDETISDVVK.S
R4/RRR4-20/2	1368.486	1369.546	-1509.300	0.434	1522.907	0.475	20	0.224	K.HLLDETISDVVK.S
R4/RRR4-20/2	1139.543	1139.197	304.000	0.459	635.682	0.466	15	0.166	R.LIDDYNTER.K
R4/RRR4-20/2	1138.963	1139.197	-206.140	0.479	633.920	0.417	15	0.161	R.LIDDYNTER.K
R4/RRR4-19/2	1140.117	1139.197	-71.050	0.460	615.789	0.413	15	0.160	R.LIDDYNTER.K
R4/RRR4-19/2	1140.001	1139.197	-172.980	0.438	557.284	0.363	14	0.153	R.LIDDYNTER.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-19/2	1138.417	1139.197	-1568.787	0.306	628.918	0.285	14	0.145	R.LIDDYNTER.K
R4/RRR4-20/2	1138.420	1139.197	-1565.987	0.325	618.270	0.200	15	0.141	R.LIDDYNTER.K
R4/RRR4-14/2	1730.262	1730.852	-921.362	0.526	2508.670	0.578	23	0.409	R.SGTALCSYIASTAQSGR.I
R4/RRR4-14/2	1730.241	1730.852	-933.757	0.511	2146.754	0.565	21	0.332	R.SGTALCSYIASTAQSGR.I
R4/RRR4-15/2	1730.318	1730.852	-888.783	0.560	2059.396	0.583	23	0.324	R.SGTALCSYIASTAQSGR.I
R4/RRR4-15/2	1729.781	1730.852	-1200.710	0.507	2011.360	0.514	23	0.295	R.SGTALCSYIASTAQSGR.I
R4/RRR4-14/2	1729.724	1730.852	-1233.806	0.476	1818.513	0.571	22	0.282	R.SGTALCSYIASTAQSGR.I
R4/RRR4-15/2	1730.259	1730.852	-922.991	0.514	1743.976	0.554	22	0.267	R.SGTALCSYIASTAQSGR.I
R4/RRR4-15/2	1930.456	1930.151	158.394	0.448	1646.107	0.593	25	0.264	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-15/2	1930.509	1930.151	186.168	0.444	1691.952	0.542	25	0.258	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-15/2	1930.203	1930.151	27.110	0.406	1657.066	0.535	25	0.251	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-14/2	1930.453	1930.151	157.125	0.486	1627.436	0.582	26	0.251	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-14/2	1929.562	1930.151	-825.943	0.394	1193.157	0.540	23	0.161	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-14/2	1929.213	1930.151	-1007.601	0.305	1072.508	0.484	22	0.140	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-15/2	1929.268	1930.151	-978.824	0.337	1087.534	0.479	22	0.138	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-14/2	1930.912	1930.151	-124.066	0.427	1016.367	0.518	21	0.134	R.ISGIPSGTVNLLAFNGNPSA.-
R4/RRR4-21/2	1305.833	1306.450	-1241.362	0.459	1403.267	0.544	18	0.225	R.TGEIVVFNVDGR.E
R4/RRR4-21/2	1306.231	1306.450	-167.932	0.524	1306.474	0.482	17	0.203	R.TGEIVVFNVDGR.E
R4/RRR4-21/2	1305.383	1306.450	-1587.513	0.378	1235.415	0.506	17	0.198	R.TGEIVVFNVDGR.E
R4/RRR4-21/2	1233.262	1233.350	-72.038	0.369	377.926	0.451	16	0.152	R.QESAEVDILTK.G
R4/RRR4-4/2	1295.120	1294.482	-280.265	0.462	961.022	0.492	17	0.176	K.NNPVIIGEPGVGK.T
R4/RRR4-28/2	1484.069	1484.624	-1050.530	0.469	1799.942	0.385	20	0.234	R.SPCSLYACEAGLR.A
R4/RRR4-28/2	1484.235	1484.624	-262.620	0.456	1775.884	0.387	20	0.231	R.SPCSLYACEAGLR.A
R4/RRR4-29/2	1484.172	1484.624	-305.281	0.409	1840.124	0.351	20	0.230	R.SPCSLYACEAGLR.A
R4/RRR4-29/2	1484.350	1484.624	-185.147	0.433	1714.628	0.364	20	0.219	R.SPCSLYACEAGLR.A
R4/RRR4-28/2	1483.227	1484.624	-1620.538	0.306	1897.280	0.269	20	0.218	R.SPCSLYACEAGLR.A
R4/RRR4-28/2	993.814	994.080	-268.279	0.369	818.837	0.281	15	0.149	R.AWCGSGVTR.C
R4/RRR4-29/2	993.956	994.080	-125.474	0.364	733.361	0.262	14	0.145	R.AWCGSGVTR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-28/2	993.796	994.080	-287.010	0.317	773.547	0.249	15	0.144	R.AWCGSGVTR.C
R4/RRR4-28/2	993.710	994.080	-373.036	0.282	712.370	0.270	14	0.144	R.AWCGSGVTR.C
R4/RRR4-29/2	993.435	994.080	-1660.563	0.248	677.453	0.271	14	0.142	R.AWCGSGVTR.C
R4/RRR4-29/2	993.356	994.080	-1740.565	0.222	774.815	0.190	14	0.137	R.AWCGSGVTR.C
R4/RRR4-29/2	993.867	994.080	-214.676	0.210	728.465	0.149	12	0.134	R.AWCGSGVTR.C
R4/RRR4-3/2	1646.475	1645.790	-192.125	0.547	2052.050	0.553	23	0.317	K.TVGAVAEVIEEEAEAK.L
R4/RRR4-6/2	901.638	901.046	-453.361	0.235	834.580	0.103	12	0.128	-.KALDALNR.-
R4/RRR4-11/3	1582.824	1581.752	45.157	0.452	714.422	0.520	26	0.119	K.TKFGFDDAFNYKK.E
R4/RRR4-8/2	1261.017	1260.374	-284.252	0.508	1041.021	0.551	15	0.197	K.SKFDNLYGCR.H
R4/RRR4-8/2	905.927	906.083	-172.197	0.427	1120.395	0.462	15	0.186	R.ATDVMLAGK.V
R4/RRR4-8/2	1260.074	1260.374	-239.088	0.483	1061.811	0.443	16	0.180	K.SKFDNLYGCR.H
R4/RRR4-8/2	905.351	906.083	-1917.803	0.344	944.986	0.406	15	0.164	R.ATDVMLAGK.V
R4/RRR4-8/2	1260.047	1260.374	-260.956	0.414	739.215	0.413	14	0.157	K.SKFDNLYGCR.H
R4/RRR4-8/2	922.130	922.082	52.397	0.403	600.508	0.356	14	0.151	R.ATDVM*LAGK.V
R4/RRR4-16/2	902.004	902.074	-77.250	0.436	1208.245	0.318	13	0.168	R.LSVQIVSR.I
R4/RRR4-16/2	902.034	902.074	-44.400	0.479	1236.016	0.290	13	0.165	R.LSVQIVSR.I
R4/RRR4-16/2	902.038	902.074	-39.106	0.415	1062.742	0.293	13	0.157	R.LSVQIVSR.I
R4/RRR4-16/2	1081.465	1082.191	-1600.683	0.429	965.600	0.207	12	0.140	-.LYQFEPER.-
R4/RRR4-8/2	1851.532	1852.017	-263.103	0.548	2334.782	0.542	22	0.362	R.M*TNFYTNFQVDEIGR.V
R4/RRR4-8/2	1851.331	1852.017	-913.827	0.530	2130.501	0.519	21	0.317	R.M*TNFYTNFQVDEIGR.V
R4/RRR4-8/2	1836.335	1836.018	172.913	0.620	2021.509	0.539	21	0.304	R.MTNFYTNFQVDEIGR.V
R4/RRR4-8/2	1834.762	1836.018	-1233.440	0.518	2157.067	0.459	22	0.303	R.MTNFYTNFQVDEIGR.V
R4/RRR4-8/2	1204.141	1204.356	-178.408	0.518	2057.825	0.428	18	0.281	R.AAELTTLLESR.M
R4/RRR4-8/2	1851.242	1852.017	-961.688	0.529	1785.405	0.548	21	0.273	R.M*TNFYTNFQVDEIGR.V
R4/RRR4-8/2	1203.958	1204.356	-331.079	0.486	1818.857	0.395	17	0.239	R.AAELTTLLESR.M
R4/RRR4-7/2	1204.053	1204.356	-251.839	0.470	1728.785	0.407	17	0.231	R.AAELTTLLESR.M
R4/RRR4-8/2	1834.623	1836.018	-1309.213	0.482	1594.029	0.465	20	0.226	R.MTNFYTNFQVDEIGR.V
R4/RRR4-7/2	1203.547	1204.356	-1506.984	0.433	1540.606	0.419	17	0.212	R.AAELTTLLESR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1203.571	1204.356	-1487.220	0.406	1623.157	0.363	17	0.209	R.AAELTTLLESR.M
R4/RRR4-4/3	1514.994	1513.812	120.197	0.489	2682.982	0.465	35	0.447	K.HLGVVGLGGLGHLGVK.F
R4/RRR4-10/3	1513.573	1513.812	-158.486	0.543	2472.257	0.528	34	0.424	K.HLGVVGLGGLGHLGVK.F
R4/RRR4-11/3	1513.869	1513.812	37.590	0.343	746.241	0.182	23	0.068	-.HLGVVGLGGLGHLGVK.-
R4/RRR4-10/2	1201.285	1201.398	-94.136	0.488	1730.933	0.541	20	0.266	K.VIALGDVTGSIR.N
R4/RRR4-10/2	1201.144	1201.398	-211.981	0.516	1666.712	0.502	20	0.249	K.VIALGDVTGSIR.N
R4/RRR4-10/2	1201.073	1201.398	-271.119	0.453	1709.283	0.433	19	0.235	K.VIALGDVTGSIR.N
R4/RRR4-10/2	1299.050	1299.414	-280.736	0.470	1273.698	0.537	18	0.211	K.DDGTLASFIGFR.V
R4/RRR4-10/2	1298.517	1299.414	-1465.506	0.432	900.100	0.517	15	0.175	K.DDGTLASFIGFR.V
R4/RRR4-10/2	1610.446	1610.920	-294.953	0.473	2461.512	0.584	26	0.404	R.TPIGALLGALSSLPATK.L
R4/RRR4-10/2	1611.410	1610.920	305.093	0.547	2130.112	0.606	25	0.348	R.TPIGALLGALSSLPATK.L
R4/RRR4-10/3	1610.749	1610.920	-106.510	0.364	815.893	0.426	27	0.103	-.TPIGALLGALSSLPATK.-
R4/RRR4-10/3	1610.686	1610.920	-145.510	0.387	943.423	0.380	28	0.102	R.TPIGALLGALSSLPATK.L
R4/RRR4-4/2	1441.268	1441.652	-267.221	0.510	1781.211	0.474	21	0.255	K.LLVSEDLQPLGEK.L
R4/RRR4-3/2	1441.123	1441.652	-1063.825	0.486	1771.948	0.428	21	0.242	K.LLVSEDLQPLGEK.L
R4/RRR4-3/2	1440.750	1441.652	-1323.973	0.435	1617.900	0.384	20	0.213	K.LLVSEDLQPLGEK.L
R4/RRR4-3/2	1441.382	1441.652	-187.778	0.502	1337.308	0.406	18	0.189	K.LLVSEDLQPLGEK.L
R4/RRR4-3/3	1948.497	1948.218	143.976	0.460	911.731	0.547	27	0.139	R.IRDPDYHVTLRPHLSK.E
R4/RRR4-23/2	1170.076	1170.256	-154.303	0.408	722.577	0.434	16	0.161	K.LQGFAEDYAR.Q
R4/RRR4-23/2	1170.216	1170.256	-34.486	0.365	628.022	0.317	15	0.146	K.LQGFAEDYAR.Q
R4/RRR4-21/2	1187.864	1187.411	382.234	0.519	1485.560	0.457	20	0.217	K.AVVVLGSSEVVK.G
R4/RRR4-20/2	1188.122	1187.411	-244.189	0.545	1313.476	0.522	19	0.214	K.AVVVLGSSEVVK.G
R4/RRR4-21/2	1186.642	1187.411	-1495.436	0.427	1323.033	0.466	19	0.202	K.AVVVLGSSEVVK.G
R4/RRR4-21/2	1187.117	1187.411	-248.728	0.437	1314.593	0.447	19	0.197	K.AVVVLGSSEVVK.G
R4/RRR4-21/2	987.582	988.157	-1599.305	0.219	902.434	0.248	13	0.072	R.VACGIIGLQG.-
R4/RRR4-21/2	987.837	988.157	-324.747	0.221	672.699	0.269	13	0.070	R.VACGIIGLQG.-
R4/RRR4-26/2	1247.379	1247.385	-5.458	0.536	971.491	0.491	16	0.183	R.HLAHLEELER.Q
R4/RRR4-26/2	1247.152	1247.385	-187.865	0.472	1005.831	0.471	16	0.181	R.HLAHLEELER.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/2	1247.148	1247.385	-191.007	0.465	933.553	0.491	16	0.180	R.HLAHLEELER.Q
R4/RRR4-26/3	1314.000	1314.561	-1191.820	0.477	1322.740	0.396	23	0.136	K.VREVPGYLKPR.L
R4/RRR4-25/3	1247.017	1247.385	-296.683	0.546	1621.217	0.291	23	0.131	R.HLAHLEELER.Q
R4/RRR4-26/3	1314.076	1314.561	-370.057	0.485	1240.910	0.387	23	0.126	-.VREVPGYLKPR.-
R4/RRR4-25/3	1247.458	1247.385	58.230	0.545	1465.397	0.266	22	0.111	R.HLAHLEELER.Q
R4/RRR4-26/3	1247.186	1247.385	-160.726	0.504	1130.597	0.353	21	0.110	R.HLAHLEELER.Q
R4/RRR4-26/3	1246.926	1247.385	-369.611	0.370	353.598	0.371	21	0.107	R.HLAHLEELER.Q
R4/RRR4-26/3	1246.800	1247.385	-1275.746	0.400	288.757	0.364	20	0.104	-.HLAHLEELER.-
R4/RRR4-26/3	1246.789	1247.385	-1284.301	0.369	309.402	0.314	21	0.104	-.HLAHLEELER.-
R4/RRR4-25/3	1247.321	1247.385	-51.457	0.553	1083.383	0.330	23	0.102	R.HLAHLEELER.Q
R4/RRR4-26/3	1247.441	1247.385	44.539	0.486	1109.317	0.308	21	0.098	-.HLAHLEELER.-
R4/RRR4-24/3	1246.888	1247.385	-400.112	0.446	469.403	0.324	21	0.097	-.HLAHLEELER.-
R4/RRR4-25/3	1247.066	1247.385	-257.056	0.458	582.420	0.412	19	0.097	-.HLAHLEELER.-
R4/RRR4-25/3	1247.588	1247.385	163.036	0.489	622.052	0.339	20	0.094	-.HLAHLEELER.-
R4/RRR4-25/3	1246.815	1247.385	-1263.652	0.386	524.354	0.363	19	0.093	-.HLAHLEELER.-
R4/RRR4-26/3	1314.065	1314.561	-378.726	0.430	731.684	0.362	19	0.091	-.VREVPGYLKPR.-
R4/RRR4-24/3	1246.793	1247.385	-1280.908	0.412	250.423	0.346	18	0.091	-.HLAHLEELER.-
R4/RRR4-26/3	1247.219	1247.385	-133.775	0.484	900.616	0.332	21	0.089	-.HLAHLEELER.-
R4/RRR4-26/3	1246.832	1247.385	-1249.642	0.246	255.521	0.347	20	0.062	-.HLAHLEELER.-
R4/RRR4-6/2	1860.519	1861.004	-261.428	0.555	1879.589	0.608	25	0.307	K.TPLTAHGADAFPFTEER.-
R4/RRR4-6/2	1226.147	1226.408	-213.051	0.410	1301.440	0.459	20	0.197	R.GIPSLVAIGADGR.T
R4/RRR4-6/2	1226.226	1226.408	-148.236	0.402	900.345	0.561	18	0.182	R.GIPSLVAIGADGR.T
R4/RRR4-6/3	1861.026	1861.004	11.696	0.440	911.807	0.426	29	0.111	K.TPLTAHGADAFPFTEER.-
R4/RRR4-6/3	1860.601	1861.004	-217.500	0.436	868.781	0.368	28	0.098	K.TPLTAHGADAFPFTEER.-
R4/RRR4-6/3	1860.622	1861.004	-205.751	0.394	984.894	0.336	27	0.098	K.TPLTAHGADAFPFTEER.-
R4/RRR4-10/2	1761.095	1761.095	-0.355	0.555	1765.611	0.562	24	0.276	R.VLVVTNTTVAPLYLEK.V
R4/RRR4-10/2	1274.921	1275.391	-369.504	0.309	1515.640	0.325	19	0.189	R.VSTVVDVDLGDR.S
R4/RRR4-10/2	1759.771	1761.095	-1324.825	0.284	776.845	0.274	18	0.137	R.VLVVTNTTVAPLYLEK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1275.232	1275.391	-124.681	0.251	648.712	0.263	16	0.137	R.VSTVVDVDLGDR.S
R4/RRR4-18/2	1849.498	1850.066	-850.378	0.481	1746.326	0.490	22	0.250	R.NVQAILDSYTTIVNAAR.S
R4/RRR4-18/2	1375.055	1375.515	-335.561	0.424	1817.646	0.420	20	0.244	K.VWSQLSSAGLGNR.V
R4/RRR4-18/2	1375.087	1375.515	-312.582	0.406	1768.587	0.401	20	0.233	K.VWSQLSSAGLGNR.V
R4/RRR4-18/2	1375.022	1375.515	-359.789	0.374	1185.904	0.449	19	0.184	K.VWSQLSSAGLGNR.V
R4/RRR4-17/2	1376.496	1375.515	-14.286	0.362	1076.554	0.461	18	0.177	K.VWSQLSSAGLGNR.V
R4/RRR4-15/2	1488.362	1488.710	-234.745	0.422	1633.357	0.524	21	0.246	K.AQDTFTPISAVIPK.S
R4/RRR4-16/2	1488.678	1488.710	-21.845	0.475	1530.452	0.525	20	0.234	K.AQDTFTPISAVIPK.S
R4/RRR4-16/2	1488.269	1488.710	-297.201	0.433	1484.220	0.513	20	0.226	K.AQDTFTPISAVIPK.S
R4/RRR4-15/2	1488.378	1488.710	-223.555	0.482	1602.853	0.436	21	0.222	K.AQDTFTPISAVIPK.S
R4/RRR4-16/2	1488.164	1488.710	-1042.045	0.380	1452.336	0.433	19	0.204	K.AQDTFTPISAVIPK.S
R4/RRR4-15/2	1487.866	1488.710	-1243.123	0.349	1394.014	0.433	19	0.197	K.AQDTFTPISAVIPK.S
R4/RRR4-16/2	1616.659	1615.766	-65.859	0.572	814.790	0.389	19	0.154	K.SDVANPDDLELWLK.V
R4/RRR4-22/2	1224.943	1225.420	-389.977	0.497	1491.611	0.463	18	0.217	R.VLLINEGPNAGK.L
R4/RRR4-22/2	1224.611	1225.420	-1481.664	0.422	1218.662	0.493	17	0.196	R.VLLINEGPNAGK.L
R4/RRR4-22/2	1131.490	1132.206	-1521.149	0.363	1508.129	0.351	18	0.195	R.VLVDGPSSDSR.L
R4/RRR4-22/2	1225.175	1225.420	-200.029	0.477	1083.069	0.486	16	0.184	R.VLLINEGPNAGK.L
R4/RRR4-22/2	1131.442	1132.206	-1563.632	0.308	1287.660	0.372	17	0.178	R.VLVDGPSSDSR.L
R4/RRR4-23/2	1226.347	1225.420	-59.165	0.422	910.540	0.473	15	0.170	R.VLLINEGPNAGK.L
R4/RRR4-23/2	1131.960	1132.206	-218.448	0.355	1158.540	0.314	16	0.162	R.VLVDGPSSDSR.L
R4/RRR4-22/2	1131.408	1132.206	-1593.980	0.314	1201.883	0.289	17	0.161	R.VLVDGPSSDSR.L
R4/RRR4-23/2	1132.163	1132.206	-38.133	0.383	986.200	0.349	15	0.158	R.VLVDGPSSDSR.L
R4/RRR4-7/2	1438.359	1438.605	-171.063	0.534	1835.626	0.512	20	0.272	R.TTDVLDGFTDLLK.A
R4/RRR4-7/2	1439.354	1438.605	-174.857	0.566	1743.561	0.524	20	0.263	R.TTDVLDGFTDLLK.A
R4/RRR4-7/2	1437.920	1438.605	-1175.014	0.455	1609.588	0.459	19	0.228	R.TTDVLDGFTDLLK.A
R4/RRR4-7/2	1758.554	1757.924	-210.584	0.483	1634.737	0.362	19	0.205	R.AGLTEELLQEQIEQR.T
R4/RRR4-22/2	1597.127	1597.684	-978.050	0.512	1400.292	0.507	20	0.215	K.VSDSGELNSLM*DDAK.Y
R4/RRR4-22/2	1597.209	1597.684	-298.056	0.493	1475.822	0.418	20	0.203	K.VSDSGELNSLM*DDAK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1596.946	1597.684	-1091.631	0.469	1388.381	0.453	20	0.202	K.VSDSGELNSLM*DDAK.Y
R4/RRR4-21/2	1597.019	1597.684	-1045.658	0.452	1409.068	0.436	20	0.200	K.VSDSGELNSLM*DDAK.Y
R4/RRR4-22/2	1148.983	1149.237	-221.498	0.373	1212.337	0.405	14	0.179	K.YADTHEWVK.V
R4/RRR4-22/2	1581.423	1581.685	-165.885	0.398	710.391	0.412	18	0.153	K.VSDSGELNSLMDDAK.Y
R4/RRR4-9/2	1296.017	1295.500	-374.070	0.435	1502.909	0.414	16	0.207	K.AAIDIVELCYK.A
R4/RRR4-9/2	1230.242	1230.436	-158.600	0.536	1105.512	0.458	18	0.186	K.TLNDQIVVLSK.R
R4/RRR4-9/2	1230.083	1230.436	-287.618	0.427	1005.559	0.472	16	0.177	K.TLNDQIVVLSK.R
R4/RRR4-9/2	1295.069	1295.500	-333.880	0.270	1017.971	0.228	14	0.141	K.AAIDIVELCYK.A
R4/RRR4-17/2	1790.362	1791.083	-964.291	0.541	1279.810	0.602	23	0.228	K.LLAVPLFELYDNVQR.Y
R4/RRR4-17/2	1790.495	1791.083	-889.889	0.558	1107.379	0.610	23	0.214	K.LLAVPLFELYDNVQR.Y
R4/RRR4-17/3	1791.712	1791.083	-207.924	0.472	1306.045	0.486	27	0.165	K.LLAVPLFELYDNVQR.Y
R4/RRR4-17/2	1559.374	1559.792	-268.260	0.424	715.538	0.349	18	0.147	R.YGPVISTIPQQLSR.F
R4/RRR4-17/2	1559.305	1559.792	-312.636	0.412	835.748	0.241	19	0.139	R.YGPVISTIPQQLSR.F
R4/RRR4-20/2	1945.559	1945.166	203.104	0.631	2273.309	0.664	25	0.392	K.VQASIAANTWVVSGSPQTK.K
R4/RRR4-20/2	1944.482	1945.166	-868.404	0.561	2004.754	0.646	24	0.335	K.VQASIAANTWVVSGSPQTK.K
R4/RRR4-20/2	1944.685	1945.166	-247.973	0.546	1551.592	0.675	21	0.270	K.VQASIAANTWVVSGSPQTK.K
R4/RRR4-13/2	1213.184	1212.424	-198.776	0.542	1750.964	0.488	22	0.257	K.VLVIGGGDGGVLR.E
R4/RRR4-13/3	1356.928	1356.595	246.084	0.498	1186.308	0.472	28	0.144	R.VSLHIGDGVAFLK.N
R4/RRR4-13/3	1356.610	1356.595	10.855	0.516	1096.721	0.430	27	0.125	R.VSLHIGDGVAFLK.N
R4/RRR4-13/3	1356.712	1356.595	86.931	0.471	832.868	0.461	23	0.114	R.VSLHIGDGVAFLK.N
R4/RRR4-17/2	1649.424	1649.825	-243.742	0.420	1674.510	0.548	26	0.257	R.CSYTVWPGALPGGGAR.L
R4/RRR4-17/2	1649.151	1649.825	-1018.128	0.428	1679.032	0.536	26	0.255	R.CSYTVWPGALPGGGAR.L
R4/RRR4-17/2	1884.489	1885.070	-841.670	0.501	1402.446	0.572	26	0.230	R.LDPGQSWSISVAAGTPAAR.I
R4/RRR4-17/2	1648.931	1649.825	-1152.066	0.380	1493.392	0.516	23	0.225	R.CSYTVWPGALPGGGAR.L
R4/RRR4-17/2	1884.469	1885.070	-852.009	0.495	1241.226	0.545	24	0.207	R.LDPGQSWSISVAAGTPAAR.I
R4/RRR4-17/2	1884.626	1885.070	-236.386	0.504	1145.056	0.527	23	0.194	R.LDPGQSWSISVAAGTPAAR.I
R4/RRR4-16/2	1884.454	1885.070	-860.332	0.508	1085.874	0.529	23	0.190	R.LDPGQSWSISVAAGTPAAR.I
R4/RRR4-16/2	1884.510	1885.070	-830.291	0.506	1005.110	0.530	23	0.184	R.LDPGQSWSISVAAGTPAAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1884.678	1885.070	-208.899	0.521	995.099	0.518	23	0.181	R.LDPGQSWSISVAAGTPAAR.I
R4/RRR4-16/2	1649.388	1649.825	-265.571	0.372	974.861	0.493	19	0.173	R.CSYTVWPGALPGGGAR.L
R4/RRR4-16/2	1649.381	1649.825	-270.026	0.383	814.784	0.384	19	0.152	-.CSYTVWPGALPGGGAR.-
R4/RRR4-17/2	1298.104	1298.427	-249.910	0.433	1337.478	0.537	23	0.217	K.EAAAASAPLPSQGK.T
R4/RRR4-17/2	1298.091	1298.427	-259.910	0.433	955.140	0.538	20	0.184	K.EAAAASAPLPSQGK.T
R4/RRR4-17/2	1298.115	1298.427	-241.513	0.424	968.281	0.528	20	0.183	K.EAAAASAPLPSQGK.T
R4/RRR4-8/2	1544.279	1544.735	-296.015	0.456	1853.349	0.523	22	0.275	K.VTALVNDTVGTLAGGR.Y
R4/RRR4-8/3	1601.844	1601.827	10.722	0.462	1485.037	0.471	27	0.185	K.LKDILGVADTSLEAR.Y
R4/RRR4-15/2	1396.229	1396.533	-218.404	0.514	1543.265	0.549	19	0.244	R.NNIQAYPSVSFR.Y
R4/RRR4-15/2	1442.189	1441.620	-299.396	0.576	1360.354	0.548	19	0.225	R.IYNQNLINHVGR.G
R4/RRR4-15/2	1441.144	1441.620	-331.218	0.543	1192.698	0.492	19	0.198	R.IYNQNLINHVGR.G
R4/RRR4-15/2	1396.122	1396.533	-295.244	0.471	1322.415	0.415	18	0.191	R.NNIQAYPSVSFR.Y
R4/RRR4-15/2	1441.206	1441.620	-287.962	0.545	1145.924	0.479	18	0.190	R.IYNQNLINHVGR.G
R4/RRR4-15/2	1396.174	1396.533	-257.612	0.468	1311.684	0.409	18	0.189	R.NNIQAYPSVSFR.Y
R4/RRR4-15/2	1396.694	1396.533	115.923	0.330	791.748	0.307	16	0.146	R.NNIQAYPSVSFR.Y
R4/RRR4-8/2	1978.616	1979.049	-219.773	0.577	1830.155	0.684	27	0.318	K.TVGGGDDAFNTFFSETGAGK.H
R4/RRR4-9/2	1978.469	1979.049	-801.318	0.563	1691.289	0.677	25	0.293	K.TVGGGDDAFNTFFSETGAGK.H
R4/RRR4-8/2	1978.445	1979.049	-813.210	0.528	1518.435	0.668	25	0.266	K.TVGGGDDAFNTFFSETGAGK.H
R4/RRR4-8/2	1978.275	1979.049	-899.431	0.541	1494.071	0.669	24	0.262	K.TVGGGDDAFNTFFSETGAGK.H
R4/RRR4-6/2	1703.860	1702.929	-40.859	0.571	1736.842	0.534	23	0.262	R.AVFVDLEPTVIDEVR.T
R4/RRR4-9/2	1978.232	1979.049	-921.236	0.495	1484.103	0.644	24	0.254	K.TVGGGDDAFNTFFSETGAGK.H
R4/RRR4-9/2	1978.382	1979.049	-845.355	0.524	1394.370	0.669	24	0.250	K.TVGGGDDAFNTFFSETGAGK.H
R4/RRR4-2/2	1979.661	1979.049	-197.021	0.560	1359.308	0.665	24	0.245	K.TVGGGDDAFNTFFSETGAGK.H
R4/RRR4-9/2	1702.358	1702.929	-925.676	0.517	1520.541	0.549	23	0.240	R.AVFVDLEPTVIDEVR.T
R4/RRR4-9/2	1703.566	1702.929	-214.219	0.602	1390.895	0.563	24	0.230	R.AVFVDLEPTVIDEVR.T
R4/RRR4-8/2	1702.944	1702.929	8.728	0.572	1388.195	0.548	24	0.226	R.AVFVDLEPTVIDEVR.T
R4/RRR4-8/2	1702.655	1702.929	-161.480	0.555	1392.754	0.540	24	0.225	R.AVFVDLEPTVIDEVR.T
R4/RRR4-1/2	1978.418	1979.049	-827.331	0.467	1186.179	0.628	21	0.214	K.TVGGGDDAFNTFFSETGAGK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1702.331	1702.929	-942.018	0.480	1200.565	0.504	23	0.199	R.AVFVDLEPTVIDEVR.T
R4/RRR4-5/2	1703.320	1702.929	230.048	0.487	1305.245	0.456	22	0.197	R.AVFVDLEPTVIDEVR.T
R4/RRR4-3/2	1703.734	1702.929	-115.098	0.531	1050.520	0.537	21	0.193	R.AVFVDLEPTVIDEVR.T
R4/RRR4-13/2	1702.461	1702.929	-276.207	0.507	1146.495	0.454	21	0.184	R.AVFVDLEPTVIDEVR.T
R4/RRR4-10/2	1703.221	1702.929	171.546	0.434	1160.940	0.452	19	0.183	R.AVFVDLEPTVIDEVR.T
R4/RRR4-13/2	1702.197	1702.929	-1020.782	0.459	1036.561	0.477	21	0.181	R.AVFVDLEPTVIDEVR.T
R4/RRR4-9/2	1701.657	1702.929	-1339.634	0.364	1199.757	0.411	22	0.180	R.AVFVDLEPTVIDEVR.T
R4/RRR4-1/2	1702.601	1702.929	-193.342	0.481	958.855	0.509	19	0.180	R.AVFVDLEPTVIDEVR.T
R4/RRR4-15/2	1703.319	1702.929	229.113	0.496	934.140	0.514	18	0.178	R.AVFVDLEPTVIDEVR.T
R4/RRR4-1/2	1702.541	1702.929	-229.090	0.516	797.531	0.519	19	0.173	R.AVFVDLEPTVIDEVR.T
R4/RRR4-3/2	1702.969	1702.929	23.538	0.489	896.588	0.480	19	0.172	R.AVFVDLEPTVIDEVR.T
R4/RRR4-13/2	1702.627	1702.929	-178.166	0.508	873.697	0.471	20	0.170	R.AVFVDLEPTVIDEVR.T
R4/RRR4-2/2	1702.353	1702.929	-928.844	0.429	917.342	0.451	19	0.168	R.AVFVDLEPTVIDEVR.T
R4/RRR4-1/2	1702.367	1702.929	-920.349	0.470	908.916	0.439	20	0.167	R.AVFVDLEPTVIDEVR.T
R4/RRR4-7/2	1703.523	1702.929	-239.092	0.510	852.753	0.454	19	0.166	R.AVFVDLEPTVIDEVR.T
R4/RRR4-3/2	1702.320	1702.929	-948.137	0.428	848.983	0.409	19	0.160	R.AVFVDLEPTVIDEVR.T
R4/RRR4-14/2	1702.142	1702.929	-1053.183	0.388	869.421	0.411	18	0.160	R.AVFVDLEPTVIDEVR.T
R4/RRR4-8/3	1702.722	1702.929	-122.041	0.404	1184.029	0.496	26	0.151	R.AVFVDLEPTVIDEVR.T
R4/RRR4-2/2	1702.045	1702.929	-1110.720	0.333	735.841	0.350	17	0.148	R.AVFVDLEPTVIDEVR.T
R4/RRR4-2/2	1704.601	1702.929	-193.402	0.344	957.716	0.253	17	0.144	R.AVFVDLEPTVIDEVR.T
R4/RRR4-14/2	1701.689	1702.929	-1320.542	0.311	644.879	0.304	16	0.142	R.AVFVDLEPTVIDEVR.T
R4/RRR4-19/2	1978.537	1979.049	-766.698	0.292	134.366	0.362	12	0.137	-.TVGGGDDAFNTFFSETGAGK.-
R4/RRR4-8/3	1702.621	1702.929	-181.698	0.411	601.049	0.441	22	0.098	R.AVFVDLEPTVIDEVR.T
R4/RRR4-17/2	1760.473	1760.924	-256.812	0.527	2581.979	0.492	25	0.394	K.LSEIQSGVEEAESLIR.K
R4/RRR4-17/2	1760.434	1760.924	-279.004	0.555	2462.953	0.514	24	0.377	K.LSEIQSGVEEAESLIR.K
R4/RRR4-23/2	1760.160	1760.924	-1005.531	0.396	456.227	0.429	15	0.145	K.LSEIQSGVEEAESLIR.K
R4/RRR4-24/2	1760.128	1760.924	-1023.774	0.386	304.973	0.433	13	0.143	K.LSEIQSGVEEAESLIR.K
R4/RRR4-23/2	1762.397	1760.924	269.299	0.390	343.650	0.450	13	0.141	-.LSEIQSGVEEAESLIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1299.419	1299.543	-96.072	0.471	1276.908	0.550	20	0.216	R.EHALLAFTLGVK.Q
R4/RRR4-8/2	1299.319	1299.543	-172.972	0.449	1125.405	0.585	19	0.208	R.EHALLAFTLGVK.Q
R4/RRR4-9/2	1299.251	1299.543	-225.942	0.404	1006.383	0.567	19	0.193	R.EHALLAFTLGVK.Q
R4/RRR4-7/2	1299.277	1299.543	-205.583	0.470	921.118	0.473	18	0.175	R.EHALLAFTLGVK.Q
R4/RRR4-1/2	1299.552	1299.543	7.009	0.413	648.348	0.530	17	0.168	R.EHALLAFTLGVK.Q
R4/RRR4-8/2	1454.014	1453.626	267.807	0.354	857.306	0.298	16	0.146	K.YYFTIIDAPGHR.D
R4/RRR4-8/2	1453.981	1453.626	244.572	0.336	664.891	0.227	14	0.135	K.YYFTIIDAPGHR.D
R4/RRR4-9/2	1452.930	1453.626	-1170.628	0.298	748.953	0.200	14	0.134	K.YYFTIIDAPGHR.D
R4/RRR4-8/3	1299.831	1299.543	221.618	0.483	1091.943	0.380	25	0.113	R.EHALLAFTLGVK.Q
R4/RRR4-8/3	1299.582	1299.543	30.174	0.509	1127.886	0.352	25	0.109	R.EHALLAFTLGVK.Q
R4/RRR4-9/3	1299.523	1299.543	-15.614	0.462	848.102	0.375	23	0.101	R.EHALLAFTLGVK.Q
R4/RRR4-9/3	1299.603	1299.543	46.142	0.465	980.378	0.339	25	0.100	R.EHALLAFTLGVK.Q
R4/RRR4-8/3	1299.201	1299.543	-264.552	0.422	602.868	0.265	21	0.085	-.EHALLAFTLGVK.-
R4/RRR4-9/3	1298.685	1299.543	-1435.487	0.392	1002.546	0.225	25	0.084	R.EHALLAFTLGVK.Q
R4/RRR4-24/2	1242.199	1242.366	-134.206	0.496	1003.297	0.559	16	0.194	K.HQYLPADAQAK.Q
R4/RRR4-24/2	1242.053	1242.366	-252.119	0.482	1031.623	0.509	16	0.187	K.HQYLPADAQAK.Q
R4/RRR4-24/2	1242.044	1242.366	-259.908	0.487	864.273	0.518	15	0.177	K.HQYLPADAQAK.Q
R4/RRR4-24/2	1232.069	1231.426	-290.632	0.489	798.501	0.361	18	0.157	R.EALGALPLYQR.T
R4/RRR4-24/2	1230.992	1231.426	-353.647	0.406	607.279	0.380	16	0.152	R.EALGALPLYQR.T
R4/RRR4-24/2	1232.123	1231.426	-246.400	0.530	717.161	0.322	17	0.148	R.EALGALPLYQR.T
R4/RRR4-18/2	1088.971	1088.237	-244.948	0.507	1362.808	0.409	16	0.193	K.GAELADGLTIK.D
R4/RRR4-18/3	1666.765	1666.811	-27.893	0.349	708.885	0.529	25	0.116	K.GAELADGLTIKDGDYK.L
R4/RRR4-18/3	1666.620	1666.811	-114.730	0.307	1065.368	0.395	25	0.112	K.GAELADGLTIKDGDYK.L
R4/RRR4-6/2	1147.204	1147.309	-91.743	0.487	1631.283	0.488	20	0.240	K.FAGVLTSAPAGR.R
R4/RRR4-6/2	1146.914	1147.309	-345.411	0.437	1366.746	0.447	19	0.202	K.FAGVLTSAPAGR.R
R4/RRR4-6/2	1417.057	1417.589	-1084.225	0.411	849.557	0.530	17	0.173	R.WVADELAVVAESK.E
R4/RRR4-21/2	1506.485	1505.698	-141.790	0.606	2580.483	0.488	22	0.392	K.ALELFLNAGNDLSK.S
R4/RRR4-17/2	1505.509	1505.698	-125.779	0.473	2181.288	0.367	21	0.281	K.ALELFLNAGNDLSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	1505.480	1505.698	-144.893	0.492	2029.323	0.418	20	0.272	K.ALELFLNAGNDLSK.S
R4/RRR4-16/2	1164.196	1164.336	-120.903	0.510	1684.056	0.493	17	0.247	R.SIGAAVIYNQK.K
R4/RRR4-16/2	1164.364	1164.336	24.331	0.520	1703.214	0.451	17	0.239	R.SIGAAVIYNQK.K
R4/RRR4-16/2	1164.118	1164.336	-187.907	0.485	1483.016	0.434	16	0.209	R.SIGAAVIYNQK.K
R4/RRR4-16/2	1902.213	1903.081	-984.893	0.355	648.558	0.501	25	0.161	K.DYTDPPPAPLFDVGELR.L
R4/RRR4-16/2	1902.553	1903.081	-805.234	0.406	474.247	0.444	22	0.153	K.DYTDPPPAPLFDVGELR.L
R4/RRR4-16/2	1901.654	1903.081	-1279.804	0.186	579.469	0.337	23	0.137	K.DYTDPPPAPLFDVGELR.L
R4/RRR4-11/2	1828.957	1829.052	-51.855	0.540	1554.394	0.532	22	0.239	K.VVYVGDGNNIVHSWLR.L
R4/RRR4-11/2	1352.006	1352.585	-1170.985	0.316	521.338	0.464	14	0.149	R.VLSGYNDIIMAR.V
R4/RRR4-11/2	1368.355	1368.584	-168.118	0.334	334.378	0.286	15	0.142	R.VLSGYNDIIM*AR.V
R4/RRR4-23/2	1300.778	1299.479	231.089	0.477	670.738	0.512	17	0.167	K.FATLAM*GTTDVR.V
R4/RRR4-23/2	901.221	902.031	-2014.153	0.394	1301.633	0.286	14	0.167	R.SAIADVVAR.E
R4/RRR4-23/2	901.746	902.031	-316.172	0.362	1009.977	0.208	13	0.142	R.SAIADVVAR.E
R4/RRR4-11/2	1368.322	1368.518	-143.490	0.454	1771.350	0.409	20	0.236	K.YIGLSEASASTIR.R
R4/RRR4-11/2	1445.333	1445.688	-246.817	0.389	1285.385	0.551	18	0.209	R.ELGIGIVAYSPLGR.G
R4/RRR4-11/2	1367.230	1368.518	-1677.967	0.324	1147.702	0.242	19	0.151	K.YIGLSEASASTIR.R
R4/RRR4-11/2	1444.284	1445.688	-1669.829	0.260	641.016	0.467	13	0.145	R.ELGIGIVAYSPLGR.G
R4/RRR4-11/2	1444.535	1445.688	-1494.851	0.308	412.422	0.427	11	0.138	R.ELGIGIVAYSPLGR.G
R4/RRR4-24/2	1229.308	1229.385	-62.771	0.430	1415.846	0.397	17	0.197	R.ISAM*IYEETR.G
R4/RRR4-24/2	1326.106	1326.527	-318.218	0.481	1149.291	0.486	17	0.191	R.DNIQGITKPAIR.R
R4/RRR4-25/2	1327.277	1326.527	-189.161	0.481	1044.563	0.493	17	0.185	R.DNIQGITKPAIR.R
R4/RRR4-24/2	1326.150	1326.527	-285.525	0.490	1174.234	0.423	18	0.182	R.DNIQGITKPAIR.R
R4/RRR4-24/2	1326.172	1326.527	-268.902	0.492	1023.399	0.464	17	0.179	R.DNIQGITKPAIR.R
R4/RRR4-25/2	1326.212	1326.527	-238.520	0.460	977.444	0.479	17	0.178	R.DNIQGITKPAIR.R
R4/RRR4-25/2	1326.177	1326.527	-265.023	0.463	1020.230	0.424	17	0.172	R.DNIQGITKPAIR.R
R4/RRR4-25/2	1327.419	1326.527	-81.409	0.367	1187.637	0.335	17	0.167	R.DNIQGITKPAIR.R
R4/RRR4-21/2	1327.138	1326.527	-294.076	0.346	1005.216	0.317	16	0.155	R.DNIQGITKPAIR.R
R4/RRR4-23/2	1325.663	1326.527	-1410.189	0.400	594.711	0.265	14	0.139	R.DNIQGITKPAIR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1455.979	1456.625	-1133.530	0.493	1702.483	0.486	19	0.246	R.NDVFQYLASSLAK.L
R4/RRR4-12/2	1456.085	1456.625	-1060.377	0.505	1643.900	0.507	19	0.244	R.NDVFQYLASSLAK.L
R4/RRR4-12/2	1457.031	1456.625	279.774	0.552	1654.789	0.473	20	0.238	R.NDVFQYLASSLAK.L
R4/RRR4-12/2	1153.080	1153.267	-162.417	0.444	1018.479	0.354	16	0.162	K.YVVNDSTNIK.S
R4/RRR4-11/2	1817.512	1818.021	-832.469	0.497	1439.534	0.539	24	0.226	K.AAANNIGLDGFDVIDAIK.S
R4/RRR4-11/2	1817.515	1818.021	-830.716	0.515	1367.183	0.556	23	0.222	K.AAANNIGLDGFDVIDAIK.S
R4/RRR4-17/2	1818.654	1818.021	-202.211	0.560	1257.520	0.554	23	0.210	K.AAANNIGLDGFDVIDAIK.S
R4/RRR4-17/2	1817.339	1818.021	-928.351	0.533	1205.098	0.567	24	0.209	K.AAANNIGLDGFDVIDAIK.S
R4/RRR4-17/2	1817.435	1818.021	-875.283	0.478	1309.665	0.512	23	0.206	K.AAANNIGLDGFDVIDAIK.S
R4/RRR4-11/2	1818.541	1818.021	-264.770	0.550	1175.924	0.572	22	0.206	K.AAANNIGLDGFDVIDAIK.S
R4/RRR4-11/3	1091.032	1091.249	-199.329	0.494	1870.556	0.315	25	0.184	K.HNPGVGAALVR.L
R4/RRR4-21/2	1714.393	1712.906	284.830	0.420	431.661	0.499	16	0.155	K.EM*PPQDIDWFYVR.A
R4/RRR4-21/2	940.159	940.124	37.492	0.367	808.049	0.285	12	0.145	K.AYAAFLKR.Q
R4/RRR4-21/3	1866.359	1867.012	-888.165	0.508	1555.426	0.507	29	0.211	R.HDVESAIPYHAELTQR.G
R4/RRR4-20/2	1465.320	1464.604	-194.319	0.479	850.740	0.517	15	0.174	R.LSYLWADDPEVR.A
R4/RRR4-21/2	1464.133	1464.604	-322.672	0.373	910.946	0.433	16	0.164	R.LSYLWADDPEVR.A
R4/RRR4-21/2	1464.109	1464.604	-338.984	0.387	782.871	0.401	15	0.155	R.LSYLWADDPEVR.A
R4/RRR4-21/2	1463.978	1464.604	-1113.956	0.324	819.945	0.264	15	0.141	R.LSYLWADDPEVR.A
R4/RRR4-16/2	1050.009	1050.233	-214.042	0.528	1458.365	0.520	16	0.229	R.SLGAAIIYNK.D
R4/RRR4-17/2	1050.097	1050.233	-130.192	0.489	1290.873	0.482	16	0.204	R.SLGAAIIYNK.D
R4/RRR4-17/2	1049.914	1050.233	-304.788	0.508	1256.096	0.491	15	0.202	R.SLGAAIIYNK.D
R4/RRR4-16/2	1049.892	1050.233	-326.136	0.532	1202.383	0.500	16	0.201	R.SLGAAIIYNK.D
R4/RRR4-17/2	1049.672	1050.233	-1491.347	0.456	1117.599	0.492	16	0.191	R.SLGAAIIYNK.D
R4/RRR4-16/2	1049.757	1050.233	-454.941	0.521	1124.914	0.481	15	0.190	R.SLGAAIIYNK.D
R4/RRR4-3/3	1329.609	1329.398	158.549	0.377	1285.075	0.286	26	0.105	R.QPIGTAAQGAGDDK.D
R4/RRR4-3/3	1329.258	1329.398	-105.715	0.364	1001.089	0.265	25	0.086	R.QPIGTAAQGAGDDK.D
R4/RRR4-5/2	1416.884	1416.601	200.338	0.412	1430.762	0.507	18	0.217	K.AIDPGLVYDIDPK.D
R4/RRR4-5/2	1340.057	1340.421	-272.694	0.450	1437.590	0.463	20	0.211	R.TVTNVGGSEANYK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1185.092	1185.304	-179.623	0.489	1631.024	0.454	16	0.232	K.FGCTDFVNPK.D
R4/RRR4-10/2	1039.930	1040.238	-297.589	0.459	697.098	0.411	17	0.160	R.IIGVDLNPAK.F
R4/RRR4-2/2	1186.274	1185.304	-25.143	0.360	780.621	0.358	16	0.153	K.FGCTDFVNPK.D
R4/RRR4-10/2	1039.986	1040.238	-243.300	0.465	652.039	0.369	15	0.153	R.IIGVDLNPAK.F
R4/RRR4-9/2	1759.693	1760.067	-213.300	0.507	1455.703	0.483	24	0.218	R.ISQAITNVVIPTFDIK.L
R4/RRR4-9/2	1760.687	1760.067	-216.865	0.558	1245.430	0.553	22	0.211	R.ISQAITNVVIPTFDIK.L
R4/RRR4-9/2	1230.587	1231.381	-1461.932	0.328	812.382	0.405	16	0.154	R.SIVQELLGDTR.I
R4/RRR4-14/2	1304.025	1304.475	-346.328	0.447	1170.756	0.531	22	0.201	K.ANTIVLSGLSGSGK.T
R4/RRR4-14/2	1273.169	1273.380	-165.754	0.489	783.568	0.519	18	0.177	R.QAEVWVGQAER.W
R4/RRR4-14/2	1304.833	1304.475	274.874	0.331	762.349	0.532	17	0.164	K.ANTIVLSGLSGSGK.T
R4/RRR4-14/2	1273.006	1273.380	-294.174	0.398	652.418	0.453	16	0.159	R.QAEVWVGQAER.W
R4/RRR4-13/2	1580.466	1580.723	-163.351	0.488	1635.450	0.476	22	0.237	R.QSDVEAFFAAELPR.Y
R4/RRR4-13/2	1579.598	1580.723	-1349.207	0.364	1185.911	0.415	19	0.178	R.QSDVEAFFAAELPR.Y
R4/RRR4-13/2	885.945	886.074	-146.506	0.393	1081.841	0.387	14	0.170	R.GLVGSAILR.H
R4/RRR4-13/2	885.354	886.074	-1948.674	0.417	1025.290	0.398	14	0.169	R.GLVGSAILR.H
R4/RRR4-13/2	885.885	886.074	-214.238	0.395	1023.055	0.374	14	0.165	R.GLVGSAILR.H
R4/RRR4-13/2	1579.829	1580.723	-1202.613	0.365	1048.044	0.333	20	0.159	R.QSDVEAFFAAELPR.Y
R4/RRR4-13/2	1582.250	1580.723	-299.513	0.416	542.522	0.365	15	0.143	R.QSDVEAFFAAELPR.Y
R4/RRR4-6/2	1745.920	1745.013	-53.059	0.561	1662.573	0.527	25	0.250	R.SFGIGAANVAGPILESIK.K
R4/RRR4-6/2	1744.598	1745.013	-238.516	0.507	1190.249	0.497	22	0.192	R.SFGIGAANVAGPILESIK.K
R4/RRR4-6/2	1744.465	1745.013	-890.138	0.455	1141.604	0.460	22	0.181	R.SFGIGAANVAGPILESIK.K
R4/RRR4-6/3	1673.655	1673.851	-117.942	0.559	979.757	0.542	29	0.146	R.KYGLLGKEEAHDNAK.R
R4/RRR4-6/3	1673.757	1673.851	-56.488	0.524	958.775	0.526	30	0.139	R.KYGLLGKEEAHDNAK.R
R4/RRR4-11/2	1072.860	1072.283	-396.300	0.534	1410.763	0.389	17	0.196	K.ISQATLALVR.N
R4/RRR4-11/2	1273.064	1273.418	-278.581	0.417	1102.323	0.463	17	0.181	K.GLIDINQDSLGK.A
R4/RRR4-11/2	1072.989	1072.283	-275.640	0.513	1222.272	0.376	17	0.179	K.ISQATLALVR.N
R4/RRR4-11/2	1072.055	1072.283	-213.523	0.394	588.300	0.377	13	0.149	K.ISQATLALVR.N
R4/RRR4-6/2	1280.219	1280.538	-250.054	0.384	1280.784	0.579	20	0.217	R.GLPTLVLIGPDGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1516.154	1516.639	-320.726	0.321	1523.288	0.313	21	0.187	K.DNQTVQSVLGTPTR.D
R4/RRR4-6/2	1281.223	1280.538	-247.182	0.410	941.836	0.480	17	0.173	R.GLPTLVLIGPDGK.T
R4/RRR4-6/2	1516.039	1516.639	-1058.339	0.323	1240.497	0.325	20	0.167	K.DNQTVQSVLGTPTR.D
R4/RRR4-6/2	1279.601	1280.538	-1518.170	0.263	948.281	0.462	18	0.165	R.GLPTLVLIGPDGK.T
R4/RRR4-7/2	1280.029	1280.538	-1182.309	0.318	648.339	0.448	14	0.151	R.GLPTLVLIGPDGK.T
R4/RRR4-5/2	1280.522	1280.538	-13.062	0.328	621.363	0.401	13	0.146	R.GLPTLVLIGPDGK.T
R4/RRR4-7/2	1281.434	1280.538	-81.751	0.308	753.026	0.285	15	0.141	R.GLPTLVLIGPDGK.T
R4/RRR4-1/2	1280.589	1280.538	39.524	0.324	747.429	0.276	14	0.139	R.GLPTLVLIGPDGK.T
R4/RRR4-17/2	1181.796	1182.353	-1321.300	0.409	1303.131	0.492	17	0.204	K.FTGAFQALAQK.V
R4/RRR4-17/2	1181.972	1182.353	-323.668	0.472	1309.275	0.478	17	0.203	K.FTGAFQALAQK.V
R4/RRR4-17/2	1181.377	1182.353	-1678.287	0.375	1377.160	0.455	17	0.202	K.FTGAFQALAQK.V
R4/RRR4-17/2	1088.076	1088.260	-169.535	0.307	608.576	0.396	17	0.149	K.VGPGSPPM*TTK.D
R4/RRR4-17/2	1087.972	1088.260	-265.770	0.224	380.565	0.291	15	0.139	K.VGPGSPPM*TTK.D
R4/RRR4-12/2	1449.075	1449.588	-1047.003	0.491	1445.440	0.501	19	0.220	K.DGTTLLWDLTEGK.M
R4/RRR4-11/3	1771.543	1771.992	-253.832	0.516	1362.945	0.622	32	0.219	K.LDAGAIIHSLCFSPNR.Y
R4/RRR4-12/2	1449.234	1449.588	-244.463	0.472	1495.993	0.468	19	0.218	K.DGTTLLWDLTEGK.M
R4/RRR4-12/2	1449.198	1449.588	-269.476	0.489	1299.648	0.475	19	0.201	K.DGTTLLWDLTEGK.M
R4/RRR4-11/2	1449.338	1449.588	-172.977	0.512	1144.024	0.497	18	0.192	K.DGTTLLWDLTEGK.M
R4/RRR4-11/2	1449.289	1449.588	-206.775	0.462	1224.733	0.431	18	0.185	K.DGTTLLWDLTEGK.M
R4/RRR4-11/3	1772.416	1771.992	239.930	0.547	1093.160	0.630	29	0.185	K.LDAGAIIHSLCFSPNR.Y
R4/RRR4-12/3	1771.591	1771.992	-226.665	0.498	1086.403	0.627	29	0.182	K.LDAGAIIHSLCFSPNR.Y
R4/RRR4-11/3	1771.770	1771.992	-125.266	0.502	998.825	0.585	26	0.160	K.LDAGAIIHSLCFSPNR.Y
R4/RRR4-11/2	1448.692	1449.588	-1312.658	0.359	889.305	0.354	16	0.153	K.DGTTLLWDLTEGK.M
R4/RRR4-12/3	1771.738	1771.992	-143.512	0.473	814.046	0.571	25	0.139	K.LDAGAIIHSLCFSPNR.Y
R4/RRR4-12/3	1771.374	1771.992	-915.883	0.477	690.449	0.605	25	0.138	K.LDAGAIIHSLCFSPNR.Y
R4/RRR4-7/2	1690.063	1688.866	116.882	0.548	1766.940	0.498	21	0.257	R.STQGILNDLWNSLAR.Y
R4/RRR4-7/2	1167.431	1167.239	164.698	0.319	756.149	0.248	12	0.138	-.TNCIDCLDR.-
R4/RRR4-21/2	1334.170	1334.500	-247.743	0.445	1088.923	0.354	18	0.165	R.IEVTEPASFNVK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1334.120	1334.500	-285.104	0.414	982.715	0.359	17	0.159	R.IEVTEPASFNVK.E
R4/RRR4-20/2	945.882	945.100	-231.003	0.382	899.583	0.300	13	0.152	R.LAVDKWGR.I
R4/RRR4-20/2	944.214	945.100	-2003.225	0.327	663.522	0.356	12	0.149	R.LAVDKWGR.I
R4/RRR4-21/2	1333.488	1334.500	-1513.380	0.339	810.812	0.330	17	0.149	R.IEVTEPASFNVK.E
R4/RRR4-20/2	944.873	945.100	-241.357	0.272	829.681	0.227	13	0.140	R.LAVDKWGR.I
R4/RRR4-9/2	1422.015	1422.469	-320.261	0.533	955.324	0.570	18	0.194	K.YGTGYCDAQCAR.D
R4/RRR4-9/2	1421.956	1422.469	-1067.315	0.475	831.567	0.564	18	0.184	K.YGTGYCDAQCAR.D
R4/RRR4-9/3	1636.522	1636.793	-166.143	0.473	866.319	0.540	24	0.134	K.FVQKHEYGTNIGSR.M
R4/RRR4-9/3	1635.832	1636.793	-1202.053	0.420	627.955	0.381	23	0.093	K.FVQKHEYGTNIGSR.M
R4/RRR4-12/2	1425.928	1426.680	-1232.121	0.461	1677.285	0.410	19	0.224	K.ILQNLCGGPNIVK.L
R4/RRR4-12/2	1787.778	1788.978	-1234.079	0.435	1359.933	0.461	20	0.200	K.TPSLIFEYVNNTDFK.V
R4/RRR4-12/2	1426.092	1426.680	-1116.677	0.423	1177.415	0.331	18	0.164	K.ILQNLCGGPNIVK.L
R4/RRR4-19/2	1508.224	1508.789	-1040.686	0.395	769.146	0.502	18	0.164	R.HYAPNVPIVLVGTK.L
R4/RRR4-19/3	905.019	905.079	-66.827	0.503	736.430	0.398	17	0.105	R.LRPLSYR.G
R4/RRR4-19/3	905.140	905.079	66.793	0.450	590.180	0.388	16	0.101	R.LRPLSYR.G
R4/RRR4-17/3	905.244	905.079	182.629	0.418	770.222	0.388	18	0.100	R.LRPLSYR.G
R4/RRR4-19/3	905.148	905.079	76.633	0.485	593.008	0.343	16	0.093	-.LRPLSYR.-
R4/RRR4-4/3	1737.559	1737.897	-195.449	0.514	1869.370	0.507	30	0.266	R.SHKDLDKDAAPHFQK.A
R4/RRR4-4/3	1737.688	1737.897	-120.818	0.487	1466.526	0.517	28	0.197	R.SHKDLDKDAAPHFQK.A
R4/RRR4-5/2	1738.748	1737.897	-86.021	0.403	581.726	0.531	16	0.157	R.SHKDLDKDAAPHFQK.A
R4/RRR4-1/2	1353.978	1353.629	258.657	0.324	809.381	0.285	16	0.140	R.CVVPLAAAISPVR.S
R4/RRR4-6/2	1191.624	1191.362	220.947	0.417	1873.979	0.461	20	0.263	R.FAATLGELVGGR.V
R4/RRR4-6/2	1191.946	1191.362	-349.927	0.454	1951.262	0.400	19	0.258	R.FAATLGELVGGR.V
R4/RRR4-6/2	1191.952	1191.362	-345.097	0.365	1248.303	0.480	17	0.193	R.FAATLGELVGGR.V
R4/RRR4-6/2	1463.410	1463.621	-144.374	0.333	1376.374	0.361	19	0.179	R.ATGGADAAAALAAYLR.G
R4/RRR4-4/2	1308.258	1308.492	-179.371	0.457	865.156	0.507	16	0.175	R.NMSVIAHVDHGK.S
R4/RRR4-4/2	1308.138	1308.492	-271.673	0.465	596.747	0.512	17	0.167	R.NMSVIAHVDHGK.S
R4/RRR4-4/2	1309.005	1308.492	-373.632	0.495	635.468	0.493	17	0.166	R.NMSVIAHVDHGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1039.679	1040.285	-1548.783	0.434	577.749	0.494	12	0.163	R.IRPVLTVNK.M
R4/RRR4-1/2	1040.049	1040.285	-227.157	0.488	851.457	0.404	13	0.162	R.IRPVLTVNK.M
R4/RRR4-4/2	1041.109	1040.285	-168.831	0.456	888.057	0.391	13	0.162	R.IRPVLTVNK.M
R4/RRR4-3/2	1041.145	1040.285	-134.486	0.417	821.875	0.383	13	0.158	R.IRPVLTVNK.M
R4/RRR4-2/2	1040.065	1040.285	-212.321	0.439	725.491	0.417	12	0.158	R.IRPVLTVNK.M
R4/RRR4-1/2	1039.631	1040.285	-1595.256	0.519	530.481	0.437	12	0.157	R.IRPVLTVNK.M
R4/RRR4-4/2	1324.246	1324.492	-186.173	0.385	540.273	0.465	16	0.157	R.NM*SVIAHVDHGK.S
R4/RRR4-3/2	1041.082	1040.285	-194.943	0.481	728.333	0.381	12	0.154	R.IRPVLTVNK.M
R4/RRR4-2/2	1308.539	1308.492	35.686	0.350	308.318	0.449	13	0.149	R.NMSVIAHVDHGK.S
R4/RRR4-2/2	1041.290	1040.285	5.102	0.350	673.835	0.313	13	0.148	R.IRPVLTVNK.M
R4/RRR4-4/2	1324.318	1324.492	-131.338	0.291	378.193	0.285	15	0.143	R.NM*SVIAHVDHGK.S
R4/RRR4-22/2	1258.182	1258.472	-230.645	0.512	1329.614	0.405	16	0.192	K.FNLFM*QQVSK.S
R4/RRR4-22/2	1257.911	1258.472	-1244.518	0.417	1349.193	0.321	16	0.177	K.FNLFM*QQVSK.S
R4/RRR4-22/2	1331.097	1331.566	-353.042	0.357	939.284	0.326	16	0.150	K.SLGM*AVPHFDIK.T
R4/RRR4-19/2	1334.345	1334.500	-116.497	0.443	1223.064	0.391	18	0.179	R.IEVTDPASFQVK.E
R4/RRR4-19/2	1334.020	1334.500	-360.568	0.351	608.211	0.334	13	0.140	-.IEVTDPASFQVK.-
R4/RRR4-19/2	1334.040	1334.500	-345.419	0.259	543.606	0.228	12	0.133	-.IEVTDPASFQVK.-
R4/RRR4-13/2	1544.737	1545.639	-1234.847	0.489	1224.177	0.414	20	0.184	K.FNDLSTNHNNQLK.T
R4/RRR4-13/2	1546.313	1545.639	-211.379	0.587	1057.701	0.452	20	0.180	K.FNDLSTNHNNQLK.T
R4/RRR4-13/2	1545.353	1545.639	-185.285	0.510	1032.516	0.412	19	0.170	K.FNDLSTNHNNQLK.T
R4/RRR4-13/3	1673.700	1673.812	-67.024	0.490	948.291	0.464	26	0.122	K.KFNDLSTNHNNQLK.T
R4/RRR4-13/3	1673.320	1673.812	-294.561	0.477	1034.500	0.412	28	0.116	K.KFNDLSTNHNNQLK.T
R4/RRR4-13/3	1673.710	1673.812	-60.660	0.465	837.382	0.442	24	0.111	K.KFNDLSTNHNNQLK.T
R4/RRR4-17/2	1333.278	1334.546	-1706.556	0.216	822.402	0.182	14	0.128	R.GAVGALLVYDISR.R
R4/RRR4-7/2	1698.554	1697.953	-235.611	0.540	2260.301	0.597	24	0.369	R.VIEVGEVDPAAYPLPK.T
R4/RRR4-7/2	1697.454	1697.953	-294.693	0.455	2134.718	0.547	23	0.327	R.VIEVGEVDPAAYPLPK.T
R4/RRR4-10/2	1223.923	1224.262	-277.761	0.493	1706.095	0.347	18	0.214	R.GDSVDQFSNVR.H
R4/RRR4-9/2	1224.061	1224.262	-165.202	0.496	1633.827	0.347	18	0.207	R.GDSVDQFSNVR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1224.145	1224.262	-95.678	0.485	1489.768	0.369	17	0.197	R.GDSVDQFSNVR.H
R4/RRR4-10/2	1224.177	1224.262	-70.072	0.442	1426.158	0.279	17	0.174	R.GDSVDQFSNVR.H
R4/RRR4-10/2	971.959	972.209	-258.187	0.416	428.288	0.476	14	0.161	K.GLPILGVFR.S
R4/RRR4-9/2	971.926	972.209	-291.579	0.435	444.946	0.447	14	0.160	K.GLPILGVFR.S
R4/RRR4-10/2	971.876	972.209	-343.245	0.394	491.034	0.450	14	0.159	K.GLPILGVFR.S
R4/RRR4-9/2	972.096	972.209	-116.204	0.376	366.610	0.423	13	0.155	K.GLPILGVFR.S
R4/RRR4-9/2	971.442	972.209	-1824.446	0.369	357.950	0.347	13	0.151	K.GLPILGVFR.S
R4/RRR4-10/2	972.031	972.209	-183.222	0.405	494.819	0.334	14	0.151	K.GLPILGVFR.S
R4/RRR4-19/2	1719.189	1719.902	-999.258	0.485	1191.944	0.517	18	0.195	R.TGGTITM*SNFFNAWR.N
R4/RRR4-19/2	1200.109	1199.342	-195.433	0.393	759.578	0.475	13	0.166	K.TFNQYWAIR.T
R4/RRR4-19/2	1199.441	1199.342	82.723	0.489	755.408	0.341	13	0.151	K.TFNQYWAIR.T
R4/RRR4-19/2	1198.800	1199.342	-1290.098	0.456	730.362	0.333	13	0.150	K.TFNQYWAIR.T
R4/RRR4-19/2	1199.062	1199.342	-234.610	0.418	689.382	0.344	12	0.149	K.TFNQYWAIR.T
R4/RRR4-19/2	1199.158	1199.342	-154.441	0.432	700.665	0.277	13	0.144	K.TFNQYWAIR.T
R4/RRR4-10/2	1615.300	1615.641	-211.674	0.475	2483.451	0.471	26	0.370	R.LDFSSGQSTGTASNSR.L
R4/RRR4-4/2	1365.274	1364.569	-216.899	0.551	1777.345	0.458	18	0.248	R.NLGFVSCIANIR.G
R4/RRR4-4/2	1364.289	1364.569	-205.389	0.440	1639.090	0.387	18	0.215	R.NLGFVSCIANIR.G
R4/RRR4-4/2	1364.206	1364.569	-266.700	0.390	851.020	0.441	16	0.163	R.NLGFVSCIANIR.G
R4/RRR4-4/2	951.744	952.091	-366.136	0.431	971.064	0.336	13	0.159	K.FSAIAWTR.D
R4/RRR4-4/2	952.402	952.091	327.417	0.476	1033.935	0.307	13	0.157	K.FSAIAWTR.D
R4/RRR4-1/2	1364.158	1364.569	-302.431	0.399	495.890	0.346	15	0.146	R.NLGFVSCIANIR.G
R4/RRR4-18/1	1115.586	1116.290	-1531.463	0.391	598.284	0.627	17	0.748	R.VVGAGGAVVACR.G
R4/RRR4-26/2	1116.041	1116.290	-223.977	0.523	2747.056	0.610	21	0.474	R.VVGAGGAVVACR.G
R4/RRR4-18/2	1116.025	1116.290	-238.352	0.524	2603.276	0.652	21	0.458	R.VVGAGGAVVACR.G
R4/RRR4-19/2	1115.976	1116.290	-281.809	0.518	2609.279	0.626	21	0.449	R.VVGAGGAVVACR.G
R4/RRR4-17/2	1115.793	1116.290	-446.231	0.519	2398.682	0.626	21	0.404	R.VVGAGGAVVACR.G
R4/RRR4-20/2	1116.122	1116.290	-150.463	0.564	2233.864	0.673	21	0.389	R.VVGAGGAVVACR.G
R4/RRR4-27/2	1115.318	1116.290	-1772.859	0.465	2389.906	0.585	21	0.386	R.VVGAGGAVVACR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/2	1115.730	1116.290	-1401.843	0.444	2351.617	0.608	21	0.386	R.VVGAGGAVVACR.G
R4/RRR4-19/2	1116.069	1116.290	-198.301	0.557	2334.378	0.605	21	0.384	R.VVGAGGAVVACR.G
R4/RRR4-27/2	1115.963	1116.290	-293.771	0.553	2217.242	0.653	21	0.379	R.VVGAGGAVVACR.G
R4/RRR4-18/2	1115.958	1116.290	-298.600	0.546	2224.122	0.649	21	0.378	R.VVGAGGAVVACR.G
R4/RRR4-18/2	1116.023	1116.290	-239.559	0.570	2290.075	0.604	21	0.376	R.VVGAGGAVVACR.G
R4/RRR4-20/2	1116.268	1116.290	-19.152	0.535	2276.898	0.591	21	0.368	R.VVGAGGAVVACR.G
R4/RRR4-19/2	1115.955	1116.290	-301.124	0.523	2226.554	0.610	21	0.365	R.VVGAGGAVVACR.G
R4/RRR4-27/2	1115.870	1116.290	-377.294	0.536	2121.095	0.621	20	0.349	R.VVGAGGAVVACR.G
R4/RRR4-20/2	1115.857	1116.290	-389.149	0.477	2045.098	0.630	20	0.337	R.VVGAGGAVVACR.G
R4/RRR4-18/2	1673.391	1673.852	-275.883	0.480	1593.816	0.578	21	0.254	R.GLVSYDFPASFWAGR.V
R4/RRR4-19/2	1674.467	1673.852	-230.518	0.577	1533.522	0.591	22	0.251	R.GLVSYDFPASFWAGR.V
R4/RRR4-19/2	1673.318	1673.852	-919.205	0.521	1228.487	0.575	20	0.213	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1673.245	1673.852	-963.003	0.502	1283.341	0.551	20	0.213	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1673.287	1673.852	-937.808	0.512	1243.949	0.554	20	0.210	R.GLVSYDFPASFWAGR.V
R4/RRR4-19/2	1674.323	1673.852	282.660	0.490	1185.571	0.580	19	0.209	R.GLVSYDFPASFWAGR.V
R4/RRR4-19/2	1673.393	1673.852	-274.639	0.535	1225.040	0.537	20	0.205	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1673.204	1673.852	-987.906	0.510	1233.164	0.524	20	0.203	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1675.196	1673.852	206.502	0.572	1091.469	0.585	19	0.203	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1674.156	1673.852	182.204	0.493	1157.051	0.554	19	0.201	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1674.128	1673.852	165.459	0.494	1174.361	0.532	19	0.199	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1672.645	1673.852	-1323.343	0.334	1322.384	0.464	20	0.196	R.GLVSYDFPASFWAGR.V
R4/RRR4-18/2	1673.600	1673.852	-150.749	0.463	982.676	0.563	18	0.189	R.GLVSYDFPASFWAGR.V
R4/RRR4-28/2	1116.014	1116.290	-247.789	0.380	777.820	0.497	17	0.169	R.VVGAGGAVVACR.G
R4/RRR4-19/2	1672.485	1673.852	-1419.516	0.301	1036.864	0.402	19	0.165	R.GLVSYDFPASFWAGR.V
R4/RRR4-17/2	1674.842	1673.852	-5.454	0.453	535.494	0.504	17	0.160	R.GLVSYDFPASFWAGR.V
R4/RRR4-1/2	1115.952	1116.290	-303.758	0.286	676.679	0.453	17	0.157	R.VVGAGGAVVACR.G
R4/RRR4-13/2	1117.204	1116.290	-76.891	0.318	561.971	0.367	15	0.149	R.VVGAGGAVVACR.G
R4/RRR4-17/2	1674.651	1673.852	-119.875	0.372	350.453	0.385	15	0.144	-.GLVSYDFPASFWAGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1116.984	1116.290	-274.978	0.214	582.911	0.302	15	0.142	R.VVGAGGAVVACR.G
R4/RRR4-19/2	1116.782	1116.290	442.084	0.287	403.083	0.303	15	0.138	-.VVGAGGAVVACR.-
R4/RRR4-5/2	1116.069	1116.290	-198.191	0.084	250.698	0.370	12	0.131	-.VVGAGGAVVACR.-
R4/RRR4-24/2	1377.239	1377.546	-224.127	0.540	1807.673	0.520	22	0.271	K.GTDPVAIDLGSM*GK.G
R4/RRR4-24/2	1377.097	1377.546	-327.462	0.515	1661.428	0.542	21	0.256	K.GTDPVAIDLGSM*GK.G
R4/RRR4-28/2	1723.198	1723.866	-970.541	0.491	1068.758	0.570	20	0.195	R.IGAQTSVFTVESGSPSR.S
R4/RRR4-28/2	1723.318	1723.866	-900.990	0.476	1028.246	0.533	19	0.184	R.IGAQTSVFTVESGSPSR.S
R4/RRR4-13/2	1240.225	1240.476	-202.932	0.436	1369.838	0.524	18	0.217	R.DVAWAPVLGLAK.A
R4/RRR4-13/2	1239.942	1240.476	-1240.479	0.356	1041.313	0.494	17	0.180	R.DVAWAPVLGLAK.A
R4/RRR4-13/2	1462.965	1463.568	-1098.993	0.427	895.916	0.405	16	0.158	K.YGTILASCSYDGR.V
R4/RRR4-13/2	1239.914	1240.476	-1263.614	0.284	767.943	0.432	14	0.152	R.DVAWAPVLGLAK.A
R4/RRR4-19/2	945.013	945.100	-92.197	0.480	861.556	0.401	14	0.164	K.AGLQFPVGR.I
R4/RRR4-22/2	944.429	945.100	-1774.862	0.447	910.254	0.382	14	0.163	K.AGLQFPVGR.I
R4/RRR4-23/2	944.591	945.100	-1602.424	0.474	859.961	0.384	14	0.162	K.AGLQFPVGR.I
R4/RRR4-20/2	944.799	945.100	-319.778	0.465	874.101	0.374	14	0.161	K.AGLQFPVGR.I
R4/RRR4-18/2	944.960	945.100	-149.341	0.501	852.575	0.370	14	0.160	K.AGLQFPVGR.I
R4/RRR4-16/2	944.883	945.100	-230.858	0.488	870.245	0.364	14	0.159	K.AGLQFPVGR.I
R4/RRR4-21/2	944.954	945.100	-155.432	0.513	886.591	0.356	14	0.158	K.AGLQFPVGR.I
R4/RRR4-24/2	944.927	945.100	-184.331	0.449	852.360	0.351	14	0.158	K.AGLQFPVGR.I
R4/RRR4-23/2	944.491	945.100	-1708.502	0.430	912.855	0.336	14	0.157	K.AGLQFPVGR.I
R4/RRR4-24/2	944.455	945.100	-1747.070	0.440	856.153	0.348	14	0.157	K.AGLQFPVGR.I
R4/RRR4-22/2	944.547	945.100	-1648.903	0.448	863.674	0.341	14	0.157	K.AGLQFPVGR.I
R4/RRR4-20/2	944.839	945.100	-277.520	0.466	862.037	0.337	14	0.156	K.AGLQFPVGR.I
R4/RRR4-20/2	821.939	822.033	-115.163	0.446	631.896	0.359	12	0.155	R.HVLLAIR.N
R4/RRR4-21/2	944.859	945.100	-256.133	0.471	856.259	0.332	14	0.155	K.AGLQFPVGR.I
R4/RRR4-17/2	944.853	945.100	-262.225	0.426	864.549	0.324	14	0.155	K.AGLQFPVGR.I
R4/RRR4-21/2	822.109	822.033	91.873	0.382	599.202	0.376	12	0.155	R.HVLLAIR.N
R4/RRR4-20/2	944.498	945.100	-1701.490	0.412	918.334	0.306	14	0.154	K.AGLQFPVGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	944.488	945.100	-1711.749	0.411	864.158	0.319	14	0.154	K.AGLQFPVGR.I
R4/RRR4-25/2	944.496	945.100	-1703.178	0.470	694.279	0.362	13	0.154	K.AGLQFPVGR.I
R4/RRR4-22/2	944.926	945.100	-184.720	0.468	861.467	0.334	14	0.153	-.AGLQFPVGR.-
R4/RRR4-25/2	944.395	945.100	-1811.227	0.384	814.305	0.315	14	0.153	K.AGLQFPVGR.I
R4/RRR4-21/2	821.566	822.033	-570.795	0.382	484.483	0.366	11	0.153	R.HVLLAIR.N
R4/RRR4-18/2	944.884	945.100	-229.433	0.448	863.222	0.301	14	0.152	K.AGLQFPVGR.I
R4/RRR4-23/2	944.480	945.100	-1721.098	0.336	860.530	0.302	14	0.152	K.AGLQFPVGR.I
R4/RRR4-17/2	945.030	945.100	-74.705	0.443	854.816	0.299	14	0.151	K.AGLQFPVGR.I
R4/RRR4-23/2	944.674	945.100	-452.797	0.420	857.933	0.290	14	0.151	K.AGLQFPVGR.I
R4/RRR4-24/2	944.386	945.100	-1820.318	0.397	896.174	0.279	14	0.151	K.AGLQFPVGR.I
R4/RRR4-25/2	944.459	945.100	-1743.304	0.413	700.018	0.320	13	0.150	K.AGLQFPVGR.I
R4/RRR4-23/2	944.428	945.100	-1775.771	0.388	876.306	0.279	14	0.150	K.AGLQFPVGR.I
R4/RRR4-23/2	944.683	945.100	-443.202	0.410	770.428	0.300	13	0.149	K.AGLQFPVGR.I
R4/RRR4-18/2	944.370	945.100	-1837.333	0.392	635.812	0.299	12	0.147	K.AGLQFPVGR.I
R4/RRR4-26/2	944.388	945.100	-1818.500	0.370	583.329	0.278	12	0.146	K.AGLQFPVGR.I
R4/RRR4-21/2	822.012	822.033	-25.486	0.288	545.093	0.315	11	0.145	R.HVLLAIR.N
R4/RRR4-19/2	944.297	945.100	-1915.401	0.353	603.019	0.304	12	0.145	-.AGLQFPVGR.-
R4/RRR4-20/2	821.431	822.033	-1956.930	0.388	520.957	0.296	11	0.145	-.HVLLAIR.-
R4/RRR4-4/2	1785.294	1784.987	172.095	0.511	1202.488	0.576	21	0.211	K.QSGVELGNSILFFGCR.N
R4/RRR4-4/2	1785.751	1784.987	-132.643	0.488	831.604	0.542	20	0.176	K.QSGVELGNSILFFGCR.N
R4/RRR4-4/3	1714.316	1713.871	260.382	0.409	1588.724	0.372	26	0.167	R.ALHTIVQEQGSLDSSK.T
R4/RRR4-24/2	1563.313	1562.620	-196.706	0.424	587.934	0.510	19	0.161	R.QSGTTPGYSYSTANK.N
R4/RRR4-24/2	923.013	923.088	-81.793	0.398	851.860	0.345	13	0.156	R.ADLISYLK.E
R4/RRR4-24/2	922.498	923.088	-1729.061	0.376	883.893	0.331	13	0.154	R.ADLISYLK.E
R4/RRR4-24/2	1563.029	1562.620	262.759	0.425	503.693	0.447	18	0.152	R.QSGTTPGYSYSTANK.N
R4/RRR4-24/2	922.660	923.088	-465.325	0.355	948.131	0.273	13	0.150	R.ADLISYLK.E
R4/RRR4-12/2	1994.580	1995.261	-845.672	0.559	1233.642	0.597	25	0.219	R.VQIANFLCPGNYAVSGGVK.G
R4/RRR4-12/2	1204.104	1204.352	-207.190	0.498	1383.167	0.458	18	0.207	R.LESALAETEIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1204.241	1204.352	-92.684	0.534	1335.646	0.452	18	0.202	R.LESALAETEIK.T
R4/RRR4-12/2	1203.171	1204.352	-1818.337	0.315	1438.155	0.292	18	0.177	R.LESALAETEIK.T
R4/RRR4-13/2	1401.078	1400.644	310.609	0.389	1609.285	0.432	19	0.221	K.VVEIYEAAPAPLK.V
R4/RRR4-13/2	1632.906	1633.912	-1231.979	0.430	1566.838	0.443	22	0.218	K.VGPALLSGPVFATFEK.V
R4/RRR4-13/2	1634.195	1633.912	173.548	0.529	1363.674	0.501	21	0.209	K.VGPALLSGPVFATFEK.V
R4/RRR4-13/2	1633.424	1633.912	-299.799	0.490	1321.965	0.506	21	0.207	K.VGPALLSGPVFATFEK.V
R4/RRR4-14/2	1633.278	1633.912	-1003.735	0.485	1291.512	0.515	21	0.206	K.VGPALLSGPVFATFEK.V
R4/RRR4-14/2	1633.443	1633.912	-287.802	0.473	1272.579	0.494	21	0.200	K.VGPALLSGPVFATFEK.V
R4/RRR4-14/2	1634.554	1633.912	-219.817	0.518	1186.167	0.511	20	0.195	K.VGPALLSGPVFATFEK.V
R4/RRR4-14/2	1633.958	1633.912	28.504	0.477	1088.340	0.526	20	0.190	K.VGPALLSGPVFATFEK.V
R4/RRR4-13/2	1633.483	1633.912	-263.660	0.448	1090.757	0.470	19	0.180	K.VGPALLSGPVFATFEK.V
R4/RRR4-14/2	1400.364	1400.644	-201.147	0.321	1065.221	0.441	17	0.170	K.VVEIYEAAPAPLK.V
R4/RRR4-16/2	1634.446	1633.912	-285.978	0.305	832.092	0.461	18	0.160	K.VGPALLSGPVFATFEK.V
R4/RRR4-13/2	1633.457	1633.912	-279.330	0.434	770.927	0.464	16	0.158	K.VGPALLSGPVFATFEK.V
R4/RRR4-13/2	1633.082	1633.912	-1124.111	0.293	833.448	0.315	17	0.144	K.VGPALLSGPVFATFEK.V
R4/RRR4-9/2	1636.385	1636.825	-269.253	0.454	1252.542	0.497	19	0.200	K.ELILNYANQLCER.L
R4/RRR4-8/3	1559.070	1559.710	-1055.131	0.394	568.435	0.527	23	0.116	K.HYKGDHTYVPVSR.K
R4/RRR4-9/3	1559.889	1559.710	115.285	0.477	663.336	0.471	24	0.112	K.HYKGDHTYVPVSR.K
R4/RRR4-8/3	1559.783	1559.710	47.119	0.484	557.854	0.481	22	0.111	K.HYKGDHTYVPVSR.K
R4/RRR4-9/3	1559.333	1559.710	-242.247	0.418	765.428	0.448	26	0.110	K.HYKGDHTYVPVSR.K
R4/RRR4-9/3	1559.683	1559.710	-17.287	0.479	622.286	0.448	23	0.108	K.HYKGDHTYVPVSR.K
R4/RRR4-8/3	1559.415	1559.710	-189.826	0.410	714.462	0.399	24	0.102	K.HYKGDHTYVPVSR.K
R4/RRR4-14/3	1559.486	1559.710	-144.006	0.395	593.025	0.408	24	0.101	K.HYKGDHTYVPVSR.K
R4/RRR4-14/3	1559.245	1559.710	-299.033	0.455	553.801	0.394	23	0.101	K.HYKGDHTYVPVSR.K
R4/RRR4-14/3	1558.363	1559.710	-1510.515	0.435	559.101	0.349	23	0.097	K.HYKGDHTYVPVSR.K
R4/RRR4-25/2	1586.218	1586.752	-970.452	0.471	2381.474	0.524	23	0.364	K.AGGAYTM*NTASAVTVR.S
R4/RRR4-25/2	1570.379	1570.753	-238.936	0.548	2225.082	0.579	23	0.353	K.AGGAYTMNTASAVTVR.S
R4/RRR4-25/2	1570.268	1570.753	-309.517	0.518	2011.494	0.571	22	0.313	K.AGGAYTMNTASAVTVR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-25/2	1570.259	1570.753	-315.757	0.519	1998.348	0.560	22	0.307	K.AGGAYTMNTASAVTVR.S
R4/RRR4-25/2	1586.299	1586.752	-286.863	0.502	1981.329	0.568	22	0.307	K.AGGAYTM*NTASAVTVR.S
R4/RRR4-25/2	1586.218	1586.752	-970.143	0.533	1928.997	0.534	22	0.289	K.AGGAYTM*NTASAVTVR.S
R4/RRR4-26/2	1586.034	1586.752	-1086.436	0.454	1854.588	0.483	21	0.263	K.AGGAYTM*NTASAVTVR.S
R4/RRR4-24/2	1274.170	1274.446	-217.417	0.467	1288.358	0.394	17	0.185	K.LNNETVTIELK.N
R4/RRR4-24/2	1436.415	1436.642	-158.253	0.527	895.800	0.490	17	0.173	K.GKNPVTLDHLSVR.G
R4/RRR4-7/2	1588.488	1587.754	-167.690	0.544	1363.852	0.453	22	0.203	R.NCPEFAFSFLGAAR.L
R4/RRR4-7/2	1587.091	1587.754	-1050.920	0.466	1345.684	0.393	22	0.190	R.NCPEFAFSFLGAAR.L
R4/RRR4-7/2	1587.239	1587.754	-957.330	0.447	1287.324	0.405	22	0.187	R.NCPEFAFSFLGAAR.L
R4/RRR4-23/2	1940.378	1940.274	54.164	0.450	960.810	0.551	21	0.183	K.YLVPADLTVGQFVYVVR.K
R4/RRR4-24/3	1319.048	1319.531	-367.409	0.432	936.721	0.355	22	0.099	K.YSDRIPVIVEK.A
R4/RRR4-13/2	1425.371	1424.628	-180.782	0.422	1064.565	0.446	15	0.175	R.VLYDFQTPVWR.L
R4/RRR4-13/2	1280.831	1281.485	-1295.036	0.322	796.943	0.433	15	0.155	R.DVAWAPNLGLPK.S
R4/RRR4-13/2	1281.478	1281.485	-5.409	0.251	469.838	0.355	12	0.136	R.DVAWAPNLGLPK.S
R4/RRR4-24/2	1308.114	1308.470	-272.988	0.487	1476.810	0.481	17	0.219	K.GVAFVNNFNIGR.F
R4/RRR4-24/2	1307.351	1308.470	-1626.237	0.383	1092.705	0.441	17	0.176	K.GVAFVNNFNIGR.F
R4/RRR4-23/2	1069.127	1069.236	-102.680	0.425	362.651	0.506	14	0.160	K.HSSSILSIPK.V
R4/RRR4-23/2	1069.160	1069.236	-72.101	0.371	415.465	0.481	15	0.157	K.HSSSILSIPK.V
R4/RRR4-16/2	1492.248	1492.574	-219.365	0.427	1195.264	0.456	18	0.187	R.SWSNASLSYASYR.F
R4/RRR4-16/2	1492.436	1492.574	-92.589	0.506	1029.387	0.499	17	0.183	R.SWSNASLSYASYR.F
R4/RRR4-16/2	1491.426	1492.574	-1444.404	0.298	1002.528	0.392	17	0.161	R.SWSNASLSYASYR.F
R4/RRR4-16/2	1180.763	1181.239	-404.154	0.396	801.786	0.303	16	0.148	R.DGAYHYELGR.A
R4/RRR4-13/2	1493.651	1492.574	51.510	0.329	153.415	0.466	14	0.147	-.SWSNASLSYASYR.-
R4/RRR4-13/2	1492.562	1492.574	-8.171	0.309	368.504	0.305	14	0.139	-.SWSNASLSYASYR.-
R4/RRR4-11/2	1785.512	1786.045	-861.386	0.483	1208.005	0.511	23	0.200	K.SNYM*SAGQISVPIVFR.G
R4/RRR4-11/2	1785.211	1786.045	-1030.453	0.456	1165.048	0.492	23	0.192	K.SNYM*SAGQISVPIVFR.G
R4/RRR4-11/2	1191.925	1192.303	-318.500	0.463	936.610	0.540	18	0.188	K.VLAPYSAEDAR.G
R4/RRR4-11/2	1191.933	1192.303	-311.410	0.379	1103.467	0.406	19	0.175	K.VLAPYSAEDAR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1770.002	1770.046	-24.599	0.454	897.469	0.486	20	0.171	K.SNYMSAGQISVPIVFR.G
R4/RRR4-11/2	1769.902	1770.046	-81.256	0.449	783.567	0.497	18	0.165	K.SNYMSAGQISVPIVFR.G
R4/RRR4-11/2	1191.459	1192.303	-1552.486	0.327	1035.596	0.362	19	0.163	K.VLAPYSAEDAR.G
R4/RRR4-10/2	1192.013	1192.303	-244.625	0.363	977.816	0.359	18	0.161	K.VLAPYSAEDAR.G
R4/RRR4-19/2	1260.135	1260.376	-191.759	0.488	1408.337	0.465	18	0.209	R.LGGGQQEVCGVR.E
R4/RRR4-18/2	1917.468	1918.182	-896.219	0.340	761.470	0.405	17	0.146	R.AENIWLATEGVYLPVNK.S
R4/RRR4-20/2	1116.942	1117.275	-298.885	0.393	866.197	0.416	16	0.164	K.LEVSDVVVEK.A
R4/RRR4-20/2	927.002	927.080	-83.884	0.494	648.581	0.353	12	0.152	R.HLDTIISK.T
R4/RRR4-20/2	1116.323	1117.275	-1753.825	0.342	915.946	0.302	16	0.151	K.LEVSDVVVEK.A
R4/RRR4-20/2	927.102	927.080	24.153	0.526	715.083	0.338	12	0.151	R.HLDTIISK.T
R4/RRR4-20/2	926.611	927.080	-507.937	0.487	581.102	0.317	11	0.146	R.HLDTIISK.T
R4/RRR4-20/2	1116.476	1117.275	-1615.408	0.315	688.558	0.250	15	0.141	K.LEVSDVVVEK.A
R4/RRR4-20/3	1699.156	1698.904	148.602	0.478	1893.558	0.419	29	0.233	R.ILVDHSIVEGFAQGGR.T
R4/RRR4-20/3	1699.322	1698.904	246.720	0.432	1515.222	0.438	28	0.179	-.ILVDHSIVEGFAQGGR.-
R4/RRR4-9/2	1954.036	1955.204	-1112.787	0.396	656.660	0.381	18	0.143	K.TGSNLLQWPVVEVENLR.M
R4/RRR4-19/2	1465.643	1465.764	-83.255	0.394	810.798	0.493	18	0.165	K.HYAPGVPIILVGTK.L
R4/RRR4-2/2	1875.759	1875.067	-164.789	0.595	2166.809	0.608	22	0.352	K.ILLLDEATSALDVESER.I
R4/RRR4-1/2	1874.553	1875.067	-810.208	0.493	1217.023	0.516	21	0.198	K.ILLLDEATSALDVESER.I
R4/RRR4-1/2	1875.170	1875.067	55.003	0.517	1084.681	0.554	20	0.194	K.ILLLDEATSALDVESER.I
R4/RRR4-9/2	1786.568	1786.063	-278.143	0.488	1411.382	0.500	23	0.216	R.DIQAWETIPLGPFLGK.S
R4/RRR4-9/2	1786.460	1786.063	222.768	0.450	1041.966	0.534	21	0.188	R.DIQAWETIPLGPFLGK.S
R4/RRR4-9/2	1785.472	1786.063	-894.175	0.324	724.218	0.481	18	0.156	R.DIQAWETIPLGPFLGK.S
R4/RRR4-10/2	1114.053	1113.289	-212.507	0.434	752.597	0.292	14	0.138	-.ILSADEPVLR.-
R4/RRR4-12/2	1935.665	1936.189	-789.815	0.487	1469.827	0.507	24	0.221	R.VCGLAAVGSFADLIVADEK.Q
R4/RRR4-12/2	1220.220	1219.369	-122.275	0.493	1058.375	0.498	17	0.186	R.GVDVLYDPVGGK.L
R4/RRR4-16/2	1085.009	1085.279	-249.792	0.421	912.583	0.496	18	0.177	K.TPIKDALAAGK.E
R4/RRR4-16/2	1084.318	1085.279	-1814.173	0.342	1008.610	0.430	18	0.169	K.TPIKDALAAGK.E
R4/RRR4-16/2	1057.424	1058.254	-1735.842	0.369	844.403	0.443	15	0.162	K.LSGIVGVPTSK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1058.060	1058.254	-183.021	0.435	790.618	0.423	15	0.160	K.LSGIVGVPTSK.R
R4/RRR4-16/2	1057.640	1058.254	-1530.006	0.409	749.610	0.425	14	0.157	K.LSGIVGVPTSK.R
R4/RRR4-26/2	1353.549	1354.536	-1472.225	0.394	1112.953	0.445	17	0.179	K.VVGNFSALDYLR.L
R4/RRR4-26/2	1499.168	1499.673	-1006.894	0.481	842.973	0.493	19	0.174	R.LM*GFFPNDSEVAR.Y
R4/RRR4-25/2	1353.472	1354.536	-1529.390	0.324	983.741	0.475	16	0.172	K.VVGNFSALDYLR.L
R4/RRR4-26/2	1498.679	1499.673	-1334.825	0.411	966.321	0.440	20	0.172	R.LM*GFFPNDSEVAR.Y
R4/RRR4-25/2	1499.165	1499.673	-1009.102	0.463	856.566	0.473	19	0.171	R.LM*GFFPNDSEVAR.Y
R4/RRR4-25/2	1499.250	1499.673	-283.204	0.443	746.485	0.502	18	0.169	R.LM*GFFPNDSEVAR.Y
R4/RRR4-25/2	1354.323	1354.536	-157.539	0.447	807.601	0.480	15	0.167	K.VVGNFSALDYLR.L
R4/RRR4-25/2	1498.599	1499.673	-1388.247	0.340	852.383	0.433	19	0.162	R.LM*GFFPNDSEVAR.Y
R4/RRR4-26/2	1498.462	1499.673	-1480.378	0.335	749.223	0.430	18	0.157	R.LM*GFFPNDSEVAR.Y
R4/RRR4-26/2	1353.893	1354.536	-1216.830	0.404	383.826	0.519	12	0.154	K.VVGNFSALDYLR.L
R4/RRR4-25/2	1354.029	1354.536	-1116.157	0.328	784.933	0.370	15	0.151	K.VVGNFSALDYLR.L
R4/RRR4-26/2	1353.950	1354.536	-1174.911	0.310	396.661	0.463	12	0.147	K.VVGNFSALDYLR.L
R4/RRR4-26/2	1353.590	1354.536	-1441.970	0.283	515.481	0.383	13	0.144	K.VVGNFSALDYLR.L
R4/RRR4-14/2	1588.398	1588.791	-248.636	0.487	1572.770	0.413	20	0.214	R.DNVQAYWPNVIIR.Y
R4/RRR4-14/2	1808.262	1808.027	129.961	0.520	936.196	0.576	23	0.193	R.EIPLNYATFQPGTTVR.D
R4/RRR4-14/2	1588.416	1588.791	-237.071	0.491	1313.532	0.413	19	0.190	R.DNVQAYWPNVIIR.Y
R4/RRR4-13/2	1589.091	1588.791	188.952	0.490	1281.737	0.409	19	0.186	R.DNVQAYWPNVIIR.Y
R4/RRR4-14/2	1808.061	1808.027	18.784	0.508	839.817	0.564	21	0.183	R.EIPLNYATFQPGTTVR.D
R4/RRR4-13/2	1807.646	1808.027	-211.638	0.455	870.209	0.512	21	0.175	R.EIPLNYATFQPGTTVR.D
R4/RRR4-14/2	1808.609	1808.027	-232.240	0.526	785.849	0.508	21	0.171	R.EIPLNYATFQPGTTVR.D
R4/RRR4-14/2	1808.432	1808.027	224.598	0.518	574.068	0.559	19	0.168	R.EIPLNYATFQPGTTVR.D
R4/RRR4-14/2	1588.132	1588.791	-1047.686	0.396	1223.912	0.326	18	0.168	R.DNVQAYWPNVIIR.Y
R4/RRR4-14/2	1588.340	1588.791	-285.337	0.437	1189.254	0.337	18	0.167	R.DNVQAYWPNVIIR.Y
R4/RRR4-14/2	1588.265	1588.791	-963.881	0.386	1207.877	0.322	18	0.166	R.DNVQAYWPNVIIR.Y
R4/RRR4-13/2	1807.451	1808.027	-874.902	0.447	683.534	0.506	20	0.165	R.EIPLNYATFQPGTTVR.D
R4/RRR4-13/2	1807.441	1808.027	-880.529	0.436	736.223	0.473	20	0.163	R.EIPLNYATFQPGTTVR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1808.451	1808.027	235.022	0.499	567.843	0.509	19	0.162	R.EIPLNYATFQPGTTVR.D
R4/RRR4-13/2	1587.615	1588.791	-1374.784	0.345	965.992	0.365	16	0.157	R.DNVQAYWPNVIIR.Y
R4/RRR4-14/2	1808.295	1808.027	148.646	0.438	500.431	0.466	18	0.154	R.EIPLNYATFQPGTTVR.D
R4/RRR4-12/2	1588.588	1588.791	-128.142	0.414	911.126	0.329	16	0.151	R.DNVQAYWPNVIIR.Y
R4/RRR4-13/2	1588.406	1588.791	-243.393	0.406	926.722	0.323	16	0.151	R.DNVQAYWPNVIIR.Y
R4/RRR4-15/2	1589.717	1588.791	-46.951	0.281	578.607	0.125	14	0.132	-.DNVQAYWPNVIIR.-
R4/RRR4-20/2	1031.811	1032.200	-377.751	0.232	1027.542	0.191	14	0.139	-.M*GKQPAAGQK.-
R4/RRR4-5/2	877.984	877.966	20.414	0.320	872.099	0.108	13	0.130	-.AKAASQSSK.-
R4/RRR4-11/2	1206.999	1206.288	-240.472	0.479	991.174	0.549	20	0.193	R.VIGSGTNLDSSR.F
R4/RRR4-11/2	1206.071	1206.288	-180.863	0.425	1027.416	0.500	20	0.185	R.VIGSGTNLDSSR.F
R4/RRR4-11/2	1205.396	1206.288	-1574.251	0.374	793.027	0.482	18	0.166	R.VIGSGTNLDSSR.F
R4/RRR4-11/2	834.343	834.943	-1922.682	0.383	746.586	0.350	13	0.153	K.LSGFPASR.V
R4/RRR4-11/2	835.023	834.943	96.024	0.353	695.473	0.322	12	0.148	K.LSGFPASR.V
R4/RRR4-11/2	834.425	834.943	-1824.330	0.229	630.827	0.147	11	0.134	-.LSGFPASR.-
R4/RRR4-25/2	1485.967	1486.719	-1182.775	0.412	1161.244	0.407	20	0.177	R.GIM*QPVPVSDALSR.F
R4/RRR4-25/2	1486.188	1486.719	-1033.569	0.434	1101.454	0.426	19	0.175	R.GIM*QPVPVSDALSR.F
R4/RRR4-26/2	1487.370	1486.719	-235.256	0.443	1015.892	0.410	19	0.168	R.GIM*QPVPVSDALSR.F
R4/RRR4-25/2	1486.188	1486.719	-1033.074	0.387	980.804	0.372	18	0.159	R.GIM*QPVPVSDALSR.F
R4/RRR4-26/2	1486.075	1486.719	-1109.940	0.408	806.824	0.386	17	0.153	R.GIM*QPVPVSDALSR.F
R4/RRR4-25/2	1039.886	1039.148	-252.235	0.370	713.601	0.344	16	0.151	R.FAGGAPEM*SR.A
R4/RRR4-25/2	1038.805	1039.148	-330.523	0.311	448.453	0.269	13	0.142	R.FAGGAPEM*SR.A
R4/RRR4-26/2	1038.930	1039.148	-210.042	0.250	619.604	0.289	13	0.140	R.FAGGAPEM*SR.A
R4/RRR4-26/2	1039.162	1039.148	13.750	0.198	578.101	0.208	14	0.136	R.FAGGAPEM*SR.A
R4/RRR4-10/2	1733.991	1733.984	4.405	0.526	1443.866	0.499	24	0.220	R.LVFDEPESGVTVISLK.Q
R4/RRR4-10/2	1734.781	1733.984	-116.990	0.584	1370.897	0.530	24	0.220	R.LVFDEPESGVTVISLK.Q
R4/RRR4-10/2	1734.213	1733.984	132.757	0.534	1297.373	0.513	23	0.208	R.LVFDEPESGVTVISLK.Q
R4/RRR4-10/3	1722.857	1722.924	-39.315	0.372	740.213	0.527	28	0.117	K.AAAVEAGGAAAAPAPAAEKK.E
R4/RRR4-7/2	1450.221	1449.677	-315.299	0.520	1312.895	0.528	19	0.208	R.ASASAVAFGLGLLSGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	996.216	996.099	117.112	0.446	777.959	0.413	15	0.162	R.AFSVLSESR.A
R4/RRR4-7/2	996.002	996.099	-98.233	0.437	990.322	0.306	15	0.156	R.AFSVLSESR.A
R4/RRR4-7/2	1449.489	1449.677	-130.133	0.220	582.549	0.421	15	0.137	R.ASASAVAFGLGLLSGK.G
R4/RRR4-15/2	1145.031	1145.336	-267.494	0.334	669.100	0.449	14	0.154	K.LSHPDHVLVK.R
R4/RRR4-15/2	1137.855	1138.169	-277.036	0.394	818.554	0.268	15	0.145	R.AVSAEDNFER.A
R4/RRR4-15/2	1137.955	1138.169	-189.323	0.358	692.563	0.290	14	0.144	R.AVSAEDNFER.A
R4/RRR4-15/2	1137.321	1138.169	-1629.939	0.262	741.591	0.191	14	0.136	R.AVSAEDNFER.A
R4/RRR4-14/2	1298.288	1298.467	-138.876	0.457	1013.339	0.513	19	0.187	K.VVLNPDEVADVK.Y
R4/RRR4-13/2	1550.356	1550.695	-219.436	0.481	1271.118	0.316	19	0.168	R.ESELIQENYLGVR.N
R4/RRR4-13/2	1549.979	1550.695	-1110.207	0.375	1186.446	0.275	18	0.157	R.ESELIQENYLGVR.N
R4/RRR4-14/2	1297.683	1298.467	-1379.457	0.310	738.989	0.392	17	0.151	K.VVLNPDEVADVK.Y
R4/RRR4-14/2	1298.071	1298.467	-306.321	0.316	701.386	0.322	15	0.143	K.VVLNPDEVADVK.Y
R4/RRR4-14/2	1550.144	1550.695	-1003.777	0.355	937.839	0.256	16	0.142	R.ESELIQENYLGVR.N
R4/RRR4-23/3	1736.543	1736.732	-109.300	0.509	1394.253	0.509	30	0.183	K.DAKEEFDDAGHSESAK.E
R4/RRR4-23/3	1737.181	1736.732	259.386	0.470	1318.617	0.504	30	0.170	K.DAKEEFDDAGHSESAK.E
R4/RRR4-23/3	1900.735	1900.078	-181.311	0.482	1055.830	0.502	31	0.141	K.YLDDHPGGADVLLEVTGK.D
R4/RRR4-23/3	1736.542	1736.732	-109.511	0.453	893.727	0.468	26	0.120	K.DAKEEFDDAGHSESAK.E
R4/RRR4-24/3	1736.059	1736.732	-966.357	0.427	842.439	0.407	25	0.104	K.DAKEEFDDAGHSESAK.E
R4/RRR4-23/2	1745.480	1745.956	-273.748	0.392	1152.690	0.468	19	0.133	R.TGDSYLSAIGVYVRPF.-
R4/RRR4-23/3	1149.537	1149.287	218.800	0.411	1055.061	0.283	21	0.091	K.LPHTAGPWGGR.G
R4/RRR4-23/3	1149.716	1149.287	374.193	0.395	1036.221	0.283	21	0.090	K.LPHTAGPWGGR.G
R4/RRR4-9/2	1892.263	1891.158	55.865	0.502	557.470	0.602	21	0.175	R.FIQYNIFGNVFEVTAK.Y
R4/RRR4-9/2	1891.686	1891.158	-250.261	0.410	856.784	0.459	18	0.162	R.FIQYNIFGNVFEVTAK.Y
R4/RRR4-9/2	1892.281	1891.158	65.311	0.308	353.326	0.339	18	0.142	R.FIQYNIFGNVFEVTAK.Y
R4/RRR4-9/3	1210.646	1210.370	228.691	0.539	964.606	0.318	23	0.098	K.YIHSANVLHR.D
R4/RRR4-9/3	1210.161	1210.370	-172.928	0.520	774.660	0.332	21	0.094	K.YIHSANVLHR.D
R4/RRR4-19/2	1293.198	1292.420	-171.992	0.428	1387.940	0.429	19	0.199	K.AVDVTGPDGSFVK.G
R4/RRR4-19/2	1292.185	1292.420	-181.791	0.400	998.485	0.476	17	0.175	K.AVDVTGPDGSFVK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-19/2	1291.964	1292.420	-353.921	0.295	772.279	0.384	15	0.148	-.AVDVTGPDGSFVK.-
R4/RRR4-18/3	1495.568	1495.567	0.801	0.399	846.398	0.488	25	0.120	R.SCYNCGEAGHIAR.D
R4/RRR4-19/3	1495.286	1495.567	-188.346	0.415	602.002	0.489	23	0.110	R.SCYNCGEAGHIAR.D
R4/RRR4-19/3	1495.543	1495.567	-15.900	0.382	576.123	0.481	22	0.108	R.SCYNCGEAGHIAR.D
R4/RRR4-18/3	1495.384	1495.567	-122.751	0.439	685.445	0.450	24	0.107	R.SCYNCGEAGHIAR.D
R4/RRR4-18/3	1495.832	1495.567	178.091	0.350	647.779	0.471	24	0.107	R.SCYNCGEAGHIAR.D
R4/RRR4-19/3	1495.502	1495.567	-43.163	0.345	767.117	0.295	25	0.088	R.SCYNCGEAGHIAR.D
R4/RRR4-12/2	1409.176	1409.656	-341.946	0.410	1143.539	0.454	17	0.181	R.IALDPQLEALIGR.H
R4/RRR4-12/2	1409.261	1409.656	-281.023	0.387	938.488	0.415	17	0.162	R.IALDPQLEALIGR.H
R4/RRR4-18/2	947.715	948.058	-363.236	0.440	1051.495	0.470	15	0.183	R.SPAAEAVFR.N
R4/RRR4-18/2	947.332	948.058	-1827.065	0.319	806.586	0.351	15	0.152	R.SPAAEAVFR.N
R4/RRR4-18/2	947.544	948.058	-1602.728	0.249	812.315	0.259	14	0.141	R.SPAAEAVFR.N
R4/RRR4-18/3	1234.193	1233.359	-134.989	0.560	1211.390	0.386	23	0.123	R.HREPLPDSGPK.K
R4/RRR4-19/3	1233.671	1233.359	254.146	0.509	1007.317	0.413	21	0.113	-.HREPLPDSGPK.-
R4/RRR4-18/3	1233.778	1233.359	340.758	0.471	1052.971	0.346	22	0.104	R.HREPLPDSGPK.K
R4/RRR4-18/3	1233.556	1233.359	160.374	0.425	845.283	0.267	20	0.085	R.HREPLPDSGPK.K
R4/RRR4-1/2	1263.224	1263.425	-159.111	0.367	1137.785	0.463	18	0.182	K.SAEPAFSVLVSR.F
R4/RRR4-15/2	1114.531	1115.350	-1637.123	0.397	761.083	0.437	14	0.159	-.VAVSFTHIIK.-
R4/RRR4-15/2	1115.157	1115.350	-173.760	0.380	783.413	0.385	14	0.155	K.VAVSFTHIIK.S
R4/RRR4-2/2	1115.079	1115.350	-244.044	0.299	529.023	0.224	12	0.137	K.VAVSFTHIIK.S
R4/RRR4-8/2	1465.284	1465.678	-270.028	0.507	1638.493	0.435	21	0.228	K.FLGNSLEVYPLGR.T
R4/RRR4-8/2	1465.290	1465.678	-265.849	0.464	1429.495	0.472	20	0.213	K.FLGNSLEVYPLGR.T
R4/RRR4-8/2	1381.589	1381.686	-70.596	0.540	986.260	0.414	17	0.165	K.SGVKLELVPPLTK.V
R4/RRR4-8/2	1465.460	1465.678	-149.352	0.366	783.889	0.436	16	0.157	K.FLGNSLEVYPLGR.T
R4/RRR4-16/2	1618.106	1617.659	277.196	0.535	1442.576	0.452	20	0.208	K.NSWGADWGDNGYFK.M
R4/RRR4-16/2	1617.347	1617.659	-193.389	0.469	1171.709	0.411	19	0.177	K.NSWGADWGDNGYFK.M
R4/RRR4-15/2	1617.090	1617.659	-972.972	0.440	744.364	0.438	16	0.155	-.NSWGADWGDNGYFK.-
R4/RRR4-16/2	1616.328	1617.659	-1446.489	0.275	695.695	0.306	17	0.141	K.NSWGADWGDNGYFK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/3	1401.503	1401.549	-33.435	0.514	1118.861	0.383	26	0.116	K.DWREDGIVSPVK.D
R4/RRR4-16/3	1401.802	1401.549	180.517	0.533	1165.201	0.362	27	0.114	K.DWREDGIVSPVK.D
R4/RRR4-15/3	1401.368	1401.549	-129.894	0.486	972.489	0.336	24	0.099	K.DWREDGIVSPVK.D
R4/RRR4-15/3	1401.233	1401.549	-226.764	0.429	1008.797	0.320	24	0.097	K.DWREDGIVSPVK.D
R4/RRR4-15/3	1401.850	1401.549	215.228	0.464	1088.884	0.290	26	0.095	K.DWREDGIVSPVK.D
R4/RRR4-16/3	1401.080	1401.549	-335.717	0.456	866.275	0.296	24	0.091	K.DWREDGIVSPVK.D
R4/RRR4-18/2	973.962	974.094	-135.592	0.366	1534.215	0.316	19	0.191	R.LSADAGAGALK.L
R4/RRR4-17/3	1256.560	1256.417	113.638	0.423	749.679	0.483	24	0.113	R.M*LGGGGVDGAIHR.A
R4/RRR4-17/3	1256.427	1256.417	7.675	0.404	917.376	0.340	25	0.096	R.M*LGGGGVDGAIHR.A
R4/RRR4-17/3	1256.290	1256.417	-101.965	0.304	456.246	0.335	19	0.083	-.M*LGGGGVDGAIHR.-
R4/RRR4-7/2	1431.041	1431.617	-1104.430	0.384	1013.987	0.401	16	0.164	R.GYISPYFITNQK.N
R4/RRR4-4/2	1463.955	1464.649	-1160.558	0.433	1352.801	0.606	20	0.231	R.LPPISADGDVPNLR.A
R4/RRR4-4/2	1119.114	1119.295	-162.205	0.316	1401.290	0.179	15	0.157	R.VFVQEVLER.E
R4/RRR4-4/2	1118.938	1119.295	-320.126	0.319	1056.604	0.149	15	0.140	-.VFVQEVLER.-
R4/RRR4-5/2	1788.373	1787.993	213.219	0.530	1422.056	0.458	23	0.206	K.LSVDNLDEVILVGGSTR.I
R4/RRR4-5/2	1787.243	1787.993	-982.073	0.403	950.672	0.430	20	0.163	K.LSVDNLDEVILVGGSTR.I
R4/RRR4-5/2	1012.526	1013.213	-1671.396	0.411	547.012	0.422	15	0.158	R.IPSVQELVK.K
R4/RRR4-5/2	1012.711	1013.213	-1487.322	0.359	533.314	0.424	15	0.155	R.IPSVQELVK.K
R4/RRR4-5/2	1013.010	1013.213	-201.131	0.374	543.711	0.391	15	0.154	R.IPSVQELVK.K
R4/RRR4-5/2	1787.100	1787.993	-1062.172	0.402	810.283	0.388	18	0.150	K.LSVDNLDEVILVGGSTR.I
R4/RRR4-9/2	1471.384	1471.768	-261.502	0.515	2321.071	0.497	21	0.345	K.TNMVMVFGEITTK.A
R4/RRR4-9/2	1470.445	1471.768	-1584.333	0.451	2343.145	0.467	21	0.339	K.TNMVMVFGEITTK.A
R4/RRR4-9/2	1503.173	1503.767	-1063.570	0.540	2286.455	0.484	21	0.334	K.TNM*VM*VFGEITTK.A
R4/RRR4-9/2	1471.161	1471.768	-1095.367	0.451	1967.658	0.437	20	0.269	K.TNMVMVFGEITTK.A
R4/RRR4-9/2	1503.072	1503.767	-1130.844	0.480	1881.783	0.396	20	0.246	K.TNM*VM*VFGEITTK.A
R4/RRR4-10/2	1472.776	1471.768	5.519	0.473	1159.593	0.433	18	0.181	K.TNMVMVFGEITTK.A
R4/RRR4-9/2	1486.541	1487.767	-1501.858	0.367	784.742	0.321	17	0.147	-.TNMVM*VFGEITTK.-
R4/RRR4-9/2	1486.385	1487.767	-1607.864	0.305	707.786	0.373	14	0.146	K.TNMVM*VFGEITTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/3	1703.000	1702.890	65.300	0.422	1716.748	0.368	30	0.182	R.RKFDLPEGGPITDEK.M
R4/RRR4-8/2	1163.969	1163.307	-290.701	0.382	965.827	0.377	14	0.162	R.SLFYNISYR.H
R4/RRR4-8/2	1163.376	1163.307	59.398	0.331	969.288	0.311	14	0.153	R.SLFYNISYR.H
R4/RRR4-17/2	916.042	916.099	-62.032	0.453	942.246	0.392	13	0.165	K.AADVLLWK.D
R4/RRR4-17/2	981.798	982.112	-321.195	0.373	645.597	0.387	13	0.150	K.SPPDIPEVK.I
R4/RRR4-20/2	1392.232	1393.574	-1687.233	0.342	1304.892	0.275	19	0.164	K.VNGATVNVGIHPSK.V
R4/RRR4-20/2	1393.041	1393.574	-1103.356	0.369	917.366	0.354	17	0.153	K.VNGATVNVGIHPSK.V
R4/RRR4-20/2	1392.294	1393.574	-1642.573	0.313	1330.112	0.187	19	0.153	K.VNGATVNVGIHPSK.V
R4/RRR4-20/2	959.903	960.024	-126.289	0.422	1008.463	0.276	12	0.151	K.DDEVQVVR.G
R4/RRR4-20/2	959.339	960.024	-1761.124	0.332	861.053	0.295	12	0.147	K.DDEVQVVR.G
R4/RRR4-21/2	1392.590	1393.574	-1428.490	0.272	229.605	0.267	14	0.141	K.VNGATVNVGIHPSK.V
R4/RRR4-10/2	1086.109	1086.224	-105.809	0.500	1466.424	0.497	18	0.224	K.EAAIQAINAGK.N
R4/RRR4-10/2	1086.008	1086.224	-199.055	0.419	1405.529	0.423	17	0.200	K.EAAIQAINAGK.N
R4/RRR4-10/2	1085.770	1086.224	-419.554	0.377	1238.396	0.443	17	0.188	K.EAAIQAINAGK.N
R4/RRR4-10/2	1476.113	1476.616	-1021.438	0.387	626.833	0.453	19	0.156	R.GYGVPELNSAIAER.F
R4/RRR4-10/2	1476.322	1476.616	-200.086	0.407	900.483	0.346	22	0.156	R.GYGVPELNSAIAER.F
R4/RRR4-6/2	1421.212	1421.581	-260.051	0.485	919.487	0.506	18	0.177	R.IVTNVGQDNAVYK.A
R4/RRR4-6/2	1824.063	1823.127	-34.878	0.465	677.977	0.538	17	0.164	K.GSLVDLNLPSITIPNLR.M
R4/RRR4-5/2	1822.399	1823.127	-951.034	0.413	800.147	0.477	19	0.162	K.GSLVDLNLPSITIPNLR.M
R4/RRR4-5/2	1822.247	1823.127	-1034.698	0.413	508.624	0.485	15	0.148	-.GSLVDLNLPSITIPNLR.-
R4/RRR4-5/2	1822.513	1823.127	-888.094	0.450	455.303	0.473	15	0.146	-.GSLVDLNLPSITIPNLR.-
R4/RRR4-1/2	1822.433	1823.127	-932.273	0.377	477.535	0.419	15	0.143	K.GSLVDLNLPSITIPNLR.M
R4/RRR4-13/2	1613.186	1613.794	-999.842	0.427	1242.639	0.418	21	0.185	K.ILNENDLITPDLSR.V
R4/RRR4-13/2	1613.339	1613.794	-283.192	0.468	977.755	0.391	20	0.164	K.ILNENDLITPDLSR.V
R4/RRR4-13/2	1691.601	1690.816	-127.287	0.450	631.735	0.452	13	0.149	R.DGYDYFFQMFNSR.L
R4/RRR4-6/2	1360.140	1360.535	-291.892	0.511	1680.290	0.440	19	0.233	R.NLSQQCLNALAK.A
R4/RRR4-6/2	1360.161	1360.535	-276.315	0.493	1633.793	0.440	19	0.228	R.NLSQQCLNALAK.A
R4/RRR4-6/2	1360.114	1360.535	-310.802	0.486	1625.151	0.409	19	0.219	R.NLSQQCLNALAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1360.214	1360.535	-237.058	0.458	1615.789	0.377	19	0.211	R.NLSQQCLNALAK.A
R4/RRR4-5/2	1361.496	1360.535	-29.192	0.395	919.270	0.393	17	0.162	R.NLSQQCLNALAK.A
R4/RRR4-5/2	1359.985	1360.535	-1143.409	0.382	1011.234	0.291	17	0.152	R.NLSQQCLNALAK.A
R4/RRR4-20/2	1076.937	1077.215	-259.623	0.432	719.900	0.425	17	0.162	R.SALPGALEYR.H
R4/RRR4-20/2	1077.028	1077.215	-174.568	0.337	508.391	0.414	14	0.147	-.SALPGALEYR.-
R4/RRR4-20/3	1791.662	1791.978	-176.802	0.466	1192.967	0.473	25	0.147	K.KPWEITGPCASPEYR.S
R4/RRR4-20/3	1791.766	1791.978	-118.675	0.456	1011.430	0.497	24	0.136	K.KPWEITGPCASPEYR.S
R4/RRR4-20/3	1792.323	1791.978	193.170	0.318	638.522	0.345	20	0.086	-.KPWEITGPCASPEYR.-
R4/RRR4-20/3	1793.450	1791.978	263.673	0.361	917.302	0.268	24	0.086	K.KPWEITGPCASPEYR.S
R4/RRR4-10/2	1623.322	1623.832	-933.411	0.440	1054.389	0.511	21	0.182	K.AGSGVATLGLPDSPGVPK.G
R4/RRR4-10/2	1333.316	1333.515	-149.645	0.471	728.028	0.556	18	0.176	K.SVGGQPIVFDSVK.G
R4/RRR4-10/2	1332.962	1333.515	-1168.150	0.394	819.481	0.477	19	0.167	K.SVGGQPIVFDSVK.G
R4/RRR4-10/2	1623.363	1623.832	-289.891	0.404	749.038	0.524	19	0.163	K.AGSGVATLGLPDSPGVPK.G
R4/RRR4-10/2	1332.445	1333.515	-1558.119	0.337	705.016	0.519	17	0.162	K.SVGGQPIVFDSVK.G
R4/RRR4-12/2	980.047	980.097	-50.922	0.374	1059.109	0.244	13	0.149	K.FSEIEQVK.Q
R4/RRR4-8/2	1349.134	1349.518	-284.835	0.466	1720.019	0.376	20	0.222	K.AREEAYAAGLLGK.N
R4/RRR4-8/3	1349.371	1349.518	-109.085	0.439	1806.659	0.375	27	0.195	K.AREEAYAAGLLGK.N
R4/RRR4-8/3	1349.688	1349.518	126.482	0.416	1857.591	0.353	28	0.194	K.AREEAYAAGLLGK.N
R4/RRR4-8/2	1310.421	1310.445	-18.276	0.501	843.985	0.543	18	0.184	R.RGPEWFASFGR.K
R4/RRR4-8/2	1310.279	1310.445	-127.046	0.541	677.235	0.498	16	0.169	R.RGPEWFASFGR.K
R4/RRR4-7/2	1311.219	1310.445	-172.616	0.251	617.000	0.386	15	0.144	R.RGPEWFASFGR.K
R4/RRR4-21/2	1176.983	1177.357	-318.469	0.391	1249.766	0.336	17	0.172	R.GIGM*LQASLDR.S
R4/RRR4-21/2	1331.209	1331.497	-217.023	0.365	752.157	0.487	18	0.164	R.QALTLQSVVEDK.T
R4/RRR4-21/2	1176.826	1177.357	-1304.391	0.368	895.280	0.327	16	0.152	R.GIGM*LQASLDR.S
R4/RRR4-21/2	1331.021	1331.497	-358.621	0.353	524.625	0.419	15	0.149	R.QALTLQSVVEDK.T
R4/RRR4-21/2	1176.961	1177.357	-337.616	0.360	732.880	0.222	14	0.137	R.GIGM*LQASLDR.S
R4/RRR4-17/2	991.856	992.111	-257.266	0.479	1393.002	0.275	13	0.172	K.FAEEVLQR.E
R4/RRR4-17/2	1278.109	1278.399	-227.955	0.492	872.751	0.419	18	0.165	R.RLEDAGYAVGAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/2	991.373	992.111	-1757.693	0.446	1252.982	0.258	13	0.161	K.FAEEVLQR.E
R4/RRR4-17/2	1277.849	1278.399	-1217.287	0.489	783.185	0.414	17	0.160	R.RLEDAGYAVGAR.V
R4/RRR4-17/2	991.954	992.111	-158.497	0.491	1107.218	0.276	13	0.156	K.FAEEVLQR.E
R4/RRR4-17/2	1278.228	1278.399	-134.159	0.484	687.787	0.405	16	0.155	R.RLEDAGYAVGAR.V
R4/RRR4-24/2	1320.253	1320.516	-200.091	0.366	837.236	0.473	15	0.162	R.TLADNPVVIYSK.S
R4/RRR4-24/2	1518.370	1518.739	-243.976	0.380	716.261	0.403	18	0.149	R.LTGQSTVPNVFIGGK.H
R4/RRR4-18/2	1588.122	1587.755	231.239	0.517	2119.811	0.575	26	0.335	K.LAFGSLGDSFSATSVK.A
R4/RRR4-19/2	1587.138	1587.755	-1022.191	0.478	1981.203	0.570	25	0.308	K.LAFGSLGDSFSATSVK.A
R4/RRR4-19/2	1588.203	1587.755	282.647	0.548	1906.443	0.582	25	0.301	K.LAFGSLGDSFSATSVK.A
R4/RRR4-1/2	1588.401	1587.755	-224.046	0.528	2026.521	0.492	25	0.293	K.LAFGSLGDSFSATSVK.A
R4/RRR4-19/2	1587.439	1587.755	-199.964	0.467	1915.021	0.542	25	0.290	K.LAFGSLGDSFSATSVK.A
R4/RRR4-18/2	1587.316	1587.755	-277.345	0.486	1884.514	0.555	25	0.289	K.LAFGSLGDSFSATSVK.A
R4/RRR4-18/2	1588.230	1587.755	299.447	0.516	1690.527	0.579	24	0.269	K.LAFGSLGDSFSATSVK.A
R4/RRR4-1/2	1587.249	1587.755	-952.079	0.428	1596.162	0.507	23	0.236	K.LAFGSLGDSFSATSVK.A
R4/RRR4-1/2	1586.962	1587.755	-1133.712	0.436	1521.223	0.514	23	0.230	K.LAFGSLGDSFSATSVK.A
R4/RRR4-2/2	1587.258	1587.755	-313.995	0.413	1594.324	0.394	23	0.211	K.LAFGSLGDSFSATSVK.A
R4/RRR4-2/2	1587.462	1587.755	-185.538	0.446	1278.863	0.418	21	0.186	K.LAFGSLGDSFSATSVK.A
R4/RRR4-2/2	1587.055	1587.755	-1074.319	0.351	1463.509	0.302	22	0.181	K.LAFGSLGDSFSATSVK.A
R4/RRR4-7/2	1904.463	1904.153	163.255	0.518	1352.973	0.477	22	0.203	R.SALDYLELQPDLSALVR.G
R4/RRR4-8/2	1903.559	1904.153	-840.056	0.464	1333.467	0.473	24	0.202	R.SALDYLELQPDLSALVR.G
R4/RRR4-8/2	1902.845	1904.153	-1216.912	0.387	1062.112	0.355	21	0.160	R.SALDYLELQPDLSALVR.G
R4/RRR4-8/2	1905.056	1904.153	-51.133	0.370	635.367	0.403	17	0.146	R.SALDYLELQPDLSALVR.G
R4/RRR4-8/3	1800.872	1800.992	-66.337	0.425	997.771	0.376	26	0.102	-.VTSGLAEGAAVIQEALDR.-
R4/RRR4-3/2	1306.276	1306.490	-163.709	0.476	1476.361	0.469	19	0.216	R.FSVGGLADVAEIK.G
R4/RRR4-10/3	1774.459	1773.025	245.588	0.433	1078.580	0.167	27	0.075	K.FYRFSVGGLADVAEIK.G
R4/RRR4-10/3	1774.189	1773.025	93.045	0.365	824.638	0.073	24	0.056	-.FYRFSVGGLADVAEIK.-
R4/RRR4-13/2	934.123	934.117	6.408	0.481	871.271	0.304	15	0.152	K.YLAGLGIAR.Q
R4/RRR4-14/2	934.111	934.117	-6.568	0.439	885.228	0.273	15	0.149	K.YLAGLGIAR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	933.873	934.117	-262.751	0.442	882.305	0.270	15	0.148	K.YLAGLGIAR.Q
R4/RRR4-13/2	1497.281	1497.677	-265.157	0.236	881.084	0.294	15	0.141	R.EQIQSYVFDVIR.A
R4/RRR4-13/2	1497.210	1497.677	-312.518	0.215	860.291	0.161	14	0.131	R.EQIQSYVFDVIR.A
R4/RRR4-14/3	1925.305	1926.061	-914.706	0.465	922.185	0.530	33	0.135	K.GGRPIQM*STDHDPNVER.G
R4/RRR4-14/3	1925.884	1926.061	-92.003	0.459	667.966	0.524	29	0.118	K.GGRPIQM*STDHDPNVER.G
R4/RRR4-14/3	1518.128	1518.721	-1052.772	0.551	876.070	0.424	26	0.111	K.VM*NNQEVVDVAKR.F
R4/RRR4-14/3	1925.672	1926.061	-202.645	0.462	447.184	0.513	25	0.108	K.GGRPIQM*STDHDPNVER.G
R4/RRR4-14/3	1517.867	1518.721	-1225.492	0.470	657.534	0.346	24	0.092	K.VM*NNQEVVDVAKR.F
R4/RRR4-20/2	1365.392	1365.620	-167.414	0.449	1223.339	0.440	17	0.187	R.VVM*ELFADTVPK.T
R4/RRR4-20/2	1365.160	1365.620	-337.847	0.371	1021.023	0.422	17	0.169	R.VVM*ELFADTVPK.T
R4/RRR4-21/2	1658.208	1656.881	198.059	0.481	373.292	0.525	19	0.165	R.IIPNFMCQGGDFTR.X
R4/RRR4-21/2	1657.137	1656.881	154.743	0.421	331.000	0.509	18	0.161	R.IIPNFMCQGGDFTR.X
R4/RRR4-21/2	1673.034	1672.880	91.864	0.377	403.847	0.506	19	0.160	R.IIPNFM*CQGGDFTR.X
R4/RRR4-21/2	1674.188	1672.880	184.532	0.369	393.836	0.493	19	0.159	R.IIPNFM*CQGGDFTR.X
R4/RRR4-21/2	1673.277	1672.880	237.828	0.376	281.785	0.520	16	0.158	R.IIPNFM*CQGGDFTR.X
R4/RRR4-21/2	1673.083	1672.880	121.572	0.399	421.493	0.447	19	0.157	R.IIPNFM*CQGGDFTR.X
R4/RRR4-22/2	1657.159	1656.881	168.187	0.424	385.576	0.446	18	0.156	R.IIPNFMCQGGDFTR.X
R4/RRR4-22/2	1656.975	1656.881	56.630	0.384	280.671	0.470	17	0.156	R.IIPNFMCQGGDFTR.X
R4/RRR4-22/2	1674.374	1672.880	295.806	0.353	394.028	0.458	19	0.156	R.IIPNFM*CQGGDFTR.X
R4/RRR4-21/2	1657.316	1656.881	263.546	0.441	327.153	0.429	18	0.156	R.IIPNFMCQGGDFTR.X
R4/RRR4-22/2	1657.142	1656.881	157.698	0.399	281.919	0.457	16	0.155	R.IIPNFMCQGGDFTR.X
R4/RRR4-21/2	1673.263	1672.880	229.123	0.335	275.894	0.491	16	0.154	R.IIPNFM*CQGGDFTR.X
R4/RRR4-22/2	1673.063	1672.880	109.279	0.320	328.122	0.468	17	0.153	R.IIPNFM*CQGGDFTR.X
R4/RRR4-21/2	1672.426	1672.880	-272.683	0.254	265.716	0.486	16	0.149	R.IIPNFM*CQGGDFTR.X
R4/RRR4-22/2	1673.262	1672.880	228.830	0.292	354.705	0.397	17	0.149	R.IIPNFM*CQGGDFTR.X
R4/RRR4-21/2	1657.601	1656.881	-169.710	0.323	290.656	0.354	15	0.147	R.IIPNFMCQGGDFTR.X
R4/RRR4-20/2	1672.350	1672.880	-918.062	0.193	189.269	0.340	17	0.147	R.IIPNFM*CQGGDFTR.X
R4/RRR4-20/2	1671.713	1672.880	-1300.212	0.156	134.037	0.312	16	0.146	R.IIPNFM*CQGGDFTR.X

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1672.481	1672.880	-239.439	0.128	129.190	0.296	15	0.143	-.IIPNFM*CQGGDFTR.-
R4/RRR4-20/2	1365.286	1365.620	-245.716	0.337	353.394	0.305	12	0.133	-.VVM*ELFADTVPK.-
R4/RRR4-22/2	1625.197	1625.757	-962.695	0.508	1968.982	0.628	22	0.325	R.YVCQDQFTGQPGPK.C
R4/RRR4-20/2	1625.196	1625.757	-963.147	0.525	1954.270	0.618	22	0.320	R.YVCQDQFTGQPGPK.C
R4/RRR4-20/2	1625.234	1625.757	-940.148	0.526	1944.355	0.618	22	0.319	R.YVCQDQFTGQPGPK.C
R4/RRR4-22/2	1626.143	1625.757	237.803	0.565	1893.216	0.631	23	0.316	R.YVCQDQFTGQPGPK.C
R4/RRR4-22/2	1624.793	1625.757	-1212.510	0.485	1875.111	0.599	22	0.301	R.YVCQDQFTGQPGPK.C
R4/RRR4-21/2	1625.285	1625.757	-291.431	0.521	1837.443	0.600	22	0.297	R.YVCQDQFTGQPGPK.C
R4/RRR4-20/2	1625.136	1625.757	-1000.777	0.511	1776.884	0.604	21	0.288	R.YVCQDQFTGQPGPK.C
R4/RRR4-21/2	1625.227	1625.757	-944.295	0.514	1759.385	0.611	21	0.287	R.YVCQDQFTGQPGPK.C
R4/RRR4-21/2	1626.281	1625.757	-293.813	0.583	1489.724	0.622	21	0.256	R.YVCQDQFTGQPGPK.C
R4/RRR4-16/2	1448.022	1448.520	-344.780	0.499	1525.640	0.508	19	0.231	R.SPSAYLNNPAEER.S
R4/RRR4-16/2	1448.282	1448.520	-164.988	0.557	1230.720	0.535	19	0.208	R.SPSAYLNNPAEER.S
R4/RRR4-16/2	1448.210	1448.520	-214.623	0.510	1174.146	0.486	18	0.192	R.SPSAYLNNPAEER.S
R4/RRR4-19/2	1535.895	1536.708	-1184.081	0.270	819.163	0.288	18	0.141	R.NDLLTDGTFALVEK.L
R4/RRR4-19/2	1535.468	1536.708	-1463.177	0.318	475.922	0.333	15	0.139	R.NDLLTDGTFALVEK.L
R4/RRR4-12/2	1188.746	1189.348	-1351.478	0.435	1217.081	0.425	14	0.186	K.HQQWYVLSK.T
R4/RRR4-12/2	1189.143	1189.348	-172.524	0.431	873.866	0.372	13	0.158	K.HQQWYVLSK.T
R4/RRR4-12/3	1428.258	1428.661	-282.909	0.396	1081.967	0.142	22	0.069	-.VAHYSELVQIIR.-
R4/RRR4-12/3	1429.063	1428.661	282.455	0.456	863.521	0.173	21	0.068	-.VAHYSELVQIIR.-
R4/RRR4-18/2	1595.442	1595.847	-254.905	0.406	513.090	0.468	20	0.159	R.VIPNFMLQGGDFTR.G
R4/RRR4-18/2	1611.532	1611.847	-196.172	0.320	352.158	0.503	20	0.156	R.VIPNFM*LQGGDFTR.G
R4/RRR4-21/2	1268.888	1269.300	-325.620	0.347	518.305	0.463	17	0.156	R.GNGTGGESIYGEK.-
R4/RRR4-19/2	1611.245	1611.847	-997.052	0.330	417.313	0.452	21	0.155	R.VIPNFM*LQGGDFTR.G
R4/RRR4-21/2	1269.348	1269.300	38.331	0.318	745.119	0.388	17	0.153	R.GNGTGGESIYGEK.-
R4/RRR4-22/2	1268.963	1269.300	-266.069	0.430	440.171	0.419	16	0.153	R.GNGTGGESIYGEK.-
R4/RRR4-21/2	1268.882	1269.300	-330.157	0.385	501.713	0.398	17	0.152	R.GNGTGGESIYGEK.-
R4/RRR4-18/2	1594.977	1595.847	-1175.915	0.358	606.306	0.359	22	0.151	R.VIPNFMLQGGDFTR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1269.906	1269.300	-310.993	0.386	537.964	0.416	15	0.151	R.GNGTGGESIYGEK.-
R4/RRR4-21/2	1269.008	1269.300	-230.844	0.424	405.157	0.413	15	0.151	R.GNGTGGESIYGEK.-
R4/RRR4-18/2	1611.372	1611.847	-295.729	0.266	322.085	0.490	19	0.150	R.VIPNFM*LQGGDFTR.G
R4/RRR4-19/2	1611.117	1611.847	-1077.155	0.285	353.988	0.408	20	0.149	R.VIPNFM*LQGGDFTR.G
R4/RRR4-21/2	1269.083	1269.300	-171.401	0.399	502.263	0.360	17	0.149	R.GNGTGGESIYGEK.-
R4/RRR4-22/2	1269.028	1269.300	-215.018	0.391	415.002	0.392	15	0.149	R.GNGTGGESIYGEK.-
R4/RRR4-18/2	1594.881	1595.847	-1236.864	0.334	412.391	0.331	19	0.147	R.VIPNFMLQGGDFTR.G
R4/RRR4-19/2	1610.562	1611.847	-1422.584	0.254	265.132	0.408	18	0.147	R.VIPNFM*LQGGDFTR.G
R4/RRR4-21/2	1269.514	1269.300	169.296	0.331	469.410	0.366	15	0.146	R.GNGTGGESIYGEK.-
R4/RRR4-22/2	1269.060	1269.300	-189.156	0.394	282.508	0.328	14	0.146	R.GNGTGGESIYGEK.-
R4/RRR4-21/2	1269.033	1269.300	-210.772	0.377	478.753	0.304	17	0.146	R.GNGTGGESIYGEK.-
R4/RRR4-22/2	1270.238	1269.300	-49.121	0.395	360.066	0.399	12	0.145	R.GNGTGGESIYGEK.-
R4/RRR4-18/2	1611.070	1611.847	-1106.141	0.232	338.615	0.377	19	0.145	R.VIPNFM*LQGGDFTR.G
R4/RRR4-21/2	1268.509	1269.300	-1415.911	0.201	437.058	0.372	17	0.143	R.GNGTGGESIYGEK.-
R4/RRR4-9/2	1131.978	1131.333	-314.332	0.404	1525.327	0.326	17	0.193	K.HFGLM*SPGLR.G
R4/RRR4-10/3	1485.683	1485.651	21.590	0.553	1557.077	0.450	29	0.180	K.SM*GHHVTVISSSAR.K
R4/RRR4-10/2	1130.972	1131.333	-319.916	0.325	866.630	0.431	15	0.162	K.HFGLM*SPGLR.G
R4/RRR4-10/3	1485.492	1485.651	-107.480	0.485	1498.496	0.407	28	0.159	K.SM*GHHVTVISSSAR.K
R4/RRR4-9/2	1131.271	1131.333	-55.103	0.319	1111.532	0.293	16	0.158	K.HFGLM*SPGLR.G
R4/RRR4-9/2	1130.993	1131.333	-301.615	0.297	1001.244	0.345	15	0.157	K.HFGLM*SPGLR.G
R4/RRR4-10/2	1115.192	1115.333	-127.203	0.259	855.274	0.360	15	0.151	K.HFGLMSPGLR.G
R4/RRR4-10/2	1130.363	1131.333	-1748.237	0.271	830.223	0.348	14	0.150	K.HFGLM*SPGLR.G
R4/RRR4-9/3	1485.584	1485.651	-45.290	0.514	1537.982	0.354	29	0.145	K.SM*GHHVTVISSSAR.K
R4/RRR4-10/3	1469.577	1469.652	-51.298	0.560	1381.106	0.390	28	0.139	-.SMGHHVTVISSSAR.-
R4/RRR4-9/3	1485.720	1485.651	46.064	0.560	1378.479	0.383	27	0.137	K.SM*GHHVTVISSSAR.K
R4/RRR4-10/3	1485.142	1485.651	-1019.302	0.543	1327.819	0.390	27	0.135	K.SM*GHHVTVISSSAR.K
R4/RRR4-9/3	1485.457	1485.651	-131.220	0.510	1061.067	0.451	25	0.129	K.SM*GHHVTVISSSAR.K
R4/RRR4-2/3	1485.158	1485.651	-333.060	0.450	844.877	0.416	23	0.110	K.SM*GHHVTVISSSAR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/3	1469.549	1469.652	-70.420	0.511	1073.878	0.302	25	0.096	-.SMGHHVTVISSSAR.-
R4/RRR4-10/3	1469.732	1469.652	54.922	0.445	1088.712	0.249	26	0.089	-.SMGHHVTVISSSAR.-
R4/RRR4-9/3	1469.874	1469.652	151.624	0.535	903.598	0.253	24	0.082	-.SMGHHVTVISSSAR.-
R4/RRR4-9/3	1469.298	1469.652	-241.800	0.494	851.819	0.250	23	0.080	-.SMGHHVTVISSSAR.-
R4/RRR4-12/2	1693.955	1694.952	-1182.376	0.408	1109.690	0.449	21	0.180	K.LYVPQDLISVYQQK.V
R4/RRR4-12/2	1694.657	1694.952	-174.597	0.474	794.482	0.421	19	0.159	K.LYVPQDLISVYQQK.V
R4/RRR4-12/3	1730.842	1730.946	-60.497	0.438	611.348	0.527	28	0.115	R.VLSIQSHTVQGYVGNK.S
R4/RRR4-12/3	1730.322	1730.946	-941.717	0.401	848.334	0.450	31	0.111	R.VLSIQSHTVQGYVGNK.S
R4/RRR4-12/3	1730.844	1730.946	-59.011	0.409	616.244	0.432	28	0.100	R.VLSIQSHTVQGYVGNK.S
R4/RRR4-10/2	1409.264	1408.708	-316.295	0.471	458.635	0.473	15	0.153	K.AIPLIDISPLVEK.I
R4/RRR4-10/2	1208.908	1209.329	-349.372	0.261	612.888	0.407	13	0.143	R.TAGDPFWVCR.L
R4/RRR4-4/2	1959.221	1959.232	-5.787	0.459	1561.208	0.459	22	0.219	R.AIAPEVLDSDFLGLQTLR.H
R4/RRR4-5/2	1321.188	1321.547	-272.418	0.442	655.684	0.424	17	0.156	K.VYTAGSIIDLLR.F
R4/RRR4-5/2	1322.071	1321.547	-361.512	0.320	476.646	0.375	14	0.143	K.VYTAGSIIDLLR.F
R4/RRR4-10/2	1601.874	1602.815	-1215.336	0.416	2355.579	0.412	23	0.324	R.AVNITINSIGTELTR.D
R4/RRR4-10/2	1602.322	1602.815	-308.598	0.473	1942.275	0.470	22	0.274	R.AVNITINSIGTELTR.D
R4/RRR4-10/2	1603.251	1602.815	272.891	0.569	1641.499	0.510	22	0.245	R.AVNITINSIGTELTR.D
R4/RRR4-20/2	1868.337	1869.018	-902.421	0.548	1980.210	0.621	24	0.326	K.LPDATLSYFDSPDGELK.T
R4/RRR4-6/2	1558.309	1558.674	-234.815	0.444	932.280	0.556	19	0.186	R.NNSTSFLIDDIYR.N
R4/RRR4-6/2	1557.300	1558.674	-1529.148	0.326	823.454	0.502	18	0.165	R.NNSTSFLIDDIYR.N
R4/RRR4-6/2	1312.494	1311.552	-44.554	0.375	402.180	0.613	17	0.164	K.VVGVPVTLNGDLK.N
R4/RRR4-6/2	1312.698	1311.552	111.588	0.336	346.727	0.534	16	0.154	K.VVGVPVTLNGDLK.N
R4/RRR4-6/2	1311.601	1311.552	37.003	0.306	296.348	0.459	14	0.146	K.VVGVPVTLNGDLK.N
R4/RRR4-6/2	1939.228	1940.232	-1036.681	0.481	945.303	0.613	24	0.196	R.VILSGAAPLATHVEEYLR.V
R4/RRR4-6/2	1939.484	1940.232	-903.785	0.505	841.758	0.599	22	0.185	R.VILSGAAPLATHVEEYLR.V
R4/RRR4-6/3	1418.972	1418.540	305.561	0.430	731.563	0.545	26	0.125	R.AAADGRPSVGPTYR.S
R4/RRR4-6/3	1418.572	1418.540	22.249	0.348	509.203	0.495	23	0.105	R.AAADGRPSVGPTYR.S
R4/RRR4-6/3	1418.009	1418.540	-1083.204	0.309	458.147	0.494	23	0.102	R.AAADGRPSVGPTYR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/3	1417.692	1418.540	-1307.559	0.349	334.188	0.473	20	0.101	R.AAADGRPSVGPTYR.S
R4/RRR4-11/2	1603.546	1602.858	-194.977	0.496	1361.478	0.416	20	0.193	R.LALYALEAGPEWIR.E
R4/RRR4-11/2	1152.090	1152.325	-205.279	0.459	1032.912	0.301	14	0.152	K.VLQENNPIPK.L
R4/RRR4-11/2	1602.399	1602.858	-287.495	0.374	1046.335	0.258	18	0.146	R.LALYALEAGPEWIR.E
R4/RRR4-13/2	1621.848	1621.773	45.853	0.417	2376.149	0.392	22	0.322	K.SLAEFFTDFGYAPR.E
R4/RRR4-13/2	1621.596	1621.773	-109.753	0.339	1275.832	0.443	18	0.187	K.SLAEFFTDFGYAPR.E
R4/RRR4-13/2	1621.772	1621.773	-1.179	0.392	1244.042	0.407	17	0.179	K.SLAEFFTDFGYAPR.E
R4/RRR4-14/2	1772.660	1772.894	-132.103	0.472	2171.718	0.516	22	0.324	R.GFTVSTVEEEVAYNAR.L
R4/RRR4-1/2	1746.548	1746.982	-249.536	0.507	1657.297	0.387	23	0.216	K.NEILAESEFAAPTIIK.L
R4/RRR4-1/2	1363.205	1363.496	-214.174	0.420	827.554	0.361	15	0.150	R.FGYSVSFEALDK.G
R4/RRR4-21/1	1219.643	1220.357	-1409.637	0.191	841.218	0.254	15	0.510	K.LNPAADAGSIYK.T
R4/RRR4-21/1	1219.668	1220.357	-1388.828	0.155	520.844	0.180	14	0.441	K.LNPAADAGSIYK.T
R4/RRR4-21/1	1219.629	1220.357	-1421.198	0.172	484.060	0.237	13	0.440	K.LNPAADAGSIYK.T
R4/RRR4-20/2	1219.848	1220.357	-1240.136	0.433	891.444	0.537	20	0.184	K.LNPAADAGSIYK.T
R4/RRR4-21/2	1220.001	1220.357	-292.102	0.454	865.609	0.530	20	0.182	K.LNPAADAGSIYK.T
R4/RRR4-21/2	1219.947	1220.357	-336.475	0.458	745.698	0.525	19	0.176	K.LNPAADAGSIYK.T
R4/RRR4-22/2	1221.163	1220.357	-159.077	0.507	709.436	0.498	19	0.172	K.LNPAADAGSIYK.T
R4/RRR4-22/2	1219.967	1220.357	-320.211	0.431	783.125	0.466	19	0.169	K.LNPAADAGSIYK.T
R4/RRR4-21/2	1219.948	1220.357	-336.074	0.419	568.695	0.504	17	0.164	K.LNPAADAGSIYK.T
R4/RRR4-20/2	1219.485	1220.357	-1539.598	0.355	691.431	0.444	18	0.159	K.LNPAADAGSIYK.T
R4/RRR4-22/2	1219.844	1220.357	-1243.854	0.477	566.217	0.427	17	0.158	K.LNPAADAGSIYK.T
R4/RRR4-20/2	1219.972	1220.357	-315.995	0.401	650.268	0.389	18	0.155	K.LNPAADAGSIYK.T
R4/RRR4-27/2	1375.118	1375.507	-283.727	0.436	2163.171	0.504	19	0.319	R.EGDILTLLESER.E
R4/RRR4-27/2	1375.162	1375.507	-251.843	0.489	1973.318	0.488	18	0.284	R.EGDILTLLESER.E
R4/RRR4-28/2	1374.930	1375.507	-1150.304	0.433	1913.966	0.439	18	0.262	R.EGDILTLLESER.E
R4/RRR4-28/2	1375.121	1375.507	-281.322	0.454	1293.379	0.497	17	0.204	R.EGDILTLLESER.E
R4/RRR4-28/2	1375.000	1375.507	-1099.133	0.416	1311.874	0.443	17	0.194	R.EGDILTLLESER.E
R4/RRR4-27/2	1374.283	1375.507	-1623.207	0.284	1448.470	0.317	18	0.181	R.EGDILTLLESER.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-12/2	1268.295	1268.491	-154.807	0.513	2178.217	0.502	20	0.323	R.IVVAGNQIAVQR.T
R4/RRR4-12/2	1268.319	1268.491	-135.593	0.508	2006.309	0.469	19	0.285	R.IVVAGNQIAVQR.T
R4/RRR4-12/2	1268.273	1268.491	-171.993	0.491	1639.777	0.501	18	0.243	R.IVVAGNQIAVQR.T
R4/RRR4-13/2	1268.065	1268.491	-336.742	0.363	1357.803	0.396	16	0.188	R.IVVAGNQIAVQR.T
R4/RRR4-19/2	1268.200	1268.491	-229.833	0.205	345.146	0.350	14	0.138	-.IVVAGNQIAVQR.-
R4/RRR4-10/2	1411.413	1411.689	-196.102	0.470	1267.070	0.420	18	0.188	K.LSISDVEYLLMK.S
R4/RRR4-10/2	1089.152	1089.309	-145.308	0.466	954.250	0.429	14	0.171	R.INEPILYVK.M
R4/RRR4-10/2	1411.333	1411.689	-253.110	0.403	715.295	0.433	13	0.153	K.LSISDVEYLLMK.S
R4/RRR4-10/2	1089.062	1089.309	-228.177	0.389	813.812	0.288	13	0.146	R.INEPILYVK.M
R4/RRR4-10/2	1411.154	1411.689	-1091.190	0.247	343.568	0.358	10	0.130	-.LSISDVEYLLMK.-
R4/RRR4-9/2	1654.560	1654.974	-251.347	0.485	2188.465	0.496	23	0.322	K.ETLIAGGPFVLPLAQK.H
R4/RRR4-18/2	995.991	995.116	-125.893	0.402	630.745	0.431	13	0.159	R.TVWTFGQR.A
R4/RRR4-18/3	1529.442	1529.724	-185.260	0.473	1285.736	0.461	29	0.152	R.GFGHIGVTVHDVYK.A
R4/RRR4-18/2	994.810	995.116	-308.440	0.318	582.152	0.396	12	0.150	R.TVWTFGQR.A
R4/RRR4-18/2	994.934	995.116	-183.865	0.292	562.788	0.365	12	0.147	R.TVWTFGQR.A
R4/RRR4-18/3	1529.368	1529.724	-233.424	0.469	1163.751	0.473	26	0.143	R.GFGHIGVTVHDVYK.A
R4/RRR4-12/2	1365.194	1365.514	-234.938	0.289	1414.605	0.336	18	0.182	K.EPYTATIVSVER.L
R4/RRR4-13/2	1364.630	1365.514	-1384.905	0.256	1100.257	0.396	16	0.165	K.EPYTATIVSVER.L
R4/RRR4-13/2	1365.201	1365.514	-230.094	0.259	1065.099	0.346	15	0.157	K.EPYTATIVSVER.L
R4/RRR4-12/2	1365.232	1365.514	-207.310	0.314	881.587	0.404	13	0.155	K.EPYTATIVSVER.L
R4/RRR4-12/2	911.049	911.037	12.215	0.326	879.651	0.285	13	0.148	R.LYSIASTR.Y
R4/RRR4-12/2	910.928	911.037	-120.848	0.336	798.742	0.270	13	0.145	R.LYSIASTR.Y
R4/RRR4-13/2	1364.601	1365.514	-1405.750	0.186	840.011	0.343	14	0.143	K.EPYTATIVSVER.L
R4/RRR4-12/2	1365.234	1365.514	-205.874	0.309	678.872	0.331	13	0.142	K.EPYTATIVSVER.L
R4/RRR4-13/2	910.521	911.037	-1670.250	0.254	632.236	0.200	12	0.137	R.LYSIASTR.Y
R4/RRR4-22/2	1355.102	1355.542	-326.222	0.538	2179.553	0.495	20	0.320	R.FSQVVSNALDM*K.L
R4/RRR4-22/2	1355.119	1355.542	-313.568	0.531	1834.349	0.488	19	0.264	R.FSQVVSNALDM*K.L
R4/RRR4-22/2	1356.238	1355.542	-224.929	0.570	1796.798	0.496	19	0.261	R.FSQVVSNALDM*K.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1356.035	1355.542	364.451	0.507	1714.105	0.516	19	0.256	R.FSQVVSNALDM*K.L
R4/RRR4-22/2	1356.133	1355.542	-302.771	0.558	1464.606	0.551	18	0.235	R.FSQVVSNALDM*K.L
R4/RRR4-21/2	1354.591	1355.542	-1444.966	0.440	1625.800	0.387	19	0.215	R.FSQVVSNALDM*K.L
R4/RRR4-22/2	1339.064	1339.543	-358.479	0.443	1289.920	0.518	18	0.209	R.FSQVVSNALDMK.L
R4/RRR4-21/2	1354.430	1355.542	-1564.010	0.372	1600.938	0.347	18	0.203	R.FSQVVSNALDM*K.L
R4/RRR4-22/2	1355.465	1355.542	-57.047	0.448	1126.184	0.481	17	0.188	R.FSQVVSNALDM*K.L
R4/RRR4-21/2	1354.490	1355.542	-1519.557	0.371	1288.744	0.401	17	0.184	R.FSQVVSNALDM*K.L
R4/RRR4-22/3	1356.075	1355.542	-345.906	0.490	1293.229	0.383	26	0.130	R.FSQVVSNALDM*K.L
R4/RRR4-22/3	1356.285	1355.542	-190.131	0.493	805.944	0.363	21	0.094	-.FSQVVSNALDM*K.-
R4/RRR4-22/3	1355.824	1355.542	208.362	0.388	1119.787	0.239	25	0.087	R.FSQVVSNALDM*K.L
R4/RRR4-5/2	1814.149	1813.124	14.064	0.498	567.064	0.534	21	0.163	K.LAFPQDSPPLAILCAAK.V
R4/RRR4-1/2	1293.934	1294.436	-1164.116	0.493	1615.875	0.495	17	0.237	K.GVADFLQEVTSK.K
R4/RRR4-2/2	1294.005	1294.436	-333.398	0.479	1465.263	0.484	18	0.219	K.GVADFLQEVTSK.K
R4/RRR4-1/2	1911.292	1910.226	34.607	0.508	805.300	0.469	22	0.164	R.GM*VLPFTPLSLSFDNVR.Y
R4/RRR4-1/2	1293.454	1294.436	-1536.556	0.221	588.853	0.333	13	0.137	K.GVADFLQEVTSK.K
R4/RRR4-20/2	1566.187	1566.784	-1022.888	0.438	1231.618	0.390	18	0.176	K.IFFVSWSPAAADVR.S
R4/RRR4-20/2	1795.507	1795.879	-207.818	0.349	758.886	0.327	19	0.140	R.DAGFDELTASLPADGCR.Y
R4/RRR4-13/3	1737.715	1737.881	-95.451	0.483	952.708	0.411	26	0.110	R.LGSAADKCNAINSQCK.G
R4/RRR4-13/3	989.252	989.156	97.068	0.466	1071.887	0.254	18	0.089	K.HLDHVVIR.L
R4/RRR4-13/3	989.501	989.156	349.278	0.479	891.674	0.264	17	0.087	K.HLDHVVIR.L
R4/RRR4-13/3	989.382	989.156	228.849	0.441	758.860	0.226	16	0.084	K.HLDHVVIR.L
R4/RRR4-4/2	1934.492	1935.166	-867.952	0.536	977.472	0.553	20	0.184	K.GVPSLFSDLSPLYEQPGK.A
R4/RRR4-4/2	1002.571	1003.263	-1692.143	0.311	811.431	0.254	14	0.141	K.ILLAFQAVK.Q
R4/RRR4-8/2	1058.831	1059.155	-307.194	0.459	1130.452	0.353	15	0.169	R.IEEELGNVR.Y
R4/RRR4-24/2	993.875	994.088	-215.598	0.335	617.791	0.402	12	0.154	K.HFSVNAYR.V
R4/RRR4-13/2	993.899	994.088	-191.078	0.415	606.605	0.362	12	0.153	K.HFSVNAYR.V
R4/RRR4-23/2	993.872	994.088	-218.309	0.428	541.862	0.362	12	0.153	K.HFSVNAYR.V
R4/RRR4-14/2	994.005	994.088	-84.265	0.307	694.238	0.383	13	0.153	K.HFSVNAYR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/2	993.839	994.088	-251.702	0.412	559.286	0.351	12	0.152	K.HFSVNAYR.V
R4/RRR4-14/2	993.978	994.088	-111.613	0.386	425.899	0.371	11	0.152	K.HFSVNAYR.V
R4/RRR4-13/2	994.025	994.088	-63.324	0.402	635.498	0.331	13	0.152	K.HFSVNAYR.V
R4/RRR4-24/2	994.046	994.088	-42.630	0.340	484.181	0.349	12	0.150	K.HFSVNAYR.V
R4/RRR4-23/2	993.670	994.088	-422.030	0.322	497.034	0.342	12	0.149	K.HFSVNAYR.V
R4/RRR4-13/3	1296.740	1296.548	148.075	0.455	1151.831	0.502	25	0.149	K.HITGGMMGGHAVK.L
R4/RRR4-13/2	993.977	994.088	-111.736	0.373	412.869	0.296	11	0.148	K.HFSVNAYR.V
R4/RRR4-14/2	993.527	994.088	-1576.303	0.327	484.462	0.308	11	0.147	K.HFSVNAYR.V
R4/RRR4-13/3	1297.633	1296.548	65.555	0.484	1177.768	0.471	24	0.144	K.HITGGMMGGHAVK.L
R4/RRR4-14/3	1296.336	1296.548	-163.983	0.458	1004.917	0.520	23	0.141	K.HITGGMMGGHAVK.L
R4/RRR4-13/3	1296.950	1296.548	310.614	0.460	1187.177	0.454	25	0.139	K.HITGGMMGGHAVK.L
R4/RRR4-14/3	1296.412	1296.548	-105.324	0.476	952.504	0.453	22	0.121	K.HITGGMMGGHAVK.L
R4/RRR4-14/3	1297.828	1296.548	216.677	0.398	959.375	0.416	23	0.113	K.HITGGMMGGHAVK.L
R4/RRR4-24/3	1297.089	1296.548	-354.656	0.310	720.235	0.182	18	0.073	-.HITGGMMGGHAVK.-
R4/RRR4-8/3	1660.932	1660.765	100.937	0.426	1335.131	0.450	26	0.157	R.DGEASDKPIDSAVLSR.M
R4/RRR4-1/2	850.774	850.961	-220.066	0.212	928.272	0.038	11	0.128	-.EENAM*LK.-
R4/RRR4-7/2	1256.979	1257.379	-318.478	0.445	1295.353	0.444	19	0.195	R.LDQSVLNASGPR.G
R4/RRR4-7/2	1257.217	1257.379	-128.708	0.494	1201.635	0.389	19	0.179	R.LDQSVLNASGPR.G
R4/RRR4-7/2	1402.111	1402.529	-298.785	0.371	593.976	0.454	17	0.154	K.IIEPVVDSDGTEK.A
R4/RRR4-7/2	1256.775	1257.379	-1279.492	0.333	773.890	0.359	15	0.148	R.LDQSVLNASGPR.G
R4/RRR4-7/2	1401.970	1402.529	-1115.717	0.360	533.276	0.349	17	0.145	K.IIEPVVDSDGTEK.A
R4/RRR4-6/2	1892.624	1892.187	231.426	0.625	1856.352	0.603	30	0.304	R.FIVSGGAPLSVAVEEFLR.V
R4/RRR4-6/2	1891.482	1892.187	-904.324	0.553	1518.358	0.578	28	0.249	R.FIVSGGAPLSVAVEEFLR.V
R4/RRR4-6/2	1891.392	1892.187	-952.205	0.553	1454.232	0.583	28	0.243	R.FIVSGGAPLSVAVEEFLR.V
R4/RRR4-1/2	1668.690	1667.581	65.184	0.450	606.440	0.440	16	0.147	R.ASSSGEDGEDDEEALR.W
R4/RRR4-17/2	1634.896	1634.686	128.989	0.549	1995.681	0.572	26	0.313	R.ASDFDSLGSDGGPGPVR.S
R4/RRR4-18/2	1635.934	1634.686	152.108	0.533	1884.048	0.563	25	0.292	R.ASDFDSLGSDGGPGPVR.S
R4/RRR4-17/2	1635.320	1634.686	-224.506	0.548	1723.880	0.591	24	0.276	R.ASDFDSLGSDGGPGPVR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1635.870	1634.686	112.820	0.522	1461.298	0.557	22	0.232	R.ASDFDSLGSDGGPGPVR.S
R4/RRR4-6/2	1121.245	1121.271	-23.653	0.421	1062.974	0.517	15	0.189	R.HADAIPVLER.A
R4/RRR4-6/2	1121.292	1121.271	18.278	0.427	953.273	0.532	15	0.184	R.HADAIPVLER.A
R4/RRR4-6/3	1557.863	1557.688	112.999	0.385	663.989	0.487	25	0.109	K.LGTANPDVEDEKLR.L
R4/RRR4-6/3	1557.540	1557.688	-94.977	0.430	728.462	0.451	25	0.107	K.LGTANPDVEDEKLR.L
R4/RRR4-6/3	1557.464	1557.688	-144.036	0.409	482.113	0.417	22	0.096	K.LGTANPDVEDEKLR.L
R4/RRR4-9/2	1578.114	1576.693	267.773	0.457	1363.868	0.417	19	0.192	R.TTGAGSNWLAQDLNK.G
R4/RRR4-8/2	1577.099	1576.693	258.629	0.492	1347.919	0.356	20	0.179	R.TTGAGSNWLAQDLNK.G
R4/RRR4-8/2	1576.940	1576.693	157.410	0.478	1225.900	0.387	20	0.176	R.TTGAGSNWLAQDLNK.G
R4/RRR4-8/2	1577.253	1576.693	-279.735	0.437	988.949	0.318	21	0.154	R.TTGAGSNWLAQDLNK.G
R4/RRR4-9/2	1577.575	1576.693	-74.709	0.332	943.863	0.307	19	0.149	R.TTGAGSNWLAQDLNK.G
R4/RRR4-9/2	1577.298	1576.693	-250.774	0.479	884.753	0.279	18	0.141	R.TTGAGSNWLAQDLNK.G
R4/RRR4-1/3	1430.789	1430.632	110.284	0.452	1548.957	0.272	25	0.126	R.VTGKDEGLTLLQR.Q
R4/RRR4-1/3	1430.669	1430.632	25.826	0.422	1313.025	0.264	25	0.103	R.VTGKDEGLTLLQR.Q
R4/RRR4-1/3	1429.789	1430.632	-1293.114	0.355	809.861	0.267	22	0.083	R.VTGKDEGLTLLQR.Q
R4/RRR4-10/2	1674.254	1672.970	169.980	0.417	718.434	0.460	16	0.154	R.EFDLIVMPGGLPGAQK.F
R4/RRR4-10/2	1247.247	1247.425	-143.578	0.337	698.660	0.415	15	0.152	K.FTAEIIPVNSR.V
R4/RRR4-10/2	1674.611	1672.970	-215.144	0.379	815.105	0.338	16	0.143	R.EFDLIVMPGGLPGAQK.F
R4/RRR4-10/2	1246.788	1247.425	-1317.434	0.358	642.753	0.229	14	0.136	K.FTAEIIPVNSR.V
R4/RRR4-10/2	1673.602	1672.970	-220.468	0.273	646.453	0.136	16	0.128	R.EFDLIVMPGGLPGAQK.F
R4/RRR4-12/2	1542.096	1542.673	-1025.370	0.333	766.766	0.454	20	0.158	R.SLVAATPSDPDLEAR.G
R4/RRR4-12/2	1542.147	1542.673	-992.786	0.340	682.213	0.398	19	0.150	R.SLVAATPSDPDLEAR.G
R4/RRR4-12/2	1349.261	1349.559	-221.560	0.279	1405.376	0.129	18	0.148	K.IFAAADAFGQPLK.D
R4/RRR4-12/2	1542.064	1542.673	-1046.591	0.317	666.070	0.359	19	0.145	R.SLVAATPSDPDLEAR.G
R4/RRR4-6/2	1443.419	1443.623	-141.368	0.427	1448.728	0.410	18	0.201	K.SIDTETFLEFLK.T
R4/RRR4-6/2	1442.852	1443.623	-1231.077	0.379	1444.924	0.363	18	0.191	K.SIDTETFLEFLK.T
R4/RRR4-6/2	1157.955	1158.287	-287.030	0.371	728.357	0.351	16	0.152	R.IVEVVQGEER.A
R4/RRR4-6/2	1157.911	1158.287	-325.953	0.373	502.736	0.362	15	0.150	R.IVEVVQGEER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1157.522	1158.287	-1528.931	0.371	325.552	0.392	15	0.149	-.IVEVVQGEER.-
R4/RRR4-6/2	1157.511	1158.287	-1538.995	0.302	420.446	0.316	15	0.146	R.IVEVVQGEER.A
R4/RRR4-12/2	1344.516	1344.496	15.061	0.426	995.678	0.343	15	0.157	R.VLDTLQEIQER.H
R4/RRR4-12/2	994.004	994.126	-123.127	0.412	1060.022	0.260	13	0.152	R.ISEFQTLR.E
R4/RRR4-12/2	993.219	994.126	-1926.207	0.337	856.310	0.265	13	0.146	R.ISEFQTLR.E
R4/RRR4-12/2	993.942	994.126	-185.958	0.374	874.778	0.224	12	0.142	R.ISEFQTLR.E
R4/RRR4-12/2	1344.207	1344.496	-215.744	0.259	902.237	0.240	15	0.140	R.VLDTLQEIQER.H
R4/RRR4-10/2	1792.534	1791.894	-201.332	0.534	837.954	0.480	22	0.170	K.VVSIDGFEDVPQNDEK.S
R4/RRR4-9/2	1791.148	1791.894	-977.471	0.445	749.768	0.435	20	0.157	K.VVSIDGFEDVPQNDEK.S
R4/RRR4-10/3	1562.578	1562.755	-114.103	0.374	1523.720	0.210	29	0.109	K.AVAHQPVSVAIEAGGR.E
R4/RRR4-13/2	945.021	945.099	-82.414	0.301	940.091	0.096	13	0.131	-.SDAIAALKR.-
R4/RRR4-13/3	1102.104	1101.285	-164.221	0.425	1288.592	0.107	20	0.074	R.RSDAIAALKR.Y
R4/RRR4-9/2	1270.118	1270.500	-301.591	0.383	1505.899	0.353	17	0.195	R.LANNLEELILK.E
R4/RRR4-9/2	1270.250	1270.500	-197.364	0.500	1507.832	0.329	18	0.191	R.LANNLEELILK.E
R4/RRR4-9/2	1270.175	1270.500	-257.140	0.504	1417.452	0.337	18	0.185	R.LANNLEELILK.E
R4/RRR4-9/3	1663.529	1663.769	-144.531	0.367	1852.721	0.277	27	0.168	R.FHLPGETEEEFATR.L
R4/RRR4-9/3	1664.500	1663.769	-162.247	0.349	1274.563	0.307	25	0.109	R.FHLPGETEEEFATR.L
R4/RRR4-11/3	1409.895	1409.570	231.238	0.500	878.238	0.406	22	0.106	R.VDRDKGYIDLSK.R
R4/RRR4-10/3	1856.921	1855.084	-88.005	0.388	1106.878	0.266	28	0.091	R.HVAETLGIDLEPLYQR.I
R4/RRR4-10/3	1856.934	1855.084	-81.279	0.418	646.509	0.265	23	0.075	-.HVAETLGIDLEPLYQR.-
R4/RRR4-20/2	1447.544	1447.616	-50.463	0.507	1970.572	0.547	21	0.302	K.TVTLQSELVGNASK.V
R4/RRR4-20/2	1447.173	1447.616	-307.333	0.483	1870.747	0.542	21	0.285	K.TVTLQSELVGNASK.V
R4/RRR4-20/2	1447.204	1447.616	-285.838	0.290	1000.988	0.456	17	0.166	K.TVTLQSELVGNASK.V
R4/RRR4-12/2	1220.632	1221.345	-1407.151	0.360	1245.068	0.345	19	0.173	K.VFGSPTSAEVAR.V
R4/RRR4-11/2	1441.436	1441.572	-94.676	0.412	746.187	0.502	20	0.168	R.QGNPDLIGTGALER.A
R4/RRR4-12/2	1221.107	1221.345	-195.281	0.454	992.982	0.400	18	0.168	K.VFGSPTSAEVAR.V
R4/RRR4-12/2	1221.074	1221.345	-221.958	0.388	974.198	0.312	18	0.154	K.VFGSPTSAEVAR.V
R4/RRR4-12/2	1441.145	1441.572	-297.319	0.396	688.400	0.408	19	0.154	R.QGNPDLIGTGALER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	1441.323	1441.572	-173.514	0.348	513.773	0.490	17	0.154	R.QGNPDLIGTGALER.A
R4/RRR4-12/2	1440.819	1441.572	-1219.982	0.413	556.269	0.414	18	0.152	R.QGNPDLIGTGALER.A
R4/RRR4-11/2	1221.042	1221.345	-248.435	0.344	834.565	0.333	17	0.151	K.VFGSPTSAEVAR.V
R4/RRR4-11/2	1221.293	1221.345	-42.167	0.369	786.720	0.308	18	0.149	K.VFGSPTSAEVAR.V
R4/RRR4-11/2	1221.399	1221.345	44.447	0.361	680.503	0.300	17	0.146	K.VFGSPTSAEVAR.V
R4/RRR4-2/2	1973.446	1972.224	112.506	0.516	1525.032	0.505	21	0.225	R.IVTSFTSLVDSADFLEVK.N
R4/RRR4-13/2	1972.844	1972.224	-193.358	0.426	713.454	0.422	17	0.147	R.IVTSFTSLVDSADFLEVK.N
R4/RRR4-2/2	1602.013	1601.785	142.566	0.423	745.072	0.342	14	0.142	K.FVYEDVFGPFPQR.A
R4/RRR4-8/2	1373.697	1374.569	-1366.494	0.461	936.777	0.472	16	0.173	R.YATNAVTAFIFR.E
R4/RRR4-8/2	1373.518	1374.569	-1497.353	0.454	634.014	0.530	16	0.168	R.YATNAVTAFIFR.E
R4/RRR4-8/2	1373.361	1374.569	-1612.172	0.329	973.056	0.410	17	0.163	R.YATNAVTAFIFR.E
R4/RRR4-8/3	1748.088	1748.020	39.032	0.415	846.718	0.411	26	0.102	K.INNQNHLVPVLATSVK.N
R4/RRR4-22/2	1332.094	1332.573	-360.538	0.474	1926.851	0.549	20	0.296	K.NVATFLVQAGIAK.K
R4/RRR4-12/2	1834.334	1834.017	173.435	0.410	640.275	0.447	16	0.151	K.DLYPQTEPYDFGFLK.V
R4/RRR4-12/2	1833.602	1834.017	-227.138	0.261	368.119	0.330	15	0.136	K.DLYPQTEPYDFGFLK.V
R4/RRR4-12/3	1719.907	1718.851	32.624	0.472	1304.130	0.333	31	0.120	K.RLTSSDADVQAEAAKR.W
R4/RRR4-13/2	1438.136	1438.522	-269.166	0.501	2020.728	0.509	21	0.300	R.ELAEEGYSGVEVR.V
R4/RRR4-23/2	1259.132	1259.439	-244.323	0.490	2080.225	0.477	21	0.299	R.FPGVNGLGISAAR.V
R4/RRR4-23/2	1259.257	1259.439	-144.931	0.465	1789.624	0.426	21	0.243	R.FPGVNGLGISAAR.V
R4/RRR4-23/2	1259.268	1259.439	-136.179	0.497	1789.334	0.402	21	0.237	R.FPGVNGLGISAAR.V
R4/RRR4-9/2	1027.294	1027.200	91.818	0.318	1171.542	0.054	16	0.133	-.VSALELAAPR.-
R4/RRR4-12/2	1189.044	1188.268	-189.323	0.546	1793.827	0.591	18	0.287	R.FDDSFSAASLK.A
R4/RRR4-16/2	1188.077	1188.268	-161.343	0.474	1829.589	0.558	18	0.282	R.FDDSFSAASLK.A
R4/RRR4-11/2	1187.972	1188.268	-249.889	0.478	1771.200	0.549	18	0.271	R.FDDSFSAASLK.A
R4/RRR4-19/2	1188.978	1188.268	-245.146	0.505	1723.254	0.567	18	0.270	R.FDDSFSAASLK.A
R4/RRR4-19/2	1189.079	1188.268	-159.457	0.502	1723.513	0.565	18	0.269	R.FDDSFSAASLK.A
R4/RRR4-12/2	1188.308	1188.268	33.320	0.496	1789.235	0.522	18	0.266	R.FDDSFSAASLK.A
R4/RRR4-20/2	1187.885	1188.268	-323.294	0.505	1740.516	0.545	18	0.266	R.FDDSFSAASLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1189.187	1188.268	-68.839	0.421	1658.918	0.595	17	0.266	R.FDDSFSAASLK.A
R4/RRR4-12/2	1187.603	1188.268	-1406.079	0.469	1704.214	0.556	18	0.264	R.FDDSFSAASLK.A
R4/RRR4-3/2	1188.262	1188.268	-5.112	0.494	1771.312	0.513	18	0.262	R.FDDSFSAASLK.A
R4/RRR4-11/2	1188.029	1188.268	-202.058	0.471	1720.831	0.529	18	0.259	R.FDDSFSAASLK.A
R4/RRR4-2/2	1187.962	1188.268	-258.651	0.483	1725.070	0.518	18	0.257	R.FDDSFSAASLK.A
R4/RRR4-3/2	1187.997	1188.268	-229.374	0.439	1742.994	0.511	18	0.257	R.FDDSFSAASLK.A
R4/RRR4-2/2	1187.990	1188.268	-235.147	0.467	1672.964	0.518	18	0.250	R.FDDSFSAASLK.A
R4/RRR4-6/2	1187.991	1188.268	-234.116	0.456	1691.576	0.487	18	0.245	R.FDDSFSAASLK.A
R4/RRR4-6/2	1188.049	1188.268	-185.462	0.448	1458.344	0.529	17	0.227	R.FDDSFSAASLK.A
R4/RRR4-4/2	1188.080	1188.268	-158.766	0.382	1492.322	0.521	17	0.227	R.FDDSFSAASLK.A
R4/RRR4-18/2	1188.051	1188.268	-183.813	0.450	1664.091	0.425	18	0.227	R.FDDSFSAASLK.A
R4/RRR4-6/2	1188.109	1188.268	-134.648	0.418	1505.722	0.495	17	0.224	R.FDDSFSAASLK.A
R4/RRR4-2/2	1188.122	1188.268	-123.930	0.446	1406.583	0.532	17	0.223	R.FDDSFSAASLK.A
R4/RRR4-20/2	1187.248	1188.268	-1706.390	0.379	1507.826	0.486	17	0.222	R.FDDSFSAASLK.A
R4/RRR4-4/2	1188.025	1188.268	-205.768	0.439	1487.871	0.488	17	0.221	R.FDDSFSAASLK.A
R4/RRR4-1/2	1188.199	1188.268	-58.180	0.465	1364.696	0.540	17	0.221	R.FDDSFSAASLK.A
R4/RRR4-9/2	1188.043	1188.268	-189.894	0.397	1375.714	0.541	16	0.219	R.FDDSFSAASLK.A
R4/RRR4-11/2	1188.241	1188.268	-23.144	0.433	1450.945	0.493	17	0.219	R.FDDSFSAASLK.A
R4/RRR4-17/2	1188.310	1188.268	35.587	0.450	1436.395	0.495	17	0.218	R.FDDSFSAASLK.A
R4/RRR4-8/2	1188.352	1188.268	71.028	0.422	1467.734	0.464	17	0.214	R.FDDSFSAASLK.A
R4/RRR4-14/2	1188.086	1188.268	-153.613	0.432	1363.389	0.480	16	0.207	R.FDDSFSAASLK.A
R4/RRR4-1/2	1188.066	1188.268	-170.929	0.449	1270.572	0.502	16	0.203	R.FDDSFSAASLK.A
R4/RRR4-8/2	1187.947	1188.268	-271.022	0.398	1215.172	0.516	17	0.201	R.FDDSFSAASLK.A
R4/RRR4-1/2	1187.353	1188.268	-1618.179	0.386	1242.245	0.493	16	0.198	R.FDDSFSAASLK.A
R4/RRR4-20/2	1188.208	1188.268	-50.966	0.504	1036.486	0.521	15	0.189	R.FDDSFSAASLK.A
R4/RRR4-14/2	1187.528	1188.268	-1469.885	0.339	1156.765	0.487	16	0.188	R.FDDSFSAASLK.A
R4/RRR4-16/2	1187.860	1188.268	-344.533	0.398	1101.040	0.496	16	0.188	R.FDDSFSAASLK.A
R4/RRR4-18/2	1187.904	1188.268	-307.519	0.466	1227.939	0.380	17	0.179	R.FDDSFSAASLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-3/2	1188.198	1188.268	-59.313	0.414	952.536	0.486	16	0.178	R.FDDSFSAASLK.A
R4/RRR4-15/2	1188.010	1188.268	-217.726	0.269	1081.407	0.451	16	0.174	R.FDDSFSAASLK.A
R4/RRR4-14/2	1187.382	1188.268	-1593.081	0.322	893.157	0.413	15	0.162	R.FDDSFSAASLK.A
R4/RRR4-16/2	1187.663	1188.268	-1355.700	0.325	965.412	0.335	16	0.157	R.FDDSFSAASLK.A
R4/RRR4-18/2	1187.351	1188.268	-1619.521	0.399	1070.711	0.217	17	0.148	R.FDDSFSAASLK.A
R4/RRR4-7/2	989.926	989.153	-230.434	0.414	553.697	0.483	15	0.161	K.LAPAYAVAGR.I
R4/RRR4-7/2	989.801	989.153	-356.759	0.374	646.061	0.452	16	0.160	K.LAPAYAVAGR.I
R4/RRR4-7/2	1130.516	1131.261	-1548.994	0.363	710.516	0.469	17	0.159	K.LAVATGEGVEGK.G
R4/RRR4-7/2	989.791	989.153	-367.277	0.463	524.319	0.356	15	0.148	-.LAPAYAVAGR.-
R4/RRR4-6/2	1211.669	1212.424	-1452.523	0.416	1482.585	0.380	17	0.197	K.DAGIIAGLNVLR.I
R4/RRR4-6/2	1212.091	1212.424	-275.220	0.478	1323.607	0.426	18	0.194	K.DAGIIAGLNVLR.I
R4/RRR4-6/2	1211.988	1212.424	-360.505	0.438	1110.946	0.381	15	0.167	K.DAGIIAGLNVLR.I
R4/RRR4-5/2	1647.482	1646.866	-233.773	0.423	592.763	0.482	19	0.155	R.IVNEPTAAAIAYGLDK.T
R4/RRR4-5/2	1211.249	1212.424	-1800.751	0.336	422.171	0.295	13	0.140	K.DAGIIAGLNVLR.I
R4/RRR4-4/2	947.959	948.101	-150.354	0.503	511.929	0.339	12	0.150	R.QGDIFLVR.G
R4/RRR4-4/2	947.974	948.101	-134.595	0.347	720.974	0.331	12	0.149	R.QGDIFLVR.G
R4/RRR4-1/2	948.056	948.101	-47.152	0.538	524.314	0.305	12	0.146	R.QGDIFLVR.G
R4/RRR4-2/2	948.389	948.101	304.919	0.388	452.668	0.259	12	0.145	R.QGDIFLVR.G
R4/RRR4-7/2	1417.578	1417.675	-68.285	0.448	1062.298	0.432	18	0.174	K.LGSILNVPESFLK.R
R4/RRR4-7/2	1418.333	1417.675	-241.847	0.336	681.743	0.389	16	0.148	K.LGSILNVPESFLK.R
R4/RRR4-7/2	1264.765	1264.388	298.767	0.313	799.077	0.234	14	0.138	K.M*QDVLDEEIR.T
R4/RRR4-9/2	1249.961	1250.384	-339.660	0.437	1168.941	0.304	16	0.158	R.AFDEGWGGVIAK.T
R4/RRR4-10/3	920.163	920.134	31.672	0.476	1019.324	0.367	20	0.104	-.AVHPIALAK.-
R4/RRR4-10/3	920.399	920.134	288.570	0.439	723.487	0.324	18	0.083	-.AVHPIALAK.-
R4/RRR4-9/3	920.029	920.134	-114.344	0.418	803.123	0.247	18	0.079	-.AVHPIALAK.-
R4/RRR4-10/3	920.345	920.134	230.318	0.362	622.640	0.254	17	0.068	-.AVHPIALAK.-
R4/RRR4-12/2	1496.585	1495.703	-78.997	0.465	996.105	0.336	16	0.154	R.SGYLYNLQYFVK.W
R4/RRR4-13/3	1228.131	1228.339	-169.750	0.497	623.233	0.516	20	0.117	R.IPESGTPYAHR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/3	1228.468	1228.339	105.823	0.470	535.796	0.465	18	0.106	R.IPESGTPYAHR.S
R4/RRR4-12/3	1228.620	1228.339	229.730	0.464	559.445	0.450	19	0.105	R.IPESGTPYAHR.S
R4/RRR4-12/3	1227.514	1228.339	-1491.287	0.442	710.161	0.421	21	0.103	R.IPESGTPYAHR.S
R4/RRR4-13/3	1228.551	1228.339	172.937	0.420	586.057	0.389	19	0.097	R.IPESGTPYAHR.S
R4/RRR4-22/2	1550.143	1549.706	282.952	0.499	1836.088	0.569	22	0.287	R.TLSDPLFFGYSSSK.N
R4/RRR4-23/2	1549.810	1549.706	67.656	0.449	1659.975	0.546	22	0.255	R.TLSDPLFFGYSSSK.N
R4/RRR4-22/2	1549.076	1549.706	-1054.816	0.451	1706.285	0.482	22	0.246	R.TLSDPLFFGYSSSK.N
R4/RRR4-22/2	1549.439	1549.706	-172.549	0.473	1605.783	0.517	21	0.242	R.TLSDPLFFGYSSSK.N
R4/RRR4-23/2	1549.340	1549.706	-236.965	0.469	1570.300	0.534	21	0.241	R.TLSDPLFFGYSSSK.N
R4/RRR4-23/2	1548.609	1549.706	-1358.022	0.320	1741.151	0.460	21	0.240	R.TLSDPLFFGYSSSK.N
R4/RRR4-22/2	1550.673	1549.706	-21.288	0.462	1041.692	0.497	18	0.183	R.TLSDPLFFGYSSSK.N
R4/RRR4-23/2	1549.433	1549.706	-176.500	0.259	882.773	0.342	17	0.149	R.TLSDPLFFGYSSSK.N
R4/RRR4-23/2	1550.040	1549.706	216.382	0.281	356.280	0.359	12	0.140	R.TLSDPLFFGYSSSK.N
R4/RRR4-23/2	1550.068	1549.706	234.230	0.359	356.815	0.325	12	0.139	R.TLSDPLFFGYSSSK.N
R4/RRR4-7/2	1197.454	1197.368	71.715	0.334	873.514	0.481	15	0.163	R.GYLLHGPPGTGK.S
R4/RRR4-7/2	1028.315	1028.231	82.678	0.347	1104.849	0.294	15	0.157	R.LQLQTLVGR.H
R4/RRR4-17/2	1694.227	1694.966	-1029.206	0.463	1981.925	0.500	21	0.289	K.GLLDLTCQTVADM*IK.G
R4/RRR4-16/2	1524.221	1524.703	-316.699	0.407	1880.495	0.531	22	0.281	K.GVNPWIEVDGGVGPK.N
R4/RRR4-18/2	1948.670	1949.023	-182.059	0.569	1814.924	0.562	23	0.280	K.YGLDTSQFTYNPSDPSR.Y
R4/RRR4-18/2	1948.590	1949.023	-223.034	0.530	1740.803	0.514	23	0.257	K.YGLDTSQFTYNPSDPSR.Y
R4/RRR4-18/2	1948.341	1949.023	-866.308	0.512	1704.793	0.494	23	0.247	K.YGLDTSQFTYNPSDPSR.Y
R4/RRR4-20/2	1238.783	1238.372	333.215	0.495	1753.905	0.583	19	0.280	K.YSGNDLLGVTAK.V
R4/RRR4-20/2	1238.446	1238.372	59.851	0.357	1541.022	0.482	19	0.223	K.YSGNDLLGVTAK.V
R4/RRR4-19/2	1238.011	1238.372	-292.303	0.368	995.307	0.440	17	0.170	K.YSGNDLLGVTAK.V
R4/RRR4-20/2	1238.544	1238.372	139.622	0.259	580.714	0.365	14	0.142	K.YSGNDLLGVTAK.V
R4/RRR4-19/2	1238.731	1238.372	290.530	0.256	503.912	0.281	14	0.139	K.YSGNDLLGVTAK.V
R4/RRR4-4/2	1420.350	1420.636	-201.592	0.476	1427.234	0.354	17	0.187	R.VNDQYITNVLLK.I
R4/RRR4-4/2	1420.112	1420.636	-1076.202	0.414	889.443	0.405	15	0.158	R.VNDQYITNVLLK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	919.994	920.131	-148.736	0.344	1004.105	0.329	14	0.156	K.FTLIVAQK.N
R4/RRR4-9/2	1667.363	1666.860	-299.351	0.601	1384.532	0.671	25	0.256	K.APVSQSQPATPVASVAR.T
R4/RRR4-9/2	1666.206	1666.860	-996.097	0.564	1433.497	0.620	25	0.248	K.APVSQSQPATPVASVAR.T
R4/RRR4-9/2	1666.316	1666.860	-929.901	0.558	1135.709	0.625	23	0.217	K.APVSQSQPATPVASVAR.T
R4/RRR4-10/2	1757.377	1756.854	-272.452	0.438	1318.821	0.493	23	0.203	R.LGFTEAAGNFQTSNNGK.G
R4/RRR4-10/2	1586.267	1586.689	-267.186	0.482	1053.134	0.581	21	0.198	K.GGLGNDAVILNSQDGR.S
R4/RRR4-10/2	1586.981	1586.689	184.420	0.542	930.543	0.587	20	0.191	K.GGLGNDAVILNSQDGR.S
R4/RRR4-10/2	1586.549	1586.689	-88.563	0.514	927.597	0.525	20	0.179	K.GGLGNDAVILNSQDGR.S
R4/RRR4-18/2	1508.028	1508.701	-1112.756	0.437	2019.805	0.466	20	0.286	K.TVYLVDKLTADNR.V
R4/RRR4-11/2	1415.213	1415.531	-225.250	0.565	1846.348	0.540	22	0.282	R.SPNELLNSEGGLGK.Q
R4/RRR4-11/2	1415.221	1415.531	-220.058	0.544	1872.525	0.491	22	0.272	R.SPNELLNSEGGLGK.Q
R4/RRR4-11/2	1414.773	1415.531	-1246.510	0.535	1657.512	0.518	21	0.250	R.SPNELLNSEGGLGK.Q
R4/RRR4-5/2	1333.890	1333.424	350.670	0.454	1046.575	0.458	17	0.178	K.LSDEAIEDALEK.V
R4/RRR4-5/2	1333.071	1333.424	-265.489	0.415	920.935	0.331	18	0.154	K.LSDEAIEDALEK.V
R4/RRR4-5/3	1398.248	1398.549	-216.040	0.388	1109.166	0.370	22	0.111	R.VGHYLHISSEQK.L
R4/RRR4-4/2	1632.462	1631.898	-267.575	0.437	1339.035	0.413	21	0.190	K.VSTPTLFLLGAQDLR.V
R4/RRR4-4/2	1601.509	1601.871	-226.723	0.406	1085.884	0.514	18	0.184	R.IPALFVVNISSGEVR.A
R4/RRR4-4/2	1631.378	1631.898	-934.205	0.451	1198.036	0.310	20	0.161	K.VSTPTLFLLGAQDLR.V
R4/RRR4-4/2	1608.700	1607.833	-83.157	0.507	1804.848	0.545	19	0.274	R.SVEQLGYITVLTQR.N
R4/RRR4-4/2	1609.221	1607.833	242.206	0.462	1778.936	0.382	20	0.229	R.SVEQLGYITVLTQR.N
R4/RRR4-4/2	1607.542	1607.833	-181.392	0.379	1495.277	0.368	19	0.195	R.SVEQLGYITVLTQR.N
R4/RRR4-11/2	975.786	975.169	-393.879	0.349	769.221	0.277	12	0.141	K.ALAFAIVNR.S
R4/RRR4-10/3	1246.288	1246.397	-88.340	0.450	1145.395	0.389	22	0.119	R.HDDVILATHPK.S
R4/RRR4-10/3	1246.964	1246.397	-348.441	0.468	846.873	0.405	19	0.106	R.HDDVILATHPK.S
R4/RRR4-11/3	1246.201	1246.397	-158.201	0.430	784.345	0.379	19	0.099	R.HDDVILATHPK.S
R4/RRR4-11/3	1246.596	1246.397	159.482	0.462	774.392	0.377	19	0.099	R.HDDVILATHPK.S
R4/RRR4-11/3	1246.869	1246.397	379.503	0.364	727.886	0.392	18	0.099	R.HDDVILATHPK.S
R4/RRR4-10/3	1246.349	1246.397	-38.530	0.470	917.242	0.347	20	0.099	R.HDDVILATHPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1807.714	1806.050	-186.434	0.586	1565.919	0.628	22	0.266	K.ALSFYDVVFDAVYAPK.V
R4/RRR4-11/2	1198.274	1198.314	-33.883	0.308	914.097	0.320	16	0.147	K.HAAATASVNSLR.E
R4/RRR4-11/3	1189.595	1189.306	243.750	0.410	1561.581	0.303	22	0.134	R.TGHQLQVYSR.E
R4/RRR4-11/3	1189.403	1189.306	81.969	0.300	757.223	0.158	17	0.074	R.TGHQLQVYSR.E
R4/RRR4-3/2	1403.106	1403.480	-267.770	0.447	1260.493	0.414	17	0.183	K.AGASQDQILNETR.L
R4/RRR4-3/2	1328.070	1328.540	-354.901	0.465	1132.247	0.390	16	0.172	K.ILNLTELELNR.V
R4/RRR4-3/2	1402.791	1403.480	-1207.668	0.481	1151.510	0.343	17	0.163	K.AGASQDQILNETR.L
R4/RRR4-3/2	1403.206	1403.480	-196.202	0.442	825.003	0.345	16	0.149	K.AGASQDQILNETR.L
R4/RRR4-2/2	1273.551	1272.436	90.215	0.477	1753.715	0.555	20	0.271	K.AAVVGGNVLTSQR.V
R4/RRR4-2/2	1273.156	1272.436	-221.148	0.410	1292.784	0.550	18	0.212	K.AAVVGGNVLTSQR.V
R4/RRR4-3/2	1273.088	1272.436	-274.440	0.387	1400.677	0.460	18	0.204	K.AAVVGGNVLTSQR.V
R4/RRR4-3/2	1273.479	1272.436	33.399	0.392	1351.528	0.451	18	0.198	K.AAVVGGNVLTSQR.V
R4/RRR4-2/2	1272.386	1272.436	-39.704	0.373	1245.227	0.273	18	0.161	K.AAVVGGNVLTSQR.V
R4/RRR4-1/2	1273.263	1272.436	-136.221	0.413	934.940	0.400	16	0.161	K.AAVVGGNVLTSQR.V
R4/RRR4-11/2	1840.652	1841.056	-219.816	0.567	1852.162	0.514	27	0.273	R.SIALSDAGALGDPAAELLR.T
R4/RRR4-11/2	1840.488	1841.056	-854.474	0.568	1546.511	0.484	26	0.225	R.SIALSDAGALGDPAAELLR.T
R4/RRR4-2/2	1809.495	1809.909	-229.352	0.461	939.224	0.527	24	0.181	K.EGDATPFTDVTVDNISK.A
R4/RRR4-2/2	1585.210	1585.658	-283.661	0.461	727.466	0.482	22	0.166	K.TSPIPQDDAQGQATR.Y
R4/RRR4-2/2	1585.380	1585.658	-175.974	0.419	718.115	0.485	22	0.165	K.TSPIPQDDAQGQATR.Y
R4/RRR4-2/2	1530.153	1528.776	247.280	0.466	1690.356	0.387	18	0.220	K.ELSSLQQEIIVLR.Q
R4/RRR4-2/2	1514.435	1513.764	-217.930	0.394	920.933	0.471	20	0.168	K.VPTGVSGTALAASLLR.D
R4/RRR4-2/2	1515.190	1513.764	281.560	0.350	651.278	0.361	19	0.143	-.VPTGVSGTALAASLLR.-
R4/RRR4-9/2	1453.183	1453.581	-274.888	0.456	734.611	0.331	16	0.146	R.NTVNSFNTWIEK.M
R4/RRR4-9/3	1177.771	1178.325	-1323.177	0.367	949.172	0.347	21	0.097	K.SKEHGFLGFR.N
R4/RRR4-9/3	1178.880	1178.325	-378.015	0.362	552.539	0.384	17	0.093	K.SKEHGFLGFR.N
R4/RRR4-9/3	1178.381	1178.325	48.136	0.401	597.380	0.351	18	0.092	K.SKEHGFLGFR.N
R4/RRR4-9/2	1690.464	1691.903	-1447.658	0.351	1833.545	0.492	25	0.262	K.FVAPDVSILESDSAIK.S
R4/RRR4-9/2	1691.466	1691.903	-259.689	0.498	1640.376	0.522	24	0.248	K.FVAPDVSILESDSAIK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1691.362	1691.903	-914.104	0.475	1690.080	0.494	24	0.247	K.FVAPDVSILESDSAIK.S
R4/RRR4-12/2	1505.842	1505.741	67.517	0.479	1894.610	0.493	20	0.276	R.TIGVLYQLVDDIR.S
R4/RRR4-16/3	1580.989	1581.717	-1096.688	0.493	1622.424	0.591	30	0.251	K.NHAVHISQIGEGYR.A
R4/RRR4-16/3	1581.432	1581.717	-180.757	0.547	1684.980	0.516	31	0.229	K.NHAVHISQIGEGYR.A
R4/RRR4-16/3	1581.577	1581.717	-89.237	0.517	1571.595	0.515	29	0.211	K.NHAVHISQIGEGYR.A
R4/RRR4-2/2	1358.398	1357.580	-134.353	0.557	1617.458	0.583	20	0.264	K.IPSVNDIPLNFK.V
R4/RRR4-2/2	1357.403	1357.580	-130.663	0.422	1351.023	0.487	18	0.207	K.IPSVNDIPLNFK.V
R4/RRR4-2/2	1357.333	1357.580	-181.906	0.522	1397.756	0.437	19	0.203	K.IPSVNDIPLNFK.V
R4/RRR4-7/2	947.050	947.199	-157.803	0.472	632.963	0.402	13	0.157	R.VLGLYLIR.F
R4/RRR4-7/3	1658.908	1657.855	31.942	0.418	1214.383	0.382	26	0.124	K.TNHVGFGLVLGSDGKR.F
R4/RRR4-7/2	1880.136	1880.094	22.688	0.532	1883.803	0.496	22	0.269	K.DSVTPTFAAAALFINNAR.W
R4/RRR4-7/2	1879.421	1880.094	-892.669	0.472	1727.249	0.466	23	0.241	K.DSVTPTFAAAALFINNAR.W
R4/RRR4-6/2	1881.393	1880.094	159.400	0.362	460.652	0.505	14	0.145	K.DSVTPTFAAAALFINNAR.W
R4/RRR4-24/2	1523.319	1523.713	-259.258	0.504	1970.461	0.458	22	0.274	R.LSYGAISDLSGIQAK.K
R4/RRR4-23/2	1523.307	1523.713	-266.976	0.464	1967.880	0.363	22	0.248	R.LSYGAISDLSGIQAK.K
R4/RRR4-24/2	1523.290	1523.713	-278.151	0.473	1809.062	0.439	21	0.247	R.LSYGAISDLSGIQAK.K
R4/RRR4-23/2	1523.278	1523.713	-286.111	0.430	1778.123	0.397	21	0.232	R.LSYGAISDLSGIQAK.K
R4/RRR4-24/2	1522.718	1523.713	-1313.892	0.337	1805.675	0.369	21	0.229	R.LSYGAISDLSGIQAK.K
R4/RRR4-23/2	1523.293	1523.713	-276.302	0.360	1358.286	0.235	19	0.160	R.LSYGAISDLSGIQAK.K
R4/RRR4-18/2	1502.203	1501.659	-304.796	0.517	1901.643	0.484	19	0.275	K.FISFLQDVSCER.N
R4/RRR4-13/2	1594.802	1594.877	-47.569	0.396	1168.930	0.345	21	0.166	R.NIEGVSLPVLTPNLK.G
R4/RRR4-13/2	1793.581	1794.039	-256.235	0.263	981.732	0.233	19	0.136	R.LATSGLSVVEATSFVSPK.W
R4/RRR4-13/2	1594.272	1594.877	-1009.861	0.274	790.461	0.209	15	0.131	R.NIEGVSLPVLTPNLK.G
R4/RRR4-16/2	1643.506	1643.908	-245.737	0.489	1674.782	0.568	25	0.265	K.NLVAPVIGEANLAAYK.A
R4/RRR4-16/2	1643.337	1643.908	-959.071	0.427	1617.563	0.553	25	0.251	K.NLVAPVIGEANLAAYK.A
R4/RRR4-14/2	1794.255	1794.001	142.303	0.537	1692.355	0.565	25	0.267	R.DIPLNYATFQPGTTVR.D
R4/RRR4-14/2	1793.263	1794.001	-971.948	0.440	1525.195	0.528	24	0.234	R.DIPLNYATFQPGTTVR.D
R4/RRR4-13/2	1793.373	1794.001	-910.102	0.471	1373.009	0.532	23	0.219	R.DIPLNYATFQPGTTVR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1793.314	1794.001	-943.177	0.515	1170.494	0.551	22	0.204	R.DIPLNYATFQPGTTVR.D
R4/RRR4-13/2	1793.418	1794.001	-885.161	0.428	1213.012	0.487	21	0.193	R.DIPLNYATFQPGTTVR.D
R4/RRR4-13/3	1570.937	1570.729	132.284	0.464	1903.718	0.477	31	0.255	R.SPSGVIHLTDTSVTR.F
R4/RRR4-13/3	1571.552	1570.729	-113.218	0.509	1696.012	0.546	35	0.241	R.SPSGVIHLTDTSVTR.F
R4/RRR4-14/3	1570.527	1570.729	-129.624	0.450	1218.132	0.479	28	0.150	R.SPSGVIHLTDTSVTR.F
R4/RRR4-13/3	1570.582	1570.729	-94.305	0.382	1233.501	0.460	29	0.144	R.SPSGVIHLTDTSVTR.F
R4/RRR4-2/2	1178.223	1178.320	-82.573	0.357	993.488	0.490	16	0.177	K.YTSDPGLVLGR.Q
R4/RRR4-2/2	1178.117	1178.320	-172.580	0.387	902.754	0.446	16	0.167	K.YTSDPGLVLGR.Q
R4/RRR4-2/2	1013.997	1014.204	-204.558	0.450	879.165	0.413	15	0.165	R.VLNINTALR.S
R4/RRR4-7/2	1178.930	1178.320	-331.981	0.300	530.810	0.371	13	0.144	K.YTSDPGLVLGR.Q
R4/RRR4-7/2	1178.395	1178.320	64.147	0.229	490.234	0.374	12	0.139	K.YTSDPGLVLGR.Q
R4/RRR4-13/2	1460.489	1459.669	-123.704	0.428	1853.159	0.490	20	0.267	R.SPWSTLDIIAEVK.Q
R4/RRR4-20/3	1582.816	1582.651	104.836	0.493	1809.244	0.513	28	0.259	R.SGAEVHTGHELCER.K
R4/RRR4-10/2	1603.319	1603.708	-243.802	0.499	1460.108	0.636	23	0.255	K.AGDTVGVGYFVDSCR.A
R4/RRR4-10/2	1603.283	1603.708	-265.877	0.513	1332.907	0.612	22	0.234	K.AGDTVGVGYFVDSCR.A
R4/RRR4-10/2	1603.144	1603.708	-978.458	0.492	1316.869	0.585	22	0.226	K.AGDTVGVGYFVDSCR.A
R4/RRR4-15/3	1568.004	1567.772	148.694	0.529	1954.066	0.448	32	0.248	R.LPLRDVLDDAGVGAR.V
R4/RRR4-12/3	1568.339	1567.772	-277.040	0.447	1478.936	0.488	28	0.186	R.LPLRDVLDDAGVGAR.V
R4/RRR4-12/3	1567.713	1567.772	-37.544	0.521	1518.727	0.435	29	0.172	R.LPLRDVLDDAGVGAR.V
R4/RRR4-15/3	1567.345	1567.772	-273.193	0.469	1290.167	0.448	26	0.150	R.LPLRDVLDDAGVGAR.V
R4/RRR4-15/3	1567.522	1567.772	-159.983	0.442	1390.240	0.364	27	0.136	R.LPLRDVLDDAGVGAR.V
R4/RRR4-16/3	1568.705	1567.772	-42.710	0.435	689.072	0.349	23	0.093	R.LPLRDVLDDAGVGAR.V
R4/RRR4-3/2	1473.989	1474.643	-1125.910	0.343	1389.262	0.375	19	0.186	R.AVQGVEFSDPVAVR.H
R4/RRR4-2/2	1474.565	1474.643	-53.108	0.396	1431.122	0.322	19	0.181	R.AVQGVEFSDPVAVR.H
R4/RRR4-2/2	1474.703	1474.643	40.714	0.433	1136.874	0.424	18	0.176	R.AVQGVEFSDPVAVR.H
R4/RRR4-2/2	1501.922	1501.774	98.834	0.386	873.487	0.288	16	0.142	K.ATPDMAVTLLEIAR.I
R4/RRR4-3/2	1473.762	1474.643	-1280.359	0.275	1031.916	0.199	19	0.141	R.AVQGVEFSDPVAVR.H
R4/RRR4-3/2	1502.394	1501.774	-253.252	0.361	568.027	0.316	14	0.137	K.ATPDMAVTLLEIAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1353.855	1352.515	251.898	0.530	1678.310	0.549	20	0.262	K.LLASGVVSYEGEK.W
R4/RRR4-9/2	1468.341	1468.679	-230.942	0.470	1743.969	0.526	20	0.263	K.LQENAFVVGSYLK.E
R4/RRR4-9/2	1468.283	1468.679	-270.727	0.440	1326.974	0.425	18	0.192	K.LQENAFVVGSYLK.E
R4/RRR4-11/2	1550.205	1548.766	284.599	0.561	1929.634	0.448	21	0.269	R.IPSFTKEQSELIR.G
R4/RRR4-5/2	1480.612	1480.645	-22.295	0.365	1160.275	0.373	18	0.165	R.DGSDFSAAIIGSLVK.A
R4/RRR4-5/2	1698.233	1696.947	168.845	0.465	513.069	0.553	17	0.158	K.M*ASTPGVSATLFDALAK.A
R4/RRR4-1/2	1466.238	1466.661	-289.392	0.326	965.196	0.432	18	0.162	K.VLAGIDTNFTVTSK.A
R4/RRR4-3/2	1344.568	1344.584	-11.711	0.330	802.179	0.213	14	0.133	R.WALGSVEILLSR.H
R4/RRR4-3/2	1589.819	1588.790	18.359	0.564	1423.488	0.603	19	0.240	K.IGGSNIQLFGESLPR.I
R4/RRR4-13/3	1659.564	1659.735	-103.635	0.472	1737.301	0.523	31	0.241	K.SGGLESEKDYPYTGR.D
R4/RRR4-14/2	1659.273	1659.735	-279.411	0.490	1477.047	0.527	20	0.228	K.SGGLESEKDYPYTGR.D
R4/RRR4-14/2	1659.315	1659.735	-253.874	0.481	999.690	0.530	19	0.184	K.SGGLESEKDYPYTGR.D
R4/RRR4-14/3	1660.700	1659.735	-21.434	0.463	1232.993	0.515	28	0.163	K.SGGLESEKDYPYTGR.D
R4/RRR4-15/3	1659.476	1659.735	-156.652	0.440	1199.504	0.480	26	0.150	K.SGGLESEKDYPYTGR.D
R4/RRR4-14/3	1659.574	1659.735	-97.659	0.519	1200.979	0.478	28	0.148	K.SGGLESEKDYPYTGR.D
R4/RRR4-14/3	1659.598	1659.735	-82.828	0.488	967.442	0.471	25	0.127	K.SGGLESEKDYPYTGR.D
R4/RRR4-15/3	1658.821	1659.735	-1157.273	0.422	1125.913	0.353	25	0.111	K.SGGLESEKDYPYTGR.D
R4/RRR4-13/3	1659.337	1659.735	-240.560	0.480	967.380	0.338	26	0.099	K.SGGLESEKDYPYTGR.D
R4/RRR4-16/2	1251.253	1250.426	-138.519	0.592	1713.073	0.507	17	0.254	K.ALEVYQAQLSK.S
R4/RRR4-16/2	1250.094	1250.426	-266.364	0.581	1550.347	0.485	17	0.229	K.ALEVYQAQLSK.S
R4/RRR4-16/2	1249.601	1250.426	-1464.378	0.451	1686.230	0.420	17	0.229	K.ALEVYQAQLSK.S
R4/RRR4-2/2	1486.115	1485.753	244.886	0.460	1711.407	0.525	21	0.257	R.LAVGEALTNLVWAK.V
R4/RRR4-7/1	949.449	950.070	-1713.237	0.303	871.782	0.170	12	0.487	R.GFEVIDAAK.A
R4/RRR4-7/1	949.468	950.070	-1693.215	0.280	905.959	0.109	12	0.477	R.GFEVIDAAK.A
R4/RRR4-8/1	949.417	950.070	-1746.694	0.249	744.333	0.201	11	0.469	-.GFEVIDAAK.-
R4/RRR4-8/1	949.415	950.070	-1749.084	0.227	674.160	0.143	11	0.449	-.GFEVIDAAK.-
R4/RRR4-7/1	949.457	950.070	-1704.195	0.214	548.706	0.157	10	0.436	-.GFEVIDAAK.-
R4/RRR4-8/1	949.500	950.070	-1658.663	0.285	528.948	0.217	10	0.421	-.GFEVIDAAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1393.201	1393.607	-291.996	0.463	2283.287	0.489	21	0.336	R.VVSCADILAFAAR.D
R4/RRR4-8/2	1394.145	1393.607	-332.108	0.531	2107.768	0.519	21	0.315	R.VVSCADILAFAAR.D
R4/RRR4-8/2	1394.222	1393.607	-277.117	0.533	1767.631	0.508	19	0.260	R.VVSCADILAFAAR.D
R4/RRR4-7/2	949.480	950.070	-1679.796	0.412	1302.966	0.434	15	0.194	R.GFEVIDAAK.A
R4/RRR4-5/2	949.716	950.070	-374.718	0.352	1211.448	0.426	15	0.184	R.GFEVIDAAK.A
R4/RRR4-7/2	950.042	950.070	-30.106	0.444	1202.597	0.380	14	0.177	R.GFEVIDAAK.A
R4/RRR4-7/2	1393.468	1393.607	-100.219	0.330	1133.585	0.433	16	0.175	R.VVSCADILAFAAR.D
R4/RRR4-7/2	949.459	950.070	-1701.884	0.409	1090.241	0.386	14	0.171	R.GFEVIDAAK.A
R4/RRR4-7/2	1394.893	1393.607	205.778	0.365	1106.411	0.407	16	0.170	R.VVSCADILAFAAR.D
R4/RRR4-12/2	950.072	950.070	1.210	0.385	1035.996	0.385	14	0.168	R.GFEVIDAAK.A
R4/RRR4-8/2	1393.038	1393.607	-1129.726	0.431	856.207	0.463	15	0.165	R.VVSCADILAFAAR.D
R4/RRR4-3/2	950.065	950.070	-5.620	0.316	906.279	0.359	13	0.156	R.GFEVIDAAK.A
R4/RRR4-7/2	1392.548	1393.607	-1482.869	0.356	605.968	0.392	14	0.147	R.VVSCADILAFAAR.D
R4/RRR4-9/2	1393.151	1393.607	-327.951	0.274	733.985	0.346	14	0.144	R.VVSCADILAFAAR.D
R4/RRR4-1/2	949.356	950.070	-1811.047	0.254	623.509	0.315	13	0.144	R.GFEVIDAAK.A
R4/RRR4-3/2	949.561	950.070	-1594.682	0.183	615.121	0.177	12	0.136	R.GFEVIDAAK.A
R4/RRR4-3/2	1370.379	1370.538	-117.007	0.369	703.139	0.456	13	0.153	K.VFEHAGDLVNIR.V
R4/RRR4-3/2	1370.455	1370.538	-60.716	0.322	636.192	0.313	13	0.138	K.VFEHAGDLVNIR.V
R4/RRR4-3/3	1417.445	1417.552	-75.946	0.449	1206.331	0.433	26	0.135	R.SPSSVSHLVSNFR.K
R4/RRR4-3/3	1416.833	1417.552	-1216.578	0.419	847.227	0.410	24	0.104	R.SPSSVSHLVSNFR.K
R4/RRR4-14/2	1726.464	1726.997	-891.051	0.502	1698.308	0.527	24	0.255	K.QGPGTAILLGPNFLAEK.G
R4/RRR4-14/2	1726.646	1726.997	-204.122	0.469	1113.116	0.470	21	0.181	K.QGPGTAILLGPNFLAEK.G
R4/RRR4-14/2	1726.896	1726.997	-59.032	0.491	943.086	0.517	20	0.178	K.QGPGTAILLGPNFLAEK.G
R4/RRR4-15/2	1728.010	1726.997	7.538	0.478	778.465	0.506	18	0.165	K.QGPGTAILLGPNFLAEK.G
R4/RRR4-15/2	1726.731	1726.997	-154.903	0.393	667.382	0.376	18	0.146	K.QGPGTAILLGPNFLAEK.G
R4/RRR4-11/2	1444.481	1444.608	-87.950	0.521	1530.551	0.574	18	0.249	R.APTYSILDTCFR.G
R4/RRR4-9/2	1486.465	1486.779	-211.900	0.393	2070.891	0.341	20	0.259	K.SEMIMVFGEITTK.A
R4/RRR4-16/2	1700.429	1700.920	-289.497	0.562	1565.272	0.566	25	0.250	R.NLAGNSAIFVAPNGLNK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-16/2	1701.513	1700.920	-239.878	0.610	1483.765	0.551	23	0.234	R.NLAGNSAIFVAPNGLNK.G
R4/RRR4-16/2	1700.529	1700.920	-230.657	0.567	1379.433	0.535	23	0.220	R.NLAGNSAIFVAPNGLNK.G
R4/RRR4-24/2	1833.093	1833.121	-15.336	0.481	1392.852	0.618	23	0.238	K.DAPSAVNVVVVPNVNLPK.E
R4/RRR4-4/2	1607.367	1607.786	-261.698	0.455	1830.283	0.477	22	0.261	K.SVFGEDALVNLSVEK.Q
R4/RRR4-8/2	1738.477	1738.882	-233.369	0.493	1559.344	0.565	23	0.245	K.AIGAAQAAGTAPDAYYAR.R
R4/RRR4-7/2	1755.483	1755.137	197.685	0.525	1393.830	0.601	24	0.238	R.AKLGVQAFADALLVIPK.V
R4/RRR4-9/3	1469.090	1468.637	308.846	0.568	1817.540	0.457	27	0.230	R.VTSHSLQELQPTK.S
R4/RRR4-9/3	1468.139	1468.637	-340.190	0.495	1169.639	0.495	24	0.150	R.VTSHSLQELQPTK.S
R4/RRR4-9/3	1468.811	1468.637	118.725	0.534	1118.527	0.440	24	0.130	R.VTSHSLQELQPTK.S
R4/RRR4-24/2	1530.563	1531.645	-1364.354	0.497	1881.270	0.441	21	0.257	R.AGDCALIHSGSWEK.A
R4/RRR4-23/2	1531.072	1531.645	-1030.834	0.510	1687.083	0.465	22	0.239	R.AGDCALIHSGSWEK.A
R4/RRR4-25/2	1531.122	1531.645	-998.175	0.506	1589.824	0.443	21	0.222	R.AGDCALIHSGSWEK.A
R4/RRR4-24/2	1531.163	1531.645	-315.903	0.520	1589.939	0.439	21	0.221	R.AGDCALIHSGSWEK.A
R4/RRR4-24/2	1530.531	1531.645	-1385.581	0.478	1559.216	0.439	21	0.218	R.AGDCALIHSGSWEK.A
R4/RRR4-25/2	1531.135	1531.645	-989.610	0.492	1485.455	0.453	21	0.214	R.AGDCALIHSGSWEK.A
R4/RRR4-24/2	1531.164	1531.645	-315.263	0.463	1450.474	0.414	19	0.200	R.AGDCALIHSGSWEK.A
R4/RRR4-25/2	1531.202	1531.645	-290.147	0.495	1342.921	0.431	20	0.195	R.AGDCALIHSGSWEK.A
R4/RRR4-23/2	1532.182	1531.645	-303.147	0.523	1335.387	0.423	20	0.192	R.AGDCALIHSGSWEK.A
R4/RRR4-24/2	1531.153	1531.645	-322.782	0.495	1164.372	0.444	18	0.182	R.AGDCALIHSGSWEK.A
R4/RRR4-23/3	1531.332	1531.645	-205.140	0.462	1297.258	0.541	27	0.179	R.AGDCALIHSGSWEK.A
R4/RRR4-23/2	1531.198	1531.645	-292.707	0.501	1210.677	0.399	19	0.178	R.AGDCALIHSGSWEK.A
R4/RRR4-24/3	1531.731	1531.645	56.056	0.480	1651.468	0.385	30	0.169	R.AGDCALIHSGSWEK.A
R4/RRR4-23/3	1530.880	1531.645	-1156.698	0.430	1331.762	0.462	27	0.158	R.AGDCALIHSGSWEK.A
R4/RRR4-24/2	1531.155	1531.645	-321.342	0.398	1446.931	0.162	20	0.155	R.AGDCALIHSGSWEK.A
R4/RRR4-25/3	1531.187	1531.645	-300.034	0.441	1355.061	0.446	28	0.155	R.AGDCALIHSGSWEK.A
R4/RRR4-25/2	1531.254	1531.645	-256.315	0.341	1294.831	0.092	20	0.140	R.AGDCALIHSGSWEK.A
R4/RRR4-24/3	1531.821	1531.645	114.800	0.478	1125.825	0.450	26	0.135	R.AGDCALIHSGSWEK.A
R4/RRR4-24/3	1531.205	1531.645	-288.397	0.418	1197.165	0.412	27	0.131	R.AGDCALIHSGSWEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-24/3	1531.808	1531.645	106.768	0.503	1205.051	0.409	27	0.130	R.AGDCALIHSGSWEK.A
R4/RRR4-21/3	1531.536	1531.645	-71.527	0.426	1463.025	0.319	29	0.129	R.AGDCALIHSGSWEK.A
R4/RRR4-25/3	1532.807	1531.645	105.940	0.417	1208.481	0.392	27	0.127	R.AGDCALIHSGSWEK.A
R4/RRR4-24/3	1532.605	1531.645	-26.221	0.407	1134.641	0.400	27	0.124	R.AGDCALIHSGSWEK.A
R4/RRR4-23/3	1532.800	1531.645	101.507	0.462	1031.549	0.425	25	0.123	R.AGDCALIHSGSWEK.A
R4/RRR4-24/3	1531.755	1531.645	71.762	0.424	983.263	0.438	26	0.123	R.AGDCALIHSGSWEK.A
R4/RRR4-25/3	1531.502	1531.645	-93.714	0.423	1021.201	0.423	25	0.122	R.AGDCALIHSGSWEK.A
R4/RRR4-26/3	1531.469	1531.645	-115.421	0.434	1038.446	0.395	25	0.117	R.AGDCALIHSGSWEK.A
R4/RRR4-26/3	1530.791	1531.645	-1214.832	0.393	1256.089	0.328	27	0.116	R.AGDCALIHSGSWEK.A
R4/RRR4-20/3	1532.153	1531.645	-322.061	0.447	1027.434	0.390	26	0.115	R.AGDCALIHSGSWEK.A
R4/RRR4-26/3	1530.684	1531.645	-1284.986	0.429	1050.487	0.357	27	0.110	R.AGDCALIHSGSWEK.A
R4/RRR4-1/3	1530.451	1531.645	-1438.303	0.434	1008.185	0.343	25	0.106	R.AGDCALIHSGSWEK.A
R4/RRR4-2/3	1531.852	1531.645	135.299	0.456	709.524	0.382	22	0.105	R.AGDCALIHSGSWEK.A
R4/RRR4-25/3	1531.475	1531.645	-111.463	0.429	1110.068	0.307	25	0.104	R.AGDCALIHSGSWEK.A
R4/RRR4-1/3	1531.625	1531.645	-13.487	0.469	1083.245	0.319	26	0.104	R.AGDCALIHSGSWEK.A
R4/RRR4-27/3	1532.114	1531.645	306.690	0.389	903.204	0.316	24	0.099	R.AGDCALIHSGSWEK.A
R4/RRR4-24/3	1531.293	1531.645	-230.452	0.318	681.971	0.214	19	0.091	-.AGDCALIHSGSWEK.-
R4/RRR4-19/3	1531.454	1531.645	-125.256	0.349	828.545	0.197	23	0.088	R.AGDCALIHSGSWEK.A
R4/RRR4-13/3	1531.317	1531.645	-215.217	0.337	789.643	0.125	22	0.087	R.AGDCALIHSGSWEK.A
R4/RRR4-27/3	1530.937	1531.645	-1119.467	0.282	920.769	0.151	23	0.085	R.AGDCALIHSGSWEK.A
R4/RRR4-25/3	1531.866	1531.645	144.290	0.373	747.388	0.176	21	0.084	-.AGDCALIHSGSWEK.-
R4/RRR4-22/3	1429.054	1429.511	-321.049	0.529	1855.940	0.447	29	0.223	K.DCRPVESSEPPR.Y
R4/RRR4-22/3	1429.604	1429.511	64.856	0.548	1224.605	0.487	25	0.152	K.DCRPVESSEPPR.Y
R4/RRR4-22/3	1429.702	1429.511	133.705	0.537	1208.627	0.458	26	0.142	K.DCRPVESSEPPR.Y
R4/RRR4-21/3	1429.660	1429.511	104.548	0.491	1154.445	0.426	26	0.128	K.DCRPVESSEPPR.Y
R4/RRR4-21/3	1430.686	1429.511	122.145	0.523	1107.262	0.435	26	0.127	K.DCRPVESSEPPR.Y
R4/RRR4-22/3	1428.982	1429.511	-1073.601	0.512	1160.349	0.412	28	0.124	K.DCRPVESSEPPR.Y
R4/RRR4-21/3	1430.479	1429.511	-22.915	0.542	1121.330	0.413	26	0.123	K.DCRPVESSEPPR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-9/2	1458.237	1458.596	-246.816	0.419	1651.640	0.520	20	0.246	R.EADPLDSQVVTVGK.F
R4/RRR4-9/2	1458.022	1458.596	-1082.817	0.385	1677.008	0.504	20	0.245	R.EADPLDSQVVTVGK.F
R4/RRR4-9/2	1458.336	1458.596	-178.878	0.398	1615.287	0.452	20	0.226	R.EADPLDSQVVTVGK.F
R4/RRR4-7/2	1754.668	1754.961	-167.788	0.485	1610.773	0.534	23	0.246	K.EGVAFYNSLIDDVIAK.G
R4/RRR4-7/2	1754.443	1754.961	-867.908	0.481	1574.467	0.551	22	0.245	K.EGVAFYNSLIDDVIAK.G
R4/RRR4-7/2	1755.551	1754.961	-234.447	0.550	923.882	0.611	19	0.194	K.EGVAFYNSLIDDVIAK.G
R4/RRR4-10/2	1934.500	1934.179	166.417	0.573	1545.269	0.540	25	0.240	K.LITELIGSPDDSSLGFLR.S
R4/RRR4-24/3	1914.586	1914.959	-195.219	0.586	1455.512	0.574	32	0.218	K.KDGEEESSGVVDYDKEK.K
R4/RRR4-24/3	1914.668	1914.959	-152.527	0.535	1083.736	0.518	30	0.149	K.KDGEEESSGVVDYDKEK.K
R4/RRR4-24/3	1914.621	1914.959	-176.991	0.314	630.428	0.262	26	0.082	K.KDGEEESSGVVDYDKEK.K
R4/RRR4-11/2	1310.076	1309.493	-319.775	0.456	1753.718	0.476	18	0.251	K.GPDPDLLAIIER.M
R4/RRR4-4/2	1782.943	1783.020	-43.030	0.403	1671.741	0.494	21	0.241	R.IIWSPDGTLFGVAYSR.H
R4/RRR4-3/2	1784.142	1783.020	68.652	0.402	803.709	0.471	18	0.161	R.IIWSPDGTLFGVAYSR.H
R4/RRR4-2/2	1783.916	1783.020	-58.175	0.298	176.771	0.305	14	0.133	-.IIWSPDGTLFGVAYSR.-
R4/RRR4-2/2	1732.353	1732.871	-878.975	0.455	1460.591	0.551	20	0.228	K.NALQELDTVASSGEVAK.L
R4/RRR4-4/2	1506.105	1504.753	234.645	0.403	756.175	0.408	18	0.153	R.ILLLPNGTDIYGSK.Y
R4/RRR4-4/3	1764.677	1765.007	-187.693	0.315	1038.803	0.325	26	0.095	R.VLQLINVTDTGVHAQR.Y
R4/RRR4-17/2	1587.204	1586.726	301.955	0.526	1177.798	0.620	25	0.222	K.DLALPVSGVSAEENGK.A
R4/RRR4-17/2	1586.448	1586.726	-175.855	0.488	1185.879	0.570	25	0.211	K.DLALPVSGVSAEENGK.A
R4/RRR4-16/2	1586.207	1586.726	-960.346	0.497	1128.194	0.544	24	0.201	K.DLALPVSGVSAEENGK.A
R4/RRR4-17/2	1585.944	1586.726	-1126.719	0.362	1231.958	0.414	25	0.182	K.DLALPVSGVSAEENGK.A
R4/RRR4-23/2	1773.064	1773.003	34.361	0.531	1684.334	0.495	21	0.246	R.AM*SILNSFVNDIFER.V
R4/RRR4-19/2	1615.890	1616.760	-1160.772	0.465	1647.172	0.509	23	0.246	K.GQQPLQGDITAANFR.T
R4/RRR4-19/2	1615.779	1616.760	-1229.808	0.427	1477.066	0.434	22	0.208	K.GQQPLQGDITAANFR.T
R4/RRR4-19/2	1616.968	1616.760	128.829	0.420	1324.152	0.434	21	0.193	K.GQQPLQGDITAANFR.T
R4/RRR4-5/3	1391.780	1391.649	94.242	0.494	1848.666	0.432	31	0.222	R.AALRPGVPFAVHR.M
R4/RRR4-5/3	1391.449	1391.649	-144.238	0.471	1626.999	0.437	29	0.188	R.AALRPGVPFAVHR.M
R4/RRR4-22/2	1159.158	1158.330	-148.362	0.316	831.733	0.207	13	0.131	-.TDNKVLDPKK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1519.919	1518.683	155.341	0.262	830.495	0.091	17	0.125	R.MNVGTNRGDAHAFK.L
R4/RRR4-12/2	1386.662	1385.593	49.833	0.446	1584.861	0.526	23	0.242	R.DVGVSPAIVGAFPR.K
R4/RRR4-12/2	1386.979	1385.593	278.986	0.453	1571.588	0.518	21	0.238	R.DVGVSPAIVGAFPR.K
R4/RRR4-12/2	1386.052	1385.593	332.173	0.405	765.439	0.502	17	0.165	R.DVGVSPAIVGAFPR.K
R4/RRR4-9/2	1753.628	1754.018	-223.184	0.539	1272.281	0.596	24	0.224	K.IQLLDLPGIIEGASEGK.G
R4/RRR4-9/2	1753.255	1754.018	-1008.513	0.494	1284.356	0.536	24	0.211	K.IQLLDLPGIIEGASEGK.G
R4/RRR4-10/2	958.936	959.082	-153.102	0.420	1740.843	0.460	16	0.245	R.AVVSAIGADR.V
R4/RRR4-4/2	1088.073	1088.346	-251.789	0.205	757.471	0.231	13	0.134	-.LLAMEELLR.-
R4/RRR4-4/3	1541.144	1540.703	286.422	0.445	803.514	0.518	24	0.122	K.STGHSVEVKPQGVSK.G
R4/RRR4-11/2	1836.343	1835.005	184.980	0.478	1452.615	0.557	21	0.230	K.NGVEEVLGLGQLSDFEK.E
R4/RRR4-11/2	1834.495	1835.005	-825.630	0.463	1363.585	0.548	21	0.218	K.NGVEEVLGLGQLSDFEK.E
R4/RRR4-11/2	1834.488	1835.005	-829.304	0.456	967.191	0.539	20	0.182	K.NGVEEVLGLGQLSDFEK.E
R4/RRR4-11/2	1835.261	1835.005	140.191	0.409	410.383	0.375	18	0.144	K.NGVEEVLGLGQLSDFEK.E
R4/RRR4-23/2	1343.238	1343.551	-234.038	0.509	1477.274	0.533	19	0.233	R.TPEGTIIELTIR.G
R4/RRR4-24/2	1342.586	1343.551	-1468.288	0.497	1302.135	0.526	18	0.212	R.TPEGTIIELTIR.G
R4/RRR4-23/2	1342.812	1343.551	-1298.994	0.449	1276.974	0.523	18	0.208	R.TPEGTIIELTIR.G
R4/RRR4-24/2	1343.177	1343.551	-279.809	0.468	1203.764	0.509	18	0.200	R.TPEGTIIELTIR.G
R4/RRR4-23/2	1342.658	1343.551	-1413.951	0.440	1076.689	0.524	18	0.192	R.TPEGTIIELTIR.G
R4/RRR4-24/2	1342.550	1343.551	-1495.231	0.430	1223.445	0.461	18	0.192	R.TPEGTIIELTIR.G
R4/RRR4-25/2	1344.583	1343.551	23.347	0.341	504.525	0.425	14	0.150	R.TPEGTIIELTIR.G
R4/RRR4-2/2	1441.108	1439.677	299.602	0.396	743.553	0.419	14	0.153	K.LPACFFILTNSR.S
R4/RRR4-1/2	1440.426	1439.677	-174.727	0.314	719.877	0.449	14	0.152	K.LPACFFILTNSR.S
R4/RRR4-2/3	1361.959	1361.615	253.311	0.465	1091.760	0.500	26	0.143	K.SPAILQVHPSALK.Q
R4/RRR4-2/3	1361.347	1361.615	-197.298	0.357	817.713	0.479	23	0.114	K.SPAILQVHPSALK.Q
R4/RRR4-2/3	1361.132	1361.615	-356.005	0.277	531.385	0.393	20	0.090	K.SPAILQVHPSALK.Q
R4/RRR4-14/3	1413.769	1413.606	115.076	0.486	1190.667	0.601	28	0.185	R.LPAAGPPSPAEHLR.E
R4/RRR4-15/3	1413.691	1413.606	59.870	0.472	1081.212	0.584	28	0.166	R.LPAAGPPSPAEHLR.E
R4/RRR4-14/3	1413.536	1413.606	-49.651	0.503	1007.873	0.599	27	0.164	R.LPAAGPPSPAEHLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/3	1413.825	1413.606	155.081	0.515	892.513	0.592	26	0.151	R.LPAAGPPSPAEHLR.E
R4/RRR4-15/3	1413.139	1413.606	-331.683	0.462	918.713	0.579	26	0.149	R.LPAAGPPSPAEHLR.E
R4/RRR4-15/3	1413.196	1413.606	-291.123	0.472	706.734	0.622	23	0.143	R.LPAAGPPSPAEHLR.E
R4/RRR4-9/3	1599.305	1598.869	273.288	0.469	1545.724	0.518	27	0.207	R.TPFYLYSKPQVVR.N
R4/RRR4-9/3	1598.975	1598.869	66.601	0.498	1190.957	0.494	26	0.151	R.TPFYLYSKPQVVR.N
R4/RRR4-9/3	1600.051	1598.869	113.922	0.369	1033.057	0.324	25	0.097	R.TPFYLYSKPQVVR.N
R4/RRR4-12/2	1353.991	1353.465	-351.090	0.509	1225.931	0.587	19	0.220	R.DNVQAYPGVSFR.Y
R4/RRR4-12/2	1353.053	1353.465	-305.094	0.437	1263.353	0.459	19	0.196	R.DNVQAYPGVSFR.Y
R4/RRR4-12/2	1353.185	1353.465	-206.983	0.489	1088.403	0.493	18	0.189	R.DNVQAYPGVSFR.Y
R4/RRR4-12/2	1352.966	1353.465	-369.908	0.412	915.153	0.488	17	0.175	R.DNVQAYPGVSFR.Y
R4/RRR4-11/2	1353.106	1353.465	-265.540	0.445	836.284	0.469	16	0.168	R.DNVQAYPGVSFR.Y
R4/RRR4-11/2	1353.210	1353.465	-188.884	0.401	819.476	0.460	16	0.165	R.DNVQAYPGVSFR.Y
R4/RRR4-11/2	1353.208	1353.465	-190.151	0.273	621.612	0.229	13	0.136	R.DNVQAYPGVSFR.Y
R4/RRR4-14/3	1737.105	1737.725	-935.503	0.335	267.650	0.617	21	0.108	R.GYGDSYQNDRDYQR.K
R4/RRR4-10/2	1985.821	1986.294	-239.137	0.482	1569.859	0.504	26	0.233	R.NEGLAQLPFLTLGGCLPGK.I
R4/RRR4-10/2	1985.340	1986.294	-987.256	0.445	932.140	0.517	23	0.176	R.NEGLAQLPFLTLGGCLPGK.I
R4/RRR4-10/2	1984.931	1986.294	-1194.097	0.430	1170.391	0.404	24	0.174	R.NEGLAQLPFLTLGGCLPGK.I
R4/RRR4-15/3	1467.509	1468.556	-1398.748	0.527	1898.400	0.366	27	0.202	R.HYNDISELSPHR.L
R4/RRR4-16/3	1468.663	1468.556	73.344	0.586	1789.167	0.339	26	0.174	R.HYNDISELSPHR.L
R4/RRR4-15/3	1468.260	1468.556	-201.944	0.426	1295.133	0.327	25	0.115	R.HYNDISELSPHR.L
R4/RRR4-17/3	1468.727	1468.556	116.981	0.417	933.583	0.204	20	0.074	-.HYNDISELSPHR.-
R4/RRR4-26/2	1540.380	1539.711	-215.054	0.510	1272.950	0.600	18	0.222	R.FLFCQSSPASAPAR.E
R4/RRR4-26/2	1539.395	1539.711	-205.886	0.446	1036.441	0.578	17	0.194	R.FLFCQSSPASAPAR.E
R4/RRR4-26/2	1539.937	1539.711	147.597	0.419	1006.658	0.515	18	0.181	R.FLFCQSSPASAPAR.E
R4/RRR4-8/3	1626.821	1626.883	-37.722	0.396	1411.243	0.541	32	0.196	K.VAQGVVGAVADKGSVLR.F
R4/RRR4-8/3	1627.228	1626.883	213.183	0.382	1239.319	0.459	32	0.145	K.VAQGVVGAVADKGSVLR.F
R4/RRR4-8/3	1625.597	1626.883	-1410.457	0.268	612.038	0.286	24	0.082	K.VAQGVVGAVADKGSVLR.F
R4/RRR4-11/2	1550.383	1550.783	-258.839	0.531	1688.225	0.453	19	0.236	K.TLFVINFDPINTR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1550.371	1550.783	-266.738	0.266	669.157	0.167	15	0.131	K.TLFVINFDPINTR.T
R4/RRR4-15/2	1662.926	1661.927	-0.413	0.472	1433.078	0.539	20	0.227	R.HVQLTVPLEQLIDR.L
R4/RRR4-11/2	1215.377	1215.298	64.513	0.473	1616.912	0.484	21	0.236	R.AVAGGGAAGEEAVR.A
R4/RRR4-11/2	1215.110	1215.298	-155.537	0.489	1446.116	0.484	20	0.216	R.AVAGGGAAGEEAVR.A
R4/RRR4-11/2	1214.459	1215.298	-1519.556	0.445	1410.407	0.450	20	0.205	R.AVAGGGAAGEEAVR.A
R4/RRR4-8/2	1553.787	1553.739	30.762	0.433	1672.731	0.461	18	0.236	K.YFYDIKDLSNFK.A
R4/RRR4-8/2	1554.918	1553.739	115.308	0.385	459.678	0.396	15	0.148	K.YFYDIKDLSNFK.A
R4/RRR4-22/3	1775.259	1774.999	146.818	0.506	1733.754	0.439	30	0.211	R.IIKDFIVQGGDPTGTGR.G
R4/RRR4-22/3	1774.584	1774.999	-234.286	0.463	1356.990	0.396	28	0.142	R.IIKDFIVQGGDPTGTGR.G
R4/RRR4-22/3	1774.465	1774.999	-867.024	0.382	1106.986	0.255	25	0.090	R.IIKDFIVQGGDPTGTGR.G
R4/RRR4-6/2	1596.613	1596.807	-121.669	0.427	1596.942	0.483	22	0.230	R.DGEAILQLIGGDVAPK.D
R4/RRR4-6/2	1597.660	1596.807	-92.085	0.499	1462.096	0.494	21	0.218	R.DGEAILQLIGGDVAPK.D
R4/RRR4-28/2	1495.369	1495.605	-158.073	0.486	1627.700	0.475	22	0.236	R.VCACVDSAGAVTER.G
R4/RRR4-16/2	1571.283	1570.861	269.638	0.465	1473.118	0.543	21	0.233	R.AVLVLQQNLTPFAR.S
R4/RRR4-16/2	1572.433	1570.861	-272.806	0.278	810.755	0.309	16	0.141	R.AVLVLQQNLTPFAR.S
R4/RRR4-2/2	1823.712	1823.037	-178.555	0.603	1311.130	0.513	20	0.205	K.YSGQINSLEETLVQIK.G
R4/RRR4-24/2	1603.537	1603.755	-135.957	0.515	1108.299	0.584	24	0.209	K.NDIPIYEAEVGSAPK.K
R4/RRR4-3/2	1576.793	1575.874	-51.762	0.452	1556.488	0.479	22	0.225	K.LLILGSPGAGTSTIFK.Q
R4/RRR4-4/2	1577.278	1575.874	257.047	0.370	421.875	0.504	15	0.148	K.LLILGSPGAGTSTIFK.Q
R4/RRR4-15/2	1793.128	1794.087	-1095.610	0.467	1047.635	0.592	25	0.201	K.LQLAPPGQEPAAVVFQK.V
R4/RRR4-17/3	1858.749	1859.081	-178.951	0.471	1210.540	0.565	30	0.179	R.AAHGGPAFEPHATVVGAIR.L
R4/RRR4-17/3	1859.024	1859.081	-30.739	0.424	1069.000	0.521	30	0.147	R.AAHGGPAFEPHATVVGAIR.L
R4/RRR4-17/3	1859.612	1859.081	-252.774	0.305	1282.799	0.404	29	0.136	R.AAHGGPAFEPHATVVGAIR.L
R4/RRR4-15/2	1757.811	1758.003	-109.746	0.516	1201.913	0.557	23	0.209	R.VEAVQLPVSDGITLCR.R
R4/RRR4-15/2	1757.320	1758.003	-960.684	0.484	1165.133	0.546	23	0.203	R.VEAVQLPVSDGITLCR.R
R4/RRR4-23/3	1716.432	1716.868	-255.135	0.490	901.899	0.597	27	0.153	R.VPDEVIDKVQEETSK.S
R4/RRR4-23/3	1716.604	1716.868	-154.327	0.503	817.590	0.516	27	0.126	R.VPDEVIDKVQEETSK.S
R4/RRR4-23/3	1716.177	1716.868	-988.253	0.432	776.056	0.475	26	0.114	R.VPDEVIDKVQEETSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/3	1716.313	1716.868	-908.563	0.328	461.874	0.457	22	0.099	R.VPDEVIDKVQEETSK.S
R4/RRR4-5/2	1732.566	1732.056	-283.138	0.555	970.619	0.566	20	0.191	K.EGILPIVLYFNEPVK.G
R4/RRR4-9/3	1902.179	1902.181	-0.754	0.519	1168.830	0.562	29	0.172	K.TPLKDLLETTLTYQHK.T
R4/RRR4-9/3	1902.256	1902.181	39.698	0.487	978.916	0.473	26	0.126	K.TPLKDLLETTLTYQHK.T
R4/RRR4-17/2	966.500	967.190	-1754.156	0.494	1374.700	0.512	15	0.219	K.AILLQGVPR.N
R4/RRR4-17/2	967.133	967.190	-59.135	0.548	1371.732	0.481	15	0.213	K.AILLQGVPR.N
R4/RRR4-17/2	966.707	967.190	-501.687	0.484	1339.962	0.442	14	0.200	K.AILLQGVPR.N
R4/RRR4-12/2	1390.152	1390.523	-267.887	0.480	1568.149	0.471	19	0.228	K.IVETSDEWIAAR.T
R4/RRR4-12/2	1390.094	1390.523	-310.088	0.485	1589.852	0.456	19	0.227	K.IVETSDEWIAAR.T
R4/RRR4-12/2	1389.998	1390.523	-1100.839	0.423	1441.069	0.365	18	0.191	K.IVETSDEWIAAR.T
R4/RRR4-13/2	1523.241	1523.630	-255.895	0.512	1471.538	0.495	20	0.223	K.VLSDNFEQLNTSR.A
R4/RRR4-13/2	1524.132	1523.630	-327.321	0.581	1443.383	0.508	20	0.223	K.VLSDNFEQLNTSR.A
R4/RRR4-13/2	1524.320	1523.630	-203.987	0.569	1260.368	0.529	20	0.211	K.VLSDNFEQLNTSR.A
R4/RRR4-17/2	1141.835	1141.346	430.133	0.472	1492.837	0.490	17	0.224	R.LVNILNAANAK.A
R4/RRR4-17/2	1141.084	1141.346	-229.791	0.454	1205.291	0.455	17	0.190	R.LVNILNAANAK.A
R4/RRR4-17/2	1141.211	1141.346	-118.510	0.308	493.028	0.420	13	0.146	R.LVNILNAANAK.A
R4/RRR4-15/2	1264.309	1264.453	-114.234	0.367	1495.706	0.484	17	0.218	K.DIGNAVYALISK.E
R4/RRR4-15/2	1264.056	1264.453	-314.854	0.431	676.870	0.456	15	0.158	K.DIGNAVYALISK.E
R4/RRR4-15/2	1263.673	1264.453	-1412.416	0.328	631.198	0.415	14	0.148	K.DIGNAVYALISK.E
R4/RRR4-10/2	1879.964	1878.979	-8.246	0.393	231.521	0.544	15	0.142	-.GASQGGYGAYNAYISAATR.-
R4/RRR4-3/2	956.568	957.109	-1616.087	0.340	928.176	0.293	13	0.148	R.AVAIENALR.L
R4/RRR4-3/2	956.486	957.109	-1702.246	0.366	721.030	0.334	12	0.147	R.AVAIENALR.L
R4/RRR4-3/3	1301.751	1300.486	203.938	0.434	1124.320	0.201	22	0.077	-.AKDTVTVIEAPR.-
R4/RRR4-19/2	1284.921	1285.409	-380.766	0.424	1338.773	0.526	19	0.214	R.AQGLYM*GSDQAK.L
R4/RRR4-19/2	1284.872	1285.409	-1199.519	0.451	980.630	0.501	17	0.181	R.AQGLYM*GSDQAK.L
R4/RRR4-19/2	1284.482	1285.409	-1504.621	0.407	935.961	0.480	17	0.174	R.AQGLYM*GSDQAK.L
R4/RRR4-7/2	1542.313	1541.731	-271.942	0.297	1834.146	0.310	20	0.218	R.ESDLAAAVAVAPVATR.K
R4/RRR4-6/2	1541.613	1541.731	-76.769	0.288	1480.357	0.258	18	0.171	R.ESDLAAAVAVAPVATR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1541.861	1541.731	84.045	0.322	1169.991	0.302	17	0.156	R.ESDLAAAVAVAPVATR.K
R4/RRR4-7/2	1542.424	1541.731	-199.608	0.305	1224.313	0.262	17	0.154	R.ESDLAAAVAVAPVATR.K
R4/RRR4-7/2	1541.853	1541.731	79.440	0.328	1027.593	0.302	16	0.148	R.ESDLAAAVAVAPVATR.K
R4/RRR4-6/2	1542.207	1541.731	309.574	0.324	957.753	0.296	15	0.144	-.ESDLAAAVAVAPVATR.-
R4/RRR4-6/2	1701.942	1702.803	-1096.758	0.466	1557.089	0.465	19	0.221	R.FTTEVSNYLAQGESR.E
R4/RRR4-5/2	1788.796	1788.034	-133.444	0.489	1371.785	0.514	21	0.213	R.ITFILDDDPDIIAVAR.D
R4/RRR4-19/2	1828.256	1828.960	-934.995	0.524	1144.424	0.551	21	0.199	R.VVGNSVSEFQSGFSDIR.T
R4/RRR4-19/2	1828.182	1828.960	-975.551	0.525	1116.721	0.541	21	0.195	R.VVGNSVSEFQSGFSDIR.T
R4/RRR4-19/2	1828.372	1828.960	-871.253	0.510	1137.698	0.532	21	0.195	R.VVGNSVSEFQSGFSDIR.T
R4/RRR4-3/2	1996.140	1995.258	-59.166	0.488	577.054	0.559	16	0.159	R.YVNLGPIVDFCVVDLDR.Q
R4/RRR4-13/2	1386.241	1385.504	-190.036	0.413	1242.323	0.540	18	0.206	K.NVYYDVAPSTQK.A
R4/RRR4-17/2	1566.262	1566.520	-165.380	0.491	1500.593	0.474	20	0.220	K.SDGSENDIESDIER.S
R4/RRR4-4/2	1267.512	1266.469	34.812	0.418	1201.440	0.547	16	0.202	K.SVGNLLYTVATK.Y
R4/RRR4-10/2	1992.701	1993.240	-774.766	0.447	300.631	0.528	16	0.151	R.QLDYVPATISCLEEVVR.E
R4/RRR4-10/2	1992.590	1993.240	-830.786	0.405	243.923	0.434	14	0.141	R.QLDYVPATISCLEEVVR.E
R4/RRR4-22/2	1585.295	1585.739	-281.251	0.505	1272.267	0.533	22	0.210	K.STGFGLIYDNLDAAK.K
R4/RRR4-22/2	1585.066	1585.739	-1059.099	0.467	1213.600	0.528	22	0.204	K.STGFGLIYDNLDAAK.K
R4/RRR4-21/2	1585.315	1585.739	-268.350	0.483	1122.499	0.549	21	0.200	K.STGFGLIYDNLDAAK.K
R4/RRR4-20/2	1585.399	1585.739	-215.203	0.507	1212.185	0.492	21	0.196	K.STGFGLIYDNLDAAK.K
R4/RRR4-21/2	1585.425	1585.739	-198.982	0.491	1127.377	0.527	21	0.196	K.STGFGLIYDNLDAAK.K
R4/RRR4-20/2	1585.189	1585.739	-981.045	0.474	1067.460	0.495	20	0.185	K.STGFGLIYDNLDAAK.K
R4/RRR4-19/2	1585.628	1585.739	-70.237	0.484	946.611	0.508	20	0.180	K.STGFGLIYDNLDAAK.K
R4/RRR4-12/2	1585.369	1585.739	-234.592	0.355	230.353	0.368	14	0.142	-.STGFGLIYDNLDAAK.-
R4/RRR4-3/2	1639.718	1638.590	78.432	0.426	440.790	0.564	16	0.156	R.NNTSQSADESLGDSGR.G
R4/RRR4-18/2	1824.147	1825.078	-1062.108	0.541	910.040	0.552	20	0.185	K.AFM*IDKDQVDWIQAK.F
R4/RRR4-17/2	1826.296	1825.078	119.665	0.450	554.938	0.502	18	0.160	K.AFM*IDKDQVDWIQAK.F
R4/RRR4-17/2	1824.657	1825.078	-231.569	0.365	506.682	0.464	17	0.151	K.AFM*IDKDQVDWIQAK.F
R4/RRR4-18/2	1825.044	1825.078	-19.056	0.358	412.095	0.450	15	0.147	K.AFM*IDKDQVDWIQAK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-17/3	1824.996	1825.078	-45.027	0.519	1246.003	0.418	24	0.137	K.AFM*IDKDQVDWIQAK.F
R4/RRR4-17/3	1825.069	1825.078	-5.176	0.344	566.593	0.309	19	0.080	-.AFM*IDKDQVDWIQAK.-
R4/RRR4-11/2	1157.946	1158.244	-257.955	0.493	1596.677	0.433	19	0.224	K.VASDDLDPAVR.E
R4/RRR4-11/2	1158.078	1158.244	-143.215	0.501	1501.801	0.465	19	0.221	K.VASDDLDPAVR.E
R4/RRR4-11/2	1158.002	1158.244	-209.306	0.476	1460.266	0.457	19	0.215	K.VASDDLDPAVR.E
R4/RRR4-8/2	1472.233	1472.671	-298.443	0.419	402.468	0.560	18	0.159	R.VAPAPPAGEPALPER.A
R4/RRR4-4/3	1950.295	1950.056	122.812	0.422	450.664	0.561	23	0.116	R.YGAIWTGDNSADWDHLK.S
R4/RRR4-4/3	1949.876	1950.056	-92.663	0.383	691.135	0.430	26	0.103	R.YGAIWTGDNSADWDHLK.S
R4/RRR4-4/3	1948.844	1950.056	-1138.406	0.357	387.469	0.457	21	0.100	R.YGAIWTGDNSADWDHLK.S
R4/RRR4-3/3	1950.407	1950.056	180.621	0.319	420.164	0.365	23	0.093	R.YGAIWTGDNSADWDHLK.S
R4/RRR4-3/3	1950.185	1950.056	66.504	0.365	664.040	0.269	24	0.085	R.YGAIWTGDNSADWDHLK.S
R4/RRR4-22/2	1235.205	1235.486	-228.141	0.496	1401.038	0.508	18	0.220	R.KVVGCSCVVVK.D
R4/RRR4-22/2	1235.064	1235.486	-342.964	0.524	1217.022	0.491	17	0.199	R.KVVGCSCVVVK.D
R4/RRR4-22/2	1236.141	1235.486	-279.671	0.535	1005.880	0.421	16	0.171	R.KVVGCSCVVVK.D
R4/RRR4-6/2	1341.121	1341.452	-247.554	0.458	266.987	0.502	14	0.154	R.TQVEHGIQDSVK.Q
R4/RRR4-15/2	1268.249	1268.444	-154.812	0.374	824.638	0.255	15	0.136	R.ATAPASSSPLLPR.T
R4/RRR4-5/3	1758.273	1756.937	191.723	0.434	929.881	0.389	25	0.103	K.GGDVPHETQFLLVESK.A
R4/RRR4-5/2	1404.152	1404.578	-304.270	0.463	1426.862	0.486	18	0.214	R.IANAAQQM*ANVTR.G
R4/RRR4-5/2	1404.388	1404.578	-135.610	0.464	1402.803	0.485	18	0.211	R.IANAAQQM*ANVTR.G
R4/RRR4-5/2	1404.329	1404.578	-177.813	0.479	1113.430	0.451	17	0.180	R.IANAAQQM*ANVTR.G
R4/RRR4-16/2	1618.267	1618.801	-951.081	0.430	1653.166	0.445	20	0.229	R.CAAEITLQCPGELR.A
R4/RRR4-9/2	1762.517	1762.985	-266.378	0.463	688.766	0.572	22	0.171	K.LLEATGISTVPGSGFGQK.E
R4/RRR4-11/2	1246.173	1245.408	-189.093	0.523	1346.044	0.494	19	0.209	K.NSLSGTIPASLGK.I
R4/RRR4-12/2	1246.386	1245.408	-17.742	0.536	1180.526	0.476	19	0.192	K.NSLSGTIPASLGK.I
R4/RRR4-11/2	1245.757	1245.408	280.931	0.460	999.515	0.448	18	0.174	K.NSLSGTIPASLGK.I
R4/RRR4-13/2	1245.211	1245.408	-158.758	0.350	975.906	0.428	18	0.167	K.NSLSGTIPASLGK.I
R4/RRR4-12/2	1245.061	1245.408	-279.339	0.338	820.867	0.368	16	0.151	K.NSLSGTIPASLGK.I
R4/RRR4-13/2	1244.849	1245.408	-1255.949	0.283	514.945	0.381	16	0.145	K.NSLSGTIPASLGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1769.543	1769.034	-278.675	0.494	730.072	0.562	19	0.177	K.QLLQWPIEEIETLR.R
R4/RRR4-6/2	1768.653	1769.034	-216.027	0.423	739.166	0.502	19	0.167	K.QLLQWPIEEIETLR.R
R4/RRR4-6/2	1769.753	1769.034	-159.163	0.480	746.082	0.479	19	0.166	K.QLLQWPIEEIETLR.R
R4/RRR4-8/2	1537.527	1536.926	-260.286	0.429	1028.271	0.563	18	0.191	R.VAPLQVIVIPVPYK.D
R4/RRR4-8/2	1536.536	1536.926	-254.079	0.277	1156.129	0.398	18	0.169	R.VAPLQVIVIPVPYK.D
R4/RRR4-8/2	1536.531	1536.926	-257.427	0.280	1023.144	0.374	17	0.158	R.VAPLQVIVIPVPYK.D
R4/RRR4-7/2	1538.052	1536.926	82.104	0.350	517.964	0.294	15	0.138	R.VAPLQVIVIPVPYK.D
R4/RRR4-16/2	1324.049	1324.508	-347.841	0.484	1545.620	0.441	18	0.218	K.SELLLSSNPVHK.K
R4/RRR4-16/2	1323.808	1324.508	-1288.139	0.446	1477.500	0.448	18	0.212	K.SELLLSSNPVHK.K
R4/RRR4-16/2	1324.093	1324.508	-314.448	0.477	1268.543	0.444	18	0.193	K.SELLLSSNPVHK.K
R4/RRR4-5/3	1602.679	1602.768	-55.709	0.364	1663.748	0.389	28	0.180	R.KIEDDDASASVPVKK.I
R4/RRR4-5/3	1602.527	1602.768	-151.064	0.490	883.684	0.449	25	0.114	R.KIEDDDASASVPVKK.I
R4/RRR4-15/2	1143.471	1142.332	122.000	0.450	1267.943	0.517	16	0.208	R.HAGIIDIQFK.R
R4/RRR4-15/2	1141.516	1142.332	-1595.955	0.336	948.238	0.503	15	0.175	R.HAGIIDIQFK.R
R4/RRR4-15/2	1141.489	1142.332	-1619.482	0.270	907.457	0.486	16	0.166	R.HAGIIDIQFK.R
R4/RRR4-15/2	1141.705	1142.332	-1429.683	0.278	701.217	0.451	15	0.154	R.HAGIIDIQFK.R
R4/RRR4-11/3	1505.588	1504.676	-58.407	0.447	1074.913	0.555	29	0.159	R.LAAALSSPAHPAGGAGR.N
R4/RRR4-11/3	1503.746	1504.676	-1287.488	0.433	852.302	0.540	28	0.134	R.LAAALSSPAHPAGGAGR.N
R4/RRR4-11/3	1504.874	1504.676	131.989	0.420	891.502	0.461	28	0.119	R.LAAALSSPAHPAGGAGR.N
R4/RRR4-10/3	1505.023	1504.676	231.306	0.376	770.994	0.474	26	0.115	R.LAAALSSPAHPAGGAGR.N
R4/RRR4-10/3	1504.191	1504.676	-323.734	0.360	593.796	0.488	24	0.110	R.LAAALSSPAHPAGGAGR.N
R4/RRR4-10/3	1504.398	1504.676	-185.252	0.329	581.052	0.339	21	0.090	-.LAAALSSPAHPAGGAGR.-
R4/RRR4-12/3	1503.629	1504.676	-1365.514	0.260	609.747	0.291	20	0.083	-.LAAALSSPAHPAGGAGR.-
R4/RRR4-16/2	1608.098	1608.731	-1018.918	0.382	1439.219	0.471	20	0.207	K.SAVSVVEGENAFDGVK.Q
R4/RRR4-14/2	1236.007	1236.399	-318.037	0.447	1743.675	0.369	18	0.225	R.VYVLSVEGDVR.E
R4/RRR4-13/2	1261.112	1261.452	-270.638	0.366	1286.801	0.506	20	0.201	R.AFTVGIGGPVGTGK.T
R4/RRR4-13/2	1260.875	1261.452	-1254.260	0.398	1120.493	0.527	20	0.192	R.AFTVGIGGPVGTGK.T
R4/RRR4-6/2	1064.773	1065.334	-1470.081	0.362	451.884	0.564	15	0.163	K.AVKPVLVGGPK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1065.468	1065.334	125.760	0.321	620.146	0.469	17	0.158	K.AVKPVLVGGPK.M
R4/RRR4-6/2	1064.696	1065.334	-1542.865	0.302	407.867	0.565	14	0.156	K.AVKPVLVGGPK.M
R4/RRR4-7/2	1065.083	1065.334	-236.417	0.290	596.930	0.479	17	0.156	K.AVKPVLVGGPK.M
R4/RRR4-6/2	1065.145	1065.334	-178.240	0.315	595.699	0.416	17	0.153	K.AVKPVLVGGPK.M
R4/RRR4-7/2	1065.112	1065.334	-208.708	0.326	406.757	0.424	14	0.150	K.AVKPVLVGGPK.M
R4/RRR4-6/3	1065.445	1065.334	103.974	0.356	1008.757	0.284	21	0.092	K.AVKPVLVGGPK.M
R4/RRR4-6/3	1065.232	1065.334	-95.827	0.398	848.450	0.301	20	0.092	K.AVKPVLVGGPK.M
R4/RRR4-5/3	1065.855	1065.334	-451.040	0.382	625.442	0.325	18	0.090	-.AVKPVLVGGPK.-
R4/RRR4-3/3	1064.831	1065.334	-1415.426	0.290	634.549	0.317	17	0.089	-.AVKPVLVGGPK.-
R4/RRR4-6/3	1065.590	1065.334	241.150	0.414	815.182	0.324	20	0.089	-.AVKPVLVGGPK.-
R4/RRR4-3/3	1065.660	1065.334	306.451	0.388	739.627	0.276	19	0.086	-.AVKPVLVGGPK.-
R4/RRR4-5/3	1065.728	1065.334	370.882	0.379	624.976	0.275	18	0.077	-.AVKPVLVGGPK.-
R4/RRR4-1/3	1065.343	1065.334	8.307	0.345	514.843	0.284	16	0.072	-.AVKPVLVGGPK.-
R4/RRR4-1/3	1065.767	1065.334	407.228	0.333	639.314	0.255	18	0.065	-.AVKPVLVGGPK.-
R4/RRR4-14/2	1442.386	1441.698	-217.272	0.505	1300.433	0.499	21	0.207	K.VTPTVLQSAGLNLK.Q
R4/RRR4-15/2	1441.335	1441.698	-252.683	0.413	1062.711	0.457	20	0.178	K.VTPTVLQSAGLNLK.Q
R4/RRR4-14/2	1441.137	1441.698	-1086.583	0.442	913.241	0.481	19	0.173	K.VTPTVLQSAGLNLK.Q
R4/RRR4-14/2	1441.301	1441.698	-276.050	0.397	719.566	0.422	18	0.156	K.VTPTVLQSAGLNLK.Q
R4/RRR4-4/2	965.289	965.088	208.129	0.376	847.469	0.216	12	0.140	K.SLNIFQSR.L
R4/RRR4-4/2	965.168	965.088	82.315	0.419	789.878	0.227	12	0.139	-.SLNIFQSR.-
R4/RRR4-4/3	1880.992	1881.080	-46.978	0.456	886.444	0.507	31	0.127	K.IAVSPGTEGTSSPLTLHGR.D
R4/RRR4-4/3	1881.005	1881.080	-40.143	0.374	737.372	0.512	29	0.117	K.IAVSPGTEGTSSPLTLHGR.D
R4/RRR4-4/3	1881.703	1881.080	-201.104	0.333	575.287	0.414	26	0.094	K.IAVSPGTEGTSSPLTLHGR.D
R4/RRR4-9/3	1692.396	1692.808	-244.144	0.417	545.353	0.560	27	0.117	R.SFDVNKPGSEVDEIR.G
R4/RRR4-9/3	1692.718	1692.808	-53.577	0.411	452.473	0.498	25	0.104	R.SFDVNKPGSEVDEIR.G
R4/RRR4-5/2	1366.185	1365.471	-209.853	0.511	1536.647	0.433	17	0.216	K.NLEDEIYAEIR.A
R4/RRR4-23/2	1345.577	1345.486	68.188	0.537	1258.467	0.491	18	0.204	R.HLVDQYLEATR.G
R4/RRR4-23/2	1344.716	1345.486	-1320.100	0.464	1150.645	0.481	18	0.192	R.HLVDQYLEATR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1344.709	1345.486	-1325.297	0.418	996.152	0.419	16	0.169	R.HLVDQYLEATR.G
R4/RRR4-15/3	1819.613	1819.141	259.949	0.464	946.233	0.557	30	0.145	K.LPNNAVAPSLFFFRPK.N
R4/RRR4-15/3	1820.171	1819.141	16.365	0.406	584.665	0.362	25	0.093	K.LPNNAVAPSLFFFRPK.N
R4/RRR4-15/3	1820.254	1819.141	62.170	0.402	515.980	0.362	22	0.093	K.LPNNAVAPSLFFFRPK.N
R4/RRR4-14/3	1819.355	1819.141	117.653	0.403	757.504	0.333	26	0.092	K.LPNNAVAPSLFFFRPK.N
R4/RRR4-14/3	1819.205	1819.141	35.285	0.402	400.828	0.367	19	0.082	-.LPNNAVAPSLFFFRPK.-
R4/RRR4-14/3	1458.618	1458.690	-49.711	0.415	1511.886	0.445	26	0.175	K.YSVRPNTGVVLPR.S
R4/RRR4-14/3	1458.673	1458.690	-12.063	0.393	1618.606	0.365	27	0.162	K.YSVRPNTGVVLPR.S
R4/RRR4-7/3	1360.480	1360.414	48.803	0.504	1223.474	0.510	21	0.161	K.HDNEGKEFVER.I
R4/RRR4-7/3	1360.338	1360.414	-56.093	0.505	1033.949	0.481	19	0.133	K.HDNEGKEFVER.I
R4/RRR4-10/3	1624.759	1624.772	-8.306	0.492	772.177	0.551	26	0.130	K.LVLHHWSDDDCVK.I
R4/RRR4-10/3	1624.289	1624.772	-298.327	0.438	845.827	0.508	25	0.124	K.LVLHHWSDDDCVK.I
R4/RRR4-10/3	1624.871	1624.772	60.867	0.451	690.844	0.513	24	0.117	K.LVLHHWSDDDCVK.I
R4/RRR4-24/2	1338.182	1338.535	-264.109	0.495	1236.729	0.507	21	0.204	K.VSGVEIVPDPVAR.G
R4/RRR4-25/2	1338.201	1338.535	-249.833	0.475	1090.694	0.487	20	0.188	K.VSGVEIVPDPVAR.G
R4/RRR4-24/2	1338.200	1338.535	-250.839	0.475	1114.600	0.466	20	0.186	K.VSGVEIVPDPVAR.G
R4/RRR4-24/2	1339.091	1338.535	-332.322	0.514	1075.331	0.478	20	0.186	K.VSGVEIVPDPVAR.G
R4/RRR4-25/2	1338.239	1338.535	-221.280	0.464	1150.671	0.445	21	0.185	K.VSGVEIVPDPVAR.G
R4/RRR4-25/2	1337.658	1338.535	-1406.971	0.377	995.407	0.421	19	0.169	K.VSGVEIVPDPVAR.G
R4/RRR4-23/2	1339.138	1338.535	-297.018	0.340	905.695	0.274	18	0.147	K.VSGVEIVPDPVAR.G
R4/RRR4-12/2	1089.858	1089.181	-297.549	0.512	1586.380	0.403	17	0.216	K.LGGELTVDER.N
R4/RRR4-14/2	1678.181	1677.840	203.727	0.526	1256.416	0.494	17	0.199	K.EFTSVFYSLQNWR.S
R4/RRR4-14/2	1678.720	1677.840	-71.885	0.333	1024.748	0.235	16	0.143	K.EFTSVFYSLQNWR.S
R4/RRR4-14/2	1678.627	1677.840	-127.103	0.361	482.253	0.261	13	0.135	K.EFTSVFYSLQNWR.S
R4/RRR4-2/3	1729.461	1727.947	-282.061	0.432	1127.670	0.526	27	0.154	R.TIAVHFTNPFHVSTR.V
R4/RRR4-2/3	1729.620	1727.947	-189.763	0.398	859.950	0.360	22	0.096	R.TIAVHFTNPFHVSTR.V
R4/RRR4-2/3	1729.139	1727.947	111.542	0.386	632.249	0.364	23	0.091	R.TIAVHFTNPFHVSTR.V
R4/RRR4-5/2	1129.015	1129.250	-209.583	0.513	1341.470	0.475	17	0.206	K.SPAGANQWVAK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/2	1129.236	1129.250	-13.294	0.449	1449.984	0.420	16	0.203	K.SPAGANQWVAK.N
R4/RRR4-5/2	1128.366	1129.250	-1674.993	0.344	1059.221	0.393	16	0.167	K.SPAGANQWVAK.N
R4/RRR4-9/2	1679.841	1678.863	-13.455	0.479	639.940	0.541	16	0.163	R.VGYTFTTDALDALYK.K
R4/RRR4-17/2	1678.192	1678.863	-998.685	0.306	539.496	0.356	18	0.142	R.VGYTFTTDALDALYK.K
R4/RRR4-20/2	1354.241	1354.446	-151.763	0.491	1249.442	0.502	17	0.202	K.AFNVEEAPSDFK.V
R4/RRR4-20/2	1353.968	1354.446	-354.261	0.443	941.925	0.450	15	0.168	K.AFNVEEAPSDFK.V
R4/RRR4-20/2	1353.968	1354.446	-354.261	0.364	924.625	0.322	15	0.150	K.AFNVEEAPSDFK.V
R4/RRR4-25/2	955.865	956.035	-178.059	0.269	886.327	0.537	14	0.123	R.GPAAAEGIVGN.-
R4/RRR4-25/2	956.067	956.035	33.282	0.346	664.342	0.540	12	0.108	R.GPAAAEGIVGN.-
R4/RRR4-25/2	956.027	956.035	-8.851	0.312	747.903	0.464	13	0.098	R.GPAAAEGIVGN.-
R4/RRR4-9/2	1128.059	1128.387	-291.923	0.382	981.317	0.550	17	0.187	K.VPILTIGSLSK.R
R4/RRR4-9/2	1128.266	1128.387	-107.281	0.365	1045.897	0.519	17	0.185	K.VPILTIGSLSK.R
R4/RRR4-9/2	1128.148	1128.387	-212.131	0.268	756.622	0.488	14	0.156	K.VPILTIGSLSK.R
R4/RRR4-12/3	1348.281	1347.457	-130.967	0.521	1839.885	0.296	24	0.173	K.AGNKTEWSYYK.V
R4/RRR4-22/2	1032.078	1032.136	-56.897	0.461	1019.404	0.533	13	0.192	K.HGWDYVVR.K
R4/RRR4-22/2	1032.005	1032.136	-127.847	0.521	1077.198	0.493	13	0.191	K.HGWDYVVR.K
R4/RRR4-22/2	1031.934	1032.136	-196.790	0.368	990.722	0.474	13	0.176	K.HGWDYVVR.K
R4/RRR4-13/2	1263.225	1262.483	-204.665	0.394	1242.283	0.513	17	0.199	R.IVNVSSGFGLLR.-
R4/RRR4-16/2	1155.452	1156.359	-1655.650	0.523	1278.350	0.476	17	0.203	R.TPLLVAWAER.V
R4/RRR4-16/2	1155.358	1156.359	-1736.746	0.365	583.893	0.359	14	0.148	R.TPLLVAWAER.V
R4/RRR4-26/2	1058.462	1059.243	-1688.333	0.370	155.932	0.452	12	0.135	-.EKVHFAISK.-
R4/RRR4-26/2	1058.657	1059.243	-1503.093	0.388	144.486	0.385	11	0.133	-.EKVHFAISK.-
R4/RRR4-5/2	1625.716	1625.893	-109.249	0.481	873.251	0.540	20	0.114	R.FRPILLEALDNLNP.-
R4/RRR4-5/2	1625.541	1625.893	-217.496	0.477	748.350	0.473	19	0.093	R.FRPILLEALDNLNP.-
R4/RRR4-6/2	1414.492	1413.514	-15.720	0.479	791.652	0.541	22	0.179	R.FGGALDGAAEEFTK.A
R4/RRR4-6/2	1414.877	1413.514	257.476	0.397	731.123	0.532	22	0.171	R.FGGALDGAAEEFTK.A
R4/RRR4-20/2	1184.102	1184.371	-227.647	0.423	439.502	0.527	14	0.161	K.NNPTLAAINKK.F
R4/RRR4-20/2	1183.967	1184.371	-342.047	0.400	607.038	0.414	16	0.155	K.NNPTLAAINKK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1184.161	1184.371	-177.386	0.425	503.857	0.376	14	0.148	K.NNPTLAAINKK.F
R4/RRR4-1/2	1542.878	1541.620	167.478	0.433	466.461	0.526	20	0.163	R.ISAEDETSGM*DLTR.H
R4/RRR4-1/2	1542.597	1541.620	-15.043	0.525	425.741	0.517	17	0.160	R.ISAEDETSGM*DLTR.H
R4/RRR4-1/2	1542.649	1541.620	18.530	0.462	324.069	0.465	17	0.154	R.ISAEDETSGM*DLTR.H
R4/RRR4-8/2	1674.499	1674.879	-227.954	0.275	1793.202	0.258	19	0.199	K.SVTGLGLVADVFGDPAR.L
R4/RRR4-16/2	1199.055	1198.310	-213.270	0.457	1385.910	0.463	16	0.208	R.ADNLYLEGFR.X
R4/RRR4-16/2	1198.195	1198.310	-95.707	0.359	810.405	0.438	13	0.159	R.ADNLYLEGFR.X
R4/RRR4-1/3	1584.827	1584.675	96.127	0.459	1286.206	0.491	26	0.161	K.HQLDDKWDGVNTR.L
R4/RRR4-1/3	1584.723	1584.675	30.771	0.427	1257.807	0.495	25	0.158	K.HQLDDKWDGVNTR.L
R4/RRR4-1/3	1584.937	1584.675	165.762	0.405	1235.567	0.465	24	0.147	K.HQLDDKWDGVNTR.L
R4/RRR4-7/3	1586.120	1584.675	281.735	0.474	1273.149	0.415	25	0.137	K.HQLDDKWDGVNTR.L
R4/RRR4-23/2	934.593	935.102	-1619.369	0.472	1397.623	0.455	15	0.208	K.SGLFVGINK.X
R4/RRR4-22/2	934.235	935.102	-2004.900	0.461	1330.520	0.482	15	0.207	K.SGLFVGINK.X
R4/RRR4-22/2	934.499	935.102	-1721.072	0.475	1398.478	0.442	15	0.206	K.SGLFVGINK.X
R4/RRR4-23/2	935.049	935.102	-56.843	0.491	1317.890	0.464	15	0.203	K.SGLFVGINK.X
R4/RRR4-23/2	934.877	935.102	-241.515	0.492	1293.243	0.432	15	0.195	K.SGLFVGINK.X
R4/RRR4-22/2	934.990	935.102	-119.964	0.503	1300.650	0.409	15	0.191	K.SGLFVGINK.X
R4/RRR4-1/3	1418.702	1418.586	81.968	0.469	568.550	0.516	21	0.109	-.NLHAVHATQALSR.-
R4/RRR4-2/3	1418.482	1418.586	-74.034	0.369	522.084	0.363	20	0.091	K.NLHAVHATQALSR.L
R4/RRR4-1/3	1417.813	1418.586	-1254.555	0.395	186.862	0.427	14	0.003	-.NLHAVHATQALSR.-
R4/RRR4-14/2	1329.462	1329.528	-49.603	0.442	1697.840	0.362	19	0.214	K.ISVDASLAGGIIGR.G
R4/RRR4-9/2	1579.205	1577.852	224.326	0.469	839.727	0.547	19	0.178	R.HALWLSNLDLAVPK.T
R4/RRR4-2/3	1995.570	1996.057	-244.914	0.534	1444.553	0.419	31	0.162	R.QSKPDEVTEDDM*PSTSGR.Q
R4/RRR4-4/2	1746.595	1746.944	-200.529	0.510	927.277	0.520	19	0.179	K.NWNFTEQGLPADLIK.R
R4/RRR4-4/2	1745.508	1746.944	-1399.973	0.297	519.487	0.402	14	0.140	K.NWNFTEQGLPADLIK.R
R4/RRR4-4/2	1747.977	1746.944	18.939	0.325	550.277	0.207	15	0.131	K.NWNFTEQGLPADLIK.R
R4/RRR4-18/2	1438.325	1437.661	-234.655	0.504	1117.732	0.504	18	0.193	R.VVFELYDDIVPK.T
R4/RRR4-19/2	1437.368	1437.661	-204.912	0.462	1218.504	0.441	18	0.188	R.VVFELYDDIVPK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1436.942	1437.661	-1200.183	0.409	1170.813	0.389	18	0.175	R.VVFELYDDIVPK.T
R4/RRR4-18/2	1437.382	1437.661	-195.200	0.355	819.095	0.287	16	0.145	R.VVFELYDDIVPK.T
R4/RRR4-6/2	1321.269	1321.416	-111.348	0.413	1062.496	0.527	18	0.187	K.ALATTITTNDGDK.K
R4/RRR4-14/2	1535.605	1534.734	-84.086	0.474	945.329	0.530	19	0.180	R.VSTTVTVDEALTGLK.T
R4/RRR4-4/2	1863.180	1864.089	-1027.737	0.422	471.905	0.515	19	0.155	R.SLEIPVIEEGQEHALAK.F
R4/RRR4-4/2	1863.389	1864.089	-915.396	0.407	530.516	0.457	19	0.151	R.SLEIPVIEEGQEHALAK.F
R4/RRR4-13/2	1217.086	1217.266	-148.745	0.404	1190.231	0.500	15	0.195	R.DLGYLDDSYR.A
R4/RRR4-13/2	1217.021	1217.266	-202.576	0.345	1196.760	0.417	16	0.180	R.DLGYLDDSYR.A
R4/RRR4-13/2	1216.316	1217.266	-1608.536	0.301	1108.376	0.407	15	0.170	R.DLGYLDDSYR.A
R4/RRR4-6/2	1258.247	1258.526	-222.601	0.437	1008.165	0.530	20	0.189	R.IPSSLCGIIGLK.T
R4/RRR4-6/2	1258.467	1258.526	-47.051	0.400	458.175	0.478	15	0.155	R.IPSSLCGIIGLK.T
R4/RRR4-6/2	1258.107	1258.526	-333.860	0.425	473.622	0.447	14	0.152	R.IPSSLCGIIGLK.T
R4/RRR4-5/2	1393.341	1393.529	-134.938	0.517	1503.506	0.412	19	0.208	R.GFVISDWQGLDR.I
R4/RRR4-5/2	1393.240	1393.529	-207.887	0.474	1503.932	0.397	19	0.205	R.GFVISDWQGLDR.I
R4/RRR4-5/2	1393.216	1393.529	-225.467	0.485	1524.686	0.303	19	0.186	R.GFVISDWQGLDR.I
R4/RRR4-7/2	1394.662	1393.529	95.549	0.328	688.443	0.197	14	0.134	-.GFVISDWQGLDR.-
R4/RRR4-14/2	1442.290	1441.698	-283.416	0.525	1012.717	0.502	22	0.187	K.ITPTVLQSAGLNVK.Q
R4/RRR4-14/2	1441.285	1441.698	-287.351	0.461	1060.572	0.444	22	0.178	K.ITPTVLQSAGLNVK.Q
R4/RRR4-14/2	1440.724	1441.698	-1374.221	0.337	968.706	0.441	21	0.168	K.ITPTVLQSAGLNVK.Q
R4/RRR4-4/2	1552.336	1550.811	-307.335	0.345	1494.920	0.410	19	0.202	R.SRATWQRMSSIVK.G
R4/RRR4-21/2	1246.229	1246.392	-131.513	0.513	1555.869	0.390	18	0.207	K.SGDVTELQIGVK.H
R4/RRR4-22/2	1245.997	1246.392	-318.435	0.474	1463.562	0.315	18	0.183	K.SGDVTELQIGVK.H
R4/RRR4-22/2	1246.072	1246.392	-257.987	0.443	1514.900	0.290	18	0.183	K.SGDVTELQIGVK.H
R4/RRR4-3/2	1911.417	1911.104	163.751	0.427	467.098	0.496	17	0.147	K.AATNNFDESLLLGVGGFGK.V
R4/RRR4-9/2	1291.267	1290.447	-139.916	0.377	1602.385	0.374	17	0.208	R.LNEDWSTLALK.R
R4/RRR4-9/2	1290.959	1290.447	-379.329	0.365	648.245	0.323	15	0.145	R.LNEDWSTLALK.R
R4/RRR4-20/3	1447.108	1447.791	-1166.336	0.416	753.822	0.539	24	0.124	K.TPVALAPIAKPLAGK.K
R4/RRR4-20/3	1447.314	1447.791	-330.026	0.391	509.443	0.576	21	0.117	K.TPVALAPIAKPLAGK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/3	1447.434	1447.791	-246.764	0.365	555.594	0.548	22	0.114	K.TPVALAPIAKPLAGK.K
R4/RRR4-8/2	1199.660	1200.410	-1462.879	0.542	1430.562	0.418	18	0.203	R.LLAAELTEIAR.A
R4/RRR4-8/2	1199.961	1200.410	-375.342	0.434	1208.014	0.364	17	0.174	R.LLAAELTEIAR.A
R4/RRR4-12/3	1951.028	1951.175	-75.822	0.460	976.847	0.520	26	0.139	K.SSAGYQAPLHAEPIKPQR.Y
R4/RRR4-12/3	1950.361	1951.175	-932.776	0.410	827.531	0.447	25	0.110	K.SSAGYQAPLHAEPIKPQR.Y
R4/RRR4-12/3	1950.790	1951.175	-197.935	0.415	900.259	0.414	28	0.108	K.SSAGYQAPLHAEPIKPQR.Y
R4/RRR4-16/2	1659.657	1659.866	-126.269	0.429	1463.989	0.439	21	0.207	R.FDPATTPLLAAWAER.F
R4/RRR4-16/2	1659.823	1659.866	-26.379	0.195	885.603	0.330	16	0.142	R.FDPATTPLLAAWAER.F
R4/RRR4-16/2	1659.588	1659.866	-168.326	0.263	633.620	0.281	15	0.135	R.FDPATTPLLAAWAER.F
R4/RRR4-16/2	1659.488	1659.866	-228.541	0.260	623.035	0.201	15	0.132	R.FDPATTPLLAAWAER.F
R4/RRR4-9/2	1385.632	1386.490	-1345.005	0.440	1261.862	0.480	18	0.195	K.TYGASTSGNSLSLK.F
R4/RRR4-9/2	1385.432	1386.490	-1490.133	0.322	890.453	0.409	15	0.154	K.TYGASTSGNSLSLK.F
R4/RRR4-10/3	1298.956	1299.420	-358.624	0.506	883.782	0.506	21	0.128	R.HLSTLTGYHNR.T
R4/RRR4-10/3	1299.613	1299.420	148.596	0.514	784.316	0.520	21	0.125	R.HLSTLTGYHNR.T
R4/RRR4-10/3	1300.701	1299.420	216.763	0.489	847.843	0.476	22	0.119	R.HLSTLTGYHNR.T
R4/RRR4-7/2	1097.089	1097.242	-139.458	0.380	392.652	0.495	11	0.154	R.SHCASFLFK.N
R4/RRR4-7/2	1097.062	1097.242	-164.126	0.342	392.681	0.464	11	0.150	R.SHCASFLFK.N
R4/RRR4-8/3	1097.206	1097.242	-33.055	0.419	729.216	0.345	17	0.091	-.SHCASFLFK.-
R4/RRR4-7/3	1097.316	1097.242	67.369	0.484	943.665	0.314	21	0.089	-.SHCASFLFK.-
R4/RRR4-7/3	1096.589	1097.242	-1512.046	0.385	597.819	0.286	16	0.086	-.SHCASFLFK.-
R4/RRR4-8/3	1097.215	1097.242	-24.100	0.389	1016.791	0.239	19	0.082	-.SHCASFLFK.-
R4/RRR4-7/3	1096.852	1097.242	-356.556	0.424	821.796	0.145	18	0.076	-.SHCASFLFK.-
R4/RRR4-26/2	1188.721	1189.384	-1403.418	0.486	1295.101	0.460	19	0.199	K.LSAGIASILESK.L
R4/RRR4-26/2	1189.041	1189.384	-289.720	0.483	1345.926	0.397	19	0.191	K.LSAGIASILESK.L
R4/RRR4-26/2	1189.051	1189.384	-281.171	0.531	1083.538	0.462	18	0.183	K.LSAGIASILESK.L
R4/RRR4-23/2	1083.154	1082.232	-72.074	0.399	979.322	0.520	17	0.183	R.YGSLTGLSGVK.V
R4/RRR4-20/2	1082.118	1082.232	-106.086	0.412	1024.846	0.486	18	0.183	R.YGSLTGLSGVK.V
R4/RRR4-20/2	1081.234	1082.232	-1853.432	0.371	759.175	0.582	16	0.176	R.YGSLTGLSGVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1083.137	1082.232	-87.900	0.447	912.160	0.463	17	0.173	R.YGSLTGLSGVK.V
R4/RRR4-13/3	1606.827	1606.808	11.718	0.463	1416.470	0.436	29	0.162	K.ALAHQPVSVAIEASGR.N
R4/RRR4-13/3	1607.246	1606.808	273.385	0.373	1133.811	0.350	25	0.109	K.ALAHQPVSVAIEASGR.N
R4/RRR4-18/2	1498.588	1498.624	-24.070	0.489	1452.821	0.418	17	0.202	K.GDWLLFEYQNGR.S
R4/RRR4-18/2	1498.284	1498.624	-227.552	0.493	1439.719	0.399	17	0.197	K.GDWLLFEYQNGR.S
R4/RRR4-22/2	1498.307	1498.624	-212.023	0.454	1288.380	0.393	16	0.182	K.GDWLLFEYQNGR.S
R4/RRR4-19/3	1517.408	1517.668	-171.964	0.452	614.459	0.513	23	0.115	K.VSDTEVIGYHQLR.V
R4/RRR4-20/3	1517.636	1517.668	-21.397	0.438	556.636	0.486	22	0.109	K.VSDTEVIGYHQLR.V
R4/RRR4-20/3	1518.513	1517.668	-102.336	0.415	759.792	0.430	24	0.106	K.VSDTEVIGYHQLR.V
R4/RRR4-19/3	1517.669	1517.668	0.265	0.367	298.478	0.432	18	0.102	K.VSDTEVIGYHQLR.V
R4/RRR4-20/3	1517.279	1517.668	-257.071	0.346	495.955	0.439	20	0.101	K.VSDTEVIGYHQLR.V
R4/RRR4-19/3	1517.372	1517.668	-195.570	0.356	644.240	0.408	23	0.099	K.VSDTEVIGYHQLR.V
R4/RRR4-9/2	1568.967	1568.750	138.857	0.372	473.173	0.515	17	0.152	K.AASVGQIFVTTTGCR.D
R4/RRR4-4/2	1417.067	1417.575	-1067.561	0.282	858.853	0.310	16	0.143	-.M*AAVANGGAAPEWR.V
R4/RRR4-1/2	1417.248	1417.575	-232.031	0.310	1026.994	0.142	16	0.134	-.M*AAVANGGAAPEWR.-
R4/RRR4-3/2	1417.269	1417.575	-216.650	0.365	944.758	0.177	17	0.131	-.M*AAVANGGAAPEWR.-
R4/RRR4-12/2	1156.773	1157.213	-381.523	0.366	1338.944	0.448	19	0.196	R.DSSVSYASAAAK.V
R4/RRR4-22/2	1123.945	1124.229	-253.230	0.467	843.418	0.512	17	0.177	K.GISSSAVPYSR.N
R4/RRR4-22/2	1123.892	1124.229	-300.740	0.368	931.570	0.456	17	0.170	K.GISSSAVPYSR.N
R4/RRR4-22/2	1123.516	1124.229	-1529.002	0.387	696.043	0.448	15	0.158	K.GISSSAVPYSR.N
R4/RRR4-9/2	1399.306	1399.578	-195.086	0.501	1237.532	0.459	17	0.194	K.LLQYVYWSNGR.E
R4/RRR4-3/2	1678.188	1676.894	176.148	0.407	739.523	0.520	18	0.163	R.VTWSPDGDLIGVAFAK.H
R4/RRR4-14/2	1488.209	1487.642	-292.277	0.345	527.867	0.518	18	0.156	R.GAGIPIPAAANTDYR.H
R4/RRR4-14/2	1487.777	1487.642	90.557	0.368	428.568	0.436	17	0.148	R.GAGIPIPAAANTDYR.H
R4/RRR4-14/2	1487.319	1487.642	-217.952	0.317	267.077	0.409	14	0.142	R.GAGIPIPAAANTDYR.H
R4/RRR4-2/2	1581.209	1580.766	281.109	0.445	1114.214	0.490	18	0.185	R.FYDPVTGQVLLDGR.D
R4/RRR4-1/2	1581.077	1580.766	197.499	0.311	424.921	0.311	13	0.134	-.FYDPVTGQVLLDGR.-
R4/RRR4-6/3	1970.957	1971.301	-175.246	0.432	1654.900	0.356	28	0.171	K.LM*STTYLVALCQAVDLR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-6/2	1970.426	1971.301	-954.361	0.466	915.027	0.418	22	0.162	K.LM*STTYLVALCQAVDLR.H
R4/RRR4-6/2	1970.756	1971.301	-786.335	0.408	625.488	0.265	17	0.132	K.LM*STTYLVALCQAVDLR.H
R4/RRR4-16/3	1512.393	1512.694	-199.422	0.423	829.724	0.523	26	0.125	R.M*HHVVM*GDDPDVK.T
R4/RRR4-27/2	1299.780	1299.502	214.714	0.242	320.653	0.474	20	0.143	R.LLAQAALTVGADR.A
R4/RRR4-24/2	1208.218	1207.361	-118.423	0.422	830.968	0.520	17	0.176	K.IVNAGSFTIER.E
R4/RRR4-24/2	1207.589	1207.361	189.536	0.312	757.577	0.363	15	0.148	K.IVNAGSFTIER.E
R4/RRR4-1/2	1658.700	1657.802	-61.828	0.473	997.461	0.504	19	0.177	K.TGGYIEGDISISGYPK.K
R4/RRR4-9/2	1960.804	1960.259	-232.322	0.490	1122.255	0.475	18	0.178	R.LYDPTLSTSFLLSQFVK.G
R4/RRR4-16/2	1279.079	1279.427	-273.059	0.435	962.051	0.514	18	0.183	K.GVVTDIIHDPGR.G
R4/RRR4-14/2	1279.124	1279.427	-237.537	0.498	893.315	0.522	17	0.181	K.GVVTDIIHDPGR.G
R4/RRR4-15/2	1279.103	1279.427	-254.484	0.422	863.552	0.527	16	0.177	K.GVVTDIIHDPGR.G
R4/RRR4-16/2	1279.239	1279.427	-147.931	0.411	880.810	0.504	17	0.175	K.GVVTDIIHDPGR.G
R4/RRR4-14/2	1278.843	1279.427	-1242.669	0.402	860.139	0.493	17	0.172	K.GVVTDIIHDPGR.G
R4/RRR4-14/2	1279.089	1279.427	-265.112	0.393	855.403	0.457	17	0.167	K.GVVTDIIHDPGR.G
R4/RRR4-15/2	1279.169	1279.427	-202.306	0.394	771.763	0.412	16	0.158	K.GVVTDIIHDPGR.G
R4/RRR4-17/2	1279.209	1279.427	-171.288	0.305	475.068	0.400	13	0.146	K.GVVTDIIHDPGR.G
R4/RRR4-17/2	1279.072	1279.427	-278.708	0.185	422.340	0.265	12	0.132	-.GVVTDIIHDPGR.-
R4/RRR4-10/2	1142.035	1142.292	-226.169	0.450	911.798	0.506	14	0.178	K.TIFHLNPSGR.F
R4/RRR4-9/2	1142.034	1142.292	-226.813	0.333	878.203	0.491	15	0.170	K.TIFHLNPSGR.F
R4/RRR4-10/2	1142.092	1142.292	-175.880	0.361	953.688	0.411	16	0.166	K.TIFHLNPSGR.F
R4/RRR4-9/2	1142.020	1142.292	-239.359	0.375	1077.615	0.328	17	0.162	K.TIFHLNPSGR.F
R4/RRR4-9/2	1141.948	1142.292	-302.740	0.401	759.949	0.439	14	0.161	K.TIFHLNPSGR.F
R4/RRR4-11/2	1142.735	1142.292	388.222	0.279	503.844	0.283	12	0.141	K.TIFHLNPSGR.F
R4/RRR4-7/2	1555.637	1555.713	-49.081	0.437	1595.179	0.367	21	0.207	K.EVVLSSVQDEFFR.A
R4/RRR4-15/2	1186.218	1186.345	-107.717	0.431	613.492	0.510	16	0.167	R.HSGIIDIQFR.R
R4/RRR4-14/2	1186.161	1186.345	-155.410	0.414	486.428	0.500	15	0.161	R.HSGIIDIQFR.R
R4/RRR4-18/2	1198.064	1197.234	-141.909	0.478	1079.704	0.487	18	0.189	R.FEDGSISDQAK.R
R4/RRR4-18/2	1196.971	1197.234	-220.188	0.446	1106.561	0.402	18	0.175	R.FEDGSISDQAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-18/2	1197.196	1197.234	-31.152	0.429	736.720	0.400	16	0.157	R.FEDGSISDQAK.R
R4/RRR4-16/2	1548.210	1546.697	-314.876	0.472	520.441	0.473	19	0.159	R.FGTICVFCGSNAGR.R
R4/RRR4-16/2	1548.136	1546.697	284.505	0.412	598.835	0.396	17	0.149	R.FGTICVFCGSNAGR.R
R4/RRR4-17/2	1547.677	1546.697	-12.389	0.376	672.695	0.404	15	0.148	R.FGTICVFCGSNAGR.R
R4/RRR4-12/2	1646.072	1645.883	115.543	0.444	493.446	0.481	17	0.154	R.HFVPGQFVDVTGITK.G
R4/RRR4-12/2	1646.782	1645.883	-61.383	0.320	253.315	0.340	14	0.137	-.HFVPGQFVDVTGITK.-
R4/RRR4-9/2	1628.893	1628.852	24.834	0.414	1061.940	0.497	22	0.181	K.SLVGVDAPASGITVVSR.Q
R4/RRR4-5/2	1758.175	1758.951	-1013.421	0.484	550.402	0.461	19	0.153	K.STAPNQLQLIESLESK.L
R4/RRR4-8/2	1911.519	1910.116	211.012	0.292	435.833	0.493	18	0.144	R.DYSAQLVVPDVVDFVSR.F
R4/RRR4-2/3	1437.947	1437.671	192.285	0.493	991.565	0.490	27	0.132	K.VAESLGHVILGWR.W
R4/RRR4-2/3	1437.676	1437.671	3.388	0.459	899.196	0.482	25	0.122	K.VAESLGHVILGWR.W
R4/RRR4-4/2	1436.666	1435.690	-16.841	0.309	477.978	0.494	15	0.146	K.SLSALSDVIFAIAK.G
R4/RRR4-3/2	1098.877	1098.278	-366.193	0.283	443.546	0.484	14	0.148	R.LPVGSENLLR.V
R4/RRR4-7/2	1055.862	1055.299	-414.971	0.422	851.427	0.513	13	0.172	R.KANIVLVAAR.S
R4/RRR4-15/2	1910.983	1910.243	-136.316	0.402	918.479	0.511	18	0.169	K.GLPALEPLQVYPIIEEK.V
R4/RRR4-20/2	1547.637	1546.685	-31.393	0.486	531.699	0.460	15	0.153	R.SILEEVESEHM*AR.A
R4/RRR4-20/2	1547.888	1546.685	131.240	0.302	401.147	0.321	13	0.137	R.SILEEVESEHM*AR.A
R4/RRR4-1/2	1422.652	1421.620	21.893	0.466	1240.198	0.461	18	0.194	K.LQAVEQSYLLEK.H
R4/RRR4-1/2	1421.417	1421.620	-143.298	0.316	536.190	0.399	13	0.144	K.LQAVEQSYLLEK.H
R4/RRR4-1/2	1422.406	1421.620	-151.290	0.320	550.732	0.349	13	0.141	K.LQAVEQSYLLEK.H
R4/RRR4-23/3	1635.813	1636.705	-1160.078	0.458	798.862	0.506	25	0.121	R.LSGDIHEEVETHNR.M
R4/RRR4-23/3	1636.735	1636.705	18.124	0.479	533.858	0.504	21	0.108	R.LSGDIHEEVETHNR.M
R4/RRR4-5/2	1498.162	1498.663	-1005.261	0.435	1459.306	0.404	22	0.201	K.ISPDIVGEAVEVNR.L
R4/RRR4-8/2	1617.079	1615.918	99.594	0.552	940.528	0.456	22	0.175	R.DFPLGDLPMLEVLR.C
R4/RRR4-8/2	1617.133	1615.918	133.283	0.522	814.261	0.490	20	0.172	R.DFPLGDLPMLEVLR.C
R4/RRR4-8/2	1616.803	1615.918	-71.836	0.486	686.162	0.449	19	0.160	R.DFPLGDLPMLEVLR.C
R4/RRR4-4/2	1200.825	1200.410	346.603	0.404	1509.416	0.386	16	0.203	R.LLNLETLDLR.G
R4/RRR4-4/2	1200.896	1200.410	405.512	0.445	1397.595	0.299	17	0.178	R.LLNLETLDLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-4/2	1200.653	1200.410	203.378	0.336	978.249	0.229	15	0.144	R.LLNLETLDLR.G
R4/RRR4-13/2	1487.575	1486.721	-98.704	0.484	664.371	0.483	17	0.161	R.NLSM*GM*NLNNM*AK.M
R4/RRR4-3/2	1303.462	1303.406	43.621	0.361	1315.694	0.435	19	0.191	R.AADPLSSWSAAAR.L
R4/RRR4-3/2	1303.091	1303.406	-242.000	0.321	563.932	0.336	14	0.139	R.AADPLSSWSAAAR.L
R4/RRR4-10/2	1218.209	1218.384	-144.086	0.468	1155.896	0.470	18	0.191	R.YIDIGIPANNK.G
R4/RRR4-10/2	1217.268	1218.384	-1743.064	0.299	1140.642	0.426	16	0.174	R.YIDIGIPANNK.G
R4/RRR4-10/2	1217.323	1218.384	-1697.927	0.323	823.310	0.388	13	0.151	R.YIDIGIPANNK.G
R4/RRR4-7/2	995.060	995.241	-182.427	0.424	655.825	0.505	16	0.167	K.VGPLTIPLGK.I
R4/RRR4-12/2	1278.841	1279.637	-1408.397	0.358	1011.896	0.498	15	0.177	K.ELLQLLLPVLK.V
R4/RRR4-12/2	1278.516	1279.637	-1663.393	0.207	371.616	0.319	12	0.134	-.ELLQLLLPVLK.-
R4/RRR4-21/3	1351.597	1351.449	109.952	0.350	888.882	0.509	22	0.126	K.YGVGDAHFEVTR.F
R4/RRR4-20/3	1352.664	1351.449	159.513	0.429	647.900	0.554	20	0.124	K.YGVGDAHFEVTR.F
R4/RRR4-20/3	1351.736	1351.449	212.791	0.458	676.697	0.525	20	0.120	K.YGVGDAHFEVTR.F
R4/RRR4-21/3	1351.360	1351.449	-65.888	0.439	518.785	0.556	19	0.119	K.YGVGDAHFEVTR.F
R4/RRR4-20/3	1351.843	1351.449	292.521	0.375	737.956	0.506	21	0.117	K.YGVGDAHFEVTR.F
R4/RRR4-21/3	1350.635	1351.449	-1346.732	0.364	872.154	0.442	22	0.112	K.YGVGDAHFEVTR.F
R4/RRR4-4/2	1238.214	1238.458	-198.021	0.381	540.896	0.502	15	0.159	K.LPSIPALEELR.K
R4/RRR4-4/2	1238.276	1238.458	-147.782	0.345	455.089	0.475	15	0.154	K.LPSIPALEELR.K
R4/RRR4-4/2	1238.350	1238.458	-87.858	0.330	536.821	0.405	16	0.150	K.LPSIPALEELR.K
R4/RRR4-8/2	1406.714	1407.512	-1282.634	0.373	950.033	0.504	16	0.176	R.HNEFEISDFLR.R
R4/RRR4-8/2	1407.168	1407.512	-245.593	0.399	795.403	0.406	16	0.158	R.HNEFEISDFLR.R
R4/RRR4-17/2	1381.447	1381.556	-79.377	0.467	1305.420	0.446	18	0.192	K.ATGDALAISSSLFK.K
R4/RRR4-1/3	1913.188	1914.066	-984.315	0.438	865.219	0.499	29	0.124	R.LGM*EKGEGM*SAVADSGEGR.G
R4/RRR4-1/3	1913.799	1914.066	-139.875	0.459	1070.597	0.426	30	0.123	R.LGM*EKGEGM*SAVADSGEGR.G
R4/RRR4-1/3	1913.825	1914.066	-126.246	0.455	829.993	0.465	28	0.114	R.LGM*EKGEGM*SAVADSGEGR.G
R4/RRR4-12/2	1001.766	1002.192	-426.442	0.382	1522.441	0.374	15	0.201	R.AFADLVLPR.G
R4/RRR4-10/2	1254.372	1254.458	-68.580	0.442	692.970	0.499	18	0.168	K.INEGIPAGILEK.I
R4/RRR4-10/2	1254.195	1254.458	-209.653	0.399	483.211	0.442	16	0.151	-.INEGIPAGILEK.-

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1253.803	1254.458	-1323.930	0.393	458.890	0.428	15	0.151	K.INEGIPAGILEK.I
R4/RRR4-4/2	1360.155	1360.580	-313.403	0.501	829.874	0.478	18	0.172	K.FTEQALPVDLVK.R
R4/RRR4-4/2	1359.490	1360.580	-1542.253	0.406	746.214	0.431	18	0.160	K.FTEQALPVDLVK.R
R4/RRR4-4/2	1359.642	1360.580	-1429.878	0.361	643.048	0.386	16	0.150	K.FTEQALPVDLVK.R
R4/RRR4-2/2	1637.819	1636.826	-4.381	0.493	907.891	0.470	20	0.172	R.LGEEFPEELANFLK.E
R4/RRR4-7/2	1872.536	1871.082	243.063	0.493	687.290	0.471	21	0.159	K.IADILGQLLASEENVER.D
R4/RRR4-1/2	1861.875	1860.102	-122.485	0.409	725.409	0.496	18	0.158	R.FQFANLPLPLDAEQAGK.R
R4/RRR4-12/2	1872.469	1873.056	-850.277	0.390	718.328	0.506	18	0.100	R.GWIPLDQSIRDTVGSDI.-
R4/RRR4-12/2	1872.072	1873.056	-1063.143	0.367	533.245	0.430	17	0.093	R.GWIPLDQSIRDTVGSDI.-
R4/RRR4-12/2	1873.221	1873.056	88.263	0.474	834.898	0.431	20	0.088	R.GWIPLDQSIRDTVGSDI.-
R4/RRR4-6/2	1354.444	1354.620	-130.406	0.464	896.929	0.491	22	0.177	R.LLVPASQAGSLIGK.Q
R4/RRR4-6/2	1354.149	1354.620	-349.241	0.306	662.323	0.419	19	0.151	R.LLVPASQAGSLIGK.Q
R4/RRR4-6/2	1354.511	1354.620	-80.865	0.323	581.263	0.355	19	0.146	R.LLVPASQAGSLIGK.Q
R4/RRR4-4/2	1021.073	1021.149	-74.417	0.476	1049.889	0.477	16	0.186	R.YADLLNSPK.K
R4/RRR4-4/2	1020.411	1021.149	-1708.455	0.382	1153.022	0.364	16	0.171	R.YADLLNSPK.K
R4/RRR4-4/2	1021.226	1021.149	75.579	0.394	941.527	0.367	14	0.160	R.YADLLNSPK.K
R4/RRR4-7/3	1373.620	1373.542	56.581	0.501	1477.666	0.382	26	0.150	K.IYAHSSIGQLQR.A
R4/RRR4-7/3	1373.777	1373.542	171.678	0.514	1257.498	0.342	24	0.117	K.IYAHSSIGQLQR.A
R4/RRR4-6/2	1496.682	1495.703	-13.957	0.448	750.960	0.495	15	0.163	R.LPVTWYPASFADK.V
R4/RRR4-6/2	1496.498	1495.703	-137.254	0.396	590.769	0.520	13	0.156	R.LPVTWYPASFADK.V
R4/RRR4-13/2	1058.739	1059.198	-434.891	0.461	1454.130	0.392	17	0.200	K.ILESAAELGR.G
R4/RRR4-15/2	1760.641	1758.955	-178.762	0.493	1308.881	0.428	20	0.188	R.GIGFELFTDAGQYAIR.F
R4/RRR4-15/2	1213.285	1213.319	-28.418	0.464	863.125	0.490	16	0.172	K.SAAAVDPVEPEK.V
R4/RRR4-15/2	1212.747	1213.319	-1300.805	0.458	740.122	0.516	15	0.168	K.SAAAVDPVEPEK.V
R4/RRR4-15/2	1213.039	1213.319	-231.603	0.472	653.072	0.509	14	0.163	K.SAAAVDPVEPEK.V
R4/RRR4-6/2	1141.020	1141.346	-286.032	0.397	506.350	0.490	16	0.160	R.AQPTLGLITAR.A
R4/RRR4-6/2	1141.102	1141.346	-213.908	0.419	500.810	0.429	16	0.156	R.AQPTLGLITAR.A
R4/RRR4-6/2	1141.101	1141.346	-214.874	0.372	448.793	0.407	15	0.151	R.AQPTLGLITAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1142.190	1141.346	-137.060	0.316	498.837	0.270	13	0.139	R.AQPTLGLITAR.A
R4/RRR4-5/3	1447.873	1447.625	172.109	0.447	1007.405	0.483	29	0.131	K.AVVHHGGAGTTAAGLK.A
R4/RRR4-16/2	1827.107	1828.100	-1094.132	0.344	875.058	0.501	22	0.169	K.GLLTDQTLPLLTDSALR.D
R4/RRR4-16/2	1827.580	1828.100	-834.114	0.288	536.600	0.355	15	0.138	K.GLLTDQTLPLLTDSALR.D
R4/RRR4-16/2	1827.890	1828.100	-115.117	0.254	415.573	0.407	14	0.137	K.GLLTDQTLPLLTDSALR.D
R4/RRR4-16/2	1828.344	1828.100	133.623	0.266	287.312	0.360	13	0.136	K.GLLTDQTLPLLTDSALR.D
R4/RRR4-16/2	1829.629	1828.100	-258.481	0.225	432.854	0.351	15	0.135	K.GLLTDQTLPLLTDSALR.D
R4/RRR4-17/2	1213.233	1212.467	-193.924	0.541	1088.610	0.438	16	0.178	R.VNIGQIILSVR.T
R4/RRR4-17/2	1213.419	1212.467	-40.120	0.429	743.059	0.339	15	0.148	R.VNIGQIILSVR.T
R4/RRR4-8/2	1108.399	1109.344	-1759.735	0.242	596.044	0.480	13	0.143	R.ALLLAGPPATGK.T
R4/RRR4-11/3	1793.589	1792.011	-235.935	0.379	1925.311	0.160	31	0.142	R.VGQM*ETQINLVGSSRR.K
R4/RRR4-7/2	1720.428	1721.077	-961.714	0.377	844.583	0.497	21	0.164	R.ILGLGDLGVQGIGIPIGK.L
R4/RRR4-7/3	1550.533	1550.615	-53.516	0.398	1468.515	0.386	26	0.152	R.SRDGSVHDSFTVSR.D
R4/RRR4-20/2	1283.011	1283.330	-248.842	0.424	597.311	0.485	16	0.157	K.GDGTGGKSIYGDR.F
R4/RRR4-14/2	1176.258	1176.347	-75.841	0.485	1423.194	0.391	19	0.198	K.IGAGIEAFEIR.N
R4/RRR4-14/2	1176.126	1176.347	-188.800	0.427	1311.448	0.387	18	0.186	K.IGAGIEAFEIR.N
R4/RRR4-14/2	1176.059	1176.347	-245.237	0.449	936.387	0.337	16	0.155	K.IGAGIEAFEIR.N
R4/RRR4-3/2	1809.564	1809.225	188.191	0.480	635.869	0.450	19	0.152	R.GLLLPSSFPDVIPVIIK.A
R4/RRR4-8/2	1518.473	1517.665	-126.963	0.508	1049.863	0.456	19	0.179	R.EVAIEDPFNVDIR.Q
R4/RRR4-8/2	1518.837	1517.665	113.614	0.466	513.112	0.380	16	0.147	R.EVAIEDPFNVDIR.Q
R4/RRR4-6/2	1732.272	1732.916	-951.887	0.385	568.586	0.489	19	0.155	K.DGAPGLWPFGPVDFEK.M
R4/RRR4-6/2	1732.159	1732.916	-1017.049	0.313	675.145	0.371	20	0.145	K.DGAPGLWPFGPVDFEK.M
R4/RRR4-8/2	1083.683	1083.222	426.551	0.365	1015.027	0.482	14	0.178	K.YSLVSNFPR.V
R4/RRR4-8/2	1084.079	1083.222	-131.984	0.323	874.246	0.310	13	0.148	K.YSLVSNFPR.V
R4/RRR4-24/2	1370.246	1370.577	-242.203	0.483	1082.512	0.461	17	0.181	K.TPIQNLKDAIEK.L
R4/RRR4-24/2	1369.566	1370.577	-1472.172	0.394	1155.705	0.418	18	0.178	K.TPIQNLKDAIEK.L
R4/RRR4-24/2	1371.203	1370.577	-273.465	0.487	904.991	0.486	17	0.175	K.TPIQNLKDAIEK.L
R4/RRR4-17/3	1388.893	1389.582	-1219.189	0.460	1044.527	0.473	23	0.132	R.LGQIVFSDPEKR.Q

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	969.993	970.191	-205.065	0.511	1129.936	0.446	15	0.186	R.ALLDVGLIR.T
R4/RRR4-13/2	969.963	970.191	-235.997	0.421	1103.272	0.403	15	0.175	R.ALLDVGLIR.T
R4/RRR4-13/2	969.882	970.191	-319.713	0.393	948.455	0.414	14	0.167	R.ALLDVGLIR.T
R4/RRR4-5/2	1916.506	1916.322	96.159	0.423	577.013	0.459	14	0.144	-.VELTLVRLSQLGKGVM*R.S
R4/RRR4-6/2	1149.052	1149.235	-160.110	0.375	435.656	0.463	15	0.156	R.HSTVVDSFEK.K
R4/RRR4-6/2	1148.918	1149.235	-276.926	0.341	371.235	0.397	14	0.149	R.HSTVVDSFEK.K
R4/RRR4-6/2	1049.024	1049.162	-132.076	0.452	1234.657	0.431	15	0.190	K.VNVFEAVDR.N
R4/RRR4-6/2	1048.996	1049.162	-158.691	0.345	1413.219	0.250	15	0.170	K.VNVFEAVDR.N
R4/RRR4-6/2	1048.497	1049.162	-1592.392	0.337	948.784	0.208	14	0.142	-.VNVFEAVDR.-
R4/RRR4-15/2	1985.544	1984.282	132.602	0.438	890.477	0.489	18	0.165	R.KVDGFEIPLDVVGQPLEK.L
R4/RRR4-15/2	1983.505	1984.282	-898.418	0.414	631.406	0.473	18	0.152	R.KVDGFEIPLDVVGQPLEK.L
R4/RRR4-3/2	1487.463	1487.637	-117.263	0.434	1168.865	0.451	18	0.183	R.ANQIQSDLEELVK.S
R4/RRR4-22/2	1383.434	1382.670	-171.394	0.484	998.793	0.467	19	0.180	R.CKQLGITALHIK.I
R4/RRR4-22/2	1383.154	1382.670	350.661	0.458	1051.740	0.392	18	0.169	R.CKQLGITALHIK.I
R4/RRR4-22/2	1383.132	1382.670	334.999	0.409	623.923	0.408	16	0.153	R.CKQLGITALHIK.I
R4/RRR4-22/3	1383.906	1382.670	170.598	0.509	1328.753	0.441	26	0.151	R.CKQLGITALHIK.I
R4/RRR4-22/3	1383.874	1382.670	147.511	0.495	1226.588	0.398	25	0.129	R.CKQLGITALHIK.I
R4/RRR4-12/2	1249.134	1249.357	-178.353	0.431	713.801	0.490	15	0.166	K.TGFTGGLNYYR.C
R4/RRR4-11/2	1249.128	1249.357	-183.255	0.459	695.565	0.437	16	0.161	K.TGFTGGLNYYR.C
R4/RRR4-12/2	1248.680	1249.357	-1347.011	0.399	652.549	0.441	14	0.156	K.TGFTGGLNYYR.C
R4/RRR4-11/2	1248.448	1249.357	-1533.203	0.362	567.064	0.432	15	0.154	K.TGFTGGLNYYR.C
R4/RRR4-11/2	1249.766	1249.357	328.915	0.283	343.969	0.442	11	0.144	K.TGFTGGLNYYR.C
R4/RRR4-4/2	1965.648	1964.245	205.388	0.403	982.157	0.485	20	0.171	K.VLTELLDQLDIGTYEIK.L
R4/RRR4-14/3	1918.491	1918.183	160.906	0.328	728.819	0.494	28	0.107	R.VATNPAIIVGLHPCGGNAR.Q
R4/RRR4-12/2	1568.370	1567.769	-254.777	0.508	1131.126	0.445	23	0.183	R.SRPSELALPVSDPAK.A
R4/RRR4-12/2	1567.240	1567.769	-978.374	0.479	977.501	0.459	21	0.174	R.SRPSELALPVSDPAK.A
R4/RRR4-12/2	1567.203	1567.769	-1002.225	0.480	820.351	0.449	20	0.164	R.SRPSELALPVSDPAK.A
R4/RRR4-13/2	1567.319	1567.769	-287.992	0.276	471.912	0.269	16	0.137	R.SRPSELALPVSDPAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1345.106	1345.569	-345.217	0.437	1307.497	0.427	18	0.192	K.DLGTVVFEPLVR.T
R4/RRR4-16/2	1592.540	1592.754	-134.572	0.480	842.586	0.474	24	0.171	-.M*DGAASVPSSNEVALK.Q
R4/RRR4-16/2	1592.067	1592.754	-1062.922	0.429	875.309	0.472	24	0.171	-.M*DGAASVPSSNEVALK.Q
R4/RRR4-16/2	1592.139	1592.754	-1017.348	0.408	780.498	0.445	23	0.162	-.M*DGAASVPSSNEVALK.Q
R4/RRR4-2/3	1756.480	1754.966	-277.444	0.434	1434.680	0.391	26	0.151	K.LRSEVEEQLHSVLSK.K
R4/RRR4-4/2	1591.380	1591.790	-258.787	0.503	1145.626	0.442	22	0.182	K.LISGDLQPTSGTVFR.S
R4/RRR4-4/2	1787.461	1787.050	230.795	0.510	1073.554	0.458	22	0.181	R.LDQLIYIPLPDDKSR.M
R4/RRR4-1/2	1788.229	1787.050	100.675	0.536	644.679	0.529	18	0.167	R.LDQLIYIPLPDDKSR.M
R4/RRR4-4/2	1786.585	1787.050	-261.077	0.405	1079.353	0.366	22	0.166	R.LDQLIYIPLPDDKSR.M
R4/RRR4-4/2	1785.672	1787.050	-1335.709	0.321	632.956	0.297	17	0.140	R.LDQLIYIPLPDDKSR.M
R4/RRR4-1/2	1786.076	1787.050	-1108.505	0.392	711.619	0.259	18	0.138	R.LDQLIYIPLPDDKSR.M
R4/RRR4-9/2	1800.329	1799.962	204.050	0.336	1296.744	0.416	19	0.152	R.GWVYGPFADQPIFQSS.-
R4/RRR4-4/2	1898.752	1899.178	-224.890	0.427	1143.328	0.453	21	0.177	K.LALGTLALEDALSTGSPIR.T
R4/RRR4-4/2	1898.503	1899.178	-885.244	0.422	1099.922	0.463	20	0.175	K.LALGTLALEDALSTGSPIR.T
R4/RRR4-18/2	1238.244	1237.518	-222.044	0.451	591.232	0.461	16	0.161	K.LPFAPVPLVQR.M
R4/RRR4-18/2	1237.202	1237.518	-256.076	0.344	591.210	0.496	16	0.160	K.LPFAPVPLVQR.M
R4/RRR4-17/2	1237.416	1237.518	-82.581	0.324	734.046	0.428	17	0.157	K.LPFAPVPLVQR.M
R4/RRR4-17/2	1237.464	1237.518	-43.793	0.302	297.136	0.375	11	0.144	K.LPFAPVPLVQR.M
R4/RRR4-18/2	1237.153	1237.518	-296.564	0.283	451.880	0.327	14	0.144	K.LPFAPVPLVQR.M
R4/RRR4-17/2	1237.209	1237.518	-250.434	0.282	339.947	0.379	12	0.142	-.LPFAPVPLVQR.-
R4/RRR4-8/2	1159.056	1159.230	-150.488	0.407	1179.623	0.444	15	0.185	R.SAVDYFEATR.A
R4/RRR4-8/2	1158.356	1159.230	-1623.172	0.275	910.685	0.269	13	0.142	R.SAVDYFEATR.A
R4/RRR4-3/2	1380.352	1379.584	-168.583	0.405	559.188	0.461	16	0.153	K.IAAEPLNPSELPK.M
R4/RRR4-23/3	1432.911	1432.567	240.811	0.404	686.773	0.487	27	0.110	R.VTGGGHTSQVYAVR.Q
R4/RRR4-23/3	1432.718	1432.567	105.991	0.397	673.759	0.444	28	0.103	R.VTGGGHTSQVYAVR.Q
R4/RRR4-23/3	1432.881	1432.567	220.180	0.401	649.861	0.392	27	0.096	R.VTGGGHTSQVYAVR.Q
R4/RRR4-22/2	1647.325	1647.860	-935.047	0.493	817.138	0.464	20	0.164	R.TVNRPYGGVLSGTAVR.E
R4/RRR4-22/2	1647.202	1647.860	-1009.744	0.458	620.906	0.445	18	0.153	R.TVNRPYGGVLSGTAVR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-22/2	1647.473	1647.860	-236.004	0.460	643.565	0.438	18	0.152	R.TVNRPYGGVLSGTAVR.E
R4/RRR4-22/3	1647.857	1647.860	-1.985	0.516	1305.127	0.393	30	0.135	R.TVNRPYGGVLSGTAVR.E
R4/RRR4-22/3	1647.975	1647.860	69.561	0.493	1016.077	0.401	28	0.113	R.TVNRPYGGVLSGTAVR.E
R4/RRR4-22/3	1646.758	1647.860	-1280.212	0.403	975.252	0.326	27	0.095	R.TVNRPYGGVLSGTAVR.E
R4/RRR4-4/2	1322.848	1323.439	-1206.237	0.459	910.945	0.468	14	0.170	R.INFVTWSQDGR.H
R4/RRR4-4/2	1322.294	1323.439	-1626.934	0.310	1128.402	0.318	13	0.156	R.INFVTWSQDGR.H
R4/RRR4-7/2	1862.881	1862.069	-101.058	0.460	820.838	0.472	16	0.159	R.YYSVDESVELFPTLAK.N
R4/RRR4-7/2	1862.736	1862.069	-179.350	0.432	679.780	0.474	16	0.154	R.YYSVDESVELFPTLAK.N
R4/RRR4-8/2	1198.567	1198.396	142.951	0.317	583.509	0.484	14	0.151	K.LPEAPLTPGFR.Q
R4/RRR4-26/2	1030.048	1030.202	-149.723	0.340	496.285	0.469	11	0.144	-.AFLNSPVGPK.-
R4/RRR4-14/2	1503.377	1502.780	-268.479	0.313	1090.226	0.458	18	0.171	K.ADALAAFPSLTLIAK.V
R4/RRR4-26/2	1334.010	1333.497	-366.133	0.485	1227.425	0.428	20	0.187	R.NLNM*GNAASIPSK.C
R4/RRR4-26/2	1334.035	1333.497	-347.403	0.508	1002.278	0.434	19	0.173	R.NLNM*GNAASIPSK.C
R4/RRR4-27/2	1333.812	1333.497	236.994	0.450	884.796	0.426	18	0.165	R.NLNM*GNAASIPSK.C
R4/RRR4-26/2	1333.024	1333.497	-355.841	0.434	882.436	0.401	18	0.162	R.NLNM*GNAASIPSK.C
R4/RRR4-26/2	1333.300	1333.497	-148.233	0.409	814.288	0.417	18	0.161	R.NLNM*GNAASIPSK.C
R4/RRR4-27/2	1333.058	1333.497	-330.115	0.393	932.141	0.375	19	0.161	R.NLNM*GNAASIPSK.C
R4/RRR4-27/2	1334.029	1333.497	-351.994	0.449	859.290	0.404	17	0.160	R.NLNM*GNAASIPSK.C
R4/RRR4-25/2	1333.105	1333.497	-295.020	0.416	908.679	0.342	19	0.156	R.NLNM*GNAASIPSK.C
R4/RRR4-26/2	1333.033	1333.497	-349.318	0.400	808.973	0.375	18	0.156	R.NLNM*GNAASIPSK.C
R4/RRR4-27/2	1332.565	1333.497	-1453.842	0.320	775.308	0.392	18	0.155	R.NLNM*GNAASIPSK.C
R4/RRR4-27/2	1333.888	1333.497	293.890	0.457	700.784	0.369	16	0.150	R.NLNM*GNAASIPSK.C
R4/RRR4-28/2	1332.873	1333.497	-1221.653	0.400	575.507	0.363	16	0.149	R.NLNM*GNAASIPSK.C
R4/RRR4-26/2	1333.025	1333.497	-354.922	0.389	696.974	0.328	17	0.148	R.NLNM*GNAASIPSK.C
R4/RRR4-25/2	1332.995	1333.497	-1129.783	0.358	676.815	0.332	17	0.148	R.NLNM*GNAASIPSK.C
R4/RRR4-27/2	1332.512	1333.497	-1493.685	0.274	840.474	0.271	18	0.145	R.NLNM*GNAASIPSK.C
R4/RRR4-17/2	1528.971	1527.750	145.292	0.509	1373.445	0.388	20	0.190	K.IFLQQPAPESQLR.R
R4/RRR4-17/2	1529.014	1527.750	173.715	0.488	1159.587	0.399	19	0.176	K.IFLQQPAPESQLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-15/2	1264.123	1263.514	-310.576	0.370	781.873	0.484	16	0.168	K.LVAPWFQVFR.G
R4/RRR4-16/2	1263.201	1263.514	-248.673	0.373	668.725	0.475	15	0.162	K.LVAPWFQVFR.G
R4/RRR4-16/2	1263.481	1263.514	-26.708	0.443	533.664	0.499	13	0.162	K.LVAPWFQVFR.G
R4/RRR4-16/2	1263.078	1263.514	-346.602	0.352	566.450	0.419	13	0.152	K.LVAPWFQVFR.G
R4/RRR4-15/2	1263.074	1263.514	-349.317	0.312	611.119	0.394	14	0.150	K.LVAPWFQVFR.G
R4/RRR4-11/2	1351.724	1351.490	172.949	0.395	1266.478	0.429	15	0.186	K.FGFNDAFNYKK.E
R4/RRR4-15/3	1343.741	1343.513	170.185	0.473	735.518	0.462	23	0.110	R.LDEALATGLFHR.I
R4/RRR4-15/3	1342.998	1343.513	-1131.215	0.436	734.998	0.426	22	0.103	R.LDEALATGLFHR.I
R4/RRR4-15/3	1343.226	1343.513	-214.225	0.436	662.718	0.389	23	0.097	R.LDEALATGLFHR.I
R4/RRR4-4/2	1234.010	1234.387	-306.348	0.466	1634.455	0.341	17	0.207	R.LLQYGEQNIR.R
R4/RRR4-4/2	1235.025	1234.387	-293.803	0.536	1271.810	0.381	17	0.183	R.LLQYGEQNIR.R
R4/RRR4-4/2	1233.659	1234.387	-1404.400	0.473	1191.625	0.274	16	0.159	R.LLQYGEQNIR.R
R4/RRR4-3/2	1600.831	1599.854	-14.425	0.402	599.552	0.465	14	0.152	K.ILVNFDPTTYFLR.D
R4/RRR4-3/2	1600.886	1599.854	19.991	0.308	447.226	0.334	12	0.135	-.ILVNFDPTTYFLR.-
R4/RRR4-13/2	1122.871	1123.286	-370.253	0.342	518.404	0.468	12	0.154	R.VPTDIFFQR.X
R4/RRR4-13/2	1122.832	1123.286	-405.269	0.348	837.031	0.229	14	0.142	R.VPTDIFFQR.X
R4/RRR4-13/2	1122.961	1123.286	-289.977	0.225	545.527	0.328	12	0.138	-.VPTDIFFQR.-
R4/RRR4-4/2	1669.196	1670.806	-2169.022	0.387	798.184	0.477	16	0.157	R.RVQDGADTSAPPIQSK.Y
R4/RRR4-23/2	1765.282	1765.063	124.857	0.468	778.785	0.465	20	0.164	K.LELFLPEEYPM*AAPK.V
R4/RRR4-23/2	1764.240	1765.063	-1035.976	0.372	717.093	0.342	19	0.145	K.LELFLPEEYPM*AAPK.V
R4/RRR4-22/2	1307.922	1308.590	-1279.164	0.482	1011.106	0.450	18	0.178	K.IPYDFLISLVK.D
R4/RRR4-23/2	1308.439	1308.590	-115.528	0.445	993.718	0.427	18	0.173	K.IPYDFLISLVK.D
R4/RRR4-22/2	1308.282	1308.590	-235.893	0.481	981.689	0.387	18	0.167	K.IPYDFLISLVK.D
R4/RRR4-22/2	1308.307	1308.590	-217.359	0.458	944.470	0.384	18	0.165	K.IPYDFLISLVK.D
R4/RRR4-23/2	1308.324	1308.590	-204.067	0.455	799.933	0.354	17	0.155	K.IPYDFLISLVK.D
R4/RRR4-8/2	1895.506	1894.192	166.094	0.371	846.246	0.476	20	0.161	-.MAEVEVAAAAAAAGVLHRR.I
R4/RRR4-8/2	1896.009	1894.192	-96.710	0.396	728.912	0.495	18	0.157	-.MAEVEVAAAAAAAGVLHRR.I
R4/RRR4-8/2	1895.157	1894.192	-18.452	0.346	748.157	0.477	20	0.156	-.MAEVEVAAAAAAAGVLHRR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-23/2	1132.001	1132.209	-185.127	0.438	804.803	0.466	16	0.169	R.NITVNEAQSR.R
R4/RRR4-23/2	1132.187	1132.209	-19.748	0.439	819.109	0.421	16	0.164	R.NITVNEAQSR.R
R4/RRR4-12/3	1505.633	1505.742	-72.676	0.387	685.242	0.479	22	0.107	R.VPVAPPAHPTYDLK.A
R4/RRR4-12/3	1504.522	1505.742	-1480.099	0.325	533.892	0.475	20	0.098	R.VPVAPPAHPTYDLK.A
R4/RRR4-19/2	1679.198	1679.861	-993.348	0.412	790.342	0.475	20	0.166	R.EALGIHQGTVPSWQR.C
R4/RRR4-18/2	1679.764	1679.861	-57.846	0.445	686.212	0.482	19	0.162	R.EALGIHQGTVPSWQR.C
R4/RRR4-18/2	1679.482	1679.861	-226.112	0.445	702.765	0.445	20	0.160	R.EALGIHQGTVPSWQR.C
R4/RRR4-19/2	1679.207	1679.861	-987.874	0.421	660.502	0.425	19	0.155	R.EALGIHQGTVPSWQR.C
R4/RRR4-18/2	1679.108	1679.861	-1047.360	0.439	585.097	0.427	19	0.154	R.EALGIHQGTVPSWQR.C
R4/RRR4-19/2	1679.360	1679.861	-896.286	0.410	591.024	0.421	19	0.153	R.EALGIHQGTVPSWQR.C
R4/RRR4-7/2	1047.942	1048.217	-263.535	0.318	554.548	0.465	13	0.152	R.ANEFGIVLGK.L
R4/RRR4-7/2	1048.084	1048.217	-127.521	0.403	635.764	0.387	11	0.144	-.ANEFGIVLGK.-
R4/RRR4-7/2	1047.312	1048.217	-1824.967	0.321	735.564	0.257	13	0.140	R.ANEFGIVLGK.L
R4/RRR4-11/2	1149.548	1150.306	-1533.892	0.445	770.242	0.467	15	0.166	K.LIDQAVEYAK.K
R4/RRR4-17/2	1182.970	1183.466	-420.581	0.343	849.508	0.476	15	0.165	K.TPIGILNITLK.Q
R4/RRR4-17/2	1183.391	1183.466	-63.072	0.386	684.751	0.516	15	0.165	K.TPIGILNITLK.Q
R4/RRR4-17/2	1183.094	1183.466	-315.185	0.370	602.917	0.495	13	0.157	K.TPIGILNITLK.Q
R4/RRR4-18/2	1161.016	1161.375	-310.317	0.475	1348.230	0.391	18	0.190	K.LLFLGLDNAGK.T
R4/RRR4-18/2	1162.171	1161.375	-176.634	0.544	1326.349	0.388	18	0.188	K.LLFLGLDNAGK.T
R4/RRR4-18/2	1161.078	1161.375	-257.153	0.564	1376.218	0.363	18	0.186	K.LLFLGLDNAGK.T
R4/RRR4-19/2	1161.152	1161.375	-193.343	0.351	565.618	0.289	12	0.139	K.LLFLGLDNAGK.T
R4/RRR4-25/2	1314.929	1314.473	347.905	0.433	1211.719	0.430	17	0.182	K.AIADILSNVNGAR.D
R4/RRR4-26/2	1314.853	1314.473	289.447	0.442	1151.259	0.324	17	0.160	K.AIADILSNVNGAR.D
R4/RRR4-6/2	1213.187	1213.364	-146.196	0.491	650.079	0.426	15	0.158	K.IVNDNYIYAK.L
R4/RRR4-25/3	1276.115	1275.396	-220.406	0.423	954.940	0.467	23	0.122	R.HGGSGGPADPVPVK.L
R4/RRR4-25/3	1275.399	1275.396	2.715	0.308	925.406	0.175	22	0.073	R.HGGSGGPADPVPVK.L
R4/RRR4-12/2	1559.796	1558.804	-5.072	0.422	1193.325	0.434	17	0.179	R.LFYGPGGPYALFAGK.D
R4/RRR4-14/2	1560.020	1558.804	139.104	0.469	1087.381	0.421	19	0.172	R.LFYGPGGPYALFAGK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-14/2	1560.069	1558.804	170.728	0.378	1197.402	0.361	19	0.169	R.LFYGPGGPYALFAGK.D
R4/RRR4-13/2	1558.334	1558.804	-302.381	0.382	1073.215	0.405	18	0.167	R.LFYGPGGPYALFAGK.D
R4/RRR4-12/2	1559.631	1558.804	-111.209	0.354	548.869	0.213	13	0.122	-.LFYGPGGPYALFAGK.-
R4/RRR4-27/2	1108.600	1109.257	-1499.324	0.470	1234.553	0.412	17	0.187	R.YIEATGIVSR.A
R4/RRR4-27/2	1108.399	1109.257	-1681.638	0.352	1267.175	0.416	17	0.186	R.YIEATGIVSR.A
R4/RRR4-27/2	1109.032	1109.257	-203.975	0.515	1085.404	0.456	17	0.185	R.YIEATGIVSR.A
R4/RRR4-12/2	821.858	821.944	-104.895	0.360	572.724	0.468	11	0.158	R.ALELGYR.L
R4/RRR4-12/2	821.890	821.944	-66.010	0.273	583.048	0.458	11	0.151	R.ALELGYR.L
R4/RRR4-9/2	1088.008	1088.280	-250.454	0.401	1090.227	0.447	16	0.178	R.LGGSLDALTIK.E
R4/RRR4-9/2	1088.185	1088.280	-87.267	0.433	1012.962	0.467	16	0.178	R.LGGSLDALTIK.E
R4/RRR4-9/2	1088.193	1088.280	-79.841	0.390	1024.868	0.447	16	0.174	R.LGGSLDALTIK.E
R4/RRR4-5/2	1616.412	1616.755	-212.741	0.386	959.842	0.467	18	0.167	R.IQNVADIVLGDSSER.K
R4/RRR4-8/2	1235.145	1235.501	-289.016	0.363	522.442	0.456	13	0.146	-.SPATILPIGPLR.-
R4/RRR4-11/2	1212.386	1212.376	8.522	0.488	590.933	0.409	13	0.152	R.FVIDIENSFK.-
R4/RRR4-6/2	968.431	969.119	-1747.371	0.430	895.011	0.442	13	0.170	R.FTDFALVR.K
R4/RRR4-6/2	968.973	969.119	-150.884	0.508	833.170	0.432	13	0.168	R.FTDFALVR.K
R4/RRR4-6/2	968.564	969.119	-1610.230	0.432	804.790	0.440	13	0.166	R.FTDFALVR.K
R4/RRR4-16/2	1336.818	1336.472	259.047	0.466	972.121	0.445	16	0.172	R.TEQFIAELEQK.L
R4/RRR4-1/2	1699.485	1699.930	-263.074	0.398	1146.609	0.438	21	0.177	R.GLGTATVTIQDIGLSPR.A
R4/RRR4-1/2	1699.519	1699.930	-242.465	0.376	745.064	0.388	18	0.147	R.GLGTATVTIQDIGLSPR.A
R4/RRR4-18/2	936.046	936.136	-97.004	0.405	799.600	0.467	14	0.169	R.HVVIIAQR.T
R4/RRR4-18/2	936.074	936.136	-66.918	0.348	500.493	0.435	11	0.153	R.HVVIIAQR.T
R4/RRR4-18/2	935.998	936.136	-148.024	0.279	332.732	0.316	9	0.132	-.HVVIIAQR.-
R4/RRR4-4/3	1331.581	1331.549	24.300	0.486	787.007	0.440	22	0.109	R.HSVILDHQLLR.F
R4/RRR4-23/2	943.887	944.111	-238.042	0.501	1237.174	0.393	14	0.182	R.GLVGEIISR.F
R4/RRR4-23/2	944.974	944.111	-145.258	0.505	1176.441	0.388	14	0.177	R.GLVGEIISR.F
R4/RRR4-23/2	944.014	944.111	-102.994	0.478	1159.778	0.386	14	0.176	R.GLVGEIISR.F
R4/RRR4-9/2	1146.080	1146.321	-211.056	0.359	1233.224	0.417	16	0.182	R.ITEGVNLPFR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1596.851	1595.738	71.260	0.438	747.905	0.454	19	0.162	R.DGLLPSFFSDVNQR.T
R4/RRR4-8/2	1596.850	1595.738	70.800	0.370	536.013	0.375	16	0.145	R.DGLLPSFFSDVNQR.T
R4/RRR4-9/2	1597.275	1595.738	-290.256	0.381	462.577	0.358	14	0.139	-.DGLLPSFFSDVNQR.-
R4/RRR4-7/2	1285.581	1286.460	-1465.680	0.405	1237.007	0.418	17	0.183	R.ELALGLELSGQR.F
R4/RRR4-7/2	1286.198	1286.460	-204.437	0.411	1044.587	0.375	17	0.164	R.ELALGLELSGQR.F
R4/RRR4-2/2	1580.366	1579.562	-124.547	0.431	793.680	0.443	18	0.158	K.SDATIDDENSTGTPR.L
R4/RRR4-4/2	1339.372	1339.519	-110.117	0.400	608.567	0.444	14	0.147	K.IGLSASTIASSFGK.T
R4/RRR4-15/1	1143.625	1144.346	-1509.761	0.180	838.836	0.409	16	0.624	K.VAVITGAASGIGK.A
R4/RRR4-15/2	1143.396	1144.346	-1711.228	0.415	2072.249	0.622	22	0.338	K.VAVITGAASGIGK.A
R4/RRR4-15/2	1144.073	1144.346	-239.786	0.465	1974.229	0.623	22	0.325	K.VAVITGAASGIGK.A
R4/RRR4-15/2	1144.000	1144.346	-303.802	0.478	1940.229	0.630	22	0.322	K.VAVITGAASGIGK.A
R4/RRR4-16/2	1144.104	1144.346	-212.598	0.341	1556.889	0.447	21	0.217	K.VAVITGAASGIGK.A
R4/RRR4-18/2	1160.961	1161.204	-210.354	0.508	1548.654	0.307	19	0.189	R.GGEGEEVGSLAR.R
R4/RRR4-18/2	1160.745	1161.204	-397.411	0.498	1371.182	0.311	18	0.174	R.GGEGEEVGSLAR.R
R4/RRR4-18/2	1160.306	1161.204	-1640.914	0.343	1156.755	0.196	17	0.146	R.GGEGEEVGSLAR.R
R4/RRR4-9/2	1556.514	1555.889	-241.694	0.467	850.300	0.447	21	0.165	R.VGFLTPVANLIGVVR.G
R4/RRR4-6/3	1358.221	1359.514	-1693.028	0.417	768.853	0.460	21	0.109	K.TNQIVITNDKGR.L
R4/RRR4-6/3	1359.463	1359.514	-37.621	0.416	480.247	0.445	19	0.098	K.TNQIVITNDKGR.L
R4/RRR4-12/3	1076.374	1076.234	130.843	0.519	1344.920	0.359	25	0.128	K.HVGHLGGALSK.N
R4/RRR4-12/3	1076.147	1076.234	-81.259	0.492	1435.898	0.296	25	0.119	K.HVGHLGGALSK.N
R4/RRR4-12/3	1076.402	1076.234	156.945	0.494	1424.621	0.275	25	0.113	K.HVGHLGGALSK.N
R4/RRR4-11/2	1309.211	1309.623	-315.591	0.398	1292.463	0.402	18	0.185	R.SLLSPVTLPIIR.D
R4/RRR4-8/2	1390.831	1390.528	218.528	0.434	1257.486	0.406	17	0.183	K.IVFANGSQDPWR.H
R4/RRR4-1/2	1676.123	1675.995	76.655	0.366	606.311	0.422	14	0.141	R.GFFPLSAALLSSPVLR.L
R4/RRR4-5/2	1245.745	1246.351	-1292.885	0.352	587.248	0.449	15	0.152	K.VPNPEFEGQTK.T
R4/RRR4-24/3	1926.640	1925.291	182.086	0.500	1718.694	0.232	28	0.133	R.RYLQMIQKNSIFNLR.S
R4/RRR4-24/3	1926.830	1925.291	-239.921	0.463	1626.781	0.221	27	0.123	-.RYLQMIQKNSIFNLR.-
R4/RRR4-23/3	1926.686	1925.291	205.722	0.436	1561.571	0.216	26	0.113	R.RYLQMIQKNSIFNLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/2	1283.231	1282.471	-187.544	0.352	645.514	0.459	18	0.154	K.DLAVLSGAHTIGK.A
R4/RRR4-1/2	1328.556	1327.510	34.503	0.331	602.965	0.453	13	0.147	R.ILGGSVSEYFVR.S
R4/RRR4-17/3	1538.214	1538.734	-991.114	0.438	1024.360	0.443	26	0.123	R.KIENVATGPNNRPK.L
R4/RRR4-17/3	1538.712	1538.734	-13.942	0.480	849.840	0.436	24	0.111	R.KIENVATGPNNRPK.L
R4/RRR4-18/3	1538.589	1538.734	-94.635	0.456	688.623	0.463	22	0.109	R.KIENVATGPNNRPK.L
R4/RRR4-17/3	1538.186	1538.734	-1009.400	0.456	773.082	0.422	23	0.105	R.KIENVATGPNNRPK.L
R4/RRR4-18/3	1538.702	1538.734	-20.865	0.490	774.351	0.391	23	0.100	R.KIENVATGPNNRPK.L
R4/RRR4-5/3	1584.871	1584.715	99.022	0.403	808.477	0.455	23	0.109	K.YKPSQQSAAFNSGAK.E
R4/RRR4-5/3	1583.866	1584.715	-1170.529	0.274	689.423	0.326	22	0.082	-.YKPSQQSAAFNSGAK.-
R4/RRR4-8/3	1462.111	1461.774	230.810	0.438	846.764	0.450	27	0.112	R.APLIKPSPLTAQPK.H
R4/RRR4-8/3	1461.955	1461.774	123.804	0.407	604.209	0.477	25	0.106	R.APLIKPSPLTAQPK.H
R4/RRR4-8/3	1462.006	1461.774	159.098	0.379	844.276	0.413	26	0.104	R.APLIKPSPLTAQPK.H
R4/RRR4-8/2	1719.799	1718.932	-77.572	0.469	1177.414	0.412	18	0.174	R.TTLFLNLANDPTIER.I
R4/RRR4-21/2	1345.063	1345.529	-347.140	0.396	645.799	0.450	18	0.158	R.NSPVPSFSGLLAR.A
R4/RRR4-21/2	1345.244	1345.529	-212.119	0.293	557.078	0.464	17	0.150	R.NSPVPSFSGLLAR.A
R4/RRR4-21/2	1345.327	1345.529	-150.675	0.273	252.356	0.349	12	0.138	-.NSPVPSFSGLLAR.-
R4/RRR4-5/2	1413.054	1413.557	-1066.414	0.324	594.120	0.444	13	0.143	K.SLVGGFYDAGDAIK.F
R4/RRR4-12/2	1524.263	1523.758	-325.687	0.444	857.644	0.446	18	0.164	R.ILGVQYSIPDYVR.V
R4/RRR4-21/2	1254.057	1253.432	-299.400	0.412	642.119	0.442	15	0.157	K.FQGSPAIITYR.V
R4/RRR4-21/2	1253.254	1253.432	-142.010	0.349	821.288	0.402	15	0.155	-.FQGSPAIITYR.-
R4/RRR4-21/2	1253.668	1253.432	189.015	0.185	595.781	0.377	15	0.139	K.FQGSPAIITYR.V
R4/RRR4-9/2	1475.315	1474.728	-280.557	0.430	1336.602	0.381	16	0.181	R.LISQVVSSITASLR.F
R4/RRR4-8/2	1475.505	1474.728	-151.322	0.418	1143.977	0.438	17	0.178	R.LISQVVSSITASLR.F
R4/RRR4-9/2	1474.399	1474.728	-223.931	0.360	1130.179	0.380	17	0.168	R.LISQVVSSITASLR.F
R4/RRR4-9/2	1474.406	1474.728	-218.781	0.344	1100.990	0.373	17	0.165	R.LISQVVSSITASLR.F
R4/RRR4-8/2	1474.417	1474.728	-211.389	0.315	1120.232	0.351	17	0.163	R.LISQVVSSITASLR.F
R4/RRR4-1/2	1475.002	1474.728	186.468	0.337	949.276	0.324	16	0.151	R.LISQVVSSITASLR.F
R4/RRR4-2/2	1474.318	1474.728	-279.252	0.298	834.734	0.369	15	0.150	R.LISQVVSSITASLR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/2	1475.539	1474.728	-128.168	0.340	822.740	0.351	15	0.148	R.LISQVVSSITASLR.F
R4/RRR4-3/2	1475.002	1474.728	186.551	0.359	859.645	0.322	15	0.146	R.LISQVVSSITASLR.F
R4/RRR4-8/2	1474.282	1474.728	-303.260	0.231	1033.045	0.115	17	0.135	R.LISQVVSSITASLR.F
R4/RRR4-9/3	1474.655	1474.728	-49.876	0.395	1241.727	0.356	28	0.118	R.LISQVVSSITASLR.F
R4/RRR4-9/3	1475.506	1474.728	-150.833	0.396	1123.314	0.374	26	0.114	R.LISQVVSSITASLR.F
R4/RRR4-2/2	1475.283	1474.728	-302.307	0.241	332.925	0.306	11	0.112	-.LISQVVSSITASLR.-
R4/RRR4-9/3	1474.875	1474.728	99.807	0.319	1353.871	0.236	28	0.099	R.LISQVVSSITASLR.F
R4/RRR4-8/3	1474.653	1474.728	-51.246	0.362	758.070	0.314	22	0.086	-.LISQVVSSITASLR.-
R4/RRR4-5/2	1780.391	1779.073	179.171	0.369	579.683	0.434	17	0.146	K.TNIVGMEANMEQLLSK.I
R4/RRR4-3/3	1282.335	1282.471	-106.290	0.432	948.360	0.437	26	0.115	K.LITHGGVTGIADK.L
R4/RRR4-3/3	1282.696	1282.471	175.946	0.483	716.327	0.487	25	0.114	K.LITHGGVTGIADK.L
R4/RRR4-3/3	1282.417	1282.471	-42.411	0.388	644.909	0.426	22	0.099	K.LITHGGVTGIADK.L
R4/RRR4-18/2	1272.038	1272.390	-277.650	0.387	959.422	0.444	18	0.171	K.VLTPISQDDQR.Q
R4/RRR4-18/2	1272.107	1272.390	-222.871	0.305	638.258	0.413	16	0.151	K.VLTPISQDDQR.Q
R4/RRR4-18/2	1271.605	1272.390	-1407.842	0.209	689.777	0.314	16	0.139	K.VLTPISQDDQR.Q
R4/RRR4-12/3	1318.367	1317.458	-69.033	0.512	853.690	0.408	20	0.107	K.FEHHEM*FPAR.T
R4/RRR4-12/3	1317.550	1317.458	70.362	0.484	926.335	0.372	20	0.103	K.FEHHEM*FPAR.T
R4/RRR4-12/3	1302.584	1301.458	96.747	0.324	741.383	0.339	19	0.089	K.FEHHEMFPAR.T
R4/RRR4-16/2	1359.547	1359.552	-4.288	0.422	780.885	0.447	17	0.162	K.GLDFDLVPVDLR.T
R4/RRR4-17/2	1358.987	1359.552	-1155.149	0.300	733.071	0.302	15	0.141	K.GLDFDLVPVDLR.T
R4/RRR4-1/2	955.700	956.078	-397.289	0.033	639.413	0.237	12	0.121	R.DIVLGSSHK.E
R4/RRR4-1/2	955.956	956.078	-127.964	0.014	845.260	0.197	13	0.121	R.DIVLGSSHK.E
R4/RRR4-20/3	1553.593	1553.788	-126.348	0.368	1523.510	0.311	25	0.137	R.LPLRDVLADTGIGGR.A
R4/RRR4-14/3	1553.984	1553.788	126.360	0.439	1209.664	0.410	24	0.131	R.LPLRDVLADTGIGGR.A
R4/RRR4-12/2	1305.354	1305.420	-50.519	0.442	927.064	0.437	15	0.167	R.TSNVFDGVYFR.E
R4/RRR4-12/2	1305.869	1305.420	345.068	0.348	815.821	0.403	15	0.155	R.TSNVFDGVYFR.E
R4/RRR4-8/2	1192.062	1192.386	-272.860	0.498	1057.811	0.410	16	0.174	R.ILVQEGIYEK.F
R4/RRR4-8/2	1192.101	1192.386	-240.293	0.475	972.931	0.430	16	0.173	R.ILVQEGIYEK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1192.213	1192.386	-145.892	0.332	710.241	0.299	13	0.143	R.ILVQEGIYEK.F
R4/RRR4-8/2	1264.531	1263.465	52.613	0.347	1013.290	0.437	17	0.169	K.IFGLSSVSDIPK.L
R4/RRR4-7/2	1264.105	1263.465	-285.592	0.308	721.374	0.279	15	0.139	K.IFGLSSVSDIPK.L
R4/RRR4-8/2	1478.512	1477.730	-148.033	0.394	1151.292	0.418	18	0.176	K.RVEGIISLSDIFK.F
R4/RRR4-2/2	1395.091	1394.601	351.786	0.317	895.887	0.425	15	0.157	R.HDSIEQLLLLGR.M
R4/RRR4-11/3	1881.942	1881.132	-101.278	0.330	1173.970	0.096	27	0.069	-.M*VGNLCQQNSACLQIK.-
R4/RRR4-4/2	1232.026	1231.335	-251.388	0.452	1068.609	0.423	18	0.175	K.TTAGIEPEDVAK.R
R4/RRR4-3/2	1230.893	1231.335	-359.444	0.358	856.711	0.339	16	0.151	K.TTAGIEPEDVAK.R
R4/RRR4-4/2	1230.374	1231.335	-1598.317	0.291	1001.861	0.287	17	0.150	K.TTAGIEPEDVAK.R
R4/RRR4-4/2	1230.430	1231.335	-1552.770	0.355	824.500	0.336	16	0.150	K.TTAGIEPEDVAK.R
R4/RRR4-14/2	1036.774	1036.163	-376.555	0.461	731.505	0.425	13	0.162	K.VLDIYEQR.L
R4/RRR4-20/2	927.315	928.066	-1894.165	0.423	685.934	0.434	11	0.160	K.CGHVLWR.E
R4/RRR4-25/2	1101.073	1101.322	-226.688	0.415	777.335	0.439	16	0.163	R.LVTIATLVDR.L
R4/RRR4-25/2	1100.872	1101.322	-409.349	0.371	471.071	0.354	13	0.146	R.LVTIATLVDR.L
R4/RRR4-17/2	1343.131	1343.548	-311.267	0.336	626.142	0.446	14	0.148	-.VNCPALLTVNGGK.-
R4/RRR4-17/2	1344.169	1343.548	-283.063	0.355	772.309	0.247	16	0.138	-.VNCPALLTVNGGK.-
R4/RRR4-10/2	893.882	894.010	-144.315	0.323	1112.224	0.395	13	0.171	K.ATVNSFVR.S
R4/RRR4-10/2	893.976	894.010	-37.884	0.345	1005.500	0.369	13	0.163	K.ATVNSFVR.S
R4/RRR4-11/2	893.936	894.010	-83.357	0.366	626.132	0.380	12	0.152	K.ATVNSFVR.S
R4/RRR4-11/2	893.875	894.010	-151.438	0.297	666.106	0.369	12	0.149	K.ATVNSFVR.S
R4/RRR4-15/2	1719.216	1718.057	92.396	0.374	564.611	0.430	16	0.144	K.LGIPLVGNAIMQTYAR.D
R4/RRR4-3/3	1164.335	1165.367	-1750.656	0.447	1151.754	0.412	19	0.125	R.HISILKDNPK.I
R4/RRR4-3/3	1165.143	1165.367	-193.008	0.437	1055.212	0.343	18	0.103	R.HISILKDNPK.I
R4/RRR4-5/2	1530.531	1530.709	-116.523	0.438	774.586	0.436	19	0.162	R.SPQFPEAIDWIAR.N
R4/RRR4-5/2	1530.331	1530.709	-247.269	0.399	558.555	0.440	17	0.153	R.SPQFPEAIDWIAR.N
R4/RRR4-7/2	1896.324	1897.161	-971.358	0.464	1076.490	0.415	18	0.167	R.EGISYYNNLINELLLK.G
R4/RRR4-8/2	1898.949	1897.161	-112.099	0.405	604.423	0.415	14	0.143	R.EGISYYNNLINELLLK.G
R4/RRR4-1/3	1513.722	1513.593	85.032	0.502	1102.103	0.397	23	0.118	-.VLYHEDPNSPDAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-2/3	1513.418	1513.593	-116.151	0.447	914.572	0.385	23	0.106	K.VLYHEDPNSPDAR.I
R4/RRR4-2/3	1513.967	1513.593	247.448	0.473	959.260	0.373	22	0.106	K.VLYHEDPNSPDAR.I
R4/RRR4-3/3	1513.707	1513.593	75.205	0.440	723.766	0.392	23	0.101	K.VLYHEDPNSPDAR.I
R4/RRR4-1/3	1512.519	1513.593	-1375.661	0.424	978.773	0.336	23	0.100	K.VLYHEDPNSPDAR.I
R4/RRR4-2/3	1513.754	1513.593	106.626	0.448	813.247	0.379	21	0.099	-.VLYHEDPNSPDAR.-
R4/RRR4-3/3	1513.315	1513.593	-184.605	0.395	533.652	0.311	22	0.094	K.VLYHEDPNSPDAR.I
R4/RRR4-3/3	1513.904	1513.593	205.727	0.387	554.462	0.309	23	0.094	K.VLYHEDPNSPDAR.I
R4/RRR4-1/3	1513.680	1513.593	57.371	0.452	607.566	0.403	18	0.085	-.VLYHEDPNSPDAR.-
R4/RRR4-19/2	1113.926	1114.146	-198.353	0.390	1347.034	0.361	15	0.184	R.FGFDEDDIR.V
R4/RRR4-18/2	1113.978	1114.146	-151.522	0.405	1150.818	0.160	15	0.142	R.FGFDEDDIR.V
R4/RRR4-10/2	1480.477	1480.774	-201.592	0.469	1258.059	0.385	20	0.179	K.IQLLDLPGIIEGAK.D
R4/RRR4-10/2	1480.369	1480.774	-274.720	0.458	1268.254	0.340	20	0.172	K.IQLLDLPGIIEGAK.D
R4/RRR4-5/2	1278.869	1279.424	-1219.762	0.460	921.127	0.426	17	0.167	R.NIEQFKVEGSK.V
R4/RRR4-13/2	1030.668	1031.187	-1478.338	0.281	603.334	0.431	12	0.146	K.FTDVPINPK.V
R4/RRR4-27/3	1068.108	1068.235	-119.836	0.481	1450.271	0.309	21	0.125	R.HPM*VGNQLR.H
R4/RRR4-27/3	1067.738	1068.235	-467.153	0.288	954.998	0.117	19	0.071	R.HPM*VGNQLR.H
R4/RRR4-12/2	1508.489	1507.674	-122.609	0.417	1414.807	0.345	18	0.183	R.GWLEWNGADFALK.T
R4/RRR4-12/3	1462.490	1462.636	-100.229	0.436	1583.218	0.277	24	0.133	R.RGDLYQLVDVQR.S
R4/RRR4-15/2	1012.927	1013.171	-241.580	0.464	851.043	0.408	13	0.164	R.SLNIYFQK.S
R4/RRR4-27/2	1087.175	1087.210	-32.616	0.447	1041.181	0.410	14	0.173	R.GYISYQSLR.R
R4/RRR4-27/2	1087.181	1087.210	-27.435	0.411	1087.663	0.370	14	0.169	R.GYISYQSLR.R
R4/RRR4-28/2	1087.029	1087.210	-167.105	0.396	1012.626	0.373	14	0.165	R.GYISYQSLR.R
R4/RRR4-28/2	1086.213	1087.210	-1844.034	0.374	895.562	0.412	14	0.164	R.GYISYQSLR.R
R4/RRR4-28/2	1086.949	1087.210	-240.785	0.449	891.066	0.370	14	0.160	R.GYISYQSLR.R
R4/RRR4-27/2	1087.035	1087.210	-161.472	0.436	909.640	0.361	14	0.160	R.GYISYQSLR.R
R4/RRR4-28/2	1087.546	1087.210	309.190	0.133	509.790	0.258	13	0.135	R.GYISYQSLR.R
R4/RRR4-20/3	1659.623	1659.933	-187.203	0.341	836.687	0.437	30	0.104	R.SAAVAGAIGGVLAGAAM*AGK.Q
R4/RRR4-21/2	1277.850	1277.451	313.159	0.353	740.839	0.442	17	0.157	K.VALTFTPAAETR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-21/2	1276.928	1277.451	-1196.783	0.262	433.082	0.383	14	0.139	-.VALTFTPAAETR.-
R4/RRR4-13/3	1553.159	1551.768	252.832	0.337	954.220	0.438	26	0.112	R.YGEITAWTGKPTVK.V
R4/RRR4-13/3	1550.996	1551.768	-1146.077	0.324	634.572	0.347	20	0.086	R.YGEITAWTGKPTVK.V
R4/RRR4-21/2	1552.177	1552.713	-992.444	0.458	699.874	0.409	15	0.149	K.DFNLAEHPDIPGVK.N
R4/RRR4-21/2	1551.238	1552.713	-1599.766	0.310	914.033	0.202	17	0.136	K.DFNLAEHPDIPGVK.N
R4/RRR4-4/2	974.982	975.083	-104.244	0.421	638.861	0.421	12	0.156	K.HGESYLLR.V
R4/RRR4-16/2	1077.092	1076.188	-88.507	0.333	700.039	0.440	14	0.157	R.NPVFDQSLR.L
R4/RRR4-16/2	1076.515	1076.188	305.420	0.261	441.042	0.258	12	0.140	R.NPVFDQSLR.L
R4/RRR4-16/2	1076.802	1076.188	-358.805	0.332	540.628	0.264	12	0.140	-.NPVFDQSLR.-
R4/RRR4-8/3	1231.565	1231.351	174.303	0.421	774.788	0.424	22	0.102	-.LHFHNNGHVR.-
R4/RRR4-12/2	940.519	941.150	-1738.694	0.432	1133.147	0.380	13	0.174	R.ILLITDPR.T
R4/RRR4-17/2	940.973	941.150	-188.424	0.419	1079.302	0.387	13	0.172	R.ILLITDPR.T
R4/RRR4-14/2	940.637	941.150	-1612.738	0.430	1131.448	0.355	13	0.170	R.ILLITDPR.T
R4/RRR4-12/2	940.505	941.150	-1753.821	0.423	966.101	0.419	12	0.170	R.ILLITDPR.T
R4/RRR4-10/2	941.017	941.150	-141.705	0.473	1022.493	0.387	13	0.170	R.ILLITDPR.T
R4/RRR4-16/2	941.036	941.150	-121.535	0.520	1093.561	0.362	13	0.168	R.ILLITDPR.T
R4/RRR4-16/2	940.990	941.150	-170.074	0.415	1032.489	0.368	13	0.167	R.ILLITDPR.T
R4/RRR4-14/2	940.550	941.150	-1705.703	0.464	986.373	0.388	12	0.167	R.ILLITDPR.T
R4/RRR4-11/2	940.932	941.150	-232.153	0.461	988.663	0.384	12	0.166	R.ILLITDPR.T
R4/RRR4-16/2	941.051	941.150	-105.661	0.490	1075.398	0.347	13	0.166	R.ILLITDPR.T
R4/RRR4-13/2	940.495	941.150	-1764.646	0.459	997.254	0.371	12	0.165	R.ILLITDPR.T
R4/RRR4-10/2	941.046	941.150	-110.996	0.482	946.240	0.383	12	0.164	R.ILLITDPR.T
R4/RRR4-12/2	940.594	941.150	-1659.414	0.432	938.992	0.384	12	0.164	R.ILLITDPR.T
R4/RRR4-11/2	941.039	941.150	-117.632	0.482	979.666	0.366	12	0.163	R.ILLITDPR.T
R4/RRR4-13/2	940.753	941.150	-422.993	0.442	966.392	0.368	12	0.163	R.ILLITDPR.T
R4/RRR4-13/2	941.074	941.150	-80.418	0.487	974.617	0.364	12	0.163	R.ILLITDPR.T
R4/RRR4-17/2	941.051	941.150	-104.880	0.487	951.607	0.366	12	0.162	R.ILLITDPR.T
R4/RRR4-10/2	941.016	941.150	-143.136	0.484	915.582	0.353	12	0.159	R.ILLITDPR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-11/2	941.153	941.150	2.848	0.500	1070.880	0.298	13	0.158	R.ILLITDPR.T
R4/RRR4-8/3	1190.624	1190.335	242.974	0.478	1059.265	0.403	19	0.116	R.RPDYFNHIK.S
R4/RRR4-8/3	1190.178	1190.335	-132.985	0.402	889.290	0.357	18	0.098	R.RPDYFNHIK.S
R4/RRR4-15/3	1190.912	1190.335	-356.873	0.297	350.877	0.293	18	0.097	R.RPDYFNHIK.S
R4/RRR4-15/3	1190.993	1190.335	-288.537	0.361	813.255	0.185	17	0.071	-.RPDYFNHIK.-
R4/RRR4-11/2	1470.917	1469.793	84.769	0.385	803.926	0.438	17	0.158	K.VLDPVPLIGFLTGK.L
R4/RRR4-11/2	1470.622	1469.793	-116.857	0.353	683.896	0.443	16	0.153	K.VLDPVPLIGFLTGK.L
R4/RRR4-11/2	1470.799	1469.793	4.361	0.283	667.902	0.360	15	0.142	K.VLDPVPLIGFLTGK.L
R4/RRR4-10/2	1252.035	1252.400	-292.452	0.421	1239.007	0.388	16	0.179	K.NFGVTEFVNPK.D
R4/RRR4-10/2	1251.462	1252.400	-1553.872	0.274	721.300	0.238	13	0.137	K.NFGVTEFVNPK.D
R4/RRR4-2/2	1253.134	1252.400	-213.250	0.257	667.019	0.194	15	0.136	K.NFGVTEFVNPK.D
R4/RRR4-10/2	1252.054	1252.400	-277.192	0.331	770.443	0.236	14	0.135	-.NFGVTEFVNPK.-
R4/RRR4-22/3	1442.827	1442.517	215.395	0.408	942.208	0.431	24	0.113	-.ALAADHDASASAVSR.-
R4/RRR4-22/3	1442.404	1442.517	-78.281	0.426	826.022	0.446	23	0.110	R.ALAADHDASASAVSR.R
R4/RRR4-23/3	1443.016	1442.517	347.220	0.364	976.320	0.404	25	0.109	R.ALAADHDASASAVSR.R
R4/RRR4-6/3	1759.929	1760.974	-1165.366	0.451	850.886	0.420	24	0.107	R.KIETYFQHNVPEVR.N
R4/RRR4-6/3	1760.849	1760.974	-71.252	0.429	992.345	0.340	26	0.099	R.KIETYFQHNVPEVR.N
R4/RRR4-6/3	1760.889	1760.974	-48.513	0.452	833.062	0.345	24	0.094	R.KIETYFQHNVPEVR.N
R4/RRR4-25/2	1559.285	1557.734	-289.005	0.396	810.689	0.437	16	0.157	R.TNYAQWVSAITFR.V
R4/RRR4-6/2	1693.168	1691.864	180.447	0.418	736.437	0.422	19	0.155	R.QQADAALSEFLQEIK.N
R4/RRR4-6/2	1691.743	1691.864	-71.476	0.287	451.721	0.364	15	0.138	R.QQADAALSEFLQEIK.N
R4/RRR4-7/2	1544.976	1545.806	-1188.454	0.360	592.201	0.420	20	0.152	K.LWPFVDQAATAVVK.E
R4/RRR4-7/2	1545.111	1545.806	-1100.233	0.334	361.794	0.342	17	0.143	K.LWPFVDQAATAVVK.E
R4/RRR4-14/2	1247.144	1246.480	-270.332	0.352	732.354	0.436	15	0.154	R.ALLVGINYPGTK.A
R4/RRR4-8/2	1247.094	1246.480	-310.595	0.166	721.698	0.351	16	0.137	R.ALLVGINYPGTK.A
R4/RRR4-8/3	1495.753	1495.626	85.317	0.456	808.152	0.415	22	0.104	K.LAHRDDIEDVRR.E
R4/RRR4-8/3	1495.695	1495.626	46.519	0.464	497.946	0.378	19	0.093	K.LAHRDDIEDVRR.E
R4/RRR4-3/2	1943.514	1944.307	-925.409	0.356	868.300	0.419	19	0.152	K.LLVFQSVLPSLGVGSLSAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/3	1689.705	1688.845	-82.897	0.479	1025.998	0.410	30	0.115	K.AAQEM*TGSHLDEVKR.M
R4/RRR4-5/3	1673.792	1672.845	-31.982	0.426	916.007	0.440	27	0.113	-.AAQEMTGSHLDEVKR.-
R4/RRR4-6/3	1688.718	1688.845	-75.296	0.477	1265.248	0.314	29	0.111	K.AAQEM*TGSHLDEVKR.M
R4/RRR4-5/3	1688.927	1688.845	49.112	0.444	732.378	0.333	27	0.092	K.AAQEM*TGSHLDEVKR.M
R4/RRR4-5/2	1321.317	1321.657	-258.051	0.452	1276.755	0.368	17	0.180	-.M*VLVALYQIVR.-
R4/RRR4-12/2	1322.044	1322.404	-273.446	0.420	1159.994	0.393	17	0.175	K.FDSGYYSNLQK.K
R4/RRR4-24/2	1173.929	1174.326	-338.922	0.397	838.451	0.429	16	0.161	R.LPEVTSTELGK.I
R4/RRR4-25/3	1445.155	1445.479	-224.744	0.446	915.980	0.417	24	0.111	K.AGHQTSAESWGTGR.A
R4/RRR4-25/3	1445.161	1445.479	-220.931	0.448	741.249	0.391	20	0.099	K.AGHQTSAESWGTGR.A
R4/RRR4-9/3	1446.405	1445.479	-51.274	0.429	896.628	0.331	24	0.095	K.AGHQTSAESWGTGR.A
R4/RRR4-9/3	1446.457	1445.479	-15.593	0.438	763.903	0.322	23	0.091	K.AGHQTSAESWGTGR.A
R4/RRR4-25/3	1445.486	1445.479	4.513	0.399	746.316	0.288	21	0.087	K.AGHQTSAESWGTGR.A
R4/RRR4-26/3	1445.834	1445.479	246.237	0.373	667.872	0.251	20	0.078	-.AGHQTSAESWGTGR.-
R4/RRR4-7/2	1622.276	1622.803	-943.975	0.447	966.078	0.414	18	0.164	R.ELGQWGLDNYLSVK.Q
R4/RRR4-7/2	1621.941	1622.803	-1151.535	0.343	876.091	0.427	17	0.159	R.ELGQWGLDNYLSVK.Q
R4/RRR4-7/2	1622.363	1622.803	-271.806	0.328	536.851	0.389	15	0.143	R.ELGQWGLDNYLSVK.Q
R4/RRR4-12/2	1562.546	1562.834	-184.814	0.450	1033.859	0.408	19	0.167	-.LFNIIEPDVAVFGK.-
R4/RRR4-9/2	1487.666	1486.731	-43.341	0.392	719.733	0.427	15	0.153	K.LPAWSVSILPDCK.N
R4/RRR4-9/2	1487.502	1486.731	-153.970	0.266	569.782	0.304	14	0.136	K.LPAWSVSILPDCK.N
R4/RRR4-6/2	1126.460	1126.280	160.471	0.302	716.037	0.424	14	0.153	K.DGFFCPALAK.A
R4/RRR4-6/2	1126.207	1126.280	-65.296	0.248	728.880	0.337	13	0.143	K.DGFFCPALAK.A
R4/RRR4-6/2	1126.200	1126.280	-70.949	0.251	544.282	0.304	12	0.138	K.DGFFCPALAK.A
R4/RRR4-9/2	984.907	985.120	-216.318	0.410	1283.649	0.370	16	0.181	R.VASLVGADPR.E
R4/RRR4-9/2	985.321	985.120	204.768	0.399	1049.613	0.344	15	0.162	R.VASLVGADPR.E
R4/RRR4-9/2	985.864	985.120	-259.575	0.283	662.991	0.154	15	0.135	R.VASLVGADPR.E
R4/RRR4-23/3	1577.485	1577.719	-148.883	0.392	948.319	0.423	21	0.110	K.STHGYHFILCEGR.K
R4/RRR4-20/2	1134.483	1135.252	-1563.867	0.352	921.097	0.420	16	0.165	K.AYGELPDTLR.L
R4/RRR4-20/2	1135.913	1135.252	-299.282	0.454	537.258	0.348	13	0.147	K.AYGELPDTLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-20/2	1134.463	1135.252	-1581.162	0.321	471.210	0.401	12	0.146	K.AYGELPDTLR.L
R4/RRR4-4/2	1694.082	1693.967	67.965	0.438	664.432	0.389	17	0.148	K.FLDEGGLFIINLVSR.S
R4/RRR4-4/2	1694.426	1693.967	271.431	0.402	726.316	0.291	18	0.140	K.FLDEGGLFIINLVSR.S
R4/RRR4-4/2	1694.874	1693.967	-55.379	0.384	448.776	0.368	14	0.140	K.FLDEGGLFIINLVSR.S
R4/RRR4-24/2	1004.955	1005.191	-235.090	0.336	960.135	0.411	15	0.162	R.LSSLGILSSK.R
R4/RRR4-30/2	1195.211	1195.503	-245.240	0.369	1734.221	0.156	16	0.178	R.FM*KIKVVGTR.-
R4/RRR4-26/2	1195.553	1195.503	41.886	0.285	1271.853	0.219	14	0.155	R.FM*KIKVVGTR.-
R4/RRR4-23/2	1196.611	1195.503	90.348	0.250	944.199	0.245	14	0.144	R.FM*KIKVVGTR.-
R4/RRR4-30/2	1195.238	1195.503	-222.493	0.340	1292.573	0.120	15	0.143	R.FM*KIKVVGTR.-
R4/RRR4-28/2	1195.078	1195.503	-357.041	0.310	600.599	0.175	13	0.137	R.FM*KIKVVGTR.-
R4/RRR4-23/2	1195.978	1195.503	397.926	0.096	508.330	0.271	11	0.130	R.FM*KIKVVGTR.-
R4/RRR4-2/3	1791.475	1791.028	249.953	0.288	1715.889	0.134	28	0.111	R.GLAARGENTGPKNFAMR.G
R4/RRR4-13/2	1213.312	1213.412	-82.304	0.493	1212.447	0.354	17	0.172	K.ALQQVLANSLR.Y
R4/RRR4-12/3	1670.677	1671.792	-1270.055	0.368	1228.891	0.373	26	0.122	R.TPGAGATEVFVHDVDR.H
R4/RRR4-12/3	1670.279	1671.792	-2109.787	0.385	789.510	0.448	23	0.106	R.TPGAGATEVFVHDVDR.H
R4/RRR4-9/2	1620.690	1619.845	-96.065	0.421	1341.471	0.347	19	0.177	R.SWVFPSSNLVDLVR.S
R4/RRR4-4/2	914.887	914.084	-216.212	0.398	1363.743	0.339	15	0.182	R.AALDIAAIR.L
R4/RRR4-4/2	914.337	914.084	276.973	0.307	661.950	0.304	14	0.145	R.AALDIAAIR.L
R4/RRR4-4/2	914.863	914.084	-242.984	0.281	571.109	0.201	12	0.137	R.AALDIAAIR.L
R4/RRR4-8/2	1162.619	1163.353	-1496.006	0.363	975.353	0.415	15	0.166	R.VFVNAWALSR.D
R4/RRR4-8/2	1162.910	1163.353	-382.458	0.277	375.894	0.317	12	0.139	-.VFVNAWALSR.-
R4/RRR4-9/2	1613.544	1612.870	-202.320	0.377	905.626	0.413	16	0.155	R.EVFSAVLM*SSDILGK.S
R4/RRR4-10/2	1248.939	1249.350	-329.841	0.464	725.162	0.387	16	0.155	R.VQIDGNCVTSR.G
R4/RRR4-10/2	1248.917	1249.350	-347.689	0.394	726.296	0.389	16	0.154	R.VQIDGNCVTSR.G
R4/RRR4-21/2	1258.109	1258.450	-271.771	0.343	1196.239	0.373	18	0.171	R.EVVGLSGQTVLR.A
R4/RRR4-11/2	1502.518	1502.697	-119.592	0.422	920.653	0.418	19	0.162	K.VASQLDVLPGAEFR.V
R4/RRR4-5/3	1457.600	1457.528	49.205	0.454	1081.539	0.387	25	0.114	R.TPEQTVTSHSVDR.R
R4/RRR4-5/3	1456.787	1457.528	-1198.634	0.424	592.573	0.470	21	0.105	R.TPEQTVTSHSVDR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-5/3	1457.565	1457.528	25.644	0.490	736.048	0.390	22	0.098	R.TPEQTVTSHSVDR.R
R4/RRR4-2/2	1252.129	1251.586	-366.647	0.416	1036.310	0.397	17	0.166	K.LIGPVILSGILR.S
R4/RRR4-8/3	1796.737	1797.006	-150.204	0.381	997.303	0.408	26	0.111	K.EVLKENDQLLADRPR.N
R4/RRR4-8/3	1796.787	1797.006	-122.398	0.413	895.879	0.378	26	0.100	K.EVLKENDQLLADRPR.N
R4/RRR4-13/2	1293.792	1293.408	297.660	0.381	925.688	0.415	16	0.165	K.FYFNPGDTGFK.A
R4/RRR4-12/2	1292.801	1293.408	-1246.868	0.399	739.200	0.395	15	0.155	K.FYFNPGDTGFK.A
R4/RRR4-17/2	1293.110	1293.408	-230.802	0.399	701.416	0.394	15	0.154	K.FYFNPGDTGFK.A
R4/RRR4-13/2	1292.249	1293.408	-1675.466	0.298	731.334	0.396	13	0.149	K.FYFNPGDTGFK.A
R4/RRR4-13/2	1293.262	1293.408	-113.097	0.293	509.136	0.356	13	0.143	K.FYFNPGDTGFK.A
R4/RRR4-5/2	1610.771	1609.799	-17.605	0.330	606.664	0.404	14	0.141	R.DLIQDCTVTLAFGR.H
R4/RRR4-15/3	1268.431	1267.503	-56.585	0.414	1554.032	0.267	27	0.127	R.SLVAALLAAAGGPR.M
R4/RRR4-13/3	1115.233	1115.267	-30.435	0.460	862.922	0.394	19	0.096	-.AHAYAAAVAAAK.-
R4/RRR4-13/3	1115.152	1115.267	-103.065	0.411	872.514	0.295	21	0.087	R.AHAYAAAVAAAK.G
R4/RRR4-3/2	1476.250	1474.788	313.951	0.350	1748.307	0.138	17	0.175	K.KMEEELILLEVK.Y
R4/RRR4-1/2	1476.196	1474.788	277.385	0.354	1402.156	0.156	17	0.153	K.KMEEELILLEVK.Y
R4/RRR4-29/2	1476.093	1474.788	206.984	0.336	1401.895	0.149	16	0.152	K.KMEEELILLEVK.Y
R4/RRR4-25/2	1476.098	1474.788	210.467	0.330	1348.202	0.163	16	0.152	K.KMEEELILLEVK.Y
R4/RRR4-13/2	1476.048	1474.788	176.630	0.331	1467.647	0.097	16	0.149	K.KMEEELILLEVK.Y
R4/RRR4-18/2	1476.112	1474.788	220.003	0.320	1350.827	0.122	16	0.146	K.KMEEELILLEVK.Y
R4/RRR4-29/2	1476.175	1474.788	262.958	0.338	1278.284	0.131	16	0.144	K.KMEEELILLEVK.Y
R4/RRR4-7/2	1476.243	1474.788	308.893	0.366	1139.683	0.155	15	0.141	-.KMEEELILLEVK.-
R4/RRR4-6/2	1476.078	1474.788	196.783	0.347	1214.590	0.122	15	0.141	-.KMEEELILLEVK.-
R4/RRR4-24/2	1476.163	1474.788	254.997	0.350	1085.090	0.155	15	0.140	-.KMEEELILLEVK.-
R4/RRR4-1/2	1476.131	1474.788	232.608	0.356	1093.278	0.143	16	0.138	K.KMEEELILLEVK.Y
R4/RRR4-23/2	1475.915	1474.788	86.141	0.315	1118.973	0.116	16	0.137	K.KMEEELILLEVK.Y
R4/RRR4-18/2	1476.106	1474.788	215.857	0.336	1075.348	0.121	15	0.136	-.KMEEELILLEVK.-
R4/RRR4-19/2	1476.192	1474.788	274.235	0.336	967.192	0.158	15	0.136	-.KMEEELILLEVK.-
R4/RRR4-26/2	1475.782	1474.788	-4.116	0.311	776.258	0.188	14	0.135	-.KMEEELILLEVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-26/2	1476.084	1474.788	201.095	0.354	954.966	0.155	15	0.132	-.KMEEELILLEVK.-
R4/RRR4-20/2	1476.228	1474.788	298.944	0.353	880.864	0.119	14	0.130	-.KMEEELILLEVK.-
R4/RRR4-21/2	1476.226	1474.788	297.202	0.327	810.920	0.110	14	0.128	-.KMEEELILLEVK.-
R4/RRR4-11/2	1367.036	1366.502	-341.919	0.343	922.382	0.409	18	0.159	K.FVGLSEASADTIR.R
R4/RRR4-7/2	1023.016	1023.125	-106.590	0.493	899.191	0.373	14	0.161	K.SGNFELVTR.E
R4/RRR4-7/2	1023.164	1023.125	38.579	0.377	757.320	0.252	13	0.141	-.SGNFELVTR.-
R4/RRR4-7/2	943.519	944.152	-1736.411	0.354	534.479	0.381	12	0.149	K.SVVFGPLPK.T
R4/RRR4-7/2	943.430	944.152	-1831.053	0.283	631.123	0.389	12	0.147	K.SVVFGPLPK.T
R4/RRR4-7/2	943.352	944.152	-1913.490	0.280	502.592	0.426	11	0.146	K.SVVFGPLPK.T
R4/RRR4-3/2	1010.880	1011.243	-360.523	0.435	668.587	0.384	15	0.154	R.LIGASLPAIR.A
R4/RRR4-3/2	1011.117	1011.243	-125.281	0.451	586.895	0.379	14	0.152	R.LIGASLPAIR.A
R4/RRR4-3/2	1011.015	1011.243	-226.293	0.421	475.965	0.408	13	0.151	R.LIGASLPAIR.A
R4/RRR4-19/2	1191.882	1192.328	-375.894	0.418	668.592	0.391	16	0.156	R.QAILNENM*SR.R
R4/RRR4-19/2	1192.008	1192.328	-269.134	0.398	437.600	0.354	15	0.150	R.QAILNENM*SR.R
R4/RRR4-19/2	1191.420	1192.328	-1606.550	0.340	436.872	0.309	15	0.146	R.QAILNENM*SR.R
R4/RRR4-1/2	1413.216	1413.562	-245.148	0.352	475.135	0.366	12	0.132	-.ETNREPIVGEIR.-
R4/RRR4-9/2	1414.430	1413.562	-93.367	0.304	858.990	0.162	14	0.131	R.ETNREPIVGEIR.L
R4/RRR4-8/2	1435.166	1435.650	-338.740	0.397	1114.865	0.385	19	0.167	R.VQLAQLGSATGVYK.T
R4/RRR4-14/2	1588.398	1587.624	-143.111	0.343	1646.638	0.173	19	0.171	K.FEETTESATSDNKK.A
R4/RRR4-2/2	1394.385	1394.683	-214.214	0.315	769.924	0.384	15	0.146	R.IPLSAVGYYIVAK.F
R4/RRR4-14/2	1240.134	1239.427	-236.277	0.257	867.784	0.385	16	0.149	R.EM*AVVGGTGVFR.W
R4/RRR4-7/3	1648.857	1648.827	18.487	0.457	903.312	0.381	29	0.102	R.LRPNSSGSQTVQM*AR.A
R4/RRR4-7/3	1316.756	1316.448	235.088	0.464	989.351	0.381	20	0.107	K.YGKDEAIQHVR.D
R4/RRR4-4/2	1388.831	1387.518	226.424	0.434	1130.342	0.370	18	0.167	K.VVNADEDVGDLLK.V
R4/RRR4-4/2	1484.700	1483.599	68.066	0.381	751.077	0.392	15	0.150	K.ESLDCIQSFVER.L
R4/RRR4-18/2	1071.924	1072.280	-333.139	0.348	1258.879	0.345	18	0.173	K.LVLLGDVGTGK.S
R4/RRR4-18/2	1072.077	1072.280	-189.993	0.389	886.530	0.397	16	0.160	K.LVLLGDVGTGK.S
R4/RRR4-23/3	1962.454	1963.199	-892.336	0.343	971.918	0.285	29	0.085	K.DLGGAAGTKEM*GDAIVAELK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-13/2	1103.273	1102.268	4.038	0.425	988.018	0.390	14	0.166	R.ILDITHAYR.A
R4/RRR4-13/2	1101.911	1102.268	-325.295	0.522	854.772	0.367	13	0.156	R.ILDITHAYR.A
R4/RRR4-13/2	1101.874	1102.268	-358.975	0.318	703.685	0.257	12	0.140	R.ILDITHAYR.A
R4/RRR4-13/2	1487.416	1487.725	-208.472	0.417	953.569	0.396	19	0.164	R.VDVLSEALPFIQR.F
R4/RRR4-13/2	1487.521	1487.725	-137.589	0.402	911.165	0.402	19	0.162	R.VDVLSEALPFIQR.F
R4/RRR4-14/2	1488.546	1487.725	-120.632	0.468	794.836	0.411	18	0.159	R.VDVLSEALPFIQR.F
R4/RRR4-13/2	1487.298	1487.725	-288.175	0.351	835.814	0.353	18	0.152	R.VDVLSEALPFIQR.F
R4/RRR4-13/2	1034.124	1034.230	-103.195	0.371	802.686	0.406	12	0.157	R.LEALLFEAK.G
R4/RRR4-13/2	1034.035	1034.230	-189.404	0.375	680.471	0.387	12	0.152	R.LEALLFEAK.G
R4/RRR4-13/2	1033.949	1034.230	-272.785	0.235	340.514	0.334	10	0.125	-.LEALLFEAK.-
R4/RRR4-11/3	1177.560	1177.378	154.899	0.433	839.872	0.392	22	0.100	R.SPIIVAPTGGHK.L
R4/RRR4-18/2	1043.984	1044.227	-232.986	0.373	1037.394	0.390	16	0.166	K.VLVLGDAATGK.T
R4/RRR4-18/2	1043.887	1044.227	-327.074	0.384	900.615	0.421	16	0.163	-.VLVLGDAATGK.-
R4/RRR4-18/2	1043.534	1044.227	-1627.304	0.296	676.480	0.391	13	0.146	K.VLVLGDAATGK.T
R4/RRR4-8/2	1073.991	1074.250	-241.411	0.453	818.114	0.380	15	0.158	K.IVCTLGPASR.S
R4/RRR4-8/2	1073.482	1074.250	-1651.707	0.402	1102.386	0.262	16	0.154	K.IVCTLGPASR.S
R4/RRR4-8/2	1073.717	1074.250	-1431.380	0.356	720.951	0.326	14	0.146	-.IVCTLGPASR.-
R4/RRR4-12/2	1484.205	1483.733	318.703	0.500	781.083	0.340	16	0.148	K.KFEDKFVDTLLK.Y
R4/RRR4-12/2	1483.420	1483.733	-211.922	0.379	739.556	0.316	15	0.144	K.KFEDKFVDTLLK.Y
R4/RRR4-3/2	1265.075	1264.645	340.807	0.416	704.329	0.390	14	0.152	R.TVVVTIIFMIK.L
R4/RRR4-3/2	1264.568	1264.645	-61.637	0.339	660.567	0.375	14	0.148	R.TVVVTIIFMIK.L
R4/RRR4-3/2	1264.869	1264.645	177.275	0.407	479.494	0.399	12	0.146	R.TVVVTIIFMIK.L
R4/RRR4-13/2	1274.389	1274.542	-120.728	0.334	1424.663	0.283	15	0.175	K.RMLQQDVMPR.Q
R4/RRR4-14/2	1275.095	1274.542	-351.689	0.357	1258.150	0.274	14	0.162	K.RMLQQDVMPR.Q
R4/RRR4-13/2	1274.336	1274.542	-162.336	0.238	1454.357	0.170	15	0.159	K.RMLQQDVMPR.Q
R4/RRR4-14/2	1274.540	1274.542	-1.500	0.329	1172.540	0.262	14	0.157	-.RMLQQDVMPR.-
R4/RRR4-13/2	1274.994	1274.542	355.153	0.387	1138.902	0.260	14	0.154	K.RMLQQDVMPR.Q
R4/RRR4-14/2	1274.819	1274.542	217.381	0.305	1013.834	0.270	13	0.148	K.RMLQQDVMPR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-7/3	1600.777	1600.804	-16.729	0.419	967.617	0.390	24	0.105	R.KNHIQQAGGPPVPEK.E
R4/RRR4-9/2	967.655	967.190	481.176	0.239	676.677	0.366	12	0.141	R.NAAVIIIPR.I
R4/RRR4-8/3	1761.498	1761.917	-238.737	0.422	1422.560	0.298	30	0.122	K.VGKPPASQEPEPSGPQR.G
R4/RRR4-9/2	1186.088	1185.402	-265.357	0.385	1398.363	0.304	16	0.176	K.IVKKDAAAVNR.A
R4/RRR4-9/2	1185.358	1185.402	-37.248	0.311	1419.153	0.284	16	0.174	K.IVKKDAAAVNR.A
R4/RRR4-9/2	1186.114	1185.402	-243.261	0.483	1189.349	0.342	15	0.167	-.IVKKDAAAVNR.-
R4/RRR4-2/2	1000.114	1000.134	-20.336	0.379	1257.421	0.343	15	0.174	R.LALDAQNVR.S
R4/RRR4-2/2	1000.617	1000.134	484.169	0.353	919.094	0.201	14	0.140	R.LALDAQNVR.S
R4/RRR4-21/2	1092.935	1092.184	-228.376	0.488	958.292	0.362	14	0.159	R.ATNLDPFADK.D
R4/RRR4-21/2	1093.230	1092.184	42.714	0.523	503.758	0.390	13	0.150	R.ATNLDPFADK.D
R4/RRR4-4/3	1310.345	1310.401	-43.516	0.395	1039.146	0.379	26	0.108	R.HGVPSAVGSANASR.G
R4/RRR4-4/3	1309.950	1310.401	-345.520	0.246	788.064	0.253	22	0.077	R.HGVPSAVGSANASR.G
R4/RRR4-7/2	1027.108	1026.125	-16.881	0.138	881.644	0.287	12	0.134	R.SRCPHSPGK.N
R4/RRR4-11/3	1775.015	1774.121	-59.687	0.452	1256.576	0.138	28	0.076	-.M*PITIETIRLAWQGK.T
R4/RRR4-11/3	1773.889	1774.121	-130.817	0.380	814.678	0.025	23	0.059	-.M*PITIETIRLAWQGK.-
R4/RRR4-17/2	1111.003	1111.275	-245.821	0.472	1150.480	0.348	15	0.170	R.FFLQDATLR.Q
R4/RRR4-17/2	1111.144	1111.275	-118.190	0.475	1089.723	0.341	15	0.166	R.FFLQDATLR.Q
R4/RRR4-18/2	1111.100	1111.275	-158.196	0.483	1073.393	0.331	15	0.163	R.FFLQDATLR.Q
R4/RRR4-17/2	1111.005	1111.275	-243.396	0.547	998.814	0.344	15	0.161	R.FFLQDATLR.Q
R4/RRR4-18/2	1111.483	1111.275	187.749	0.427	920.522	0.224	14	0.143	R.FFLQDATLR.Q
R4/RRR4-19/2	1111.018	1111.275	-232.484	0.216	515.041	0.231	12	0.138	R.FFLQDATLR.Q
R4/RRR4-22/2	963.217	964.097	-1957.412	0.475	886.788	0.351	13	0.157	-.AFLVEEQK.-
R4/RRR4-22/2	963.356	964.097	-1812.497	0.438	854.147	0.231	13	0.143	R.AFLVEEQK.I
R4/RRR4-22/2	963.927	964.097	-177.078	0.447	812.578	0.249	13	0.143	-.AFLVEEQK.-
R4/RRR4-17/2	1314.896	1314.513	292.138	0.446	755.476	0.373	15	0.151	K.DVVLNQVVSNVK.S
R4/RRR4-17/2	1313.988	1314.513	-1164.053	0.239	726.598	0.321	13	0.140	K.DVVLNQVVSNVK.S
R4/RRR4-16/2	1314.159	1314.513	-270.614	0.287	798.573	0.183	14	0.134	K.DVVLNQVVSNVK.S
R4/RRR4-16/2	1315.129	1314.513	-293.038	0.365	555.203	0.281	13	0.128	-.DVVLNQVVSNVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-10/2	1483.510	1483.735	-152.239	0.356	897.307	0.396	18	0.098	R.LPSSPDVFPWLKP.-
R4/RRR4-9/2	1484.532	1483.735	-137.288	0.275	681.090	0.379	16	0.094	R.LPSSPDVFPWLKP.-
R4/RRR4-10/2	1483.243	1483.735	-332.713	0.376	654.647	0.338	16	0.089	R.LPSSPDVFPWLKP.-
R4/RRR4-10/2	1483.034	1483.735	-1150.498	0.370	684.078	0.276	16	0.082	R.LPSSPDVFPWLKP.-
R4/RRR4-23/3	1456.304	1455.688	-264.430	0.370	579.412	0.373	20	0.087	-.DQLRSVAGLLLNR.-
R4/RRR4-23/3	1456.785	1455.688	66.966	0.438	918.413	0.297	24	0.084	-.DQLRSVAGLLLNR.-
R4/RRR4-5/2	1045.387	1045.170	207.935	0.272	906.412	0.378	15	0.152	K.SAFTASSFVK.E
R4/RRR4-2/3	1507.763	1508.834	-1377.971	0.416	1728.085	0.136	28	0.109	R.LILLNNKILNSPR.I
R4/RRR4-19/2	1697.757	1697.782	-14.684	0.397	1062.766	0.377	18	0.159	K.DGDGIVSLSETYDGLR.A
R4/RRR4-9/2	1242.372	1242.490	-94.866	0.423	681.746	0.372	17	0.154	R.LATNLENLILK.E
R4/RRR4-9/2	1242.342	1242.490	-119.408	0.475	727.426	0.343	18	0.153	R.LATNLENLILK.E
R4/RRR4-9/2	1241.611	1242.490	-1518.078	0.332	580.712	0.319	16	0.145	R.LATNLENLILK.E
R4/RRR4-23/2	981.842	982.244	-410.217	0.427	900.878	0.378	13	0.163	K.LAVLKFYK.V
R4/RRR4-23/2	981.856	982.244	-396.245	0.448	739.284	0.403	13	0.161	K.LAVLKFYK.V
R4/RRR4-25/2	982.179	982.244	-66.270	0.459	763.662	0.381	13	0.159	K.LAVLKFYK.V
R4/RRR4-23/2	982.118	982.244	-128.108	0.449	787.129	0.373	13	0.159	K.LAVLKFYK.V
R4/RRR4-24/2	982.070	982.244	-177.734	0.501	751.295	0.375	13	0.159	K.LAVLKFYK.V
R4/RRR4-24/2	982.035	982.244	-213.397	0.490	742.782	0.376	13	0.159	K.LAVLKFYK.V
R4/RRR4-25/2	981.499	982.244	-1782.799	0.323	784.789	0.399	13	0.157	K.LAVLKFYK.V
R4/RRR4-25/2	981.443	982.244	-1839.787	0.429	784.279	0.352	13	0.156	K.LAVLKFYK.V
R4/RRR4-24/2	981.611	982.244	-1668.343	0.427	679.678	0.349	13	0.154	K.LAVLKFYK.V
R4/RRR4-16/2	1338.085	1337.610	355.727	0.390	885.021	0.389	14	0.155	R.SLTLIESM*WLK.G
R4/RRR4-11/2	1177.220	1177.289	-58.722	0.358	980.899	0.388	15	0.161	K.GYDPEVIDIR.S
R4/RRR4-9/2	883.011	883.070	-67.403	0.439	734.285	0.364	12	0.152	-.LVDVLPAR.-
R4/RRR4-9/2	882.709	883.070	-411.000	0.247	577.605	0.354	10	0.141	R.LVDVLPAR.G
R4/RRR4-9/2	883.027	883.070	-49.515	0.375	600.745	0.333	11	0.137	-.LVDVLPAR.-
R4/RRR4-15/2	1457.255	1456.666	-283.278	0.434	853.668	0.381	15	0.151	R.LGIDEELVELLGR.Y
R4/RRR4-8/2	1020.440	1021.066	-1597.841	0.446	798.181	0.374	14	0.158	K.FGDPTEQAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R4/RRR4-8/2	1020.827	1021.066	-234.493	0.467	798.196	0.345	14	0.154	K.FGDPTEQAR.A
R4/RRR4-8/2	1020.727	1021.066	-332.515	0.464	798.601	0.339	14	0.154	K.FGDPTEQAR.A
R4/RRR4-9/2	1020.736	1021.066	-323.996	0.436	661.575	0.304	13	0.147	K.FGDPTEQAR.A
R4/RRR4-9/2	1021.580	1021.066	-476.897	0.297	477.960	0.335	12	0.143	-.FGDPTEQAR.-
R4/RRR4-4/2	1899.485	1900.165	-886.720	0.327	639.684	0.381	17	0.140	R.ILPNVVVLTFDPDSDVR.T
R5/RRR5-2/2	1846.619	1847.062	-240.721	0.655	3789.509	0.632	29	0.749	K.YKEAAELAAESPQGLLR.T
R5/RRR5-2/2	1846.589	1847.062	-256.704	0.634	3454.378	0.619	29	0.638	K.YKEAAELAAESPQGLLR.T
R5/RRR5-2/2	1846.457	1847.062	-871.737	0.632	3258.683	0.624	28	0.583	K.YKEAAELAAESPQGLLR.T
R5/RRR5-2/3	1674.806	1673.876	-42.417	0.574	2890.556	0.408	34	0.453	R.RPITADSALM*NPNTR.I
R5/RRR5-2/2	1842.552	1843.120	-853.118	0.586	2636.075	0.509	24	0.381	K.FNLNVQAVNVLLDNIR.S
R5/RRR5-1/2	1565.354	1565.711	-228.831	0.485	2587.575	0.531	24	0.381	R.SQALEAHAASFASFK.V
R5/RRR5-2/2	1564.677	1565.711	-1303.855	0.532	2601.224	0.520	24	0.380	R.SQALEAHAASFASFK.V
R5/RRR5-2/2	1566.292	1565.711	-268.717	0.541	2520.732	0.522	24	0.364	R.SQALEAHAASFASFK.V
R5/RRR5-2/2	1565.301	1565.711	-262.708	0.579	2475.053	0.527	24	0.355	R.SQALEAHAASFASFK.V
R5/RRR5-2/2	1842.236	1843.120	-1025.265	0.581	2528.878	0.491	24	0.353	K.FNLNVQAVNVLLDNIR.S
R5/RRR5-2/3	1847.213	1847.062	81.943	0.555	2406.386	0.472	35	0.348	K.YKEAAELAAESPQGLLR.T
R5/RRR5-1/2	1566.163	1565.711	289.204	0.490	2477.706	0.480	23	0.341	R.SQALEAHAASFASFK.V
R5/RRR5-2/2	1842.747	1843.120	-202.823	0.589	2364.801	0.529	23	0.334	K.FNLNVQAVNVLLDNIR.S
R5/RRR5-2/2	1694.399	1694.979	-935.079	0.505	2145.178	0.630	22	0.328	R.AHM*GIFTELGVLYAR.Y
R5/RRR5-2/2	1694.614	1694.979	-215.708	0.539	2059.862	0.558	22	0.291	R.AHM*GIFTELGVLYAR.Y
R5/RRR5-2/2	1507.324	1506.591	-177.613	0.532	2180.561	0.460	20	0.283	R.GQCDDELINVTNK.N
R5/RRR5-2/2	1779.369	1779.076	165.168	0.577	1899.443	0.570	25	0.270	K.LHVIELGAQPGKPGFSK.K
R5/RRR5-2/2	1140.556	1141.346	-1573.681	0.519	1888.220	0.567	17	0.267	R.GNLQIVVQAAK.E
R5/RRR5-2/2	1632.038	1632.740	-1046.209	0.462	2077.365	0.449	20	0.264	K.EVCFACVDAEEFR.L
R5/RRR5-2/3	1516.308	1516.749	-291.189	0.466	2578.017	0.207	27	0.263	K.SHQMPEQVVFWK.W
R5/RRR5-2/2	1507.070	1506.591	318.742	0.541	2048.017	0.432	20	0.253	R.GQCDDELINVTNK.N
R5/RRR5-2/2	1437.186	1437.534	-242.678	0.499	1881.366	0.499	20	0.248	R.AAEEANVYDDLVK.Y
R5/RRR5-2/3	1846.910	1847.062	-82.715	0.590	1973.625	0.465	33	0.241	K.YKEAAELAAESPQGLLR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1226.064	1226.403	-277.077	0.553	1767.715	0.518	18	0.238	K.VDGELIFAYAK.I
R5/RRR5-1/2	1842.528	1843.120	-866.419	0.553	1927.240	0.445	21	0.237	K.FNLNVQAVNVLLDNIR.S
R5/RRR5-2/2	1227.183	1226.403	-179.648	0.543	1712.715	0.540	18	0.236	K.VDGELIFAYAK.I
R5/RRR5-2/2	1480.087	1480.648	-1057.575	0.501	1692.844	0.550	20	0.236	R.GKLNAYESLELSR.L
R5/RRR5-2/2	1436.682	1437.534	-1292.951	0.450	1879.457	0.449	20	0.235	R.AAEEANVYDDLVK.Y
R5/RRR5-2/2	1226.016	1226.403	-316.434	0.570	1741.823	0.513	18	0.233	K.VDGELIFAYAK.I
R5/RRR5-2/3	1674.417	1673.876	-275.174	0.558	2308.606	0.280	33	0.232	R.RPITADSALM*NPNTR.I
R5/RRR5-1/2	1437.227	1437.534	-213.877	0.450	1788.156	0.479	20	0.230	R.AAEEANVYDDLVK.Y
R5/RRR5-2/2	1305.115	1304.480	-280.745	0.466	1856.001	0.438	19	0.230	K.LKQFQGAVDAAR.K
R5/RRR5-2/2	1555.305	1555.715	-264.081	0.441	1956.294	0.367	22	0.225	K.EAAELAAESPQGLLR.T
R5/RRR5-2/2	1362.326	1361.482	-115.093	0.530	1587.441	0.544	19	0.222	R.VEEDAVWSQVAK.A
R5/RRR5-2/2	1451.068	1450.619	310.624	0.542	1564.782	0.555	19	0.220	R.EGLVSEAIESFIR.A
R5/RRR5-2/2	1479.962	1480.648	-1142.545	0.513	1611.079	0.519	20	0.218	R.GKLNAYESLELSR.L
R5/RRR5-2/2	1141.216	1141.346	-114.540	0.516	1615.682	0.516	17	0.218	R.GNLQIVVQAAK.E
R5/RRR5-2/2	1326.194	1326.567	-281.914	0.447	1748.458	0.445	18	0.218	K.IIYAFISNWAK.L
R5/RRR5-1/2	1227.144	1226.403	-211.381	0.545	1538.893	0.551	17	0.217	K.VDGELIFAYAK.I
R5/RRR5-1/2	1451.107	1450.619	337.278	0.542	1716.098	0.462	20	0.216	R.EGLVSEAIESFIR.A
R5/RRR5-1/3	1846.244	1847.062	-987.401	0.515	1916.591	0.422	33	0.215	K.YKEAAELAAESPQGLLR.T
R5/RRR5-1/2	1437.122	1437.534	-286.906	0.483	1605.775	0.508	20	0.214	R.AAEEANVYDDLVK.Y
R5/RRR5-2/2	1304.007	1304.480	-363.891	0.427	1799.705	0.397	19	0.213	K.LKQFQGAVDAAR.K
R5/RRR5-1/2	1140.940	1141.346	-356.448	0.424	1551.147	0.523	17	0.211	R.GNLQIVVQAAK.E
R5/RRR5-2/2	1555.451	1555.715	-169.914	0.468	1774.440	0.387	22	0.206	K.EAAELAAESPQGLLR.T
R5/RRR5-1/2	1629.366	1628.849	-297.014	0.452	1516.324	0.511	23	0.205	R.QLIDQVVSTALPESK.S
R5/RRR5-2/2	1505.863	1506.591	-1150.944	0.420	1795.778	0.364	19	0.204	R.GQCDDELINVTNK.N
R5/RRR5-2/2	1479.583	1480.648	-1399.530	0.444	1449.699	0.534	19	0.202	R.GKLNAYESLELSR.L
R5/RRR5-2/2	1628.647	1628.849	-124.088	0.456	1630.380	0.438	23	0.202	R.QLIDQVVSTALPESK.S
R5/RRR5-2/2	1437.247	1437.534	-199.818	0.536	1557.760	0.466	20	0.200	R.AAEEANVYDDLVK.Y
R5/RRR5-1/2	1450.184	1450.619	-300.278	0.439	1610.632	0.440	19	0.199	R.EGLVSEAIESFIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1628.536	1628.849	-192.963	0.457	1587.152	0.439	23	0.197	R.QLIDQVVSTALPESK.S
R5/RRR5-1/2	1362.299	1361.482	-134.687	0.397	1586.921	0.432	17	0.195	R.VEEDAVWSQVAK.A
R5/RRR5-2/3	1847.707	1847.062	-192.744	0.558	1667.884	0.477	31	0.190	K.YKEAAELAAESPQGLLR.T
R5/RRR5-2/2	1373.197	1373.496	-218.055	0.458	1500.755	0.436	18	0.187	R.ADDATHFLDVIR.A
R5/RRR5-2/2	1515.980	1516.749	-1169.996	0.395	1399.907	0.493	18	0.187	K.SHQMPEQVVFWK.W
R5/RRR5-1/2	1449.820	1450.619	-1244.415	0.409	1593.756	0.389	19	0.187	R.EGLVSEAIESFIR.A
R5/RRR5-2/2	1345.123	1344.448	-242.813	0.590	1254.351	0.533	18	0.186	R.LYDEELYEAAK.I
R5/RRR5-2/2	1373.333	1373.496	-118.895	0.483	1475.142	0.431	18	0.184	R.ADDATHFLDVIR.A
R5/RRR5-2/2	1631.600	1632.740	-1315.586	0.250	1864.793	0.224	20	0.183	K.EVCFACVDAEEFR.L
R5/RRR5-2/2	1736.447	1736.941	-285.185	0.503	1124.164	0.596	21	0.182	K.VVGNENPSTLICFASK.T
R5/RRR5-2/2	1631.496	1632.740	-1379.458	0.278	1684.272	0.323	19	0.182	K.EVCFACVDAEEFR.L
R5/RRR5-1/2	1227.102	1226.403	-245.512	0.509	1369.933	0.472	16	0.182	K.VDGELIFAYAK.I
R5/RRR5-1/2	1737.495	1736.941	-257.460	0.508	1182.725	0.561	21	0.181	K.VVGNENPSTLICFASK.T
R5/RRR5-2/2	1736.443	1736.941	-287.653	0.481	1156.802	0.573	21	0.180	K.VVGNENPSTLICFASK.T
R5/RRR5-2/3	1305.523	1304.480	32.850	0.533	1893.203	0.353	29	0.180	K.LKQFQGAVDAAR.K
R5/RRR5-2/2	1736.127	1736.941	-1047.871	0.491	1145.315	0.565	21	0.178	K.VVGNENPSTLICFASK.T
R5/RRR5-2/3	1304.724	1304.480	187.896	0.545	1722.171	0.425	28	0.178	K.LKQFQGAVDAAR.K
R5/RRR5-1/3	1673.827	1673.876	-29.897	0.526	1946.432	0.307	32	0.176	R.RPITADSALM*NPNTR.I
R5/RRR5-1/2	1450.413	1450.619	-142.544	0.495	1222.210	0.507	18	0.175	R.EGLVSEAIESFIR.A
R5/RRR5-2/2	1344.113	1344.448	-249.827	0.519	1218.998	0.480	18	0.173	R.LYDEELYEAAK.I
R5/RRR5-1/2	1437.181	1437.534	-245.746	0.448	1326.547	0.440	18	0.171	R.AAEEANVYDDLVK.Y
R5/RRR5-1/2	1374.080	1373.496	-303.455	0.473	1290.169	0.444	18	0.170	R.ADDATHFLDVIR.A
R5/RRR5-2/2	1440.104	1439.579	-330.843	0.498	1281.911	0.455	16	0.170	K.GNM*QLFSVDQQR.S
R5/RRR5-2/3	1516.000	1516.749	-1156.865	0.474	2056.113	0.236	26	0.170	K.SHQMPEQVVFWK.W
R5/RRR5-1/2	1140.882	1141.346	-407.550	0.385	1243.669	0.466	17	0.169	R.GNLQIVVQAAK.E
R5/RRR5-2/2	1326.359	1326.567	-157.076	0.437	1354.351	0.405	16	0.168	K.IIYAFISNWAK.L
R5/RRR5-1/2	1736.181	1736.941	-1016.809	0.446	1103.760	0.527	21	0.168	K.VVGNENPSTLICFASK.T
R5/RRR5-2/2	1069.669	1070.306	-1534.548	0.409	1016.704	0.553	14	0.166	K.YGLIYVITK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1513.083	1512.637	295.870	0.510	1186.645	0.467	19	0.166	K.EYSEQLGVDACIK.L
R5/RRR5-2/3	1674.782	1673.876	-56.564	0.536	1779.626	0.348	31	0.163	R.RPITADSALM*NPNTR.I
R5/RRR5-2/2	1628.388	1628.849	-283.658	0.418	1180.412	0.457	20	0.162	R.QLIDQVVSTALPESK.S
R5/RRR5-2/2	1512.342	1512.637	-195.887	0.458	1145.994	0.461	19	0.162	K.EYSEQLGVDACIK.L
R5/RRR5-2/2	1422.915	1423.580	-1173.896	0.353	1755.190	0.166	18	0.161	K.GNMQLFSVDQQR.S
R5/RRR5-2/2	1344.237	1344.448	-157.264	0.504	1201.270	0.420	18	0.161	R.LYDEELYEAAK.I
R5/RRR5-1/2	1736.373	1736.941	-905.568	0.496	968.694	0.546	19	0.161	K.VVGNENPSTLICFASK.T
R5/RRR5-2/2	1344.185	1344.448	-196.619	0.471	1065.654	0.465	17	0.159	R.LYDEELYEAAK.I
R5/RRR5-2/2	1537.403	1537.749	-225.505	0.533	941.505	0.522	21	0.158	K.RANLPGAENLVVQR.F
R5/RRR5-2/2	1449.501	1450.619	-1465.573	0.362	1410.543	0.317	18	0.157	R.EGLVSEAIESFIR.A
R5/RRR5-2/2	1070.096	1070.306	-196.523	0.431	970.447	0.498	14	0.157	K.YGLIYVITK.L
R5/RRR5-1/2	1225.915	1226.403	-399.256	0.378	1120.087	0.443	16	0.156	K.VDGELIFAYAK.I
R5/RRR5-2/2	1099.262	1099.261	1.269	0.551	939.867	0.482	14	0.155	K.VANVELYYK.A
R5/RRR5-2/2	1070.158	1070.306	-138.734	0.446	991.287	0.471	14	0.154	K.YGLIYVITK.L
R5/RRR5-2/3	1532.488	1532.748	-170.447	0.527	1556.772	0.417	25	0.153	K.SHQM*PEQVVFWK.W
R5/RRR5-2/2	1098.639	1099.261	-1481.045	0.457	891.371	0.486	14	0.152	K.VANVELYYK.A
R5/RRR5-2/2	1372.815	1373.496	-1227.884	0.408	1118.581	0.412	17	0.152	R.ADDATHFLDVIR.A
R5/RRR5-2/2	1325.578	1326.567	-1504.768	0.385	1162.961	0.397	15	0.152	K.IIYAFISNWAK.L
R5/RRR5-2/2	1678.823	1678.979	-93.468	0.402	841.616	0.550	17	0.150	R.AHMGIFTELGVLYAR.Y
R5/RRR5-1/2	1325.702	1326.567	-1411.349	0.419	961.033	0.452	16	0.149	K.IIYAFISNWAK.L
R5/RRR5-1/2	1449.372	1450.619	-1554.740	0.397	793.548	0.538	15	0.148	R.EGLVSEAIESFIR.A
R5/RRR5-1/2	1098.604	1099.261	-1512.743	0.369	886.534	0.474	14	0.147	K.VANVELYYK.A
R5/RRR5-2/2	1362.143	1361.482	-249.576	0.401	975.598	0.446	16	0.147	R.VEEDAVWSQVAK.A
R5/RRR5-2/3	1843.786	1843.120	-181.699	0.531	1512.404	0.405	31	0.146	K.FNLNVQAVNVLLDNIR.S
R5/RRR5-2/2	1098.424	1099.261	-1677.738	0.371	957.279	0.434	14	0.146	K.VANVELYYK.A
R5/RRR5-2/2	1112.180	1112.260	-71.624	0.497	1026.386	0.390	14	0.146	R.FQELFAQTK.Y
R5/RRR5-2/2	1516.302	1516.749	-295.663	0.396	902.397	0.467	16	0.146	K.SHQMPEQVVFWK.W
R5/RRR5-1/3	1845.346	1847.062	-2019.473	0.491	1511.294	0.404	29	0.145	K.YKEAAELAAESPQGLLR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1373.120	1373.496	-274.688	0.399	1038.460	0.396	16	0.144	R.ADDATHFLDVIR.A
R5/RRR5-1/2	1373.110	1373.496	-282.180	0.371	1189.936	0.324	17	0.144	R.ADDATHFLDVIR.A
R5/RRR5-1/2	1627.611	1628.849	-1379.065	0.341	1047.786	0.400	19	0.143	R.QLIDQVVSTALPESK.S
R5/RRR5-1/2	1304.172	1304.480	-236.636	0.344	1150.100	0.340	16	0.142	K.LKQFQGAVDAAR.K
R5/RRR5-2/2	862.833	862.996	-189.737	0.412	644.583	0.490	13	0.142	K.VVAAFAER.R
R5/RRR5-1/2	1099.268	1099.261	5.947	0.410	894.336	0.406	14	0.141	K.VANVELYYK.A
R5/RRR5-2/2	1382.232	1381.563	-240.103	0.402	782.546	0.446	19	0.140	R.ANLPGAENLVVQR.F
R5/RRR5-2/2	1112.081	1112.260	-161.469	0.503	830.026	0.401	14	0.140	R.FQELFAQTK.Y
R5/RRR5-2/2	1844.152	1843.120	17.354	0.486	663.380	0.516	17	0.139	K.FNLNVQAVNVLLDNIR.S
R5/RRR5-2/2	1784.447	1785.026	-887.072	0.419	713.829	0.471	20	0.139	R.SLLPVEPLVDECEKR.N
R5/RRR5-2/2	1295.448	1295.424	19.128	0.474	789.529	0.451	14	0.138	K.LNAYESLELSR.L
R5/RRR5-2/2	1261.054	1261.455	-318.808	0.406	685.824	0.464	16	0.138	K.RDPTLAVVAYR.R
R5/RRR5-1/2	1628.485	1628.849	-224.396	0.353	1084.426	0.333	19	0.138	R.QLIDQVVSTALPESK.S
R5/RRR5-1/2	1343.975	1344.448	-353.343	0.356	804.482	0.419	17	0.137	R.LYDEELYEAAK.I
R5/RRR5-1/2	1381.383	1381.563	-130.168	0.368	710.051	0.459	17	0.136	R.ANLPGAENLVVQR.F
R5/RRR5-1/2	1382.218	1381.563	-250.203	0.390	643.135	0.468	17	0.136	R.ANLPGAENLVVQR.F
R5/RRR5-2/2	1382.132	1381.563	-312.317	0.435	684.965	0.435	18	0.136	R.ANLPGAENLVVQR.F
R5/RRR5-2/2	862.647	862.996	-406.365	0.379	635.005	0.427	13	0.135	K.VVAAFAER.R
R5/RRR5-1/2	1111.931	1112.260	-296.267	0.463	781.774	0.364	14	0.134	R.FQELFAQTK.Y
R5/RRR5-2/2	1784.714	1785.026	-174.911	0.425	561.094	0.481	18	0.134	R.SLLPVEPLVDECEKR.N
R5/RRR5-1/2	1566.372	1565.711	-217.270	0.419	1077.843	0.308	19	0.134	R.SQALEAHAASFASFK.V
R5/RRR5-2/2	1451.438	1450.619	-124.560	0.456	775.040	0.389	17	0.133	R.EGLVSEAIESFIR.A
R5/RRR5-1/2	863.108	862.996	129.782	0.365	527.308	0.441	12	0.133	K.VVAAFAER.R
R5/RRR5-2/2	969.346	970.190	-1908.029	0.357	670.254	0.439	12	0.132	R.IAAYIYKK.A
R5/RRR5-1/2	1111.955	1112.260	-274.680	0.398	907.838	0.317	14	0.132	R.FQELFAQTK.Y
R5/RRR5-2/3	1532.649	1532.748	-64.740	0.479	1387.890	0.407	23	0.131	K.SHQM*PEQVVFWK.W
R5/RRR5-2/2	1423.081	1423.580	-352.027	0.388	1455.925	0.129	17	0.131	K.GNMQLFSVDQQR.S
R5/RRR5-1/3	1673.285	1673.876	-954.208	0.464	1580.450	0.322	29	0.130	R.RPITADSALM*NPNTR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1016.160	1016.130	29.145	0.342	734.449	0.357	17	0.130	K.SPEQVSAAVK.A
R5/RRR5-1/2	1675.032	1673.876	93.078	0.341	182.815	0.534	15	0.129	R.RPITADSALM*NPNTR.I
R5/RRR5-2/2	1450.223	1450.619	-273.423	0.340	831.292	0.362	14	0.129	R.EGLVSEAIESFIR.A
R5/RRR5-1/2	1380.791	1381.563	-1287.029	0.292	702.715	0.400	18	0.129	R.ANLPGAENLVVQR.F
R5/RRR5-1/2	1631.308	1632.740	-1495.050	0.219	1376.804	0.126	17	0.128	K.EVCFACVDAEEFR.L
R5/RRR5-2/2	1673.417	1673.876	-275.440	0.320	245.833	0.464	17	0.128	R.RPITADSALM*NPNTR.I
R5/RRR5-2/2	1784.687	1785.026	-190.212	0.401	590.999	0.403	18	0.127	R.SLLPVEPLVDECEKR.N
R5/RRR5-2/2	1111.205	1112.260	-1854.235	0.329	844.615	0.295	14	0.127	R.FQELFAQTK.Y
R5/RRR5-1/2	1141.135	1141.346	-184.932	0.360	632.456	0.398	13	0.127	-.GNLQIVVQAAK.-
R5/RRR5-2/2	1674.218	1673.876	204.721	0.297	207.850	0.503	16	0.127	R.RPITADSALM*NPNTR.I
R5/RRR5-2/2	1016.865	1016.130	-262.137	0.341	491.597	0.359	15	0.126	K.SPEQVSAAVK.A
R5/RRR5-2/2	1511.601	1512.637	-1351.176	0.267	950.648	0.298	17	0.126	K.EYSEQLGVDACIK.L
R5/RRR5-2/2	1427.883	1428.615	-1216.715	0.436	992.882	0.295	15	0.126	R.ALQHYTELPDIK.R
R5/RRR5-1/2	1111.556	1112.260	-1537.745	0.393	819.046	0.276	14	0.126	R.FQELFAQTK.Y
R5/RRR5-1/2	1673.125	1673.876	-1050.228	0.282	285.709	0.463	18	0.126	R.RPITADSALM*NPNTR.I
R5/RRR5-2/2	1262.282	1261.455	-137.503	0.429	462.800	0.416	13	0.125	-.RDPTLAVVAYR.-
R5/RRR5-1/2	1673.187	1673.876	-1012.649	0.244	334.061	0.463	19	0.124	R.RPITADSALM*NPNTR.I
R5/RRR5-2/2	1449.752	1450.619	-1291.091	0.379	532.800	0.333	17	0.124	-.EGLVSEAIESFIR.-
R5/RRR5-2/2	1016.810	1016.130	-316.096	0.254	289.339	0.342	15	0.121	-.SPEQVSAAVK.-
R5/RRR5-2/3	1584.902	1584.801	63.986	0.472	1379.368	0.369	27	0.119	R.ALQHYTELPDIKR.V
R5/RRR5-1/2	1516.412	1516.749	-222.894	0.341	433.314	0.290	13	0.119	K.SHQMPEQVVFWK.W
R5/RRR5-3/2	1450.662	1450.619	30.164	0.309	609.574	0.279	13	0.118	R.EGLVSEAIESFIR.A
R5/RRR5-1/3	1480.287	1480.648	-244.802	0.464	1414.932	0.343	27	0.117	R.GKLNAYESLELSR.L
R5/RRR5-2/2	1303.609	1304.480	-1439.682	0.253	488.855	0.255	13	0.117	K.LKQFQGAVDAAR.K
R5/RRR5-2/3	1480.750	1480.648	69.190	0.508	1456.802	0.321	28	0.115	R.GKLNAYESLELSR.L
R5/RRR5-2/2	1422.275	1423.580	-1625.250	0.259	1034.904	0.082	16	0.112	K.GNMQLFSVDQQR.S
R5/RRR5-2/3	1929.338	1930.109	-921.078	0.443	937.232	0.493	24	0.110	K.VDELVKDRIESQNEVR.A
R5/RRR5-1/3	1584.548	1584.801	-160.041	0.465	1027.793	0.445	25	0.108	R.ALQHYTELPDIKR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1479.723	1480.648	-1304.501	0.454	1259.543	0.357	26	0.107	R.GKLNAYESLELSR.L
R5/RRR5-2/3	1930.302	1930.109	100.108	0.461	1009.021	0.448	26	0.106	K.VDELVKDRIESQNEVR.A
R5/RRR5-2/3	1480.674	1480.648	17.843	0.476	1268.078	0.340	26	0.104	R.GKLNAYESLELSR.L
R5/RRR5-2/3	1583.940	1584.801	-1178.745	0.430	1263.519	0.345	27	0.104	R.ALQHYTELPDIKR.V
R5/RRR5-2/3	1778.371	1779.076	-961.575	0.442	1071.998	0.401	32	0.102	K.LHVIELGAQPGKPGFSK.K
R5/RRR5-2/3	1516.111	1516.749	-1083.736	0.451	1666.289	0.182	24	0.102	K.SHQMPEQVVFWK.W
R5/RRR5-1/3	1674.741	1673.876	-81.020	0.521	1229.727	0.349	26	0.102	R.RPITADSALM*NPNTR.I
R5/RRR5-2/3	1584.360	1584.801	-279.107	0.463	1184.999	0.358	27	0.101	R.ALQHYTELPDIKR.V
R5/RRR5-1/3	1304.621	1304.480	108.515	0.498	1162.288	0.349	26	0.098	K.LKQFQGAVDAAR.K
R5/RRR5-1/3	1778.234	1779.076	-1038.799	0.429	920.246	0.421	30	0.097	K.LHVIELGAQPGKPGFSK.K
R5/RRR5-2/3	1531.584	1532.748	-1417.069	0.396	1136.127	0.351	23	0.096	K.SHQM*PEQVVFWK.W
R5/RRR5-1/3	1778.868	1779.076	-116.955	0.429	681.196	0.473	27	0.096	K.LHVIELGAQPGKPGFSK.K
R5/RRR5-2/3	1929.424	1930.109	-876.299	0.430	949.518	0.405	27	0.095	K.VDELVKDRIESQNEVR.A
R5/RRR5-2/3	1450.293	1450.619	-225.045	0.462	1232.810	0.300	25	0.093	R.EGLVSEAIESFIR.A
R5/RRR5-2/3	1373.235	1373.496	-190.910	0.467	762.200	0.454	25	0.093	-.ADDATHFLDVIR.-
R5/RRR5-2/3	1373.315	1373.496	-131.923	0.481	671.169	0.429	24	0.093	R.ADDATHFLDVIR.A
R5/RRR5-1/3	1779.152	1779.076	42.858	0.434	597.918	0.461	25	0.092	K.LHVIELGAQPGKPGFSK.K
R5/RRR5-1/3	1373.632	1373.496	99.542	0.499	518.852	0.415	21	0.092	R.ADDATHFLDVIR.A
R5/RRR5-1/3	1373.189	1373.496	-224.485	0.431	544.676	0.438	22	0.091	R.ADDATHFLDVIR.A
R5/RRR5-1/3	1373.485	1373.496	-8.355	0.411	628.217	0.443	23	0.091	R.ADDATHFLDVIR.A
R5/RRR5-2/3	1428.839	1428.615	157.650	0.411	921.844	0.395	22	0.091	R.ALQHYTELPDIK.R
R5/RRR5-1/3	1846.116	1847.062	-1057.207	0.405	976.732	0.381	23	0.091	K.YKEAAELAAESPQGLLR.T
R5/RRR5-2/3	1373.351	1373.496	-105.575	0.442	611.650	0.417	23	0.090	R.ADDATHFLDVIR.A
R5/RRR5-2/3	1428.932	1428.615	222.545	0.448	834.823	0.387	21	0.088	R.ALQHYTELPDIK.R
R5/RRR5-1/3	1479.438	1480.648	-1498.159	0.365	1279.024	0.259	23	0.088	R.GKLNAYESLELSR.L
R5/RRR5-2/3	1450.378	1450.619	-166.278	0.394	903.709	0.350	24	0.084	R.EGLVSEAIESFIR.A
R5/RRR5-1/3	1584.236	1584.801	-990.608	0.401	858.515	0.342	22	0.083	R.ALQHYTELPDIKR.V
R5/RRR5-2/3	1779.060	1779.076	-8.652	0.439	673.291	0.364	27	0.083	K.LHVIELGAQPGKPGFSK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1778.970	1779.076	-59.445	0.380	742.716	0.361	28	0.082	K.LHVIELGAQPGKPGFSK.K
R5/RRR5-1/3	1304.832	1304.480	270.923	0.418	833.924	0.327	24	0.081	K.LKQFQGAVDAAR.K
R5/RRR5-1/3	1584.626	1584.801	-110.545	0.392	600.490	0.330	21	0.081	R.ALQHYTELPDIKR.V
R5/RRR5-2/3	1450.160	1450.619	-317.516	0.395	1121.725	0.268	25	0.081	R.EGLVSEAIESFIR.A
R5/RRR5-2/3	1305.300	1304.480	-138.516	0.519	887.184	0.338	23	0.080	-.LKQFQGAVDAAR.-
R5/RRR5-2/3	1428.999	1428.615	269.702	0.410	725.964	0.332	20	0.078	R.ALQHYTELPDIK.R
R5/RRR5-2/3	1842.156	1843.120	-1069.050	0.367	750.985	0.299	25	0.073	K.FNLNVQAVNVLLDNIR.S
R5/RRR5-1/3	1479.653	1480.648	-1352.225	0.341	1114.601	0.165	23	0.065	R.GKLNAYESLELSR.L
R5/RRR5-2/3	1584.480	1584.801	-202.934	0.363	751.901	0.166	19	0.063	-.ALQHYTELPDIKR.-
R5/RRR5-1/3	1842.177	1843.120	-1057.673	0.418	615.643	0.333	20	0.061	-.FNLNVQAVNVLLDNIR.-
R5/RRR5-1/3	1305.137	1304.480	-263.208	0.375	469.156	0.300	21	0.058	-.LKQFQGAVDAAR.-
R5/RRR5-7/2	1489.138	1489.700	-1052.052	0.531	1703.208	0.555	20	0.239	K.VVVADNVHDFVFK.S
R5/RRR5-7/2	1446.224	1446.542	-220.844	0.597	1685.776	0.472	20	0.214	K.SPEDATNLIDDKK.I
R5/RRR5-7/2	1489.823	1489.700	83.036	0.548	1448.925	0.558	20	0.209	K.VVVADNVHDFVFK.S
R5/RRR5-7/3	1881.762	1881.000	-126.956	0.505	1519.277	0.592	31	0.208	R.SDYDFGHTLHANHLPR.G
R5/RRR5-7/2	1522.883	1522.730	101.252	0.487	1464.629	0.541	20	0.206	K.AHVEPDQIVSWLK.Q
R5/RRR5-7/2	1489.112	1489.700	-1069.089	0.524	1383.348	0.565	19	0.202	K.VVVADNVHDFVFK.S
R5/RRR5-7/2	1877.221	1878.071	-988.417	0.482	1458.982	0.503	20	0.195	K.SVYYGAAEEFKDKEIK.F
R5/RRR5-7/2	1522.502	1522.730	-150.109	0.493	1318.253	0.534	19	0.189	K.AHVEPDQIVSWLK.Q
R5/RRR5-7/2	1880.066	1881.110	-1090.533	0.499	1214.848	0.591	20	0.189	K.NVLVEFYAPWCGHCK.K
R5/RRR5-7/2	1446.161	1446.542	-264.201	0.560	1435.049	0.469	19	0.187	K.SPEDATNLIDDKK.I
R5/RRR5-7/2	1278.552	1279.464	-1499.881	0.444	1462.318	0.440	17	0.185	R.TADEIVDFIKK.N
R5/RRR5-7/2	1877.384	1878.071	-901.463	0.473	1328.229	0.516	19	0.183	K.SVYYGAAEEFKDKEIK.F
R5/RRR5-7/2	1278.406	1279.464	-1614.692	0.436	1388.081	0.444	16	0.178	R.TADEIVDFIKK.N
R5/RRR5-7/2	1877.612	1878.071	-245.094	0.544	1276.055	0.512	19	0.177	K.SVYYGAAEEFKDKEIK.F
R5/RRR5-7/2	1196.192	1196.377	-154.824	0.395	1373.424	0.426	16	0.174	K.YEIQGFPTLK.I
R5/RRR5-7/2	1446.066	1446.542	-330.429	0.513	1338.627	0.408	19	0.167	K.SPEDATNLIDDKK.I
R5/RRR5-7/3	1880.349	1881.000	-880.775	0.537	1234.660	0.597	31	0.166	R.SDYDFGHTLHANHLPR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	976.956	976.063	-110.299	0.522	1318.530	0.391	15	0.164	K.SDEDVVIAK.M
R5/RRR5-7/2	1279.278	1279.464	-146.108	0.482	1242.963	0.427	15	0.162	R.TADEIVDFIKK.N
R5/RRR5-1/2	1279.558	1279.464	73.812	0.426	1386.409	0.338	16	0.159	R.TADEIVDFIKK.N
R5/RRR5-7/2	1196.148	1196.377	-191.679	0.362	1147.484	0.453	15	0.159	K.YEIQGFPTLK.I
R5/RRR5-7/2	1521.773	1522.730	-1289.445	0.337	1223.991	0.396	19	0.155	K.AHVEPDQIVSWLK.Q
R5/RRR5-7/2	1150.941	1151.291	-305.268	0.408	1141.250	0.384	16	0.150	R.TADEIVDFIK.K
R5/RRR5-7/2	1538.591	1537.781	-124.109	0.497	874.557	0.473	21	0.150	R.LFKPFDELVVDSK.D
R5/RRR5-7/2	1150.946	1151.291	-300.798	0.438	1068.594	0.403	16	0.149	R.TADEIVDFIK.K
R5/RRR5-7/3	1446.704	1446.542	112.203	0.575	1487.050	0.436	28	0.149	K.SPEDATNLIDDKK.I
R5/RRR5-7/2	1196.021	1196.377	-298.164	0.321	1104.059	0.394	15	0.146	K.YEIQGFPTLK.I
R5/RRR5-7/2	1523.171	1522.730	290.695	0.383	993.327	0.441	16	0.146	K.AHVEPDQIVSWLK.Q
R5/RRR5-1/3	1446.698	1446.542	108.014	0.489	1527.610	0.383	26	0.140	K.SPEDATNLIDDKK.I
R5/RRR5-7/2	1538.453	1537.781	-213.732	0.508	734.858	0.432	20	0.139	R.LFKPFDELVVDSK.D
R5/RRR5-7/2	1453.064	1452.591	326.123	0.397	629.304	0.458	20	0.137	K.SEPIPEVNNEPVK.V
R5/RRR5-7/2	1453.001	1452.591	282.825	0.431	418.506	0.509	17	0.136	K.SEPIPEVNNEPVK.V
R5/RRR5-7/2	966.908	966.070	-168.174	0.420	629.179	0.395	16	0.134	K.FIDASSTPK.V
R5/RRR5-7/2	989.768	990.181	-418.931	0.377	425.461	0.442	13	0.132	K.HDPPIVLAK.V
R5/RRR5-7/2	989.631	990.181	-1571.064	0.343	383.025	0.486	12	0.132	K.HDPPIVLAK.V
R5/RRR5-7/2	1452.165	1452.591	-294.388	0.375	368.697	0.466	16	0.130	K.SEPIPEVNNEPVK.V
R5/RRR5-7/2	1538.712	1537.781	-45.245	0.494	622.711	0.391	18	0.130	R.LFKPFDELVVDSK.D
R5/RRR5-7/3	1522.618	1522.730	-73.675	0.453	1623.541	0.297	27	0.130	K.AHVEPDQIVSWLK.Q
R5/RRR5-7/2	1717.388	1717.990	-935.755	0.432	440.548	0.523	16	0.130	K.AAQELSKHDPPIVLAK.V
R5/RRR5-7/2	1037.833	1038.133	-289.460	0.337	913.094	0.309	15	0.128	K.DFDVTALEK.F
R5/RRR5-7/2	1278.366	1279.464	-1646.349	0.304	360.870	0.401	17	0.128	R.EAEGIVEYLKK.Q
R5/RRR5-7/2	1279.136	1279.464	-256.870	0.303	346.625	0.417	16	0.128	R.EAEGIVEYLKK.Q
R5/RRR5-7/3	1880.475	1881.000	-813.425	0.460	941.413	0.574	28	0.127	R.SDYDFGHTLHANHLPR.G
R5/RRR5-7/2	990.084	990.181	-98.387	0.352	420.568	0.352	13	0.127	K.HDPPIVLAK.V
R5/RRR5-8/2	976.924	976.063	-143.139	0.381	927.276	0.265	14	0.126	K.SDEDVVIAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	990.221	990.181	40.728	0.314	326.787	0.376	11	0.125	K.HDPPIVLAK.V
R5/RRR5-7/2	1523.648	1522.730	-54.049	0.294	287.287	0.375	14	0.124	K.AHVEPDQIVSWLK.Q
R5/RRR5-7/3	1446.532	1446.542	-6.748	0.554	1168.389	0.465	27	0.124	K.SPEDATNLIDDKK.I
R5/RRR5-7/2	1370.070	1370.487	-305.415	0.442	1100.705	0.468	19	0.123	K.AESAPAEPLKDEL.-
R5/RRR5-2/2	1280.298	1279.464	-129.926	0.283	1007.471	0.206	15	0.122	R.TADEIVDFIKK.N
R5/RRR5-7/2	1451.646	1452.591	-1344.399	0.261	479.047	0.350	18	0.122	K.SEPIPEVNNEPVK.V
R5/RRR5-7/2	1278.564	1279.464	-1490.674	0.229	407.743	0.352	17	0.122	R.EAEGIVEYLKK.Q
R5/RRR5-2/2	1522.537	1522.730	-127.187	0.278	371.571	0.359	14	0.120	-.AHVEPDQIVSWLK.-
R5/RRR5-7/2	1279.415	1279.464	-38.050	0.291	909.654	0.230	14	0.120	R.EAEGIVEYLKK.Q
R5/RRR5-7/3	1522.764	1522.730	22.455	0.442	1780.930	0.193	27	0.120	K.AHVEPDQIVSWLK.Q
R5/RRR5-1/2	1523.466	1522.730	-173.803	0.270	295.383	0.367	13	0.120	-.AHVEPDQIVSWLK.-
R5/RRR5-1/2	1279.438	1279.464	-20.250	0.294	643.740	0.220	14	0.118	R.TADEIVDFIKK.N
R5/RRR5-7/3	1522.809	1522.730	52.123	0.436	1751.292	0.194	27	0.117	K.AHVEPDQIVSWLK.Q
R5/RRR5-2/2	1279.199	1279.464	-208.139	0.209	765.619	0.165	13	0.114	R.TADEIVDFIKK.N
R5/RRR5-7/2	1627.438	1627.775	-207.613	0.433	839.964	0.591	21	0.110	K.EKAESAPAEPLKDEL.-
R5/RRR5-6/2	965.320	966.070	-1818.196	0.275	372.997	0.328	12	0.108	-.FIDASSTPK.-
R5/RRR5-7/3	1446.133	1446.542	-283.984	0.515	1189.635	0.388	26	0.108	K.SPEDATNLIDDKK.I
R5/RRR5-5/3	1446.168	1446.542	-259.595	0.469	1023.754	0.429	23	0.105	K.SPEDATNLIDDKK.I
R5/RRR5-7/3	1538.664	1537.781	-76.289	0.473	1039.431	0.427	23	0.104	-.LFKPFDELVVDSK.-
R5/RRR5-7/2	1150.413	1151.291	-1637.465	0.236	405.278	0.267	10	0.103	-.TADEIVDFIK.-
R5/RRR5-7/2	1628.221	1627.775	274.873	0.435	684.480	0.599	20	0.102	K.EKAESAPAEPLKDEL.-
R5/RRR5-7/2	1628.275	1627.775	-307.589	0.517	631.603	0.601	20	0.100	K.EKAESAPAEPLKDEL.-
R5/RRR5-7/2	1370.257	1370.487	-168.127	0.411	840.668	0.401	17	0.094	K.AESAPAEPLKDEL.-
R5/RRR5-7/2	1369.980	1370.487	-1103.340	0.422	802.298	0.405	16	0.091	K.AESAPAEPLKDEL.-
R5/RRR5-7/3	1717.335	1717.990	-966.983	0.405	708.097	0.444	27	0.090	K.AAQELSKHDPPIVLAK.V
R5/RRR5-3/3	1446.967	1446.542	294.318	0.401	612.319	0.412	18	0.086	K.SPEDATNLIDDKK.I
R5/RRR5-7/3	1718.009	1717.990	10.924	0.403	693.505	0.370	26	0.081	K.AAQELSKHDPPIVLAK.V
R5/RRR5-7/3	1580.601	1580.764	-103.506	0.425	991.055	0.299	27	0.079	R.KSEPIPEVNNEPVK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/3	1716.678	1717.990	-1350.886	0.430	510.671	0.415	23	0.078	-.AAQELSKHDPPIVLAK.-
R5/RRR5-7/3	1537.641	1537.781	-91.229	0.356	881.454	0.266	21	0.070	R.LFKPFDELVVDSK.D
R5/RRR5-5/3	1446.905	1446.542	251.682	0.336	899.185	0.210	22	0.068	K.SPEDATNLIDDKK.I
R5/RRR5-5/2	1557.278	1556.618	-218.932	0.583	3485.270	0.578	25	0.629	K.DEAYFAANAAAQASR.R
R5/RRR5-5/2	1556.251	1556.618	-237.014	0.511	3254.473	0.519	24	0.538	K.DEAYFAANAAAQASR.R
R5/RRR5-5/2	1968.511	1969.179	-849.967	0.630	3146.912	0.557	26	0.522	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/2	1968.664	1969.179	-771.849	0.635	2989.647	0.569	25	0.486	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/2	1968.602	1969.179	-803.655	0.645	2916.708	0.585	26	0.475	K.KISEDEYVSAIKEEISK.V
R5/RRR5-6/2	1807.547	1808.137	-882.328	0.574	2880.554	0.587	25	0.462	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/2	1556.156	1556.618	-298.162	0.460	2888.855	0.514	23	0.443	K.DEAYFAANAAAQASR.R
R5/RRR5-5/2	1807.570	1808.137	-869.379	0.574	2592.031	0.626	24	0.411	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-1/2	1808.289	1808.137	84.370	0.612	2623.694	0.604	24	0.409	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/2	1807.533	1808.137	-890.260	0.581	2540.372	0.592	24	0.387	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-4/2	1807.396	1808.137	-965.995	0.541	2559.400	0.577	24	0.386	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/1	1021.472	1022.181	-1678.679	0.198	805.947	0.208	12	0.377	K.SWLAFAAQK.V
R5/RRR5-2/2	1807.951	1808.137	-103.337	0.582	2494.550	0.589	24	0.377	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/2	1791.390	1792.138	-978.500	0.546	2536.399	0.542	24	0.369	K.GMLTGPVTILNWSFVR.N
R5/RRR5-5/2	1807.535	1808.137	-888.836	0.560	2422.248	0.570	23	0.355	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/3	1978.398	1978.201	100.212	0.567	2205.069	0.577	30	0.353	R.KAEHAFYLDWAVHSFR.I
R5/RRR5-5/3	1978.286	1978.201	43.031	0.552	2307.553	0.512	30	0.348	R.KAEHAFYLDWAVHSFR.I
R5/RRR5-5/2	1807.527	1808.137	-893.718	0.592	2289.044	0.607	23	0.342	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/2	1790.933	1792.138	-1234.981	0.446	2414.977	0.521	23	0.339	K.GMLTGPVTILNWSFVR.N
R5/RRR5-1/2	1809.493	1808.137	197.379	0.602	2163.907	0.663	23	0.338	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/2	1791.675	1792.138	-258.900	0.526	2322.350	0.572	23	0.337	K.GMLTGPVTILNWSFVR.N
R5/RRR5-1/2	1809.596	1808.137	254.270	0.602	2217.047	0.612	23	0.330	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/2	1792.195	1792.138	32.067	0.592	2278.720	0.575	23	0.329	K.GMLTGPVTILNWSFVR.N
R5/RRR5-2/2	1807.325	1808.137	-1005.867	0.526	2163.446	0.561	22	0.305	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/2	1851.809	1850.028	-118.721	0.543	2097.560	0.573	22	0.303	K.AEHAFYLDWAVHSFR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1807.565	1808.137	-872.091	0.546	2089.708	0.579	23	0.298	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/3	1970.349	1969.179	86.764	0.610	1911.649	0.632	34	0.297	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/2	1791.580	1792.138	-872.060	0.521	2085.908	0.554	22	0.290	K.GMLTGPVTILNWSFVR.N
R5/RRR5-5/3	1978.175	1978.201	-13.228	0.552	1998.911	0.537	30	0.283	R.KAEHAFYLDWAVHSFR.I
R5/RRR5-6/2	1807.518	1808.137	-898.463	0.558	1964.362	0.583	22	0.279	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/3	1969.258	1969.179	40.026	0.597	1869.665	0.605	35	0.275	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/3	1970.338	1969.179	80.986	0.572	1796.017	0.622	34	0.268	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/1	1021.454	1022.181	-1696.389	0.186	622.360	0.331	11	0.267	K.SWLAFAAQK.V
R5/RRR5-5/1	1021.489	1022.181	-1661.991	0.199	610.635	0.314	11	0.252	K.SWLAFAAQK.V
R5/RRR5-2/2	1807.279	1808.137	-1031.230	0.499	1898.195	0.493	21	0.244	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/2	1740.323	1740.015	177.764	0.587	1566.008	0.597	25	0.232	K.YTEVKPALTNM*VSAAK.L
R5/RRR5-6/3	1969.668	1969.179	249.159	0.571	1545.583	0.604	32	0.214	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/2	1486.336	1486.653	-213.895	0.505	1673.440	0.427	20	0.204	R.IPSTEEIADRINK.M
R5/RRR5-2/3	1969.165	1969.179	-7.164	0.536	1508.954	0.587	32	0.202	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/3	1723.710	1724.015	-177.486	0.451	1653.093	0.518	32	0.202	K.YTEVKPALTNMVSAAK.L
R5/RRR5-6/3	1969.623	1969.179	226.133	0.548	1482.185	0.595	33	0.200	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/2	1486.163	1486.653	-330.247	0.493	1632.712	0.425	20	0.199	R.IPSTEEIADRINK.M
R5/RRR5-1/3	1967.960	1969.179	-1131.175	0.420	1652.624	0.508	32	0.199	K.KISEDEYVSAIKEEISK.V
R5/RRR5-6/2	1660.326	1659.826	302.004	0.514	1349.419	0.515	22	0.187	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/2	1867.415	1868.188	-952.049	0.465	1218.697	0.551	25	0.183	R.KYTEVKPALTNM*VSAAK.L
R5/RRR5-5/2	1840.643	1841.006	-198.132	0.554	1382.617	0.469	21	0.180	K.ISEDEYVSAIKEEISK.V
R5/RRR5-3/2	1806.556	1808.137	-1988.400	0.367	1560.710	0.359	20	0.176	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/2	1867.378	1868.188	-972.065	0.484	1079.908	0.568	25	0.175	R.KYTEVKPALTNM*VSAAK.L
R5/RRR5-5/2	1659.338	1659.826	-295.043	0.504	1193.264	0.519	21	0.174	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1740.039	1740.015	13.978	0.481	1494.720	0.511	34	0.173	K.YTEVKPALTNM*VSAAK.L
R5/RRR5-5/2	1660.436	1659.826	-236.005	0.520	1204.633	0.506	21	0.172	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/2	1739.463	1740.015	-894.572	0.522	1051.765	0.561	22	0.171	K.YTEVKPALTNM*VSAAK.L
R5/RRR5-6/3	1968.729	1969.179	-229.093	0.540	1361.692	0.553	32	0.169	K.KISEDEYVSAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1660.282	1659.826	275.095	0.508	1206.707	0.483	21	0.168	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/2	1486.144	1486.653	-1018.169	0.489	1275.494	0.423	19	0.165	R.IPSTEEIADRINK.M
R5/RRR5-6/2	1659.449	1659.826	-227.882	0.489	1105.825	0.503	20	0.164	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-6/2	1021.903	1022.181	-273.425	0.517	1162.269	0.437	15	0.162	K.SWLAFAAQK.V
R5/RRR5-1/3	1969.518	1969.179	172.900	0.515	1298.895	0.556	32	0.162	K.KISEDEYVSAIKEEISK.V
R5/RRR5-5/2	1131.028	1131.218	-168.832	0.482	1098.332	0.460	17	0.161	R.IPSTEEIADR.I
R5/RRR5-5/2	1458.603	1457.689	-59.649	0.514	1061.356	0.478	19	0.160	R.FETCYQIALAIK.K
R5/RRR5-6/2	1791.574	1792.138	-875.206	0.450	1048.259	0.513	17	0.158	K.GMLTGPVTILNWSFVR.N
R5/RRR5-3/2	1659.887	1659.826	36.393	0.434	929.143	0.544	18	0.156	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1739.846	1740.015	-97.173	0.464	1558.345	0.425	33	0.156	K.YTEVKPALTNM*VSAAK.L
R5/RRR5-6/2	1194.358	1194.362	-3.240	0.544	1193.171	0.397	16	0.156	R.SDEKLLSVFR.E
R5/RRR5-6/2	1658.745	1659.826	-1258.848	0.409	894.657	0.538	18	0.153	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/2	1840.471	1841.006	-836.454	0.515	1164.008	0.425	19	0.153	K.ISEDEYVSAIKEEISK.V
R5/RRR5-5/3	1723.859	1724.015	-91.123	0.442	1364.728	0.498	31	0.153	K.YTEVKPALTNMVSAAK.L
R5/RRR5-4/2	1791.878	1792.138	-145.172	0.495	881.532	0.510	21	0.152	K.GMLTGPVTILNWSFVR.N
R5/RRR5-5/2	1707.337	1707.951	-947.933	0.483	1090.392	0.452	18	0.152	K.LDSEIKSWLAFAAQK.V
R5/RRR5-5/2	1194.114	1194.362	-208.205	0.517	1155.275	0.384	16	0.152	R.SDEKLLSVFR.E
R5/RRR5-5/2	1193.653	1194.362	-1436.495	0.472	1078.125	0.406	16	0.151	R.SDEKLLSVFR.E
R5/RRR5-4/2	1132.174	1131.218	-39.430	0.490	987.457	0.428	16	0.150	R.IPSTEEIADR.I
R5/RRR5-5/2	1840.389	1841.006	-881.397	0.499	1139.906	0.410	19	0.149	K.ISEDEYVSAIKEEISK.V
R5/RRR5-2/2	1194.584	1194.362	185.757	0.477	982.341	0.426	15	0.148	R.SDEKLLSVFR.E
R5/RRR5-5/2	1021.857	1022.181	-318.728	0.416	1260.759	0.299	15	0.146	K.SWLAFAAQK.V
R5/RRR5-4/3	1969.271	1969.179	46.834	0.439	1320.746	0.491	30	0.146	K.KISEDEYVSAIKEEISK.V
R5/RRR5-1/2	1194.313	1194.362	-41.787	0.481	941.887	0.423	15	0.146	R.SDEKLLSVFR.E
R5/RRR5-5/2	1254.202	1254.368	-132.824	0.426	961.136	0.441	15	0.146	K.ISEDEYVSAIK.E
R5/RRR5-5/2	1021.997	1022.181	-181.033	0.477	1093.457	0.364	14	0.145	K.SWLAFAAQK.V
R5/RRR5-9/2	1809.337	1808.137	110.847	0.409	700.514	0.550	16	0.144	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-5/2	1021.516	1022.181	-1635.471	0.371	1252.644	0.279	15	0.143	K.SWLAFAAQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1660.132	1659.826	184.849	0.385	814.205	0.490	17	0.142	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-1/2	1130.818	1131.218	-354.983	0.457	699.436	0.450	16	0.141	R.IPSTEEIADR.I
R5/RRR5-6/2	1021.335	1022.181	-1813.061	0.376	1133.387	0.313	14	0.140	K.SWLAFAAQK.V
R5/RRR5-5/2	1457.316	1457.689	-257.053	0.386	994.420	0.386	17	0.140	R.FETCYQIALAIK.K
R5/RRR5-5/2	1193.562	1194.362	-1512.616	0.498	927.146	0.380	15	0.139	R.SDEKLLSVFR.E
R5/RRR5-2/2	1659.975	1659.826	89.792	0.381	982.474	0.392	18	0.139	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-1/2	942.940	943.123	-194.198	0.424	537.610	0.460	14	0.139	K.VVEVNALAK.A
R5/RRR5-5/2	1254.662	1254.368	234.926	0.463	689.616	0.461	15	0.138	K.ISEDEYVSAIK.E
R5/RRR5-6/2	1021.993	1022.181	-184.508	0.404	973.981	0.353	13	0.137	K.SWLAFAAQK.V
R5/RRR5-5/2	942.634	943.123	-519.500	0.378	704.256	0.420	15	0.137	K.VVEVNALAK.A
R5/RRR5-1/2	1132.110	1131.218	-95.886	0.460	700.314	0.405	16	0.137	R.IPSTEEIADR.I
R5/RRR5-2/2	1131.165	1131.218	-46.825	0.434	740.464	0.396	16	0.137	R.IPSTEEIADR.I
R5/RRR5-6/2	1130.856	1131.218	-321.408	0.456	699.641	0.401	16	0.137	R.IPSTEEIADR.I
R5/RRR5-4/3	1659.058	1659.826	-1069.103	0.459	855.568	0.637	29	0.136	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-2/2	943.086	943.123	-39.157	0.430	341.856	0.465	12	0.136	K.VVEVNALAK.A
R5/RRR5-1/2	1132.124	1131.218	-83.556	0.522	601.929	0.418	15	0.136	R.IPSTEEIADR.I
R5/RRR5-5/2	942.511	943.123	-1715.210	0.392	501.461	0.425	14	0.135	K.VVEVNALAK.A
R5/RRR5-5/2	942.997	943.123	-133.293	0.376	530.029	0.423	14	0.134	K.VVEVNALAK.A
R5/RRR5-1/2	942.991	943.123	-140.045	0.411	463.391	0.420	13	0.134	K.VVEVNALAK.A
R5/RRR5-2/2	942.828	943.123	-313.044	0.382	386.602	0.441	12	0.133	K.VVEVNALAK.A
R5/RRR5-1/2	1809.361	1808.137	124.041	0.400	563.961	0.471	16	0.132	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/2	1809.179	1808.137	23.015	0.401	390.799	0.504	15	0.132	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-3/2	942.944	943.123	-190.432	0.361	407.845	0.390	13	0.131	K.VVEVNALAK.A
R5/RRR5-3/2	942.990	943.123	-141.084	0.344	430.272	0.404	13	0.131	K.VVEVNALAK.A
R5/RRR5-3/2	1659.844	1659.826	10.429	0.371	664.706	0.446	15	0.130	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-7/2	1131.073	1131.218	-128.990	0.408	590.195	0.363	14	0.129	R.IPSTEEIADR.I
R5/RRR5-6/2	1131.470	1131.218	222.847	0.396	659.561	0.314	16	0.128	R.IPSTEEIADR.I
R5/RRR5-4/2	942.273	943.123	-1969.152	0.298	393.185	0.325	12	0.126	K.VVEVNALAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	943.082	943.123	-42.922	0.306	353.752	0.325	11	0.126	K.VVEVNALAK.A
R5/RRR5-4/2	942.954	943.123	-179.393	0.306	359.081	0.330	11	0.126	K.VVEVNALAK.A
R5/RRR5-1/2	942.477	943.123	-1750.866	0.299	394.028	0.311	12	0.126	K.VVEVNALAK.A
R5/RRR5-6/2	1808.617	1808.137	266.322	0.326	481.337	0.418	15	0.125	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/3	1807.325	1808.137	-1005.908	0.449	1379.175	0.383	27	0.125	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/3	1660.830	1659.826	1.900	0.467	749.587	0.606	29	0.123	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-4/2	1659.281	1659.826	-934.065	0.337	763.475	0.324	16	0.123	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1194.528	1194.362	139.323	0.525	1431.143	0.361	22	0.123	R.SDEKLLSVFR.E
R5/RRR5-6/2	1193.441	1194.362	-1614.643	0.332	665.873	0.285	13	0.122	R.SDEKLLSVFR.E
R5/RRR5-5/3	1660.870	1659.826	26.227	0.450	708.400	0.606	27	0.121	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-6/2	1791.345	1792.138	-1003.677	0.276	537.165	0.357	13	0.120	K.GMLTGPVTILNWSFVR.N
R5/RRR5-1/2	1659.548	1659.826	-168.478	0.272	660.868	0.320	15	0.120	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1194.634	1194.362	228.015	0.529	1226.192	0.420	21	0.118	R.SDEKLLSVFR.E
R5/RRR5-1/3	1659.648	1659.826	-107.724	0.460	639.875	0.590	26	0.115	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-4/2	1658.654	1659.826	-1313.837	0.324	895.914	0.185	17	0.115	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1852.958	1852.188	-124.667	0.522	874.110	0.526	30	0.115	R.KYTEVKPALTNMVSAAK.L
R5/RRR5-2/3	1661.062	1659.826	142.428	0.448	718.661	0.571	24	0.115	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-6/3	1739.656	1740.015	-206.871	0.377	1292.199	0.382	31	0.114	K.YTEVKPALTNM*VSAAK.L
R5/RRR5-1/2	1659.606	1659.826	-133.134	0.292	570.239	0.216	14	0.114	-.YGAGIGPGVYDIHSPR.-
R5/RRR5-6/3	1660.832	1659.826	3.559	0.430	616.116	0.584	25	0.113	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-4/3	1659.211	1659.826	-976.801	0.412	560.117	0.598	25	0.113	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-6/3	1660.757	1659.826	-42.002	0.463	649.263	0.559	27	0.111	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-6/3	1194.550	1194.362	157.462	0.481	1342.684	0.347	21	0.111	R.SDEKLLSVFR.E
R5/RRR5-2/3	1659.607	1659.826	-132.404	0.399	481.349	0.598	23	0.110	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1852.172	1852.188	-8.773	0.517	688.743	0.545	27	0.109	R.KYTEVKPALTNMVSAAK.L
R5/RRR5-4/3	1659.812	1659.826	-8.462	0.416	480.981	0.582	22	0.108	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1739.638	1740.015	-217.324	0.418	1140.696	0.407	32	0.107	K.YTEVKPALTNM*VSAAK.L
R5/RRR5-1/3	1659.121	1659.826	-1030.984	0.422	577.636	0.557	22	0.107	K.YGAGIGPGVYDIHSPR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/3	1194.705	1194.362	288.107	0.489	1287.830	0.347	21	0.106	R.SDEKLLSVFR.E
R5/RRR5-3/3	1659.863	1659.826	22.186	0.463	572.489	0.537	25	0.106	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1849.056	1850.028	-1069.564	0.443	1148.297	0.391	24	0.105	K.AEHAFYLDWAVHSFR.I
R5/RRR5-2/3	1661.106	1659.826	168.848	0.494	621.023	0.499	26	0.102	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-5/3	1868.799	1868.188	-208.529	0.507	859.735	0.449	30	0.100	R.KYTEVKPALTNM*VSAAK.L
R5/RRR5-5/3	1849.282	1850.028	-946.584	0.426	996.470	0.413	23	0.098	-.AEHAFYLDWAVHSFR.-
R5/RRR5-6/3	1867.828	1868.188	-193.167	0.516	521.377	0.491	26	0.098	R.KYTEVKPALTNM*VSAAK.L
R5/RRR5-5/3	1658.632	1659.826	-1326.817	0.444	566.841	0.477	23	0.097	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-6/3	1992.072	1992.176	-52.533	0.473	661.099	0.475	29	0.095	K.IQEELDIDVLVHGEPER.N
R5/RRR5-5/3	1659.314	1659.826	-914.316	0.382	510.519	0.433	23	0.092	K.YGAGIGPGVYDIHSPR.I
R5/RRR5-6/3	1867.798	1868.188	-209.296	0.511	786.707	0.404	29	0.091	R.KYTEVKPALTNM*VSAAK.L
R5/RRR5-5/3	1867.509	1868.188	-901.493	0.452	726.521	0.413	28	0.090	R.KYTEVKPALTNM*VSAAK.L
R5/RRR5-5/3	1659.701	1659.826	-75.963	0.346	425.846	0.443	22	0.089	-.YGAGIGPGVYDIHSPR.-
R5/RRR5-5/3	1851.521	1852.188	-903.218	0.440	560.891	0.411	26	0.088	R.KYTEVKPALTNMVSAAK.L
R5/RRR5-5/3	1869.078	1868.188	-58.848	0.464	498.664	0.409	24	0.088	R.KYTEVKPALTNM*VSAAK.L
R5/RRR5-5/3	1194.087	1194.362	-231.600	0.376	1025.717	0.341	19	0.088	R.SDEKLLSVFR.E
R5/RRR5-6/3	1992.916	1992.176	-130.780	0.378	531.306	0.442	28	0.086	K.IQEELDIDVLVHGEPER.N
R5/RRR5-6/3	1194.882	1194.362	-403.181	0.445	1125.185	0.291	20	0.085	R.SDEKLLSVFR.E
R5/RRR5-6/3	1585.454	1585.862	-258.064	0.402	885.745	0.354	26	0.084	R.FETCYQIALAIKK.E
R5/RRR5-6/3	1991.227	1992.176	-981.638	0.440	293.268	0.476	21	0.082	-.IQEELDIDVLVHGEPER.-
R5/RRR5-5/3	1808.611	1808.137	262.829	0.354	664.289	0.348	22	0.076	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/3	1585.615	1585.862	-156.227	0.279	602.275	0.315	22	0.073	R.FETCYQIALAIKK.E
R5/RRR5-6/3	1739.799	1740.015	-124.094	0.228	657.200	0.267	24	0.070	K.YTEVKPALTNM*VSAAK.L
R5/RRR5-6/3	1586.778	1585.862	-53.373	0.350	996.642	0.226	27	0.070	R.FETCYQIALAIKK.E
R5/RRR5-5/3	1848.644	1850.028	-1293.529	0.238	807.184	0.292	22	0.070	-.AEHAFYLDWAVHSFR.-
R5/RRR5-5/3	1808.954	1808.137	-101.528	0.366	861.914	0.248	25	0.069	K.GM*LTGPVTILNWSFVR.N
R5/RRR5-6/2	1967.671	1968.236	-797.564	0.622	2639.709	0.551	26	0.399	R.VQQLLQDFFNGKELCK.S
R5/RRR5-6/2	1413.265	1413.562	-210.660	0.469	2171.445	0.560	21	0.311	K.SSVHDVVLVGGSTR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1412.687	1413.562	-1330.685	0.425	2105.945	0.574	21	0.303	K.SSVHDVVLVGGSTR.I
R5/RRR5-6/2	1437.850	1437.625	156.969	0.548	2227.695	0.498	19	0.301	R.VQQLLQDFFNGK.E
R5/RRR5-6/2	1437.236	1437.625	-271.038	0.582	2296.427	0.462	19	0.300	R.VQQLLQDFFNGK.E
R5/RRR5-6/2	1967.493	1968.236	-888.616	0.603	2124.360	0.550	24	0.299	R.VQQLLQDFFNGKELCK.S
R5/RRR5-6/2	1676.199	1676.683	-289.738	0.486	2051.691	0.541	24	0.285	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/2	1437.276	1437.625	-243.174	0.560	2174.342	0.457	18	0.279	R.VQQLLQDFFNGK.E
R5/RRR5-6/2	1216.062	1216.436	-308.251	0.535	1987.281	0.532	20	0.273	K.DAGVIAGLNVMR.I
R5/RRR5-6/2	1412.781	1413.562	-1263.866	0.416	2022.742	0.502	21	0.269	K.SSVHDVVLVGGSTR.I
R5/RRR5-6/2	1437.235	1437.625	-271.805	0.566	2028.065	0.481	18	0.263	R.VQQLLQDFFNGK.E
R5/RRR5-6/2	1309.279	1309.490	-161.837	0.431	1869.008	0.508	19	0.248	R.EIAEAYLGTTIK.N
R5/RRR5-6/2	1966.725	1968.236	-1790.651	0.559	1770.006	0.543	23	0.243	R.VQQLLQDFFNGKELCK.S
R5/RRR5-6/2	1231.394	1232.436	-1662.748	0.504	1799.055	0.493	20	0.236	K.DAGVIAGLNVM*R.I
R5/RRR5-6/2	1196.910	1197.277	-307.046	0.507	1795.440	0.484	18	0.233	R.FSDASVQSDIK.L
R5/RRR5-6/2	1233.220	1232.436	-175.425	0.549	1872.638	0.444	21	0.233	K.DAGVIAGLNVM*R.I
R5/RRR5-6/2	1676.163	1676.683	-909.098	0.458	1665.326	0.547	23	0.230	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/2	1215.971	1216.436	-383.490	0.426	1776.646	0.478	20	0.228	K.DAGVIAGLNVMR.I
R5/RRR5-6/2	1197.026	1197.277	-209.847	0.550	1743.227	0.492	18	0.228	R.FSDASVQSDIK.L
R5/RRR5-6/2	1309.240	1309.490	-191.300	0.395	1737.198	0.499	19	0.227	R.EIAEAYLGTTIK.N
R5/RRR5-6/3	1669.914	1669.929	-9.511	0.559	2017.232	0.402	27	0.224	R.ARFEELNMDLFRK.C
R5/RRR5-6/2	1217.068	1216.436	-303.772	0.581	1598.355	0.517	20	0.217	K.DAGVIAGLNVMR.I
R5/RRR5-6/2	1677.160	1676.683	285.467	0.493	1591.861	0.526	22	0.216	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/2	1437.730	1437.625	73.100	0.555	1573.480	0.518	17	0.212	R.VQQLLQDFFNGK.E
R5/RRR5-6/2	1232.065	1232.436	-301.398	0.552	1578.176	0.477	19	0.205	K.DAGVIAGLNVM*R.I
R5/RRR5-6/2	1309.300	1309.490	-145.563	0.371	1569.176	0.489	18	0.204	R.EIAEAYLGTTIK.N
R5/RRR5-6/2	1197.089	1197.277	-157.060	0.579	1418.318	0.487	18	0.191	R.FSDASVQSDIK.L
R5/RRR5-6/2	1596.501	1596.874	-234.183	0.556	1319.548	0.459	20	0.174	K.MREIAEAYLGTTIK.N
R5/RRR5-6/2	1374.995	1375.492	-362.844	0.473	1169.908	0.489	16	0.168	K.NALENYAYNM*R.N
R5/RRR5-1/2	1437.413	1437.625	-147.581	0.515	1289.915	0.434	16	0.166	R.VQQLLQDFFNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1596.184	1596.874	-1061.962	0.511	1387.280	0.384	20	0.166	K.MREIAEAYLGTTIK.N
R5/RRR5-6/2	1375.015	1375.492	-348.236	0.462	1152.067	0.483	16	0.166	K.NALENYAYNM*R.N
R5/RRR5-6/2	1596.281	1596.874	-1000.382	0.521	1359.071	0.376	21	0.163	K.MREIAEAYLGTTIK.N
R5/RRR5-6/2	1567.510	1566.844	-213.832	0.576	1024.489	0.451	22	0.154	K.QFAAEEISSMVLIK.M
R5/RRR5-6/3	1670.022	1669.929	55.373	0.493	1782.707	0.302	26	0.150	R.ARFEELNMDLFRK.C
R5/RRR5-6/3	1670.060	1669.929	78.245	0.530	1686.122	0.339	25	0.147	R.ARFEELNMDLFRK.C
R5/RRR5-6/2	1567.357	1566.844	-311.655	0.565	967.637	0.432	20	0.146	K.QFAAEEISSMVLIK.M
R5/RRR5-6/2	1868.610	1869.109	-267.766	0.507	785.558	0.495	18	0.142	R.FSDASVQSDIKLWPFK.V
R5/RRR5-3/2	1197.980	1197.277	-248.108	0.341	767.131	0.490	16	0.141	R.FSDASVQSDIK.L
R5/RRR5-6/2	1868.655	1869.109	-243.582	0.492	662.840	0.528	16	0.139	R.FSDASVQSDIKLWPFK.V
R5/RRR5-6/2	1868.603	1869.109	-808.463	0.488	620.105	0.518	16	0.136	R.FSDASVQSDIKLWPFK.V
R5/RRR5-6/2	1682.184	1681.830	210.666	0.427	624.681	0.449	21	0.136	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-6/2	1296.146	1295.492	-267.585	0.513	515.617	0.437	14	0.134	R.M*VNHFVQEFK.R
R5/RRR5-1/2	1681.115	1681.830	-1023.313	0.383	398.383	0.513	17	0.134	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-6/2	1294.623	1295.492	-1448.173	0.480	573.245	0.424	14	0.133	R.M*VNHFVQEFK.R
R5/RRR5-6/2	1331.511	1330.491	14.826	0.402	576.123	0.455	13	0.133	R.FEELNM*DLFR.K
R5/RRR5-6/2	1331.523	1330.491	23.929	0.443	485.296	0.438	13	0.132	R.FEELNM*DLFR.K
R5/RRR5-6/2	1582.181	1582.844	-1053.781	0.421	743.991	0.381	19	0.132	K.QFAAEEISSM*VLIK.M
R5/RRR5-5/2	1681.167	1681.830	-992.330	0.334	422.553	0.482	18	0.131	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-6/2	1682.464	1681.830	-218.506	0.416	329.484	0.489	15	0.131	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-6/2	1294.611	1295.492	-1457.454	0.438	618.512	0.392	14	0.131	R.M*VNHFVQEFK.R
R5/RRR5-6/2	1612.600	1612.873	-169.674	0.492	513.159	0.381	21	0.131	K.M*REIAEAYLGTTIK.N
R5/RRR5-1/2	1681.450	1681.830	-226.721	0.397	472.744	0.417	18	0.129	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-5/2	1681.261	1681.830	-936.491	0.354	476.012	0.417	19	0.129	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-6/2	1681.302	1681.830	-911.563	0.298	490.105	0.446	19	0.129	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-6/2	1582.299	1582.844	-979.110	0.473	821.247	0.321	20	0.128	K.QFAAEEISSM*VLIK.M
R5/RRR5-6/3	1676.799	1676.683	69.607	0.394	801.445	0.626	29	0.127	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/2	1329.957	1330.491	-1157.272	0.383	576.494	0.371	11	0.124	R.FEELNM*DLFR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1197.722	1197.277	372.750	0.265	442.032	0.410	12	0.122	R.FSDASVQSDIK.L
R5/RRR5-6/2	1581.632	1582.844	-1402.189	0.349	609.869	0.301	18	0.122	K.QFAAEEISSM*VLIK.M
R5/RRR5-6/2	1356.978	1357.571	-1177.973	0.333	935.798	0.261	16	0.122	K.ELEGICNPIIAK.M
R5/RRR5-6/2	1565.662	1566.844	-1397.814	0.408	637.711	0.263	20	0.122	K.QFAAEEISSMVLIK.M
R5/RRR5-2/2	1438.273	1437.625	-245.219	0.338	547.825	0.278	15	0.121	R.VQQLLQDFFNGK.E
R5/RRR5-6/2	1681.159	1681.830	-997.287	0.251	305.164	0.379	14	0.121	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-4/2	1681.806	1681.830	-14.459	0.360	228.970	0.344	13	0.121	-.NAVVTVPAYFNDSQR.-
R5/RRR5-6/3	1676.810	1676.683	75.959	0.442	810.106	0.579	30	0.120	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/2	1353.208	1353.463	-188.975	0.363	937.583	0.219	18	0.120	R.RFSDASVQSDIK.L
R5/RRR5-5/2	1680.478	1681.830	-1404.240	0.192	448.560	0.285	18	0.118	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-5/3	1676.497	1676.683	-111.133	0.416	679.150	0.596	28	0.115	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/3	1682.144	1681.830	187.044	0.348	1136.740	0.438	28	0.109	K.NAVVTVPAYFNDSQR.Q
R5/RRR5-6/3	1868.990	1869.109	-63.788	0.376	831.515	0.530	29	0.107	R.FSDASVQSDIKLWPFK.V
R5/RRR5-6/3	1676.956	1676.683	163.675	0.385	559.523	0.567	26	0.106	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/3	1968.526	1968.236	147.922	0.495	749.094	0.487	30	0.102	R.VQQLLQDFFNGKELCK.S
R5/RRR5-6/3	1969.160	1968.236	-38.595	0.495	647.262	0.501	27	0.101	R.VQQLLQDFFNGKELCK.S
R5/RRR5-6/3	1279.671	1279.492	139.669	0.436	380.357	0.512	17	0.099	R.MVNHFVQEFK.R
R5/RRR5-5/3	1676.906	1676.683	133.452	0.389	499.297	0.497	25	0.097	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-16/3	1676.665	1676.683	-10.787	0.371	532.531	0.494	24	0.096	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/3	1295.374	1295.492	-90.864	0.525	609.831	0.422	21	0.094	R.M*VNHFVQEFK.R
R5/RRR5-6/3	1295.503	1295.492	8.663	0.421	601.839	0.472	22	0.093	R.M*VNHFVQEFK.R
R5/RRR5-14/3	1676.464	1676.683	-130.854	0.370	471.479	0.503	24	0.093	-.ATAGDTHLGGEDFDNR.-
R5/RRR5-6/3	1279.468	1279.492	-19.208	0.435	613.981	0.449	20	0.093	R.MVNHFVQEFK.R
R5/RRR5-6/3	1868.335	1869.109	-952.660	0.394	738.791	0.453	26	0.092	R.FSDASVQSDIKLWPFK.V
R5/RRR5-5/3	1676.370	1676.683	-187.392	0.375	406.047	0.430	23	0.091	K.ATAGDTHLGGEDFDNR.M
R5/RRR5-6/3	1295.285	1295.492	-160.488	0.429	488.879	0.420	20	0.091	R.M*VNHFVQEFK.R
R5/RRR5-6/3	1868.326	1869.109	-957.382	0.404	552.002	0.475	23	0.089	R.FSDASVQSDIKLWPFK.V
R5/RRR5-8/3	1676.156	1676.683	-913.676	0.351	436.651	0.422	23	0.089	K.ATAGDTHLGGEDFDNR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/3	1685.734	1685.929	-116.197	0.434	529.356	0.402	24	0.089	R.ARFEELNM*DLFRK.C
R5/RRR5-6/3	1542.279	1541.757	-310.578	0.509	1202.486	0.281	22	0.087	R.ARFEELNMDLFR.K
R5/RRR5-6/3	1279.604	1279.492	87.720	0.428	397.121	0.488	17	0.087	-.MVNHFVQEFK.-
R5/RRR5-6/3	1969.916	1968.236	-162.700	0.352	350.677	0.355	23	0.087	R.VQQLLQDFFNGKELCK.S
R5/RRR5-6/3	1968.584	1968.236	177.585	0.373	728.011	0.396	27	0.086	R.VQQLLQDFFNGKELCK.S
R5/RRR5-6/3	1685.930	1685.929	0.485	0.441	472.904	0.317	21	0.084	R.ARFEELNM*DLFRK.C
R5/RRR5-7/3	1676.747	1676.683	38.393	0.424	457.678	0.392	22	0.084	-.ATAGDTHLGGEDFDNR.-
R5/RRR5-6/3	1685.335	1685.929	-948.264	0.470	656.109	0.310	27	0.082	R.ARFEELNM*DLFRK.C
R5/RRR5-6/3	1968.235	1968.236	-0.511	0.306	350.073	0.366	21	0.081	-.VQQLLQDFFNGKELCK.-
R5/RRR5-6/3	1968.159	1968.236	-38.863	0.417	351.209	0.385	21	0.080	-.VQQLLQDFFNGKELCK.-
R5/RRR5-6/3	1582.417	1582.844	-270.617	0.314	1038.016	0.291	25	0.078	K.QFAAEEISSM*VLIK.M
R5/RRR5-6/3	1557.137	1557.756	-1042.609	0.448	1284.445	0.202	22	0.078	R.ARFEELNM*DLFR.K
R5/RRR5-6/3	1582.716	1582.844	-81.076	0.394	940.898	0.175	23	0.063	K.QFAAEEISSM*VLIK.M
R5/RRR5-6/3	1541.381	1541.757	-244.115	0.392	618.421	0.330	18	0.058	-.ARFEELNMDLFR.-
R5/RRR5-6/3	1582.965	1582.844	76.955	0.281	895.094	0.090	20	0.053	K.QFAAEEISSM*VLIK.M
R5/RRR5-5/1	963.468	964.097	-1695.996	0.312	947.792	0.179	12	0.484	R.FQELGLEK.G
R5/RRR5-5/3	1928.151	1927.150	0.431	0.562	2546.222	0.587	37	0.443	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/3	1928.034	1927.150	-60.437	0.588	2381.799	0.594	37	0.397	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-1/3	1928.583	1927.150	225.263	0.527	2254.735	0.612	34	0.376	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-1/3	1928.249	1927.150	51.100	0.569	2135.594	0.579	35	0.325	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/1	963.581	964.097	-1578.072	0.337	756.579	0.166	11	0.300	R.FQELGLEK.G
R5/RRR5-5/1	963.478	964.097	-1685.176	0.311	744.817	0.171	11	0.294	R.FQELGLEK.G
R5/RRR5-5/3	1928.173	1927.150	11.956	0.576	2078.656	0.519	35	0.282	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-4/3	1927.136	1927.150	-7.257	0.512	1910.563	0.572	33	0.272	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/2	1863.712	1864.118	-218.082	0.602	1814.044	0.573	23	0.258	K.MFDLIEQYNLNGHIR.W
R5/RRR5-3/3	1927.127	1927.150	-11.926	0.531	1844.375	0.572	33	0.258	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-4/3	1927.208	1927.150	30.099	0.528	1876.075	0.554	34	0.256	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/2	1879.560	1880.117	-830.914	0.614	1749.343	0.574	25	0.251	K.M*FDLIEQYNLNGHIR.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/3	1927.502	1927.150	182.926	0.527	1697.787	0.606	32	0.243	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/2	1234.752	1235.414	-1350.802	0.476	1694.512	0.496	19	0.223	K.NLTGLVELYGR.N
R5/RRR5-1/3	1927.032	1927.150	-61.485	0.507	1577.031	0.578	31	0.211	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-4/3	1926.382	1927.150	-920.903	0.506	1615.219	0.558	30	0.210	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/2	1416.439	1416.712	-193.678	0.488	1417.917	0.504	18	0.193	R.LMTLTGVYGFWK.Y
R5/RRR5-4/2	1235.162	1235.414	-205.251	0.448	1386.272	0.495	18	0.189	K.NLTGLVELYGR.N
R5/RRR5-5/2	1267.793	1268.491	-1343.024	0.454	1348.515	0.514	17	0.188	R.IKQQGLNITPR.I
R5/RRR5-5/2	1926.530	1927.150	-843.385	0.561	1086.767	0.639	24	0.188	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-2/3	1927.203	1927.150	27.431	0.402	1700.214	0.449	32	0.186	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/2	1748.212	1747.949	150.933	0.537	1033.067	0.638	25	0.185	R.TM*ASTVPLAVEGEPSNK.-
R5/RRR5-5/2	1267.784	1268.491	-1350.470	0.462	1311.236	0.506	16	0.183	R.IKQQGLNITPR.I
R5/RRR5-5/2	1143.857	1144.350	-431.751	0.393	1683.829	0.311	18	0.182	R.SLSALQGALRK.A
R5/RRR5-5/2	1235.220	1235.414	-158.258	0.540	1312.270	0.484	17	0.180	K.NLTGLVELYGR.N
R5/RRR5-5/2	1927.459	1927.150	160.418	0.542	1003.307	0.626	23	0.178	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/2	1433.258	1432.712	-317.494	0.532	1329.606	0.460	18	0.176	R.LM*TLTGVYGFWK.Y
R5/RRR5-5/2	1267.610	1268.491	-1488.391	0.430	1171.776	0.519	16	0.173	R.IKQQGLNITPR.I
R5/RRR5-5/2	1748.469	1747.949	-275.191	0.510	912.853	0.625	23	0.172	R.TM*ASTVPLAVEGEPSNK.-
R5/RRR5-4/2	1926.561	1927.150	-827.548	0.530	925.913	0.621	22	0.171	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-1/2	1206.064	1205.349	-236.293	0.538	1145.974	0.462	19	0.165	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1747.430	1747.949	-871.832	0.458	915.712	0.580	23	0.164	R.TM*ASTVPLAVEGEPSNK.-
R5/RRR5-5/2	1205.590	1205.349	200.514	0.519	1143.595	0.455	18	0.163	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1205.409	1205.349	50.420	0.461	1095.761	0.473	17	0.161	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1926.606	1927.150	-804.205	0.518	715.691	0.644	20	0.159	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-3/3	1926.600	1927.150	-806.979	0.451	1302.239	0.544	29	0.159	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-5/2	1416.227	1416.712	-343.702	0.516	858.781	0.540	18	0.158	R.LMTLTGVYGFWK.Y
R5/RRR5-5/2	1204.557	1205.349	-1492.000	0.445	1097.086	0.435	18	0.156	K.SIGNGVQFLNR.H
R5/RRR5-1/2	1204.984	1205.349	-303.261	0.457	1012.104	0.457	18	0.155	K.SIGNGVQFLNR.H
R5/RRR5-1/2	1016.102	1016.177	-74.179	0.393	1521.086	0.236	17	0.154	R.SLSALQGALR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1204.724	1205.349	-1352.457	0.466	988.137	0.457	17	0.153	K.SIGNGVQFLNR.H
R5/RRR5-3/2	1016.018	1016.177	-157.214	0.418	1567.901	0.215	16	0.153	R.SLSALQGALR.K
R5/RRR5-3/2	1234.843	1235.414	-1276.041	0.420	923.107	0.503	14	0.152	K.NLTGLVELYGR.N
R5/RRR5-5/2	1205.853	1205.349	-411.787	0.424	1242.280	0.343	17	0.150	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1416.107	1416.712	-1136.655	0.447	922.187	0.467	18	0.150	R.LMTLTGVYGFWK.Y
R5/RRR5-5/2	1022.173	1022.094	78.144	0.411	1541.925	0.204	15	0.150	K.DGAFEDVLR.S
R5/RRR5-5/2	1235.231	1235.414	-148.939	0.426	900.988	0.478	16	0.150	K.NLTGLVELYGR.N
R5/RRR5-5/2	1416.034	1416.712	-1188.939	0.446	851.165	0.472	18	0.148	R.LMTLTGVYGFWK.Y
R5/RRR5-5/2	1206.175	1205.349	-143.899	0.431	1196.622	0.343	17	0.148	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1015.954	1016.177	-219.529	0.474	1520.966	0.213	16	0.147	R.SLSALQGALR.K
R5/RRR5-5/2	1226.175	1226.406	-188.582	0.367	744.794	0.535	16	0.147	R.VVHGIDVFDPK.F
R5/RRR5-5/2	1226.103	1226.406	-247.510	0.359	832.219	0.499	16	0.146	R.VVHGIDVFDPK.F
R5/RRR5-5/2	1205.101	1205.349	-206.002	0.471	900.223	0.435	17	0.146	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1225.465	1226.406	-1588.834	0.351	782.499	0.518	16	0.146	R.VVHGIDVFDPK.F
R5/RRR5-1/2	1206.071	1205.349	-231.114	0.433	749.952	0.488	16	0.145	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1193.114	1193.444	-277.627	0.364	727.812	0.516	16	0.145	R.NKPIIFSM*AR.L
R5/RRR5-4/2	1226.932	1226.406	-387.349	0.344	810.187	0.495	17	0.145	R.VVHGIDVFDPK.F
R5/RRR5-1/2	1204.627	1205.349	-1433.674	0.444	808.934	0.447	16	0.143	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1416.114	1416.712	-1132.154	0.389	807.855	0.454	18	0.142	R.LMTLTGVYGFWK.Y
R5/RRR5-2/2	1016.172	1016.177	-4.893	0.395	1443.740	0.197	16	0.142	R.SLSALQGALR.K
R5/RRR5-4/2	1206.061	1205.349	-239.339	0.427	713.472	0.465	16	0.142	K.SIGNGVQFLNR.H
R5/RRR5-3/2	1016.677	1016.177	493.080	0.426	1410.775	0.203	16	0.140	R.SLSALQGALR.K
R5/RRR5-4/2	1390.087	1390.518	-311.411	0.388	415.280	0.542	20	0.140	R.LLPDATGTTCGQR.L
R5/RRR5-3/2	1204.737	1205.349	-1341.670	0.402	628.744	0.473	15	0.139	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1415.986	1415.574	291.256	0.430	738.143	0.440	16	0.138	K.TKYPNSDLYWK.K
R5/RRR5-5/2	1144.000	1144.408	-358.064	0.434	814.265	0.393	14	0.137	R.YLEMLYALK.Y
R5/RRR5-5/2	1015.433	1016.177	-1722.497	0.390	1374.782	0.193	16	0.137	R.SLSALQGALR.K
R5/RRR5-3/2	1204.549	1205.349	-1498.820	0.424	804.911	0.395	16	0.137	K.SIGNGVQFLNR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1015.685	1016.177	-485.270	0.359	1350.519	0.191	16	0.136	R.SLSALQGALR.K
R5/RRR5-5/2	1732.196	1731.949	142.807	0.488	506.698	0.505	19	0.136	R.TMASTVPLAVEGEPSNK.-
R5/RRR5-5/2	1015.590	1016.177	-1567.195	0.396	1275.826	0.220	16	0.135	R.SLSALQGALR.K
R5/RRR5-4/2	1226.343	1226.406	-51.777	0.343	738.497	0.438	15	0.135	R.VVHGIDVFDPK.F
R5/RRR5-5/2	1138.439	1139.329	-1664.638	0.417	1240.002	0.231	15	0.135	R.AM*ENEM*LLR.I
R5/RRR5-5/2	1192.486	1193.444	-1646.819	0.312	577.657	0.499	14	0.135	R.NKPIIFSM*AR.L
R5/RRR5-1/2	1205.695	1205.349	288.640	0.394	681.976	0.414	15	0.134	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1159.861	1160.408	-1337.125	0.378	782.229	0.378	14	0.134	R.YLEM*LYALK.Y
R5/RRR5-5/2	1205.241	1205.349	-89.357	0.455	633.399	0.409	15	0.134	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1390.014	1390.518	-1085.412	0.327	487.711	0.482	21	0.134	R.LLPDATGTTCGQR.L
R5/RRR5-4/2	1389.898	1390.518	-1169.629	0.334	365.217	0.509	19	0.133	R.LLPDATGTTCGQR.L
R5/RRR5-5/2	1205.617	1205.349	223.258	0.422	869.203	0.353	15	0.133	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1138.697	1139.329	-1437.710	0.434	826.873	0.351	14	0.133	R.AM*ENEM*LLR.I
R5/RRR5-5/2	1160.144	1160.408	-228.358	0.446	724.707	0.365	14	0.133	R.YLEM*LYALK.Y
R5/RRR5-5/2	1263.140	1263.425	-226.294	0.402	657.572	0.411	15	0.133	K.LKDGAFEDVLR.S
R5/RRR5-2/2	1204.937	1205.349	-342.191	0.380	648.856	0.401	15	0.133	K.SIGNGVQFLNR.H
R5/RRR5-1/2	1390.105	1390.518	-298.283	0.323	517.274	0.462	21	0.132	R.LLPDATGTTCGQR.L
R5/RRR5-4/2	1416.424	1416.712	-204.053	0.383	527.421	0.459	14	0.132	R.LMTLTGVYGFWK.Y
R5/RRR5-4/2	1205.446	1205.349	80.787	0.378	650.043	0.395	15	0.132	K.SIGNGVQFLNR.H
R5/RRR5-1/2	1389.921	1390.518	-1152.432	0.332	367.644	0.481	19	0.132	R.LLPDATGTTCGQR.L
R5/RRR5-5/2	1416.396	1416.712	-223.679	0.366	448.759	0.524	11	0.132	R.LMTLTGVYGFWK.Y
R5/RRR5-5/2	1262.562	1263.425	-1479.893	0.436	736.895	0.361	16	0.131	K.LKDGAFEDVLR.S
R5/RRR5-5/2	1205.135	1205.349	-177.753	0.346	553.708	0.449	12	0.131	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1177.064	1177.445	-324.289	0.379	497.001	0.401	14	0.131	R.NKPIIFSMAR.L
R5/RRR5-5/2	1415.592	1415.574	12.575	0.491	592.516	0.412	14	0.130	K.TKYPNSDLYWK.K
R5/RRR5-5/2	1414.861	1415.574	-1214.327	0.367	647.041	0.401	15	0.130	K.TKYPNSDLYWK.K
R5/RRR5-1/2	1206.233	1205.349	-96.084	0.359	722.724	0.347	16	0.130	K.SIGNGVQFLNR.H
R5/RRR5-5/2	1021.687	1022.094	-398.653	0.355	1284.697	0.174	14	0.130	K.DGAFEDVLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1732.345	1731.949	229.232	0.449	463.377	0.457	18	0.130	R.TMASTVPLAVEGEPSNK.-
R5/RRR5-5/3	1415.897	1415.574	228.658	0.520	1269.649	0.455	25	0.130	K.TKYPNSDLYWK.K
R5/RRR5-5/2	1262.890	1263.425	-1218.811	0.380	609.731	0.386	15	0.129	K.LKDGAFEDVLR.S
R5/RRR5-5/2	1140.194	1139.329	-118.350	0.503	858.599	0.309	14	0.129	R.AM*ENEM*LLR.I
R5/RRR5-5/2	1144.025	1144.408	-335.795	0.399	764.401	0.303	15	0.128	R.YLEMLYALK.Y
R5/RRR5-5/2	1193.053	1193.444	-328.543	0.262	628.618	0.417	15	0.128	R.NKPIIFSM*AR.L
R5/RRR5-1/2	1235.254	1235.414	-130.302	0.320	687.607	0.390	13	0.128	K.NLTGLVELYGR.N
R5/RRR5-5/3	1584.763	1584.816	-33.967	0.518	950.073	0.564	28	0.127	K.M*GVTHCTIAHALEK.T
R5/RRR5-5/2	1178.224	1177.445	-188.048	0.328	593.055	0.337	15	0.127	R.NKPIIFSMAR.L
R5/RRR5-3/2	1015.937	1016.177	-236.405	0.405	1147.094	0.195	16	0.127	R.SLSALQGALR.K
R5/RRR5-2/3	1926.937	1927.150	-111.049	0.438	974.033	0.548	26	0.126	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-1/2	1263.043	1263.425	-303.474	0.334	714.002	0.338	15	0.126	K.LKDGAFEDVLR.S
R5/RRR5-4/2	1206.365	1205.349	13.640	0.308	395.978	0.354	13	0.126	K.SIGNGVQFLNR.H
R5/RRR5-5/3	1584.714	1584.816	-64.911	0.544	821.597	0.599	26	0.126	K.M*GVTHCTIAHALEK.T
R5/RRR5-1/2	1205.253	1205.349	-79.807	0.353	515.943	0.341	13	0.125	K.SIGNGVQFLNR.H
R5/RRR5-1/2	1226.173	1226.406	-190.280	0.275	796.703	0.313	16	0.125	R.VVHGIDVFDPK.F
R5/RRR5-5/2	1143.518	1144.408	-1657.830	0.368	643.727	0.368	13	0.125	-.YLEMLYALK.-
R5/RRR5-1/2	1417.540	1416.712	-121.665	0.402	429.774	0.360	13	0.125	R.LMTLTGVYGFWK.Y
R5/RRR5-4/2	1193.412	1193.444	-27.332	0.247	608.539	0.365	15	0.124	R.NKPIIFSM*AR.L
R5/RRR5-1/2	1206.068	1205.349	-233.044	0.298	351.589	0.286	12	0.124	K.SIGNGVQFLNR.H
R5/RRR5-4/2	1431.508	1432.712	-1543.609	0.285	670.139	0.325	15	0.124	R.LM*TLTGVYGFWK.Y
R5/RRR5-5/2	1730.778	1731.949	-1258.521	0.292	442.363	0.411	18	0.124	R.TMASTVPLAVEGEPSNK.-
R5/RRR5-1/2	1747.532	1747.949	-239.046	0.406	384.928	0.434	15	0.123	-.TM*ASTVPLAVEGEPSNK.-
R5/RRR5-5/2	1177.013	1177.445	-368.305	0.278	580.811	0.271	15	0.122	R.NKPIIFSMAR.L
R5/RRR5-1/2	1192.713	1193.444	-1456.084	0.201	671.854	0.346	14	0.121	R.NKPIIFSM*AR.L
R5/RRR5-5/3	1415.580	1415.574	3.873	0.519	1088.509	0.486	23	0.121	K.TKYPNSDLYWK.K
R5/RRR5-5/2	1021.429	1022.094	-1634.111	0.338	910.055	0.216	13	0.121	K.DGAFEDVLR.S
R5/RRR5-2/2	1416.809	1416.712	68.390	0.302	447.844	0.284	12	0.118	-.LMTLTGVYGFWK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1016.834	1016.177	-337.702	0.373	962.075	0.154	15	0.118	R.SLSALQGALR.K
R5/RRR5-4/2	1234.853	1235.414	-1268.297	0.283	470.276	0.279	12	0.116	-.NLTGLVELYGR.-
R5/RRR5-5/2	1144.188	1144.350	-141.850	0.286	533.884	0.222	13	0.115	-.SLSALQGALRK.-
R5/RRR5-5/2	1263.547	1263.425	97.228	0.249	702.180	0.199	12	0.114	K.LKDGAFEDVLR.S
R5/RRR5-5/3	1584.955	1584.816	87.937	0.520	786.844	0.543	26	0.112	K.M*GVTHCTIAHALEK.T
R5/RRR5-5/3	1415.008	1415.574	-1110.031	0.493	901.486	0.488	23	0.108	K.TKYPNSDLYWK.K
R5/RRR5-3/3	1263.464	1263.425	31.182	0.472	1605.619	0.211	23	0.103	-.LKDGAFEDVLR.-
R5/RRR5-5/3	1879.957	1880.117	-85.299	0.485	798.944	0.477	25	0.103	K.M*FDLIEQYNLNGHIR.W
R5/RRR5-5/3	1881.665	1880.117	-241.059	0.472	739.162	0.488	26	0.102	K.M*FDLIEQYNLNGHIR.W
R5/RRR5-5/3	1864.858	1864.118	-139.399	0.450	468.238	0.512	24	0.100	K.MFDLIEQYNLNGHIR.W
R5/RRR5-5/3	1263.707	1263.425	224.465	0.544	1467.795	0.263	23	0.100	K.LKDGAFEDVLR.S
R5/RRR5-5/3	1568.376	1568.817	-282.108	0.494	805.941	0.443	25	0.096	K.MGVTHCTIAHALEK.T
R5/RRR5-2/3	1262.614	1263.425	-1438.096	0.426	1306.935	0.294	23	0.095	K.LKDGAFEDVLR.S
R5/RRR5-5/3	1262.890	1263.425	-1219.064	0.492	1496.700	0.225	24	0.094	K.LKDGAFEDVLR.S
R5/RRR5-4/3	1415.244	1415.574	-234.382	0.431	732.177	0.455	21	0.094	K.TKYPNSDLYWK.K
R5/RRR5-5/3	1879.937	1880.117	-96.241	0.392	835.392	0.398	27	0.090	K.M*FDLIEQYNLNGHIR.W
R5/RRR5-5/3	1863.420	1864.118	-913.876	0.327	428.736	0.439	21	0.090	K.MFDLIEQYNLNGHIR.W
R5/RRR5-5/3	1864.376	1864.118	138.782	0.340	606.837	0.438	23	0.090	K.MFDLIEQYNLNGHIR.W
R5/RRR5-4/3	1263.306	1263.425	-93.983	0.497	1261.875	0.278	22	0.089	-.LKDGAFEDVLR.-
R5/RRR5-2/3	1263.701	1263.425	219.380	0.434	1327.982	0.248	22	0.089	-.LKDGAFEDVLR.-
R5/RRR5-1/3	1268.213	1268.491	-220.042	0.493	1119.970	0.308	22	0.088	R.IKQQGLNITPR.I
R5/RRR5-5/3	1879.988	1880.117	-68.885	0.367	699.240	0.392	23	0.086	K.M*FDLIEQYNLNGHIR.W
R5/RRR5-1/3	1263.273	1263.425	-120.590	0.487	1145.651	0.292	21	0.086	K.LKDGAFEDVLR.S
R5/RRR5-2/3	1926.810	1927.150	-177.301	0.322	611.347	0.404	21	0.085	R.IGDSLSAHPNELVAVFTR.L
R5/RRR5-1/3	1263.796	1263.425	294.494	0.482	1304.566	0.240	22	0.085	-.LKDGAFEDVLR.-
R5/RRR5-5/3	1864.492	1864.118	201.125	0.366	452.417	0.327	22	0.084	K.MFDLIEQYNLNGHIR.W
R5/RRR5-5/3	1863.752	1864.118	-196.997	0.278	439.749	0.375	21	0.084	K.MFDLIEQYNLNGHIR.W
R5/RRR5-5/3	1263.225	1263.425	-158.540	0.503	1206.527	0.235	22	0.079	K.LKDGAFEDVLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1881.971	1880.117	-78.051	0.359	823.277	0.313	24	0.078	K.M*FDLIEQYNLNGHIR.W
R5/RRR5-4/3	1263.579	1263.425	122.311	0.498	1078.111	0.280	21	0.076	-.LKDGAFEDVLR.-
R5/RRR5-4/3	1177.511	1177.445	56.490	0.377	957.398	0.220	18	0.070	R.NKPIIFSMAR.L
R5/RRR5-2/3	1269.077	1268.491	-326.740	0.464	974.917	0.207	21	0.068	-.IKQQGLNITPR.-
R5/RRR5-5/3	1177.486	1177.445	34.655	0.341	696.477	0.260	15	0.068	-.NKPIIFSMAR.-
R5/RRR5-5/3	1192.626	1193.444	-1528.988	0.324	995.441	0.207	20	0.068	R.NKPIIFSM*AR.L
R5/RRR5-5/3	1176.657	1177.445	-1524.006	0.357	898.300	0.214	17	0.068	-.NKPIIFSMAR.-
R5/RRR5-5/3	1177.320	1177.445	-106.047	0.335	924.154	0.208	18	0.067	R.NKPIIFSMAR.L
R5/RRR5-2/3	1267.931	1268.491	-1234.206	0.339	881.021	0.199	20	0.066	-.IKQQGLNITPR.-
R5/RRR5-5/3	1268.802	1268.491	246.289	0.439	803.236	0.159	19	0.057	-.IKQQGLNITPR.-
R5/RRR5-5/3	1269.642	1268.491	119.364	0.428	840.798	0.081	20	0.057	-.IKQQGLNITPR.-
R5/RRR5-1/3	1263.676	1263.425	199.764	0.509	994.272	0.245	20	0.056	-.LKDGAFEDVLR.-
R5/RRR5-5/3	1269.412	1268.491	-62.618	0.397	766.621	0.125	19	0.055	-.IKQQGLNITPR.-
R5/RRR5-11/2	1760.384	1760.969	-903.023	0.607	2974.173	0.530	24	0.466	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/2	1761.114	1760.969	82.411	0.601	2735.895	0.449	24	0.380	R.FKDIFQEVYEAGWK.S
R5/RRR5-10/3	1777.710	1777.908	-111.693	0.551	2574.978	0.428	34	0.372	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1762.562	1760.969	-231.917	0.624	2528.615	0.529	23	0.366	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/2	1761.769	1760.969	-114.086	0.601	2520.072	0.516	23	0.360	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/2	1760.448	1760.969	-866.478	0.592	2466.476	0.513	23	0.349	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/3	1777.498	1777.908	-231.767	0.588	2333.393	0.464	34	0.323	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1436.970	1436.569	279.588	0.571	2168.201	0.572	20	0.313	R.AFAEASM*TTAYEK.K
R5/RRR5-11/2	1321.069	1321.453	-291.349	0.528	2050.647	0.631	22	0.312	K.LEAACVGTVESGK.M
R5/RRR5-11/2	1436.085	1436.569	-337.757	0.542	2170.090	0.549	20	0.306	R.AFAEASM*TTAYEK.K
R5/RRR5-10/2	1436.038	1436.569	-1069.555	0.499	2144.097	0.555	20	0.304	R.AFAEASM*TTAYEK.K
R5/RRR5-10/2	1321.006	1321.453	-339.188	0.515	2036.052	0.599	22	0.300	K.LEAACVGTVESGK.M
R5/RRR5-11/2	1436.215	1436.569	-247.021	0.507	2143.938	0.538	20	0.298	R.AFAEASM*TTAYEK.K
R5/RRR5-10/2	1436.051	1436.569	-1060.252	0.481	2121.872	0.542	20	0.296	R.AFAEASM*TTAYEK.K
R5/RRR5-10/2	1322.000	1321.453	-343.379	0.529	1863.980	0.633	21	0.282	K.LEAACVGTVESGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1321.119	1321.453	-253.526	0.520	1887.556	0.602	21	0.277	K.LEAACVGTVESGK.M
R5/RRR5-10/2	1437.189	1436.569	-265.596	0.568	1909.318	0.572	20	0.271	R.AFAEASM*TTAYEK.K
R5/RRR5-11/2	1321.030	1321.453	-321.109	0.513	1903.302	0.568	22	0.270	K.LEAACVGTVESGK.M
R5/RRR5-11/2	1486.468	1485.622	-103.916	0.510	2123.036	0.418	19	0.262	K.DIFQEVYEAGWK.S
R5/RRR5-11/2	1496.335	1496.694	-240.368	0.554	1939.247	0.463	23	0.246	K.DLALLIHGSSNVTR.S
R5/RRR5-11/2	1777.408	1777.908	-282.126	0.563	1907.895	0.478	25	0.244	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1798.512	1798.934	-235.314	0.513	1893.022	0.474	24	0.241	K.GGETSTNSIASIFAWTR.G
R5/RRR5-10/2	1760.476	1760.969	-280.805	0.434	2057.844	0.374	20	0.240	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/3	1778.870	1777.908	-21.524	0.552	1828.786	0.525	30	0.239	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1320.552	1321.453	-1443.369	0.451	1710.048	0.555	21	0.238	K.LEAACVGTVESGK.M
R5/RRR5-10/3	1778.060	1777.908	85.612	0.512	1920.723	0.460	31	0.231	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1798.480	1798.934	-253.495	0.480	1808.853	0.474	23	0.229	K.GGETSTNSIASIFAWTR.G
R5/RRR5-10/2	1799.425	1798.934	273.487	0.525	1788.580	0.484	22	0.228	K.GGETSTNSIASIFAWTR.G
R5/RRR5-11/2	1420.018	1420.570	-1095.673	0.496	1672.856	0.529	19	0.227	R.AFAEASMTTAYEK.K
R5/RRR5-11/2	1419.951	1420.570	-1143.321	0.495	1697.595	0.509	19	0.225	R.AFAEASMTTAYEK.K
R5/RRR5-10/2	1777.481	1777.908	-241.198	0.563	1743.541	0.491	24	0.225	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1777.370	1777.908	-868.010	0.535	1653.384	0.523	24	0.222	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1777.425	1777.908	-272.548	0.578	1666.290	0.514	24	0.221	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/2	1798.573	1798.934	-201.269	0.500	1701.798	0.495	22	0.220	K.GGETSTNSIASIFAWTR.G
R5/RRR5-10/2	1777.566	1777.908	-193.247	0.572	1617.941	0.502	24	0.213	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-10/2	1777.507	1777.908	-226.178	0.554	1641.217	0.483	24	0.211	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-11/3	1777.681	1777.908	-128.018	0.557	1903.856	0.407	29	0.206	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-10/2	1496.306	1496.694	-259.765	0.525	1617.117	0.448	23	0.203	K.DLALLIHGSSNVTR.S
R5/RRR5-11/2	1485.532	1485.622	-60.711	0.425	1886.777	0.296	18	0.200	K.DIFQEVYEAGWK.S
R5/RRR5-10/2	1798.467	1798.934	-260.713	0.470	1604.646	0.442	21	0.196	K.GGETSTNSIASIFAWTR.G
R5/RRR5-10/2	1496.270	1496.694	-284.320	0.513	1467.543	0.487	22	0.195	K.DLALLIHGSSNVTR.S
R5/RRR5-10/2	1496.235	1496.694	-307.566	0.493	1434.267	0.465	22	0.187	K.DLALLIHGSSNVTR.S
R5/RRR5-11/2	1057.130	1057.226	-91.105	0.474	1623.638	0.331	18	0.179	R.ATDAVLKGPGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1057.070	1057.226	-147.981	0.433	1590.451	0.289	18	0.168	R.ATDAVLKGPGK.L
R5/RRR5-11/3	1760.710	1760.969	-147.436	0.473	1686.725	0.391	28	0.166	R.FKDIFQEVYEAGWK.S
R5/RRR5-10/2	1137.063	1136.285	-195.070	0.481	1341.873	0.386	15	0.165	K.YYDLGVLHR.D
R5/RRR5-10/2	1136.267	1136.285	-15.151	0.430	1273.964	0.419	15	0.165	K.YYDLGVLHR.D
R5/RRR5-11/2	1269.037	1268.505	-369.550	0.508	973.497	0.533	18	0.165	R.LIDDM*VAYALK.S
R5/RRR5-11/2	1251.900	1252.505	-1286.431	0.524	1061.600	0.466	18	0.160	R.LIDDMVAYALK.S
R5/RRR5-11/2	1419.548	1420.570	-1428.445	0.361	1300.369	0.378	19	0.159	R.AFAEASMTTAYEK.K
R5/RRR5-11/3	1760.780	1760.969	-107.482	0.516	1590.155	0.410	29	0.157	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/2	1252.163	1252.505	-274.430	0.514	1014.628	0.462	18	0.156	R.LIDDMVAYALK.S
R5/RRR5-11/2	1268.180	1268.505	-256.649	0.482	954.270	0.471	18	0.154	R.LIDDM*VAYALK.S
R5/RRR5-10/2	1252.341	1252.505	-131.751	0.411	1135.486	0.406	18	0.154	R.LIDDMVAYALK.S
R5/RRR5-11/2	1268.162	1268.505	-271.231	0.466	953.109	0.466	18	0.153	R.LIDDM*VAYALK.S
R5/RRR5-11/2	1056.732	1057.226	-468.390	0.407	1197.136	0.361	16	0.149	R.ATDAVLKGPGK.L
R5/RRR5-10/2	1268.114	1268.505	-308.702	0.430	935.029	0.438	18	0.148	R.LIDDM*VAYALK.S
R5/RRR5-1/2	1496.075	1496.694	-1085.228	0.405	1077.668	0.394	19	0.146	K.DLALLIHGSSNVTR.S
R5/RRR5-11/2	993.383	994.045	-1678.584	0.384	730.550	0.498	12	0.143	R.HAFGDQYR.C
R5/RRR5-11/3	1761.786	1760.969	-104.224	0.559	1584.958	0.368	30	0.143	R.FKDIFQEVYEAGWK.S
R5/RRR5-10/2	1158.050	1157.251	-173.667	0.412	949.527	0.406	15	0.143	K.SEGGYVWACK.N
R5/RRR5-11/2	993.547	994.045	-502.922	0.355	677.768	0.481	12	0.138	R.HAFGDQYR.C
R5/RRR5-11/2	993.594	994.045	-455.457	0.364	713.923	0.441	12	0.136	R.HAFGDQYR.C
R5/RRR5-10/2	1268.000	1268.505	-1189.925	0.386	786.046	0.400	16	0.136	R.LIDDM*VAYALK.S
R5/RRR5-10/3	1777.492	1777.908	-234.867	0.534	1380.115	0.425	27	0.134	R.DATDDKVTVEAAEATLK.Y
R5/RRR5-10/2	1380.771	1379.504	193.962	0.396	832.739	0.398	14	0.132	K.FEAAGIWYEHR.L
R5/RRR5-10/2	1797.242	1798.934	-2060.404	0.283	1116.269	0.280	18	0.131	K.GGETSTNSIASIFAWTR.G
R5/RRR5-10/2	1157.275	1157.251	21.201	0.360	697.595	0.379	13	0.128	K.SEGGYVWACK.N
R5/RRR5-10/2	1132.660	1132.289	328.115	0.309	622.934	0.414	13	0.126	K.VTVEAAEATLK.Y
R5/RRR5-10/2	1158.135	1157.251	-100.709	0.374	710.391	0.313	14	0.125	K.SEGGYVWACK.N
R5/RRR5-10/2	1577.830	1577.888	-37.372	0.494	857.758	0.327	16	0.124	K.DKLIFPFLDLDIK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1799.081	1798.934	82.101	0.296	798.830	0.300	19	0.122	K.GGETSTNSIASIFAWTR.G
R5/RRR5-10/2	1132.479	1132.289	167.727	0.279	393.847	0.395	13	0.121	K.VTVEAAEATLK.Y
R5/RRR5-10/2	1268.351	1268.505	-121.083	0.295	492.294	0.280	13	0.121	R.LIDDM*VAYALK.S
R5/RRR5-8/2	1798.017	1798.934	-1069.615	0.301	574.277	0.272	16	0.117	K.GGETSTNSIASIFAWTR.G
R5/RRR5-10/2	1799.149	1798.934	119.799	0.345	575.286	0.210	16	0.114	K.GGETSTNSIASIFAWTR.G
R5/RRR5-11/3	1594.894	1594.755	87.844	0.570	1007.943	0.458	27	0.111	K.SKFEAAGIWYEHR.L
R5/RRR5-11/3	1760.820	1760.969	-85.159	0.352	1062.914	0.413	25	0.102	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/3	1594.053	1594.755	-1070.494	0.530	763.058	0.470	25	0.100	K.SKFEAAGIWYEHR.L
R5/RRR5-11/3	1594.237	1594.755	-954.941	0.487	903.347	0.437	26	0.099	K.SKFEAAGIWYEHR.L
R5/RRR5-10/3	1761.216	1760.969	140.411	0.467	1227.194	0.329	27	0.099	R.FKDIFQEVYEAGWK.S
R5/RRR5-11/2	1918.612	1918.175	228.228	0.636	2932.377	0.569	24	0.471	K.SLVEEDKLELATSLIEK.A
R5/RRR5-11/2	1917.613	1918.175	-817.107	0.618	2837.880	0.587	25	0.457	K.SLVEEDKLELATSLIEK.A
R5/RRR5-11/2	1917.582	1918.175	-833.210	0.635	2743.209	0.588	24	0.434	K.SLVEEDKLELATSLIEK.A
R5/RRR5-11/3	1751.790	1752.048	-147.803	0.458	2659.954	0.422	34	0.404	K.LAATLPDGGVLLLENVR.F
R5/RRR5-11/1	1042.735	1043.282	-1488.517	0.139	825.287	0.136	13	0.389	-.IGVIESLLAK.-
R5/RRR5-11/2	1803.596	1804.016	-233.593	0.538	2323.083	0.543	29	0.333	K.M*SHISTGGGASLELLEGK.T
R5/RRR5-11/2	1804.462	1804.016	248.134	0.531	2112.076	0.579	28	0.306	K.M*SHISTGGGASLELLEGK.T
R5/RRR5-11/2	1803.302	1804.016	-953.054	0.558	2020.959	0.563	26	0.286	K.M*SHISTGGGASLELLEGK.T
R5/RRR5-11/3	1919.274	1918.175	51.531	0.514	2052.226	0.508	33	0.283	K.SLVEEDKLELATSLIEK.A
R5/RRR5-11/2	1389.182	1389.578	-286.495	0.457	2178.509	0.447	22	0.279	K.ELDYLVGAVANPK.K
R5/RRR5-11/2	1390.432	1389.578	-105.810	0.554	1950.232	0.541	21	0.269	K.ELDYLVGAVANPK.K
R5/RRR5-11/2	1389.195	1389.578	-277.062	0.471	1902.911	0.498	20	0.250	K.ELDYLVGAVANPK.K
R5/RRR5-11/2	1920.437	1921.103	-869.650	0.556	1674.022	0.614	23	0.247	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-11/2	1920.561	1921.103	-804.824	0.532	1491.526	0.595	22	0.218	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-11/2	1921.054	1921.103	-25.214	0.503	1745.899	0.455	22	0.216	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-11/2	1920.652	1921.103	-235.330	0.540	1350.531	0.582	21	0.199	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-12/2	1390.367	1389.578	-152.310	0.403	1479.269	0.475	19	0.192	K.ELDYLVGAVANPK.K
R5/RRR5-11/2	1786.688	1788.016	-1306.990	0.403	1582.744	0.381	25	0.184	K.MSHISTGGGASLELLEGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1787.336	1788.016	-942.907	0.421	1562.773	0.389	25	0.183	K.MSHISTGGGASLELLEGK.T
R5/RRR5-11/2	1774.341	1774.908	-885.984	0.532	1094.514	0.582	22	0.181	R.FYKEEEKNDPEFAK.K
R5/RRR5-11/2	1774.422	1774.908	-274.734	0.558	1036.038	0.579	21	0.175	R.FYKEEEKNDPEFAK.K
R5/RRR5-11/2	1573.792	1574.758	-1253.048	0.313	1423.432	0.439	20	0.175	K.GVTTIIGGGDSVAAVEK.A
R5/RRR5-11/2	1042.702	1043.282	-1520.222	0.445	1220.143	0.496	17	0.175	K.IGVIESLLAK.V
R5/RRR5-11/2	1527.318	1526.800	-316.458	0.511	1119.224	0.532	24	0.174	K.GVSLLLPTDVVVADK.F
R5/RRR5-11/2	1150.174	1150.261	-75.858	0.485	1111.981	0.503	17	0.168	R.SVGTLTESDLK.G
R5/RRR5-11/2	1774.417	1774.908	-277.357	0.553	924.970	0.564	20	0.164	R.FYKEEEKNDPEFAK.K
R5/RRR5-11/2	1093.952	1093.258	-280.543	0.495	1281.195	0.395	17	0.161	K.FAAGTDAIAKK.L
R5/RRR5-11/2	1042.681	1043.282	-1540.332	0.448	1102.523	0.468	16	0.161	K.IGVIESLLAK.V
R5/RRR5-11/2	1150.118	1150.261	-125.150	0.433	1017.780	0.508	17	0.161	R.SVGTLTESDLK.G
R5/RRR5-11/2	1043.124	1043.282	-151.837	0.465	1091.643	0.463	16	0.160	K.IGVIESLLAK.V
R5/RRR5-12/2	1389.113	1389.578	-336.396	0.334	1464.717	0.303	17	0.159	K.ELDYLVGAVANPK.K
R5/RRR5-12/2	1752.498	1752.048	257.266	0.516	777.792	0.534	23	0.151	K.LAATLPDGGVLLLENVR.F
R5/RRR5-12/2	1751.553	1752.048	-283.494	0.476	696.731	0.550	22	0.148	K.LAATLPDGGVLLLENVR.F
R5/RRR5-11/2	1769.900	1771.029	-1206.517	0.394	1219.492	0.360	18	0.148	K.TVIWNGPM*GVFEFEK.F
R5/RRR5-11/2	964.844	965.085	-250.827	0.400	1037.659	0.372	17	0.144	K.FAAGTDAIAK.K
R5/RRR5-11/2	1751.655	1752.048	-225.183	0.487	577.261	0.549	21	0.144	K.LAATLPDGGVLLLENVR.F
R5/RRR5-11/2	1752.433	1752.048	220.107	0.500	572.892	0.547	21	0.143	K.LAATLPDGGVLLLENVR.F
R5/RRR5-11/2	1092.395	1093.258	-1710.309	0.333	1140.652	0.344	17	0.143	K.FAAGTDAIAKK.L
R5/RRR5-12/2	1751.176	1752.048	-1072.356	0.442	561.025	0.561	20	0.142	K.LAATLPDGGVLLLENVR.F
R5/RRR5-11/2	1074.617	1075.286	-1557.790	0.411	502.416	0.527	17	0.141	K.KPFAAIVGGSK.V
R5/RRR5-11/2	964.593	965.085	-511.608	0.393	1171.135	0.289	18	0.140	K.FAAGTDAIAK.K
R5/RRR5-11/2	1073.156	1073.313	-147.018	0.431	410.620	0.500	14	0.139	K.YSLKPLVPR.L
R5/RRR5-11/2	1073.095	1073.313	-204.303	0.393	499.287	0.487	15	0.138	K.YSLKPLVPR.L
R5/RRR5-11/2	1075.009	1075.286	-257.924	0.349	627.056	0.482	18	0.137	K.KPFAAIVGGSK.V
R5/RRR5-11/2	1388.953	1389.578	-1173.774	0.325	1030.384	0.360	15	0.137	K.ELDYLVGAVANPK.K
R5/RRR5-11/2	1092.333	1093.258	-1767.571	0.357	1053.643	0.322	16	0.136	K.FAAGTDAIAKK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1149.215	1150.261	-1785.769	0.333	795.910	0.407	17	0.134	R.SVGTLTESDLK.G
R5/RRR5-11/2	1526.349	1526.800	-295.963	0.397	661.197	0.469	19	0.134	-.GVSLLLPTDVVVADK.-
R5/RRR5-11/2	1770.152	1771.029	-1063.653	0.378	851.524	0.394	16	0.132	K.TVIWNGPM*GVFEFEK.F
R5/RRR5-11/2	964.838	965.085	-256.412	0.329	812.367	0.366	15	0.131	K.FAAGTDAIAK.K
R5/RRR5-11/3	1774.913	1774.908	2.641	0.449	1134.844	0.503	25	0.129	R.FYKEEEKNDPEFAK.K
R5/RRR5-11/2	1753.245	1752.048	112.460	0.445	313.179	0.453	16	0.127	K.LAATLPDGGVLLLENVR.F
R5/RRR5-11/2	1074.598	1075.286	-1575.477	0.317	471.234	0.392	16	0.126	K.KPFAAIVGGSK.V
R5/RRR5-11/2	1073.008	1073.313	-285.449	0.316	448.916	0.343	14	0.125	K.YSLKPLVPR.L
R5/RRR5-11/2	1753.952	1755.030	-1188.282	0.309	718.162	0.372	15	0.124	K.TVIWNGPMGVFEFEK.F
R5/RRR5-11/1	1043.781	1043.282	479.878	0.137	447.539	0.057	10	0.123	-.IGVIESLLAK.-
R5/RRR5-11/2	1526.453	1526.800	-228.005	0.346	525.879	0.401	17	0.123	-.GVSLLLPTDVVVADK.-
R5/RRR5-12/3	1751.273	1752.048	-1016.933	0.359	1206.501	0.433	29	0.118	K.LAATLPDGGVLLLENVR.F
R5/RRR5-6/2	1576.131	1574.758	237.426	0.323	379.176	0.295	18	0.118	K.GVTTIIGGGDSVAAVEK.A
R5/RRR5-11/2	1388.419	1389.578	-1560.296	0.238	714.432	0.186	15	0.115	K.ELDYLVGAVANPK.K
R5/RRR5-11/2	1769.595	1771.029	-1379.351	0.264	531.560	0.285	13	0.115	K.TVIWNGPM*GVFEFEK.F
R5/RRR5-11/3	1075.642	1075.286	332.234	0.409	1313.943	0.356	24	0.109	K.KPFAAIVGGSK.V
R5/RRR5-11/3	1920.830	1921.103	-142.413	0.391	932.091	0.478	31	0.106	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-11/3	1389.467	1389.578	-80.162	0.362	1437.210	0.275	26	0.104	K.ELDYLVGAVANPK.K
R5/RRR5-11/3	1774.614	1774.908	-166.255	0.500	777.473	0.472	22	0.099	R.FYKEEEKNDPEFAK.K
R5/RRR5-11/3	1074.731	1075.286	-1451.062	0.334	1382.917	0.265	23	0.095	K.KPFAAIVGGSK.V
R5/RRR5-10/3	1921.463	1921.103	187.961	0.453	455.975	0.508	24	0.095	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-11/3	1921.516	1921.103	215.961	0.397	500.445	0.478	26	0.091	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-12/3	1775.129	1774.908	125.033	0.357	624.157	0.480	24	0.091	R.FYKEEEKNDPEFAK.K
R5/RRR5-11/3	1921.490	1921.103	202.009	0.377	589.637	0.467	27	0.091	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-12/3	1922.619	1921.103	-252.100	0.337	619.262	0.440	27	0.087	K.LASVADLYVNDAFGTAHR.A
R5/RRR5-11/2	1084.032	1084.248	-199.644	0.354	805.308	0.380	13	0.084	K.TLPGVLALNDA.-
R5/RRR5-11/3	1804.310	1804.016	163.460	0.427	1004.819	0.334	26	0.084	K.M*SHISTGGGASLELLEGK.T
R5/RRR5-13/3	1775.363	1774.908	257.428	0.326	546.089	0.401	20	0.081	R.FYKEEEKNDPEFAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1083.945	1084.248	-279.857	0.232	762.132	0.276	13	0.079	-.TLPGVLALNDA.-
R5/RRR5-10/3	1917.124	1918.175	-1073.164	0.316	1072.716	0.276	26	0.077	K.SLVEEDKLELATSLIEK.A
R5/RRR5-11/3	1751.291	1752.048	-1006.751	0.304	581.497	0.358	25	0.076	K.LAATLPDGGVLLLENVR.F
R5/RRR5-11/3	1074.695	1075.286	-1484.434	0.306	1100.432	0.206	21	0.069	K.KPFAAIVGGSK.V
R5/RRR5-11/3	1803.366	1804.016	-917.723	0.348	828.603	0.251	25	0.065	-.M*SHISTGGGASLELLEGK.-
R5/RRR5-11/3	1917.683	1918.175	-257.346	0.334	984.015	0.180	23	0.060	K.SLVEEDKLELATSLIEK.A
R5/RRR5-11/3	1803.820	1804.016	-108.950	0.347	902.529	0.162	24	0.058	-.M*SHISTGGGASLELLEGK.-
R5/RRR5-5/2	1846.544	1847.057	-821.635	0.613	2581.050	0.583	25	0.399	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/2	1846.548	1847.057	-819.711	0.590	2453.455	0.570	25	0.368	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/2	1846.524	1847.057	-832.518	0.623	2237.209	0.573	24	0.327	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1321.794	1321.463	251.606	0.636	2102.752	0.518	26	0.291	K.HFSVEGQLEFK.A
R5/RRR5-5/3	1322.389	1321.463	-55.480	0.632	2013.527	0.470	25	0.252	K.HFSVEGQLEFK.A
R5/RRR5-5/3	1321.283	1321.463	-136.655	0.613	1835.539	0.489	24	0.225	K.HFSVEGQLEFK.A
R5/RRR5-5/2	1542.326	1542.675	-226.611	0.524	1562.586	0.411	20	0.188	K.SLTNDWEEHLAVK.H
R5/RRR5-5/2	1837.618	1838.052	-236.836	0.509	1364.131	0.482	20	0.182	K.HSEFISYPISLWTEK.T
R5/RRR5-5/2	1273.200	1273.421	-174.597	0.502	1438.127	0.431	18	0.180	K.SDLVNNLGTIAR.S
R5/RRR5-1/2	1529.401	1528.689	-189.059	0.558	1405.978	0.447	22	0.180	K.GIVDSEDLPLNISR.Q
R5/RRR5-5/2	1273.062	1273.421	-283.005	0.457	1348.707	0.469	18	0.179	K.SDLVNNLGTIAR.S
R5/RRR5-5/3	1846.523	1847.057	-833.289	0.547	1445.386	0.552	29	0.179	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1847.083	1847.057	14.038	0.563	1343.861	0.586	30	0.176	R.KPEEITKEEYAAFYK.S
R5/RRR5-6/2	1528.353	1528.689	-220.993	0.496	1418.808	0.401	22	0.173	K.GIVDSEDLPLNISR.Q
R5/RRR5-1/2	1528.273	1528.689	-273.399	0.506	1395.226	0.401	22	0.171	K.GIVDSEDLPLNISR.Q
R5/RRR5-6/2	1529.154	1528.689	304.450	0.532	1390.382	0.400	22	0.169	K.GIVDSEDLPLNISR.Q
R5/RRR5-6/2	1273.354	1273.421	-53.039	0.481	1390.245	0.383	19	0.167	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1542.269	1542.675	-263.694	0.504	1256.535	0.433	19	0.165	K.SLTNDWEEHLAVK.H
R5/RRR5-5/2	1584.448	1584.710	-165.877	0.524	1241.172	0.447	19	0.165	K.SGDELTSLKDYVTR.M
R5/RRR5-3/2	1529.429	1528.689	-170.563	0.493	1285.639	0.415	21	0.164	K.GIVDSEDLPLNISR.Q
R5/RRR5-5/2	1837.272	1838.052	-971.524	0.454	1130.948	0.482	20	0.163	K.HSEFISYPISLWTEK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1543.036	1542.675	235.059	0.558	1119.666	0.478	18	0.162	K.SLTNDWEEHLAVK.H
R5/RRR5-4/2	1528.417	1528.689	-178.687	0.505	1285.314	0.395	22	0.161	K.GIVDSEDLPLNISR.Q
R5/RRR5-2/2	1529.490	1528.689	-131.012	0.543	1188.712	0.425	21	0.158	K.GIVDSEDLPLNISR.Q
R5/RRR5-4/2	1273.073	1273.421	-274.251	0.443	1234.163	0.404	17	0.158	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1836.640	1838.052	-1317.375	0.440	1020.716	0.503	19	0.158	K.HSEFISYPISLWTEK.T
R5/RRR5-6/2	1584.604	1584.710	-66.960	0.538	1168.242	0.441	18	0.157	K.SGDELTSLKDYVTR.M
R5/RRR5-3/2	1529.545	1528.689	-94.905	0.469	1231.439	0.392	21	0.157	K.GIVDSEDLPLNISR.Q
R5/RRR5-4/2	1272.531	1273.421	-1489.755	0.396	1212.461	0.383	17	0.153	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1584.279	1584.710	-272.544	0.518	1027.841	0.474	17	0.153	K.SGDELTSLKDYVTR.M
R5/RRR5-4/2	1274.000	1273.421	-331.425	0.485	1024.319	0.459	16	0.153	K.SDLVNNLGTIAR.S
R5/RRR5-3/2	1274.147	1273.421	-215.499	0.483	955.920	0.468	17	0.152	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1529.222	1528.689	-306.616	0.546	1178.959	0.388	21	0.151	K.GIVDSEDLPLNISR.Q
R5/RRR5-6/2	1273.431	1273.421	7.537	0.432	964.158	0.439	16	0.147	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1528.377	1528.689	-204.807	0.505	1116.250	0.381	20	0.147	K.GIVDSEDLPLNISR.Q
R5/RRR5-5/2	1529.215	1528.689	-311.021	0.539	1007.945	0.425	19	0.146	K.GIVDSEDLPLNISR.Q
R5/RRR5-5/3	1528.634	1528.689	-36.381	0.478	1525.218	0.389	28	0.144	K.GIVDSEDLPLNISR.Q
R5/RRR5-5/2	1528.349	1528.689	-223.156	0.493	1098.775	0.366	20	0.144	K.GIVDSEDLPLNISR.Q
R5/RRR5-3/2	1527.492	1528.689	-1442.603	0.323	1251.208	0.296	20	0.143	K.GIVDSEDLPLNISR.Q
R5/RRR5-1/3	1846.845	1847.057	-115.335	0.498	1207.903	0.518	27	0.140	R.KPEEITKEEYAAFYK.S
R5/RRR5-6/2	1527.630	1528.689	-1352.146	0.359	1044.103	0.354	20	0.140	K.GIVDSEDLPLNISR.Q
R5/RRR5-5/2	1322.144	1321.463	-241.569	0.435	792.268	0.425	16	0.138	K.HFSVEGQLEFK.A
R5/RRR5-5/2	1134.085	1134.264	-158.444	0.437	729.220	0.445	14	0.138	K.AVENSPFLEK.L
R5/RRR5-5/2	1837.495	1838.052	-849.802	0.510	712.268	0.480	17	0.138	K.HSEFISYPISLWTEK.T
R5/RRR5-5/2	1272.668	1273.421	-1382.038	0.399	1083.636	0.323	16	0.137	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1262.201	1262.437	-186.886	0.534	951.278	0.368	16	0.137	K.KAVENSPFLEK.L
R5/RRR5-4/3	1846.702	1847.057	-192.716	0.547	1223.344	0.499	30	0.137	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1527.753	1528.689	-1271.624	0.421	1600.824	0.323	28	0.135	K.GIVDSEDLPLNISR.Q
R5/RRR5-1/3	1847.447	1847.057	211.762	0.513	1084.467	0.545	28	0.135	R.KPEEITKEEYAAFYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1134.115	1134.264	-131.342	0.451	603.675	0.429	14	0.134	K.AVENSPFLEK.L
R5/RRR5-5/2	1584.597	1584.710	-71.364	0.540	734.545	0.453	15	0.134	K.SGDELTSLKDYVTR.M
R5/RRR5-5/2	1082.057	1082.191	-123.970	0.437	760.031	0.366	14	0.133	R.APFDLFDTR.K
R5/RRR5-7/2	1528.310	1528.689	-248.878	0.487	979.798	0.337	18	0.133	K.GIVDSEDLPLNISR.Q
R5/RRR5-7/2	1322.013	1321.463	-341.431	0.310	686.110	0.443	15	0.132	K.HFSVEGQLEFK.A
R5/RRR5-3/2	1273.288	1273.421	-105.255	0.444	652.298	0.389	16	0.132	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1262.080	1262.437	-283.333	0.503	770.705	0.385	14	0.131	K.KAVENSPFLEK.L
R5/RRR5-1/2	1321.751	1321.463	218.833	0.353	825.420	0.356	15	0.130	K.HFSVEGQLEFK.A
R5/RRR5-5/2	1262.075	1262.437	-287.409	0.503	795.058	0.357	15	0.130	K.KAVENSPFLEK.L
R5/RRR5-6/2	1542.249	1542.675	-276.717	0.500	620.941	0.405	16	0.130	K.SLTNDWEEHLAVK.H
R5/RRR5-5/2	1133.912	1134.264	-311.148	0.434	513.689	0.396	13	0.129	K.AVENSPFLEK.L
R5/RRR5-15/2	1273.611	1273.421	149.140	0.291	365.779	0.391	17	0.128	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1082.131	1082.191	-55.623	0.357	814.903	0.317	14	0.128	R.APFDLFDTR.K
R5/RRR5-2/2	1528.162	1528.689	-1002.752	0.370	1028.291	0.250	19	0.127	K.GIVDSEDLPLNISR.Q
R5/RRR5-5/3	1584.571	1584.710	-87.948	0.506	1298.330	0.426	28	0.127	K.SGDELTSLKDYVTR.M
R5/RRR5-6/2	1272.613	1273.421	-1425.296	0.347	751.212	0.341	14	0.127	K.SDLVNNLGTIAR.S
R5/RRR5-1/2	1542.350	1542.675	-210.890	0.480	673.127	0.364	16	0.127	K.SLTNDWEEHLAVK.H
R5/RRR5-3/2	1272.275	1273.421	-1691.762	0.264	307.798	0.430	14	0.126	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1081.509	1082.191	-1559.069	0.348	816.177	0.284	14	0.125	R.APFDLFDTR.K
R5/RRR5-1/2	1272.383	1273.421	-1606.940	0.379	763.158	0.271	17	0.124	K.SDLVNNLGTIAR.S
R5/RRR5-5/2	1357.203	1357.621	-309.303	0.418	944.907	0.269	16	0.123	K.VIKEVLGDKVEK.V
R5/RRR5-5/2	1274.089	1273.421	-261.539	0.317	600.352	0.294	15	0.123	K.SDLVNNLGTIAR.S
R5/RRR5-2/2	1528.242	1528.689	-293.834	0.367	817.804	0.271	17	0.122	K.GIVDSEDLPLNISR.Q
R5/RRR5-4/3	1846.788	1847.057	-146.166	0.508	950.169	0.530	26	0.121	R.KPEEITKEEYAAFYK.S
R5/RRR5-4/3	1847.227	1847.057	92.083	0.566	882.034	0.544	27	0.120	R.KPEEITKEEYAAFYK.S
R5/RRR5-7/2	1272.278	1273.421	-1689.448	0.307	633.916	0.275	13	0.120	K.SDLVNNLGTIAR.S
R5/RRR5-5/3	1966.877	1966.225	-177.393	0.481	1075.410	0.487	27	0.120	K.KHSEFISYPISLWTEK.T
R5/RRR5-3/3	1584.662	1584.710	-30.575	0.457	1012.259	0.506	24	0.119	K.SGDELTSLKDYVTR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/3	1846.192	1847.057	-1013.393	0.487	847.932	0.541	25	0.117	R.KPEEITKEEYAAFYK.S
R5/RRR5-6/3	1846.405	1847.057	-897.498	0.483	914.714	0.518	26	0.116	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1846.432	1847.057	-882.963	0.556	868.508	0.526	26	0.115	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1966.505	1966.225	143.031	0.435	1268.493	0.391	28	0.115	K.KHSEFISYPISLWTEK.T
R5/RRR5-3/3	1846.938	1847.057	-64.616	0.453	1008.731	0.476	28	0.113	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1569.777	1569.786	-6.062	0.533	722.756	0.535	23	0.108	K.IKEVSHEWSLVNK.Q
R5/RRR5-5/3	1568.389	1569.786	-1533.295	0.472	825.167	0.506	23	0.106	K.IKEVSHEWSLVNK.Q
R5/RRR5-5/3	1569.701	1569.786	-54.617	0.499	819.712	0.494	24	0.105	K.IKEVSHEWSLVNK.Q
R5/RRR5-3/3	1846.496	1847.057	-848.121	0.473	809.123	0.451	26	0.099	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1141.873	1142.204	-291.245	0.476	562.453	0.528	20	0.098	K.LGIHEDSTNR.N
R5/RRR5-5/3	1892.884	1893.065	-95.730	0.452	812.118	0.430	23	0.090	R.M*KEGQNDIYYITGESK.K
R5/RRR5-5/3	1585.291	1584.710	-264.964	0.398	698.447	0.413	21	0.087	K.SGDELTSLKDYVTR.M
R5/RRR5-5/3	1366.469	1366.550	-59.559	0.490	1129.243	0.291	23	0.086	K.RAPFDLFDTRK.K
R5/RRR5-7/3	1585.151	1584.710	279.243	0.417	744.099	0.383	22	0.085	K.SGDELTSLKDYVTR.M
R5/RRR5-5/3	1893.213	1893.065	78.414	0.440	666.361	0.430	21	0.083	-.M*KEGQNDIYYITGESK.-
R5/RRR5-5/3	1142.643	1142.204	384.652	0.363	501.676	0.376	19	0.080	K.LGIHEDSTNR.N
R5/RRR5-5/3	1366.950	1366.550	293.677	0.482	792.826	0.276	20	0.075	K.RAPFDLFDTRK.K
R5/RRR5-5/3	1584.833	1584.710	77.779	0.413	866.694	0.266	25	0.074	K.SGDELTSLKDYVTR.M
R5/RRR5-7/3	1846.237	1847.057	-988.698	0.312	672.195	0.255	22	0.073	R.KPEEITKEEYAAFYK.S
R5/RRR5-5/3	1366.773	1366.550	163.913	0.476	791.553	0.215	20	0.070	K.RAPFDLFDTRK.K
R5/RRR5-5/2	1971.742	1971.200	-232.959	0.621	3055.915	0.655	26	0.542	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-5/2	1970.541	1971.200	-844.245	0.596	2791.432	0.631	26	0.465	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-5/2	1970.844	1971.200	-181.253	0.639	2336.360	0.650	24	0.371	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-5/3	1961.621	1961.210	210.110	0.602	2146.998	0.567	33	0.322	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-4/3	1960.657	1961.210	-794.242	0.524	2125.521	0.540	33	0.307	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/3	1960.560	1961.210	-844.116	0.537	2085.420	0.523	33	0.289	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1968.513	1969.312	-916.704	0.600	2160.094	0.468	24	0.278	K.LFQDKESLYPLLNFLK.A
R5/RRR5-4/3	1971.142	1971.200	-29.673	0.590	2054.238	0.517	35	0.277	R.HQLLAEFDALIEADKEK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1972.161	1971.200	-19.911	0.582	2001.572	0.543	35	0.277	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-5/3	1969.896	1969.312	-211.865	0.484	2315.798	0.374	35	0.275	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/3	1971.024	1971.200	-89.588	0.583	1871.707	0.557	35	0.256	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-4/3	1972.272	1971.200	36.706	0.586	1856.031	0.561	35	0.254	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-4/2	1968.752	1969.312	-794.701	0.574	1849.096	0.509	23	0.244	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/2	1840.387	1841.009	-884.259	0.580	1651.202	0.609	23	0.243	R.DLANLVIVCGDHGNQSK.D
R5/RRR5-5/2	1968.022	1969.312	-1167.029	0.524	1897.261	0.479	23	0.243	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/3	1970.995	1971.200	-104.405	0.588	1808.672	0.556	34	0.243	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-4/3	1971.073	1971.200	-64.336	0.552	1859.196	0.495	34	0.229	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-4/3	1960.630	1961.210	-808.304	0.509	1826.544	0.505	31	0.228	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-4/3	1960.990	1961.210	-112.555	0.539	1806.178	0.505	31	0.223	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1841.355	1841.009	188.067	0.562	1536.974	0.587	22	0.223	R.DLANLVIVCGDHGNQSK.D
R5/RRR5-5/2	1541.159	1541.768	-1047.365	0.509	1799.944	0.425	20	0.217	K.LGVTQCTIAHALEK.T
R5/RRR5-5/3	1962.085	1961.210	-64.037	0.583	1614.127	0.539	30	0.201	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/3	1970.929	1969.312	-194.826	0.412	2056.408	0.288	32	0.189	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/2	1841.358	1841.009	190.194	0.553	1264.863	0.553	20	0.184	R.DLANLVIVCGDHGNQSK.D
R5/RRR5-2/3	1961.061	1961.210	-76.027	0.503	1527.898	0.525	31	0.184	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1542.302	1541.768	-303.222	0.547	1578.159	0.385	19	0.181	K.LGVTQCTIAHALEK.T
R5/RRR5-5/2	1242.154	1241.462	-248.550	0.510	1505.166	0.365	18	0.174	R.IKQQGLDITPK.I
R5/RRR5-5/2	1541.402	1541.768	-237.947	0.471	1340.493	0.419	18	0.168	K.LGVTQCTIAHALEK.T
R5/RRR5-5/2	1241.206	1241.462	-206.718	0.478	1455.300	0.343	18	0.166	R.IKQQGLDITPK.I
R5/RRR5-1/2	1241.139	1241.462	-260.887	0.440	1407.509	0.350	18	0.164	R.IKQQGLDITPK.I
R5/RRR5-5/2	1253.697	1254.418	-1376.387	0.542	1012.493	0.504	18	0.163	K.VIGTEHTDILR.V
R5/RRR5-5/3	1970.897	1969.312	-211.323	0.455	1783.762	0.342	32	0.162	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/2	1962.980	1961.210	-117.424	0.524	793.732	0.616	20	0.160	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1240.701	1241.462	-1423.666	0.442	1306.431	0.332	17	0.153	R.IKQQGLDITPK.I
R5/RRR5-4/2	1241.123	1241.462	-273.715	0.449	1264.234	0.343	17	0.152	R.IKQQGLDITPK.I
R5/RRR5-5/2	1389.092	1388.546	-327.499	0.459	572.432	0.555	20	0.148	R.LLPDAVGTTCGQR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1254.125	1254.418	-234.267	0.471	954.439	0.424	18	0.148	K.VIGTEHTDILR.V
R5/RRR5-1/2	1240.531	1241.462	-1561.247	0.445	1063.391	0.388	17	0.147	R.IKQQGLDITPK.I
R5/RRR5-5/2	1962.590	1961.210	194.042	0.460	700.648	0.561	19	0.146	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1253.473	1254.418	-1555.872	0.416	858.055	0.459	17	0.146	K.VIGTEHTDILR.V
R5/RRR5-4/3	1969.741	1971.200	-1252.076	0.463	1398.403	0.458	31	0.146	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-4/2	1241.259	1241.462	-163.801	0.487	1116.668	0.352	16	0.143	R.IKQQGLDITPK.I
R5/RRR5-5/3	1961.943	1961.210	-136.589	0.526	1327.212	0.483	27	0.143	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-4/2	1388.119	1388.546	-308.500	0.405	614.120	0.487	20	0.141	R.LLPDAVGTTCGQR.V
R5/RRR5-1/2	1388.321	1388.546	-162.412	0.361	643.780	0.495	20	0.140	R.LLPDAVGTTCGQR.V
R5/RRR5-4/2	1388.077	1388.546	-338.323	0.399	769.572	0.417	21	0.139	R.LLPDAVGTTCGQR.V
R5/RRR5-5/2	1227.701	1228.332	-1332.530	0.416	1242.523	0.257	16	0.138	K.YPNSDIYLDK.F
R5/RRR5-1/2	1388.038	1388.546	-1089.339	0.424	543.226	0.472	19	0.138	R.LLPDAVGTTCGQR.V
R5/RRR5-4/2	1254.229	1254.418	-151.076	0.472	932.366	0.354	18	0.138	K.VIGTEHTDILR.V
R5/RRR5-1/2	1388.080	1388.546	-336.647	0.373	691.351	0.446	20	0.138	R.LLPDAVGTTCGQR.V
R5/RRR5-5/2	1962.624	1961.210	211.506	0.433	486.264	0.569	17	0.138	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-4/2	1388.101	1388.546	-321.470	0.385	629.056	0.456	20	0.138	R.LLPDAVGTTCGQR.V
R5/RRR5-5/2	1388.989	1388.546	320.188	0.363	586.133	0.474	20	0.137	R.LLPDAVGTTCGQR.V
R5/RRR5-5/2	1228.020	1228.332	-255.100	0.463	1164.308	0.269	16	0.135	K.YPNSDIYLDK.F
R5/RRR5-5/2	1540.685	1541.768	-1355.867	0.372	1346.696	0.194	17	0.132	K.LGVTQCTIAHALEK.T
R5/RRR5-4/2	1253.874	1254.418	-1234.507	0.413	738.463	0.373	16	0.132	K.VIGTEHTDILR.V
R5/RRR5-5/2	1337.282	1337.588	-230.045	0.364	495.903	0.455	16	0.132	K.ESLYPLLNFLK.A
R5/RRR5-5/2	1227.379	1228.332	-1596.232	0.437	1050.249	0.268	16	0.131	K.YPNSDIYLDK.F
R5/RRR5-4/2	1253.962	1254.418	-364.158	0.434	611.220	0.382	15	0.130	K.VIGTEHTDILR.V
R5/RRR5-4/2	1241.306	1241.462	-126.017	0.438	1086.695	0.264	15	0.130	R.IKQQGLDITPK.I
R5/RRR5-5/2	1389.555	1388.546	6.731	0.340	301.870	0.464	18	0.129	-.LLPDAVGTTCGQR.-
R5/RRR5-5/2	1337.246	1337.588	-256.695	0.333	364.571	0.460	14	0.128	K.ESLYPLLNFLK.A
R5/RRR5-5/2	1387.434	1388.546	-1526.634	0.301	527.523	0.388	20	0.128	R.LLPDAVGTTCGQR.V
R5/RRR5-5/2	1389.338	1388.546	-150.044	0.368	263.313	0.378	17	0.127	-.LLPDAVGTTCGQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1089.653	1089.291	333.537	0.391	483.292	0.334	13	0.127	R.ALENEMLLR.I
R5/RRR5-1/2	1969.143	1969.312	-86.154	0.406	653.093	0.372	19	0.127	K.LFQDKESLYPLLNFLK.A
R5/RRR5-1/3	1961.511	1961.210	154.038	0.422	1135.967	0.484	26	0.126	-.LGATFSSHPNELIALFSR.-
R5/RRR5-1/2	1968.492	1969.312	-927.039	0.328	888.743	0.302	20	0.126	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/2	1105.991	1105.291	-271.332	0.467	821.997	0.291	12	0.124	R.ALENEM*LLR.I
R5/RRR5-2/3	1961.220	1961.210	5.074	0.507	1207.338	0.458	27	0.124	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1337.573	1337.588	-11.773	0.328	416.559	0.306	15	0.123	K.ESLYPLLNFLK.A
R5/RRR5-1/2	1960.983	1961.210	-116.107	0.335	313.065	0.428	15	0.123	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1969.353	1969.312	20.976	0.362	501.060	0.342	18	0.123	K.LFQDKESLYPLLNFLK.A
R5/RRR5-1/2	1960.235	1961.210	-1010.581	0.331	385.371	0.407	16	0.122	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/3	1457.686	1457.610	52.646	0.489	1371.281	0.376	25	0.122	K.TKYPNSDIYLDK.F
R5/RRR5-5/2	1961.776	1961.210	-221.597	0.300	229.131	0.397	14	0.121	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-3/2	1960.332	1961.210	-960.815	0.316	256.782	0.384	14	0.121	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/2	1089.791	1089.291	459.999	0.432	451.713	0.293	13	0.120	-.ALENEMLLR.-
R5/RRR5-5/3	1457.169	1457.610	-303.133	0.496	1244.577	0.414	24	0.119	K.TKYPNSDIYLDK.F
R5/RRR5-1/2	1968.910	1969.312	-204.813	0.304	509.433	0.259	18	0.119	K.LFQDKESLYPLLNFLK.A
R5/RRR5-7/2	1959.960	1961.210	-1151.590	0.242	364.725	0.333	15	0.118	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-5/3	1962.484	1961.210	140.173	0.530	1075.964	0.475	25	0.116	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-4/2	1105.068	1105.291	-201.868	0.249	633.008	0.125	12	0.115	R.ALENEM*LLR.I
R5/RRR5-5/3	1457.628	1457.610	12.833	0.508	1253.388	0.382	24	0.113	K.TKYPNSDIYLDK.F
R5/RRR5-2/3	1972.770	1971.200	-218.321	0.376	1007.259	0.457	27	0.109	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-2/3	1970.918	1971.200	-143.639	0.447	836.752	0.495	25	0.106	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-5/2	1105.076	1105.291	-194.665	0.416	681.408	0.220	12	0.105	-.ALENEM*LLR.-
R5/RRR5-5/3	1840.335	1841.009	-912.500	0.380	871.729	0.469	29	0.101	R.DLANLVIVCGDHGNQSK.D
R5/RRR5-5/3	1969.358	1969.312	23.394	0.393	1355.616	0.294	29	0.100	K.LFQDKESLYPLLNFLK.A
R5/RRR5-3/3	1972.034	1971.200	-84.358	0.371	872.888	0.446	26	0.099	R.HQLLAEFDALIEADKEK.Y
R5/RRR5-1/3	1960.698	1961.210	-773.337	0.456	967.334	0.411	25	0.097	R.LGATFSSHPNELIALFSR.Y
R5/RRR5-2/3	1961.621	1961.210	210.391	0.342	1133.713	0.348	27	0.095	R.LGATFSSHPNELIALFSR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1961.397	1961.210	95.525	0.440	766.435	0.433	23	0.091	-.LGATFSSHPNELIALFSR.-
R5/RRR5-4/3	1241.645	1241.462	147.496	0.490	995.507	0.340	22	0.088	R.IKQQGLDITPK.I
R5/RRR5-5/3	1841.010	1841.009	0.251	0.378	497.216	0.463	23	0.088	R.DLANLVIVCGDHGNQSK.D
R5/RRR5-4/3	1841.960	1841.009	-27.102	0.350	464.619	0.451	22	0.085	R.DLANLVIVCGDHGNQSK.D
R5/RRR5-4/3	1241.535	1241.462	59.050	0.518	1144.559	0.287	23	0.085	R.IKQQGLDITPK.I
R5/RRR5-5/3	1969.081	1969.312	-117.346	0.398	1161.323	0.277	29	0.084	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/3	1840.668	1841.009	-185.831	0.393	520.313	0.387	23	0.081	R.DLANLVIVCGDHGNQSK.D
R5/RRR5-5/3	1241.773	1241.462	251.157	0.503	999.165	0.279	22	0.079	R.IKQQGLDITPK.I
R5/RRR5-2/3	1241.238	1241.462	-181.077	0.485	959.894	0.283	22	0.079	R.IKQQGLDITPK.I
R5/RRR5-5/3	1241.594	1241.462	106.529	0.474	811.112	0.287	20	0.078	R.IKQQGLDITPK.I
R5/RRR5-4/3	1969.182	1969.312	-65.952	0.373	1167.483	0.247	24	0.078	K.LFQDKESLYPLLNFLK.A
R5/RRR5-4/3	1241.895	1241.462	349.918	0.544	1130.879	0.243	23	0.077	R.IKQQGLDITPK.I
R5/RRR5-3/3	1241.174	1241.462	-232.727	0.479	968.391	0.263	21	0.076	R.IKQQGLDITPK.I
R5/RRR5-2/3	1241.446	1241.462	-12.843	0.438	813.974	0.243	21	0.075	R.IKQQGLDITPK.I
R5/RRR5-3/3	1240.337	1241.462	-1718.504	0.402	849.919	0.255	20	0.074	R.IKQQGLDITPK.I
R5/RRR5-3/3	1242.124	1241.462	-273.407	0.506	706.645	0.257	19	0.073	-.IKQQGLDITPK.-
R5/RRR5-5/3	1241.988	1241.462	-382.565	0.507	1017.208	0.225	22	0.072	R.IKQQGLDITPK.I
R5/RRR5-2/3	1241.566	1241.462	83.603	0.461	996.331	0.228	21	0.072	R.IKQQGLDITPK.I
R5/RRR5-5/3	1241.695	1241.462	187.869	0.401	831.371	0.200	22	0.065	-.IKQQGLDITPK.-
R5/RRR5-5/3	1968.617	1969.312	-863.642	0.346	768.829	0.174	23	0.064	-.LFQDKESLYPLLNFLK.-
R5/RRR5-1/3	1968.477	1969.312	-935.077	0.265	1117.571	0.135	24	0.060	K.LFQDKESLYPLLNFLK.A
R5/RRR5-5/3	1968.966	1969.312	-176.303	0.327	941.851	0.125	26	0.059	K.LFQDKESLYPLLNFLK.A
R5/RRR5-3/2	1569.181	1569.783	-1024.370	0.560	2439.901	0.466	22	0.329	K.YLLQSGLQEYLNK.Q
R5/RRR5-4/2	1569.329	1569.783	-290.120	0.566	2412.938	0.430	22	0.312	K.YLLQSGLQEYLNK.Q
R5/RRR5-4/2	1569.341	1569.783	-282.472	0.607	2312.922	0.475	22	0.308	K.YLLQSGLQEYLNK.Q
R5/RRR5-4/2	1569.254	1569.783	-977.196	0.575	2286.353	0.447	22	0.295	K.YLLQSGLQEYLNK.Q
R5/RRR5-4/2	1545.213	1545.656	-287.520	0.498	1664.549	0.546	20	0.232	K.M*FVDYNEPQTER.V
R5/RRR5-4/2	1545.051	1545.656	-1041.957	0.491	1526.665	0.543	19	0.214	K.M*FVDYNEPQTER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1498.361	1498.684	-216.264	0.402	1832.878	0.389	19	0.214	R.SDETVAMIEAYLR.A
R5/RRR5-4/2	1498.174	1498.684	-1010.974	0.405	1719.402	0.403	19	0.203	R.SDETVAMIEAYLR.A
R5/RRR5-4/2	1280.041	1280.431	-305.290	0.460	1429.090	0.511	18	0.196	K.FVEFYGEGM*GK.L
R5/RRR5-4/2	1280.049	1280.431	-299.167	0.406	1444.248	0.511	18	0.196	K.FVEFYGEGM*GK.L
R5/RRR5-4/2	1497.526	1498.684	-1444.898	0.382	1740.452	0.349	19	0.194	R.SDETVAMIEAYLR.A
R5/RRR5-4/2	1528.998	1528.563	285.503	0.479	1436.203	0.500	20	0.193	K.AGEDADSLGLTGHER.Y
R5/RRR5-4/2	1528.122	1528.563	-289.931	0.451	1418.113	0.475	21	0.186	K.AGEDADSLGLTGHER.Y
R5/RRR5-4/2	1724.124	1724.761	-952.125	0.630	1523.160	0.412	23	0.183	R.NCDNFQVNQNDVEK.I
R5/RRR5-4/2	1724.076	1724.761	-980.416	0.613	1519.557	0.408	23	0.182	R.NCDNFQVNQNDVEK.I
R5/RRR5-4/2	1724.210	1724.761	-902.370	0.618	1488.176	0.421	23	0.182	R.NCDNFQVNQNDVEK.I
R5/RRR5-4/2	1280.013	1280.431	-327.010	0.422	1223.686	0.521	17	0.178	K.FVEFYGEGM*GK.L
R5/RRR5-4/2	1527.547	1528.563	-1323.846	0.444	1255.552	0.501	19	0.175	K.AGEDADSLGLTGHER.Y
R5/RRR5-4/2	1515.157	1514.683	313.963	0.504	1297.510	0.412	19	0.164	R.SDETVAM*IEAYLR.A
R5/RRR5-4/2	1294.269	1293.453	-142.240	0.380	1033.298	0.538	17	0.164	K.FYSLPALNDPR.I
R5/RRR5-4/2	1514.247	1514.683	-288.471	0.413	1114.731	0.450	18	0.157	R.SDETVAM*IEAYLR.A
R5/RRR5-4/2	1565.327	1565.896	-1005.387	0.484	665.906	0.586	18	0.152	R.SNLVGM*GIIPLCFK.A
R5/RRR5-4/2	1565.296	1565.896	-1025.040	0.497	597.680	0.612	17	0.151	R.SNLVGM*GIIPLCFK.A
R5/RRR5-4/2	1514.220	1514.683	-306.508	0.356	1178.670	0.381	17	0.150	R.SDETVAM*IEAYLR.A
R5/RRR5-4/3	1993.480	1994.066	-797.748	0.457	1303.528	0.507	32	0.150	K.SEGHDTIVLAGAEYGSGSSR.D
R5/RRR5-4/2	1548.471	1549.897	-1571.235	0.352	979.821	0.455	19	0.147	R.SNLVGMGIIPLCFK.A
R5/RRR5-4/2	1289.101	1289.421	-248.331	0.371	1110.077	0.361	16	0.144	K.FDFHGQPAELK.H
R5/RRR5-4/3	1528.391	1528.563	-112.890	0.503	1226.329	0.524	30	0.143	K.AGEDADSLGLTGHER.Y
R5/RRR5-4/2	1570.404	1569.783	-242.285	0.421	1231.150	0.291	19	0.141	K.YLLQSGLQEYLNK.Q
R5/RRR5-1/2	1293.370	1293.453	-63.956	0.324	820.826	0.454	15	0.139	K.FYSLPALNDPR.I
R5/RRR5-3/2	1203.072	1203.326	-211.540	0.479	752.959	0.402	16	0.138	K.IIDWENTSPK.L
R5/RRR5-4/2	1645.608	1645.881	-166.706	0.468	556.963	0.524	18	0.137	K.NILTTLPKPGGGEYGK.F
R5/RRR5-4/2	1289.059	1289.421	-281.488	0.375	1050.990	0.340	15	0.137	K.FDFHGQPAELK.H
R5/RRR5-4/3	1750.692	1750.958	-152.441	0.522	1120.490	0.534	28	0.136	R.SPNAVQSNMELEFKR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1289.125	1289.421	-230.091	0.345	1114.948	0.289	16	0.135	K.FDFHGQPAELK.H
R5/RRR5-4/2	1117.095	1117.278	-163.813	0.388	680.823	0.421	18	0.135	K.TSLAPGSGVVTK.Y
R5/RRR5-4/2	1203.168	1203.326	-132.047	0.477	732.770	0.376	16	0.135	K.IIDWENTSPK.L
R5/RRR5-4/2	1766.270	1766.957	-958.297	0.507	375.709	0.517	17	0.134	R.SPNAVQSNM*ELEFKR.N
R5/RRR5-4/2	1766.434	1766.957	-864.843	0.528	480.017	0.477	18	0.132	R.SPNAVQSNM*ELEFKR.N
R5/RRR5-4/2	1202.501	1203.326	-1522.041	0.463	731.079	0.352	16	0.132	K.IIDWENTSPK.L
R5/RRR5-1/2	1203.221	1203.326	-87.675	0.388	779.259	0.350	16	0.132	K.IIDWENTSPK.L
R5/RRR5-4/3	1994.128	1994.066	31.330	0.477	1300.534	0.444	33	0.132	K.SEGHDTIVLAGAEYGSGSSR.D
R5/RRR5-4/2	1203.124	1203.326	-168.484	0.486	716.773	0.351	16	0.132	K.IIDWENTSPK.L
R5/RRR5-4/3	1751.030	1750.958	41.623	0.528	1032.411	0.545	28	0.131	R.SPNAVQSNMELEFKR.N
R5/RRR5-4/2	1645.295	1645.881	-966.711	0.411	423.034	0.510	16	0.130	K.NILTTLPKPGGGEYGK.F
R5/RRR5-4/2	814.746	815.059	-386.150	0.377	951.033	0.314	12	0.130	K.GPMLLGVK.A
R5/RRR5-4/2	1645.294	1645.881	-967.307	0.430	442.351	0.485	16	0.129	K.NILTTLPKPGGGEYGK.F
R5/RRR5-1/2	1293.985	1293.453	-362.546	0.276	756.787	0.385	15	0.129	K.FYSLPALNDPR.I
R5/RRR5-4/2	1292.755	1293.453	-1316.997	0.204	785.017	0.433	16	0.129	K.FYSLPALNDPR.I
R5/RRR5-3/2	1293.238	1293.453	-166.685	0.250	691.719	0.437	14	0.129	K.FYSLPALNDPR.I
R5/RRR5-4/2	1117.238	1117.278	-36.012	0.384	503.652	0.425	16	0.128	-.TSLAPGSGVVTK.-
R5/RRR5-4/2	1118.023	1117.278	-228.508	0.388	500.981	0.413	16	0.128	-.TSLAPGSGVVTK.-
R5/RRR5-4/2	1292.627	1293.453	-1416.583	0.328	859.349	0.307	15	0.127	K.FYSLPALNDPR.I
R5/RRR5-4/2	1570.476	1569.783	-196.276	0.461	910.259	0.304	17	0.127	K.YLLQSGLQEYLNK.Q
R5/RRR5-3/2	1566.781	1565.896	-73.510	0.365	357.392	0.441	14	0.126	R.SNLVGM*GIIPLCFK.A
R5/RRR5-3/2	1292.507	1293.453	-1510.116	0.275	599.398	0.355	14	0.124	K.FYSLPALNDPR.I
R5/RRR5-3/2	1515.000	1514.683	210.146	0.376	699.837	0.311	14	0.121	R.SDETVAM*IEAYLR.A
R5/RRR5-4/2	1564.848	1565.896	-1312.481	0.248	465.053	0.384	15	0.120	R.SNLVGM*GIIPLCFK.A
R5/RRR5-4/3	1993.439	1994.066	-818.217	0.450	1064.583	0.498	27	0.120	K.SEGHDTIVLAGAEYGSGSSR.D
R5/RRR5-3/2	1293.096	1293.453	-276.727	0.270	512.818	0.288	12	0.119	K.FYSLPALNDPR.I
R5/RRR5-3/2	1202.543	1203.326	-1486.963	0.317	613.839	0.173	14	0.118	K.IIDWENTSPK.L
R5/RRR5-4/3	1750.957	1750.958	-0.540	0.526	872.089	0.526	27	0.115	R.SPNAVQSNMELEFKR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/3	1528.056	1528.563	-989.129	0.481	877.686	0.521	27	0.114	K.AGEDADSLGLTGHER.Y
R5/RRR5-3/2	1202.263	1203.326	-1721.437	0.299	863.633	0.087	16	0.114	K.IIDWENTSPK.L
R5/RRR5-1/3	1528.657	1528.563	61.335	0.427	953.294	0.465	26	0.107	K.AGEDADSLGLTGHER.Y
R5/RRR5-1/3	1528.294	1528.563	-176.467	0.460	953.608	0.460	26	0.107	K.AGEDADSLGLTGHER.Y
R5/RRR5-1/3	1528.121	1528.563	-290.541	0.427	956.646	0.429	26	0.101	K.AGEDADSLGLTGHER.Y
R5/RRR5-4/3	1767.930	1766.957	-15.617	0.545	582.493	0.493	25	0.100	R.SPNAVQSNM*ELEFKR.N
R5/RRR5-2/3	1528.262	1528.563	-197.381	0.424	758.072	0.468	23	0.099	K.AGEDADSLGLTGHER.Y
R5/RRR5-3/2	1117.960	1117.278	-285.470	0.380	276.858	0.347	12	0.097	-.TSLAPGSGVVTK.-
R5/RRR5-2/3	1528.409	1528.563	-101.113	0.403	660.673	0.456	22	0.094	K.AGEDADSLGLTGHER.Y
R5/RRR5-4/3	1386.701	1386.580	87.373	0.389	535.007	0.505	23	0.093	K.DM*TM*SPPGPHGVK.N
R5/RRR5-3/2	1117.352	1117.278	66.337	0.321	294.168	0.345	12	0.092	-.TSLAPGSGVVTK.-
R5/RRR5-4/3	1766.512	1766.957	-252.530	0.444	434.839	0.442	22	0.092	R.SPNAVQSNM*ELEFKR.N
R5/RRR5-4/3	1386.833	1386.580	183.109	0.403	490.379	0.467	22	0.089	K.DM*TM*SPPGPHGVK.N
R5/RRR5-4/3	1657.370	1657.972	-969.206	0.468	1203.661	0.290	26	0.089	K.KACELGLEVKPWVK.T
R5/RRR5-4/3	1766.893	1766.957	-36.380	0.419	501.934	0.423	22	0.089	R.SPNAVQSNM*ELEFKR.N
R5/RRR5-4/3	1528.639	1528.563	49.802	0.429	819.078	0.380	26	0.088	K.AGEDADSLGLTGHER.Y
R5/RRR5-3/3	1767.106	1766.957	84.287	0.431	619.312	0.407	24	0.088	R.SPNAVQSNM*ELEFKR.N
R5/RRR5-4/3	1386.057	1386.580	-1102.363	0.373	505.022	0.455	22	0.087	K.DM*TM*SPPGPHGVK.N
R5/RRR5-5/3	1528.617	1528.563	35.024	0.380	487.588	0.372	21	0.086	K.AGEDADSLGLTGHER.Y
R5/RRR5-3/3	1528.856	1528.563	192.023	0.448	757.354	0.370	24	0.085	K.AGEDADSLGLTGHER.Y
R5/RRR5-2/3	1528.769	1528.563	135.091	0.326	525.992	0.345	20	0.081	K.AGEDADSLGLTGHER.Y
R5/RRR5-1/3	1658.462	1657.972	296.319	0.391	725.694	0.240	19	0.066	K.KACELGLEVKPWVK.T
R5/RRR5-1/3	1657.535	1657.972	-264.274	0.263	1070.902	0.184	22	0.064	K.KACELGLEVKPWVK.T
R5/RRR5-7/2	1599.554	1599.899	-215.978	0.483	2259.680	0.541	26	0.320	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/2	1599.383	1599.899	-950.367	0.510	2213.688	0.531	26	0.309	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/2	1599.516	1599.899	-240.248	0.522	1968.377	0.551	25	0.274	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/2	1618.806	1619.792	-1230.684	0.475	1951.878	0.518	22	0.263	K.IGDTAGTIDNIIQCK.L
R5/RRR5-7/2	1619.335	1619.792	-283.580	0.531	1720.795	0.549	21	0.238	K.IGDTAGTIDNIIQCK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1817.462	1817.977	-836.399	0.507	1519.376	0.618	24	0.228	R.ETPSVAGIINPGSDGFQK.L
R5/RRR5-7/2	1817.600	1817.977	-208.256	0.507	1560.475	0.593	25	0.228	R.ETPSVAGIINPGSDGFQK.L
R5/RRR5-7/2	1529.382	1528.729	-227.488	0.540	1358.432	0.625	23	0.214	R.VVAIIAEGVPESDTK.Q
R5/RRR5-7/2	1818.222	1817.977	135.107	0.524	1354.248	0.595	22	0.203	R.ETPSVAGIINPGSDGFQK.L
R5/RRR5-7/2	1528.317	1528.729	-270.747	0.414	1325.935	0.585	23	0.198	R.VVAIIAEGVPESDTK.Q
R5/RRR5-6/2	1601.029	1599.899	81.704	0.518	1400.291	0.538	23	0.197	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/2	1528.290	1528.729	-288.377	0.412	1378.556	0.518	23	0.191	R.VVAIIAEGVPESDTK.Q
R5/RRR5-7/2	1563.199	1563.696	-318.707	0.501	1375.700	0.473	19	0.181	K.SGGM*SNEM*YNTIAR.V
R5/RRR5-7/2	1658.429	1658.920	-297.050	0.462	1269.290	0.514	23	0.180	K.VQKPVVAWVSGTCAR.L
R5/RRR5-6/2	1619.566	1619.792	-140.432	0.422	1370.370	0.474	19	0.180	K.IGDTAGTIDNIIQCK.L
R5/RRR5-7/2	1249.491	1249.396	75.588	0.503	1330.591	0.464	15	0.178	K.TTQALFYNYK.Q
R5/RRR5-7/2	1618.447	1619.792	-1453.219	0.326	1392.705	0.440	20	0.174	K.IGDTAGTIDNIIQCK.L
R5/RRR5-7/2	1562.991	1563.696	-1094.186	0.468	1208.633	0.423	18	0.158	K.SGGM*SNEM*YNTIAR.V
R5/RRR5-7/2	1563.041	1563.696	-1061.956	0.464	1139.629	0.432	18	0.155	K.SGGM*SNEM*YNTIAR.V
R5/RRR5-7/2	1472.052	1472.674	-1104.935	0.412	1073.572	0.458	18	0.153	R.SIGLIGHTFDQKR.L
R5/RRR5-7/2	992.335	993.055	-1738.531	0.382	1220.293	0.298	16	0.143	R.FGGAIDDAAR.Y
R5/RRR5-7/2	1249.049	1249.396	-278.741	0.414	1048.394	0.360	15	0.141	K.TTQALFYNYK.Q
R5/RRR5-7/2	1316.204	1316.488	-215.869	0.454	1014.858	0.369	18	0.140	R.SIGLIGHTFDQK.R
R5/RRR5-7/2	992.907	993.055	-149.528	0.433	1088.638	0.319	16	0.139	R.FGGAIDDAAR.Y
R5/RRR5-7/2	1310.197	1310.526	-252.182	0.442	966.169	0.365	17	0.137	K.LYRPGSVGFVSK.S
R5/RRR5-7/2	1187.400	1187.332	57.990	0.429	739.621	0.412	15	0.135	K.YAHTHFPSVK.Y
R5/RRR5-7/2	1187.148	1187.332	-154.869	0.426	603.907	0.406	15	0.132	K.YAHTHFPSVK.Y
R5/RRR5-7/2	1310.383	1310.526	-109.564	0.475	871.968	0.356	16	0.132	K.LYRPGSVGFVSK.S
R5/RRR5-7/2	1309.923	1310.526	-1227.485	0.439	884.365	0.326	16	0.129	K.LYRPGSVGFVSK.S
R5/RRR5-7/2	992.339	993.055	-1735.070	0.333	672.805	0.333	16	0.126	R.FGGAIDDAAR.Y
R5/RRR5-7/2	1289.491	1290.464	-1534.780	0.294	1226.663	0.181	15	0.126	R.M*LDFDFLCGR.E
R5/RRR5-15/2	1601.094	1599.899	122.153	0.350	200.480	0.452	13	0.124	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/2	1248.403	1249.396	-1601.813	0.309	900.724	0.240	15	0.122	K.TTQALFYNYK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1599.965	1599.899	41.659	0.314	448.621	0.291	18	0.120	K.VILGPATVGGIQAGAFK.I
R5/RRR5-3/2	1564.902	1563.696	131.749	0.433	408.692	0.308	14	0.119	K.SGGM*SNEM*YNTIAR.V
R5/RRR5-6/2	1598.569	1599.899	-1461.946	0.261	561.215	0.228	18	0.116	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/3	1636.884	1635.868	9.573	0.512	733.241	0.510	28	0.103	R.SAAASSM*SALKQPTIR.V
R5/RRR5-7/3	1599.349	1599.899	-971.946	0.355	1393.647	0.264	28	0.098	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/3	1078.006	1078.159	-142.479	0.399	664.913	0.464	15	0.091	R.YFKDAYDR.N
R5/RRR5-7/3	1077.258	1078.159	-1769.986	0.411	590.190	0.448	14	0.089	R.YFKDAYDR.N
R5/RRR5-7/3	1636.204	1635.868	205.593	0.433	636.294	0.424	26	0.087	R.SAAASSM*SALKQPTIR.V
R5/RRR5-7/3	1883.830	1884.210	-202.176	0.330	1390.149	0.207	27	0.084	R.AGKDLVSSLVSGLLTIGPR.F
R5/RRR5-7/3	1636.021	1635.868	93.584	0.371	767.592	0.385	29	0.083	R.SAAASSM*SALKQPTIR.V
R5/RRR5-7/3	1078.499	1078.159	316.255	0.420	470.627	0.445	13	0.081	-.YFKDAYDR.-
R5/RRR5-7/3	1599.682	1599.899	-136.025	0.233	894.893	0.272	25	0.067	K.VILGPATVGGIQAGAFK.I
R5/RRR5-7/3	1883.779	1884.210	-229.675	0.280	1081.618	0.142	25	0.056	R.AGKDLVSSLVSGLLTIGPR.F
R5/RRR5-4/2	1815.441	1815.062	209.635	0.613	2241.488	0.569	26	0.321	K.AYLPVIESFGFSSQLR.A
R5/RRR5-14/2	1815.298	1815.062	130.806	0.582	2155.010	0.593	25	0.314	K.AYLPVIESFGFSSQLR.A
R5/RRR5-5/2	1814.502	1815.062	-862.123	0.499	2309.348	0.470	25	0.304	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1814.295	1815.062	-976.810	0.511	2269.369	0.486	25	0.301	K.AYLPVIESFGFSSQLR.A
R5/RRR5-3/2	1814.425	1815.062	-904.672	0.509	2172.186	0.523	25	0.296	K.AYLPVIESFGFSSQLR.A
R5/RRR5-5/2	1814.306	1815.062	-970.663	0.490	2207.132	0.487	25	0.291	K.AYLPVIESFGFSSQLR.A
R5/RRR5-3/2	1814.999	1815.062	-34.445	0.550	2012.433	0.559	24	0.280	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1814.545	1815.062	-838.351	0.533	2044.479	0.529	24	0.277	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/3	1819.867	1819.945	-43.039	0.455	2044.794	0.517	35	0.276	K.NATLTNEKESDACPIR.A
R5/RRR5-4/3	1821.022	1819.945	42.377	0.516	1945.792	0.556	36	0.270	K.NATLTNEKESDACPIR.A
R5/RRR5-2/2	1815.225	1815.062	90.476	0.594	1941.898	0.559	24	0.269	K.AYLPVIESFGFSSQLR.A
R5/RRR5-14/2	1814.562	1815.062	-276.012	0.508	2017.875	0.514	23	0.268	K.AYLPVIESFGFSSQLR.A
R5/RRR5-3/2	1814.345	1815.062	-948.777	0.495	2046.483	0.492	25	0.267	K.AYLPVIESFGFSSQLR.A
R5/RRR5-1/2	1815.797	1815.062	-146.091	0.550	1986.238	0.522	24	0.266	K.AYLPVIESFGFSSQLR.A
R5/RRR5-2/2	1815.267	1815.062	113.272	0.571	1883.690	0.569	24	0.263	K.AYLPVIESFGFSSQLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1816.506	1815.062	245.438	0.579	1812.098	0.577	24	0.255	K.AYLPVIESFGFSSQLR.A
R5/RRR5-14/2	1815.606	1815.062	-251.576	0.573	1851.814	0.556	24	0.255	K.AYLPVIESFGFSSQLR.A
R5/RRR5-2/2	1814.145	1815.062	-1059.768	0.480	1870.690	0.535	24	0.253	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1820.257	1819.945	171.951	0.536	1806.208	0.547	22	0.249	K.NATLTNEKESDACPIR.A
R5/RRR5-8/3	1820.829	1819.945	-63.929	0.469	1955.329	0.486	35	0.243	K.NATLTNEKESDACPIR.A
R5/RRR5-1/2	1815.413	1815.062	194.464	0.566	1657.928	0.586	23	0.237	K.AYLPVIESFGFSSQLR.A
R5/RRR5-1/2	1815.551	1815.062	270.519	0.563	1714.771	0.546	23	0.234	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/3	1814.816	1815.062	-135.923	0.529	1812.766	0.518	31	0.232	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1819.270	1819.945	-923.327	0.545	1696.077	0.533	21	0.230	K.NATLTNEKESDACPIR.A
R5/RRR5-4/2	1388.131	1388.586	-328.520	0.483	1578.657	0.469	17	0.203	R.GFVQFCYEPIK.Q
R5/RRR5-4/2	1651.355	1651.841	-295.135	0.509	1756.900	0.379	19	0.200	K.ILSEEFGWDKDLAK.K
R5/RRR5-4/2	1388.256	1388.586	-238.091	0.481	1552.084	0.456	17	0.198	R.GFVQFCYEPIK.Q
R5/RRR5-4/2	1347.268	1347.588	-238.064	0.465	1321.082	0.562	18	0.195	R.VIYASQLTAKPR.L
R5/RRR5-4/2	1347.220	1347.588	-274.152	0.485	1325.804	0.554	18	0.194	R.VIYASQLTAKPR.L
R5/RRR5-4/2	1388.129	1388.586	-330.020	0.468	1492.580	0.446	17	0.189	R.GFVQFCYEPIK.Q
R5/RRR5-5/2	1813.791	1815.062	-1255.802	0.311	1753.094	0.313	23	0.187	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1815.657	1815.062	-223.651	0.501	1412.785	0.488	22	0.187	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1347.133	1347.588	-338.699	0.440	1266.363	0.537	18	0.184	R.VIYASQLTAKPR.L
R5/RRR5-10/2	1815.946	1815.062	-63.554	0.438	1290.583	0.512	20	0.179	K.AYLPVIESFGFSSQLR.A
R5/RRR5-2/2	1426.185	1425.569	-270.477	0.479	1166.479	0.544	18	0.178	R.LWGENFFDPATK.K
R5/RRR5-4/2	1426.013	1425.569	312.132	0.520	1253.978	0.494	19	0.177	R.LWGENFFDPATK.K
R5/RRR5-4/2	1425.118	1425.569	-317.502	0.492	1290.526	0.467	19	0.175	R.LWGENFFDPATK.K
R5/RRR5-4/2	1425.224	1425.569	-243.341	0.485	1212.210	0.502	19	0.175	R.LWGENFFDPATK.K
R5/RRR5-4/3	1814.675	1815.062	-213.659	0.461	1375.198	0.538	27	0.168	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1553.581	1553.742	-104.155	0.470	1306.672	0.412	21	0.166	R.LWGENFFDPATKK.W
R5/RRR5-4/2	1623.425	1623.846	-260.014	0.527	980.981	0.550	20	0.166	R.NCDPEGPLMLYVSK.M
R5/RRR5-3/2	1347.200	1347.588	-288.516	0.447	1091.434	0.505	17	0.165	R.VIYASQLTAKPR.L
R5/RRR5-4/2	1816.223	1815.062	89.011	0.330	1152.781	0.513	18	0.164	K.AYLPVIESFGFSSQLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1652.368	1651.841	-287.248	0.549	1406.990	0.377	18	0.163	K.ILSEEFGWDKDLAK.K
R5/RRR5-1/2	1347.297	1347.588	-216.430	0.424	1014.019	0.529	17	0.162	R.VIYASQLTAKPR.L
R5/RRR5-4/2	1652.461	1651.841	-230.476	0.537	1388.701	0.377	18	0.162	K.ILSEEFGWDKDLAK.K
R5/RRR5-3/3	1819.423	1819.945	-839.005	0.408	1567.519	0.434	32	0.160	K.NATLTNEKESDACPIR.A
R5/RRR5-4/2	1623.216	1623.846	-1007.014	0.517	1010.101	0.499	20	0.159	R.NCDPEGPLMLYVSK.M
R5/RRR5-8/2	1816.799	1815.062	-144.730	0.491	891.870	0.573	18	0.159	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1624.195	1623.846	215.398	0.565	1040.442	0.482	20	0.158	R.NCDPEGPLMLYVSK.M
R5/RRR5-3/2	1424.666	1425.569	-1340.209	0.479	970.415	0.499	16	0.156	R.LWGENFFDPATK.K
R5/RRR5-1/2	1815.285	1815.062	123.320	0.478	1045.936	0.477	19	0.154	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	1867.384	1868.098	-920.447	0.502	1235.705	0.571	21	0.150	K.GLKEQM*TPLSDFEDKL.-
R5/RRR5-4/2	1639.194	1639.845	-1010.502	0.467	974.870	0.443	20	0.149	R.NCDPEGPLM*LYVSK.M
R5/RRR5-4/2	1639.295	1639.845	-948.523	0.495	1076.420	0.389	20	0.146	R.NCDPEGPLM*LYVSK.M
R5/RRR5-4/2	1639.197	1639.845	-1008.857	0.482	1102.707	0.370	21	0.146	R.NCDPEGPLM*LYVSK.M
R5/RRR5-4/3	1819.709	1819.945	-129.939	0.431	1389.210	0.465	32	0.146	K.NATLTNEKESDACPIR.A
R5/RRR5-4/2	1503.431	1503.774	-228.809	0.585	603.155	0.491	19	0.141	R.RVIYASQLTAKPR.L
R5/RRR5-4/2	1503.117	1503.774	-1106.129	0.577	730.235	0.455	20	0.141	R.RVIYASQLTAKPR.L
R5/RRR5-3/2	1425.106	1425.569	-326.182	0.416	788.116	0.439	16	0.139	R.LWGENFFDPATK.K
R5/RRR5-3/2	891.004	891.049	-50.996	0.369	652.770	0.443	12	0.137	K.FSVSPVVR.V
R5/RRR5-4/2	744.758	744.863	-140.496	0.387	343.973	0.474	9	0.134	-.FFAFGR.-
R5/RRR5-4/2	890.985	891.049	-72.434	0.347	643.479	0.402	12	0.132	K.FSVSPVVR.V
R5/RRR5-1/2	1640.299	1639.845	277.170	0.446	889.020	0.341	19	0.131	R.NCDPEGPLM*LYVSK.M
R5/RRR5-1/3	1819.565	1819.945	-209.687	0.421	1120.364	0.517	28	0.131	K.NATLTNEKESDACPIR.A
R5/RRR5-5/2	1650.947	1651.841	-1150.659	0.416	1100.052	0.280	17	0.130	K.ILSEEFGWDKDLAK.K
R5/RRR5-2/2	1503.910	1503.774	90.562	0.512	261.374	0.413	16	0.130	R.RVIYASQLTAKPR.L
R5/RRR5-8/2	744.779	744.863	-112.710	0.362	346.339	0.399	9	0.130	-.FFAFGR.-
R5/RRR5-11/2	1816.627	1815.062	-239.910	0.367	599.321	0.422	17	0.129	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/2	744.413	744.863	-605.858	0.316	339.070	0.453	9	0.129	-.FFAFGR.-
R5/RRR5-8/2	745.065	744.863	271.866	0.435	344.055	0.420	9	0.129	-.FFAFGR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	891.021	891.049	-32.444	0.346	523.834	0.364	11	0.128	K.FSVSPVVR.V
R5/RRR5-2/2	1425.125	1425.569	-312.517	0.294	693.273	0.392	14	0.128	R.LWGENFFDPATK.K
R5/RRR5-1/2	744.932	744.863	93.091	0.318	281.950	0.375	9	0.128	-.FFAFGR.-
R5/RRR5-5/2	744.906	744.863	58.414	0.339	365.421	0.361	9	0.127	-.FFAFGR.-
R5/RRR5-4/2	890.944	891.049	-119.024	0.305	555.002	0.372	11	0.127	K.FSVSPVVR.V
R5/RRR5-5/2	1425.308	1425.569	-184.140	0.437	333.862	0.391	12	0.126	R.LWGENFFDPATK.K
R5/RRR5-13/3	1503.428	1503.774	-231.099	0.480	1411.429	0.386	26	0.126	R.RVIYASQLTAKPR.L
R5/RRR5-3/2	1425.150	1425.569	-295.416	0.350	728.275	0.339	14	0.126	R.LWGENFFDPATK.K
R5/RRR5-8/2	891.119	891.049	78.576	0.324	558.423	0.361	11	0.125	-.FSVSPVVR.-
R5/RRR5-4/2	1119.628	1120.219	-1425.176	0.334	738.458	0.335	14	0.125	K.EGALAEENMR.G
R5/RRR5-4/2	1119.191	1120.219	-1817.814	0.295	858.873	0.296	15	0.125	K.EGALAEENMR.G
R5/RRR5-1/2	744.434	744.863	-577.716	0.224	355.366	0.323	9	0.124	R.FFAFGR.V
R5/RRR5-3/3	1503.487	1503.774	-191.635	0.481	1215.045	0.452	25	0.124	R.RVIYASQLTAKPR.L
R5/RRR5-3/2	891.000	891.049	-55.531	0.367	459.431	0.340	10	0.124	-.FSVSPVVR.-
R5/RRR5-10/2	1816.509	1815.062	246.920	0.353	530.521	0.376	15	0.124	K.AYLPVIESFGFSSQLR.A
R5/RRR5-2/2	1425.138	1425.569	-303.838	0.371	496.399	0.338	13	0.123	R.LWGENFFDPATK.K
R5/RRR5-4/2	744.462	744.863	-540.526	0.252	351.753	0.350	9	0.123	-.FFAFGR.-
R5/RRR5-8/2	1425.159	1425.569	-288.884	0.294	457.187	0.375	12	0.123	R.LWGENFFDPATK.K
R5/RRR5-7/2	891.048	891.049	-2.076	0.282	610.792	0.295	11	0.123	K.FSVSPVVR.V
R5/RRR5-10/2	1814.128	1815.062	-1069.024	0.298	530.003	0.348	16	0.122	K.AYLPVIESFGFSSQLR.A
R5/RRR5-5/2	744.726	744.863	-183.740	0.337	416.054	0.244	10	0.121	-.FFAFGR.-
R5/RRR5-2/3	1819.556	1819.945	-214.735	0.429	943.119	0.533	26	0.120	K.NATLTNEKESDACPIR.A
R5/RRR5-7/2	890.867	891.049	-205.206	0.284	404.375	0.377	9	0.120	-.FSVSPVVR.-
R5/RRR5-3/2	744.904	744.863	55.784	0.243	355.716	0.252	9	0.119	-.FFAFGR.-
R5/RRR5-5/2	1424.878	1425.569	-1190.409	0.279	755.761	0.226	14	0.118	R.LWGENFFDPATK.K
R5/RRR5-2/3	1814.664	1815.062	-219.935	0.483	1164.441	0.444	26	0.118	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/3	1503.389	1503.774	-256.759	0.541	1182.466	0.436	25	0.117	R.RVIYASQLTAKPR.L
R5/RRR5-1/2	1425.390	1425.569	-126.321	0.270	320.711	0.350	10	0.116	-.LWGENFFDPATK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	890.322	891.049	-1946.465	0.313	611.635	0.269	11	0.116	-.FSVSPVVR.-
R5/RRR5-10/2	1814.018	1815.062	-1130.172	0.268	795.375	0.208	16	0.116	K.AYLPVIESFGFSSQLR.A
R5/RRR5-8/2	1425.184	1425.569	-271.526	0.306	312.452	0.329	10	0.112	-.LWGENFFDPATK.-
R5/RRR5-4/2	1868.177	1868.098	42.172	0.528	1027.241	0.536	20	0.110	K.GLKEQM*TPLSDFEDKL.-
R5/RRR5-2/2	744.454	744.863	-550.235	0.191	347.104	0.296	9	0.109	-.FFAFGR.-
R5/RRR5-3/2	744.361	744.863	-2023.270	0.129	280.429	0.350	8	0.108	-.FFAFGR.-
R5/RRR5-1/3	1819.658	1819.945	-158.405	0.371	1073.446	0.421	28	0.106	K.NATLTNEKESDACPIR.A
R5/RRR5-3/3	1820.017	1819.945	39.407	0.415	1054.283	0.424	29	0.105	K.NATLTNEKESDACPIR.A
R5/RRR5-7/2	890.488	891.049	-1758.698	0.182	464.136	0.235	9	0.100	-.FSVSPVVR.-
R5/RRR5-6/3	1503.771	1503.774	-1.931	0.416	1388.955	0.282	27	0.099	R.RVIYASQLTAKPR.L
R5/RRR5-4/3	1680.217	1681.012	-1071.885	0.431	878.902	0.415	25	0.090	K.LGVVM*KADEKELM*GK.A
R5/RRR5-1/3	1503.162	1503.774	-1075.926	0.432	696.725	0.396	23	0.089	R.RVIYASQLTAKPR.L
R5/RRR5-3/3	1502.882	1503.774	-1262.728	0.443	915.636	0.368	22	0.089	R.RVIYASQLTAKPR.L
R5/RRR5-3/3	1819.399	1819.945	-852.138	0.430	896.522	0.371	25	0.088	K.NATLTNEKESDACPIR.A
R5/RRR5-1/3	1503.586	1503.774	-125.420	0.445	828.439	0.354	23	0.086	R.RVIYASQLTAKPR.L
R5/RRR5-3/3	1814.727	1815.062	-184.810	0.404	1026.362	0.322	27	0.085	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/3	1814.600	1815.062	-255.164	0.297	946.307	0.349	23	0.084	K.AYLPVIESFGFSSQLR.A
R5/RRR5-4/3	1421.188	1421.624	-307.836	0.347	808.578	0.373	21	0.082	K.FGVDEFKM*M*ER.L
R5/RRR5-5/3	1502.916	1503.774	-1239.848	0.378	1118.049	0.275	24	0.082	R.RVIYASQLTAKPR.L
R5/RRR5-4/3	1421.630	1421.624	3.857	0.376	595.345	0.364	18	0.080	K.FGVDEFKM*M*ER.L
R5/RRR5-2/3	1815.001	1815.062	-33.508	0.368	742.377	0.353	21	0.079	K.AYLPVIESFGFSSQLR.A
R5/RRR5-1/3	1504.869	1503.774	62.955	0.371	711.505	0.289	22	0.078	R.RVIYASQLTAKPR.L
R5/RRR5-5/3	1502.591	1503.774	-1457.066	0.381	662.210	0.293	19	0.077	R.RVIYASQLTAKPR.L
R5/RRR5-4/3	1421.330	1421.624	-207.665	0.369	807.738	0.319	21	0.077	K.FGVDEFKM*M*ER.L
R5/RRR5-11/3	1502.849	1503.774	-1284.753	0.350	676.505	0.239	21	0.074	R.RVIYASQLTAKPR.L
R5/RRR5-4/2	1569.134	1569.715	-1010.646	0.399	754.964	0.270	16	0.073	K.EQM*TPLSDFEDKL.-
R5/RRR5-11/3	1503.507	1503.774	-178.318	0.371	787.487	0.218	22	0.071	R.RVIYASQLTAKPR.L
R5/RRR5-1/2	1569.691	1569.715	-15.471	0.416	695.515	0.276	15	0.071	K.EQM*TPLSDFEDKL.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1502.423	1503.774	-1569.567	0.340	745.422	0.195	21	0.058	-.RVIYASQLTAKPR.-
R5/RRR5-3/2	1213.026	1213.324	-246.948	0.521	1727.053	0.412	17	0.208	K.FYVQTVGDQR.V
R5/RRR5-3/2	1213.247	1213.324	-63.639	0.522	1656.152	0.393	17	0.195	K.FYVQTVGDQR.V
R5/RRR5-5/2	1418.759	1419.565	-1276.664	0.451	1676.464	0.380	17	0.194	K.AALQNLEQFQEK.A
R5/RRR5-3/2	1287.406	1286.503	-75.190	0.455	1335.330	0.532	19	0.191	R.VASIQQQLASLK.L
R5/RRR5-3/2	1433.962	1434.684	-1204.605	0.398	1618.312	0.394	21	0.191	K.TNM*ASVLLEAGLAK.L
R5/RRR5-3/2	1274.247	1274.359	-88.169	0.408	1484.876	0.404	16	0.179	R.DVEIEVEAVDR.T
R5/RRR5-5/2	1286.294	1286.503	-163.301	0.352	1411.901	0.433	17	0.176	R.VASIQQQLASLK.L
R5/RRR5-3/2	1212.461	1213.324	-1541.448	0.432	1428.773	0.406	16	0.176	K.FYVQTVGDQR.V
R5/RRR5-5/2	1213.083	1213.324	-199.802	0.460	1311.621	0.432	16	0.171	K.FYVQTVGDQR.V
R5/RRR5-3/2	1286.382	1286.503	-94.666	0.420	1267.143	0.461	18	0.171	R.VASIQQQLASLK.L
R5/RRR5-3/3	1547.720	1547.738	-11.488	0.504	1688.348	0.396	28	0.169	R.KAALQNLEQFQEK.A
R5/RRR5-3/2	1433.973	1434.684	-1197.167	0.482	1306.306	0.432	19	0.168	K.TNM*ASVLLEAGLAK.L
R5/RRR5-3/2	1462.259	1461.595	-230.479	0.424	1194.596	0.450	18	0.162	K.ETCSIAFSFSGVR.C
R5/RRR5-3/2	1502.126	1502.659	-1023.311	0.527	861.624	0.550	21	0.159	R.HSAIVEYVFSGHR.F
R5/RRR5-3/3	1502.712	1502.659	35.506	0.575	1460.936	0.460	27	0.153	R.HSAIVEYVFSGHR.F
R5/RRR5-4/2	1286.533	1286.503	23.829	0.320	1250.069	0.371	17	0.153	R.VASIQQQLASLK.L
R5/RRR5-5/2	1418.968	1419.565	-1128.409	0.370	1347.818	0.294	17	0.149	K.AALQNLEQFQEK.A
R5/RRR5-3/2	1285.739	1286.503	-1376.273	0.278	1117.140	0.413	18	0.148	R.VASIQQQLASLK.L
R5/RRR5-3/2	1419.168	1419.565	-280.614	0.500	1301.848	0.309	18	0.147	K.AALQNLEQFQEK.A
R5/RRR5-3/2	1461.516	1461.595	-54.001	0.391	1077.086	0.399	18	0.146	K.ETCSIAFSFSGVR.C
R5/RRR5-3/2	1647.233	1647.726	-300.259	0.477	917.008	0.449	23	0.146	R.ISTVDGQPTTNTADAR.V
R5/RRR5-3/2	1433.448	1434.684	-1564.630	0.368	939.128	0.469	17	0.146	K.TNM*ASVLLEAGLAK.L
R5/RRR5-3/3	1502.134	1502.659	-1018.058	0.534	1534.917	0.402	28	0.145	R.HSAIVEYVFSGHR.F
R5/RRR5-3/2	1057.356	1058.254	-1799.756	0.316	852.157	0.503	16	0.144	K.VVVTEVLGGGK.F
R5/RRR5-3/2	1263.152	1263.473	-254.693	0.437	1031.224	0.385	14	0.143	K.ARDFLPFLQR.N
R5/RRR5-3/2	1647.256	1647.726	-286.058	0.464	706.739	0.508	21	0.143	R.ISTVDGQPTTNTADAR.V
R5/RRR5-3/3	1547.289	1547.738	-290.661	0.439	1687.078	0.302	26	0.141	R.KAALQNLEQFQEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1274.047	1274.359	-245.884	0.332	1346.930	0.236	15	0.140	R.DVEIEVEAVDR.T
R5/RRR5-5/2	1286.312	1286.503	-148.545	0.339	914.303	0.418	16	0.140	R.VASIQQQLASLK.L
R5/RRR5-3/2	1326.266	1326.479	-161.426	0.466	762.056	0.429	17	0.138	R.TGTFLGSLWESK.T
R5/RRR5-3/2	1274.399	1274.359	31.454	0.375	1173.144	0.289	15	0.137	R.DVEIEVEAVDR.T
R5/RRR5-3/2	1418.314	1419.565	-1591.807	0.361	1177.995	0.261	17	0.134	K.AALQNLEQFQEK.A
R5/RRR5-3/2	1045.006	1045.238	-222.763	0.462	692.366	0.376	15	0.134	R.IPDANVLM*R.A
R5/RRR5-4/2	1326.257	1326.479	-168.074	0.463	616.495	0.437	15	0.133	R.TGTFLGSLWESK.T
R5/RRR5-4/2	1286.155	1286.503	-271.557	0.279	1070.628	0.297	17	0.133	R.VASIQQQLASLK.L
R5/RRR5-4/2	1213.085	1213.324	-197.581	0.338	918.064	0.314	15	0.130	K.FYVQTVGDQR.V
R5/RRR5-3/2	1648.538	1647.726	-114.124	0.445	529.416	0.440	18	0.129	R.ISTVDGQPTTNTADAR.V
R5/RRR5-3/2	1418.184	1418.685	-1061.175	0.335	976.847	0.285	18	0.128	K.TNMASVLLEAGLAK.L
R5/RRR5-3/2	1418.140	1418.685	-1092.203	0.366	969.455	0.281	18	0.127	K.TNMASVLLEAGLAK.L
R5/RRR5-3/2	1044.287	1045.238	-1873.948	0.338	639.263	0.327	15	0.126	R.IPDANVLM*R.A
R5/RRR5-3/2	1325.757	1326.479	-1302.961	0.320	616.316	0.375	15	0.126	R.TGTFLGSLWESK.T
R5/RRR5-3/2	1044.549	1045.238	-1622.052	0.344	659.884	0.303	15	0.125	R.IPDANVLM*R.A
R5/RRR5-3/2	1264.149	1263.473	-256.816	0.398	711.373	0.323	12	0.123	K.ARDFLPFLQR.N
R5/RRR5-3/2	1462.350	1461.595	-168.005	0.370	589.168	0.353	14	0.122	K.ETCSIAFSFSGVR.C
R5/RRR5-5/2	1326.962	1326.479	364.773	0.434	430.283	0.387	13	0.120	-.TGTFLGSLWESK.-
R5/RRR5-3/2	1325.972	1326.479	-1140.328	0.248	408.836	0.347	13	0.119	-.TGTFLGSLWESK.-
R5/RRR5-3/2	1264.524	1263.473	40.510	0.407	689.895	0.312	12	0.112	-.ARDFLPFLQR.-
R5/RRR5-3/3	1921.278	1921.211	35.099	0.411	1146.464	0.423	29	0.112	K.LSSFGLDRIPDANVLM*R.A
R5/RRR5-4/2	1057.852	1058.254	-380.510	0.224	504.230	0.278	12	0.109	-.VVVTEVLGGGK.-
R5/RRR5-3/3	1469.508	1469.753	-167.279	0.458	1342.004	0.319	26	0.106	K.LKDAPVIGAFNPVK.G
R5/RRR5-5/3	1502.788	1502.659	86.221	0.510	984.563	0.423	23	0.102	R.HSAIVEYVFSGHR.F
R5/RRR5-3/3	1502.897	1502.659	159.413	0.488	1225.112	0.334	24	0.099	R.HSAIVEYVFSGHR.F
R5/RRR5-5/3	1502.614	1502.659	-29.637	0.424	982.510	0.368	23	0.091	R.HSAIVEYVFSGHR.F
R5/RRR5-5/3	1502.804	1502.659	96.975	0.443	990.399	0.337	23	0.087	R.HSAIVEYVFSGHR.F
R5/RRR5-3/3	1468.870	1469.753	-1285.799	0.383	1173.464	0.259	23	0.083	-.LKDAPVIGAFNPVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/3	1248.362	1248.330	25.822	0.471	926.471	0.324	18	0.081	R.RDEKPDNFAR.E
R5/RRR5-2/3	1922.369	1921.211	82.433	0.364	620.915	0.330	21	0.075	K.LSSFGLDRIPDANVLM*R.A
R5/RRR5-4/3	1502.903	1502.659	163.201	0.421	963.362	0.244	22	0.072	R.HSAIVEYVFSGHR.F
R5/RRR5-3/3	1419.654	1419.565	63.112	0.410	1046.391	0.221	22	0.070	K.AALQNLEQFQEK.A
R5/RRR5-3/3	1920.414	1921.211	-938.460	0.309	1059.955	0.221	27	0.070	K.LSSFGLDRIPDANVLM*R.A
R5/RRR5-3/3	1920.670	1921.211	-804.754	0.312	795.234	0.288	23	0.069	-.LSSFGLDRIPDANVLM*R.-
R5/RRR5-3/3	1905.059	1905.211	-80.158	0.305	533.088	0.289	21	0.062	-.LSSFGLDRIPDANVLMR.-
R5/RRR5-3/3	1974.834	1974.290	-231.733	0.554	3481.968	0.531	41	0.773	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-3/2	1974.502	1974.290	107.671	0.627	2632.165	0.562	29	0.398	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-2/3	1974.764	1974.290	240.828	0.541	2462.686	0.510	36	0.389	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-3/2	1973.959	1974.290	-168.128	0.599	2395.792	0.563	28	0.350	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-3/2	1974.577	1974.290	145.615	0.608	2398.644	0.559	28	0.349	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-3/2	1644.922	1645.938	-1229.156	0.482	2668.004	0.386	23	0.347	K.IFM*VGSGALGCEFLK.N
R5/RRR5-3/2	1571.259	1570.728	-299.114	0.596	2405.865	0.523	24	0.342	R.YDAQISVFGSNLQK.K
R5/RRR5-3/2	1646.156	1645.938	133.092	0.568	2498.081	0.453	24	0.335	K.IFM*VGSGALGCEFLK.N
R5/RRR5-3/2	1571.353	1570.728	-239.567	0.598	2249.375	0.511	24	0.309	R.YDAQISVFGSNLQK.K
R5/RRR5-3/2	1645.468	1645.938	-286.217	0.498	2341.244	0.439	21	0.303	K.IFM*VGSGALGCEFLK.N
R5/RRR5-3/2	1975.865	1974.290	-215.866	0.572	1931.015	0.479	28	0.246	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-3/2	1975.350	1974.290	30.643	0.562	1851.832	0.475	26	0.233	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-3/2	1569.523	1570.728	-1408.807	0.425	1900.437	0.370	23	0.219	R.YDAQISVFGSNLQK.K
R5/RRR5-3/2	1629.382	1629.939	-957.892	0.494	1877.889	0.378	22	0.216	K.IFMVGSGALGCEFLK.N
R5/RRR5-3/2	1448.093	1448.566	-327.684	0.437	1740.731	0.380	20	0.202	R.RFPIAGSSDDVQR.L
R5/RRR5-3/2	1448.271	1448.566	-204.638	0.466	1568.981	0.396	19	0.186	R.RFPIAGSSDDVQR.L
R5/RRR5-3/2	1292.209	1292.380	-132.802	0.508	1413.253	0.432	19	0.179	R.FPIAGSSDDVQR.L
R5/RRR5-3/2	1291.462	1292.380	-1489.248	0.400	1420.911	0.421	19	0.177	R.FPIAGSSDDVQR.L
R5/RRR5-3/2	1448.229	1448.566	-233.134	0.420	1511.456	0.355	19	0.173	R.RFPIAGSSDDVQR.L
R5/RRR5-3/2	1247.986	1248.362	-301.740	0.476	1130.679	0.450	18	0.161	K.LTVTDDDVIEK.S
R5/RRR5-3/2	1080.142	1080.223	-74.655	0.415	1259.645	0.377	15	0.158	K.LHVEALQNR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1282.110	1282.342	-181.214	0.455	1283.468	0.359	17	0.156	R.APEIDEDLHSR.Q
R5/RRR5-3/2	1247.606	1248.362	-1411.567	0.426	1144.525	0.388	18	0.152	K.LTVTDDDVIEK.S
R5/RRR5-3/2	1291.393	1292.380	-1543.275	0.432	1192.287	0.360	18	0.149	R.FPIAGSSDDVQR.L
R5/RRR5-3/2	1247.981	1248.362	-306.254	0.453	1009.274	0.426	17	0.149	K.LTVTDDDVIEK.S
R5/RRR5-3/2	957.962	958.053	-94.976	0.466	1106.135	0.370	13	0.146	R.DWNIGQPK.S
R5/RRR5-3/2	1079.588	1080.223	-1518.975	0.412	982.806	0.413	14	0.145	K.LHVEALQNR.A
R5/RRR5-3/2	1282.079	1282.342	-205.475	0.430	1100.389	0.370	16	0.145	R.APEIDEDLHSR.Q
R5/RRR5-3/2	1318.413	1319.447	-1547.400	0.415	839.081	0.457	15	0.144	R.LKFEDYFSNR.V
R5/RRR5-3/2	1282.052	1282.342	-226.394	0.448	1027.034	0.373	15	0.141	R.APEIDEDLHSR.Q
R5/RRR5-3/2	1080.052	1080.223	-158.776	0.434	923.218	0.379	15	0.140	K.LHVEALQNR.A
R5/RRR5-3/2	1319.148	1319.447	-227.453	0.487	878.318	0.390	16	0.140	R.LKFEDYFSNR.V
R5/RRR5-3/2	1473.262	1473.697	-295.824	0.408	746.926	0.449	19	0.139	R.AETFGIPIPDWVK.N
R5/RRR5-3/2	1474.992	1473.697	200.497	0.494	709.442	0.431	19	0.137	R.AETFGIPIPDWVK.N
R5/RRR5-3/2	1318.340	1319.447	-1603.023	0.390	676.454	0.441	13	0.134	R.LKFEDYFSNR.V
R5/RRR5-3/2	1052.148	1052.160	-10.777	0.395	790.411	0.379	14	0.134	R.SEFEGLLEK.T
R5/RRR5-3/2	1473.457	1473.697	-163.083	0.377	617.127	0.427	17	0.131	R.AETFGIPIPDWVK.N
R5/RRR5-3/2	1051.610	1052.160	-1477.888	0.334	759.272	0.363	13	0.130	R.SEFEGLLEK.T
R5/RRR5-4/2	1571.790	1570.728	39.680	0.396	712.754	0.349	17	0.126	R.YDAQISVFGSNLQK.K
R5/RRR5-3/2	1051.501	1052.160	-1582.022	0.318	518.055	0.367	12	0.125	R.SEFEGLLEK.T
R5/RRR5-3/2	1630.896	1629.939	-25.946	0.350	757.860	0.349	16	0.125	K.IFMVGSGALGCEFLK.N
R5/RRR5-2/2	1974.877	1974.290	-209.960	0.449	572.607	0.388	18	0.122	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-1/2	1320.400	1319.447	-35.386	0.366	546.202	0.330	12	0.121	-.LKFEDYFSNR.-
R5/RRR5-3/3	1846.495	1844.990	-268.726	0.421	1275.486	0.412	24	0.121	R.EKCETFQDCITWAR.L
R5/RRR5-3/3	1883.869	1882.198	-175.168	0.384	1579.098	0.272	26	0.120	K.FDRPPLLHLAFQALDK.F
R5/RRR5-1/2	1975.166	1974.290	-62.708	0.279	588.496	0.206	15	0.111	R.LFASNVLVSGLNGLGAEIAK.N
R5/RRR5-1/2	1052.145	1052.160	-14.152	0.285	307.626	0.304	10	0.109	-.SEFEGLLEK.-
R5/RRR5-3/3	1973.570	1974.290	-874.068	0.345	955.253	0.406	27	0.095	-.LFASNVLVSGLNGLGAEIAK.-
R5/RRR5-3/3	1974.257	1974.290	-16.789	0.424	1096.418	0.323	30	0.087	R.LFASNVLVSGLNGLGAEIAK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/3	1125.273	1125.265	6.776	0.353	250.282	0.294	14	0.087	-.LLHHFASGSR.-
R5/RRR5-3/3	1125.231	1125.265	-30.273	0.362	474.432	0.368	17	0.084	K.LLHHFASGSR.A
R5/RRR5-3/3	1125.321	1125.265	50.025	0.370	849.089	0.371	21	0.084	K.LLHHFASGSR.A
R5/RRR5-1/3	1124.805	1125.265	-410.067	0.337	555.281	0.362	19	0.081	K.LLHHFASGSR.A
R5/RRR5-3/3	1125.411	1125.265	130.473	0.325	695.758	0.309	19	0.076	K.LLHHFASGSR.A
R5/RRR5-3/3	1319.870	1319.447	321.593	0.462	865.221	0.311	20	0.073	-.LKFEDYFSNR.-
R5/RRR5-3/3	1846.723	1844.990	-144.779	0.311	773.283	0.140	21	0.059	R.EKCETFQDCITWAR.L
R5/RRR5-3/3	1974.822	1974.290	-237.686	0.319	685.477	0.153	24	0.057	-.LFASNVLVSGLNGLGAEIAK.-
R5/RRR5-3/3	1319.565	1319.447	89.518	0.446	724.844	0.232	18	0.056	-.LKFEDYFSNR.-
R5/RRR5-11/2	1449.219	1449.629	-283.497	0.526	1927.776	0.511	22	0.258	R.VATVQCLSGTGSLR.V
R5/RRR5-12/2	1449.206	1449.629	-292.708	0.522	1844.929	0.541	22	0.254	R.VATVQCLSGTGSLR.V
R5/RRR5-11/2	1449.276	1449.629	-243.949	0.529	1762.196	0.574	22	0.251	R.VATVQCLSGTGSLR.V
R5/RRR5-12/2	1574.367	1574.798	-274.415	0.498	1807.860	0.553	23	0.251	R.VGALSIVCGSADVAVR.V
R5/RRR5-11/2	1531.394	1531.695	-196.808	0.493	1867.359	0.457	22	0.235	K.LIFGADSPAIQENR.V
R5/RRR5-11/2	1575.340	1574.798	-291.578	0.526	1735.630	0.527	22	0.234	R.VGALSIVCGSADVAVR.V
R5/RRR5-11/2	1575.478	1574.798	-203.502	0.549	1521.062	0.593	21	0.222	R.VGALSIVCGSADVAVR.V
R5/RRR5-12/2	1532.233	1531.695	-302.578	0.539	1606.944	0.492	22	0.211	K.LIFGADSPAIQENR.V
R5/RRR5-12/2	1531.252	1531.695	-290.218	0.504	1735.371	0.429	21	0.211	K.LIFGADSPAIQENR.V
R5/RRR5-12/2	1587.059	1586.748	197.067	0.524	1643.546	0.473	18	0.210	K.DSAM*FNEWTVELK.G
R5/RRR5-11/2	1532.178	1531.695	316.475	0.545	1583.823	0.483	21	0.206	K.LIFGADSPAIQENR.V
R5/RRR5-12/2	1573.887	1574.798	-1217.499	0.408	1556.408	0.488	22	0.202	R.VGALSIVCGSADVAVR.V
R5/RRR5-12/2	1530.743	1531.695	-1278.689	0.338	1774.860	0.334	22	0.195	K.LIFGADSPAIQENR.V
R5/RRR5-11/2	1708.647	1708.979	-194.736	0.517	1373.771	0.487	24	0.186	R.VKEYLPITGLADFNK.L
R5/RRR5-11/2	1574.638	1574.798	-101.751	0.483	1335.030	0.497	21	0.182	R.VGALSIVCGSADVAVR.V
R5/RRR5-12/2	1481.941	1481.674	180.720	0.513	1136.557	0.493	20	0.168	K.EYLPITGLADFNK.L
R5/RRR5-12/2	1481.279	1481.674	-267.442	0.474	1168.401	0.479	20	0.167	K.EYLPITGLADFNK.L
R5/RRR5-12/2	1481.189	1481.674	-328.628	0.413	1205.624	0.443	20	0.163	K.EYLPITGLADFNK.L
R5/RRR5-11/2	1482.016	1481.674	231.354	0.477	1148.182	0.455	20	0.162	K.EYLPITGLADFNK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1448.700	1449.629	-1335.554	0.414	1097.365	0.485	19	0.160	R.VATVQCLSGTGSLR.V
R5/RRR5-11/2	1481.534	1481.674	-95.171	0.452	1217.711	0.413	20	0.160	K.EYLPITGLADFNK.L
R5/RRR5-11/2	1708.310	1708.979	-980.003	0.482	1184.709	0.423	23	0.159	R.VKEYLPITGLADFNK.L
R5/RRR5-11/2	1708.601	1708.979	-221.828	0.483	1142.916	0.431	23	0.158	R.VKEYLPITGLADFNK.L
R5/RRR5-12/2	948.525	949.089	-1654.058	0.449	945.855	0.462	15	0.152	K.VNLGVGAYR.D
R5/RRR5-12/2	948.532	949.089	-1646.301	0.445	934.593	0.455	15	0.151	K.VNLGVGAYR.D
R5/RRR5-12/2	1077.298	1077.302	-3.820	0.422	846.753	0.487	17	0.150	K.VFTLAGLTVR.S
R5/RRR5-12/2	1453.795	1454.697	-1312.261	0.518	616.645	0.539	19	0.148	R.TEEGKPLVLNVVR.R
R5/RRR5-12/3	1531.604	1531.695	-59.453	0.489	1702.450	0.326	29	0.147	K.LIFGADSPAIQENR.V
R5/RRR5-12/2	848.910	848.969	-70.039	0.527	1108.925	0.368	13	0.147	R.VGGEFLAR.H
R5/RRR5-11/2	948.315	949.089	-1876.622	0.462	742.941	0.474	14	0.145	K.VNLGVGAYR.D
R5/RRR5-12/2	1454.237	1454.697	-316.785	0.522	836.224	0.432	21	0.143	R.TEEGKPLVLNVVR.R
R5/RRR5-12/2	1708.439	1708.979	-903.963	0.526	1003.038	0.400	21	0.143	R.VKEYLPITGLADFNK.L
R5/RRR5-11/2	948.477	949.089	-1704.097	0.413	632.733	0.506	13	0.142	K.VNLGVGAYR.D
R5/RRR5-11/2	848.309	848.969	-1963.700	0.451	1113.615	0.324	13	0.142	R.VGGEFLAR.H
R5/RRR5-12/2	1077.150	1077.302	-141.699	0.442	841.166	0.382	17	0.138	K.VFTLAGLTVR.S
R5/RRR5-12/2	1077.139	1077.302	-151.589	0.446	823.132	0.379	17	0.137	K.VFTLAGLTVR.S
R5/RRR5-12/2	1455.731	1454.697	23.246	0.504	693.449	0.422	20	0.137	R.TEEGKPLVLNVVR.R
R5/RRR5-12/2	848.838	848.969	-154.713	0.525	1044.524	0.318	13	0.137	R.VGGEFLAR.H
R5/RRR5-11/2	848.856	848.969	-133.363	0.527	1062.159	0.314	13	0.137	R.VGGEFLAR.H
R5/RRR5-11/2	948.261	949.089	-1933.540	0.398	661.428	0.444	13	0.137	K.VNLGVGAYR.D
R5/RRR5-12/2	848.815	848.969	-182.701	0.537	1078.187	0.309	13	0.137	R.VGGEFLAR.H
R5/RRR5-12/2	907.943	908.059	-127.477	0.357	967.686	0.378	13	0.137	R.ISM*AGLSGR.T
R5/RRR5-11/2	1454.372	1454.697	-224.321	0.461	594.803	0.444	19	0.136	R.TEEGKPLVLNVVR.R
R5/RRR5-12/2	1559.269	1558.807	297.314	0.478	489.400	0.491	20	0.136	R.TIPHLADAIHAAVTK.L
R5/RRR5-11/2	1530.671	1531.695	-1326.023	0.285	1187.854	0.270	19	0.136	K.LIFGADSPAIQENR.V
R5/RRR5-11/2	848.950	848.969	-23.452	0.500	1080.268	0.293	13	0.135	R.VGGEFLAR.H
R5/RRR5-12/2	948.196	949.089	-2002.238	0.395	530.813	0.422	12	0.132	K.VNLGVGAYR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1653.268	1652.877	237.086	0.405	563.341	0.437	18	0.131	R.TIYIPQPTWGNHPK.V
R5/RRR5-12/2	1709.424	1708.979	260.956	0.478	1069.996	0.288	21	0.131	R.VKEYLPITGLADFNK.L
R5/RRR5-12/2	1558.469	1558.807	-217.508	0.406	613.439	0.393	21	0.129	R.TIPHLADAIHAAVTK.L
R5/RRR5-11/2	1077.085	1077.302	-201.386	0.425	824.551	0.290	17	0.128	K.VFTLAGLTVR.S
R5/RRR5-12/2	1652.162	1652.877	-1041.024	0.333	587.456	0.396	19	0.127	R.TIYIPQPTWGNHPK.V
R5/RRR5-11/2	1481.011	1481.674	-1126.276	0.363	825.386	0.316	17	0.127	K.EYLPITGLADFNK.L
R5/RRR5-13/2	1531.942	1531.695	161.475	0.368	653.346	0.319	16	0.123	K.LIFGADSPAIQENR.V
R5/RRR5-12/2	1652.403	1652.877	-287.908	0.251	269.060	0.360	13	0.119	R.TIYIPQPTWGNHPK.V
R5/RRR5-1/2	1531.252	1531.695	-290.218	0.358	523.356	0.233	15	0.117	K.LIFGADSPAIQENR.V
R5/RRR5-12/3	1531.722	1531.695	17.888	0.500	1351.342	0.303	26	0.102	K.LIFGADSPAIQENR.V
R5/RRR5-12/3	1500.389	1500.618	-153.146	0.375	710.401	0.470	23	0.092	R.QEYHIYMTSDGR.I
R5/RRR5-12/3	1500.431	1500.618	-125.112	0.341	551.177	0.497	20	0.089	R.QEYHIYMTSDGR.I
R5/RRR5-11/3	1531.055	1531.695	-1074.077	0.338	1142.284	0.285	24	0.083	K.LIFGADSPAIQENR.V
R5/RRR5-12/3	1531.014	1531.695	-1101.337	0.428	995.093	0.294	24	0.079	K.LIFGADSPAIQENR.V
R5/RRR5-12/3	1517.143	1516.618	-313.452	0.310	275.174	0.416	20	0.075	-.QEYHIYM*TSDGR.-
R5/RRR5-1/2	1485.488	1485.708	-147.997	0.459	3088.669	0.536	23	0.501	K.ILVLDEATAAVDVR.T
R5/RRR5-1/2	1486.398	1485.708	-208.614	0.553	2980.469	0.578	23	0.490	K.ILVLDEATAAVDVR.T
R5/RRR5-1/2	1486.448	1485.708	-175.495	0.546	2855.468	0.588	23	0.464	K.ILVLDEATAAVDVR.T
R5/RRR5-1/2	1952.933	1954.172	-1150.153	0.497	2629.767	0.486	25	0.375	R.SPVYAQFSEALNGLSTIR.A
R5/RRR5-1/2	1487.231	1487.641	-275.922	0.527	2593.462	0.497	22	0.371	R.LASLAENSLNAVER.V
R5/RRR5-1/2	1487.284	1487.641	-240.266	0.499	2534.379	0.478	22	0.353	R.LASLAENSLNAVER.V
R5/RRR5-2/2	1485.156	1485.708	-1047.947	0.337	2006.102	0.357	19	0.229	K.ILVLDEATAAVDVR.T
R5/RRR5-1/2	1486.712	1487.641	-1301.324	0.372	1706.368	0.403	20	0.202	R.LASLAENSLNAVER.V
R5/RRR5-1/2	1356.583	1357.538	-1445.105	0.410	1361.236	0.442	17	0.175	K.RLEDLLLAEER.L
R5/RRR5-1/2	1356.933	1357.538	-1186.133	0.409	1324.363	0.381	17	0.162	K.RLEDLLLAEER.L
R5/RRR5-1/2	1357.040	1357.538	-367.895	0.387	1240.980	0.360	17	0.153	K.RLEDLLLAEER.L
R5/RRR5-2/2	1358.084	1357.538	-335.337	0.424	1110.273	0.417	16	0.152	K.RLEDLLLAEER.L
R5/RRR5-1/2	1201.165	1201.352	-155.610	0.389	1287.841	0.307	15	0.147	R.LEDLLLAEER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1489.830	1488.672	106.786	0.415	1021.057	0.434	17	0.146	R.DNILFGSPFQPPR.Y
R5/RRR5-1/2	1850.303	1851.007	-923.987	0.500	708.409	0.551	20	0.145	R.HDLDLLPGGDLTEIGER.G
R5/RRR5-1/2	844.294	844.941	-1956.506	0.352	902.932	0.439	12	0.143	R.HANIFSR.I
R5/RRR5-1/2	844.827	844.941	-135.593	0.384	848.332	0.433	12	0.142	R.HANIFSR.I
R5/RRR5-1/2	1123.020	1123.198	-158.479	0.386	848.517	0.423	15	0.140	K.TLVFGDGEER.L
R5/RRR5-1/2	1754.507	1754.109	227.384	0.441	582.762	0.508	22	0.139	K.VLGIIPQAPVLFSGSVR.F
R5/RRR5-1/2	1955.224	1954.172	26.325	0.448	787.869	0.489	18	0.138	R.SPVYAQFSEALNGLSTIR.A
R5/RRR5-1/2	1122.459	1123.198	-1553.676	0.277	965.435	0.383	16	0.136	K.TLVFGDGEER.L
R5/RRR5-1/2	1642.278	1642.705	-260.533	0.418	827.280	0.442	16	0.136	K.LDSWDETETLYNR.F
R5/RRR5-1/3	1943.125	1941.343	-112.771	0.429	1329.566	0.446	30	0.136	R.LLLPNPPLDPELPAISIK.N
R5/RRR5-1/2	1754.178	1754.109	39.253	0.419	476.198	0.493	20	0.134	K.VLGIIPQAPVLFSGSVR.F
R5/RRR5-1/2	1941.986	1941.343	-184.640	0.398	387.860	0.520	20	0.133	R.LLLPNPPLDPELPAISIK.N
R5/RRR5-1/2	844.412	844.941	-1815.876	0.340	703.185	0.400	11	0.132	R.HANIFSR.I
R5/RRR5-2/2	1753.596	1754.109	-865.255	0.382	492.156	0.478	20	0.132	K.VLGIIPQAPVLFSGSVR.F
R5/RRR5-2/2	1940.478	1941.343	-964.020	0.363	306.358	0.555	18	0.132	R.LLLPNPPLDPELPAISIK.N
R5/RRR5-2/2	1939.745	1941.343	-1860.435	0.346	307.408	0.534	18	0.130	R.LLLPNPPLDPELPAISIK.N
R5/RRR5-2/2	1941.331	1941.343	-6.219	0.392	256.275	0.513	17	0.130	R.LLLPNPPLDPELPAISIK.N
R5/RRR5-1/2	1753.312	1754.109	-1027.963	0.365	522.061	0.432	21	0.129	K.VLGIIPQAPVLFSGSVR.F
R5/RRR5-2/2	1753.363	1754.109	-998.745	0.374	446.083	0.451	19	0.128	K.VLGIIPQAPVLFSGSVR.F
R5/RRR5-1/2	1665.415	1665.998	-952.828	0.301	979.792	0.335	16	0.127	R.ISLM*NEILAAMDTVK.C
R5/RRR5-1/3	1679.719	1679.815	-56.798	0.526	1207.303	0.464	27	0.127	K.VQDIRDDEISWFR.S
R5/RRR5-1/2	1940.634	1941.343	-883.312	0.285	474.180	0.445	21	0.126	R.LLLPNPPLDPELPAISIK.N
R5/RRR5-1/2	1940.824	1941.343	-785.066	0.325	226.693	0.406	15	0.120	-.LLLPNPPLDPELPAISIK.-
R5/RRR5-2/2	1122.864	1123.198	-298.071	0.214	552.420	0.327	12	0.118	-.TLVFGDGEER.-
R5/RRR5-2/2	1201.164	1201.352	-156.731	0.352	951.432	0.169	14	0.117	-.LEDLLLAEER.-
R5/RRR5-1/2	1122.241	1123.198	-1749.377	0.205	471.122	0.303	12	0.116	-.TLVFGDGEER.-
R5/RRR5-1/3	1503.995	1503.753	161.546	0.448	938.838	0.500	26	0.112	R.APM*VFFHTNPLGR.I
R5/RRR5-1/3	1503.743	1503.753	-6.847	0.469	778.816	0.541	23	0.111	R.APM*VFFHTNPLGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/3	1503.522	1503.753	-154.405	0.485	608.950	0.547	22	0.105	R.APM*VFFHTNPLGR.I
R5/RRR5-2/3	1504.559	1503.753	-129.560	0.450	604.932	0.496	21	0.097	R.APM*VFFHTNPLGR.I
R5/RRR5-1/3	1272.398	1272.478	-62.808	0.457	1253.650	0.301	20	0.095	K.RPITDKDIWK.L
R5/RRR5-2/3	1503.811	1503.753	38.706	0.399	577.171	0.435	21	0.089	R.APM*VFFHTNPLGR.I
R5/RRR5-1/3	1941.205	1941.343	-71.570	0.400	697.228	0.371	25	0.071	-.LLLPNPPLDPELPAISIK.-
R5/RRR5-15/2	1803.244	1804.124	-1045.541	0.549	4303.174	0.596	28	0.904	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-15/3	1804.808	1804.124	-175.489	0.544	3816.666	0.491	36	0.903	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-16/2	1819.373	1820.123	-964.675	0.578	3800.396	0.604	27	0.732	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-15/2	1819.256	1820.123	-1029.750	0.563	3688.055	0.614	27	0.701	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-15/2	1819.337	1820.123	-984.816	0.559	3707.842	0.601	27	0.701	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-15/2	1804.275	1804.124	83.757	0.616	3696.342	0.607	28	0.698	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-16/2	1803.578	1804.124	-859.613	0.584	3715.662	0.590	28	0.697	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-15/2	1803.378	1804.124	-970.985	0.562	3619.892	0.596	27	0.671	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-16/2	1820.687	1820.123	-240.599	0.592	3477.370	0.603	27	0.630	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-16/2	1819.443	1820.123	-926.079	0.569	3372.571	0.594	26	0.596	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-15/2	1818.878	1820.123	-1238.099	0.516	3240.193	0.594	27	0.560	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-2/2	1820.392	1820.123	147.914	0.568	3057.110	0.560	26	0.496	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-15/2	1804.214	1804.124	50.236	0.604	2747.378	0.622	26	0.445	K.NFM*IDFLMGGVSAAVSK.T
R5/RRR5-15/2	1803.542	1804.124	-879.929	0.581	2675.656	0.607	26	0.423	K.NFM*IDFLMGGVSAAVSK.T
R5/RRR5-15/2	1803.392	1804.124	-963.170	0.554	2292.493	0.581	25	0.336	K.NFM*IDFLMGGVSAAVSK.T
R5/RRR5-16/2	1803.945	1804.124	-99.753	0.574	2254.265	0.585	25	0.330	K.NFM*IDFLMGGVSAAVSK.T
R5/RRR5-15/2	1498.244	1498.745	-1004.961	0.470	2095.912	0.513	20	0.284	R.GFNISCVGIIVYR.G
R5/RRR5-15/2	1498.384	1498.745	-241.346	0.451	2058.605	0.508	20	0.276	R.GFNISCVGIIVYR.G
R5/RRR5-15/2	1498.798	1498.745	35.649	0.501	2037.200	0.512	20	0.274	R.GFNISCVGIIVYR.G
R5/RRR5-16/2	1498.654	1498.745	-60.751	0.505	2013.112	0.508	20	0.269	R.GFNISCVGIIVYR.G
R5/RRR5-16/2	1227.147	1227.413	-216.968	0.467	1661.158	0.458	18	0.209	K.SSMDAFSQILK.N
R5/RRR5-16/2	1497.817	1498.745	-1290.695	0.337	1728.107	0.430	19	0.209	R.GFNISCVGIIVYR.G
R5/RRR5-16/2	1362.003	1361.590	304.188	0.534	1653.005	0.378	18	0.189	K.LLIQNQDEM*IK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1227.095	1227.413	-259.283	0.488	1470.439	0.439	17	0.185	K.SSMDAFSQILK.N
R5/RRR5-16/2	1243.241	1243.412	-137.949	0.443	1450.080	0.432	17	0.182	K.SSM*DAFSQILK.N
R5/RRR5-15/2	1227.178	1227.413	-191.371	0.456	1520.247	0.390	17	0.180	K.SSMDAFSQILK.N
R5/RRR5-15/2	1242.579	1243.412	-1479.960	0.406	1476.973	0.406	17	0.179	K.SSM*DAFSQILK.N
R5/RRR5-16/2	1243.078	1243.412	-269.655	0.479	1392.106	0.437	16	0.177	K.SSM*DAFSQILK.N
R5/RRR5-1/2	1804.001	1804.124	-68.258	0.509	1218.147	0.526	22	0.176	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-16/2	1243.100	1243.412	-251.921	0.470	1336.848	0.449	16	0.174	K.SSM*DAFSQILK.N
R5/RRR5-15/2	1243.133	1243.412	-224.829	0.473	1277.254	0.473	16	0.174	K.SSM*DAFSQILK.N
R5/RRR5-15/2	1362.012	1361.590	310.928	0.536	1361.717	0.423	18	0.172	K.LLIQNQDEM*IK.S
R5/RRR5-1/2	1243.512	1243.412	80.367	0.353	1423.698	0.375	18	0.168	K.SSM*DAFSQILK.N
R5/RRR5-15/2	1226.681	1227.413	-1415.883	0.353	1519.069	0.321	17	0.167	K.SSMDAFSQILK.N
R5/RRR5-16/2	1226.891	1227.413	-1244.095	0.451	1453.389	0.352	17	0.167	K.SSMDAFSQILK.N
R5/RRR5-15/2	1361.148	1361.590	-326.087	0.522	1389.121	0.374	17	0.164	K.LLIQNQDEM*IK.S
R5/RRR5-16/2	1361.152	1361.590	-322.488	0.514	1281.657	0.413	17	0.164	K.LLIQNQDEM*IK.S
R5/RRR5-15/2	1345.135	1345.591	-339.567	0.500	1336.762	0.382	17	0.162	K.LLIQNQDEMIK.S
R5/RRR5-15/2	1242.947	1243.412	-374.985	0.360	1249.036	0.402	16	0.159	K.SSM*DAFSQILK.N
R5/RRR5-15/2	1361.176	1361.590	-304.852	0.527	1356.592	0.358	17	0.159	K.LLIQNQDEM*IK.S
R5/RRR5-16/2	1345.226	1345.591	-271.828	0.510	1331.078	0.357	17	0.157	K.LLIQNQDEMIK.S
R5/RRR5-15/2	1447.111	1447.661	-1074.568	0.483	874.217	0.508	20	0.156	R.YFPTQALNFAFK.D
R5/RRR5-15/2	1361.112	1361.590	-352.452	0.530	1333.697	0.348	17	0.155	K.LLIQNQDEM*IK.S
R5/RRR5-15/2	1345.262	1345.591	-245.063	0.492	1362.260	0.322	18	0.154	K.LLIQNQDEMIK.S
R5/RRR5-16/2	1345.138	1345.591	-337.746	0.503	1314.842	0.344	17	0.154	K.LLIQNQDEMIK.S
R5/RRR5-15/2	1345.102	1345.591	-363.969	0.483	1368.569	0.318	17	0.153	K.LLIQNQDEMIK.S
R5/RRR5-15/2	1424.261	1423.598	-237.144	0.474	992.220	0.456	19	0.153	R.TIKDEGFASLWR.G
R5/RRR5-16/2	1362.144	1361.590	-328.635	0.541	1255.070	0.368	17	0.153	K.LLIQNQDEM*IK.S
R5/RRR5-1/2	1360.778	1361.590	-1335.519	0.474	1274.472	0.350	17	0.153	K.LLIQNQDEM*IK.S
R5/RRR5-14/2	1820.023	1820.123	-55.218	0.417	1010.879	0.481	20	0.153	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-15/2	1423.213	1423.598	-271.472	0.439	1126.365	0.397	19	0.152	R.TIKDEGFASLWR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1423.188	1423.598	-288.768	0.443	1112.641	0.401	19	0.152	R.TIKDEGFASLWR.G
R5/RRR5-16/2	1361.906	1361.590	233.008	0.517	1356.482	0.318	17	0.152	K.LLIQNQDEM*IK.S
R5/RRR5-16/2	1448.088	1447.661	295.283	0.465	850.963	0.482	20	0.151	R.YFPTQALNFAFK.D
R5/RRR5-16/2	1423.447	1423.598	-106.710	0.448	1113.147	0.387	19	0.150	R.TIKDEGFASLWR.G
R5/RRR5-16/2	1361.710	1361.590	88.640	0.483	1329.600	0.310	17	0.150	K.LLIQNQDEM*IK.S
R5/RRR5-15/2	1447.244	1447.661	-289.468	0.429	956.006	0.440	20	0.149	R.YFPTQALNFAFK.D
R5/RRR5-16/2	1344.616	1345.591	-1473.083	0.399	1270.285	0.321	17	0.149	K.LLIQNQDEMIK.S
R5/RRR5-15/2	1424.285	1423.598	-220.291	0.476	924.550	0.449	18	0.148	R.TIKDEGFASLWR.G
R5/RRR5-3/2	1361.179	1361.590	-302.603	0.450	1256.303	0.322	17	0.148	K.LLIQNQDEM*IK.S
R5/RRR5-15/2	1447.741	1447.661	55.004	0.399	963.857	0.434	18	0.147	R.YFPTQALNFAFK.D
R5/RRR5-15/2	1448.003	1447.661	236.450	0.479	690.618	0.497	19	0.146	R.YFPTQALNFAFK.D
R5/RRR5-1/2	1422.561	1423.598	-1436.091	0.414	1021.919	0.402	18	0.146	R.TIKDEGFASLWR.G
R5/RRR5-1/2	1242.969	1243.412	-357.543	0.255	1411.411	0.246	16	0.146	K.SSM*DAFSQILK.N
R5/RRR5-15/2	951.842	952.046	-215.085	0.448	768.233	0.475	14	0.146	K.SDGIAGLYR.G
R5/RRR5-15/2	951.955	952.046	-96.347	0.438	869.767	0.436	15	0.146	K.SDGIAGLYR.G
R5/RRR5-16/2	1424.257	1423.598	-240.239	0.486	889.945	0.430	18	0.144	R.TIKDEGFASLWR.G
R5/RRR5-1/2	1448.561	1447.661	-69.276	0.453	600.632	0.502	18	0.143	R.YFPTQALNFAFK.D
R5/RRR5-16/2	1423.059	1423.598	-1085.072	0.404	887.377	0.429	17	0.142	R.TIKDEGFASLWR.G
R5/RRR5-16/2	1447.022	1447.661	-1136.316	0.446	711.689	0.463	19	0.142	R.YFPTQALNFAFK.D
R5/RRR5-16/2	1743.471	1742.932	-265.707	0.434	967.459	0.432	20	0.142	K.SSMDAFSQILKNEGSK.S
R5/RRR5-16/2	1086.039	1085.345	-282.474	0.415	758.416	0.457	15	0.142	R.MMMTSGEAVK.Y
R5/RRR5-1/2	1361.336	1361.590	-187.087	0.452	1264.824	0.279	17	0.141	K.LLIQNQDEM*IK.S
R5/RRR5-15/2	1361.112	1361.590	-352.182	0.511	1180.707	0.315	17	0.141	K.LLIQNQDEM*IK.S
R5/RRR5-15/2	1423.717	1423.598	84.053	0.486	789.510	0.431	17	0.140	R.TIKDEGFASLWR.G
R5/RRR5-1/2	1361.750	1361.590	117.679	0.505	1175.359	0.291	17	0.137	K.LLIQNQDEM*IK.S
R5/RRR5-1/2	1423.173	1423.598	-299.439	0.423	899.000	0.372	17	0.137	R.TIKDEGFASLWR.G
R5/RRR5-15/2	1423.220	1423.598	-266.825	0.457	941.975	0.358	17	0.136	R.TIKDEGFASLWR.G
R5/RRR5-15/2	881.892	881.950	-66.100	0.347	479.048	0.507	11	0.135	K.GIGDCFGR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	881.692	881.950	-293.021	0.334	622.632	0.456	12	0.135	K.GIGDCFGR.T
R5/RRR5-2/2	1361.364	1361.590	-166.577	0.461	1137.432	0.277	16	0.134	K.LLIQNQDEM*IK.S
R5/RRR5-16/2	1361.083	1361.590	-1110.332	0.457	1126.886	0.270	17	0.133	K.LLIQNQDEM*IK.S
R5/RRR5-15/2	1212.253	1211.351	-81.164	0.340	453.847	0.479	16	0.133	R.QFNGLVDVYR.K
R5/RRR5-1/2	1804.282	1804.124	87.828	0.384	652.270	0.460	17	0.133	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-1/2	1424.225	1423.598	-263.112	0.442	745.150	0.370	17	0.132	R.TIKDEGFASLWR.G
R5/RRR5-15/3	1802.933	1804.124	-1218.967	0.490	1283.847	0.450	29	0.132	K.NFM*IDFLMGGVSAAVSK.T
R5/RRR5-15/2	951.945	952.046	-107.024	0.439	716.486	0.338	14	0.131	K.SDGIAGLYR.G
R5/RRR5-16/2	771.158	771.888	-2249.783	0.344	969.322	0.285	13	0.131	K.GAGANILR.A
R5/RRR5-2/2	951.787	952.046	-273.371	0.303	236.934	0.410	12	0.130	K.SDGIAGLYR.G
R5/RRR5-3/2	1361.347	1361.590	-178.811	0.450	1219.348	0.216	17	0.130	K.LLIQNQDEM*IK.S
R5/RRR5-2/2	1360.656	1361.590	-1425.893	0.362	1255.463	0.177	17	0.129	K.LLIQNQDEM*IK.S
R5/RRR5-16/2	881.912	881.950	-43.053	0.282	718.132	0.362	13	0.128	K.GIGDCFGR.T
R5/RRR5-15/2	1085.195	1085.345	-138.730	0.282	854.786	0.316	15	0.128	R.MMMTSGEAVK.Y
R5/RRR5-16/2	951.604	952.046	-466.033	0.265	434.428	0.416	14	0.128	K.SDGIAGLYR.G
R5/RRR5-15/2	1212.393	1211.351	34.375	0.322	348.633	0.406	14	0.127	R.QFNGLVDVYR.K
R5/RRR5-15/2	771.456	771.888	-561.845	0.437	1056.837	0.220	13	0.126	K.GAGANILR.A
R5/RRR5-16/2	772.075	771.888	243.404	0.497	988.390	0.247	13	0.126	K.GAGANILR.A
R5/RRR5-16/2	881.838	881.950	-127.195	0.237	609.872	0.422	12	0.126	K.GIGDCFGR.T
R5/RRR5-16/2	1086.220	1085.345	-115.379	0.349	433.725	0.408	12	0.126	-.MMMTSGEAVK.-
R5/RRR5-15/2	1212.084	1211.351	-221.180	0.303	371.102	0.340	14	0.124	R.QFNGLVDVYR.K
R5/RRR5-15/2	952.394	952.046	366.115	0.307	347.669	0.316	12	0.124	-.SDGIAGLYR.-
R5/RRR5-2/2	951.646	952.046	-421.754	0.291	196.028	0.454	12	0.124	-.SDGIAGLYR.-
R5/RRR5-16/2	1100.837	1101.344	-1373.328	0.359	903.990	0.234	15	0.124	R.MMM*TSGEAVK.Y
R5/RRR5-15/2	1085.681	1085.345	311.074	0.265	423.041	0.371	12	0.124	R.MMMTSGEAVK.Y
R5/RRR5-16/2	1447.211	1447.661	-312.147	0.367	554.229	0.295	16	0.123	R.YFPTQALNFAFK.D
R5/RRR5-12/2	952.314	952.046	281.806	0.402	499.066	0.264	12	0.123	K.SDGIAGLYR.G
R5/RRR5-15/2	951.892	952.046	-162.853	0.270	319.002	0.270	12	0.123	-.SDGIAGLYR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1084.920	1085.345	-392.233	0.297	580.892	0.314	13	0.123	R.MMMTSGEAVK.Y
R5/RRR5-15/2	1100.765	1101.344	-1438.931	0.302	878.374	0.238	15	0.123	R.MMM*TSGEAVK.Y
R5/RRR5-16/2	881.727	881.950	-252.879	0.234	617.859	0.350	12	0.123	K.GIGDCFGR.T
R5/RRR5-16/2	951.814	952.046	-244.935	0.273	218.785	0.378	12	0.122	-.SDGIAGLYR.-
R5/RRR5-15/2	1821.179	1820.123	30.535	0.356	360.176	0.396	13	0.122	K.NFM*IDFLM*GGVSAAVSK.T
R5/RRR5-16/2	771.814	771.888	-96.150	0.452	697.896	0.236	12	0.121	K.GAGANILR.A
R5/RRR5-15/2	1499.033	1498.745	192.626	0.329	802.644	0.287	14	0.121	R.GFNISCVGIIVYR.G
R5/RRR5-16/2	952.045	952.046	-1.686	0.347	413.844	0.258	11	0.121	-.SDGIAGLYR.-
R5/RRR5-15/2	881.390	881.950	-1774.489	0.252	639.798	0.275	12	0.121	K.GIGDCFGR.T
R5/RRR5-3/2	1361.470	1361.590	-88.595	0.411	1352.482	0.089	17	0.120	K.LLIQNQDEM*IK.S
R5/RRR5-10/2	1244.535	1243.412	99.288	0.246	517.383	0.288	12	0.120	K.SSM*DAFSQILK.N
R5/RRR5-14/2	951.840	952.046	-217.787	0.276	218.411	0.355	12	0.119	-.SDGIAGLYR.-
R5/RRR5-1/2	772.289	771.888	520.143	0.403	899.813	0.172	13	0.119	K.GAGANILR.A
R5/RRR5-15/2	771.376	771.888	-1966.778	0.421	833.270	0.194	12	0.119	K.GAGANILR.A
R5/RRR5-15/2	771.853	771.888	-45.702	0.427	746.888	0.185	12	0.118	K.GAGANILR.A
R5/RRR5-1/2	772.090	771.888	261.954	0.428	716.598	0.180	12	0.118	K.GAGANILR.A
R5/RRR5-2/2	1242.937	1243.412	-382.967	0.323	818.849	0.176	15	0.118	K.SSM*DAFSQILK.N
R5/RRR5-16/2	1100.678	1101.344	-1517.800	0.360	687.633	0.180	13	0.116	R.M*MMTSGEAVK.Y
R5/RRR5-1/2	772.112	771.888	290.648	0.354	803.319	0.136	12	0.116	K.GAGANILR.A
R5/RRR5-14/2	1243.531	1243.412	95.627	0.313	722.659	0.176	13	0.116	K.SSM*DAFSQILK.N
R5/RRR5-15/2	1101.200	1101.344	-130.831	0.338	485.826	0.229	12	0.109	-.MMM*TSGEAVK.-
R5/RRR5-16/3	1294.873	1294.482	303.169	0.402	1072.228	0.383	22	0.097	K.TLKSDGIAGLYR.G
R5/RRR5-16/3	1804.018	1804.124	-58.967	0.398	1158.726	0.350	30	0.097	K.NFMIDFLM*GGVSAAVSK.T
R5/RRR5-15/3	1294.674	1294.482	148.737	0.330	1043.389	0.284	21	0.078	K.TLKSDGIAGLYR.G
R5/RRR5-16/3	1424.758	1423.598	112.341	0.432	855.153	0.277	21	0.072	-.TIKDEGFASLWR.-
R5/RRR5-16/3	1294.203	1294.482	-216.332	0.321	1131.286	0.193	22	0.069	K.TLKSDGIAGLYR.G
R5/RRR5-15/3	1423.428	1423.598	-119.881	0.456	964.862	0.267	22	0.066	-.TIKDEGFASLWR.-
R5/RRR5-1/3	1423.728	1423.598	91.439	0.466	1003.127	0.235	21	0.066	-.TIKDEGFASLWR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1423.196	1423.598	-283.658	0.388	753.985	0.193	19	0.064	-.TIKDEGFASLWR.-
R5/RRR5-15/3	1423.609	1423.598	7.592	0.411	878.680	0.237	21	0.060	-.TIKDEGFASLWR.-
R5/RRR5-16/3	1423.584	1423.598	-10.082	0.403	786.308	0.243	20	0.057	-.TIKDEGFASLWR.-
R5/RRR5-15/3	1423.829	1423.598	162.762	0.418	638.194	0.198	19	0.034	-.TIKDEGFASLWR.-
R5/RRR5-5/3	1950.986	1951.170	-94.839	0.532	2638.615	0.583	33	0.486	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-5/2	1240.492	1241.379	-1525.962	0.473	2114.150	0.513	20	0.287	K.IDNPIGATNIGR.A
R5/RRR5-5/2	1950.598	1951.170	-808.437	0.605	1961.735	0.566	23	0.276	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-5/2	1508.586	1508.695	-72.606	0.512	1665.605	0.537	22	0.229	R.IVSFVGGLDLCDGR.Y
R5/RRR5-5/2	1859.423	1860.057	-881.725	0.559	1645.485	0.533	24	0.225	R.AYLPVQELLNGEEIDR.W
R5/RRR5-4/2	1951.834	1951.170	-172.606	0.576	1493.766	0.554	21	0.209	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-5/2	1240.186	1241.379	-1773.544	0.440	1628.023	0.464	19	0.207	K.IDNPIGATNIGR.A
R5/RRR5-5/2	1950.688	1951.170	-247.900	0.585	1454.466	0.551	21	0.204	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-5/2	1951.421	1951.170	129.022	0.603	1427.473	0.551	21	0.201	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-4/2	1241.160	1241.379	-177.427	0.439	1428.008	0.535	19	0.200	K.IDNPIGATNIGR.A
R5/RRR5-5/2	1859.419	1860.057	-883.834	0.563	1344.087	0.552	23	0.195	R.AYLPVQELLNGEEIDR.W
R5/RRR5-5/2	1288.634	1287.449	143.886	0.430	1482.281	0.403	17	0.180	R.SIQDAYIHAIR.R
R5/RRR5-5/2	1287.073	1287.449	-293.623	0.401	1467.809	0.398	17	0.177	R.SIQDAYIHAIR.R
R5/RRR5-5/2	1951.165	1951.170	-2.486	0.546	1197.545	0.497	21	0.170	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-1/2	1241.467	1241.379	71.145	0.389	1152.187	0.502	18	0.168	K.IDNPIGATNIGR.A
R5/RRR5-5/2	1163.574	1163.372	174.071	0.404	1179.726	0.447	14	0.162	R.VLM*LVWDDR.T
R5/RRR5-1/2	1949.992	1951.170	-1120.306	0.396	1209.670	0.452	19	0.162	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-5/2	1200.833	1201.378	-1290.714	0.519	1284.029	0.372	16	0.158	-.M*ITNEPINPR.W
R5/RRR5-5/2	1880.343	1880.989	-878.101	0.474	913.662	0.560	22	0.158	R.SIDGGAAFGFPDTPEEAAK.A
R5/RRR5-4/2	1407.023	1406.561	329.659	0.419	1156.081	0.410	16	0.154	R.DYLTFFCLGNR.E
R5/RRR5-5/2	1879.830	1880.989	-1151.894	0.447	818.401	0.576	21	0.153	R.SIDGGAAFGFPDTPEEAAK.A
R5/RRR5-5/2	1880.388	1880.989	-854.119	0.434	858.697	0.529	21	0.149	R.SIDGGAAFGFPDTPEEAAK.A
R5/RRR5-5/2	1877.108	1877.193	-45.437	0.410	1247.450	0.347	19	0.147	R.TMEMMYTDITEALQAK.G
R5/RRR5-2/2	1242.118	1241.379	-211.100	0.419	955.261	0.415	17	0.144	K.IDNPIGATNIGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1201.188	1201.378	-158.915	0.466	1091.419	0.358	15	0.143	-.M*ITNEPINPR.W
R5/RRR5-5/2	1407.389	1406.561	-122.543	0.424	698.042	0.453	16	0.139	R.DYLTFFCLGNR.E
R5/RRR5-4/2	1950.031	1951.170	-1100.443	0.419	956.985	0.403	18	0.139	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-5/2	1201.066	1201.378	-260.565	0.417	902.625	0.376	15	0.136	-.M*ITNEPINPR.-
R5/RRR5-5/2	1462.444	1462.633	-129.734	0.381	606.872	0.447	19	0.135	K.YPGVPYTFFSQR.Q
R5/RRR5-5/2	1950.267	1951.170	-978.957	0.451	784.019	0.420	19	0.135	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-1/2	1241.045	1241.379	-270.180	0.393	822.802	0.379	17	0.134	K.IDNPIGATNIGR.A
R5/RRR5-5/2	1406.719	1406.561	112.834	0.386	663.630	0.398	16	0.132	R.DYLTFFCLGNR.E
R5/RRR5-5/2	1462.052	1462.633	-1084.606	0.343	512.680	0.444	18	0.131	K.YPGVPYTFFSQR.Q
R5/RRR5-5/2	1164.143	1163.372	-196.854	0.343	871.728	0.344	13	0.129	-.VLM*LVWDDR.-
R5/RRR5-5/2	1509.659	1508.695	-23.731	0.385	665.617	0.422	16	0.129	R.IVSFVGGLDLCDGR.Y
R5/RRR5-1/2	1286.737	1287.449	-1334.860	0.396	687.485	0.358	14	0.127	R.SIQDAYIHAIR.R
R5/RRR5-5/2	1163.394	1163.372	18.973	0.384	522.179	0.372	12	0.127	R.VLM*LVWDDR.T
R5/RRR5-5/2	1892.798	1893.193	-209.510	0.435	796.991	0.377	17	0.127	-.TM*EMMYTDITEALQAK.-
R5/RRR5-4/2	1407.461	1406.561	-71.386	0.337	630.958	0.357	14	0.126	R.DYLTFFCLGNR.E
R5/RRR5-5/2	1461.563	1462.633	-1420.136	0.288	441.216	0.441	16	0.126	K.YPGVPYTFFSQR.Q
R5/RRR5-4/2	1407.069	1406.561	-351.073	0.352	775.713	0.304	14	0.124	R.DYLTFFCLGNR.E
R5/RRR5-3/2	1240.958	1241.379	-340.151	0.293	507.331	0.341	16	0.124	K.IDNPIGATNIGR.A
R5/RRR5-5/2	1240.699	1241.379	-1358.142	0.301	620.379	0.351	14	0.124	K.IDNPIGATNIGR.A
R5/RRR5-5/2	1405.863	1406.561	-1211.125	0.300	810.375	0.285	14	0.123	R.DYLTFFCLGNR.E
R5/RRR5-5/2	1288.194	1287.449	-199.273	0.254	546.684	0.317	15	0.121	R.SIQDAYIHAIR.R
R5/RRR5-5/3	1950.964	1951.170	-105.948	0.429	1110.310	0.454	25	0.115	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-5/3	1820.125	1820.000	69.171	0.425	1060.283	0.471	29	0.114	K.IVVVDHELPNQGSQQR.R
R5/RRR5-5/3	1897.493	1897.122	195.788	0.429	1226.876	0.385	29	0.109	R.DSNRPKPGGDVTLGELLK.K
R5/RRR5-5/3	1819.816	1820.000	-101.372	0.439	643.116	0.472	26	0.093	K.IVVVDHELPNQGSQQR.R
R5/RRR5-5/3	1857.871	1858.086	-116.495	0.412	635.210	0.478	28	0.093	K.VTLYQDAHVPDNFIPK.I
R5/RRR5-5/3	1857.817	1858.086	-145.562	0.422	489.122	0.463	26	0.090	K.VTLYQDAHVPDNFIPK.I
R5/RRR5-5/3	1820.029	1820.000	16.097	0.355	620.962	0.448	26	0.087	K.IVVVDHELPNQGSQQR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1857.899	1858.086	-101.172	0.398	391.111	0.420	22	0.085	K.VTLYQDAHVPDNFIPK.I
R5/RRR5-5/3	1950.986	1951.170	-94.744	0.375	675.835	0.334	25	0.076	R.LEGPIAWDVLYNFEQR.W
R5/RRR5-6/2	1496.277	1496.694	-279.573	0.559	2876.998	0.578	23	0.468	K.SQIHEIVLVGGSTR.I
R5/RRR5-6/2	1537.110	1537.620	-985.365	0.498	1662.434	0.520	20	0.224	K.NGHVEIIANDQGNR.I
R5/RRR5-6/2	1418.963	1419.585	-1146.578	0.490	1764.466	0.452	17	0.221	R.NQLETYVYNM*K.N
R5/RRR5-6/2	1538.217	1537.620	-262.637	0.513	1319.498	0.520	19	0.186	K.NGHVEIIANDQGNR.I
R5/RRR5-6/2	1418.850	1419.585	-1226.576	0.464	1664.748	0.325	17	0.181	R.NQLETYVYNM*K.N
R5/RRR5-6/2	1296.992	1297.398	-314.222	0.512	1263.255	0.489	15	0.177	R.FEELNNDLFR.K
R5/RRR5-6/2	1524.086	1523.776	203.733	0.437	1327.026	0.464	20	0.176	K.VFSPEEVSAM*ILGK.M
R5/RRR5-6/2	1524.462	1524.663	-132.247	0.522	1292.095	0.449	19	0.172	R.ARFEELNNDLFR.K
R5/RRR5-6/2	1506.759	1507.777	-1343.004	0.323	1536.883	0.337	20	0.171	K.VFSPEEVSAMILGK.M
R5/RRR5-6/2	1524.314	1524.663	-229.369	0.530	1276.206	0.425	19	0.166	R.ARFEELNNDLFR.K
R5/RRR5-6/2	1524.287	1524.663	-247.125	0.487	1245.345	0.396	19	0.159	R.ARFEELNNDLFR.K
R5/RRR5-6/2	1144.145	1144.305	-140.143	0.513	906.722	0.527	18	0.159	K.FDLSGIPAAPR.G
R5/RRR5-6/2	1536.466	1537.620	-1405.649	0.291	1228.213	0.374	19	0.150	K.NGHVEIIANDQGNR.I
R5/RRR5-6/2	1156.114	1156.317	-176.076	0.402	1264.549	0.332	16	0.148	K.DAGVIAGLNVAR.I
R5/RRR5-6/3	1537.863	1537.620	158.575	0.513	1665.995	0.337	27	0.147	K.NGHVEIIANDQGNR.I
R5/RRR5-6/3	1369.374	1369.612	-174.191	0.514	1441.066	0.433	27	0.142	K.MKETAEAYLGKK.I
R5/RRR5-6/2	1296.943	1297.398	-352.090	0.523	996.413	0.374	14	0.139	R.FEELNNDLFR.K
R5/RRR5-6/2	1507.284	1507.777	-327.812	0.288	1122.816	0.328	18	0.138	K.VFSPEEVSAMILGK.M
R5/RRR5-6/2	1155.404	1156.317	-1661.229	0.272	1158.489	0.305	16	0.136	K.DAGVIAGLNVAR.I
R5/RRR5-6/3	1525.073	1524.663	270.012	0.552	1507.100	0.373	27	0.136	R.ARFEELNNDLFR.K
R5/RRR5-6/2	1509.222	1509.645	-280.825	0.328	530.206	0.541	18	0.136	R.ITPSWVAFTDSER.L
R5/RRR5-6/3	1385.424	1385.612	-136.132	0.507	1399.036	0.411	25	0.133	K.M*KETAEAYLGKK.I
R5/RRR5-6/2	1509.382	1509.645	-174.370	0.338	416.891	0.532	16	0.132	R.ITPSWVAFTDSER.L
R5/RRR5-6/2	1228.065	1227.305	-195.869	0.381	787.523	0.377	14	0.132	R.DYFEGKEPNK.G
R5/RRR5-6/3	1385.243	1385.612	-266.608	0.484	1771.362	0.248	26	0.131	K.M*KETAEAYLGKK.I
R5/RRR5-5/2	1509.393	1509.645	-167.555	0.308	457.321	0.481	17	0.129	R.ITPSWVAFTDSER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/3	1652.047	1652.835	-1086.091	0.533	1519.116	0.331	24	0.126	R.ARFEELNNDLFRK.T
R5/RRR5-6/2	1226.546	1227.305	-1437.800	0.373	730.392	0.334	13	0.126	R.DYFEGKEPNK.G
R5/RRR5-6/2	1296.350	1297.398	-1584.597	0.346	825.637	0.304	12	0.124	R.FEELNNDLFR.K
R5/RRR5-6/2	1507.423	1507.777	-235.270	0.263	1139.484	0.180	19	0.124	K.VFSPEEVSAMILGK.M
R5/RRR5-6/2	1226.945	1227.305	-294.341	0.327	714.035	0.258	13	0.119	R.DYFEGKEPNK.G
R5/RRR5-6/2	1523.272	1523.776	-990.485	0.272	1037.178	0.077	18	0.112	K.VFSPEEVSAM*ILGK.M
R5/RRR5-6/2	1970.499	1970.856	-181.844	0.458	961.674	0.522	23	0.108	R.TGGAPGGGADGEGGGDDEHDEL.-
R5/RRR5-6/3	1369.636	1369.612	17.591	0.481	1205.680	0.382	25	0.108	K.MKETAEAYLGKK.I
R5/RRR5-6/3	1524.474	1524.663	-124.183	0.563	1250.104	0.355	24	0.106	R.ARFEELNNDLFR.K
R5/RRR5-6/3	1652.439	1652.835	-240.453	0.562	1283.667	0.336	23	0.103	R.ARFEELNNDLFRK.T
R5/RRR5-6/3	1652.822	1652.835	-8.165	0.547	1320.722	0.317	24	0.103	R.ARFEELNNDLFRK.T
R5/RRR5-6/2	1971.143	1970.856	146.180	0.504	885.511	0.516	23	0.097	R.TGGAPGGGADGEGGGDDEHDEL.-
R5/RRR5-6/3	1538.521	1537.620	-64.398	0.450	1325.571	0.259	24	0.093	-.NGHVEIIANDQGNR.-
R5/RRR5-6/2	1970.270	1970.856	-807.387	0.421	752.398	0.470	23	0.089	R.TGGAPGGGADGEGGGDDEHDEL.-
R5/RRR5-6/3	1385.118	1385.612	-357.192	0.488	983.612	0.331	22	0.086	K.M*KETAEAYLGKK.I
R5/RRR5-6/3	1524.693	1524.663	20.138	0.540	1164.362	0.262	24	0.083	R.ARFEELNNDLFR.K
R5/RRR5-6/3	1369.195	1369.612	-305.799	0.444	857.833	0.308	22	0.080	K.MKETAEAYLGKK.I
R5/RRR5-6/3	1537.958	1537.620	220.900	0.425	1164.490	0.242	24	0.079	-.NGHVEIIANDQGNR.-
R5/RRR5-6/3	1503.965	1502.783	121.526	0.344	942.361	0.310	21	0.078	K.IVNKDGKPYIQVK.I
R5/RRR5-6/3	1502.634	1502.783	-99.425	0.326	684.203	0.303	20	0.071	-.IVNKDGKPYIQVK.-
R5/RRR5-6/3	1503.961	1502.783	118.962	0.336	805.875	0.279	21	0.071	-.IVNKDGKPYIQVK.-
R5/RRR5-4/3	1803.984	1803.946	21.025	0.498	2033.826	0.496	35	0.268	K.NATLTNEKEADACPIR.A
R5/RRR5-4/3	1803.630	1803.946	-175.697	0.479	1911.777	0.537	35	0.258	K.NATLTNEKEADACPIR.A
R5/RRR5-4/3	1802.962	1803.946	-1103.767	0.473	1470.278	0.502	32	0.169	K.NATLTNEKEADACPIR.A
R5/RRR5-3/3	1803.647	1803.946	-166.124	0.438	1098.049	0.399	26	0.103	K.NATLTNEKEADACPIR.A
R5/RRR5-2/3	1803.798	1803.946	-82.316	0.315	665.664	0.256	26	0.072	K.NATLTNEKEADACPIR.A
R5/RRR5-11/3	1450.638	1450.816	-123.076	0.578	3137.190	0.436	31	0.553	K.FLKPAVAGFLMQK.E
R5/RRR5-11/3	1450.821	1450.816	3.019	0.552	3060.529	0.424	30	0.520	K.FLKPAVAGFLMQK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/3	1466.896	1466.816	54.934	0.535	2936.117	0.483	30	0.514	K.FLKPAVAGFLM*QK.E
R5/RRR5-11/3	1450.756	1450.816	-41.541	0.576	2734.130	0.401	29	0.400	K.FLKPAVAGFLMQK.E
R5/RRR5-11/3	1735.378	1736.049	-965.642	0.544	2456.820	0.380	33	0.322	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/3	1466.610	1466.816	-140.530	0.529	2407.700	0.415	27	0.320	K.FLKPAVAGFLM*QK.E
R5/RRR5-11/2	1546.313	1546.705	-253.819	0.487	2175.793	0.530	24	0.302	K.GATTIIGGGDSVAAVEK.A
R5/RRR5-11/2	1546.312	1546.705	-255.007	0.476	2128.038	0.507	24	0.287	K.GATTIIGGGDSVAAVEK.A
R5/RRR5-11/2	1546.288	1546.705	-269.976	0.471	2180.247	0.458	24	0.282	K.GATTIIGGGDSVAAVEK.A
R5/RRR5-11/3	1466.227	1466.816	-1086.672	0.517	1947.155	0.435	26	0.225	K.FLKPAVAGFLM*QK.E
R5/RRR5-11/3	1736.294	1736.049	141.827	0.572	1977.560	0.410	31	0.224	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/3	1735.811	1736.049	-137.666	0.474	1967.138	0.350	30	0.202	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1734.997	1736.049	-1186.303	0.500	1174.538	0.568	26	0.183	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1735.024	1736.049	-1170.689	0.509	1178.757	0.551	26	0.181	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1734.952	1736.049	-1212.163	0.516	1040.100	0.544	24	0.168	K.LAAALPEGGVLLLENVR.F
R5/RRR5-10/2	1736.460	1736.049	237.291	0.573	998.809	0.523	24	0.162	K.LAAALPEGGVLLLENVR.F
R5/RRR5-2/2	1735.573	1736.049	-274.958	0.507	894.653	0.527	23	0.156	K.LAAALPEGGVLLLENVR.F
R5/RRR5-12/2	1735.878	1736.049	-98.719	0.514	892.169	0.508	23	0.153	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1735.735	1736.049	-181.328	0.529	905.922	0.502	23	0.153	K.LAAALPEGGVLLLENVR.F
R5/RRR5-12/2	1736.294	1736.049	141.624	0.516	951.944	0.465	24	0.150	K.LAAALPEGGVLLLENVR.F
R5/RRR5-1/2	1735.253	1736.049	-1038.309	0.449	935.443	0.475	23	0.150	K.LAAALPEGGVLLLENVR.F
R5/RRR5-10/2	1735.366	1736.049	-972.767	0.456	782.095	0.521	22	0.148	K.LAAALPEGGVLLLENVR.F
R5/RRR5-2/2	1736.183	1736.049	77.247	0.503	811.166	0.502	22	0.148	K.LAAALPEGGVLLLENVR.F
R5/RRR5-15/2	1735.974	1736.049	-43.489	0.435	875.277	0.431	22	0.141	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1736.198	1736.049	86.273	0.530	727.757	0.471	22	0.140	K.LAAALPEGGVLLLENVR.F
R5/RRR5-10/2	1735.631	1736.049	-241.370	0.484	716.412	0.478	21	0.140	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1450.396	1450.816	-290.949	0.490	688.247	0.429	20	0.138	K.FLKPAVAGFLMQK.E
R5/RRR5-2/2	1736.693	1736.049	-205.338	0.427	535.863	0.490	18	0.134	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1466.290	1466.816	-1043.655	0.408	576.074	0.413	19	0.133	K.FLKPAVAGFLM*QK.E
R5/RRR5-11/2	1465.803	1466.816	-1377.197	0.441	528.971	0.416	18	0.132	K.FLKPAVAGFLM*QK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1735.730	1736.049	-184.361	0.402	478.740	0.500	16	0.132	K.LAAALPEGGVLLLENVR.F
R5/RRR5-11/2	1467.251	1466.816	297.592	0.421	593.269	0.387	19	0.131	K.FLKPAVAGFLM*QK.E
R5/RRR5-11/2	1450.045	1450.816	-1225.054	0.483	549.976	0.383	18	0.130	K.FLKPAVAGFLMQK.E
R5/RRR5-11/2	1449.457	1450.816	-1632.361	0.351	477.635	0.325	16	0.123	K.FLKPAVAGFLMQK.E
R5/RRR5-4/2	1431.382	1431.767	-269.666	0.558	2658.301	0.554	22	0.403	R.IVSQLLTLMDGLK.Q
R5/RRR5-4/2	1448.292	1447.766	-328.217	0.584	2149.139	0.601	21	0.319	R.IVSQLLTLM*DGLK.Q
R5/RRR5-4/2	1845.537	1846.969	-1321.970	0.457	2127.464	0.554	23	0.301	K.YTQGFSGADITEICQR.A
R5/RRR5-4/2	1846.451	1846.969	-824.528	0.547	1818.501	0.558	23	0.254	K.YTQGFSGADITEICQR.A
R5/RRR5-4/2	1844.012	1844.098	-46.950	0.527	1977.718	0.469	24	0.251	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-4/2	1430.777	1431.767	-1394.557	0.393	1838.988	0.504	19	0.241	R.IVSQLLTLMDGLK.Q
R5/RRR5-4/2	1447.397	1447.766	-255.841	0.481	1658.265	0.560	19	0.232	R.IVSQLLTLM*DGLK.Q
R5/RRR5-4/2	1843.607	1844.098	-266.815	0.497	1857.453	0.429	24	0.225	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-4/2	1843.448	1844.098	-897.867	0.482	1854.561	0.430	23	0.224	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-4/2	1843.172	1844.098	-1047.795	0.463	1744.328	0.462	23	0.218	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-4/2	1584.424	1584.750	-206.372	0.440	1576.618	0.452	20	0.198	R.LGDVVSVHQCQDVK.Y
R5/RRR5-4/2	1447.313	1447.766	-313.803	0.480	1440.573	0.500	19	0.194	R.IVSQLLTLM*DGLK.Q
R5/RRR5-4/2	1846.237	1846.969	-941.076	0.501	1369.722	0.537	19	0.192	K.YTQGFSGADITEICQR.A
R5/RRR5-4/2	1188.085	1188.316	-195.040	0.478	1399.071	0.473	20	0.186	K.TALGTSNPSALR.E
R5/RRR5-4/2	1843.402	1844.098	-922.597	0.468	1630.865	0.373	22	0.185	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-1/2	1188.060	1188.316	-216.274	0.480	1412.771	0.442	19	0.181	K.TALGTSNPSALR.E
R5/RRR5-1/2	1843.278	1844.098	-990.544	0.448	1487.229	0.411	21	0.178	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-4/2	1431.499	1431.767	-187.449	0.422	1225.591	0.516	17	0.175	R.IVSQLLTLMDGLK.Q
R5/RRR5-4/2	1952.351	1953.165	-932.081	0.517	1175.748	0.528	21	0.173	K.GPELLTM*WFGESEANVR.E
R5/RRR5-4/2	1187.734	1188.316	-1336.446	0.450	1219.878	0.467	19	0.169	K.TALGTSNPSALR.E
R5/RRR5-2/2	1188.197	1188.316	-100.531	0.452	1464.711	0.346	19	0.167	K.TALGTSNPSALR.E
R5/RRR5-4/2	1584.224	1584.750	-966.108	0.416	1269.963	0.451	18	0.167	R.LGDVVSVHQCQDVK.Y
R5/RRR5-4/2	1844.549	1844.098	245.423	0.503	1490.497	0.352	20	0.165	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-4/2	1252.024	1252.437	-330.886	0.438	1016.379	0.534	17	0.163	K.GVLFYGPPGCGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1801.485	1801.033	251.562	0.534	981.483	0.506	21	0.158	R.LDQLIYIPLPDEQSR.L
R5/RRR5-4/2	1802.648	1801.033	-214.126	0.529	962.087	0.505	21	0.157	R.LDQLIYIPLPDEQSR.L
R5/RRR5-4/2	1188.051	1188.316	-224.005	0.431	1133.180	0.417	19	0.155	K.TALGTSNPSALR.E
R5/RRR5-3/2	1187.986	1188.316	-278.331	0.407	1311.403	0.333	19	0.154	K.TALGTSNPSALR.E
R5/RRR5-3/2	1843.216	1844.098	-1023.790	0.407	1161.963	0.427	19	0.154	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-4/2	1564.681	1565.746	-1324.197	0.368	1184.768	0.407	18	0.153	K.AIANECQANFISVK.G
R5/RRR5-4/2	1565.245	1565.746	-962.178	0.463	1103.802	0.435	17	0.152	K.AIANECQANFISVK.G
R5/RRR5-4/2	1566.153	1565.746	260.124	0.482	1137.951	0.421	17	0.152	K.AIANECQANFISVK.G
R5/RRR5-4/2	1802.443	1801.033	227.993	0.500	924.128	0.462	21	0.149	R.LDQLIYIPLPDEQSR.L
R5/RRR5-4/2	1952.271	1953.165	-972.883	0.513	926.205	0.472	19	0.145	K.GPELLTM*WFGESEANVR.E
R5/RRR5-5/2	1447.293	1447.766	-328.105	0.417	976.704	0.429	16	0.145	R.IVSQLLTLM*DGLK.Q
R5/RRR5-1/2	1187.918	1188.316	-336.477	0.461	1104.928	0.351	19	0.144	K.TALGTSNPSALR.E
R5/RRR5-2/2	1188.004	1188.316	-263.486	0.469	1068.184	0.358	18	0.143	K.TALGTSNPSALR.E
R5/RRR5-3/2	1842.991	1844.098	-1146.818	0.369	1131.123	0.356	19	0.142	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-2/2	1187.970	1188.316	-292.042	0.445	1051.647	0.349	19	0.141	K.TALGTSNPSALR.E
R5/RRR5-1/2	1844.747	1844.098	-190.789	0.443	859.455	0.452	18	0.140	K.NAPSIIFIDEIDSIAPK.R
R5/RRR5-3/2	1188.059	1188.316	-217.511	0.442	956.025	0.365	18	0.139	K.TALGTSNPSALR.E
R5/RRR5-4/2	1802.492	1801.033	255.361	0.538	693.633	0.459	19	0.137	R.LDQLIYIPLPDEQSR.L
R5/RRR5-4/2	1159.025	1159.360	-289.300	0.395	788.035	0.449	15	0.137	K.GILLYGPPGSGK.T
R5/RRR5-1/2	1187.589	1188.316	-1458.985	0.419	875.786	0.367	19	0.137	K.TALGTSNPSALR.E
R5/RRR5-4/2	958.946	959.079	-139.247	0.390	807.428	0.392	14	0.136	K.DVDLNALAK.Y
R5/RRR5-4/2	969.040	969.160	-124.404	0.331	746.001	0.394	12	0.133	R.ELVELPLR.H
R5/RRR5-4/2	959.120	959.079	42.559	0.374	920.195	0.322	15	0.132	K.DVDLNALAK.Y
R5/RRR5-4/2	1894.959	1894.054	-50.630	0.358	854.614	0.413	18	0.132	K.DTICIVLADETCEEPK.I
R5/RRR5-4/2	969.042	969.160	-122.003	0.302	760.820	0.390	12	0.131	R.ELVELPLR.H
R5/RRR5-4/2	968.958	969.160	-209.328	0.297	718.766	0.400	12	0.131	R.ELVELPLR.H
R5/RRR5-4/2	959.177	959.079	102.806	0.425	781.189	0.309	14	0.128	K.DVDLNALAK.Y
R5/RRR5-3/2	1187.363	1188.316	-1650.028	0.341	686.777	0.315	17	0.126	K.TALGTSNPSALR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1799.379	1801.033	-2037.000	0.295	683.313	0.365	17	0.125	R.LDQLIYIPLPDEQSR.L
R5/RRR5-2/2	1800.543	1801.033	-273.333	0.397	485.999	0.390	15	0.124	R.LDQLIYIPLPDEQSR.L
R5/RRR5-3/2	1800.490	1801.033	-859.584	0.329	466.168	0.309	15	0.120	R.LDQLIYIPLPDEQSR.L
R5/RRR5-2/2	1446.864	1447.766	-1318.194	0.287	515.799	0.295	14	0.120	R.IVSQLLTLM*DGLK.Q
R5/RRR5-3/2	969.111	969.160	-50.613	0.335	529.288	0.225	10	0.120	R.ELVELPLR.H
R5/RRR5-5/2	1446.401	1447.766	-1639.775	0.316	662.748	0.272	14	0.119	R.IVSQLLTLM*DGLK.Q
R5/RRR5-4/2	1799.436	1801.033	-2005.024	0.241	640.898	0.262	18	0.118	R.LDQLIYIPLPDEQSR.L
R5/RRR5-4/2	1252.559	1252.437	97.787	0.303	619.622	0.266	14	0.117	K.GVLFYGPPGCGK.T
R5/RRR5-4/2	1951.256	1953.165	-2009.289	0.287	647.116	0.228	19	0.115	K.GPELLTM*WFGESEANVR.E
R5/RRR5-5/2	968.580	969.160	-1636.686	0.335	910.113	0.109	12	0.114	R.ELVELPLR.H
R5/RRR5-3/2	968.837	969.160	-334.212	0.211	1037.494	0.062	12	0.113	R.ELVELPLR.H
R5/RRR5-3/2	1158.302	1159.360	-1781.590	0.153	601.556	0.027	12	0.109	-.GILLYGPPGSGK.-
R5/RRR5-4/3	1587.571	1587.953	-240.984	0.463	895.747	0.349	24	0.082	R.RIVSQLLTLMDGLK.Q
R5/RRR5-4/2	1568.853	1569.746	-1210.480	0.580	2513.650	0.544	22	0.372	R.KYQAFAQTLQQSR.G
R5/RRR5-4/2	1569.232	1569.746	-967.769	0.607	2443.879	0.569	22	0.366	R.KYQAFAQTLQQSR.G
R5/RRR5-4/2	1569.301	1569.746	-284.898	0.612	2250.413	0.559	22	0.326	R.KYQAFAQTLQQSR.G
R5/RRR5-4/2	1441.241	1441.574	-231.716	0.550	2198.544	0.513	20	0.302	K.YQAFAQTLQQSR.G
R5/RRR5-4/2	1441.238	1441.574	-233.756	0.536	1989.930	0.533	19	0.274	K.YQAFAQTLQQSR.G
R5/RRR5-4/2	1441.127	1441.574	-310.831	0.516	1999.849	0.486	19	0.262	K.YQAFAQTLQQSR.G
R5/RRR5-4/2	1353.250	1353.503	-187.702	0.490	1829.470	0.458	18	0.231	K.LAEDVDLEHIAK.D
R5/RRR5-1/2	1353.448	1353.503	-40.854	0.362	952.008	0.382	16	0.137	K.LAEDVDLEHIAK.D
R5/RRR5-4/2	1352.394	1353.503	-1564.197	0.294	771.467	0.328	16	0.124	K.LAEDVDLEHIAK.D
R5/RRR5-4/2	1552.555	1553.736	-1408.590	0.277	935.317	0.211	17	0.116	R.LGDVVSVHQCPDVK.Y
R5/RRR5-4/3	1354.059	1353.503	-328.929	0.519	625.829	0.439	25	0.092	K.LAEDVDLEHIAK.D
R5/RRR5-4/3	1353.232	1353.503	-201.105	0.425	499.342	0.444	23	0.087	K.LAEDVDLEHIAK.D
R5/RRR5-8/3	1911.867	1911.020	-80.353	0.543	3659.589	0.476	36	0.811	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1911.311	1911.020	153.062	0.608	3121.129	0.511	28	0.493	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1910.497	1911.020	-799.194	0.612	3004.351	0.540	27	0.476	R.TGELIAHVAEGDAEDINR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1910.410	1911.020	-844.990	0.602	3009.607	0.508	27	0.464	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1481.159	1481.550	-264.571	0.524	2676.494	0.558	26	0.410	K.YGVDSGANLVTGGDR.L
R5/RRR5-8/2	1910.440	1911.020	-829.147	0.569	2628.510	0.503	25	0.376	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/3	1910.371	1911.020	-865.459	0.501	2524.366	0.438	32	0.370	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-8/3	1911.067	1911.020	24.972	0.527	2435.082	0.435	32	0.342	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1480.955	1481.550	-1080.352	0.454	2387.855	0.531	25	0.341	K.YGVDSGANLVTGGDR.L
R5/RRR5-9/2	1481.199	1481.550	-237.286	0.518	2199.604	0.586	24	0.324	K.YGVDSGANLVTGGDR.L
R5/RRR5-8/2	1481.210	1481.550	-229.762	0.492	2200.460	0.552	25	0.313	K.YGVDSGANLVTGGDR.L
R5/RRR5-8/2	1481.190	1481.550	-243.404	0.520	2109.190	0.557	24	0.299	K.YGVDSGANLVTGGDR.L
R5/RRR5-8/2	1910.592	1911.020	-224.330	0.528	2316.655	0.409	25	0.287	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-8/2	1481.197	1481.550	-238.857	0.480	2050.628	0.523	23	0.280	K.YGVDSGANLVTGGDR.L
R5/RRR5-9/3	1673.220	1672.947	163.784	0.521	2043.584	0.450	31	0.253	K.IAQEEIFGPVQSILK.F
R5/RRR5-2/2	1912.445	1911.020	223.010	0.536	2062.686	0.430	24	0.252	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1818.313	1818.879	-863.885	0.568	1663.754	0.555	23	0.232	K.NGVEQGPQIDDEQFNK.I
R5/RRR5-9/2	1818.392	1818.879	-268.966	0.537	1673.805	0.542	23	0.230	K.NGVEQGPQIDDEQFNK.I
R5/RRR5-8/2	1910.288	1911.020	-909.009	0.543	1730.726	0.472	22	0.217	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1818.380	1818.879	-275.095	0.550	1507.522	0.564	22	0.215	K.NGVEQGPQIDDEQFNK.I
R5/RRR5-9/2	1398.588	1399.655	-1482.243	0.478	1356.312	0.574	21	0.201	K.VGPALACGNTVVLK.T
R5/RRR5-8/2	1464.486	1464.645	-108.987	0.492	1228.886	0.565	19	0.186	K.TAEQTPLSALFASK.L
R5/RRR5-8/2	1818.145	1818.879	-956.694	0.527	1338.162	0.514	21	0.185	K.NGVEQGPQIDDEQFNK.I
R5/RRR5-9/3	1910.754	1911.020	-139.671	0.534	1773.025	0.408	30	0.184	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1465.588	1464.645	-39.399	0.545	1182.343	0.566	20	0.184	K.TAEQTPLSALFASK.L
R5/RRR5-9/2	1464.532	1464.645	-77.633	0.495	1214.177	0.540	20	0.181	K.TAEQTPLSALFASK.L
R5/RRR5-8/2	1818.244	1818.879	-901.963	0.551	1218.001	0.539	21	0.180	K.NGVEQGPQIDDEQFNK.I
R5/RRR5-8/2	1465.341	1464.645	-208.019	0.532	1130.214	0.560	20	0.178	K.TAEQTPLSALFASK.L
R5/RRR5-1/2	1464.316	1464.645	-225.724	0.447	1193.732	0.506	20	0.172	K.TAEQTPLSALFASK.L
R5/RRR5-8/2	1399.329	1399.655	-233.494	0.473	1078.990	0.536	19	0.169	K.VGPALACGNTVVLK.T
R5/RRR5-8/2	1674.582	1672.947	-218.219	0.582	1413.510	0.399	20	0.167	K.IAQEEIFGPVQSILK.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1399.263	1399.655	-280.493	0.484	1048.901	0.497	19	0.160	K.VGPALACGNTVVLK.T
R5/RRR5-9/2	1378.640	1378.599	30.052	0.486	1491.361	0.306	17	0.160	K.GIDSLKNYLQVK.A
R5/RRR5-9/2	1464.223	1464.645	-289.037	0.347	1117.625	0.454	18	0.155	K.TAEQTPLSALFASK.L
R5/RRR5-9/2	1247.601	1248.413	-1457.109	0.451	1120.771	0.378	16	0.149	K.FNDLNEVIKR.A
R5/RRR5-8/2	1399.018	1399.655	-1173.556	0.461	964.952	0.435	18	0.145	K.VGPALACGNTVVLK.T
R5/RRR5-9/2	1398.757	1399.655	-1360.569	0.407	993.145	0.426	17	0.145	K.VGPALACGNTVVLK.T
R5/RRR5-8/2	1377.708	1378.599	-1376.557	0.387	1081.058	0.372	17	0.144	K.GIDSLKNYLQVK.A
R5/RRR5-8/2	1464.223	1464.645	-289.205	0.341	968.054	0.401	18	0.140	K.TAEQTPLSALFASK.L
R5/RRR5-9/2	1378.598	1378.599	-0.498	0.480	1263.854	0.286	16	0.140	K.GIDSLKNYLQVK.A
R5/RRR5-9/2	1097.985	1098.188	-186.067	0.382	1032.013	0.337	17	0.138	K.IAFTGSTDTGK.I
R5/RRR5-9/2	1398.549	1399.655	-1509.861	0.435	815.267	0.434	17	0.138	K.VGPALACGNTVVLK.T
R5/RRR5-8/2	1091.906	1092.227	-295.197	0.445	1162.353	0.281	14	0.137	K.FNDLNEVIK.R
R5/RRR5-2/2	1674.446	1672.947	299.019	0.503	970.107	0.376	18	0.136	K.IAQEEIFGPVQSILK.F
R5/RRR5-9/2	1248.028	1248.413	-309.578	0.442	893.501	0.356	15	0.135	K.FNDLNEVIKR.A
R5/RRR5-8/2	1247.544	1248.413	-1502.516	0.435	819.767	0.374	15	0.135	K.FNDLNEVIKR.A
R5/RRR5-9/2	885.049	885.086	-42.209	0.470	617.016	0.383	13	0.134	K.IVLELAAR.S
R5/RRR5-8/2	885.154	885.086	76.892	0.456	597.572	0.384	13	0.134	K.IVLELAAR.S
R5/RRR5-9/2	1098.162	1098.188	-23.593	0.375	676.109	0.428	15	0.134	K.IAFTGSTDTGK.I
R5/RRR5-8/2	1247.457	1248.413	-1572.699	0.406	775.804	0.366	15	0.133	K.FNDLNEVIKR.A
R5/RRR5-9/2	1377.985	1378.599	-1174.765	0.475	1035.866	0.304	17	0.133	K.GIDSLKNYLQVK.A
R5/RRR5-9/2	885.068	885.086	-20.766	0.469	597.262	0.365	13	0.133	K.IVLELAAR.S
R5/RRR5-8/2	1248.140	1248.413	-219.303	0.468	949.485	0.311	15	0.132	K.FNDLNEVIKR.A
R5/RRR5-9/2	1247.605	1248.413	-1454.062	0.452	868.021	0.328	15	0.132	K.FNDLNEVIKR.A
R5/RRR5-9/2	884.503	885.086	-1794.821	0.412	712.247	0.343	13	0.131	K.IVLELAAR.S
R5/RRR5-8/2	884.507	885.086	-1790.938	0.363	771.598	0.334	13	0.130	K.IVLELAAR.S
R5/RRR5-8/2	884.469	885.086	-1834.205	0.405	702.518	0.334	13	0.130	K.IVLELAAR.S
R5/RRR5-9/2	1097.462	1098.188	-1577.797	0.274	733.101	0.403	16	0.129	K.IAFTGSTDTGK.I
R5/RRR5-8/2	1097.986	1098.188	-184.952	0.361	697.933	0.365	15	0.129	K.IAFTGSTDTGK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1378.579	1378.599	-14.353	0.449	876.960	0.310	16	0.128	K.GIDSLKNYLQVK.A
R5/RRR5-8/2	1674.605	1672.947	-204.763	0.454	708.609	0.397	15	0.126	-.IAQEEIFGPVQSILK.-
R5/RRR5-8/2	1672.200	1672.947	-1047.513	0.423	757.318	0.345	17	0.126	K.IAQEEIFGPVQSILK.F
R5/RRR5-8/2	1091.979	1092.227	-227.567	0.284	1137.338	0.188	14	0.125	K.FNDLNEVIK.R
R5/RRR5-7/2	1378.428	1378.599	-124.496	0.334	475.332	0.352	15	0.125	K.GIDSLKNYLQVK.A
R5/RRR5-9/2	1671.842	1672.947	-1262.314	0.344	635.492	0.360	15	0.122	-.IAQEEIFGPVQSILK.-
R5/RRR5-7/2	1399.013	1399.655	-1176.711	0.270	431.633	0.296	15	0.120	K.VGPALACGNTVVLK.T
R5/RRR5-9/2	1092.186	1092.227	-37.174	0.454	957.724	0.205	13	0.119	K.FNDLNEVIK.R
R5/RRR5-9/3	1910.740	1911.020	-146.785	0.428	1295.307	0.391	29	0.118	R.TGELIAHVAEGDAEDINR.A
R5/RRR5-9/2	1091.416	1092.227	-1663.942	0.367	1313.054	0.064	14	0.118	K.FNDLNEVIK.R
R5/RRR5-8/2	1377.503	1378.599	-1525.641	0.378	643.764	0.224	14	0.117	K.GIDSLKNYLQVK.A
R5/RRR5-8/2	1097.928	1098.188	-238.155	0.270	652.116	0.171	15	0.116	K.IAFTGSTDTGK.I
R5/RRR5-8/3	1673.714	1672.947	-139.591	0.417	1085.668	0.458	24	0.114	K.IAQEEIFGPVQSILK.F
R5/RRR5-8/2	1673.986	1672.947	23.507	0.330	622.328	0.141	16	0.112	K.IAQEEIFGPVQSILK.F
R5/RRR5-7/2	1673.450	1672.947	-297.750	0.402	592.737	0.209	15	0.112	-.IAQEEIFGPVQSILK.-
R5/RRR5-8/2	1091.395	1092.227	-1683.382	0.312	979.252	0.055	13	0.110	-.FNDLNEVIK.-
R5/RRR5-9/3	1176.061	1175.318	-218.596	0.476	1087.489	0.398	20	0.103	R.KAFDEGPWPK.M
R5/RRR5-8/3	1175.479	1175.318	137.415	0.517	947.058	0.428	19	0.101	R.KAFDEGPWPK.M
R5/RRR5-8/3	1673.843	1672.947	-61.898	0.424	1248.768	0.332	25	0.100	K.IAQEEIFGPVQSILK.F
R5/RRR5-8/3	1175.430	1175.318	96.015	0.526	819.781	0.447	18	0.098	R.KAFDEGPWPK.M
R5/RRR5-8/3	1673.178	1672.947	138.982	0.305	1189.248	0.329	23	0.097	-.IAQEEIFGPVQSILK.-
R5/RRR5-8/3	1175.336	1175.318	16.019	0.528	1095.301	0.328	21	0.091	R.KAFDEGPWPK.M
R5/RRR5-26/3	1439.109	1439.642	-1068.726	0.359	1231.936	0.150	27	0.067	R.ADGTQGLLPGILQR.F
R5/RRR5-26/3	1439.217	1439.642	-296.323	0.325	862.724	0.189	24	0.064	-.ADGTQGLLPGILQR.-
R5/RRR5-26/3	1439.380	1439.642	-182.732	0.337	1123.731	0.126	26	0.061	R.ADGTQGLLPGILQR.F
R5/RRR5-7/2	1779.414	1779.974	-879.467	0.509	2174.776	0.584	25	0.318	K.SVGPVVDGDAVVTFNFR.A
R5/RRR5-7/2	1780.318	1779.974	194.033	0.597	2053.528	0.591	24	0.298	K.SVGPVVDGDAVVTFNFR.A
R5/RRR5-7/2	1404.239	1404.570	-236.371	0.446	2238.578	0.467	20	0.295	R.YAGM*LQYDGELK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1780.464	1779.974	276.262	0.534	2004.081	0.566	24	0.283	K.SVGPVVDGDAVVTFNFR.A
R5/RRR5-6/2	1780.201	1779.974	127.677	0.523	1955.806	0.570	23	0.276	K.SVGPVVDGDAVVTFNFR.A
R5/RRR5-6/2	1779.365	1779.974	-907.084	0.497	1976.661	0.529	24	0.269	K.SVGPVVDGDAVVTFNFR.A
R5/RRR5-7/2	1433.552	1434.578	-1417.138	0.341	2045.457	0.414	20	0.249	R.GWDAQVLGEAPYK.F
R5/RRR5-7/2	1434.264	1434.578	-219.527	0.446	1977.563	0.436	20	0.246	R.GWDAQVLGEAPYK.F
R5/RRR5-7/2	1779.404	1779.974	-885.114	0.514	1740.659	0.533	23	0.236	K.SVGPVVDGDAVVTFNFR.A
R5/RRR5-7/2	1433.664	1434.578	-1338.800	0.319	1848.591	0.354	19	0.208	R.GWDAQVLGEAPYK.F
R5/RRR5-7/2	1403.815	1404.570	-1254.265	0.451	1641.300	0.446	18	0.205	R.YAGM*LQYDGELK.L
R5/RRR5-6/2	1490.113	1490.598	-326.660	0.389	1476.451	0.417	17	0.180	K.ALEYADFDKFDR.V
R5/RRR5-7/2	1070.198	1070.307	-102.234	0.518	1537.330	0.293	14	0.162	R.LDQVQLLLK.G
R5/RRR5-6/2	1070.068	1070.307	-224.790	0.452	1422.468	0.329	14	0.161	R.LDQVQLLLK.G
R5/RRR5-7/2	1349.233	1349.518	-211.673	0.470	1147.438	0.446	18	0.160	R.DAILSGKFDQVR.V
R5/RRR5-6/2	987.070	987.175	-107.309	0.560	970.357	0.491	17	0.160	K.LVDLALASGK.I
R5/RRR5-6/2	987.094	987.175	-82.250	0.503	1098.398	0.441	17	0.159	K.LVDLALASGK.I
R5/RRR5-7/2	986.509	987.175	-1693.879	0.435	1024.963	0.466	17	0.157	K.LVDLALASGK.I
R5/RRR5-7/2	986.394	987.175	-1811.002	0.387	1012.453	0.465	17	0.154	K.LVDLALASGK.I
R5/RRR5-7/3	1576.641	1576.782	-89.672	0.539	1404.827	0.476	28	0.154	K.ARDAILSGKFDQVR.V
R5/RRR5-6/2	1070.449	1070.307	132.266	0.482	1412.749	0.292	14	0.153	R.LDQVQLLLK.G
R5/RRR5-6/2	1070.101	1070.307	-193.433	0.474	1373.373	0.283	14	0.150	-.LDQVQLLLK.-
R5/RRR5-7/2	1590.032	1590.764	-1092.867	0.439	1008.005	0.460	18	0.149	K.RGWDAQVLGEAPYK.F
R5/RRR5-6/2	987.373	987.175	200.994	0.525	962.816	0.424	17	0.149	K.LVDLALASGK.I
R5/RRR5-7/2	1349.288	1349.518	-171.013	0.397	994.930	0.440	17	0.148	R.DAILSGKFDQVR.V
R5/RRR5-7/2	1069.556	1070.307	-1642.087	0.420	1257.010	0.253	14	0.139	R.LDQVQLLLK.G
R5/RRR5-7/2	1388.649	1388.571	56.198	0.368	995.072	0.357	17	0.137	R.YAGMLQYDGELK.L
R5/RRR5-7/2	1069.607	1070.307	-1594.504	0.439	1201.073	0.267	14	0.137	R.LDQVQLLLK.G
R5/RRR5-7/2	1388.827	1388.571	185.167	0.354	965.141	0.336	17	0.134	R.YAGMLQYDGELK.L
R5/RRR5-7/2	1865.432	1866.060	-875.406	0.359	603.350	0.466	22	0.133	K.ASDQYLPPFVIVDESGK.S
R5/RRR5-7/2	1349.292	1349.518	-167.745	0.423	752.499	0.396	15	0.131	R.DAILSGKFDQVR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1865.009	1866.060	-1103.276	0.380	449.892	0.490	19	0.131	K.ASDQYLPPFVIVDESGK.S
R5/RRR5-7/2	1864.939	1866.060	-1140.871	0.378	496.175	0.465	20	0.131	K.ASDQYLPPFVIVDESGK.S
R5/RRR5-6/2	1865.538	1866.060	-818.257	0.414	360.737	0.468	17	0.128	K.ASDQYLPPFVIVDESGK.S
R5/RRR5-7/2	1483.505	1482.629	-84.150	0.394	661.626	0.394	16	0.127	K.FGHVTFFWNGNR.S
R5/RRR5-6/2	1006.147	1006.137	9.539	0.431	728.248	0.316	15	0.127	-.FQNAVEAVK.-
R5/RRR5-6/2	1865.304	1866.060	-944.584	0.361	394.999	0.438	18	0.126	K.ASDQYLPPFVIVDESGK.S
R5/RRR5-7/2	1005.920	1006.137	-216.850	0.450	708.305	0.305	15	0.126	-.FQNAVEAVK.-
R5/RRR5-6/2	1006.007	1006.137	-129.812	0.472	856.378	0.250	16	0.126	K.FQNAVEAVK.T
R5/RRR5-7/2	1005.988	1006.137	-149.166	0.432	727.187	0.272	15	0.124	-.FQNAVEAVK.-
R5/RRR5-6/2	1006.106	1006.137	-31.106	0.478	687.271	0.277	15	0.123	-.FQNAVEAVK.-
R5/RRR5-7/2	1005.902	1006.137	-234.260	0.458	846.237	0.265	15	0.122	-.FQNAVEAVK.-
R5/RRR5-7/3	1733.089	1732.965	71.443	0.400	814.358	0.490	27	0.097	K.GTLHLIGLLSDGGVHSR.L
R5/RRR5-7/3	1482.388	1482.629	-162.852	0.438	1066.303	0.312	22	0.085	K.FGHVTFFWNGNR.S
R5/RRR5-7/3	1575.405	1576.782	-1513.527	0.431	607.462	0.426	22	0.085	K.ARDAILSGKFDQVR.V
R5/RRR5-7/3	1482.252	1482.629	-254.803	0.426	1064.934	0.223	21	0.072	K.FGHVTFFWNGNR.S
R5/RRR5-7/3	1482.872	1482.629	164.414	0.414	939.924	0.184	21	0.065	K.FGHVTFFWNGNR.S
R5/RRR5-2/2	1592.346	1592.644	-187.506	0.547	2323.393	0.556	22	0.339	R.TQDLENELSTANEK.F
R5/RRR5-2/2	1611.178	1611.732	-967.652	0.506	2343.618	0.497	22	0.323	K.VSQLSDELEAYQTK.A
R5/RRR5-2/2	1610.747	1611.732	-1236.386	0.369	2353.274	0.473	21	0.317	K.VSQLSDELEAYQTK.A
R5/RRR5-2/2	1508.470	1507.625	-103.212	0.572	1795.390	0.574	22	0.256	K.INELQASLDSTTSK.N
R5/RRR5-2/2	1507.196	1507.625	-285.833	0.491	1754.406	0.491	21	0.229	K.INELQASLDSTTSK.N
R5/RRR5-2/2	1203.008	1203.328	-266.713	0.505	1862.833	0.381	19	0.217	K.TAALEEQALTR.E
R5/RRR5-2/2	1202.833	1203.328	-412.719	0.437	1809.898	0.317	18	0.196	K.TAALEEQALTR.E
R5/RRR5-2/2	1160.395	1161.248	-1600.904	0.419	1412.505	0.473	18	0.186	R.GLELQSAAESR.S
R5/RRR5-2/2	1160.331	1161.248	-1656.812	0.395	1475.480	0.433	18	0.184	R.GLELQSAAESR.S
R5/RRR5-2/2	1160.309	1161.248	-1675.626	0.428	1408.349	0.427	18	0.178	R.GLELQSAAESR.S
R5/RRR5-2/2	1388.106	1388.509	-291.215	0.421	1493.314	0.386	18	0.176	R.TIANQEEQISVR.E
R5/RRR5-2/2	1506.527	1507.625	-1397.012	0.380	1419.876	0.373	19	0.167	K.INELQASLDSTTSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1074.104	1074.253	-138.795	0.392	1158.656	0.299	15	0.138	K.LALVNTEVSK.L
R5/RRR5-2/2	1537.457	1536.663	-134.394	0.331	663.241	0.440	18	0.128	K.LSSISSEKEEVAEK.L
R5/RRR5-2/3	1527.156	1527.660	-988.069	0.459	1613.779	0.273	24	0.122	K.FKEVEADLEQYR.S
R5/RRR5-2/3	1588.776	1588.707	44.063	0.502	1228.939	0.396	25	0.114	R.QNLHYTSLQEAQR.S
R5/RRR5-2/3	1322.449	1322.452	-2.613	0.496	719.782	0.514	21	0.103	K.TIEHLTEVHSR.G
R5/RRR5-2/3	1834.045	1834.018	14.472	0.454	1064.991	0.405	27	0.101	R.SLADKDKELADATQSLK.E
R5/RRR5-2/3	1322.522	1322.452	52.657	0.468	495.197	0.474	18	0.093	K.TIEHLTEVHSR.G
R5/RRR5-2/3	1425.296	1425.529	-164.265	0.538	1020.761	0.355	22	0.091	K.AIDHQQVEESLR.S
R5/RRR5-10/3	1317.937	1318.502	-1191.233	0.382	413.897	0.372	20	0.090	K.RTSLEASLLEAK.Q
R5/RRR5-2/3	1527.093	1527.660	-1029.480	0.444	1233.798	0.270	23	0.089	-.FKEVEADLEQYR.-
R5/RRR5-2/3	1588.293	1588.707	-261.534	0.492	797.593	0.375	24	0.087	R.QNLHYTSLQEAQR.S
R5/RRR5-2/3	1425.190	1425.529	-238.760	0.501	1084.207	0.308	23	0.087	K.AIDHQQVEESLR.S
R5/RRR5-2/3	1526.950	1527.660	-1123.271	0.474	1284.284	0.247	23	0.086	K.FKEVEADLEQYR.S
R5/RRR5-2/3	1426.474	1425.529	-39.029	0.552	720.940	0.383	20	0.083	-.AIDHQQVEESLR.-
R5/RRR5-2/3	1416.978	1416.602	265.984	0.489	1302.019	0.220	22	0.083	R.RIEELELEKEK.L
R5/RRR5-2/3	1321.686	1322.452	-1340.241	0.333	484.519	0.405	17	0.082	K.TIEHLTEVHSR.G
R5/RRR5-1/3	1318.121	1318.502	-289.828	0.372	701.074	0.324	23	0.081	K.RTSLEASLLEAK.Q
R5/RRR5-2/3	1588.654	1588.707	-33.388	0.547	735.578	0.349	23	0.080	-.QNLHYTSLQEAQR.-
R5/RRR5-6/3	1317.958	1318.502	-1174.910	0.349	718.201	0.302	24	0.078	K.RTSLEASLLEAK.Q
R5/RRR5-10/3	1317.370	1318.502	-1623.220	0.327	810.031	0.310	25	0.077	K.RTSLEASLLEAK.Q
R5/RRR5-3/3	1317.185	1318.502	-1764.272	0.308	676.298	0.290	22	0.077	K.RTSLEASLLEAK.Q
R5/RRR5-2/3	1416.991	1416.602	275.443	0.482	1259.497	0.201	21	0.077	R.RIEELELEKEK.L
R5/RRR5-1/3	1317.981	1318.502	-1157.192	0.362	664.954	0.247	23	0.077	K.RTSLEASLLEAK.Q
R5/RRR5-8/3	1317.776	1318.502	-1313.464	0.379	952.428	0.267	25	0.076	K.RTSLEASLLEAK.Q
R5/RRR5-10/3	1317.729	1318.502	-1349.608	0.326	679.825	0.220	23	0.074	K.RTSLEASLLEAK.Q
R5/RRR5-9/3	1317.742	1318.502	-1339.560	0.306	757.032	0.230	24	0.069	-.RTSLEASLLEAK.-
R5/RRR5-2/3	1832.517	1834.018	-1916.320	0.338	754.135	0.278	25	0.068	R.SLADKDKELADATQSLK.E
R5/RRR5-6/3	1317.297	1318.502	-1679.077	0.285	756.065	0.224	25	0.068	-.RTSLEASLLEAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1415.253	1416.602	-1664.945	0.435	964.813	0.171	20	0.064	-.RIEELELEKEK.-
R5/RRR5-26/3	1317.844	1318.502	-1261.414	0.245	802.735	0.085	21	0.062	K.RTSLEASLLEAK.Q
R5/RRR5-2/3	1426.170	1425.529	-252.417	0.398	553.565	0.268	17	0.036	-.AIDHQQVEESLR.-
R5/RRR5-23/2	1923.524	1924.095	-819.306	0.625	3384.167	0.606	26	0.608	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-23/2	1923.481	1924.095	-841.858	0.623	3298.645	0.601	26	0.581	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-22/2	1923.654	1924.095	-230.062	0.642	3226.698	0.606	26	0.563	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-22/2	1923.598	1924.095	-259.157	0.636	3119.555	0.597	26	0.530	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-22/2	1924.577	1924.095	250.995	0.646	3072.296	0.617	26	0.526	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-22/2	1638.217	1638.823	-982.965	0.483	2328.826	0.576	22	0.518	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1924.411	1924.095	164.681	0.634	2959.157	0.627	25	0.502	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-23/2	1978.464	1979.086	-822.051	0.598	2568.994	0.687	27	0.435	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-24/2	1639.250	1638.823	261.775	0.521	2083.974	0.630	21	0.423	K.M*IEDYLVAHPAEYA.-
R5/RRR5-20/2	1639.296	1638.823	289.403	0.532	2057.942	0.596	21	0.404	K.M*IEDYLVAHPAEYA.-
R5/RRR5-22/2	1622.606	1622.823	-134.057	0.438	2040.355	0.593	22	0.404	K.MIEDYLVAHPAEYA.-
R5/RRR5-20/2	1638.500	1638.823	-197.363	0.512	2053.399	0.564	21	0.396	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1623.365	1622.823	-283.404	0.483	2046.102	0.555	22	0.393	K.MIEDYLVAHPAEYA.-
R5/RRR5-23/2	1978.548	1979.086	-779.442	0.599	2231.116	0.676	26	0.359	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-21/2	1638.333	1638.823	-299.468	0.453	1950.220	0.514	20	0.354	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1682.200	1682.764	-932.693	0.536	2486.250	0.477	23	0.342	K.VEYELEDGSSLSPEK.E
R5/RRR5-21/2	1638.459	1638.823	-222.327	0.429	1881.375	0.560	20	0.342	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1624.254	1622.823	265.745	0.575	1895.987	0.604	21	0.342	K.MIEDYLVAHPAEYA.-
R5/RRR5-22/2	1638.221	1638.823	-980.347	0.478	1889.621	0.558	20	0.340	K.M*IEDYLVAHPAEYA.-
R5/RRR5-22/2	1638.262	1638.823	-955.136	0.467	1883.568	0.552	20	0.338	K.M*IEDYLVAHPAEYA.-
R5/RRR5-22/1	1177.557	1178.320	-1501.503	0.291	618.122	0.531	15	0.338	K.LNPAAGVGSTYK.T
R5/RRR5-23/2	1638.190	1638.823	-999.573	0.467	1856.877	0.571	20	0.333	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1979.274	1979.086	95.349	0.616	2052.176	0.689	25	0.329	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-20/2	1639.335	1638.823	-298.165	0.521	1836.409	0.598	19	0.327	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/3	1978.260	1979.086	-925.656	0.488	2088.564	0.605	36	0.326	K.SHSTETKLEATGDGSCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1638.171	1638.823	-1011.469	0.470	1829.596	0.574	19	0.325	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1638.252	1638.823	-961.420	0.476	1827.748	0.568	20	0.322	K.M*IEDYLVAHPAEYA.-
R5/RRR5-19/2	1638.484	1638.823	-207.304	0.436	1827.490	0.529	20	0.317	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/1	1177.629	1178.320	-1440.174	0.328	581.798	0.515	15	0.300	K.LNPAAGVGSTYK.T
R5/RRR5-23/2	1683.130	1682.764	218.040	0.568	2156.799	0.501	22	0.290	K.VEYELEDGSSLSPEK.E
R5/RRR5-23/2	1638.434	1638.823	-237.650	0.457	1713.762	0.570	19	0.289	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1682.131	1682.764	-973.783	0.471	2162.619	0.460	22	0.280	K.VEYELEDGSSLSPEK.E
R5/RRR5-23/2	1638.279	1638.823	-944.738	0.403	1651.748	0.485	19	0.260	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1622.469	1622.823	-218.738	0.453	1622.816	0.528	19	0.256	K.MIEDYLVAHPAEYA.-
R5/RRR5-23/3	1978.665	1979.086	-213.339	0.483	1736.413	0.605	34	0.248	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-24/2	1638.164	1638.823	-1015.359	0.416	1589.713	0.506	19	0.246	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/1	1177.589	1178.320	-1474.534	0.307	498.627	0.506	14	0.246	K.LNPAAGVGSTYK.T
R5/RRR5-23/1	1177.626	1178.320	-1442.361	0.332	461.672	0.562	14	0.246	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1622.202	1622.823	-1002.285	0.360	1555.569	0.521	19	0.243	K.MIEDYLVAHPAEYA.-
R5/RRR5-22/3	1979.408	1979.086	163.160	0.499	1689.156	0.594	36	0.233	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1622.244	1622.823	-976.447	0.445	1503.168	0.559	19	0.232	K.MIEDYLVAHPAEYA.-
R5/RRR5-20/3	1978.298	1979.086	-906.421	0.452	1628.747	0.598	35	0.225	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-24/3	1978.642	1979.086	-225.037	0.506	1803.306	0.517	35	0.224	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/3	1978.792	1979.086	-149.007	0.504	1618.208	0.597	36	0.221	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-22/3	1978.486	1979.086	-811.281	0.486	1697.412	0.559	36	0.221	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-22/1	1177.643	1178.320	-1427.784	0.278	477.337	0.454	14	0.215	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1270.092	1270.454	-285.788	0.417	1738.631	0.428	19	0.212	R.VAVCDAASHVLK.S
R5/RRR5-1/2	1638.291	1638.823	-937.781	0.336	1446.441	0.467	18	0.211	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1208.045	1208.295	-207.426	0.456	1635.141	0.445	20	0.204	K.LEATGDGSCVAK.L
R5/RRR5-22/2	1269.976	1270.454	-377.691	0.466	1682.935	0.409	19	0.201	R.VAVCDAASHVLK.S
R5/RRR5-23/2	1207.957	1208.295	-280.520	0.445	1586.498	0.450	20	0.200	K.LEATGDGSCVAK.L
R5/RRR5-22/2	1207.916	1208.295	-314.486	0.403	1513.597	0.483	20	0.198	K.LEATGDGSCVAK.L
R5/RRR5-23/2	1623.274	1622.823	278.426	0.507	1371.848	0.530	18	0.194	K.MIEDYLVAHPAEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/3	1924.786	1924.095	-160.980	0.496	1833.522	0.406	33	0.192	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-23/3	1978.412	1979.086	-848.536	0.491	1485.765	0.573	35	0.191	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-20/2	1270.225	1270.454	-180.886	0.389	1546.095	0.434	18	0.191	R.VAVCDAASHVLK.S
R5/RRR5-21/3	1979.604	1979.086	-244.348	0.518	1453.745	0.584	33	0.190	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-22/3	1978.914	1979.086	-87.189	0.492	1522.752	0.548	35	0.188	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1270.057	1270.454	-313.656	0.464	1503.392	0.434	19	0.188	R.VAVCDAASHVLK.S
R5/RRR5-23/3	1978.509	1979.086	-799.483	0.504	1374.070	0.608	32	0.187	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-22/3	1977.781	1979.086	-1168.892	0.485	1506.800	0.547	34	0.186	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-22/2	1270.354	1270.454	-78.801	0.452	1544.382	0.400	19	0.185	R.VAVCDAASHVLK.S
R5/RRR5-22/2	1289.945	1290.467	-1183.828	0.466	1364.826	0.485	17	0.185	K.DIVDGYYGM*LK.M
R5/RRR5-22/3	1924.030	1924.095	-33.677	0.504	1770.724	0.411	33	0.184	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-23/3	1924.111	1924.095	8.513	0.482	1718.224	0.434	33	0.184	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-23/2	1270.028	1270.454	-336.704	0.448	1473.831	0.425	19	0.183	R.VAVCDAASHVLK.S
R5/RRR5-23/2	1207.971	1208.295	-268.456	0.445	1388.224	0.465	19	0.183	K.LEATGDGSCVAK.L
R5/RRR5-22/2	1207.816	1208.295	-397.129	0.456	1397.073	0.441	19	0.179	K.LEATGDGSCVAK.L
R5/RRR5-22/2	1622.122	1622.823	-1052.227	0.282	1317.400	0.380	18	0.177	K.MIEDYLVAHPAEYA.-
R5/RRR5-24/3	1979.281	1979.086	98.683	0.486	1330.310	0.593	34	0.176	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/3	1977.920	1979.086	-1098.242	0.453	1375.156	0.571	33	0.176	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-18/3	1979.106	1979.086	10.163	0.499	1451.309	0.540	34	0.175	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-22/2	1208.764	1208.295	389.806	0.440	1219.045	0.497	19	0.174	K.LEATGDGSCVAK.L
R5/RRR5-24/3	1978.449	1979.086	-830.048	0.434	1449.423	0.530	34	0.172	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1177.987	1178.320	-283.500	0.398	1040.672	0.566	20	0.170	K.LNPAAGVGSTYK.T
R5/RRR5-22/1	1177.519	1178.320	-1533.577	0.237	378.728	0.443	12	0.168	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1291.552	1290.467	65.756	0.411	1206.484	0.471	17	0.168	K.DIVDGYYGM*LK.M
R5/RRR5-23/3	1978.467	1979.086	-820.572	0.470	1344.199	0.557	33	0.167	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-20/2	1084.083	1083.240	-145.420	0.419	1125.402	0.493	15	0.165	K.AFM*DASSLPK.A
R5/RRR5-23/3	1978.356	1979.086	-876.874	0.463	1260.637	0.584	31	0.165	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1269.976	1270.454	-377.402	0.469	1322.458	0.400	18	0.165	R.VAVCDAASHVLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1531.236	1531.755	-994.742	0.467	1176.964	0.455	21	0.165	K.EKDIVDGYYGMLK.M
R5/RRR5-23/2	1547.216	1547.755	-997.253	0.469	1174.120	0.444	22	0.163	K.EKDIVDGYYGM*LK.M
R5/RRR5-21/2	1177.865	1178.320	-387.685	0.453	829.880	0.589	19	0.163	K.LNPAAGVGSTYK.T
R5/RRR5-19/3	1978.905	1979.086	-91.644	0.439	1274.518	0.567	31	0.162	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-24/2	1177.991	1178.320	-279.861	0.376	903.709	0.580	19	0.162	K.LNPAAGVGSTYK.T
R5/RRR5-20/2	1083.346	1083.240	98.033	0.464	1071.520	0.480	15	0.161	K.AFM*DASSLPK.A
R5/RRR5-20/2	1082.896	1083.240	-318.680	0.391	1175.381	0.439	16	0.160	K.AFM*DASSLPK.A
R5/RRR5-23/2	1273.794	1274.468	-1317.569	0.380	1150.757	0.453	17	0.160	K.DIVDGYYGMLK.M
R5/RRR5-22/2	1178.043	1178.320	-235.678	0.395	894.701	0.557	20	0.160	K.LNPAAGVGSTYK.T
R5/RRR5-22/3	1923.414	1924.095	-876.842	0.465	1578.054	0.424	31	0.160	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-23/3	1924.232	1924.095	71.218	0.468	1574.769	0.424	32	0.159	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-20/2	1178.072	1178.320	-211.144	0.439	813.867	0.572	19	0.159	K.LNPAAGVGSTYK.T
R5/RRR5-21/2	1178.945	1178.320	-318.683	0.405	859.129	0.562	20	0.159	K.LNPAAGVGSTYK.T
R5/RRR5-23/2	1177.535	1178.320	-1520.103	0.364	968.181	0.531	20	0.159	K.LNPAAGVGSTYK.T
R5/RRR5-17/2	1177.808	1178.320	-1287.312	0.342	915.339	0.559	20	0.158	K.LNPAAGVGSTYK.T
R5/RRR5-21/2	1084.168	1083.240	-67.147	0.445	1001.082	0.489	15	0.158	K.AFM*DASSLPK.A
R5/RRR5-23/2	1547.267	1547.755	-316.221	0.469	1138.313	0.424	21	0.157	K.EKDIVDGYYGM*LK.M
R5/RRR5-23/2	1177.994	1178.320	-277.782	0.426	862.574	0.535	20	0.157	K.LNPAAGVGSTYK.T
R5/RRR5-23/3	1978.520	1979.086	-793.538	0.489	1285.929	0.547	32	0.157	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-20/2	1177.953	1178.320	-312.403	0.381	913.938	0.519	20	0.155	K.LNPAAGVGSTYK.T
R5/RRR5-18/2	1082.957	1083.240	-261.908	0.351	1044.642	0.466	15	0.154	K.AFM*DASSLPK.A
R5/RRR5-24/2	1084.170	1083.240	-64.550	0.454	1046.264	0.444	15	0.154	K.AFM*DASSLPK.A
R5/RRR5-23/3	1923.615	1924.095	-250.219	0.435	1659.819	0.367	32	0.153	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-19/2	1083.052	1083.240	-173.934	0.381	1069.097	0.434	15	0.152	K.AFM*DASSLPK.A
R5/RRR5-19/2	1177.908	1178.320	-350.771	0.453	714.799	0.547	18	0.152	K.LNPAAGVGSTYK.T
R5/RRR5-1/2	1638.369	1638.823	-277.491	0.374	1144.359	0.405	17	0.150	K.M*IEDYLVAHPAEYA.-
R5/RRR5-23/2	1531.121	1531.755	-1070.264	0.475	1071.502	0.408	20	0.150	K.EKDIVDGYYGMLK.M
R5/RRR5-18/2	1177.977	1178.320	-291.921	0.370	854.766	0.505	19	0.150	K.LNPAAGVGSTYK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	977.980	978.036	-56.977	0.465	1101.802	0.375	15	0.148	K.SDVLEAESK.V
R5/RRR5-22/2	1083.204	1083.240	-33.750	0.431	1108.671	0.381	15	0.148	K.AFM*DASSLPK.A
R5/RRR5-19/2	1177.965	1178.320	-302.110	0.385	684.869	0.547	18	0.148	K.LNPAAGVGSTYK.T
R5/RRR5-18/2	1178.147	1178.320	-147.322	0.337	895.715	0.472	20	0.147	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1083.196	1083.240	-41.210	0.435	1094.405	0.377	15	0.147	K.AFM*DASSLPK.A
R5/RRR5-18/2	1177.856	1178.320	-395.276	0.423	592.625	0.555	17	0.147	K.LNPAAGVGSTYK.T
R5/RRR5-20/2	1177.465	1178.320	-1579.775	0.315	792.327	0.531	19	0.147	K.LNPAAGVGSTYK.T
R5/RRR5-19/2	1178.167	1178.320	-129.757	0.433	719.071	0.500	18	0.146	K.LNPAAGVGSTYK.T
R5/RRR5-23/2	1547.285	1547.755	-304.189	0.472	1060.023	0.383	20	0.146	K.EKDIVDGYYGM*LK.M
R5/RRR5-21/2	1177.478	1178.320	-1569.152	0.356	688.865	0.536	18	0.145	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1178.011	1178.320	-262.811	0.411	669.498	0.515	18	0.145	K.LNPAAGVGSTYK.T
R5/RRR5-24/2	1177.995	1178.320	-276.534	0.353	653.564	0.543	18	0.145	K.LNPAAGVGSTYK.T
R5/RRR5-23/2	1178.420	1178.320	85.134	0.398	583.117	0.527	18	0.143	K.LNPAAGVGSTYK.T
R5/RRR5-18/3	1978.969	1979.086	-59.439	0.394	1038.458	0.597	32	0.143	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-22/2	1289.852	1290.467	-1256.149	0.441	866.635	0.435	16	0.143	K.DIVDGYYGM*LK.M
R5/RRR5-23/2	1290.036	1290.467	-334.969	0.386	1090.892	0.356	16	0.143	K.DIVDGYYGM*LK.M
R5/RRR5-23/2	977.964	978.036	-73.378	0.464	1052.350	0.360	14	0.143	K.SDVLEAESK.V
R5/RRR5-25/2	1178.090	1178.320	-195.968	0.366	529.741	0.541	16	0.140	K.LNPAAGVGSTYK.T
R5/RRR5-1/2	1638.297	1638.823	-934.116	0.334	1009.879	0.416	18	0.140	K.M*IEDYLVAHPAEYA.-
R5/RRR5-12/2	1178.628	1178.320	262.027	0.400	567.161	0.501	16	0.139	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1177.553	1178.320	-1505.316	0.283	681.937	0.525	18	0.139	K.LNPAAGVGSTYK.T
R5/RRR5-27/2	1084.163	1083.240	-71.213	0.383	699.838	0.470	13	0.139	K.AFM*DASSLPK.A
R5/RRR5-22/2	1084.267	1083.240	25.002	0.384	853.862	0.408	14	0.139	K.AFM*DASSLPK.A
R5/RRR5-17/2	1177.882	1178.320	-372.503	0.305	779.960	0.451	19	0.138	K.LNPAAGVGSTYK.T
R5/RRR5-23/2	1179.026	1178.320	-250.227	0.430	564.094	0.456	18	0.138	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1547.349	1547.755	-263.189	0.471	823.962	0.398	19	0.137	K.EKDIVDGYYGM*LK.M
R5/RRR5-24/2	1177.921	1178.320	-339.333	0.334	579.655	0.500	16	0.137	K.LNPAAGVGSTYK.T
R5/RRR5-22/2	1066.929	1067.241	-293.272	0.337	616.508	0.477	13	0.136	K.AFMDASSLPK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1084.304	1083.240	59.328	0.359	619.324	0.438	14	0.135	K.AFM*DASSLPK.A
R5/RRR5-23/2	1066.753	1067.241	-459.055	0.337	578.942	0.470	13	0.135	K.AFMDASSLPK.A
R5/RRR5-19/2	1082.885	1083.240	-328.633	0.351	825.661	0.370	14	0.133	K.AFM*DASSLPK.A
R5/RRR5-21/2	1269.408	1270.454	-1616.299	0.285	972.312	0.328	17	0.132	R.VAVCDAASHVLK.S
R5/RRR5-22/3	1978.442	1979.086	-833.114	0.428	1051.403	0.541	31	0.131	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1066.916	1067.241	-305.325	0.335	575.637	0.420	13	0.131	K.AFMDASSLPK.A
R5/RRR5-18/3	1978.841	1979.086	-124.223	0.463	993.924	0.558	29	0.131	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-20/3	1978.844	1979.086	-122.553	0.443	864.167	0.592	30	0.129	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1082.830	1083.240	-379.645	0.383	550.066	0.343	13	0.127	K.AFM*DASSLPK.A
R5/RRR5-21/2	1547.884	1547.755	84.148	0.423	668.382	0.333	18	0.127	K.EKDIVDGYYGM*LK.M
R5/RRR5-21/3	1979.344	1979.086	130.598	0.500	969.724	0.550	30	0.127	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1274.217	1274.468	-197.711	0.348	598.541	0.391	13	0.126	-.DIVDGYYGMLK.-
R5/RRR5-1/2	1177.844	1178.320	-405.467	0.302	491.901	0.337	15	0.125	K.LNPAAGVGSTYK.T
R5/RRR5-21/3	1978.134	1979.086	-989.404	0.447	1072.047	0.506	30	0.125	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/2	1082.256	1083.240	-1838.895	0.254	453.772	0.378	12	0.124	K.AFM*DASSLPK.A
R5/RRR5-1/2	1178.034	1178.320	-243.682	0.307	510.257	0.287	16	0.124	K.LNPAAGVGSTYK.T
R5/RRR5-19/2	1083.087	1083.240	-141.710	0.334	456.650	0.326	11	0.124	K.AFM*DASSLPK.A
R5/RRR5-21/2	1547.304	1547.755	-292.079	0.393	802.694	0.265	19	0.124	K.EKDIVDGYYGM*LK.M
R5/RRR5-22/2	1067.091	1067.241	-141.199	0.272	557.346	0.319	13	0.124	K.AFMDASSLPK.A
R5/RRR5-23/2	977.417	978.036	-1661.284	0.252	1057.770	0.208	14	0.123	K.SDVLEAESK.V
R5/RRR5-2/2	1178.054	1178.320	-226.529	0.248	626.878	0.262	17	0.122	K.LNPAAGVGSTYK.T
R5/RRR5-21/3	1925.077	1924.095	-9.363	0.443	1333.091	0.393	28	0.122	K.LKVEYELEDGSSLSPEK.E
R5/RRR5-22/2	1066.958	1067.241	-265.493	0.270	430.759	0.397	12	0.121	-.AFMDASSLPK.-
R5/RRR5-14/2	1177.331	1178.320	-1694.037	0.264	398.744	0.349	14	0.119	-.LNPAAGVGSTYK.-
R5/RRR5-21/2	1637.532	1638.823	-1402.905	0.161	835.721	0.206	16	0.119	K.M*IEDYLVAHPAEYA.-
R5/RRR5-2/2	1623.921	1622.823	60.346	0.241	602.345	0.199	14	0.117	K.MIEDYLVAHPAEYA.-
R5/RRR5-23/2	1289.521	1290.467	-1513.969	0.243	659.548	0.160	14	0.115	K.DIVDGYYGM*LK.M
R5/RRR5-27/3	1979.177	1979.086	46.259	0.363	1040.154	0.469	28	0.114	K.SHSTETKLEATGDGSCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/3	1978.583	1979.086	-762.046	0.465	820.432	0.525	29	0.113	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-12/3	1979.899	1979.086	-94.598	0.379	481.788	0.558	29	0.107	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-12/3	1980.709	1979.086	-190.649	0.329	239.173	0.372	23	0.098	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-25/3	1978.580	1979.086	-763.347	0.364	667.357	0.447	26	0.094	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-11/3	1979.695	1979.086	-197.952	0.182	287.506	0.431	29	0.092	K.SHSTETKLEATGDGSCVAK.L
R5/RRR5-23/3	1178.139	1178.320	-154.090	0.352	958.945	0.391	23	0.087	K.LNPAAGVGSTYK.T
R5/RRR5-21/3	1924.078	1924.095	-8.764	0.323	587.795	0.338	22	0.072	-.LKVEYELEDGSSLSPEK.-
R5/RRR5-20/3	1914.291	1915.135	-965.766	0.578	3151.646	0.441	38	0.552	K.VKDELVLDGNDIELVSR.S
R5/RRR5-22/2	1914.658	1915.135	-249.688	0.585	2639.247	0.567	26	0.403	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1845.625	1844.996	-201.777	0.528	2067.187	0.556	25	0.392	K.FLDGIYVSDKGTITEDA.-
R5/RRR5-20/2	1914.649	1915.135	-254.357	0.631	2584.170	0.557	26	0.386	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1844.473	1844.996	-828.599	0.494	2029.207	0.553	25	0.381	K.FLDGIYVSDKGTITEDA.-
R5/RRR5-20/2	1914.639	1915.135	-259.730	0.641	2512.309	0.577	26	0.378	K.VKDELVLDGNDIELVSR.S
R5/RRR5-20/2	1914.483	1915.135	-865.192	0.638	2529.757	0.558	26	0.375	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1914.691	1915.135	-232.354	0.636	2474.698	0.586	26	0.374	K.VKDELVLDGNDIELVSR.S
R5/RRR5-20/3	1916.461	1915.135	170.723	0.598	2444.746	0.517	34	0.372	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/3	1914.703	1915.135	-225.997	0.583	2411.437	0.517	33	0.364	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/3	1914.060	1915.135	-1086.876	0.590	2570.639	0.438	35	0.364	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1915.808	1915.135	-170.803	0.640	2494.714	0.544	26	0.363	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1844.485	1844.996	-821.955	0.486	1995.126	0.511	25	0.359	K.FLDGIYVSDKGTITEDA.-
R5/RRR5-19/2	1915.362	1915.135	118.986	0.635	2425.037	0.567	26	0.357	K.VKDELVLDGNDIELVSR.S
R5/RRR5-20/3	1916.640	1915.135	-258.891	0.611	2442.932	0.474	35	0.347	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1582.397	1582.827	-272.017	0.514	2332.026	0.574	22	0.342	R.TAISHVQNLITGVTK.G
R5/RRR5-20/2	1844.342	1844.996	-899.756	0.486	1920.412	0.517	24	0.334	K.FLDGIYVSDKGTITEDA.-
R5/RRR5-19/2	1582.467	1582.827	-227.826	0.518	2116.122	0.617	22	0.316	R.TAISHVQNLITGVTK.G
R5/RRR5-20/2	1844.302	1844.996	-921.616	0.472	1814.287	0.562	24	0.309	K.FLDGIYVSDKGTITEDA.-
R5/RRR5-20/2	1582.435	1582.827	-248.412	0.513	2039.639	0.615	21	0.302	R.TAISHVQNLITGVTK.G
R5/RRR5-19/2	1582.267	1582.827	-988.427	0.531	2045.137	0.583	22	0.294	R.TAISHVQNLITGVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1582.348	1582.827	-303.208	0.517	2020.344	0.594	22	0.293	R.TAISHVQNLITGVTK.G
R5/RRR5-27/3	1915.364	1915.135	120.226	0.530	2307.008	0.425	33	0.293	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1375.355	1374.675	-233.202	0.551	2127.393	0.486	20	0.280	R.KVDMLEGVTILR.S
R5/RRR5-19/2	1374.209	1374.675	-340.134	0.552	2061.722	0.500	20	0.274	R.KVDMLEGVTILR.S
R5/RRR5-19/3	1914.662	1915.135	-247.392	0.573	2142.577	0.465	32	0.271	K.VKDELVLDGNDIELVSR.S
R5/RRR5-27/3	1915.131	1915.135	-1.836	0.563	1980.827	0.534	34	0.267	K.VKDELVLDGNDIELVSR.S
R5/RRR5-24/2	1582.502	1582.827	-205.694	0.528	1837.694	0.594	21	0.264	R.TAISHVQNLITGVTK.G
R5/RRR5-18/2	1582.366	1582.827	-291.676	0.529	1825.742	0.593	21	0.262	R.TAISHVQNLITGVTK.G
R5/RRR5-20/2	1375.332	1374.675	-250.388	0.568	1903.696	0.516	20	0.255	R.KVDMLEGVTILR.S
R5/RRR5-19/2	1513.408	1512.695	-190.005	0.579	1684.903	0.579	22	0.243	K.HLNLDFQLLEGGR.K
R5/RRR5-20/2	1512.322	1512.695	-247.380	0.541	1663.681	0.588	22	0.242	K.HLNLDFQLLEGGR.K
R5/RRR5-18/2	1582.499	1582.827	-207.706	0.484	1633.814	0.611	20	0.239	R.TAISHVQNLITGVTK.G
R5/RRR5-22/2	1581.947	1582.827	-1191.483	0.494	1741.782	0.535	21	0.236	R.TAISHVQNLITGVTK.G
R5/RRR5-19/2	1513.247	1512.695	-296.988	0.580	1596.113	0.579	22	0.232	K.HLNLDFQLLEGGR.K
R5/RRR5-20/2	1844.431	1844.996	-851.453	0.471	1575.257	0.519	22	0.231	K.FLDGIYVSDKGTITEDA.-
R5/RRR5-20/2	1511.814	1512.695	-1248.214	0.526	1691.125	0.524	22	0.229	K.HLNLDFQLLEGGR.K
R5/RRR5-20/2	1512.326	1512.695	-244.546	0.524	1659.016	0.531	22	0.227	K.HLNLDFQLLEGGR.K
R5/RRR5-24/2	1581.992	1582.827	-1163.045	0.479	1571.263	0.584	21	0.226	R.TAISHVQNLITGVTK.G
R5/RRR5-22/2	1582.609	1582.827	-138.141	0.499	1634.444	0.542	20	0.223	R.TAISHVQNLITGVTK.G
R5/RRR5-19/2	1583.177	1582.827	222.139	0.546	1441.801	0.636	20	0.223	R.TAISHVQNLITGVTK.G
R5/RRR5-22/2	1582.232	1582.827	-1010.581	0.492	1714.241	0.497	20	0.222	R.TAISHVQNLITGVTK.G
R5/RRR5-20/2	1373.624	1374.675	-1497.683	0.474	1676.746	0.484	19	0.217	R.KVDMLEGVTILR.S
R5/RRR5-20/3	1914.378	1915.135	-920.537	0.573	1931.989	0.438	32	0.216	K.VKDELVLDGNDIELVSR.S
R5/RRR5-20/2	1373.587	1374.675	-1524.731	0.517	1752.187	0.422	19	0.211	R.KVDMLEGVTILR.S
R5/RRR5-18/2	1582.219	1582.827	-1019.179	0.487	1510.627	0.542	20	0.209	R.TAISHVQNLITGVTK.G
R5/RRR5-19/2	1511.694	1512.695	-1327.361	0.487	1483.620	0.533	21	0.207	K.HLNLDFQLLEGGR.K
R5/RRR5-19/2	1261.508	1262.502	-1584.890	0.365	1756.322	0.347	18	0.196	K.VDM*LEGVTILR.S
R5/RRR5-19/2	1262.120	1262.502	-303.317	0.439	1744.948	0.351	18	0.196	K.VDM*LEGVTILR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1511.865	1512.695	-1213.996	0.513	1310.257	0.551	20	0.193	K.HLNLDFQLLEGGR.K
R5/RRR5-19/2	1320.456	1321.509	-1559.563	0.457	1469.243	0.446	17	0.187	R.KLQVDAWFGTR.R
R5/RRR5-20/2	1582.281	1582.827	-979.443	0.510	1034.558	0.583	22	0.175	R.TAISHVQNLITGVTK.G
R5/RRR5-19/2	1320.727	1321.509	-1353.626	0.445	1372.109	0.426	17	0.174	R.KLQVDAWFGTR.R
R5/RRR5-22/3	1914.047	1915.135	-1093.984	0.457	1768.521	0.380	32	0.170	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/2	1262.029	1262.502	-375.713	0.399	1332.951	0.395	16	0.164	K.VDM*LEGVTILR.S
R5/RRR5-19/2	1391.375	1390.675	-216.051	0.534	1048.332	0.495	19	0.163	R.KVDM*LEGVTILR.S
R5/RRR5-19/2	1390.188	1390.675	-350.898	0.486	1014.165	0.494	19	0.160	R.KVDM*LEGVTILR.S
R5/RRR5-19/3	1640.715	1640.868	-93.259	0.462	1389.932	0.501	28	0.157	K.HLNLDFQLLEGGRK.L
R5/RRR5-20/2	1390.367	1390.675	-221.932	0.516	1043.453	0.453	19	0.156	R.KVDM*LEGVTILR.S
R5/RRR5-21/3	1914.585	1915.135	-811.948	0.464	1526.879	0.438	30	0.155	K.VKDELVLDGNDIELVSR.S
R5/RRR5-20/2	1321.235	1321.509	-207.726	0.443	1127.819	0.414	16	0.153	R.KLQVDAWFGTR.R
R5/RRR5-20/2	1390.076	1390.675	-1153.061	0.479	1039.348	0.434	19	0.153	R.KVDM*LEGVTILR.S
R5/RRR5-19/2	1156.907	1157.297	-338.724	0.506	1085.902	0.411	16	0.152	K.FLDGIYVSDK.G
R5/RRR5-20/2	1320.441	1321.509	-1570.708	0.403	1139.227	0.409	15	0.152	R.KLQVDAWFGTR.R
R5/RRR5-19/3	1389.966	1390.675	-1233.101	0.400	1917.930	0.245	26	0.151	R.KVDM*LEGVTILR.S
R5/RRR5-20/2	1389.665	1390.675	-1450.228	0.484	989.953	0.433	19	0.150	R.KVDM*LEGVTILR.S
R5/RRR5-19/2	1193.118	1193.336	-183.545	0.451	943.159	0.442	17	0.150	K.LQVDAWFGTR.R
R5/RRR5-19/2	1156.542	1157.297	-1522.500	0.439	1125.873	0.377	16	0.149	K.FLDGIYVSDK.G
R5/RRR5-20/2	1156.887	1157.297	-355.345	0.490	1095.885	0.384	16	0.149	K.FLDGIYVSDK.G
R5/RRR5-19/2	1156.578	1157.297	-1490.905	0.414	1119.850	0.369	16	0.148	K.FLDGIYVSDK.G
R5/RRR5-20/2	1157.220	1157.297	-66.720	0.558	1028.773	0.403	16	0.148	K.FLDGIYVSDK.G
R5/RRR5-24/2	1513.449	1512.695	-163.061	0.410	671.963	0.560	17	0.147	K.HLNLDFQLLEGGR.K
R5/RRR5-19/2	1193.202	1193.336	-112.936	0.449	867.825	0.450	16	0.147	K.LQVDAWFGTR.R
R5/RRR5-19/2	1320.429	1321.509	-1579.809	0.415	1074.445	0.365	15	0.143	R.KLQVDAWFGTR.R
R5/RRR5-19/2	1389.710	1390.675	-1417.848	0.392	935.209	0.403	18	0.142	R.KVDM*LEGVTILR.S
R5/RRR5-20/2	1157.090	1157.297	-179.525	0.509	1032.605	0.357	16	0.142	K.FLDGIYVSDK.G
R5/RRR5-19/3	1640.400	1640.868	-285.731	0.506	1306.975	0.471	28	0.139	K.HLNLDFQLLEGGRK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	857.220	856.990	269.575	0.425	661.455	0.414	13	0.138	K.VVTVEGPR.G
R5/RRR5-20/2	856.344	856.990	-1927.402	0.362	426.690	0.457	12	0.135	K.VVTVEGPR.G
R5/RRR5-19/3	1640.504	1640.868	-222.238	0.461	1081.844	0.548	26	0.135	K.HLNLDFQLLEGGRK.L
R5/RRR5-19/2	856.706	856.990	-331.794	0.314	372.760	0.483	11	0.133	K.VVTVEGPR.G
R5/RRR5-19/2	856.740	856.990	-292.624	0.336	290.274	0.460	10	0.133	K.VVTVEGPR.G
R5/RRR5-19/2	856.666	856.990	-379.546	0.303	483.690	0.453	12	0.132	K.VVTVEGPR.G
R5/RRR5-19/2	856.358	856.990	-1911.214	0.316	449.426	0.438	12	0.132	K.VVTVEGPR.G
R5/RRR5-20/2	856.835	856.990	-181.277	0.324	315.178	0.461	10	0.132	K.VVTVEGPR.G
R5/RRR5-19/2	857.579	856.990	-479.937	0.419	574.077	0.359	12	0.131	K.VVTVEGPR.G
R5/RRR5-20/2	1192.957	1193.336	-319.045	0.353	583.748	0.431	13	0.131	K.LQVDAWFGTR.R
R5/RRR5-18/2	857.109	856.990	139.904	0.303	411.634	0.441	11	0.131	K.VVTVEGPR.G
R5/RRR5-22/2	857.031	856.990	48.343	0.351	531.719	0.362	12	0.130	K.VVTVEGPR.G
R5/RRR5-19/2	856.257	856.990	-2029.979	0.304	387.966	0.415	11	0.130	K.VVTVEGPR.G
R5/RRR5-24/2	856.662	856.990	-384.121	0.320	433.776	0.362	12	0.129	K.VVTVEGPR.G
R5/RRR5-20/2	856.344	856.990	-1927.688	0.272	354.833	0.451	11	0.129	K.VVTVEGPR.G
R5/RRR5-20/2	1192.960	1193.336	-315.863	0.368	666.287	0.364	14	0.129	K.LQVDAWFGTR.R
R5/RRR5-20/2	1320.405	1321.509	-1598.569	0.401	715.879	0.359	14	0.128	R.KLQVDAWFGTR.R
R5/RRR5-20/2	856.888	856.990	-118.682	0.282	352.187	0.420	10	0.128	K.VVTVEGPR.G
R5/RRR5-26/2	856.670	856.990	-374.399	0.262	444.718	0.412	11	0.127	K.VVTVEGPR.G
R5/RRR5-20/2	1193.318	1193.336	-15.555	0.405	475.855	0.368	12	0.126	K.LQVDAWFGTR.R
R5/RRR5-22/2	856.948	856.990	-48.379	0.312	639.625	0.274	13	0.125	K.VVTVEGPR.G
R5/RRR5-20/3	1640.739	1640.868	-78.482	0.490	1163.585	0.468	24	0.124	K.HLNLDFQLLEGGRK.L
R5/RRR5-20/2	856.637	856.990	-412.860	0.216	329.020	0.376	10	0.124	K.VVTVEGPR.G
R5/RRR5-21/2	856.633	856.990	-417.722	0.336	378.000	0.255	11	0.124	-.VVTVEGPR.-
R5/RRR5-19/2	1192.895	1193.336	-370.997	0.333	635.536	0.316	13	0.124	K.LQVDAWFGTR.R
R5/RRR5-20/2	856.909	856.990	-94.389	0.306	296.831	0.349	10	0.122	-.VVTVEGPR.-
R5/RRR5-19/2	1246.687	1246.502	148.629	0.459	833.687	0.274	14	0.121	K.VDMLEGVTILR.S
R5/RRR5-18/2	856.488	856.990	-1758.251	0.208	356.569	0.319	10	0.121	-.VVTVEGPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/3	1391.837	1390.675	116.968	0.454	1783.251	0.200	27	0.118	R.KVDM*LEGVTILR.S
R5/RRR5-18/3	1914.859	1915.135	-144.167	0.439	1164.839	0.434	27	0.115	K.VKDELVLDGNDIELVSR.S
R5/RRR5-25/2	856.439	856.990	-1816.108	0.165	319.698	0.376	10	0.115	-.VVTVEGPR.-
R5/RRR5-20/3	1641.078	1640.868	128.346	0.465	876.310	0.532	24	0.115	K.HLNLDFQLLEGGRK.L
R5/RRR5-20/3	1512.985	1512.695	191.974	0.501	1418.663	0.293	25	0.107	-.HLNLDFQLLEGGR.-
R5/RRR5-20/3	1512.709	1512.695	9.290	0.461	1474.665	0.250	26	0.103	-.HLNLDFQLLEGGR.-
R5/RRR5-19/3	1321.942	1321.509	328.220	0.451	1139.320	0.380	22	0.102	R.KLQVDAWFGTR.R
R5/RRR5-20/3	1914.389	1915.135	-914.776	0.434	1313.860	0.313	30	0.100	K.VKDELVLDGNDIELVSR.S
R5/RRR5-20/3	1640.814	1640.868	-32.812	0.410	841.544	0.461	24	0.100	K.HLNLDFQLLEGGRK.L
R5/RRR5-19/3	1512.558	1512.695	-90.880	0.470	1301.234	0.309	24	0.099	K.HLNLDFQLLEGGR.K
R5/RRR5-19/3	1582.458	1582.827	-233.562	0.453	1021.987	0.398	30	0.099	R.TAISHVQNLITGVTK.G
R5/RRR5-20/3	1513.661	1512.695	-22.545	0.456	1199.984	0.337	23	0.097	-.HLNLDFQLLEGGR.-
R5/RRR5-20/3	1584.031	1582.827	129.296	0.488	872.117	0.419	29	0.097	R.TAISHVQNLITGVTK.G
R5/RRR5-19/3	1390.627	1390.675	-34.498	0.431	1708.371	0.149	28	0.097	R.KVDM*LEGVTILR.S
R5/RRR5-19/3	1582.570	1582.827	-162.640	0.434	1008.160	0.376	30	0.094	R.TAISHVQNLITGVTK.G
R5/RRR5-19/3	1583.853	1582.827	16.603	0.416	558.041	0.437	23	0.093	R.TAISHVQNLITGVTK.G
R5/RRR5-18/3	1914.976	1915.135	-83.259	0.399	984.242	0.373	25	0.092	K.VKDELVLDGNDIELVSR.S
R5/RRR5-26/3	1584.231	1582.827	256.336	0.439	822.610	0.398	26	0.092	R.TAISHVQNLITGVTK.G
R5/RRR5-22/3	1582.925	1582.827	62.596	0.468	786.565	0.399	27	0.091	R.TAISHVQNLITGVTK.G
R5/RRR5-25/3	1582.600	1582.827	-143.837	0.445	694.011	0.409	25	0.091	R.TAISHVQNLITGVTK.G
R5/RRR5-19/3	1512.709	1512.695	9.169	0.431	1200.663	0.292	24	0.090	-.HLNLDFQLLEGGR.-
R5/RRR5-19/3	1583.536	1582.827	-184.151	0.424	985.058	0.352	29	0.089	R.TAISHVQNLITGVTK.G
R5/RRR5-20/3	1390.854	1390.675	129.507	0.499	1305.633	0.261	23	0.089	R.KVDM*LEGVTILR.S
R5/RRR5-20/3	1582.929	1582.827	65.149	0.448	775.833	0.382	27	0.089	R.TAISHVQNLITGVTK.G
R5/RRR5-19/3	1583.023	1582.827	124.429	0.465	740.065	0.375	26	0.088	R.TAISHVQNLITGVTK.G
R5/RRR5-22/3	1582.186	1582.827	-1040.025	0.425	574.480	0.376	23	0.087	R.TAISHVQNLITGVTK.G
R5/RRR5-20/3	1915.275	1915.135	73.437	0.377	648.893	0.395	24	0.087	K.VKDELVLDGNDIELVSR.S
R5/RRR5-24/3	1582.556	1582.827	-171.345	0.411	651.238	0.354	25	0.085	R.TAISHVQNLITGVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/3	1374.828	1374.675	111.211	0.490	1338.099	0.232	25	0.085	-.KVDMLEGVTILR.-
R5/RRR5-19/3	1321.534	1321.509	18.694	0.379	971.360	0.336	22	0.083	R.KLQVDAWFGTR.R
R5/RRR5-26/3	1582.720	1582.827	-67.473	0.345	511.102	0.373	22	0.083	-.TAISHVQNLITGVTK.-
R5/RRR5-20/3	1582.182	1582.827	-1042.465	0.420	865.578	0.326	29	0.083	R.TAISHVQNLITGVTK.G
R5/RRR5-25/3	1582.347	1582.827	-304.262	0.382	675.619	0.274	26	0.078	R.TAISHVQNLITGVTK.G
R5/RRR5-22/3	1914.181	1915.135	-1023.580	0.291	662.893	0.285	22	0.075	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/3	1512.247	1512.695	-297.356	0.388	983.205	0.278	21	0.074	-.HLNLDFQLLEGGR.-
R5/RRR5-19/3	1913.914	1915.135	-1163.725	0.380	668.118	0.256	24	0.074	K.VKDELVLDGNDIELVSR.S
R5/RRR5-19/3	1321.510	1321.509	1.045	0.343	718.689	0.266	19	0.071	R.KLQVDAWFGTR.R
R5/RRR5-23/3	1583.272	1582.827	282.049	0.316	732.226	0.229	21	0.065	-.TAISHVQNLITGVTK.-
R5/RRR5-19/3	1390.519	1390.675	-112.294	0.427	939.396	0.165	21	0.063	-.KVDM*LEGVTILR.-
R5/RRR5-20/3	1374.590	1374.675	-62.459	0.410	974.784	0.161	22	0.062	-.KVDMLEGVTILR.-
R5/RRR5-23/2	1930.586	1931.131	-802.230	0.636	3441.519	0.698	29	0.673	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-23/2	1913.241	1914.037	-941.927	0.604	3487.939	0.641	27	0.657	K.M*NVEYELEDGGSLSPEK.E
R5/RRR5-23/2	1913.414	1914.037	-850.850	0.598	3416.052	0.602	27	0.617	K.M*NVEYELEDGGSLSPEK.E
R5/RRR5-23/2	1914.489	1914.037	236.758	0.645	3315.834	0.658	27	0.613	K.M*NVEYELEDGGSLSPEK.E
R5/RRR5-23/3	1950.878	1951.170	-150.323	0.525	2912.463	0.517	38	0.543	R.DNAAHVIKSEVLDVPAGSK.V
R5/RRR5-23/2	1930.543	1931.131	-824.635	0.633	3006.382	0.685	28	0.541	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-23/2	1930.487	1931.131	-853.961	0.628	2940.319	0.670	28	0.518	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-23/3	1950.984	1951.170	-95.529	0.511	2721.128	0.513	36	0.475	R.DNAAHVIKSEVLDVPAGSK.V
R5/RRR5-24/3	1931.177	1931.131	23.856	0.528	2399.896	0.649	37	0.443	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-24/3	1930.619	1931.131	-785.513	0.496	2379.001	0.651	37	0.439	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-23/2	1653.212	1652.849	220.135	0.545	2130.620	0.625	22	0.435	K.MIEDYLVAHPTEYA.-
R5/RRR5-23/2	1897.545	1898.038	-260.779	0.548	2656.958	0.551	25	0.402	K.MNVEYELEDGGSLSPEK.E
R5/RRR5-23/3	1931.885	1931.131	-127.433	0.525	2161.937	0.660	36	0.380	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-23/2	1668.216	1668.849	-981.718	0.513	1977.468	0.614	21	0.377	K.M*IEDYLVAHPTEYA.-
R5/RRR5-23/2	1653.348	1652.849	302.760	0.506	1957.116	0.635	21	0.375	K.MIEDYLVAHPTEYA.-
R5/RRR5-23/2	1653.251	1652.849	243.458	0.522	1963.161	0.627	21	0.374	K.MIEDYLVAHPTEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1897.170	1898.038	-987.511	0.528	2465.027	0.551	24	0.362	K.MNVEYELEDGGSLSPEK.E
R5/RRR5-23/2	1653.308	1652.849	278.329	0.567	1959.845	0.585	21	0.358	K.MIEDYLVAHPTEYA.-
R5/RRR5-23/2	1897.120	1898.038	-1013.933	0.547	2459.245	0.536	25	0.355	K.MNVEYELEDGGSLSPEK.E
R5/RRR5-23/3	1931.806	1931.131	-168.318	0.561	2087.654	0.639	36	0.348	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-24/2	1668.129	1668.849	-1034.101	0.450	1888.032	0.600	21	0.348	K.M*IEDYLVAHPTEYA.-
R5/RRR5-23/2	1669.300	1668.849	271.083	0.586	1838.931	0.618	21	0.322	K.M*IEDYLVAHPTEYA.-
R5/RRR5-24/3	1932.110	1931.131	-10.692	0.545	1913.607	0.661	34	0.317	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-23/2	1667.998	1668.849	-1112.650	0.433	1800.520	0.556	20	0.311	K.M*IEDYLVAHPTEYA.-
R5/RRR5-23/2	1669.066	1668.849	130.571	0.501	1776.418	0.613	21	0.309	K.M*IEDYLVAHPTEYA.-
R5/RRR5-23/2	1652.473	1652.849	-228.325	0.483	1746.087	0.645	20	0.308	K.MIEDYLVAHPTEYA.-
R5/RRR5-23/3	1930.993	1931.131	-71.631	0.516	1876.722	0.650	35	0.303	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-22/2	1668.257	1668.849	-956.960	0.487	1743.052	0.615	19	0.301	K.M*IEDYLVAHPTEYA.-
R5/RRR5-24/2	1668.244	1668.849	-964.674	0.508	1744.461	0.612	21	0.299	K.M*IEDYLVAHPTEYA.-
R5/RRR5-22/2	1669.415	1668.849	-260.291	0.554	1691.318	0.647	20	0.286	K.M*IEDYLVAHPTEYA.-
R5/RRR5-23/3	1950.552	1951.170	-832.158	0.548	1992.846	0.519	34	0.274	R.DNAAHVIKSEVLDVPAGSK.V
R5/RRR5-24/2	1339.424	1339.455	-23.546	0.506	1932.098	0.552	22	0.269	K.VEGDGGAGTVTTM*K.L
R5/RRR5-23/2	1323.076	1323.456	-288.039	0.494	1740.341	0.605	23	0.255	K.VEGDGGAGTVTTMK.L
R5/RRR5-23/2	1338.980	1339.455	-355.482	0.481	1746.679	0.574	22	0.248	K.VEGDGGAGTVTTM*K.L
R5/RRR5-23/2	1338.546	1339.455	-1430.367	0.503	1774.879	0.544	21	0.244	K.VEGDGGAGTVTTM*K.L
R5/RRR5-23/2	1323.086	1323.456	-280.449	0.494	1637.163	0.584	22	0.236	K.VEGDGGAGTVTTMK.L
R5/RRR5-24/2	1668.396	1668.849	-272.045	0.527	1467.029	0.617	20	0.225	K.M*IEDYLVAHPTEYA.-
R5/RRR5-23/2	1338.614	1339.455	-1379.257	0.473	1617.019	0.513	21	0.216	K.VEGDGGAGTVTTM*K.L
R5/RRR5-23/2	1322.528	1323.456	-1461.857	0.390	1499.872	0.574	21	0.214	K.VEGDGGAGTVTTMK.L
R5/RRR5-22/2	1669.296	1668.849	268.957	0.557	1375.552	0.637	19	0.206	K.M*IEDYLVAHPTEYA.-
R5/RRR5-24/2	1338.918	1339.455	-1151.522	0.499	1340.693	0.573	20	0.199	K.VEGDGGAGTVTTM*K.L
R5/RRR5-22/3	1930.806	1931.131	-168.659	0.475	1326.322	0.616	30	0.186	K.SHVTETKIEAAGAGSCLAK.M
R5/RRR5-23/2	1147.969	1148.285	-276.301	0.453	1401.895	0.468	19	0.185	K.IEAAGAGSCLAK.M
R5/RRR5-23/2	1147.888	1148.285	-347.571	0.451	1414.122	0.448	19	0.182	K.IEAAGAGSCLAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1147.447	1148.285	-1607.339	0.401	1286.728	0.451	18	0.170	K.IEAAGAGSCLAK.M
R5/RRR5-24/2	1148.138	1148.285	-128.459	0.482	1134.374	0.511	18	0.170	K.IEAAGAGSCLAK.M
R5/RRR5-22/2	1147.981	1148.285	-265.633	0.447	1142.001	0.480	18	0.165	K.IEAAGAGSCLAK.M
R5/RRR5-24/2	1148.021	1148.285	-231.069	0.454	1230.099	0.422	18	0.162	K.IEAAGAGSCLAK.M
R5/RRR5-22/2	1286.054	1286.565	-1178.341	0.471	1104.682	0.461	18	0.161	K.LILDGYFGM*LK.M
R5/RRR5-24/2	1148.858	1148.285	-373.495	0.472	1051.166	0.485	17	0.159	K.IEAAGAGSCLAK.M
R5/RRR5-23/2	1286.138	1286.565	-332.915	0.499	1099.815	0.448	18	0.159	K.LILDGYFGM*LK.M
R5/RRR5-24/2	1287.130	1286.565	-339.127	0.494	1128.541	0.437	18	0.159	K.LILDGYFGM*LK.M
R5/RRR5-23/2	1286.970	1286.565	316.029	0.490	949.269	0.504	17	0.158	K.LILDGYFGM*LK.M
R5/RRR5-23/2	1285.978	1286.565	-1237.250	0.411	1067.196	0.458	18	0.157	K.LILDGYFGM*LK.M
R5/RRR5-23/2	1147.830	1148.285	-398.149	0.404	1184.951	0.412	18	0.157	K.IEAAGAGSCLAK.M
R5/RRR5-23/2	1543.228	1543.852	-1055.903	0.486	1245.411	0.380	20	0.156	K.EKLILDGYFGM*LK.M
R5/RRR5-23/2	1270.145	1270.565	-331.756	0.477	902.408	0.493	18	0.155	K.LILDGYFGMLK.M
R5/RRR5-23/2	1285.695	1286.565	-1458.837	0.377	1069.893	0.450	17	0.155	K.LILDGYFGM*LK.M
R5/RRR5-24/2	1286.127	1286.565	-341.009	0.416	1107.007	0.421	18	0.154	K.LILDGYFGM*LK.M
R5/RRR5-22/2	1285.961	1286.565	-1250.786	0.414	1110.789	0.418	18	0.154	K.LILDGYFGM*LK.M
R5/RRR5-22/2	1101.858	1102.220	-329.533	0.422	1268.339	0.352	17	0.153	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1270.031	1270.565	-1212.055	0.529	958.938	0.455	18	0.152	K.LILDGYFGMLK.M
R5/RRR5-25/2	1668.339	1668.849	-907.890	0.430	1069.276	0.545	19	0.152	K.M*IEDYLVAHPTEYA.-
R5/RRR5-23/2	1270.086	1270.565	-378.333	0.479	910.333	0.471	18	0.152	K.LILDGYFGMLK.M
R5/RRR5-24/2	1271.238	1270.565	-257.984	0.542	887.335	0.468	18	0.151	K.LILDGYFGMLK.M
R5/RRR5-23/2	1270.201	1270.565	-287.595	0.520	905.812	0.462	18	0.151	K.LILDGYFGMLK.M
R5/RRR5-23/2	1101.963	1102.220	-234.394	0.415	1319.214	0.299	17	0.149	K.SEVLDVPAGSK.V
R5/RRR5-24/2	1285.551	1286.565	-1571.193	0.352	1000.898	0.435	17	0.148	K.LILDGYFGM*LK.M
R5/RRR5-23/2	1093.969	1094.279	-284.904	0.418	1086.481	0.376	16	0.147	K.VCAGFIDAIK.V
R5/RRR5-23/2	1285.712	1286.565	-1445.581	0.341	1017.892	0.405	18	0.145	K.LILDGYFGM*LK.M
R5/RRR5-23/2	1543.678	1543.852	-113.256	0.516	1026.701	0.401	19	0.145	K.EKLILDGYFGM*LK.M
R5/RRR5-23/2	1668.401	1668.849	-269.402	0.401	419.161	0.623	20	0.145	K.M*IEDYLVAHPTEYA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1286.142	1286.565	-329.867	0.402	844.620	0.449	16	0.144	K.LILDGYFGM*LK.M
R5/RRR5-22/2	1147.876	1148.285	-358.028	0.395	1035.819	0.377	17	0.143	K.IEAAGAGSCLAK.M
R5/RRR5-27/2	1101.853	1102.220	-333.757	0.349	1244.081	0.284	16	0.142	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1285.766	1286.565	-1403.526	0.402	961.949	0.376	17	0.141	K.LILDGYFGM*LK.M
R5/RRR5-22/2	1102.053	1102.220	-151.828	0.416	1202.572	0.293	16	0.140	K.SEVLDVPAGSK.V
R5/RRR5-24/2	1101.969	1102.220	-228.837	0.434	1095.823	0.330	16	0.140	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1093.588	1094.279	-1551.478	0.335	1062.791	0.327	16	0.138	K.VCAGFIDAIK.V
R5/RRR5-24/2	1101.574	1102.220	-1499.218	0.330	1084.883	0.317	16	0.137	K.SEVLDVPAGSK.V
R5/RRR5-22/2	1102.093	1102.220	-115.273	0.449	1117.803	0.306	16	0.137	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1270.258	1270.565	-242.569	0.434	920.416	0.352	18	0.137	K.LILDGYFGMLK.M
R5/RRR5-23/2	1101.933	1102.220	-261.289	0.383	992.693	0.342	16	0.137	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1543.205	1543.852	-1070.279	0.487	879.151	0.371	19	0.135	K.EKLILDGYFGM*LK.M
R5/RRR5-27/2	1101.989	1102.220	-210.279	0.343	1058.129	0.305	15	0.135	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1101.898	1102.220	-293.187	0.356	1128.594	0.265	16	0.134	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1270.079	1270.565	-384.119	0.430	684.598	0.386	16	0.133	K.LILDGYFGMLK.M
R5/RRR5-24/2	1078.595	1079.252	-1540.233	0.319	612.750	0.443	14	0.133	K.VFSDAPAM*PK.V
R5/RRR5-24/2	1270.309	1270.565	-202.753	0.351	538.272	0.431	15	0.133	K.LILDGYFGMLK.M
R5/RRR5-24/2	1079.030	1079.252	-205.897	0.319	653.627	0.406	14	0.131	K.VFSDAPAM*PK.V
R5/RRR5-24/2	1101.979	1102.220	-219.502	0.401	1049.381	0.272	15	0.130	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1078.903	1079.252	-324.170	0.301	742.810	0.343	14	0.128	K.VFSDAPAM*PK.V
R5/RRR5-23/2	1270.280	1270.565	-225.215	0.417	664.436	0.318	16	0.128	K.LILDGYFGMLK.M
R5/RRR5-25/2	1286.572	1286.565	5.794	0.412	515.035	0.334	14	0.126	K.LILDGYFGM*LK.M
R5/RRR5-22/2	1093.857	1094.279	-387.014	0.314	940.307	0.268	15	0.126	K.VCAGFIDAIK.V
R5/RRR5-22/2	1079.039	1079.252	-197.158	0.361	554.778	0.302	14	0.125	K.VFSDAPAM*PK.V
R5/RRR5-24/2	1269.956	1270.565	-1270.839	0.290	672.469	0.324	14	0.125	K.LILDGYFGMLK.M
R5/RRR5-26/2	1101.947	1102.220	-248.397	0.279	849.992	0.292	13	0.124	-.SEVLDVPAGSK.-
R5/RRR5-22/2	1079.007	1079.252	-227.007	0.353	528.461	0.300	13	0.124	K.VFSDAPAM*PK.V
R5/RRR5-23/2	1078.953	1079.252	-277.743	0.305	625.987	0.297	14	0.124	K.VFSDAPAM*PK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1102.344	1102.220	112.445	0.263	910.160	0.266	14	0.123	-.SEVLDVPAGSK.-
R5/RRR5-23/2	1102.092	1102.220	-116.384	0.313	818.425	0.267	14	0.123	K.SEVLDVPAGSK.V
R5/RRR5-24/2	1078.972	1079.252	-260.149	0.366	587.283	0.262	14	0.123	K.VFSDAPAM*PK.V
R5/RRR5-24/2	1078.402	1079.252	-1720.008	0.250	414.465	0.309	12	0.122	K.VFSDAPAM*PK.V
R5/RRR5-28/2	1338.812	1339.455	-1230.901	0.295	339.465	0.373	12	0.121	K.VEGDGGAGTVTTM*K.L
R5/RRR5-21/2	1079.469	1079.252	201.829	0.322	517.593	0.261	13	0.120	-.VFSDAPAM*PK.-
R5/RRR5-23/2	1093.456	1094.279	-1672.595	0.284	1164.728	0.122	16	0.120	K.VCAGFIDAIK.V
R5/RRR5-22/2	1079.190	1079.252	-57.584	0.316	582.435	0.209	13	0.119	K.VFSDAPAM*PK.V
R5/RRR5-21/2	1102.251	1102.220	27.702	0.216	586.207	0.207	13	0.118	K.SEVLDVPAGSK.V
R5/RRR5-23/2	1078.241	1079.252	-1869.926	0.260	836.501	0.130	16	0.116	K.VFSDAPAM*PK.V
R5/RRR5-21/2	1101.902	1102.220	-289.408	0.221	535.469	0.263	12	0.116	-.SEVLDVPAGSK.-
R5/RRR5-24/2	1669.218	1668.849	222.026	0.354	820.607	0.259	17	0.115	K.M*IEDYLVAHPTEYA.-
R5/RRR5-21/2	1102.033	1102.220	-170.496	0.350	796.894	0.200	13	0.111	-.SEVLDVPAGSK.-
R5/RRR5-26/2	1102.036	1102.220	-167.940	0.340	667.762	0.273	12	0.106	-.SEVLDVPAGSK.-
R5/RRR5-20/2	1101.451	1102.220	-1611.100	0.227	500.467	0.172	11	0.079	-.SEVLDVPAGSK.-
R5/RRR5-19/2	1784.137	1783.021	65.015	0.629	2389.756	0.621	25	0.373	K.HLNLDFQLLEVEGVR.K
R5/RRR5-19/2	1783.755	1783.021	-149.677	0.635	2393.066	0.607	25	0.368	K.HLNLDFQLLEVEGVR.K
R5/RRR5-19/2	1902.386	1902.048	178.172	0.532	1993.181	0.592	27	0.364	K.FLDGIYVSDKGTITEDQ.-
R5/RRR5-19/2	1783.473	1783.021	254.103	0.624	2275.985	0.626	25	0.353	K.HLNLDFQLLEVEGVR.K
R5/RRR5-19/2	1902.432	1902.048	202.238	0.536	1931.329	0.576	26	0.338	K.FLDGIYVSDKGTITEDQ.-
R5/RRR5-19/2	1901.282	1902.048	-931.733	0.490	1652.736	0.571	25	0.251	K.FLDGIYVSDKGTITEDQ.-
R5/RRR5-19/3	1910.913	1911.194	-147.669	0.539	1262.863	0.451	30	0.130	K.HLNLDFQLLEVEGVRK.L
R5/RRR5-19/3	1910.981	1911.194	-111.528	0.551	1060.568	0.462	28	0.114	K.HLNLDFQLLEVEGVRK.L
R5/RRR5-19/3	1909.834	1911.194	-1239.231	0.450	789.436	0.470	24	0.097	K.HLNLDFQLLEVEGVRK.L
R5/RRR5-19/3	1781.976	1783.021	-1151.257	0.331	1029.226	0.198	24	0.065	-.HLNLDFQLLEVEGVR.-
R5/RRR5-1/2	1633.469	1633.746	-169.894	0.514	1803.430	0.504	21	0.238	R.TALTYIDADGNWHR.A
R5/RRR5-2/2	1406.676	1407.643	-1402.609	0.515	1744.931	0.493	20	0.229	K.GVDKDHVLLLAAR.A
R5/RRR5-2/2	1559.196	1559.743	-995.515	0.452	1704.382	0.509	21	0.225	K.IDQSALTGESLPVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1492.605	1492.742	-91.676	0.509	1556.269	0.511	20	0.209	K.LSVDKNLVEVFTK.G
R5/RRR5-2/2	1634.166	1633.746	257.989	0.532	1509.737	0.529	20	0.208	R.TALTYIDADGNWHR.A
R5/RRR5-1/2	1633.442	1633.746	-186.537	0.488	1496.171	0.512	20	0.202	R.TALTYIDADGNWHR.A
R5/RRR5-1/2	1492.434	1492.742	-207.032	0.501	1497.821	0.505	19	0.201	K.LSVDKNLVEVFTK.G
R5/RRR5-1/3	1429.197	1429.649	-316.905	0.559	1797.659	0.448	28	0.199	R.KVHAVIDKYAER.G
R5/RRR5-3/2	1559.390	1559.743	-227.586	0.454	1563.021	0.468	20	0.199	K.IDQSALTGESLPVTK.G
R5/RRR5-3/2	1492.344	1492.742	-267.593	0.524	1479.512	0.500	20	0.199	K.LSVDKNLVEVFTK.G
R5/RRR5-4/2	1940.483	1940.229	131.390	0.593	1509.964	0.474	26	0.193	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-1/2	1493.650	1492.742	-61.529	0.547	1229.105	0.560	19	0.187	K.LSVDKNLVEVFTK.G
R5/RRR5-1/2	1163.086	1163.370	-244.524	0.443	1573.630	0.387	18	0.185	K.M*ITGDQLAIGK.E
R5/RRR5-3/2	1559.117	1559.743	-1046.059	0.366	1520.132	0.401	20	0.181	K.IDQSALTGESLPVTK.G
R5/RRR5-1/2	1559.090	1559.743	-1063.433	0.391	1489.444	0.412	20	0.180	K.IDQSALTGESLPVTK.G
R5/RRR5-1/2	1940.272	1940.229	22.300	0.558	1368.318	0.468	25	0.179	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-1/2	1914.335	1915.182	-967.262	0.525	1353.383	0.475	23	0.178	R.LGM*GTNM*YPSSALLGQNK.D
R5/RRR5-3/2	1492.190	1492.742	-1043.418	0.493	1261.137	0.501	19	0.178	K.LSVDKNLVEVFTK.G
R5/RRR5-1/2	1942.092	1940.229	-70.773	0.635	1282.087	0.510	24	0.177	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-1/2	1940.434	1940.229	106.281	0.596	1257.509	0.507	25	0.176	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-2/2	1492.319	1492.742	-284.334	0.480	1308.708	0.469	19	0.176	K.LSVDKNLVEVFTK.G
R5/RRR5-1/2	1941.860	1940.229	-190.390	0.583	1281.962	0.467	25	0.170	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-1/2	1407.326	1407.643	-225.990	0.512	1251.458	0.470	18	0.170	K.GVDKDHVLLLAAR.A
R5/RRR5-2/3	1406.767	1407.643	-1337.818	0.537	1730.417	0.393	28	0.168	K.GVDKDHVLLLAAR.A
R5/RRR5-4/2	1940.443	1940.229	110.445	0.604	1183.770	0.491	24	0.166	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-2/2	1940.578	1940.229	180.596	0.550	1175.966	0.492	22	0.166	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-3/2	1492.556	1492.742	-124.984	0.494	1074.750	0.506	18	0.164	K.LSVDKNLVEVFTK.G
R5/RRR5-2/2	1939.660	1940.229	-811.417	0.512	1116.939	0.494	24	0.164	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-4/3	1407.855	1407.643	151.042	0.534	1667.570	0.403	27	0.162	K.GVDKDHVLLLAAR.A
R5/RRR5-1/3	1429.178	1429.649	-330.916	0.541	1739.146	0.363	28	0.161	R.KVHAVIDKYAER.G
R5/RRR5-1/2	1938.735	1940.229	-1289.997	0.416	1148.237	0.439	23	0.156	R.WGEQEAAILVPGDIISIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1162.901	1163.370	-404.913	0.448	1284.287	0.354	18	0.156	K.M*ITGDQLAIGK.E
R5/RRR5-2/2	1162.978	1163.370	-338.034	0.483	1273.965	0.347	18	0.153	K.M*ITGDQLAIGK.E
R5/RRR5-2/2	1643.469	1642.829	-220.115	0.496	1001.400	0.458	21	0.152	K.DASLEALPVDELIEK.A
R5/RRR5-1/3	1429.348	1429.649	-210.997	0.526	1596.178	0.396	27	0.152	R.KVHAVIDKYAER.G
R5/RRR5-2/3	1429.672	1429.649	16.039	0.544	1570.683	0.405	27	0.151	R.KVHAVIDKYAER.G
R5/RRR5-2/2	1163.160	1163.370	-180.825	0.421	1186.166	0.357	18	0.150	K.M*ITGDQLAIGK.E
R5/RRR5-3/3	1406.631	1407.643	-1434.695	0.508	1771.401	0.313	28	0.148	K.GVDKDHVLLLAAR.A
R5/RRR5-1/2	1026.422	1027.156	-1694.991	0.390	916.972	0.437	17	0.146	K.LGDIVPADAR.L
R5/RRR5-2/2	1939.449	1940.229	-920.404	0.467	1038.149	0.424	21	0.146	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-2/2	1914.404	1915.182	-931.156	0.524	900.070	0.478	21	0.145	R.LGM*GTNM*YPSSALLGQNK.D
R5/RRR5-3/2	1633.267	1633.746	-293.830	0.389	925.437	0.462	17	0.145	R.TALTYIDADGNWHR.A
R5/RRR5-4/2	1940.623	1940.229	203.494	0.555	1048.430	0.415	22	0.144	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-2/2	1643.448	1642.829	-232.857	0.484	918.693	0.421	21	0.143	K.DASLEALPVDELIEK.A
R5/RRR5-4/3	1429.924	1429.649	193.150	0.540	1511.245	0.400	27	0.142	R.KVHAVIDKYAER.G
R5/RRR5-1/2	1026.471	1027.156	-1647.318	0.418	796.632	0.438	16	0.142	K.LGDIVPADAR.L
R5/RRR5-2/2	1163.110	1163.370	-224.413	0.479	1058.361	0.347	17	0.141	K.M*ITGDQLAIGK.E
R5/RRR5-2/2	1914.442	1915.182	-911.312	0.535	866.262	0.463	20	0.140	R.LGM*GTNM*YPSSALLGQNK.D
R5/RRR5-4/2	1643.684	1642.829	-88.315	0.513	1049.551	0.350	22	0.139	K.DASLEALPVDELIEK.A
R5/RRR5-3/2	1642.341	1642.829	-298.395	0.424	922.386	0.362	21	0.136	K.DASLEALPVDELIEK.A
R5/RRR5-4/3	1407.578	1407.643	-46.599	0.542	1392.942	0.426	25	0.135	K.GVDKDHVLLLAAR.A
R5/RRR5-2/3	1406.879	1407.643	-1257.690	0.532	1420.152	0.414	25	0.135	K.GVDKDHVLLLAAR.A
R5/RRR5-2/2	1146.970	1147.371	-350.305	0.362	674.943	0.435	15	0.135	K.MITGDQLAIGK.E
R5/RRR5-4/3	1407.283	1407.643	-256.980	0.524	1384.851	0.425	26	0.134	K.GVDKDHVLLLAAR.A
R5/RRR5-1/2	1162.386	1163.370	-1711.631	0.347	1145.175	0.258	17	0.134	K.M*ITGDQLAIGK.E
R5/RRR5-4/2	1642.460	1642.829	-225.617	0.458	861.211	0.338	21	0.131	K.DASLEALPVDELIEK.A
R5/RRR5-4/2	1026.424	1027.156	-1693.198	0.352	501.096	0.417	13	0.130	K.LGDIVPADAR.L
R5/RRR5-1/2	1642.702	1642.829	-77.933	0.429	859.144	0.334	20	0.130	K.DASLEALPVDELIEK.A
R5/RRR5-3/2	1940.489	1940.229	134.608	0.472	812.121	0.377	20	0.129	R.WGEQEAAILVPGDIISIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1642.306	1642.829	-930.375	0.367	829.324	0.335	20	0.129	K.DASLEALPVDELIEK.A
R5/RRR5-1/2	1026.379	1027.156	-1736.813	0.387	505.926	0.422	13	0.129	-.LGDIVPADAR.-
R5/RRR5-8/2	1939.596	1940.229	-844.206	0.375	702.195	0.388	20	0.129	R.WGEQEAAILVPGDIISIK.L
R5/RRR5-4/2	1026.425	1027.156	-1691.406	0.373	505.685	0.413	13	0.128	-.LGDIVPADAR.-
R5/RRR5-4/2	1642.480	1642.829	-213.240	0.405	676.148	0.358	19	0.128	K.DASLEALPVDELIEK.A
R5/RRR5-2/2	1026.992	1027.156	-160.779	0.471	604.162	0.360	14	0.127	-.LGDIVPADAR.-
R5/RRR5-1/3	1407.173	1407.643	-335.177	0.510	1493.618	0.353	26	0.126	K.GVDKDHVLLLAAR.A
R5/RRR5-3/2	1163.153	1163.370	-186.931	0.386	935.153	0.265	15	0.126	K.M*ITGDQLAIGK.E
R5/RRR5-1/2	1643.268	1642.829	267.513	0.456	646.866	0.348	18	0.125	K.DASLEALPVDELIEK.A
R5/RRR5-4/2	1642.403	1642.829	-260.439	0.353	751.068	0.315	19	0.125	K.DASLEALPVDELIEK.A
R5/RRR5-3/2	1642.678	1642.829	-92.245	0.393	621.675	0.341	18	0.125	K.DASLEALPVDELIEK.A
R5/RRR5-4/2	1990.829	1991.233	-203.849	0.338	846.652	0.369	19	0.125	R.TENQDAIDAAMVGMLADPK.E
R5/RRR5-3/2	1027.094	1027.156	-60.630	0.411	582.220	0.316	14	0.124	-.LGDIVPADAR.-
R5/RRR5-4/2	1491.565	1492.742	-1463.889	0.296	729.662	0.307	16	0.123	K.LSVDKNLVEVFTK.G
R5/RRR5-2/2	1026.934	1027.156	-217.421	0.440	430.038	0.389	12	0.123	-.LGDIVPADAR.-
R5/RRR5-3/2	1026.418	1027.156	-1698.695	0.411	442.948	0.419	12	0.122	-.LGDIVPADAR.-
R5/RRR5-3/2	1026.382	1027.156	-1733.467	0.297	540.491	0.328	13	0.120	-.LGDIVPADAR.-
R5/RRR5-2/3	1407.821	1407.643	126.390	0.526	1333.858	0.383	26	0.119	-.GVDKDHVLLLAAR.-
R5/RRR5-4/2	1026.870	1027.156	-279.435	0.365	547.994	0.368	13	0.118	-.LGDIVPADAR.-
R5/RRR5-3/2	1147.115	1147.371	-223.780	0.192	586.960	0.190	14	0.117	K.MITGDQLAIGK.E
R5/RRR5-2/2	1146.452	1147.371	-1678.471	0.174	586.506	0.170	15	0.116	K.MITGDQLAIGK.E
R5/RRR5-5/2	1643.475	1642.829	-216.464	0.430	436.142	0.275	15	0.116	-.DASLEALPVDELIEK.-
R5/RRR5-1/3	1407.686	1407.643	30.249	0.522	1294.856	0.387	25	0.116	K.GVDKDHVLLLAAR.A
R5/RRR5-1/2	1147.141	1147.371	-200.508	0.143	566.794	0.148	14	0.115	-.MITGDQLAIGK.-
R5/RRR5-2/2	1027.061	1027.156	-93.415	0.414	415.853	0.360	11	0.110	-.LGDIVPADAR.-
R5/RRR5-2/3	1493.023	1492.742	189.087	0.479	1187.776	0.384	27	0.106	K.LSVDKNLVEVFTK.G
R5/RRR5-2/3	1839.784	1840.094	-169.395	0.482	1140.442	0.398	30	0.106	K.KHIVGM*TGDGVNDAPALK.K
R5/RRR5-2/3	1840.161	1840.094	36.335	0.476	1343.818	0.310	33	0.104	K.KHIVGM*TGDGVNDAPALK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/3	1492.391	1492.742	-235.885	0.436	963.839	0.430	25	0.101	K.LSVDKNLVEVFTK.G
R5/RRR5-1/3	1407.749	1407.643	75.517	0.516	1041.684	0.379	22	0.096	K.GVDKDHVLLLAAR.A
R5/RRR5-4/3	1492.242	1492.742	-335.967	0.435	645.815	0.459	22	0.096	K.LSVDKNLVEVFTK.G
R5/RRR5-4/3	1492.920	1492.742	119.842	0.406	945.360	0.390	25	0.093	K.LSVDKNLVEVFTK.G
R5/RRR5-4/3	1492.850	1492.742	72.360	0.465	791.318	0.383	24	0.089	K.LSVDKNLVEVFTK.G
R5/RRR5-1/3	1492.617	1492.742	-84.199	0.474	861.332	0.371	24	0.089	K.LSVDKNLVEVFTK.G
R5/RRR5-2/3	1492.641	1492.742	-67.649	0.483	869.874	0.363	23	0.088	K.LSVDKNLVEVFTK.G
R5/RRR5-2/3	1492.252	1492.742	-329.318	0.388	645.130	0.394	21	0.087	K.LSVDKNLVEVFTK.G
R5/RRR5-1/3	1492.383	1492.742	-240.931	0.396	820.259	0.370	23	0.087	K.LSVDKNLVEVFTK.G
R5/RRR5-3/3	1492.237	1492.742	-1011.313	0.378	636.540	0.384	21	0.086	K.LSVDKNLVEVFTK.G
R5/RRR5-3/3	1492.328	1492.742	-278.352	0.397	658.278	0.330	21	0.081	K.LSVDKNLVEVFTK.G
R5/RRR5-4/3	1969.277	1968.267	4.823	0.294	962.230	0.309	28	0.073	K.KHIVGM*TGDGVNDAPALKK.A
R5/RRR5-6/3	1465.320	1465.683	-248.473	0.533	1722.225	0.556	31	0.228	K.KVLTTGPAGGLHSAR.F
R5/RRR5-1/2	1707.015	1707.826	-1064.020	0.535	1549.629	0.575	22	0.223	R.EVNSVNDNPVIDVHR.G
R5/RRR5-5/2	1707.165	1707.826	-976.286	0.517	1494.977	0.570	22	0.215	R.EVNSVNDNPVIDVHR.G
R5/RRR5-5/2	1707.412	1707.826	-243.639	0.530	1479.117	0.566	22	0.213	R.EVNSVNDNPVIDVHR.G
R5/RRR5-3/2	1707.343	1707.826	-283.664	0.524	1403.775	0.572	21	0.205	R.EVNSVNDNPVIDVHR.G
R5/RRR5-6/3	1465.082	1465.683	-1096.328	0.505	1598.646	0.551	30	0.205	K.KVLTTGPAGGLHSAR.F
R5/RRR5-6/2	1377.115	1377.528	-301.008	0.487	1493.817	0.510	20	0.202	R.VAFETGTAPITNR.I
R5/RRR5-2/2	1708.245	1707.826	245.869	0.572	1342.856	0.559	22	0.197	R.EVNSVNDNPVIDVHR.G
R5/RRR5-6/2	1377.105	1377.528	-308.123	0.489	1472.529	0.485	20	0.195	R.VAFETGTAPITNR.I
R5/RRR5-6/2	1709.301	1707.826	278.810	0.580	1217.761	0.598	22	0.193	R.EVNSVNDNPVIDVHR.G
R5/RRR5-6/2	1377.070	1377.528	-333.114	0.429	1453.515	0.461	20	0.188	R.VAFETGTAPITNR.I
R5/RRR5-2/2	1707.451	1707.826	-220.687	0.513	1188.369	0.533	20	0.176	R.EVNSVNDNPVIDVHR.G
R5/RRR5-5/2	1377.185	1377.528	-249.873	0.460	1246.598	0.486	20	0.174	R.VAFETGTAPITNR.I
R5/RRR5-1/2	1378.143	1377.528	-280.083	0.484	1208.010	0.500	20	0.174	R.VAFETGTAPITNR.I
R5/RRR5-1/2	1377.033	1377.528	-360.420	0.401	1262.672	0.425	20	0.164	R.VAFETGTAPITNR.I
R5/RRR5-6/2	1708.215	1707.826	228.313	0.492	949.759	0.555	19	0.162	R.EVNSVNDNPVIDVHR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/3	1801.087	1801.027	33.465	0.450	1513.629	0.449	29	0.160	R.FVREELGCVYLTGEK.L
R5/RRR5-5/2	1376.991	1377.528	-1119.774	0.430	1004.515	0.489	19	0.157	R.VAFETGTAPITNR.I
R5/RRR5-6/2	1337.252	1337.510	-193.885	0.375	1117.538	0.447	19	0.154	K.VLTTGPAGGLHSAR.F
R5/RRR5-5/2	1377.209	1377.528	-232.266	0.389	1156.714	0.396	18	0.152	R.VAFETGTAPITNR.I
R5/RRR5-6/2	1624.849	1624.865	-9.917	0.456	935.512	0.470	20	0.150	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	1398.484	1398.534	-36.124	0.379	1001.553	0.464	15	0.148	R.EELGCVYLTGEK.L
R5/RRR5-1/2	1625.838	1624.865	-16.915	0.439	906.210	0.460	19	0.147	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	1252.212	1252.485	-218.492	0.569	974.791	0.426	16	0.146	K.VNEVDPLLKPK.Q
R5/RRR5-5/2	1625.089	1624.865	138.206	0.490	831.538	0.471	19	0.145	R.TSPQWLGPQIEVIR.A
R5/RRR5-2/2	1625.451	1624.865	-255.773	0.515	836.863	0.477	17	0.144	R.TSPQWLGPQIEVIR.A
R5/RRR5-5/2	1624.493	1624.865	-229.469	0.469	800.996	0.457	19	0.143	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	1252.308	1252.485	-141.922	0.560	950.293	0.404	16	0.142	K.VNEVDPLLKPK.Q
R5/RRR5-6/2	1624.335	1624.865	-944.889	0.412	768.059	0.463	19	0.141	R.TSPQWLGPQIEVIR.A
R5/RRR5-4/2	1624.328	1624.865	-949.265	0.443	758.007	0.461	19	0.141	R.TSPQWLGPQIEVIR.A
R5/RRR5-2/2	1624.404	1624.865	-284.957	0.470	836.453	0.435	19	0.141	R.TSPQWLGPQIEVIR.A
R5/RRR5-2/2	1625.440	1624.865	-262.554	0.465	865.529	0.423	19	0.141	R.TSPQWLGPQIEVIR.A
R5/RRR5-1/2	1624.356	1624.865	-931.762	0.431	685.173	0.482	18	0.140	R.TSPQWLGPQIEVIR.A
R5/RRR5-3/2	1625.601	1624.865	-163.033	0.467	712.963	0.462	19	0.140	R.TSPQWLGPQIEVIR.A
R5/RRR5-4/2	1624.479	1624.865	-238.591	0.471	661.397	0.483	17	0.139	R.TSPQWLGPQIEVIR.A
R5/RRR5-5/2	1624.287	1624.865	-974.315	0.424	819.573	0.426	19	0.139	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	1624.318	1624.865	-955.603	0.366	803.447	0.436	19	0.139	R.TSPQWLGPQIEVIR.A
R5/RRR5-1/2	1624.522	1624.865	-211.679	0.415	766.636	0.429	20	0.139	R.TSPQWLGPQIEVIR.A
R5/RRR5-3/2	1625.281	1624.865	256.763	0.510	731.844	0.450	18	0.138	R.TSPQWLGPQIEVIR.A
R5/RRR5-1/2	1625.309	1624.865	273.708	0.476	782.564	0.418	19	0.137	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	1625.420	1624.865	-274.836	0.500	678.640	0.450	18	0.137	R.TSPQWLGPQIEVIR.A
R5/RRR5-3/2	1624.213	1624.865	-1020.418	0.424	698.884	0.447	18	0.137	R.TSPQWLGPQIEVIR.A
R5/RRR5-5/2	934.449	935.102	-1774.754	0.447	1040.259	0.318	13	0.137	K.VFLAISER.K
R5/RRR5-9/2	1625.176	1624.865	192.064	0.443	707.017	0.436	17	0.135	R.TSPQWLGPQIEVIR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1251.627	1252.485	-1488.811	0.484	874.721	0.366	16	0.135	K.VNEVDPLLKPK.Q
R5/RRR5-6/2	934.920	935.102	-195.668	0.502	871.007	0.350	13	0.135	K.VFLAISER.K
R5/RRR5-5/3	1465.622	1465.683	-41.788	0.490	1140.918	0.512	27	0.133	K.KVLTTGPAGGLHSAR.F
R5/RRR5-1/2	1377.112	1377.528	-303.053	0.314	1064.056	0.290	18	0.133	R.VAFETGTAPITNR.I
R5/RRR5-6/3	1465.651	1465.683	-21.863	0.523	1187.586	0.492	28	0.132	K.KVLTTGPAGGLHSAR.F
R5/RRR5-6/3	1800.187	1801.027	-1024.804	0.407	1564.654	0.328	28	0.132	R.FVREELGCVYLTGEK.L
R5/RRR5-2/2	1708.573	1707.826	-148.452	0.405	532.258	0.461	17	0.132	R.EVNSVNDNPVIDVHR.G
R5/RRR5-6/2	959.925	960.107	-189.805	0.437	709.442	0.366	14	0.132	K.TAEAVDILK.L
R5/RRR5-6/2	959.469	960.107	-1712.523	0.341	1030.990	0.270	15	0.130	K.TAEAVDILK.L
R5/RRR5-7/2	1624.715	1624.865	-92.963	0.435	607.362	0.389	17	0.129	R.TSPQWLGPQIEVIR.A
R5/RRR5-5/2	873.049	873.032	18.847	0.329	808.402	0.338	12	0.129	K.ALLTAIDR.E
R5/RRR5-1/3	1465.117	1465.683	-1071.733	0.486	1050.495	0.531	26	0.129	K.KVLTTGPAGGLHSAR.F
R5/RRR5-6/2	1624.991	1624.865	77.485	0.433	393.605	0.411	15	0.129	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	1625.457	1624.865	-252.006	0.478	724.575	0.348	18	0.128	R.TSPQWLGPQIEVIR.A
R5/RRR5-5/2	872.893	873.032	-160.409	0.283	894.566	0.293	13	0.127	K.ALLTAIDR.E
R5/RRR5-5/2	1251.917	1252.485	-1255.899	0.463	772.049	0.323	15	0.127	K.VNEVDPLLKPK.Q
R5/RRR5-6/2	1108.284	1108.226	52.629	0.409	830.375	0.284	14	0.126	K.ITAFEEELR.E
R5/RRR5-17/2	1626.246	1624.865	234.777	0.441	638.062	0.350	16	0.125	R.TSPQWLGPQIEVIR.A
R5/RRR5-8/2	1624.241	1624.865	-1002.685	0.344	603.235	0.333	17	0.125	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	960.009	960.107	-101.661	0.430	857.322	0.251	15	0.124	K.TAEAVDILK.L
R5/RRR5-6/2	1108.090	1108.226	-123.157	0.401	776.144	0.281	14	0.124	K.ITAFEEELR.E
R5/RRR5-7/2	1625.536	1624.865	-203.111	0.373	547.900	0.328	16	0.124	R.TSPQWLGPQIEVIR.A
R5/RRR5-7/2	1623.925	1624.865	-1198.230	0.305	374.305	0.369	13	0.123	R.TSPQWLGPQIEVIR.A
R5/RRR5-6/2	872.276	873.032	-2019.087	0.253	536.470	0.361	11	0.123	K.ALLTAIDR.E
R5/RRR5-1/3	1466.015	1465.683	227.063	0.494	979.833	0.531	25	0.123	K.KVLTTGPAGGLHSAR.F
R5/RRR5-8/2	1624.222	1624.865	-1014.909	0.342	510.027	0.319	15	0.123	R.TSPQWLGPQIEVIR.A
R5/RRR5-2/2	1376.680	1377.528	-1346.369	0.231	1025.591	0.184	19	0.121	R.VAFETGTAPITNR.I
R5/RRR5-6/2	872.765	873.032	-307.311	0.270	591.173	0.293	10	0.120	K.ALLTAIDR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	872.471	873.032	-1794.524	0.246	682.928	0.267	11	0.120	K.ALLTAIDR.E
R5/RRR5-9/2	1626.238	1624.865	229.884	0.420	731.538	0.267	16	0.119	R.TSPQWLGPQIEVIR.A
R5/RRR5-5/2	1252.136	1252.485	-279.814	0.424	449.180	0.293	13	0.119	-.VNEVDPLLKPK.-
R5/RRR5-6/3	1251.625	1252.485	-1490.438	0.408	803.243	0.460	20	0.098	K.VNEVDPLLKPK.Q
R5/RRR5-6/3	1252.374	1252.485	-88.742	0.327	855.974	0.383	21	0.086	K.VNEVDPLLKPK.Q
R5/RRR5-6/3	1252.580	1252.485	75.928	0.363	659.951	0.397	18	0.083	-.VNEVDPLLKPK.-
R5/RRR5-2/3	1253.177	1252.485	-246.277	0.401	468.232	0.418	17	0.082	-.VNEVDPLLKPK.-
R5/RRR5-5/3	1252.202	1252.485	-226.473	0.332	518.665	0.361	17	0.080	-.VNEVDPLLKPK.-
R5/RRR5-1/3	1252.570	1252.485	68.011	0.373	432.293	0.328	17	0.070	-.VNEVDPLLKPK.-
R5/RRR5-1/3	1252.887	1252.485	321.587	0.329	460.667	0.344	16	0.067	-.VNEVDPLLKPK.-
R5/RRR5-8/2	1983.631	1983.204	215.686	0.615	2950.892	0.589	26	0.483	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-8/2	1983.121	1983.204	-41.897	0.616	2769.522	0.573	26	0.434	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-8/2	1744.868	1745.940	-1190.679	0.517	2589.470	0.589	26	0.402	R.HMDGFGVNTYTFVTR.D
R5/RRR5-8/2	1745.322	1745.940	-929.477	0.517	2585.973	0.572	26	0.395	R.HMDGFGVNTYTFVTR.D
R5/RRR5-8/2	1983.427	1983.204	112.990	0.597	2514.772	0.587	25	0.384	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-7/2	1981.582	1983.204	-1833.328	0.413	2719.492	0.437	25	0.376	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-7/2	1982.551	1983.204	-836.043	0.551	2364.902	0.566	25	0.347	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-7/2	1745.097	1745.940	-1059.042	0.513	2277.486	0.584	24	0.337	R.HMDGFGVNTYTFVTR.D
R5/RRR5-7/2	1981.879	1983.204	-1176.662	0.453	2268.511	0.488	25	0.305	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-7/2	1540.455	1540.785	-214.964	0.575	1958.903	0.543	20	0.270	R.GPILLEDYHLIEK.L
R5/RRR5-7/2	1540.541	1540.785	-158.763	0.607	1915.075	0.551	20	0.265	R.GPILLEDYHLIEK.L
R5/RRR5-7/2	1540.191	1540.785	-1038.086	0.569	1909.559	0.548	20	0.264	R.GPILLEDYHLIEK.L
R5/RRR5-1/2	1540.039	1540.785	-1137.089	0.554	1934.365	0.498	20	0.253	R.GPILLEDYHLIEK.L
R5/RRR5-8/2	1529.325	1527.856	307.218	0.605	1750.379	0.589	21	0.250	R.LGPNYLMLPVNAPK.C
R5/RRR5-8/2	1541.181	1540.785	257.507	0.614	1842.639	0.536	20	0.250	R.GPILLEDYHLIEK.L
R5/RRR5-8/2	1540.481	1540.785	-198.111	0.558	1868.420	0.514	20	0.249	R.GPILLEDYHLIEK.L
R5/RRR5-8/2	1540.409	1540.785	-244.857	0.558	1842.220	0.514	20	0.245	R.GPILLEDYHLIEK.L
R5/RRR5-7/2	1745.450	1745.940	-281.469	0.511	1641.941	0.583	22	0.236	R.HMDGFGVNTYTFVTR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1528.278	1527.856	276.825	0.572	1417.283	0.560	19	0.202	R.LGPNYLMLPVNAPK.C
R5/RRR5-6/2	1540.614	1540.785	-110.992	0.508	1465.707	0.493	18	0.194	R.GPILLEDYHLIEK.L
R5/RRR5-8/2	1273.939	1273.287	-273.968	0.494	1632.476	0.383	16	0.191	R.DEEVDYYPSR.H
R5/RRR5-7/2	1544.286	1543.855	279.603	0.585	1397.789	0.508	20	0.189	R.LGPNYLM*LPVNAPK.C
R5/RRR5-6/2	1540.265	1540.785	-989.547	0.507	1449.908	0.472	18	0.188	R.GPILLEDYHLIEK.L
R5/RRR5-7/2	970.059	970.107	-49.301	0.488	1322.881	0.492	15	0.184	R.FAGELAHPK.V
R5/RRR5-8/2	1125.484	1125.303	161.154	0.463	1279.217	0.500	18	0.180	R.SPGAQTPVIVR.F
R5/RRR5-8/2	1125.160	1125.303	-127.273	0.501	1326.003	0.463	18	0.177	R.SPGAQTPVIVR.F
R5/RRR5-7/2	1527.488	1527.856	-241.958	0.478	1284.547	0.498	18	0.177	R.LGPNYLMLPVNAPK.C
R5/RRR5-7/2	1543.489	1543.855	-238.322	0.528	1279.298	0.497	19	0.177	R.LGPNYLM*LPVNAPK.C
R5/RRR5-8/2	1543.388	1543.855	-303.863	0.523	1177.933	0.537	19	0.176	R.LGPNYLM*LPVNAPK.C
R5/RRR5-8/2	1761.135	1761.939	-1027.192	0.568	934.586	0.604	23	0.174	R.HM*DGFGVNTYTFVTR.D
R5/RRR5-6/2	1125.039	1125.303	-235.136	0.529	1188.438	0.502	18	0.174	R.SPGAQTPVIVR.F
R5/RRR5-1/2	1543.364	1543.855	-319.100	0.491	1370.661	0.424	19	0.171	R.LGPNYLM*LPVNAPK.C
R5/RRR5-2/2	1125.075	1125.303	-203.787	0.494	1167.808	0.500	17	0.171	R.SPGAQTPVIVR.F
R5/RRR5-1/2	1125.116	1125.303	-166.781	0.518	1160.167	0.492	18	0.170	R.SPGAQTPVIVR.F
R5/RRR5-1/2	1543.335	1543.855	-988.196	0.516	1258.807	0.461	19	0.168	R.LGPNYLM*LPVNAPK.C
R5/RRR5-7/2	1527.208	1527.856	-1082.346	0.461	1164.837	0.498	19	0.168	R.LGPNYLMLPVNAPK.C
R5/RRR5-8/2	969.941	970.107	-171.246	0.508	1134.908	0.490	14	0.168	R.FAGELAHPK.V
R5/RRR5-1/2	1528.726	1527.856	-85.586	0.536	1214.577	0.488	17	0.168	R.LGPNYLMLPVNAPK.C
R5/RRR5-3/2	1125.148	1125.303	-138.701	0.531	1074.378	0.512	18	0.168	R.SPGAQTPVIVR.F
R5/RRR5-7/2	1070.489	1071.168	-1572.832	0.479	953.301	0.549	15	0.166	R.VFAYADTQR.Y
R5/RRR5-2/2	1124.782	1125.303	-1356.600	0.464	1310.667	0.406	17	0.165	R.SPGAQTPVIVR.F
R5/RRR5-6/2	1543.470	1543.855	-250.223	0.480	1244.280	0.444	19	0.165	R.LGPNYLM*LPVNAPK.C
R5/RRR5-6/2	1124.546	1125.303	-1567.233	0.456	1088.282	0.491	17	0.163	R.SPGAQTPVIVR.F
R5/RRR5-6/2	1125.077	1125.303	-201.610	0.475	1092.398	0.477	18	0.163	R.SPGAQTPVIVR.F
R5/RRR5-8/3	1982.448	1983.204	-888.651	0.448	1729.787	0.350	29	0.161	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-7/2	1126.390	1125.303	77.327	0.537	1049.893	0.483	18	0.161	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1124.665	1125.303	-1460.706	0.447	1103.086	0.469	17	0.161	R.SPGAQTPVIVR.F
R5/RRR5-9/2	1124.579	1125.303	-1538.010	0.466	1070.919	0.474	17	0.160	R.SPGAQTPVIVR.F
R5/RRR5-7/2	1542.879	1543.855	-1284.882	0.482	1054.611	0.494	18	0.159	R.LGPNYLM*LPVNAPK.C
R5/RRR5-2/2	1543.501	1543.855	-230.387	0.420	1318.663	0.380	18	0.159	R.LGPNYLM*LPVNAPK.C
R5/RRR5-3/2	1124.629	1125.303	-1492.978	0.483	1080.559	0.462	17	0.159	R.SPGAQTPVIVR.F
R5/RRR5-5/2	1126.108	1125.303	-174.244	0.499	1000.040	0.482	18	0.158	R.SPGAQTPVIVR.F
R5/RRR5-7/2	971.026	970.107	-83.170	0.524	1051.553	0.455	15	0.158	R.FAGELAHPK.V
R5/RRR5-2/2	1543.507	1543.855	-226.103	0.524	1122.461	0.469	17	0.158	R.LGPNYLM*LPVNAPK.C
R5/RRR5-6/2	1071.982	1071.168	-174.019	0.466	903.846	0.514	15	0.158	R.VFAYADTQR.Y
R5/RRR5-8/2	969.328	970.107	-1840.045	0.436	1062.443	0.458	15	0.158	R.FAGELAHPK.V
R5/RRR5-8/2	1273.005	1273.287	-222.040	0.392	1433.891	0.294	15	0.156	R.DEEVDYYPSR.H
R5/RRR5-8/2	1125.637	1125.303	297.748	0.475	1146.772	0.418	17	0.156	R.SPGAQTPVIVR.F
R5/RRR5-2/2	1540.604	1540.785	-117.669	0.367	1231.023	0.388	18	0.155	R.GPILLEDYHLIEK.L
R5/RRR5-2/2	1543.713	1543.855	-92.668	0.454	1072.546	0.461	17	0.154	R.LGPNYLM*LPVNAPK.C
R5/RRR5-10/2	1125.042	1125.303	-233.286	0.461	1103.205	0.424	17	0.154	R.SPGAQTPVIVR.F
R5/RRR5-2/2	1072.221	1071.168	49.717	0.443	1033.306	0.443	14	0.153	R.VFAYADTQR.Y
R5/RRR5-3/2	1124.847	1125.303	-406.393	0.502	943.804	0.470	17	0.153	R.SPGAQTPVIVR.F
R5/RRR5-8/2	1761.292	1761.939	-937.704	0.518	830.254	0.510	22	0.152	R.HM*DGFGVNTYTFVTR.D
R5/RRR5-1/2	1124.379	1125.303	-1716.649	0.443	952.687	0.463	17	0.152	R.SPGAQTPVIVR.F
R5/RRR5-8/2	1761.299	1761.939	-933.738	0.553	731.918	0.526	22	0.150	R.HM*DGFGVNTYTFVTR.D
R5/RRR5-5/2	1125.248	1125.303	-48.813	0.472	953.994	0.449	17	0.150	R.SPGAQTPVIVR.F
R5/RRR5-1/2	1983.087	1983.204	-59.247	0.416	1092.817	0.431	18	0.149	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-8/2	1104.960	1105.188	-206.278	0.475	793.484	0.487	12	0.148	R.SHVQEYWR.V
R5/RRR5-5/2	1125.303	1125.303	-0.610	0.514	877.933	0.453	17	0.147	R.SPGAQTPVIVR.F
R5/RRR5-4/2	1125.024	1125.303	-249.288	0.498	929.961	0.444	16	0.147	R.SPGAQTPVIVR.F
R5/RRR5-4/2	1125.071	1125.303	-206.835	0.469	924.067	0.437	17	0.147	R.SPGAQTPVIVR.F
R5/RRR5-10/2	1125.107	1125.303	-175.161	0.376	989.361	0.426	17	0.147	R.SPGAQTPVIVR.F
R5/RRR5-8/2	1125.931	1125.303	-331.949	0.421	1049.434	0.394	17	0.147	R.SPGAQTPVIVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1542.637	1543.855	-1442.312	0.397	1122.097	0.383	18	0.147	R.LGPNYLM*LPVNAPK.C
R5/RRR5-7/2	1125.993	1125.303	-276.039	0.501	941.068	0.427	17	0.147	R.SPGAQTPVIVR.F
R5/RRR5-2/2	1124.424	1125.303	-1676.292	0.401	890.908	0.448	17	0.146	R.SPGAQTPVIVR.F
R5/RRR5-7/2	969.925	970.107	-187.280	0.446	940.375	0.420	14	0.146	R.FAGELAHPK.V
R5/RRR5-7/2	1071.092	1071.168	-70.713	0.483	902.709	0.420	15	0.146	R.VFAYADTQR.Y
R5/RRR5-7/2	1070.403	1071.168	-1653.828	0.373	971.286	0.415	15	0.146	R.VFAYADTQR.Y
R5/RRR5-1/2	1072.134	1071.168	-31.360	0.412	845.868	0.453	14	0.145	R.VFAYADTQR.Y
R5/RRR5-8/2	1544.350	1543.855	321.292	0.479	1227.692	0.339	17	0.144	R.LGPNYLM*LPVNAPK.C
R5/RRR5-8/2	1273.040	1273.287	-194.431	0.380	1332.813	0.245	15	0.141	R.DEEVDYYPSR.H
R5/RRR5-2/2	1071.129	1071.168	-36.648	0.402	956.653	0.368	15	0.140	R.VFAYADTQR.Y
R5/RRR5-1/2	1071.154	1071.168	-12.415	0.461	753.373	0.420	14	0.140	R.VFAYADTQR.Y
R5/RRR5-7/2	1105.978	1105.188	-189.815	0.496	738.361	0.428	12	0.140	R.SHVQEYWR.V
R5/RRR5-1/2	970.055	970.107	-53.593	0.418	864.618	0.392	14	0.139	R.FAGELAHPK.V
R5/RRR5-2/2	1543.194	1543.855	-1079.844	0.442	1076.174	0.355	17	0.139	R.LGPNYLM*LPVNAPK.C
R5/RRR5-7/2	1070.407	1071.168	-1649.474	0.397	966.896	0.354	15	0.139	R.VFAYADTQR.Y
R5/RRR5-3/2	1070.933	1071.168	-219.692	0.386	931.779	0.366	15	0.139	R.VFAYADTQR.Y
R5/RRR5-9/2	1124.576	1125.303	-1540.081	0.458	625.816	0.459	15	0.138	R.SPGAQTPVIVR.F
R5/RRR5-7/2	1070.531	1071.168	-1533.312	0.374	959.373	0.354	15	0.138	R.VFAYADTQR.Y
R5/RRR5-1/2	969.757	970.107	-361.418	0.409	896.134	0.374	14	0.138	R.FAGELAHPK.V
R5/RRR5-21/2	1126.012	1125.303	-259.834	0.460	664.611	0.441	15	0.138	R.SPGAQTPVIVR.F
R5/RRR5-8/2	1603.154	1603.755	-1001.287	0.432	1067.730	0.328	18	0.136	-.LFVQVIDPEEEER.-
R5/RRR5-8/2	1104.890	1105.188	-270.452	0.469	652.050	0.437	11	0.134	-.SHVQEYWR.-
R5/RRR5-1/2	1070.964	1071.168	-190.990	0.406	688.905	0.384	13	0.133	R.VFAYADTQR.Y
R5/RRR5-7/2	988.974	989.110	-137.619	0.387	603.402	0.420	11	0.133	R.FSTVIHER.G
R5/RRR5-2/2	1071.231	1071.168	59.021	0.396	714.691	0.376	13	0.133	R.VFAYADTQR.Y
R5/RRR5-7/2	988.808	989.110	-306.536	0.374	623.006	0.416	11	0.133	R.FSTVIHER.G
R5/RRR5-7/2	1526.615	1527.856	-1472.144	0.415	611.816	0.441	16	0.133	R.LGPNYLMLPVNAPK.C
R5/RRR5-3/2	1071.180	1071.168	11.932	0.366	716.180	0.381	13	0.133	R.VFAYADTQR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	988.468	989.110	-1666.059	0.392	623.073	0.401	11	0.132	R.FSTVIHER.G
R5/RRR5-8/2	1104.974	1105.188	-193.422	0.456	632.096	0.398	11	0.130	-.SHVQEYWR.-
R5/RRR5-8/2	988.456	989.110	-1678.094	0.398	482.529	0.409	10	0.130	R.FSTVIHER.G
R5/RRR5-7/2	1104.943	1105.188	-222.238	0.338	689.972	0.392	11	0.129	-.SHVQEYWR.-
R5/RRR5-7/2	988.343	989.110	-1792.627	0.336	448.601	0.405	10	0.128	R.FSTVIHER.G
R5/RRR5-8/2	988.278	989.110	-1859.647	0.361	456.057	0.432	10	0.128	-.FSTVIHER.-
R5/RRR5-1/2	969.707	970.107	-413.457	0.364	750.221	0.318	13	0.128	R.FAGELAHPK.V
R5/RRR5-1/2	989.214	989.110	105.749	0.330	478.487	0.387	10	0.127	R.FSTVIHER.G
R5/RRR5-6/2	1070.309	1071.168	-1741.369	0.321	692.344	0.306	13	0.126	R.VFAYADTQR.Y
R5/RRR5-8/2	1070.341	1071.168	-1711.346	0.343	797.157	0.256	14	0.125	R.VFAYADTQR.Y
R5/RRR5-4/2	1543.352	1543.855	-976.919	0.261	385.232	0.373	16	0.124	R.LGPNYLM*LPVNAPK.C
R5/RRR5-6/2	1070.824	1071.168	-322.390	0.350	557.190	0.281	12	0.124	R.VFAYADTQR.Y
R5/RRR5-8/2	1543.663	1543.855	-124.873	0.386	1103.132	0.212	17	0.124	R.LGPNYLM*LPVNAPK.C
R5/RRR5-5/2	1543.430	1543.855	-276.725	0.316	237.577	0.330	13	0.122	-.LGPNYLM*LPVNAPK.-
R5/RRR5-3/3	1541.633	1540.785	-98.935	0.426	1080.770	0.497	25	0.122	R.GPILLEDYHLIEK.L
R5/RRR5-7/3	1541.077	1540.785	189.825	0.453	797.255	0.573	23	0.119	R.GPILLEDYHLIEK.L
R5/RRR5-7/2	1273.224	1273.287	-49.198	0.408	843.835	0.235	13	0.119	-.DEEVDYYPSR.-
R5/RRR5-21/2	1125.631	1125.303	291.985	0.293	586.101	0.194	14	0.116	-.SPGAQTPVIVR.-
R5/RRR5-5/3	1541.785	1540.785	0.181	0.422	737.100	0.541	22	0.110	R.GPILLEDYHLIEK.L
R5/RRR5-9/3	1540.881	1540.785	62.795	0.390	974.489	0.475	24	0.110	R.GPILLEDYHLIEK.L
R5/RRR5-9/3	1541.120	1540.785	218.063	0.476	816.137	0.510	22	0.109	R.GPILLEDYHLIEK.L
R5/RRR5-2/3	1539.715	1540.785	-1348.500	0.364	822.641	0.480	23	0.102	R.GPILLEDYHLIEK.L
R5/RRR5-1/3	1541.321	1540.785	-301.755	0.434	789.914	0.471	21	0.101	R.GPILLEDYHLIEK.L
R5/RRR5-7/3	1126.139	1126.293	-136.905	0.524	1067.896	0.389	21	0.100	R.RFAGELAHPK.V
R5/RRR5-1/3	1540.674	1540.785	-72.136	0.437	829.972	0.442	21	0.098	R.GPILLEDYHLIEK.L
R5/RRR5-9/3	1540.861	1540.785	49.565	0.414	730.278	0.459	21	0.097	R.GPILLEDYHLIEK.L
R5/RRR5-3/3	1540.730	1540.785	-35.777	0.374	710.304	0.468	20	0.097	R.GPILLEDYHLIEK.L
R5/RRR5-2/3	1541.399	1540.785	-250.983	0.417	764.220	0.442	22	0.096	R.GPILLEDYHLIEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/3	1126.846	1126.293	-397.644	0.494	1064.002	0.365	21	0.095	R.RFAGELAHPK.V
R5/RRR5-8/3	1126.761	1126.293	416.207	0.513	1022.131	0.374	21	0.095	R.RFAGELAHPK.V
R5/RRR5-7/3	1540.925	1540.785	90.921	0.439	861.014	0.409	24	0.094	R.GPILLEDYHLIEK.L
R5/RRR5-2/3	1983.420	1983.204	109.341	0.455	904.333	0.412	25	0.092	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-7/3	1541.006	1540.785	144.069	0.390	677.795	0.418	20	0.091	R.GPILLEDYHLIEK.L
R5/RRR5-6/3	1539.749	1540.785	-1326.046	0.311	687.614	0.411	20	0.088	R.GPILLEDYHLIEK.L
R5/RRR5-8/3	1126.677	1126.293	341.908	0.472	1028.774	0.322	21	0.087	R.RFAGELAHPK.V
R5/RRR5-2/3	1983.045	1983.204	-80.216	0.399	984.542	0.342	24	0.084	R.AIWVNYLSQCDESLGVK.I
R5/RRR5-6/3	1540.647	1540.785	-89.541	0.345	641.063	0.339	19	0.082	R.GPILLEDYHLIEK.L
R5/RRR5-5/3	1127.012	1126.293	-250.272	0.437	985.710	0.295	21	0.081	R.RFAGELAHPK.V
R5/RRR5-5/3	1540.389	1540.785	-257.904	0.334	584.887	0.299	19	0.080	R.GPILLEDYHLIEK.L
R5/RRR5-6/3	1126.596	1126.293	270.042	0.431	917.332	0.156	20	0.066	R.RFAGELAHPK.V
R5/RRR5-6/2	1427.254	1427.588	-234.845	0.514	2489.608	0.576	22	0.378	K.STVHDVVLVGGSTR.I
R5/RRR5-6/2	1428.083	1427.588	347.517	0.585	2251.077	0.628	21	0.348	K.STVHDVVLVGGSTR.I
R5/RRR5-6/2	1427.331	1427.588	-180.619	0.519	2289.934	0.604	21	0.347	K.STVHDVVLVGGSTR.I
R5/RRR5-6/2	1248.059	1248.435	-302.277	0.533	1451.204	0.522	20	0.202	K.DAGVISGLNVM*R.I
R5/RRR5-6/2	1232.184	1232.436	-205.151	0.519	1420.724	0.512	20	0.197	K.DAGVISGLNVMR.I
R5/RRR5-6/2	1233.065	1232.436	-301.618	0.463	1425.502	0.511	20	0.196	K.DAGVISGLNVMR.I
R5/RRR5-6/2	1248.054	1248.435	-306.300	0.532	1402.511	0.502	19	0.192	K.DAGVISGLNVM*R.I
R5/RRR5-6/2	1248.151	1248.435	-227.997	0.509	1350.421	0.493	19	0.186	K.DAGVISGLNVM*R.I
R5/RRR5-6/2	1545.138	1544.752	250.403	0.514	1309.766	0.484	19	0.177	K.M*KETAEAYLGSTVK.N
R5/RRR5-6/2	1544.457	1544.752	-191.602	0.495	1257.260	0.451	20	0.168	K.M*KETAEAYLGSTVK.N
R5/RRR5-6/2	1584.261	1583.788	299.038	0.569	1159.595	0.451	22	0.162	K.QFSAEEISSMVLNK.M
R5/RRR5-6/2	1583.391	1583.788	-252.051	0.505	1186.352	0.381	22	0.153	K.QFSAEEISSMVLNK.M
R5/RRR5-6/2	1584.388	1583.788	-253.747	0.571	951.901	0.461	21	0.151	K.QFSAEEISSMVLNK.M
R5/RRR5-6/3	1528.425	1528.753	-215.303	0.470	1528.298	0.367	31	0.135	K.MKETAEAYLGSTVK.N
R5/RRR5-6/2	1599.256	1599.788	-960.734	0.530	888.535	0.377	20	0.134	-.QFSAEEISSM*VLNK.-
R5/RRR5-6/2	1599.263	1599.788	-956.596	0.461	708.821	0.368	18	0.128	K.QFSAEEISSM*VLNK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1232.246	1232.436	-154.566	0.316	573.884	0.201	14	0.108	-.DAGVISGLNVMR.-
R5/RRR5-6/3	1544.661	1544.752	-59.452	0.485	1391.694	0.286	28	0.102	K.M*KETAEAYLGSTVK.N
R5/RRR5-6/3	1544.697	1544.752	-35.790	0.457	1347.000	0.292	29	0.099	K.M*KETAEAYLGSTVK.N
R5/RRR5-6/3	1528.772	1528.753	12.636	0.429	1189.945	0.319	29	0.093	K.MKETAEAYLGSTVK.N
R5/RRR5-6/3	1527.823	1528.753	-1266.757	0.424	845.479	0.321	25	0.081	K.MKETAEAYLGSTVK.N
R5/RRR5-6/3	1545.634	1544.752	-77.039	0.498	725.565	0.316	23	0.079	K.M*KETAEAYLGSTVK.N
R5/RRR5-4/2	1832.409	1831.958	247.049	0.596	2292.995	0.521	25	0.319	K.TEDLWAALEEGSGEPVK.T
R5/RRR5-4/2	1582.390	1582.787	-251.746	0.518	2044.059	0.551	21	0.286	R.GVGAAGHEVAWTWLK.E
R5/RRR5-4/2	1831.433	1831.958	-834.966	0.527	2065.583	0.538	24	0.286	K.TEDLWAALEEGSGEPVK.T
R5/RRR5-4/2	1582.435	1582.787	-223.266	0.488	1950.559	0.522	20	0.263	R.GVGAAGHEVAWTWLK.E
R5/RRR5-4/2	1516.253	1516.744	-324.420	0.471	2084.761	0.434	21	0.262	R.MLQSYLGAETFQK.S
R5/RRR5-4/2	1831.173	1831.958	-977.836	0.480	1923.329	0.530	24	0.262	K.TEDLWAALEEGSGEPVK.T
R5/RRR5-4/2	1581.535	1582.787	-1427.912	0.454	1579.529	0.515	19	0.211	R.GVGAAGHEVAWTWLK.E
R5/RRR5-4/2	1211.444	1212.339	-1569.120	0.441	1551.350	0.447	17	0.196	K.LNVNQTGFYR.V
R5/RRR5-4/2	1168.964	1169.223	-222.635	0.462	1490.247	0.325	17	0.167	R.VSYDEELASR.L
R5/RRR5-4/2	1169.213	1169.223	-9.070	0.473	1297.130	0.399	16	0.164	R.VSYDEELASR.L
R5/RRR5-4/2	1211.486	1212.339	-1534.199	0.443	1212.641	0.397	17	0.158	K.LNVNQTGFYR.V
R5/RRR5-4/2	1029.311	1029.172	135.174	0.497	1168.785	0.389	16	0.153	R.AEANLGNVLK.E
R5/RRR5-4/2	1029.071	1029.172	-99.062	0.453	1220.039	0.350	17	0.151	R.AEANLGNVLK.E
R5/RRR5-4/2	1310.060	1309.560	-382.770	0.397	1420.206	0.260	18	0.148	K.AAYVALMQTVNK.S
R5/RRR5-4/2	1325.007	1324.548	347.661	0.376	561.006	0.512	16	0.137	K.EYFAVPYPLPK.M
R5/RRR5-4/2	1833.421	1834.148	-944.783	0.488	512.505	0.488	20	0.133	R.FNEVLPVGEGTLVIAFK.G
R5/RRR5-4/2	1169.177	1169.223	-39.858	0.446	953.920	0.329	14	0.133	R.VSYDEELASR.L
R5/RRR5-4/2	1105.854	1106.257	-365.544	0.414	785.491	0.288	13	0.125	R.NQDSIFLLR.G
R5/RRR5-4/2	1496.271	1496.734	-310.505	0.397	819.950	0.288	17	0.125	K.FLIDFLEPFAQR.I
R5/RRR5-4/2	1105.981	1106.257	-250.259	0.370	765.918	0.291	13	0.124	R.NQDSIFLLR.G
R5/RRR5-4/2	1496.318	1496.734	-278.583	0.469	865.552	0.272	17	0.123	K.FLIDFLEPFAQR.I
R5/RRR5-4/2	1323.644	1324.548	-1442.958	0.284	342.824	0.456	11	0.120	-.EYFAVPYPLPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1105.510	1106.257	-1584.917	0.373	749.625	0.234	13	0.120	R.NQDSIFLLR.G
R5/RRR5-4/2	1832.848	1834.148	-1258.509	0.347	444.260	0.337	19	0.120	R.FNEVLPVGEGTLVIAFK.G
R5/RRR5-4/2	1496.921	1496.734	125.501	0.503	887.539	0.239	17	0.119	K.FLIDFLEPFAQR.I
R5/RRR5-4/3	1745.670	1745.914	-140.220	0.446	587.362	0.514	26	0.095	R.ETALLFDEKHSAAANK.Q
R5/RRR5-4/3	1833.974	1834.148	-95.115	0.424	1086.782	0.361	28	0.093	R.FNEVLPVGEGTLVIAFK.G
R5/RRR5-4/3	1168.153	1168.285	-113.063	0.479	488.651	0.465	18	0.092	K.SGEGHLDALLR.G
R5/RRR5-4/3	1168.350	1168.285	55.623	0.472	388.664	0.521	17	0.092	-.SGEGHLDALLR.-
R5/RRR5-4/3	1745.455	1745.914	-263.974	0.394	524.146	0.491	25	0.086	-.ETALLFDEKHSAAANK.-
R5/RRR5-4/3	1168.141	1168.285	-123.441	0.345	618.357	0.357	20	0.078	K.SGEGHLDALLR.G
R5/RRR5-9/2	1984.423	1985.085	-840.499	0.573	2728.504	0.637	26	0.450	R.GNPTVEVDVCCSDGTFAR.A
R5/RRR5-9/2	1985.407	1985.085	162.335	0.590	2680.674	0.662	26	0.449	R.GNPTVEVDVCCSDGTFAR.A
R5/RRR5-8/2	1985.359	1985.085	137.979	0.566	2419.664	0.640	25	0.383	R.GNPTVEVDVCCSDGTFAR.A
R5/RRR5-8/2	1984.285	1985.085	-910.158	0.577	2331.587	0.669	26	0.376	R.GNPTVEVDVCCSDGTFAR.A
R5/RRR5-9/2	1984.304	1985.085	-900.401	0.558	2353.474	0.646	26	0.372	R.GNPTVEVDVCCSDGTFAR.A
R5/RRR5-9/2	1492.226	1492.656	-288.536	0.520	2529.984	0.533	24	0.367	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1984.201	1985.085	-952.403	0.539	2246.140	0.628	25	0.345	R.GNPTVEVDVCCSDGTFAR.A
R5/RRR5-9/2	1492.171	1492.656	-325.553	0.495	2262.117	0.551	23	0.322	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1581.527	1581.839	-197.769	0.489	2115.186	0.588	24	0.307	K.AVDNVNSVIAPALIGK.D
R5/RRR5-9/2	1492.334	1492.656	-215.907	0.506	2053.413	0.569	23	0.291	R.IEEELGAAAVYAGAK.F
R5/RRR5-1/2	1493.454	1492.656	-135.157	0.586	2051.894	0.565	22	0.288	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1887.280	1888.241	-1042.157	0.581	1868.938	0.621	26	0.277	K.LAM*QEFM*ILPTGAASFK.E
R5/RRR5-8/2	1492.262	1492.656	-264.325	0.532	1952.255	0.548	23	0.269	R.IEEELGAAAVYAGAK.F
R5/RRR5-9/2	1582.426	1581.839	-261.335	0.520	1852.571	0.586	24	0.265	K.AVDNVNSVIAPALIGK.D
R5/RRR5-8/3	1574.410	1574.758	-221.613	0.526	1959.571	0.512	30	0.263	K.VNQIGSVTESIEAVK.M
R5/RRR5-9/2	1888.559	1888.241	169.067	0.625	1784.375	0.599	25	0.257	K.LAM*QEFM*ILPTGAASFK.E
R5/RRR5-8/2	1580.931	1581.839	-1210.371	0.396	1981.704	0.484	23	0.256	K.AVDNVNSVIAPALIGK.D
R5/RRR5-9/2	1582.318	1581.839	303.971	0.498	1905.738	0.518	25	0.255	K.AVDNVNSVIAPALIGK.D
R5/RRR5-8/2	1872.351	1872.241	58.585	0.608	1746.259	0.603	25	0.253	K.LAM*QEFMILPTGAASFK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1902.403	1902.953	-816.882	0.565	1685.300	0.591	22	0.244	K.TYDLNFKEENNDGSQK.I
R5/RRR5-8/2	1492.208	1492.656	-300.930	0.532	1759.655	0.556	22	0.244	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1493.251	1492.656	-271.448	0.587	1747.688	0.558	22	0.242	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1872.373	1872.241	70.747	0.594	1627.442	0.616	24	0.240	K.LAM*QEFMILPTGAASFK.E
R5/RRR5-9/2	1581.442	1581.839	-251.665	0.436	1770.120	0.524	22	0.236	K.AVDNVNSVIAPALIGK.D
R5/RRR5-1/2	1492.408	1492.656	-166.262	0.492	1770.116	0.506	22	0.232	R.IEEELGAAAVYAGAK.F
R5/RRR5-9/2	1887.626	1888.241	-858.275	0.563	1642.987	0.558	25	0.228	K.LAM*QEFM*ILPTGAASFK.E
R5/RRR5-2/2	1493.162	1492.656	-331.405	0.548	1746.016	0.505	22	0.228	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1887.498	1888.241	-926.249	0.573	1651.066	0.537	26	0.225	K.LAM*QEFM*ILPTGAASFK.E
R5/RRR5-8/2	1552.403	1552.802	-257.950	0.496	1787.937	0.457	21	0.225	K.IPLYQHIANLAGNK.Q
R5/RRR5-8/2	1871.396	1872.241	-988.974	0.553	1495.726	0.588	24	0.218	K.LAMQEFM*ILPTGAASFK.E
R5/RRR5-1/2	1575.280	1574.758	-304.336	0.547	1576.221	0.544	23	0.217	K.VNQIGSVTESIEAVK.M
R5/RRR5-9/3	1574.897	1574.758	88.648	0.487	1909.364	0.422	29	0.217	K.VNQIGSVTESIEAVK.M
R5/RRR5-7/2	1491.640	1492.656	-1355.550	0.351	1913.188	0.355	23	0.215	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1575.161	1574.758	256.382	0.548	1561.016	0.541	23	0.215	K.VNQIGSVTESIEAVK.M
R5/RRR5-7/2	1581.794	1581.839	-27.990	0.440	1586.392	0.515	23	0.212	K.AVDNVNSVIAPALIGK.D
R5/RRR5-8/2	1553.902	1552.802	64.247	0.505	1699.811	0.446	22	0.212	K.IPLYQHIANLAGNK.Q
R5/RRR5-2/2	1493.131	1492.656	319.094	0.515	1645.763	0.486	21	0.211	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1553.442	1552.802	-232.793	0.522	1698.668	0.434	21	0.208	K.IPLYQHIANLAGNK.Q
R5/RRR5-2/2	1582.357	1581.839	-305.373	0.468	1525.376	0.520	23	0.206	K.AVDNVNSVIAPALIGK.D
R5/RRR5-8/2	1902.294	1902.953	-874.855	0.537	1484.859	0.538	21	0.206	K.TYDLNFKEENNDGSQK.I
R5/RRR5-1/2	1581.221	1581.839	-1025.939	0.399	1671.371	0.442	22	0.205	K.AVDNVNSVIAPALIGK.D
R5/RRR5-8/2	1580.580	1581.839	-1433.346	0.404	1524.332	0.508	22	0.202	K.AVDNVNSVIAPALIGK.D
R5/RRR5-3/2	1492.412	1492.656	-163.554	0.394	1669.878	0.430	21	0.202	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/3	1492.721	1492.656	43.864	0.511	1793.255	0.441	30	0.202	R.IEEELGAAAVYAGAK.F
R5/RRR5-9/2	1887.588	1888.241	-878.270	0.577	1507.777	0.514	24	0.202	K.LAM*QEFM*ILPTGAASFK.E
R5/RRR5-6/2	1574.229	1574.758	-974.420	0.481	1420.236	0.549	22	0.201	K.VNQIGSVTESIEAVK.M
R5/RRR5-9/3	1575.477	1574.758	-178.720	0.493	1579.475	0.539	27	0.201	K.VNQIGSVTESIEAVK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/3	1492.740	1492.656	56.536	0.481	1835.967	0.415	29	0.201	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1870.995	1872.241	-1204.153	0.486	1427.622	0.545	23	0.200	K.LAMQEFM*ILPTGAASFK.E
R5/RRR5-9/2	1573.960	1574.758	-1145.644	0.436	1553.605	0.477	23	0.200	K.VNQIGSVTESIEAVK.M
R5/RRR5-8/2	1871.069	1872.241	-1164.320	0.547	1388.060	0.562	23	0.200	K.LAM*QEFMILPTGAASFK.E
R5/RRR5-8/2	1854.898	1856.242	-1267.443	0.467	1539.281	0.488	23	0.200	K.LAMQEFMILPTGAASFK.E
R5/RRR5-7/2	1574.312	1574.758	-284.302	0.507	1472.291	0.513	22	0.199	K.VNQIGSVTESIEAVK.M
R5/RRR5-4/2	1491.997	1492.656	-1115.111	0.351	1812.245	0.331	21	0.198	R.IEEELGAAAVYAGAK.F
R5/RRR5-7/2	1492.178	1492.656	-321.038	0.422	1596.253	0.443	22	0.197	R.IEEELGAAAVYAGAK.F
R5/RRR5-9/2	1856.619	1856.242	203.865	0.623	1327.039	0.575	23	0.196	K.LAMQEFMILPTGAASFK.E
R5/RRR5-7/2	1581.660	1581.839	-113.453	0.441	1382.282	0.535	21	0.193	K.AVDNVNSVIAPALIGK.D
R5/RRR5-8/2	1574.311	1574.758	-284.924	0.513	1406.688	0.507	22	0.191	K.VNQIGSVTESIEAVK.M
R5/RRR5-8/2	1856.372	1856.242	70.531	0.597	1249.633	0.587	22	0.190	K.LAMQEFMILPTGAASFK.E
R5/RRR5-9/2	1855.294	1856.242	-1053.025	0.497	1261.599	0.572	23	0.190	K.LAMQEFMILPTGAASFK.E
R5/RRR5-4/2	1574.248	1574.758	-962.119	0.509	1302.017	0.549	21	0.189	K.VNQIGSVTESIEAVK.M
R5/RRR5-7/2	1574.294	1574.758	-295.582	0.502	1374.164	0.503	22	0.187	K.VNQIGSVTESIEAVK.M
R5/RRR5-6/2	1574.361	1574.758	-252.719	0.492	1400.243	0.491	22	0.187	K.VNQIGSVTESIEAVK.M
R5/RRR5-2/2	1574.169	1574.758	-1012.724	0.483	1308.994	0.532	21	0.186	K.VNQIGSVTESIEAVK.M
R5/RRR5-8/2	1190.091	1190.397	-258.292	0.514	1443.444	0.435	16	0.183	K.MGVEVYHNLK.S
R5/RRR5-10/2	1574.268	1574.758	-312.542	0.508	1207.523	0.554	21	0.182	K.VNQIGSVTESIEAVK.M
R5/RRR5-3/2	1574.715	1574.758	-27.649	0.531	1232.458	0.542	21	0.182	K.VNQIGSVTESIEAVK.M
R5/RRR5-1/2	1574.485	1574.758	-173.848	0.498	1291.192	0.514	21	0.181	K.VNQIGSVTESIEAVK.M
R5/RRR5-9/2	1855.535	1856.242	-922.899	0.558	1153.935	0.567	22	0.179	K.LAMQEFMILPTGAASFK.E
R5/RRR5-8/2	1190.083	1190.397	-265.186	0.512	1511.219	0.385	16	0.179	K.MGVEVYHNLK.S
R5/RRR5-8/2	1574.164	1574.758	-1015.605	0.486	1260.234	0.512	21	0.178	K.VNQIGSVTESIEAVK.M
R5/RRR5-2/2	1491.610	1492.656	-1375.769	0.368	1580.038	0.356	21	0.178	R.IEEELGAAAVYAGAK.F
R5/RRR5-2/2	1581.458	1581.839	-241.288	0.437	1252.169	0.513	21	0.177	K.AVDNVNSVIAPALIGK.D
R5/RRR5-5/2	1574.277	1574.758	-306.707	0.509	1117.237	0.561	20	0.175	K.VNQIGSVTESIEAVK.M
R5/RRR5-9/2	1552.515	1552.802	-185.614	0.389	1726.000	0.248	21	0.173	K.IPLYQHIANLAGNK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1574.293	1574.758	-296.127	0.480	1239.285	0.484	21	0.172	K.VNQIGSVTESIEAVK.M
R5/RRR5-1/2	1575.267	1574.758	-312.810	0.537	1244.157	0.480	21	0.171	K.VNQIGSVTESIEAVK.M
R5/RRR5-2/2	1574.295	1574.758	-295.116	0.487	1271.814	0.461	21	0.170	K.VNQIGSVTESIEAVK.M
R5/RRR5-4/2	1574.912	1574.758	97.830	0.483	1347.238	0.427	21	0.170	K.VNQIGSVTESIEAVK.M
R5/RRR5-6/2	1574.247	1574.758	-962.509	0.448	1202.939	0.482	21	0.168	K.VNQIGSVTESIEAVK.M
R5/RRR5-8/2	1189.602	1190.397	-1513.947	0.490	1298.536	0.407	16	0.166	K.MGVEVYHNLK.S
R5/RRR5-8/3	1493.001	1492.656	232.185	0.481	1645.018	0.402	29	0.165	R.IEEELGAAAVYAGAK.F
R5/RRR5-9/2	1573.623	1574.758	-1360.710	0.361	1240.596	0.449	21	0.164	K.VNQIGSVTESIEAVK.M
R5/RRR5-8/2	1888.521	1888.241	148.843	0.623	1110.870	0.508	23	0.164	K.LAM*QEFM*ILPTGAASFK.E
R5/RRR5-9/2	1573.845	1574.758	-1219.243	0.361	1254.945	0.430	21	0.163	K.VNQIGSVTESIEAVK.M
R5/RRR5-4/2	1575.349	1574.758	-260.566	0.503	1095.214	0.493	20	0.162	K.VNQIGSVTESIEAVK.M
R5/RRR5-7/2	1581.557	1581.839	-178.722	0.359	1310.680	0.360	21	0.156	K.AVDNVNSVIAPALIGK.D
R5/RRR5-9/2	1792.349	1791.983	204.617	0.542	677.055	0.587	24	0.154	R.AAVPSGASTGVYEALELR.D
R5/RRR5-7/2	1574.127	1574.758	-1039.507	0.456	1093.038	0.444	20	0.154	K.VNQIGSVTESIEAVK.M
R5/RRR5-3/2	1574.347	1574.758	-261.665	0.441	1216.912	0.360	21	0.150	K.VNQIGSVTESIEAVK.M
R5/RRR5-9/2	1792.441	1791.983	256.383	0.547	570.893	0.580	23	0.149	R.AAVPSGASTGVYEALELR.D
R5/RRR5-8/2	1791.407	1791.983	-882.669	0.468	655.079	0.559	24	0.149	R.AAVPSGASTGVYEALELR.D
R5/RRR5-8/2	1870.710	1872.241	-1893.190	0.423	820.360	0.515	20	0.147	K.LAMQEFM*ILPTGAASFK.E
R5/RRR5-5/2	1492.106	1492.656	-1041.261	0.301	1210.732	0.349	19	0.146	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1680.468	1680.975	-899.702	0.500	769.576	0.496	21	0.146	K.KIPLYQHIANLAGNK.Q
R5/RRR5-8/2	1681.015	1680.975	23.991	0.545	732.531	0.500	21	0.146	K.KIPLYQHIANLAGNK.Q
R5/RRR5-9/2	1791.403	1791.983	-884.995	0.474	649.374	0.525	24	0.145	R.AAVPSGASTGVYEALELR.D
R5/RRR5-11/2	1574.109	1574.758	-1050.875	0.399	937.142	0.437	20	0.145	K.VNQIGSVTESIEAVK.M
R5/RRR5-8/2	1791.366	1791.983	-905.313	0.465	512.294	0.560	22	0.143	R.AAVPSGASTGVYEALELR.D
R5/RRR5-10/2	1574.258	1574.758	-318.299	0.406	998.297	0.407	19	0.143	K.VNQIGSVTESIEAVK.M
R5/RRR5-9/2	1680.466	1680.975	-900.650	0.495	744.621	0.474	21	0.143	K.KIPLYQHIANLAGNK.Q
R5/RRR5-8/2	1791.347	1791.983	-916.258	0.479	594.628	0.508	23	0.141	R.AAVPSGASTGVYEALELR.D
R5/RRR5-9/2	1680.488	1680.975	-290.601	0.529	716.754	0.473	20	0.141	K.KIPLYQHIANLAGNK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1491.188	1492.656	-1659.673	0.334	1308.225	0.249	20	0.140	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1205.970	1206.397	-354.680	0.475	1052.667	0.333	16	0.140	K.M*GVEVYHNLK.S
R5/RRR5-8/2	1205.932	1206.397	-386.774	0.498	1020.050	0.343	16	0.139	K.M*GVEVYHNLK.S
R5/RRR5-7/2	1791.225	1791.983	-984.606	0.426	617.555	0.500	22	0.139	R.AAVPSGASTGVYEALELR.D
R5/RRR5-9/2	1855.970	1856.242	-147.019	0.480	844.388	0.445	19	0.139	K.LAMQEFMILPTGAASFK.E
R5/RRR5-9/2	1207.096	1206.397	-249.673	0.539	936.968	0.363	16	0.138	K.M*GVEVYHNLK.S
R5/RRR5-9/2	1680.408	1680.975	-935.509	0.493	687.462	0.440	21	0.137	K.KIPLYQHIANLAGNK.Q
R5/RRR5-1/2	1792.403	1791.983	235.213	0.482	473.304	0.511	21	0.137	R.AAVPSGASTGVYEALELR.D
R5/RRR5-8/2	1680.582	1680.975	-234.560	0.490	691.261	0.445	20	0.137	K.KIPLYQHIANLAGNK.Q
R5/RRR5-8/2	1855.861	1856.242	-205.678	0.428	897.902	0.404	19	0.136	K.LAMQEFMILPTGAASFK.E
R5/RRR5-2/2	1793.304	1791.983	179.383	0.431	275.883	0.527	19	0.135	R.AAVPSGASTGVYEALELR.D
R5/RRR5-3/2	1580.728	1581.839	-1339.025	0.292	1085.396	0.314	19	0.135	K.AVDNVNSVIAPALIGK.D
R5/RRR5-9/2	1207.210	1206.397	-154.719	0.521	828.825	0.348	15	0.132	K.M*GVEVYHNLK.S
R5/RRR5-2/2	1580.965	1581.839	-1188.971	0.357	833.261	0.369	19	0.131	K.AVDNVNSVIAPALIGK.D
R5/RRR5-8/2	1117.781	1118.251	-421.916	0.422	748.761	0.343	16	0.131	R.AGWGVM*TSHR.S
R5/RRR5-1/2	1491.443	1492.656	-1488.144	0.286	1189.184	0.213	20	0.130	R.IEEELGAAAVYAGAK.F
R5/RRR5-8/2	1206.040	1206.397	-296.793	0.471	821.570	0.319	15	0.129	K.M*GVEVYHNLK.S
R5/RRR5-2/2	1790.952	1791.983	-1137.412	0.327	203.878	0.479	18	0.129	R.AAVPSGASTGVYEALELR.D
R5/RRR5-3/2	1791.243	1791.983	-974.617	0.400	384.119	0.426	20	0.129	R.AAVPSGASTGVYEALELR.D
R5/RRR5-9/2	1117.892	1118.251	-322.426	0.434	646.719	0.351	14	0.128	R.AGWGVM*TSHR.S
R5/RRR5-8/2	1117.845	1118.251	-364.389	0.392	775.704	0.317	15	0.128	R.AGWGVM*TSHR.S
R5/RRR5-1/2	1790.599	1791.983	-1335.658	0.300	234.582	0.429	19	0.127	R.AAVPSGASTGVYEALELR.D
R5/RRR5-9/2	918.390	919.094	-1861.446	0.403	796.112	0.299	13	0.127	-.SCNALLLK.-
R5/RRR5-9/2	1855.732	1856.242	-816.314	0.376	709.489	0.374	17	0.126	K.LAMQEFMILPTGAASFK.E
R5/RRR5-8/2	918.923	919.094	-186.749	0.509	732.736	0.290	13	0.124	-.SCNALLLK.-
R5/RRR5-8/2	918.833	919.094	-284.974	0.479	730.471	0.301	13	0.123	-.SCNALLLK.-
R5/RRR5-8/2	918.423	919.094	-1824.984	0.405	675.135	0.310	12	0.122	-.SCNALLLK.-
R5/RRR5-8/2	1117.861	1118.251	-350.255	0.377	570.881	0.266	14	0.122	R.AGWGVM*TSHR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	918.895	919.094	-217.934	0.531	724.640	0.260	13	0.120	-.SCNALLLK.-
R5/RRR5-2/2	1790.502	1791.983	-1390.093	0.297	136.013	0.434	16	0.118	-.AAVPSGASTGVYEALELR.-
R5/RRR5-1/2	1887.984	1888.241	-136.457	0.342	471.261	0.293	14	0.118	K.LAM*QEFM*ILPTGAASFK.E
R5/RRR5-1/2	1793.039	1791.983	31.301	0.284	114.841	0.421	15	0.114	-.AAVPSGASTGVYEALELR.-
R5/RRR5-8/3	1902.146	1902.953	-952.912	0.405	479.824	0.585	26	0.105	K.TYDLNFKEENNDGSQK.I
R5/RRR5-9/3	1553.633	1552.802	-109.164	0.385	839.827	0.499	26	0.104	K.IPLYQHIANLAGNK.Q
R5/RRR5-8/3	1902.760	1902.953	-101.553	0.406	440.437	0.563	26	0.101	K.TYDLNFKEENNDGSQK.I
R5/RRR5-9/3	1903.164	1902.953	111.250	0.394	515.100	0.556	26	0.101	K.TYDLNFKEENNDGSQK.I
R5/RRR5-8/3	1553.534	1552.802	-173.245	0.379	946.019	0.438	27	0.099	K.IPLYQHIANLAGNK.Q
R5/RRR5-9/3	1792.152	1791.983	94.640	0.448	670.054	0.519	28	0.098	R.AAVPSGASTGVYEALELR.D
R5/RRR5-9/3	1902.906	1902.953	-24.721	0.372	379.546	0.546	24	0.098	K.TYDLNFKEENNDGSQK.I
R5/RRR5-8/3	1902.491	1902.953	-243.473	0.340	554.138	0.524	28	0.096	K.TYDLNFKEENNDGSQK.I
R5/RRR5-8/3	1856.211	1856.242	-16.637	0.464	994.893	0.391	29	0.095	-.LAMQEFMILPTGAASFK.-
R5/RRR5-9/3	1553.219	1552.802	269.218	0.402	846.634	0.429	27	0.094	K.IPLYQHIANLAGNK.Q
R5/RRR5-9/3	1792.057	1791.983	41.149	0.423	657.400	0.490	28	0.093	R.AAVPSGASTGVYEALELR.D
R5/RRR5-9/3	1903.109	1902.953	82.302	0.371	424.303	0.453	23	0.090	K.TYDLNFKEENNDGSQK.I
R5/RRR5-8/3	1552.913	1552.802	71.651	0.334	855.534	0.401	27	0.088	K.IPLYQHIANLAGNK.Q
R5/RRR5-2/3	1552.869	1552.802	43.505	0.317	549.101	0.348	22	0.079	K.IPLYQHIANLAGNK.Q
R5/RRR5-8/3	1857.547	1856.242	164.570	0.428	629.678	0.333	25	0.066	-.LAMQEFMILPTGAASFK.-
R5/RRR5-9/3	1855.554	1856.242	-912.604	0.348	813.455	0.255	26	0.061	-.LAMQEFMILPTGAASFK.-
R5/RRR5-4/2	1647.167	1646.869	181.621	0.599	2813.572	0.577	24	0.449	K.LLVAGDLQSFGEQLR.N
R5/RRR5-4/2	1646.278	1646.869	-969.555	0.520	2760.542	0.568	24	0.434	K.LLVAGDLQSFGEQLR.N
R5/RRR5-4/2	1645.936	1646.869	-1177.743	0.503	2804.860	0.531	24	0.430	K.LLVAGDLQSFGEQLR.N
R5/RRR5-4/2	1860.569	1860.958	-209.501	0.604	1898.559	0.478	24	0.242	K.DITADDKQELDEALQR.E
R5/RRR5-4/2	1861.226	1860.958	144.813	0.622	1831.444	0.500	23	0.238	K.DITADDKQELDEALQR.E
R5/RRR5-3/2	1861.275	1860.958	170.990	0.604	1794.072	0.491	23	0.231	K.DITADDKQELDEALQR.E
R5/RRR5-4/2	1269.181	1268.444	-208.046	0.547	1572.723	0.529	21	0.216	K.LADLEAAPAAVAR.L
R5/RRR5-4/2	1269.185	1268.444	-205.055	0.542	1574.087	0.519	21	0.214	K.LADLEAAPAAVAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1267.998	1268.444	-352.789	0.411	1724.901	0.435	21	0.212	K.LADLEAAPAAVAR.L
R5/RRR5-3/2	1269.148	1268.444	-233.906	0.516	1588.363	0.485	21	0.208	K.LADLEAAPAAVAR.L
R5/RRR5-3/2	1861.439	1860.958	259.180	0.602	1562.484	0.498	22	0.204	K.DITADDKQELDEALQR.E
R5/RRR5-3/2	1860.409	1860.958	-834.926	0.584	1574.807	0.485	22	0.203	K.DITADDKQELDEALQR.E
R5/RRR5-4/2	1860.210	1860.958	-942.168	0.558	1530.474	0.463	22	0.194	K.DITADDKQELDEALQR.E
R5/RRR5-4/2	1268.179	1268.444	-209.851	0.457	1512.736	0.381	21	0.179	K.LADLEAAPAAVAR.L
R5/RRR5-4/2	1316.660	1316.491	129.200	0.463	1301.321	0.310	16	0.149	K.RQDWLLSELR.G
R5/RRR5-3/3	1861.818	1860.958	-75.246	0.494	1586.432	0.386	33	0.149	K.DITADDKQELDEALQR.E
R5/RRR5-4/2	1114.200	1114.299	-88.934	0.416	985.821	0.374	14	0.141	R.LSAAWQM*YK.A
R5/RRR5-4/2	1113.996	1114.299	-273.375	0.438	1029.171	0.351	14	0.141	R.LSAAWQM*YK.A
R5/RRR5-4/2	1119.979	1120.237	-230.733	0.340	579.372	0.541	17	0.140	K.GDPGIAALYDK.L
R5/RRR5-4/2	1114.050	1114.299	-224.455	0.379	1044.857	0.331	14	0.138	R.LSAAWQM*YK.A
R5/RRR5-3/2	1119.960	1120.237	-248.338	0.351	569.524	0.515	17	0.138	K.GDPGIAALYDK.L
R5/RRR5-4/3	1742.659	1742.932	-157.198	0.440	1550.528	0.339	29	0.137	-.INGKQEVM*IGYSDSGK.-
R5/RRR5-3/2	1113.868	1114.299	-388.383	0.373	982.979	0.337	14	0.136	R.LSAAWQM*YK.A
R5/RRR5-4/2	1119.977	1120.237	-232.482	0.397	576.980	0.456	17	0.136	K.GDPGIAALYDK.L
R5/RRR5-4/2	1097.758	1098.300	-1408.621	0.332	950.527	0.356	14	0.136	R.LSAAWQMYK.A
R5/RRR5-4/2	1490.266	1490.733	-314.138	0.359	681.279	0.431	18	0.135	R.AIPWIFAWTQTR.F
R5/RRR5-3/2	976.099	976.154	-56.585	0.421	805.161	0.393	12	0.135	-.SIVFKEPR.-
R5/RRR5-4/2	1023.065	1023.168	-101.140	0.431	856.192	0.349	11	0.134	K.HYIEFWK.K
R5/RRR5-4/2	1023.058	1023.168	-107.603	0.408	820.334	0.353	11	0.134	K.HYIEFWK.K
R5/RRR5-4/2	975.845	976.154	-318.199	0.403	838.303	0.341	12	0.131	R.SIVFKEPR.F
R5/RRR5-4/2	1490.085	1490.733	-1108.818	0.378	600.797	0.396	17	0.131	R.AIPWIFAWTQTR.F
R5/RRR5-4/2	1490.347	1490.733	-259.654	0.368	656.438	0.379	18	0.131	R.AIPWIFAWTQTR.F
R5/RRR5-3/2	1490.370	1490.733	-244.123	0.390	609.853	0.385	17	0.131	R.AIPWIFAWTQTR.F
R5/RRR5-4/2	1490.419	1490.733	-210.927	0.379	580.477	0.391	17	0.131	R.AIPWIFAWTQTR.F
R5/RRR5-2/2	1489.861	1490.733	-1259.867	0.340	580.704	0.398	17	0.130	R.AIPWIFAWTQTR.F
R5/RRR5-4/2	1163.013	1163.391	-326.207	0.325	259.333	0.504	14	0.130	R.QVSTFGLALVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1490.333	1490.733	-268.611	0.352	485.902	0.393	14	0.127	R.AIPWIFAWTQTR.F
R5/RRR5-3/2	1120.204	1120.237	-29.359	0.300	483.159	0.408	16	0.127	K.GDPGIAALYDK.L
R5/RRR5-4/2	1490.275	1490.733	-308.221	0.323	663.601	0.329	18	0.127	R.AIPWIFAWTQTR.F
R5/RRR5-3/2	1163.243	1163.391	-127.948	0.314	247.813	0.354	14	0.126	R.QVSTFGLALVK.L
R5/RRR5-3/2	1022.747	1023.168	-412.306	0.336	857.140	0.266	11	0.125	K.HYIEFWK.K
R5/RRR5-3/2	976.112	976.154	-43.539	0.406	786.826	0.282	12	0.125	R.SIVFKEPR.F
R5/RRR5-4/3	1860.581	1860.958	-202.992	0.503	1280.240	0.426	29	0.125	K.DITADDKQELDEALQR.E
R5/RRR5-3/2	1490.106	1490.733	-1094.916	0.307	644.611	0.306	17	0.124	R.AIPWIFAWTQTR.F
R5/RRR5-3/2	1490.002	1490.733	-1165.250	0.283	558.792	0.316	17	0.124	R.AIPWIFAWTQTR.F
R5/RRR5-4/2	1022.283	1023.168	-1849.707	0.376	809.652	0.248	11	0.124	K.HYIEFWK.K
R5/RRR5-4/2	1097.946	1098.300	-323.236	0.242	740.126	0.204	13	0.118	R.LSAAWQMYK.A
R5/RRR5-3/2	1162.628	1163.391	-1521.164	0.243	144.969	0.407	11	0.114	-.QVSTFGLALVK.-
R5/RRR5-3/2	1315.416	1316.491	-1582.386	0.317	919.760	0.137	14	0.114	K.RQDWLLSELR.G
R5/RRR5-3/3	1742.579	1742.932	-203.261	0.468	1131.879	0.424	28	0.111	R.INGKQEVM*IGYSDSGK.D
R5/RRR5-3/2	1316.526	1316.491	26.820	0.320	641.996	0.136	12	0.111	-.RQDWLLSELR.-
R5/RRR5-3/3	1861.628	1860.958	-177.557	0.540	1143.857	0.397	28	0.106	K.DITADDKQELDEALQR.E
R5/RRR5-4/3	1860.941	1860.958	-8.732	0.520	1136.651	0.396	30	0.106	K.DITADDKQELDEALQR.E
R5/RRR5-4/3	1742.592	1742.932	-196.093	0.462	1120.599	0.356	27	0.096	R.INGKQEVM*IGYSDSGK.D
R5/RRR5-4/3	1861.020	1860.958	33.900	0.521	1014.085	0.388	27	0.096	K.DITADDKQELDEALQR.E
R5/RRR5-3/3	1646.327	1646.869	-939.377	0.401	978.741	0.421	25	0.096	K.LLVAGDLQSFGEQLR.N
R5/RRR5-4/3	1831.723	1832.114	-213.822	0.436	1035.120	0.381	25	0.095	R.IRDPSFEVM*PQPALSK.E
R5/RRR5-3/3	1980.918	1980.162	-123.259	0.353	873.821	0.410	24	0.085	K.VSEDDKLVEYDALLVDR.F
R5/RRR5-4/3	1831.666	1832.114	-245.212	0.438	680.558	0.388	25	0.084	R.IRDPSFEVM*PQPALSK.E
R5/RRR5-3/3	1860.890	1860.958	-36.366	0.427	580.167	0.337	22	0.069	-.DITADDKQELDEALQR.-
R5/RRR5-4/3	1832.777	1832.114	-184.573	0.456	428.246	0.351	19	0.057	-.IRDPSFEVM*PQPALSK.-
R5/RRR5-3/3	1833.194	1832.114	44.087	0.420	359.094	0.361	19	0.053	-.IRDPSFEVM*PQPALSK.-
R5/RRR5-7/2	1707.321	1705.937	225.994	0.596	2600.799	0.576	22	0.402	K.WPYEAAALAFEAIPR.T
R5/RRR5-7/2	1158.038	1158.327	-250.533	0.472	1584.142	0.485	17	0.207	K.ALEDALAVLDK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1157.981	1158.327	-299.817	0.448	1614.028	0.470	17	0.207	K.ALEDALAVLDK.I
R5/RRR5-7/2	1157.616	1158.327	-1482.376	0.443	1608.781	0.470	17	0.206	K.ALEDALAVLDK.I
R5/RRR5-7/2	1317.335	1317.516	-137.612	0.484	1375.228	0.477	18	0.184	K.GLSDLAIHYLSK.A
R5/RRR5-7/2	1317.221	1317.516	-224.533	0.443	1153.829	0.511	17	0.170	K.GLSDLAIHYLSK.A
R5/RRR5-7/2	1120.920	1121.250	-295.506	0.431	1270.098	0.417	16	0.165	R.NLQDAM*SVAR.N
R5/RRR5-7/2	1360.074	1359.551	-351.231	0.507	1264.620	0.416	18	0.162	R.TLAQNCGLNVIR.I
R5/RRR5-7/2	1120.764	1121.250	-434.942	0.466	1183.997	0.425	16	0.160	R.NLQDAM*SVAR.N
R5/RRR5-7/2	1120.296	1121.250	-1749.110	0.359	1382.837	0.336	16	0.159	R.NLQDAM*SVAR.N
R5/RRR5-7/2	1363.231	1363.618	-284.404	0.475	1243.887	0.369	16	0.153	R.IILLDCPVEYK.K
R5/RRR5-7/2	819.172	819.048	151.216	0.370	1253.631	0.333	13	0.149	R.AAM*LGLVK.S
R5/RRR5-7/2	1317.085	1317.431	-263.227	0.402	1153.136	0.364	18	0.147	R.GASKDVLNEVER.N
R5/RRR5-7/2	1317.016	1317.431	-316.231	0.416	1204.923	0.322	18	0.144	R.GASKDVLNEVER.N
R5/RRR5-7/2	959.871	960.107	-246.833	0.399	1111.497	0.344	15	0.144	R.IDDIVSGIK.K
R5/RRR5-7/2	1316.367	1317.431	-1572.872	0.367	1092.841	0.344	17	0.140	R.GASKDVLNEVER.N
R5/RRR5-7/2	1057.902	1058.127	-213.486	0.388	939.999	0.374	16	0.139	K.VPGGQLEDSR.V
R5/RRR5-7/2	960.097	960.107	-9.706	0.442	920.133	0.349	15	0.137	R.IDDIVSGIK.K
R5/RRR5-7/2	959.423	960.107	-1760.076	0.409	799.441	0.398	14	0.136	R.IDDIVSGIK.K
R5/RRR5-7/2	1363.170	1363.618	-329.146	0.362	985.358	0.328	15	0.132	R.IILLDCPVEYK.K
R5/RRR5-7/2	1058.040	1058.127	-82.579	0.390	586.938	0.374	15	0.129	K.VPGGQLEDSR.V
R5/RRR5-7/2	1058.880	1058.127	-234.565	0.396	616.625	0.326	15	0.126	K.VPGGQLEDSR.V
R5/RRR5-7/2	1104.895	1105.251	-322.644	0.313	720.840	0.189	14	0.117	R.NLQDAMSVAR.N
R5/RRR5-7/3	1414.499	1414.546	-33.690	0.500	1130.809	0.253	24	0.079	K.VEKVPGGQLEDSR.V
R5/RRR5-7/3	1378.793	1378.622	124.143	0.419	992.411	0.275	22	0.076	K.GVM*FNKDVVAPGK.M
R5/RRR5-7/3	1378.551	1378.622	-51.690	0.356	659.564	0.326	18	0.072	K.GVM*FNKDVVAPGK.M
R5/RRR5-9/2	1996.248	1997.392	-1077.296	0.537	3196.862	0.538	29	0.528	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/2	1666.644	1666.881	-142.196	0.578	3219.469	0.517	27	0.523	R.GLLYLGMGVSGGEEGAR.N
R5/RRR5-9/2	1996.595	1997.392	-902.646	0.516	2922.831	0.543	28	0.461	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/2	1666.342	1666.881	-926.360	0.589	3017.923	0.485	27	0.458	R.GLLYLGMGVSGGEEGAR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1996.095	1997.392	-1154.235	0.570	2624.161	0.601	27	0.413	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/2	1666.376	1666.881	-905.988	0.558	2855.992	0.444	26	0.405	R.GLLYLGMGVSGGEEGAR.N
R5/RRR5-9/2	1683.241	1682.880	214.752	0.580	2679.427	0.477	26	0.378	R.GLLYLGM*GVSGGEEGAR.N
R5/RRR5-9/2	1682.100	1682.880	-1061.730	0.517	2681.779	0.423	25	0.361	R.GLLYLGM*GVSGGEEGAR.N
R5/RRR5-9/3	1997.266	1997.392	-63.001	0.517	2486.263	0.446	39	0.359	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/2	1683.272	1682.880	233.732	0.580	2536.358	0.462	25	0.344	R.GLLYLGM*GVSGGEEGAR.N
R5/RRR5-9/2	1998.190	1997.392	-101.016	0.370	2562.546	0.429	27	0.342	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/3	1996.719	1997.392	-840.174	0.452	2079.989	0.462	36	0.268	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/2	1997.914	1997.392	-239.712	0.525	1741.209	0.529	22	0.231	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/2	1110.036	1110.292	-231.255	0.530	1547.770	0.510	17	0.210	R.LPANLVQAQR.D
R5/RRR5-9/2	1110.060	1110.292	-209.191	0.521	1399.901	0.535	17	0.200	R.LPANLVQAQR.D
R5/RRR5-9/2	1110.252	1110.292	-35.467	0.527	1396.581	0.445	17	0.181	R.LPANLVQAQR.D
R5/RRR5-10/2	1553.824	1553.697	81.822	0.471	1297.716	0.438	21	0.170	K.VFQGDFSSNLPVDK.A
R5/RRR5-9/2	1215.657	1216.371	-1414.219	0.381	1380.605	0.358	17	0.162	K.GWSLNLGELAR.I
R5/RRR5-9/2	1414.023	1414.646	-1151.248	0.460	1209.075	0.424	18	0.160	K.ICSYAQGM*NIIK.A
R5/RRR5-9/2	1258.462	1259.308	-1471.482	0.390	934.085	0.485	15	0.151	R.DYFGAHTYER.V
R5/RRR5-9/2	1553.146	1553.697	-1002.073	0.434	1112.382	0.382	19	0.146	K.VFQGDFSSNLPVDK.A
R5/RRR5-9/3	1998.939	1997.392	-227.284	0.396	1563.995	0.378	33	0.146	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/2	1763.365	1762.978	219.853	0.490	691.770	0.530	22	0.145	K.VAAQVPDSGPCVTYIGK.G
R5/RRR5-9/2	1598.337	1597.775	-275.045	0.471	705.630	0.519	18	0.145	R.VDM*PGSFHTEWFK.I
R5/RRR5-9/2	1260.019	1259.308	-230.547	0.383	894.672	0.455	15	0.145	R.DYFGAHTYER.V
R5/RRR5-9/2	1762.409	1762.978	-893.302	0.490	723.561	0.516	22	0.145	K.VAAQVPDSGPCVTYIGK.G
R5/RRR5-9/2	943.370	944.067	-1804.433	0.360	828.852	0.426	13	0.139	K.AQLIEDVR.Q
R5/RRR5-9/2	1258.529	1259.308	-1418.384	0.338	822.408	0.448	15	0.139	R.DYFGAHTYER.V
R5/RRR5-9/2	1216.201	1216.371	-140.095	0.432	1042.904	0.342	15	0.138	K.GWSLNLGELAR.I
R5/RRR5-9/2	1762.335	1762.978	-935.371	0.471	729.026	0.450	22	0.137	K.VAAQVPDSGPCVTYIGK.G
R5/RRR5-9/2	1572.253	1571.736	-308.212	0.449	535.712	0.510	18	0.137	R.NGPSLM*PGGSFEAYK.Y
R5/RRR5-9/2	1571.149	1571.736	-1013.132	0.379	658.731	0.459	20	0.135	R.NGPSLM*PGGSFEAYK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1571.304	1571.736	-276.217	0.369	565.502	0.480	19	0.133	R.NGPSLM*PGGSFEAYK.Y
R5/RRR5-9/2	943.677	944.067	-415.455	0.380	728.578	0.356	12	0.130	K.AQLIEDVR.Q
R5/RRR5-1/2	1215.330	1216.371	-1684.189	0.371	1043.510	0.272	15	0.130	K.GWSLNLGELAR.I
R5/RRR5-9/2	1597.213	1597.775	-981.320	0.404	604.481	0.412	17	0.129	R.VDM*PGSFHTEWFK.I
R5/RRR5-7/2	1111.254	1110.292	-34.223	0.343	518.580	0.386	14	0.129	R.LPANLVQAQR.D
R5/RRR5-9/2	943.335	944.067	-1842.010	0.354	746.760	0.339	12	0.128	K.AQLIEDVR.Q
R5/RRR5-7/2	1111.104	1110.292	-169.104	0.302	529.154	0.311	13	0.123	R.LPANLVQAQR.D
R5/RRR5-6/2	1111.194	1110.292	-88.215	0.263	384.327	0.321	12	0.122	R.LPANLVQAQR.D
R5/RRR5-9/2	1215.221	1216.371	-1774.817	0.240	820.588	0.259	14	0.120	K.GWSLNLGELAR.I
R5/RRR5-10/2	1216.088	1216.371	-233.540	0.251	485.910	0.268	13	0.119	K.GWSLNLGELAR.I
R5/RRR5-8/2	1109.740	1110.292	-1402.349	0.254	204.835	0.308	10	0.116	-.LPANLVQAQR.-
R5/RRR5-9/2	1552.605	1553.697	-1351.608	0.335	866.555	0.183	17	0.115	K.VFQGDFSSNLPVDK.A
R5/RRR5-9/3	1998.256	1997.392	-68.331	0.463	1077.828	0.456	30	0.113	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/3	1997.346	1997.392	-23.093	0.395	1052.629	0.373	32	0.095	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/3	1998.995	1997.392	-199.165	0.359	959.416	0.327	30	0.082	R.IGLAGLAVMGQNLALNIAEK.G
R5/RRR5-9/3	1381.789	1381.566	161.777	0.512	901.366	0.343	22	0.077	-.DRLPANLVQAQR.-
R5/RRR5-9/3	1381.825	1381.566	187.823	0.490	799.141	0.298	20	0.072	-.DRLPANLVQAQR.-
R5/RRR5-9/3	1381.608	1381.566	30.200	0.443	870.165	0.267	22	0.071	-.DRLPANLVQAQR.-
R5/RRR5-8/3	1381.593	1381.566	19.698	0.402	954.249	0.156	22	0.061	-.DRLPANLVQAQR.-
R5/RRR5-8/3	1381.364	1381.566	-146.621	0.390	744.195	0.185	20	0.060	-.DRLPANLVQAQR.-
R5/RRR5-9/2	1619.173	1619.796	-1005.068	0.544	1924.503	0.486	25	0.251	K.FLNASVGFGGSCFQK.D
R5/RRR5-9/2	1619.410	1619.796	-238.733	0.545	1698.501	0.539	25	0.235	K.FLNASVGFGGSCFQK.D
R5/RRR5-8/2	1619.086	1619.796	-1059.191	0.557	1704.047	0.530	24	0.232	K.FLNASVGFGGSCFQK.D
R5/RRR5-1/2	1476.097	1476.699	-1088.635	0.439	1834.101	0.467	21	0.231	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1475.449	1476.699	-1529.419	0.398	1890.016	0.437	21	0.231	R.IITTNLWSAELSK.L
R5/RRR5-6/2	1476.300	1476.699	-271.247	0.454	1732.209	0.509	21	0.228	R.IITTNLWSAELSK.L
R5/RRR5-9/2	1476.391	1476.699	-209.448	0.519	1766.921	0.480	21	0.226	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1619.306	1619.796	-303.244	0.549	1631.115	0.538	24	0.225	K.FLNASVGFGGSCFQK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1355.097	1354.450	-260.722	0.569	1657.527	0.530	18	0.225	K.AADLTYWESAAR.M
R5/RRR5-2/2	1477.269	1476.699	-291.955	0.539	1708.687	0.505	21	0.225	R.IITTNLWSAELSK.L
R5/RRR5-4/2	1074.922	1075.246	-302.709	0.449	1813.781	0.436	17	0.222	K.LAANAFLAQR.I
R5/RRR5-9/2	1354.116	1354.450	-246.987	0.537	1680.907	0.474	18	0.215	K.AADLTYWESAAR.M
R5/RRR5-8/2	1354.070	1354.450	-281.355	0.508	1625.491	0.493	18	0.213	K.AADLTYWESAAR.M
R5/RRR5-7/2	1476.170	1476.699	-1038.733	0.443	1644.021	0.468	21	0.209	R.IITTNLWSAELSK.L
R5/RRR5-9/2	1074.284	1075.246	-1831.687	0.451	1693.161	0.433	17	0.207	K.LAANAFLAQR.I
R5/RRR5-8/2	1075.071	1075.246	-163.497	0.535	1639.867	0.450	17	0.205	K.LAANAFLAQR.I
R5/RRR5-9/2	1354.103	1354.450	-256.664	0.550	1675.207	0.437	18	0.205	K.AADLTYWESAAR.M
R5/RRR5-8/2	1074.553	1075.246	-1580.215	0.472	1677.480	0.423	17	0.203	K.LAANAFLAQR.I
R5/RRR5-8/2	1475.661	1476.699	-1385.162	0.408	1612.830	0.451	20	0.201	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1272.137	1272.453	-249.315	0.469	1333.490	0.560	20	0.197	R.VVSSM*FNTVSGK.K
R5/RRR5-8/2	1353.570	1354.450	-1393.055	0.441	1681.821	0.386	18	0.196	K.AADLTYWESAAR.M
R5/RRR5-7/2	1074.460	1075.246	-1667.639	0.438	1547.393	0.448	17	0.195	K.LAANAFLAQR.I
R5/RRR5-8/2	1074.960	1075.246	-267.276	0.527	1566.157	0.438	17	0.195	K.LAANAFLAQR.I
R5/RRR5-6/2	1074.919	1075.246	-304.646	0.471	1501.666	0.466	17	0.194	K.LAANAFLAQR.I
R5/RRR5-9/3	1683.228	1682.979	148.044	0.560	1528.389	0.536	27	0.191	K.CPAIEVVVVDISKPR.I
R5/RRR5-8/2	1353.551	1354.450	-1407.095	0.412	1675.144	0.365	18	0.191	K.AADLTYWESAAR.M
R5/RRR5-8/2	1257.208	1256.454	-196.198	0.461	1199.612	0.594	20	0.191	R.VVSSMFNTVSGK.K
R5/RRR5-9/2	1476.183	1476.699	-1030.098	0.441	1538.283	0.437	20	0.190	R.IITTNLWSAELSK.L
R5/RRR5-7/2	1075.308	1075.246	58.114	0.559	1551.985	0.422	17	0.189	K.LAANAFLAQR.I
R5/RRR5-9/2	1476.449	1476.699	-169.884	0.522	1470.343	0.459	20	0.188	R.IITTNLWSAELSK.L
R5/RRR5-6/2	1076.070	1075.246	-164.142	0.564	1332.082	0.502	17	0.186	K.LAANAFLAQR.I
R5/RRR5-1/2	1075.020	1075.246	-210.429	0.530	1452.243	0.444	17	0.185	K.LAANAFLAQR.I
R5/RRR5-3/2	1476.513	1476.699	-126.342	0.463	1497.571	0.428	20	0.185	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1271.962	1272.453	-387.768	0.372	1273.501	0.535	20	0.183	R.VVSSM*FNTVSGK.K
R5/RRR5-1/2	1476.508	1476.699	-129.908	0.485	1392.427	0.467	20	0.183	R.IITTNLWSAELSK.L
R5/RRR5-9/2	1272.172	1272.453	-222.168	0.427	1289.356	0.500	20	0.180	R.VVSSM*FNTVSGK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1074.482	1075.246	-1646.638	0.395	1470.615	0.411	17	0.179	K.LAANAFLAQR.I
R5/RRR5-7/2	1475.603	1476.699	-1424.961	0.368	1577.921	0.351	21	0.178	R.IITTNLWSAELSK.L
R5/RRR5-10/2	1074.736	1075.246	-1408.948	0.519	1343.183	0.454	16	0.177	K.LAANAFLAQR.I
R5/RRR5-5/2	1075.019	1075.246	-211.568	0.446	1420.489	0.399	17	0.174	K.LAANAFLAQR.I
R5/RRR5-9/2	1272.065	1272.453	-306.309	0.456	1108.264	0.532	19	0.172	R.VVSSM*FNTVSGK.K
R5/RRR5-9/3	1682.401	1682.979	-941.250	0.498	1466.174	0.500	28	0.170	K.CPAIEVVVVDISKPR.I
R5/RRR5-8/2	1272.006	1272.453	-352.622	0.438	977.129	0.543	18	0.163	R.VVSSM*FNTVSGK.K
R5/RRR5-6/2	1075.572	1075.246	304.208	0.444	1241.700	0.418	16	0.163	K.LAANAFLAQR.I
R5/RRR5-3/2	1476.320	1476.699	-257.476	0.399	1272.455	0.415	19	0.163	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1476.362	1476.699	-228.775	0.460	1248.807	0.419	19	0.162	R.IITTNLWSAELSK.L
R5/RRR5-7/2	1475.742	1476.699	-1330.246	0.361	1388.154	0.354	19	0.161	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1497.349	1496.646	-198.666	0.486	804.205	0.588	20	0.161	K.QVSVVWDAYEATK.G
R5/RRR5-6/2	1476.288	1476.699	-279.211	0.421	1185.470	0.409	19	0.156	R.IITTNLWSAELSK.L
R5/RRR5-2/2	1476.382	1476.699	-215.586	0.480	1147.687	0.410	18	0.153	R.IITTNLWSAELSK.L
R5/RRR5-6/2	1075.854	1075.246	-365.153	0.528	1113.077	0.406	16	0.153	K.LAANAFLAQR.I
R5/RRR5-1/2	1477.709	1476.699	6.909	0.507	964.382	0.476	18	0.153	R.IITTNLWSAELSK.L
R5/RRR5-11/2	1476.408	1476.699	-197.504	0.429	1240.514	0.362	19	0.152	R.IITTNLWSAELSK.L
R5/RRR5-1/2	1074.355	1075.246	-1765.239	0.380	1074.593	0.410	15	0.149	K.LAANAFLAQR.I
R5/RRR5-6/2	1475.989	1476.699	-1162.377	0.399	973.686	0.430	18	0.146	R.IITTNLWSAELSK.L
R5/RRR5-5/2	1074.895	1075.246	-327.092	0.394	693.825	0.516	13	0.144	K.LAANAFLAQR.I
R5/RRR5-10/2	1476.296	1476.699	-273.819	0.401	947.712	0.415	17	0.142	R.IITTNLWSAELSK.L
R5/RRR5-9/2	1497.238	1496.646	-273.424	0.418	781.296	0.464	19	0.141	K.QVSVVWDAYEATK.G
R5/RRR5-8/2	1069.525	1070.224	-1593.825	0.378	1000.046	0.374	14	0.139	R.NVVDPEKLR.E
R5/RRR5-9/2	1271.434	1272.453	-1593.002	0.264	963.409	0.411	18	0.139	R.VVSSM*FNTVSGK.K
R5/RRR5-8/2	1200.047	1200.322	-229.928	0.436	958.766	0.354	15	0.137	R.NLFFSTDVEK.H
R5/RRR5-9/2	1200.828	1200.322	-413.001	0.412	972.997	0.337	15	0.136	R.NLFFSTDVEK.H
R5/RRR5-3/2	1475.552	1476.699	-1459.446	0.340	861.915	0.375	17	0.134	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1401.831	1400.626	146.650	0.396	453.888	0.540	16	0.134	R.VVSSM*FNTVSGKK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1074.286	1075.246	-1830.203	0.350	788.551	0.351	16	0.132	K.LAANAFLAQR.I
R5/RRR5-8/2	1256.025	1256.454	-342.602	0.303	710.353	0.390	16	0.129	R.VVSSMFNTVSGK.K
R5/RRR5-9/2	1201.051	1200.322	-226.779	0.399	839.474	0.325	14	0.129	R.NLFFSTDVEK.H
R5/RRR5-9/3	1801.394	1802.046	-920.013	0.501	1039.546	0.530	28	0.128	R.IFDNM*QKPAFVFDGR.N
R5/RRR5-4/2	1074.940	1075.246	-285.163	0.267	286.018	0.378	12	0.127	K.LAANAFLAQR.I
R5/RRR5-10/2	1476.496	1476.699	-138.202	0.365	679.150	0.353	15	0.127	R.IITTNLWSAELSK.L
R5/RRR5-8/3	1801.935	1802.046	-61.835	0.440	940.954	0.556	26	0.125	R.IFDNM*QKPAFVFDGR.N
R5/RRR5-8/3	1802.068	1802.046	11.853	0.474	1055.766	0.511	25	0.125	R.IFDNM*QKPAFVFDGR.N
R5/RRR5-8/2	1200.305	1200.322	-14.751	0.302	839.647	0.275	14	0.124	R.NLFFSTDVEK.H
R5/RRR5-15/2	1076.129	1075.246	-108.952	0.279	552.778	0.300	13	0.123	K.LAANAFLAQR.I
R5/RRR5-1/2	1475.837	1476.699	-1265.617	0.248	568.319	0.270	16	0.121	R.IITTNLWSAELSK.L
R5/RRR5-8/2	1199.696	1200.322	-1359.350	0.305	825.138	0.214	14	0.119	R.NLFFSTDVEK.H
R5/RRR5-9/3	1802.310	1802.046	146.665	0.532	917.041	0.531	28	0.119	R.IFDNM*QKPAFVFDGR.N
R5/RRR5-1/2	1353.637	1354.450	-1343.239	0.192	716.697	0.121	13	0.112	K.AADLTYWESAAR.M
R5/RRR5-9/3	1802.082	1802.046	19.904	0.497	733.097	0.548	26	0.112	R.IFDNM*QKPAFVFDGR.N
R5/RRR5-9/3	1786.707	1786.047	-191.067	0.511	800.811	0.521	27	0.110	R.IFDNMQKPAFVFDGR.N
R5/RRR5-9/3	1786.390	1786.047	192.921	0.484	785.613	0.526	27	0.110	R.IFDNMQKPAFVFDGR.N
R5/RRR5-8/3	1801.195	1802.046	-1030.846	0.382	722.738	0.486	24	0.098	R.IFDNM*QKPAFVFDGR.N
R5/RRR5-8/3	1842.534	1842.085	244.090	0.448	1134.269	0.378	23	0.098	K.HVAEADIIFVSVNTPTK.T
R5/RRR5-6/2	1582.593	1582.844	-158.644	0.507	843.661	0.364	20	0.132	K.QFSAEEISSMVLIK.M
R5/RRR5-6/2	1598.526	1598.843	-198.666	0.404	494.697	0.351	16	0.120	-.QFSAEEISSM*VLIK.-
R5/RRR5-2/3	1802.370	1803.135	-982.669	0.525	2687.610	0.391	34	0.386	R.HVEPPLSALLELDKLK.V
R5/RRR5-2/2	1646.618	1646.909	-177.385	0.530	2049.401	0.540	23	0.284	R.LDQPIILTGYSALNK.L
R5/RRR5-2/2	1646.450	1646.909	-279.579	0.512	2016.745	0.497	23	0.267	R.LDQPIILTGYSALNK.L
R5/RRR5-2/2	1282.249	1281.483	-183.200	0.497	1807.112	0.484	18	0.234	K.IIEEGPVTVAPR.E
R5/RRR5-2/2	1280.655	1281.483	-1432.120	0.323	1835.666	0.458	18	0.229	K.IIEEGPVTVAPR.E
R5/RRR5-1/2	1646.259	1646.909	-1005.563	0.503	1738.192	0.500	22	0.228	R.LDQPIILTGYSALNK.L
R5/RRR5-1/2	1646.399	1646.909	-919.807	0.458	1737.360	0.430	22	0.212	R.LDQPIILTGYSALNK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1802.520	1803.135	-898.631	0.561	1892.476	0.405	32	0.203	R.HVEPPLSALLELDKLK.V
R5/RRR5-1/2	1281.253	1281.483	-179.902	0.427	1633.181	0.416	17	0.197	K.IIEEGPVTVAPR.E
R5/RRR5-2/2	1281.066	1281.483	-326.634	0.387	1477.174	0.454	18	0.188	K.IIEEGPVTVAPR.E
R5/RRR5-2/2	1205.079	1205.216	-113.651	0.414	1706.803	0.314	18	0.185	R.VGWSDDGSPER.G
R5/RRR5-2/2	1646.057	1646.909	-1128.639	0.487	1380.092	0.484	20	0.184	R.LDQPIILTGYSALNK.L
R5/RRR5-2/2	1906.010	1905.095	-44.748	0.553	1121.396	0.591	23	0.181	K.TVTANTATVSDYVGYLTK.G
R5/RRR5-2/2	1726.434	1727.019	-920.710	0.425	1468.446	0.425	18	0.179	R.SLMTAIEELELHAIR.T
R5/RRR5-1/2	1905.447	1905.095	185.275	0.571	908.942	0.653	21	0.175	K.TVTANTATVSDYVGYLTK.G
R5/RRR5-2/2	1905.333	1905.095	125.139	0.516	1079.977	0.579	22	0.174	K.TVTANTATVSDYVGYLTK.G
R5/RRR5-1/2	1904.850	1905.095	-129.170	0.516	1008.074	0.592	22	0.171	K.TVTANTATVSDYVGYLTK.G
R5/RRR5-1/2	1280.951	1281.483	-1199.810	0.362	1208.076	0.449	16	0.162	K.IIEEGPVTVAPR.E
R5/RRR5-1/2	1430.130	1429.691	307.895	0.442	1118.979	0.452	16	0.157	R.EGLPLFILANWR.-
R5/RRR5-2/3	1802.619	1803.135	-843.973	0.524	1518.421	0.436	30	0.156	R.HVEPPLSALLELDKLK.V
R5/RRR5-2/2	1904.299	1905.095	-946.073	0.496	832.055	0.555	21	0.154	K.TVTANTATVSDYVGYLTK.G
R5/RRR5-1/2	1021.133	1021.195	-60.444	0.416	997.745	0.378	16	0.142	R.TVGIGAYLAR.L
R5/RRR5-1/3	1802.408	1803.135	-961.352	0.523	1462.238	0.405	29	0.139	R.HVEPPLSALLELDKLK.V
R5/RRR5-1/2	1430.634	1429.691	-39.420	0.465	982.421	0.362	16	0.136	R.EGLPLFILANWR.-
R5/RRR5-2/2	1180.956	1181.357	-340.949	0.276	759.394	0.441	15	0.131	K.VVEFCTALGGK.T
R5/RRR5-1/2	1711.525	1710.935	-240.263	0.419	1003.700	0.325	18	0.129	K.FDSGIINDFPANMLR.V
R5/RRR5-3/2	1905.222	1905.095	66.924	0.390	294.626	0.486	16	0.127	K.TVTANTATVSDYVGYLTK.G
R5/RRR5-1/2	1180.836	1181.357	-1292.306	0.319	599.707	0.406	14	0.126	K.VVEFCTALGGK.T
R5/RRR5-2/2	994.120	994.123	-3.093	0.366	862.251	0.285	14	0.125	K.ATELVFADK.H
R5/RRR5-2/2	1208.221	1207.466	-203.443	0.350	827.188	0.333	15	0.124	R.SAAITTM*ALALK.E
R5/RRR5-2/2	1957.085	1955.149	-33.133	0.498	622.612	0.443	15	0.124	-.TTYCYDFPLAFETAVR.-
R5/RRR5-1/2	1645.776	1646.909	-1299.864	0.306	804.182	0.298	17	0.122	R.LDQPIILTGYSALNK.L
R5/RRR5-2/2	1204.789	1205.216	-355.648	0.342	1311.794	0.097	17	0.122	R.VGWSDDGSPER.G
R5/RRR5-2/2	1106.951	1107.307	-321.712	0.382	1043.298	0.183	15	0.119	K.SLESLSMAIR.F
R5/RRR5-1/2	1204.784	1205.216	-359.307	0.329	1312.185	0.061	17	0.118	R.VGWSDDGSPER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1020.900	1021.195	-289.404	0.206	541.926	0.285	12	0.115	R.TVGIGAYLAR.L
R5/RRR5-1/3	1802.214	1803.135	-1069.577	0.491	1032.826	0.440	28	0.108	R.HVEPPLSALLELDKLK.V
R5/RRR5-2/3	1904.808	1905.095	-151.259	0.390	815.919	0.457	24	0.090	K.TVTANTATVSDYVGYLTK.G
R5/RRR5-2/2	1805.044	1806.059	-1119.647	0.498	2354.936	0.584	26	0.354	R.HNEAALGTVNQLVAVLR.L
R5/RRR5-2/2	1887.918	1886.184	-141.743	0.586	2388.518	0.555	24	0.349	R.LLAALALGDLFQNEGLAR.S
R5/RRR5-2/2	1805.542	1806.059	-842.667	0.589	2201.112	0.644	26	0.345	R.HNEAALGTVNQLVAVLR.L
R5/RRR5-2/2	1938.637	1939.113	-246.347	0.505	2422.730	0.505	23	0.339	K.TGSEATQEAALDSLYLLR.Q
R5/RRR5-2/2	1155.108	1155.372	-229.545	0.418	1729.585	0.463	16	0.219	R.LIEALLNNVR.I
R5/RRR5-2/2	1155.164	1155.372	-180.991	0.486	1796.848	0.414	17	0.217	R.LIEALLNNVR.I
R5/RRR5-2/2	1155.144	1155.372	-197.952	0.524	1585.858	0.481	17	0.208	R.LIEALLNNVR.I
R5/RRR5-2/2	1216.205	1216.414	-172.309	0.538	1516.037	0.467	17	0.196	K.ALNALLSNFPR.L
R5/RRR5-2/2	1786.773	1786.087	-176.354	0.474	1181.034	0.512	21	0.170	R.QAIQPLVEILSTGMER.E
R5/RRR5-1/2	960.089	960.112	-23.288	0.414	1220.709	0.315	13	0.146	K.APFLVQER.V
R5/RRR5-2/2	960.130	960.112	18.923	0.438	1060.075	0.366	13	0.145	K.APFLVQER.V
R5/RRR5-2/2	960.056	960.112	-58.614	0.415	1137.616	0.307	13	0.140	K.APFLVQER.V
R5/RRR5-2/2	1806.306	1806.089	120.002	0.368	1108.596	0.373	18	0.140	R.VIEALASLYSNPVLCR.T
R5/RRR5-2/2	959.894	960.112	-227.248	0.430	1160.797	0.290	13	0.139	K.APFLVQER.V
R5/RRR5-2/2	1233.927	1233.399	-383.466	0.477	656.543	0.441	17	0.138	K.LLGPGNETYIR.A
R5/RRR5-2/2	1937.704	1939.113	-1246.959	0.335	1105.562	0.355	18	0.137	K.TGSEATQEAALDSLYLLR.Q
R5/RRR5-2/2	1902.509	1903.210	-897.023	0.434	722.837	0.482	19	0.136	K.IFSTENVVPVLWEQLK.V
R5/RRR5-2/2	1567.317	1567.857	-985.670	0.344	1058.342	0.327	19	0.134	K.ALANLALAWPNTIAK.E
R5/RRR5-2/2	1568.000	1567.857	91.702	0.410	886.119	0.395	17	0.133	K.ALANLALAWPNTIAK.E
R5/RRR5-2/2	1705.683	1705.983	-176.483	0.461	582.733	0.478	17	0.132	R.SNAALHSIPVLSNLLR.S
R5/RRR5-2/2	1231.308	1231.509	-163.335	0.294	653.870	0.459	16	0.131	K.VVQPLFSLLSK.A
R5/RRR5-1/2	959.848	960.112	-275.731	0.382	1136.129	0.216	13	0.129	K.APFLVQER.V
R5/RRR5-2/2	921.903	921.115	-230.902	0.386	794.568	0.312	13	0.128	K.VYVLDALK.S
R5/RRR5-1/2	1234.156	1233.399	-197.184	0.376	377.921	0.370	14	0.126	K.LLGPGNETYIR.A
R5/RRR5-1/2	1155.131	1155.372	-209.614	0.311	696.945	0.334	13	0.124	R.LIEALLNNVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1706.222	1705.983	140.747	0.387	539.331	0.402	15	0.122	R.SNAALHSIPVLSNLLR.S
R5/RRR5-1/2	1233.181	1233.399	-177.285	0.346	565.361	0.271	16	0.122	K.LLGPGNETYIR.A
R5/RRR5-2/2	1231.146	1231.509	-295.823	0.248	373.780	0.350	13	0.119	K.VVQPLFSLLSK.A
R5/RRR5-2/2	920.353	921.115	-1920.133	0.277	597.752	0.297	12	0.118	-.VYVLDALK.-
R5/RRR5-2/2	920.880	921.115	-256.819	0.283	479.612	0.311	11	0.109	-.VYVLDALK.-
R5/RRR5-2/3	1805.635	1806.059	-235.783	0.423	1242.685	0.253	27	0.083	R.HNEAALGTVNQLVAVLR.L
R5/RRR5-2/3	1806.395	1806.059	186.141	0.355	559.509	0.253	21	0.047	-.HNEAALGTVNQLVAVLR.-
R5/RRR5-6/2	1941.384	1940.214	87.939	0.614	3392.481	0.569	30	0.594	K.GVNPDEAVAMGAAIQGGILR.G
R5/RRR5-6/2	1812.673	1813.042	-204.567	0.552	3195.604	0.591	27	0.556	K.IPAEVATEIETAIADLR.S
R5/RRR5-6/2	1955.586	1956.213	-834.611	0.553	3164.383	0.564	29	0.530	K.GVNPDEAVAM*GAAIQGGILR.G
R5/RRR5-6/2	1941.641	1940.214	220.476	0.589	2919.935	0.550	28	0.461	K.GVNPDEAVAMGAAIQGGILR.G
R5/RRR5-6/2	1956.713	1956.213	256.008	0.601	2845.989	0.565	28	0.449	K.GVNPDEAVAM*GAAIQGGILR.G
R5/RRR5-6/2	1939.419	1940.214	-928.120	0.542	2827.287	0.552	28	0.441	K.GVNPDEAVAMGAAIQGGILR.G
R5/RRR5-6/2	1822.279	1822.957	-923.482	0.488	1920.998	0.507	22	0.254	K.SQVFSTAADNQTQVGIR.V
R5/RRR5-6/2	1522.123	1522.728	-1057.728	0.497	1762.571	0.562	20	0.248	R.SKFESLVNSLIER.T
R5/RRR5-6/2	1460.824	1461.515	-1160.949	0.517	1572.649	0.604	21	0.233	K.APNGDAWVETTDGK.Q
R5/RRR5-6/2	1777.343	1777.956	-910.251	0.541	1581.999	0.589	25	0.231	R.IINEPTAAALSYGTNNK.E
R5/RRR5-6/2	1777.214	1777.956	-983.619	0.561	1543.989	0.585	24	0.224	R.IINEPTAAALSYGTNNK.E
R5/RRR5-6/2	1522.957	1522.728	150.850	0.479	1739.708	0.462	20	0.220	R.SKFESLVNSLIER.T
R5/RRR5-6/2	1461.074	1461.515	-303.236	0.536	1497.745	0.584	20	0.219	K.APNGDAWVETTDGK.Q
R5/RRR5-6/2	1777.279	1777.956	-946.727	0.516	1426.076	0.579	23	0.209	R.IINEPTAAALSYGTNNK.E
R5/RRR5-6/2	1355.053	1355.433	-281.242	0.478	1585.090	0.439	19	0.198	R.NNADTTIYSVEK.S
R5/RRR5-6/2	1354.968	1355.433	-343.608	0.474	1444.084	0.453	18	0.186	R.NNADTTIYSVEK.S
R5/RRR5-6/2	1249.205	1249.438	-186.968	0.568	1266.070	0.512	18	0.183	K.VQEIVSEIFGK.S
R5/RRR5-6/2	1248.711	1249.438	-1387.374	0.517	1294.481	0.493	18	0.181	K.VQEIVSEIFGK.S
R5/RRR5-6/2	1354.955	1355.433	-353.552	0.480	1313.272	0.435	18	0.171	R.NNADTTIYSVEK.S
R5/RRR5-6/2	1205.955	1206.285	-274.387	0.542	1311.876	0.354	19	0.155	R.SSGGLSEAEIQK.M
R5/RRR5-6/2	1540.233	1539.757	309.653	0.478	544.454	0.520	19	0.140	K.QYSPSQIGAFVLTK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1206.025	1206.285	-216.606	0.473	1048.546	0.327	17	0.136	R.SSGGLSEAEIQK.M
R5/RRR5-6/2	1205.345	1206.285	-1614.441	0.436	973.548	0.343	17	0.135	R.SSGGLSEAEIQK.M
R5/RRR5-6/2	1778.902	1777.956	-30.808	0.441	568.630	0.484	19	0.134	R.IINEPTAAALSYGTNNK.E
R5/RRR5-6/2	1553.163	1553.701	-993.312	0.409	364.111	0.515	15	0.129	R.QAVTNPQNTFFGTK.R
R5/RRR5-6/2	1540.952	1539.757	126.921	0.415	324.342	0.441	16	0.127	K.QYSPSQIGAFVLTK.M
R5/RRR5-6/3	1954.906	1956.213	-1183.697	0.384	1257.888	0.395	28	0.113	K.GVNPDEAVAM*GAAIQGGILR.G
R5/RRR5-9/2	993.957	994.276	-321.797	0.431	1043.617	0.078	13	0.109	K.M*VPYKIVK.A
R5/RRR5-6/3	1522.595	1522.728	-87.628	0.531	1357.432	0.320	26	0.108	R.SKFESLVNSLIER.T
R5/RRR5-6/3	1522.643	1522.728	-56.265	0.541	1012.405	0.353	24	0.090	R.SKFESLVNSLIER.T
R5/RRR5-8/2	1296.235	1296.501	-205.687	0.519	1840.208	0.591	21	0.267	K.VVAAGANPVQITR.G
R5/RRR5-7/2	1296.056	1296.501	-344.112	0.503	1831.889	0.567	21	0.259	K.VVAAGANPVQITR.G
R5/RRR5-7/2	1296.119	1296.501	-295.919	0.511	1787.406	0.572	21	0.254	K.VVAAGANPVQITR.G
R5/RRR5-8/2	1183.439	1183.423	13.800	0.480	1946.413	0.462	20	0.248	K.LADLVGVTLGPK.G
R5/RRR5-8/2	1297.256	1296.501	-189.197	0.549	1675.643	0.593	20	0.244	K.VVAAGANPVQITR.G
R5/RRR5-7/2	1296.201	1296.501	-232.330	0.514	1699.329	0.567	20	0.241	K.VVAAGANPVQITR.G
R5/RRR5-8/2	1296.216	1296.501	-220.237	0.534	1593.817	0.589	20	0.233	K.VVAAGANPVQITR.G
R5/RRR5-7/2	1183.529	1183.423	90.146	0.467	1789.873	0.449	19	0.224	K.LADLVGVTLGPK.G
R5/RRR5-7/2	1284.691	1285.472	-1390.261	0.464	1667.650	0.484	17	0.216	R.DLINVLEEAIR.G
R5/RRR5-7/2	1285.071	1285.472	-312.850	0.442	1581.760	0.479	17	0.205	R.DLINVLEEAIR.G
R5/RRR5-7/2	1088.174	1088.240	-61.052	0.467	1356.504	0.490	17	0.185	R.KGVVTLEEGR.S
R5/RRR5-7/2	1285.060	1285.472	-321.046	0.454	1480.900	0.412	17	0.181	R.DLINVLEEAIR.G
R5/RRR5-7/2	1284.482	1285.472	-1553.484	0.312	1598.494	0.323	17	0.174	R.DLINVLEEAIR.G
R5/RRR5-7/2	1542.415	1542.670	-165.793	0.502	1460.207	0.380	22	0.173	R.EVELEDPVENIGAK.L
R5/RRR5-8/2	1321.056	1321.504	-340.288	0.426	1252.341	0.439	17	0.166	-.NVVLESKYGSPK.-
R5/RRR5-7/2	1506.242	1506.638	-263.091	0.398	1169.806	0.454	20	0.162	R.GYISPYFVTDSEK.M
R5/RRR5-7/2	1043.427	1044.187	-1691.421	0.441	1083.786	0.442	17	0.157	K.IVNDGVTVAR.E
R5/RRR5-7/2	1507.056	1506.638	278.205	0.438	1064.702	0.460	19	0.156	R.GYISPYFVTDSEK.M
R5/RRR5-8/2	1542.316	1542.670	-230.106	0.463	1330.552	0.335	21	0.154	R.EVELEDPVENIGAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1284.188	1285.472	-1783.995	0.341	1391.529	0.291	16	0.152	R.DLINVLEEAIR.G
R5/RRR5-7/2	1542.102	1542.670	-1019.332	0.482	1257.832	0.351	20	0.151	R.EVELEDPVENIGAK.L
R5/RRR5-7/2	1937.623	1938.040	-215.892	0.524	796.307	0.563	20	0.150	K.ESTTIVGDGSTQEEVTKR.V
R5/RRR5-8/2	1284.819	1285.472	-1290.445	0.465	1233.504	0.346	16	0.149	R.DLINVLEEAIR.G
R5/RRR5-7/2	1284.960	1285.472	-1179.773	0.354	1144.972	0.361	16	0.146	R.DLINVLEEAIR.G
R5/RRR5-7/2	1043.480	1044.187	-1640.999	0.408	1093.521	0.352	17	0.144	K.IVNDGVTVAR.E
R5/RRR5-7/2	1505.944	1506.638	-1127.792	0.271	1020.914	0.421	19	0.143	R.GYISPYFVTDSEK.M
R5/RRR5-7/2	1176.041	1175.274	-199.016	0.441	781.927	0.484	15	0.143	K.NAGVNGSVVTEK.V
R5/RRR5-7/2	1176.038	1175.274	-201.411	0.455	840.527	0.454	16	0.143	K.NAGVNGSVVTEK.V
R5/RRR5-7/2	1542.290	1542.670	-246.622	0.482	1385.304	0.247	21	0.142	R.EVELEDPVENIGAK.L
R5/RRR5-7/2	1043.411	1044.187	-1706.936	0.392	873.830	0.430	16	0.142	K.IVNDGVTVAR.E
R5/RRR5-7/2	1175.009	1175.274	-226.283	0.459	823.902	0.416	17	0.139	K.NAGVNGSVVTEK.V
R5/RRR5-7/2	959.228	960.067	-1922.410	0.460	942.206	0.342	14	0.136	K.GVVTLEEGR.S
R5/RRR5-7/2	1175.957	1175.274	-270.558	0.425	600.367	0.425	15	0.131	K.NAGVNGSVVTEK.V
R5/RRR5-7/2	959.395	960.067	-1747.749	0.415	854.344	0.329	13	0.130	K.GVVTLEEGR.S
R5/RRR5-8/2	1182.657	1183.423	-1497.680	0.314	774.689	0.395	15	0.130	K.LADLVGVTLGPK.G
R5/RRR5-8/2	1183.006	1183.423	-352.985	0.279	1149.715	0.235	17	0.130	K.LADLVGVTLGPK.G
R5/RRR5-8/2	1230.266	1230.396	-106.348	0.375	768.802	0.368	14	0.128	K.LRVEDALNATK.A
R5/RRR5-7/2	959.834	960.067	-243.782	0.320	681.601	0.328	13	0.125	K.GVVTLEEGR.S
R5/RRR5-8/2	1285.299	1285.472	-135.136	0.328	503.298	0.297	15	0.124	R.DLINVLEEAIR.G
R5/RRR5-10/2	1284.484	1285.472	-1552.147	0.237	670.397	0.191	15	0.117	R.DLINVLEEAIR.G
R5/RRR5-8/2	1505.691	1506.638	-1296.956	0.152	521.303	0.254	15	0.114	R.GYISPYFVTDSEK.M
R5/RRR5-8/2	1505.604	1506.638	-1354.606	0.156	550.536	0.245	14	0.113	-.GYISPYFVTDSEK.-
R5/RRR5-7/2	1230.195	1230.396	-164.478	0.379	675.064	0.187	14	0.113	-.LRVEDALNATK.-
R5/RRR5-8/2	1284.925	1285.472	-1207.439	0.193	603.185	0.180	11	0.110	-.DLINVLEEAIR.-
R5/RRR5-9/2	1968.445	1968.196	126.911	0.628	3430.357	0.546	27	0.595	K.EYVFVANSDNLGAIVDIK.I
R5/RRR5-9/2	1967.548	1968.196	-839.867	0.583	3198.654	0.536	26	0.528	K.EYVFVANSDNLGAIVDIK.I
R5/RRR5-9/2	1967.548	1968.196	-840.053	0.570	3119.509	0.511	26	0.497	K.EYVFVANSDNLGAIVDIK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1476.186	1476.704	-1031.755	0.511	2766.416	0.355	20	0.354	K.IFNTNNLWVNLK.A
R5/RRR5-2/2	1477.647	1476.704	-38.911	0.513	2265.031	0.396	19	0.276	K.IFNTNNLWVNLK.A
R5/RRR5-8/2	1477.606	1476.704	-66.920	0.563	2182.601	0.426	18	0.270	K.IFNTNNLWVNLK.A
R5/RRR5-9/2	1314.247	1313.528	-214.420	0.510	2023.989	0.501	20	0.269	K.VLQLETAAGAAIR.F
R5/RRR5-8/2	1477.521	1476.704	-124.101	0.555	2033.427	0.390	18	0.237	K.IFNTNNLWVNLK.A
R5/RRR5-7/2	1312.863	1313.528	-1272.299	0.453	1968.982	0.406	19	0.236	K.VLQLETAAGAAIR.F
R5/RRR5-9/2	1476.162	1476.704	-1047.946	0.499	1968.141	0.347	19	0.220	K.IFNTNNLWVNLK.A
R5/RRR5-9/2	1452.291	1452.636	-238.468	0.534	1651.933	0.501	21	0.218	K.VSGDVWFGSGVTLK.G
R5/RRR5-8/2	1452.343	1452.636	-202.715	0.472	1720.075	0.424	22	0.209	K.VSGDVWFGSGVTLK.G
R5/RRR5-9/2	1359.253	1359.592	-250.647	0.442	1890.467	0.299	20	0.201	R.IVTEDFLPLPSK.G
R5/RRR5-9/2	1359.298	1359.592	-217.492	0.469	1786.369	0.350	20	0.200	R.IVTEDFLPLPSK.G
R5/RRR5-8/2	1453.904	1452.636	184.542	0.519	1533.712	0.483	20	0.200	K.VSGDVWFGSGVTLK.G
R5/RRR5-9/2	1476.347	1476.704	-242.793	0.511	1788.185	0.327	18	0.192	K.IFNTNNLWVNLK.A
R5/RRR5-8/2	1477.415	1476.704	-196.375	0.555	1498.624	0.410	18	0.180	K.IFNTNNLWVNLK.A
R5/RRR5-9/2	1477.188	1476.704	328.754	0.509	1454.948	0.327	18	0.161	K.IFNTNNLWVNLK.A
R5/RRR5-8/2	1453.156	1452.636	-331.682	0.481	1201.166	0.438	19	0.161	K.VSGDVWFGSGVTLK.G
R5/RRR5-9/2	1630.220	1630.780	-960.104	0.449	581.726	0.585	19	0.147	R.TNPSNPSIELGPEFK.K
R5/RRR5-8/2	1758.310	1758.953	-937.164	0.486	550.614	0.580	19	0.145	R.TNPSNPSIELGPEFKK.V
R5/RRR5-7/2	1477.858	1476.704	104.254	0.424	1275.332	0.298	17	0.145	K.IFNTNNLWVNLK.A
R5/RRR5-9/2	1630.276	1630.780	-925.224	0.440	561.829	0.560	19	0.143	R.TNPSNPSIELGPEFK.K
R5/RRR5-9/2	1359.330	1359.592	-193.348	0.412	1297.604	0.275	17	0.143	R.IVTEDFLPLPSK.G
R5/RRR5-9/2	1758.423	1758.953	-872.907	0.459	461.362	0.570	18	0.140	R.TNPSNPSIELGPEFKK.V
R5/RRR5-9/2	1758.455	1758.953	-284.331	0.439	475.117	0.549	18	0.138	R.TNPSNPSIELGPEFKK.V
R5/RRR5-8/2	1316.055	1315.538	-368.188	0.342	379.966	0.571	18	0.137	K.SIPSIVELDTLK.V
R5/RRR5-8/2	1630.618	1630.780	-99.910	0.430	508.883	0.482	19	0.135	R.TNPSNPSIELGPEFK.K
R5/RRR5-9/2	1629.770	1630.780	-1237.130	0.384	603.866	0.476	19	0.135	R.TNPSNPSIELGPEFK.K
R5/RRR5-9/2	790.870	790.933	-79.745	0.447	743.097	0.368	11	0.134	K.VANFLAR.F
R5/RRR5-8/2	1758.380	1758.953	-897.089	0.403	494.304	0.512	18	0.134	R.TNPSNPSIELGPEFKK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	839.390	840.006	-1930.230	0.348	624.653	0.428	13	0.134	K.AIGINVPR.S
R5/RRR5-8/2	1313.377	1313.528	-115.467	0.381	920.233	0.356	17	0.134	K.VLQLETAAGAAIR.F
R5/RRR5-8/2	1359.100	1359.592	-363.464	0.321	1058.429	0.293	17	0.133	R.IVTEDFLPLPSK.G
R5/RRR5-9/2	790.386	790.933	-1962.846	0.393	762.998	0.353	11	0.133	K.VANFLAR.F
R5/RRR5-8/2	790.540	790.933	-498.256	0.398	652.994	0.365	11	0.132	K.VANFLAR.F
R5/RRR5-8/2	839.878	840.006	-152.209	0.398	506.339	0.394	12	0.132	K.AIGINVPR.S
R5/RRR5-8/2	790.765	790.933	-213.687	0.371	618.966	0.365	11	0.131	K.VANFLAR.F
R5/RRR5-9/2	790.908	790.933	-31.907	0.430	598.693	0.336	11	0.130	K.VANFLAR.F
R5/RRR5-9/2	839.423	840.006	-1891.065	0.333	429.311	0.411	11	0.129	K.AIGINVPR.S
R5/RRR5-8/2	790.438	790.933	-628.590	0.378	529.332	0.334	10	0.128	K.VANFLAR.F
R5/RRR5-8/2	839.975	840.006	-36.311	0.353	504.249	0.316	12	0.126	K.AIGINVPR.S
R5/RRR5-8/2	840.201	840.006	232.995	0.339	530.640	0.314	12	0.125	K.AIGINVPR.S
R5/RRR5-9/2	791.716	790.933	-274.670	0.281	470.056	0.328	10	0.124	K.VANFLAR.F
R5/RRR5-9/2	1315.239	1315.538	-227.570	0.251	363.982	0.400	17	0.123	K.SIPSIVELDTLK.V
R5/RRR5-9/2	1314.956	1315.538	-1206.399	0.226	285.434	0.418	16	0.121	K.SIPSIVELDTLK.V
R5/RRR5-18/2	1312.344	1313.528	-1669.497	0.363	495.705	0.243	15	0.118	K.VLQLETAAGAAIR.F
R5/RRR5-8/2	1358.582	1359.592	-1484.345	0.248	807.151	0.149	14	0.114	-.IVTEDFLPLPSK.-
R5/RRR5-1/2	1312.788	1313.528	-1329.449	0.341	386.388	0.292	14	0.114	-.VLQLETAAGAAIR.-
R5/RRR5-9/2	1359.403	1359.592	-139.658	0.238	646.897	0.146	13	0.112	-.IVTEDFLPLPSK.-
R5/RRR5-8/3	1812.062	1812.164	-56.427	0.282	1232.024	0.240	25	0.078	R.LVEAEALKM*EIIPNPK.E
R5/RRR5-12/2	1747.459	1748.146	-968.277	0.525	2381.057	0.563	28	0.349	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-12/2	1747.638	1748.146	-865.403	0.546	2193.643	0.545	25	0.307	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-12/2	1747.316	1748.146	-1050.410	0.436	2087.931	0.490	25	0.275	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-13/2	1748.634	1748.146	279.891	0.554	2004.589	0.541	24	0.274	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-13/2	1746.926	1748.146	-1274.502	0.380	2119.244	0.432	26	0.264	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-13/2	1470.195	1469.649	-309.683	0.479	1707.663	0.609	22	0.250	K.AGAGSATLSMAYAAAR.F
R5/RRR5-13/3	1747.848	1748.146	-171.077	0.527	1936.984	0.483	37	0.246	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-12/2	1348.258	1348.616	-266.495	0.547	1887.551	0.474	20	0.242	K.KLFGVTTLDVVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/3	1982.802	1983.123	-162.322	0.471	1975.006	0.427	31	0.242	-.TRPSVTFTNEETEELTK.-
R5/RRR5-12/2	1348.425	1348.616	-142.248	0.511	1932.499	0.427	20	0.237	K.KLFGVTTLDVVR.A
R5/RRR5-13/2	1747.681	1748.146	-267.098	0.544	1793.976	0.511	26	0.236	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-13/2	1469.355	1469.649	-200.368	0.482	1615.617	0.536	22	0.221	K.AGAGSATLSMAYAAAR.F
R5/RRR5-13/2	1349.325	1348.616	-216.196	0.575	1732.525	0.456	20	0.217	K.KLFGVTTLDVVR.A
R5/RRR5-13/2	1348.258	1348.616	-266.131	0.506	1721.319	0.450	20	0.215	K.KLFGVTTLDVVR.A
R5/RRR5-12/2	1348.178	1348.616	-325.904	0.524	1712.269	0.432	20	0.210	K.KLFGVTTLDVVR.A
R5/RRR5-13/2	1348.313	1348.616	-225.439	0.515	1669.148	0.452	20	0.210	K.KLFGVTTLDVVR.A
R5/RRR5-13/2	1485.242	1485.648	-274.094	0.466	1425.838	0.479	22	0.187	K.AGAGSATLSM*AYAAAR.F
R5/RRR5-13/2	1277.665	1278.526	-1460.482	0.323	1522.568	0.429	19	0.185	K.GVDVVVIPAGVPR.K
R5/RRR5-13/2	1349.146	1349.514	-273.670	0.515	1663.511	0.305	19	0.176	R.DDLFNINASIVK.S
R5/RRR5-13/2	1278.146	1278.526	-297.685	0.387	1419.699	0.408	19	0.174	K.GVDVVVIPAGVPR.K
R5/RRR5-13/2	1469.227	1469.649	-287.886	0.479	1194.253	0.516	20	0.173	K.AGAGSATLSMAYAAAR.F
R5/RRR5-13/2	1485.231	1485.648	-281.598	0.474	1235.501	0.444	21	0.164	K.AGAGSATLSM*AYAAAR.F
R5/RRR5-13/2	1259.096	1259.391	-234.995	0.495	1032.502	0.503	19	0.163	R.IQNAGTEVVEAK.A
R5/RRR5-13/2	1349.233	1349.514	-209.405	0.536	1391.672	0.349	18	0.160	R.DDLFNINASIVK.S
R5/RRR5-13/2	1220.215	1220.443	-187.497	0.547	1286.210	0.377	19	0.159	K.LFGVTTLDVVR.A
R5/RRR5-13/2	1259.430	1259.391	30.953	0.498	991.112	0.492	19	0.159	R.IQNAGTEVVEAK.A
R5/RRR5-12/2	1220.081	1220.443	-297.301	0.505	1334.421	0.337	19	0.156	K.LFGVTTLDVVR.A
R5/RRR5-13/2	1259.099	1259.391	-233.147	0.511	907.701	0.499	18	0.155	R.IQNAGTEVVEAK.A
R5/RRR5-13/2	1485.136	1485.648	-1020.949	0.426	1044.963	0.473	19	0.154	K.AGAGSATLSM*AYAAAR.F
R5/RRR5-13/2	1220.130	1220.443	-257.150	0.518	1261.714	0.345	19	0.153	K.LFGVTTLDVVR.A
R5/RRR5-12/2	1259.346	1259.391	-35.643	0.501	941.939	0.451	19	0.150	R.IQNAGTEVVEAK.A
R5/RRR5-13/2	1277.595	1278.526	-1515.955	0.320	1209.044	0.372	17	0.149	K.GVDVVVIPAGVPR.K
R5/RRR5-13/3	1982.774	1983.123	-176.403	0.528	1482.162	0.423	30	0.149	K.TRPSVTFTNEETEELTK.R
R5/RRR5-12/2	1220.387	1220.443	-45.910	0.409	1312.537	0.277	18	0.146	K.LFGVTTLDVVR.A
R5/RRR5-13/2	1415.082	1415.578	-351.075	0.430	1030.841	0.404	19	0.145	K.RIQNAGTEVVEAK.A
R5/RRR5-12/2	1259.098	1259.391	-233.244	0.511	870.999	0.443	18	0.145	R.IQNAGTEVVEAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1220.256	1220.443	-154.078	0.434	1016.188	0.333	17	0.138	K.LFGVTTLDVVR.A
R5/RRR5-14/2	1220.403	1220.443	-33.068	0.354	856.168	0.380	15	0.134	K.LFGVTTLDVVR.A
R5/RRR5-13/2	1220.220	1220.443	-183.583	0.382	985.361	0.305	17	0.133	K.LFGVTTLDVVR.A
R5/RRR5-13/2	1415.071	1415.578	-1067.490	0.435	930.308	0.332	18	0.131	K.RIQNAGTEVVEAK.A
R5/RRR5-13/2	1128.045	1128.344	-265.335	0.453	1111.953	0.260	15	0.130	K.ALESLKPELK.A
R5/RRR5-12/2	1349.079	1349.514	-323.872	0.390	725.539	0.311	14	0.122	R.DDLFNINASIVK.S
R5/RRR5-13/2	1348.410	1348.616	-153.236	0.340	676.016	0.260	14	0.119	-.KLFGVTTLDVVR.-
R5/RRR5-14/2	1748.765	1748.146	-218.624	0.377	679.397	0.269	20	0.117	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-13/3	1748.318	1748.146	98.623	0.419	1199.692	0.415	31	0.114	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-13/3	1747.274	1748.146	-1074.373	0.370	1343.810	0.301	36	0.101	K.VAVLGAAGGIGQPLGLLIK.M
R5/RRR5-13/3	1888.315	1888.221	49.993	0.309	803.953	0.498	27	0.093	K.M*SPLVSALHLYDIANVK.G
R5/RRR5-13/3	1348.564	1348.616	-38.787	0.539	955.892	0.319	26	0.069	-.KLFGVTTLDVVR.-
R5/RRR5-12/3	1348.392	1348.616	-166.823	0.426	922.389	0.212	25	0.066	-.KLFGVTTLDVVR.-
R5/RRR5-12/3	1348.681	1348.616	48.095	0.528	974.772	0.308	26	0.064	-.KLFGVTTLDVVR.-
R5/RRR5-13/3	1348.909	1348.616	218.275	0.489	928.549	0.250	26	0.064	-.KLFGVTTLDVVR.-
R5/RRR5-13/3	1348.570	1348.616	-34.293	0.509	803.715	0.307	24	0.063	-.KLFGVTTLDVVR.-
R5/RRR5-12/3	1347.813	1348.616	-1341.376	0.412	726.605	0.150	24	0.039	-.KLFGVTTLDVVR.-
R5/RRR5-8/2	1841.610	1841.100	-267.104	0.623	2954.175	0.639	26	0.511	K.HVAEANIIFVSVNTPTK.T
R5/RRR5-8/2	965.650	966.201	-1611.285	0.389	1048.528	0.413	15	0.150	K.IAVLGFAFK.K
R5/RRR5-9/2	965.506	966.201	-1760.908	0.451	1020.482	0.397	15	0.147	K.IAVLGFAFK.K
R5/RRR5-8/2	965.736	966.201	-483.048	0.449	984.908	0.374	15	0.143	K.IAVLGFAFK.K
R5/RRR5-9/2	965.760	966.201	-457.807	0.422	945.282	0.381	15	0.142	K.IAVLGFAFK.K
R5/RRR5-8/2	966.053	966.201	-153.241	0.488	930.957	0.380	15	0.142	K.IAVLGFAFK.K
R5/RRR5-9/2	965.528	966.201	-1737.534	0.391	971.871	0.364	15	0.140	K.IAVLGFAFK.K
R5/RRR5-7/2	965.941	966.201	-269.999	0.367	854.670	0.381	14	0.136	K.IAVLGFAFK.K
R5/RRR5-3/2	965.544	966.201	-1721.656	0.254	760.911	0.322	13	0.125	K.IAVLGFAFK.K
R5/RRR5-4/2	1650.550	1650.813	-159.902	0.509	2040.911	0.452	21	0.258	K.GILQNDPFEVFDQK.G
R5/RRR5-4/2	1344.611	1344.495	87.268	0.570	1741.900	0.548	20	0.243	K.VFANAETTISYK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1650.438	1650.813	-228.162	0.506	1749.067	0.458	20	0.219	K.GILQNDPFEVFDQK.G
R5/RRR5-5/2	1651.148	1650.813	203.429	0.561	1622.685	0.497	19	0.212	K.GILQNDPFEVFDQK.G
R5/RRR5-4/2	1345.139	1344.495	-265.110	0.535	1422.263	0.580	19	0.211	K.VFANAETTISYK.I
R5/RRR5-5/2	1824.408	1824.025	210.417	0.604	1386.597	0.594	23	0.209	R.LLSSGNVYTQEEILTR.I
R5/RRR5-4/2	1650.146	1650.813	-1013.062	0.474	1755.711	0.387	20	0.203	K.GILQNDPFEVFDQK.G
R5/RRR5-4/2	1823.408	1824.025	-889.673	0.546	1391.566	0.558	23	0.201	R.LLSSGNVYTQEEILTR.I
R5/RRR5-5/2	1344.402	1344.495	-69.361	0.516	1429.773	0.494	19	0.193	K.VFANAETTISYK.I
R5/RRR5-5/2	1824.462	1824.025	239.938	0.609	1256.601	0.580	22	0.192	R.LLSSGNVYTQEEILTR.I
R5/RRR5-5/2	1344.135	1344.495	-268.314	0.520	1394.557	0.501	19	0.192	K.VFANAETTISYK.I
R5/RRR5-5/2	1651.670	1650.813	-86.850	0.546	1415.341	0.488	18	0.187	K.GILQNDPFEVFDQK.G
R5/RRR5-4/2	1823.577	1824.025	-246.582	0.549	1186.658	0.575	22	0.185	R.LLSSGNVYTQEEILTR.I
R5/RRR5-5/2	1650.578	1650.813	-143.135	0.495	1554.031	0.402	19	0.184	K.GILQNDPFEVFDQK.G
R5/RRR5-5/2	1596.399	1595.842	-278.374	0.481	1486.164	0.428	22	0.184	R.AIFEAAISMTEQGVK.V
R5/RRR5-5/2	1823.366	1824.025	-912.456	0.528	1206.956	0.520	22	0.176	R.LLSSGNVYTQEEILTR.I
R5/RRR5-5/2	1343.770	1344.495	-1286.861	0.458	1166.850	0.488	18	0.168	K.VFANAETTISYK.I
R5/RRR5-4/2	1287.211	1287.361	-117.528	0.446	1017.086	0.554	20	0.168	K.ANADTPADALTAR.N
R5/RRR5-4/2	1823.158	1824.025	-1027.129	0.523	970.038	0.542	20	0.161	R.LLSSGNVYTQEEILTR.I
R5/RRR5-5/2	1287.016	1287.361	-269.567	0.408	810.493	0.545	18	0.152	K.ANADTPADALTAR.N
R5/RRR5-4/2	1288.146	1287.361	-167.439	0.459	829.915	0.490	18	0.147	K.ANADTPADALTAR.N
R5/RRR5-5/2	1567.244	1566.804	281.303	0.503	599.973	0.556	18	0.146	R.LGISYPELTAM*QAR.A
R5/RRR5-4/2	1287.103	1287.361	-201.058	0.402	841.955	0.483	18	0.146	K.ANADTPADALTAR.N
R5/RRR5-5/2	1279.285	1279.491	-161.509	0.479	796.736	0.431	16	0.141	K.LSEVNPM*LGFR.G
R5/RRR5-4/2	1278.995	1279.491	-388.805	0.438	815.624	0.414	16	0.139	K.LSEVNPM*LGFR.G
R5/RRR5-5/2	1566.061	1566.804	-1116.208	0.473	504.402	0.527	17	0.139	R.LGISYPELTAM*QAR.A
R5/RRR5-5/2	1286.613	1287.361	-1363.157	0.328	747.773	0.479	18	0.138	K.ANADTPADALTAR.N
R5/RRR5-4/2	1595.994	1595.842	95.003	0.423	1064.702	0.344	19	0.138	R.AIFEAAISMTEQGVK.V
R5/RRR5-4/2	1088.433	1089.291	-1712.153	0.385	804.502	0.407	15	0.136	R.AM*DGLPVTIR.L
R5/RRR5-5/2	1263.259	1263.491	-184.403	0.435	715.729	0.433	13	0.135	K.LSEVNPMLGFR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1566.358	1566.804	-285.713	0.410	595.901	0.464	18	0.135	R.LGISYPELTAM*QAR.A
R5/RRR5-5/2	996.447	997.129	-1693.267	0.405	808.736	0.352	13	0.134	R.LDFEGIFR.A
R5/RRR5-4/2	996.864	997.129	-266.598	0.462	749.896	0.368	12	0.133	R.LDFEGIFR.A
R5/RRR5-4/2	1263.345	1263.491	-116.454	0.447	662.347	0.423	13	0.133	K.LSEVNPMLGFR.G
R5/RRR5-5/2	997.065	997.129	-64.543	0.441	657.656	0.371	12	0.132	R.LDFEGIFR.A
R5/RRR5-5/2	1566.443	1566.804	-231.297	0.379	554.472	0.448	18	0.132	R.LGISYPELTAM*QAR.A
R5/RRR5-4/2	1595.236	1595.842	-1010.172	0.334	1107.377	0.274	19	0.131	R.AIFEAAISMTEQGVK.V
R5/RRR5-5/2	1278.793	1279.491	-1331.656	0.394	685.236	0.370	15	0.130	K.LSEVNPM*LGFR.G
R5/RRR5-4/2	1278.575	1279.491	-1502.911	0.357	883.102	0.316	16	0.130	K.LSEVNPM*LGFR.G
R5/RRR5-4/2	996.973	997.129	-156.410	0.427	753.052	0.333	12	0.130	R.LDFEGIFR.A
R5/RRR5-5/2	996.605	997.129	-1533.780	0.436	632.571	0.348	12	0.130	R.LDFEGIFR.A
R5/RRR5-5/2	1019.025	1018.213	-184.772	0.375	892.147	0.280	15	0.128	K.IGSM*IEVPR.A
R5/RRR5-5/2	1262.598	1263.491	-1504.288	0.428	584.393	0.367	13	0.127	K.LSEVNPMLGFR.G
R5/RRR5-4/2	1263.307	1263.491	-146.114	0.345	749.760	0.330	14	0.127	K.LSEVNPMLGFR.G
R5/RRR5-1/2	1278.518	1279.491	-1547.412	0.348	648.218	0.346	14	0.126	K.LSEVNPM*LGFR.G
R5/RRR5-4/2	1278.540	1279.491	-1530.340	0.337	756.552	0.300	15	0.125	K.LSEVNPM*LGFR.G
R5/RRR5-4/2	1018.142	1018.213	-70.209	0.313	1012.571	0.233	14	0.125	K.IGSM*IEVPR.A
R5/RRR5-5/2	1550.431	1550.805	-242.010	0.369	328.092	0.445	13	0.125	R.LGISYPELTAMQAR.A
R5/RRR5-5/2	1611.051	1611.842	-1115.021	0.324	968.733	0.256	19	0.124	R.AIFEAAISM*TEQGVK.V
R5/RRR5-4/2	996.493	997.129	-1646.129	0.357	705.684	0.265	12	0.123	R.LDFEGIFR.A
R5/RRR5-5/2	1278.522	1279.491	-1544.535	0.323	702.125	0.284	14	0.123	K.LSEVNPM*LGFR.G
R5/RRR5-5/2	1017.897	1018.213	-311.155	0.320	563.061	0.250	13	0.120	K.IGSM*IEVPR.A
R5/RRR5-5/2	1611.139	1611.842	-1060.016	0.258	927.635	0.169	19	0.116	R.AIFEAAISM*TEQGVK.V
R5/RRR5-4/2	1263.022	1263.491	-372.403	0.389	564.051	0.309	12	0.115	-.LSEVNPMLGFR.-
R5/RRR5-6/2	1089.763	1089.291	434.053	0.271	539.821	0.265	12	0.107	-.AM*DGLPVTIR.-
R5/RRR5-4/3	1515.042	1514.666	249.091	0.517	854.049	0.499	24	0.107	K.VKANADTPADALTAR.N
R5/RRR5-5/3	1515.043	1514.666	249.455	0.419	1150.262	0.370	26	0.101	K.VKANADTPADALTAR.N
R5/RRR5-5/3	1514.146	1514.666	-1006.909	0.412	925.692	0.398	24	0.092	K.VKANADTPADALTAR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	954.434	954.195	250.763	0.418	1262.404	0.286	17	0.091	R.RPLLLSVR.S
R5/RRR5-4/3	954.196	954.195	0.998	0.410	1020.848	0.194	16	0.068	-.RPLLLSVR.-
R5/RRR5-4/3	954.528	954.195	350.018	0.416	766.739	0.199	15	0.065	-.RPLLLSVR.-
R5/RRR5-5/3	953.957	954.195	-250.335	0.383	718.114	0.197	14	0.053	-.RPLLLSVR.-
R5/RRR5-3/2	1469.114	1469.645	-1045.602	0.491	2274.762	0.478	23	0.304	R.FIGTAGAASSTM*NPK.N
R5/RRR5-4/3	1422.923	1422.655	188.809	0.502	2358.374	0.331	29	0.267	K.HANPVLLSSDLKK.K
R5/RRR5-3/2	1469.085	1469.645	-1065.458	0.505	2094.949	0.437	23	0.262	R.FIGTAGAASSTM*NPK.N
R5/RRR5-3/2	1885.388	1885.881	-262.266	0.588	1548.431	0.641	26	0.237	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-3/2	1568.556	1567.796	-153.039	0.549	1657.536	0.547	21	0.230	R.GCALECAILSPTFK.V
R5/RRR5-3/2	1468.666	1469.645	-1351.874	0.379	1892.102	0.353	22	0.213	R.FIGTAGAASSTM*NPK.N
R5/RRR5-3/3	1422.900	1422.655	173.065	0.502	2107.489	0.303	29	0.202	K.HANPVLLSSDLKK.K
R5/RRR5-4/2	1469.200	1469.645	-303.855	0.503	1502.104	0.491	21	0.198	R.FIGTAGAASSTM*NPK.N
R5/RRR5-4/3	1423.062	1422.655	287.131	0.503	1977.028	0.323	28	0.187	K.HANPVLLSSDLKK.K
R5/RRR5-3/3	1422.607	1422.655	-33.972	0.499	1929.460	0.311	27	0.175	K.HANPVLLSSDLKK.K
R5/RRR5-3/2	1541.354	1541.811	-297.212	0.239	1727.618	0.234	20	0.171	R.AVLDAATIAGLCPLR.L
R5/RRR5-3/2	1567.160	1567.796	-1047.098	0.375	1320.912	0.419	19	0.166	R.GCALECAILSPTFK.V
R5/RRR5-3/2	1885.048	1885.881	-975.415	0.445	853.068	0.619	25	0.163	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-3/2	1481.288	1481.638	-236.941	0.478	806.237	0.550	19	0.154	R.VSEGPDGFPLVHAR.Y
R5/RRR5-4/3	1422.511	1422.655	-101.496	0.526	1871.778	0.275	27	0.153	K.HANPVLLSSDLKK.K
R5/RRR5-4/2	1541.528	1541.811	-184.395	0.229	1377.427	0.284	19	0.147	R.AVLDAATIAGLCPLR.L
R5/RRR5-3/2	1541.314	1541.811	-323.752	0.243	1323.940	0.299	19	0.146	R.AVLDAATIAGLCPLR.L
R5/RRR5-3/3	1885.345	1885.881	-817.072	0.481	1336.342	0.463	35	0.141	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-3/2	936.556	937.077	-1628.133	0.360	631.563	0.499	11	0.139	R.DIAAFPFR.V
R5/RRR5-8/2	936.697	937.077	-406.918	0.326	714.848	0.445	11	0.135	R.DIAAFPFR.V
R5/RRR5-3/2	1381.781	1381.558	162.010	0.412	807.259	0.435	16	0.135	K.ISTYTVGPFNPGK.G
R5/RRR5-3/3	1886.181	1885.881	159.638	0.534	1197.198	0.495	34	0.134	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-3/2	1481.138	1481.638	-1015.824	0.406	646.246	0.462	17	0.134	R.VSEGPDGFPLVHAR.Y
R5/RRR5-3/2	898.752	899.070	-355.097	0.379	565.720	0.432	12	0.133	K.ISAPILER.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	936.898	937.077	-190.811	0.392	572.988	0.429	10	0.132	R.DIAAFPFR.V
R5/RRR5-3/2	936.769	937.077	-329.642	0.339	547.081	0.437	11	0.132	R.DIAAFPFR.V
R5/RRR5-3/2	936.910	937.077	-178.133	0.356	553.555	0.442	10	0.132	R.DIAAFPFR.V
R5/RRR5-3/2	1040.989	1041.183	-186.728	0.436	886.856	0.323	14	0.131	K.IQQQDALPK.H
R5/RRR5-3/2	1041.110	1041.183	-70.751	0.476	974.638	0.283	15	0.130	K.IQQQDALPK.H
R5/RRR5-3/2	1323.254	1323.522	-203.060	0.367	981.651	0.296	15	0.129	K.ILTDFFGKEPR.R
R5/RRR5-3/2	1481.313	1481.638	-219.580	0.430	604.653	0.426	16	0.129	R.VSEGPDGFPLVHAR.Y
R5/RRR5-4/2	936.984	937.077	-99.194	0.364	661.623	0.359	11	0.129	R.DIAAFPFR.V
R5/RRR5-3/2	1323.510	1323.522	-8.845	0.393	548.252	0.425	13	0.129	K.ILTDFFGKEPR.R
R5/RRR5-8/2	936.586	937.077	-525.796	0.292	578.199	0.412	11	0.129	R.DIAAFPFR.V
R5/RRR5-3/2	1885.166	1885.881	-912.290	0.354	190.316	0.540	19	0.128	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-4/2	1541.377	1541.811	-282.513	0.278	916.982	0.336	16	0.127	R.AVLDAATIAGLCPLR.L
R5/RRR5-8/2	936.723	937.077	-379.066	0.233	736.276	0.382	11	0.126	R.DIAAFPFR.V
R5/RRR5-3/2	898.535	899.070	-1713.652	0.284	541.200	0.321	12	0.123	K.ISAPILER.V
R5/RRR5-3/3	1422.519	1422.655	-95.944	0.486	1622.249	0.269	26	0.120	K.HANPVLLSSDLKK.K
R5/RRR5-3/2	1322.806	1323.522	-1301.147	0.311	613.670	0.278	13	0.118	K.ILTDFFGKEPR.R
R5/RRR5-7/2	1543.212	1541.811	260.500	0.264	435.114	0.298	14	0.117	R.AVLDAATIAGLCPLR.L
R5/RRR5-4/2	898.435	899.070	-1825.317	0.234	670.313	0.221	12	0.117	K.ISAPILER.V
R5/RRR5-4/3	1885.177	1885.881	-906.674	0.449	1051.456	0.479	32	0.116	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-3/3	1886.217	1885.881	178.816	0.512	1023.674	0.468	33	0.112	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-1/3	1480.991	1481.638	-1115.554	0.378	970.885	0.479	25	0.110	R.VSEGPDGFPLVHAR.Y
R5/RRR5-4/3	1482.957	1481.638	215.883	0.403	610.472	0.497	22	0.098	R.VSEGPDGFPLVHAR.Y
R5/RRR5-7/3	1481.520	1481.638	-79.520	0.399	841.972	0.448	24	0.098	R.VSEGPDGFPLVHAR.Y
R5/RRR5-3/3	1482.558	1481.638	-53.616	0.437	623.739	0.479	22	0.097	R.VSEGPDGFPLVHAR.Y
R5/RRR5-4/3	1482.125	1481.638	330.045	0.397	609.565	0.473	22	0.095	R.VSEGPDGFPLVHAR.Y
R5/RRR5-4/3	1801.307	1800.047	144.933	0.408	1144.732	0.340	26	0.093	R.LFHETTATALAYGIYK.T
R5/RRR5-1/3	1481.129	1481.638	-1021.956	0.370	923.935	0.382	25	0.091	R.VSEGPDGFPLVHAR.Y
R5/RRR5-3/3	1481.340	1481.638	-201.525	0.373	578.861	0.433	22	0.090	R.VSEGPDGFPLVHAR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/3	1481.024	1481.638	-1092.711	0.355	752.063	0.411	23	0.089	R.VSEGPDGFPLVHAR.Y
R5/RRR5-3/3	1480.784	1481.638	-1255.858	0.344	677.657	0.395	22	0.086	R.VSEGPDGFPLVHAR.Y
R5/RRR5-2/3	1481.619	1481.638	-12.703	0.342	764.844	0.333	22	0.080	R.VSEGPDGFPLVHAR.Y
R5/RRR5-4/3	1885.360	1885.881	-809.078	0.380	743.574	0.338	29	0.078	K.APADAAADGAENGAPNSEEK.S
R5/RRR5-3/3	1799.800	1800.047	-137.669	0.340	733.865	0.239	21	0.063	-.LFHETTATALAYGIYK.-
R5/RRR5-11/2	1319.142	1318.495	-268.571	0.507	2266.923	0.463	21	0.299	K.CDVIASGIVNAAK.Q
R5/RRR5-11/3	1619.673	1619.824	-93.449	0.547	1695.342	0.507	28	0.206	R.LNIHEYQGAELM*GK.Y
R5/RRR5-11/2	1318.089	1318.495	-309.471	0.468	1643.141	0.441	19	0.203	K.CDVIASGIVNAAK.Q
R5/RRR5-11/2	1317.876	1318.495	-1232.527	0.370	1647.902	0.411	18	0.197	K.CDVIASGIVNAAK.Q
R5/RRR5-11/2	1474.435	1474.642	-140.720	0.501	1394.550	0.478	22	0.185	R.GAAAGSVEEVKNTLK.N
R5/RRR5-11/2	1474.224	1474.642	-284.170	0.480	1368.180	0.409	21	0.169	R.GAAAGSVEEVKNTLK.N
R5/RRR5-11/2	1183.093	1183.255	-137.185	0.496	1153.068	0.431	17	0.160	K.LNFDDNAAFR.Q
R5/RRR5-11/3	1603.946	1603.825	75.936	0.493	1364.997	0.511	26	0.158	R.LNIHEYQGAELMGK.Y
R5/RRR5-11/2	1183.144	1183.255	-94.130	0.472	1208.386	0.393	17	0.158	K.LNFDDNAAFR.Q
R5/RRR5-11/2	1474.246	1474.642	-269.217	0.443	1145.762	0.423	20	0.154	R.GAAAGSVEEVKNTLK.N
R5/RRR5-11/2	1095.135	1095.277	-129.757	0.434	1033.183	0.456	16	0.153	K.SGLQGGVHIVK.A
R5/RRR5-11/3	1620.673	1619.824	-93.429	0.545	1426.692	0.467	27	0.153	R.LNIHEYQGAELM*GK.Y
R5/RRR5-11/2	1019.050	1019.284	-230.538	0.495	1079.909	0.381	16	0.149	K.M*LGQILVTK.Q
R5/RRR5-11/2	1003.115	1003.285	-169.122	0.510	933.865	0.430	15	0.148	K.MLGQILVTK.Q
R5/RRR5-12/2	1183.924	1183.255	-280.010	0.436	954.451	0.425	16	0.147	K.LNFDDNAAFR.Q
R5/RRR5-11/2	1018.523	1019.284	-1733.761	0.437	1017.077	0.396	15	0.147	K.M*LGQILVTK.Q
R5/RRR5-11/2	1018.530	1019.284	-1727.379	0.401	1065.923	0.368	16	0.145	K.M*LGQILVTK.Q
R5/RRR5-11/2	1095.099	1095.277	-163.302	0.413	1037.557	0.374	16	0.142	K.SGLQGGVHIVK.A
R5/RRR5-11/2	1183.285	1183.255	25.391	0.450	931.368	0.385	16	0.141	K.LNFDDNAAFR.Q
R5/RRR5-11/2	818.206	817.995	258.936	0.442	404.528	0.497	11	0.140	K.VPIDVFK.G
R5/RRR5-11/2	1245.132	1245.444	-251.102	0.352	739.582	0.488	18	0.140	R.NTAGPLIIACSK.G
R5/RRR5-11/2	1002.948	1003.285	-336.273	0.442	806.163	0.401	14	0.138	K.MLGQILVTK.Q
R5/RRR5-11/2	1094.735	1095.277	-1413.071	0.434	812.254	0.424	14	0.137	K.SGLQGGVHIVK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1389.130	1389.622	-354.901	0.396	907.891	0.370	17	0.135	K.NVFPSEKEIVVK.S
R5/RRR5-11/2	1245.172	1245.444	-219.432	0.442	472.482	0.490	15	0.134	R.NTAGPLIIACSK.G
R5/RRR5-11/3	1605.142	1603.825	198.267	0.506	1319.381	0.444	27	0.134	R.LNIHEYQGAELMGK.Y
R5/RRR5-12/2	1183.366	1183.255	93.986	0.448	999.133	0.292	17	0.133	K.LNFDDNAAFR.Q
R5/RRR5-11/2	1531.249	1531.607	-234.727	0.448	699.879	0.401	20	0.133	R.DTTQEDPREVAAAK.A
R5/RRR5-11/2	817.976	817.995	-24.041	0.397	389.412	0.471	11	0.132	-.VPIDVFK.-
R5/RRR5-11/2	817.678	817.995	-388.658	0.399	363.291	0.390	11	0.132	K.VPIDVFK.G
R5/RRR5-11/2	1531.153	1531.607	-297.273	0.405	673.259	0.372	20	0.129	R.DTTQEDPREVAAAK.A
R5/RRR5-12/2	1183.221	1183.255	-28.519	0.440	774.124	0.323	14	0.128	K.LNFDDNAAFR.Q
R5/RRR5-11/2	1389.368	1389.622	-182.823	0.382	773.435	0.343	16	0.127	K.NVFPSEKEIVVK.S
R5/RRR5-10/2	1183.749	1183.255	418.936	0.260	370.101	0.319	14	0.124	K.LNFDDNAAFR.Q
R5/RRR5-11/2	1530.469	1531.607	-1401.318	0.328	625.628	0.284	19	0.121	R.DTTQEDPREVAAAK.A
R5/RRR5-11/3	1619.428	1619.824	-245.202	0.507	1541.525	0.298	27	0.119	R.LNIHEYQGAELM*GK.Y
R5/RRR5-11/3	1252.330	1252.531	-160.848	0.402	1171.080	0.243	23	0.078	K.QVDLKVPVVVR.L
R5/RRR5-17/2	1435.432	1435.650	-152.646	0.476	2563.069	0.493	23	0.364	K.YIGLLATGLTADAR.S
R5/RRR5-17/2	1849.573	1850.063	-265.425	0.610	2416.298	0.494	24	0.332	K.ATSAGLKEQEAINFLEK.K
R5/RRR5-17/2	1849.234	1850.063	-991.922	0.553	2341.865	0.488	24	0.318	K.ATSAGLKEQEAINFLEK.K
R5/RRR5-17/2	1435.348	1435.650	-211.087	0.510	2276.266	0.473	23	0.303	K.YIGLLATGLTADAR.S
R5/RRR5-17/2	1849.627	1850.063	-236.026	0.576	2142.885	0.486	23	0.281	K.ATSAGLKEQEAINFLEK.K
R5/RRR5-16/2	1435.343	1435.650	-214.755	0.516	1872.420	0.521	21	0.252	K.YIGLLATGLTADAR.S
R5/RRR5-17/2	1072.908	1073.225	-295.974	0.490	1677.128	0.409	16	0.201	K.ATEIEVGVVR.K
R5/RRR5-17/3	1849.561	1850.063	-814.444	0.500	1556.457	0.502	34	0.184	K.ATSAGLKEQEAINFLEK.K
R5/RRR5-17/2	1409.172	1408.647	-338.124	0.439	1085.949	0.565	18	0.174	K.WGYEMPVDVLAK.W
R5/RRR5-17/2	1423.306	1424.646	-1649.308	0.475	1256.010	0.477	18	0.173	K.WGYEM*PVDVLAK.W
R5/RRR5-17/2	1072.475	1073.225	-1636.933	0.437	1525.914	0.340	16	0.172	K.ATEIEVGVVR.K
R5/RRR5-17/2	1713.514	1713.999	-283.642	0.455	1141.114	0.462	21	0.159	K.LLDQTSVTHLFPITK.Y
R5/RRR5-17/2	947.969	947.071	-108.054	0.534	1007.254	0.444	17	0.154	K.SAGVTSIGVR.G
R5/RRR5-17/2	947.868	947.071	-215.277	0.491	945.162	0.456	16	0.152	K.SAGVTSIGVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1072.445	1073.225	-1665.178	0.433	1092.705	0.404	15	0.150	K.ATEIEVGVVR.K
R5/RRR5-15/2	1157.241	1157.304	-54.869	0.365	921.603	0.470	16	0.148	R.HITIFSPEGR.L
R5/RRR5-17/2	1162.151	1161.331	-155.250	0.419	952.587	0.438	14	0.147	-.LYQVEYAFK.-
R5/RRR5-17/2	1157.333	1157.304	25.326	0.345	654.868	0.527	15	0.141	R.HITIFSPEGR.L
R5/RRR5-16/2	1157.353	1157.304	42.569	0.409	633.540	0.495	15	0.141	R.HITIFSPEGR.L
R5/RRR5-16/2	946.155	947.071	-2031.857	0.363	1170.866	0.300	17	0.141	K.SAGVTSIGVR.G
R5/RRR5-16/2	1162.069	1161.331	-226.379	0.450	840.719	0.398	14	0.139	R.LYQVEYAFK.A
R5/RRR5-15/2	946.760	947.071	-329.720	0.367	875.653	0.399	15	0.139	K.SAGVTSIGVR.G
R5/RRR5-16/2	1162.364	1161.331	28.692	0.477	868.324	0.350	14	0.134	R.LYQVEYAFK.A
R5/RRR5-15/2	946.863	947.071	-220.678	0.331	936.510	0.324	16	0.133	K.SAGVTSIGVR.G
R5/RRR5-15/2	946.468	947.071	-1698.595	0.335	617.337	0.471	13	0.133	-.SAGVTSIGVR.-
R5/RRR5-16/2	1160.987	1161.331	-296.826	0.302	960.865	0.312	14	0.131	R.LYQVEYAFK.A
R5/RRR5-16/2	946.213	947.071	-1969.491	0.344	626.419	0.374	14	0.129	K.SAGVTSIGVR.G
R5/RRR5-16/2	1156.354	1157.304	-1691.098	0.256	557.389	0.422	14	0.126	R.HITIFSPEGR.L
R5/RRR5-17/2	1435.222	1435.650	-299.485	0.304	567.343	0.326	14	0.118	-.YIGLLATGLTADAR.-
R5/RRR5-17/2	1156.985	1157.304	-276.370	0.219	623.790	0.192	14	0.116	R.HITIFSPEGR.L
R5/RRR5-16/3	1221.500	1221.380	99.110	0.487	1382.636	0.340	21	0.114	R.GKDSVCVVTQK.K
R5/RRR5-21/2	946.909	947.071	-172.050	0.308	681.243	0.077	14	0.114	K.SAGVTSIGVR.G
R5/RRR5-17/3	1979.326	1978.235	45.947	0.462	977.866	0.437	28	0.101	K.ATSAGLKEQEAINFLEKK.M
R5/RRR5-17/3	1978.037	1978.235	-100.505	0.480	782.582	0.482	27	0.098	K.ATSAGLKEQEAINFLEKK.M
R5/RRR5-17/3	1713.539	1713.999	-268.927	0.377	483.007	0.521	27	0.096	K.LLDQTSVTHLFPITK.Y
R5/RRR5-16/3	1715.081	1713.999	48.243	0.417	485.214	0.456	28	0.093	K.LLDQTSVTHLFPITK.Y
R5/RRR5-16/3	1713.642	1713.999	-208.894	0.350	393.395	0.470	24	0.091	K.LLDQTSVTHLFPITK.Y
R5/RRR5-17/3	1713.758	1713.999	-140.723	0.357	370.087	0.433	25	0.090	K.LLDQTSVTHLFPITK.Y
R5/RRR5-17/3	1221.324	1221.380	-45.686	0.482	1334.478	0.242	21	0.090	-.GKDSVCVVTQK.-
R5/RRR5-17/3	1714.153	1713.999	90.304	0.357	460.784	0.387	28	0.086	K.LLDQTSVTHLFPITK.Y
R5/RRR5-17/3	1220.599	1221.380	-1463.123	0.425	1061.271	0.331	19	0.086	-.GKDSVCVVTQK.-
R5/RRR5-17/3	1221.504	1221.380	102.417	0.505	1099.182	0.343	20	0.086	-.GKDSVCVVTQK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/3	1714.306	1713.999	179.964	0.350	465.903	0.386	25	0.085	K.LLDQTSVTHLFPITK.Y
R5/RRR5-17/3	1849.630	1850.063	-234.511	0.323	597.703	0.330	21	0.068	-.ATSAGLKEQEAINFLEK.-
R5/RRR5-15/2	1609.241	1609.806	-975.360	0.470	2186.168	0.513	24	0.297	K.LDISGHTVSAVGPDIK.H
R5/RRR5-15/2	1312.094	1312.497	-308.459	0.460	1842.715	0.601	21	0.265	R.VLVGVVASPEADR.D
R5/RRR5-15/2	1311.491	1312.497	-1534.188	0.376	1867.651	0.525	21	0.247	R.VLVGVVASPEADR.D
R5/RRR5-25/2	1263.562	1264.456	-1503.139	0.479	1675.441	0.589	19	0.240	R.LQAALSTGLFSR.I
R5/RRR5-22/2	1263.764	1264.456	-1342.753	0.474	1709.881	0.569	19	0.239	R.LQAALSTGLFSR.I
R5/RRR5-3/2	1313.038	1312.497	-351.131	0.460	1696.359	0.578	20	0.239	R.VLVGVVASPEADR.D
R5/RRR5-23/2	1264.349	1264.456	-85.083	0.414	1746.876	0.549	19	0.238	R.LQAALSTGLFSR.I
R5/RRR5-15/2	1264.220	1264.456	-187.072	0.499	1680.475	0.576	19	0.237	R.LQAALSTGLFSR.I
R5/RRR5-14/2	1264.304	1264.456	-120.723	0.529	1657.454	0.575	19	0.235	R.LQAALSTGLFSR.I
R5/RRR5-24/2	1609.316	1609.806	-305.431	0.481	1831.727	0.475	23	0.233	K.LDISGHTVSAVGPDIK.H
R5/RRR5-23/2	1263.397	1264.456	-1634.359	0.450	1575.319	0.613	18	0.232	R.LQAALSTGLFSR.I
R5/RRR5-23/2	1311.973	1312.497	-1165.094	0.434	1744.894	0.519	20	0.231	R.VLVGVVASPEADR.D
R5/RRR5-16/2	1609.327	1609.806	-298.277	0.436	1791.268	0.481	22	0.229	K.LDISGHTVSAVGPDIK.H
R5/RRR5-25/2	1264.040	1264.456	-329.969	0.497	1624.848	0.568	19	0.229	R.LQAALSTGLFSR.I
R5/RRR5-16/2	1609.364	1609.806	-275.371	0.456	1662.279	0.548	21	0.228	K.LDISGHTVSAVGPDIK.H
R5/RRR5-24/2	1264.215	1264.456	-191.334	0.421	1637.517	0.555	19	0.226	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1263.396	1264.456	-1634.941	0.434	1551.838	0.600	19	0.225	R.LQAALSTGLFSR.I
R5/RRR5-23/2	1264.147	1264.456	-245.194	0.489	1650.937	0.542	18	0.225	R.LQAALSTGLFSR.I
R5/RRR5-15/2	1609.400	1609.806	-252.770	0.462	1708.664	0.509	22	0.225	K.LDISGHTVSAVGPDIK.H
R5/RRR5-24/2	1313.075	1312.497	-322.588	0.537	1581.921	0.566	20	0.223	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1312.141	1312.497	-272.057	0.464	1514.206	0.605	19	0.222	R.VLVGVVASPEADR.D
R5/RRR5-16/2	1264.243	1264.456	-168.571	0.514	1589.823	0.552	19	0.221	R.LQAALSTGLFSR.I
R5/RRR5-16/2	1263.679	1264.456	-1410.569	0.516	1554.751	0.559	19	0.218	R.LQAALSTGLFSR.I
R5/RRR5-14/2	1264.278	1264.456	-141.450	0.490	1654.341	0.507	19	0.218	R.LQAALSTGLFSR.I
R5/RRR5-24/2	1264.119	1264.456	-267.573	0.470	1566.593	0.546	19	0.216	R.LQAALSTGLFSR.I
R5/RRR5-24/2	1311.593	1312.497	-1456.216	0.411	1606.656	0.532	20	0.216	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1311.994	1312.497	-1149.305	0.413	1605.313	0.532	20	0.216	R.VLVGVVASPEADR.D
R5/RRR5-2/2	1264.462	1264.456	5.170	0.414	1630.340	0.501	19	0.213	R.LQAALSTGLFSR.I
R5/RRR5-15/2	1608.796	1609.806	-1252.725	0.481	1648.906	0.486	22	0.212	K.LDISGHTVSAVGPDIK.H
R5/RRR5-16/2	1312.026	1312.497	-360.174	0.398	1594.612	0.515	20	0.211	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1312.315	1312.497	-138.884	0.456	1467.696	0.571	20	0.210	R.VLVGVVASPEADR.D
R5/RRR5-16/2	1312.252	1312.497	-187.595	0.431	1549.443	0.529	20	0.210	R.VLVGVVASPEADR.D
R5/RRR5-15/2	1263.462	1264.456	-1582.430	0.454	1482.523	0.560	18	0.209	R.LQAALSTGLFSR.I
R5/RRR5-16/2	1312.053	1312.497	-339.637	0.463	1474.774	0.562	20	0.209	R.VLVGVVASPEADR.D
R5/RRR5-24/2	1609.227	1609.806	-983.737	0.406	1780.978	0.400	22	0.209	K.LDISGHTVSAVGPDIK.H
R5/RRR5-16/2	1610.290	1609.806	301.504	0.508	1565.844	0.512	22	0.209	K.LDISGHTVSAVGPDIK.H
R5/RRR5-15/2	1263.538	1264.456	-1521.966	0.456	1533.187	0.526	19	0.208	R.LQAALSTGLFSR.I
R5/RRR5-14/2	1312.053	1312.497	-339.263	0.440	1438.780	0.580	19	0.208	R.VLVGVVASPEADR.D
R5/RRR5-25/2	1263.942	1264.456	-1201.329	0.474	1519.568	0.520	19	0.206	R.LQAALSTGLFSR.I
R5/RRR5-22/2	1264.068	1264.456	-307.393	0.464	1494.256	0.533	18	0.205	R.LQAALSTGLFSR.I
R5/RRR5-14/2	1311.651	1312.497	-1411.719	0.419	1501.545	0.535	19	0.205	R.VLVGVVASPEADR.D
R5/RRR5-24/2	1263.712	1264.456	-1384.179	0.426	1444.340	0.553	18	0.203	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1264.144	1264.456	-247.229	0.487	1437.960	0.550	18	0.203	R.LQAALSTGLFSR.I
R5/RRR5-14/2	1311.610	1312.497	-1442.941	0.399	1482.381	0.536	19	0.202	R.VLVGVVASPEADR.D
R5/RRR5-17/2	1312.497	1312.497	-0.430	0.487	1449.353	0.538	20	0.202	R.VLVGVVASPEADR.D
R5/RRR5-23/2	1312.170	1312.497	-250.310	0.459	1402.630	0.562	20	0.201	R.VLVGVVASPEADR.D
R5/RRR5-16/2	1264.132	1264.456	-256.626	0.481	1450.000	0.531	18	0.200	R.LQAALSTGLFSR.I
R5/RRR5-24/2	1610.119	1609.806	195.229	0.548	1487.693	0.508	22	0.199	K.LDISGHTVSAVGPDIK.H
R5/RRR5-14/2	1263.612	1264.456	-1463.159	0.419	1447.219	0.529	18	0.198	R.LQAALSTGLFSR.I
R5/RRR5-19/2	1264.568	1264.456	89.016	0.491	1428.649	0.531	18	0.198	R.LQAALSTGLFSR.I
R5/RRR5-13/2	1264.045	1264.456	-325.996	0.458	1503.211	0.497	17	0.198	R.LQAALSTGLFSR.I
R5/RRR5-13/2	1263.558	1264.456	-1506.439	0.438	1364.185	0.551	18	0.195	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1264.191	1264.456	-209.739	0.522	1394.328	0.531	18	0.195	R.LQAALSTGLFSR.I
R5/RRR5-1/2	1263.367	1264.456	-1658.044	0.356	1485.066	0.485	18	0.192	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1313.164	1312.497	-254.689	0.539	1250.427	0.571	19	0.189	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1312.150	1312.497	-265.524	0.445	1247.359	0.579	19	0.189	R.VLVGVVASPEADR.D
R5/RRR5-1/2	1264.003	1264.456	-359.619	0.474	1306.975	0.548	17	0.189	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1609.267	1609.806	-958.986	0.411	1428.526	0.484	22	0.188	K.LDISGHTVSAVGPDIK.H
R5/RRR5-25/2	1049.038	1049.270	-221.604	0.493	1648.648	0.370	17	0.188	R.LGVM*LTATAR.C
R5/RRR5-27/2	1312.288	1312.497	-159.693	0.461	1292.454	0.543	19	0.187	R.VLVGVVASPEADR.D
R5/RRR5-19/2	1312.676	1312.497	136.867	0.451	1310.521	0.537	18	0.186	R.VLVGVVASPEADR.D
R5/RRR5-27/2	1312.086	1312.497	-314.433	0.435	1287.626	0.549	18	0.186	R.VLVGVVASPEADR.D
R5/RRR5-18/2	1312.867	1312.497	282.797	0.515	1229.269	0.564	19	0.186	R.VLVGVVASPEADR.D
R5/RRR5-25/2	1311.627	1312.497	-1430.227	0.383	1564.788	0.407	20	0.186	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1263.990	1264.456	-369.696	0.508	1303.070	0.526	18	0.185	R.LQAALSTGLFSR.I
R5/RRR5-25/2	1609.294	1609.806	-941.852	0.407	1572.009	0.396	22	0.185	K.LDISGHTVSAVGPDIK.H
R5/RRR5-18/2	1312.102	1312.497	-302.299	0.404	1344.026	0.504	19	0.183	R.VLVGVVASPEADR.D
R5/RRR5-20/2	1311.580	1312.497	-1466.125	0.400	1324.108	0.511	19	0.182	R.VLVGVVASPEADR.D
R5/RRR5-17/2	1312.092	1312.497	-309.486	0.444	1275.624	0.527	19	0.182	R.VLVGVVASPEADR.D
R5/RRR5-18/2	1311.453	1312.497	-1563.267	0.399	1395.775	0.471	19	0.182	R.VLVGVVASPEADR.D
R5/RRR5-16/2	1311.681	1312.497	-1388.911	0.397	1270.525	0.530	19	0.181	R.VLVGVVASPEADR.D
R5/RRR5-24/2	1312.222	1312.497	-210.459	0.463	1277.656	0.516	19	0.180	R.VLVGVVASPEADR.D
R5/RRR5-20/2	1311.674	1312.497	-1393.771	0.379	1541.601	0.389	20	0.180	R.VLVGVVASPEADR.D
R5/RRR5-25/2	1312.035	1312.497	-353.079	0.439	1288.601	0.511	19	0.180	R.VLVGVVASPEADR.D
R5/RRR5-16/2	1263.757	1264.456	-1348.379	0.481	1257.635	0.517	18	0.180	R.LQAALSTGLFSR.I
R5/RRR5-15/2	1311.685	1312.497	-1385.359	0.425	1336.901	0.484	19	0.179	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1049.054	1049.270	-206.895	0.508	1460.779	0.413	16	0.178	R.LGVM*LTATAR.C
R5/RRR5-20/2	1264.061	1264.456	-313.303	0.424	1187.750	0.544	18	0.178	R.LQAALSTGLFSR.I
R5/RRR5-2/2	1312.296	1312.497	-153.721	0.464	1236.224	0.516	18	0.176	R.VLVGVVASPEADR.D
R5/RRR5-27/2	1312.161	1312.497	-257.030	0.459	1147.043	0.555	18	0.176	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1109.759	1110.271	-1365.806	0.406	1420.956	0.416	16	0.176	K.WMAAYPQSR.V
R5/RRR5-25/2	1312.051	1312.497	-341.037	0.399	1284.297	0.492	19	0.176	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/2	1609.490	1609.806	-196.768	0.474	1337.497	0.464	21	0.175	K.LDISGHTVSAVGPDIK.H
R5/RRR5-22/2	1049.465	1049.270	186.116	0.408	1465.753	0.394	16	0.175	R.LGVM*LTATAR.C
R5/RRR5-13/2	1264.430	1264.456	-20.781	0.468	1211.538	0.514	17	0.175	R.LQAALSTGLFSR.I
R5/RRR5-3/2	1264.089	1264.456	-291.310	0.446	1163.943	0.536	17	0.174	R.LQAALSTGLFSR.I
R5/RRR5-15/2	1049.072	1049.270	-189.385	0.484	1493.861	0.377	16	0.174	R.LGVM*LTATAR.C
R5/RRR5-21/2	1312.185	1312.497	-238.831	0.417	1158.135	0.535	18	0.173	R.VLVGVVASPEADR.D
R5/RRR5-24/2	1048.815	1049.270	-434.815	0.445	1380.555	0.417	16	0.172	R.LGVM*LTATAR.C
R5/RRR5-28/2	1312.124	1312.497	-285.497	0.455	1304.617	0.459	18	0.172	R.VLVGVVASPEADR.D
R5/RRR5-22/2	1311.649	1312.497	-1413.214	0.347	1286.402	0.472	19	0.171	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1312.114	1312.497	-292.871	0.414	1330.794	0.435	20	0.170	R.VLVGVVASPEADR.D
R5/RRR5-20/2	1312.048	1312.497	-343.744	0.446	1269.547	0.462	19	0.170	R.VLVGVVASPEADR.D
R5/RRR5-22/2	1312.274	1312.497	-170.518	0.443	1136.680	0.521	18	0.169	R.VLVGVVASPEADR.D
R5/RRR5-16/2	1531.905	1531.733	112.165	0.482	1465.162	0.360	18	0.169	K.DLYYDVLQFINK.L
R5/RRR5-16/2	1048.527	1049.270	-1667.676	0.441	1395.701	0.391	16	0.169	R.LGVM*LTATAR.C
R5/RRR5-16/2	1110.092	1110.271	-161.538	0.461	1254.242	0.444	15	0.168	K.WMAAYPQSR.V
R5/RRR5-13/2	1311.414	1312.497	-1593.190	0.348	1348.762	0.421	19	0.168	R.VLVGVVASPEADR.D
R5/RRR5-1/2	1312.170	1312.497	-249.750	0.423	1158.034	0.505	18	0.168	R.VLVGVVASPEADR.D
R5/RRR5-25/2	1048.635	1049.270	-1563.939	0.431	1397.117	0.381	16	0.167	R.LGVM*LTATAR.C
R5/RRR5-25/2	1049.057	1049.270	-203.510	0.451	1338.698	0.405	16	0.167	R.LGVM*LTATAR.C
R5/RRR5-17/2	1049.336	1049.270	63.275	0.389	1478.106	0.342	16	0.167	R.LGVM*LTATAR.C
R5/RRR5-2/2	1312.252	1312.497	-187.689	0.397	1246.292	0.450	18	0.165	R.VLVGVVASPEADR.D
R5/RRR5-15/2	1049.072	1049.270	-189.852	0.515	1394.003	0.372	16	0.165	R.LGVM*LTATAR.C
R5/RRR5-16/2	1048.498	1049.270	-1695.514	0.476	1318.034	0.399	16	0.164	R.LGVM*LTATAR.C
R5/RRR5-14/2	1050.108	1049.270	-155.269	0.460	1320.013	0.392	16	0.163	R.LGVM*LTATAR.C
R5/RRR5-25/2	1110.797	1110.271	-427.406	0.424	1132.965	0.471	14	0.163	K.WMAAYPQSR.V
R5/RRR5-15/2	1048.988	1049.270	-269.819	0.432	1330.307	0.384	16	0.163	R.LGVM*LTATAR.C
R5/RRR5-3/2	1312.030	1312.497	-357.280	0.344	1228.338	0.449	18	0.163	R.VLVGVVASPEADR.D
R5/RRR5-1/2	1312.106	1312.497	-298.658	0.385	1071.484	0.517	17	0.162	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-28/2	1312.245	1312.497	-192.448	0.427	996.020	0.537	17	0.161	R.VLVGVVASPEADR.D
R5/RRR5-5/2	1312.469	1312.497	-21.420	0.409	1145.364	0.469	18	0.161	R.VLVGVVASPEADR.D
R5/RRR5-1/2	1263.469	1264.456	-1576.898	0.432	1192.171	0.438	18	0.161	R.LQAALSTGLFSR.I
R5/RRR5-16/2	1048.711	1049.270	-1490.740	0.446	1369.617	0.353	16	0.160	R.LGVM*LTATAR.C
R5/RRR5-24/2	1048.950	1049.270	-305.780	0.481	1347.622	0.362	16	0.160	R.LGVM*LTATAR.C
R5/RRR5-16/2	1532.049	1531.733	206.297	0.505	1464.689	0.313	18	0.159	K.DLYYDVLQFINK.L
R5/RRR5-10/2	1312.265	1312.497	-177.237	0.421	1212.193	0.425	18	0.159	R.VLVGVVASPEADR.D
R5/RRR5-3/2	1312.453	1312.497	-34.014	0.417	1019.071	0.510	17	0.159	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1264.073	1264.456	-303.614	0.464	935.350	0.533	16	0.158	R.LQAALSTGLFSR.I
R5/RRR5-21/2	1312.030	1312.497	-357.093	0.362	1023.463	0.512	18	0.158	R.VLVGVVASPEADR.D
R5/RRR5-15/2	1109.862	1110.271	-369.519	0.406	1163.131	0.421	16	0.158	K.WMAAYPQSR.V
R5/RRR5-26/2	1126.162	1126.270	-96.076	0.438	1067.871	0.453	15	0.157	K.WM*AAYPQSR.V
R5/RRR5-26/2	1263.583	1264.456	-1486.642	0.353	1115.530	0.458	17	0.157	R.LQAALSTGLFSR.I
R5/RRR5-18/2	1264.094	1264.456	-287.241	0.397	1070.746	0.472	16	0.156	R.LQAALSTGLFSR.I
R5/RRR5-22/2	1263.582	1264.456	-1487.419	0.435	992.981	0.499	16	0.156	R.LQAALSTGLFSR.I
R5/RRR5-16/2	1109.983	1110.271	-260.277	0.432	1331.033	0.340	15	0.156	K.WMAAYPQSR.V
R5/RRR5-15/2	1109.956	1110.271	-283.889	0.396	1198.163	0.395	15	0.156	K.WMAAYPQSR.V
R5/RRR5-14/2	1048.631	1049.270	-1567.798	0.346	1428.027	0.291	16	0.155	R.LGVM*LTATAR.C
R5/RRR5-1/2	1312.175	1312.497	-246.390	0.368	1124.562	0.436	18	0.154	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1126.033	1126.270	-211.452	0.418	990.289	0.470	14	0.154	K.WM*AAYPQSR.V
R5/RRR5-15/2	1532.296	1531.733	-286.185	0.479	1407.997	0.302	18	0.154	K.DLYYDVLQFINK.L
R5/RRR5-25/2	1126.012	1126.270	-229.724	0.459	920.678	0.479	15	0.154	K.WM*AAYPQSR.V
R5/RRR5-16/2	1530.874	1531.733	-1217.956	0.326	1624.732	0.185	18	0.154	K.DLYYDVLQFINK.L
R5/RRR5-15/2	1109.899	1110.271	-335.530	0.463	1141.639	0.391	16	0.153	K.WMAAYPQSR.V
R5/RRR5-26/2	1048.468	1049.270	-1724.406	0.390	1210.491	0.375	15	0.152	R.LGVM*LTATAR.C
R5/RRR5-16/2	1109.417	1110.271	-1675.901	0.361	1195.270	0.378	15	0.152	K.WMAAYPQSR.V
R5/RRR5-14/2	1048.447	1049.270	-1744.059	0.416	1311.503	0.324	16	0.152	R.LGVM*LTATAR.C
R5/RRR5-26/2	1034.036	1033.271	-227.768	0.529	1063.676	0.428	15	0.152	R.LGVMLTATAR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1125.504	1126.270	-1573.741	0.381	1051.103	0.431	15	0.152	K.WM*AAYPQSR.V
R5/RRR5-16/2	1033.007	1033.271	-256.204	0.492	996.713	0.446	15	0.151	R.LGVMLTATAR.C
R5/RRR5-5/2	1264.038	1264.456	-331.422	0.346	1008.873	0.465	17	0.151	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1125.496	1126.270	-1580.824	0.413	899.637	0.474	15	0.151	K.WM*AAYPQSR.V
R5/RRR5-25/2	1134.180	1133.194	-12.912	0.553	1231.544	0.364	16	0.151	R.NTDQLEGSLR.E
R5/RRR5-26/2	1754.463	1754.945	-275.338	0.439	942.858	0.479	19	0.151	R.EELEKWM*AAYPQSR.V
R5/RRR5-14/2	1048.874	1049.270	-379.109	0.431	1268.781	0.330	16	0.150	R.LGVM*LTATAR.C
R5/RRR5-16/2	1125.914	1126.270	-317.283	0.343	957.131	0.470	14	0.150	K.WM*AAYPQSR.V
R5/RRR5-25/2	1109.446	1110.271	-1649.150	0.315	1134.537	0.395	15	0.149	K.WMAAYPQSR.V
R5/RRR5-2/2	1312.091	1312.497	-310.886	0.332	1084.786	0.421	17	0.149	R.VLVGVVASPEADR.D
R5/RRR5-25/2	1110.115	1110.271	-140.469	0.395	934.002	0.453	14	0.149	K.WMAAYPQSR.V
R5/RRR5-26/2	1109.871	1110.271	-361.132	0.392	1061.313	0.402	14	0.148	K.WMAAYPQSR.V
R5/RRR5-26/2	1126.304	1126.270	30.688	0.478	956.522	0.435	15	0.148	-.WM*AAYPQSR.-
R5/RRR5-28/2	1312.000	1312.497	-379.778	0.367	1008.790	0.439	17	0.148	R.VLVGVVASPEADR.D
R5/RRR5-13/2	1311.753	1312.497	-1333.765	0.332	1075.979	0.415	17	0.147	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1754.236	1754.945	-977.300	0.442	758.299	0.530	18	0.147	R.EELEKWM*AAYPQSR.V
R5/RRR5-16/2	1033.475	1033.271	197.892	0.485	986.608	0.419	15	0.147	R.LGVMLTATAR.C
R5/RRR5-15/2	1125.974	1126.270	-263.875	0.469	958.331	0.415	15	0.147	K.WM*AAYPQSR.V
R5/RRR5-26/2	1033.171	1033.271	-96.417	0.486	1042.470	0.399	15	0.147	R.LGVMLTATAR.C
R5/RRR5-25/2	1125.954	1126.270	-281.387	0.368	922.680	0.445	15	0.147	K.WM*AAYPQSR.V
R5/RRR5-21/2	1049.010	1049.270	-248.455	0.429	1169.205	0.350	15	0.147	R.LGVM*LTATAR.C
R5/RRR5-26/2	1110.161	1110.271	-98.995	0.396	1085.834	0.367	16	0.146	K.WMAAYPQSR.V
R5/RRR5-25/3	1911.077	1911.131	-28.395	0.484	1027.225	0.604	26	0.145	R.REELEKWM*AAYPQSR.V
R5/RRR5-16/2	1126.911	1126.270	-319.175	0.473	786.562	0.452	14	0.144	K.WM*AAYPQSR.V
R5/RRR5-25/2	1609.293	1609.806	-943.070	0.417	1152.832	0.337	22	0.143	K.LDISGHTVSAVGPDIK.H
R5/RRR5-16/2	1126.983	1126.270	-255.600	0.357	862.375	0.434	15	0.143	K.WM*AAYPQSR.V
R5/RRR5-26/2	1032.455	1033.271	-1764.303	0.425	924.729	0.399	15	0.142	R.LGVMLTATAR.C
R5/RRR5-17/2	1312.030	1312.497	-357.373	0.374	929.103	0.427	16	0.142	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1033.158	1033.271	-109.573	0.446	963.466	0.385	15	0.142	R.LGVMLTATAR.C
R5/RRR5-2/2	1263.389	1264.456	-1640.571	0.336	1117.165	0.343	17	0.142	R.LQAALSTGLFSR.I
R5/RRR5-25/2	1032.860	1033.271	-398.845	0.393	988.879	0.374	15	0.141	R.LGVMLTATAR.C
R5/RRR5-22/2	1311.602	1312.497	-1449.391	0.328	903.820	0.438	16	0.141	R.VLVGVVASPEADR.D
R5/RRR5-2/2	1263.708	1264.456	-1386.895	0.366	892.259	0.419	16	0.140	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1311.962	1312.497	-1173.410	0.342	1083.915	0.339	19	0.140	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1125.822	1126.270	-398.982	0.374	756.332	0.433	14	0.139	K.WM*AAYPQSR.V
R5/RRR5-25/2	1125.958	1126.270	-277.580	0.420	767.286	0.414	14	0.139	K.WM*AAYPQSR.V
R5/RRR5-1/2	1610.465	1609.806	-212.158	0.440	840.959	0.424	19	0.138	K.LDISGHTVSAVGPDIK.H
R5/RRR5-25/2	1133.295	1133.194	89.604	0.461	959.472	0.346	16	0.137	R.NTDQLEGSLR.E
R5/RRR5-26/2	1126.959	1126.270	-276.790	0.420	620.961	0.434	13	0.137	K.WM*AAYPQSR.V
R5/RRR5-21/2	1132.939	1133.194	-225.824	0.472	749.994	0.391	16	0.137	R.NTDQLEGSLR.E
R5/RRR5-21/2	1132.530	1133.194	-1474.022	0.370	764.819	0.404	16	0.137	R.NTDQLEGSLR.E
R5/RRR5-16/2	1033.127	1033.271	-139.322	0.368	887.221	0.369	15	0.136	R.LGVMLTATAR.C
R5/RRR5-14/2	1134.040	1133.194	-136.534	0.511	613.671	0.413	15	0.136	R.NTDQLEGSLR.E
R5/RRR5-25/2	1134.298	1133.194	92.007	0.499	745.987	0.392	15	0.136	R.NTDQLEGSLR.E
R5/RRR5-15/2	1033.380	1033.271	105.613	0.294	950.314	0.360	14	0.135	-.LGVMLTATAR.-
R5/RRR5-18/2	1132.781	1133.194	-365.609	0.339	734.509	0.395	16	0.134	R.NTDQLEGSLR.E
R5/RRR5-22/2	1132.925	1133.194	-238.579	0.486	773.658	0.359	16	0.134	R.NTDQLEGSLR.E
R5/RRR5-13/2	1134.260	1133.194	58.332	0.513	637.562	0.388	15	0.134	R.NTDQLEGSLR.E
R5/RRR5-15/2	1532.653	1531.733	-52.773	0.496	1020.446	0.329	16	0.134	K.DLYYDVLQFINK.L
R5/RRR5-27/2	1132.995	1133.194	-176.319	0.486	719.736	0.360	16	0.133	R.NTDQLEGSLR.E
R5/RRR5-15/2	921.460	922.014	-1691.014	0.365	806.026	0.345	12	0.133	R.CVFPDQR.L
R5/RRR5-15/2	1132.915	1133.194	-247.443	0.469	780.520	0.346	16	0.133	R.NTDQLEGSLR.E
R5/RRR5-15/2	1133.020	1133.194	-154.379	0.412	605.819	0.383	15	0.133	R.NTDQLEGSLR.E
R5/RRR5-25/2	1264.170	1264.456	-226.982	0.365	1000.262	0.306	17	0.133	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1110.127	1110.271	-130.100	0.373	826.445	0.342	14	0.133	K.WMAAYPQSR.V
R5/RRR5-26/2	921.804	922.014	-228.669	0.393	642.674	0.369	11	0.133	R.CVFPDQR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1132.975	1133.194	-193.721	0.493	724.053	0.352	16	0.132	R.NTDQLEGSLR.E
R5/RRR5-16/2	1132.857	1133.194	-298.901	0.395	755.315	0.348	16	0.132	R.NTDQLEGSLR.E
R5/RRR5-24/2	1133.009	1133.194	-163.782	0.465	781.606	0.340	16	0.132	R.NTDQLEGSLR.E
R5/RRR5-3/2	1132.916	1133.194	-245.930	0.405	752.733	0.344	16	0.132	R.NTDQLEGSLR.E
R5/RRR5-16/3	1609.979	1609.806	107.858	0.455	1053.555	0.545	29	0.132	K.LDISGHTVSAVGPDIK.H
R5/RRR5-19/2	1311.414	1312.497	-1593.003	0.289	842.548	0.387	15	0.132	R.VLVGVVASPEADR.D
R5/RRR5-23/2	1132.938	1133.194	-226.905	0.483	713.117	0.347	16	0.132	R.NTDQLEGSLR.E
R5/RRR5-25/2	921.847	922.014	-181.508	0.363	643.833	0.368	11	0.132	R.CVFPDQR.L
R5/RRR5-2/2	1132.989	1133.194	-181.723	0.404	724.056	0.344	16	0.132	R.NTDQLEGSLR.E
R5/RRR5-27/2	1132.390	1133.194	-1598.437	0.425	652.590	0.353	15	0.131	R.NTDQLEGSLR.E
R5/RRR5-1/2	1134.004	1133.194	-168.281	0.412	712.028	0.336	16	0.131	R.NTDQLEGSLR.E
R5/RRR5-1/2	1132.997	1133.194	-175.022	0.379	588.077	0.361	15	0.131	R.NTDQLEGSLR.E
R5/RRR5-21/2	1312.006	1312.497	-375.577	0.259	768.498	0.396	18	0.131	R.VLVGVVASPEADR.D
R5/RRR5-26/2	1132.428	1133.194	-1564.326	0.385	804.122	0.319	16	0.130	R.NTDQLEGSLR.E
R5/RRR5-19/2	1132.981	1133.194	-188.425	0.402	765.523	0.324	16	0.130	R.NTDQLEGSLR.E
R5/RRR5-26/2	1133.005	1133.194	-167.889	0.459	719.657	0.329	16	0.130	R.NTDQLEGSLR.E
R5/RRR5-23/2	1132.820	1133.194	-331.335	0.430	694.582	0.342	15	0.130	R.NTDQLEGSLR.E
R5/RRR5-1/2	1132.998	1133.194	-173.617	0.498	736.680	0.331	16	0.130	R.NTDQLEGSLR.E
R5/RRR5-28/2	1133.118	1133.194	-67.275	0.474	726.837	0.339	15	0.130	R.NTDQLEGSLR.E
R5/RRR5-27/2	1132.518	1133.194	-1484.200	0.398	643.943	0.345	15	0.130	R.NTDQLEGSLR.E
R5/RRR5-25/2	1132.944	1133.194	-221.392	0.465	746.915	0.321	16	0.130	R.NTDQLEGSLR.E
R5/RRR5-15/2	1125.381	1126.270	-1683.470	0.282	655.825	0.405	12	0.130	K.WM*AAYPQSR.V
R5/RRR5-21/2	1132.855	1133.194	-299.982	0.398	577.780	0.341	15	0.130	R.NTDQLEGSLR.E
R5/RRR5-15/2	921.940	922.014	-80.560	0.353	736.045	0.318	12	0.130	R.CVFPDQR.L
R5/RRR5-25/2	1132.992	1133.194	-179.129	0.491	794.262	0.314	16	0.129	R.NTDQLEGSLR.E
R5/RRR5-19/2	1132.219	1133.194	-1750.181	0.322	757.405	0.330	16	0.129	R.NTDQLEGSLR.E
R5/RRR5-25/2	921.973	922.014	-44.303	0.399	429.391	0.357	9	0.129	R.CVFPDQR.L
R5/RRR5-15/2	1264.266	1264.456	-150.555	0.359	373.758	0.414	13	0.129	R.LQAALSTGLFSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1530.785	1531.733	-1276.575	0.319	1308.203	0.157	17	0.129	K.DLYYDVLQFINK.L
R5/RRR5-16/2	1132.820	1133.194	-331.119	0.413	668.020	0.321	15	0.129	R.NTDQLEGSLR.E
R5/RRR5-26/2	922.038	922.014	26.477	0.425	453.279	0.336	9	0.128	R.CVFPDQR.L
R5/RRR5-17/2	1048.931	1049.270	-324.111	0.357	811.732	0.308	14	0.128	R.LGVM*LTATAR.C
R5/RRR5-15/2	1132.417	1133.194	-1574.397	0.352	699.761	0.308	16	0.128	R.NTDQLEGSLR.E
R5/RRR5-28/2	1132.463	1133.194	-1533.357	0.396	659.413	0.313	15	0.128	R.NTDQLEGSLR.E
R5/RRR5-16/2	921.905	922.014	-118.812	0.365	596.431	0.306	11	0.128	R.CVFPDQR.L
R5/RRR5-22/2	1132.282	1133.194	-1693.962	0.312	614.218	0.336	15	0.128	R.NTDQLEGSLR.E
R5/RRR5-1/2	921.540	922.014	-516.113	0.397	547.097	0.311	10	0.127	R.CVFPDQR.L
R5/RRR5-24/2	1132.990	1133.194	-180.859	0.391	684.686	0.301	15	0.127	R.NTDQLEGSLR.E
R5/RRR5-12/2	1312.204	1312.497	-223.991	0.287	749.328	0.366	14	0.127	R.VLVGVVASPEADR.D
R5/RRR5-28/2	1132.389	1133.194	-1598.546	0.381	513.804	0.351	15	0.127	-.NTDQLEGSLR.-
R5/RRR5-25/2	1132.994	1133.194	-177.400	0.389	395.629	0.288	13	0.127	R.NTDQLEGSLR.E
R5/RRR5-17/2	1049.125	1049.270	-139.076	0.317	653.546	0.343	13	0.127	R.LGVM*LTATAR.C
R5/RRR5-26/2	921.789	922.014	-244.346	0.322	590.689	0.308	11	0.127	R.CVFPDQR.L
R5/RRR5-24/3	1609.404	1609.806	-250.420	0.454	1035.015	0.527	28	0.127	K.LDISGHTVSAVGPDIK.H
R5/RRR5-19/2	1132.251	1133.194	-1721.258	0.300	625.100	0.322	15	0.126	R.NTDQLEGSLR.E
R5/RRR5-3/2	1133.100	1133.194	-83.376	0.357	727.221	0.281	16	0.126	R.NTDQLEGSLR.E
R5/RRR5-26/2	1110.957	1110.271	-282.972	0.281	684.114	0.323	13	0.126	K.WMAAYPQSR.V
R5/RRR5-25/2	1132.537	1133.194	-1467.743	0.396	692.333	0.277	15	0.125	R.NTDQLEGSLR.E
R5/RRR5-25/2	1033.113	1033.271	-153.427	0.336	770.623	0.272	15	0.125	R.LGVMLTATAR.C
R5/RRR5-20/2	1132.501	1133.194	-1499.358	0.336	670.829	0.276	15	0.125	R.NTDQLEGSLR.E
R5/RRR5-23/2	921.872	922.014	-154.277	0.351	511.433	0.262	10	0.125	R.CVFPDQR.L
R5/RRR5-6/2	1313.285	1312.497	-161.996	0.316	376.557	0.281	15	0.125	R.VLVGVVASPEADR.D
R5/RRR5-15/2	921.775	922.014	-259.492	0.329	834.423	0.241	12	0.125	R.CVFPDQR.L
R5/RRR5-2/2	1132.812	1133.194	-338.254	0.449	581.966	0.329	14	0.125	-.NTDQLEGSLR.-
R5/RRR5-22/2	1132.395	1133.194	-1593.889	0.347	633.923	0.265	15	0.125	R.NTDQLEGSLR.E
R5/RRR5-22/2	1126.652	1126.270	339.961	0.333	314.810	0.438	11	0.124	-.WM*AAYPQSR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	921.944	922.014	-75.513	0.383	519.988	0.249	10	0.124	R.CVFPDQR.L
R5/RRR5-26/2	1311.483	1312.497	-1540.172	0.299	839.015	0.275	17	0.124	R.VLVGVVASPEADR.D
R5/RRR5-25/2	1126.293	1126.270	20.578	0.200	298.309	0.296	11	0.124	K.WM*AAYPQSR.V
R5/RRR5-26/2	1132.513	1133.194	-1488.964	0.381	662.055	0.258	15	0.124	R.NTDQLEGSLR.E
R5/RRR5-20/2	1132.596	1133.194	-1415.345	0.383	449.858	0.296	14	0.124	-.NTDQLEGSLR.-
R5/RRR5-22/2	1048.665	1049.270	-1535.407	0.270	779.902	0.286	13	0.124	R.LGVM*LTATAR.C
R5/RRR5-17/2	1132.964	1133.194	-203.773	0.394	611.208	0.246	15	0.124	R.NTDQLEGSLR.E
R5/RRR5-20/2	1132.150	1133.194	-1810.956	0.312	700.602	0.254	15	0.123	R.NTDQLEGSLR.E
R5/RRR5-2/2	1132.479	1133.194	-1519.172	0.356	585.129	0.243	14	0.123	R.NTDQLEGSLR.E
R5/RRR5-25/2	1264.191	1264.456	-209.739	0.328	672.083	0.268	16	0.123	R.LQAALSTGLFSR.I
R5/RRR5-26/2	1048.451	1049.270	-1740.550	0.331	783.850	0.245	14	0.123	R.LGVM*LTATAR.C
R5/RRR5-16/2	1311.508	1312.497	-1521.285	0.331	802.234	0.266	16	0.123	R.VLVGVVASPEADR.D
R5/RRR5-16/3	1610.058	1609.806	156.902	0.496	943.451	0.538	28	0.122	K.LDISGHTVSAVGPDIK.H
R5/RRR5-18/2	1132.331	1133.194	-1650.530	0.296	606.960	0.260	13	0.122	R.NTDQLEGSLR.E
R5/RRR5-5/2	1263.615	1264.456	-1461.024	0.308	604.123	0.288	14	0.122	R.LQAALSTGLFSR.I
R5/RRR5-1/2	921.954	922.014	-65.021	0.372	435.413	0.257	9	0.122	-.CVFPDQR.-
R5/RRR5-16/2	921.596	922.014	-454.171	0.358	398.405	0.333	9	0.122	-.CVFPDQR.-
R5/RRR5-5/2	1610.434	1609.806	-231.321	0.315	376.477	0.308	16	0.122	K.LDISGHTVSAVGPDIK.H
R5/RRR5-16/3	1910.916	1911.131	-113.068	0.486	788.727	0.582	24	0.122	R.REELEKWM*AAYPQSR.V
R5/RRR5-16/3	1609.730	1609.806	-47.288	0.459	1084.740	0.488	29	0.121	K.LDISGHTVSAVGPDIK.H
R5/RRR5-25/2	921.696	922.014	-345.460	0.365	401.012	0.301	9	0.121	-.CVFPDQR.-
R5/RRR5-25/3	1609.937	1609.806	81.738	0.473	1087.608	0.482	29	0.120	K.LDISGHTVSAVGPDIK.H
R5/RRR5-24/3	1610.017	1609.806	131.810	0.463	1053.167	0.494	29	0.120	K.LDISGHTVSAVGPDIK.H
R5/RRR5-13/2	1048.947	1049.270	-308.582	0.217	1017.107	0.163	15	0.120	R.LGVM*LTATAR.C
R5/RRR5-15/2	1740.105	1738.945	92.060	0.207	233.044	0.382	13	0.118	R.EELEKWMAAYPQSR.V
R5/RRR5-16/2	1313.464	1312.497	-25.319	0.255	587.057	0.237	14	0.118	-.VLVGVVASPEADR.-
R5/RRR5-23/2	921.171	922.014	-2006.951	0.344	446.316	0.292	9	0.117	-.CVFPDQR.-
R5/RRR5-25/3	1610.732	1609.806	-46.157	0.490	852.238	0.534	27	0.116	K.LDISGHTVSAVGPDIK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/3	1910.025	1911.131	-1105.934	0.386	1059.662	0.468	25	0.115	R.REELEKWM*AAYPQSR.V
R5/RRR5-14/2	1034.090	1033.271	-175.305	0.257	823.044	0.210	14	0.114	-.LGVMLTATAR.-
R5/RRR5-26/3	1911.014	1911.131	-61.455	0.443	797.458	0.540	24	0.114	R.REELEKWM*AAYPQSR.V
R5/RRR5-26/3	1911.056	1911.131	-39.543	0.462	796.324	0.538	25	0.114	R.REELEKWM*AAYPQSR.V
R5/RRR5-15/3	1910.668	1911.131	-243.134	0.472	885.340	0.503	24	0.112	R.REELEKWM*AAYPQSR.V
R5/RRR5-15/3	1911.839	1911.131	-153.200	0.465	759.948	0.528	24	0.110	R.REELEKWM*AAYPQSR.V
R5/RRR5-15/2	1740.164	1738.945	126.111	0.238	145.171	0.371	10	0.110	-.EELEKWMAAYPQSR.-
R5/RRR5-19/3	1610.723	1609.806	-51.288	0.483	774.219	0.523	25	0.110	K.LDISGHTVSAVGPDIK.H
R5/RRR5-16/3	1909.461	1911.131	-1927.875	0.392	873.188	0.487	23	0.107	R.REELEKWM*AAYPQSR.V
R5/RRR5-25/3	1609.979	1609.806	107.744	0.465	882.797	0.479	28	0.107	K.LDISGHTVSAVGPDIK.H
R5/RRR5-26/3	1911.196	1911.131	33.780	0.501	675.559	0.523	24	0.107	R.REELEKWM*AAYPQSR.V
R5/RRR5-16/3	1755.511	1754.945	-247.633	0.447	1013.995	0.442	26	0.106	R.EELEKWM*AAYPQSR.V
R5/RRR5-26/3	1910.551	1911.131	-829.650	0.393	695.635	0.520	23	0.105	R.REELEKWM*AAYPQSR.V
R5/RRR5-24/3	1609.441	1609.806	-227.135	0.445	756.786	0.496	25	0.104	K.LDISGHTVSAVGPDIK.H
R5/RRR5-2/3	1610.726	1609.806	-49.691	0.447	881.033	0.458	27	0.103	K.LDISGHTVSAVGPDIK.H
R5/RRR5-25/3	1910.743	1911.131	-203.717	0.437	758.994	0.480	23	0.102	R.REELEKWM*AAYPQSR.V
R5/RRR5-15/3	1608.454	1609.806	-1466.633	0.364	658.113	0.499	25	0.101	K.LDISGHTVSAVGPDIK.H
R5/RRR5-26/3	1313.058	1312.497	-335.424	0.496	892.468	0.443	24	0.101	R.VLVGVVASPEADR.D
R5/RRR5-26/3	1312.629	1312.497	100.764	0.461	920.798	0.426	25	0.098	R.VLVGVVASPEADR.D
R5/RRR5-16/3	1909.394	1911.131	-1963.146	0.396	560.291	0.487	19	0.097	R.REELEKWM*AAYPQSR.V
R5/RRR5-25/3	1909.536	1911.131	-1888.173	0.340	650.927	0.475	22	0.097	R.REELEKWM*AAYPQSR.V
R5/RRR5-21/3	1610.561	1609.806	-152.211	0.412	646.495	0.461	24	0.096	K.LDISGHTVSAVGPDIK.H
R5/RRR5-27/3	1609.287	1609.806	-946.734	0.438	652.474	0.453	25	0.096	K.LDISGHTVSAVGPDIK.H
R5/RRR5-16/3	1755.780	1754.945	-93.937	0.461	780.610	0.458	22	0.095	R.EELEKWM*AAYPQSR.V
R5/RRR5-24/3	1909.536	1911.131	-1888.366	0.402	838.581	0.426	23	0.095	R.REELEKWM*AAYPQSR.V
R5/RRR5-24/3	1912.652	1911.131	-251.204	0.373	502.491	0.448	21	0.093	R.REELEKWM*AAYPQSR.V
R5/RRR5-26/3	1312.452	1312.497	-34.817	0.432	728.041	0.443	22	0.093	R.VLVGVVASPEADR.D
R5/RRR5-16/3	1312.654	1312.497	119.790	0.432	722.845	0.442	22	0.093	R.VLVGVVASPEADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/3	1609.440	1609.806	-227.706	0.373	691.144	0.400	25	0.089	K.LDISGHTVSAVGPDIK.H
R5/RRR5-14/3	1909.876	1911.131	-1184.583	0.332	559.859	0.401	20	0.087	R.REELEKWM*AAYPQSR.V
R5/RRR5-27/3	1609.591	1609.806	-133.894	0.350	967.286	0.341	27	0.086	K.LDISGHTVSAVGPDIK.H
R5/RRR5-26/3	1909.485	1911.131	-1915.347	0.345	730.122	0.370	23	0.085	R.REELEKWM*AAYPQSR.V
R5/RRR5-17/3	1610.955	1609.806	93.276	0.350	591.600	0.395	24	0.085	-.LDISGHTVSAVGPDIK.-
R5/RRR5-25/3	1909.944	1911.131	-1148.578	0.279	559.214	0.374	19	0.084	R.REELEKWM*AAYPQSR.V
R5/RRR5-25/3	1910.686	1911.131	-233.808	0.364	545.797	0.337	21	0.083	R.REELEKWM*AAYPQSR.V
R5/RRR5-16/3	1312.528	1312.497	23.813	0.347	789.220	0.372	21	0.083	R.VLVGVVASPEADR.D
R5/RRR5-23/3	1609.317	1609.806	-304.298	0.315	728.579	0.326	25	0.080	K.LDISGHTVSAVGPDIK.H
R5/RRR5-17/3	1609.923	1609.806	73.297	0.319	667.573	0.298	23	0.078	K.LDISGHTVSAVGPDIK.H
R5/RRR5-17/3	1609.737	1609.806	-42.724	0.297	662.370	0.208	22	0.062	-.LDISGHTVSAVGPDIK.-
R5/RRR5-16/3	1754.481	1754.945	-265.434	0.277	971.975	0.143	24	0.059	R.EELEKWM*AAYPQSR.V
R5/RRR5-16/2	1794.337	1795.025	-943.458	0.464	2548.887	0.528	26	0.371	K.LTVSTVSSSGVGLTSTAVK.K
R5/RRR5-15/2	1795.549	1795.025	-266.319	0.491	2369.802	0.603	25	0.360	K.LTVSTVSSSGVGLTSTAVK.K
R5/RRR5-16/2	1794.542	1795.025	-270.017	0.450	2229.079	0.590	24	0.328	K.LTVSTVSSSGVGLTSTAVK.K
R5/RRR5-15/2	1795.443	1795.025	233.587	0.498	2038.780	0.631	25	0.307	K.LTVSTVSSSGVGLTSTAVK.K
R5/RRR5-15/2	1766.409	1766.977	-890.448	0.579	2026.867	0.583	24	0.294	R.RLSTNENTLTVGGLYK.V
R5/RRR5-15/2	1795.252	1795.025	126.402	0.538	1935.362	0.583	24	0.276	K.LTVSTVSSSGVGLTSTAVK.K
R5/RRR5-16/2	1794.384	1795.025	-917.437	0.422	1796.270	0.593	24	0.257	K.LTVSTVSSSGVGLTSTAVK.K
R5/RRR5-15/2	1530.478	1530.747	-176.206	0.493	1851.378	0.536	21	0.253	K.KGGLYTLDVSSVYK.Y
R5/RRR5-15/2	1530.337	1530.747	-268.950	0.465	1626.620	0.504	21	0.216	K.KGGLYTLDVSSVYK.Y
R5/RRR5-15/2	1297.210	1297.436	-175.235	0.471	1485.911	0.562	18	0.212	K.SVLTISGEFDTK.A
R5/RRR5-15/2	1297.183	1297.436	-195.815	0.469	1404.120	0.558	18	0.203	K.SVLTISGEFDTK.A
R5/RRR5-15/2	1610.229	1610.790	-972.860	0.495	1235.997	0.531	19	0.179	R.LSTNENTLTVGGLYK.V
R5/RRR5-16/2	1610.489	1610.790	-187.827	0.473	1199.237	0.541	20	0.178	R.LSTNENTLTVGGLYK.V
R5/RRR5-16/2	1610.400	1610.790	-243.262	0.478	1266.371	0.502	21	0.178	R.LSTNENTLTVGGLYK.V
R5/RRR5-15/2	1147.099	1147.309	-183.330	0.467	1266.874	0.496	16	0.177	K.GPGLFSDIGKR.A
R5/RRR5-15/2	1347.332	1347.631	-222.513	0.487	1442.706	0.401	18	0.175	K.LAALLQHEVKPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1347.439	1347.631	-143.079	0.485	1293.159	0.462	17	0.173	K.LAALLQHEVKPK.S
R5/RRR5-15/2	1297.038	1297.436	-308.264	0.446	1214.262	0.480	18	0.170	K.SVLTISGEFDTK.A
R5/RRR5-15/2	1611.202	1610.790	256.498	0.513	1029.571	0.551	19	0.167	R.LSTNENTLTVGGLYK.V
R5/RRR5-16/2	961.443	962.083	-1710.342	0.401	1619.095	0.252	15	0.164	K.SSVVAELTR.R
R5/RRR5-15/2	1610.074	1610.790	-1069.378	0.476	989.146	0.520	19	0.159	R.LSTNENTLTVGGLYK.V
R5/RRR5-16/3	1530.791	1530.747	29.096	0.446	1811.371	0.311	28	0.159	K.KGGLYTLDVSSVYK.Y
R5/RRR5-15/2	1147.021	1147.309	-251.979	0.430	1222.302	0.405	16	0.158	K.GPGLFSDIGKR.A
R5/RRR5-15/2	1403.975	1402.574	286.509	0.474	916.111	0.521	17	0.154	K.GGLYTLDVSSVYK.Y
R5/RRR5-16/2	1531.303	1530.747	-290.848	0.494	933.234	0.488	19	0.152	K.KGGLYTLDVSSVYK.Y
R5/RRR5-15/2	961.300	962.083	-1860.252	0.390	1389.409	0.269	14	0.149	K.SSVVAELTR.R
R5/RRR5-16/2	1297.194	1297.436	-187.224	0.346	824.901	0.549	15	0.149	K.SVLTISGEFDTK.A
R5/RRR5-15/2	961.994	962.083	-92.224	0.439	1449.596	0.225	15	0.146	K.SSVVAELTR.R
R5/RRR5-15/3	1530.951	1530.747	133.459	0.466	1773.196	0.290	28	0.146	K.KGGLYTLDVSSVYK.Y
R5/RRR5-15/2	961.323	962.083	-1835.626	0.378	1466.545	0.212	14	0.146	K.SSVVAELTR.R
R5/RRR5-16/2	962.028	962.083	-56.967	0.421	1399.416	0.230	14	0.143	K.SSVVAELTR.R
R5/RRR5-15/2	1146.497	1147.309	-1584.856	0.416	857.160	0.437	14	0.140	K.GPGLFSDIGKR.A
R5/RRR5-16/2	1610.211	1610.790	-983.592	0.444	835.480	0.447	18	0.140	R.LSTNENTLTVGGLYK.V
R5/RRR5-16/2	961.443	962.083	-1710.980	0.394	1417.123	0.190	14	0.139	K.SSVVAELTR.R
R5/RRR5-16/2	1297.133	1297.436	-234.239	0.291	965.383	0.382	16	0.136	K.SVLTISGEFDTK.A
R5/RRR5-15/3	1530.829	1530.747	53.569	0.476	1570.324	0.342	28	0.134	K.KGGLYTLDVSSVYK.Y
R5/RRR5-16/2	1146.886	1147.309	-369.546	0.392	868.583	0.353	14	0.131	K.GPGLFSDIGKR.A
R5/RRR5-15/2	1401.653	1402.574	-1374.792	0.396	679.397	0.438	14	0.130	K.GGLYTLDVSSVYK.Y
R5/RRR5-17/2	962.159	962.083	79.837	0.303	683.900	0.156	15	0.118	K.SSVVAELTR.R
R5/RRR5-15/3	1530.658	1530.747	-58.010	0.475	1564.583	0.279	27	0.117	K.KGGLYTLDVSSVYK.Y
R5/RRR5-15/2	957.920	958.182	-274.433	0.435	724.068	0.539	15	0.116	K.FGLALALRP.-
R5/RRR5-15/2	957.966	958.182	-226.747	0.363	597.218	0.477	14	0.111	K.FGLALALRP.-
R5/RRR5-16/2	958.023	958.182	-166.667	0.349	583.032	0.518	13	0.109	K.FGLALALRP.-
R5/RRR5-15/2	957.986	958.182	-205.654	0.343	548.037	0.445	13	0.108	K.FGLALALRP.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1147.463	1147.309	134.954	0.355	671.243	0.516	22	0.096	K.GPGLFSDIGKR.A
R5/RRR5-16/3	1530.610	1530.747	-89.809	0.455	1101.542	0.350	23	0.094	-.KGGLYTLDVSSVYK.-
R5/RRR5-15/3	1147.052	1147.309	-224.605	0.352	533.657	0.520	20	0.094	K.GPGLFSDIGKR.A
R5/RRR5-15/3	1147.116	1147.309	-168.557	0.297	452.439	0.489	19	0.088	K.GPGLFSDIGKR.A
R5/RRR5-16/3	1147.500	1147.309	167.120	0.341	306.247	0.492	16	0.084	-.GPGLFSDIGKR.-
R5/RRR5-16/3	1147.897	1147.309	-360.326	0.184	508.743	0.334	19	0.072	K.GPGLFSDIGKR.A
R5/RRR5-6/2	1880.424	1880.002	224.854	0.561	2459.608	0.472	24	0.335	K.SWEDLTSDKDAIETIR.A
R5/RRR5-6/2	1879.279	1880.002	-919.904	0.515	2386.459	0.449	23	0.314	K.SWEDLTSDKDAIETIR.A
R5/RRR5-6/2	1880.329	1880.002	174.272	0.526	2298.810	0.444	24	0.297	K.SWEDLTSDKDAIETIR.A
R5/RRR5-6/2	1855.328	1855.901	-850.411	0.559	2180.864	0.468	24	0.285	R.TAWWDGSAVYGNNEER.A
R5/RRR5-6/3	1455.814	1455.770	30.679	0.449	1992.554	0.325	27	0.196	K.VPVPIGLLYLNTR.R
R5/RRR5-6/2	1751.669	1752.050	-217.982	0.506	1347.878	0.543	24	0.193	K.DTFGHIGGPILGGLVGLK.K
R5/RRR5-6/3	1454.453	1454.695	-166.822	0.516	1662.915	0.478	26	0.190	K.VHTIDWTVELLK.T
R5/RRR5-6/2	1751.518	1752.050	-877.117	0.513	1277.602	0.556	24	0.188	K.DTFGHIGGPILGGLVGLK.K
R5/RRR5-6/2	1634.974	1633.915	35.825	0.561	1471.820	0.468	20	0.188	R.NSWAGVSILQALFVK.E
R5/RRR5-6/2	1750.839	1752.050	-1266.478	0.460	1368.800	0.449	24	0.176	K.DTFGHIGGPILGGLVGLK.K
R5/RRR5-6/2	1628.523	1628.720	-121.240	0.524	974.677	0.573	20	0.170	R.FFTSNFNEETYTK.K
R5/RRR5-6/2	1520.801	1521.700	-1252.753	0.404	1240.164	0.453	20	0.167	R.SDRIDLAALEVYR.D
R5/RRR5-6/2	1455.480	1455.770	-199.755	0.374	915.272	0.581	18	0.161	K.VPVPIGLLYLNTR.R
R5/RRR5-6/2	1021.807	1022.181	-367.272	0.432	1116.436	0.461	15	0.161	R.ANWYGLLGK.K
R5/RRR5-6/2	1521.306	1521.700	-259.601	0.451	1088.518	0.481	19	0.161	R.SDRIDLAALEVYR.D
R5/RRR5-6/3	1456.367	1455.770	-277.449	0.474	1780.001	0.324	25	0.160	K.VPVPIGLLYLNTR.R
R5/RRR5-6/3	1455.766	1455.770	-2.247	0.436	1887.858	0.271	26	0.160	K.VPVPIGLLYLNTR.R
R5/RRR5-6/2	1455.319	1455.770	-310.829	0.395	874.534	0.574	19	0.160	K.VPVPIGLLYLNTR.R
R5/RRR5-1/2	1456.361	1455.770	-281.182	0.381	747.760	0.579	18	0.152	K.VPVPIGLLYLNTR.R
R5/RRR5-6/2	1021.897	1022.181	-279.657	0.410	979.389	0.459	15	0.152	R.ANWYGLLGK.K
R5/RRR5-6/2	1455.577	1455.770	-132.449	0.428	624.576	0.532	17	0.144	K.VPVPIGLLYLNTR.R
R5/RRR5-6/2	1021.381	1022.181	-1768.028	0.352	850.500	0.468	14	0.143	R.ANWYGLLGK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1454.426	1454.695	-185.925	0.476	518.439	0.525	18	0.143	K.VHTIDWTVELLK.T
R5/RRR5-6/2	1521.022	1521.700	-1106.873	0.460	933.990	0.401	19	0.141	R.SDRIDLAALEVYR.D
R5/RRR5-6/2	1293.431	1293.537	-82.223	0.381	750.771	0.497	17	0.140	K.LVIGDDGLLLHK.E
R5/RRR5-6/2	1627.657	1628.720	-1271.232	0.458	627.592	0.491	18	0.139	R.FFTSNFNEETYTK.K
R5/RRR5-6/2	1635.190	1633.915	168.725	0.510	996.078	0.371	17	0.134	-.NSWAGVSILQALFVK.-
R5/RRR5-2/2	1455.143	1455.770	-1121.477	0.355	444.624	0.507	14	0.133	K.VPVPIGLLYLNTR.R
R5/RRR5-1/2	1456.199	1455.770	296.077	0.356	524.658	0.476	15	0.132	K.VPVPIGLLYLNTR.R
R5/RRR5-6/3	1993.347	1993.381	-17.089	0.474	1163.391	0.506	34	0.132	K.IKDTFGHIGGPILGGLVGLK.K
R5/RRR5-6/2	1456.123	1455.770	243.708	0.349	447.712	0.483	15	0.132	K.VPVPIGLLYLNTR.R
R5/RRR5-6/2	1454.115	1454.695	-1090.189	0.410	333.296	0.430	15	0.129	K.VHTIDWTVELLK.T
R5/RRR5-5/2	1455.669	1455.770	-69.106	0.319	440.681	0.452	15	0.129	K.VPVPIGLLYLNTR.R
R5/RRR5-2/2	1454.576	1455.770	-1512.478	0.339	579.060	0.380	16	0.127	K.VPVPIGLLYLNTR.R
R5/RRR5-1/2	1455.941	1455.770	117.849	0.273	424.050	0.430	14	0.125	K.VPVPIGLLYLNTR.R
R5/RRR5-6/2	1453.861	1454.695	-1265.293	0.315	296.483	0.367	14	0.124	K.VHTIDWTVELLK.T
R5/RRR5-3/2	1455.423	1455.770	-238.628	0.284	419.598	0.427	12	0.123	K.VPVPIGLLYLNTR.R
R5/RRR5-6/3	1879.848	1880.002	-82.568	0.386	1228.221	0.456	32	0.123	K.SWEDLTSDKDAIETIR.A
R5/RRR5-6/2	1456.531	1455.770	-164.137	0.313	272.358	0.467	11	0.123	-.VPVPIGLLYLNTR.-
R5/RRR5-3/2	1455.591	1455.770	-123.027	0.231	363.846	0.329	13	0.120	K.VPVPIGLLYLNTR.R
R5/RRR5-6/3	1454.466	1454.695	-158.234	0.504	1246.321	0.413	24	0.119	K.VHTIDWTVELLK.T
R5/RRR5-6/3	1521.163	1521.700	-1013.170	0.468	1380.061	0.328	26	0.111	R.SDRIDLAALEVYR.D
R5/RRR5-6/3	1521.362	1521.700	-222.661	0.481	1203.341	0.378	24	0.107	-.SDRIDLAALEVYR.-
R5/RRR5-6/3	1453.871	1454.695	-1258.473	0.497	1082.667	0.405	24	0.103	-.VHTIDWTVELLK.-
R5/RRR5-6/3	1521.205	1521.700	-326.632	0.486	1158.025	0.350	23	0.098	-.SDRIDLAALEVYR.-
R5/RRR5-15/2	1367.101	1367.556	-334.174	0.559	1891.468	0.579	22	0.272	K.FDVGNVVM*VTGGR.N
R5/RRR5-15/2	1351.300	1351.557	-190.601	0.480	1700.013	0.545	22	0.235	K.FDVGNVVMVTGGR.N
R5/RRR5-15/2	1366.648	1367.556	-1400.483	0.496	1726.976	0.514	21	0.231	K.FDVGNVVM*VTGGR.N
R5/RRR5-15/3	1883.833	1884.186	-187.812	0.442	1837.109	0.431	27	0.209	R.TDKTYPAGFMDVISIPK.T
R5/RRR5-15/2	1366.508	1367.556	-1503.575	0.437	1321.355	0.481	20	0.179	K.FDVGNVVM*VTGGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	949.118	949.129	-11.689	0.493	1009.331	0.579	15	0.175	R.LGNVFTIGK.G
R5/RRR5-15/2	1350.369	1351.557	-1624.933	0.411	1308.529	0.460	18	0.173	K.FDVGNVVMVTGGR.N
R5/RRR5-16/2	948.781	949.129	-367.602	0.454	1046.627	0.555	15	0.172	R.LGNVFTIGK.G
R5/RRR5-15/2	948.479	949.129	-1744.434	0.442	1060.185	0.527	15	0.168	R.LGNVFTIGK.G
R5/RRR5-15/2	1351.190	1351.557	-272.350	0.506	1184.257	0.482	18	0.168	K.FDVGNVVMVTGGR.N
R5/RRR5-15/2	1899.535	1900.185	-871.369	0.486	1097.113	0.535	21	0.167	R.TDKTYPAGFM*DVISIPK.T
R5/RRR5-15/2	948.623	949.129	-1592.387	0.464	1024.657	0.527	15	0.167	R.LGNVFTIGK.G
R5/RRR5-14/2	1368.041	1367.556	355.635	0.455	1149.683	0.470	18	0.163	K.FDVGNVVM*VTGGR.N
R5/RRR5-15/2	948.614	949.129	-1601.565	0.512	1076.716	0.471	15	0.162	R.LGNVFTIGK.G
R5/RRR5-15/3	1483.810	1483.818	-5.340	0.542	1882.867	0.294	25	0.161	K.SRECLPLILIIR.N
R5/RRR5-16/2	948.766	949.129	-383.997	0.510	926.900	0.523	14	0.160	R.LGNVFTIGK.G
R5/RRR5-15/2	1483.997	1483.818	120.736	0.565	1194.491	0.345	17	0.143	K.SRECLPLILIIR.N
R5/RRR5-15/2	1484.456	1483.818	-244.601	0.541	1169.301	0.327	17	0.140	K.SRECLPLILIIR.N
R5/RRR5-15/2	1126.109	1126.333	-199.577	0.430	533.362	0.507	14	0.139	K.GNKPWVSLPK.G
R5/RRR5-15/3	1483.160	1483.818	-1121.434	0.552	1594.113	0.344	25	0.139	-.SRECLPLILIIR.-
R5/RRR5-15/3	1484.023	1483.818	138.587	0.569	1699.120	0.300	26	0.139	-.SRECLPLILIIR.-
R5/RRR5-15/2	1126.019	1126.333	-279.404	0.456	719.602	0.439	14	0.138	K.GNKPWVSLPK.G
R5/RRR5-15/2	1482.880	1483.818	-1310.549	0.489	1057.515	0.346	16	0.138	K.SRECLPLILIIR.N
R5/RRR5-16/2	1483.849	1483.818	21.073	0.503	1060.470	0.333	16	0.135	K.SRECLPLILIIR.N
R5/RRR5-15/2	1105.058	1105.334	-249.998	0.382	810.513	0.400	13	0.133	R.EVISILM*QR.H
R5/RRR5-16/2	1126.204	1126.333	-114.544	0.374	461.622	0.421	13	0.129	K.GNKPWVSLPK.G
R5/RRR5-15/2	1126.000	1126.333	-296.806	0.376	606.212	0.386	14	0.129	K.GNKPWVSLPK.G
R5/RRR5-15/2	987.972	988.120	-150.585	0.453	927.114	0.263	13	0.128	K.LSIIEEQR.K
R5/RRR5-15/2	987.575	988.120	-1568.817	0.457	963.021	0.248	13	0.127	K.LSIIEEQR.K
R5/RRR5-16/2	988.003	988.120	-118.732	0.428	940.549	0.248	13	0.126	K.LSIIEEQR.K
R5/RRR5-15/2	987.826	988.120	-298.474	0.440	945.134	0.229	13	0.124	K.LSIIEEQR.K
R5/RRR5-15/2	1548.381	1548.805	-274.751	0.423	873.494	0.286	18	0.124	K.IDLETNKIVDFIK.F
R5/RRR5-16/2	988.935	988.120	-187.828	0.523	981.598	0.237	13	0.124	K.LSIIEEQR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	987.304	988.120	-1844.800	0.335	1053.056	0.151	13	0.120	K.LSIIEEQR.K
R5/RRR5-15/2	1548.423	1548.805	-248.017	0.461	941.571	0.181	18	0.114	K.IDLETNKIVDFIK.F
R5/RRR5-15/3	1216.664	1216.454	172.966	0.450	1504.784	0.301	25	0.111	R.TIRYPDPIIK.A
R5/RRR5-15/3	1475.554	1475.626	-49.431	0.435	907.295	0.456	23	0.101	K.ANDTIKIDLETNK.I
R5/RRR5-15/3	1475.738	1475.626	76.020	0.470	755.892	0.482	22	0.099	K.ANDTIKIDLETNK.I
R5/RRR5-15/3	1475.179	1475.626	-304.537	0.438	770.304	0.468	23	0.097	K.ANDTIKIDLETNK.I
R5/RRR5-15/3	1900.442	1900.185	135.427	0.381	901.445	0.441	23	0.096	R.TDKTYPAGFM*DVISIPK.T
R5/RRR5-15/3	1216.696	1216.454	199.075	0.493	1247.792	0.287	23	0.091	R.TIRYPDPIIK.A
R5/RRR5-16/3	1483.813	1483.818	-3.236	0.493	1161.397	0.293	22	0.087	-.SRECLPLILIIR.-
R5/RRR5-15/3	1216.562	1216.454	88.895	0.462	812.623	0.349	20	0.085	R.TIRYPDPIIK.A
R5/RRR5-16/3	1216.421	1216.454	-27.802	0.330	457.940	0.231	21	0.084	R.TIRYPDPIIK.A
R5/RRR5-16/3	1216.286	1216.454	-138.335	0.364	494.876	0.271	19	0.083	R.TIRYPDPIIK.A
R5/RRR5-15/3	1900.916	1900.185	-141.824	0.387	519.161	0.362	20	0.076	R.TDKTYPAGFM*DVISIPK.T
R5/RRR5-16/3	1483.856	1483.818	26.097	0.421	905.898	0.269	22	0.075	K.SRECLPLILIIR.N
R5/RRR5-15/3	1216.398	1216.454	-46.223	0.351	922.440	0.261	20	0.074	R.TIRYPDPIIK.A
R5/RRR5-15/3	1216.204	1216.454	-206.146	0.384	775.955	0.156	20	0.069	R.TIRYPDPIIK.A
R5/RRR5-4/2	1291.144	1291.478	-259.317	0.536	2033.237	0.548	19	0.283	R.AIADGSLLDFLR.Q
R5/RRR5-3/2	1290.905	1291.478	-1222.522	0.458	2083.775	0.462	19	0.267	R.AIADGSLLDFLR.Q
R5/RRR5-2/2	1291.996	1291.478	-374.571	0.457	1929.799	0.549	19	0.267	R.AIADGSLLDFLR.Q
R5/RRR5-4/2	1290.509	1291.478	-1530.100	0.413	1994.764	0.497	19	0.262	R.AIADGSLLDFLR.Q
R5/RRR5-4/2	1290.669	1291.478	-1406.020	0.415	1992.719	0.498	19	0.262	R.AIADGSLLDFLR.Q
R5/RRR5-2/2	1291.746	1291.478	208.277	0.503	1513.089	0.533	18	0.209	R.AIADGSLLDFLR.Q
R5/RRR5-4/2	1328.154	1328.497	-259.098	0.501	1531.203	0.510	20	0.207	K.LADLESAPAALTR.L
R5/RRR5-3/2	1077.418	1077.212	191.185	0.455	1479.303	0.534	16	0.206	K.SPAEVFDALK.S
R5/RRR5-4/2	1329.238	1328.497	-195.514	0.518	1464.310	0.510	20	0.199	K.LADLESAPAALTR.L
R5/RRR5-4/2	1886.330	1886.995	-885.245	0.521	1462.384	0.491	23	0.194	K.DITPDDKQELDEALQR.E
R5/RRR5-4/2	1076.528	1077.212	-1569.241	0.388	1484.547	0.482	16	0.194	K.SPAEVFDALK.S
R5/RRR5-3/2	1077.664	1077.212	420.980	0.383	1420.665	0.443	15	0.180	K.SPAEVFDALK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1078.259	1077.212	43.420	0.451	1226.359	0.518	15	0.178	K.SPAEVFDALK.S
R5/RRR5-4/2	1852.458	1853.070	-872.681	0.506	1158.339	0.573	20	0.178	K.SQTVDLVLTAHPTQSVR.R
R5/RRR5-1/2	1291.568	1291.478	69.997	0.549	1332.076	0.472	17	0.177	R.AIADGSLLDFLR.Q
R5/RRR5-4/2	1886.498	1886.995	-264.189	0.500	1294.069	0.481	22	0.176	K.DITPDDKQELDEALQR.E
R5/RRR5-4/2	1328.118	1328.497	-285.931	0.356	1412.024	0.377	19	0.167	K.LADLESAPAALTR.L
R5/RRR5-4/2	1077.042	1077.212	-158.424	0.399	1133.979	0.500	15	0.167	K.SPAEVFDALK.S
R5/RRR5-4/2	1077.199	1077.212	-12.118	0.468	1156.072	0.449	15	0.162	K.SPAEVFDALK.S
R5/RRR5-4/2	1886.429	1886.995	-832.367	0.507	1110.571	0.458	21	0.157	K.DITPDDKQELDEALQR.E
R5/RRR5-3/2	1328.158	1328.497	-255.686	0.428	1136.494	0.430	18	0.156	K.LADLESAPAALTR.L
R5/RRR5-2/2	1291.681	1291.478	157.860	0.357	1018.289	0.427	17	0.147	R.AIADGSLLDFLR.Q
R5/RRR5-3/2	1327.576	1328.497	-1451.411	0.356	966.027	0.404	17	0.141	K.LADLESAPAALTR.L
R5/RRR5-1/2	1076.470	1077.212	-1622.896	0.380	956.128	0.377	14	0.139	K.SPAEVFDALK.S
R5/RRR5-3/2	1208.205	1207.404	-165.749	0.376	621.997	0.436	17	0.135	R.QVSTFGLSLVR.L
R5/RRR5-4/3	1886.927	1886.995	-36.221	0.519	1499.035	0.379	29	0.135	K.DITPDDKQELDEALQR.E
R5/RRR5-1/2	1291.958	1291.478	372.950	0.325	683.099	0.408	15	0.130	R.AIADGSLLDFLR.Q
R5/RRR5-4/2	1207.322	1207.404	-68.718	0.383	444.151	0.377	16	0.130	R.QVSTFGLSLVR.L
R5/RRR5-3/2	1290.459	1291.478	-1569.060	0.351	637.753	0.395	15	0.129	R.AIADGSLLDFLR.Q
R5/RRR5-3/2	1208.272	1207.404	-110.108	0.359	351.110	0.423	14	0.129	R.QVSTFGLSLVR.L
R5/RRR5-4/2	1207.304	1207.404	-83.424	0.392	514.906	0.351	17	0.129	R.QVSTFGLSLVR.L
R5/RRR5-1/2	1328.206	1328.497	-219.357	0.304	1099.820	0.245	17	0.129	K.LADLESAPAALTR.L
R5/RRR5-3/2	1207.286	1207.404	-98.028	0.308	330.704	0.411	15	0.128	R.QVSTFGLSLVR.L
R5/RRR5-4/2	1207.164	1207.404	-199.565	0.345	428.330	0.363	16	0.128	R.QVSTFGLSLVR.L
R5/RRR5-3/2	1327.506	1328.497	-1503.782	0.312	1019.473	0.268	16	0.127	K.LADLESAPAALTR.L
R5/RRR5-3/2	1290.427	1291.478	-1593.862	0.292	632.708	0.372	14	0.125	R.AIADGSLLDFLR.Q
R5/RRR5-4/3	1996.157	1996.209	-26.388	0.444	1129.967	0.491	27	0.124	R.HTDVLDAITTYLGIGSYR.E
R5/RRR5-4/3	1886.230	1886.995	-938.656	0.493	1190.739	0.424	28	0.116	K.DITPDDKQELDEALQR.E
R5/RRR5-3/3	1886.889	1886.995	-56.272	0.492	1209.055	0.416	28	0.116	K.DITPDDKQELDEALQR.E
R5/RRR5-1/2	1291.294	1291.478	-142.852	0.187	584.046	0.160	14	0.115	R.AIADGSLLDFLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1328.163	1328.497	-252.366	0.176	817.773	0.134	14	0.112	K.LADLESAPAALTR.L
R5/RRR5-3/3	1886.736	1886.995	-137.750	0.458	1248.702	0.343	27	0.102	K.DITPDDKQELDEALQR.E
R5/RRR5-3/3	1886.426	1886.995	-834.387	0.469	963.002	0.401	26	0.096	K.DITPDDKQELDEALQR.E
R5/RRR5-4/3	1168.281	1168.373	-79.252	0.422	1117.350	0.350	20	0.095	K.RPLFGPDLPR.T
R5/RRR5-4/3	1886.653	1886.995	-181.756	0.467	1045.406	0.357	27	0.092	K.DITPDDKQELDEALQR.E
R5/RRR5-4/3	1168.444	1168.373	60.648	0.420	1143.201	0.312	21	0.089	K.RPLFGPDLPR.T
R5/RRR5-4/3	1168.499	1168.373	107.797	0.425	851.426	0.332	19	0.080	-.RPLFGPDLPR.-
R5/RRR5-3/3	1168.425	1168.373	44.302	0.388	991.132	0.298	20	0.080	K.RPLFGPDLPR.T
R5/RRR5-3/3	1168.481	1168.373	92.552	0.359	992.130	0.243	19	0.073	K.RPLFGPDLPR.T
R5/RRR5-1/3	1886.878	1886.995	-62.210	0.345	710.573	0.276	22	0.069	-.DITPDDKQELDEALQR.-
R5/RRR5-12/3	1790.743	1789.922	-100.351	0.595	2725.048	0.506	40	0.472	R.KQSSALSAASSACDHIR.D
R5/RRR5-12/2	1347.294	1347.648	-263.777	0.521	2559.452	0.373	20	0.320	K.MELVDAAFPLLK.G
R5/RRR5-12/2	1347.162	1347.648	-362.050	0.455	2587.185	0.338	20	0.316	K.MELVDAAFPLLK.G
R5/RRR5-12/2	1346.609	1347.648	-1518.454	0.394	2537.217	0.312	20	0.300	K.MELVDAAFPLLK.G
R5/RRR5-12/3	1651.552	1650.987	-264.416	0.466	2023.923	0.556	34	0.300	K.VLVVANPANTNALILK.E
R5/RRR5-13/2	1650.582	1650.987	-246.241	0.505	2151.318	0.486	25	0.283	K.VLVVANPANTNALILK.E
R5/RRR5-12/2	1555.186	1555.668	-311.181	0.516	1829.526	0.604	24	0.268	K.SQASALEAHAAPNCK.V
R5/RRR5-13/2	1555.206	1555.668	-298.029	0.526	1833.913	0.601	24	0.268	K.SQASALEAHAAPNCK.V
R5/RRR5-12/2	1555.215	1555.668	-292.359	0.523	1828.691	0.595	24	0.266	K.SQASALEAHAAPNCK.V
R5/RRR5-12/2	1651.329	1650.987	207.410	0.549	1906.109	0.547	26	0.262	K.VLVVANPANTNALILK.E
R5/RRR5-13/2	1650.297	1650.987	-1027.214	0.478	1856.935	0.542	26	0.254	K.VLVVANPANTNALILK.E
R5/RRR5-12/2	1651.410	1650.987	256.852	0.583	1779.448	0.576	25	0.252	K.VLVVANPANTNALILK.E
R5/RRR5-13/2	1348.383	1347.648	-197.188	0.550	2099.930	0.397	20	0.250	K.MELVDAAFPLLK.G
R5/RRR5-13/2	1346.858	1347.648	-1333.182	0.350	2193.281	0.320	18	0.247	K.MELVDAAFPLLK.G
R5/RRR5-13/2	1555.196	1555.668	-304.487	0.542	1644.170	0.602	23	0.242	K.SQASALEAHAAPNCK.V
R5/RRR5-12/2	1555.223	1555.668	-287.241	0.534	1603.798	0.621	23	0.241	K.SQASALEAHAAPNCK.V
R5/RRR5-12/2	1352.108	1352.451	-254.236	0.569	1874.885	0.477	19	0.241	K.MDATAQELSEEK.T
R5/RRR5-13/2	1555.009	1555.668	-1070.318	0.538	1540.576	0.595	22	0.227	K.SQASALEAHAAPNCK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1351.987	1352.451	-343.732	0.516	1761.315	0.456	20	0.222	K.MDATAQELSEEK.T
R5/RRR5-12/2	1650.642	1650.987	-210.035	0.531	1568.928	0.532	24	0.214	K.VLVVANPANTNALILK.E
R5/RRR5-12/2	1352.011	1352.451	-325.976	0.513	1663.850	0.468	19	0.213	K.MDATAQELSEEK.T
R5/RRR5-14/2	1651.522	1650.987	-282.724	0.537	1502.488	0.544	23	0.209	K.VLVVANPANTNALILK.E
R5/RRR5-13/2	1650.495	1650.987	-299.220	0.455	1491.661	0.546	24	0.208	K.VLVVANPANTNALILK.E
R5/RRR5-11/2	1651.540	1650.987	-271.453	0.531	1438.969	0.524	24	0.198	K.VLVVANPANTNALILK.E
R5/RRR5-11/2	1651.727	1650.987	-158.009	0.529	1413.874	0.508	23	0.192	K.VLVVANPANTNALILK.E
R5/RRR5-12/2	1367.949	1368.450	-1100.574	0.505	1430.179	0.468	20	0.189	K.M*DATAQELSEEK.T
R5/RRR5-3/2	1651.371	1650.987	233.355	0.502	1475.224	0.446	23	0.185	K.VLVVANPANTNALILK.E
R5/RRR5-1/2	1650.545	1650.987	-268.797	0.530	1233.014	0.535	22	0.180	K.VLVVANPANTNALILK.E
R5/RRR5-12/2	1015.981	1016.174	-190.300	0.514	1513.839	0.352	15	0.172	K.LNVQVTDVK.N
R5/RRR5-12/3	1842.875	1843.115	-130.266	0.462	1482.306	0.491	30	0.170	R.ALGQISEKLNVQVTDVK.N
R5/RRR5-11/2	1649.857	1650.987	-1295.017	0.382	1184.367	0.470	22	0.164	K.VLVVANPANTNALILK.E
R5/RRR5-12/2	1016.075	1016.174	-97.015	0.545	1509.015	0.314	15	0.163	K.LNVQVTDVK.N
R5/RRR5-13/2	1017.075	1016.174	-97.522	0.568	1320.571	0.378	15	0.161	K.LNVQVTDVK.N
R5/RRR5-13/2	1362.848	1363.648	-1324.147	0.451	1383.468	0.336	18	0.158	K.M*ELVDAAFPLLK.G
R5/RRR5-13/2	1016.265	1016.174	90.585	0.517	1297.692	0.353	15	0.156	K.LNVQVTDVK.N
R5/RRR5-7/2	1651.848	1650.987	-84.617	0.493	1109.389	0.453	20	0.155	K.VLVVANPANTNALILK.E
R5/RRR5-12/2	1363.526	1363.648	-89.539	0.461	1375.283	0.320	18	0.155	K.M*ELVDAAFPLLK.G
R5/RRR5-7/2	1651.597	1650.987	-236.749	0.468	1097.655	0.432	20	0.152	K.VLVVANPANTNALILK.E
R5/RRR5-11/2	1015.839	1016.174	-330.138	0.467	1273.930	0.301	15	0.146	K.LNVQVTDVK.N
R5/RRR5-13/2	1347.100	1347.648	-1152.618	0.382	1340.688	0.270	16	0.146	-.MELVDAAFPLLK.-
R5/RRR5-12/2	1651.099	1650.987	67.732	0.477	991.772	0.434	20	0.146	K.VLVVANPANTNALILK.E
R5/RRR5-13/3	1624.060	1624.796	-1072.112	0.438	1511.933	0.402	26	0.145	R.KKM*DATAQELSEEK.T
R5/RRR5-12/3	1624.821	1624.796	15.671	0.494	1337.794	0.478	27	0.145	R.KKM*DATAQELSEEK.T
R5/RRR5-9/2	1650.431	1650.987	-945.676	0.389	1153.804	0.340	21	0.143	K.VLVVANPANTNALILK.E
R5/RRR5-11/2	1015.845	1016.174	-323.989	0.507	1018.905	0.362	14	0.141	K.LNVQVTDVK.N
R5/RRR5-10/2	1649.942	1650.987	-1243.451	0.304	1073.336	0.358	21	0.140	K.VLVVANPANTNALILK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1650.297	1650.987	-1027.066	0.386	774.363	0.439	19	0.137	K.VLVVANPANTNALILK.E
R5/RRR5-10/2	1015.920	1016.174	-249.967	0.462	844.081	0.320	13	0.130	K.LNVQVTDVK.N
R5/RRR5-10/2	1015.826	1016.174	-342.677	0.433	853.564	0.290	14	0.129	K.LNVQVTDVK.N
R5/RRR5-2/2	1016.948	1016.174	-222.385	0.398	346.535	0.293	12	0.128	K.LNVQVTDVK.N
R5/RRR5-10/2	1015.496	1016.174	-1656.499	0.385	703.570	0.314	13	0.128	K.LNVQVTDVK.N
R5/RRR5-2/2	1016.262	1016.174	86.971	0.417	483.016	0.302	13	0.127	K.LNVQVTDVK.N
R5/RRR5-2/2	1016.984	1016.174	-187.102	0.359	358.385	0.269	12	0.127	K.LNVQVTDVK.N
R5/RRR5-3/2	1016.217	1016.174	42.517	0.404	443.227	0.269	13	0.126	K.LNVQVTDVK.N
R5/RRR5-1/2	1016.049	1016.174	-123.287	0.369	431.530	0.255	13	0.126	K.LNVQVTDVK.N
R5/RRR5-3/2	1556.501	1555.668	-108.207	0.395	754.333	0.360	16	0.126	K.SQASALEAHAAPNCK.V
R5/RRR5-6/2	1016.343	1016.174	166.835	0.422	509.987	0.312	13	0.125	-.LNVQVTDVK.-
R5/RRR5-13/2	1017.144	1016.174	-29.264	0.493	583.433	0.283	13	0.124	K.LNVQVTDVK.N
R5/RRR5-3/2	1016.220	1016.174	45.650	0.404	589.261	0.222	14	0.123	K.LNVQVTDVK.N
R5/RRR5-20/2	1326.751	1326.526	169.984	0.353	1075.062	0.206	16	0.122	K.EGM*ERKDVMSK.N
R5/RRR5-3/2	1016.007	1016.174	-164.145	0.375	524.268	0.243	14	0.122	-.LNVQVTDVK.-
R5/RRR5-5/2	1016.028	1016.174	-143.294	0.349	814.715	0.223	13	0.122	K.LNVQVTDVK.N
R5/RRR5-12/2	1650.927	1650.987	-36.459	0.351	468.945	0.291	14	0.117	-.VLVVANPANTNALILK.-
R5/RRR5-13/2	1362.995	1363.648	-1215.760	0.314	646.653	0.163	15	0.115	-.M*ELVDAAFPLLK.-
R5/RRR5-12/3	1624.038	1624.796	-1085.810	0.474	1306.061	0.371	25	0.114	R.KKM*DATAQELSEEK.T
R5/RRR5-13/3	1662.866	1661.749	70.374	0.386	878.421	0.505	28	0.103	K.QSSALSAASSACDHIR.D
R5/RRR5-12/3	1624.423	1624.796	-230.002	0.457	1007.302	0.371	24	0.093	R.KKM*DATAQELSEEK.T
R5/RRR5-13/3	1624.013	1624.796	-1100.754	0.378	837.543	0.386	24	0.087	R.KKM*DATAQELSEEK.T
R5/RRR5-12/3	1843.312	1843.115	107.589	0.361	849.651	0.347	22	0.077	-.ALGQISEKLNVQVTDVK.-
R5/RRR5-9/1	975.531	976.154	-1669.000	0.229	767.316	0.313	15	0.373	K.IGLFGGAGVGK.T
R5/RRR5-9/2	1708.583	1709.007	-248.846	0.579	2375.048	0.619	23	0.369	R.LVLEVAQHLGENMVR.T
R5/RRR5-8/2	1493.319	1493.647	-219.946	0.541	2608.898	0.476	24	0.363	R.FTQANSEVSALLGR.I
R5/RRR5-8/2	1474.342	1474.791	-305.930	0.490	2512.726	0.424	20	0.328	K.TVLIM*ELINNVAK.A
R5/RRR5-8/2	1707.506	1709.007	-2056.540	0.489	2283.911	0.544	23	0.326	R.LVLEVAQHLGENMVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1493.238	1493.647	-274.402	0.532	2361.418	0.488	23	0.320	R.FTQANSEVSALLGR.I
R5/RRR5-9/2	1474.466	1474.791	-221.288	0.541	2419.308	0.448	20	0.317	K.TVLIM*ELINNVAK.A
R5/RRR5-8/2	1492.964	1493.647	-1130.216	0.469	2345.203	0.475	22	0.314	R.FTQANSEVSALLGR.I
R5/RRR5-8/2	1493.381	1493.647	-178.452	0.523	2362.724	0.466	22	0.313	R.FTQANSEVSALLGR.I
R5/RRR5-9/2	1474.323	1474.791	-318.723	0.484	2449.226	0.403	20	0.309	K.TVLIM*ELINNVAK.A
R5/RRR5-8/2	1459.347	1458.792	-305.776	0.583	2425.875	0.404	20	0.302	K.TVLIMELINNVAK.A
R5/RRR5-8/2	1494.144	1493.647	333.791	0.548	2231.355	0.498	23	0.300	R.FTQANSEVSALLGR.I
R5/RRR5-9/2	1458.358	1458.792	-298.679	0.521	2330.887	0.429	20	0.296	K.TVLIMELINNVAK.A
R5/RRR5-8/2	1474.228	1474.791	-1063.547	0.410	2537.699	0.299	20	0.295	K.TVLIM*ELINNVAK.A
R5/RRR5-9/2	1493.262	1493.647	-258.737	0.528	2168.196	0.514	22	0.295	R.FTQANSEVSALLGR.I
R5/RRR5-9/2	1865.502	1866.064	-839.407	0.556	2038.620	0.567	23	0.291	R.DAEGQDVLLFIDNIFR.F
R5/RRR5-9/2	1458.304	1458.792	-335.632	0.550	2304.831	0.423	20	0.289	K.TVLIMELINNVAK.A
R5/RRR5-9/2	1458.279	1458.792	-1040.478	0.544	2284.279	0.421	20	0.285	K.TVLIMELINNVAK.A
R5/RRR5-9/2	1474.237	1474.791	-1057.229	0.462	2276.843	0.404	20	0.281	K.TVLIM*ELINNVAK.A
R5/RRR5-9/2	1492.732	1493.647	-1286.808	0.431	2213.781	0.411	22	0.273	R.FTQANSEVSALLGR.I
R5/RRR5-8/2	1474.349	1474.791	-301.029	0.460	2278.932	0.347	20	0.264	K.TVLIM*ELINNVAK.A
R5/RRR5-9/2	1391.849	1391.516	240.008	0.561	1601.441	0.637	23	0.247	K.AHGGFSVFAGVGER.T
R5/RRR5-8/2	1279.038	1279.446	-319.846	0.411	1576.645	0.446	20	0.197	R.TIAM*DGTEGLVR.G
R5/RRR5-9/2	1410.259	1410.644	-273.531	0.430	1473.771	0.454	22	0.188	R.VLNTGSPITVPVGR.A
R5/RRR5-9/2	1856.428	1857.040	-870.988	0.556	1142.962	0.597	24	0.186	R.M*LSPHVLGEDHYNTAR.G
R5/RRR5-8/2	1390.620	1391.516	-1367.650	0.503	1115.782	0.595	22	0.184	K.AHGGFSVFAGVGER.T
R5/RRR5-9/2	1279.116	1279.446	-259.045	0.408	1332.097	0.499	19	0.183	R.TIAM*DGTEGLVR.G
R5/RRR5-9/2	1391.261	1391.516	-183.982	0.477	1094.011	0.596	23	0.183	K.AHGGFSVFAGVGER.T
R5/RRR5-9/2	1279.114	1279.446	-259.907	0.429	1425.450	0.434	19	0.180	R.TIAM*DGTEGLVR.G
R5/RRR5-9/2	1410.363	1410.644	-199.547	0.429	1272.969	0.500	21	0.178	R.VLNTGSPITVPVGR.A
R5/RRR5-9/2	1400.320	1400.608	-206.049	0.470	1162.734	0.545	18	0.177	R.VGLTGLTVAEHFR.D
R5/RRR5-9/2	1391.047	1391.516	-338.481	0.510	1011.829	0.573	24	0.174	K.AHGGFSVFAGVGER.T
R5/RRR5-8/2	1279.002	1279.446	-347.999	0.414	1298.875	0.451	20	0.172	R.TIAM*DGTEGLVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1400.025	1400.608	-1133.708	0.445	1168.907	0.517	18	0.172	R.VGLTGLTVAEHFR.D
R5/RRR5-9/2	1410.254	1410.644	-277.178	0.383	1260.215	0.468	21	0.170	R.VLNTGSPITVPVGR.A
R5/RRR5-8/2	1390.525	1391.516	-1436.599	0.429	968.638	0.586	22	0.169	K.AHGGFSVFAGVGER.T
R5/RRR5-9/2	1262.522	1263.447	-1528.622	0.381	1173.267	0.487	18	0.167	R.TIAMDGTEGLVR.G
R5/RRR5-8/2	1411.415	1410.644	-162.791	0.408	938.993	0.595	19	0.166	R.VLNTGSPITVPVGR.A
R5/RRR5-9/2	1264.143	1263.447	-241.030	0.528	1038.078	0.508	18	0.164	R.TIAMDGTEGLVR.G
R5/RRR5-9/2	975.956	976.154	-204.000	0.461	1168.515	0.432	17	0.160	K.IGLFGGAGVGK.T
R5/RRR5-8/2	1410.097	1410.644	-1100.517	0.366	1205.396	0.414	20	0.157	R.VLNTGSPITVPVGR.A
R5/RRR5-9/2	1263.149	1263.447	-236.374	0.463	1160.033	0.420	18	0.157	R.TIAMDGTEGLVR.G
R5/RRR5-8/2	975.364	976.154	-1841.149	0.391	1113.511	0.423	16	0.153	K.IGLFGGAGVGK.T
R5/RRR5-9/2	975.878	976.154	-283.936	0.408	1114.124	0.406	17	0.152	K.IGLFGGAGVGK.T
R5/RRR5-8/2	976.052	976.154	-105.384	0.443	1071.239	0.424	16	0.152	K.IGLFGGAGVGK.T
R5/RRR5-8/2	1391.238	1391.516	-200.442	0.420	608.356	0.618	19	0.151	K.AHGGFSVFAGVGER.T
R5/RRR5-8/2	975.907	976.154	-253.943	0.420	1129.775	0.388	17	0.150	K.IGLFGGAGVGK.T
R5/RRR5-2/2	976.183	976.154	29.210	0.428	1213.429	0.351	17	0.150	K.IGLFGGAGVGK.T
R5/RRR5-9/2	976.043	976.154	-114.291	0.404	1119.505	0.384	17	0.149	K.IGLFGGAGVGK.T
R5/RRR5-8/2	1409.713	1410.644	-1373.618	0.294	1144.091	0.399	20	0.149	R.VLNTGSPITVPVGR.A
R5/RRR5-8/2	1174.303	1174.374	-61.058	0.506	918.434	0.453	15	0.149	K.VVDLLAPYQR.G
R5/RRR5-9/2	1493.200	1493.647	-300.238	0.480	1107.047	0.407	17	0.148	R.FTQANSEVSALLGR.I
R5/RRR5-8/3	1856.395	1857.040	-889.082	0.491	1364.403	0.474	30	0.147	R.M*LSPHVLGEDHYNTAR.G
R5/RRR5-9/3	1709.558	1709.007	-263.287	0.507	1121.133	0.591	35	0.146	R.LVLEVAQHLGENMVR.T
R5/RRR5-8/2	1173.739	1174.374	-1397.444	0.384	926.667	0.440	15	0.145	K.VVDLLAPYQR.G
R5/RRR5-1/2	976.416	976.154	269.081	0.435	997.263	0.404	16	0.145	K.IGLFGGAGVGK.T
R5/RRR5-9/2	1399.397	1400.608	-1584.540	0.388	829.136	0.501	15	0.144	R.VGLTGLTVAEHFR.D
R5/RRR5-9/3	1858.130	1857.040	48.243	0.511	1132.217	0.550	29	0.141	R.M*LSPHVLGEDHYNTAR.G
R5/RRR5-8/2	1400.359	1400.608	-178.153	0.415	1015.200	0.386	17	0.141	R.VGLTGLTVAEHFR.D
R5/RRR5-8/2	1278.534	1279.446	-1499.871	0.297	1096.544	0.350	19	0.141	R.TIAM*DGTEGLVR.G
R5/RRR5-9/2	1278.634	1279.446	-1421.617	0.300	1033.537	0.362	18	0.139	R.TIAM*DGTEGLVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/3	1725.094	1725.007	51.022	0.493	1037.089	0.580	32	0.137	R.LVLEVAQHLGENM*VR.T
R5/RRR5-9/3	1856.356	1857.040	-910.273	0.504	1256.903	0.483	29	0.137	R.M*LSPHVLGEDHYNTAR.G
R5/RRR5-16/2	1493.773	1493.647	84.865	0.445	1007.548	0.326	18	0.133	R.FTQANSEVSALLGR.I
R5/RRR5-12/2	1475.000	1474.791	142.034	0.305	1014.331	0.309	16	0.131	K.TVLIM*ELINNVAK.A
R5/RRR5-8/2	1726.340	1725.007	193.902	0.444	802.599	0.351	19	0.128	-.LVLEVAQHLGENM*VR.-
R5/RRR5-8/2	1726.414	1725.007	236.800	0.406	706.385	0.372	18	0.127	R.LVLEVAQHLGENM*VR.T
R5/RRR5-9/3	1725.955	1725.007	-29.803	0.516	1032.843	0.533	33	0.127	R.LVLEVAQHLGENM*VR.T
R5/RRR5-8/2	1173.802	1174.374	-1343.651	0.357	654.032	0.339	13	0.125	K.VVDLLAPYQR.G
R5/RRR5-8/2	1458.170	1458.792	-1115.874	0.305	452.253	0.307	14	0.122	K.TVLIMELINNVAK.A
R5/RRR5-1/2	1493.053	1493.647	-1070.696	0.305	552.713	0.318	15	0.121	R.FTQANSEVSALLGR.I
R5/RRR5-12/2	1476.063	1474.791	184.816	0.354	687.295	0.297	14	0.121	K.TVLIM*ELINNVAK.A
R5/RRR5-8/2	1410.975	1410.644	235.193	0.200	193.830	0.351	13	0.120	R.VLNTGSPITVPVGR.A
R5/RRR5-8/3	1856.890	1857.040	-81.257	0.510	1053.213	0.489	27	0.120	R.M*LSPHVLGEDHYNTAR.G
R5/RRR5-8/3	1856.632	1857.040	-220.446	0.535	1128.979	0.461	28	0.119	R.M*LSPHVLGEDHYNTAR.G
R5/RRR5-9/2	1175.266	1174.374	-92.782	0.292	561.629	0.305	11	0.119	-.VVDLLAPYQR.-
R5/RRR5-16/2	1494.054	1493.647	273.496	0.322	529.093	0.245	15	0.118	R.FTQANSEVSALLGR.I
R5/RRR5-15/2	1493.502	1493.647	-97.114	0.314	491.795	0.258	14	0.118	R.FTQANSEVSALLGR.I
R5/RRR5-15/2	1493.045	1493.647	-1075.786	0.318	551.315	0.213	14	0.116	R.FTQANSEVSALLGR.I
R5/RRR5-9/3	1856.446	1857.040	-861.556	0.490	981.534	0.494	26	0.115	R.M*LSPHVLGEDHYNTAR.G
R5/RRR5-9/3	1708.846	1709.007	-94.628	0.374	910.885	0.534	30	0.113	R.LVLEVAQHLGENMVR.T
R5/RRR5-9/2	976.928	976.154	-232.623	0.160	290.895	0.360	13	0.112	-.IGLFGGAGVGK.-
R5/RRR5-9/3	1400.855	1400.608	177.056	0.486	957.033	0.476	26	0.110	R.VGLTGLTVAEHFR.D
R5/RRR5-8/3	1400.673	1400.608	47.009	0.462	996.396	0.449	27	0.106	R.VGLTGLTVAEHFR.D
R5/RRR5-9/3	1724.942	1725.007	-37.663	0.458	753.712	0.522	30	0.106	R.LVLEVAQHLGENM*VR.T
R5/RRR5-8/3	1840.614	1841.041	-232.467	0.419	988.650	0.443	26	0.105	R.MLSPHVLGEDHYNTAR.G
R5/RRR5-9/3	1709.044	1709.007	21.441	0.394	665.903	0.531	29	0.101	R.LVLEVAQHLGENMVR.T
R5/RRR5-8/3	1400.751	1400.608	102.335	0.489	864.407	0.454	25	0.101	R.VGLTGLTVAEHFR.D
R5/RRR5-9/3	1840.327	1841.041	-934.292	0.477	788.857	0.465	24	0.099	R.MLSPHVLGEDHYNTAR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/3	1401.688	1400.608	57.282	0.485	794.663	0.448	24	0.098	R.VGLTGLTVAEHFR.D
R5/RRR5-9/3	1401.736	1400.608	92.000	0.468	758.035	0.452	24	0.097	R.VGLTGLTVAEHFR.D
R5/RRR5-9/3	1400.591	1400.608	-11.864	0.425	944.735	0.378	26	0.091	R.VGLTGLTVAEHFR.D
R5/RRR5-8/3	1493.680	1493.647	22.401	0.427	950.904	0.375	24	0.089	R.FTQANSEVSALLGR.I
R5/RRR5-9/3	1410.466	1410.644	-126.756	0.365	996.853	0.349	25	0.086	R.VLNTGSPITVPVGR.A
R5/RRR5-8/3	1410.424	1410.644	-156.578	0.338	1140.929	0.250	26	0.078	R.VLNTGSPITVPVGR.A
R5/RRR5-9/3	1493.405	1493.647	-162.061	0.348	815.500	0.304	22	0.072	-.FTQANSEVSALLGR.-
R5/RRR5-9/3	1410.068	1410.644	-1120.997	0.279	840.052	0.170	23	0.061	R.VLNTGSPITVPVGR.A
R5/RRR5-14/2	1565.085	1565.732	-1055.117	0.499	1983.916	0.513	23	0.267	R.LAIAGM*GTDENSLTR.I
R5/RRR5-14/2	1566.322	1565.732	-262.206	0.544	1764.949	0.548	22	0.244	R.LAIAGM*GTDENSLTR.I
R5/RRR5-14/2	1369.019	1369.416	-290.804	0.494	1774.583	0.448	19	0.222	R.SITDEISGDFER.A
R5/RRR5-14/2	1549.161	1549.732	-1017.217	0.479	1558.521	0.541	22	0.216	R.LAIAGMGTDENSLTR.I
R5/RRR5-14/2	1564.509	1565.732	-1425.122	0.370	1643.194	0.470	22	0.208	R.LAIAGM*GTDENSLTR.I
R5/RRR5-14/2	1369.082	1369.416	-245.002	0.457	1430.368	0.446	19	0.183	R.SITDEISGDFER.A
R5/RRR5-14/2	1401.189	1401.503	-224.621	0.455	1461.613	0.397	18	0.176	R.AYADTYGEELLR.S
R5/RRR5-14/2	959.074	959.127	-55.355	0.517	1167.805	0.527	14	0.176	R.GPAQLFAVR.Q
R5/RRR5-14/2	1058.153	1058.171	-16.964	0.442	1333.892	0.391	16	0.164	R.DAVLANEVAR.K
R5/RRR5-14/2	1030.551	1031.225	-1629.271	0.393	1208.018	0.402	15	0.156	R.VLVEIACAR.G
R5/RRR5-14/2	1350.012	1350.418	-301.519	0.476	1170.740	0.409	17	0.155	R.YNDEYGHPINK.D
R5/RRR5-14/2	1383.361	1384.605	-1626.715	0.281	1289.583	0.301	17	0.145	R.AVILWTLDPAER.D
R5/RRR5-14/2	1400.440	1401.503	-1477.573	0.345	1230.199	0.297	17	0.141	R.AYADTYGEELLR.S
R5/RRR5-14/2	1146.194	1145.419	-196.935	0.422	630.815	0.450	16	0.136	K.LLVPLISAYR.Y
R5/RRR5-14/2	1122.330	1122.299	27.534	0.408	984.003	0.315	14	0.132	K.LITEAYQKR.N
R5/RRR5-14/2	1384.276	1384.605	-238.598	0.263	822.786	0.310	13	0.121	R.AVILWTLDPAER.D
R5/RRR5-14/2	1384.366	1384.605	-173.224	0.335	509.138	0.404	11	0.121	-.AVILWTLDPAER.-
R5/RRR5-15/2	1819.407	1820.040	-900.108	0.539	2217.316	0.583	23	0.325	K.SAQDIALADLPTTHPIR.L
R5/RRR5-16/2	1819.372	1820.040	-919.237	0.520	2023.649	0.568	24	0.287	K.SAQDIALADLPTTHPIR.L
R5/RRR5-16/2	1820.492	1820.040	249.272	0.558	1833.517	0.584	23	0.262	K.SAQDIALADLPTTHPIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1819.358	1820.040	-926.916	0.487	1827.133	0.526	23	0.246	K.SAQDIALADLPTTHPIR.L
R5/RRR5-15/2	1819.885	1820.040	-85.449	0.540	1738.303	0.558	23	0.242	K.SAQDIALADLPTTHPIR.L
R5/RRR5-15/2	1336.551	1337.504	-1465.207	0.533	1589.494	0.546	19	0.223	R.KEAAENTLVAYK.S
R5/RRR5-15/2	1336.736	1337.504	-1326.515	0.533	1607.246	0.527	20	0.221	R.KEAAENTLVAYK.S
R5/RRR5-15/2	1319.078	1319.400	-244.729	0.520	1694.004	0.477	19	0.218	K.TADVGELTVEER.N
R5/RRR5-15/2	1638.861	1639.832	-1205.912	0.466	1540.962	0.500	25	0.205	K.LLDSHLVPSATAAESK.V
R5/RRR5-15/2	1337.182	1337.504	-240.867	0.521	1457.210	0.526	19	0.203	R.KEAAENTLVAYK.S
R5/RRR5-16/2	1319.066	1319.400	-254.292	0.478	1596.505	0.446	19	0.200	K.TADVGELTVEER.N
R5/RRR5-16/2	1337.148	1337.504	-266.603	0.525	1409.107	0.534	19	0.200	R.KEAAENTLVAYK.S
R5/RRR5-15/2	1639.310	1639.832	-931.179	0.458	1424.254	0.508	24	0.194	K.LLDSHLVPSATAAESK.V
R5/RRR5-15/2	1318.624	1319.400	-1351.328	0.384	1650.297	0.388	18	0.193	K.TADVGELTVEER.N
R5/RRR5-15/2	1419.251	1419.563	-220.555	0.485	1401.251	0.505	19	0.192	R.IISSIEQKEESR.G
R5/RRR5-16/2	1419.131	1419.563	-305.210	0.476	1506.680	0.449	19	0.191	R.IISSIEQKEESR.G
R5/RRR5-16/2	1639.524	1639.832	-188.085	0.484	1272.436	0.559	23	0.189	K.LLDSHLVPSATAAESK.V
R5/RRR5-15/2	1419.106	1419.563	-322.729	0.464	1458.307	0.456	19	0.188	R.IISSIEQKEESR.G
R5/RRR5-15/2	1639.459	1639.832	-228.346	0.481	1323.552	0.520	23	0.187	K.LLDSHLVPSATAAESK.V
R5/RRR5-16/2	1418.670	1419.563	-1338.451	0.492	1448.632	0.450	19	0.186	R.IISSIEQKEESR.G
R5/RRR5-16/2	1639.223	1639.832	-984.484	0.450	1362.237	0.485	24	0.184	K.LLDSHLVPSATAAESK.V
R5/RRR5-14/2	1419.085	1419.563	-338.178	0.479	1422.094	0.448	19	0.183	R.IISSIEQKEESR.G
R5/RRR5-16/2	1639.377	1639.832	-277.948	0.476	1299.861	0.498	24	0.181	K.LLDSHLVPSATAAESK.V
R5/RRR5-16/2	1319.151	1319.400	-189.584	0.511	1366.657	0.430	18	0.174	K.TADVGELTVEER.N
R5/RRR5-14/2	1419.089	1419.563	-335.157	0.506	1227.908	0.481	19	0.173	R.IISSIEQKEESR.G
R5/RRR5-16/2	1318.992	1319.400	-310.745	0.456	1421.575	0.390	18	0.171	K.TADVGELTVEER.N
R5/RRR5-15/2	1051.856	1052.163	-292.935	0.384	1074.008	0.541	15	0.168	R.GNEAYVASIK.E
R5/RRR5-15/2	1419.200	1419.563	-256.279	0.468	1164.804	0.469	19	0.166	R.IISSIEQKEESR.G
R5/RRR5-16/2	1419.206	1419.563	-252.396	0.470	1133.897	0.464	18	0.162	R.IISSIEQKEESR.G
R5/RRR5-15/2	1051.805	1052.163	-340.675	0.378	949.800	0.551	15	0.160	R.GNEAYVASIK.E
R5/RRR5-16/2	1191.070	1190.439	-310.505	0.449	1720.732	0.193	16	0.160	K.DSTLIMQLLR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1051.505	1052.163	-1581.200	0.398	910.573	0.549	15	0.159	R.GNEAYVASIK.E
R5/RRR5-15/2	1051.457	1052.163	-1627.035	0.395	825.977	0.578	15	0.157	R.GNEAYVASIK.E
R5/RRR5-15/2	1207.504	1206.438	55.054	0.434	1554.019	0.248	16	0.157	K.DSTLIM*QLLR.D
R5/RRR5-16/2	1051.541	1052.163	-1547.264	0.406	937.633	0.493	15	0.153	R.GNEAYVASIK.E
R5/RRR5-16/2	1210.149	1209.331	-150.306	0.413	931.388	0.475	16	0.150	K.EAAENTLVAYK.S
R5/RRR5-16/2	1051.523	1052.163	-1564.174	0.399	934.626	0.461	15	0.149	R.GNEAYVASIK.E
R5/RRR5-16/2	1190.731	1190.439	246.408	0.543	1641.914	0.189	16	0.148	K.DSTLIMQLLR.D
R5/RRR5-15/2	1190.252	1190.439	-156.831	0.449	1605.806	0.173	16	0.147	K.DSTLIMQLLR.D
R5/RRR5-16/2	1209.060	1209.331	-224.264	0.374	795.401	0.470	15	0.141	K.EAAENTLVAYK.S
R5/RRR5-15/2	1191.300	1190.439	-116.919	0.564	1537.912	0.179	16	0.137	K.DSTLIMQLLR.D
R5/RRR5-15/2	1209.109	1209.331	-184.257	0.348	735.810	0.423	15	0.134	K.EAAENTLVAYK.S
R5/RRR5-15/2	1208.964	1209.331	-304.187	0.311	738.253	0.435	15	0.133	K.EAAENTLVAYK.S
R5/RRR5-15/3	1640.749	1639.832	-50.312	0.405	1337.466	0.435	32	0.132	K.LLDSHLVPSATAAESK.V
R5/RRR5-16/2	1206.138	1206.438	-249.417	0.399	1128.260	0.213	15	0.127	K.DSTLIM*QLLR.D
R5/RRR5-16/2	1518.697	1518.786	-58.498	0.428	783.117	0.368	17	0.127	R.NLLSVAYKNVIGAR.R
R5/RRR5-16/3	1639.859	1639.832	16.671	0.424	1403.743	0.382	31	0.127	K.LLDSHLVPSATAAESK.V
R5/RRR5-15/2	1419.105	1419.563	-323.938	0.349	325.606	0.341	13	0.125	R.IISSIEQKEESR.G
R5/RRR5-15/2	1420.131	1419.563	-305.167	0.379	442.942	0.315	13	0.122	R.IISSIEQKEESR.G
R5/RRR5-16/2	1205.973	1206.438	-386.510	0.294	537.600	0.244	13	0.121	K.DSTLIM*QLLR.D
R5/RRR5-16/2	1206.408	1206.438	-25.274	0.448	986.299	0.193	14	0.118	-.DSTLIM*QLLR.-
R5/RRR5-16/2	1189.508	1190.439	-1627.907	0.405	843.483	0.171	15	0.117	K.DSTLIMQLLR.D
R5/RRR5-15/2	1206.091	1206.438	-288.510	0.322	697.613	0.168	13	0.117	K.DSTLIM*QLLR.D
R5/RRR5-15/2	1206.194	1206.438	-203.220	0.435	631.297	0.211	13	0.113	-.DSTLIM*QLLR.-
R5/RRR5-16/3	1639.715	1639.832	-71.139	0.362	1216.996	0.396	30	0.110	K.LLDSHLVPSATAAESK.V
R5/RRR5-15/2	1190.422	1190.439	-13.742	0.341	742.927	0.098	12	0.104	-.DSTLIMQLLR.-
R5/RRR5-16/3	1337.612	1337.504	81.170	0.449	884.906	0.398	24	0.090	R.KEAAENTLVAYK.S
R5/RRR5-15/2	1025.568	1025.054	-475.460	0.210	981.701	0.182	13	0.086	K.EAAKPEGEGH.-
R5/RRR5-16/2	1026.000	1025.054	-53.415	0.259	835.838	0.242	13	0.081	-.EAAKPEGEGH.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/3	1337.673	1337.504	127.435	0.419	820.316	0.269	21	0.072	R.KEAAENTLVAYK.S
R5/RRR5-15/3	1639.825	1639.832	-3.936	0.268	683.392	0.284	26	0.071	K.LLDSHLVPSATAAESK.V
R5/RRR5-24/1	1549.828	1548.681	95.353	0.461	1148.974	0.579	19	1.000	R.AWSAADAVASWVGEK.K
R5/RRR5-24/1	1548.795	1548.681	74.151	0.364	838.167	0.539	17	0.568	R.AWSAADAVASWVGEK.K
R5/RRR5-24/1	1549.794	1548.681	73.393	0.461	756.705	0.588	16	0.500	R.AWSAADAVASWVGEK.K
R5/RRR5-24/1	1549.809	1548.681	82.872	0.442	675.616	0.599	16	0.427	R.AWSAADAVASWVGEK.K
R5/RRR5-24/3	1383.754	1384.522	-1281.629	0.547	2131.107	0.636	29	0.342	R.RADGVGPVSWDPK.V
R5/RRR5-25/2	1549.108	1548.681	276.581	0.539	2285.821	0.583	23	0.333	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1549.209	1548.681	-305.505	0.532	2259.926	0.594	23	0.332	R.AWSAADAVASWVGEK.K
R5/RRR5-24/3	1384.265	1384.522	-186.027	0.561	2101.706	0.625	27	0.332	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1549.166	1548.681	314.348	0.533	2317.410	0.545	23	0.327	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1548.961	1548.681	181.279	0.505	2344.932	0.513	23	0.322	R.AWSAADAVASWVGEK.K
R5/RRR5-19/2	1548.219	1548.681	-299.453	0.445	2356.973	0.493	23	0.318	R.AWSAADAVASWVGEK.K
R5/RRR5-1/2	1548.325	1548.681	-230.715	0.455	2361.108	0.471	23	0.312	R.AWSAADAVASWVGEK.K
R5/RRR5-24/3	1384.553	1384.522	22.530	0.564	2133.579	0.568	29	0.310	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1549.163	1548.681	312.136	0.539	2109.090	0.581	23	0.301	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1549.190	1548.681	-317.996	0.573	2140.088	0.556	23	0.298	R.AWSAADAVASWVGEK.K
R5/RRR5-24/1	1548.747	1548.681	42.532	0.351	550.139	0.535	16	0.298	R.AWSAADAVASWVGEK.K
R5/RRR5-2/2	1549.331	1548.681	-226.772	0.532	2132.524	0.544	23	0.294	R.AWSAADAVASWVGEK.K
R5/RRR5-20/2	1548.093	1548.681	-1028.675	0.413	2216.587	0.494	23	0.294	R.AWSAADAVASWVGEK.K
R5/RRR5-3/2	1549.349	1548.681	-214.995	0.547	2081.609	0.564	23	0.292	R.AWSAADAVASWVGEK.K
R5/RRR5-25/2	1549.381	1548.681	-194.286	0.579	2046.530	0.579	23	0.290	R.AWSAADAVASWVGEK.K
R5/RRR5-26/2	1548.459	1548.681	-143.956	0.508	2095.311	0.549	23	0.290	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1548.216	1548.681	-301.510	0.415	2179.153	0.494	23	0.288	R.AWSAADAVASWVGEK.K
R5/RRR5-18/2	1549.142	1548.681	298.467	0.524	2136.293	0.516	23	0.286	R.AWSAADAVASWVGEK.K
R5/RRR5-18/2	1548.190	1548.681	-317.965	0.437	2170.792	0.491	22	0.285	R.AWSAADAVASWVGEK.K
R5/RRR5-16/2	1549.345	1548.681	-217.682	0.536	2086.891	0.535	23	0.284	R.AWSAADAVASWVGEK.K
R5/RRR5-15/2	1549.139	1548.681	296.808	0.533	2099.461	0.528	23	0.284	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1549.437	1548.681	-158.009	0.555	2012.872	0.572	23	0.283	R.AWSAADAVASWVGEK.K
R5/RRR5-13/2	1549.452	1548.681	-148.288	0.535	1971.257	0.584	23	0.280	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1548.064	1548.681	-1047.913	0.416	2046.336	0.541	23	0.279	R.AWSAADAVASWVGEK.K
R5/RRR5-21/2	1548.423	1548.681	-167.206	0.477	2102.770	0.507	22	0.279	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1549.196	1548.681	-313.648	0.528	1965.975	0.580	23	0.278	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1548.116	1548.681	-1013.949	0.509	2031.104	0.543	23	0.278	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1548.241	1548.681	-285.135	0.450	2061.179	0.524	23	0.277	R.AWSAADAVASWVGEK.K
R5/RRR5-20/2	1549.310	1548.681	-240.368	0.518	1979.394	0.542	23	0.270	R.AWSAADAVASWVGEK.K
R5/RRR5-17/2	1549.247	1548.681	-280.920	0.539	2003.855	0.530	22	0.269	R.AWSAADAVASWVGEK.K
R5/RRR5-4/2	1548.069	1548.681	-1044.588	0.364	2288.469	0.356	23	0.267	R.AWSAADAVASWVGEK.K
R5/RRR5-20/3	1384.789	1384.522	193.345	0.558	1798.746	0.626	27	0.263	R.RADGVGPVSWDPK.V
R5/RRR5-14/2	1548.249	1548.681	-279.836	0.395	2140.566	0.422	23	0.262	R.AWSAADAVASWVGEK.K
R5/RRR5-22/2	1549.226	1548.681	-294.359	0.540	1935.615	0.524	23	0.258	R.AWSAADAVASWVGEK.K
R5/RRR5-22/2	1547.621	1548.681	-1334.759	0.400	2029.609	0.466	23	0.256	R.AWSAADAVASWVGEK.K
R5/RRR5-14/2	1548.269	1548.681	-266.863	0.422	1953.886	0.507	23	0.256	R.AWSAADAVASWVGEK.K
R5/RRR5-1/2	1676.346	1676.854	-901.914	0.509	1896.829	0.530	24	0.254	R.AWSAADAVASWVGEKK.N
R5/RRR5-2/2	1549.049	1548.681	238.178	0.518	1914.724	0.507	22	0.250	R.AWSAADAVASWVGEK.K
R5/RRR5-26/2	1548.497	1548.681	-119.125	0.529	1865.054	0.532	21	0.249	R.AWSAADAVASWVGEK.K
R5/RRR5-13/2	1549.465	1548.681	-139.911	0.558	1790.702	0.565	22	0.248	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1548.527	1548.681	-99.988	0.447	1940.957	0.481	22	0.247	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1548.238	1548.681	-286.955	0.487	1746.423	0.579	22	0.246	R.AWSAADAVASWVGEK.K
R5/RRR5-19/2	1547.617	1548.681	-1337.452	0.403	1947.554	0.469	23	0.245	R.AWSAADAVASWVGEK.K
R5/RRR5-22/2	1548.116	1548.681	-1014.108	0.420	1958.841	0.460	22	0.245	R.AWSAADAVASWVGEK.K
R5/RRR5-1/2	1548.205	1548.681	-308.630	0.486	1855.241	0.513	22	0.244	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1548.258	1548.681	-273.824	0.509	1964.562	0.457	22	0.244	R.AWSAADAVASWVGEK.K
R5/RRR5-20/2	1675.997	1676.854	-1111.399	0.508	1882.981	0.498	23	0.243	R.AWSAADAVASWVGEKK.N
R5/RRR5-4/2	1548.599	1548.681	-53.178	0.466	1822.445	0.502	22	0.237	R.AWSAADAVASWVGEK.K
R5/RRR5-14/2	1549.005	1548.681	209.887	0.525	1795.771	0.513	22	0.235	R.AWSAADAVASWVGEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1548.440	1548.681	-155.976	0.450	1800.831	0.508	22	0.235	R.AWSAADAVASWVGEK.K
R5/RRR5-26/2	1548.072	1548.681	-1042.213	0.437	1793.889	0.506	22	0.234	R.AWSAADAVASWVGEK.K
R5/RRR5-3/2	1548.498	1548.681	-118.729	0.458	1848.081	0.468	22	0.231	R.AWSAADAVASWVGEK.K
R5/RRR5-25/2	1547.953	1548.681	-1119.332	0.397	1924.383	0.423	22	0.231	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1676.344	1676.854	-903.596	0.511	1680.263	0.548	23	0.229	R.AWSAADAVASWVGEKK.N
R5/RRR5-23/3	1384.201	1384.522	-232.606	0.563	1712.918	0.581	27	0.228	R.RADGVGPVSWDPK.V
R5/RRR5-22/2	1676.142	1676.854	-1024.304	0.500	1739.888	0.509	23	0.227	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1548.510	1548.681	-110.742	0.481	1745.269	0.493	22	0.224	R.AWSAADAVASWVGEK.K
R5/RRR5-15/2	1677.782	1676.854	-43.100	0.538	1692.861	0.518	23	0.223	R.AWSAADAVASWVGEKK.N
R5/RRR5-21/2	1548.203	1548.681	-309.579	0.387	1889.808	0.407	22	0.222	R.AWSAADAVASWVGEK.K
R5/RRR5-23/3	1384.091	1384.522	-312.504	0.539	1740.424	0.547	27	0.220	R.RADGVGPVSWDPK.V
R5/RRR5-2/2	1676.340	1676.854	-905.862	0.489	1720.679	0.488	23	0.220	R.AWSAADAVASWVGEKK.N
R5/RRR5-23/2	1548.189	1548.681	-318.914	0.487	1650.843	0.519	21	0.219	R.AWSAADAVASWVGEK.K
R5/RRR5-22/3	1385.447	1384.522	-54.413	0.566	1608.486	0.592	26	0.215	R.RADGVGPVSWDPK.V
R5/RRR5-23/3	1384.424	1384.522	-71.257	0.558	1542.022	0.614	25	0.212	R.RADGVGPVSWDPK.V
R5/RRR5-23/2	1676.496	1676.854	-214.026	0.535	1514.205	0.558	23	0.212	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1677.350	1676.854	296.676	0.536	1550.013	0.538	23	0.211	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1405.120	1405.579	-328.295	0.508	1657.635	0.447	18	0.208	K.VCGHYTQVVWR.K
R5/RRR5-24/2	1405.222	1405.579	-255.343	0.507	1720.861	0.411	18	0.207	K.VCGHYTQVVWR.K
R5/RRR5-24/2	1548.038	1548.681	-1064.777	0.376	1681.258	0.437	21	0.204	R.AWSAADAVASWVGEK.K
R5/RRR5-25/2	1676.203	1676.854	-988.038	0.502	1514.816	0.508	23	0.201	R.AWSAADAVASWVGEKK.N
R5/RRR5-23/2	1677.216	1676.854	216.911	0.555	1466.135	0.532	22	0.200	R.AWSAADAVASWVGEKK.N
R5/RRR5-1/2	1548.106	1548.681	-1020.045	0.384	1634.789	0.422	21	0.195	R.AWSAADAVASWVGEK.K
R5/RRR5-1/2	1676.106	1676.854	-1046.022	0.497	1477.115	0.494	21	0.193	R.AWSAADAVASWVGEKK.N
R5/RRR5-7/3	1385.061	1384.522	-333.545	0.547	1571.370	0.550	27	0.193	R.RADGVGPVSWDPK.V
R5/RRR5-23/2	1676.293	1676.854	-934.081	0.538	1307.105	0.558	21	0.190	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1676.369	1676.854	-290.000	0.549	1312.140	0.550	21	0.188	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1676.191	1676.854	-995.057	0.481	1435.607	0.490	21	0.188	R.AWSAADAVASWVGEKK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1675.981	1676.854	-1120.834	0.491	1398.052	0.504	22	0.188	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1676.378	1676.854	-284.594	0.533	1228.878	0.580	21	0.187	R.AWSAADAVASWVGEKK.N
R5/RRR5-21/2	1548.847	1548.681	107.855	0.462	1422.649	0.484	21	0.187	R.AWSAADAVASWVGEK.K
R5/RRR5-16/2	1548.252	1548.681	-278.095	0.401	1521.125	0.434	21	0.186	R.AWSAADAVASWVGEK.K
R5/RRR5-20/3	1384.662	1384.522	101.181	0.537	1521.125	0.540	26	0.183	R.RADGVGPVSWDPK.V
R5/RRR5-26/2	1676.096	1676.854	-1051.579	0.494	1364.924	0.496	21	0.183	R.AWSAADAVASWVGEKK.N
R5/RRR5-22/2	1676.305	1676.854	-926.624	0.534	1375.037	0.491	22	0.183	R.AWSAADAVASWVGEKK.N
R5/RRR5-20/2	1676.175	1676.854	-1004.416	0.467	1362.646	0.492	22	0.182	R.AWSAADAVASWVGEKK.N
R5/RRR5-2/2	1547.401	1548.681	-1477.609	0.356	1547.185	0.403	21	0.182	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1676.412	1676.854	-264.139	0.520	1427.624	0.465	21	0.182	R.AWSAADAVASWVGEKK.N
R5/RRR5-20/2	1547.974	1548.681	-1105.713	0.366	1487.145	0.425	20	0.181	R.AWSAADAVASWVGEK.K
R5/RRR5-6/2	1548.139	1548.681	-999.224	0.314	1729.578	0.294	21	0.180	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1676.184	1676.854	-999.444	0.514	1376.771	0.474	22	0.180	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1547.544	1548.681	-1385.065	0.364	1433.257	0.445	20	0.179	R.AWSAADAVASWVGEK.K
R5/RRR5-18/3	1384.413	1384.522	-79.084	0.552	1448.264	0.559	25	0.179	R.RADGVGPVSWDPK.V
R5/RRR5-24/3	1384.243	1384.522	-202.084	0.535	1352.946	0.593	24	0.178	R.RADGVGPVSWDPK.V
R5/RRR5-23/2	1228.085	1228.336	-204.938	0.451	1385.463	0.439	19	0.178	R.ADGVGPVSWDPK.V
R5/RRR5-24/2	1675.743	1676.854	-1263.468	0.520	1205.440	0.534	21	0.176	R.AWSAADAVASWVGEKK.N
R5/RRR5-3/3	1384.714	1384.522	139.375	0.526	1443.954	0.551	25	0.176	R.RADGVGPVSWDPK.V
R5/RRR5-10/2	1143.034	1143.274	-210.654	0.495	996.318	0.598	18	0.176	K.VASFAQSYAAK.R
R5/RRR5-10/2	1548.855	1548.681	112.993	0.437	1323.880	0.480	18	0.175	R.AWSAADAVASWVGEK.K
R5/RRR5-2/2	1143.017	1143.274	-225.547	0.508	1018.051	0.583	18	0.175	K.VASFAQSYAAK.R
R5/RRR5-9/2	1143.027	1143.274	-216.868	0.472	960.134	0.613	18	0.175	K.VASFAQSYAAK.R
R5/RRR5-2/2	1143.057	1143.274	-189.977	0.506	1054.266	0.562	18	0.174	K.VASFAQSYAAK.R
R5/RRR5-24/2	1404.556	1405.579	-1445.261	0.515	1408.513	0.408	17	0.174	K.VCGHYTQVVWR.K
R5/RRR5-24/2	1143.025	1143.274	-218.154	0.474	1028.568	0.571	18	0.173	K.VASFAQSYAAK.R
R5/RRR5-21/2	1142.772	1143.274	-1318.208	0.494	1024.039	0.566	18	0.172	K.VASFAQSYAAK.R
R5/RRR5-18/3	1384.574	1384.522	37.519	0.558	1378.633	0.564	24	0.171	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/3	1384.831	1384.522	223.709	0.513	1425.678	0.545	26	0.171	R.RADGVGPVSWDPK.V
R5/RRR5-26/3	1384.705	1384.522	132.877	0.548	1426.294	0.543	25	0.171	R.RADGVGPVSWDPK.V
R5/RRR5-4/2	1142.998	1143.274	-241.939	0.423	972.325	0.595	18	0.171	K.VASFAQSYAAK.R
R5/RRR5-24/2	1143.050	1143.274	-196.619	0.456	1045.641	0.554	18	0.171	K.VASFAQSYAAK.R
R5/RRR5-23/2	1142.931	1143.274	-300.658	0.443	997.574	0.577	18	0.170	K.VASFAQSYAAK.R
R5/RRR5-28/2	1143.140	1143.274	-117.453	0.504	972.414	0.574	18	0.170	K.VASFAQSYAAK.R
R5/RRR5-23/2	1547.841	1548.681	-1192.583	0.407	1607.314	0.311	20	0.170	R.AWSAADAVASWVGEK.K
R5/RRR5-14/2	1143.010	1143.274	-231.225	0.508	995.401	0.561	18	0.170	K.VASFAQSYAAK.R
R5/RRR5-24/2	1550.227	1548.681	-293.379	0.578	1133.516	0.536	19	0.170	R.AWSAADAVASWVGEK.K
R5/RRR5-20/2	1143.048	1143.274	-197.905	0.504	1003.083	0.557	18	0.170	K.VASFAQSYAAK.R
R5/RRR5-22/3	1384.858	1384.522	243.597	0.549	1507.777	0.507	26	0.170	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1675.837	1676.854	-1207.287	0.437	1182.961	0.513	19	0.169	R.AWSAADAVASWVGEKK.N
R5/RRR5-1/2	1143.024	1143.274	-219.654	0.479	1007.469	0.551	18	0.168	K.VASFAQSYAAK.R
R5/RRR5-23/2	1229.031	1228.336	-248.913	0.431	1233.058	0.454	19	0.168	R.ADGVGPVSWDPK.V
R5/RRR5-28/2	1142.904	1143.274	-324.662	0.488	989.555	0.551	18	0.168	K.VASFAQSYAAK.R
R5/RRR5-14/2	1143.163	1143.274	-97.101	0.475	975.886	0.558	18	0.167	K.VASFAQSYAAK.R
R5/RRR5-1/2	1143.907	1143.274	-321.487	0.519	892.451	0.578	18	0.167	K.VASFAQSYAAK.R
R5/RRR5-4/2	1143.076	1143.274	-173.586	0.500	966.179	0.552	18	0.167	K.VASFAQSYAAK.R
R5/RRR5-23/2	1144.169	1143.274	-91.986	0.426	1014.703	0.544	18	0.166	K.VASFAQSYAAK.R
R5/RRR5-21/2	1142.896	1143.274	-331.949	0.439	1013.501	0.541	18	0.166	K.VASFAQSYAAK.R
R5/RRR5-7/2	1143.038	1143.274	-206.797	0.420	963.100	0.567	18	0.166	K.VASFAQSYAAK.R
R5/RRR5-24/2	1585.019	1585.607	-1004.710	0.404	1202.190	0.468	18	0.166	K.NYHYDTNTCDPGK.V
R5/RRR5-1/2	1142.906	1143.274	-322.840	0.456	1012.138	0.534	18	0.166	K.VASFAQSYAAK.R
R5/RRR5-2/3	1384.636	1384.522	82.348	0.516	1301.749	0.575	24	0.165	R.RADGVGPVSWDPK.V
R5/RRR5-4/2	1142.953	1143.274	-281.585	0.531	921.637	0.551	18	0.164	K.VASFAQSYAAK.R
R5/RRR5-3/2	1142.914	1143.274	-316.196	0.495	955.097	0.542	18	0.164	K.VASFAQSYAAK.R
R5/RRR5-23/2	1142.998	1143.274	-242.261	0.456	970.585	0.542	18	0.164	K.VASFAQSYAAK.R
R5/RRR5-24/2	1676.342	1676.854	-904.473	0.472	1221.826	0.461	20	0.164	R.AWSAADAVASWVGEKK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1142.904	1143.274	-324.340	0.458	969.481	0.541	18	0.164	K.VASFAQSYAAK.R
R5/RRR5-26/2	1142.932	1143.274	-299.694	0.449	986.594	0.532	18	0.163	K.VASFAQSYAAK.R
R5/RRR5-11/2	1143.017	1143.274	-225.225	0.448	963.019	0.541	18	0.163	K.VASFAQSYAAK.R
R5/RRR5-24/2	1143.435	1143.274	141.706	0.443	1051.030	0.499	18	0.162	K.VASFAQSYAAK.R
R5/RRR5-3/2	1143.054	1143.274	-192.870	0.510	899.040	0.545	18	0.162	K.VASFAQSYAAK.R
R5/RRR5-24/2	1142.507	1143.274	-1551.383	0.396	1012.460	0.524	18	0.162	K.VASFAQSYAAK.R
R5/RRR5-2/2	1143.106	1143.274	-147.125	0.477	863.218	0.560	18	0.162	K.VASFAQSYAAK.R
R5/RRR5-17/2	1547.865	1548.681	-1176.744	0.292	1425.621	0.348	21	0.162	R.AWSAADAVASWVGEK.K
R5/RRR5-25/2	1675.944	1676.854	-1143.214	0.471	1216.219	0.448	20	0.161	R.AWSAADAVASWVGEKK.N
R5/RRR5-22/2	1142.919	1143.274	-311.481	0.430	964.097	0.531	18	0.161	K.VASFAQSYAAK.R
R5/RRR5-8/2	1143.016	1143.274	-226.725	0.486	960.224	0.521	18	0.161	K.VASFAQSYAAK.R
R5/RRR5-13/2	1143.001	1143.274	-239.154	0.502	944.293	0.524	18	0.161	K.VASFAQSYAAK.R
R5/RRR5-24/3	1548.557	1548.681	-80.031	0.499	1464.443	0.476	28	0.161	R.AWSAADAVASWVGEK.K
R5/RRR5-20/2	1143.234	1143.274	-34.979	0.451	945.145	0.531	18	0.161	K.VASFAQSYAAK.R
R5/RRR5-10/2	1144.162	1143.274	-98.407	0.512	828.953	0.558	18	0.161	K.VASFAQSYAAK.R
R5/RRR5-25/2	1142.984	1143.274	-254.154	0.483	959.065	0.515	18	0.160	K.VASFAQSYAAK.R
R5/RRR5-18/2	1142.783	1143.274	-430.871	0.511	774.416	0.580	17	0.160	K.VASFAQSYAAK.R
R5/RRR5-24/2	1676.257	1676.854	-955.283	0.466	1232.018	0.434	20	0.160	R.AWSAADAVASWVGEKK.N
R5/RRR5-20/2	1142.523	1143.274	-1536.786	0.400	977.032	0.525	18	0.160	K.VASFAQSYAAK.R
R5/RRR5-24/2	1228.070	1228.336	-216.606	0.408	1185.412	0.432	18	0.160	R.ADGVGPVSWDPK.V
R5/RRR5-24/3	1548.833	1548.681	98.796	0.531	1417.968	0.493	29	0.160	R.AWSAADAVASWVGEK.K
R5/RRR5-25/2	1675.694	1676.854	-1292.585	0.501	1105.095	0.482	20	0.159	R.AWSAADAVASWVGEKK.N
R5/RRR5-15/2	1547.715	1548.681	-1273.923	0.292	1480.188	0.304	21	0.159	R.AWSAADAVASWVGEK.K
R5/RRR5-8/2	1143.243	1143.274	-27.268	0.419	994.174	0.504	18	0.159	K.VASFAQSYAAK.R
R5/RRR5-14/2	1142.917	1143.274	-312.981	0.484	861.007	0.546	17	0.159	K.VASFAQSYAAK.R
R5/RRR5-23/2	1142.516	1143.274	-1543.012	0.388	983.788	0.515	18	0.159	K.VASFAQSYAAK.R
R5/RRR5-25/2	1229.519	1228.336	149.908	0.459	1192.628	0.419	17	0.158	R.ADGVGPVSWDPK.V
R5/RRR5-27/2	1143.041	1143.274	-204.119	0.429	895.792	0.531	18	0.158	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1143.036	1143.274	-208.511	0.453	794.148	0.567	17	0.158	K.VASFAQSYAAK.R
R5/RRR5-16/2	1677.789	1676.854	-38.429	0.522	1078.172	0.483	20	0.157	R.AWSAADAVASWVGEKK.N
R5/RRR5-10/2	1548.168	1548.681	-980.383	0.360	1253.304	0.407	18	0.157	R.AWSAADAVASWVGEK.K
R5/RRR5-2/2	1676.626	1676.854	-136.164	0.504	1116.386	0.470	19	0.157	R.AWSAADAVASWVGEKK.N
R5/RRR5-23/2	1405.250	1405.579	-234.863	0.485	1284.775	0.367	17	0.157	K.VCGHYTQVVWR.K
R5/RRR5-8/2	1142.796	1143.274	-419.402	0.451	861.543	0.537	17	0.157	K.VASFAQSYAAK.R
R5/RRR5-12/2	1142.837	1143.274	-383.176	0.475	814.671	0.546	17	0.157	K.VASFAQSYAAK.R
R5/RRR5-19/2	1142.455	1143.274	-1596.679	0.441	946.572	0.498	18	0.156	K.VASFAQSYAAK.R
R5/RRR5-9/2	1143.376	1143.274	89.135	0.474	779.284	0.550	17	0.156	K.VASFAQSYAAK.R
R5/RRR5-6/2	1143.317	1143.274	37.737	0.414	869.334	0.533	17	0.155	K.VASFAQSYAAK.R
R5/RRR5-18/3	1384.111	1384.522	-298.037	0.492	1335.770	0.526	24	0.155	R.RADGVGPVSWDPK.V
R5/RRR5-13/2	1142.394	1143.274	-1650.781	0.362	950.093	0.512	18	0.155	K.VASFAQSYAAK.R
R5/RRR5-26/3	1384.711	1384.522	137.120	0.534	1375.498	0.512	25	0.155	R.RADGVGPVSWDPK.V
R5/RRR5-15/2	1143.083	1143.274	-167.587	0.497	908.719	0.491	18	0.155	K.VASFAQSYAAK.R
R5/RRR5-24/2	1143.377	1143.274	90.313	0.396	957.220	0.492	18	0.154	K.VASFAQSYAAK.R
R5/RRR5-21/3	1384.227	1384.522	-213.496	0.506	1202.732	0.578	25	0.154	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1143.262	1143.274	-10.132	0.475	804.127	0.526	18	0.154	K.VASFAQSYAAK.R
R5/RRR5-25/2	1142.990	1143.274	-249.440	0.468	788.103	0.538	17	0.154	K.VASFAQSYAAK.R
R5/RRR5-24/3	1384.365	1384.522	-113.978	0.534	1241.617	0.561	24	0.154	R.RADGVGPVSWDPK.V
R5/RRR5-13/2	1142.663	1143.274	-1413.804	0.395	949.671	0.487	18	0.154	K.VASFAQSYAAK.R
R5/RRR5-26/2	1142.515	1143.274	-1544.299	0.399	869.744	0.517	18	0.153	K.VASFAQSYAAK.R
R5/RRR5-26/2	1142.924	1143.274	-307.088	0.458	821.921	0.516	18	0.153	K.VASFAQSYAAK.R
R5/RRR5-21/3	1383.755	1384.522	-1280.898	0.530	1153.093	0.587	23	0.152	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1676.200	1676.854	-989.646	0.381	1210.438	0.387	20	0.152	R.AWSAADAVASWVGEKK.N
R5/RRR5-20/2	1675.793	1676.854	-1233.182	0.508	1057.105	0.454	20	0.152	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1143.017	1143.274	-225.868	0.465	848.310	0.498	17	0.151	K.VASFAQSYAAK.R
R5/RRR5-24/2	1585.086	1585.607	-962.184	0.400	1087.798	0.431	17	0.151	K.NYHYDTNTCDPGK.V
R5/RRR5-24/2	1143.606	1143.274	291.036	0.427	839.534	0.501	18	0.151	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/3	1385.243	1384.522	-201.850	0.555	1194.408	0.568	24	0.151	R.RADGVGPVSWDPK.V
R5/RRR5-17/2	1677.525	1676.854	-196.524	0.539	1088.090	0.449	20	0.151	-.AWSAADAVASWVGEKK.-
R5/RRR5-17/2	1547.258	1548.681	-1570.488	0.354	1199.766	0.385	19	0.151	R.AWSAADAVASWVGEK.K
R5/RRR5-22/2	1676.094	1676.854	-1053.334	0.455	876.050	0.515	19	0.150	R.AWSAADAVASWVGEKK.N
R5/RRR5-21/2	1228.284	1228.336	-42.226	0.339	1218.962	0.358	18	0.150	R.ADGVGPVSWDPK.V
R5/RRR5-23/2	1228.018	1228.336	-259.387	0.429	1155.267	0.375	18	0.150	R.ADGVGPVSWDPK.V
R5/RRR5-24/2	1142.497	1143.274	-1559.862	0.361	884.468	0.479	18	0.148	K.VASFAQSYAAK.R
R5/RRR5-22/2	1227.584	1228.336	-1431.498	0.298	1264.408	0.323	18	0.147	R.ADGVGPVSWDPK.V
R5/RRR5-24/2	1143.225	1143.274	-43.119	0.435	818.116	0.475	17	0.147	K.VASFAQSYAAK.R
R5/RRR5-22/2	1228.132	1228.336	-166.549	0.397	1025.219	0.413	17	0.147	R.ADGVGPVSWDPK.V
R5/RRR5-1/3	1384.682	1384.522	115.769	0.516	1179.581	0.557	23	0.147	R.RADGVGPVSWDPK.V
R5/RRR5-22/2	1142.455	1143.274	-1596.464	0.367	814.184	0.479	18	0.145	K.VASFAQSYAAK.R
R5/RRR5-24/2	1228.117	1228.336	-178.315	0.366	1025.013	0.403	17	0.145	R.ADGVGPVSWDPK.V
R5/RRR5-24/3	1384.858	1384.522	243.729	0.520	1248.776	0.527	27	0.144	R.RADGVGPVSWDPK.V
R5/RRR5-6/2	1144.005	1143.274	-235.519	0.386	787.657	0.472	17	0.144	K.VASFAQSYAAK.R
R5/RRR5-24/2	1142.441	1143.274	-1609.238	0.346	796.978	0.475	18	0.143	K.VASFAQSYAAK.R
R5/RRR5-24/2	1227.490	1228.336	-1508.312	0.342	1083.996	0.366	17	0.143	R.ADGVGPVSWDPK.V
R5/RRR5-5/2	1548.405	1548.681	-178.911	0.355	1179.429	0.328	21	0.143	R.AWSAADAVASWVGEK.K
R5/RRR5-6/2	1142.339	1143.274	-1699.307	0.317	949.554	0.418	18	0.142	K.VASFAQSYAAK.R
R5/RRR5-23/2	1144.036	1143.274	-208.864	0.383	913.081	0.402	18	0.142	K.VASFAQSYAAK.R
R5/RRR5-18/2	1142.398	1143.274	-1646.809	0.363	766.714	0.449	18	0.141	K.VASFAQSYAAK.R
R5/RRR5-19/2	1385.167	1384.522	-257.095	0.437	573.248	0.475	20	0.140	R.RADGVGPVSWDPK.V
R5/RRR5-19/2	1142.197	1143.274	-1824.077	0.338	798.771	0.442	18	0.140	K.VASFAQSYAAK.R
R5/RRR5-24/2	1300.013	1299.460	-344.760	0.400	937.336	0.420	16	0.140	K.VASFAQSYAAKR.A
R5/RRR5-3/2	1676.507	1676.854	-207.598	0.456	917.975	0.425	18	0.140	R.AWSAADAVASWVGEKK.N
R5/RRR5-12/2	1142.321	1143.274	-1714.982	0.352	754.229	0.445	17	0.139	K.VASFAQSYAAK.R
R5/RRR5-21/2	1229.263	1228.336	-59.423	0.389	1084.413	0.330	17	0.139	R.ADGVGPVSWDPK.V
R5/RRR5-3/3	1384.512	1384.522	-7.581	0.471	1181.274	0.524	23	0.138	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1383.732	1384.522	-1297.566	0.423	404.621	0.503	17	0.138	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1585.144	1585.607	-292.787	0.410	927.899	0.388	16	0.137	K.NYHYDTNTCDPGK.V
R5/RRR5-22/3	1384.123	1384.522	-289.144	0.479	1015.554	0.577	22	0.137	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1585.011	1585.607	-1009.813	0.403	884.429	0.402	16	0.137	K.NYHYDTNTCDPGK.V
R5/RRR5-3/3	1384.280	1384.522	-175.146	0.488	1015.681	0.581	22	0.136	-.RADGVGPVSWDPK.-
R5/RRR5-19/2	1385.161	1384.522	-261.428	0.400	491.993	0.452	19	0.136	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1384.223	1384.522	-216.937	0.426	622.677	0.417	20	0.136	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1675.780	1676.854	-1241.375	0.394	952.510	0.379	18	0.136	R.AWSAADAVASWVGEKK.N
R5/RRR5-17/3	1384.525	1384.522	2.368	0.471	1283.760	0.477	24	0.136	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1675.264	1676.854	-2148.960	0.396	1004.750	0.354	19	0.136	R.AWSAADAVASWVGEKK.N
R5/RRR5-23/2	1383.634	1384.522	-1368.449	0.415	542.784	0.436	19	0.136	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1584.960	1585.607	-1042.136	0.337	944.088	0.376	16	0.135	K.NYHYDTNTCDPGK.V
R5/RRR5-24/1	1547.821	1548.681	-1205.047	0.138	373.226	0.311	13	0.135	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1384.191	1384.522	-239.674	0.412	561.034	0.417	20	0.135	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1385.125	1384.522	-287.157	0.391	569.681	0.424	20	0.135	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1585.081	1585.607	-965.354	0.413	943.748	0.360	16	0.134	K.NYHYDTNTCDPGK.V
R5/RRR5-23/2	1384.284	1384.522	-172.704	0.424	528.979	0.415	19	0.134	R.RADGVGPVSWDPK.V
R5/RRR5-21/2	1384.103	1384.522	-303.823	0.429	587.433	0.394	20	0.134	R.RADGVGPVSWDPK.V
R5/RRR5-18/2	1676.298	1676.854	-931.157	0.454	807.549	0.401	19	0.134	R.AWSAADAVASWVGEKK.N
R5/RRR5-20/2	1384.144	1384.522	-274.181	0.440	399.876	0.490	17	0.134	-.RADGVGPVSWDPK.-
R5/RRR5-19/2	1547.976	1548.681	-1104.683	0.264	1081.871	0.305	19	0.134	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1142.423	1143.274	-1625.125	0.320	630.092	0.436	15	0.133	K.VASFAQSYAAK.R
R5/RRR5-4/2	1547.669	1548.681	-1303.944	0.327	1059.468	0.305	18	0.133	R.AWSAADAVASWVGEK.K
R5/RRR5-23/2	1384.051	1384.522	-341.342	0.405	626.396	0.380	20	0.133	R.RADGVGPVSWDPK.V
R5/RRR5-19/3	1384.310	1384.522	-153.783	0.530	983.978	0.570	22	0.133	R.RADGVGPVSWDPK.V
R5/RRR5-22/2	1384.177	1384.522	-250.203	0.385	461.223	0.412	18	0.132	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1384.196	1384.522	-236.489	0.394	568.225	0.380	20	0.132	R.RADGVGPVSWDPK.V
R5/RRR5-20/2	1384.395	1384.522	-91.678	0.464	512.216	0.430	19	0.132	-.RADGVGPVSWDPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1384.233	1384.522	-209.329	0.377	562.278	0.375	20	0.131	R.RADGVGPVSWDPK.V
R5/RRR5-1/2	1384.123	1384.522	-289.311	0.402	520.162	0.378	19	0.131	R.RADGVGPVSWDPK.V
R5/RRR5-22/2	1143.029	1143.274	-215.261	0.357	296.577	0.417	13	0.131	K.VASFAQSYAAK.R
R5/RRR5-18/2	1676.511	1676.854	-204.968	0.467	563.618	0.433	18	0.131	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1384.172	1384.522	-253.919	0.407	480.605	0.369	19	0.131	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1384.095	1384.522	-309.486	0.399	529.251	0.372	19	0.131	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1383.652	1384.522	-1355.690	0.370	439.479	0.381	18	0.131	R.RADGVGPVSWDPK.V
R5/RRR5-22/2	1384.195	1384.522	-237.109	0.462	533.642	0.407	19	0.130	-.RADGVGPVSWDPK.-
R5/RRR5-21/2	1384.200	1384.522	-233.304	0.394	522.777	0.364	19	0.130	R.RADGVGPVSWDPK.V
R5/RRR5-21/2	1677.042	1676.854	112.460	0.473	671.980	0.380	21	0.130	R.AWSAADAVASWVGEKK.N
R5/RRR5-1/2	1385.117	1384.522	-293.435	0.374	339.770	0.386	16	0.130	R.RADGVGPVSWDPK.V
R5/RRR5-19/3	1383.922	1384.522	-1159.250	0.521	992.191	0.557	22	0.130	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1675.238	1676.854	-2164.560	0.381	676.111	0.386	19	0.130	R.AWSAADAVASWVGEKK.N
R5/RRR5-23/3	1384.751	1384.522	166.162	0.562	915.371	0.579	23	0.129	R.RADGVGPVSWDPK.V
R5/RRR5-17/3	1383.856	1384.522	-1207.614	0.462	1076.257	0.529	25	0.129	R.RADGVGPVSWDPK.V
R5/RRR5-22/2	1227.432	1228.336	-1555.565	0.287	972.719	0.293	16	0.129	R.ADGVGPVSWDPK.V
R5/RRR5-10/2	1675.911	1676.854	-1162.449	0.414	784.309	0.361	18	0.128	R.AWSAADAVASWVGEKK.N
R5/RRR5-19/2	1384.245	1384.522	-200.482	0.385	525.763	0.326	19	0.128	R.RADGVGPVSWDPK.V
R5/RRR5-22/2	1384.099	1384.522	-306.654	0.348	574.207	0.323	20	0.128	R.RADGVGPVSWDPK.V
R5/RRR5-25/2	1384.057	1384.522	-337.271	0.396	467.897	0.323	18	0.128	R.RADGVGPVSWDPK.V
R5/RRR5-25/2	1385.008	1384.522	351.960	0.438	471.254	0.377	18	0.127	-.RADGVGPVSWDPK.-
R5/RRR5-20/2	1228.328	1228.336	-6.540	0.345	934.674	0.280	16	0.127	R.ADGVGPVSWDPK.V
R5/RRR5-24/2	1677.637	1676.854	-129.879	0.418	330.604	0.439	14	0.127	R.AWSAADAVASWVGEKK.N
R5/RRR5-3/2	1383.978	1384.522	-1118.809	0.328	476.251	0.315	18	0.126	R.RADGVGPVSWDPK.V
R5/RRR5-13/2	1384.385	1384.522	-99.196	0.348	426.198	0.302	17	0.126	R.RADGVGPVSWDPK.V
R5/RRR5-1/2	1384.150	1384.522	-269.314	0.351	441.334	0.285	18	0.126	R.RADGVGPVSWDPK.V
R5/RRR5-14/2	1384.309	1384.522	-154.481	0.392	521.266	0.305	18	0.126	R.RADGVGPVSWDPK.V
R5/RRR5-10/2	1143.007	1143.274	-234.225	0.291	462.571	0.351	14	0.126	K.VASFAQSYAAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1385.062	1384.522	-333.137	0.308	430.818	0.289	18	0.126	R.RADGVGPVSWDPK.V
R5/RRR5-18/2	1228.076	1228.336	-211.919	0.287	900.715	0.286	15	0.126	R.ADGVGPVSWDPK.V
R5/RRR5-24/2	1678.081	1676.854	135.957	0.374	402.328	0.419	14	0.125	R.AWSAADAVASWVGEKK.N
R5/RRR5-20/2	1384.136	1384.522	-279.578	0.351	376.230	0.263	16	0.125	R.RADGVGPVSWDPK.V
R5/RRR5-24/3	1384.598	1384.522	55.159	0.526	1044.391	0.520	23	0.125	R.RADGVGPVSWDPK.V
R5/RRR5-18/2	1384.232	1384.522	-210.125	0.408	505.691	0.327	19	0.125	-.RADGVGPVSWDPK.-
R5/RRR5-6/2	1547.945	1548.681	-1125.113	0.288	1084.811	0.216	18	0.125	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1384.211	1384.522	-225.253	0.363	479.878	0.264	18	0.125	R.RADGVGPVSWDPK.V
R5/RRR5-17/2	1676.370	1676.854	-289.489	0.480	821.549	0.346	18	0.125	-.AWSAADAVASWVGEKK.-
R5/RRR5-3/2	1384.420	1384.522	-73.547	0.358	362.810	0.334	16	0.124	-.RADGVGPVSWDPK.-
R5/RRR5-26/2	1384.033	1384.522	-354.085	0.371	316.408	0.328	15	0.124	-.RADGVGPVSWDPK.-
R5/RRR5-15/2	1384.196	1384.522	-236.047	0.332	461.720	0.255	17	0.124	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1384.187	1384.522	-242.683	0.360	405.822	0.297	17	0.123	-.RADGVGPVSWDPK.-
R5/RRR5-14/2	1676.851	1676.854	-1.505	0.324	539.790	0.352	16	0.123	R.AWSAADAVASWVGEKK.N
R5/RRR5-22/2	1675.763	1676.854	-1251.105	0.359	669.193	0.303	19	0.123	R.AWSAADAVASWVGEKK.N
R5/RRR5-24/2	1228.039	1228.336	-242.134	0.360	566.084	0.312	14	0.123	R.ADGVGPVSWDPK.V
R5/RRR5-5/2	1548.382	1548.681	-193.937	0.349	758.196	0.291	17	0.123	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1384.167	1384.522	-257.193	0.295	582.896	0.219	20	0.122	R.RADGVGPVSWDPK.V
R5/RRR5-17/2	1383.963	1384.522	-1130.145	0.406	413.524	0.359	17	0.122	-.RADGVGPVSWDPK.-
R5/RRR5-2/3	1384.810	1384.522	208.593	0.513	903.231	0.550	21	0.122	R.RADGVGPVSWDPK.V
R5/RRR5-26/2	1384.100	1384.522	-305.769	0.403	393.494	0.348	17	0.122	-.RADGVGPVSWDPK.-
R5/RRR5-19/3	1384.494	1384.522	-20.580	0.570	946.940	0.536	21	0.121	R.RADGVGPVSWDPK.V
R5/RRR5-26/2	1384.046	1384.522	-345.059	0.362	333.206	0.292	16	0.121	-.RADGVGPVSWDPK.-
R5/RRR5-24/3	1383.797	1384.522	-1250.533	0.434	862.920	0.555	23	0.120	R.RADGVGPVSWDPK.V
R5/RRR5-17/2	1677.076	1676.854	132.972	0.448	606.836	0.371	17	0.120	-.AWSAADAVASWVGEKK.-
R5/RRR5-24/2	1547.554	1548.681	-1378.251	0.289	682.320	0.238	17	0.119	R.AWSAADAVASWVGEK.K
R5/RRR5-24/2	1675.311	1676.854	-2120.909	0.300	520.739	0.265	15	0.119	R.AWSAADAVASWVGEKK.N
R5/RRR5-3/2	1384.761	1384.522	173.067	0.354	359.352	0.275	16	0.117	-.RADGVGPVSWDPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/3	1384.758	1384.522	170.803	0.484	912.968	0.516	22	0.116	R.RADGVGPVSWDPK.V
R5/RRR5-2/2	1385.044	1384.522	-346.490	0.361	267.857	0.307	15	0.115	-.RADGVGPVSWDPK.-
R5/RRR5-5/3	1384.822	1384.522	217.212	0.446	928.995	0.508	21	0.114	-.RADGVGPVSWDPK.-
R5/RRR5-8/3	1384.502	1384.522	-14.744	0.497	730.366	0.539	21	0.112	R.RADGVGPVSWDPK.V
R5/RRR5-24/2	1678.471	1676.854	-228.655	0.424	218.121	0.349	13	0.111	-.AWSAADAVASWVGEKK.-
R5/RRR5-5/3	1384.863	1384.522	246.646	0.471	877.393	0.501	22	0.111	R.RADGVGPVSWDPK.V
R5/RRR5-17/3	1384.271	1384.522	-181.781	0.503	979.258	0.472	24	0.111	R.RADGVGPVSWDPK.V
R5/RRR5-24/3	1549.423	1548.681	-167.146	0.512	984.573	0.475	24	0.111	R.AWSAADAVASWVGEK.K
R5/RRR5-20/3	1383.531	1384.522	-1443.251	0.449	972.506	0.472	24	0.110	R.RADGVGPVSWDPK.V
R5/RRR5-16/2	1384.374	1384.522	-106.892	0.378	340.973	0.322	15	0.110	-.RADGVGPVSWDPK.-
R5/RRR5-19/2	1676.071	1676.854	-1067.009	0.382	298.106	0.379	12	0.109	-.AWSAADAVASWVGEKK.-
R5/RRR5-5/3	1384.975	1384.522	327.781	0.499	804.516	0.509	20	0.109	R.RADGVGPVSWDPK.V
R5/RRR5-26/3	1406.076	1405.579	354.078	0.545	1220.103	0.393	24	0.108	K.VCGHYTQVVWR.K
R5/RRR5-10/3	1384.630	1384.522	78.370	0.465	1011.706	0.451	22	0.107	-.RADGVGPVSWDPK.-
R5/RRR5-23/3	1384.664	1384.522	103.038	0.482	829.681	0.490	22	0.107	R.RADGVGPVSWDPK.V
R5/RRR5-16/3	1384.804	1384.522	204.615	0.461	854.955	0.486	27	0.106	R.RADGVGPVSWDPK.V
R5/RRR5-13/3	1383.991	1384.522	-1109.165	0.480	617.710	0.508	22	0.105	R.RADGVGPVSWDPK.V
R5/RRR5-22/3	1548.696	1548.681	9.983	0.443	961.021	0.450	25	0.104	R.AWSAADAVASWVGEK.K
R5/RRR5-9/3	1384.295	1384.522	-164.133	0.440	990.367	0.427	23	0.102	R.RADGVGPVSWDPK.V
R5/RRR5-12/3	1384.802	1384.522	203.024	0.471	726.136	0.482	20	0.102	R.RADGVGPVSWDPK.V
R5/RRR5-23/3	1405.346	1405.579	-166.509	0.532	1173.560	0.371	24	0.101	K.VCGHYTQVVWR.K
R5/RRR5-23/3	1713.681	1713.780	-57.995	0.477	901.932	0.438	28	0.100	K.KNYHYDTNTCDPGK.V
R5/RRR5-8/3	1384.371	1384.522	-109.201	0.464	584.494	0.507	21	0.099	-.RADGVGPVSWDPK.-
R5/RRR5-22/3	1405.068	1405.579	-1078.803	0.555	1233.239	0.345	24	0.098	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1406.058	1405.579	341.152	0.566	1102.652	0.377	23	0.098	K.VCGHYTQVVWR.K
R5/RRR5-6/2	1548.002	1548.681	-1087.897	0.281	574.193	0.129	14	0.098	-.AWSAADAVASWVGEK.-
R5/RRR5-24/3	1585.855	1585.607	157.173	0.440	766.871	0.460	27	0.098	K.NYHYDTNTCDPGK.V
R5/RRR5-14/3	1384.889	1384.522	266.003	0.432	560.310	0.444	25	0.097	R.RADGVGPVSWDPK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-28/3	1384.445	1384.522	-56.000	0.444	497.786	0.426	21	0.096	R.RADGVGPVSWDPK.V
R5/RRR5-3/3	1405.311	1405.579	-191.736	0.468	637.299	0.430	19	0.095	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1713.861	1713.780	47.348	0.507	613.592	0.450	25	0.094	K.KNYHYDTNTCDPGK.V
R5/RRR5-20/3	1405.590	1405.579	7.690	0.530	869.607	0.397	21	0.094	K.VCGHYTQVVWR.K
R5/RRR5-23/3	1405.432	1405.579	-105.213	0.555	1138.374	0.341	24	0.093	K.VCGHYTQVVWR.K
R5/RRR5-16/3	1384.478	1384.522	-31.591	0.262	369.277	0.348	22	0.092	R.RADGVGPVSWDPK.V
R5/RRR5-28/3	1384.629	1384.522	77.707	0.449	516.482	0.383	21	0.092	R.RADGVGPVSWDPK.V
R5/RRR5-24/3	1405.690	1405.579	79.025	0.565	1127.969	0.340	23	0.092	K.VCGHYTQVVWR.K
R5/RRR5-1/3	1406.405	1405.579	-124.379	0.517	926.752	0.375	22	0.092	K.VCGHYTQVVWR.K
R5/RRR5-2/3	1405.018	1405.579	-1114.395	0.467	559.527	0.385	18	0.091	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1713.241	1713.780	-900.830	0.504	547.852	0.424	24	0.091	K.KNYHYDTNTCDPGK.V
R5/RRR5-24/3	1405.063	1405.579	-1082.597	0.537	1114.700	0.333	23	0.090	K.VCGHYTQVVWR.K
R5/RRR5-23/3	1405.490	1405.579	-63.655	0.534	1150.206	0.323	24	0.090	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1585.784	1585.607	112.013	0.337	736.479	0.434	25	0.090	K.NYHYDTNTCDPGK.V
R5/RRR5-19/3	1405.426	1405.579	-109.395	0.487	729.337	0.377	21	0.090	K.VCGHYTQVVWR.K
R5/RRR5-14/3	1384.878	1384.522	257.916	0.303	281.889	0.419	20	0.090	-.RADGVGPVSWDPK.-
R5/RRR5-23/3	1405.251	1405.579	-234.219	0.552	1067.758	0.338	23	0.089	K.VCGHYTQVVWR.K
R5/RRR5-1/3	1405.219	1405.579	-257.096	0.509	699.028	0.372	20	0.089	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1713.848	1713.780	40.169	0.480	754.916	0.391	27	0.089	K.KNYHYDTNTCDPGK.V
R5/RRR5-22/3	1405.699	1405.579	85.034	0.557	865.087	0.365	21	0.088	K.VCGHYTQVVWR.K
R5/RRR5-9/3	1384.785	1384.522	190.825	0.405	792.930	0.373	23	0.088	R.RADGVGPVSWDPK.V
R5/RRR5-24/3	1585.777	1585.607	107.728	0.317	792.815	0.420	27	0.088	K.NYHYDTNTCDPGK.V
R5/RRR5-23/3	1713.631	1713.780	-87.147	0.464	567.978	0.402	23	0.088	K.KNYHYDTNTCDPGK.V
R5/RRR5-26/3	1406.403	1405.579	-125.816	0.487	850.066	0.352	22	0.087	K.VCGHYTQVVWR.K
R5/RRR5-22/3	1405.515	1405.579	-46.014	0.561	951.879	0.342	22	0.087	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1405.494	1405.579	-61.042	0.529	936.455	0.339	22	0.086	K.VCGHYTQVVWR.K
R5/RRR5-26/3	1585.813	1585.607	130.193	0.375	651.471	0.390	24	0.086	K.NYHYDTNTCDPGK.V
R5/RRR5-3/3	1405.701	1405.579	86.863	0.462	398.335	0.401	16	0.086	-.VCGHYTQVVWR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/3	1405.700	1405.579	86.079	0.519	880.525	0.340	21	0.085	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1586.523	1585.607	-52.803	0.344	530.929	0.376	23	0.085	K.NYHYDTNTCDPGK.V
R5/RRR5-24/3	1405.787	1405.579	148.390	0.559	997.621	0.325	22	0.085	K.VCGHYTQVVWR.K
R5/RRR5-19/3	1405.377	1405.579	-144.159	0.401	788.601	0.342	22	0.084	K.VCGHYTQVVWR.K
R5/RRR5-20/3	1405.899	1405.579	228.194	0.514	865.652	0.332	21	0.084	K.VCGHYTQVVWR.K
R5/RRR5-19/3	1586.468	1585.607	-87.650	0.435	471.923	0.420	22	0.084	-.NYHYDTNTCDPGK.-
R5/RRR5-28/3	1384.394	1384.522	-93.015	0.383	327.580	0.383	17	0.083	-.RADGVGPVSWDPK.-
R5/RRR5-25/3	1405.431	1405.579	-105.866	0.469	945.979	0.312	22	0.083	K.VCGHYTQVVWR.K
R5/RRR5-4/3	1384.053	1384.522	-339.715	0.416	787.019	0.348	21	0.082	-.RADGVGPVSWDPK.-
R5/RRR5-26/3	1405.851	1405.579	193.453	0.528	972.309	0.303	22	0.082	K.VCGHYTQVVWR.K
R5/RRR5-23/3	1405.448	1405.579	-93.973	0.526	799.737	0.308	20	0.081	K.VCGHYTQVVWR.K
R5/RRR5-2/3	1404.894	1405.579	-1202.994	0.443	604.369	0.316	19	0.081	-.VCGHYTQVVWR.-
R5/RRR5-24/3	1405.603	1405.579	16.575	0.549	968.594	0.298	22	0.080	K.VCGHYTQVVWR.K
R5/RRR5-25/3	1405.498	1405.579	-58.036	0.462	743.438	0.283	20	0.079	K.VCGHYTQVVWR.K
R5/RRR5-22/3	1585.152	1585.607	-287.773	0.271	555.893	0.333	22	0.079	K.NYHYDTNTCDPGK.V
R5/RRR5-19/3	1405.636	1405.579	40.484	0.517	881.488	0.288	22	0.079	K.VCGHYTQVVWR.K
R5/RRR5-18/3	1406.762	1405.579	130.358	0.549	644.476	0.366	19	0.079	-.VCGHYTQVVWR.-
R5/RRR5-24/3	1586.509	1585.607	-61.949	0.318	676.604	0.328	26	0.079	K.NYHYDTNTCDPGK.V
R5/RRR5-17/3	1405.672	1405.579	66.222	0.476	583.742	0.325	19	0.078	-.VCGHYTQVVWR.-
R5/RRR5-1/3	1383.455	1384.522	-1498.821	0.393	580.328	0.411	18	0.077	-.RADGVGPVSWDPK.-
R5/RRR5-16/3	1384.726	1384.522	147.862	0.379	367.700	0.424	20	0.077	-.RADGVGPVSWDPK.-
R5/RRR5-18/3	1405.817	1405.579	169.289	0.475	892.094	0.269	21	0.077	K.VCGHYTQVVWR.K
R5/RRR5-24/3	1585.398	1585.607	-132.269	0.300	744.178	0.290	25	0.075	K.NYHYDTNTCDPGK.V
R5/RRR5-25/3	1384.579	1384.522	40.967	0.390	635.766	0.348	21	0.074	-.RADGVGPVSWDPK.-
R5/RRR5-25/3	1384.236	1384.522	-206.861	0.313	798.307	0.237	24	0.073	R.RADGVGPVSWDPK.V
R5/RRR5-3/3	1405.061	1405.579	-1083.644	0.387	517.427	0.318	17	0.073	-.VCGHYTQVVWR.-
R5/RRR5-2/3	1406.065	1405.579	346.636	0.464	550.347	0.277	18	0.072	-.VCGHYTQVVWR.-
R5/RRR5-25/3	1405.446	1405.579	-95.542	0.533	518.593	0.316	18	0.070	-.VCGHYTQVVWR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/3	1405.549	1405.579	-21.579	0.436	587.281	0.301	16	0.067	-.VCGHYTQVVWR.-
R5/RRR5-6/2	1740.500	1740.944	-256.242	0.598	2399.519	0.567	24	0.356	R.NIIHFNTLANQAVER.A
R5/RRR5-6/2	1740.600	1740.944	-198.336	0.604	2339.459	0.592	24	0.353	R.NIIHFNTLANQAVER.A
R5/RRR5-6/2	1563.252	1562.774	306.364	0.526	2293.750	0.462	22	0.302	R.TTLVANTSNM*PVAAR.E
R5/RRR5-6/2	1562.167	1562.774	-1031.851	0.469	2290.868	0.432	22	0.293	R.TTLVANTSNM*PVAAR.E
R5/RRR5-6/2	1519.370	1519.635	-174.513	0.484	2037.966	0.557	24	0.289	K.FEDPAEGEDVLVAK.F
R5/RRR5-6/2	1519.131	1519.635	-993.078	0.463	2078.324	0.530	24	0.287	K.FEDPAEGEDVLVAK.F
R5/RRR5-6/2	1562.217	1562.774	-999.842	0.483	2224.456	0.447	22	0.286	R.TTLVANTSNM*PVAAR.E
R5/RRR5-6/2	1741.326	1740.944	219.964	0.595	1934.703	0.570	24	0.276	R.NIIHFNTLANQAVER.A
R5/RRR5-6/2	1519.055	1519.635	-1043.261	0.489	1867.750	0.555	23	0.262	K.FEDPAEGEDVLVAK.F
R5/RRR5-6/2	1796.420	1797.025	-896.155	0.582	1638.950	0.631	26	0.249	R.LAEMPADSGYPAYLAAR.L
R5/RRR5-6/2	1734.507	1734.930	-244.492	0.476	1775.334	0.530	22	0.241	R.EASIYTGITIAEYFR.D
R5/RRR5-6/2	1812.359	1813.024	-921.561	0.558	1707.621	0.560	25	0.239	R.LAEM*PADSGYPAYLAAR.L
R5/RRR5-6/2	1812.381	1813.024	-909.525	0.563	1643.761	0.581	25	0.236	R.LAEM*PADSGYPAYLAAR.L
R5/RRR5-6/2	1604.781	1605.769	-1242.279	0.524	1727.345	0.519	22	0.232	K.DALAESDKITLETAK.L
R5/RRR5-6/2	1605.334	1605.769	-271.791	0.534	1672.819	0.520	22	0.225	K.DALAESDKITLETAK.L
R5/RRR5-6/2	1605.418	1605.769	-219.231	0.547	1570.296	0.525	22	0.214	K.DALAESDKITLETAK.L
R5/RRR5-6/2	1796.331	1797.025	-945.546	0.515	1451.481	0.548	25	0.206	R.LAEMPADSGYPAYLAAR.L
R5/RRR5-6/2	1796.529	1797.025	-276.737	0.510	1343.426	0.602	24	0.205	R.LAEMPADSGYPAYLAAR.L
R5/RRR5-6/2	1813.434	1813.024	226.359	0.575	1277.645	0.624	23	0.203	R.LAEM*PADSGYPAYLAAR.L
R5/RRR5-6/2	1472.889	1472.623	181.249	0.472	1571.327	0.434	20	0.195	R.EDDLNEIVQLVGK.D
R5/RRR5-6/2	1472.308	1472.623	-214.270	0.453	1540.437	0.429	20	0.190	R.EDDLNEIVQLVGK.D
R5/RRR5-6/2	1734.364	1734.930	-905.912	0.430	1268.474	0.512	18	0.177	R.EASIYTGITIAEYFR.D
R5/RRR5-6/2	1200.958	1201.310	-293.879	0.530	1227.963	0.451	17	0.169	K.LYDDLTTGFR.N
R5/RRR5-6/3	1740.045	1740.944	-1094.739	0.500	1543.315	0.459	28	0.168	R.NIIHFNTLANQAVER.A
R5/RRR5-6/2	1201.007	1201.310	-253.191	0.528	1129.083	0.450	17	0.162	K.LYDDLTTGFR.N
R5/RRR5-6/2	1471.653	1472.623	-1342.594	0.378	1278.318	0.381	18	0.157	R.EDDLNEIVQLVGK.D
R5/RRR5-6/2	917.995	918.052	-62.396	0.433	685.245	0.416	11	0.137	R.M*GDLFYR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1201.229	1201.310	-67.741	0.431	978.469	0.331	16	0.136	K.LYDDLTTGFR.N
R5/RRR5-6/2	917.893	918.052	-173.382	0.360	654.449	0.344	11	0.128	R.M*GDLFYR.L
R5/RRR5-6/2	918.040	918.052	-12.514	0.385	708.197	0.321	11	0.128	R.M*GDLFYR.L
R5/RRR5-6/3	1741.520	1740.944	-244.253	0.486	1048.268	0.456	25	0.111	R.NIIHFNTLANQAVER.A
R5/RRR5-6/3	1562.949	1562.774	112.570	0.472	1042.474	0.445	27	0.108	R.TTLVANTSNM*PVAAR.E
R5/RRR5-6/3	1578.509	1578.795	-181.557	0.424	1734.572	0.151	26	0.107	K.HFPSVNWLISYSK.Y
R5/RRR5-6/3	1741.350	1740.944	233.734	0.364	914.560	0.400	23	0.090	R.NIIHFNTLANQAVER.A
R5/RRR5-6/3	1562.749	1562.774	-16.217	0.362	775.662	0.367	25	0.080	R.TTLVANTSNM*PVAAR.E
R5/RRR5-12/1	1436.839	1435.607	161.648	0.366	830.070	0.497	18	0.529	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/1	1291.817	1292.463	-1277.899	0.305	968.637	0.123	16	0.504	R.LEKPASYDQIK.A
R5/RRR5-13/2	1500.386	1499.734	-232.783	0.554	2373.602	0.674	22	0.383	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1499.546	1499.734	-126.034	0.564	2343.003	0.624	22	0.360	R.VPTVDVSVVDLTVR.I
R5/RRR5-1/2	1499.257	1499.734	-319.359	0.525	2204.483	0.640	23	0.339	R.VPTVDVSVVDLTVR.I
R5/RRR5-3/2	1499.054	1499.734	-1124.236	0.438	2340.803	0.546	22	0.333	R.VPTVDVSVVDLTVR.I
R5/RRR5-2/2	1499.744	1499.734	6.563	0.536	2181.633	0.628	21	0.330	R.VPTVDVSVVDLTVR.I
R5/RRR5-2/2	1500.585	1499.734	-99.593	0.575	2111.976	0.638	22	0.322	R.VPTVDVSVVDLTVR.I
R5/RRR5-10/2	1500.033	1499.734	199.599	0.527	2097.415	0.600	22	0.307	R.VPTVDVSVVDLTVR.I
R5/RRR5-3/2	1500.453	1499.734	-188.382	0.544	1914.873	0.682	22	0.302	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1499.359	1499.734	-251.070	0.531	1938.957	0.649	21	0.295	R.VPTVDVSVVDLTVR.I
R5/RRR5-16/2	1500.468	1499.734	-177.935	0.540	1927.188	0.655	21	0.295	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1756.434	1757.017	-904.148	0.546	1982.624	0.568	22	0.282	K.TLLFGEKEVTVFGCR.N
R5/RRR5-5/2	1499.721	1499.734	-9.193	0.459	2005.119	0.553	21	0.278	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/1	1434.803	1435.607	-1261.483	0.115	624.798	0.282	17	0.270	R.AASFNIIPSSTGAAK.A
R5/RRR5-10/2	1499.670	1499.734	-42.830	0.467	1926.826	0.540	20	0.262	R.VPTVDVSVVDLTVR.I
R5/RRR5-14/2	1498.735	1499.734	-1338.349	0.435	1769.591	0.631	20	0.262	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1756.522	1757.017	-282.692	0.532	1713.368	0.633	21	0.259	K.TLLFGEKEVTVFGCR.N
R5/RRR5-1/2	1499.304	1499.734	-288.154	0.502	1793.757	0.598	20	0.258	R.VPTVDVSVVDLTVR.I
R5/RRR5-5/2	1499.324	1499.734	-274.758	0.486	1864.519	0.557	21	0.258	R.VPTVDVSVVDLTVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/1	1436.816	1435.607	145.971	0.367	509.460	0.499	16	0.254	R.AASFNIIPSSTGAAK.A
R5/RRR5-1/2	1498.797	1499.734	-1296.468	0.459	1834.447	0.507	21	0.241	R.VPTVDVSVVDLTVR.I
R5/RRR5-14/2	1499.752	1499.734	12.033	0.506	1598.856	0.614	20	0.236	R.VPTVDVSVVDLTVR.I
R5/RRR5-4/2	1499.080	1499.734	-1106.575	0.490	1665.460	0.561	20	0.232	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1757.535	1757.017	-275.145	0.550	1524.882	0.626	20	0.231	K.TLLFGEKEVTVFGCR.N
R5/RRR5-12/1	1436.796	1435.607	131.828	0.355	497.370	0.442	16	0.225	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1762.232	1762.859	-926.047	0.510	1680.888	0.517	20	0.225	K.LVSWYDNEWGYSSR.V
R5/RRR5-12/2	1762.245	1762.859	-918.606	0.486	1621.351	0.540	19	0.222	K.LVSWYDNEWGYSSR.V
R5/RRR5-12/1	1434.703	1435.607	-1331.037	0.134	556.320	0.280	16	0.222	R.AASFNIIPSSTGAAK.A
R5/RRR5-23/2	1499.856	1499.734	81.419	0.472	1480.810	0.617	18	0.221	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1764.361	1762.859	-282.893	0.559	1471.080	0.591	19	0.217	K.LVSWYDNEWGYSSR.V
R5/RRR5-12/2	1762.475	1762.859	-218.660	0.502	1331.071	0.567	18	0.195	K.LVSWYDNEWGYSSR.V
R5/RRR5-12/3	1499.749	1499.734	9.860	0.430	1972.589	0.339	27	0.195	R.VPTVDVSVVDLTVR.I
R5/RRR5-11/2	1162.088	1162.320	-200.141	0.449	1494.438	0.421	16	0.182	K.AGIALNDNFVK.-
R5/RRR5-17/2	1498.437	1499.734	-1537.659	0.349	1399.826	0.470	19	0.181	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1762.225	1762.859	-929.732	0.494	1198.742	0.543	17	0.178	K.LVSWYDNEWGYSSR.V
R5/RRR5-12/2	1162.029	1162.320	-251.253	0.473	1357.615	0.457	17	0.178	K.AGIALNDNFVK.-
R5/RRR5-12/2	1162.083	1162.320	-205.094	0.441	1399.178	0.428	17	0.175	K.AGIALNDNFVK.-
R5/RRR5-12/2	1763.247	1762.859	220.563	0.548	1023.002	0.592	16	0.172	K.LVSWYDNEWGYSSR.V
R5/RRR5-1/2	1161.890	1162.320	-371.835	0.411	1458.011	0.376	16	0.171	K.AGIALNDNFVK.-
R5/RRR5-5/2	1499.113	1499.734	-1084.989	0.403	1199.508	0.501	17	0.169	R.VPTVDVSVVDLTVR.I
R5/RRR5-11/2	1162.075	1162.320	-211.838	0.423	1349.027	0.409	16	0.167	K.AGIALNDNFVK.-
R5/RRR5-12/2	1162.066	1162.320	-219.321	0.474	1209.654	0.460	17	0.167	K.AGIALNDNFVK.-
R5/RRR5-1/2	1161.441	1162.320	-1622.865	0.361	1400.170	0.369	16	0.164	K.AGIALNDNFVK.-
R5/RRR5-9/2	1163.290	1162.320	-25.956	0.430	1276.348	0.417	17	0.164	K.AGIALNDNFVK.-
R5/RRR5-12/2	1162.195	1162.320	-107.731	0.453	1224.520	0.430	17	0.162	K.AGIALNDNFVK.-
R5/RRR5-11/2	1162.272	1162.320	-41.358	0.486	1169.011	0.455	16	0.162	K.AGIALNDNFVK.-
R5/RRR5-12/3	1757.972	1757.017	-25.471	0.493	1409.301	0.496	28	0.160	K.TLLFGEKEVTVFGCR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1162.142	1162.320	-154.092	0.412	1214.880	0.414	16	0.158	K.AGIALNDNFVK.-
R5/RRR5-11/2	1436.451	1435.607	-108.898	0.489	868.955	0.524	22	0.155	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1163.063	1162.320	-221.764	0.473	1120.418	0.424	17	0.155	K.AGIALNDNFVK.-
R5/RRR5-12/1	1434.797	1435.607	-1265.242	0.154	418.500	0.317	15	0.153	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1133.922	1134.226	-268.819	0.458	1022.068	0.443	14	0.153	K.YDTVHGQWK.H
R5/RRR5-12/2	1161.526	1162.320	-1549.170	0.409	1297.092	0.342	16	0.153	K.AGIALNDNFVK.-
R5/RRR5-3/2	1162.174	1162.320	-125.854	0.362	1225.937	0.373	16	0.152	K.AGIALNDNFVK.-
R5/RRR5-12/2	1435.269	1435.607	-236.519	0.477	887.881	0.503	21	0.152	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1162.217	1162.320	-89.083	0.447	1069.880	0.429	16	0.152	K.AGIALNDNFVK.-
R5/RRR5-12/2	1134.139	1134.226	-76.390	0.447	1022.880	0.429	14	0.151	K.YDTVHGQWK.H
R5/RRR5-12/2	1163.181	1162.320	-120.482	0.395	966.791	0.459	15	0.149	K.AGIALNDNFVK.-
R5/RRR5-12/2	1498.904	1499.734	-1224.820	0.349	928.276	0.482	20	0.149	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/2	1435.257	1435.607	-244.369	0.457	886.602	0.464	22	0.148	R.AASFNIIPSSTGAAK.A
R5/RRR5-14/2	1436.287	1435.607	-223.821	0.473	691.864	0.522	21	0.147	R.AASFNIIPSSTGAAK.A
R5/RRR5-11/2	833.422	833.958	-1847.900	0.397	1066.387	0.382	13	0.147	K.IGINGFGR.I
R5/RRR5-12/2	1162.263	1162.320	-49.260	0.451	1084.121	0.389	15	0.146	K.AGIALNDNFVK.-
R5/RRR5-2/2	1161.247	1162.320	-1790.885	0.299	1173.883	0.343	16	0.144	K.AGIALNDNFVK.-
R5/RRR5-12/2	1435.183	1435.607	-296.507	0.436	747.074	0.475	22	0.144	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1435.403	1435.607	-143.011	0.468	763.026	0.480	20	0.143	R.AASFNIIPSSTGAAK.A
R5/RRR5-17/2	1498.518	1499.734	-1483.160	0.356	903.221	0.457	17	0.143	-.VPTVDVSVVDLTVR.-
R5/RRR5-12/2	929.042	929.139	-104.984	0.452	791.910	0.441	14	0.142	K.KVVISAPSK.D
R5/RRR5-17/2	1499.332	1499.734	-269.204	0.402	653.074	0.515	18	0.142	R.VPTVDVSVVDLTVR.I
R5/RRR5-10/2	1162.160	1162.320	-138.708	0.374	1159.189	0.323	16	0.142	K.AGIALNDNFVK.-
R5/RRR5-12/2	928.900	929.139	-258.293	0.413	845.223	0.424	14	0.141	K.KVVISAPSK.D
R5/RRR5-2/2	833.667	833.958	-350.069	0.356	1158.433	0.310	13	0.141	K.IGINGFGR.I
R5/RRR5-12/2	1133.955	1134.226	-239.334	0.371	969.500	0.383	14	0.141	K.YDTVHGQWK.H
R5/RRR5-13/2	1134.156	1134.226	-61.600	0.424	857.736	0.419	13	0.141	K.YDTVHGQWK.H
R5/RRR5-11/2	1133.500	1134.226	-1527.093	0.416	840.071	0.424	13	0.141	K.YDTVHGQWK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1162.066	1162.320	-219.215	0.423	869.230	0.428	14	0.141	K.AGIALNDNFVK.-
R5/RRR5-12/2	1306.009	1306.513	-1155.322	0.305	1039.884	0.369	17	0.139	K.DAPMFVVGVNEK.E
R5/RRR5-12/2	929.335	929.139	211.109	0.379	858.783	0.401	14	0.138	K.KVVISAPSK.D
R5/RRR5-12/2	1436.219	1435.607	-271.315	0.500	693.599	0.460	19	0.138	R.AASFNIIPSSTGAAK.A
R5/RRR5-1/2	1162.123	1162.320	-169.898	0.413	1130.846	0.311	15	0.138	K.AGIALNDNFVK.-
R5/RRR5-11/2	1133.978	1134.226	-219.031	0.411	793.291	0.407	13	0.138	K.YDTVHGQWK.H
R5/RRR5-13/2	1293.391	1292.463	-55.530	0.501	693.441	0.402	18	0.137	R.LEKPASYDQIK.A
R5/RRR5-12/2	833.811	833.958	-176.591	0.402	760.503	0.390	12	0.136	K.IGINGFGR.I
R5/RRR5-10/2	833.897	833.958	-72.915	0.418	771.137	0.383	12	0.136	K.IGINGFGR.I
R5/RRR5-12/2	833.925	833.958	-39.584	0.456	766.305	0.380	12	0.136	K.IGINGFGR.I
R5/RRR5-11/2	833.923	833.958	-41.933	0.442	778.249	0.377	12	0.135	K.IGINGFGR.I
R5/RRR5-10/2	1435.330	1435.607	-193.346	0.356	700.910	0.437	20	0.135	R.AASFNIIPSSTGAAK.A
R5/RRR5-14/2	1435.372	1435.607	-164.168	0.370	653.587	0.451	19	0.135	R.AASFNIIPSSTGAAK.A
R5/RRR5-11/2	833.869	833.958	-106.541	0.446	823.753	0.362	12	0.135	K.IGINGFGR.I
R5/RRR5-12/2	1436.196	1435.607	-286.835	0.419	626.259	0.440	19	0.135	R.AASFNIIPSSTGAAK.A
R5/RRR5-11/2	1435.210	1435.607	-277.307	0.452	653.887	0.422	20	0.135	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1292.122	1292.463	-264.238	0.478	680.517	0.374	18	0.134	R.LEKPASYDQIK.A
R5/RRR5-12/2	1435.381	1435.607	-157.855	0.410	541.311	0.466	17	0.134	R.AASFNIIPSSTGAAK.A
R5/RRR5-14/2	1435.230	1435.607	-263.483	0.422	570.077	0.437	19	0.134	R.AASFNIIPSSTGAAK.A
R5/RRR5-8/2	1436.150	1435.607	-319.070	0.465	437.413	0.484	16	0.134	R.AASFNIIPSSTGAAK.A
R5/RRR5-28/2	833.959	833.958	1.085	0.396	674.616	0.395	11	0.133	K.IGINGFGR.I
R5/RRR5-2/2	1161.516	1162.320	-1557.722	0.364	814.455	0.383	14	0.133	K.AGIALNDNFVK.-
R5/RRR5-12/2	833.901	833.958	-68.803	0.442	764.319	0.357	12	0.133	K.IGINGFGR.I
R5/RRR5-13/2	1436.050	1435.607	309.098	0.450	522.981	0.449	17	0.132	R.AASFNIIPSSTGAAK.A
R5/RRR5-8/2	1161.823	1162.320	-429.395	0.328	1067.559	0.283	15	0.132	K.AGIALNDNFVK.-
R5/RRR5-16/2	1435.274	1435.607	-232.936	0.403	448.002	0.460	17	0.132	R.AASFNIIPSSTGAAK.A
R5/RRR5-27/2	833.865	833.958	-111.534	0.355	762.262	0.356	12	0.132	K.IGINGFGR.I
R5/RRR5-13/2	1133.955	1134.226	-239.550	0.344	718.655	0.380	13	0.132	K.YDTVHGQWK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1162.111	1162.320	-181.068	0.347	1056.732	0.278	15	0.131	K.AGIALNDNFVK.-
R5/RRR5-12/2	1306.046	1306.513	-358.354	0.239	1118.262	0.275	17	0.131	K.DAPMFVVGVNEK.E
R5/RRR5-14/2	1161.870	1162.320	-388.491	0.332	945.583	0.313	15	0.131	K.AGIALNDNFVK.-
R5/RRR5-12/2	1162.195	1162.320	-107.731	0.318	742.965	0.397	13	0.131	K.AGIALNDNFVK.-
R5/RRR5-13/2	1133.960	1134.226	-234.798	0.348	789.377	0.351	13	0.131	K.YDTVHGQWK.H
R5/RRR5-27/2	833.926	833.958	-38.703	0.387	763.721	0.331	12	0.130	K.IGINGFGR.I
R5/RRR5-3/2	1162.013	1162.320	-264.849	0.339	723.121	0.387	13	0.130	K.AGIALNDNFVK.-
R5/RRR5-12/2	1292.084	1292.463	-294.190	0.472	703.792	0.327	18	0.130	R.LEKPASYDQIK.A
R5/RRR5-12/2	1762.614	1762.859	-139.107	0.361	557.110	0.442	16	0.130	K.LVSWYDNEWGYSSR.V
R5/RRR5-2/2	833.937	833.958	-25.195	0.378	698.129	0.346	11	0.130	K.IGINGFGR.I
R5/RRR5-3/2	1435.116	1435.607	-343.102	0.458	522.907	0.414	17	0.130	R.AASFNIIPSSTGAAK.A
R5/RRR5-14/2	833.533	833.958	-510.968	0.380	752.754	0.320	12	0.129	K.IGINGFGR.I
R5/RRR5-16/2	1435.257	1435.607	-244.881	0.375	523.941	0.398	18	0.129	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1306.114	1306.513	-306.591	0.262	1079.363	0.256	18	0.129	K.DAPMFVVGVNEK.E
R5/RRR5-18/2	1436.348	1435.607	-181.276	0.358	389.919	0.480	16	0.128	-.AASFNIIPSSTGAAK.-
R5/RRR5-4/2	1435.353	1435.607	-177.307	0.395	315.581	0.413	15	0.128	R.AASFNIIPSSTGAAK.A
R5/RRR5-11/2	1133.284	1134.226	-1717.960	0.363	638.730	0.331	13	0.128	K.YDTVHGQWK.H
R5/RRR5-12/2	1434.646	1435.607	-1371.253	0.299	471.308	0.404	18	0.127	R.AASFNIIPSSTGAAK.A
R5/RRR5-14/2	833.890	833.958	-81.725	0.354	722.197	0.316	11	0.127	K.IGINGFGR.I
R5/RRR5-12/3	1756.785	1757.017	-132.294	0.471	1107.642	0.505	27	0.127	K.TLLFGEKEVTVFGCR.N
R5/RRR5-12/2	1322.276	1322.512	-179.252	0.405	678.116	0.337	17	0.127	K.DAPM*FVVGVNEK.E
R5/RRR5-1/2	1435.640	1435.607	22.804	0.373	514.227	0.363	18	0.127	R.AASFNIIPSSTGAAK.A
R5/RRR5-1/2	1292.061	1292.463	-311.820	0.451	655.200	0.303	17	0.127	R.LEKPASYDQIK.A
R5/RRR5-10/2	833.507	833.958	-542.713	0.386	704.049	0.307	11	0.127	K.IGINGFGR.I
R5/RRR5-10/2	1435.030	1435.607	-1102.043	0.315	478.991	0.408	16	0.127	R.AASFNIIPSSTGAAK.A
R5/RRR5-15/2	1162.142	1162.320	-154.092	0.304	646.437	0.349	14	0.127	K.AGIALNDNFVK.-
R5/RRR5-15/2	1435.017	1435.607	-1111.353	0.350	430.360	0.368	17	0.126	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/3	1500.078	1499.734	229.865	0.454	1577.828	0.310	25	0.126	R.VPTVDVSVVDLTVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1436.022	1435.607	290.005	0.423	353.471	0.439	15	0.126	-.AASFNIIPSSTGAAK.-
R5/RRR5-15/2	1435.389	1435.607	-152.480	0.343	393.722	0.395	15	0.126	R.AASFNIIPSSTGAAK.A
R5/RRR5-2/2	1161.182	1162.320	-1846.763	0.285	887.195	0.287	14	0.126	K.AGIALNDNFVK.-
R5/RRR5-16/2	1435.227	1435.607	-265.360	0.312	521.575	0.388	16	0.126	R.AASFNIIPSSTGAAK.A
R5/RRR5-13/2	1291.701	1292.463	-1368.214	0.443	585.711	0.282	17	0.125	R.LEKPASYDQIK.A
R5/RRR5-12/2	929.220	929.139	86.883	0.341	606.589	0.330	13	0.125	K.KVVISAPSK.D
R5/RRR5-6/2	1435.322	1435.607	-199.148	0.350	426.874	0.340	17	0.125	R.AASFNIIPSSTGAAK.A
R5/RRR5-12/2	1292.602	1292.463	108.019	0.491	498.809	0.358	15	0.125	-.LEKPASYDQIK.-
R5/RRR5-27/2	833.553	833.958	-487.455	0.329	650.949	0.312	10	0.125	K.IGINGFGR.I
R5/RRR5-3/2	833.991	833.958	39.842	0.365	579.810	0.307	10	0.125	K.IGINGFGR.I
R5/RRR5-2/2	833.982	833.958	29.272	0.373	719.371	0.282	11	0.125	K.IGINGFGR.I
R5/RRR5-19/2	1434.626	1435.607	-1385.183	0.395	335.383	0.390	16	0.125	-.AASFNIIPSSTGAAK.-
R5/RRR5-12/2	1499.198	1499.734	-1027.597	0.227	627.928	0.385	16	0.124	R.VPTVDVSVVDLTVR.I
R5/RRR5-11/2	1434.697	1435.607	-1335.361	0.298	406.893	0.330	16	0.124	R.AASFNIIPSSTGAAK.A
R5/RRR5-16/2	1162.222	1162.320	-84.974	0.334	616.332	0.287	14	0.123	K.AGIALNDNFVK.-
R5/RRR5-12/2	834.284	833.958	392.484	0.390	690.240	0.243	12	0.123	K.IGINGFGR.I
R5/RRR5-10/2	833.565	833.958	-473.200	0.351	673.205	0.280	10	0.123	K.IGINGFGR.I
R5/RRR5-12/2	1763.270	1762.859	233.822	0.379	331.948	0.378	13	0.123	K.LVSWYDNEWGYSSR.V
R5/RRR5-24/2	833.731	833.958	-272.650	0.242	757.520	0.282	11	0.123	K.IGINGFGR.I
R5/RRR5-15/2	1434.636	1435.607	-1378.261	0.298	316.758	0.387	15	0.123	-.AASFNIIPSSTGAAK.-
R5/RRR5-13/2	833.974	833.958	19.730	0.280	648.218	0.263	11	0.123	K.IGINGFGR.I
R5/RRR5-3/2	833.892	833.958	-79.375	0.347	642.009	0.268	10	0.123	K.IGINGFGR.I
R5/RRR5-11/2	1499.905	1499.734	114.395	0.237	683.753	0.362	14	0.122	-.VPTVDVSVVDLTVR.-
R5/RRR5-11/2	1292.084	1292.463	-294.379	0.456	584.578	0.259	16	0.122	R.LEKPASYDQIK.A
R5/RRR5-12/2	1134.374	1134.226	131.613	0.364	699.816	0.303	13	0.122	-.YDTVHGQWK.-
R5/RRR5-12/2	834.371	833.958	496.922	0.335	658.146	0.214	12	0.122	K.IGINGFGR.I
R5/RRR5-28/2	833.479	833.958	-576.812	0.203	496.782	0.318	11	0.122	K.IGINGFGR.I
R5/RRR5-1/2	1133.842	1134.226	-338.919	0.253	606.927	0.277	13	0.122	K.YDTVHGQWK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	833.869	833.958	-106.835	0.312	701.515	0.232	11	0.122	K.IGINGFGR.I
R5/RRR5-12/3	1756.893	1757.017	-71.029	0.448	1079.574	0.493	26	0.121	K.TLLFGEKEVTVFGCR.N
R5/RRR5-4/2	834.231	833.958	328.079	0.300	752.460	0.230	11	0.121	K.IGINGFGR.I
R5/RRR5-8/2	1435.309	1435.607	-208.107	0.327	256.557	0.431	14	0.121	-.AASFNIIPSSTGAAK.-
R5/RRR5-12/2	1292.090	1292.463	-289.450	0.410	646.180	0.219	17	0.121	R.LEKPASYDQIK.A
R5/RRR5-1/2	1161.476	1162.320	-1592.562	0.267	848.371	0.230	14	0.121	K.AGIALNDNFVK.-
R5/RRR5-13/2	1292.176	1292.463	-222.631	0.483	560.762	0.240	16	0.121	R.LEKPASYDQIK.A
R5/RRR5-3/2	833.419	833.958	-1852.610	0.254	591.277	0.200	11	0.120	K.IGINGFGR.I
R5/RRR5-16/2	1161.998	1162.320	-277.918	0.287	677.706	0.249	13	0.120	K.AGIALNDNFVK.-
R5/RRR5-15/2	1161.820	1162.320	-1295.437	0.241	824.531	0.225	14	0.120	K.AGIALNDNFVK.-
R5/RRR5-10/2	1434.615	1435.607	-1392.875	0.314	261.409	0.374	14	0.120	-.AASFNIIPSSTGAAK.-
R5/RRR5-2/2	1292.111	1292.463	-272.863	0.420	611.148	0.192	17	0.120	R.LEKPASYDQIK.A
R5/RRR5-12/2	834.597	833.958	-433.739	0.328	649.264	0.164	12	0.120	K.IGINGFGR.I
R5/RRR5-7/2	1162.273	1162.320	-40.516	0.298	779.417	0.229	13	0.120	K.AGIALNDNFVK.-
R5/RRR5-1/2	833.185	833.958	-2134.244	0.277	848.543	0.162	12	0.119	K.IGINGFGR.I
R5/RRR5-8/2	1435.043	1435.607	-1093.160	0.347	410.445	0.366	14	0.119	-.AASFNIIPSSTGAAK.-
R5/RRR5-8/2	1162.360	1162.320	33.959	0.286	851.139	0.190	13	0.118	K.AGIALNDNFVK.-
R5/RRR5-1/2	833.824	833.958	-160.876	0.308	710.117	0.151	11	0.118	K.IGINGFGR.I
R5/RRR5-7/2	1161.897	1162.320	-365.721	0.246	686.929	0.185	13	0.117	K.AGIALNDNFVK.-
R5/RRR5-20/2	1435.136	1435.607	-329.362	0.318	211.694	0.348	12	0.116	-.AASFNIIPSSTGAAK.-
R5/RRR5-12/2	1292.163	1292.463	-232.866	0.160	602.046	0.164	15	0.115	R.LEKPASYDQIK.A
R5/RRR5-3/2	1435.043	1435.607	-1092.989	0.344	376.928	0.296	16	0.115	-.AASFNIIPSSTGAAK.-
R5/RRR5-16/2	1162.296	1162.320	-21.027	0.330	506.215	0.280	12	0.115	-.AGIALNDNFVK.-
R5/RRR5-19/2	1435.010	1435.607	-1116.478	0.390	273.461	0.404	14	0.112	-.AASFNIIPSSTGAAK.-
R5/RRR5-12/3	1292.571	1292.463	84.235	0.546	1140.492	0.432	24	0.112	R.LEKPASYDQIK.A
R5/RRR5-5/2	1435.104	1435.607	-1050.712	0.278	287.532	0.348	13	0.111	-.AASFNIIPSSTGAAK.-
R5/RRR5-12/3	1292.772	1292.463	239.781	0.499	1028.326	0.429	25	0.104	R.LEKPASYDQIK.A
R5/RRR5-10/3	1291.344	1292.463	-1645.837	0.502	757.474	0.458	21	0.100	R.LEKPASYDQIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/3	1292.491	1292.463	22.288	0.490	504.625	0.465	19	0.100	R.LEKPASYDQIK.A
R5/RRR5-11/3	1292.490	1292.463	21.009	0.505	876.277	0.431	23	0.099	R.LEKPASYDQIK.A
R5/RRR5-2/3	1292.284	1292.463	-138.869	0.489	624.605	0.449	21	0.098	R.LEKPASYDQIK.A
R5/RRR5-14/3	1292.611	1292.463	114.638	0.478	631.393	0.436	21	0.096	R.LEKPASYDQIK.A
R5/RRR5-25/3	1292.847	1292.463	298.294	0.435	646.195	0.442	20	0.096	R.LEKPASYDQIK.A
R5/RRR5-10/3	1292.061	1292.463	-312.020	0.425	468.972	0.428	17	0.096	R.LEKPASYDQIK.A
R5/RRR5-13/3	1292.488	1292.463	19.588	0.477	859.135	0.413	22	0.095	R.LEKPASYDQIK.A
R5/RRR5-6/3	1292.803	1292.463	264.067	0.455	532.940	0.474	19	0.095	-.LEKPASYDQIK.-
R5/RRR5-3/3	1292.479	1292.463	12.626	0.455	971.922	0.394	24	0.095	R.LEKPASYDQIK.A
R5/RRR5-27/3	1293.480	1292.463	13.136	0.438	430.717	0.468	17	0.095	-.LEKPASYDQIK.-
R5/RRR5-12/3	1499.411	1499.734	-216.612	0.418	1333.657	0.274	25	0.094	R.VPTVDVSVVDLTVR.I
R5/RRR5-11/3	1292.525	1292.463	48.432	0.481	710.765	0.417	21	0.094	R.LEKPASYDQIK.A
R5/RRR5-13/3	1293.324	1292.463	-107.564	0.448	667.802	0.415	21	0.093	R.LEKPASYDQIK.A
R5/RRR5-10/3	1291.921	1292.463	-1196.740	0.487	481.819	0.495	18	0.093	-.LEKPASYDQIK.-
R5/RRR5-14/3	1292.494	1292.463	24.135	0.459	694.262	0.409	22	0.093	R.LEKPASYDQIK.A
R5/RRR5-16/3	1292.262	1292.463	-155.783	0.423	963.550	0.382	23	0.093	R.LEKPASYDQIK.A
R5/RRR5-2/3	1293.651	1292.463	145.873	0.484	641.757	0.400	21	0.093	R.LEKPASYDQIK.A
R5/RRR5-6/3	1292.852	1292.463	302.270	0.491	453.831	0.438	17	0.092	-.LEKPASYDQIK.-
R5/RRR5-12/3	1292.933	1292.463	364.467	0.510	994.488	0.365	24	0.092	R.LEKPASYDQIK.A
R5/RRR5-16/3	1292.501	1292.463	29.534	0.461	670.254	0.399	20	0.092	R.LEKPASYDQIK.A
R5/RRR5-3/3	1292.124	1292.463	-262.684	0.471	672.729	0.395	21	0.092	R.LEKPASYDQIK.A
R5/RRR5-13/3	1292.756	1292.463	227.424	0.481	701.163	0.389	22	0.091	R.LEKPASYDQIK.A
R5/RRR5-11/3	1291.991	1292.463	-366.480	0.487	564.551	0.432	20	0.091	-.LEKPASYDQIK.-
R5/RRR5-11/3	1499.252	1499.734	-322.472	0.432	1254.590	0.283	22	0.089	R.VPTVDVSVVDLTVR.I
R5/RRR5-12/3	1292.644	1292.463	140.635	0.515	989.042	0.351	23	0.089	R.LEKPASYDQIK.A
R5/RRR5-9/2	1434.972	1435.607	-1143.043	0.340	273.227	0.362	12	0.088	-.AASFNIIPSSTGAAK.-
R5/RRR5-11/3	1500.017	1499.734	189.103	0.390	1258.277	0.264	24	0.087	R.VPTVDVSVVDLTVR.I
R5/RRR5-8/3	1292.685	1292.463	172.171	0.349	557.234	0.344	19	0.087	R.LEKPASYDQIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/3	1291.956	1292.463	-1169.841	0.409	461.638	0.335	18	0.086	-.LEKPASYDQIK.-
R5/RRR5-16/3	1292.846	1292.463	297.300	0.320	464.126	0.336	16	0.084	-.LEKPASYDQIK.-
R5/RRR5-14/3	1291.406	1292.463	-1597.405	0.424	613.995	0.360	19	0.084	-.LEKPASYDQIK.-
R5/RRR5-17/2	1436.111	1435.607	-346.360	0.244	172.652	0.430	11	0.082	-.AASFNIIPSSTGAAK.-
R5/RRR5-12/3	1292.451	1292.463	-8.973	0.509	953.305	0.354	21	0.081	-.LEKPASYDQIK.-
R5/RRR5-12/3	1293.369	1292.463	-72.771	0.476	706.710	0.317	21	0.079	-.LEKPASYDQIK.-
R5/RRR5-11/3	1498.996	1499.734	-1163.045	0.368	1190.991	0.229	22	0.076	-.VPTVDVSVVDLTVR.-
R5/RRR5-7/2	1407.202	1407.722	-1083.639	0.524	2252.457	0.471	20	0.300	K.MLIAMVETELEK.R
R5/RRR5-7/2	1415.244	1414.577	-235.540	0.526	1917.007	0.528	18	0.261	K.SVTDYITDIVCK.R
R5/RRR5-7/2	1653.507	1652.828	-194.343	0.528	1583.897	0.570	21	0.228	K.YVELTADYVYPYR.N
R5/RRR5-7/2	1414.253	1414.577	-229.212	0.471	1688.149	0.507	18	0.224	K.SVTDYITDIVCK.R
R5/RRR5-7/2	1653.031	1652.828	123.278	0.492	1595.207	0.531	21	0.219	K.YVELTADYVYPYR.N
R5/RRR5-7/2	1413.701	1414.577	-1330.858	0.372	1695.021	0.401	18	0.200	K.SVTDYITDIVCK.R
R5/RRR5-7/2	1285.099	1285.349	-195.275	0.432	1226.996	0.528	16	0.179	R.GQSHFFGYEGR.C
R5/RRR5-7/2	1285.292	1285.349	-44.163	0.483	1145.716	0.486	16	0.166	R.GQSHFFGYEGR.C
R5/RRR5-7/2	1285.198	1285.349	-117.903	0.403	1021.658	0.521	15	0.160	R.GQSHFFGYEGR.C
R5/RRR5-7/2	1571.352	1570.763	-262.008	0.486	1147.810	0.450	17	0.158	K.SVTDYITDIVCKR.A
R5/RRR5-7/2	1414.286	1414.577	-206.266	0.298	1105.074	0.487	17	0.157	K.SVTDYITDIVCK.R
R5/RRR5-7/2	1570.343	1570.763	-267.946	0.391	1275.763	0.371	16	0.154	K.SVTDYITDIVCKR.A
R5/RRR5-7/2	1351.717	1352.520	-1337.991	0.420	1350.028	0.294	16	0.149	K.FASLRDEWSLK.N
R5/RRR5-7/2	1570.336	1570.763	-272.391	0.451	897.885	0.444	16	0.142	K.SVTDYITDIVCKR.A
R5/RRR5-7/2	1351.884	1352.520	-1213.385	0.462	1092.282	0.314	15	0.136	K.FASLRDEWSLK.N
R5/RRR5-7/2	1352.004	1352.520	-1124.530	0.446	1090.141	0.274	15	0.130	K.FASLRDEWSLK.N
R5/RRR5-7/2	1243.050	1243.435	-310.916	0.391	1169.600	0.211	16	0.128	K.TIQEQLLLER.D
R5/RRR5-7/2	1234.938	1235.368	-349.047	0.413	989.291	0.246	15	0.124	R.DKIETPEQFK.Q
R5/RRR5-7/2	1458.941	1459.576	-1123.844	0.242	313.835	0.563	16	0.122	K.EVPTSFGFDTACK.I
R5/RRR5-7/2	1651.294	1652.828	-2146.493	0.189	597.215	0.291	15	0.115	K.YVELTADYVYPYR.N
R5/RRR5-7/3	1176.380	1176.309	61.071	0.436	997.360	0.431	21	0.100	K.AEGKYPAHFR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/3	1176.732	1176.309	361.023	0.431	492.512	0.432	18	0.087	K.AEGKYPAHFR.G
R5/RRR5-9/2	1522.334	1522.682	-229.266	0.561	3102.885	0.567	24	0.517	R.IEEELGAAAVYAGTK.F
R5/RRR5-9/2	1523.163	1522.682	317.062	0.612	2871.812	0.580	25	0.464	R.IEEELGAAAVYAGTK.F
R5/RRR5-9/2	1522.218	1522.682	-305.453	0.479	2362.579	0.551	24	0.344	R.IEEELGAAAVYAGTK.F
R5/RRR5-9/2	1515.629	1514.829	-132.452	0.514	2165.423	0.535	22	0.303	K.LGANAILAVSLALCK.A
R5/RRR5-9/2	1514.108	1514.829	-1139.986	0.367	2311.968	0.407	22	0.290	K.LGANAILAVSLALCK.A
R5/RRR5-8/2	1998.327	1999.112	-896.104	0.511	1952.843	0.611	25	0.289	R.GNPTVEVDICCSDGTFAR.A
R5/RRR5-8/2	1998.551	1999.112	-783.403	0.581	1897.125	0.641	24	0.288	R.GNPTVEVDICCSDGTFAR.A
R5/RRR5-8/2	1998.373	1999.112	-873.047	0.541	1733.839	0.622	24	0.258	R.GNPTVEVDICCSDGTFAR.A
R5/RRR5-8/2	1871.298	1872.241	-1041.795	0.420	1124.000	0.465	21	0.157	K.LAMQEFMILPTGASSFK.E
R5/RRR5-8/2	1871.556	1872.241	-903.420	0.386	913.508	0.420	18	0.136	K.LAMQEFMILPTGASSFK.E
R5/RRR5-11/2	1560.495	1559.788	-188.430	0.546	2235.936	0.501	23	0.303	K.ATAELLFGADNPVLK.Q
R5/RRR5-11/3	1697.329	1696.958	219.116	0.503	2403.272	0.339	35	0.293	R.LARPM*YSNPPIHGAR.I
R5/RRR5-11/2	1560.243	1559.788	292.577	0.525	1958.771	0.489	22	0.255	K.ATAELLFGADNPVLK.Q
R5/RRR5-11/2	1560.608	1559.788	-115.768	0.523	1742.319	0.477	21	0.222	K.ATAELLFGADNPVLK.Q
R5/RRR5-11/2	1700.411	1700.912	-885.478	0.506	1566.625	0.533	21	0.214	R.IGAINVVCSTPEVANR.V
R5/RRR5-11/2	1700.390	1700.912	-897.802	0.540	1472.257	0.566	21	0.210	R.IGAINVVCSTPEVANR.V
R5/RRR5-11/2	1700.479	1700.912	-255.072	0.498	1451.205	0.572	21	0.209	R.IGAINVVCSTPEVANR.V
R5/RRR5-11/2	1391.140	1390.568	-308.623	0.524	1352.430	0.599	22	0.208	R.VATLQSLSGTGSLR.L
R5/RRR5-11/2	1391.166	1390.568	-290.047	0.567	1354.678	0.586	22	0.206	R.VATLQSLSGTGSLR.L
R5/RRR5-11/2	1390.289	1390.568	-201.548	0.510	1497.348	0.519	22	0.205	R.VATLQSLSGTGSLR.L
R5/RRR5-10/2	1561.008	1559.788	141.369	0.393	1465.548	0.456	18	0.185	K.ATAELLFGADNPVLK.Q
R5/RRR5-11/2	1327.470	1328.495	-1529.925	0.362	1526.592	0.410	17	0.183	R.GLEVFVAQSYSK.N
R5/RRR5-11/2	1532.613	1532.763	-97.751	0.542	1194.957	0.482	20	0.170	R.TEELQPYVLNVVK.K
R5/RRR5-11/2	972.367	973.192	-1882.205	0.390	1397.682	0.365	17	0.166	R.ISLAGLSLAK.C
R5/RRR5-11/2	973.047	973.192	-148.994	0.481	1359.246	0.378	17	0.166	R.ISLAGLSLAK.C
R5/RRR5-11/2	973.184	973.192	-7.814	0.481	1290.291	0.407	17	0.166	R.ISLAGLSLAK.C
R5/RRR5-11/2	889.847	890.065	-245.412	0.455	901.228	0.404	13	0.142	R.LAAAFIQR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	889.571	890.065	-556.269	0.442	935.638	0.390	13	0.142	R.LAAAFIQR.Y
R5/RRR5-11/2	889.526	890.065	-1734.378	0.428	850.122	0.400	13	0.140	R.LAAAFIQR.Y
R5/RRR5-10/2	1560.813	1559.788	16.190	0.392	891.405	0.417	15	0.136	K.ATAELLFGADNPVLK.Q
R5/RRR5-11/2	1532.099	1532.763	-1089.200	0.402	1077.568	0.304	20	0.135	R.TEELQPYVLNVVK.K
R5/RRR5-11/2	1854.318	1854.988	-903.565	0.473	1098.297	0.597	21	0.133	K.CEYLADAIIDSFHNVS.-
R5/RRR5-1/2	1560.646	1559.788	-91.523	0.220	595.745	0.216	15	0.114	K.ATAELLFGADNPVLK.Q
R5/RRR5-11/3	1439.647	1439.554	64.319	0.432	1114.257	0.330	23	0.091	K.DDSGKDWSFILR.Q
R5/RRR5-11/3	1439.491	1439.554	-43.865	0.362	845.522	0.319	22	0.076	-.DDSGKDWSFILR.-
R5/RRR5-11/3	1439.990	1439.554	303.056	0.396	992.505	0.263	22	0.075	K.DDSGKDWSFILR.Q
R5/RRR5-8/2	1156.995	1157.302	-266.632	0.491	2004.025	0.549	20	0.281	R.DPAAATSGVVIR.R
R5/RRR5-8/3	1454.867	1453.581	197.034	0.457	2299.487	0.213	25	0.214	R.RFDSVDDPLFNK.L
R5/RRR5-8/2	1242.113	1242.447	-269.849	0.404	1532.999	0.552	18	0.214	R.NLVVVSSPDLAK.E
R5/RRR5-8/2	1164.978	1164.290	-268.589	0.459	1242.357	0.543	18	0.185	K.LAGYDIPAESK.I
R5/RRR5-8/2	1163.916	1164.290	-322.272	0.468	1342.835	0.423	18	0.172	K.LAGYDIPAESK.I
R5/RRR5-8/2	1164.070	1164.290	-189.072	0.469	1157.108	0.483	17	0.167	K.LAGYDIPAESK.I
R5/RRR5-8/2	1242.338	1242.447	-88.265	0.439	999.508	0.494	17	0.156	R.NLVVVSSPDLAK.E
R5/RRR5-9/2	1157.371	1157.302	59.600	0.440	1071.972	0.425	18	0.152	R.DPAAATSGVVIR.R
R5/RRR5-8/2	1479.569	1478.786	-146.674	0.406	962.841	0.456	15	0.146	R.LQLM*MYNDMFR.I
R5/RRR5-8/2	1102.622	1103.342	-1564.972	0.485	1098.173	0.339	16	0.144	R.RFGDILLLR.M
R5/RRR5-8/2	1241.624	1242.447	-1472.702	0.383	889.830	0.464	15	0.143	R.NLVVVSSPDLAK.E
R5/RRR5-8/2	1102.312	1103.342	-1847.203	0.461	1242.900	0.275	16	0.142	R.RFGDILLLR.M
R5/RRR5-8/2	1103.228	1103.342	-103.834	0.492	1075.204	0.300	16	0.137	R.RFGDILLLR.M
R5/RRR5-8/2	1459.169	1459.589	-288.444	0.323	582.403	0.483	19	0.131	K.EVLHTQGVEFGSR.T
R5/RRR5-8/2	1156.717	1157.302	-1374.293	0.365	770.076	0.293	18	0.125	R.DPAAATSGVVIR.R
R5/RRR5-8/3	1891.653	1892.018	-193.444	0.491	1224.901	0.385	33	0.110	R.FLEEEKAVEAHGNDFR.F
R5/RRR5-8/3	1468.899	1469.675	-1212.340	0.446	986.293	0.358	26	0.089	R.RDPAAATSGVVIRR.R
R5/RRR5-8/2	1211.160	1211.386	-187.483	0.427	651.431	0.557	16	0.086	K.HATVVCKPIDA.-
R5/RRR5-8/3	1468.750	1469.675	-1314.497	0.442	924.510	0.355	27	0.086	R.RDPAAATSGVVIRR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/3	1452.766	1453.581	-1252.814	0.354	1131.404	0.090	23	0.057	R.RFDSVDDPLFNK.L
R5/RRR5-9/3	1824.103	1824.025	42.708	0.491	2118.514	0.406	34	0.256	R.EILHIQGGQCGNQIGAK.F
R5/RRR5-9/2	1343.146	1343.427	-209.624	0.568	1780.404	0.546	20	0.247	R.INVYYNEASGGR.Y
R5/RRR5-9/3	1823.883	1824.025	-78.019	0.443	2016.750	0.428	31	0.244	R.EILHIQGGQCGNQIGAK.F
R5/RRR5-9/2	1343.153	1343.427	-204.154	0.571	1806.963	0.524	20	0.244	R.INVYYNEASGGR.Y
R5/RRR5-9/2	1343.038	1343.427	-290.321	0.499	1677.599	0.535	20	0.230	R.INVYYNEASGGR.Y
R5/RRR5-9/2	1972.535	1974.161	-1843.598	0.477	1666.819	0.534	24	0.226	K.GHYTEGAELIDSVLDVVR.K
R5/RRR5-9/2	1385.230	1385.720	-354.928	0.567	1511.875	0.597	17	0.224	R.MMLTFSVFPSPK.V
R5/RRR5-9/2	1385.188	1385.720	-1109.258	0.510	1496.589	0.571	17	0.216	R.MMLTFSVFPSPK.V
R5/RRR5-9/2	1232.098	1232.391	-238.787	0.526	1584.780	0.427	17	0.196	R.VSEQFTAM*FR.R
R5/RRR5-9/2	1231.855	1232.391	-1250.445	0.530	1468.594	0.448	16	0.188	R.VSEQFTAM*FR.R
R5/RRR5-9/2	1385.401	1385.720	-230.716	0.488	1232.797	0.526	17	0.180	R.MMLTFSVFPSPK.V
R5/RRR5-9/2	1216.135	1216.391	-211.382	0.454	1505.502	0.381	16	0.178	R.VSEQFTAMFR.R
R5/RRR5-1/2	1141.124	1140.403	-244.912	0.500	1184.964	0.499	17	0.174	K.LAVNLIPFPR.L
R5/RRR5-9/2	1697.413	1697.871	-271.185	0.496	1136.497	0.479	21	0.165	K.NSSYFVEWIPNNVK.S
R5/RRR5-8/2	1140.183	1140.403	-192.926	0.536	1050.711	0.497	17	0.165	K.LAVNLIPFPR.L
R5/RRR5-9/2	1139.706	1140.403	-1493.317	0.525	963.535	0.527	17	0.164	K.LAVNLIPFPR.L
R5/RRR5-9/2	1140.236	1140.403	-146.207	0.558	1048.845	0.493	17	0.164	K.LAVNLIPFPR.L
R5/RRR5-10/2	1140.226	1140.403	-155.228	0.550	1020.160	0.479	17	0.160	K.LAVNLIPFPR.L
R5/RRR5-8/2	1140.173	1140.403	-202.163	0.585	1092.906	0.448	17	0.159	K.LAVNLIPFPR.L
R5/RRR5-1/2	1140.323	1140.403	-70.178	0.459	994.447	0.469	17	0.156	K.LAVNLIPFPR.L
R5/RRR5-9/2	1140.220	1140.403	-160.276	0.574	1053.774	0.440	17	0.155	K.LAVNLIPFPR.L
R5/RRR5-2/2	1141.415	1140.403	10.769	0.535	966.362	0.461	17	0.155	K.LAVNLIPFPR.L
R5/RRR5-13/2	1141.365	1140.403	-33.105	0.526	962.499	0.450	17	0.153	K.LAVNLIPFPR.L
R5/RRR5-9/2	1698.482	1697.871	-229.782	0.476	932.281	0.482	19	0.151	K.NSSYFVEWIPNNVK.S
R5/RRR5-8/2	1140.256	1140.403	-128.702	0.483	855.222	0.476	16	0.150	K.LAVNLIPFPR.L
R5/RRR5-8/2	1697.517	1697.871	-209.572	0.491	918.326	0.466	19	0.148	K.NSSYFVEWIPNNVK.S
R5/RRR5-3/2	1140.192	1140.403	-185.408	0.445	854.592	0.462	15	0.147	K.LAVNLIPFPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1140.177	1140.403	-198.189	0.420	943.284	0.423	17	0.147	K.LAVNLIPFPR.L
R5/RRR5-9/2	1972.627	1974.161	-1796.838	0.457	813.477	0.510	21	0.146	K.GHYTEGAELIDSVLDVVR.K
R5/RRR5-9/2	1731.289	1731.994	-987.717	0.415	774.988	0.495	21	0.144	R.ALTVPELTQQMWDAK.N
R5/RRR5-9/2	1748.216	1747.994	127.384	0.496	644.955	0.520	19	0.143	R.ALTVPELTQQM*WDAK.N
R5/RRR5-8/2	1344.207	1343.427	-163.643	0.427	948.341	0.406	17	0.142	R.INVYYNEASGGR.Y
R5/RRR5-9/2	1731.383	1731.994	-933.566	0.396	734.605	0.478	20	0.140	R.ALTVPELTQQMWDAK.N
R5/RRR5-8/2	1697.159	1697.871	-1011.980	0.401	884.875	0.415	18	0.139	K.NSSYFVEWIPNNVK.S
R5/RRR5-9/2	1417.795	1417.719	54.241	0.382	1238.390	0.261	17	0.138	R.M*M*LTFSVFPSPK.V
R5/RRR5-9/2	1696.863	1697.871	-1186.915	0.381	840.473	0.418	18	0.137	K.NSSYFVEWIPNNVK.S
R5/RRR5-3/2	1140.024	1140.403	-333.107	0.436	717.214	0.437	14	0.136	-.LAVNLIPFPR.-
R5/RRR5-1/2	1139.802	1140.403	-1408.115	0.494	710.179	0.410	14	0.136	K.LAVNLIPFPR.L
R5/RRR5-9/2	1731.368	1731.994	-942.343	0.382	692.877	0.445	19	0.134	R.ALTVPELTQQMWDAK.N
R5/RRR5-9/2	1402.150	1401.719	308.258	0.405	828.103	0.381	15	0.133	R.MM*LTFSVFPSPK.V
R5/RRR5-7/2	1140.227	1140.403	-154.369	0.442	690.781	0.374	14	0.132	K.LAVNLIPFPR.L
R5/RRR5-10/2	1697.186	1697.871	-995.949	0.384	725.912	0.396	16	0.130	K.NSSYFVEWIPNNVK.S
R5/RRR5-9/2	1147.455	1147.266	165.324	0.374	832.083	0.318	16	0.129	R.FPGQLNSDLR.K
R5/RRR5-10/2	1232.148	1232.391	-197.639	0.334	853.633	0.328	14	0.129	R.VSEQFTAM*FR.R
R5/RRR5-8/2	1343.184	1343.427	-180.996	0.364	718.180	0.348	17	0.129	R.INVYYNEASGGR.Y
R5/RRR5-11/2	1140.195	1140.403	-182.830	0.335	613.167	0.374	13	0.129	K.LAVNLIPFPR.L
R5/RRR5-9/3	1640.391	1639.945	272.846	0.449	1525.025	0.331	31	0.128	R.LHFFM*VGFAPLTSR.G
R5/RRR5-11/2	1140.096	1140.403	-269.725	0.278	662.832	0.355	14	0.127	K.LAVNLIPFPR.L
R5/RRR5-21/2	1344.767	1343.427	253.965	0.322	373.005	0.403	13	0.125	R.INVYYNEASGGR.Y
R5/RRR5-9/2	1973.233	1974.161	-979.600	0.361	293.051	0.455	16	0.124	K.GHYTEGAELIDSVLDVVR.K
R5/RRR5-9/2	1147.071	1147.266	-170.313	0.355	799.595	0.264	16	0.124	R.FPGQLNSDLR.K
R5/RRR5-9/2	1401.053	1401.719	-1193.105	0.304	485.225	0.408	12	0.123	R.MM*LTFSVFPSPK.V
R5/RRR5-1/2	1343.923	1343.427	370.190	0.263	246.111	0.345	12	0.123	R.INVYYNEASGGR.Y
R5/RRR5-13/2	1140.415	1140.403	10.993	0.341	628.599	0.256	13	0.122	K.LAVNLIPFPR.L
R5/RRR5-8/2	1343.013	1343.427	-309.016	0.326	735.920	0.265	16	0.122	R.INVYYNEASGGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1147.290	1147.266	20.958	0.338	833.729	0.224	16	0.121	R.FPGQLNSDLR.K
R5/RRR5-2/2	1140.181	1140.403	-194.859	0.256	554.456	0.301	12	0.118	-.LAVNLIPFPR.-
R5/RRR5-7/2	1972.862	1974.161	-1168.324	0.326	314.582	0.335	14	0.117	K.GHYTEGAELIDSVLDVVR.K
R5/RRR5-6/2	1141.126	1140.403	-242.873	0.320	486.556	0.299	11	0.115	-.LAVNLIPFPR.-
R5/RRR5-8/2	1231.638	1232.391	-1427.814	0.234	697.649	0.157	12	0.114	R.VSEQFTAM*FR.R
R5/RRR5-8/3	1973.218	1974.161	-987.154	0.387	1346.105	0.346	28	0.112	K.GHYTEGAELIDSVLDVVR.K
R5/RRR5-9/3	1974.224	1974.161	32.391	0.404	944.904	0.339	24	0.080	K.GHYTEGAELIDSVLDVVR.K
R5/RRR5-7/2	1726.256	1726.956	-987.476	0.543	2701.095	0.438	24	0.370	R.LDQLQLLLNGASANGAK.K
R5/RRR5-7/2	1726.427	1726.956	-888.091	0.546	2631.087	0.406	25	0.345	R.LDQLQLLLNGASANGAK.K
R5/RRR5-7/2	1133.879	1134.219	-300.791	0.568	2400.577	0.506	21	0.336	K.GIDACIASGGGR.M
R5/RRR5-7/2	1133.999	1134.219	-194.734	0.538	2256.103	0.501	20	0.308	K.GIDACIASGGGR.M
R5/RRR5-7/2	1133.444	1134.219	-1570.269	0.468	2046.478	0.461	19	0.262	K.GIDACIASGGGR.M
R5/RRR5-7/2	1548.514	1548.635	-77.929	0.467	1799.321	0.521	18	0.242	K.ALEYEDFDKFDR.V
R5/RRR5-7/2	1726.452	1726.956	-873.611	0.549	1924.922	0.407	23	0.227	R.LDQLQLLLNGASANGAK.K
R5/RRR5-7/2	1548.221	1548.635	-268.057	0.428	1640.150	0.507	18	0.217	K.ALEYEDFDKFDR.V
R5/RRR5-6/2	1549.750	1548.635	74.532	0.422	1204.129	0.436	16	0.161	K.ALEYEDFDKFDR.V
R5/RRR5-7/2	974.628	975.121	-507.597	0.473	828.726	0.566	16	0.160	K.LVDTALASGK.I
R5/RRR5-7/2	1548.134	1548.635	-972.021	0.432	1150.902	0.451	16	0.159	K.ALEYEDFDKFDR.V
R5/RRR5-6/2	1133.694	1134.219	-1349.175	0.375	1283.869	0.376	19	0.158	K.GIDACIASGGGR.M
R5/RRR5-7/2	974.920	975.121	-207.043	0.445	930.299	0.494	17	0.156	K.LVDTALASGK.I
R5/RRR5-7/2	975.034	975.121	-90.111	0.455	834.360	0.504	17	0.153	K.LVDTALASGK.I
R5/RRR5-7/2	1777.422	1778.001	-891.199	0.376	1108.904	0.439	20	0.150	K.AVGPIVDGDAVVTFNFR.A
R5/RRR5-6/2	974.951	975.121	-175.389	0.409	689.225	0.505	15	0.144	K.LVDTALASGK.I
R5/RRR5-7/2	1727.289	1726.956	193.327	0.414	848.082	0.422	19	0.135	R.LDQLQLLLNGASANGAK.K
R5/RRR5-6/2	974.341	975.121	-1832.463	0.341	708.879	0.439	15	0.135	K.LVDTALASGK.I
R5/RRR5-12/2	1918.543	1919.128	-828.964	0.592	3706.789	0.561	29	0.685	K.VQQVDTTGAGDAFVGALLR.R
R5/RRR5-13/2	1919.585	1919.128	238.700	0.614	3584.828	0.597	30	0.664	K.VQQVDTTGAGDAFVGALLR.R
R5/RRR5-12/2	1918.507	1919.128	-847.806	0.601	3420.729	0.588	30	0.611	K.VQQVDTTGAGDAFVGALLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1918.532	1919.128	-834.585	0.561	3414.687	0.581	29	0.607	K.VQQVDTTGAGDAFVGALLR.R
R5/RRR5-12/2	1919.652	1919.128	-248.592	0.618	3318.033	0.614	29	0.593	K.VQQVDTTGAGDAFVGALLR.R
R5/RRR5-13/2	1919.700	1919.128	-223.520	0.637	3190.390	0.614	28	0.556	K.VQQVDTTGAGDAFVGALLR.R
R5/RRR5-13/2	1578.175	1578.622	-284.382	0.567	2445.899	0.618	27	0.383	R.DNGVDDAGVVFDAGAR.T
R5/RRR5-12/2	1579.047	1578.622	269.863	0.579	2485.208	0.593	27	0.382	R.DNGVDDAGVVFDAGAR.T
R5/RRR5-13/2	1578.160	1578.622	-294.005	0.545	1943.189	0.583	25	0.280	R.DNGVDDAGVVFDAGAR.T
R5/RRR5-12/2	1577.668	1578.622	-1242.442	0.412	1741.479	0.505	24	0.229	R.DNGVDDAGVVFDAGAR.T
R5/RRR5-12/2	991.932	992.197	-267.738	0.544	1747.587	0.487	15	0.228	R.TALAFVTLR.A
R5/RRR5-13/2	992.089	992.197	-108.987	0.555	1737.132	0.477	15	0.224	R.TALAFVTLR.A
R5/RRR5-12/2	991.489	992.197	-1727.604	0.475	1713.986	0.462	15	0.218	R.TALAFVTLR.A
R5/RRR5-13/2	992.105	992.197	-93.189	0.508	1692.672	0.469	15	0.217	R.TALAFVTLR.A
R5/RRR5-13/2	991.946	992.197	-253.170	0.485	1644.571	0.453	15	0.208	R.TALAFVTLR.A
R5/RRR5-13/3	1918.716	1919.128	-215.538	0.461	1749.240	0.454	32	0.200	K.VQQVDTTGAGDAFVGALLR.R
R5/RRR5-12/2	991.972	992.197	-226.873	0.460	1583.574	0.429	15	0.196	R.TALAFVTLR.A
R5/RRR5-12/2	1401.382	1401.632	-179.246	0.534	1432.720	0.482	20	0.192	K.ILSIWDQADIVK.V
R5/RRR5-13/2	1358.137	1358.480	-253.107	0.505	1437.320	0.457	20	0.187	R.IVQDPSSLQDQK.K
R5/RRR5-12/2	1225.081	1225.370	-236.523	0.522	1452.283	0.432	18	0.182	K.FANACGAITATK.K
R5/RRR5-12/2	1224.925	1225.370	-364.294	0.514	1518.091	0.394	19	0.181	K.FANACGAITATK.K
R5/RRR5-13/2	1224.870	1225.370	-408.992	0.459	1426.847	0.410	19	0.176	K.FANACGAITATK.K
R5/RRR5-13/2	1401.319	1401.632	-224.600	0.432	1271.194	0.477	19	0.175	K.ILSIWDQADIVK.V
R5/RRR5-12/2	1358.124	1358.480	-262.846	0.502	1250.165	0.479	19	0.174	R.IVQDPSSLQDQK.K
R5/RRR5-12/2	1358.211	1358.480	-198.104	0.494	1305.116	0.444	19	0.172	R.IVQDPSSLQDQK.K
R5/RRR5-13/2	1316.306	1317.550	-1710.328	0.361	1320.377	0.403	18	0.164	K.LLLVTLGDQGCK.Y
R5/RRR5-13/2	1358.182	1358.480	-219.924	0.486	1185.641	0.449	18	0.163	R.IVQDPSSLQDQK.K
R5/RRR5-12/2	1577.229	1578.622	-1521.703	0.369	1280.165	0.413	21	0.161	R.DNGVDDAGVVFDAGAR.T
R5/RRR5-12/2	1400.726	1401.632	-1365.213	0.417	1026.604	0.488	18	0.158	K.ILSIWDQADIVK.V
R5/RRR5-13/2	1400.903	1401.632	-1238.050	0.415	1164.623	0.413	18	0.156	K.ILSIWDQADIVK.V
R5/RRR5-12/3	1919.159	1919.128	16.095	0.449	1431.406	0.464	30	0.154	K.VQQVDTTGAGDAFVGALLR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1358.019	1358.480	-340.312	0.454	1113.694	0.403	18	0.151	R.IVQDPSSLQDQK.K
R5/RRR5-12/2	1400.576	1401.632	-1472.621	0.361	928.639	0.493	17	0.150	K.ILSIWDQADIVK.V
R5/RRR5-13/2	1358.057	1358.480	-311.903	0.477	1097.830	0.399	18	0.150	R.IVQDPSSLQDQK.K
R5/RRR5-13/2	1401.015	1401.632	-1157.551	0.389	1028.824	0.371	17	0.141	K.ILSIWDQADIVK.V
R5/RRR5-12/2	1419.127	1419.565	-309.352	0.426	838.174	0.429	17	0.139	K.EAGALLSYDPNLR.E
R5/RRR5-13/2	1317.472	1317.550	-59.534	0.377	638.504	0.488	14	0.135	K.LLLVTLGDQGCK.Y
R5/RRR5-12/2	1419.254	1419.565	-219.433	0.397	778.834	0.417	16	0.135	K.EAGALLSYDPNLR.E
R5/RRR5-13/2	1419.061	1419.565	-1062.849	0.385	823.610	0.347	16	0.129	K.EAGALLSYDPNLR.E
R5/RRR5-12/2	1317.485	1317.550	-49.961	0.436	409.346	0.400	13	0.125	K.LLLVTLGDQGCK.Y
R5/RRR5-13/2	1419.195	1419.565	-261.025	0.370	833.675	0.280	16	0.123	K.EAGALLSYDPNLR.E
R5/RRR5-13/2	1418.648	1419.565	-1355.388	0.265	735.018	0.292	16	0.121	K.EAGALLSYDPNLR.E
R5/RRR5-12/2	1418.939	1419.565	-1149.401	0.300	366.732	0.412	11	0.120	-.EAGALLSYDPNLR.-
R5/RRR5-13/3	1514.559	1514.666	-70.712	0.446	1240.872	0.365	28	0.106	R.RIVQDPSSLQDQK.K
R5/RRR5-12/3	1918.609	1919.128	-794.035	0.360	1139.526	0.370	27	0.099	K.VQQVDTTGAGDAFVGALLR.R
R5/RRR5-13/3	1918.719	1919.128	-214.006	0.306	614.737	0.295	23	0.066	-.VQQVDTTGAGDAFVGALLR.-
R5/RRR5-7/3	1868.987	1869.112	-67.522	0.426	1893.680	0.468	28	0.235	K.WGAPNKIDFLSLSYTR.H
R5/RRR5-1/2	1322.316	1321.504	-142.834	0.525	1446.174	0.550	19	0.207	K.LGDLSQTQIFAK.I
R5/RRR5-7/2	1321.101	1321.504	-306.449	0.535	1412.638	0.485	19	0.190	K.LGDLSQTQIFAK.I
R5/RRR5-7/2	1321.111	1321.504	-298.291	0.531	1365.161	0.485	19	0.185	K.LGDLSQTQIFAK.I
R5/RRR5-8/2	1321.213	1321.504	-220.981	0.508	1408.495	0.460	19	0.184	K.LGDLSQTQIFAK.I
R5/RRR5-7/2	1569.297	1569.808	-965.656	0.456	1302.545	0.486	18	0.177	-.M*HSTNLLLEEPIR.M
R5/RRR5-8/2	1321.123	1321.504	-289.113	0.506	1270.134	0.485	18	0.176	K.LGDLSQTQIFAK.I
R5/RRR5-7/2	1320.586	1321.504	-1457.147	0.392	1374.880	0.429	19	0.174	K.LGDLSQTQIFAK.I
R5/RRR5-8/3	1644.683	1645.006	-196.979	0.497	1518.837	0.444	27	0.158	K.YRPTM*PVLSVVIPR.L
R5/RRR5-7/2	1215.243	1215.380	-113.305	0.357	1244.938	0.369	15	0.154	K.IDFLSLSYTR.H
R5/RRR5-8/2	1215.088	1215.380	-241.289	0.329	941.259	0.396	14	0.139	K.IDFLSLSYTR.H
R5/RRR5-8/2	1171.786	1172.274	-417.908	0.322	1093.993	0.327	14	0.138	R.WSFTGAFEAR.Q
R5/RRR5-1/2	1321.053	1321.504	-342.235	0.360	796.411	0.392	16	0.133	K.LGDLSQTQIFAK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1377.326	1376.623	-215.801	0.377	679.143	0.451	19	0.133	R.GLYPVETISIVGK.I
R5/RRR5-7/2	1154.195	1153.310	-100.522	0.382	749.514	0.431	15	0.133	R.GNLGIDLPPEK.V
R5/RRR5-8/2	1171.681	1172.274	-1363.220	0.252	1198.188	0.236	14	0.132	R.WSFTGAFEAR.Q
R5/RRR5-7/2	1214.596	1215.380	-1472.812	0.313	970.613	0.317	13	0.131	K.IDFLSLSYTR.H
R5/RRR5-7/2	1171.916	1172.274	-305.968	0.319	880.984	0.316	15	0.129	R.WSFTGAFEAR.Q
R5/RRR5-2/2	1321.206	1321.504	-225.987	0.386	804.273	0.293	16	0.125	K.LGDLSQTQIFAK.I
R5/RRR5-7/2	1215.354	1215.380	-21.419	0.386	557.273	0.309	13	0.123	K.IDFLSLSYTR.H
R5/RRR5-8/2	1171.774	1172.274	-427.420	0.278	755.170	0.304	13	0.123	R.WSFTGAFEAR.Q
R5/RRR5-8/2	1214.865	1215.380	-1250.867	0.306	740.367	0.289	13	0.122	K.IDFLSLSYTR.H
R5/RRR5-7/2	1172.285	1172.274	9.963	0.256	677.582	0.314	13	0.121	R.WSFTGAFEAR.Q
R5/RRR5-7/3	1599.048	1598.697	220.691	0.513	864.049	0.529	28	0.114	R.HPAESTNATNESVLK.V
R5/RRR5-8/3	1304.907	1304.538	283.386	0.469	1021.585	0.375	22	0.093	K.CNMAGKPAVVTR.V
R5/RRR5-7/3	1645.016	1645.006	5.805	0.416	1046.572	0.347	24	0.090	K.YRPTM*PVLSVVIPR.L
R5/RRR5-7/3	1598.684	1598.697	-8.212	0.405	588.448	0.444	24	0.089	R.HPAESTNATNESVLK.V
R5/RRR5-8/3	1598.438	1598.697	-162.289	0.385	903.594	0.374	27	0.087	-.HPAESTNATNESVLK.-
R5/RRR5-8/3	1599.788	1598.697	56.962	0.443	788.432	0.391	26	0.085	-.HPAESTNATNESVLK.-
R5/RRR5-7/3	1645.115	1645.006	66.200	0.303	955.594	0.302	22	0.077	K.YRPTM*PVLSVVIPR.L
R5/RRR5-8/3	1628.774	1629.007	-143.067	0.330	699.609	0.234	22	0.070	K.YRPTMPVLSVVIPR.L
R5/RRR5-8/3	1628.781	1629.007	-138.894	0.400	468.756	0.372	19	0.065	-.YRPTMPVLSVVIPR.-
R5/RRR5-8/3	1869.152	1869.112	21.111	0.224	982.281	0.169	22	0.057	K.WGAPNKIDFLSLSYTR.H
R5/RRR5-7/2	1702.437	1701.940	292.736	0.577	2532.698	0.536	25	0.371	K.AAVEEGIVVGGGCTLLR.L
R5/RRR5-9/2	1703.555	1701.940	-226.438	0.552	1663.377	0.490	24	0.216	K.AAVEEGIVVGGGCTLLR.L
R5/RRR5-9/2	1702.658	1701.940	-166.226	0.421	1777.919	0.413	24	0.213	K.AAVEEGIVVGGGCTLLR.L
R5/RRR5-9/2	1272.325	1272.473	-116.401	0.434	1847.208	0.365	18	0.211	R.DLITILEDAIR.G
R5/RRR5-9/2	1272.787	1272.473	247.741	0.494	1568.532	0.393	17	0.186	R.DLITILEDAIR.G
R5/RRR5-7/2	1271.415	1272.473	-1623.764	0.360	1204.213	0.327	15	0.144	R.DLITILEDAIR.G
R5/RRR5-7/2	1272.138	1272.473	-264.058	0.517	1023.794	0.383	16	0.143	R.DLITILEDAIR.G
R5/RRR5-8/2	1618.857	1617.737	74.451	0.442	917.505	0.450	18	0.143	K.VDAIIETLENDEQK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1272.682	1272.473	164.930	0.176	729.537	0.316	15	0.119	R.DLITILEDAIR.G
R5/RRR5-8/1	1030.441	1031.142	-1655.870	0.146	1026.507	0.169	12	0.648	K.AIDDAEGLVK.V
R5/RRR5-8/2	1835.399	1836.033	-892.732	0.549	2448.184	0.566	28	0.365	R.VPYTAGIGLESVGVETDK.A
R5/RRR5-8/2	1947.614	1948.118	-774.659	0.532	2397.158	0.595	29	0.364	K.LASPSEVSVDLSDGGSTVVK.G
R5/RRR5-7/2	1948.405	1948.118	147.823	0.565	2216.828	0.632	29	0.341	K.LASPSEVSVDLSDGGSTVVK.G
R5/RRR5-8/2	1835.448	1836.033	-866.026	0.574	2270.172	0.558	27	0.328	R.VPYTAGIGLESVGVETDK.A
R5/RRR5-8/2	1834.769	1836.033	-1237.372	0.559	2081.006	0.566	27	0.297	R.VPYTAGIGLESVGVETDK.A
R5/RRR5-8/2	1947.380	1948.118	-895.090	0.487	1955.527	0.615	28	0.290	K.LASPSEVSVDLSDGGSTVVK.G
R5/RRR5-7/2	1947.302	1948.118	-935.618	0.472	1825.006	0.626	27	0.271	K.LASPSEVSVDLSDGGSTVVK.G
R5/RRR5-8/2	1948.606	1948.118	251.356	0.567	1867.210	0.594	26	0.269	K.LASPSEVSVDLSDGGSTVVK.G
R5/RRR5-8/2	1131.002	1131.305	-268.213	0.459	1325.644	0.486	17	0.181	K.NIIIATGSDVK.S
R5/RRR5-8/2	1130.409	1131.305	-1682.256	0.394	1260.118	0.468	17	0.171	K.NIIIATGSDVK.S
R5/RRR5-7/2	1131.235	1131.305	-61.434	0.430	1200.001	0.441	17	0.163	K.NIIIATGSDVK.S
R5/RRR5-8/2	1575.520	1575.823	-192.850	0.359	1382.865	0.354	21	0.160	K.IVSSTGALCLSEIPK.K
R5/RRR5-8/2	1130.475	1131.305	-1623.347	0.379	1052.327	0.451	16	0.153	K.NIIIATGSDVK.S
R5/RRR5-7/2	1131.219	1131.305	-75.722	0.393	959.210	0.422	16	0.145	K.NIIIATGSDVK.S
R5/RRR5-8/2	1030.765	1031.142	-366.991	0.415	856.653	0.437	17	0.144	K.AIDDAEGLVK.V
R5/RRR5-7/2	1030.880	1031.142	-255.188	0.462	843.432	0.411	17	0.142	K.AIDDAEGLVK.V
R5/RRR5-8/2	1030.481	1031.142	-1616.312	0.416	924.297	0.381	17	0.141	K.AIDDAEGLVK.V
R5/RRR5-7/2	1132.986	1133.234	-219.871	0.390	566.609	0.532	16	0.140	K.VVGVDTSGDGVK.L
R5/RRR5-8/2	1132.869	1133.234	-323.215	0.416	680.347	0.478	17	0.140	K.VVGVDTSGDGVK.L
R5/RRR5-8/2	1030.341	1031.142	-1753.188	0.385	805.898	0.395	16	0.137	K.AIDDAEGLVK.V
R5/RRR5-7/2	1030.787	1031.142	-345.127	0.398	754.059	0.398	16	0.136	K.AIDDAEGLVK.V
R5/RRR5-8/2	1132.986	1133.234	-219.222	0.426	543.653	0.450	16	0.134	K.VVGVDTSGDGVK.L
R5/RRR5-7/2	1031.024	1031.142	-114.431	0.436	703.417	0.373	16	0.133	K.AIDDAEGLVK.V
R5/RRR5-7/2	1132.890	1133.234	-305.052	0.355	458.352	0.473	15	0.132	K.VVGVDTSGDGVK.L
R5/RRR5-8/2	917.937	918.075	-150.136	0.463	908.958	0.319	13	0.129	-.FPLLANSR.-
R5/RRR5-8/2	917.944	918.075	-142.799	0.491	799.812	0.343	12	0.129	-.FPLLANSR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1132.424	1133.234	-1603.038	0.289	526.498	0.437	15	0.127	K.VVGVDTSGDGVK.L
R5/RRR5-7/2	1133.071	1133.234	-144.214	0.290	407.478	0.430	14	0.123	-.VVGVDTSGDGVK.-
R5/RRR5-2/2	1727.367	1726.996	215.534	0.427	702.681	0.374	16	0.123	K.FSNLEVDLPAM*M*AQK.D
R5/RRR5-7/2	917.873	918.075	-220.444	0.240	897.651	0.249	13	0.122	-.FPLLANSR.-
R5/RRR5-8/2	1574.815	1575.823	-1278.668	0.226	769.937	0.019	18	0.107	K.IVSSTGALCLSEIPK.K
R5/RRR5-7/3	1452.066	1451.603	319.339	0.467	1001.633	0.363	23	0.091	R.TCHAHPTVSEALK.E
R5/RRR5-8/3	1452.772	1451.603	116.369	0.452	703.826	0.358	21	0.083	R.TCHAHPTVSEALK.E
R5/RRR5-8/3	1202.126	1202.431	-254.138	0.457	1129.956	0.263	22	0.081	-.VGKFPLLANSR.-
R5/RRR5-7/3	1452.088	1451.603	335.017	0.445	464.403	0.338	19	0.079	-.TCHAHPTVSEALK.-
R5/RRR5-7/3	1451.953	1451.603	241.827	0.431	1035.054	0.212	23	0.070	R.TCHAHPTVSEALK.E
R5/RRR5-8/3	1451.929	1451.603	224.628	0.388	881.292	0.191	21	0.065	R.TCHAHPTVSEALK.E
R5/RRR5-16/1	1131.649	1132.377	-1531.688	0.257	770.828	0.427	14	0.430	K.SGLLLVTGPFK.I
R5/RRR5-17/2	1740.403	1740.890	-280.315	0.607	1748.714	0.581	23	0.251	K.KTEGELFETEKEATK.N
R5/RRR5-16/2	1311.115	1311.466	-268.815	0.495	1688.476	0.550	20	0.236	R.VNQSYVIATSTK.V
R5/RRR5-16/2	1311.063	1311.466	-308.235	0.480	1594.265	0.576	19	0.229	R.VNQSYVIATSTK.V
R5/RRR5-16/3	1211.693	1211.350	284.523	0.515	2002.307	0.403	27	0.221	K.AEKPDAAAAAAPK.F
R5/RRR5-16/2	1310.651	1311.466	-1389.255	0.407	1606.841	0.535	19	0.219	R.VNQSYVIATSTK.V
R5/RRR5-21/2	1311.144	1311.466	-246.584	0.486	1546.792	0.542	19	0.216	R.VNQSYVIATSTK.V
R5/RRR5-15/2	1132.322	1132.377	-48.832	0.448	1630.048	0.428	17	0.199	K.SGLLLVTGPFK.I
R5/RRR5-16/2	1059.981	1060.183	-190.890	0.517	1231.933	0.557	16	0.188	K.VDISGVNVEK.F
R5/RRR5-16/3	1211.379	1211.350	24.286	0.505	1710.547	0.417	26	0.175	K.AEKPDAAAAAAPK.F
R5/RRR5-20/2	1059.991	1060.183	-181.532	0.411	1179.656	0.510	16	0.172	K.VDISGVNVEK.F
R5/RRR5-16/2	1132.148	1132.377	-202.838	0.485	1259.037	0.470	15	0.171	K.SGLLLVTGPFK.I
R5/RRR5-16/3	1211.745	1211.350	327.554	0.521	1667.254	0.422	25	0.171	K.AEKPDAAAAAAPK.F
R5/RRR5-16/2	1059.440	1060.183	-1650.370	0.406	1188.991	0.455	16	0.164	K.VDISGVNVEK.F
R5/RRR5-16/2	1131.518	1132.377	-1647.820	0.425	1072.649	0.483	14	0.158	K.SGLLLVTGPFK.I
R5/RRR5-21/3	1211.166	1211.350	-151.910	0.514	1624.188	0.401	26	0.157	K.AEKPDAAAAAAPK.F
R5/RRR5-17/2	1612.340	1612.717	-234.237	0.506	953.337	0.513	18	0.155	K.TEGELFETEKEATK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1131.336	1132.377	-1809.879	0.390	975.549	0.445	14	0.147	K.SGLLLVTGPFK.I
R5/RRR5-15/2	1498.422	1498.793	-248.368	0.369	990.476	0.398	22	0.143	R.SSITPGTVLILLAGR.F
R5/RRR5-16/2	1059.845	1060.183	-319.954	0.450	834.033	0.440	14	0.142	K.VDISGVNVEK.F
R5/RRR5-15/3	1211.167	1211.350	-151.455	0.479	1463.855	0.414	25	0.141	K.AEKPDAAAAAAPK.F
R5/RRR5-15/3	1211.422	1211.350	59.760	0.511	1513.626	0.384	25	0.138	K.AEKPDAAAAAAPK.F
R5/RRR5-15/2	1131.749	1132.377	-1443.342	0.379	851.895	0.418	14	0.138	K.SGLLLVTGPFK.I
R5/RRR5-17/2	1207.970	1208.348	-313.560	0.397	505.068	0.493	15	0.137	K.FYPADDVKPR.Q
R5/RRR5-17/2	1207.810	1208.348	-1276.826	0.361	400.822	0.552	14	0.137	K.FYPADDVKPR.Q
R5/RRR5-17/2	1207.974	1208.348	-310.315	0.354	472.365	0.500	15	0.135	K.FYPADDVKPR.Q
R5/RRR5-16/2	1497.788	1498.793	-1342.546	0.332	876.924	0.378	21	0.134	R.SSITPGTVLILLAGR.F
R5/RRR5-15/2	1498.388	1498.793	-270.680	0.401	800.580	0.390	20	0.134	R.SSITPGTVLILLAGR.F
R5/RRR5-15/2	955.555	956.118	-1640.864	0.381	923.973	0.342	14	0.134	K.AIEAVPDLK.T
R5/RRR5-15/2	1060.091	1060.183	-86.808	0.389	612.651	0.429	13	0.133	K.VDISGVNVEK.F
R5/RRR5-15/2	1060.473	1060.183	274.250	0.329	709.980	0.415	13	0.132	K.VDISGVNVEK.F
R5/RRR5-15/2	1497.967	1498.793	-1222.235	0.350	710.033	0.410	19	0.131	R.SSITPGTVLILLAGR.F
R5/RRR5-19/2	1612.918	1612.717	124.901	0.458	474.721	0.477	14	0.129	K.TEGELFETEKEATK.N
R5/RRR5-15/2	1132.249	1132.377	-113.717	0.336	574.417	0.423	12	0.128	K.SGLLLVTGPFK.I
R5/RRR5-16/2	1498.060	1498.793	-1159.963	0.329	782.703	0.328	20	0.127	R.SSITPGTVLILLAGR.F
R5/RRR5-15/2	955.857	956.118	-273.872	0.359	768.265	0.320	13	0.126	K.AIEAVPDLK.T
R5/RRR5-16/2	1498.033	1498.793	-1178.455	0.341	721.149	0.331	19	0.125	R.SSITPGTVLILLAGR.F
R5/RRR5-16/2	1499.930	1498.793	91.863	0.320	422.800	0.374	15	0.122	R.SSITPGTVLILLAGR.F
R5/RRR5-14/2	1132.007	1132.377	-328.328	0.355	772.873	0.262	13	0.120	K.SGLLLVTGPFK.I
R5/RRR5-17/3	1740.963	1740.890	42.356	0.526	1058.811	0.461	29	0.114	K.KTEGELFETEKEATK.N
R5/RRR5-20/3	1740.840	1740.890	-28.957	0.463	1101.533	0.444	30	0.113	K.KTEGELFETEKEATK.N
R5/RRR5-20/3	1740.604	1740.890	-164.755	0.488	1000.269	0.468	28	0.111	K.KTEGELFETEKEATK.N
R5/RRR5-21/3	1211.598	1211.350	205.268	0.464	1292.058	0.367	24	0.111	K.AEKPDAAAAAAPK.F
R5/RRR5-16/3	1742.130	1740.890	138.541	0.526	958.303	0.468	28	0.109	K.KTEGELFETEKEATK.N
R5/RRR5-15/2	1060.457	1060.183	259.360	0.252	402.476	0.281	12	0.108	-.VDISGVNVEK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/3	1740.400	1740.890	-282.223	0.525	921.306	0.471	27	0.108	K.KTEGELFETEKEATK.N
R5/RRR5-16/3	1740.624	1740.890	-153.252	0.517	848.423	0.485	26	0.107	K.KTEGELFETEKEATK.N
R5/RRR5-15/3	1740.177	1740.890	-986.971	0.484	812.539	0.490	26	0.106	K.KTEGELFETEKEATK.N
R5/RRR5-16/3	1740.977	1740.890	50.479	0.503	1084.962	0.400	29	0.103	K.KTEGELFETEKEATK.N
R5/RRR5-15/3	1741.005	1740.890	66.407	0.536	913.970	0.444	27	0.102	K.KTEGELFETEKEATK.N
R5/RRR5-16/3	1741.227	1740.890	194.233	0.518	698.691	0.487	24	0.102	K.KTEGELFETEKEATK.N
R5/RRR5-15/3	1740.599	1740.890	-167.815	0.534	730.592	0.464	25	0.099	K.KTEGELFETEKEATK.N
R5/RRR5-17/3	1741.049	1740.890	91.721	0.496	842.429	0.435	26	0.098	K.KTEGELFETEKEATK.N
R5/RRR5-20/3	1741.112	1740.890	127.793	0.519	729.114	0.451	25	0.097	K.KTEGELFETEKEATK.N
R5/RRR5-21/3	1210.387	1211.350	-1626.593	0.440	976.776	0.400	22	0.097	K.AEKPDAAAAAAPK.F
R5/RRR5-19/3	1740.035	1740.890	-1069.273	0.392	441.014	0.412	20	0.087	-.KTEGELFETEKEATK.-
R5/RRR5-19/3	1740.198	1740.890	-975.140	0.387	540.643	0.325	24	0.084	K.KTEGELFETEKEATK.N
R5/RRR5-16/3	1498.639	1498.793	-102.917	0.347	1106.496	0.288	26	0.082	R.SSITPGTVLILLAGR.F
R5/RRR5-16/3	1498.447	1498.793	-231.499	0.386	840.972	0.232	25	0.068	R.SSITPGTVLILLAGR.F
R5/RRR5-16/3	1498.013	1498.793	-1191.680	0.297	786.665	0.216	24	0.065	R.SSITPGTVLILLAGR.F
R5/RRR5-14/2	1699.257	1699.843	-935.724	0.540	2098.666	0.623	23	0.318	K.GNAYAQVAIGTEDVYK.S
R5/RRR5-14/2	1699.421	1699.843	-248.963	0.535	1869.414	0.611	24	0.277	K.GNAYAQVAIGTEDVYK.S
R5/RRR5-14/2	1699.215	1699.843	-960.822	0.530	1948.625	0.545	23	0.270	K.GNAYAQVAIGTEDVYK.S
R5/RRR5-14/2	1047.036	1047.184	-142.617	0.482	1913.835	0.484	17	0.250	K.SAEAVELVTK.E
R5/RRR5-14/2	1046.960	1047.184	-215.250	0.502	1685.413	0.525	16	0.229	K.SAEAVELVTK.E
R5/RRR5-14/2	1046.944	1047.184	-229.988	0.429	1635.927	0.485	15	0.212	K.SAEAVELVTK.E
R5/RRR5-14/2	1183.994	1184.366	-314.946	0.442	1495.490	0.439	16	0.188	K.SPEVVLEWPK.K
R5/RRR5-14/2	1232.543	1233.438	-1542.359	0.366	1319.635	0.504	17	0.181	K.VVLVDNADFLK.E
R5/RRR5-14/2	1233.320	1233.438	-96.555	0.488	1232.403	0.518	17	0.180	K.VVLVDNADFLK.E
R5/RRR5-14/2	1184.049	1184.366	-268.295	0.424	1247.751	0.475	15	0.171	K.SPEVVLEWPK.K
R5/RRR5-14/2	1248.744	1249.396	-1327.038	0.485	1024.677	0.455	17	0.154	K.IASFLDPDGWK.V
R5/RRR5-14/2	1515.266	1514.766	-330.665	0.436	464.394	0.558	17	0.142	R.GPTPEPLCQVM*LR.V
R5/RRR5-14/2	1498.069	1498.767	-1136.908	0.419	648.166	0.500	18	0.141	R.GPTPEPLCQVMLR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1249.197	1249.396	-159.820	0.451	997.035	0.350	17	0.138	K.IASFLDPDGWK.V
R5/RRR5-14/2	1499.345	1498.767	-281.940	0.429	475.712	0.494	17	0.136	R.GPTPEPLCQVMLR.V
R5/RRR5-14/2	1499.365	1498.767	-268.544	0.436	393.654	0.509	16	0.136	R.GPTPEPLCQVMLR.V
R5/RRR5-14/2	1249.102	1249.396	-236.091	0.351	938.126	0.348	17	0.134	K.IASFLDPDGWK.V
R5/RRR5-14/2	1514.166	1514.766	-1059.945	0.325	528.365	0.483	16	0.132	R.GPTPEPLCQVM*LR.V
R5/RRR5-14/2	1515.277	1514.766	-323.552	0.372	369.167	0.471	16	0.131	R.GPTPEPLCQVM*LR.V
R5/RRR5-14/2	1604.261	1603.841	262.722	0.475	1108.803	0.398	21	0.127	K.VVLVDNADFLKELQ.-
R5/RRR5-14/2	1603.454	1603.841	-242.331	0.450	1101.302	0.370	21	0.125	K.VVLVDNADFLKELQ.-
R5/RRR5-14/2	1232.471	1233.438	-1600.862	0.264	877.862	0.240	16	0.121	K.VVLVDNADFLK.E
R5/RRR5-14/2	1602.747	1603.841	-1310.699	0.299	844.616	0.268	18	0.102	K.VVLVDNADFLKELQ.-
R5/RRR5-13/2	1603.846	1603.841	2.778	0.380	705.932	0.218	17	0.095	K.VVLVDNADFLKELQ.-
R5/RRR5-14/3	1028.578	1028.236	333.628	0.520	843.014	0.412	17	0.094	K.RLLHAVYR.V
R5/RRR5-14/3	1028.580	1028.236	335.949	0.507	771.293	0.429	17	0.094	K.RLLHAVYR.V
R5/RRR5-14/2	1605.305	1603.841	290.161	0.462	797.788	0.274	16	0.090	-.VVLVDNADFLKELQ.-
R5/RRR5-14/3	1028.686	1028.236	439.106	0.516	724.308	0.396	16	0.089	K.RLLHAVYR.V
R5/RRR5-14/3	1504.633	1504.802	-112.760	0.412	962.602	0.320	25	0.081	K.ILRQPGPLPGLNTK.I
R5/RRR5-14/3	1504.982	1504.802	119.979	0.501	952.605	0.318	24	0.081	K.ILRQPGPLPGLNTK.I
R5/RRR5-6/2	1316.030	1316.355	-247.436	0.488	1937.070	0.537	20	0.267	R.YDYENVDAGAAK.E
R5/RRR5-6/2	1315.459	1316.355	-1445.607	0.348	2058.068	0.455	20	0.261	R.YDYENVDAGAAK.E
R5/RRR5-6/2	1743.379	1743.940	-897.926	0.543	1844.088	0.515	23	0.246	K.DNLGGDKLVTVEDIVR.Q
R5/RRR5-6/2	1489.430	1489.609	-120.478	0.492	1862.888	0.469	19	0.239	R.VYIEQYEKDSSK.T
R5/RRR5-6/2	1315.495	1316.355	-1418.484	0.394	1718.393	0.472	19	0.219	R.YDYENVDAGAAK.E
R5/RRR5-6/3	1986.929	1986.216	-145.069	0.554	1662.361	0.526	31	0.210	K.NKDNLGGDKLVTVEDIVR.Q
R5/RRR5-6/3	1985.681	1986.216	-775.199	0.482	1685.505	0.495	29	0.204	K.NKDNLGGDKLVTVEDIVR.Q
R5/RRR5-6/3	1985.802	1986.216	-209.027	0.492	1539.375	0.469	30	0.171	K.NKDNLGGDKLVTVEDIVR.Q
R5/RRR5-6/2	1556.234	1555.755	309.066	0.434	1229.079	0.413	22	0.160	R.DSQDALAPLVDVALK.L
R5/RRR5-6/2	1031.132	1032.133	-1945.981	0.426	1051.485	0.449	16	0.153	K.GATIVVSGDGR.Y
R5/RRR5-6/2	1306.106	1306.511	-311.286	0.449	739.986	0.559	20	0.153	R.SM*PTSAALDVVAK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1031.288	1032.133	-1794.555	0.360	965.809	0.449	16	0.147	K.GATIVVSGDGR.Y
R5/RRR5-6/2	1305.602	1306.511	-1466.936	0.391	692.021	0.526	19	0.144	R.SM*PTSAALDVVAK.N
R5/RRR5-6/2	1306.063	1306.511	-344.575	0.446	647.184	0.509	19	0.143	R.SM*PTSAALDVVAK.N
R5/RRR5-6/2	1555.306	1555.755	-289.666	0.393	996.472	0.391	20	0.141	R.DSQDALAPLVDVALK.L
R5/RRR5-6/2	1555.262	1555.755	-317.542	0.294	1101.443	0.321	21	0.136	R.DSQDALAPLVDVALK.L
R5/RRR5-6/2	1031.423	1032.133	-1663.031	0.345	934.279	0.361	16	0.135	K.GATIVVSGDGR.Y
R5/RRR5-6/2	888.773	888.044	-305.014	0.479	1009.285	0.318	13	0.134	K.DAVQIITK.M
R5/RRR5-6/2	1044.004	1044.227	-213.983	0.333	743.617	0.371	15	0.131	K.LVTVEDIVR.Q
R5/RRR5-6/2	1291.244	1290.512	-207.905	0.383	438.460	0.432	17	0.130	R.SMPTSAALDVVAK.N
R5/RRR5-6/2	1043.980	1044.227	-237.092	0.301	634.531	0.321	15	0.124	K.LVTVEDIVR.Q
R5/RRR5-6/2	1044.083	1044.227	-137.978	0.303	587.435	0.253	14	0.121	K.LVTVEDIVR.Q
R5/RRR5-6/3	1743.654	1743.940	-164.256	0.412	1143.763	0.388	26	0.102	K.DNLGGDKLVTVEDIVR.Q
R5/RRR5-6/3	1761.437	1761.960	-867.424	0.409	980.279	0.311	26	0.079	K.KATTPFDGQKPGTSGLR.K
R5/RRR5-6/3	1761.935	1761.960	-14.087	0.427	832.184	0.337	25	0.077	K.KATTPFDGQKPGTSGLR.K
R5/RRR5-11/2	1593.689	1593.752	-39.612	0.445	1739.266	0.475	21	0.223	K.YVFTIDDDCFVAK.D
R5/RRR5-12/2	1594.067	1593.752	198.424	0.485	1576.880	0.519	21	0.214	K.YVFTIDDDCFVAK.D
R5/RRR5-12/2	1593.065	1593.752	-1061.965	0.411	1587.976	0.481	21	0.206	K.YVFTIDDDCFVAK.D
R5/RRR5-11/2	1239.155	1239.397	-195.697	0.510	1581.307	0.459	17	0.203	K.CYLSLAEQVR.E
R5/RRR5-11/2	1238.562	1239.397	-1485.536	0.471	1601.587	0.446	17	0.202	K.CYLSLAEQVR.E
R5/RRR5-11/2	1239.045	1239.397	-284.945	0.498	1482.057	0.465	17	0.193	K.CYLSLAEQVR.E
R5/RRR5-11/2	1593.221	1593.752	-963.649	0.415	1509.129	0.450	20	0.191	K.YVFTIDDDCFVAK.D
R5/RRR5-11/2	1502.403	1502.609	-137.856	0.489	1146.338	0.578	19	0.184	R.VPEGFDYELYNR.N
R5/RRR5-12/2	1502.156	1502.609	-302.197	0.485	1185.296	0.555	19	0.183	R.VPEGFDYELYNR.N
R5/RRR5-11/2	1503.170	1502.609	-293.033	0.482	1152.601	0.569	19	0.182	R.VPEGFDYELYNR.N
R5/RRR5-11/2	1180.569	1181.324	-1491.099	0.480	1494.133	0.388	15	0.177	K.DINALEQHIK.N
R5/RRR5-12/2	1123.141	1123.348	-184.843	0.587	879.299	0.608	16	0.173	R.YVDAVMTVPK.G
R5/RRR5-12/2	1502.246	1502.609	-242.356	0.494	1122.623	0.506	19	0.170	R.VPEGFDYELYNR.N
R5/RRR5-10/2	1504.089	1502.609	319.943	0.523	947.657	0.566	18	0.167	R.VPEGFDYELYNR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1181.394	1181.324	60.150	0.517	1383.912	0.363	15	0.163	K.DINALEQHIK.N
R5/RRR5-12/2	1502.286	1502.609	-215.944	0.480	849.348	0.583	17	0.162	R.VPEGFDYELYNR.N
R5/RRR5-11/2	1139.171	1139.347	-155.160	0.582	852.341	0.545	16	0.161	R.YVDAVM*TVPK.G
R5/RRR5-12/2	1138.985	1139.347	-318.472	0.547	870.906	0.533	16	0.160	R.YVDAVM*TVPK.G
R5/RRR5-12/2	1138.978	1139.347	-324.494	0.566	877.700	0.521	16	0.159	R.YVDAVM*TVPK.G
R5/RRR5-11/2	1139.092	1139.347	-224.715	0.567	829.135	0.529	16	0.157	R.YVDAVM*TVPK.G
R5/RRR5-11/2	1123.144	1123.348	-181.572	0.485	820.141	0.540	15	0.156	R.YVDAVMTVPK.G
R5/RRR5-12/2	1181.112	1181.324	-179.295	0.438	1223.885	0.393	14	0.156	K.DINALEQHIK.N
R5/RRR5-11/2	1502.252	1502.609	-238.606	0.466	961.727	0.490	18	0.156	R.VPEGFDYELYNR.N
R5/RRR5-11/2	1123.077	1123.348	-241.216	0.501	861.639	0.509	16	0.155	R.YVDAVMTVPK.G
R5/RRR5-12/2	1138.554	1139.347	-1579.678	0.454	875.795	0.496	16	0.153	R.YVDAVM*TVPK.G
R5/RRR5-12/2	1122.984	1123.348	-324.642	0.412	907.858	0.463	16	0.149	R.YVDAVMTVPK.G
R5/RRR5-11/2	1122.915	1123.348	-385.940	0.443	854.891	0.457	16	0.147	R.YVDAVMTVPK.G
R5/RRR5-12/2	1240.651	1241.456	-1459.054	0.468	835.216	0.467	16	0.146	K.VICDHLSLGVK.T
R5/RRR5-12/2	1122.439	1123.348	-1705.873	0.399	831.568	0.423	16	0.141	R.YVDAVMTVPK.G
R5/RRR5-1/2	1138.943	1139.347	-355.464	0.372	644.473	0.458	14	0.137	R.YVDAVM*TVPK.G
R5/RRR5-12/2	1202.148	1202.386	-198.360	0.399	582.153	0.470	14	0.137	K.TGLPYIWHSK.A
R5/RRR5-12/2	1238.679	1239.397	-1390.900	0.378	756.586	0.429	14	0.136	K.CYLSLAEQVR.E
R5/RRR5-12/2	1242.212	1241.456	-196.595	0.471	790.482	0.397	16	0.136	K.VICDHLSLGVK.T
R5/RRR5-12/2	992.932	992.167	-238.122	0.420	588.888	0.424	13	0.135	R.CFGYMVSK.K
R5/RRR5-12/2	1241.058	1241.456	-321.182	0.413	813.417	0.388	15	0.134	K.VICDHLSLGVK.T
R5/RRR5-12/2	1203.045	1202.386	-284.719	0.397	556.008	0.437	14	0.133	K.TGLPYIWHSK.A
R5/RRR5-11/2	1202.149	1202.386	-197.545	0.361	604.287	0.432	15	0.133	K.TGLPYIWHSK.A
R5/RRR5-12/2	990.301	990.138	165.473	0.427	548.505	0.422	14	0.131	-.ASNPFVNLK.-
R5/RRR5-12/2	989.412	990.138	-1749.111	0.376	595.380	0.385	14	0.130	K.ASNPFVNLK.K
R5/RRR5-1/2	1138.898	1139.347	-395.685	0.325	599.329	0.392	14	0.130	R.YVDAVM*TVPK.G
R5/RRR5-12/2	992.398	992.167	233.534	0.379	491.964	0.383	11	0.126	-.CFGYMVSK.-
R5/RRR5-11/2	1202.976	1202.386	-341.934	0.356	449.790	0.342	13	0.125	K.TGLPYIWHSK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	989.858	990.138	-283.328	0.347	458.923	0.330	13	0.125	K.ASNPFVNLK.K
R5/RRR5-12/2	1007.908	1008.167	-257.055	0.274	382.373	0.378	10	0.123	R.CFGYM*VSK.K
R5/RRR5-11/2	1592.687	1593.752	-1300.220	0.234	958.713	0.232	17	0.121	K.YVFTIDDDCFVAK.D
R5/RRR5-11/2	1202.129	1202.386	-214.150	0.231	471.063	0.358	13	0.121	K.TGLPYIWHSK.A
R5/RRR5-2/2	1502.881	1502.609	181.705	0.345	308.477	0.318	12	0.118	-.VPEGFDYELYNR.-
R5/RRR5-4/2	1832.446	1833.143	-929.116	0.506	2906.945	0.540	26	0.456	R.NGVTATDLVLTVTQMLR.K
R5/RRR5-4/2	1832.323	1833.143	-996.199	0.521	2516.252	0.528	23	0.364	R.NGVTATDLVLTVTQMLR.K
R5/RRR5-4/2	1833.318	1833.143	95.728	0.532	2379.743	0.548	23	0.344	R.NGVTATDLVLTVTQMLR.K
R5/RRR5-4/2	1894.493	1895.082	-841.481	0.557	1927.775	0.578	24	0.276	K.FVEFYGGGM*SELSLADR.A
R5/RRR5-4/2	1559.094	1558.589	-318.646	0.551	1700.474	0.542	24	0.235	K.SGEDADTLGLTGHER.F
R5/RRR5-4/2	1515.085	1515.630	-1022.252	0.513	1619.214	0.542	20	0.226	K.M*FVDYNQPEAER.V
R5/RRR5-4/2	1501.346	1500.656	-207.271	0.480	1924.133	0.376	20	0.223	R.SDDTVAMIESYLR.A
R5/RRR5-4/2	1517.388	1516.656	-176.751	0.566	1525.235	0.504	20	0.205	R.SDDTVAM*IESYLR.A
R5/RRR5-4/2	1516.338	1516.656	-209.898	0.488	1471.320	0.451	20	0.188	R.SDDTVAM*IESYLR.A
R5/RRR5-4/2	1850.469	1849.143	176.807	0.504	1253.901	0.555	22	0.186	R.NGVTATDLVLTVTQM*LR.K
R5/RRR5-4/2	1515.198	1515.630	-285.956	0.474	1291.946	0.477	18	0.176	K.M*FVDYNQPEAER.V
R5/RRR5-4/2	1558.055	1558.589	-987.678	0.497	1111.790	0.535	22	0.172	K.SGEDADTLGLTGHER.F
R5/RRR5-4/2	1544.144	1543.825	206.742	0.526	1231.916	0.479	18	0.170	K.ACELGLEVKPWIK.T
R5/RRR5-4/2	1558.070	1558.589	-978.396	0.484	1149.106	0.506	22	0.170	K.SGEDADTLGLTGHER.F
R5/RRR5-2/2	1516.108	1515.630	316.583	0.429	1327.338	0.403	18	0.166	K.M*FVDYNQPEAER.V
R5/RRR5-4/2	1850.457	1849.143	170.192	0.488	994.579	0.515	18	0.155	R.NGVTATDLVLTVTQM*LR.K
R5/RRR5-4/2	1537.367	1537.843	-310.172	0.487	744.578	0.566	19	0.153	R.SNLAGM*GIIPLCFK.S
R5/RRR5-4/2	1538.334	1537.843	320.299	0.516	654.572	0.581	18	0.151	R.SNLAGM*GIIPLCFK.S
R5/RRR5-4/2	1173.100	1173.300	-171.439	0.541	846.624	0.421	16	0.142	K.ILDWENSAPK.Q
R5/RRR5-3/2	1616.691	1616.793	-63.586	0.424	926.541	0.402	21	0.140	R.DIWPSTEEIAEVVK.S
R5/RRR5-4/2	1172.987	1173.300	-267.486	0.497	749.477	0.421	16	0.139	K.ILDWENSAPK.Q
R5/RRR5-4/2	1174.112	1173.300	-160.759	0.548	816.937	0.369	16	0.135	K.ILDWENSAPK.Q
R5/RRR5-4/2	1197.850	1198.258	-341.865	0.353	885.030	0.363	15	0.133	R.NCDEFQVTGK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1849.107	1849.143	-19.586	0.394	347.550	0.488	16	0.128	R.NGVTATDLVLTVTQM*LR.K
R5/RRR5-4/2	1536.397	1537.843	-1596.814	0.328	486.371	0.364	15	0.122	R.SNLAGM*GIIPLCFK.S
R5/RRR5-4/2	1616.423	1616.793	-230.161	0.313	512.597	0.311	17	0.119	R.DIWPSTEEIAEVVK.S
R5/RRR5-3/2	1538.506	1537.843	-219.776	0.313	268.828	0.338	11	0.112	-.SNLAGM*GIIPLCFK.-
R5/RRR5-4/2	1197.869	1198.258	-325.710	0.142	731.620	0.159	15	0.110	R.NCDEFQVTGK.D
R5/RRR5-13/3	1982.899	1983.123	-113.040	0.569	2112.789	0.495	34	0.296	K.TRPSVTFTDEETEQLTK.R
R5/RRR5-7/3	1541.536	1540.767	-150.429	0.595	2869.624	0.473	35	0.484	K.HAVM*AIGVDEEPKK.S
R5/RRR5-7/2	1719.397	1719.960	-912.017	0.481	2525.391	0.551	24	0.375	R.ALDSGIVAQAALDVFTK.E
R5/RRR5-7/2	1183.162	1183.426	-223.792	0.511	2451.590	0.554	22	0.363	R.LAVQLVAGGGGIK.S
R5/RRR5-7/2	1183.138	1183.426	-243.873	0.557	2461.372	0.535	22	0.358	R.LAVQLVAGGGGIK.S
R5/RRR5-7/2	1183.113	1183.426	-264.782	0.583	2356.991	0.533	22	0.337	R.LAVQLVAGGGGIK.S
R5/RRR5-7/2	1719.292	1719.960	-973.245	0.511	2204.854	0.544	22	0.310	R.ALDSGIVAQAALDVFTK.E
R5/RRR5-7/2	1651.334	1651.796	-280.606	0.519	1931.167	0.546	26	0.268	K.FPSAISESGEITVEGK.V
R5/RRR5-7/2	1652.240	1651.796	269.469	0.535	1469.431	0.580	23	0.215	K.FPSAISESGEITVEGK.V
R5/RRR5-7/2	1718.473	1719.960	-1451.778	0.291	1804.659	0.369	20	0.204	R.ALDSGIVAQAALDVFTK.E
R5/RRR5-7/2	1651.312	1651.796	-293.808	0.497	1267.483	0.474	22	0.172	K.FPSAISESGEITVEGK.V
R5/RRR5-7/2	1606.756	1605.899	-89.126	0.480	873.774	0.523	19	0.153	K.IGEIPAIEEFVFLK.-
R5/RRR5-7/2	1605.430	1605.899	-292.977	0.493	967.813	0.444	23	0.150	K.IGEIPAIEEFVFLK.-
R5/RRR5-7/3	1540.228	1540.767	-1002.399	0.490	1479.829	0.426	28	0.148	K.HAVM*AIGVDEEPKK.S
R5/RRR5-7/2	1605.896	1605.899	-1.648	0.477	760.534	0.485	21	0.145	K.IGEIPAIEEFVFLK.-
R5/RRR5-7/3	1164.090	1164.379	-249.295	0.464	1831.688	0.204	24	0.134	-.NKYVGVSLVGK.-
R5/RRR5-6/2	1650.811	1651.796	-1206.231	0.458	1018.722	0.347	19	0.134	K.FPSAISESGEITVEGK.V
R5/RRR5-6/2	1651.200	1651.796	-969.780	0.467	702.730	0.323	17	0.120	K.FPSAISESGEITVEGK.V
R5/RRR5-7/3	1164.142	1164.379	-204.164	0.444	1770.089	0.194	24	0.119	R.NKYVGVSLVGK.T
R5/RRR5-6/2	1145.282	1144.260	18.750	0.408	842.293	0.281	14	0.118	-.GGVIDEDALVR.-
R5/RRR5-6/2	1144.033	1144.260	-198.805	0.280	745.883	0.198	14	0.116	-.GGVIDEDALVR.-
R5/RRR5-6/2	1718.575	1719.960	-1391.847	0.214	413.970	0.367	16	0.116	R.ALDSGIVAQAALDVFTK.E
R5/RRR5-2/2	1145.153	1144.260	-93.832	0.378	701.094	0.227	13	0.116	-.GGVIDEDALVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/3	1164.411	1164.379	27.421	0.466	1556.918	0.257	22	0.112	R.NKYVGVSLVGK.T
R5/RRR5-9/2	1144.060	1144.260	-175.791	0.303	528.013	0.238	12	0.110	-.GGVIDEDALVR.-
R5/RRR5-7/3	1523.682	1524.767	-1372.734	0.403	1039.121	0.445	25	0.107	K.HAVMAIGVDEEPKK.S
R5/RRR5-7/3	1668.405	1668.940	-922.527	0.414	1183.659	0.381	30	0.105	R.KHAVM*AIGVDEEPKK.S
R5/RRR5-7/3	1826.822	1827.014	-105.359	0.475	1003.264	0.414	28	0.099	K.GLGM*HVIAHDPYASADR.A
R5/RRR5-7/3	1668.123	1668.940	-1092.342	0.438	1086.971	0.384	29	0.099	R.KHAVM*AIGVDEEPKK.S
R5/RRR5-7/3	1825.968	1827.014	-1123.908	0.442	949.980	0.404	29	0.095	K.GLGM*HVIAHDPYASADR.A
R5/RRR5-7/3	1668.411	1668.940	-919.221	0.490	844.814	0.421	29	0.094	R.KHAVM*AIGVDEEPKK.S
R5/RRR5-2/2	1145.269	1144.260	7.632	0.315	482.719	0.183	12	0.087	-.GGVIDEDALVR.-
R5/RRR5-7/3	1719.344	1719.960	-942.745	0.384	999.749	0.368	28	0.087	R.ALDSGIVAQAALDVFTK.E
R5/RRR5-7/3	1825.732	1827.014	-1254.019	0.396	958.672	0.334	29	0.083	K.GLGM*HVIAHDPYASADR.A
R5/RRR5-6/3	1541.374	1540.767	-255.893	0.312	863.320	0.224	23	0.067	K.HAVM*AIGVDEEPKK.S
R5/RRR5-11/3	1769.517	1769.891	-211.847	0.593	2965.436	0.496	33	0.533	R.HYAHVDCPGHADYVK.N
R5/RRR5-10/3	1769.654	1769.891	-134.410	0.576	2477.570	0.475	31	0.368	R.HYAHVDCPGHADYVK.N
R5/RRR5-10/3	1769.349	1769.891	-874.340	0.566	2424.716	0.486	31	0.359	R.HYAHVDCPGHADYVK.N
R5/RRR5-10/3	1769.451	1769.891	-249.531	0.569	2370.578	0.513	30	0.359	R.HYAHVDCPGHADYVK.N
R5/RRR5-11/2	1692.136	1692.898	-1044.434	0.528	2381.329	0.543	25	0.345	K.ILDHGEAGDNVGLLLR.G
R5/RRR5-11/2	1693.551	1692.898	-205.726	0.560	2288.982	0.558	24	0.332	K.ILDHGEAGDNVGLLLR.G
R5/RRR5-11/3	1769.377	1769.891	-858.549	0.561	2322.511	0.459	30	0.319	R.HYAHVDCPGHADYVK.N
R5/RRR5-11/2	1562.420	1562.703	-181.459	0.528	2511.927	0.387	22	0.319	K.AVAFDEIDKAPEEK.A
R5/RRR5-11/2	1692.249	1692.898	-977.294	0.519	2180.803	0.547	24	0.309	K.ILDHGEAGDNVGLLLR.G
R5/RRR5-11/3	1769.173	1769.891	-973.979	0.508	2049.439	0.473	28	0.264	R.HYAHVDCPGHADYVK.N
R5/RRR5-11/2	1728.596	1726.949	-204.955	0.553	1316.180	0.575	22	0.196	K.TGEDVEILGLTPSGPLK.T
R5/RRR5-11/2	1726.314	1726.949	-949.924	0.416	1514.810	0.448	23	0.190	K.TGEDVEILGLTPSGPLK.T
R5/RRR5-11/2	1158.114	1157.344	-198.819	0.533	1230.566	0.414	17	0.162	K.FPGDEIPIIR.G
R5/RRR5-11/2	1649.282	1649.847	-951.744	0.450	1193.231	0.443	20	0.161	K.LM*DAVDEYIPDPVR.Q
R5/RRR5-11/2	1157.291	1157.344	-45.768	0.428	1240.466	0.385	17	0.158	K.FPGDEIPIIR.G
R5/RRR5-11/2	1649.331	1649.847	-921.874	0.462	1146.330	0.431	20	0.156	K.LM*DAVDEYIPDPVR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1560.581	1561.676	-1346.348	0.355	1220.257	0.377	21	0.151	R.GSALSALQGTNDEIGK.N
R5/RRR5-11/2	1562.189	1561.676	-313.078	0.460	957.161	0.492	19	0.151	R.GSALSALQGTNDEIGK.N
R5/RRR5-11/2	1755.377	1756.016	-936.416	0.427	682.760	0.496	18	0.139	K.SFLM*PIEDVFSIQGR.G
R5/RRR5-11/2	1739.245	1740.016	-1021.635	0.402	790.062	0.422	20	0.136	K.SFLMPIEDVFSIQGR.G
R5/RRR5-11/2	1156.981	1157.344	-314.892	0.382	850.950	0.377	16	0.135	K.FPGDEIPIIR.G
R5/RRR5-11/2	1756.263	1756.016	141.211	0.385	733.082	0.440	17	0.133	K.SFLM*PIEDVFSIQGR.G
R5/RRR5-11/2	1726.277	1726.949	-971.931	0.357	987.420	0.346	19	0.132	K.TGEDVEILGLTPSGPLK.T
R5/RRR5-13/2	1726.908	1726.949	-23.795	0.408	619.157	0.370	17	0.123	K.TGEDVEILGLTPSGPLK.T
R5/RRR5-11/3	1796.797	1797.011	-119.365	0.491	548.751	0.568	30	0.107	R.TKPHVNVGTIGHVDHGK.T
R5/RRR5-11/3	1797.311	1797.011	167.191	0.416	426.824	0.524	27	0.097	R.TKPHVNVGTIGHVDHGK.T
R5/RRR5-10/3	1796.918	1797.011	-51.901	0.421	328.806	0.524	24	0.097	R.TKPHVNVGTIGHVDHGK.T
R5/RRR5-11/3	1796.340	1797.011	-933.349	0.353	399.403	0.432	26	0.088	R.TKPHVNVGTIGHVDHGK.T
R5/RRR5-10/3	1796.328	1797.011	-939.694	0.341	431.913	0.399	26	0.085	R.TKPHVNVGTIGHVDHGK.T
R5/RRR5-11/3	1692.656	1692.898	-143.346	0.350	917.549	0.339	25	0.080	K.ILDHGEAGDNVGLLLR.G
R5/RRR5-11/3	1692.329	1692.898	-929.651	0.422	742.609	0.306	25	0.073	K.ILDHGEAGDNVGLLLR.G
R5/RRR5-5/2	1997.772	1997.232	-231.333	0.640	3084.458	0.584	26	0.517	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/2	1996.505	1997.232	-867.792	0.634	2381.466	0.600	24	0.361	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/2	1997.553	1997.232	160.919	0.609	2340.466	0.589	24	0.350	K.KISEEEYISAIKEEISK.V
R5/RRR5-6/2	1869.376	1869.059	169.856	0.586	1904.722	0.520	23	0.254	K.ISEEEYISAIKEEISK.V
R5/RRR5-6/2	1868.509	1869.059	-832.290	0.588	1842.454	0.537	23	0.250	K.ISEEEYISAIKEEISK.V
R5/RRR5-5/2	1869.432	1869.059	199.651	0.601	1684.864	0.554	23	0.234	K.ISEEEYISAIKEEISK.V
R5/RRR5-5/2	1868.607	1869.059	-242.802	0.581	1730.190	0.521	23	0.231	K.ISEEEYISAIKEEISK.V
R5/RRR5-5/2	1869.070	1869.059	5.790	0.591	1619.151	0.545	22	0.222	K.ISEEEYISAIKEEISK.V
R5/RRR5-6/2	1868.592	1869.059	-250.733	0.555	1665.483	0.499	22	0.217	K.ISEEEYISAIKEEISK.V
R5/RRR5-1/3	1996.778	1997.232	-228.420	0.568	1737.152	0.526	33	0.216	K.KISEEEYISAIKEEISK.V
R5/RRR5-3/3	1997.384	1997.232	76.272	0.503	1660.979	0.514	34	0.200	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/3	1997.433	1997.232	100.820	0.604	1473.581	0.583	33	0.193	K.KISEEEYISAIKEEISK.V
R5/RRR5-3/3	1996.796	1997.232	-218.944	0.511	1744.269	0.457	35	0.192	K.KISEEEYISAIKEEISK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1997.598	1997.232	183.740	0.474	1493.682	0.542	33	0.183	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/3	1997.856	1997.232	-188.799	0.567	1486.313	0.537	33	0.180	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/2	1282.476	1282.422	42.425	0.443	1526.070	0.278	17	0.160	K.ISEEEYISAIK.E
R5/RRR5-5/2	1283.191	1282.422	-180.489	0.481	1301.635	0.375	17	0.159	K.ISEEEYISAIK.E
R5/RRR5-6/3	1996.763	1997.232	-235.779	0.481	1376.641	0.468	30	0.146	K.KISEEEYISAIKEEISK.V
R5/RRR5-4/3	1997.321	1997.232	44.368	0.510	1493.439	0.419	33	0.144	K.KISEEEYISAIKEEISK.V
R5/RRR5-6/3	1996.781	1997.232	-226.672	0.539	1070.527	0.491	29	0.121	K.KISEEEYISAIKEEISK.V
R5/RRR5-1/3	1997.087	1997.232	-73.061	0.491	805.187	0.453	28	0.099	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/3	1868.429	1869.059	-875.320	0.424	540.714	0.506	27	0.097	K.ISEEEYISAIKEEISK.V
R5/RRR5-6/3	1868.527	1869.059	-822.394	0.448	528.416	0.481	26	0.095	K.ISEEEYISAIKEEISK.V
R5/RRR5-4/3	1996.520	1997.232	-860.342	0.399	872.843	0.412	27	0.094	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/3	1868.745	1869.059	-168.920	0.419	430.407	0.450	24	0.091	K.ISEEEYISAIKEEISK.V
R5/RRR5-6/3	1868.860	1869.059	-106.901	0.360	459.453	0.448	24	0.089	K.ISEEEYISAIKEEISK.V
R5/RRR5-6/3	1867.600	1869.059	-1320.980	0.413	491.703	0.401	27	0.088	K.ISEEEYISAIKEEISK.V
R5/RRR5-4/3	1996.748	1997.232	-243.415	0.418	826.764	0.374	25	0.086	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/3	1996.725	1997.232	-757.330	0.369	507.850	0.372	22	0.085	K.KISEEEYISAIKEEISK.V
R5/RRR5-5/3	1868.426	1869.059	-876.796	0.365	566.714	0.310	27	0.079	K.ISEEEYISAIKEEISK.V
R5/RRR5-1/3	1997.209	1997.232	-11.631	0.341	574.515	0.301	23	0.078	K.KISEEEYISAIKEEISK.V
R5/RRR5-3/2	1852.619	1851.071	-244.436	0.600	2476.452	0.591	24	0.381	K.EIAWM*EEVIAAESSLR.A
R5/RRR5-3/2	1941.902	1941.152	-129.244	0.584	1401.006	0.578	19	0.203	R.SFITTDM*NPFYDAFVR.W
R5/RRR5-3/2	1307.293	1307.481	-144.288	0.390	1495.775	0.339	17	0.168	R.AALSLAYQNLSR.V
R5/RRR5-3/2	1196.129	1196.380	-210.721	0.451	1299.166	0.375	15	0.159	K.LGFYDLQLAR.D
R5/RRR5-3/2	1196.170	1196.380	-175.912	0.441	1311.847	0.337	16	0.154	K.LGFYDLQLAR.D
R5/RRR5-3/2	1354.082	1354.405	-238.855	0.455	815.937	0.440	20	0.143	R.QAIEEFSSDATR.F
R5/RRR5-3/2	1353.971	1354.405	-321.074	0.450	711.519	0.471	19	0.142	R.QAIEEFSSDATR.F
R5/RRR5-3/2	1355.110	1354.405	-218.255	0.436	714.784	0.423	20	0.138	R.QAIEEFSSDATR.F
R5/RRR5-3/2	1619.278	1618.813	288.488	0.530	687.148	0.421	18	0.131	R.ASGEGVQPQEYVLIK.M
R5/RRR5-3/2	1196.306	1196.380	-62.289	0.372	1015.817	0.289	14	0.130	K.LGFYDLQLAR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1618.498	1618.813	-194.840	0.470	782.112	0.345	19	0.127	R.ASGEGVQPQEYVLIK.M
R5/RRR5-3/2	1482.510	1481.719	-141.440	0.394	826.226	0.301	16	0.124	K.YGVKDEWVLPFK.V
R5/RRR5-3/2	1618.210	1618.813	-993.030	0.463	679.234	0.347	18	0.124	R.ASGEGVQPQEYVLIK.M
R5/RRR5-3/2	1452.204	1452.640	-301.126	0.296	678.050	0.380	17	0.122	K.AGWPIAGTPDPTLR.I
R5/RRR5-3/3	1882.085	1882.025	32.025	0.466	1047.197	0.501	32	0.121	R.QVGLEHAEVLSASNEAAR.A
R5/RRR5-3/2	1941.001	1941.152	-78.210	0.462	417.035	0.336	16	0.114	-.SFITTDM*NPFYDAFVR.-
R5/RRR5-3/2	1481.486	1481.719	-157.571	0.327	790.734	0.147	14	0.111	K.YGVKDEWVLPFK.V
R5/RRR5-3/3	1882.801	1882.025	-119.212	0.446	925.040	0.461	27	0.102	R.QVGLEHAEVLSASNEAAR.A
R5/RRR5-3/2	1307.258	1307.481	-170.798	0.191	459.134	0.256	11	0.096	-.AALSLAYQNLSR.-
R5/RRR5-3/3	1881.771	1882.025	-135.349	0.459	681.780	0.448	26	0.090	R.QVGLEHAEVLSASNEAAR.A
R5/RRR5-9/3	1076.915	1077.261	-322.157	0.322	1150.723	0.138	19	0.063	-.AGMHASM*LDK.-
R5/RRR5-10/2	1650.361	1650.767	-246.497	0.551	2847.218	0.551	25	0.447	K.SVIGETGSDVTTDQLK.E
R5/RRR5-10/2	1650.111	1650.767	-1006.332	0.521	2764.589	0.528	25	0.420	K.SVIGETGSDVTTDQLK.E
R5/RRR5-10/2	1651.147	1650.767	231.310	0.591	1913.525	0.553	23	0.266	K.SVIGETGSDVTTDQLK.E
R5/RRR5-10/2	1554.435	1553.781	-223.113	0.581	1791.627	0.534	22	0.245	K.YLTEDPLFQLVSK.L
R5/RRR5-10/2	1553.260	1553.781	-981.583	0.498	1629.432	0.484	20	0.212	K.YLTEDPLFQLVSK.L
R5/RRR5-10/2	1554.417	1553.781	-234.301	0.594	1482.223	0.527	21	0.206	K.YLTEDPLFQLVSK.L
R5/RRR5-10/2	1139.243	1139.328	-74.973	0.415	1300.943	0.462	17	0.175	R.LPAVASYVYR.R
R5/RRR5-10/2	1345.288	1345.529	-179.439	0.474	1188.544	0.505	18	0.173	R.SIGIGSQLIWDR.A
R5/RRR5-10/2	1552.576	1553.781	-1424.264	0.383	1319.471	0.413	19	0.166	K.YLTEDPLFQLVSK.L
R5/RRR5-10/2	1345.171	1345.529	-267.106	0.499	1130.460	0.488	17	0.165	R.SIGIGSQLIWDR.A
R5/RRR5-10/2	1139.082	1139.328	-216.974	0.383	1284.269	0.384	17	0.160	R.LPAVASYVYR.R
R5/RRR5-10/2	1345.437	1345.529	-68.306	0.400	1048.526	0.473	17	0.155	R.SIGIGSQLIWDR.A
R5/RRR5-10/2	1719.528	1720.052	-888.764	0.487	1019.233	0.482	19	0.152	K.VQLGNITVDMVLGGM*R.G
R5/RRR5-10/2	1138.893	1139.328	-382.998	0.378	978.048	0.445	16	0.148	R.LPAVASYVYR.R
R5/RRR5-10/2	1094.205	1094.332	-116.663	0.438	592.153	0.517	15	0.143	R.ALGLPLERPK.S
R5/RRR5-10/2	1094.160	1094.332	-157.735	0.420	600.031	0.523	15	0.143	R.ALGLPLERPK.S
R5/RRR5-10/2	1571.753	1571.882	-82.386	0.370	586.232	0.472	19	0.135	K.LYEVVPPILTELGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1094.112	1094.332	-201.609	0.415	502.011	0.462	14	0.134	R.ALGLPLERPK.S
R5/RRR5-10/2	1571.407	1571.882	-302.982	0.355	558.043	0.483	18	0.134	K.LYEVVPPILTELGK.V
R5/RRR5-10/2	1554.673	1553.781	-69.273	0.436	565.372	0.458	15	0.133	K.YLTEDPLFQLVSK.L
R5/RRR5-10/2	1571.599	1571.882	-180.633	0.373	435.482	0.462	16	0.130	K.LYEVVPPILTELGK.V
R5/RRR5-10/2	1204.702	1205.387	-1402.484	0.362	641.270	0.396	14	0.127	R.YYTVLFGVSR.S
R5/RRR5-10/2	1554.207	1553.781	275.516	0.473	776.595	0.349	16	0.127	K.YLTEDPLFQLVSK.L
R5/RRR5-10/2	1570.640	1571.882	-1431.503	0.247	351.895	0.329	15	0.120	K.LYEVVPPILTELGK.V
R5/RRR5-11/2	1571.623	1571.882	-165.283	0.262	246.802	0.430	12	0.117	-.LYEVVPPILTELGK.-
R5/RRR5-9/2	1572.436	1571.882	-284.719	0.288	405.181	0.389	13	0.115	-.LYEVVPPILTELGK.-
R5/RRR5-10/2	1138.029	1138.347	-280.006	0.122	175.634	0.573	15	0.105	-.VVPGFGHGVLR.-
R5/RRR5-20/3	1274.218	1274.574	-280.117	0.538	2555.666	0.225	25	0.266	R.VRFPCIQIIK.T
R5/RRR5-20/3	1274.437	1274.574	-107.284	0.535	2541.438	0.175	25	0.241	R.VRFPCIQIIK.T
R5/RRR5-20/2	1577.438	1576.776	-214.504	0.583	1587.876	0.501	21	0.210	K.SNGQILAINEIFEK.N
R5/RRR5-20/2	1576.249	1576.776	-971.151	0.559	1502.828	0.452	20	0.189	K.SNGQILAINEIFEK.N
R5/RRR5-20/2	1576.257	1576.776	-966.330	0.560	1387.645	0.447	20	0.177	K.SNGQILAINEIFEK.N
R5/RRR5-20/2	1133.959	1134.272	-276.692	0.397	1157.203	0.396	15	0.153	R.FHQYQVVGR.G
R5/RRR5-20/2	1133.996	1134.272	-243.968	0.399	980.832	0.417	14	0.146	R.FHQYQVVGR.G
R5/RRR5-20/2	1133.991	1134.272	-248.504	0.419	805.922	0.392	14	0.137	R.FHQYQVVGR.G
R5/RRR5-19/2	1576.496	1576.776	-177.664	0.444	939.138	0.392	16	0.136	K.SNGQILAINEIFEK.N
R5/RRR5-20/2	1274.955	1274.574	299.850	0.446	1176.144	0.275	15	0.136	R.VRFPCIQIIK.T
R5/RRR5-20/2	1191.875	1192.303	-360.323	0.333	327.501	0.600	14	0.135	R.GLPTPTDEHPK.I
R5/RRR5-21/2	1133.745	1134.272	-1351.275	0.353	840.453	0.319	14	0.129	R.FHQYQVVGR.G
R5/RRR5-20/3	1274.351	1274.574	-175.459	0.522	1958.949	0.153	24	0.129	R.VRFPCIQIIK.T
R5/RRR5-20/2	1192.158	1192.303	-122.380	0.280	378.665	0.539	15	0.129	R.GLPTPTDEHPK.I
R5/RRR5-20/2	1263.944	1264.479	-1218.108	0.429	1237.423	0.184	16	0.128	R.M*KLWATNEVR.A
R5/RRR5-20/2	1274.068	1274.574	-1185.631	0.432	1113.914	0.224	15	0.126	R.VRFPCIQIIK.T
R5/RRR5-20/2	1264.054	1264.479	-337.155	0.448	1037.448	0.223	15	0.124	R.M*KLWATNEVR.A
R5/RRR5-20/2	1191.488	1192.303	-1528.094	0.220	312.739	0.529	14	0.122	R.GLPTPTDEHPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	951.805	952.113	-325.004	0.349	713.597	0.404	12	0.121	K.ASRPNLFM*.-
R5/RRR5-20/2	951.839	952.113	-288.719	0.394	623.607	0.414	11	0.119	K.ASRPNLFM*.-
R5/RRR5-20/2	951.491	952.113	-1709.822	0.308	581.111	0.400	11	0.119	K.ASRPNLFM*.-
R5/RRR5-19/2	1577.757	1576.776	-11.532	0.408	491.275	0.324	14	0.118	-.SNGQILAINEIFEK.-
R5/RRR5-20/2	951.950	952.113	-171.644	0.264	565.579	0.277	10	0.114	K.ASRPNLFM*.-
R5/RRR5-20/2	951.801	952.113	-328.865	0.258	712.250	0.273	11	0.113	K.ASRPNLFM*.-
R5/RRR5-20/2	951.831	952.113	-296.696	0.223	679.712	0.255	11	0.112	K.ASRPNLFM*.-
R5/RRR5-20/2	1248.017	1248.480	-372.270	0.349	606.338	0.175	12	0.108	-.MKLWATNEVR.-
R5/RRR5-20/3	1238.612	1238.460	122.947	0.488	753.281	0.526	19	0.106	K.SDIKFPLVYR.K
R5/RRR5-20/3	1366.679	1366.633	34.068	0.549	916.526	0.406	23	0.096	K.SDIKFPLVYRK.V
R5/RRR5-20/3	1238.361	1238.460	-79.760	0.441	799.678	0.449	19	0.095	K.SDIKFPLVYR.K
R5/RRR5-20/3	1238.672	1238.460	171.573	0.432	845.008	0.437	20	0.094	K.SDIKFPLVYR.K
R5/RRR5-20/3	1366.523	1366.633	-80.433	0.414	406.903	0.308	17	0.077	-.SDIKFPLVYRK.-
R5/RRR5-7/2	1914.630	1915.178	-810.770	0.479	2712.262	0.541	26	0.413	K.DLGLLVESTTVEQLGIAR.K
R5/RRR5-7/2	1915.214	1915.178	18.756	0.551	2668.434	0.539	26	0.401	K.DLGLLVESTTVEQLGIAR.K
R5/RRR5-7/2	1914.391	1915.178	-936.225	0.490	2493.699	0.510	26	0.355	K.DLGLLVESTTVEQLGIAR.K
R5/RRR5-7/2	1637.288	1637.688	-244.876	0.497	2231.289	0.542	26	0.316	K.TNDSAGDGTTTASVLAR.E
R5/RRR5-7/2	1638.122	1637.688	266.036	0.558	2185.448	0.533	25	0.305	K.TNDSAGDGTTTASVLAR.E
R5/RRR5-7/2	1789.642	1789.066	-237.233	0.510	2097.629	0.513	23	0.284	K.ALLQDIAIVTGAEFQAK.D
R5/RRR5-7/2	1637.199	1637.688	-299.781	0.503	1913.925	0.538	25	0.263	K.TNDSAGDGTTTASVLAR.E
R5/RRR5-7/3	1788.748	1789.066	-177.980	0.490	2028.126	0.462	32	0.258	K.ALLQDIAIVTGAEFQAK.D
R5/RRR5-7/2	1788.443	1789.066	-909.736	0.465	1765.579	0.516	22	0.235	K.ALLQDIAIVTGAEFQAK.D
R5/RRR5-7/3	1789.286	1789.066	123.428	0.496	2029.820	0.391	31	0.229	K.ALLQDIAIVTGAEFQAK.D
R5/RRR5-7/2	1480.239	1480.646	-275.902	0.463	1366.249	0.496	20	0.187	R.GYISPQFVTNPEK.S
R5/RRR5-7/2	1480.175	1480.646	-319.258	0.452	1349.647	0.501	20	0.186	R.GYISPQFVTNPEK.S
R5/RRR5-7/2	1291.042	1291.347	-237.241	0.493	1414.235	0.458	19	0.185	K.VGAATETELEDR.K
R5/RRR5-7/2	1480.463	1480.646	-124.103	0.484	1215.403	0.471	19	0.169	R.GYISPQFVTNPEK.S
R5/RRR5-7/2	1291.119	1291.347	-177.105	0.548	1193.582	0.447	18	0.163	K.VGAATETELEDR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1064.963	1065.161	-187.238	0.366	1230.985	0.350	15	0.151	K.SLVEFENAR.I
R5/RRR5-7/2	1788.550	1789.066	-849.988	0.262	1165.085	0.431	17	0.150	K.ALLQDIAIVTGAEFQAK.D
R5/RRR5-7/2	898.653	899.113	-513.044	0.473	922.897	0.443	14	0.148	R.GILNVAAIK.A
R5/RRR5-7/2	1473.079	1473.478	-271.840	0.375	969.713	0.454	19	0.148	R.ELSQTDSAYDSEK.L
R5/RRR5-7/2	1064.558	1065.161	-1511.093	0.351	1110.849	0.374	14	0.146	K.SLVEFENAR.I
R5/RRR5-7/2	899.042	899.113	-78.798	0.467	831.182	0.457	14	0.145	R.GILNVAAIK.A
R5/RRR5-7/2	1065.097	1065.161	-60.421	0.439	1176.013	0.328	15	0.145	K.SLVEFENAR.I
R5/RRR5-7/2	1290.553	1291.347	-1394.193	0.434	1088.110	0.340	18	0.141	K.VGAATETELEDR.K
R5/RRR5-7/2	1472.986	1473.478	-335.113	0.320	849.034	0.430	18	0.137	R.ELSQTDSAYDSEK.L
R5/RRR5-7/2	898.565	899.113	-1727.423	0.401	742.230	0.438	13	0.136	-.GILNVAAIK.-
R5/RRR5-7/2	1472.414	1473.478	-1406.178	0.238	644.188	0.338	17	0.120	R.ELSQTDSAYDSEK.L
R5/RRR5-7/2	857.869	858.018	-174.208	0.517	992.145	0.192	13	0.119	R.LGADIIQK.A
R5/RRR5-7/2	857.950	858.018	-79.718	0.539	1036.324	0.186	13	0.118	R.LGADIIQK.A
R5/RRR5-7/2	857.870	858.018	-173.066	0.571	1061.141	0.167	13	0.114	R.LGADIIQK.A
R5/RRR5-7/3	1788.423	1789.066	-921.221	0.281	870.381	0.235	24	0.065	-.ALLQDIAIVTGAEFQAK.-
R5/RRR5-6/2	1690.189	1689.801	230.314	0.538	1860.350	0.620	21	0.277	K.YSNSQAVVYVGCGER.G
R5/RRR5-6/2	1256.240	1256.434	-154.343	0.463	1128.704	0.500	19	0.168	K.LAADTPLLTGQR.V
R5/RRR5-6/2	1256.225	1256.434	-166.430	0.444	1109.220	0.434	19	0.156	K.LAADTPLLTGQR.V
R5/RRR5-6/2	1256.208	1256.434	-180.468	0.445	987.305	0.470	18	0.153	K.LAADTPLLTGQR.V
R5/RRR5-6/2	1171.550	1171.284	227.868	0.491	895.327	0.334	16	0.132	K.LYDDLTAGFR.N
R5/RRR5-6/2	1596.639	1596.852	-133.323	0.559	2317.645	0.639	25	0.363	R.TGAATNVIFGLALGYK.S
R5/RRR5-6/2	1489.751	1490.598	-1243.276	0.423	2454.541	0.539	25	0.354	K.TDALDAAGNTTAAIGK.G
R5/RRR5-5/2	1489.509	1490.598	-1406.397	0.384	2316.280	0.478	24	0.309	K.TDALDAAGNTTAAIGK.G
R5/RRR5-5/2	1491.114	1490.598	-325.455	0.526	2005.603	0.593	24	0.291	K.TDALDAAGNTTAAIGK.G
R5/RRR5-6/2	1490.078	1490.598	-1022.875	0.418	2198.977	0.483	25	0.290	K.TDALDAAGNTTAAIGK.G
R5/RRR5-1/2	1490.138	1490.598	-309.893	0.474	2073.674	0.511	24	0.278	K.TDALDAAGNTTAAIGK.G
R5/RRR5-7/2	1489.542	1490.598	-1384.748	0.380	2254.646	0.397	24	0.275	K.TDALDAAGNTTAAIGK.G
R5/RRR5-3/2	1490.176	1490.598	-284.250	0.424	2012.156	0.534	24	0.274	K.TDALDAAGNTTAAIGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1491.058	1490.598	309.519	0.518	2026.998	0.521	24	0.273	K.TDALDAAGNTTAAIGK.G
R5/RRR5-2/2	1490.132	1490.598	-314.002	0.434	1985.739	0.509	23	0.263	K.TDALDAAGNTTAAIGK.G
R5/RRR5-1/2	1490.050	1490.598	-1042.040	0.455	1942.056	0.528	23	0.262	K.TDALDAAGNTTAAIGK.G
R5/RRR5-6/2	1490.141	1490.598	-307.509	0.461	1871.476	0.527	24	0.252	K.TDALDAAGNTTAAIGK.G
R5/RRR5-5/2	1491.128	1490.598	-315.927	0.549	1893.267	0.514	24	0.251	K.TDALDAAGNTTAAIGK.G
R5/RRR5-6/2	1596.574	1596.852	-174.510	0.534	1709.702	0.605	23	0.250	R.TGAATNVIFGLALGYK.S
R5/RRR5-2/2	1490.250	1490.598	-234.037	0.444	1789.714	0.526	23	0.240	K.TDALDAAGNTTAAIGK.G
R5/RRR5-1/2	1596.333	1596.852	-953.947	0.508	1709.131	0.557	23	0.238	R.TGAATNVIFGLALGYK.S
R5/RRR5-1/2	1400.189	1400.563	-267.716	0.485	1777.478	0.502	22	0.234	K.AADVGADLVGKVER.N
R5/RRR5-2/2	1400.233	1400.563	-236.054	0.458	1791.923	0.478	22	0.230	K.AADVGADLVGKVER.N
R5/RRR5-3/2	1490.103	1490.598	-333.235	0.426	1666.375	0.553	23	0.230	K.TDALDAAGNTTAAIGK.G
R5/RRR5-6/2	1596.255	1596.852	-1003.390	0.490	1585.851	0.581	21	0.227	R.TGAATNVIFGLALGYK.S
R5/RRR5-3/2	1490.216	1490.598	-256.801	0.435	1793.011	0.469	23	0.226	K.TDALDAAGNTTAAIGK.G
R5/RRR5-1/2	1399.697	1400.563	-1336.912	0.483	1669.114	0.508	22	0.222	K.AADVGADLVGKVER.N
R5/RRR5-1/3	1332.761	1332.447	236.445	0.539	1634.042	0.584	26	0.221	K.KYIEAGASEHAR.T
R5/RRR5-2/2	1490.199	1490.598	-268.306	0.457	1666.137	0.513	23	0.221	K.TDALDAAGNTTAAIGK.G
R5/RRR5-5/2	1400.204	1400.563	-257.395	0.489	1607.157	0.512	22	0.215	K.AADVGADLVGKVER.N
R5/RRR5-6/2	1400.077	1400.563	-348.104	0.466	1672.966	0.477	21	0.214	K.AADVGADLVGKVER.N
R5/RRR5-6/2	1400.344	1400.563	-157.083	0.463	1547.604	0.529	22	0.212	K.AADVGADLVGKVER.N
R5/RRR5-5/2	1596.032	1596.852	-1143.532	0.416	1501.869	0.564	21	0.212	R.TGAATNVIFGLALGYK.S
R5/RRR5-6/2	1270.170	1270.457	-227.066	0.361	1751.492	0.420	19	0.211	K.AAVIGDTIGDPLK.D
R5/RRR5-6/2	1401.104	1400.563	-328.362	0.537	1557.271	0.515	22	0.210	K.AADVGADLVGKVER.N
R5/RRR5-6/2	1270.033	1270.457	-335.256	0.393	1690.025	0.449	19	0.210	K.AAVIGDTIGDPLK.D
R5/RRR5-2/2	1400.254	1400.563	-221.448	0.479	1638.244	0.470	22	0.209	K.AADVGADLVGKVER.N
R5/RRR5-1/3	1332.781	1332.447	251.324	0.532	1492.175	0.594	25	0.201	K.KYIEAGASEHAR.T
R5/RRR5-2/2	1270.108	1270.457	-275.951	0.348	1720.454	0.374	19	0.197	K.AAVIGDTIGDPLK.D
R5/RRR5-2/2	1270.106	1270.457	-277.205	0.334	1615.764	0.390	19	0.189	K.AAVIGDTIGDPLK.D
R5/RRR5-1/2	1400.116	1400.563	-320.111	0.484	1529.679	0.429	21	0.188	K.AADVGADLVGKVER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1597.493	1596.852	-224.994	0.510	1226.480	0.584	19	0.187	R.TGAATNVIFGLALGYK.S
R5/RRR5-5/2	1400.302	1400.563	-186.991	0.461	1298.556	0.511	20	0.182	K.AADVGADLVGKVER.N
R5/RRR5-1/2	1595.919	1596.852	-1214.577	0.406	1263.355	0.472	19	0.169	R.TGAATNVIFGLALGYK.S
R5/RRR5-5/2	1595.823	1596.852	-1275.108	0.363	1268.070	0.472	19	0.169	R.TGAATNVIFGLALGYK.S
R5/RRR5-2/2	1399.519	1400.563	-1464.460	0.447	1125.913	0.493	20	0.165	K.AADVGADLVGKVER.N
R5/RRR5-2/2	1015.413	1016.130	-1696.667	0.422	1253.665	0.426	18	0.165	K.AADVGADLVGK.V
R5/RRR5-5/2	1400.024	1400.563	-1102.751	0.476	1151.905	0.449	19	0.159	K.AADVGADLVGKVER.N
R5/RRR5-3/2	1015.933	1016.130	-195.009	0.347	1262.536	0.387	18	0.158	K.AADVGADLVGK.V
R5/RRR5-1/3	1332.753	1332.447	230.245	0.524	1235.092	0.570	26	0.156	K.KYIEAGASEHAR.T
R5/RRR5-6/2	1015.143	1016.130	-1964.150	0.370	1143.952	0.424	17	0.155	K.AADVGADLVGK.V
R5/RRR5-1/2	1203.417	1204.274	-1547.640	0.318	1129.250	0.457	17	0.154	K.YIEAGASEHAR.T
R5/RRR5-2/2	1015.342	1016.130	-1767.088	0.380	1183.549	0.392	17	0.154	K.AADVGADLVGK.V
R5/RRR5-6/2	1015.936	1016.130	-191.995	0.447	1197.273	0.375	17	0.153	K.AADVGADLVGK.V
R5/RRR5-1/2	1015.406	1016.130	-1703.069	0.358	1021.778	0.416	17	0.147	K.AADVGADLVGK.V
R5/RRR5-5/3	1332.486	1332.447	29.062	0.594	1048.510	0.598	24	0.145	K.KYIEAGASEHAR.T
R5/RRR5-6/2	1230.971	1231.381	-334.158	0.379	1012.668	0.397	15	0.144	K.FTIFNFGEQK.E
R5/RRR5-1/2	1015.647	1016.130	-477.634	0.399	984.757	0.406	16	0.144	K.AADVGADLVGK.V
R5/RRR5-2/2	1015.363	1016.130	-1745.466	0.376	1015.417	0.369	17	0.142	K.AADVGADLVGK.V
R5/RRR5-1/2	1015.180	1016.130	-1926.689	0.368	1052.616	0.355	17	0.141	K.AADVGADLVGK.V
R5/RRR5-6/2	1232.206	1231.381	-142.548	0.500	997.590	0.373	15	0.141	K.FTIFNFGEQK.E
R5/RRR5-1/2	1258.202	1258.446	-194.973	0.285	1069.648	0.373	17	0.141	K.DTSGPSLNILIK.L
R5/RRR5-6/2	1015.236	1016.130	-1871.590	0.367	1035.219	0.359	16	0.140	K.AADVGADLVGK.V
R5/RRR5-3/2	1016.130	1016.130	-0.013	0.360	1064.708	0.333	17	0.139	K.AADVGADLVGK.V
R5/RRR5-2/2	1259.107	1258.446	-270.000	0.369	910.622	0.392	17	0.138	K.DTSGPSLNILIK.L
R5/RRR5-1/2	1231.105	1231.381	-225.321	0.399	845.922	0.383	14	0.136	K.FTIFNFGEQK.E
R5/RRR5-2/2	1258.545	1258.446	78.935	0.358	805.388	0.363	15	0.130	K.DTSGPSLNILIK.L
R5/RRR5-2/2	1231.281	1231.381	-81.401	0.347	839.888	0.314	14	0.128	K.FTIFNFGEQK.E
R5/RRR5-1/2	1231.003	1231.381	-308.389	0.346	920.650	0.273	15	0.127	K.FTIFNFGEQK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1231.254	1231.381	-103.678	0.292	701.467	0.353	13	0.126	K.FTIFNFGEQK.E
R5/RRR5-5/2	1230.610	1231.381	-1443.200	0.289	725.586	0.334	13	0.125	-.FTIFNFGEQK.-
R5/RRR5-6/2	1230.745	1231.381	-1333.314	0.301	571.529	0.337	13	0.124	K.FTIFNFGEQK.E
R5/RRR5-1/2	1595.952	1596.852	-1194.069	0.323	799.872	0.300	19	0.124	R.TGAATNVIFGLALGYK.S
R5/RRR5-1/2	1258.108	1258.446	-269.435	0.297	728.871	0.316	15	0.123	K.DTSGPSLNILIK.L
R5/RRR5-1/2	1231.024	1231.381	-290.780	0.369	817.079	0.245	14	0.122	K.FTIFNFGEQK.E
R5/RRR5-1/2	1258.227	1258.446	-174.631	0.242	826.408	0.251	17	0.120	K.DTSGPSLNILIK.L
R5/RRR5-6/3	1332.654	1332.447	155.844	0.495	897.940	0.507	23	0.112	K.KYIEAGASEHAR.T
R5/RRR5-7/3	1828.542	1829.068	-837.302	0.539	2482.361	0.365	33	0.323	K.GKVTEQVVDDPM*QIPR.S
R5/RRR5-7/2	1502.766	1502.732	23.170	0.519	1640.037	0.490	20	0.214	R.GCVLVASSPEILTR.V
R5/RRR5-7/2	1167.578	1168.368	-1537.365	0.365	1254.181	0.633	21	0.197	R.AALPVGTVSGAPK.V
R5/RRR5-7/2	1167.960	1168.368	-350.404	0.350	1395.358	0.552	21	0.196	R.AALPVGTVSGAPK.V
R5/RRR5-7/2	1167.409	1168.368	-1682.740	0.348	1119.836	0.577	21	0.174	R.AALPVGTVSGAPK.V
R5/RRR5-7/3	1829.364	1829.068	162.316	0.453	1665.156	0.410	28	0.172	K.GKVTEQVVDDPM*QIPR.S
R5/RRR5-7/2	1320.116	1320.347	-175.626	0.534	751.727	0.577	19	0.159	R.HATTEDAFQDGK.S
R5/RRR5-7/2	1320.098	1320.347	-188.706	0.521	765.151	0.565	19	0.157	R.HATTEDAFQDGK.S
R5/RRR5-7/2	1259.892	1260.379	-388.003	0.387	933.384	0.383	14	0.138	R.TYANPFEVYR.A
R5/RRR5-7/2	1260.250	1260.379	-103.041	0.300	797.594	0.467	13	0.137	R.TYANPFEVYR.A
R5/RRR5-7/2	1610.653	1609.874	-137.941	0.380	736.161	0.345	18	0.125	R.IVNPSPYMAYVQAR.G
R5/RRR5-7/2	1610.314	1609.874	274.128	0.385	672.516	0.338	18	0.124	R.IVNPSPYMAYVQAR.G
R5/RRR5-10/2	1645.346	1643.844	-303.597	0.386	880.275	0.302	17	0.123	K.VTEQVVDDPM*QIPR.S
R5/RRR5-7/2	1259.902	1260.379	-380.322	0.212	496.241	0.398	11	0.118	-.TYANPFEVYR.-
R5/RRR5-7/2	1434.510	1435.626	-1479.639	0.315	874.421	0.114	13	0.108	-.AM*ELIDELEVTR.-
R5/RRR5-7/3	1320.324	1320.347	-17.547	0.475	977.056	0.414	22	0.097	R.HATTEDAFQDGK.S
R5/RRR5-7/3	1211.617	1210.454	134.933	0.397	584.603	0.509	23	0.091	K.IINRPLAGTVR.R
R5/RRR5-7/3	1610.244	1609.874	230.410	0.391	1017.510	0.327	22	0.083	-.IVNPSPYMAYVQAR.-
R5/RRR5-7/3	1211.167	1210.454	-238.038	0.238	342.536	0.339	20	0.075	K.IINRPLAGTVR.R
R5/RRR5-9/2	1505.198	1504.744	302.463	0.500	1711.670	0.510	21	0.228	K.ECILSGLLSVDGLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/3	1625.925	1626.798	-1155.122	0.483	1744.216	0.468	31	0.202	R.FRGEDKPPAHLGSSK.D
R5/RRR5-9/2	1503.989	1504.744	-1170.776	0.298	1641.808	0.420	20	0.196	K.ECILSGLLSVDGLK.V
R5/RRR5-9/2	1503.781	1504.744	-1309.513	0.317	1220.543	0.420	18	0.156	K.ECILSGLLSVDGLK.V
R5/RRR5-9/2	1072.987	1073.180	-181.159	0.459	645.071	0.497	15	0.143	K.AVDGSYVFSK.G
R5/RRR5-9/2	1072.788	1073.180	-366.995	0.428	698.388	0.453	16	0.140	K.AVDGSYVFSK.G
R5/RRR5-9/2	1072.880	1073.180	-281.260	0.447	707.033	0.437	16	0.139	K.AVDGSYVFSK.G
R5/RRR5-9/2	1863.721	1864.003	-151.795	0.449	841.510	0.457	18	0.139	R.NFFIYVQDYNEADPK.T
R5/RRR5-9/2	1419.215	1419.608	-277.413	0.471	923.935	0.376	19	0.137	R.YLNEPAIDTVKR.M
R5/RRR5-9/2	922.979	923.048	-74.898	0.393	609.148	0.402	13	0.133	K.LYAESLAR.F
R5/RRR5-9/2	1072.954	1073.180	-211.747	0.386	600.656	0.425	15	0.133	K.AVDGSYVFSK.G
R5/RRR5-9/2	1090.986	1091.261	-252.509	0.341	398.596	0.517	14	0.130	K.VPATDM*EALK.S
R5/RRR5-9/2	922.997	923.048	-55.264	0.376	622.330	0.352	13	0.129	K.LYAESLAR.F
R5/RRR5-9/2	922.437	923.048	-1752.271	0.376	547.986	0.359	12	0.128	K.LYAESLAR.F
R5/RRR5-9/3	1628.103	1626.798	188.214	0.454	1231.977	0.445	29	0.125	R.FRGEDKPPAHLGSSK.D
R5/RRR5-9/2	922.403	923.048	-1788.439	0.328	548.110	0.249	12	0.120	-.LYAESLAR.-
R5/RRR5-9/3	1626.819	1626.798	13.192	0.482	1432.622	0.325	29	0.116	R.FRGEDKPPAHLGSSK.D
R5/RRR5-9/3	1469.214	1469.732	-1036.313	0.500	1121.631	0.364	25	0.099	K.IHKVPATDM*EALK.S
R5/RRR5-9/3	1468.308	1469.732	-1655.594	0.406	1078.651	0.367	24	0.095	K.IHKVPATDM*EALK.S
R5/RRR5-9/3	1805.873	1805.970	-53.542	0.469	1163.717	0.334	27	0.095	R.DDRYLNEPAIDTVKR.M
R5/RRR5-9/3	1469.377	1469.732	-241.981	0.464	996.731	0.357	25	0.090	K.IHKVPATDM*EALK.S
R5/RRR5-9/3	1805.368	1805.970	-890.093	0.459	1027.478	0.321	26	0.084	R.DDRYLNEPAIDTVKR.M
R5/RRR5-7/3	1901.971	1902.181	-110.543	0.456	2167.813	0.479	35	0.298	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-7/3	1861.840	1862.072	-124.599	0.509	2195.080	0.421	35	0.278	K.VTVSKDDTVILDGAGDKK.S
R5/RRR5-7/2	1434.202	1434.684	-337.138	0.476	2284.321	0.342	21	0.265	R.GISM*AVDAVVTNLK.G
R5/RRR5-7/2	1433.983	1434.684	-1189.987	0.465	2158.803	0.363	21	0.252	R.GISM*AVDAVVTNLK.G
R5/RRR5-7/2	1321.104	1321.461	-271.323	0.466	1805.275	0.535	19	0.247	R.NVVIEQSYGSPK.V
R5/RRR5-7/2	1321.029	1321.461	-327.782	0.464	1804.156	0.527	19	0.245	R.NVVIEQSYGSPK.V
R5/RRR5-7/2	1418.254	1418.685	-304.363	0.448	1982.181	0.378	20	0.231	R.GISMAVDAVVTNLK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1434.231	1434.684	-316.814	0.433	2077.042	0.324	20	0.230	R.GISM*AVDAVVTNLK.G
R5/RRR5-7/2	1321.047	1321.461	-314.617	0.475	1642.321	0.529	18	0.224	R.NVVIEQSYGSPK.V
R5/RRR5-7/2	1901.511	1902.181	-880.817	0.454	1478.703	0.585	29	0.215	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-7/2	1901.441	1902.181	-917.875	0.502	1393.405	0.624	27	0.215	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-7/2	1147.052	1147.218	-144.485	0.510	1500.373	0.483	19	0.198	K.IGGASEAEVGEK.K
R5/RRR5-7/2	1386.117	1386.576	-332.088	0.494	1329.398	0.557	19	0.196	R.GYISPYFVTNPK.T
R5/RRR5-7/2	1386.154	1386.576	-305.405	0.461	1209.676	0.563	18	0.185	R.GYISPYFVTNPK.T
R5/RRR5-7/2	1387.146	1386.576	-311.012	0.475	1185.442	0.561	18	0.183	R.GYISPYFVTNPK.T
R5/RRR5-7/2	1147.141	1147.218	-67.199	0.483	1301.893	0.489	18	0.179	K.IGGASEAEVGEK.K
R5/RRR5-7/2	1268.140	1268.447	-242.616	0.450	1388.853	0.399	19	0.171	K.SVAAGM*NAM*DLR.R
R5/RRR5-8/2	1901.062	1902.181	-1118.033	0.434	1131.114	0.534	25	0.170	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-7/2	1586.396	1586.679	-178.871	0.533	1110.759	0.507	18	0.165	R.SAIELSTSDYDKEK.L
R5/RRR5-7/2	1586.184	1586.679	-313.359	0.482	1187.189	0.467	19	0.165	R.SAIELSTSDYDKEK.L
R5/RRR5-7/2	1268.231	1268.447	-170.675	0.462	1231.374	0.389	18	0.156	K.SVAAGM*NAM*DLR.R
R5/RRR5-7/2	1900.856	1902.181	-1226.623	0.384	931.623	0.543	25	0.156	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-7/2	1586.150	1586.679	-967.328	0.497	1097.550	0.444	18	0.154	R.SAIELSTSDYDKEK.L
R5/RRR5-7/2	1030.877	1031.142	-257.445	0.467	1151.042	0.362	16	0.148	-.GVEELADAVK.-
R5/RRR5-7/2	1031.020	1031.142	-118.588	0.437	1106.478	0.371	16	0.147	R.GVEELADAVK.V
R5/RRR5-1/2	1900.881	1902.181	-1213.403	0.332	513.823	0.388	20	0.122	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-7/3	1861.599	1862.072	-254.444	0.485	1350.079	0.383	31	0.122	K.VTVSKDDTVILDGAGDKK.S
R5/RRR5-7/3	1901.478	1902.181	-898.161	0.354	1198.344	0.439	30	0.119	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-8/2	1032.044	1031.142	-95.574	0.263	718.591	0.233	14	0.118	R.GVEELADAVK.V
R5/RRR5-8/3	1901.812	1902.181	-194.277	0.397	1104.945	0.458	29	0.116	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-7/3	1862.371	1862.072	161.317	0.521	1041.701	0.434	28	0.105	K.VTVSKDDTVILDGAGDKK.S
R5/RRR5-7/3	1901.466	1902.181	-904.348	0.289	997.738	0.373	29	0.089	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-8/3	1901.192	1902.181	-1049.185	0.326	701.158	0.429	27	0.086	K.AAVEEGIVPGGGVALLYASK.E
R5/RRR5-8/2	1444.091	1444.573	-334.611	0.425	2327.230	0.331	20	0.270	K.AESLDDAIQIVNR.N
R5/RRR5-9/2	1967.726	1968.071	-176.252	0.530	1855.603	0.597	24	0.269	R.ADEHVDVTNPATQEVVSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1443.565	1444.573	-1395.181	0.380	2182.664	0.313	19	0.244	K.AESLDDAIQIVNR.N
R5/RRR5-9/2	1443.706	1444.573	-1296.752	0.376	2127.743	0.275	19	0.226	K.AESLDDAIQIVNR.N
R5/RRR5-9/3	1967.875	1968.071	-100.091	0.410	1854.820	0.464	32	0.223	R.ADEHVDVTNPATQEVVSR.I
R5/RRR5-9/2	1203.997	1204.312	-262.935	0.572	1583.208	0.508	18	0.213	K.LAENITTEQGK.T
R5/RRR5-9/2	1163.049	1163.305	-221.241	0.441	1599.397	0.430	17	0.197	R.IPLTTADEFR.A
R5/RRR5-8/2	1162.477	1163.305	-1577.183	0.390	1628.075	0.417	17	0.197	R.IPLTTADEFR.A
R5/RRR5-8/2	1163.037	1163.305	-231.349	0.435	1595.361	0.412	17	0.193	R.IPLTTADEFR.A
R5/RRR5-9/2	1162.520	1163.305	-1540.158	0.394	1538.431	0.428	16	0.190	R.IPLTTADEFR.A
R5/RRR5-8/2	1162.843	1163.305	-398.695	0.455	1449.957	0.442	16	0.185	R.IPLTTADEFR.A
R5/RRR5-9/2	1203.399	1204.312	-1594.363	0.489	1286.627	0.489	18	0.179	K.LAENITTEQGK.T
R5/RRR5-9/3	1967.406	1968.071	-848.989	0.438	1271.095	0.537	27	0.154	R.ADEHVDVTNPATQEVVSR.I
R5/RRR5-9/2	1162.531	1163.305	-1530.348	0.396	1286.247	0.337	15	0.152	R.IPLTTADEFR.A
R5/RRR5-8/2	1220.364	1220.400	-29.257	0.393	1125.352	0.392	18	0.150	R.LLIGGEFVESR.A
R5/RRR5-9/3	1967.741	1968.071	-168.324	0.424	1240.190	0.496	29	0.139	R.ADEHVDVTNPATQEVVSR.I
R5/RRR5-8/2	1588.707	1588.703	2.265	0.452	780.733	0.483	17	0.137	K.YGNGASIFTTSGVSAR.K
R5/RRR5-8/2	1934.912	1933.303	-202.873	0.397	1025.058	0.345	20	0.131	K.DPGAAM*MLAELAMEAGLPK.G
R5/RRR5-8/2	1444.345	1444.573	-157.723	0.327	1180.312	0.224	15	0.128	K.AESLDDAIQIVNR.N
R5/RRR5-9/2	1093.579	1094.265	-1546.369	0.345	699.177	0.362	14	0.125	R.VSLSM*PTSQK.-
R5/RRR5-9/2	1444.342	1444.573	-159.927	0.269	937.544	0.256	16	0.123	K.AESLDDAIQIVNR.N
R5/RRR5-8/2	1220.767	1220.400	301.325	0.267	530.688	0.278	16	0.119	R.LLIGGEFVESR.A
R5/RRR5-13/2	1101.945	1102.183	-217.176	0.398	833.507	0.234	15	0.117	-.LIQSGADNGAR.-
R5/RRR5-8/3	1967.436	1968.071	-833.574	0.418	1066.327	0.471	27	0.115	R.ADEHVDVTNPATQEVVSR.I
R5/RRR5-13/2	1101.532	1102.183	-1503.275	0.281	740.540	0.134	15	0.112	K.LIQSGADNGAR.V
R5/RRR5-8/3	1967.355	1968.071	-875.243	0.375	864.721	0.401	25	0.089	R.ADEHVDVTNPATQEVVSR.I
R5/RRR5-13/3	1940.205	1940.190	7.306	0.589	3637.679	0.628	38	0.923	K.VLIAVADNVGSNQLQEIR.K
R5/RRR5-13/3	1940.557	1940.190	189.393	0.574	3556.831	0.640	38	0.895	K.VLIAVADNVGSNQLQEIR.K
R5/RRR5-13/3	1940.496	1940.190	157.977	0.603	3587.197	0.601	37	0.876	K.VLIAVADNVGSNQLQEIR.K
R5/RRR5-13/2	1939.644	1940.190	-799.873	0.549	2848.402	0.542	28	0.443	K.VLIAVADNVGSNQLQEIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1743.494	1743.942	-257.487	0.520	2656.252	0.620	33	0.430	K.FAVAAPVAADSGAAAPSAAK.E
R5/RRR5-13/2	1743.443	1743.942	-287.130	0.564	2450.267	0.603	32	0.379	K.FAVAAPVAADSGAAAPSAAK.E
R5/RRR5-13/2	1743.328	1743.942	-928.222	0.549	2206.725	0.651	31	0.347	K.FAVAAPVAADSGAAAPSAAK.E
R5/RRR5-13/2	1939.657	1940.190	-793.050	0.562	2332.131	0.544	26	0.334	K.VLIAVADNVGSNQLQEIR.K
R5/RRR5-13/2	1940.402	1940.190	109.564	0.584	2302.541	0.514	27	0.318	K.VLIAVADNVGSNQLQEIR.K
R5/RRR5-13/2	1767.000	1768.131	-1209.510	0.503	1990.776	0.492	22	0.261	K.INKGTVEIITPVELIK.K
R5/RRR5-13/2	1768.382	1768.131	142.170	0.537	1730.566	0.504	21	0.227	K.INKGTVEIITPVELIK.K
R5/RRR5-13/2	1411.023	1411.619	-1134.416	0.512	1401.506	0.469	17	0.185	K.KLCQLLDEYTK.V
R5/RRR5-13/2	1411.200	1411.619	-297.815	0.508	1281.054	0.459	16	0.172	K.KLCQLLDEYTK.V
R5/RRR5-13/2	1540.482	1540.870	-252.316	0.478	1442.390	0.371	19	0.168	K.GTVEIITPVELIKK.G
R5/RRR5-13/2	1411.967	1411.619	247.514	0.553	1114.226	0.488	16	0.165	K.KLCQLLDEYTK.V
R5/RRR5-13/2	1540.060	1540.870	-1178.733	0.440	1054.830	0.408	18	0.145	K.GTVEIITPVELIKK.G
R5/RRR5-16/2	1411.721	1412.697	-1403.842	0.354	1078.847	0.332	17	0.138	K.GTVEIITPVELIK.K
R5/RRR5-13/2	1412.328	1412.697	-261.600	0.382	922.117	0.370	16	0.135	K.GTVEIITPVELIK.K
R5/RRR5-15/2	1411.916	1412.697	-1265.075	0.275	943.691	0.372	16	0.134	K.GTVEIITPVELIK.K
R5/RRR5-13/2	1061.952	1062.199	-233.310	0.420	755.078	0.362	17	0.133	K.VGSSESALLAK.L
R5/RRR5-13/2	1362.232	1362.511	-205.789	0.389	760.223	0.426	18	0.132	K.GDKVGSSESALLAK.L
R5/RRR5-14/2	1411.937	1412.697	-1250.054	0.336	741.427	0.419	15	0.132	K.GTVEIITPVELIK.K
R5/RRR5-13/2	1061.937	1062.199	-247.956	0.413	725.275	0.340	17	0.130	K.VGSSESALLAK.L
R5/RRR5-13/2	1061.615	1062.199	-1496.829	0.346	699.035	0.324	17	0.127	K.VGSSESALLAK.L
R5/RRR5-13/2	1940.187	1940.190	-1.742	0.392	734.912	0.392	18	0.127	K.VLIAVADNVGSNQLQEIR.K
R5/RRR5-12/2	1061.419	1062.199	-1682.476	0.295	650.212	0.340	16	0.125	K.VGSSESALLAK.L
R5/RRR5-12/2	1061.795	1062.199	-381.519	0.302	713.028	0.288	17	0.124	K.VGSSESALLAK.L
R5/RRR5-12/2	1413.443	1412.697	-179.795	0.359	731.005	0.320	13	0.122	K.GTVEIITPVELIK.K
R5/RRR5-15/2	1061.963	1062.199	-223.392	0.330	754.482	0.234	17	0.121	K.VGSSESALLAK.L
R5/RRR5-13/2	1411.729	1412.697	-1398.023	0.288	669.528	0.279	14	0.119	K.GTVEIITPVELIK.K
R5/RRR5-14/2	1412.457	1412.697	-169.866	0.224	589.230	0.285	13	0.117	K.GTVEIITPVELIK.K
R5/RRR5-15/2	1412.369	1412.697	-232.812	0.313	510.847	0.270	12	0.116	-.GTVEIITPVELIK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/3	1767.520	1768.131	-914.209	0.392	1460.079	0.297	30	0.112	K.INKGTVEIITPVELIK.K
R5/RRR5-13/2	1412.193	1412.697	-1068.192	0.300	818.900	0.105	14	0.110	K.GTVEIITPVELIK.K
R5/RRR5-13/3	1743.731	1743.942	-121.102	0.434	1302.914	0.347	34	0.108	K.FAVAAPVAADSGAAAPSAAK.E
R5/RRR5-16/2	1411.502	1412.697	-1559.501	0.215	423.769	0.264	11	0.108	-.GTVEIITPVELIK.-
R5/RRR5-13/3	1362.140	1362.511	-273.226	0.440	685.925	0.433	25	0.086	-.GDKVGSSESALLAK.-
R5/RRR5-13/3	1362.328	1362.511	-135.009	0.406	828.772	0.369	27	0.083	K.GDKVGSSESALLAK.L
R5/RRR5-16/3	1940.864	1940.190	-168.541	0.400	801.412	0.382	22	0.082	K.VLIAVADNVGSNQLQEIR.K
R5/RRR5-13/2	1817.401	1817.036	201.796	0.605	2614.971	0.681	35	0.446	K.FAVAAPVAAADSGAAAVAASK.E
R5/RRR5-13/3	1816.947	1817.036	-49.240	0.420	1472.193	0.473	33	0.163	K.FAVAAPVAAADSGAAAVAASK.E
R5/RRR5-7/2	1473.749	1474.730	-1347.829	0.412	2302.647	0.498	23	0.314	R.LGANSLLDIVVFGR.A
R5/RRR5-7/2	1475.068	1474.730	230.202	0.552	2040.781	0.572	22	0.292	R.LGANSLLDIVVFGR.A
R5/RRR5-7/2	1474.565	1474.730	-112.144	0.535	2055.304	0.552	21	0.288	R.LGANSLLDIVVFGR.A
R5/RRR5-7/2	1475.167	1474.730	297.084	0.549	1839.476	0.588	22	0.266	R.LGANSLLDIVVFGR.A
R5/RRR5-7/2	1791.496	1790.992	-277.857	0.534	1658.738	0.616	22	0.246	R.AAIGLSEHGFNTACITK.L
R5/RRR5-7/2	1474.288	1474.730	-300.601	0.495	1695.825	0.491	20	0.220	R.LGANSLLDIVVFGR.A
R5/RRR5-7/2	1474.273	1474.730	-310.985	0.513	1564.440	0.518	20	0.211	R.LGANSLLDIVVFGR.A
R5/RRR5-7/2	1295.126	1295.427	-233.184	0.504	1452.168	0.539	20	0.205	R.ATNTILATGGYGR.A
R5/RRR5-7/2	1294.279	1295.427	-1664.514	0.389	1461.452	0.464	20	0.188	R.ATNTILATGGYGR.A
R5/RRR5-7/2	1609.405	1608.819	-258.399	0.552	1051.527	0.563	20	0.173	K.AVIELENYGLPFSR.T
R5/RRR5-7/2	1609.389	1608.819	-267.911	0.507	1079.031	0.551	20	0.172	K.AVIELENYGLPFSR.T
R5/RRR5-7/2	1165.906	1166.336	-369.296	0.528	1200.420	0.481	17	0.172	R.VM*QNNAAVFR.T
R5/RRR5-7/2	1294.711	1295.427	-1329.098	0.325	1413.454	0.399	19	0.170	R.ATNTILATGGYGR.A
R5/RRR5-6/2	1608.513	1608.819	-190.798	0.381	1166.555	0.485	21	0.166	K.AVIELENYGLPFSR.T
R5/RRR5-7/2	1165.983	1166.336	-303.327	0.469	1373.568	0.367	16	0.164	R.VM*QNNAAVFR.T
R5/RRR5-7/2	1128.056	1127.231	-156.035	0.501	1065.353	0.468	18	0.160	R.AFGGQSLDFGK.G
R5/RRR5-6/2	1608.969	1608.819	93.019	0.476	1064.116	0.478	20	0.159	K.AVIELENYGLPFSR.T
R5/RRR5-7/2	1165.970	1166.336	-314.462	0.487	1238.291	0.383	17	0.158	R.VM*QNNAAVFR.T
R5/RRR5-7/2	1127.107	1127.231	-110.977	0.477	1084.980	0.445	18	0.157	R.AFGGQSLDFGK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1608.249	1608.819	-979.539	0.344	1174.290	0.414	20	0.154	K.AVIELENYGLPFSR.T
R5/RRR5-7/2	1116.054	1116.338	-255.240	0.342	1025.234	0.398	14	0.143	K.TIAWLDKLR.N
R5/RRR5-7/2	1115.601	1116.338	-1561.142	0.393	1012.926	0.367	14	0.140	K.TIAWLDKLR.N
R5/RRR5-6/2	1294.888	1295.427	-1191.624	0.361	951.239	0.378	18	0.137	R.ATNTILATGGYGR.A
R5/RRR5-6/2	1264.049	1263.340	-231.072	0.399	524.426	0.472	16	0.134	K.HSLGYWENEK.V
R5/RRR5-1/2	1476.200	1474.730	319.601	0.295	501.515	0.356	14	0.121	R.LGANSLLDIVVFGR.A
R5/RRR5-6/2	1607.431	1608.819	-1490.066	0.218	696.371	0.265	16	0.117	K.AVIELENYGLPFSR.T
R5/RRR5-7/3	1791.087	1790.992	53.168	0.409	778.977	0.554	27	0.108	R.AAIGLSEHGFNTACITK.L
R5/RRR5-7/3	1790.823	1790.992	-94.296	0.400	775.425	0.556	26	0.108	R.AAIGLSEHGFNTACITK.L
R5/RRR5-6/3	1518.976	1518.658	210.199	0.566	802.894	0.421	22	0.092	K.HSLGYWENEKVR.L
R5/RRR5-2/3	1861.835	1861.132	-159.913	0.518	2262.010	0.457	35	0.315	R.ATLAQLGFEKLDDIIGR.T
R5/RRR5-2/2	1459.101	1459.670	-1078.492	0.426	1950.215	0.562	24	0.274	K.LVAEAGIGTVASGVSK.G
R5/RRR5-2/2	1906.741	1907.199	-240.900	0.523	1794.482	0.499	26	0.236	R.FGVTPTFLVNAEQIEIK.I
R5/RRR5-2/2	1906.511	1907.199	-887.819	0.499	1694.090	0.475	26	0.217	R.FGVTPTFLVNAEQIEIK.I
R5/RRR5-2/2	1459.315	1459.670	-244.452	0.424	1429.033	0.609	22	0.213	K.LVAEAGIGTVASGVSK.G
R5/RRR5-2/2	1276.252	1276.379	-99.255	0.444	1408.762	0.520	19	0.194	K.GLQNGDTATSAIK.Q
R5/RRR5-2/2	1907.765	1907.199	-228.320	0.513	1542.594	0.438	24	0.191	R.FGVTPTFLVNAEQIEIK.I
R5/RRR5-2/2	1853.393	1852.985	220.537	0.559	1105.443	0.619	22	0.185	K.SVASANPYGSWLQQSTR.S
R5/RRR5-2/2	1144.484	1144.303	158.158	0.441	1537.469	0.392	18	0.183	K.IGGLTLDELGR.E
R5/RRR5-2/3	1908.480	1907.199	147.604	0.508	1526.616	0.503	29	0.181	R.FGVTPTFLVNAEQIEIK.I
R5/RRR5-2/2	1219.174	1219.321	-120.773	0.488	1305.197	0.436	18	0.171	K.VLCDEADAAVR.N
R5/RRR5-2/2	1520.850	1521.699	-1219.141	0.284	1414.988	0.374	19	0.165	K.VFTDEGLEVLGWR.T
R5/RRR5-2/2	1156.085	1156.273	-162.736	0.448	1294.731	0.400	15	0.163	K.TFQIYNVDR.A
R5/RRR5-2/3	1907.797	1907.199	-211.509	0.448	1583.923	0.413	31	0.160	R.FGVTPTFLVNAEQIEIK.I
R5/RRR5-2/2	1458.604	1459.670	-1421.171	0.347	1068.905	0.493	20	0.156	K.LVAEAGIGTVASGVSK.G
R5/RRR5-2/2	1853.369	1852.985	207.856	0.512	755.764	0.558	19	0.148	K.SVASANPYGSWLQQSTR.S
R5/RRR5-2/2	1219.978	1219.321	-281.871	0.407	980.640	0.379	16	0.139	K.VLCDEADAAVR.N
R5/RRR5-2/2	1048.980	1049.245	-253.936	0.358	780.677	0.412	16	0.135	K.YLLSSAGLPK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1520.846	1521.699	-1221.559	0.273	1282.561	0.195	18	0.131	K.VFTDEGLEVLGWR.T
R5/RRR5-2/2	1520.771	1521.699	-1271.052	0.264	1036.340	0.260	17	0.126	K.VFTDEGLEVLGWR.T
R5/RRR5-2/2	1049.043	1049.245	-193.697	0.214	386.479	0.407	11	0.112	-.YLLSSAGLPK.-
R5/RRR5-15/2	1940.433	1940.234	103.063	0.629	4465.121	0.551	30	0.942	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-15/2	1939.589	1940.234	-850.711	0.584	4565.303	0.475	30	0.938	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-15/2	1939.587	1940.234	-851.469	0.607	4028.626	0.528	29	0.773	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-15/3	1865.576	1866.072	-266.535	0.545	2950.997	0.420	38	0.494	R.GLRDAADLVALSGGHTVGR.T
R5/RRR5-14/2	1939.363	1940.234	-967.605	0.571	3088.642	0.486	27	0.476	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-4/2	1941.267	1940.234	16.991	0.564	2735.654	0.483	27	0.393	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-15/3	1939.741	1940.234	-254.672	0.438	2073.551	0.409	35	0.247	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-15/3	1940.506	1940.234	140.846	0.495	1837.736	0.488	34	0.230	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-14/2	1276.631	1277.451	-1430.112	0.428	1843.100	0.420	18	0.223	R.VQDLIDLFASR.G
R5/RRR5-16/2	1277.249	1277.451	-158.898	0.571	1550.863	0.539	18	0.216	R.VQDLIDLFASR.G
R5/RRR5-16/2	1277.242	1277.451	-164.267	0.514	1548.358	0.509	18	0.209	R.VQDLIDLFASR.G
R5/RRR5-16/2	1276.974	1277.451	-375.046	0.508	1588.782	0.471	18	0.205	R.VQDLIDLFASR.G
R5/RRR5-16/2	1539.275	1539.676	-261.263	0.474	1490.040	0.490	22	0.196	R.DAADLVALSGGHTVGR.T
R5/RRR5-15/2	1277.148	1277.451	-237.905	0.586	1478.173	0.487	17	0.195	R.VQDLIDLFASR.G
R5/RRR5-15/2	1277.020	1277.451	-338.983	0.507	1527.393	0.450	18	0.194	R.VQDLIDLFASR.G
R5/RRR5-15/2	1539.345	1539.676	-215.279	0.486	1325.981	0.557	22	0.194	R.DAADLVALSGGHTVGR.T
R5/RRR5-14/2	1278.113	1277.451	-265.410	0.561	1357.385	0.520	17	0.191	R.VQDLIDLFASR.G
R5/RRR5-15/2	1277.304	1277.451	-115.373	0.545	1486.148	0.458	18	0.191	R.VQDLIDLFASR.G
R5/RRR5-15/2	1539.348	1539.676	-213.290	0.475	1332.230	0.533	22	0.189	R.DAADLVALSGGHTVGR.T
R5/RRR5-15/2	1860.354	1859.999	190.936	0.541	1375.097	0.488	20	0.180	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-15/2	1539.262	1539.676	-269.697	0.480	1217.014	0.535	21	0.179	R.DAADLVALSGGHTVGR.T
R5/RRR5-14/2	1277.068	1277.451	-301.388	0.519	1306.755	0.457	17	0.175	R.VQDLIDLFASR.G
R5/RRR5-15/3	1859.650	1859.999	-188.328	0.489	1409.628	0.541	31	0.174	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-15/2	1744.469	1744.970	-862.974	0.506	1061.428	0.578	23	0.174	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-15/2	1859.350	1859.999	-890.006	0.485	1339.506	0.466	20	0.174	R.GGSNSEQGM*GPNLTLQPR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1939.648	1940.234	-819.888	0.337	1828.150	0.325	33	0.170	R.SSVQAALQQEIALAAGLLR.I
R5/RRR5-14/2	1745.509	1744.970	-264.485	0.525	971.661	0.579	22	0.167	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-16/2	1539.185	1539.676	-319.666	0.475	1091.175	0.500	21	0.163	R.DAADLVALSGGHTVGR.T
R5/RRR5-16/2	1744.700	1744.970	-155.273	0.495	1020.571	0.512	23	0.160	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-15/2	1859.388	1859.999	-869.114	0.495	1242.298	0.441	19	0.160	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-15/2	1744.382	1744.970	-912.851	0.444	892.800	0.546	22	0.156	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-16/2	1744.527	1744.970	-254.597	0.489	814.097	0.533	21	0.150	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-15/3	1859.879	1859.999	-64.774	0.483	1365.825	0.478	31	0.149	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-15/2	1744.424	1744.970	-888.685	0.461	848.184	0.489	21	0.145	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-14/2	1056.980	1057.226	-233.365	0.447	1144.577	0.336	13	0.143	R.ALQLVEDIR.A
R5/RRR5-16/2	1744.209	1744.970	-1012.480	0.388	834.687	0.477	21	0.142	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-16/2	1057.002	1057.226	-212.510	0.460	1092.069	0.337	13	0.141	R.ALQLVEDIR.A
R5/RRR5-12/2	1057.952	1057.226	-259.421	0.397	1009.209	0.357	13	0.140	R.ALQLVEDIR.A
R5/RRR5-15/2	1057.061	1057.226	-156.669	0.467	1128.396	0.330	13	0.139	-.ALQLVEDIR.-
R5/RRR5-16/2	1056.552	1057.226	-1589.292	0.369	1108.610	0.314	13	0.139	-.ALQLVEDIR.-
R5/RRR5-15/2	1057.026	1057.226	-189.570	0.429	1072.474	0.321	13	0.138	-.ALQLVEDIR.-
R5/RRR5-14/2	1744.497	1744.970	-271.727	0.447	832.075	0.428	21	0.137	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-14/2	1744.337	1744.970	-938.986	0.425	669.228	0.479	19	0.135	R.DAVVVSGGPSYAVPLGQK.D
R5/RRR5-15/2	1056.521	1057.226	-1618.774	0.384	1008.588	0.323	13	0.135	-.ALQLVEDIR.-
R5/RRR5-16/2	1057.950	1057.226	-261.736	0.497	1079.740	0.297	13	0.133	-.ALQLVEDIR.-
R5/RRR5-1/2	1057.103	1057.226	-116.357	0.385	1029.995	0.244	13	0.128	R.ALQLVEDIR.A
R5/RRR5-15/2	1030.956	1031.188	-226.192	0.293	955.751	0.294	14	0.126	K.AAFFTQFAK.S
R5/RRR5-14/2	1058.141	1057.226	-80.257	0.506	1065.337	0.260	13	0.125	-.ALQLVEDIR.-
R5/RRR5-1/2	1056.532	1057.226	-1607.515	0.310	1015.403	0.225	13	0.121	-.ALQLVEDIR.-
R5/RRR5-15/3	1539.892	1539.676	141.033	0.433	1060.266	0.486	28	0.119	R.DAADLVALSGGHTVGR.T
R5/RRR5-15/3	1859.068	1859.999	-1041.854	0.354	1237.830	0.416	30	0.118	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-14/3	1541.057	1539.676	248.144	0.442	1052.509	0.470	29	0.115	R.DAADLVALSGGHTVGR.T
R5/RRR5-11/2	1058.064	1057.226	-153.628	0.385	850.826	0.251	12	0.111	-.ALQLVEDIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/3	1540.255	1539.676	-273.864	0.331	1097.824	0.438	27	0.110	R.DAADLVALSGGHTVGR.T
R5/RRR5-15/3	1540.691	1539.676	10.035	0.478	993.659	0.458	29	0.109	R.DAADLVALSGGHTVGR.T
R5/RRR5-15/3	1540.751	1539.676	49.013	0.428	958.882	0.470	28	0.108	R.DAADLVALSGGHTVGR.T
R5/RRR5-11/2	1057.243	1057.226	16.490	0.278	724.585	0.145	12	0.103	-.ALQLVEDIR.-
R5/RRR5-2/2	1056.523	1057.226	-1615.988	0.311	594.022	0.246	11	0.100	-.ALQLVEDIR.-
R5/RRR5-16/3	1859.589	1859.999	-221.419	0.376	1005.966	0.360	26	0.089	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-16/3	1867.570	1866.072	267.697	0.340	955.174	0.311	26	0.077	R.GLRDAADLVALSGGHTVGR.T
R5/RRR5-14/3	1539.082	1539.676	-1038.365	0.310	830.333	0.313	23	0.076	R.DAADLVALSGGHTVGR.T
R5/RRR5-14/3	1859.975	1859.999	-13.425	0.262	836.722	0.287	28	0.072	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-15/3	1276.850	1277.451	-1258.236	0.351	1060.595	0.220	20	0.070	-.VQDLIDLFASR.-
R5/RRR5-16/3	1858.899	1859.999	-1133.535	0.298	815.074	0.230	25	0.066	R.GGSNSEQGM*GPNLTLQPR.A
R5/RRR5-16/3	1867.933	1866.072	-74.246	0.265	687.174	0.175	25	0.058	-.GLRDAADLVALSGGHTVGR.-
R5/RRR5-14/3	1584.827	1584.823	2.797	0.552	1969.726	0.415	29	0.220	R.KKIEYSM*QLNASR.I
R5/RRR5-14/3	1584.720	1584.823	-64.883	0.536	1878.836	0.375	28	0.189	R.KKIEYSM*QLNASR.I
R5/RRR5-14/2	1152.790	1153.307	-1319.710	0.435	1269.472	0.534	18	0.185	R.FCSGGVVLASR.D
R5/RRR5-14/2	1153.126	1153.307	-157.633	0.481	1114.718	0.481	17	0.164	R.FCSGGVVLASR.D
R5/RRR5-14/2	1191.301	1191.310	-7.874	0.386	1306.567	0.389	17	0.162	K.IVCENTLDAR.L
R5/RRR5-14/2	1152.513	1153.307	-1561.286	0.402	1065.064	0.472	17	0.157	R.FCSGGVVLASR.D
R5/RRR5-15/2	1191.130	1191.310	-152.192	0.467	1149.079	0.402	17	0.155	K.IVCENTLDAR.L
R5/RRR5-15/2	1190.865	1191.310	-374.919	0.418	1127.003	0.389	17	0.151	K.IVCENTLDAR.L
R5/RRR5-16/2	1191.119	1191.310	-161.239	0.458	1161.968	0.337	17	0.146	K.IVCENTLDAR.L
R5/RRR5-14/2	1783.309	1782.884	239.022	0.550	850.737	0.464	20	0.142	K.ASEISVSAEEEFNIEK.L
R5/RRR5-14/2	1027.073	1027.243	-165.416	0.400	1088.917	0.341	14	0.142	K.ELVVQGLLR.L
R5/RRR5-14/2	1783.496	1782.884	-217.799	0.525	896.986	0.437	19	0.140	K.ASEISVSAEEEFNIEK.L
R5/RRR5-16/2	1191.276	1191.310	-29.046	0.408	973.892	0.369	16	0.138	-.IVCENTLDAR.-
R5/RRR5-14/2	1027.277	1027.243	33.776	0.370	996.541	0.306	14	0.133	K.ELVVQGLLR.L
R5/RRR5-14/2	1782.551	1782.884	-186.868	0.489	815.964	0.406	18	0.132	K.ASEISVSAEEEFNIEK.L
R5/RRR5-14/2	1026.747	1027.243	-483.858	0.371	860.226	0.324	13	0.130	K.ELVVQGLLR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/3	1584.692	1584.823	-82.732	0.536	1294.265	0.421	25	0.125	R.KKIEYSM*QLNASR.I
R5/RRR5-15/2	1026.550	1027.243	-1653.750	0.311	716.339	0.301	12	0.121	-.ELVVQGLLR.-
R5/RRR5-14/3	1457.673	1456.650	16.229	0.572	1193.296	0.421	26	0.116	K.KIEYSM*QLNASR.I
R5/RRR5-14/3	1619.682	1619.809	-78.180	0.489	1136.682	0.393	26	0.105	R.VSHNHHEYKNLLK.E
R5/RRR5-14/3	1456.980	1456.650	227.037	0.509	1222.715	0.335	26	0.100	K.KIEYSM*QLNASR.I
R5/RRR5-14/2	976.992	977.182	-195.450	0.351	668.100	0.540	12	0.099	R.KLLFGQVTA.-
R5/RRR5-14/2	976.602	977.182	-1623.116	0.308	638.396	0.531	12	0.098	R.KLLFGQVTA.-
R5/RRR5-14/3	1457.683	1456.650	22.780	0.490	1057.160	0.348	24	0.092	K.KIEYSM*QLNASR.I
R5/RRR5-14/2	977.035	977.182	-150.579	0.307	727.490	0.284	12	0.088	R.KLLFGQVTA.-
R5/RRR5-14/3	1567.289	1568.823	-2261.941	0.475	1057.750	0.320	23	0.087	R.KKIEYSMQLNASR.I
R5/RRR5-14/3	1619.741	1619.809	-42.120	0.483	783.676	0.343	23	0.081	R.VSHNHHEYKNLLK.E
R5/RRR5-14/3	1569.707	1568.823	-74.624	0.408	980.241	0.270	23	0.076	R.KKIEYSMQLNASR.I
R5/RRR5-15/2	1686.806	1687.833	-1205.679	0.414	3343.185	0.445	26	0.530	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-16/3	1773.241	1773.021	124.545	0.544	3129.778	0.356	35	0.509	R.ARVEAELSNICAGILR.L
R5/RRR5-16/2	1687.089	1687.833	-1037.253	0.401	2973.339	0.481	26	0.450	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-15/2	1687.546	1687.833	-170.761	0.482	2901.891	0.520	26	0.447	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-15/3	1773.662	1773.021	-203.241	0.594	2792.939	0.413	35	0.429	R.ARVEAELSNICAGILR.L
R5/RRR5-16/2	1773.446	1773.021	240.489	0.556	2781.033	0.540	24	0.425	R.ARVEAELSNICAGILR.L
R5/RRR5-15/3	1772.758	1773.021	-148.817	0.507	2929.248	0.319	35	0.422	R.ARVEAELSNICAGILR.L
R5/RRR5-16/2	1771.834	1773.021	-1237.858	0.511	2708.188	0.519	23	0.402	R.ARVEAELSNICAGILR.L
R5/RRR5-15/2	1687.217	1687.833	-960.543	0.430	2745.327	0.488	25	0.400	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-16/2	1687.310	1687.833	-905.197	0.460	2763.702	0.455	25	0.391	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-16/2	1687.263	1687.833	-933.595	0.475	2720.227	0.480	24	0.391	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-15/2	1954.142	1955.136	-1023.263	0.495	2470.028	0.591	26	0.379	K.DAADATLAAYQAAQDIAM*K.E
R5/RRR5-16/2	1771.399	1773.021	-2050.858	0.473	2520.784	0.514	22	0.361	R.ARVEAELSNICAGILR.L
R5/RRR5-15/2	1772.328	1773.021	-958.352	0.520	2381.549	0.492	23	0.326	R.ARVEAELSNICAGILR.L
R5/RRR5-15/2	1545.392	1545.757	-236.382	0.511	2410.787	0.460	23	0.322	R.VEAELSNICAGILR.L
R5/RRR5-15/2	1545.226	1545.757	-993.739	0.487	2381.020	0.418	23	0.304	R.VEAELSNICAGILR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1545.341	1545.757	-269.745	0.534	2293.953	0.449	23	0.298	R.VEAELSNICAGILR.L
R5/RRR5-16/2	1545.365	1545.757	-254.292	0.532	2312.180	0.425	23	0.293	R.VEAELSNICAGILR.L
R5/RRR5-15/2	1545.316	1545.757	-286.151	0.486	2276.390	0.425	23	0.288	R.VEAELSNICAGILR.L
R5/RRR5-16/2	1544.898	1545.757	-1206.742	0.407	2354.982	0.372	23	0.287	R.VEAELSNICAGILR.L
R5/RRR5-15/2	1773.513	1773.021	278.381	0.521	2006.020	0.487	22	0.261	R.ARVEAELSNICAGILR.L
R5/RRR5-15/2	1772.475	1773.021	-874.828	0.521	1927.373	0.521	21	0.258	R.ARVEAELSNICAGILR.L
R5/RRR5-16/3	1938.499	1939.136	-847.280	0.511	1829.816	0.525	33	0.242	K.DAADATLAAYQAAQDIAMK.E
R5/RRR5-15/3	1773.694	1773.021	-184.703	0.490	1914.064	0.405	31	0.210	R.ARVEAELSNICAGILR.L
R5/RRR5-16/3	1939.814	1939.136	-166.739	0.544	1682.728	0.504	33	0.205	K.DAADATLAAYQAAQDIAMK.E
R5/RRR5-16/2	1375.979	1375.510	341.990	0.466	1120.428	0.505	18	0.168	R.IVSSIEQKEEGR.G
R5/RRR5-15/2	1025.923	1026.212	-282.199	0.363	331.582	0.625	16	0.142	R.LVPAAAAVDAK.V
R5/RRR5-16/2	1025.967	1026.212	-238.748	0.384	333.779	0.590	16	0.141	R.LVPAAAAVDAK.V
R5/RRR5-16/2	1025.629	1026.212	-1547.796	0.271	458.413	0.480	16	0.128	R.LVPAAAAVDAK.V
R5/RRR5-15/2	1025.818	1026.212	-384.635	0.305	280.938	0.434	14	0.128	R.LVPAAAAVDAK.V
R5/RRR5-16/3	1955.189	1955.136	27.343	0.436	1257.362	0.433	33	0.124	K.DAADATLAAYQAAQDIAM*K.E
R5/RRR5-16/2	1375.161	1375.510	-254.960	0.449	800.480	0.274	16	0.121	R.IVSSIEQKEEGR.G
R5/RRR5-16/2	1375.029	1375.510	-350.794	0.411	768.932	0.249	16	0.119	R.IVSSIEQKEEGR.G
R5/RRR5-16/3	1687.817	1687.833	-9.483	0.424	954.958	0.429	29	0.099	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-16/2	1025.861	1026.212	-342.607	0.196	142.754	0.418	10	0.098	-.LVPAAAAVDAK.-
R5/RRR5-15/3	1687.826	1687.833	-4.260	0.381	882.652	0.407	24	0.089	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-16/3	1687.771	1687.833	-37.122	0.417	687.907	0.420	26	0.086	K.VVTAAAAGGGGELTVEER.N
R5/RRR5-15/3	1954.486	1955.136	-846.654	0.264	656.538	0.269	22	0.066	K.DAADATLAAYQAAQDIAM*K.E
R5/RRR5-7/2	1629.341	1629.877	-945.668	0.463	1950.963	0.523	24	0.265	R.SLAIGQCDVALVVGAR.L
R5/RRR5-7/2	1908.161	1908.144	9.136	0.542	1727.133	0.477	21	0.218	R.GDFQELDQIAATKPFVK.I
R5/RRR5-7/2	1629.485	1629.877	-241.014	0.492	1614.821	0.523	22	0.218	R.SLAIGQCDVALVVGAR.L
R5/RRR5-7/2	1687.432	1687.988	-924.918	0.421	1243.299	0.484	22	0.170	R.HM*FGVVGIPVTSLASR.A
R5/RRR5-7/2	1492.141	1492.662	-1022.118	0.351	385.562	0.566	17	0.130	K.GVVPDTHPLSATAAR.S
R5/RRR5-7/2	1703.437	1704.024	-934.613	0.389	464.839	0.522	17	0.128	-.LVDTTGIPFLPTPM*GK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1025.875	1026.172	-289.612	0.329	892.943	0.303	13	0.125	R.AVLVQNEPR.T
R5/RRR5-7/3	1121.668	1121.315	316.364	0.452	996.030	0.451	22	0.106	R.KPHVGIVGDAK.R
R5/RRR5-7/3	1121.420	1121.315	93.871	0.434	902.469	0.457	22	0.100	R.KPHVGIVGDAK.R
R5/RRR5-7/3	1120.885	1121.315	-384.521	0.419	705.871	0.456	20	0.092	R.KPHVGIVGDAK.R
R5/RRR5-7/3	1971.889	1971.246	-181.909	0.368	1227.019	0.306	27	0.091	R.KPAVINVIIDPYAGAESGR.M
R5/RRR5-7/3	1451.919	1451.696	154.005	0.391	986.785	0.332	23	0.082	R.LNWLLHFGEPPK.W
R5/RRR5-5/2	1879.476	1880.066	-848.660	0.561	1339.309	0.611	25	0.209	R.M*KEGQSEIYYITGESK.K
R5/RRR5-5/2	1879.437	1880.066	-869.458	0.555	976.878	0.584	22	0.170	R.M*KEGQSEIYYITGESK.K
R5/RRR5-5/3	1880.466	1880.066	213.589	0.554	1409.139	0.526	26	0.169	R.M*KEGQSEIYYITGESK.K
R5/RRR5-5/3	1879.766	1880.066	-159.842	0.512	1532.678	0.468	27	0.169	R.M*KEGQSEIYYITGESK.K
R5/RRR5-5/3	1865.745	1864.066	-172.834	0.500	1609.227	0.421	29	0.165	R.MKEGQSEIYYITGESK.K
R5/RRR5-5/2	1604.101	1604.696	-997.261	0.433	1033.294	0.473	18	0.152	K.EGQSEIYYITGESK.K
R5/RRR5-5/3	1879.756	1880.066	-165.314	0.512	1225.338	0.521	25	0.144	R.M*KEGQSEIYYITGESK.K
R5/RRR5-6/2	1309.267	1309.414	-112.650	0.381	685.135	0.515	19	0.138	K.VNPAHAAAAASGGSK.N
R5/RRR5-5/2	1772.173	1771.950	125.768	0.602	2435.062	0.502	24	0.339	R.LYLDQYGGSGDVWIGK.V
R5/RRR5-5/2	1771.541	1771.950	-231.778	0.527	2212.873	0.513	24	0.304	R.LYLDQYGGSGDVWIGK.V
R5/RRR5-5/2	1772.583	1771.950	-207.743	0.571	2142.375	0.498	23	0.286	R.LYLDQYGGSGDVWIGK.V
R5/RRR5-5/2	1386.668	1386.581	62.813	0.462	1490.446	0.432	18	0.185	R.VALLADAVSSHFR.R
R5/RRR5-5/2	1417.604	1418.677	-1466.506	0.478	904.351	0.446	15	0.144	R.MTLFCNDLYLK.A
R5/RRR5-5/2	1417.355	1418.677	-1642.640	0.427	997.924	0.386	16	0.141	R.MTLFCNDLYLK.A
R5/RRR5-5/2	1381.408	1381.585	-128.304	0.422	963.918	0.410	15	0.141	R.GLSFIQENMWR.L
R5/RRR5-5/2	1243.965	1244.412	-360.293	0.387	843.839	0.453	14	0.140	K.CFEYLDGIVK.K
R5/RRR5-5/2	1618.255	1617.778	295.405	0.450	892.248	0.377	21	0.138	K.DLDLDIPYDEPALK.A
R5/RRR5-5/2	1617.295	1617.778	-299.457	0.432	717.545	0.424	19	0.136	K.DLDLDIPYDEPALK.A
R5/RRR5-5/2	1118.967	1118.263	-265.299	0.438	814.983	0.380	15	0.135	R.VLQGCSAINR.L
R5/RRR5-5/2	1617.419	1617.778	-222.903	0.365	869.430	0.340	19	0.131	K.DLDLDIPYDEPALK.A
R5/RRR5-1/2	1118.629	1118.263	328.509	0.370	745.688	0.349	14	0.129	R.VLQGCSAINR.L
R5/RRR5-5/2	1118.076	1118.263	-167.283	0.375	837.361	0.324	14	0.129	R.VLQGCSAINR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1618.145	1617.778	227.175	0.455	548.718	0.423	17	0.129	-.DLDLDIPYDEPALK.-
R5/RRR5-5/2	1033.126	1033.120	6.564	0.330	868.875	0.295	15	0.127	K.FPGDDGVLGR.A
R5/RRR5-5/2	1118.069	1118.263	-173.855	0.365	799.806	0.284	15	0.125	R.VLQGCSAINR.L
R5/RRR5-6/2	1617.484	1617.778	-182.397	0.435	432.218	0.378	15	0.125	K.DLDLDIPYDEPALK.A
R5/RRR5-5/2	1111.090	1111.232	-128.555	0.372	879.353	0.250	15	0.123	R.LYGYQVDPR.V
R5/RRR5-2/2	1618.308	1617.778	-291.553	0.332	416.304	0.333	14	0.120	-.DLDLDIPYDEPALK.-
R5/RRR5-4/2	1617.396	1617.778	-237.289	0.323	529.518	0.265	15	0.119	K.DLDLDIPYDEPALK.A
R5/RRR5-1/2	1617.471	1617.778	-190.271	0.352	463.760	0.288	15	0.119	-.DLDLDIPYDEPALK.-
R5/RRR5-5/2	1032.962	1033.120	-153.094	0.305	524.282	0.264	13	0.117	-.FPGDDGVLGR.-
R5/RRR5-3/2	1618.213	1617.778	269.536	0.356	421.228	0.293	14	0.116	-.DLDLDIPYDEPALK.-
R5/RRR5-6/2	1033.058	1033.120	-59.569	0.267	1213.456	0.048	16	0.115	K.FPGDDGVLGR.A
R5/RRR5-3/2	1387.667	1386.581	62.061	0.242	357.314	0.361	11	0.115	R.VALLADAVSSHFR.R
R5/RRR5-4/2	1032.409	1033.120	-1661.798	0.259	492.488	0.225	11	0.107	-.FPGDDGVLGR.-
R5/RRR5-14/2	1594.290	1594.754	-292.182	0.546	2796.680	0.598	26	0.454	R.VADHAGVALAGLTADGR.V
R5/RRR5-14/2	1594.349	1594.754	-254.696	0.539	2604.421	0.573	26	0.401	R.VADHAGVALAGLTADGR.V
R5/RRR5-14/2	1595.463	1594.754	-182.919	0.562	2383.646	0.632	24	0.375	R.VADHAGVALAGLTADGR.V
R5/RRR5-14/2	1717.192	1717.856	-972.368	0.551	2531.622	0.503	24	0.362	R.FEGYNDYTPEQLIK.D
R5/RRR5-14/2	1429.283	1428.678	-277.343	0.589	2166.514	0.488	19	0.287	R.LFQVEYAMEAVK.Q
R5/RRR5-14/2	1712.436	1711.770	-196.021	0.586	1902.387	0.598	23	0.279	R.NQYDTDVTTWSPAGR.L
R5/RRR5-14/2	1718.361	1717.856	-288.827	0.580	1955.939	0.522	23	0.266	R.FEGYNDYTPEQLIK.D
R5/RRR5-14/2	1377.997	1378.551	-1131.218	0.443	2122.886	0.413	21	0.261	K.LTSSNCTVAIVGR.K
R5/RRR5-14/2	1444.181	1444.678	-344.601	0.544	2081.450	0.404	19	0.250	R.LFQVEYAM*EAVK.Q
R5/RRR5-14/2	1428.205	1428.678	-332.247	0.477	2114.369	0.377	20	0.249	R.LFQVEYAMEAVK.Q
R5/RRR5-14/2	1712.269	1711.770	292.271	0.569	1681.166	0.547	21	0.232	R.NQYDTDVTTWSPAGR.L
R5/RRR5-14/2	1379.106	1378.551	-323.745	0.495	1780.740	0.473	20	0.228	K.LTSSNCTVAIVGR.K
R5/RRR5-14/2	1444.186	1444.678	-341.040	0.501	1780.502	0.419	18	0.214	R.LFQVEYAM*EAVK.Q
R5/RRR5-14/2	1711.244	1711.770	-894.397	0.491	1610.175	0.497	21	0.212	R.NQYDTDVTTWSPAGR.L
R5/RRR5-14/2	1503.155	1503.680	-1017.724	0.468	1633.474	0.439	21	0.202	K.DALSAIKETLQGEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1443.586	1444.678	-1453.180	0.421	1801.206	0.317	18	0.194	R.LFQVEYAM*EAVK.Q
R5/RRR5-14/2	1378.016	1378.551	-1116.986	0.454	1598.362	0.420	19	0.194	K.LTSSNCTVAIVGR.K
R5/RRR5-14/2	1504.292	1503.680	-258.793	0.503	1497.894	0.469	20	0.193	K.DALSAIKETLQGEK.L
R5/RRR5-14/2	1428.553	1428.678	-88.073	0.448	1345.046	0.420	18	0.170	R.LFQVEYAMEAVK.Q
R5/RRR5-14/2	1503.390	1503.680	-193.470	0.442	1175.229	0.446	18	0.159	K.DALSAIKETLQGEK.L
R5/RRR5-14/2	1873.072	1874.043	-1055.124	0.509	1006.181	0.467	19	0.151	R.RFEGYNDYTPEQLIK.D
R5/RRR5-14/2	1872.698	1874.043	-1255.985	0.490	611.207	0.435	16	0.129	R.RFEGYNDYTPEQLIK.D
R5/RRR5-14/2	1872.528	1874.043	-1882.690	0.480	660.659	0.407	17	0.128	R.RFEGYNDYTPEQLIK.D
R5/RRR5-14/3	1503.647	1503.680	-22.044	0.398	960.465	0.480	28	0.107	K.DALSAIKETLQGEK.L
R5/RRR5-14/3	1503.079	1503.680	-1068.614	0.459	805.326	0.486	27	0.101	K.DALSAIKETLQGEK.L
R5/RRR5-14/3	1895.834	1896.112	-147.100	0.478	1008.927	0.424	27	0.100	R.KDDGTVEPFEM*IDVKR.I
R5/RRR5-14/3	1503.355	1503.680	-217.021	0.411	758.679	0.484	25	0.097	K.DALSAIKETLQGEK.L
R5/RRR5-14/3	1595.862	1594.754	67.881	0.440	1071.327	0.344	24	0.088	R.VADHAGVALAGLTADGR.V
R5/RRR5-14/3	1594.651	1594.754	-64.704	0.338	798.108	0.364	24	0.079	-.VADHAGVALAGLTADGR.-
R5/RRR5-14/3	1594.756	1594.754	1.288	0.328	885.833	0.299	23	0.073	R.VADHAGVALAGLTADGR.V
R5/RRR5-4/2	1579.437	1579.672	-149.001	0.557	1948.192	0.508	24	0.260	K.VM*ANADTPEDATTAR.Q
R5/RRR5-4/2	1578.763	1579.672	-1212.965	0.507	1893.124	0.486	24	0.247	K.VM*ANADTPEDATTAR.Q
R5/RRR5-1/2	1579.784	1579.672	71.370	0.581	1714.979	0.534	23	0.234	K.VM*ANADTPEDATTAR.Q
R5/RRR5-4/2	1445.323	1445.667	-238.771	0.429	1703.361	0.391	19	0.199	K.IAVDMVNEGLVER.R
R5/RRR5-4/2	1372.038	1372.501	-338.441	0.425	1339.426	0.417	18	0.169	K.AGLDYVSCSPFR.V
R5/RRR5-4/2	970.962	971.048	-88.976	0.413	1019.933	0.392	13	0.145	R.SDFEGIFR.A
R5/RRR5-4/2	970.504	971.048	-1595.845	0.312	1085.739	0.334	13	0.138	R.SDFEGIFR.A
R5/RRR5-4/3	1976.023	1976.215	-97.447	0.459	1506.383	0.372	30	0.138	K.VGICGEHGGEPLSVAFFAK.A
R5/RRR5-4/2	1372.090	1372.501	-300.772	0.440	819.669	0.424	15	0.136	-.AGLDYVSCSPFR.-
R5/RRR5-4/2	973.937	974.180	-250.246	0.399	742.628	0.325	15	0.129	R.SINKITGLK.G
R5/RRR5-5/2	973.925	974.180	-262.694	0.351	838.115	0.298	15	0.128	R.SINKITGLK.G
R5/RRR5-4/2	973.903	974.180	-284.701	0.415	682.324	0.323	14	0.128	R.SINKITGLK.G
R5/RRR5-4/2	974.134	974.180	-47.335	0.433	661.096	0.316	14	0.127	R.SINKITGLK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1371.923	1372.501	-1154.075	0.323	492.036	0.267	11	0.114	-.AGLDYVSCSPFR.-
R5/RRR5-4/3	1386.620	1386.472	107.395	0.489	998.965	0.336	20	0.086	R.TEHM*FFASDER.I
R5/RRR5-6/2	1717.359	1717.987	-950.742	0.483	1816.105	0.612	25	0.269	K.KVPVVVGNCTGFAVNR.T
R5/RRR5-6/2	1635.485	1635.906	-258.771	0.421	2021.031	0.482	23	0.262	R.ASDLDIASILGMGFPK.F
R5/RRR5-6/2	1650.806	1651.906	-1275.615	0.376	1761.160	0.528	23	0.235	R.ASDLDIASILGM*GFPK.F
R5/RRR5-6/2	1248.802	1249.443	-1317.956	0.550	1726.755	0.480	16	0.223	R.LWALEIANYR.K
R5/RRR5-6/2	1248.768	1249.443	-1345.445	0.446	1652.357	0.491	16	0.216	R.LWALEIANYR.K
R5/RRR5-6/2	1635.247	1635.906	-1018.025	0.345	1811.396	0.376	22	0.208	R.ASDLDIASILGMGFPK.F
R5/RRR5-6/2	1652.451	1651.906	-276.079	0.533	1455.857	0.557	22	0.207	R.ASDLDIASILGM*GFPK.F
R5/RRR5-6/2	1249.049	1249.443	-316.088	0.507	1535.771	0.415	17	0.188	R.LWALEIANYR.K
R5/RRR5-6/2	1628.209	1628.769	-961.064	0.523	1119.088	0.606	25	0.187	R.SLPLSAPNATQQASSR.S
R5/RRR5-6/2	1628.282	1628.769	-300.069	0.513	1121.976	0.572	25	0.181	R.SLPLSAPNATQQASSR.S
R5/RRR5-5/2	1653.105	1651.906	120.869	0.539	1196.380	0.552	20	0.179	R.ASDLDIASILGM*GFPK.F
R5/RRR5-6/2	1651.257	1651.906	-1001.440	0.383	1275.630	0.521	20	0.179	R.ASDLDIASILGM*GFPK.F
R5/RRR5-6/2	1628.357	1628.769	-253.813	0.497	1067.050	0.544	25	0.171	R.SLPLSAPNATQQASSR.S
R5/RRR5-6/2	1530.357	1530.739	-249.825	0.451	1217.584	0.411	19	0.158	R.GLVDALCSPDELIK.M
R5/RRR5-1/2	1651.703	1651.906	-123.427	0.442	1192.407	0.428	20	0.157	R.ASDLDIASILGM*GFPK.F
R5/RRR5-6/3	1457.006	1456.709	204.308	0.507	1601.109	0.389	28	0.154	K.TSPQAILDLITVGK.M
R5/RRR5-6/2	1530.520	1530.739	-143.083	0.420	1209.329	0.381	18	0.152	R.GLVDALCSPDELIK.M
R5/RRR5-5/2	1531.885	1530.739	95.782	0.451	1083.331	0.417	17	0.148	R.GLVDALCSPDELIK.M
R5/RRR5-6/2	1530.135	1530.739	-1050.989	0.398	1056.689	0.387	17	0.142	R.GLVDALCSPDELIK.M
R5/RRR5-2/2	1653.511	1651.906	-239.619	0.362	851.358	0.461	18	0.140	R.ASDLDIASILGM*GFPK.F
R5/RRR5-6/2	1455.939	1456.709	-1219.927	0.382	628.191	0.487	19	0.138	K.TSPQAILDLITVGK.M
R5/RRR5-5/2	1457.320	1456.709	-268.143	0.344	727.297	0.467	19	0.138	K.TSPQAILDLITVGK.M
R5/RRR5-6/2	1456.076	1456.709	-1125.467	0.414	748.005	0.437	19	0.138	K.TSPQAILDLITVGK.M
R5/RRR5-6/2	1175.176	1175.424	-211.659	0.366	887.814	0.367	16	0.134	K.M*IAANLEGLVK.R
R5/RRR5-6/3	1456.562	1456.709	-101.771	0.489	1397.209	0.406	27	0.133	K.TSPQAILDLITVGK.M
R5/RRR5-6/2	1309.209	1309.540	-253.588	0.316	672.645	0.488	15	0.132	K.VPGVTDVQLKPR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1457.403	1456.709	-210.917	0.324	691.596	0.371	18	0.128	K.TSPQAILDLITVGK.M
R5/RRR5-2/2	1455.851	1456.709	-1280.552	0.325	428.290	0.464	14	0.127	K.TSPQAILDLITVGK.M
R5/RRR5-5/2	1456.430	1456.709	-192.563	0.330	323.817	0.410	14	0.123	-.TSPQAILDLITVGK.-
R5/RRR5-6/2	1175.186	1175.424	-203.322	0.354	626.590	0.303	15	0.123	K.M*IAANLEGLVK.R
R5/RRR5-3/2	1248.596	1249.443	-1483.894	0.259	460.674	0.347	11	0.120	R.LWALEIANYR.K
R5/RRR5-2/2	1455.762	1456.709	-1341.522	0.320	473.307	0.283	15	0.120	K.TSPQAILDLITVGK.M
R5/RRR5-1/2	1457.144	1456.709	299.414	0.218	432.695	0.373	14	0.119	K.TSPQAILDLITVGK.M
R5/RRR5-6/2	1158.937	1159.425	-421.801	0.316	750.109	0.207	14	0.116	-.MIAANLEGLVK.-
R5/RRR5-6/3	1160.459	1160.353	91.926	0.476	917.551	0.479	21	0.106	K.ALVHAFFAQR.L
R5/RRR5-6/3	1160.673	1160.353	276.723	0.496	878.823	0.494	23	0.106	K.ALVHAFFAQR.L
R5/RRR5-6/3	1160.454	1160.353	87.495	0.440	753.474	0.440	20	0.092	K.ALVHAFFAQR.L
R5/RRR5-6/3	1456.267	1456.709	-304.456	0.488	915.783	0.387	23	0.090	-.TSPQAILDLITVGK.-
R5/RRR5-15/3	1529.700	1529.764	-41.718	0.528	2462.262	0.526	32	0.395	K.VKIQLGEGSAAQVTK.N
R5/RRR5-16/2	1461.488	1460.637	-102.382	0.580	2109.548	0.500	20	0.281	K.NM*LANEGIGSFYK.G
R5/RRR5-16/2	1460.285	1460.637	-241.899	0.522	2078.702	0.450	20	0.263	K.NM*LANEGIGSFYK.G
R5/RRR5-15/2	1461.088	1460.637	309.291	0.553	2077.674	0.444	20	0.260	K.NM*LANEGIGSFYK.G
R5/RRR5-15/2	1461.139	1460.637	-342.144	0.556	2004.220	0.450	20	0.251	K.NM*LANEGIGSFYK.G
R5/RRR5-16/2	1329.222	1328.581	-270.956	0.569	1548.112	0.528	20	0.214	R.IIADEGVLALWK.G
R5/RRR5-16/2	1302.210	1302.459	-192.239	0.521	1603.810	0.493	22	0.212	K.IQLGEGSAAQVTK.N
R5/RRR5-16/3	1529.259	1529.764	-986.549	0.467	1596.254	0.546	30	0.204	K.VKIQLGEGSAAQVTK.N
R5/RRR5-15/2	1328.351	1328.581	-174.261	0.546	1465.782	0.488	20	0.196	R.IIADEGVLALWK.G
R5/RRR5-15/2	1301.635	1302.459	-1405.368	0.437	1574.635	0.436	22	0.196	K.IQLGEGSAAQVTK.N
R5/RRR5-15/2	1328.189	1328.581	-296.609	0.491	1501.649	0.467	20	0.195	R.IIADEGVLALWK.G
R5/RRR5-15/2	1328.318	1328.581	-199.245	0.575	1460.214	0.469	20	0.191	R.IIADEGVLALWK.G
R5/RRR5-16/2	1327.945	1328.581	-1235.628	0.476	1363.845	0.516	19	0.191	R.IIADEGVLALWK.G
R5/RRR5-15/2	1301.689	1302.459	-1364.112	0.504	1379.472	0.504	21	0.191	K.IQLGEGSAAQVTK.N
R5/RRR5-16/2	1302.208	1302.459	-193.367	0.491	1404.258	0.472	21	0.187	K.IQLGEGSAAQVTK.N
R5/RRR5-15/2	1302.105	1302.459	-272.932	0.523	1301.099	0.505	21	0.184	K.IQLGEGSAAQVTK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1302.170	1302.459	-223.085	0.493	1299.146	0.479	20	0.178	K.IQLGEGSAAQVTK.N
R5/RRR5-15/3	1529.792	1529.764	18.310	0.530	1486.988	0.514	28	0.176	K.VKIQLGEGSAAQVTK.N
R5/RRR5-15/3	1530.291	1529.764	-309.971	0.540	1381.646	0.554	29	0.173	K.VKIQLGEGSAAQVTK.N
R5/RRR5-16/2	1410.453	1409.607	-109.516	0.462	999.384	0.491	17	0.158	K.FYTGFPVYCVR.I
R5/RRR5-16/2	1327.811	1328.581	-1337.460	0.406	1117.128	0.361	18	0.145	R.IIADEGVLALWK.G
R5/RRR5-16/2	1347.408	1347.523	-86.027	0.462	865.302	0.411	17	0.137	R.M*QADSTLPIAQR.R
R5/RRR5-15/2	1327.985	1328.581	-1205.535	0.453	948.442	0.360	17	0.137	R.IIADEGVLALWK.G
R5/RRR5-16/2	991.928	992.115	-189.174	0.344	871.378	0.342	13	0.131	K.NAFHALYR.I
R5/RRR5-15/2	1410.192	1409.607	-294.729	0.354	584.833	0.384	14	0.127	K.FYTGFPVYCVR.I
R5/RRR5-15/2	1410.018	1409.607	292.923	0.320	648.407	0.334	14	0.124	K.FYTGFPVYCVR.I
R5/RRR5-15/2	1410.335	1409.607	-193.387	0.349	734.504	0.287	14	0.122	K.FYTGFPVYCVR.I
R5/RRR5-16/2	991.289	992.115	-1848.069	0.318	685.095	0.190	13	0.118	K.NAFHALYR.I
R5/RRR5-16/2	1329.471	1328.581	-83.401	0.254	624.268	0.190	15	0.117	R.IIADEGVLALWK.G
R5/RRR5-15/2	1460.272	1460.637	-250.621	0.329	751.819	0.154	16	0.113	K.NM*LANEGIGSFYK.G
R5/RRR5-15/3	1650.681	1650.944	-159.563	0.451	1064.314	0.359	29	0.094	K.AIEKNDGKPLPLVQK.A
R5/RRR5-15/3	1651.945	1650.944	0.725	0.443	636.033	0.375	24	0.084	K.AIEKNDGKPLPLVQK.A
R5/RRR5-16/3	1650.871	1650.944	-44.181	0.453	505.261	0.415	23	0.081	-.AIEKNDGKPLPLVQK.-
R5/RRR5-16/3	1650.539	1650.944	-246.145	0.415	567.386	0.349	22	0.081	K.AIEKNDGKPLPLVQK.A
R5/RRR5-16/3	1652.059	1650.944	69.648	0.405	625.844	0.320	24	0.079	K.AIEKNDGKPLPLVQK.A
R5/RRR5-15/3	1651.079	1650.944	82.074	0.416	501.857	0.395	22	0.076	-.AIEKNDGKPLPLVQK.-
R5/RRR5-10/2	1887.221	1886.970	133.196	0.614	2885.903	0.649	24	0.498	K.TM*ISDSDYAEFDNFSK.W
R5/RRR5-10/2	1712.613	1711.936	-189.423	0.620	2659.037	0.567	25	0.410	K.KLEEVYGTFEAPSLK.K
R5/RRR5-10/2	1710.731	1711.936	-1292.807	0.569	2208.450	0.599	23	0.331	K.KLEEVYGTFEAPSLK.K
R5/RRR5-10/2	1712.379	1711.936	259.075	0.600	2172.120	0.593	23	0.322	K.KLEEVYGTFEAPSLK.K
R5/RRR5-10/2	1349.218	1349.557	-252.693	0.455	1725.219	0.515	20	0.231	R.KGPLIVYGTEGSK.I
R5/RRR5-10/2	1349.124	1349.557	-321.955	0.475	1379.534	0.566	19	0.202	R.KGPLIVYGTEGSK.I
R5/RRR5-10/2	1348.687	1349.557	-1391.381	0.479	1394.938	0.546	19	0.199	R.KGPLIVYGTEGSK.I
R5/RRR5-10/3	1797.976	1797.132	-86.941	0.482	1573.868	0.453	39	0.169	R.VAVASALAATSVPSLVLAR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1445.684	1446.680	-1384.751	0.523	1061.264	0.526	21	0.168	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/2	1797.443	1797.132	173.384	0.448	1199.664	0.490	23	0.168	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-10/2	1446.289	1446.680	-270.696	0.555	1028.804	0.491	21	0.160	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/2	1797.549	1797.132	232.496	0.442	1144.234	0.459	21	0.157	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-10/2	1446.304	1446.680	-260.788	0.465	917.238	0.516	20	0.156	R.LNLLDLAPGGHLGR.F
R5/RRR5-7/3	1446.599	1446.680	-56.176	0.400	1645.714	0.385	29	0.152	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/2	1228.240	1228.420	-146.996	0.460	805.082	0.480	15	0.146	R.FVIWTESAFK.K
R5/RRR5-10/3	1446.795	1446.680	79.911	0.485	1645.842	0.361	30	0.143	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/3	1839.824	1840.109	-155.637	0.473	1299.776	0.478	29	0.141	K.KLEEVYGTFEAPSLKK.K
R5/RRR5-9/2	1283.088	1283.416	-256.270	0.389	443.210	0.519	18	0.139	R.NLPGVDVANVER.L
R5/RRR5-10/2	1228.051	1228.420	-301.453	0.446	801.918	0.404	15	0.137	R.FVIWTESAFK.K
R5/RRR5-6/3	1446.978	1446.680	207.204	0.429	1549.650	0.373	28	0.136	R.LNLLDLAPGGHLGR.F
R5/RRR5-14/2	1284.308	1283.416	-84.428	0.358	450.490	0.494	18	0.135	R.NLPGVDVANVER.L
R5/RRR5-10/2	1283.099	1283.416	-247.489	0.356	477.042	0.449	19	0.133	R.NLPGVDVANVER.L
R5/RRR5-10/2	1284.136	1283.416	-218.781	0.346	282.955	0.474	16	0.132	R.NLPGVDVANVER.L
R5/RRR5-11/3	1446.933	1446.680	175.479	0.452	1476.976	0.381	28	0.130	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/2	1282.551	1283.416	-1458.546	0.299	331.206	0.447	17	0.129	R.NLPGVDVANVER.L
R5/RRR5-10/2	1796.555	1797.132	-880.412	0.276	828.458	0.366	19	0.126	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-10/3	1447.397	1446.680	-196.016	0.474	1387.906	0.400	28	0.125	R.LNLLDLAPGGHLGR.F
R5/RRR5-1/2	1447.372	1446.680	-212.801	0.388	567.036	0.380	16	0.125	R.LNLLDLAPGGHLGR.F
R5/RRR5-13/2	1797.541	1797.132	228.070	0.317	852.232	0.333	19	0.125	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-10/2	1227.967	1228.420	-370.371	0.293	824.322	0.288	15	0.124	R.FVIWTESAFK.K
R5/RRR5-14/2	1283.131	1283.416	-222.578	0.296	400.253	0.270	17	0.124	R.NLPGVDVANVER.L
R5/RRR5-2/2	1797.880	1797.132	-141.010	0.276	808.280	0.312	18	0.121	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-3/2	1797.299	1797.132	93.218	0.273	780.449	0.272	18	0.118	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-9/3	1446.295	1446.680	-266.598	0.448	1163.728	0.440	25	0.117	R.LNLLDLAPGGHLGR.F
R5/RRR5-14/3	1446.511	1446.680	-116.995	0.446	1422.786	0.347	27	0.116	R.LNLLDLAPGGHLGR.F
R5/RRR5-11/3	1445.643	1446.680	-1413.045	0.413	1322.099	0.375	27	0.114	R.LNLLDLAPGGHLGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1447.197	1446.680	-334.241	0.433	1407.876	0.343	27	0.114	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/3	1350.014	1349.557	339.352	0.357	1453.621	0.311	26	0.114	R.KGPLIVYGTEGSK.I
R5/RRR5-9/3	1446.735	1446.680	38.657	0.388	1395.762	0.344	27	0.113	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/3	1796.591	1797.132	-860.230	0.460	1395.892	0.325	39	0.112	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-12/3	1446.402	1446.680	-192.553	0.407	1305.095	0.370	26	0.112	R.LNLLDLAPGGHLGR.F
R5/RRR5-1/3	1447.036	1446.680	246.921	0.401	1334.748	0.358	26	0.111	R.LNLLDLAPGGHLGR.F
R5/RRR5-7/3	1446.448	1446.680	-160.804	0.429	1268.660	0.375	25	0.110	R.LNLLDLAPGGHLGR.F
R5/RRR5-13/3	1446.340	1446.680	-235.734	0.364	1226.563	0.389	26	0.109	R.LNLLDLAPGGHLGR.F
R5/RRR5-2/3	1446.314	1446.680	-253.262	0.440	1334.296	0.343	26	0.107	R.LNLLDLAPGGHLGR.F
R5/RRR5-8/3	1446.694	1446.680	10.222	0.438	1236.189	0.374	25	0.107	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/3	1796.848	1797.132	-158.610	0.401	1095.707	0.414	34	0.106	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-10/3	1840.319	1840.109	114.251	0.473	982.479	0.446	27	0.104	K.KLEEVYGTFEAPSLKK.K
R5/RRR5-11/3	1446.026	1446.680	-1147.100	0.409	1265.008	0.343	26	0.102	R.LNLLDLAPGGHLGR.F
R5/RRR5-14/3	1446.606	1446.680	-50.780	0.384	1189.765	0.365	25	0.102	R.LNLLDLAPGGHLGR.F
R5/RRR5-9/3	1446.511	1446.680	-116.868	0.377	1156.807	0.374	25	0.102	R.LNLLDLAPGGHLGR.F
R5/RRR5-6/3	1446.510	1446.680	-117.376	0.359	1356.247	0.302	26	0.100	R.LNLLDLAPGGHLGR.F
R5/RRR5-6/3	1446.429	1446.680	-173.504	0.428	1163.076	0.356	24	0.098	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/3	1446.278	1446.680	-278.538	0.432	1251.404	0.315	25	0.095	R.LNLLDLAPGGHLGR.F
R5/RRR5-1/3	1446.666	1446.680	-9.328	0.376	1177.460	0.328	25	0.094	R.LNLLDLAPGGHLGR.F
R5/RRR5-1/3	1446.731	1446.680	35.737	0.427	1082.379	0.344	23	0.091	R.LNLLDLAPGGHLGR.F
R5/RRR5-13/3	1446.492	1446.680	-130.201	0.355	1056.935	0.335	24	0.089	R.LNLLDLAPGGHLGR.F
R5/RRR5-8/3	1446.937	1446.680	178.271	0.377	941.584	0.349	23	0.087	R.LNLLDLAPGGHLGR.F
R5/RRR5-10/3	1841.111	1840.109	0.750	0.472	727.136	0.387	23	0.083	K.KLEEVYGTFEAPSLKK.K
R5/RRR5-5/3	1446.217	1446.680	-320.964	0.348	674.686	0.288	20	0.078	R.LNLLDLAPGGHLGR.F
R5/RRR5-13/3	1797.318	1797.132	103.837	0.243	941.343	0.176	28	0.060	R.VAVASALAATSVPSLVLAR.G
R5/RRR5-18/2	1375.048	1375.547	-364.146	0.505	2029.695	0.483	19	0.265	K.VIACVGETLEQR.E
R5/RRR5-18/2	1375.108	1375.547	-319.967	0.512	1995.073	0.456	19	0.252	K.VIACVGETLEQR.E
R5/RRR5-17/2	1340.127	1340.501	-280.080	0.505	1810.263	0.549	22	0.252	R.IIYGGSVTGANCK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1375.286	1375.547	-190.125	0.537	1741.234	0.506	19	0.231	K.VIACVGETLEQR.E
R5/RRR5-17/2	1340.117	1340.501	-287.665	0.482	1663.201	0.518	22	0.225	R.IIYGGSVTGANCK.E
R5/RRR5-18/2	1340.074	1340.501	-319.195	0.508	1570.059	0.558	21	0.223	R.IIYGGSVTGANCK.E
R5/RRR5-17/2	1375.116	1375.547	-314.089	0.509	1698.285	0.480	19	0.219	K.VIACVGETLEQR.E
R5/RRR5-17/2	1375.131	1375.547	-303.401	0.515	1632.766	0.491	19	0.214	K.VIACVGETLEQR.E
R5/RRR5-18/2	1340.066	1340.501	-325.593	0.476	1540.426	0.532	21	0.213	R.IIYGGSVTGANCK.E
R5/RRR5-17/2	1604.257	1604.746	-305.860	0.523	1326.255	0.600	20	0.202	K.WLAANVSAEVAESTR.I
R5/RRR5-17/2	1341.120	1340.501	-284.528	0.539	1375.940	0.551	20	0.200	R.IIYGGSVTGANCK.E
R5/RRR5-18/2	1375.503	1375.547	-31.921	0.503	1586.227	0.436	19	0.196	K.VIACVGETLEQR.E
R5/RRR5-17/2	1396.027	1395.497	-337.625	0.499	1198.123	0.599	19	0.191	R.SLLGESNEFVGDK.V
R5/RRR5-18/2	1395.185	1395.497	-224.008	0.446	1258.832	0.529	19	0.182	R.SLLGESNEFVGDK.V
R5/RRR5-17/2	1395.199	1395.497	-214.177	0.455	1216.609	0.521	19	0.177	R.SLLGESNEFVGDK.V
R5/RRR5-18/2	1395.029	1395.497	-336.286	0.409	1228.577	0.507	19	0.175	R.SLLGESNEFVGDK.V
R5/RRR5-17/2	1636.326	1636.748	-258.638	0.471	1119.011	0.528	21	0.170	K.VATPDQAQEVHDGLR.K
R5/RRR5-17/2	1423.969	1424.560	-1120.319	0.446	1357.678	0.416	19	0.169	R.ESGSTMDVVAAQTK.A
R5/RRR5-17/2	1423.989	1424.560	-1106.375	0.479	1303.626	0.419	19	0.165	R.ESGSTMDVVAAQTK.A
R5/RRR5-18/2	1424.063	1424.560	-350.236	0.421	1210.966	0.452	18	0.163	R.ESGSTMDVVAAQTK.A
R5/RRR5-17/2	1637.163	1636.748	254.002	0.497	1115.366	0.479	20	0.161	K.VATPDQAQEVHDGLR.K
R5/RRR5-17/2	1394.542	1395.497	-1405.770	0.371	1087.688	0.499	18	0.161	R.SLLGESNEFVGDK.V
R5/RRR5-17/2	1764.426	1764.921	-281.217	0.450	1066.867	0.497	19	0.159	K.VATPDQAQEVHDGLRK.W
R5/RRR5-17/2	1423.933	1424.560	-1146.316	0.431	1171.525	0.442	18	0.159	R.ESGSTMDVVAAQTK.A
R5/RRR5-18/2	1339.431	1340.501	-1549.718	0.314	1354.229	0.353	21	0.158	R.IIYGGSVTGANCK.E
R5/RRR5-17/2	1440.151	1440.559	-284.316	0.390	1057.399	0.482	18	0.156	R.ESGSTM*DVVAAQTK.A
R5/RRR5-17/2	1636.163	1636.748	-971.658	0.473	924.720	0.521	20	0.156	K.VATPDQAQEVHDGLR.K
R5/RRR5-18/2	1424.123	1424.560	-307.923	0.427	1099.592	0.436	17	0.152	R.ESGSTMDVVAAQTK.A
R5/RRR5-18/2	1394.527	1395.497	-1416.848	0.300	1079.995	0.433	19	0.149	R.SLLGESNEFVGDK.V
R5/RRR5-18/2	1764.312	1764.921	-914.615	0.459	710.774	0.572	17	0.148	K.VATPDQAQEVHDGLRK.W
R5/RRR5-17/2	1441.201	1440.559	-249.108	0.455	928.894	0.463	17	0.147	R.ESGSTM*DVVAAQTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1764.469	1764.921	-256.924	0.462	845.389	0.498	19	0.147	K.VATPDQAQEVHDGLRK.W
R5/RRR5-17/2	1440.990	1440.559	300.082	0.392	1044.850	0.414	18	0.147	R.ESGSTM*DVVAAQTK.A
R5/RRR5-17/2	1375.495	1375.547	-37.974	0.358	1281.994	0.274	18	0.144	-.VIACVGETLEQR.-
R5/RRR5-18/2	1440.093	1440.559	-325.052	0.391	918.297	0.449	17	0.144	R.ESGSTM*DVVAAQTK.A
R5/RRR5-18/2	1424.188	1424.560	-262.173	0.437	1054.233	0.386	18	0.143	R.ESGSTMDVVAAQTK.A
R5/RRR5-17/2	1440.117	1440.559	-307.873	0.429	1045.796	0.381	18	0.142	R.ESGSTM*DVVAAQTK.A
R5/RRR5-17/2	1441.085	1440.559	-330.096	0.470	954.277	0.404	18	0.141	R.ESGSTM*DVVAAQTK.A
R5/RRR5-18/2	1439.622	1440.559	-1349.643	0.383	1008.051	0.378	18	0.140	R.ESGSTM*DVVAAQTK.A
R5/RRR5-17/2	1764.224	1764.921	-964.767	0.432	803.420	0.462	18	0.139	K.VATPDQAQEVHDGLRK.W
R5/RRR5-17/2	1440.005	1440.559	-1082.901	0.374	1023.231	0.362	18	0.139	R.ESGSTM*DVVAAQTK.A
R5/RRR5-17/2	1764.350	1764.921	-893.291	0.448	798.009	0.456	18	0.138	K.VATPDQAQEVHDGLRK.W
R5/RRR5-18/2	1764.408	1764.921	-860.161	0.442	582.865	0.520	17	0.137	K.VATPDQAQEVHDGLRK.W
R5/RRR5-17/2	1440.158	1440.559	-279.214	0.413	989.405	0.358	18	0.137	R.ESGSTM*DVVAAQTK.A
R5/RRR5-17/2	1637.164	1636.748	254.824	0.494	658.341	0.444	17	0.132	K.VATPDQAQEVHDGLR.K
R5/RRR5-18/2	1440.157	1440.559	-280.405	0.403	749.427	0.395	16	0.131	R.ESGSTM*DVVAAQTK.A
R5/RRR5-18/2	1440.129	1440.559	-299.454	0.392	841.554	0.358	17	0.131	R.ESGSTM*DVVAAQTK.A
R5/RRR5-3/2	1441.356	1440.559	-141.455	0.326	536.167	0.377	18	0.127	R.ESGSTM*DVVAAQTK.A
R5/RRR5-2/2	1766.153	1764.921	132.020	0.260	272.207	0.411	13	0.120	K.VATPDQAQEVHDGLRK.W
R5/RRR5-18/2	1604.430	1604.746	-197.465	0.234	738.111	0.223	18	0.114	K.WLAANVSAEVAESTR.I
R5/RRR5-17/3	1375.641	1375.547	68.691	0.505	1273.033	0.371	27	0.111	K.VIACVGETLEQR.E
R5/RRR5-17/3	1375.399	1375.547	-107.554	0.474	1281.502	0.316	28	0.099	K.VIACVGETLEQR.E
R5/RRR5-17/3	1375.389	1375.547	-115.033	0.464	1100.828	0.340	26	0.092	K.VIACVGETLEQR.E
R5/RRR5-17/3	1478.684	1478.624	40.596	0.420	1195.164	0.304	26	0.091	K.CNGTTDQVDKIVK.I
R5/RRR5-18/3	1478.103	1478.624	-1031.959	0.407	922.864	0.314	23	0.081	K.CNGTTDQVDKIVK.I
R5/RRR5-17/3	1478.988	1478.624	247.216	0.416	870.362	0.318	23	0.080	K.CNGTTDQVDKIVK.I
R5/RRR5-17/3	1479.441	1478.624	-123.701	0.433	697.360	0.326	21	0.080	K.CNGTTDQVDKIVK.I
R5/RRR5-17/3	1478.256	1478.624	-249.611	0.419	858.090	0.300	24	0.078	K.CNGTTDQVDKIVK.I
R5/RRR5-17/3	1478.506	1478.624	-79.765	0.392	762.092	0.321	21	0.078	K.CNGTTDQVDKIVK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/3	1775.361	1775.858	-280.458	0.583	2437.060	0.444	33	0.348	K.FEANRDVDNPDVIDR.L
R5/RRR5-25/3	1775.895	1775.858	21.392	0.561	1993.585	0.377	32	0.215	K.FEANRDVDNPDVIDR.L
R5/RRR5-25/3	1424.759	1424.632	88.967	0.508	1985.524	0.362	27	0.207	R.ALKDTLNWAVHR.H
R5/RRR5-25/2	1413.619	1414.542	-1364.454	0.380	1432.949	0.477	17	0.185	K.GIEIIYNYGKED.-
R5/RRR5-25/3	1622.457	1622.763	-189.053	0.541	1579.429	0.461	29	0.171	R.HLFYQDASDLREK.F
R5/RRR5-25/2	1424.510	1424.632	-86.260	0.471	1267.554	0.450	18	0.169	R.ALKDTLNWAVHR.H
R5/RRR5-25/2	1194.047	1194.276	-192.529	0.487	1165.286	0.438	17	0.162	R.LIDDAEAQYR.N
R5/RRR5-25/2	1193.985	1194.276	-244.529	0.533	1158.544	0.433	17	0.161	R.LIDDAEAQYR.N
R5/RRR5-25/2	1365.563	1365.476	64.501	0.479	1223.768	0.411	16	0.159	R.HLFYQDASDLR.E
R5/RRR5-25/2	1366.124	1365.476	-258.439	0.412	1129.224	0.449	16	0.158	R.HLFYQDASDLR.E
R5/RRR5-25/2	1365.204	1365.476	-199.332	0.397	1152.464	0.391	16	0.151	R.HLFYQDASDLR.E
R5/RRR5-25/2	1193.430	1194.276	-1551.152	0.421	1010.125	0.401	16	0.146	R.LIDDAEAQYR.N
R5/RRR5-25/2	1157.847	1158.201	-306.408	0.497	912.970	0.435	15	0.146	R.DVDNPDVIDR.L
R5/RRR5-25/2	1157.976	1158.201	-194.931	0.467	1070.460	0.356	16	0.143	R.DVDNPDVIDR.L
R5/RRR5-25/2	1157.816	1158.201	-332.853	0.415	1038.087	0.376	15	0.143	R.DVDNPDVIDR.L
R5/RRR5-25/2	1775.432	1775.858	-240.580	0.466	1008.255	0.422	18	0.143	K.FEANRDVDNPDVIDR.L
R5/RRR5-25/2	1414.303	1414.542	-169.124	0.369	1153.650	0.483	16	0.135	K.GIEIIYNYGKED.-
R5/RRR5-25/3	1622.489	1622.763	-169.693	0.426	1228.057	0.473	26	0.130	R.HLFYQDASDLREK.F
R5/RRR5-25/3	1424.339	1424.632	-206.667	0.522	1287.995	0.431	23	0.128	R.ALKDTLNWAVHR.H
R5/RRR5-25/3	1621.813	1622.763	-1206.292	0.362	961.544	0.391	22	0.091	R.HLFYQDASDLREK.F
R5/RRR5-25/2	1413.552	1414.542	-1411.897	0.260	634.454	0.347	13	0.085	K.GIEIIYNYGKED.-
R5/RRR5-15/2	1237.163	1237.387	-181.761	0.493	1523.695	0.514	19	0.207	K.TLASDGLAGLYR.G
R5/RRR5-16/2	1236.631	1237.387	-1424.193	0.457	1413.377	0.564	18	0.205	K.TLASDGLAGLYR.G
R5/RRR5-15/2	1236.515	1237.387	-1518.889	0.449	1520.948	0.486	19	0.200	K.TLASDGLAGLYR.G
R5/RRR5-15/2	1238.175	1237.387	-171.625	0.524	1483.158	0.479	19	0.195	K.TLASDGLAGLYR.G
R5/RRR5-16/2	1237.151	1237.387	-191.363	0.494	1414.045	0.499	18	0.192	K.TLASDGLAGLYR.G
R5/RRR5-15/2	1236.814	1237.387	-1275.789	0.457	1492.637	0.430	19	0.186	K.TLASDGLAGLYR.G
R5/RRR5-15/2	1361.064	1361.590	-1124.471	0.495	1487.438	0.422	17	0.184	K.LLVQNQEEM*LK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1362.055	1361.590	342.200	0.535	1338.449	0.444	17	0.175	K.LLVQNQEEM*LK.A
R5/RRR5-15/2	1361.087	1361.590	-1107.360	0.476	1385.057	0.387	17	0.168	K.LLVQNQEEM*LK.A
R5/RRR5-15/2	1323.364	1322.537	-131.249	0.461	875.319	0.541	16	0.154	R.GFGPSVAGIVVYR.G
R5/RRR5-15/2	1475.440	1475.675	-159.627	0.480	725.556	0.527	19	0.150	R.YFPTQALNFAFR.D
R5/RRR5-15/2	1045.904	1046.115	-202.239	0.327	1032.343	0.436	15	0.146	K.YSSSLDAFR.Q
R5/RRR5-15/2	1476.133	1475.675	311.156	0.477	638.017	0.518	18	0.145	R.YFPTQALNFAFR.D
R5/RRR5-15/2	1322.307	1322.537	-174.780	0.385	723.393	0.539	16	0.143	R.GFGPSVAGIVVYR.G
R5/RRR5-15/2	1476.177	1475.675	-338.204	0.423	657.092	0.483	18	0.141	R.YFPTQALNFAFR.D
R5/RRR5-15/2	1237.073	1237.387	-254.717	0.336	917.772	0.378	15	0.135	K.TLASDGLAGLYR.G
R5/RRR5-16/2	1236.993	1237.387	-319.664	0.286	841.496	0.361	15	0.129	K.TLASDGLAGLYR.G
R5/RRR5-16/2	1474.877	1475.675	-1222.775	0.278	417.381	0.409	16	0.125	R.YFPTQALNFAFR.D
R5/RRR5-5/2	1031.092	1030.160	-66.094	0.514	2201.997	0.391	17	0.267	K.TAIAEGLAQR.I
R5/RRR5-4/2	1030.018	1030.160	-138.554	0.473	2087.990	0.413	17	0.256	K.TAIAEGLAQR.I
R5/RRR5-5/2	1160.155	1160.260	-90.824	0.478	1752.403	0.533	18	0.239	K.AIDLIDEAGSR.V
R5/RRR5-5/2	1160.040	1160.260	-189.623	0.537	1774.389	0.508	19	0.237	K.AIDLIDEAGSR.V
R5/RRR5-5/2	1160.153	1160.260	-92.091	0.502	1726.108	0.509	18	0.231	K.AIDLIDEAGSR.V
R5/RRR5-4/2	1159.947	1160.260	-270.598	0.427	1853.996	0.418	18	0.224	K.AIDLIDEAGSR.V
R5/RRR5-5/2	1610.459	1610.834	-233.294	0.517	1535.624	0.565	22	0.220	K.VPEPTVDETIQILR.G
R5/RRR5-4/2	1159.143	1159.315	-148.470	0.418	1666.458	0.421	17	0.203	R.VLELSLEEAR.Q
R5/RRR5-4/2	1029.885	1030.160	-268.512	0.435	1676.374	0.387	17	0.197	K.TAIAEGLAQR.I
R5/RRR5-5/2	1030.865	1030.160	-287.022	0.461	1799.338	0.307	17	0.193	K.TAIAEGLAQR.I
R5/RRR5-5/2	1611.510	1610.834	-201.459	0.472	1297.721	0.503	21	0.182	K.VPEPTVDETIQILR.G
R5/RRR5-5/2	1610.282	1610.834	-966.746	0.499	1199.389	0.514	20	0.175	K.VPEPTVDETIQILR.G
R5/RRR5-5/2	1478.408	1477.689	-190.860	0.473	1146.072	0.534	18	0.172	R.GSGFVAVEIPFTPR.A
R5/RRR5-5/3	1960.398	1960.225	88.360	0.430	1416.758	0.512	27	0.167	K.NPNRPIASFIFSGPTGVGK.S
R5/RRR5-5/2	1159.174	1159.315	-121.638	0.406	1532.116	0.299	17	0.166	R.VLELSLEEAR.Q
R5/RRR5-5/2	1159.021	1159.315	-254.441	0.418	1284.779	0.378	16	0.159	R.VLELSLEEAR.Q
R5/RRR5-4/2	1159.186	1159.315	-111.285	0.394	1220.670	0.333	15	0.147	R.VLELSLEEAR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1398.129	1398.547	-300.162	0.430	1086.192	0.360	19	0.141	R.VLESLGADPNNIR.T
R5/RRR5-5/3	1959.637	1960.225	-812.649	0.429	1388.467	0.424	28	0.136	K.NPNRPIASFIFSGPTGVGK.S
R5/RRR5-5/2	1477.268	1477.689	-285.822	0.350	802.193	0.391	16	0.131	R.GSGFVAVEIPFTPR.A
R5/RRR5-4/2	1612.055	1610.834	137.804	0.385	850.697	0.366	17	0.131	K.VPEPTVDETIQILR.G
R5/RRR5-4/3	1959.126	1960.225	-1074.686	0.406	1280.929	0.438	27	0.128	K.NPNRPIASFIFSGPTGVGK.S
R5/RRR5-5/3	1208.665	1208.349	262.038	0.524	1369.113	0.398	22	0.127	K.HIEKDPALER.R
R5/RRR5-5/2	1476.287	1477.689	-1632.055	0.188	1105.220	0.145	17	0.118	R.GSGFVAVEIPFTPR.A
R5/RRR5-4/2	1477.380	1477.689	-209.556	0.194	744.466	0.214	16	0.115	R.GSGFVAVEIPFTPR.A
R5/RRR5-4/2	1476.924	1477.689	-1198.946	0.204	658.152	0.213	16	0.115	R.GSGFVAVEIPFTPR.A
R5/RRR5-4/2	1476.621	1477.689	-1404.410	0.229	694.394	0.175	16	0.114	R.GSGFVAVEIPFTPR.A
R5/RRR5-5/3	1960.065	1960.225	-81.875	0.361	1255.516	0.379	29	0.111	K.NPNRPIASFIFSGPTGVGK.S
R5/RRR5-5/3	1208.448	1208.349	82.146	0.535	1087.281	0.384	21	0.101	K.HIEKDPALER.R
R5/RRR5-5/3	1208.708	1208.349	297.735	0.544	1054.041	0.393	21	0.101	K.HIEKDPALER.R
R5/RRR5-5/2	1891.718	1890.213	-262.618	0.339	604.869	0.502	16	0.081	K.VIVLNGGSGVPEPLAPALSV.-
R5/RRR5-8/2	1359.181	1359.471	-214.178	0.461	1483.345	0.455	16	0.189	K.SVYAHWVPEDR.I
R5/RRR5-9/2	1359.074	1359.471	-293.022	0.447	1442.461	0.466	16	0.188	K.SVYAHWVPEDR.I
R5/RRR5-8/2	1359.172	1359.471	-220.935	0.448	1426.438	0.405	16	0.174	K.SVYAHWVPEDR.I
R5/RRR5-8/2	1359.205	1359.471	-196.609	0.425	1437.326	0.349	16	0.165	K.SVYAHWVPEDR.I
R5/RRR5-3/2	1477.481	1476.703	-150.291	0.588	2112.012	0.544	19	0.295	R.VLQQASQIFQSVK.I
R5/RRR5-1/2	1476.238	1476.703	-315.796	0.404	2217.528	0.432	20	0.281	R.VLQQASQIFQSVK.I
R5/RRR5-4/2	1476.307	1476.703	-268.592	0.463	1977.531	0.516	20	0.266	R.VLQQASQIFQSVK.I
R5/RRR5-3/2	1476.096	1476.703	-1091.871	0.443	1955.360	0.488	19	0.255	R.VLQQASQIFQSVK.I
R5/RRR5-3/2	1565.755	1564.767	-7.164	0.551	1766.775	0.544	20	0.244	K.IATELSLWQEAFR.S
R5/RRR5-3/2	1845.772	1846.109	-183.187	0.551	1935.932	0.430	23	0.236	R.IVCQQVNVSSLEEVIK.H
R5/RRR5-3/2	1566.314	1564.767	-289.740	0.593	1563.202	0.564	18	0.221	K.IATELSLWQEAFR.S
R5/RRR5-3/3	1266.892	1266.433	363.212	0.492	1561.395	0.479	26	0.174	K.VNHLSGAVHFGK.M
R5/RRR5-1/2	1476.389	1476.703	-212.848	0.449	1257.808	0.486	17	0.173	R.VLQQASQIFQSVK.I
R5/RRR5-2/2	1565.866	1564.767	63.756	0.445	1265.818	0.424	17	0.163	K.IATELSLWQEAFR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1476.702	1477.690	-1350.606	0.414	871.756	0.528	17	0.150	R.IANLVNFSLDSKR.E
R5/RRR5-3/3	1266.238	1266.433	-154.537	0.424	1313.011	0.509	26	0.146	K.VNHLSGAVHFGK.M
R5/RRR5-1/2	1565.430	1564.767	-215.680	0.413	827.469	0.501	15	0.145	K.IATELSLWQEAFR.S
R5/RRR5-3/2	1036.793	1037.191	-385.523	0.349	1286.542	0.290	16	0.145	R.ASLFSELAAK.G
R5/RRR5-3/2	1331.250	1330.509	-195.495	0.496	1007.185	0.390	18	0.144	K.EKIEAEELLQK.Q
R5/RRR5-1/2	1566.231	1564.767	297.165	0.468	956.983	0.395	16	0.139	K.IATELSLWQEAFR.S
R5/RRR5-3/2	1476.937	1475.733	138.527	0.469	557.636	0.447	19	0.135	R.M*IPFFDFSVVEK.I
R5/RRR5-3/3	1969.522	1970.007	-246.998	0.421	1108.544	0.532	33	0.134	R.GGDGGSSAGGQRPAVAPEQDR.W
R5/RRR5-4/2	1565.595	1564.767	-109.925	0.309	654.851	0.425	13	0.127	K.IATELSLWQEAFR.S
R5/RRR5-3/2	1036.784	1037.191	-393.911	0.289	627.383	0.316	14	0.121	R.ASLFSELAAK.G
R5/RRR5-4/2	1846.029	1846.109	-43.483	0.436	454.352	0.340	16	0.118	R.IVCQQVNVSSLEEVIK.H
R5/RRR5-3/3	1476.570	1476.703	-90.152	0.474	1389.828	0.322	27	0.111	R.VLQQASQIFQSVK.I
R5/RRR5-3/3	1969.856	1970.007	-77.086	0.490	837.545	0.526	30	0.111	R.GGDGGSSAGGQRPAVAPEQDR.W
R5/RRR5-3/3	1971.686	1970.007	-163.702	0.433	1000.474	0.445	29	0.104	R.GGDGGSSAGGQRPAVAPEQDR.W
R5/RRR5-3/3	1265.686	1266.433	-1384.981	0.313	1003.597	0.452	21	0.102	K.VNHLSGAVHFGK.M
R5/RRR5-12/3	1969.817	1970.007	-96.946	0.376	543.315	0.376	24	0.078	R.GGDGGSSAGGQRPAVAPEQDR.W
R5/RRR5-3/3	1476.515	1476.703	-127.470	0.451	1096.404	0.252	24	0.077	R.VLQQASQIFQSVK.I
R5/RRR5-3/3	1969.408	1970.007	-814.306	0.254	787.871	0.297	29	0.071	R.GGDGGSSAGGQRPAVAPEQDR.W
R5/RRR5-11/3	1749.792	1748.915	-70.792	0.564	2487.630	0.414	34	0.344	K.SYELPDGQVITIGAER.F
R5/RRR5-1/2	1749.721	1748.915	-111.303	0.589	1878.812	0.600	27	0.274	K.SYELPDGQVITIGAER.F
R5/RRR5-10/2	1748.169	1748.915	-1001.712	0.556	1849.657	0.565	27	0.260	K.SYELPDGQVITIGAER.F
R5/RRR5-11/2	1748.459	1748.915	-261.377	0.533	1855.938	0.535	27	0.253	K.SYELPDGQVITIGAER.F
R5/RRR5-11/2	1826.504	1827.024	-834.672	0.538	1892.876	0.509	21	0.250	K.LAYVALDYEQELEAAK.S
R5/RRR5-11/2	1748.367	1748.915	-888.362	0.556	1696.697	0.570	26	0.240	K.SYELPDGQVITIGAER.F
R5/RRR5-11/2	1826.446	1827.024	-866.607	0.527	1902.234	0.470	21	0.240	K.LAYVALDYEQELEAAK.S
R5/RRR5-10/2	1826.554	1827.024	-258.179	0.564	1830.114	0.510	21	0.240	K.LAYVALDYEQELEAAK.S
R5/RRR5-10/2	1748.336	1748.915	-906.025	0.516	1720.317	0.547	26	0.237	K.SYELPDGQVITIGAER.F
R5/RRR5-10/2	1748.362	1748.915	-890.815	0.521	1725.607	0.519	26	0.231	K.SYELPDGQVITIGAER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1826.247	1827.024	-976.317	0.503	1748.874	0.496	21	0.227	K.LAYVALDYEQELEAAK.S
R5/RRR5-10/2	1825.620	1827.024	-1320.766	0.356	1955.205	0.375	21	0.226	K.LAYVALDYEQELEAAK.S
R5/RRR5-12/2	1748.227	1748.915	-968.693	0.509	1670.371	0.498	26	0.219	K.SYELPDGQVITIGAER.F
R5/RRR5-12/2	1748.428	1748.915	-279.589	0.539	1552.202	0.558	25	0.219	K.SYELPDGQVITIGAER.F
R5/RRR5-10/2	1826.137	1827.024	-1036.449	0.446	1884.248	0.383	22	0.218	K.LAYVALDYEQELEAAK.S
R5/RRR5-11/3	1748.605	1748.915	-177.935	0.430	1845.204	0.429	29	0.209	K.SYELPDGQVITIGAER.F
R5/RRR5-10/2	1430.098	1430.504	-285.062	0.440	1570.390	0.500	18	0.207	K.GEYDESGPAIVHR.K
R5/RRR5-13/2	1748.316	1748.915	-917.521	0.523	1417.724	0.563	24	0.205	K.SYELPDGQVITIGAER.F
R5/RRR5-11/2	1747.985	1748.915	-1107.585	0.513	1479.770	0.523	25	0.203	K.SYELPDGQVITIGAER.F
R5/RRR5-2/2	1748.466	1748.915	-257.385	0.501	1424.690	0.522	24	0.197	K.SYELPDGQVITIGAER.F
R5/RRR5-12/2	1749.454	1748.915	-264.378	0.597	1298.998	0.578	24	0.197	K.SYELPDGQVITIGAER.F
R5/RRR5-1/2	1748.261	1748.915	-949.064	0.484	1331.890	0.529	24	0.189	K.SYELPDGQVITIGAER.F
R5/RRR5-13/2	1748.388	1748.915	-876.236	0.524	1283.864	0.474	24	0.175	K.SYELPDGQVITIGAER.F
R5/RRR5-10/2	976.650	977.013	-372.281	0.442	1404.228	0.402	16	0.173	K.AGFAGDDAPR.A
R5/RRR5-10/3	1749.062	1748.915	84.196	0.545	1593.294	0.452	29	0.173	K.SYELPDGQVITIGAER.F
R5/RRR5-11/2	976.751	977.013	-269.079	0.483	1199.200	0.451	16	0.166	K.AGFAGDDAPR.A
R5/RRR5-10/2	976.709	977.013	-311.837	0.465	1239.997	0.418	16	0.163	K.AGFAGDDAPR.A
R5/RRR5-13/2	1132.950	1133.193	-214.799	0.479	930.999	0.538	16	0.163	R.GYSFTTTAER.E
R5/RRR5-10/2	1132.995	1133.193	-175.022	0.433	847.337	0.571	16	0.161	R.GYSFTTTAER.E
R5/RRR5-10/2	976.226	977.013	-1835.320	0.406	1305.090	0.362	16	0.158	K.AGFAGDDAPR.A
R5/RRR5-11/2	976.601	977.013	-423.075	0.417	1230.733	0.388	16	0.157	K.AGFAGDDAPR.A
R5/RRR5-9/2	976.320	977.013	-1738.707	0.341	1248.081	0.377	16	0.155	K.AGFAGDDAPR.A
R5/RRR5-10/2	976.320	977.013	-1738.958	0.341	1242.695	0.357	16	0.152	K.AGFAGDDAPR.A
R5/RRR5-10/2	976.736	977.013	-284.502	0.391	1004.681	0.408	15	0.146	K.AGFAGDDAPR.A
R5/RRR5-11/2	1163.910	1164.355	-383.542	0.373	749.873	0.493	16	0.143	K.EITALAPSSM*K.I
R5/RRR5-11/2	976.376	977.013	-1681.677	0.277	1097.578	0.361	15	0.141	K.AGFAGDDAPR.A
R5/RRR5-10/2	1163.944	1164.355	-353.972	0.349	917.509	0.413	17	0.141	K.EITALAPSSM*K.I
R5/RRR5-13/2	1132.455	1133.193	-1539.531	0.368	793.024	0.443	16	0.141	R.GYSFTTTAER.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1132.910	1133.193	-249.930	0.427	797.617	0.417	16	0.140	R.GYSFTTTAER.E
R5/RRR5-11/2	1163.208	1164.355	-1851.170	0.346	702.429	0.437	16	0.135	K.EITALAPSSM*K.I
R5/RRR5-10/2	1133.209	1133.193	14.736	0.402	813.220	0.369	16	0.135	R.GYSFTTTAER.E
R5/RRR5-10/2	1164.014	1164.355	-293.680	0.386	709.285	0.420	15	0.135	K.EITALAPSSM*K.I
R5/RRR5-13/2	1132.439	1133.193	-1553.174	0.350	761.425	0.375	16	0.133	R.GYSFTTTAER.E
R5/RRR5-13/2	1164.091	1164.355	-227.714	0.336	522.408	0.477	14	0.133	K.EITALAPSSM*K.I
R5/RRR5-9/2	1132.742	1133.193	-399.237	0.305	613.476	0.435	15	0.132	R.GYSFTTTAER.E
R5/RRR5-1/2	976.324	977.013	-1735.315	0.293	930.530	0.317	14	0.130	K.AGFAGDDAPR.A
R5/RRR5-11/2	1163.380	1164.355	-1702.821	0.243	734.489	0.383	16	0.127	K.EITALAPSSM*K.I
R5/RRR5-10/2	1133.030	1133.193	-144.111	0.339	850.606	0.248	16	0.124	R.GYSFTTTAER.E
R5/RRR5-16/2	1132.668	1133.193	-1350.506	0.303	714.150	0.246	16	0.122	R.GYSFTTTAER.E
R5/RRR5-24/2	1748.952	1748.915	21.239	0.287	514.964	0.385	15	0.122	K.SYELPDGQVITIGAER.F
R5/RRR5-10/2	1163.374	1164.355	-1707.987	0.233	615.015	0.336	15	0.122	K.EITALAPSSM*K.I
R5/RRR5-16/2	1134.069	1133.193	-109.432	0.405	547.509	0.238	14	0.120	-.GYSFTTTAER.-
R5/RRR5-10/2	1148.031	1148.355	-283.005	0.333	593.904	0.210	13	0.117	K.EITALAPSSMK.I
R5/RRR5-11/3	1515.790	1516.687	-1255.085	0.504	1096.555	0.432	23	0.110	K.IWHHTFYNELR.V
R5/RRR5-10/3	1516.661	1516.687	-17.495	0.508	930.659	0.476	21	0.109	K.IWHHTFYNELR.V
R5/RRR5-10/3	1516.665	1516.687	-14.710	0.515	1005.632	0.437	23	0.106	K.IWHHTFYNELR.V
R5/RRR5-11/3	1516.347	1516.687	-224.729	0.539	982.480	0.434	22	0.104	K.IWHHTFYNELR.V
R5/RRR5-10/3	1516.539	1516.687	-97.666	0.477	879.780	0.423	21	0.097	K.IWHHTFYNELR.V
R5/RRR5-10/3	1430.445	1430.504	-41.788	0.286	466.431	0.555	24	0.094	K.GEYDESGPAIVHR.K
R5/RRR5-11/3	1429.633	1430.504	-1312.609	0.319	325.118	0.472	20	0.092	K.GEYDESGPAIVHR.K
R5/RRR5-11/3	1161.707	1161.381	281.374	0.452	1156.298	0.316	22	0.091	R.HTGVM*VGMGQK.D
R5/RRR5-11/3	1430.862	1430.504	250.996	0.297	404.248	0.477	24	0.089	K.GEYDESGPAIVHR.K
R5/RRR5-10/3	1145.485	1145.381	90.723	0.447	871.582	0.377	20	0.089	R.HTGVMVGMGQK.D
R5/RRR5-10/3	1429.664	1430.504	-1291.000	0.308	214.159	0.360	17	0.084	-.GEYDESGPAIVHR.-
R5/RRR5-11/3	1430.737	1430.504	163.345	0.258	579.003	0.442	26	0.082	K.GEYDESGPAIVHR.K
R5/RRR5-10/3	1429.729	1430.504	-1245.726	0.246	407.653	0.360	23	0.082	K.GEYDESGPAIVHR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/3	1145.210	1145.381	-150.288	0.372	763.910	0.350	20	0.079	-.HTGVMVGMGQK.-
R5/RRR5-10/3	1430.169	1430.504	-234.932	0.212	586.080	0.392	26	0.076	K.GEYDESGPAIVHR.K
R5/RRR5-11/3	1515.306	1516.687	-1575.696	0.344	782.520	0.290	19	0.075	K.IWHHTFYNELR.V
R5/RRR5-11/3	1161.028	1161.381	-305.162	0.401	846.601	0.255	19	0.071	-.HTGVM*VGMGQK.-
R5/RRR5-10/3	1144.894	1145.381	-426.719	0.382	730.742	0.247	17	0.062	-.HTGVMVGMGQK.-
R5/RRR5-10/2	1907.480	1907.088	206.335	0.623	2134.065	0.577	24	0.309	K.LSYIALDYDQEM*ETAK.T
R5/RRR5-10/2	1906.527	1907.088	-821.462	0.573	2054.038	0.483	23	0.267	K.LSYIALDYDQEM*ETAK.T
R5/RRR5-10/2	1460.170	1460.531	-247.327	0.406	1761.150	0.518	19	0.234	K.AEYDESGPSIVHR.K
R5/RRR5-10/2	1906.468	1907.088	-852.057	0.570	1710.175	0.508	22	0.225	K.LSYIALDYDQEM*ETAK.T
R5/RRR5-11/2	1460.090	1460.531	-302.518	0.397	1570.222	0.480	18	0.202	K.AEYDESGPSIVHR.K
R5/RRR5-10/2	1460.057	1460.531	-325.082	0.426	1309.786	0.500	17	0.180	K.AEYDESGPSIVHR.K
R5/RRR5-11/2	1460.168	1460.531	-249.172	0.399	1288.272	0.454	17	0.169	K.AEYDESGPSIVHR.K
R5/RRR5-11/2	1460.172	1460.531	-246.489	0.417	1183.013	0.487	16	0.166	K.AEYDESGPSIVHR.K
R5/RRR5-10/2	1460.051	1460.531	-329.444	0.409	1155.873	0.447	17	0.158	K.AEYDESGPSIVHR.K
R5/RRR5-8/2	1663.430	1663.805	-226.527	0.569	3575.486	0.512	26	0.624	K.ATDSESTEVILDAALK.S
R5/RRR5-8/2	1664.087	1663.805	169.547	0.602	2942.054	0.502	24	0.448	K.ATDSESTEVILDAALK.S
R5/RRR5-8/2	1664.171	1663.805	220.598	0.614	2888.342	0.529	24	0.446	K.ATDSESTEVILDAALK.S
R5/RRR5-8/2	1761.637	1761.914	-157.324	0.571	1633.204	0.491	22	0.212	K.VENQEGVVNFDEILR.E
R5/RRR5-1/2	1761.583	1761.914	-188.606	0.487	1453.872	0.397	20	0.173	K.VENQEGVVNFDEILR.E
R5/RRR5-8/2	955.927	956.208	-294.409	0.484	1266.718	0.448	15	0.171	K.AALIVVLTR.G
R5/RRR5-8/2	956.177	956.208	-32.090	0.505	1314.822	0.411	14	0.167	K.AALIVVLTR.G
R5/RRR5-8/2	1155.171	1155.369	-171.874	0.409	863.215	0.589	19	0.161	R.GLVPLLAEGSAK.A
R5/RRR5-8/2	1814.422	1814.097	179.725	0.478	761.871	0.610	24	0.160	R.SAPLPMSPLESLASSAVR.T
R5/RRR5-8/2	955.981	956.208	-238.296	0.460	1179.474	0.415	14	0.158	K.AALIVVLTR.G
R5/RRR5-8/2	1813.355	1814.097	-963.475	0.484	737.708	0.587	23	0.155	R.SAPLPMSPLESLASSAVR.T
R5/RRR5-8/2	1186.560	1187.285	-1458.393	0.400	1205.739	0.361	17	0.151	K.ILAGLENDDAR.V
R5/RRR5-8/2	1187.019	1187.285	-224.819	0.481	1184.036	0.361	17	0.149	K.ILAGLENDDAR.V
R5/RRR5-8/2	1814.786	1814.097	-171.742	0.530	665.849	0.560	23	0.149	R.SAPLPMSPLESLASSAVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1761.114	1761.914	-1025.078	0.463	1072.396	0.401	19	0.146	K.VENQEGVVNFDEILR.E
R5/RRR5-8/2	1204.082	1204.376	-244.652	0.469	972.806	0.411	17	0.145	R.GDLGM*EIPVEK.I
R5/RRR5-8/2	1830.338	1830.096	132.432	0.473	459.648	0.590	22	0.145	R.SAPLPM*SPLESLASSAVR.T
R5/RRR5-1/2	1761.335	1761.914	-899.269	0.447	1185.290	0.337	19	0.143	K.VENQEGVVNFDEILR.E
R5/RRR5-8/2	1187.049	1187.285	-199.130	0.443	1069.360	0.351	17	0.142	K.ILAGLENDDAR.V
R5/RRR5-8/2	786.974	786.983	-11.063	0.446	786.350	0.370	13	0.135	R.IGVASVIK.I
R5/RRR5-8/2	787.133	786.983	191.306	0.398	828.783	0.342	13	0.132	R.IGVASVIK.I
R5/RRR5-8/2	1829.157	1830.096	-1063.160	0.423	228.987	0.527	16	0.131	R.SAPLPM*SPLESLASSAVR.T
R5/RRR5-8/2	1829.513	1830.096	-867.940	0.377	310.894	0.481	19	0.130	R.SAPLPM*SPLESLASSAVR.T
R5/RRR5-1/2	1829.839	1830.096	-140.863	0.364	277.332	0.506	18	0.130	R.SAPLPM*SPLESLASSAVR.T
R5/RRR5-8/2	1204.083	1204.376	-244.041	0.365	855.061	0.314	16	0.127	R.GDLGM*EIPVEK.I
R5/RRR5-3/2	1761.521	1761.914	-223.574	0.447	963.991	0.302	18	0.127	K.VENQEGVVNFDEILR.E
R5/RRR5-8/2	786.473	786.983	-1925.443	0.371	668.647	0.274	12	0.123	R.IGVASVIK.I
R5/RRR5-1/2	1828.858	1830.096	-1227.623	0.290	220.698	0.425	16	0.121	-.SAPLPM*SPLESLASSAVR.-
R5/RRR5-1/2	1829.353	1830.096	-955.827	0.309	204.591	0.314	15	0.120	-.SAPLPM*SPLESLASSAVR.-
R5/RRR5-7/2	1761.740	1761.914	-99.146	0.399	661.346	0.308	16	0.120	K.VENQEGVVNFDEILR.E
R5/RRR5-7/2	1155.728	1155.369	311.502	0.083	743.349	0.244	16	0.108	R.GLVPLLAEGSAK.A
R5/RRR5-8/3	1760.777	1761.914	-1217.130	0.379	1060.188	0.186	24	0.063	K.VENQEGVVNFDEILR.E
R5/RRR5-10/2	1870.463	1871.077	-865.524	0.521	2381.090	0.533	23	0.341	K.LAYIALDYEQELETAK.S
R5/RRR5-10/2	1870.739	1871.077	-181.135	0.508	2409.709	0.504	24	0.338	K.LAYIALDYEQELETAK.S
R5/RRR5-10/3	1969.902	1969.270	-187.500	0.442	1127.146	0.342	31	0.094	R.VAPEEHPILLTEAPLNPK.A
R5/RRR5-10/3	1969.336	1969.270	33.403	0.448	786.595	0.359	27	0.081	R.VAPEEHPILLTEAPLNPK.A
R5/RRR5-11/3	1970.047	1969.270	-113.560	0.422	923.797	0.294	30	0.077	R.VAPEEHPILLTEAPLNPK.A
R5/RRR5-11/3	1969.033	1969.270	-120.956	0.386	891.600	0.263	29	0.072	R.VAPEEHPILLTEAPLNPK.A
R5/RRR5-10/3	1669.346	1669.773	-256.537	0.480	2637.571	0.460	34	1.000	K.KLESSAHYSADFGKE.-
R5/RRR5-10/3	1669.553	1669.773	-132.422	0.461	2223.313	0.429	31	0.671	K.KLESSAHYSADFGKE.-
R5/RRR5-11/2	1670.488	1669.773	-171.479	0.590	2097.226	0.570	24	0.402	K.KLESSAHYSADFGKE.-
R5/RRR5-10/2	1163.291	1163.265	22.565	0.536	2207.330	0.388	19	0.266	K.LAEGFNGADLR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1260.251	1260.378	-100.709	0.557	1825.450	0.560	18	0.257	K.HGEIDYEAVVK.L
R5/RRR5-11/2	1260.431	1260.378	42.779	0.603	1777.259	0.583	18	0.257	K.HGEIDYEAVVK.L
R5/RRR5-10/2	1259.481	1260.378	-1510.538	0.558	1801.265	0.553	18	0.252	K.HGEIDYEAVVK.L
R5/RRR5-10/2	1162.739	1163.265	-1316.737	0.506	2176.430	0.341	19	0.249	K.LAEGFNGADLR.N
R5/RRR5-11/2	1276.891	1277.451	-1225.775	0.467	1683.367	0.518	19	0.226	R.AIASNIDANFLK.I
R5/RRR5-11/2	1277.055	1277.451	-311.170	0.473	1844.910	0.371	19	0.212	R.AIASNIDANFLK.I
R5/RRR5-10/2	1259.736	1260.378	-1307.392	0.546	1404.263	0.530	17	0.198	K.HGEIDYEAVVK.L
R5/RRR5-10/2	1276.508	1277.451	-1527.125	0.347	1515.656	0.445	18	0.189	R.AIASNIDANFLK.I
R5/RRR5-11/2	1276.992	1277.451	-360.563	0.453	1342.942	0.482	18	0.182	R.AIASNIDANFLK.I
R5/RRR5-10/2	1276.385	1277.451	-1623.868	0.414	1302.911	0.445	18	0.171	R.AIASNIDANFLK.I
R5/RRR5-10/2	1162.945	1163.265	-276.007	0.398	1393.893	0.321	17	0.158	K.LAEGFNGADLR.N
R5/RRR5-10/2	1158.311	1159.360	-1773.648	0.362	1192.576	0.410	17	0.156	K.GVLLYGPPGTGK.T
R5/RRR5-10/2	1159.118	1159.360	-208.893	0.418	966.303	0.476	17	0.152	K.GVLLYGPPGTGK.T
R5/RRR5-9/2	1158.567	1159.360	-1551.859	0.387	952.619	0.488	16	0.151	K.GVLLYGPPGTGK.T
R5/RRR5-11/2	1159.143	1159.360	-187.024	0.397	863.432	0.490	16	0.147	K.GVLLYGPPGTGK.T
R5/RRR5-9/2	1159.023	1159.360	-291.625	0.421	858.619	0.484	16	0.147	K.GVLLYGPPGTGK.T
R5/RRR5-10/2	1817.736	1818.127	-215.858	0.456	784.610	0.449	21	0.139	R.ESIELPLM*NPELFLR.V
R5/RRR5-9/2	1159.148	1159.360	-183.326	0.295	810.165	0.372	15	0.129	K.GVLLYGPPGTGK.T
R5/RRR5-11/2	1160.247	1159.360	-97.465	0.332	586.134	0.453	13	0.126	-.GVLLYGPPGTGK.-
R5/RRR5-11/2	1817.424	1818.127	-939.969	0.369	387.253	0.310	16	0.119	R.ESIELPLM*NPELFLR.V
R5/RRR5-11/3	1652.654	1652.751	-58.432	0.461	1096.186	0.407	23	0.105	R.RFSEGTSADREIQR.T
R5/RRR5-11/3	1652.427	1652.751	-196.701	0.464	1058.229	0.413	25	0.104	R.RFSEGTSADREIQR.T
R5/RRR5-10/2	1163.978	1163.265	-247.361	0.340	477.052	0.223	12	0.094	-.LAEGFNGADLR.-
R5/RRR5-11/3	1723.136	1722.964	100.065	0.425	930.755	0.413	30	0.094	K.IVSSAIIDKYIGESAR.L
R5/RRR5-11/3	1652.557	1652.751	-117.336	0.426	968.570	0.363	22	0.089	R.RFSEGTSADREIQR.T
R5/RRR5-10/3	1653.819	1652.751	41.183	0.440	896.012	0.346	23	0.084	R.RFSEGTSADREIQR.T
R5/RRR5-10/3	1652.318	1652.751	-262.849	0.394	964.719	0.325	22	0.083	R.RFSEGTSADREIQR.T
R5/RRR5-11/3	1723.210	1722.964	143.544	0.343	644.843	0.404	24	0.080	K.IVSSAIIDKYIGESAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/3	1652.555	1652.751	-118.893	0.426	734.153	0.336	21	0.079	R.RFSEGTSADREIQR.T
R5/RRR5-23/2	1992.564	1993.113	-779.428	0.623	3133.058	0.696	27	0.584	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-21/3	1992.483	1993.113	-820.115	0.492	2416.153	0.540	38	0.378	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-24/3	1992.926	1993.113	-94.010	0.519	2183.754	0.566	36	0.330	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-22/3	1993.817	1993.113	-148.898	0.536	2036.198	0.633	37	0.325	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-24/3	1993.968	1993.113	-72.531	0.551	1955.408	0.634	36	0.306	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-23/3	1994.026	1993.113	-43.332	0.561	1812.476	0.644	36	0.278	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-22/3	1993.893	1993.113	-110.298	0.524	1791.768	0.631	35	0.270	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-23/3	1992.890	1993.113	-112.074	0.515	1787.971	0.617	35	0.263	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-21/3	1992.931	1993.113	-91.522	0.514	1989.124	0.517	36	0.262	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-23/3	1993.104	1993.113	-4.344	0.507	1857.159	0.565	36	0.255	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-24/3	1993.944	1993.113	-84.966	0.531	1689.023	0.584	35	0.230	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-24/2	1222.959	1222.321	-297.102	0.508	1631.001	0.531	20	0.223	K.LEATGDASCVAK.L
R5/RRR5-22/2	1222.082	1222.321	-196.327	0.466	1652.663	0.509	20	0.220	K.LEATGDASCVAK.L
R5/RRR5-22/2	1222.016	1222.321	-250.141	0.461	1611.814	0.515	20	0.217	K.LEATGDASCVAK.L
R5/RRR5-23/2	1221.986	1222.321	-275.396	0.477	1625.816	0.504	20	0.216	K.LEATGDASCVAK.L
R5/RRR5-22/2	1221.656	1222.321	-1366.885	0.464	1556.388	0.502	20	0.208	K.LEATGDASCVAK.L
R5/RRR5-22/3	1993.786	1993.113	-164.191	0.569	1485.341	0.611	35	0.204	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-23/3	1992.821	1993.113	-146.822	0.473	1511.351	0.539	32	0.185	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-24/2	1222.066	1222.321	-209.054	0.457	1335.361	0.488	19	0.182	K.LEATGDASCVAK.L
R5/RRR5-23/2	1221.972	1222.321	-286.321	0.449	1332.948	0.453	19	0.176	K.LEATGDASCVAK.L
R5/RRR5-24/2	1221.861	1222.321	-377.333	0.440	1286.020	0.445	19	0.170	K.LEATGDASCVAK.L
R5/RRR5-23/2	1221.497	1222.321	-1497.770	0.403	1239.884	0.411	19	0.161	K.LEATGDASCVAK.L
R5/RRR5-22/3	1993.207	1993.113	47.439	0.474	1360.650	0.524	31	0.160	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-23/3	1992.995	1993.113	-59.082	0.501	1395.117	0.511	32	0.159	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-24/2	1222.072	1222.329	-211.156	0.414	945.600	0.506	20	0.157	K.LNPSADAGSVYK.T
R5/RRR5-22/3	1992.531	1993.113	-796.038	0.469	1304.197	0.515	31	0.150	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-22/3	1993.014	1993.113	-49.406	0.469	1229.636	0.536	31	0.147	K.SHSTETKLEATGDASCVAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1221.960	1222.329	-303.157	0.342	837.163	0.481	19	0.145	K.LNPSADAGSVYK.T
R5/RRR5-23/2	1221.961	1222.329	-302.756	0.354	995.715	0.406	20	0.145	K.LNPSADAGSVYK.T
R5/RRR5-20/3	1992.441	1993.113	-841.425	0.460	1349.332	0.477	30	0.144	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-23/2	1221.904	1222.321	-342.550	0.409	948.414	0.414	16	0.143	K.LEATGDASCVAK.L
R5/RRR5-23/2	1221.970	1222.329	-295.239	0.377	757.355	0.468	19	0.142	K.LNPSADAGSVYK.T
R5/RRR5-23/2	1160.927	1161.201	-236.727	0.409	1274.881	0.274	17	0.142	K.DGASLSPEQEK.M
R5/RRR5-22/2	1221.973	1222.329	-292.533	0.388	741.059	0.470	18	0.142	K.LNPSADAGSVYK.T
R5/RRR5-24/2	1221.975	1222.329	-291.129	0.383	824.350	0.434	19	0.141	K.LNPSADAGSVYK.T
R5/RRR5-23/2	1221.998	1222.329	-272.288	0.303	860.237	0.436	19	0.139	K.LNPSADAGSVYK.T
R5/RRR5-24/2	1221.608	1222.329	-1413.243	0.262	827.133	0.443	19	0.136	K.LNPSADAGSVYK.T
R5/RRR5-20/3	1992.163	1993.113	-981.300	0.413	1238.181	0.488	31	0.136	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-21/2	1221.906	1222.329	-347.258	0.373	627.180	0.440	17	0.135	K.LNPSADAGSVYK.T
R5/RRR5-23/2	1221.778	1222.321	-1266.537	0.363	914.350	0.361	16	0.135	K.LEATGDASCVAK.L
R5/RRR5-23/2	994.960	995.151	-193.028	0.374	577.453	0.424	13	0.134	K.LTVEYELK.D
R5/RRR5-23/2	1161.007	1161.201	-167.847	0.417	898.134	0.343	16	0.132	-.DGASLSPEQEK.-
R5/RRR5-23/2	1343.730	1342.560	127.052	0.464	847.541	0.368	15	0.131	K.IVVCDSATHVLK.A
R5/RRR5-23/2	1167.955	1168.361	-348.623	0.470	848.152	0.336	14	0.130	K.VCLDVHSLPK.V
R5/RRR5-23/2	1160.343	1161.201	-1606.146	0.329	931.819	0.305	16	0.129	K.DGASLSPEQEK.M
R5/RRR5-23/3	1993.244	1993.113	65.958	0.461	1045.864	0.529	29	0.128	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-23/2	994.458	995.151	-1708.104	0.277	645.420	0.390	13	0.128	K.LTVEYELK.D
R5/RRR5-24/2	995.017	995.151	-135.061	0.356	585.634	0.332	13	0.128	K.LTVEYELK.D
R5/RRR5-22/2	1168.065	1168.361	-254.672	0.501	757.065	0.335	14	0.128	K.VCLDVHSLPK.V
R5/RRR5-23/2	1221.963	1222.321	-294.138	0.364	882.162	0.301	16	0.128	K.LEATGDASCVAK.L
R5/RRR5-24/2	994.815	995.151	-339.146	0.315	605.883	0.347	13	0.127	K.LTVEYELK.D
R5/RRR5-23/2	1168.111	1168.361	-214.832	0.472	692.832	0.329	14	0.127	K.VCLDVHSLPK.V
R5/RRR5-22/2	1168.127	1168.361	-201.203	0.424	826.735	0.302	14	0.127	K.VCLDVHSLPK.V
R5/RRR5-23/2	1343.388	1342.560	-128.654	0.440	715.863	0.329	17	0.127	K.IVVCDSATHVLK.A
R5/RRR5-22/2	1221.421	1222.329	-1567.431	0.235	545.360	0.460	16	0.127	K.LNPSADAGSVYK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1168.069	1168.361	-250.897	0.464	763.205	0.312	14	0.126	K.VCLDVHSLPK.V
R5/RRR5-22/2	1168.122	1168.361	-205.606	0.468	760.492	0.309	14	0.126	K.VCLDVHSLPK.V
R5/RRR5-22/2	1343.592	1342.560	24.275	0.405	906.822	0.270	17	0.125	-.IVVCDSATHVLK.-
R5/RRR5-24/2	994.369	995.151	-1797.772	0.256	536.582	0.383	12	0.125	K.LTVEYELK.D
R5/RRR5-23/2	994.334	995.151	-1832.558	0.260	653.292	0.331	13	0.124	K.LTVEYELK.D
R5/RRR5-23/3	1992.243	1993.113	-941.068	0.444	1003.777	0.509	30	0.120	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-24/2	1343.691	1342.560	98.171	0.344	254.644	0.286	12	0.117	-.IVVCDSATHVLK.-
R5/RRR5-20/3	1992.529	1993.113	-797.053	0.467	979.235	0.497	29	0.116	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-20/3	1992.805	1993.113	-154.748	0.440	899.193	0.504	30	0.112	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-21/3	1993.412	1993.113	150.528	0.450	993.318	0.451	29	0.107	K.SHSTETKLEATGDASCVAK.L
R5/RRR5-9/3	1638.356	1638.812	-279.325	0.506	1594.323	0.473	31	0.179	R.FRGEDKPPAHLGASR.D
R5/RRR5-9/3	1638.446	1638.812	-223.937	0.537	1459.582	0.529	30	0.177	R.FRGEDKPPAHLGASR.D
R5/RRR5-9/3	1639.947	1638.812	82.743	0.526	1363.162	0.503	30	0.155	R.FRGEDKPPAHLGASR.D
R5/RRR5-10/2	1730.425	1730.933	-874.436	0.498	2355.646	0.440	24	0.308	R.FFYASSACIYPEFK.Q
R5/RRR5-10/2	1283.064	1283.370	-238.907	0.496	1797.266	0.577	22	0.258	K.TQGVDIAGYGSSK.V
R5/RRR5-10/2	1558.545	1557.779	-150.487	0.532	1834.801	0.534	23	0.250	R.ISITGAGGFIGSHIAR.R
R5/RRR5-10/2	1558.236	1557.779	294.525	0.526	1715.945	0.506	22	0.226	R.ISITGAGGFIGSHIAR.R
R5/RRR5-10/2	1282.856	1283.370	-1183.330	0.459	1506.158	0.584	20	0.219	K.TQGVDIAGYGSSK.V
R5/RRR5-10/2	1674.369	1672.854	-290.274	0.539	1708.588	0.449	20	0.212	R.SFTFIDECVEGVLR.Y
R5/RRR5-10/2	1557.463	1557.779	-203.105	0.451	1678.329	0.442	22	0.207	R.ISITGAGGFIGSHIAR.R
R5/RRR5-10/3	1468.173	1467.654	-328.965	0.438	1794.134	0.451	27	0.201	R.FHNIYGPFGTWK.G
R5/RRR5-10/2	1283.114	1283.370	-200.062	0.539	1250.950	0.601	19	0.197	K.TQGVDIAGYGSSK.V
R5/RRR5-10/2	1673.423	1672.854	-257.952	0.515	1510.352	0.481	19	0.196	R.SFTFIDECVEGVLR.Y
R5/RRR5-10/2	1455.275	1455.685	-282.654	0.513	1371.649	0.459	20	0.179	K.VVSTQAPVQLGSLR.A
R5/RRR5-10/3	1468.634	1467.654	-14.108	0.524	1296.737	0.521	26	0.151	R.FHNIYGPFGTWK.G
R5/RRR5-11/2	1732.092	1730.933	92.133	0.457	970.380	0.445	20	0.148	R.FFYASSACIYPEFK.Q
R5/RRR5-10/2	1906.414	1906.983	-825.503	0.455	634.549	0.521	22	0.142	K.ESDAWPAEPQDAYGLEK.L
R5/RRR5-10/2	1907.340	1906.983	187.852	0.498	590.216	0.532	21	0.141	K.ESDAWPAEPQDAYGLEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1468.289	1467.654	-249.545	0.464	758.107	0.455	16	0.140	R.FHNIYGPFGTWK.G
R5/RRR5-10/3	1455.212	1455.685	-325.627	0.418	1499.761	0.360	26	0.133	K.VVSTQAPVQLGSLR.A
R5/RRR5-10/2	1906.347	1906.983	-860.921	0.396	544.500	0.466	21	0.132	K.ESDAWPAEPQDAYGLEK.L
R5/RRR5-10/2	1729.660	1730.933	-1318.371	0.358	976.703	0.313	19	0.131	R.FFYASSACIYPEFK.Q
R5/RRR5-10/2	1468.869	1467.654	146.736	0.446	669.487	0.377	15	0.129	R.FHNIYGPFGTWK.G
R5/RRR5-11/2	1468.241	1467.654	-282.409	0.402	717.193	0.365	14	0.127	R.FHNIYGPFGTWK.G
R5/RRR5-10/2	1468.398	1467.654	-175.318	0.428	678.220	0.347	15	0.125	-.FHNIYGPFGTWK.-
R5/RRR5-9/2	1455.075	1455.685	-1109.917	0.367	1020.605	0.241	18	0.123	K.VVSTQAPVQLGSLR.A
R5/RRR5-11/2	1468.334	1467.654	-218.519	0.339	605.993	0.290	13	0.119	R.FHNIYGPFGTWK.G
R5/RRR5-10/2	1467.348	1467.654	-209.654	0.291	622.377	0.244	15	0.119	R.FHNIYGPFGTWK.G
R5/RRR5-10/3	1406.681	1406.524	111.522	0.443	995.000	0.385	21	0.094	K.SEGHYIIASDWK.K
R5/RRR5-10/3	1672.186	1672.854	-1000.304	0.395	1046.398	0.369	25	0.091	R.SFTFIDECVEGVLR.Y
R5/RRR5-10/3	1466.876	1467.654	-1216.057	0.389	999.520	0.347	23	0.087	R.FHNIYGPFGTWK.G
R5/RRR5-10/3	1406.666	1406.524	100.817	0.478	787.396	0.375	19	0.084	K.SEGHYIIASDWK.K
R5/RRR5-10/3	1406.830	1406.524	217.774	0.449	690.597	0.398	18	0.082	-.SEGHYIIASDWK.-
R5/RRR5-10/3	1455.335	1455.685	-241.176	0.398	943.953	0.326	23	0.081	K.VVSTQAPVQLGSLR.A
R5/RRR5-10/3	1454.735	1455.685	-1344.077	0.381	700.860	0.299	21	0.073	K.VVSTQAPVQLGSLR.A
R5/RRR5-10/3	1466.828	1467.654	-1248.775	0.312	866.921	0.139	20	0.061	-.FHNIYGPFGTWK.-
R5/RRR5-10/2	1550.638	1549.792	-99.457	0.432	345.730	0.451	20	0.135	K.YLPEDPLFQLVSK.L
R5/RRR5-10/2	1549.248	1549.792	-999.694	0.229	237.380	0.362	16	0.121	K.YLPEDPLFQLVSK.L
R5/RRR5-10/2	1550.360	1549.792	-279.376	0.189	395.209	0.339	20	0.118	K.YLPEDPLFQLVSK.L
R5/RRR5-9/2	1793.813	1794.107	-164.331	0.567	2607.598	0.593	23	0.406	R.IHFMLSSYAPVISAEK.A
R5/RRR5-9/2	1793.451	1794.107	-926.106	0.559	2534.176	0.566	23	0.381	R.IHFMLSSYAPVISAEK.A
R5/RRR5-10/2	1532.695	1532.807	-73.621	0.499	2364.050	0.521	22	0.334	R.LISQIISSLTTSLR.F
R5/RRR5-9/2	1809.028	1810.107	-1152.353	0.563	1985.765	0.610	23	0.294	R.IHFM*LSSYAPVISAEK.A
R5/RRR5-9/2	1793.716	1794.107	-218.606	0.543	1985.810	0.591	21	0.287	R.IHFMLSSYAPVISAEK.A
R5/RRR5-9/2	1809.214	1810.107	-1049.099	0.562	1768.903	0.611	24	0.261	R.IHFM*LSSYAPVISAEK.A
R5/RRR5-9/2	1532.403	1532.807	-264.992	0.449	1911.336	0.436	20	0.235	R.LISQIISSLTTSLR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1717.350	1716.956	229.951	0.564	1755.929	0.521	23	0.235	R.AIFVDLEPTVIDEVR.T
R5/RRR5-9/2	1531.960	1532.807	-1209.501	0.359	1695.193	0.457	21	0.212	R.LISQIISSLTTSLR.F
R5/RRR5-9/2	1809.428	1810.107	-930.357	0.554	1353.316	0.621	21	0.210	R.IHFM*LSSYAPVISAEK.A
R5/RRR5-9/2	1531.727	1532.807	-1362.038	0.376	1729.170	0.411	20	0.206	R.LISQIISSLTTSLR.F
R5/RRR5-9/2	1001.502	1002.147	-1647.555	0.391	1385.840	0.536	17	0.194	K.DVNAAVATIK.T
R5/RRR5-10/2	1717.352	1716.956	231.447	0.586	1442.347	0.467	24	0.188	R.AIFVDLEPTVIDEVR.T
R5/RRR5-9/2	1716.366	1716.956	-929.178	0.536	1393.849	0.460	24	0.183	R.AIFVDLEPTVIDEVR.T
R5/RRR5-9/2	1001.514	1002.147	-1635.310	0.471	1246.275	0.526	16	0.182	K.DVNAAVATIK.T
R5/RRR5-9/2	1001.470	1002.147	-1679.517	0.470	1200.952	0.535	16	0.180	K.DVNAAVATIK.T
R5/RRR5-10/2	1716.409	1716.956	-904.117	0.513	1409.392	0.439	24	0.180	R.AIFVDLEPTVIDEVR.T
R5/RRR5-9/2	1716.864	1716.956	-53.779	0.514	1376.393	0.426	24	0.174	R.AIFVDLEPTVIDEVR.T
R5/RRR5-10/2	1001.966	1002.147	-181.414	0.460	1159.112	0.521	16	0.174	K.DVNAAVATIK.T
R5/RRR5-10/2	1002.013	1002.147	-133.629	0.469	1111.859	0.540	16	0.174	K.DVNAAVATIK.T
R5/RRR5-9/2	1001.898	1002.147	-248.883	0.489	1109.969	0.508	16	0.169	K.DVNAAVATIK.T
R5/RRR5-8/2	1001.874	1002.147	-273.331	0.473	1135.796	0.494	17	0.169	K.DVNAAVATIK.T
R5/RRR5-9/2	1873.433	1873.093	182.298	0.509	988.973	0.536	24	0.162	K.CGINYQPPSVVPGGDLAK.V
R5/RRR5-1/2	1001.870	1002.147	-276.998	0.332	1106.216	0.492	16	0.161	K.DVNAAVATIK.T
R5/RRR5-10/2	1716.458	1716.956	-290.860	0.508	1161.512	0.437	21	0.158	R.AIFVDLEPTVIDEVR.T
R5/RRR5-9/2	1872.365	1873.093	-925.393	0.457	958.405	0.528	24	0.158	K.CGINYQPPSVVPGGDLAK.V
R5/RRR5-10/2	1001.444	1002.147	-1705.112	0.400	934.162	0.503	14	0.154	K.DVNAAVATIK.T
R5/RRR5-8/2	1717.873	1716.956	-48.295	0.504	1043.882	0.454	21	0.154	R.AIFVDLEPTVIDEVR.T
R5/RRR5-7/2	1002.894	1002.147	-252.909	0.431	1075.001	0.428	15	0.153	K.DVNAAVATIK.T
R5/RRR5-1/2	1001.610	1002.147	-1538.583	0.285	1086.566	0.415	16	0.148	K.DVNAAVATIK.T
R5/RRR5-9/2	1872.574	1873.093	-813.418	0.460	778.082	0.517	22	0.146	K.CGINYQPPSVVPGGDLAK.V
R5/RRR5-22/2	1001.860	1002.147	-286.900	0.395	780.214	0.426	15	0.139	K.DVNAAVATIK.T
R5/RRR5-7/2	1002.101	1002.147	-45.525	0.352	1233.273	0.260	15	0.138	K.DVNAAVATIK.T
R5/RRR5-8/2	1001.916	1002.147	-230.793	0.363	1248.989	0.246	15	0.134	-.DVNAAVATIK.-
R5/RRR5-7/2	1002.485	1002.147	338.722	0.306	827.414	0.312	14	0.128	K.DVNAAVATIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1001.722	1002.147	-425.788	0.244	654.980	0.389	13	0.126	K.DVNAAVATIK.T
R5/RRR5-9/3	1717.751	1716.956	-119.797	0.480	1129.054	0.491	28	0.125	R.AIFVDLEPTVIDEVR.T
R5/RRR5-9/2	1132.992	1133.271	-247.102	0.298	816.960	0.306	13	0.123	K.EIVDLCLDR.V
R5/RRR5-20/2	1716.337	1716.956	-946.244	0.437	529.226	0.330	17	0.118	-.AIFVDLEPTVIDEVR.-
R5/RRR5-9/3	1811.382	1810.107	152.666	0.427	1160.337	0.394	27	0.107	R.IHFM*LSSYAPVISAEK.A
R5/RRR5-1/3	1693.152	1692.855	176.355	0.429	379.213	0.510	23	0.102	R.SLDIERPTYTNLNR.L
R5/RRR5-8/3	1692.950	1692.855	56.720	0.387	334.681	0.474	22	0.098	R.SLDIERPTYTNLNR.L
R5/RRR5-2/3	1693.501	1692.855	-209.246	0.368	319.295	0.434	23	0.097	R.SLDIERPTYTNLNR.L
R5/RRR5-8/3	1692.610	1692.855	-144.760	0.427	429.943	0.436	25	0.096	R.SLDIERPTYTNLNR.L
R5/RRR5-9/3	1693.000	1692.855	86.008	0.422	668.313	0.454	29	0.095	R.SLDIERPTYTNLNR.L
R5/RRR5-8/3	1692.835	1692.855	-11.516	0.404	393.062	0.393	23	0.093	R.SLDIERPTYTNLNR.L
R5/RRR5-9/3	1692.517	1692.855	-200.217	0.388	500.685	0.436	27	0.093	R.SLDIERPTYTNLNR.L
R5/RRR5-9/3	1810.822	1810.107	-157.736	0.413	1144.545	0.329	28	0.093	R.IHFM*LSSYAPVISAEK.A
R5/RRR5-2/3	1693.036	1692.855	107.484	0.378	380.600	0.343	24	0.092	R.SLDIERPTYTNLNR.L
R5/RRR5-9/3	1397.445	1397.604	-113.918	0.374	292.123	0.542	19	0.091	R.QLFHPEQLISGK.E
R5/RRR5-10/3	1692.919	1692.855	38.062	0.391	545.597	0.418	27	0.091	R.SLDIERPTYTNLNR.L
R5/RRR5-10/3	1692.156	1692.855	-1006.696	0.383	457.520	0.397	24	0.091	R.SLDIERPTYTNLNR.L
R5/RRR5-9/3	1693.004	1692.855	88.177	0.376	536.251	0.414	27	0.090	R.SLDIERPTYTNLNR.L
R5/RRR5-10/3	1692.789	1692.855	-38.748	0.389	532.751	0.391	26	0.089	R.SLDIERPTYTNLNR.L
R5/RRR5-14/3	1692.567	1692.855	-170.697	0.347	553.141	0.402	27	0.088	R.SLDIERPTYTNLNR.L
R5/RRR5-9/3	1397.753	1397.604	107.241	0.307	214.289	0.434	17	0.081	-.QLFHPEQLISGK.-
R5/RRR5-9/3	1811.769	1810.107	-186.982	0.378	932.163	0.275	25	0.074	R.IHFM*LSSYAPVISAEK.A
R5/RRR5-9/3	1794.441	1794.107	186.460	0.366	982.062	0.234	27	0.071	R.IHFMLSSYAPVISAEK.A
R5/RRR5-9/3	1794.044	1794.107	-35.537	0.288	828.584	0.172	26	0.063	R.IHFMLSSYAPVISAEK.A
R5/RRR5-3/2	1559.068	1558.757	199.816	0.517	1835.809	0.513	20	0.245	K.LVYELFTDTLTSR.L
R5/RRR5-3/2	1558.418	1558.757	-218.222	0.406	1615.139	0.468	19	0.206	K.LVYELFTDTLTSR.L
R5/RRR5-3/2	1558.224	1558.757	-986.943	0.366	1789.326	0.369	19	0.204	K.LVYELFTDTLTSR.L
R5/RRR5-3/2	1095.942	1096.219	-253.557	0.388	1399.819	0.441	14	0.177	R.HDNVQLLEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1226.829	1227.392	-1278.289	0.452	1156.147	0.491	18	0.168	K.IIGLDGSEAPVR.V
R5/RRR5-3/2	1508.449	1508.761	-208.014	0.468	1176.465	0.462	20	0.165	R.LTEPSFLESLM*PK.K
R5/RRR5-3/2	1508.336	1508.761	-282.953	0.452	1017.645	0.488	20	0.158	R.LTEPSFLESLM*PK.K
R5/RRR5-3/2	1509.382	1508.761	-252.500	0.507	1000.335	0.483	19	0.157	R.LTEPSFLESLM*PK.K
R5/RRR5-2/2	1558.455	1558.757	-194.648	0.332	1305.357	0.359	18	0.155	K.LVYELFTDTLTSR.L
R5/RRR5-3/2	1237.074	1237.409	-271.297	0.443	1114.006	0.387	20	0.150	R.LGSM*ETGTGLVR.A
R5/RRR5-3/2	1226.365	1227.392	-1658.253	0.321	1302.815	0.300	20	0.147	K.IIGLDGSEAPVR.V
R5/RRR5-3/2	1492.829	1492.762	45.141	0.423	1081.956	0.379	21	0.147	R.LTEPSFLESLMPK.K
R5/RRR5-2/2	1227.233	1227.392	-130.356	0.398	1194.614	0.332	18	0.146	K.IIGLDGSEAPVR.V
R5/RRR5-3/2	1226.357	1227.392	-1664.553	0.353	1209.769	0.293	18	0.141	K.IIGLDGSEAPVR.V
R5/RRR5-3/2	1493.027	1492.762	177.984	0.415	1083.287	0.334	20	0.140	R.LTEPSFLESLMPK.K
R5/RRR5-3/2	909.190	909.065	137.681	0.357	563.683	0.422	13	0.134	K.YGSLTVLR.E
R5/RRR5-3/2	1237.078	1237.409	-268.723	0.431	734.097	0.388	18	0.133	R.LGSM*ETGTGLVR.A
R5/RRR5-3/2	1237.062	1237.409	-281.197	0.453	822.878	0.350	18	0.132	R.LGSM*ETGTGLVR.A
R5/RRR5-27/2	908.404	909.065	-1833.927	0.335	422.757	0.487	12	0.131	-.YGSLTVLR.-
R5/RRR5-2/2	908.982	909.065	-90.733	0.310	370.639	0.462	11	0.131	K.YGSLTVLR.E
R5/RRR5-26/2	909.070	909.065	5.305	0.331	457.783	0.384	12	0.129	K.YGSLTVLR.E
R5/RRR5-27/2	908.510	909.065	-1716.601	0.300	349.638	0.405	12	0.129	K.YGSLTVLR.E
R5/RRR5-2/2	1226.408	1227.392	-1622.553	0.281	972.060	0.272	17	0.127	K.IIGLDGSEAPVR.V
R5/RRR5-3/2	1236.099	1236.396	-241.348	0.451	837.742	0.327	15	0.126	R.FIDLASEVVDK.H
R5/RRR5-27/2	909.025	909.065	-44.126	0.250	384.404	0.429	12	0.126	K.YGSLTVLR.E
R5/RRR5-3/2	909.024	909.065	-44.934	0.315	392.206	0.376	12	0.126	-.YGSLTVLR.-
R5/RRR5-3/2	1492.012	1492.762	-1176.235	0.276	704.333	0.349	16	0.124	R.LTEPSFLESLMPK.K
R5/RRR5-3/2	909.112	909.065	52.307	0.262	333.591	0.278	11	0.122	-.YGSLTVLR.-
R5/RRR5-3/2	1056.525	1056.153	352.687	0.268	995.390	0.253	12	0.122	R.AFEYAQQAK.E
R5/RRR5-3/3	1403.546	1403.608	-44.421	0.447	734.125	0.432	23	0.092	K.FKLEDGAEIKPR.V
R5/RRR5-3/3	1404.041	1403.608	308.897	0.456	841.718	0.374	22	0.088	K.FKLEDGAEIKPR.V
R5/RRR5-2/3	1403.599	1403.608	-6.474	0.444	498.856	0.350	20	0.085	K.FKLEDGAEIKPR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/3	1404.128	1403.608	-343.447	0.449	794.690	0.348	22	0.083	K.FKLEDGAEIKPR.V
R5/RRR5-2/3	1403.487	1403.608	-86.559	0.420	753.382	0.309	21	0.078	K.FKLEDGAEIKPR.V
R5/RRR5-7/2	1815.500	1815.103	219.407	0.624	2856.180	0.583	25	0.459	R.TLKEWIVSSLGPDAVAK.H
R5/RRR5-7/2	1814.429	1815.103	-925.521	0.576	2603.788	0.529	25	0.382	R.TLKEWIVSSLGPDAVAK.H
R5/RRR5-7/2	1814.741	1815.103	-200.083	0.596	2258.514	0.588	23	0.333	R.TLKEWIVSSLGPDAVAK.H
R5/RRR5-7/2	1896.321	1896.130	101.070	0.538	1030.267	0.526	25	0.165	R.YLAVEPSTPYNTTTLPK.-
R5/RRR5-7/2	1896.163	1896.130	17.588	0.542	961.764	0.542	24	0.163	R.YLAVEPSTPYNTTTLPK.-
R5/RRR5-7/2	1371.780	1372.530	-1279.678	0.405	1083.660	0.479	19	0.160	K.TFTTAETM*LNAR.T
R5/RRR5-7/2	1372.041	1372.530	-357.529	0.490	908.809	0.523	18	0.157	K.TFTTAETM*LNAR.T
R5/RRR5-7/2	1844.352	1844.139	115.402	0.550	881.505	0.510	23	0.151	R.SIKDLDPETTLVVVVSK.T
R5/RRR5-7/2	1372.122	1372.530	-297.812	0.497	784.708	0.498	17	0.147	K.TFTTAETM*LNAR.T
R5/RRR5-7/3	1703.796	1703.901	-61.834	0.494	1356.500	0.469	31	0.145	K.FAPHIQQLSM*ESNGK.G
R5/RRR5-8/2	1316.230	1316.488	-196.051	0.440	1005.120	0.390	18	0.144	R.FLANVDPVDVAR.S
R5/RRR5-7/2	1895.416	1896.130	-906.646	0.485	631.403	0.529	20	0.141	R.YLAVEPSTPYNTTTLPK.-
R5/RRR5-7/2	949.919	950.031	-117.370	0.416	498.027	0.511	15	0.137	R.SGSWVGATGK.A
R5/RRR5-8/2	1316.134	1316.488	-269.743	0.427	836.236	0.393	17	0.137	R.FLANVDPVDVAR.S
R5/RRR5-8/2	1316.005	1316.488	-368.109	0.426	880.824	0.370	17	0.136	R.FLANVDPVDVAR.S
R5/RRR5-7/2	1233.058	1233.438	-309.464	0.429	602.132	0.413	18	0.135	R.AILPYSQALEK.F
R5/RRR5-7/2	1232.994	1233.438	-361.712	0.447	532.745	0.395	17	0.132	R.AILPYSQALEK.F
R5/RRR5-7/2	1316.210	1316.488	-211.217	0.393	881.934	0.330	16	0.130	-.FLANVDPVDVAR.-
R5/RRR5-8/2	1233.201	1233.438	-193.167	0.422	472.904	0.368	16	0.129	R.AILPYSQALEK.F
R5/RRR5-7/2	1315.630	1316.488	-1416.011	0.351	720.620	0.379	15	0.124	-.FLANVDPVDVAR.-
R5/RRR5-1/2	1316.486	1316.488	-0.987	0.405	689.404	0.327	15	0.124	-.FLANVDPVDVAR.-
R5/RRR5-8/2	1232.868	1233.438	-1277.390	0.294	471.860	0.302	16	0.123	R.AILPYSQALEK.F
R5/RRR5-7/2	1315.761	1316.488	-1316.303	0.416	917.702	0.275	17	0.122	-.FLANVDPVDVAR.-
R5/RRR5-12/2	1815.311	1815.103	114.955	0.419	1011.133	0.228	17	0.117	R.TLKEWIVSSLGPDAVAK.H
R5/RRR5-12/2	1814.416	1815.103	-932.748	0.372	1038.427	0.150	17	0.112	R.TLKEWIVSSLGPDAVAK.H
R5/RRR5-7/3	1843.888	1844.139	-136.668	0.494	1062.239	0.427	26	0.104	R.SIKDLDPETTLVVVVSK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/3	1815.224	1815.103	66.760	0.420	926.350	0.411	29	0.091	R.TLKEWIVSSLGPDAVAK.H
R5/RRR5-7/3	1703.294	1703.901	-946.471	0.385	1069.209	0.313	28	0.085	K.FAPHIQQLSM*ESNGK.G
R5/RRR5-7/3	1704.556	1703.901	-202.987	0.399	756.599	0.250	25	0.070	K.FAPHIQQLSM*ESNGK.G
R5/RRR5-7/2	1567.187	1567.722	-982.782	0.533	2277.041	0.620	26	0.352	K.IAVFAGGVDTSATETK.G
R5/RRR5-7/2	1289.029	1289.457	-332.975	0.507	1998.338	0.320	18	0.219	K.TEEAKVEELIK.A
R5/RRR5-7/2	1259.672	1260.341	-1328.841	0.413	1180.667	0.510	17	0.172	K.NPANFNVDNVR.V
R5/RRR5-7/2	1260.191	1260.341	-119.077	0.463	1143.684	0.498	17	0.169	K.NPANFNVDNVR.V
R5/RRR5-7/2	1288.389	1288.469	-62.778	0.487	1253.665	0.387	16	0.156	K.TVEILEDLVEK.G
R5/RRR5-7/2	1182.179	1182.352	-146.613	0.472	1003.560	0.458	18	0.154	K.HLSGLDEAVLK.N
R5/RRR5-8/2	1259.147	1260.341	-1747.323	0.366	954.508	0.466	17	0.149	K.NPANFNVDNVR.V
R5/RRR5-8/2	1322.262	1321.373	-84.041	0.447	1032.777	0.401	17	0.146	R.GSTDSILDDLER.A
R5/RRR5-7/2	1182.270	1182.352	-69.138	0.374	836.063	0.447	17	0.141	K.HLSGLDEAVLK.N
R5/RRR5-8/2	1425.304	1425.656	-247.364	0.427	497.543	0.530	19	0.139	R.IIPGAAATEIELAR.R
R5/RRR5-8/2	1321.446	1321.373	55.165	0.394	1093.401	0.322	16	0.137	R.GSTDSILDDLER.A
R5/RRR5-8/2	1425.379	1425.656	-194.438	0.364	478.138	0.505	19	0.134	R.IIPGAAATEIELAR.R
R5/RRR5-7/2	1226.947	1227.343	-323.778	0.320	866.034	0.417	15	0.134	K.YSADAACTVLR.V
R5/RRR5-8/2	1322.109	1321.373	-200.365	0.449	811.993	0.380	15	0.132	R.GSTDSILDDLER.A
R5/RRR5-7/2	1321.233	1321.373	-106.440	0.264	921.888	0.278	17	0.125	R.GSTDSILDDLER.A
R5/RRR5-7/2	1320.615	1321.373	-1335.291	0.264	718.305	0.279	15	0.120	R.GSTDSILDDLER.A
R5/RRR5-7/2	1424.908	1425.656	-1230.254	0.249	387.286	0.332	14	0.117	R.IIPGAAATEIELAR.R
R5/RRR5-13/2	1330.000	1330.456	-343.799	0.490	1893.768	0.522	20	0.256	K.FSNACGAICTTK.K
R5/RRR5-13/2	1331.054	1330.456	-303.514	0.494	1612.449	0.511	19	0.217	K.FSNACGAICTTK.K
R5/RRR5-13/2	1452.064	1452.588	-1052.774	0.531	1649.072	0.496	19	0.216	K.SAGILCSYDPNVR.L
R5/RRR5-12/2	1453.237	1452.588	-242.441	0.517	1613.594	0.494	19	0.212	K.SAGILCSYDPNVR.L
R5/RRR5-12/2	1452.986	1452.588	274.401	0.519	1630.526	0.481	19	0.211	K.SAGILCSYDPNVR.L
R5/RRR5-12/2	1331.070	1330.456	-290.724	0.482	1628.437	0.475	19	0.210	K.FSNACGAICTTK.K
R5/RRR5-12/2	1451.997	1452.588	-1099.284	0.467	1609.293	0.485	19	0.209	K.SAGILCSYDPNVR.L
R5/RRR5-13/2	1452.158	1452.588	-297.172	0.463	1531.486	0.491	19	0.202	K.SAGILCSYDPNVR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1329.956	1330.456	-1131.665	0.496	1526.365	0.474	19	0.199	K.FSNACGAICTTK.K
R5/RRR5-12/2	1330.104	1330.456	-265.345	0.492	1494.898	0.455	20	0.192	K.FSNACGAICTTK.K
R5/RRR5-13/2	1452.128	1452.588	-318.089	0.487	1391.406	0.490	18	0.187	K.SAGILCSYDPNVR.L
R5/RRR5-13/2	1906.611	1907.287	-881.351	0.525	872.496	0.605	22	0.163	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-13/2	1907.807	1907.287	-252.061	0.497	855.372	0.606	23	0.163	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-12/2	1778.376	1779.114	-980.360	0.412	871.685	0.603	24	0.162	K.GAIPALPTVAVAQELISK.A
R5/RRR5-13/2	1906.798	1907.287	-257.267	0.512	827.795	0.597	22	0.159	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-13/2	1778.605	1779.114	-851.024	0.405	808.439	0.594	24	0.157	K.GAIPALPTVAVAQELISK.A
R5/RRR5-12/2	1778.443	1779.114	-942.321	0.403	813.657	0.576	24	0.155	K.GAIPALPTVAVAQELISK.A
R5/RRR5-13/3	1906.361	1907.287	-1012.943	0.453	1316.386	0.513	30	0.153	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-13/2	1778.509	1779.114	-905.111	0.434	661.055	0.595	22	0.150	K.GAIPALPTVAVAQELISK.A
R5/RRR5-12/2	1906.462	1907.287	-959.770	0.434	813.568	0.531	22	0.148	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-12/2	1906.180	1907.287	-1108.544	0.426	802.252	0.537	22	0.148	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-12/2	1778.288	1779.114	-1030.050	0.361	883.831	0.466	24	0.144	K.GAIPALPTVAVAQELISK.A
R5/RRR5-13/3	1907.137	1907.287	-78.883	0.467	1421.885	0.435	28	0.143	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-12/2	1254.505	1255.404	-1518.383	0.442	491.792	0.519	15	0.141	R.LPLWPSEDAAR.A
R5/RRR5-13/2	1255.070	1255.404	-266.771	0.425	703.830	0.460	16	0.140	R.LPLWPSEDAAR.A
R5/RRR5-13/2	1235.022	1234.254	-188.619	0.424	1090.066	0.325	16	0.140	K.DDSIFHNEEK.L
R5/RRR5-12/2	1256.158	1255.404	-196.460	0.475	488.623	0.479	15	0.138	R.LPLWPSEDAAR.A
R5/RRR5-12/2	1255.203	1255.404	-160.616	0.393	568.643	0.479	16	0.138	R.LPLWPSEDAAR.A
R5/RRR5-13/2	1503.234	1503.599	-243.011	0.354	760.298	0.440	16	0.135	K.DDSIFHNEEKLR.E
R5/RRR5-13/2	1254.532	1255.404	-1496.880	0.413	800.162	0.382	15	0.134	R.LPLWPSEDAAR.A
R5/RRR5-13/2	1504.145	1503.599	-302.449	0.398	683.630	0.424	17	0.133	K.DDSIFHNEEKLR.E
R5/RRR5-13/2	1778.602	1779.114	-852.471	0.397	636.655	0.443	21	0.133	K.GAIPALPTVAVAQELISK.A
R5/RRR5-13/2	1254.657	1255.404	-1396.999	0.419	458.453	0.438	14	0.132	R.LPLWPSEDAAR.A
R5/RRR5-17/2	1256.635	1255.404	184.574	0.350	370.419	0.495	13	0.132	R.LPLWPSEDAAR.A
R5/RRR5-10/2	1778.753	1779.114	-203.374	0.367	604.318	0.437	20	0.130	K.GAIPALPTVAVAQELISK.A
R5/RRR5-13/2	1254.935	1255.404	-374.998	0.329	407.886	0.426	13	0.128	R.LPLWPSEDAAR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1779.669	1779.114	-250.464	0.353	408.590	0.420	18	0.126	K.GAIPALPTVAVAQELISK.A
R5/RRR5-13/2	1233.741	1234.254	-1230.241	0.418	777.393	0.293	14	0.124	K.DDSIFHNEEK.L
R5/RRR5-17/2	1256.605	1255.404	160.512	0.288	423.660	0.331	13	0.123	R.LPLWPSEDAAR.A
R5/RRR5-13/2	1778.401	1779.114	-965.957	0.286	289.736	0.429	15	0.122	K.GAIPALPTVAVAQELISK.A
R5/RRR5-3/2	1778.033	1779.114	-1173.565	0.318	401.830	0.297	18	0.120	K.GAIPALPTVAVAQELISK.A
R5/RRR5-17/2	1256.127	1255.404	-221.222	0.218	425.276	0.343	12	0.120	R.LPLWPSEDAAR.A
R5/RRR5-13/2	1233.933	1234.254	-260.724	0.388	598.228	0.259	13	0.119	K.DDSIFHNEEK.L
R5/RRR5-12/3	1907.246	1907.287	-21.488	0.382	777.788	0.467	27	0.095	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-12/3	1908.287	1907.287	0.339	0.281	948.020	0.268	25	0.070	K.KGAIPALPTVAVAQELISK.A
R5/RRR5-18/3	1806.686	1807.001	-174.926	0.584	3553.410	0.556	40	0.811	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/3	1808.136	1807.001	74.945	0.588	3302.610	0.523	40	0.677	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-18/3	1806.919	1807.001	-45.516	0.600	2934.114	0.542	38	0.550	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/3	1807.236	1807.001	130.298	0.594	2819.368	0.563	37	0.524	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-18/3	1806.911	1807.001	-50.090	0.589	2635.610	0.536	36	0.447	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/2	1806.653	1807.001	-193.050	0.575	2334.702	0.669	27	0.378	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/2	1806.472	1807.001	-848.875	0.566	2322.211	0.620	26	0.358	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/3	1805.874	1807.001	-1181.244	0.535	2219.827	0.570	33	0.349	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/2	1807.318	1807.001	176.163	0.597	2023.401	0.655	25	0.314	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/2	1507.360	1506.644	-189.143	0.565	1808.466	0.524	22	0.245	R.LAWHSAGTFDVSSK.T
R5/RRR5-17/2	1499.353	1498.663	-207.873	0.560	1534.619	0.538	18	0.214	K.AFFEDYKEAHLK.L
R5/RRR5-17/2	1506.257	1506.644	-258.049	0.493	1533.547	0.524	22	0.210	R.LAWHSAGTFDVSSK.T
R5/RRR5-17/2	1506.217	1506.644	-284.068	0.466	1242.292	0.455	21	0.168	R.LAWHSAGTFDVSSK.T
R5/RRR5-17/2	1498.206	1498.663	-306.099	0.531	1177.888	0.465	18	0.166	K.AFFEDYKEAHLK.L
R5/RRR5-17/2	1556.458	1556.831	-240.050	0.496	992.250	0.541	21	0.165	K.ALLSDPAFRPLVEK.Y
R5/RRR5-14/3	1808.199	1807.001	109.780	0.435	1364.878	0.489	30	0.151	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/3	1808.154	1807.001	84.796	0.466	1284.698	0.518	31	0.150	K.TPAELSHAANAGLDIAVR.M
R5/RRR5-17/2	1498.417	1498.663	-165.105	0.486	892.957	0.481	16	0.149	K.AFFEDYKEAHLK.L
R5/RRR5-17/2	1008.685	1009.096	-408.647	0.447	997.181	0.392	14	0.145	R.SGFEGPWTK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1009.041	1009.096	-55.284	0.488	1018.213	0.362	14	0.142	R.SGFEGPWTK.N
R5/RRR5-15/2	1099.491	1100.247	-1601.833	0.372	1091.737	0.331	15	0.140	K.EGLLQLPSDK.A
R5/RRR5-18/2	1556.339	1556.831	-316.614	0.451	777.249	0.445	19	0.140	K.ALLSDPAFRPLVEK.Y
R5/RRR5-17/2	1008.914	1009.096	-181.257	0.470	982.783	0.357	14	0.140	R.SGFEGPWTK.N
R5/RRR5-16/2	1100.099	1100.247	-135.515	0.473	964.234	0.359	16	0.139	K.EGLLQLPSDK.A
R5/RRR5-17/2	1101.032	1100.247	-196.450	0.475	835.375	0.399	15	0.139	K.EGLLQLPSDK.A
R5/RRR5-17/2	1100.073	1100.247	-158.557	0.417	917.377	0.373	15	0.138	K.EGLLQLPSDK.A
R5/RRR5-17/2	1556.351	1556.831	-309.296	0.454	792.479	0.420	19	0.138	K.ALLSDPAFRPLVEK.Y
R5/RRR5-17/2	1557.355	1556.831	-306.266	0.457	663.242	0.458	18	0.137	K.ALLSDPAFRPLVEK.Y
R5/RRR5-17/2	1008.538	1009.096	-1549.867	0.399	976.450	0.338	14	0.137	R.SGFEGPWTK.N
R5/RRR5-17/2	1008.960	1009.096	-135.864	0.417	930.489	0.343	14	0.136	R.SGFEGPWTK.N
R5/RRR5-17/2	1008.905	1009.096	-190.117	0.434	938.020	0.340	14	0.136	R.SGFEGPWTK.N
R5/RRR5-18/2	1556.448	1556.831	-246.896	0.424	662.164	0.430	18	0.134	K.ALLSDPAFRPLVEK.Y
R5/RRR5-19/2	1557.315	1556.831	311.681	0.315	1101.205	0.270	18	0.131	K.ALLSDPAFRPLVEK.Y
R5/RRR5-16/2	1100.112	1100.247	-123.160	0.438	899.189	0.306	15	0.130	K.EGLLQLPSDK.A
R5/RRR5-15/2	1556.215	1556.831	-1041.480	0.341	598.444	0.428	17	0.130	K.ALLSDPAFRPLVEK.Y
R5/RRR5-18/2	1008.710	1009.096	-383.754	0.332	936.921	0.267	14	0.127	R.SGFEGPWTK.N
R5/RRR5-15/2	1100.107	1100.247	-128.057	0.362	842.204	0.278	14	0.125	K.EGLLQLPSDK.A
R5/RRR5-18/2	1008.486	1009.096	-1601.909	0.295	750.342	0.209	13	0.119	R.SGFEGPWTK.N
R5/RRR5-15/2	1556.123	1556.831	-1100.552	0.261	493.728	0.284	15	0.119	K.ALLSDPAFRPLVEK.Y
R5/RRR5-15/3	1310.130	1310.441	-238.374	0.449	926.065	0.473	25	0.105	R.LPDATKGSDHLR.Q
R5/RRR5-17/3	1506.527	1506.644	-77.957	0.409	996.746	0.386	27	0.094	R.LAWHSAGTFDVSSK.T
R5/RRR5-16/3	1309.488	1310.441	-1496.153	0.483	639.119	0.441	23	0.093	R.LPDATKGSDHLR.Q
R5/RRR5-16/3	1309.594	1310.441	-1415.115	0.417	559.306	0.403	22	0.087	R.LPDATKGSDHLR.Q
R5/RRR5-16/3	1310.013	1310.441	-327.839	0.351	685.658	0.420	23	0.085	R.LPDATKGSDHLR.Q
R5/RRR5-17/3	1505.721	1506.644	-1281.042	0.406	728.896	0.393	23	0.084	R.LAWHSAGTFDVSSK.T
R5/RRR5-17/3	1507.239	1506.644	-269.750	0.431	575.848	0.362	23	0.082	R.LAWHSAGTFDVSSK.T
R5/RRR5-7/2	1704.738	1705.010	-160.224	0.533	2291.387	0.549	23	0.328	K.SALGILM*NLGLIEESK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1704.484	1705.010	-898.323	0.503	2289.444	0.481	23	0.306	K.SALGILM*NLGLIEESK.I
R5/RRR5-8/2	1705.487	1705.010	280.133	0.554	2158.783	0.553	23	0.305	K.SALGILM*NLGLIEESK.I
R5/RRR5-8/2	1704.385	1705.010	-956.202	0.472	1992.914	0.490	22	0.260	K.SALGILM*NLGLIEESK.I
R5/RRR5-7/2	1845.409	1845.946	-835.543	0.486	1495.941	0.564	24	0.212	R.SDSTSVGWGGPGGYVYQK.A
R5/RRR5-7/2	1846.486	1845.946	-250.021	0.559	1293.392	0.562	23	0.190	R.SDSTSVGWGGPGGYVYQK.A
R5/RRR5-8/2	1888.517	1889.052	-815.692	0.496	1349.790	0.515	21	0.186	K.LTSSPWSELDGLQPETK.I
R5/RRR5-7/2	1888.580	1889.052	-250.996	0.469	1342.256	0.518	21	0.186	K.LTSSPWSELDGLQPETK.I
R5/RRR5-7/2	1889.290	1889.052	126.137	0.542	1315.133	0.525	20	0.183	K.LTSSPWSELDGLQPETK.I
R5/RRR5-8/2	1845.394	1845.946	-843.577	0.516	1187.459	0.575	22	0.183	R.SDSTSVGWGGPGGYVYQK.A
R5/RRR5-8/2	1846.449	1845.946	-270.250	0.539	1159.826	0.585	22	0.182	R.SDSTSVGWGGPGGYVYQK.A
R5/RRR5-7/2	1603.999	1603.761	148.572	0.472	1458.966	0.428	21	0.181	K.GFLTINSQPAVNGER.S
R5/RRR5-7/2	1845.244	1845.946	-925.459	0.485	1140.127	0.558	22	0.175	R.SDSTSVGWGGPGGYVYQK.A
R5/RRR5-8/2	1887.790	1889.052	-1202.166	0.465	1320.672	0.457	21	0.172	K.LTSSPWSELDGLQPETK.I
R5/RRR5-7/2	1200.092	1199.381	-241.244	0.475	1371.304	0.394	16	0.169	K.LQEEWAVPVK.S
R5/RRR5-8/2	1845.450	1845.946	-269.601	0.461	1082.603	0.551	21	0.169	R.SDSTSVGWGGPGGYVYQK.A
R5/RRR5-8/2	1198.524	1199.381	-1553.550	0.353	1427.209	0.365	16	0.167	K.LQEEWAVPVK.S
R5/RRR5-8/2	1888.123	1889.052	-1024.925	0.445	1339.141	0.414	21	0.166	K.LTSSPWSELDGLQPETK.I
R5/RRR5-8/2	1703.768	1705.010	-1319.740	0.313	1310.172	0.437	18	0.165	K.SALGILM*NLGLIEESK.I
R5/RRR5-7/2	1704.324	1705.010	-992.228	0.345	1307.598	0.396	19	0.160	K.SALGILM*NLGLIEESK.I
R5/RRR5-7/2	1603.206	1603.761	-972.998	0.442	1213.336	0.395	22	0.156	K.GFLTINSQPAVNGER.S
R5/RRR5-8/2	1199.033	1199.381	-290.471	0.383	1206.028	0.392	15	0.155	K.LQEEWAVPVK.S
R5/RRR5-7/2	1603.164	1603.761	-999.219	0.491	1086.781	0.423	20	0.151	K.GFLTINSQPAVNGER.S
R5/RRR5-8/2	1604.112	1603.761	219.393	0.474	988.642	0.444	20	0.148	K.GFLTINSQPAVNGER.S
R5/RRR5-8/2	1603.274	1603.761	-304.596	0.495	1061.603	0.414	20	0.148	K.GFLTINSQPAVNGER.S
R5/RRR5-7/2	990.041	990.133	-92.888	0.467	1019.018	0.392	15	0.147	K.IDDALTTIK.S
R5/RRR5-8/2	1604.123	1603.761	226.108	0.516	1001.025	0.425	20	0.146	K.GFLTINSQPAVNGER.S
R5/RRR5-7/2	990.007	990.133	-127.891	0.509	985.895	0.393	15	0.146	K.IDDALTTIK.S
R5/RRR5-7/2	1888.610	1889.052	-235.174	0.482	983.615	0.436	18	0.143	K.LTSSPWSELDGLQPETK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1200.127	1199.381	-211.855	0.543	1000.729	0.396	14	0.143	K.LQEEWAVPVK.S
R5/RRR5-8/2	1603.511	1603.761	-156.575	0.499	949.699	0.420	19	0.142	K.GFLTINSQPAVNGER.S
R5/RRR5-7/2	990.178	990.133	45.366	0.438	816.274	0.409	14	0.140	K.IDDALTTIK.S
R5/RRR5-8/2	1199.037	1199.381	-287.304	0.406	953.331	0.384	14	0.140	K.LQEEWAVPVK.S
R5/RRR5-7/2	1603.057	1603.761	-1066.039	0.421	941.822	0.398	19	0.139	K.GFLTINSQPAVNGER.S
R5/RRR5-8/2	1886.452	1887.045	-846.765	0.449	604.826	0.464	19	0.133	R.NPSYGALTDYQFTRPR.G
R5/RRR5-8/2	989.472	990.133	-1683.114	0.361	892.364	0.337	14	0.133	K.IDDALTTIK.S
R5/RRR5-8/2	1886.489	1887.045	-827.148	0.475	649.876	0.433	20	0.132	R.NPSYGALTDYQFTRPR.G
R5/RRR5-8/2	989.575	990.133	-1579.010	0.399	872.878	0.325	14	0.132	K.IDDALTTIK.S
R5/RRR5-27/2	989.751	990.133	-386.961	0.379	659.493	0.381	13	0.132	K.IDDALTTIK.S
R5/RRR5-16/2	1889.497	1889.052	236.021	0.438	778.069	0.416	17	0.131	K.LTSSPWSELDGLQPETK.I
R5/RRR5-27/2	989.932	990.133	-203.099	0.379	661.478	0.369	13	0.131	K.IDDALTTIK.S
R5/RRR5-7/2	1198.506	1199.381	-1568.897	0.281	1006.135	0.272	14	0.129	-.LQEEWAVPVK.-
R5/RRR5-8/2	989.915	990.133	-220.542	0.350	755.651	0.326	13	0.128	K.IDDALTTIK.S
R5/RRR5-11/2	990.936	990.133	-199.063	0.364	722.603	0.280	13	0.125	K.IDDALTTIK.S
R5/RRR5-7/2	1886.427	1887.045	-860.017	0.384	459.452	0.409	17	0.124	R.NPSYGALTDYQFTRPR.G
R5/RRR5-8/2	1165.068	1165.313	-210.769	0.326	763.720	0.315	11	0.123	K.AYLEFFCSK.E
R5/RRR5-11/2	990.765	990.133	-372.848	0.293	583.182	0.258	12	0.121	K.IDDALTTIK.S
R5/RRR5-8/2	1165.374	1165.313	52.362	0.304	1004.713	0.208	13	0.121	K.AYLEFFCSK.E
R5/RRR5-1/2	989.889	990.133	-247.017	0.260	700.899	0.222	12	0.119	K.IDDALTTIK.S
R5/RRR5-7/3	1885.539	1887.045	-1865.031	0.310	736.865	0.463	24	0.092	R.NPSYGALTDYQFTRPR.G
R5/RRR5-8/3	1886.458	1887.045	-843.524	0.340	610.517	0.471	24	0.091	R.NPSYGALTDYQFTRPR.G
R5/RRR5-8/3	1886.664	1887.045	-202.294	0.328	736.224	0.423	24	0.088	R.NPSYGALTDYQFTRPR.G
R5/RRR5-9/3	1885.438	1887.045	-1918.411	0.285	590.839	0.440	21	0.085	R.NPSYGALTDYQFTRPR.G
R5/RRR5-8/3	1886.909	1887.045	-72.331	0.309	468.329	0.389	20	0.081	R.NPSYGALTDYQFTRPR.G
R5/RRR5-7/3	1885.692	1887.045	-1251.460	0.335	492.019	0.352	21	0.080	R.NPSYGALTDYQFTRPR.G
R5/RRR5-22/2	1567.187	1566.739	286.281	0.575	2198.838	0.538	23	0.309	K.VYFDVEIDGKPAGR.V
R5/RRR5-21/2	1566.130	1566.739	-1030.978	0.498	1741.850	0.540	21	0.239	K.VYFDVEIDGKPAGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1565.726	1566.739	-1289.766	0.503	1676.201	0.539	21	0.230	K.VYFDVEIDGKPAGR.V
R5/RRR5-21/2	1566.219	1566.739	-973.931	0.503	1696.916	0.490	21	0.221	K.VYFDVEIDGKPAGR.V
R5/RRR5-22/2	1566.310	1566.739	-274.811	0.522	1499.032	0.564	20	0.214	K.VYFDVEIDGKPAGR.V
R5/RRR5-22/2	1925.716	1925.198	-251.052	0.598	1244.459	0.615	26	0.199	R.IIPSFMIQGGDFTLGDGR.G
R5/RRR5-22/3	1639.535	1639.905	-226.516	0.474	1753.907	0.425	30	0.193	K.IKHTGPGLLSM*ANAGR.D
R5/RRR5-21/2	1926.426	1925.198	119.066	0.549	850.442	0.661	24	0.174	R.IIPSFMIQGGDFTLGDGR.G
R5/RRR5-22/2	1924.348	1925.198	-964.339	0.520	1063.103	0.558	26	0.172	R.IIPSFMIQGGDFTLGDGR.G
R5/RRR5-22/2	1924.919	1925.198	-145.315	0.557	915.682	0.575	25	0.165	R.IIPSFMIQGGDFTLGDGR.G
R5/RRR5-22/2	1940.518	1941.197	-867.860	0.483	784.079	0.568	26	0.157	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-21/2	1942.560	1941.197	187.392	0.555	628.599	0.600	25	0.155	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-21/2	1940.604	1941.197	-823.594	0.498	713.273	0.567	26	0.154	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-22/2	1640.675	1639.905	-140.456	0.488	736.717	0.579	23	0.154	K.IKHTGPGLLSM*ANAGR.D
R5/RRR5-22/2	1940.550	1941.197	-851.252	0.502	599.317	0.569	25	0.150	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-22/2	1940.359	1941.197	-950.150	0.451	653.819	0.571	24	0.150	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-21/2	1940.664	1941.197	-792.339	0.497	625.542	0.552	25	0.148	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-21/2	1398.015	1398.574	-1118.230	0.385	557.623	0.607	21	0.148	K.HTGPGLLSM*ANAGR.D
R5/RRR5-22/2	1399.203	1398.574	-265.512	0.427	389.272	0.576	20	0.143	K.HTGPGLLSM*ANAGR.D
R5/RRR5-21/2	1924.630	1925.198	-817.054	0.464	536.056	0.530	20	0.139	R.IIPSFMIQGGDFTLGDGR.G
R5/RRR5-22/2	1398.159	1398.574	-297.410	0.396	389.970	0.533	19	0.138	K.HTGPGLLSM*ANAGR.D
R5/RRR5-22/2	1398.262	1398.574	-223.310	0.398	512.179	0.506	19	0.137	K.HTGPGLLSM*ANAGR.D
R5/RRR5-21/2	866.986	867.091	-121.100	0.364	438.231	0.441	11	0.132	R.VVM*GLFGK.T
R5/RRR5-19/2	1940.593	1941.197	-829.214	0.405	316.089	0.533	17	0.132	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-21/2	1398.219	1398.574	-254.140	0.333	355.836	0.496	19	0.132	K.HTGPGLLSM*ANAGR.D
R5/RRR5-22/2	866.949	867.091	-164.603	0.414	651.214	0.338	13	0.130	R.VVM*GLFGK.T
R5/RRR5-21/2	866.972	867.091	-137.625	0.330	703.299	0.343	13	0.129	R.VVM*GLFGK.T
R5/RRR5-21/2	1398.178	1398.574	-284.096	0.286	423.915	0.467	20	0.129	K.HTGPGLLSM*ANAGR.D
R5/RRR5-21/2	867.082	867.091	-10.381	0.392	796.654	0.293	13	0.128	R.VVM*GLFGK.T
R5/RRR5-22/2	866.830	867.091	-301.775	0.324	829.440	0.286	13	0.127	R.VVM*GLFGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	866.955	867.091	-157.116	0.351	601.829	0.274	13	0.125	R.VVM*GLFGK.T
R5/RRR5-22/2	1941.355	1941.197	81.492	0.273	237.800	0.378	16	0.123	R.IIPSFM*IQGGDFTLGDGR.G
R5/RRR5-22/2	850.633	851.092	-540.998	0.186	312.814	0.418	11	0.121	R.VVMGLFGK.T
R5/RRR5-22/2	850.854	851.092	-280.114	0.141	229.672	0.392	9	0.117	R.VVMGLFGK.T
R5/RRR5-21/3	1996.388	1995.378	5.475	0.377	1024.067	0.445	29	0.103	R.VVMGLFGKTVPKTAENFR.A
R5/RRR5-22/3	1399.550	1398.574	-17.136	0.468	1020.300	0.412	24	0.100	K.HTGPGLLSM*ANAGR.D
R5/RRR5-22/3	1228.897	1229.365	-382.407	0.505	1168.793	0.327	20	0.095	-.SKADLTEVTHK.-
R5/RRR5-22/3	1230.414	1229.365	39.533	0.483	1037.731	0.285	21	0.081	K.SKADLTEVTHK.V
R5/RRR5-22/3	1229.335	1229.365	-24.323	0.428	927.153	0.304	20	0.078	-.SKADLTEVTHK.-
R5/RRR5-22/3	1399.596	1398.574	15.932	0.351	815.985	0.304	23	0.073	K.HTGPGLLSM*ANAGR.D
R5/RRR5-25/3	1457.638	1456.668	-20.724	0.495	1779.167	0.467	29	0.401	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/3	1457.320	1456.668	-239.629	0.485	1765.936	0.445	28	0.389	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/2	1535.698	1536.798	-1371.671	0.474	2234.775	0.521	24	0.310	K.KLLGVTIYSSDAIR.S
R5/RRR5-26/2	1535.491	1536.798	-1506.932	0.444	2247.922	0.479	23	0.299	K.KLLGVTIYSSDAIR.S
R5/RRR5-25/2	1536.507	1536.798	-189.619	0.530	2049.020	0.568	23	0.293	K.KLLGVTIYSSDAIR.S
R5/RRR5-26/2	1537.249	1536.798	294.643	0.551	2043.292	0.561	23	0.290	K.KLLGVTIYSSDAIR.S
R5/RRR5-26/2	1456.263	1456.668	-279.267	0.446	1669.737	0.531	21	0.273	R.SGTLIDAIGIYVHP.-
R5/RRR5-20/2	1457.064	1456.668	272.793	0.475	1603.617	0.577	21	0.261	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1838.296	1838.014	154.279	0.556	1832.795	0.585	27	0.260	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1536.406	1536.798	-255.535	0.534	1869.408	0.532	22	0.255	K.KLLGVTIYSSDAIR.S
R5/RRR5-24/2	1457.428	1456.668	-165.380	0.494	1555.277	0.615	21	0.254	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/2	1456.295	1456.668	-256.897	0.441	1590.647	0.497	21	0.247	R.SGTLIDAIGIYVHP.-
R5/RRR5-20/2	1456.280	1456.668	-266.989	0.416	1550.582	0.545	20	0.246	R.SGTLIDAIGIYVHP.-
R5/RRR5-24/2	1457.222	1456.668	-307.146	0.497	1525.520	0.600	21	0.245	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/2	1839.714	1838.014	-163.159	0.532	1708.472	0.562	26	0.236	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1838.516	1838.014	-271.283	0.572	1623.708	0.575	26	0.228	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/2	1456.250	1456.668	-287.845	0.441	1500.190	0.490	20	0.225	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1408.236	1408.625	-277.054	0.576	1594.749	0.548	21	0.222	K.LLGVTIYSSDAIR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	1839.365	1838.014	191.532	0.571	1556.359	0.578	25	0.220	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1456.259	1456.668	-281.790	0.429	1493.664	0.459	20	0.219	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1408.293	1408.625	-236.616	0.565	1585.938	0.534	21	0.218	K.LLGVTIYSSDAIR.S
R5/RRR5-26/2	1408.335	1408.625	-206.529	0.534	1531.301	0.544	21	0.214	K.LLGVTIYSSDAIR.S
R5/RRR5-25/2	1408.124	1408.625	-1068.843	0.517	1611.798	0.504	21	0.214	K.LLGVTIYSSDAIR.S
R5/RRR5-26/2	1408.208	1408.625	-296.709	0.489	1581.833	0.516	21	0.213	K.LLGVTIYSSDAIR.S
R5/RRR5-25/2	1536.337	1536.798	-300.733	0.515	1629.031	0.488	21	0.212	K.KLLGVTIYSSDAIR.S
R5/RRR5-24/2	1456.278	1456.668	-268.334	0.428	1472.203	0.446	19	0.212	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1456.183	1456.668	-333.935	0.434	1458.862	0.463	20	0.212	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1838.542	1838.014	-257.494	0.537	1487.029	0.574	25	0.212	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1839.368	1838.014	193.329	0.515	1563.038	0.515	25	0.207	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-22/2	1456.212	1456.668	-314.422	0.449	1410.997	0.495	20	0.206	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/2	1408.317	1408.625	-219.050	0.534	1638.011	0.452	21	0.205	K.LLGVTIYSSDAIR.S
R5/RRR5-25/2	1838.487	1838.014	258.153	0.535	1470.146	0.544	25	0.203	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/3	1456.099	1456.668	-1080.851	0.410	1335.845	0.422	25	0.202	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1838.002	1838.014	-6.103	0.558	1322.944	0.605	24	0.201	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-24/2	1408.135	1408.625	-349.155	0.465	1568.061	0.461	21	0.200	K.LLGVTIYSSDAIR.S
R5/RRR5-26/2	1838.749	1838.014	-144.068	0.514	1426.661	0.548	24	0.199	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-15/2	1456.684	1456.668	11.128	0.428	1387.399	0.463	19	0.198	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/2	1839.174	1838.014	87.634	0.515	1521.781	0.493	25	0.198	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/2	1837.171	1838.014	-1006.166	0.482	1421.970	0.537	25	0.197	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1735.354	1735.876	-880.066	0.499	1271.557	0.601	25	0.197	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1456.478	1456.668	-131.106	0.444	1314.603	0.555	19	0.196	R.SGTLIDAIGIYVHP.-
R5/RRR5-24/2	1408.150	1408.625	-338.544	0.466	1549.710	0.450	21	0.195	K.LLGVTIYSSDAIR.S
R5/RRR5-25/2	1837.493	1838.014	-829.880	0.553	1351.352	0.552	25	0.193	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-19/2	1456.315	1456.668	-243.274	0.399	1331.683	0.492	19	0.193	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1838.229	1838.014	117.518	0.541	1358.059	0.550	24	0.193	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1837.566	1838.014	-244.372	0.541	1252.656	0.589	24	0.191	K.IGPWGGNGGSAQDISVPPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1408.187	1408.625	-311.755	0.502	1492.904	0.455	21	0.191	K.LLGVTIYSSDAIR.S
R5/RRR5-25/2	1839.477	1838.014	252.823	0.543	1337.137	0.544	24	0.189	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-3/2	1457.380	1456.668	-198.402	0.392	1394.779	0.351	19	0.187	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1993.439	1993.210	115.063	0.545	1104.068	0.630	23	0.187	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1837.454	1838.014	-851.221	0.479	1277.954	0.554	24	0.186	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1838.537	1838.014	-259.893	0.568	1219.281	0.580	24	0.186	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-22/2	1456.451	1456.668	-149.435	0.404	1277.177	0.510	19	0.185	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1839.351	1838.014	183.746	0.525	1247.870	0.559	24	0.184	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/2	1837.353	1838.014	-906.643	0.481	1220.267	0.573	23	0.184	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/2	1993.619	1993.210	205.393	0.527	1007.815	0.656	23	0.183	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1837.615	1838.014	-217.381	0.544	1155.212	0.589	23	0.182	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/2	1992.514	1993.210	-853.800	0.480	1079.724	0.621	22	0.181	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1735.257	1735.876	-936.350	0.502	1114.355	0.583	23	0.179	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-24/2	1992.457	1993.210	-882.890	0.493	958.645	0.654	23	0.179	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-26/2	1735.271	1735.876	-927.734	0.452	1164.288	0.558	24	0.178	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/3	1456.405	1456.668	-180.974	0.412	1304.181	0.366	27	0.178	R.SGTLIDAIGIYVHP.-
R5/RRR5-24/2	1993.625	1993.210	208.402	0.521	955.401	0.641	22	0.176	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1838.427	1838.014	225.728	0.483	1151.767	0.557	24	0.176	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/2	1837.497	1838.014	-828.013	0.472	1186.602	0.544	23	0.176	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1838.304	1838.014	158.674	0.473	1206.183	0.532	23	0.175	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1838.354	1838.014	185.843	0.548	1114.509	0.571	23	0.175	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/2	1736.361	1735.876	279.965	0.473	1284.185	0.479	25	0.175	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1993.211	1993.210	0.515	0.533	955.431	0.629	22	0.174	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1737.154	1735.876	160.090	0.502	1136.046	0.534	24	0.173	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-26/2	1992.188	1993.210	-1018.402	0.476	991.994	0.609	22	0.172	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1838.528	1838.014	-264.689	0.525	1063.495	0.571	23	0.171	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-24/2	1992.497	1993.210	-862.656	0.480	965.100	0.610	22	0.171	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-26/2	1736.350	1735.876	273.409	0.471	1214.548	0.491	24	0.171	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1456.076	1456.668	-1096.793	0.437	1205.600	0.493	18	0.170	R.SGTLIDAIGIYVHP.-
R5/RRR5-14/2	1992.894	1993.210	-159.158	0.510	914.024	0.620	22	0.170	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1838.468	1838.014	248.166	0.520	1063.804	0.563	22	0.169	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-15/2	1457.253	1456.668	-285.463	0.385	1145.491	0.543	18	0.169	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1737.209	1735.876	192.223	0.511	1084.651	0.535	23	0.168	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1992.522	1993.210	-850.171	0.502	879.175	0.631	21	0.168	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1993.656	1993.210	224.366	0.515	922.456	0.604	22	0.168	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-19/2	1457.117	1456.668	309.082	0.418	1120.704	0.568	18	0.167	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/2	1736.249	1735.876	215.389	0.471	1205.358	0.472	24	0.167	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1736.363	1735.876	281.305	0.447	1293.451	0.430	25	0.167	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-26/2	1837.398	1838.014	-881.966	0.439	1135.677	0.512	23	0.166	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/2	1993.307	1993.210	48.610	0.510	879.212	0.617	21	0.166	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-27/2	1407.839	1408.625	-1272.478	0.475	1243.112	0.441	19	0.165	K.LLGVTIYSSDAIR.S
R5/RRR5-1/2	1735.241	1735.876	-945.531	0.419	1031.765	0.543	23	0.165	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1735.354	1735.876	-879.854	0.460	1002.557	0.543	23	0.164	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-22/2	1408.384	1408.625	-171.748	0.424	1267.256	0.420	18	0.163	K.LLGVTIYSSDAIR.S
R5/RRR5-22/2	1456.351	1456.668	-218.467	0.391	1200.395	0.414	18	0.163	R.SGTLIDAIGIYVHP.-
R5/RRR5-24/2	1737.414	1735.876	-266.844	0.453	1121.398	0.485	24	0.163	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1736.381	1735.876	-286.112	0.441	1230.817	0.435	24	0.162	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-20/2	1456.326	1456.668	-235.538	0.431	1130.613	0.512	18	0.162	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1838.530	1838.014	-263.689	0.466	1188.348	0.469	22	0.162	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-23/2	1456.148	1456.668	-1047.299	0.328	1208.008	0.357	18	0.161	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1992.653	1993.210	-783.755	0.498	847.616	0.597	21	0.161	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-22/2	1735.364	1735.876	-873.922	0.418	1005.624	0.528	23	0.161	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-15/2	1735.419	1735.876	-264.117	0.467	873.920	0.577	21	0.160	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1737.272	1735.876	228.582	0.441	1120.863	0.448	24	0.157	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-24/2	1735.512	1735.876	-210.840	0.466	887.072	0.546	22	0.157	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-26/2	1736.113	1735.876	136.843	0.486	935.283	0.524	22	0.157	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1992.504	1993.210	-859.027	0.440	815.644	0.592	20	0.156	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-15/2	1992.473	1993.210	-874.587	0.457	722.757	0.620	19	0.155	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-26/2	1735.302	1735.876	-909.796	0.435	944.311	0.513	22	0.155	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-21/2	1736.119	1735.876	140.298	0.490	890.078	0.527	21	0.154	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-24/2	1736.315	1735.876	253.247	0.452	888.141	0.512	22	0.152	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-15/2	1735.274	1735.876	-926.392	0.448	865.993	0.521	21	0.151	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-18/2	1735.469	1735.876	-235.255	0.477	826.414	0.526	21	0.151	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-21/2	1456.043	1456.668	-1119.270	0.333	1007.380	0.518	17	0.150	R.SGTLIDAIGIYVHP.-
R5/RRR5-27/2	1735.255	1735.876	-936.986	0.422	843.245	0.519	21	0.150	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-23/2	1735.396	1735.876	-277.738	0.456	763.119	0.539	20	0.148	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-11/2	1456.342	1456.668	-224.437	0.425	1067.971	0.443	17	0.147	R.SGTLIDAIGIYVHP.-
R5/RRR5-27/2	1735.110	1735.876	-1021.318	0.432	832.880	0.501	21	0.147	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-21/2	1735.039	1735.876	-1062.359	0.404	822.642	0.497	21	0.146	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-24/2	1734.745	1735.876	-1232.281	0.298	1066.843	0.407	23	0.145	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-27/2	1735.356	1735.876	-879.007	0.432	768.695	0.510	20	0.145	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-22/2	1735.915	1735.876	22.104	0.456	837.547	0.476	21	0.144	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-19/2	1409.018	1408.625	280.183	0.520	818.438	0.473	16	0.143	K.LLGVTIYSSDAIR.S
R5/RRR5-25/2	1992.760	1993.210	-226.877	0.475	487.452	0.609	17	0.143	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-23/2	1408.091	1408.625	-1092.694	0.367	936.155	0.418	17	0.142	K.LLGVTIYSSDAIR.S
R5/RRR5-20/2	1735.266	1735.876	-930.841	0.395	806.118	0.450	21	0.140	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-24/2	1838.153	1838.014	76.293	0.441	794.469	0.456	19	0.137	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-23/2	1408.192	1408.625	-308.102	0.401	631.877	0.492	14	0.137	K.LLGVTIYSSDAIR.S
R5/RRR5-20/2	1991.721	1993.210	-1253.466	0.354	804.571	0.457	18	0.137	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-20/2	1408.336	1408.625	-205.659	0.447	861.000	0.394	17	0.137	K.LLGVTIYSSDAIR.S
R5/RRR5-11/2	1456.123	1456.668	-1064.133	0.393	917.507	0.438	16	0.134	R.SGTLIDAIGIYVHP.-
R5/RRR5-21/2	1455.750	1456.668	-1321.264	0.321	823.044	0.498	16	0.134	R.SGTLIDAIGIYVHP.-
R5/RRR5-2/2	1992.676	1993.210	-772.133	0.429	534.444	0.488	18	0.133	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-26/3	1736.707	1735.876	-98.080	0.511	961.829	0.575	27	0.132	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1457.083	1456.668	285.562	0.345	841.312	0.432	16	0.131	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/3	1966.371	1966.187	93.945	0.441	1195.465	0.488	40	0.130	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/2	1456.229	1456.668	-302.563	0.329	872.487	0.374	16	0.130	R.SGTLIDAIGIYVHP.-
R5/RRR5-23/2	1456.140	1456.668	-1052.265	0.380	759.253	0.497	15	0.128	R.SGTLIDAIGIYVHP.-
R5/RRR5-6/2	1457.306	1456.668	-248.906	0.268	705.876	0.462	16	0.128	R.SGTLIDAIGIYVHP.-
R5/RRR5-16/2	1456.198	1456.668	-324.010	0.347	729.144	0.497	15	0.128	R.SGTLIDAIGIYVHP.-
R5/RRR5-26/3	1966.804	1966.187	-194.830	0.455	1087.725	0.516	37	0.128	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-23/2	1456.188	1456.668	-330.991	0.334	838.373	0.386	15	0.126	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/2	1456.192	1456.668	-327.711	0.259	815.510	0.315	16	0.126	R.SGTLIDAIGIYVHP.-
R5/RRR5-19/2	1736.538	1735.876	-195.768	0.396	374.470	0.427	15	0.126	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/2	1455.973	1456.668	-1168.013	0.251	578.749	0.269	15	0.126	R.SGTLIDAIGIYVHP.-
R5/RRR5-19/2	1456.215	1456.668	-312.235	0.301	715.187	0.437	15	0.126	R.SGTLIDAIGIYVHP.-
R5/RRR5-3/2	1456.040	1456.668	-1121.711	0.401	735.794	0.447	15	0.125	R.SGTLIDAIGIYVHP.-
R5/RRR5-22/2	1455.560	1456.668	-1452.405	0.216	762.033	0.425	15	0.125	R.SGTLIDAIGIYVHP.-
R5/RRR5-18/2	1456.266	1456.668	-276.744	0.329	705.084	0.482	14	0.125	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/3	1966.881	1966.187	-155.605	0.465	1065.601	0.505	37	0.124	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-6/2	1457.318	1456.668	-240.922	0.292	616.045	0.406	14	0.123	R.SGTLIDAIGIYVHP.-
R5/RRR5-11/2	1992.992	1993.210	-109.758	0.349	335.911	0.408	14	0.123	K.EFSIPLQDSGHVVGFFGR.S
R5/RRR5-25/2	1408.358	1408.625	-190.355	0.289	796.649	0.275	16	0.122	K.LLGVTIYSSDAIR.S
R5/RRR5-16/2	1456.393	1456.668	-189.457	0.257	686.971	0.384	14	0.121	R.SGTLIDAIGIYVHP.-
R5/RRR5-2/2	1456.217	1456.668	-310.890	0.355	644.830	0.392	14	0.121	R.SGTLIDAIGIYVHP.-
R5/RRR5-21/2	1456.110	1456.668	-1073.561	0.280	779.167	0.241	15	0.121	R.SGTLIDAIGIYVHP.-
R5/RRR5-1/2	1455.995	1456.668	-1152.607	0.309	610.079	0.449	13	0.121	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/3	1967.765	1966.187	-215.019	0.424	1038.713	0.475	36	0.115	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1966.723	1966.187	-236.299	0.437	1114.891	0.445	39	0.113	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1967.902	1966.187	-145.197	0.439	1142.251	0.415	39	0.109	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1966.549	1966.187	184.804	0.428	1034.383	0.445	39	0.108	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1735.507	1735.876	-213.247	0.522	752.908	0.539	26	0.108	-.IVTSANNTYEAGVPNGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/3	1966.731	1966.187	-232.283	0.416	1043.924	0.432	38	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1965.970	1966.187	-110.246	0.443	890.109	0.469	35	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1967.580	1966.187	200.730	0.439	990.675	0.442	37	0.106	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1966.337	1966.187	76.761	0.434	937.038	0.455	36	0.105	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1966.939	1966.187	-126.469	0.439	876.750	0.457	36	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1966.864	1966.187	-164.290	0.410	1058.338	0.410	39	0.103	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1967.238	1966.187	26.095	0.433	993.012	0.420	38	0.101	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1965.805	1966.187	-194.804	0.415	964.556	0.425	36	0.101	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1967.740	1966.187	-227.528	0.420	761.732	0.465	32	0.100	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1456.809	1456.668	97.053	0.397	1042.699	0.359	24	0.100	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/3	1966.793	1966.187	-200.620	0.395	817.573	0.446	33	0.099	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1966.249	1966.187	32.117	0.434	737.615	0.457	31	0.098	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1966.325	1966.187	70.597	0.401	729.639	0.452	32	0.097	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1736.668	1735.876	-120.607	0.442	723.359	0.467	26	0.097	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-26/3	1735.698	1735.876	-102.863	0.438	679.171	0.480	24	0.097	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/3	1965.288	1966.187	-968.740	0.405	577.790	0.441	31	0.095	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1966.424	1966.187	121.307	0.416	733.645	0.421	33	0.093	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1966.544	1966.187	182.376	0.415	702.867	0.428	30	0.093	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1966.850	1966.187	-171.668	0.461	805.374	0.411	32	0.093	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1736.731	1735.876	-83.803	0.412	786.331	0.431	25	0.093	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-26/3	1967.187	1966.187	0.235	0.440	871.737	0.394	35	0.092	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1966.968	1966.187	-111.341	0.458	590.618	0.416	30	0.092	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1967.440	1966.187	129.148	0.333	954.622	0.374	32	0.091	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1966.965	1966.187	-113.209	0.380	534.070	0.410	28	0.091	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-24/3	1456.786	1456.668	81.296	0.434	1001.080	0.381	25	0.090	R.SGTLIDAIGIYVHP.-
R5/RRR5-25/3	1965.895	1966.187	-148.926	0.397	622.122	0.401	31	0.090	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1736.375	1735.876	287.888	0.377	842.774	0.404	25	0.090	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-24/3	1735.806	1735.876	-40.644	0.409	827.087	0.396	26	0.089	K.IVTSANNTYEAGVPNGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/3	1966.973	1966.187	-108.727	0.353	949.808	0.360	35	0.089	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1967.503	1966.187	161.254	0.442	795.437	0.372	36	0.088	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1967.359	1966.187	87.892	0.351	470.125	0.333	29	0.087	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1967.893	1966.187	-149.770	0.409	614.124	0.362	30	0.086	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1839.074	1838.014	33.040	0.296	800.709	0.394	29	0.083	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-26/3	1967.667	1966.187	245.150	0.297	781.134	0.347	29	0.083	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-26/3	1966.721	1966.187	-237.233	0.310	736.000	0.337	30	0.082	K.IGPWGGNGGSAQDISVPPKK.L
R5/RRR5-25/3	1736.775	1735.876	-58.633	0.430	590.919	0.327	24	0.079	K.IVTSANNTYEAGVPNGK.E
R5/RRR5-25/3	1838.594	1838.014	-229.060	0.264	1048.468	0.294	28	0.078	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/3	1837.817	1838.014	-107.407	0.315	567.209	0.338	27	0.076	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-25/3	1838.752	1838.014	-142.843	0.290	590.655	0.305	25	0.072	K.IGPWGGNGGSAQDISVPPK.K
R5/RRR5-14/2	1709.142	1708.932	122.741	0.525	2028.131	0.570	26	0.290	R.GWVPTLLGYSAQGACK.F
R5/RRR5-14/2	1708.619	1708.932	-184.062	0.516	1642.647	0.602	25	0.242	R.GWVPTLLGYSAQGACK.F
R5/RRR5-15/2	1708.047	1708.932	-1107.390	0.474	1660.450	0.566	25	0.234	R.GWVPTLLGYSAQGACK.F
R5/RRR5-15/2	1709.048	1708.932	67.656	0.491	1546.526	0.588	25	0.226	R.GWVPTLLGYSAQGACK.F
R5/RRR5-14/2	1504.645	1505.610	-1309.494	0.391	1602.917	0.519	21	0.215	K.YYSDIAGPEYAQK.Y
R5/RRR5-14/2	1506.245	1505.610	-243.013	0.557	1317.326	0.596	20	0.204	K.YYSDIAGPEYAQK.Y
R5/RRR5-14/2	1505.330	1505.610	-186.145	0.516	1438.187	0.527	20	0.201	K.YYSDIAGPEYAQK.Y
R5/RRR5-14/2	1707.752	1708.932	-1280.365	0.445	1442.539	0.522	24	0.198	R.GWVPTLLGYSAQGACK.F
R5/RRR5-15/2	1707.942	1708.932	-1169.109	0.467	1356.669	0.535	23	0.192	R.GWVPTLLGYSAQGACK.F
R5/RRR5-14/2	1709.484	1708.932	-263.326	0.471	1304.949	0.511	23	0.183	R.GWVPTLLGYSAQGACK.F
R5/RRR5-14/2	1213.080	1213.407	-270.656	0.452	1042.597	0.426	13	0.150	K.FGFYEFFKK.C
R5/RRR5-14/2	1084.828	1085.234	-376.014	0.436	954.329	0.452	12	0.150	K.FGFYEFFK.K
R5/RRR5-14/2	1213.530	1213.407	100.932	0.473	1038.575	0.416	13	0.148	K.FGFYEFFKK.C
R5/RRR5-14/2	1062.568	1063.277	-1613.249	0.424	942.018	0.436	14	0.148	K.LGLWGLFTR.G
R5/RRR5-14/2	937.553	938.060	-1612.168	0.415	757.903	0.491	15	0.147	K.SEGALGLYK.G
R5/RRR5-14/2	1063.283	1063.277	6.263	0.468	699.677	0.491	13	0.145	K.LGLWGLFTR.G
R5/RRR5-14/2	1084.680	1085.234	-1437.458	0.484	887.187	0.428	12	0.144	K.FGFYEFFK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	937.307	938.060	-1875.279	0.436	691.018	0.481	14	0.144	K.SEGALGLYK.G
R5/RRR5-14/2	1085.742	1085.234	-454.973	0.329	884.513	0.454	12	0.142	K.FGFYEFFK.K
R5/RRR5-14/2	937.533	938.060	-1633.227	0.365	790.915	0.434	15	0.140	K.SEGALGLYK.G
R5/RRR5-14/2	1063.289	1063.277	11.329	0.445	691.235	0.451	13	0.140	K.LGLWGLFTR.G
R5/RRR5-14/2	1062.786	1063.277	-463.418	0.399	541.530	0.514	12	0.139	K.LGLWGLFTR.G
R5/RRR5-14/2	1063.257	1063.277	-18.840	0.437	669.275	0.436	13	0.138	K.LGLWGLFTR.G
R5/RRR5-14/2	1063.157	1063.277	-112.815	0.440	790.550	0.388	14	0.137	K.LGLWGLFTR.G
R5/RRR5-14/2	1062.984	1063.277	-276.046	0.376	696.473	0.416	13	0.135	K.LGLWGLFTR.G
R5/RRR5-14/2	1063.044	1063.277	-219.249	0.413	702.562	0.411	12	0.134	K.LGLWGLFTR.G
R5/RRR5-14/2	1094.041	1094.286	-224.340	0.418	821.022	0.378	16	0.132	K.SITSGFGILAK.E
R5/RRR5-15/2	937.946	938.060	-121.153	0.450	614.837	0.349	14	0.131	K.SEGALGLYK.G
R5/RRR5-15/2	937.928	938.060	-140.736	0.418	721.744	0.278	15	0.126	K.SEGALGLYK.G
R5/RRR5-16/2	938.063	938.060	4.032	0.303	536.539	0.271	13	0.121	-.SEGALGLYK.-
R5/RRR5-1/2	937.672	938.060	-414.721	0.278	621.623	0.265	12	0.121	K.SEGALGLYK.G
R5/RRR5-14/2	1062.435	1063.277	-1738.487	0.281	273.228	0.362	9	0.119	-.LGLWGLFTR.-
R5/RRR5-13/2	937.742	938.060	-339.353	0.199	605.114	0.267	12	0.117	-.SEGALGLYK.-
R5/RRR5-14/3	1708.169	1708.932	-1035.247	0.429	857.811	0.464	24	0.098	R.GWVPTLLGYSAQGACK.F
R5/RRR5-14/3	1213.617	1213.407	172.845	0.430	548.535	0.480	17	0.092	K.FGFYEFFKK.C
R5/RRR5-14/3	1213.579	1213.407	141.525	0.439	661.255	0.424	19	0.088	K.FGFYEFFKK.C
R5/RRR5-14/3	1213.591	1213.407	151.511	0.458	534.362	0.392	18	0.087	K.FGFYEFFKK.C
R5/RRR5-14/3	1708.897	1708.932	-20.471	0.371	394.547	0.368	20	0.060	-.GWVPTLLGYSAQGACK.-
R5/RRR5-4/2	1433.253	1433.508	-178.592	0.552	2762.079	0.466	20	0.396	R.WSNEVQEAVQSR.A
R5/RRR5-4/2	1433.023	1433.508	-339.759	0.530	2588.932	0.453	20	0.356	R.WSNEVQEAVQSR.A
R5/RRR5-4/2	1402.202	1402.619	-298.155	0.502	2137.019	0.438	19	0.269	R.IIDSTLLTQIER.Y
R5/RRR5-3/2	1402.282	1402.619	-240.599	0.513	2227.651	0.359	18	0.260	R.IIDSTLLTQIER.Y
R5/RRR5-4/2	1403.273	1402.619	-247.234	0.574	2052.899	0.431	19	0.253	R.IIDSTLLTQIER.Y
R5/RRR5-4/2	1402.184	1402.619	-311.256	0.447	1782.277	0.382	17	0.206	R.IIDSTLLTQIER.Y
R5/RRR5-4/2	1171.198	1171.408	-179.872	0.557	1646.538	0.425	17	0.201	R.SPLAQCLLIR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1171.080	1171.408	-281.722	0.530	1411.659	0.450	16	0.183	R.SPLAQCLLIR.Y
R5/RRR5-3/2	1402.822	1402.619	145.179	0.378	1469.090	0.368	17	0.171	R.IIDSTLLTQIER.Y
R5/RRR5-4/2	1160.924	1161.291	-317.091	0.402	1147.850	0.483	18	0.165	R.AITELNGVTSR.E
R5/RRR5-4/2	1527.262	1526.758	-326.009	0.499	1400.491	0.375	18	0.165	K.LLYLLNQGDTFTK.V
R5/RRR5-4/2	1171.294	1171.408	-97.905	0.544	1287.218	0.372	16	0.158	R.SPLAQCLLIR.Y
R5/RRR5-3/2	1528.212	1526.758	297.588	0.466	1354.810	0.323	19	0.153	K.LLYLLNQGDTFTK.V
R5/RRR5-4/2	1160.678	1161.291	-1393.971	0.414	1050.217	0.434	17	0.152	R.AITELNGVTSR.E
R5/RRR5-4/2	1160.960	1161.291	-285.443	0.470	994.541	0.422	17	0.148	R.AITELNGVTSR.E
R5/RRR5-3/2	1161.533	1161.291	209.173	0.395	988.925	0.411	18	0.146	R.AITELNGVTSR.E
R5/RRR5-3/2	1171.108	1171.408	-257.042	0.479	1208.747	0.316	16	0.145	R.SPLAQCLLIR.Y
R5/RRR5-4/2	1367.351	1366.587	-173.051	0.407	655.527	0.514	20	0.142	K.LLSSIPEFAGFGK.L
R5/RRR5-4/2	1015.994	1015.189	-191.984	0.452	712.294	0.402	15	0.137	R.VILENATVR.A
R5/RRR5-4/2	1366.234	1366.587	-258.687	0.362	566.325	0.474	18	0.133	K.LLSSIPEFAGFGK.L
R5/RRR5-4/2	1015.037	1015.189	-150.430	0.406	651.554	0.365	15	0.132	R.VILENATVR.A
R5/RRR5-4/2	1015.291	1015.189	100.923	0.366	817.595	0.333	15	0.131	R.VILENATVR.A
R5/RRR5-4/2	1202.526	1203.416	-1575.972	0.384	902.636	0.314	16	0.128	K.FGALVDSLKPR.I
R5/RRR5-4/2	1525.449	1526.758	-1518.618	0.322	606.319	0.362	15	0.123	K.LLYLLNQGDTFTK.V
R5/RRR5-3/2	1015.244	1015.189	54.135	0.317	493.034	0.226	13	0.117	-.VILENATVR.-
R5/RRR5-11/2	1819.119	1818.927	105.561	0.632	3226.784	0.658	28	0.589	R.HETADINTFSWGVANR.G
R5/RRR5-12/2	1818.390	1818.927	-848.093	0.612	3010.882	0.720	26	0.558	R.HETADINTFSWGVANR.G
R5/RRR5-12/2	1819.373	1818.927	245.858	0.638	2965.663	0.703	27	0.538	R.HETADINTFSWGVANR.G
R5/RRR5-11/2	1819.040	1818.927	62.421	0.620	2931.883	0.657	27	0.509	R.HETADINTFSWGVANR.G
R5/RRR5-12/2	1819.384	1818.927	251.981	0.632	2453.176	0.683	27	0.408	R.HETADINTFSWGVANR.G
R5/RRR5-12/2	1810.155	1811.095	-1074.638	0.418	2652.240	0.410	25	0.353	K.IIAEYIWIGGSGM*DLR.S
R5/RRR5-12/2	1811.366	1811.095	150.468	0.587	2404.750	0.546	25	0.348	K.IIAEYIWIGGSGM*DLR.S
R5/RRR5-11/3	1627.790	1627.700	55.756	0.551	2265.753	0.524	30	0.335	R.HKEHISAYGEGNER.R
R5/RRR5-11/2	1811.038	1811.095	-31.364	0.572	2195.608	0.563	25	0.316	K.IIAEYIWIGGSGM*DLR.S
R5/RRR5-11/2	1810.180	1811.095	-1061.096	0.477	2114.226	0.528	23	0.291	K.IIAEYIWIGGSGM*DLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/3	1627.929	1627.700	141.265	0.545	2004.027	0.535	30	0.277	R.HKEHISAYGEGNER.R
R5/RRR5-11/3	1627.686	1627.700	-8.329	0.568	1962.040	0.547	30	0.273	R.HKEHISAYGEGNER.R
R5/RRR5-12/3	1627.118	1627.700	-974.885	0.489	2116.869	0.453	29	0.269	R.HKEHISAYGEGNER.R
R5/RRR5-12/3	1627.131	1627.700	-966.864	0.505	1841.326	0.516	29	0.236	R.HKEHISAYGEGNER.R
R5/RRR5-12/3	1627.215	1627.700	-299.070	0.498	1818.916	0.499	28	0.226	R.HKEHISAYGEGNER.R
R5/RRR5-12/2	1810.265	1811.095	-1013.973	0.480	1618.647	0.449	21	0.201	K.IIAEYIWIGGSGM*DLR.S
R5/RRR5-12/2	1440.273	1440.667	-274.377	0.441	1025.680	0.399	18	0.143	R.TLSGPVTDPSKLPK.W
R5/RRR5-11/2	1440.335	1440.667	-231.437	0.413	945.749	0.367	18	0.135	-.TLSGPVTDPSKLPK.-
R5/RRR5-11/2	1809.752	1811.095	-1298.406	0.287	1212.961	0.268	19	0.135	K.IIAEYIWIGGSGM*DLR.S
R5/RRR5-12/3	1399.337	1399.555	-156.539	0.508	1424.313	0.397	26	0.131	K.SM*RNDGGYEIIK.S
R5/RRR5-11/2	1439.659	1440.667	-1399.136	0.402	902.898	0.322	17	0.128	-.TLSGPVTDPSKLPK.-
R5/RRR5-12/2	1441.180	1440.667	-338.728	0.433	745.875	0.364	17	0.127	-.TLSGPVTDPSKLPK.-
R5/RRR5-11/2	1441.024	1440.667	248.810	0.402	638.258	0.356	15	0.118	-.TLSGPVTDPSKLPK.-
R5/RRR5-12/3	1399.117	1399.555	-313.950	0.481	1259.113	0.409	24	0.118	K.SM*RNDGGYEIIK.S
R5/RRR5-12/3	1817.693	1818.927	-1233.007	0.479	1020.730	0.445	25	0.106	R.HETADINTFSWGVANR.G
R5/RRR5-12/3	1783.777	1783.886	-61.344	0.452	996.916	0.453	32	0.105	R.HKEHISAYGEGNERR.L
R5/RRR5-11/3	1399.616	1399.555	43.600	0.504	1000.377	0.426	23	0.103	K.SM*RNDGGYEIIK.S
R5/RRR5-11/3	1399.768	1399.555	152.625	0.489	1007.394	0.405	23	0.100	K.SM*RNDGGYEIIK.S
R5/RRR5-11/3	1783.655	1783.886	-129.717	0.424	744.505	0.465	27	0.093	R.HKEHISAYGEGNERR.L
R5/RRR5-12/3	1399.978	1399.555	302.939	0.508	926.607	0.370	22	0.090	K.SM*RNDGGYEIIK.S
R5/RRR5-11/3	1399.392	1399.555	-116.636	0.502	761.992	0.367	22	0.087	K.SM*RNDGGYEIIK.S
R5/RRR5-12/3	1817.817	1818.927	-1164.626	0.394	946.466	0.362	24	0.086	R.HETADINTFSWGVANR.G
R5/RRR5-12/3	1817.900	1818.927	-1118.505	0.361	722.614	0.355	23	0.077	R.HETADINTFSWGVANR.G
R5/RRR5-12/3	1400.811	1399.555	183.409	0.353	1159.632	0.226	24	0.075	K.SM*RNDGGYEIIK.S
R5/RRR5-12/3	1362.638	1362.387	184.852	0.460	1012.984	0.251	22	0.073	-.EHISAYGEGNER.-
R5/RRR5-12/3	1362.756	1362.387	271.356	0.425	692.522	0.220	19	0.064	-.EHISAYGEGNER.-
R5/RRR5-11/3	1362.633	1362.387	180.944	0.431	773.489	0.175	21	0.063	-.EHISAYGEGNER.-
R5/RRR5-11/3	1362.480	1362.387	68.141	0.429	815.544	0.219	20	0.058	-.EHISAYGEGNER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/3	1361.758	1362.387	-1199.742	0.329	914.330	0.066	20	0.055	-.EHISAYGEGNER.-
R5/RRR5-3/2	1602.122	1601.825	185.963	0.589	2637.444	0.422	24	0.352	R.FNAILEELGIEQPK.G
R5/RRR5-3/2	1601.341	1601.825	-303.435	0.467	2218.936	0.437	22	0.283	R.FNAILEELGIEQPK.G
R5/RRR5-3/2	1142.081	1142.331	-219.406	0.468	1580.968	0.576	19	0.228	K.VPIITTVDGAR.A
R5/RRR5-3/2	1141.487	1142.331	-1620.129	0.378	1611.504	0.511	19	0.214	K.VPIITTVDGAR.A
R5/RRR5-3/2	1142.162	1142.331	-147.997	0.470	1369.254	0.582	17	0.204	K.VPIITTVDGAR.A
R5/RRR5-3/2	1600.458	1601.825	-1483.323	0.350	1891.396	0.208	21	0.183	R.FNAILEELGIEQPK.G
R5/RRR5-3/2	1535.684	1534.865	-118.205	0.513	1144.858	0.518	21	0.171	K.VLQLEGIPVEPVLK.I
R5/RRR5-3/2	1905.409	1906.169	-926.502	0.427	1191.049	0.449	20	0.158	K.LSVGYTLDQIPNDITKK.T
R5/RRR5-3/2	1778.319	1777.996	182.134	0.527	932.197	0.509	21	0.154	K.LSVGYTLDQIPNDITK.K
R5/RRR5-3/2	1777.561	1777.996	-245.664	0.493	770.259	0.476	20	0.141	K.LSVGYTLDQIPNDITK.K
R5/RRR5-3/2	1106.342	1105.309	29.813	0.419	900.810	0.385	13	0.135	R.LALEVAPTYK.R
R5/RRR5-3/2	1206.320	1206.419	-82.883	0.424	1156.179	0.267	15	0.134	R.LRDYSVAIIR.E
R5/RRR5-3/2	1206.299	1206.419	-100.139	0.439	952.003	0.266	14	0.125	R.LRDYSVAIIR.E
R5/RRR5-3/2	1776.711	1777.996	-1290.211	0.327	665.688	0.349	18	0.122	K.LSVGYTLDQIPNDITK.K
R5/RRR5-3/2	1207.026	1206.419	-326.890	0.510	986.136	0.241	14	0.121	R.LRDYSVAIIR.E
R5/RRR5-3/2	1656.518	1656.818	-181.277	0.452	708.393	0.358	14	0.120	R.GLDQLSKDDFYQVK.R
R5/RRR5-3/2	1105.104	1105.309	-185.644	0.278	544.748	0.300	12	0.116	-.LALEVAPTYK.-
R5/RRR5-13/2	1307.661	1308.457	-1377.450	0.412	2196.394	0.389	19	0.264	K.VSCADITTLATR.D
R5/RRR5-12/2	1309.287	1308.457	-130.415	0.478	1945.692	0.517	19	0.261	K.VSCADITTLATR.D
R5/RRR5-12/2	1308.062	1308.457	-303.139	0.450	2081.430	0.440	20	0.260	K.VSCADITTLATR.D
R5/RRR5-13/2	1308.207	1308.457	-191.544	0.461	2010.478	0.410	19	0.242	K.VSCADITTLATR.D
R5/RRR5-14/2	1308.141	1308.457	-242.283	0.452	1938.538	0.430	19	0.237	K.VSCADITTLATR.D
R5/RRR5-12/2	1308.152	1308.457	-233.670	0.420	1993.000	0.395	19	0.236	K.VSCADITTLATR.D
R5/RRR5-11/2	1735.155	1734.933	128.451	0.486	1648.653	0.546	25	0.226	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-14/2	1308.033	1308.457	-325.517	0.417	1925.765	0.388	19	0.225	K.VSCADITTLATR.D
R5/RRR5-13/2	1735.389	1734.933	263.260	0.552	1473.318	0.615	24	0.221	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-13/2	1735.547	1734.933	-222.969	0.550	1540.385	0.574	25	0.220	R.DAIVASGGPYFDVPLGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1307.567	1308.457	-1450.025	0.344	1848.269	0.372	19	0.211	K.VSCADITTLATR.D
R5/RRR5-14/2	1307.653	1308.457	-1383.451	0.318	1875.057	0.352	19	0.210	K.VSCADITTLATR.D
R5/RRR5-15/2	1308.317	1308.457	-107.771	0.397	1714.445	0.371	19	0.196	K.VSCADITTLATR.D
R5/RRR5-13/2	1734.320	1734.933	-933.255	0.494	1404.738	0.533	24	0.195	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-12/2	1735.135	1734.933	116.739	0.542	1340.824	0.557	23	0.193	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-18/2	1308.044	1308.457	-317.090	0.379	1751.151	0.340	18	0.193	K.VSCADITTLATR.D
R5/RRR5-14/2	1735.309	1734.933	216.917	0.553	1350.024	0.552	23	0.193	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-19/2	1308.245	1308.457	-162.620	0.347	1956.944	0.225	19	0.193	K.VSCADITTLATR.D
R5/RRR5-18/2	1735.110	1734.933	102.345	0.557	1279.829	0.537	23	0.184	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-13/2	1735.646	1734.933	-165.888	0.534	1276.263	0.529	23	0.182	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-15/2	1734.254	1734.933	-971.414	0.458	1262.876	0.531	23	0.181	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-14/2	1733.771	1734.933	-1250.628	0.335	1442.674	0.427	23	0.177	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-14/2	984.987	985.163	-179.010	0.428	1330.686	0.457	17	0.177	R.DIGIAAGLVR.I
R5/RRR5-15/2	1734.593	1734.933	-196.764	0.506	1126.684	0.567	22	0.176	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-11/2	1735.320	1734.933	223.265	0.532	1170.169	0.543	22	0.175	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-19/2	985.006	985.163	-159.988	0.494	1325.884	0.440	17	0.174	R.DIGIAAGLVR.I
R5/RRR5-18/2	984.894	985.163	-273.381	0.526	1266.890	0.460	16	0.172	R.DIGIAAGLVR.I
R5/RRR5-16/2	1734.521	1734.933	-238.207	0.467	1310.349	0.457	23	0.172	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-12/2	984.695	985.163	-476.234	0.490	1258.951	0.459	16	0.171	R.DIGIAAGLVR.I
R5/RRR5-15/2	985.187	985.163	24.345	0.483	1338.043	0.416	16	0.170	R.DIGIAAGLVR.I
R5/RRR5-18/2	1735.448	1734.933	-280.481	0.556	1132.859	0.524	22	0.169	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-15/2	984.348	985.163	-1849.097	0.465	1425.541	0.366	16	0.168	R.DIGIAAGLVR.I
R5/RRR5-15/2	1734.383	1734.933	-896.654	0.474	1236.006	0.468	23	0.168	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-18/2	985.000	985.163	-165.831	0.484	1223.484	0.452	16	0.168	R.DIGIAAGLVR.I
R5/RRR5-12/2	985.139	985.163	-24.249	0.506	1224.400	0.448	16	0.167	R.DIGIAAGLVR.I
R5/RRR5-14/2	984.803	985.163	-366.775	0.464	1258.597	0.429	16	0.166	R.DIGIAAGLVR.I
R5/RRR5-13/2	984.966	985.163	-200.767	0.539	1287.618	0.419	16	0.166	R.DIGIAAGLVR.I
R5/RRR5-14/2	985.040	985.163	-124.683	0.498	1233.930	0.437	16	0.166	R.DIGIAAGLVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	985.089	985.163	-74.836	0.488	1211.728	0.441	16	0.165	R.DIGIAAGLVR.I
R5/RRR5-19/2	1734.195	1734.933	-1005.053	0.437	1097.859	0.513	22	0.164	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-14/2	1734.299	1734.933	-944.915	0.442	1240.151	0.448	22	0.164	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-18/2	985.014	985.163	-151.535	0.492	1152.867	0.451	16	0.163	R.DIGIAAGLVR.I
R5/RRR5-13/2	985.091	985.163	-73.220	0.461	1225.339	0.421	16	0.162	R.DIGIAAGLVR.I
R5/RRR5-3/2	1736.607	1734.933	-188.216	0.518	913.160	0.561	21	0.160	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-12/2	1734.340	1734.933	-921.526	0.467	1065.359	0.502	21	0.160	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-16/2	1734.351	1734.933	-915.237	0.466	1353.117	0.365	23	0.158	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-3/2	1735.375	1734.933	255.501	0.482	904.007	0.559	20	0.158	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-18/2	1307.573	1308.457	-1445.242	0.282	1673.300	0.162	19	0.154	K.VSCADITTLATR.D
R5/RRR5-19/2	1734.215	1734.933	-993.534	0.427	989.159	0.476	21	0.151	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-2/2	1734.254	1734.933	-971.273	0.467	932.467	0.494	20	0.150	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-5/2	1734.517	1734.933	-240.961	0.397	1198.703	0.381	21	0.150	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-12/2	1571.342	1571.714	-237.465	0.464	781.699	0.483	22	0.147	K.DVPVNSVTQELDVR.T
R5/RRR5-15/2	1571.493	1571.714	-141.066	0.481	802.846	0.471	22	0.147	K.DVPVNSVTQELDVR.T
R5/RRR5-14/2	1572.262	1571.714	-288.333	0.492	737.919	0.485	22	0.147	K.DVPVNSVTQELDVR.T
R5/RRR5-13/2	1571.429	1571.714	-181.977	0.472	762.544	0.473	22	0.146	K.DVPVNSVTQELDVR.T
R5/RRR5-12/2	1734.053	1734.933	-1087.605	0.397	982.948	0.435	21	0.145	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-12/2	1572.172	1571.714	291.681	0.511	766.411	0.456	22	0.144	K.DVPVNSVTQELDVR.T
R5/RRR5-11/2	1734.132	1734.933	-1041.592	0.320	915.258	0.452	23	0.143	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-12/2	1572.173	1571.714	292.304	0.503	738.583	0.442	22	0.142	K.DVPVNSVTQELDVR.T
R5/RRR5-3/2	1734.494	1734.933	-253.811	0.446	936.299	0.426	20	0.141	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-15/2	1571.446	1571.714	-170.989	0.438	691.219	0.452	21	0.140	K.DVPVNSVTQELDVR.T
R5/RRR5-13/2	1573.231	1571.714	-307.923	0.472	211.927	0.506	18	0.140	K.DVPVNSVTQELDVR.T
R5/RRR5-13/2	1572.353	1571.714	-230.616	0.518	349.920	0.524	17	0.139	K.DVPVNSVTQELDVR.T
R5/RRR5-13/2	1571.285	1571.714	-274.330	0.439	673.635	0.445	21	0.139	K.DVPVNSVTQELDVR.T
R5/RRR5-1/2	1572.205	1571.714	313.168	0.478	648.090	0.451	20	0.139	K.DVPVNSVTQELDVR.T
R5/RRR5-12/2	1308.102	1308.457	-272.148	0.365	916.609	0.383	16	0.137	K.VSCADITTLATR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1571.545	1571.714	-107.795	0.459	796.281	0.392	21	0.137	K.DVPVNSVTQELDVR.T
R5/RRR5-2/2	1734.193	1734.933	-1006.325	0.413	868.059	0.411	19	0.136	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-1/2	1571.165	1571.714	-988.866	0.391	639.401	0.432	21	0.136	K.DVPVNSVTQELDVR.T
R5/RRR5-11/2	1571.047	1571.714	-1064.379	0.385	489.037	0.437	20	0.134	K.DVPVNSVTQELDVR.T
R5/RRR5-13/2	1570.665	1571.714	-1308.394	0.334	690.755	0.383	22	0.132	K.DVPVNSVTQELDVR.T
R5/RRR5-9/2	1734.525	1734.933	-236.089	0.405	639.315	0.449	16	0.131	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-11/2	1571.207	1571.714	-962.111	0.398	602.587	0.373	20	0.131	K.DVPVNSVTQELDVR.T
R5/RRR5-2/2	1571.792	1571.714	49.806	0.420	442.371	0.408	17	0.130	K.DVPVNSVTQELDVR.T
R5/RRR5-15/2	1571.209	1571.714	-960.707	0.361	559.486	0.380	20	0.130	K.DVPVNSVTQELDVR.T
R5/RRR5-13/2	1563.208	1562.856	226.427	0.413	748.961	0.386	17	0.130	R.FDGSKPIM*DPVLVK.K
R5/RRR5-13/2	1562.376	1562.856	-307.985	0.391	857.053	0.344	18	0.129	R.FDGSKPIM*DPVLVK.K
R5/RRR5-1/2	1733.661	1734.933	-1314.834	0.326	759.046	0.394	17	0.129	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-6/2	984.408	985.163	-1787.542	0.378	695.161	0.338	14	0.128	R.DIGIAAGLVR.I
R5/RRR5-2/2	1571.386	1571.714	-209.798	0.422	496.832	0.394	18	0.127	-.DVPVNSVTQELDVR.-
R5/RRR5-10/2	1571.336	1571.714	-241.752	0.370	353.762	0.355	16	0.127	K.DVPVNSVTQELDVR.T
R5/RRR5-2/2	1571.068	1571.714	-1051.039	0.380	708.923	0.309	20	0.126	K.DVPVNSVTQELDVR.T
R5/RRR5-1/2	1570.678	1571.714	-1300.277	0.321	416.976	0.319	18	0.126	K.DVPVNSVTQELDVR.T
R5/RRR5-10/2	1734.351	1734.933	-915.166	0.294	846.787	0.269	18	0.122	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-13/2	1562.393	1562.856	-297.089	0.357	683.076	0.300	17	0.121	R.FDGSKPIM*DPVLVK.K
R5/RRR5-18/2	1307.594	1308.457	-1429.489	0.280	793.839	0.216	16	0.120	K.VSCADITTLATR.D
R5/RRR5-1/2	1733.539	1734.933	-1385.484	0.262	626.065	0.193	16	0.115	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-12/3	1735.449	1734.933	-279.712	0.426	762.458	0.497	25	0.100	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-14/3	1734.577	1734.933	-206.232	0.360	711.289	0.456	23	0.089	R.DAIVASGGPYFDVPLGR.R
R5/RRR5-13/3	1141.127	1141.349	-195.299	0.400	1121.071	0.309	22	0.086	R.RDIGIAAGLVR.I
R5/RRR5-13/3	982.414	982.121	299.641	0.516	1092.185	0.265	18	0.081	R.WHVAEALR.R
R5/RRR5-13/3	982.146	982.121	26.339	0.508	1126.973	0.241	18	0.079	R.WHVAEALR.R
R5/RRR5-13/3	982.260	982.121	142.165	0.515	983.957	0.213	17	0.072	R.WHVAEALR.R
R5/RRR5-12/3	1734.461	1734.933	-273.272	0.287	647.328	0.332	22	0.072	R.DAIVASGGPYFDVPLGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/3	982.527	982.121	414.563	0.456	871.336	0.237	17	0.071	-.WHVAEALR.-
R5/RRR5-18/2	1384.094	1384.476	-276.756	0.498	1481.504	0.536	20	0.207	K.GPGLYYVDSEGAR.L
R5/RRR5-18/2	1332.915	1333.429	-1138.981	0.518	1530.583	0.478	18	0.200	K.LSGDDVGELHYK.Y
R5/RRR5-18/2	1332.928	1333.429	-1128.866	0.512	1448.497	0.489	18	0.193	K.LSGDDVGELHYK.Y
R5/RRR5-18/2	1373.964	1373.518	326.046	0.498	1427.531	0.489	19	0.191	R.ASM*GGYISSQTVR.K
R5/RRR5-18/2	1225.429	1226.449	-1653.925	0.453	1364.244	0.500	16	0.188	K.LLANILYSYR.G
R5/RRR5-18/2	1226.005	1226.449	-363.374	0.533	1392.165	0.453	17	0.183	K.LLANILYSYR.G
R5/RRR5-18/2	1226.053	1226.449	-324.214	0.429	1360.730	0.419	17	0.173	K.LLANILYSYR.G
R5/RRR5-18/2	1333.268	1333.429	-120.999	0.514	1205.945	0.477	18	0.170	K.LSGDDVGELHYK.Y
R5/RRR5-18/2	1479.005	1478.696	209.970	0.461	1044.587	0.538	21	0.169	R.YVMPVEEAAELAR.R
R5/RRR5-18/2	1479.049	1478.696	239.848	0.435	965.535	0.510	21	0.159	R.YVMPVEEAAELAR.R
R5/RRR5-18/2	1373.048	1373.518	-343.146	0.473	1018.099	0.487	20	0.158	R.ASM*GGYISSQTVR.K
R5/RRR5-18/2	1478.812	1478.696	78.935	0.448	1017.725	0.473	21	0.157	R.YVMPVEEAAELAR.R
R5/RRR5-18/2	1372.978	1373.518	-1124.700	0.474	936.155	0.508	19	0.156	R.ASM*GGYISSQTVR.K
R5/RRR5-18/2	1494.006	1494.695	-1133.832	0.388	865.497	0.411	20	0.140	R.YVM*PVEEAAELAR.R
R5/RRR5-18/2	969.901	970.107	-212.659	0.347	770.970	0.408	13	0.135	R.AIYQATFR.D
R5/RRR5-18/2	1127.019	1126.293	-243.414	0.543	530.693	0.412	14	0.135	R.RAIYQATFR.D
R5/RRR5-18/2	1126.995	1126.293	-264.930	0.549	482.592	0.406	14	0.134	R.RAIYQATFR.D
R5/RRR5-18/2	1493.691	1494.695	-1345.880	0.355	765.236	0.388	19	0.133	R.YVM*PVEEAAELAR.R
R5/RRR5-18/2	970.074	970.107	-33.776	0.361	840.966	0.350	13	0.133	R.AIYQATFR.D
R5/RRR5-18/2	1494.038	1494.695	-1112.009	0.375	807.244	0.366	19	0.132	R.YVM*PVEEAAELAR.R
R5/RRR5-18/2	1126.077	1126.293	-192.516	0.497	508.429	0.375	14	0.131	R.RAIYQATFR.D
R5/RRR5-18/2	969.714	970.107	-406.510	0.350	688.451	0.354	12	0.129	R.AIYQATFR.D
R5/RRR5-17/2	969.235	970.107	-1936.479	0.135	463.745	0.280	10	0.113	R.AIYQATFR.D
R5/RRR5-12/3	1955.427	1955.204	114.413	0.515	1943.606	0.535	36	0.270	K.KGGTEHLGLPVFNSVAEAK.A
R5/RRR5-12/2	1823.582	1824.159	-867.767	0.531	1651.239	0.580	25	0.236	K.TQKPVVAFIAGLTAPPGR.R
R5/RRR5-12/2	1823.698	1824.159	-253.615	0.531	1513.365	0.591	24	0.221	K.TQKPVVAFIAGLTAPPGR.R
R5/RRR5-12/2	1824.272	1824.159	61.705	0.574	1432.168	0.621	24	0.219	K.TQKPVVAFIAGLTAPPGR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1187.351	1187.325	22.107	0.486	1360.930	0.517	20	0.192	R.EAGVTVVESPAK.I
R5/RRR5-12/2	1186.927	1187.325	-335.933	0.486	1317.727	0.508	20	0.186	R.EAGVTVVESPAK.I
R5/RRR5-11/2	1186.988	1187.325	-284.960	0.412	1248.722	0.467	19	0.171	R.EAGVTVVESPAK.I
R5/RRR5-12/3	1827.278	1827.031	135.838	0.394	1517.455	0.440	30	0.159	K.GGTEHLGLPVFNSVAEAK.A
R5/RRR5-12/3	1954.700	1955.204	-771.388	0.490	1398.492	0.491	32	0.157	K.KGGTEHLGLPVFNSVAEAK.A
R5/RRR5-12/3	1954.764	1955.204	-225.656	0.495	1379.648	0.498	32	0.157	K.KGGTEHLGLPVFNSVAEAK.A
R5/RRR5-12/2	1186.629	1187.325	-1433.544	0.310	959.300	0.477	17	0.147	R.EAGVTVVESPAK.I
R5/RRR5-11/2	1187.178	1187.325	-124.234	0.354	913.512	0.463	17	0.145	R.EAGVTVVESPAK.I
R5/RRR5-12/2	1954.376	1955.204	-937.932	0.517	966.083	0.464	20	0.144	-.KGGTEHLGLPVFNSVAEAK.-
R5/RRR5-12/2	1189.089	1189.406	-267.310	0.404	385.512	0.500	13	0.135	K.IGSTM*FEIFK.Q
R5/RRR5-12/2	1172.984	1173.406	-361.637	0.356	527.501	0.472	15	0.134	K.IGSTMFEIFK.Q
R5/RRR5-12/2	1188.897	1189.406	-1273.191	0.404	386.305	0.392	13	0.129	K.IGSTM*FEIFK.Q
R5/RRR5-12/2	1084.424	1085.263	-1700.413	0.273	679.485	0.419	15	0.127	R.MGHAGAIVSGGK.G
R5/RRR5-12/2	1084.485	1085.263	-1644.433	0.240	764.950	0.367	16	0.125	R.MGHAGAIVSGGK.G
R5/RRR5-12/2	1172.644	1173.406	-1507.754	0.247	419.674	0.358	14	0.122	K.IGSTMFEIFK.Q
R5/RRR5-12/2	1084.551	1085.263	-1583.146	0.241	516.977	0.411	14	0.121	R.MGHAGAIVSGGK.G
R5/RRR5-12/3	1455.706	1455.753	-32.570	0.385	810.368	0.401	23	0.087	K.IGIM*PGYIHKPGR.V
R5/RRR5-12/3	1455.331	1455.753	-290.899	0.315	693.916	0.400	21	0.081	K.IGIM*PGYIHKPGR.V
R5/RRR5-12/3	1455.055	1455.753	-1170.612	0.302	735.214	0.334	21	0.075	K.IGIM*PGYIHKPGR.V
R5/RRR5-10/2	1807.400	1807.939	-854.333	0.569	3179.723	0.625	29	0.563	K.GTVAVGFDADANGDVTAVK.L
R5/RRR5-10/2	1916.454	1916.121	173.989	0.579	2586.183	0.607	24	0.406	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/2	1916.694	1916.121	-223.679	0.588	2591.643	0.594	24	0.402	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/2	1994.700	1995.225	-766.501	0.570	2696.936	0.516	26	0.397	K.LTDFGVQGAEANNILYLR.D
R5/RRR5-10/2	1915.383	1916.121	-910.107	0.514	2648.750	0.539	24	0.395	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/2	1807.415	1807.939	-846.129	0.579	2412.052	0.636	26	0.381	K.GTVAVGFDADANGDVTAVK.L
R5/RRR5-10/2	1807.461	1807.939	-265.512	0.579	2427.833	0.623	26	0.380	K.GTVAVGFDADANGDVTAVK.L
R5/RRR5-10/2	1916.515	1916.121	205.990	0.588	2382.267	0.613	24	0.366	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/2	1915.606	1916.121	-793.548	0.522	2434.668	0.558	24	0.358	R.LFTSGLAAFYEGYYANK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1994.656	1995.225	-788.923	0.591	2409.879	0.569	25	0.356	K.LTDFGVQGAEANNILYLR.D
R5/RRR5-9/2	1994.827	1995.225	-200.127	0.528	2467.549	0.527	25	0.354	K.LTDFGVQGAEANNILYLR.D
R5/RRR5-10/2	1914.991	1916.121	-1115.591	0.489	2403.178	0.513	24	0.337	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/2	1995.540	1995.225	158.381	0.621	2224.729	0.553	24	0.314	K.LTDFGVQGAEANNILYLR.D
R5/RRR5-10/3	1995.624	1995.225	200.640	0.492	1726.005	0.527	35	0.223	K.LTDFGVQGAEANNILYLR.D
R5/RRR5-10/2	1620.466	1620.807	-210.833	0.535	1005.512	0.552	22	0.167	R.DIDDADKLVAAM*QAK.K
R5/RRR5-10/2	1315.148	1315.581	-329.993	0.480	1091.908	0.511	17	0.165	K.GIELILSTEIVK.A
R5/RRR5-10/2	1448.119	1447.618	-345.940	0.472	527.165	0.510	18	0.140	K.ESVAPYERPALSK.G
R5/RRR5-1/2	1917.987	1916.121	-70.195	0.455	720.465	0.478	17	0.136	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/2	1474.040	1474.597	-1059.339	0.361	945.276	0.372	22	0.136	R.LPGFHTCVGSGGER.L
R5/RRR5-10/2	1447.239	1447.618	-262.396	0.396	527.563	0.477	18	0.135	K.ESVAPYERPALSK.G
R5/RRR5-10/2	1446.790	1447.618	-1267.331	0.421	559.527	0.407	18	0.130	K.ESVAPYERPALSK.G
R5/RRR5-3/2	1997.041	1995.225	-92.185	0.416	762.074	0.349	19	0.124	K.LTDFGVQGAEANNILYLR.D
R5/RRR5-10/3	1915.431	1916.121	-885.002	0.452	1181.097	0.427	27	0.115	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/3	1995.292	1995.225	33.981	0.438	979.246	0.429	29	0.099	K.LTDFGVQGAEANNILYLR.D
R5/RRR5-10/3	1915.562	1916.121	-816.391	0.429	823.012	0.482	27	0.099	R.LFTSGLAAFYEGYYANK.G
R5/RRR5-10/3	1474.109	1474.597	-332.292	0.471	630.954	0.501	23	0.097	R.LPGFHTCVGSGGER.L
R5/RRR5-10/3	1474.207	1474.597	-265.620	0.427	684.615	0.472	24	0.094	R.LPGFHTCVGSGGER.L
R5/RRR5-10/3	1474.331	1474.597	-181.141	0.452	536.277	0.414	22	0.086	R.LPGFHTCVGSGGER.L
R5/RRR5-10/3	1619.196	1620.807	-2236.901	0.269	1034.760	0.176	24	0.061	R.DIDDADKLVAAM*QAK.K
R5/RRR5-10/3	1620.913	1620.807	65.261	0.273	672.267	0.185	20	0.058	-.DIDDADKLVAAM*QAK.-
R5/RRR5-15/2	1420.155	1419.517	-255.158	0.580	2177.226	0.568	19	0.314	K.TVDVEELTVEER.N
R5/RRR5-16/2	1419.155	1419.517	-255.424	0.512	2213.893	0.501	19	0.300	K.TVDVEELTVEER.N
R5/RRR5-16/2	1419.228	1419.517	-204.081	0.535	2154.531	0.527	19	0.298	K.TVDVEELTVEER.N
R5/RRR5-15/2	1418.670	1419.517	-1305.224	0.483	2115.998	0.511	19	0.287	K.TVDVEELTVEER.N
R5/RRR5-15/2	1419.139	1419.517	-266.643	0.501	1988.791	0.564	19	0.282	K.TVDVEELTVEER.N
R5/RRR5-16/2	1419.173	1419.517	-242.998	0.529	2059.593	0.502	19	0.275	K.TVDVEELTVEER.N
R5/RRR5-16/2	1773.549	1774.014	-262.788	0.568	1482.708	0.585	22	0.216	K.AAQDIALADLAPTHPIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1773.373	1774.014	-927.961	0.536	1473.996	0.565	22	0.210	K.AAQDIALADLAPTHPIR.L
R5/RRR5-16/2	1774.434	1774.014	237.043	0.538	1449.083	0.575	22	0.209	K.AAQDIALADLAPTHPIR.L
R5/RRR5-16/2	1774.569	1774.014	-251.736	0.563	1406.639	0.586	22	0.207	K.AAQDIALADLAPTHPIR.L
R5/RRR5-15/2	1773.370	1774.014	-930.103	0.545	1378.797	0.574	22	0.202	K.AAQDIALADLAPTHPIR.L
R5/RRR5-15/2	1773.766	1774.014	-140.235	0.572	1431.261	0.535	22	0.198	K.AAQDIALADLAPTHPIR.L
R5/RRR5-15/3	1655.974	1655.831	86.378	0.412	1692.661	0.486	33	0.198	K.LLDSHLVPSSTAAESK.V
R5/RRR5-15/2	1655.299	1655.831	-928.101	0.458	1352.606	0.509	23	0.187	K.LLDSHLVPSSTAAESK.V
R5/RRR5-15/2	1215.930	1216.343	-341.242	0.428	1257.819	0.510	17	0.179	K.EAAESTM*VAYK.A
R5/RRR5-15/2	1655.384	1655.831	-270.970	0.458	1328.679	0.459	24	0.176	K.LLDSHLVPSSTAAESK.V
R5/RRR5-15/3	1774.983	1774.014	-17.708	0.458	1468.220	0.516	29	0.175	K.AAQDIALADLAPTHPIR.L
R5/RRR5-16/2	1655.348	1655.831	-293.017	0.447	1297.120	0.464	23	0.173	K.LLDSHLVPSSTAAESK.V
R5/RRR5-15/3	1656.122	1655.831	175.973	0.391	1521.869	0.468	31	0.165	K.LLDSHLVPSSTAAESK.V
R5/RRR5-16/2	1655.409	1655.831	-255.878	0.480	1187.512	0.461	22	0.164	K.LLDSHLVPSSTAAESK.V
R5/RRR5-16/2	1656.395	1655.831	-264.300	0.516	1043.796	0.515	21	0.162	K.LLDSHLVPSSTAAESK.V
R5/RRR5-16/2	1215.921	1216.343	-348.192	0.408	1090.216	0.482	17	0.161	K.EAAESTM*VAYK.A
R5/RRR5-15/2	1216.065	1216.343	-229.749	0.467	1104.370	0.455	17	0.159	K.EAAESTM*VAYK.A
R5/RRR5-14/3	1774.951	1774.014	-35.506	0.384	1513.124	0.443	31	0.157	K.AAQDIALADLAPTHPIR.L
R5/RRR5-15/3	1773.973	1774.014	-23.067	0.347	1370.609	0.507	29	0.157	K.AAQDIALADLAPTHPIR.L
R5/RRR5-15/2	1655.478	1655.831	-213.711	0.447	1189.479	0.413	22	0.156	K.LLDSHLVPSSTAAESK.V
R5/RRR5-16/2	1216.061	1216.343	-233.072	0.440	1108.282	0.416	17	0.153	K.EAAESTM*VAYK.A
R5/RRR5-15/3	1774.787	1774.014	-128.123	0.449	1229.608	0.520	28	0.144	K.AAQDIALADLAPTHPIR.L
R5/RRR5-15/2	1215.710	1216.343	-1347.718	0.403	992.065	0.399	15	0.143	K.EAAESTM*VAYK.A
R5/RRR5-16/3	1773.566	1774.014	-253.474	0.436	1212.635	0.495	28	0.135	K.AAQDIALADLAPTHPIR.L
R5/RRR5-16/2	1215.894	1216.343	-370.555	0.392	798.670	0.402	15	0.135	K.EAAESTM*VAYK.A
R5/RRR5-15/3	1656.087	1655.831	155.128	0.374	1117.808	0.400	28	0.104	K.LLDSHLVPSSTAAESK.V
R5/RRR5-16/3	1655.977	1655.831	88.596	0.379	1139.285	0.387	28	0.103	K.LLDSHLVPSSTAAESK.V
R5/RRR5-16/3	1655.771	1655.831	-36.508	0.269	1173.697	0.306	29	0.087	K.LLDSHLVPSSTAAESK.V
R5/RRR5-16/3	1419.589	1419.517	51.298	0.377	937.127	0.312	23	0.079	K.TVDVEELTVEER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1419.912	1419.517	279.447	0.416	751.552	0.342	21	0.078	-.TVDVEELTVEER.-
R5/RRR5-15/3	1419.603	1419.517	60.871	0.286	695.242	0.169	21	0.058	-.TVDVEELTVEER.-
R5/RRR5-3/2	1555.266	1553.785	309.966	0.486	2152.197	0.559	23	0.308	K.VHISDLVQGLSGTVK.L
R5/RRR5-4/2	1343.320	1343.599	-208.321	0.460	1768.420	0.363	17	0.201	R.IIWSNLLQSLR.S
R5/RRR5-4/2	1957.230	1958.163	-990.488	0.497	1224.565	0.504	18	0.169	K.DGVSVANVEHNLFEWLK.G
R5/RRR5-4/2	1343.215	1343.599	-287.275	0.398	1342.531	0.393	15	0.164	R.IIWSNLLQSLR.S
R5/RRR5-4/2	1352.228	1352.561	-247.422	0.445	1128.394	0.483	18	0.163	K.YVVTLSSGGSILR.A
R5/RRR5-4/2	1343.583	1343.599	-11.811	0.392	1444.195	0.326	16	0.162	R.IIWSNLLQSLR.S
R5/RRR5-1/2	1343.709	1343.599	81.678	0.445	1439.127	0.329	16	0.162	R.IIWSNLLQSLR.S
R5/RRR5-3/2	1342.402	1343.599	-1642.057	0.304	1615.621	0.221	17	0.159	R.IIWSNLLQSLR.S
R5/RRR5-1/2	1351.921	1352.561	-1216.884	0.397	1201.935	0.423	18	0.158	K.YVVTLSSGGSILR.A
R5/RRR5-4/2	1351.744	1352.561	-1348.833	0.327	1348.443	0.357	17	0.157	K.YVVTLSSGGSILR.A
R5/RRR5-4/2	1580.155	1579.735	266.885	0.498	851.992	0.511	17	0.149	K.ELWSIVFPSDTER.I
R5/RRR5-3/2	1039.288	1039.212	73.558	0.484	706.021	0.332	12	0.129	K.VFLNNYIR.T
R5/RRR5-4/2	1038.528	1039.212	-1626.778	0.432	716.191	0.362	12	0.127	-.VFLNNYIR.-
R5/RRR5-4/2	1038.584	1039.212	-1572.225	0.356	589.546	0.305	12	0.125	K.VFLNNYIR.T
R5/RRR5-3/2	1038.428	1039.212	-1723.263	0.399	629.125	0.263	12	0.123	K.VFLNNYIR.T
R5/RRR5-4/2	1078.080	1077.259	-166.221	0.431	977.492	0.223	14	0.123	-.LNLYQLNAK.-
R5/RRR5-4/2	1038.901	1039.212	-300.241	0.413	535.185	0.312	12	0.121	-.VFLNNYIR.-
R5/RRR5-4/2	1078.340	1078.203	126.757	0.321	1018.064	0.198	14	0.119	K.DNLVFVSAGR.W
R5/RRR5-4/2	1077.381	1077.259	114.369	0.399	715.580	0.228	13	0.119	K.LNLYQLNAK.T
R5/RRR5-3/2	1552.652	1553.785	-1378.379	0.266	627.572	0.242	16	0.114	-.VHISDLVQGLSGTVK.-
R5/RRR5-16/2	1407.129	1407.463	-237.595	0.446	2017.482	0.413	20	0.245	K.TVDSEELTVEER.N
R5/RRR5-14/2	1407.081	1407.463	-272.061	0.440	1971.523	0.362	19	0.226	K.TVDSEELTVEER.N
R5/RRR5-15/2	1407.018	1407.463	-316.713	0.438	1927.610	0.381	19	0.225	K.TVDSEELTVEER.N
R5/RRR5-15/2	1407.151	1407.463	-221.929	0.442	1780.709	0.393	19	0.209	K.TVDSEELTVEER.N
R5/RRR5-16/2	1406.580	1407.463	-1342.470	0.341	1870.750	0.320	19	0.204	K.TVDSEELTVEER.N
R5/RRR5-15/2	1814.542	1814.078	256.095	0.546	1309.130	0.514	22	0.182	K.AAQDIALAELPPTHPIR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1229.017	1229.342	-265.577	0.493	1231.678	0.451	17	0.168	K.DAAENTM*VAYK.A
R5/RRR5-16/2	1406.617	1407.463	-1315.886	0.329	1504.831	0.292	18	0.161	K.TVDSEELTVEER.N
R5/RRR5-15/2	1681.295	1681.869	-938.803	0.473	860.095	0.596	21	0.161	K.LLDSHLVPSSTAPESK.V
R5/RRR5-15/2	1229.086	1229.342	-209.379	0.468	1139.531	0.423	17	0.156	K.DAAENTM*VAYK.A
R5/RRR5-15/2	1813.371	1814.078	-944.494	0.543	1006.586	0.496	22	0.156	K.AAQDIALAELPPTHPIR.L
R5/RRR5-15/2	1228.289	1229.342	-1676.413	0.291	779.569	0.314	15	0.124	K.DAAENTM*VAYK.A
R5/RRR5-16/3	1813.777	1814.078	-166.479	0.417	1238.379	0.440	33	0.123	K.AAQDIALAELPPTHPIR.L
R5/RRR5-15/2	1813.956	1814.078	-67.808	0.296	416.067	0.349	18	0.120	K.AAQDIALAELPPTHPIR.L
R5/RRR5-15/3	1991.071	1991.106	-17.570	0.413	1072.551	0.488	31	0.119	R.IISSIEQKEESRGNEDR.V
R5/RRR5-16/3	1814.128	1814.078	27.623	0.346	1139.307	0.442	30	0.114	K.AAQDIALAELPPTHPIR.L
R5/RRR5-16/3	1813.933	1814.078	-80.304	0.343	946.440	0.438	29	0.098	K.AAQDIALAELPPTHPIR.L
R5/RRR5-15/3	1990.764	1991.106	-172.558	0.373	522.467	0.479	25	0.090	R.IISSIEQKEESRGNEDR.V
R5/RRR5-15/3	1991.850	1991.106	-129.159	0.398	514.572	0.454	25	0.088	R.IISSIEQKEESRGNEDR.V
R5/RRR5-16/3	1990.553	1991.106	-782.744	0.368	466.898	0.444	26	0.087	R.IISSIEQKEESRGNEDR.V
R5/RRR5-14/3	1814.145	1814.078	36.835	0.335	557.797	0.352	23	0.075	-.AAQDIALAELPPTHPIR.-
R5/RRR5-13/2	1603.437	1603.887	-281.505	0.539	2385.678	0.580	24	0.359	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/2	1456.186	1456.618	-297.864	0.514	2515.482	0.457	20	0.343	R.YWLCAATQDSIK.I
R5/RRR5-13/3	1941.667	1940.104	-225.728	0.507	2148.039	0.489	35	0.302	R.FSPNTFQPTIVSGSWDR.T
R5/RRR5-13/2	1322.034	1322.449	-315.123	0.451	2144.460	0.503	19	0.290	K.DVLSVAFSVDNR.Q
R5/RRR5-13/2	1603.336	1603.887	-970.781	0.525	1892.001	0.589	22	0.275	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/2	1417.009	1417.589	-1117.873	0.425	1711.008	0.499	19	0.224	K.DGVTLLWDLAEGK.R
R5/RRR5-13/2	1417.152	1417.589	-309.092	0.491	1733.566	0.482	19	0.224	K.DGVTLLWDLAEGK.R
R5/RRR5-14/2	1248.960	1249.398	-351.402	0.519	1716.291	0.466	19	0.219	R.LWDLSTGVTTR.R
R5/RRR5-13/2	1249.078	1249.398	-256.876	0.548	1570.757	0.535	19	0.219	R.LWDLSTGVTTR.R
R5/RRR5-13/2	1604.454	1603.887	-271.101	0.557	1468.592	0.586	20	0.216	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/2	1416.877	1417.589	-1211.389	0.424	1610.238	0.502	19	0.213	K.DGVTLLWDLAEGK.R
R5/RRR5-13/2	1939.490	1940.104	-834.972	0.522	1360.758	0.568	25	0.201	R.FSPNTFQPTIVSGSWDR.T
R5/RRR5-13/2	1455.967	1456.618	-1137.829	0.371	1739.246	0.356	18	0.196	R.YWLCAATQDSIK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1939.523	1940.104	-817.535	0.465	1304.361	0.577	24	0.195	R.FSPNTFQPTIVSGSWDR.T
R5/RRR5-13/2	1940.263	1940.104	81.932	0.523	1214.378	0.573	24	0.187	R.FSPNTFQPTIVSGSWDR.T
R5/RRR5-13/2	1938.843	1940.104	-1169.752	0.451	1243.300	0.553	24	0.185	R.FSPNTFQPTIVSGSWDR.T
R5/RRR5-13/2	1248.654	1249.398	-1400.969	0.449	1370.251	0.471	17	0.182	R.LWDLSTGVTTR.R
R5/RRR5-13/2	1321.527	1322.449	-1458.888	0.355	1273.794	0.503	17	0.175	K.DVLSVAFSVDNR.Q
R5/RRR5-13/2	1574.278	1573.775	-316.973	0.513	1083.603	0.497	19	0.163	K.DGVTLLWDLAEGKR.L
R5/RRR5-12/2	1322.165	1322.449	-215.266	0.335	1229.165	0.420	17	0.158	K.DVLSVAFSVDNR.Q
R5/RRR5-13/2	1940.648	1940.104	-235.619	0.493	934.140	0.535	21	0.157	R.FSPNTFQPTIVSGSWDR.T
R5/RRR5-13/2	1573.352	1573.775	-269.846	0.498	972.524	0.509	18	0.156	K.DGVTLLWDLAEGKR.L
R5/RRR5-13/2	1248.441	1249.398	-1571.950	0.328	1313.076	0.353	17	0.155	R.LWDLSTGVTTR.R
R5/RRR5-13/2	1573.147	1573.775	-1037.898	0.465	939.059	0.487	18	0.151	K.DGVTLLWDLAEGKR.L
R5/RRR5-14/2	1573.293	1573.775	-307.444	0.369	915.937	0.404	17	0.137	K.DGVTLLWDLAEGKR.L
R5/RRR5-14/2	1573.043	1573.775	-1104.281	0.414	999.958	0.346	18	0.135	K.DGVTLLWDLAEGKR.L
R5/RRR5-13/3	1604.341	1603.887	283.763	0.439	746.649	0.461	23	0.098	K.HIVQDLKPEIPVSK.N
R5/RRR5-14/3	1604.265	1603.887	236.039	0.366	834.441	0.447	24	0.097	K.HIVQDLKPEIPVSK.N
R5/RRR5-14/3	1603.866	1603.887	-13.300	0.416	716.847	0.464	22	0.097	K.HIVQDLKPEIPVSK.N
R5/RRR5-12/3	1604.210	1603.887	201.817	0.427	774.141	0.443	23	0.096	K.HIVQDLKPEIPVSK.N
R5/RRR5-12/3	1604.003	1603.887	72.231	0.385	836.257	0.412	24	0.092	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/3	1604.166	1603.887	174.460	0.446	721.598	0.418	23	0.091	K.HIVQDLKPEIPVSK.N
R5/RRR5-14/3	1573.718	1573.775	-36.195	0.380	953.212	0.378	28	0.090	K.DGVTLLWDLAEGKR.L
R5/RRR5-13/3	1604.077	1603.887	118.368	0.423	496.036	0.426	19	0.090	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/3	1604.080	1603.887	120.544	0.355	854.474	0.385	23	0.088	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/3	1574.603	1573.775	-109.577	0.387	782.606	0.399	26	0.088	K.DGVTLLWDLAEGKR.L
R5/RRR5-12/3	1603.718	1603.887	-105.832	0.322	871.240	0.376	25	0.087	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/3	1574.034	1573.775	164.965	0.358	796.519	0.363	27	0.082	K.DGVTLLWDLAEGKR.L
R5/RRR5-13/3	1604.948	1603.887	37.593	0.321	630.272	0.329	21	0.079	K.HIVQDLKPEIPVSK.N
R5/RRR5-13/3	1573.621	1573.775	-98.052	0.316	735.219	0.326	26	0.077	K.DGVTLLWDLAEGKR.L
R5/RRR5-13/3	1573.693	1573.775	-52.183	0.350	771.365	0.255	27	0.072	K.DGVTLLWDLAEGKR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1619.245	1617.885	223.089	0.625	2534.007	0.448	22	0.337	R.SFCYVADMVNGLIK.L
R5/RRR5-11/2	1618.559	1617.885	-202.019	0.573	2485.135	0.419	22	0.320	R.SFCYVADMVNGLIK.L
R5/RRR5-12/2	1203.648	1204.404	-1463.017	0.467	2307.936	0.472	19	0.307	R.VVSNFIAQAVR.G
R5/RRR5-11/2	1446.671	1445.753	-56.841	0.563	2122.353	0.557	23	0.300	K.TNVIGTLNMLGLAK.R
R5/RRR5-11/2	1445.464	1445.753	-201.054	0.571	2114.649	0.549	23	0.296	K.TNVIGTLNMLGLAK.R
R5/RRR5-11/2	1446.267	1445.753	-337.494	0.605	2074.611	0.540	23	0.286	K.TNVIGTLNMLGLAK.R
R5/RRR5-12/2	1444.531	1445.753	-1542.744	0.451	2112.151	0.514	23	0.285	K.TNVIGTLNMLGLAK.R
R5/RRR5-12/2	1462.314	1461.753	-300.837	0.561	1992.867	0.576	23	0.285	K.TNVIGTLNM*LGLAK.R
R5/RRR5-11/2	1462.359	1461.753	-269.766	0.558	1961.387	0.593	23	0.285	K.TNVIGTLNM*LGLAK.R
R5/RRR5-12/2	1445.345	1445.753	-283.579	0.563	2129.101	0.498	23	0.283	K.TNVIGTLNMLGLAK.R
R5/RRR5-11/2	1204.151	1204.404	-210.435	0.559	2158.059	0.476	19	0.283	R.VVSNFIAQAVR.G
R5/RRR5-12/2	1462.452	1461.753	-205.954	0.557	2009.571	0.544	23	0.278	K.TNVIGTLNM*LGLAK.R
R5/RRR5-11/2	1461.129	1461.753	-1114.739	0.477	2057.482	0.484	23	0.269	K.TNVIGTLNM*LGLAK.R
R5/RRR5-11/2	1462.517	1461.753	-161.994	0.551	1874.283	0.556	23	0.261	K.TNVIGTLNM*LGLAK.R
R5/RRR5-12/2	1461.373	1461.753	-260.313	0.502	1956.645	0.485	23	0.254	K.TNVIGTLNM*LGLAK.R
R5/RRR5-12/2	1617.296	1617.885	-985.340	0.447	2045.215	0.348	21	0.232	R.SFCYVADMVNGLIK.L
R5/RRR5-11/2	1617.150	1617.885	-1076.131	0.453	1584.847	0.400	18	0.187	R.SFCYVADMVNGLIK.L
R5/RRR5-12/2	1512.327	1512.693	-242.926	0.431	1149.410	0.569	22	0.180	R.GEPLTVQKPGTQTR.S
R5/RRR5-11/2	1512.214	1512.693	-317.675	0.478	1103.762	0.578	22	0.180	R.GEPLTVQKPGTQTR.S
R5/RRR5-12/3	1446.110	1445.753	247.164	0.445	1785.523	0.364	28	0.173	K.TNVIGTLNMLGLAK.R
R5/RRR5-12/2	1512.246	1512.693	-296.375	0.464	1006.139	0.586	21	0.173	R.GEPLTVQKPGTQTR.S
R5/RRR5-11/2	1512.416	1512.693	-183.978	0.461	970.861	0.576	21	0.169	R.GEPLTVQKPGTQTR.S
R5/RRR5-12/2	1157.202	1157.344	-123.220	0.508	1335.147	0.392	16	0.165	K.AKEVLGWEPK.I
R5/RRR5-12/2	1512.306	1512.693	-256.774	0.472	920.244	0.574	20	0.165	R.GEPLTVQKPGTQTR.S
R5/RRR5-12/2	1157.287	1157.344	-49.260	0.478	1304.794	0.398	16	0.164	K.AKEVLGWEPK.I
R5/RRR5-11/2	1203.278	1204.404	-1771.572	0.345	1470.196	0.290	17	0.158	R.VVSNFIAQAVR.G
R5/RRR5-13/2	1204.440	1204.404	29.926	0.434	1155.956	0.415	17	0.156	R.VVSNFIAQAVR.G
R5/RRR5-11/2	1157.105	1157.344	-206.611	0.461	1226.012	0.377	15	0.155	K.AKEVLGWEPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1444.454	1445.753	-1596.906	0.417	1267.459	0.368	19	0.154	K.TNVIGTLNMLGLAK.R
R5/RRR5-11/2	1158.316	1157.344	-24.165	0.508	1212.185	0.379	15	0.153	K.AKEVLGWEPK.I
R5/RRR5-12/2	1157.186	1157.344	-136.977	0.498	1161.930	0.395	15	0.153	K.AKEVLGWEPK.I
R5/RRR5-11/2	1617.160	1617.885	-1069.840	0.409	1353.572	0.316	19	0.152	R.SFCYVADMVNGLIK.L
R5/RRR5-11/2	1512.369	1512.693	-214.990	0.446	706.308	0.538	18	0.147	R.GEPLTVQKPGTQTR.S
R5/RRR5-11/2	1157.210	1157.344	-116.025	0.446	1167.311	0.347	15	0.146	K.AKEVLGWEPK.I
R5/RRR5-1/2	1462.733	1461.753	-13.647	0.441	974.291	0.399	18	0.141	K.TNVIGTLNM*LGLAK.R
R5/RRR5-11/2	967.720	968.091	-384.700	0.403	750.839	0.375	12	0.134	R.IFNTYGPR.M
R5/RRR5-12/2	1616.963	1617.885	-1192.259	0.363	911.587	0.360	19	0.134	R.SFCYVADMVNGLIK.L
R5/RRR5-13/2	968.015	968.091	-78.496	0.405	577.016	0.404	11	0.133	R.IFNTYGPR.M
R5/RRR5-12/2	967.831	968.091	-269.409	0.449	592.217	0.381	11	0.132	R.IFNTYGPR.M
R5/RRR5-11/2	967.575	968.091	-1571.699	0.427	623.590	0.341	12	0.130	R.IFNTYGPR.M
R5/RRR5-12/2	967.858	968.091	-240.811	0.454	634.943	0.366	12	0.129	-.IFNTYGPR.-
R5/RRR5-13/2	968.193	968.091	106.022	0.427	547.466	0.390	11	0.129	-.IFNTYGPR.-
R5/RRR5-11/3	1445.725	1445.753	-19.285	0.466	1456.734	0.364	27	0.128	K.TNVIGTLNMLGLAK.R
R5/RRR5-14/2	968.127	968.091	38.116	0.389	582.445	0.372	11	0.128	-.IFNTYGPR.-
R5/RRR5-12/2	967.423	968.091	-1728.752	0.372	650.763	0.322	11	0.127	R.IFNTYGPR.M
R5/RRR5-11/3	1445.025	1445.753	-1199.919	0.452	1229.764	0.454	27	0.127	-.TNVIGTLNMLGLAK.-
R5/RRR5-10/2	1204.119	1204.404	-237.387	0.290	397.475	0.355	15	0.126	R.VVSNFIAQAVR.G
R5/RRR5-14/2	1204.031	1204.404	-310.111	0.288	616.228	0.347	16	0.126	R.VVSNFIAQAVR.G
R5/RRR5-10/2	968.015	968.091	-78.370	0.322	681.665	0.315	12	0.125	-.IFNTYGPR.-
R5/RRR5-12/2	1205.051	1204.404	-293.288	0.347	368.145	0.350	12	0.124	R.VVSNFIAQAVR.G
R5/RRR5-14/2	1462.277	1461.753	-326.383	0.345	575.195	0.356	15	0.124	K.TNVIGTLNM*LGLAK.R
R5/RRR5-13/2	968.300	968.091	216.776	0.428	614.252	0.350	11	0.124	-.IFNTYGPR.-
R5/RRR5-11/2	967.603	968.091	-505.588	0.337	676.816	0.274	12	0.123	-.IFNTYGPR.-
R5/RRR5-10/2	968.404	968.091	324.093	0.313	624.531	0.291	11	0.122	-.IFNTYGPR.-
R5/RRR5-14/2	1203.850	1204.404	-1294.145	0.249	669.150	0.261	16	0.120	R.VVSNFIAQAVR.G
R5/RRR5-12/3	1383.900	1382.570	239.165	0.485	771.009	0.584	23	0.118	R.VAETLMFDYHR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1513.357	1512.693	-222.940	0.292	806.917	0.144	18	0.114	R.GEPLTVQKPGTQTR.S
R5/RRR5-10/2	968.278	968.091	194.020	0.270	485.959	0.295	11	0.112	-.IFNTYGPR.-
R5/RRR5-12/3	1383.816	1382.570	178.263	0.552	852.301	0.502	24	0.110	R.VAETLMFDYHR.Q
R5/RRR5-11/3	1382.558	1382.570	-8.698	0.453	813.503	0.529	23	0.110	R.VAETLMFDYHR.Q
R5/RRR5-11/3	1382.791	1382.570	160.642	0.473	638.851	0.530	21	0.106	R.VAETLMFDYHR.Q
R5/RRR5-11/3	1398.643	1398.569	53.153	0.478	528.860	0.533	21	0.104	R.VAETLM*FDYHR.Q
R5/RRR5-12/3	1382.219	1382.570	-254.376	0.505	746.099	0.486	23	0.103	R.VAETLMFDYHR.Q
R5/RRR5-12/2	1203.288	1204.404	-1763.826	0.306	573.786	0.198	13	0.102	-.VVSNFIAQAVR.-
R5/RRR5-11/3	1398.504	1398.569	-46.647	0.409	331.599	0.498	18	0.100	R.VAETLM*FDYHR.Q
R5/RRR5-12/3	1399.838	1398.569	192.920	0.382	405.627	0.476	21	0.096	R.VAETLM*FDYHR.Q
R5/RRR5-12/3	1398.528	1398.569	-29.181	0.357	340.165	0.495	18	0.092	-.VAETLM*FDYHR.-
R5/RRR5-11/3	1382.776	1382.570	149.753	0.398	812.383	0.408	24	0.090	R.VAETLMFDYHR.Q
R5/RRR5-12/3	1397.963	1398.569	-1152.082	0.281	391.722	0.435	19	0.089	R.VAETLM*FDYHR.Q
R5/RRR5-12/3	1445.282	1445.753	-327.314	0.371	1083.431	0.324	24	0.089	-.TNVIGTLNMLGLAK.-
R5/RRR5-12/2	1739.152	1739.942	-1032.179	0.578	2248.154	0.524	23	0.314	R.LYEALDKCEEILSR.Q
R5/RRR5-13/2	1739.461	1739.942	-277.089	0.614	2134.164	0.501	23	0.286	R.LYEALDKCEEILSR.Q
R5/RRR5-12/2	1739.201	1739.942	-1003.639	0.598	2040.283	0.515	22	0.275	R.LYEALDKCEEILSR.Q
R5/RRR5-12/2	1739.562	1739.942	-218.865	0.600	2042.192	0.499	23	0.271	R.LYEALDKCEEILSR.Q
R5/RRR5-12/2	1497.191	1497.546	-237.532	0.494	1889.521	0.562	22	0.266	R.SALDEVTDTGAFDR.S
R5/RRR5-12/2	1497.049	1497.546	-332.752	0.481	1903.235	0.542	22	0.262	R.SALDEVTDTGAFDR.S
R5/RRR5-12/2	1497.115	1497.546	-288.903	0.503	1825.945	0.538	21	0.250	R.SALDEVTDTGAFDR.S
R5/RRR5-13/2	1497.230	1497.546	-211.357	0.517	1875.077	0.508	22	0.249	R.SALDEVTDTGAFDR.S
R5/RRR5-13/2	1497.164	1497.546	-256.100	0.521	1774.844	0.537	22	0.243	R.SALDEVTDTGAFDR.S
R5/RRR5-13/2	1497.362	1497.546	-122.947	0.527	1749.386	0.545	21	0.241	R.SALDEVTDTGAFDR.S
R5/RRR5-13/2	1540.222	1539.666	-288.925	0.574	1702.293	0.497	20	0.224	R.YICGNQLTEADVR.L
R5/RRR5-13/2	1361.196	1361.484	-212.152	0.453	1629.590	0.456	19	0.206	K.TVVNNESSEIIR.M
R5/RRR5-13/2	1539.427	1539.666	-155.776	0.499	1591.053	0.442	20	0.198	R.YICGNQLTEADVR.L
R5/RRR5-12/2	1361.088	1361.484	-291.419	0.450	1579.496	0.447	19	0.198	K.TVVNNESSEIIR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1361.285	1361.484	-146.031	0.452	1514.271	0.419	18	0.185	K.TVVNNESSEIIR.M
R5/RRR5-12/2	1361.132	1361.484	-259.387	0.458	1360.363	0.485	19	0.184	K.TVVNNESSEIIR.M
R5/RRR5-12/3	1255.553	1255.403	119.679	0.424	1710.716	0.450	24	0.182	R.FDEVYAVHFK.C
R5/RRR5-12/2	1360.556	1361.484	-1420.908	0.313	1549.987	0.392	19	0.182	K.TVVNNESSEIIR.M
R5/RRR5-13/2	1361.135	1361.484	-257.047	0.412	1559.054	0.364	18	0.179	K.TVVNNESSEIIR.M
R5/RRR5-12/3	1335.596	1336.432	-1379.177	0.486	1599.823	0.410	26	0.155	K.KQEPYDEAVTR.L
R5/RRR5-12/3	1887.674	1888.159	-257.610	0.508	1346.480	0.502	29	0.154	K.GLDHAIGFTSVKPIFER.T
R5/RRR5-12/3	1255.566	1255.403	130.356	0.421	1578.660	0.414	24	0.151	R.FDEVYAVHFK.C
R5/RRR5-12/2	1336.210	1336.432	-167.372	0.451	1209.037	0.334	18	0.148	K.KQEPYDEAVTR.L
R5/RRR5-13/3	1739.070	1739.942	-1079.617	0.524	1310.141	0.485	29	0.144	R.LYEALDKCEEILSR.Q
R5/RRR5-12/2	1336.088	1336.432	-258.659	0.516	1031.802	0.370	17	0.142	K.KQEPYDEAVTR.L
R5/RRR5-13/2	1336.075	1336.432	-268.466	0.469	1029.766	0.359	17	0.141	K.KQEPYDEAVTR.L
R5/RRR5-12/2	1336.125	1336.432	-230.611	0.445	1013.589	0.356	17	0.140	K.KQEPYDEAVTR.L
R5/RRR5-13/3	1739.830	1739.942	-64.160	0.486	1335.283	0.445	28	0.136	R.LYEALDKCEEILSR.Q
R5/RRR5-13/2	1335.939	1336.432	-370.773	0.467	887.385	0.364	16	0.135	K.KQEPYDEAVTR.L
R5/RRR5-13/3	1739.976	1739.942	19.969	0.541	1190.333	0.490	28	0.132	R.LYEALDKCEEILSR.Q
R5/RRR5-13/2	1336.068	1336.432	-273.325	0.434	879.304	0.307	16	0.129	K.KQEPYDEAVTR.L
R5/RRR5-12/3	1336.719	1336.432	214.953	0.537	1613.554	0.293	24	0.125	K.KQEPYDEAVTR.L
R5/RRR5-12/3	1887.842	1888.159	-168.573	0.367	1292.387	0.415	28	0.123	K.GLDHAIGFTSVKPIFER.T
R5/RRR5-12/3	1255.165	1255.403	-190.188	0.372	1186.179	0.389	21	0.104	R.FDEVYAVHFK.C
R5/RRR5-13/3	1336.131	1336.432	-226.176	0.480	1239.640	0.325	22	0.099	-.KQEPYDEAVTR.-
R5/RRR5-12/3	1888.481	1888.159	171.275	0.355	994.957	0.425	26	0.099	K.GLDHAIGFTSVKPIFER.T
R5/RRR5-12/3	1336.068	1336.432	-273.747	0.450	1288.043	0.300	22	0.097	K.KQEPYDEAVTR.L
R5/RRR5-13/3	1336.147	1336.432	-213.940	0.446	1338.982	0.271	23	0.094	K.KQEPYDEAVTR.L
R5/RRR5-13/3	1255.050	1255.403	-281.956	0.420	775.414	0.326	18	0.078	-.FDEVYAVHFK.-
R5/RRR5-11/2	1948.588	1949.109	-783.006	0.513	1338.580	0.559	26	0.197	K.YTSLPPFDAIEQNPEAR.F
R5/RRR5-11/2	1480.431	1480.711	-190.153	0.474	1407.688	0.467	20	0.184	R.ASIYNAM*PLAGVEK.L
R5/RRR5-11/2	1481.081	1480.711	250.380	0.488	1359.231	0.451	20	0.177	R.ASIYNAM*PLAGVEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1283.381	1283.502	-94.983	0.445	1158.499	0.538	18	0.174	K.NVGPSGVTIAIVR.K
R5/RRR5-11/2	1480.239	1480.711	-319.956	0.469	1325.764	0.442	20	0.172	R.ASIYNAM*PLAGVEK.L
R5/RRR5-11/2	1068.347	1068.250	90.582	0.490	1158.051	0.403	16	0.155	R.FGLIYAGAQK.N
R5/RRR5-11/2	1283.198	1283.502	-237.546	0.464	955.960	0.490	17	0.152	K.NVGPSGVTIAIVR.K
R5/RRR5-11/2	1068.052	1068.250	-185.894	0.492	1100.614	0.404	16	0.152	R.FGLIYAGAQK.N
R5/RRR5-11/2	1947.957	1949.109	-1108.214	0.437	775.043	0.523	22	0.147	K.YTSLPPFDAIEQNPEAR.F
R5/RRR5-11/2	1067.518	1068.250	-1627.904	0.398	1021.990	0.382	15	0.143	R.FGLIYAGAQK.N
R5/RRR5-11/2	1949.300	1949.109	97.946	0.538	614.269	0.507	21	0.139	K.YTSLPPFDAIEQNPEAR.F
R5/RRR5-11/2	1238.378	1239.405	-1641.276	0.403	895.382	0.416	17	0.138	K.KFSAASVAWSGK.D
R5/RRR5-11/2	1282.505	1283.502	-1561.798	0.344	630.884	0.512	15	0.135	K.NVGPSGVTIAIVR.K
R5/RRR5-11/2	1238.455	1237.494	-31.271	0.593	698.085	0.421	16	0.132	-.SLM*NVPFTLAK.-
R5/RRR5-11/2	1110.765	1111.232	-421.356	0.282	810.239	0.361	15	0.127	K.FSAASVAWSGK.D
R5/RRR5-11/2	1111.007	1111.232	-203.282	0.277	623.489	0.426	13	0.125	K.FSAASVAWSGK.D
R5/RRR5-11/2	1236.627	1237.494	-1513.869	0.318	705.667	0.280	16	0.122	R.SLM*NVPFTLAK.G
R5/RRR5-11/2	1067.806	1068.250	-417.209	0.202	694.964	0.199	13	0.115	R.FGLIYAGAQK.N
R5/RRR5-11/2	1220.674	1221.494	-1496.072	0.345	712.456	0.019	14	0.105	-.SLMNVPFTLAK.-
R5/RRR5-15/2	1400.689	1401.636	-1394.182	0.420	1371.589	0.422	18	0.173	R.TIKDEGVIALWR.G
R5/RRR5-16/2	1402.053	1401.636	298.866	0.489	1185.922	0.491	18	0.171	R.TIKDEGVIALWR.G
R5/RRR5-15/2	1400.419	1401.636	-1587.492	0.447	948.299	0.471	18	0.152	R.TIKDEGVIALWR.G
R5/RRR5-16/2	1401.312	1401.636	-231.504	0.474	1047.103	0.416	18	0.150	R.TIKDEGVIALWR.G
R5/RRR5-15/2	1401.331	1401.636	-217.696	0.434	978.748	0.443	17	0.149	R.TIKDEGVIALWR.G
R5/RRR5-16/2	1402.006	1401.636	265.166	0.501	869.956	0.443	17	0.144	R.TIKDEGVIALWR.G
R5/RRR5-1/2	1401.233	1401.636	-288.487	0.418	1049.172	0.336	17	0.138	R.TIKDEGVIALWR.G
R5/RRR5-9/2	1968.735	1969.163	-217.642	0.522	3072.760	0.549	26	0.505	R.TMLELLNQLDGFSSDER.I
R5/RRR5-9/2	1661.304	1661.947	-992.138	0.416	1267.375	0.483	19	0.171	K.LAGPQLVQM*FIGDGAK.L
R5/RRR5-9/2	1669.407	1669.986	-948.348	0.455	1041.955	0.442	22	0.152	R.QTIFLPVIGLVDPEK.L
R5/RRR5-9/2	1660.771	1661.947	-1314.034	0.392	1015.688	0.478	17	0.150	K.LAGPQLVQM*FIGDGAK.L
R5/RRR5-9/2	1669.605	1669.986	-228.476	0.415	1035.468	0.415	22	0.147	R.QTIFLPVIGLVDPEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1195.134	1196.249	-1775.040	0.363	1035.095	0.411	17	0.146	R.STDDFNGAQLK.A
R5/RRR5-9/2	1668.997	1669.986	-1194.921	0.360	1077.816	0.377	22	0.144	R.QTIFLPVIGLVDPEK.L
R5/RRR5-9/2	1645.375	1645.948	-958.628	0.415	733.894	0.471	20	0.139	K.LAGPQLVQMFIGDGAK.L
R5/RRR5-9/2	1195.156	1196.249	-1756.567	0.316	734.503	0.422	16	0.132	R.STDDFNGAQLK.A
R5/RRR5-10/3	1680.243	1680.761	-906.389	0.484	1427.669	0.376	24	0.127	K.RFDSEVSGDREVQR.T
R5/RRR5-9/2	1195.372	1196.249	-1574.649	0.363	556.306	0.378	15	0.127	R.STDDFNGAQLK.A
R5/RRR5-10/3	1680.550	1680.761	-125.800	0.456	1381.331	0.378	25	0.123	K.RFDSEVSGDREVQR.T
R5/RRR5-9/2	1645.751	1645.948	-120.120	0.312	697.804	0.328	16	0.120	K.LAGPQLVQMFIGDGAK.L
R5/RRR5-9/3	1679.710	1680.761	-1224.410	0.460	1364.501	0.367	24	0.119	K.RFDSEVSGDREVQR.T
R5/RRR5-9/3	1680.133	1680.761	-971.597	0.436	1317.518	0.369	23	0.115	K.RFDSEVSGDREVQR.T
R5/RRR5-10/3	1441.421	1440.586	-114.605	0.475	952.608	0.411	23	0.097	R.KIEFPHPSEEAR.A
R5/RRR5-9/3	1440.409	1440.586	-122.930	0.463	843.343	0.431	19	0.095	R.KIEFPHPSEEAR.A
R5/RRR5-10/3	1440.454	1440.586	-91.307	0.411	321.373	0.308	19	0.089	R.KIEFPHPSEEAR.A
R5/RRR5-9/3	1440.761	1440.586	122.353	0.434	1143.962	0.301	22	0.088	R.KIEFPHPSEEAR.A
R5/RRR5-9/3	1680.302	1680.761	-273.809	0.436	1105.701	0.315	23	0.087	K.RFDSEVSGDREVQR.T
R5/RRR5-12/3	1643.936	1643.995	-35.617	0.496	1933.468	0.573	34	0.270	K.TLLLGEKPVTVFGIR.N
R5/RRR5-11/3	1643.787	1643.995	-126.901	0.494	1746.609	0.570	32	0.233	K.TLLLGEKPVTVFGIR.N
R5/RRR5-11/3	1643.966	1643.995	-17.183	0.486	1776.329	0.535	34	0.223	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/3	1644.285	1643.995	177.277	0.503	1689.386	0.538	34	0.209	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/3	1644.288	1643.995	178.729	0.499	1568.407	0.562	31	0.199	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/3	1643.468	1643.995	-931.438	0.431	1521.720	0.502	31	0.172	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/2	1643.816	1643.995	-109.089	0.510	1023.641	0.519	22	0.164	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/3	1643.378	1643.995	-986.473	0.463	1337.186	0.552	31	0.163	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/3	1643.613	1643.995	-232.619	0.473	1361.621	0.543	32	0.162	K.TLLLGEKPVTVFGIR.N
R5/RRR5-11/2	1644.442	1643.995	272.757	0.467	1012.455	0.526	19	0.161	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/2	1643.633	1643.995	-220.391	0.443	884.716	0.521	20	0.153	K.TLLLGEKPVTVFGIR.N
R5/RRR5-14/3	1645.174	1643.995	109.495	0.442	1399.897	0.491	30	0.153	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/2	1644.513	1643.995	-293.459	0.524	888.007	0.500	21	0.152	K.TLLLGEKPVTVFGIR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/3	1643.275	1643.995	-1049.344	0.439	1289.022	0.533	30	0.152	K.TLLLGEKPVTVFGIR.N
R5/RRR5-11/2	1644.571	1643.995	-258.160	0.513	778.948	0.521	20	0.150	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/2	1643.703	1643.995	-177.923	0.493	775.796	0.518	20	0.149	K.TLLLGEKPVTVFGIR.N
R5/RRR5-11/2	1643.098	1643.995	-1158.019	0.480	739.715	0.488	19	0.143	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/3	1643.484	1643.995	-922.155	0.442	1163.540	0.528	29	0.137	K.TLLLGEKPVTVFGIR.N
R5/RRR5-14/2	1643.546	1643.995	-273.890	0.466	598.621	0.491	17	0.137	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/2	1643.104	1643.995	-1154.214	0.448	525.320	0.457	17	0.132	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/2	1644.384	1643.995	237.623	0.473	450.756	0.458	16	0.131	K.TLLLGEKPVTVFGIR.N
R5/RRR5-2/2	1642.580	1643.995	-1474.430	0.323	636.778	0.366	16	0.125	K.TLLLGEKPVTVFGIR.N
R5/RRR5-12/2	1643.715	1643.995	-170.473	0.214	390.251	0.334	12	0.116	-.TLLLGEKPVTVFGIR.-
R5/RRR5-10/3	1643.770	1643.995	-136.957	0.439	844.679	0.437	26	0.098	K.TLLLGEKPVTVFGIR.N
R5/RRR5-1/3	1643.180	1643.995	-1107.860	0.431	594.781	0.444	23	0.094	K.TLLLGEKPVTVFGIR.N
R5/RRR5-2/3	1642.676	1643.995	-1415.656	0.352	847.886	0.417	26	0.094	K.TLLLGEKPVTVFGIR.N
R5/RRR5-24/3	1644.172	1643.995	108.259	0.459	856.990	0.397	26	0.092	K.TLLLGEKPVTVFGIR.N
R5/RRR5-9/3	1643.219	1643.995	-1083.916	0.350	522.735	0.421	21	0.090	K.TLLLGEKPVTVFGIR.N
R5/RRR5-9/3	1643.768	1643.995	-138.522	0.327	679.582	0.339	24	0.082	K.TLLLGEKPVTVFGIR.N
R5/RRR5-14/3	1643.230	1643.995	-1076.867	0.269	781.085	0.224	23	0.069	-.TLLLGEKPVTVFGIR.-
R5/RRR5-3/2	1965.192	1965.190	0.834	0.552	1627.961	0.552	26	0.226	K.TGLYLEGSVSPAISDVDIK.I
R5/RRR5-3/2	1664.358	1664.798	-265.390	0.527	1750.021	0.479	24	0.225	K.FTPSAVAIDLNSGESR.E
R5/RRR5-3/2	1664.185	1664.798	-972.144	0.507	1736.380	0.469	25	0.222	K.FTPSAVAIDLNSGESR.E
R5/RRR5-3/2	1663.923	1664.798	-1130.575	0.421	1754.458	0.385	25	0.204	K.FTPSAVAIDLNSGESR.E
R5/RRR5-3/2	1155.139	1155.288	-129.164	0.451	1581.723	0.403	19	0.190	K.FQVTGFSVGGR.V
R5/RRR5-3/2	1172.056	1172.272	-185.068	0.413	1420.059	0.433	16	0.180	R.AVTDNLGYYR.L
R5/RRR5-3/2	1154.978	1155.288	-269.112	0.471	1253.789	0.368	18	0.156	K.FQVTGFSVGGR.V
R5/RRR5-3/2	1172.178	1172.272	-80.179	0.431	1087.036	0.429	16	0.154	R.AVTDNLGYYR.L
R5/RRR5-3/2	1154.996	1155.288	-253.313	0.412	1307.861	0.316	18	0.151	K.FQVTGFSVGGR.V
R5/RRR5-3/2	1588.805	1587.797	5.039	0.404	1050.951	0.322	18	0.134	K.EQCNQNILLSLVR.L
R5/RRR5-3/2	798.916	798.997	-100.934	0.436	1050.795	0.229	11	0.126	K.LGQILVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1171.448	1172.272	-1561.656	0.268	933.368	0.289	16	0.126	R.AVTDNLGYYR.L
R5/RRR5-3/2	981.722	982.109	-395.676	0.314	893.728	0.276	12	0.125	R.YDVCGIVR.T
R5/RRR5-1/2	1903.129	1902.116	6.958	0.426	808.696	0.356	18	0.124	R.GELHVEM*GSLQEIDLSK.N
R5/RRR5-3/2	981.649	982.109	-470.166	0.402	768.994	0.289	11	0.123	-.YDVCGIVR.-
R5/RRR5-3/2	798.979	798.997	-21.701	0.374	791.291	0.199	11	0.119	K.LGQILVR.I
R5/RRR5-3/2	798.886	798.997	-138.486	0.359	810.184	0.184	11	0.118	K.LGQILVR.I
R5/RRR5-2/2	1155.197	1155.288	-78.919	0.281	582.252	0.258	13	0.118	K.FQVTGFSVGGR.V
R5/RRR5-5/2	1213.144	1213.406	-216.243	0.408	1101.964	0.430	16	0.153	K.AVDEIEPALKK.Q
R5/RRR5-5/2	1213.344	1213.406	-50.516	0.326	670.486	0.339	15	0.124	K.AVDEIEPALKK.Q
R5/RRR5-5/2	1427.207	1426.728	336.664	0.558	2059.281	0.598	19	0.305	R.LPLLDLNIYVPR.D
R5/RRR5-5/2	1426.490	1426.728	-167.336	0.446	1803.873	0.550	17	0.249	R.LPLLDLNIYVPR.D
R5/RRR5-5/2	1087.140	1087.252	-103.344	0.420	1666.361	0.436	18	0.206	K.VANASALAEIK.K
R5/RRR5-5/2	1181.263	1180.465	-171.809	0.418	1508.368	0.435	18	0.188	K.AIVEGVLPIIR.T
R5/RRR5-5/2	1403.155	1402.576	-300.570	0.530	1360.738	0.447	18	0.177	R.VFFANDTYLPSK.M
R5/RRR5-4/2	1402.219	1402.576	-255.453	0.476	1375.327	0.428	18	0.175	R.VFFANDTYLPSK.M
R5/RRR5-5/2	1426.587	1426.728	-99.180	0.488	1075.815	0.542	15	0.168	R.LPLLDLNIYVPR.D
R5/RRR5-4/2	1402.241	1402.576	-239.383	0.454	1355.107	0.400	18	0.168	R.VFFANDTYLPSK.M
R5/RRR5-4/2	1161.958	1161.353	-340.307	0.500	1168.016	0.467	15	0.166	K.MSDFLGYSLK.A
R5/RRR5-4/2	1160.426	1161.353	-1664.906	0.332	964.719	0.495	15	0.152	K.MSDFLGYSLK.A
R5/RRR5-4/2	1161.302	1161.353	-43.713	0.396	985.324	0.431	14	0.147	K.MSDFLGYSLK.A
R5/RRR5-5/2	1155.426	1156.273	-1602.702	0.411	954.477	0.427	16	0.145	K.LDGNFIYASR.T
R5/RRR5-5/2	1401.545	1402.576	-1452.908	0.345	1006.049	0.388	15	0.140	R.VFFANDTYLPSK.M
R5/RRR5-3/2	1162.469	1161.353	100.521	0.379	802.291	0.438	13	0.138	K.MSDFLGYSLK.A
R5/RRR5-5/2	1087.163	1087.252	-81.606	0.411	943.732	0.382	16	0.138	-.VANASALAEIK.-
R5/RRR5-5/3	1782.319	1782.079	134.662	0.540	1200.646	0.496	31	0.135	K.LVRPVLGGSQELPYPR.R
R5/RRR5-4/2	1402.277	1402.576	-213.969	0.440	1016.533	0.317	16	0.133	R.VFFANDTYLPSK.M
R5/RRR5-3/2	1161.934	1161.353	-361.283	0.304	616.787	0.259	12	0.119	K.MSDFLGYSLK.A
R5/RRR5-5/2	1177.985	1177.352	-312.683	0.253	359.929	0.299	11	0.119	-.M*SDFLGYSLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1177.225	1177.352	-108.621	0.166	707.020	0.181	14	0.114	K.M*SDFLGYSLK.A
R5/RRR5-4/3	1781.300	1782.079	-1002.197	0.491	1027.403	0.447	30	0.109	K.LVRPVLGGSQELPYPR.R
R5/RRR5-5/3	1781.927	1782.079	-85.765	0.490	1105.981	0.395	30	0.104	K.LVRPVLGGSQELPYPR.R
R5/RRR5-5/3	1782.941	1782.079	-77.716	0.558	850.391	0.455	29	0.101	K.LVRPVLGGSQELPYPR.R
R5/RRR5-10/2	1689.028	1688.818	124.275	0.564	1634.131	0.515	19	0.219	K.FLQSLEFFEENER.K
R5/RRR5-10/2	1255.899	1255.316	-333.180	0.535	1516.464	0.515	17	0.207	K.SIESSDLNFSR.Y
R5/RRR5-10/2	1254.399	1255.316	-1532.860	0.418	1449.477	0.456	17	0.186	K.SIESSDLNFSR.Y
R5/RRR5-10/2	1254.359	1255.316	-1565.413	0.371	1447.353	0.424	17	0.179	K.SIESSDLNFSR.Y
R5/RRR5-10/3	1406.296	1406.526	-164.351	0.496	1688.336	0.402	26	0.169	K.RTSEALSEHFTK.E
R5/RRR5-10/3	1406.453	1406.526	-52.164	0.517	1573.211	0.403	26	0.153	K.RTSEALSEHFTK.E
R5/RRR5-10/2	1542.489	1541.750	-169.913	0.460	1088.845	0.439	15	0.149	K.MEDNLLEFFPSAK.R
R5/RRR5-10/2	1688.780	1688.818	-22.809	0.456	1033.769	0.436	16	0.148	K.FLQSLEFFEENER.K
R5/RRR5-10/2	1374.087	1374.650	-1141.030	0.404	614.892	0.435	16	0.133	R.EAILPSVLYIQK.T
R5/RRR5-10/2	1639.264	1639.960	-1037.489	0.373	562.840	0.493	19	0.133	K.LSGLPPETVFQPLLK.D
R5/RRR5-10/2	1639.164	1639.960	-1098.428	0.366	685.176	0.435	20	0.132	K.LSGLPPETVFQPLLK.D
R5/RRR5-10/2	1374.233	1374.650	-304.045	0.415	637.500	0.391	17	0.131	R.EAILPSVLYIQK.T
R5/RRR5-11/2	1374.007	1374.650	-1199.374	0.373	664.804	0.391	16	0.130	R.EAILPSVLYIQK.T
R5/RRR5-11/2	1374.301	1374.650	-254.674	0.317	563.859	0.430	15	0.128	R.EAILPSVLYIQK.T
R5/RRR5-10/2	1374.205	1374.650	-325.078	0.356	569.408	0.335	16	0.125	R.EAILPSVLYIQK.T
R5/RRR5-10/2	974.662	975.123	-474.102	0.466	781.943	0.287	13	0.122	-.FPDIEVVR.-
R5/RRR5-10/2	974.687	975.123	-449.092	0.431	767.397	0.285	13	0.120	-.FPDIEVVR.-
R5/RRR5-10/2	974.929	975.123	-199.945	0.445	748.071	0.310	13	0.119	-.FPDIEVVR.-
R5/RRR5-10/3	1405.481	1406.526	-1459.434	0.506	1157.312	0.413	23	0.111	K.RTSEALSEHFTK.E
R5/RRR5-14/2	1689.370	1688.864	-293.349	0.560	1969.727	0.651	26	0.303	K.VDGLVSGIGTGGTITGAGR.Y
R5/RRR5-14/2	1688.410	1688.864	-269.876	0.532	1836.518	0.598	26	0.267	K.VDGLVSGIGTGGTITGAGR.Y
R5/RRR5-14/2	1357.203	1357.512	-228.473	0.488	1977.318	0.475	19	0.255	R.IGYSMITDAEEK.G
R5/RRR5-14/2	1358.082	1357.512	-317.577	0.526	1805.219	0.542	19	0.249	R.IGYSMITDAEEK.G
R5/RRR5-14/3	1818.664	1818.064	-220.192	0.532	1739.794	0.569	30	0.244	K.DVTELIGNTPLVYLNR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1689.333	1688.864	278.047	0.503	1589.502	0.620	25	0.237	K.VDGLVSGIGTGGTITGAGR.Y
R5/RRR5-14/2	1819.321	1818.064	141.756	0.571	1735.756	0.535	22	0.235	K.DVTELIGNTPLVYLNR.V
R5/RRR5-14/2	1819.363	1818.064	165.171	0.558	1677.337	0.525	22	0.225	K.DVTELIGNTPLVYLNR.V
R5/RRR5-14/2	1356.568	1357.512	-1437.631	0.381	1755.697	0.476	19	0.224	R.IGYSMITDAEEK.G
R5/RRR5-14/2	1705.373	1706.040	-980.089	0.407	1622.394	0.462	20	0.203	K.AFGAELILTDPLLGM*K.G
R5/RRR5-14/2	1286.239	1285.513	-213.663	0.486	1553.313	0.421	18	0.191	R.YLSSVLFQSIK.K
R5/RRR5-14/2	1818.623	1818.064	-243.282	0.553	1502.368	0.459	21	0.189	K.DVTELIGNTPLVYLNR.V
R5/RRR5-14/2	1373.166	1373.511	-251.998	0.448	1368.664	0.491	18	0.185	R.IGYSM*ITDAEEK.G
R5/RRR5-14/2	1372.884	1373.511	-1188.549	0.396	1476.038	0.419	18	0.181	R.IGYSM*ITDAEEK.G
R5/RRR5-14/2	1286.241	1285.513	-212.330	0.444	1331.072	0.414	17	0.168	R.YLSSVLFQSIK.K
R5/RRR5-14/2	1475.147	1474.642	-336.614	0.526	768.202	0.548	17	0.153	K.IHYETTGPEIWK.S
R5/RRR5-14/2	1475.170	1474.642	-321.088	0.528	709.157	0.574	16	0.153	K.IHYETTGPEIWK.S
R5/RRR5-14/2	1474.359	1474.642	-192.630	0.485	808.361	0.523	17	0.151	K.IHYETTGPEIWK.S
R5/RRR5-14/2	1372.457	1373.511	-1501.243	0.332	1206.720	0.376	17	0.151	R.IGYSM*ITDAEEK.G
R5/RRR5-3/2	1819.328	1818.064	145.726	0.355	525.240	0.251	16	0.115	K.DVTELIGNTPLVYLNR.V
R5/RRR5-14/2	1285.172	1285.513	-266.715	0.251	591.807	0.179	12	0.113	-.YLSSVLFQSIK.-
R5/RRR5-14/3	1988.049	1986.176	-63.971	0.349	1020.108	0.353	27	0.085	K.THNSFILQQFENPANPK.I
R5/RRR5-11/2	1545.400	1545.760	-233.370	0.484	1712.951	0.526	19	0.232	K.TYVVQDGDIIFFK.F
R5/RRR5-10/2	1067.283	1067.307	-22.669	0.436	1041.879	0.551	17	0.169	K.IGIVGLPNVGK.S
R5/RRR5-11/2	1067.067	1067.307	-225.766	0.441	929.157	0.525	17	0.158	K.IGIVGLPNVGK.S
R5/RRR5-11/3	1707.712	1707.874	-95.336	0.509	1204.495	0.539	30	0.147	R.GAHAGEGLGNAFLSHIR.A
R5/RRR5-11/2	1067.097	1067.307	-197.649	0.378	846.736	0.424	16	0.139	K.IGIVGLPNVGK.S
R5/RRR5-10/2	1128.252	1127.321	-61.054	0.486	918.263	0.377	15	0.137	R.AVDGIFHVLR.A
R5/RRR5-11/3	1707.208	1707.874	-979.030	0.493	1176.602	0.495	30	0.132	R.GAHAGEGLGNAFLSHIR.A
R5/RRR5-11/2	1066.898	1067.307	-384.284	0.395	540.847	0.442	12	0.125	-.IGIVGLPNVGK.-
R5/RRR5-11/3	1514.508	1514.625	-77.424	0.445	903.204	0.585	25	0.125	K.APQAAGTIHTDFER.G
R5/RRR5-11/3	1948.226	1948.206	10.230	0.536	964.993	0.525	31	0.120	R.LKDIEFVQNKIDDLEK.S
R5/RRR5-11/3	1948.468	1948.206	135.024	0.505	1034.480	0.494	31	0.119	R.LKDIEFVQNKIDDLEK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/3	1514.636	1514.625	7.702	0.490	756.110	0.593	22	0.117	K.APQAAGTIHTDFER.G
R5/RRR5-11/3	1707.426	1707.874	-263.149	0.466	670.596	0.479	25	0.094	R.GAHAGEGLGNAFLSHIR.A
R5/RRR5-11/3	1539.200	1538.681	-313.268	0.371	854.603	0.433	25	0.091	K.FDDLKELGSESAVK.A
R5/RRR5-11/3	1948.010	1948.206	-101.111	0.517	636.520	0.440	27	0.091	R.LKDIEFVQNKIDDLEK.S
R5/RRR5-11/3	1538.516	1538.681	-107.332	0.353	737.240	0.264	22	0.069	K.FDDLKELGSESAVK.A
R5/RRR5-3/2	1497.128	1497.637	-1010.780	0.429	1119.572	0.540	20	0.173	R.QGNVGIVEYAYQR.T
R5/RRR5-3/2	1497.350	1497.637	-192.534	0.504	996.791	0.554	19	0.167	R.QGNVGIVEYAYQR.T
R5/RRR5-3/2	1252.393	1252.528	-107.793	0.354	1160.242	0.452	15	0.158	R.LILGELQAPAVK.Y
R5/RRR5-3/2	1497.065	1497.637	-1053.187	0.457	865.351	0.487	18	0.148	R.QGNVGIVEYAYQR.T
R5/RRR5-3/2	1192.204	1191.402	-166.330	0.408	702.224	0.405	16	0.136	K.TLDVPIYITR.V
R5/RRR5-3/3	1298.275	1298.434	-123.092	0.522	1591.255	0.339	26	0.135	R.RPGSVSLNQSPR.T
R5/RRR5-1/2	1252.143	1252.528	-308.463	0.377	866.890	0.390	14	0.133	R.LILGELQAPAVK.Y
R5/RRR5-1/2	1497.128	1497.637	-1010.944	0.353	702.811	0.426	17	0.132	R.QGNVGIVEYAYQR.T
R5/RRR5-3/2	1192.154	1191.402	-208.548	0.420	534.886	0.368	14	0.129	K.TLDVPIYITR.V
R5/RRR5-3/2	1119.989	1120.283	-263.745	0.386	853.715	0.289	13	0.124	-.VTIFDLQQR.-
R5/RRR5-2/2	771.954	771.928	34.241	0.422	1043.965	0.200	11	0.124	R.LGIEALR.Q
R5/RRR5-3/2	1251.786	1252.528	-1395.605	0.335	569.159	0.377	13	0.123	-.LILGELQAPAVK.-
R5/RRR5-5/2	771.431	771.928	-646.299	0.319	889.422	0.216	11	0.122	R.LGIEALR.Q
R5/RRR5-4/2	1190.711	1191.402	-1424.414	0.333	471.278	0.266	13	0.122	K.TLDVPIYITR.V
R5/RRR5-1/2	772.224	771.928	384.151	0.406	1007.793	0.175	11	0.121	R.LGIEALR.Q
R5/RRR5-2/2	771.317	771.928	-2095.505	0.310	995.708	0.167	11	0.120	R.LGIEALR.Q
R5/RRR5-4/2	1190.701	1191.402	-1432.343	0.347	402.201	0.329	12	0.119	-.TLDVPIYITR.-
R5/RRR5-1/2	771.443	771.928	-630.418	0.328	977.914	0.144	11	0.118	R.LGIEALR.Q
R5/RRR5-1/2	1191.221	1191.402	-151.769	0.331	537.494	0.205	13	0.118	-.TLDVPIYITR.-
R5/RRR5-2/2	771.848	771.928	-104.553	0.424	697.120	0.176	10	0.117	R.LGIEALR.Q
R5/RRR5-4/2	1251.724	1252.528	-1445.560	0.194	472.328	0.344	13	0.116	R.LILGELQAPAVK.Y
R5/RRR5-5/3	1298.530	1298.434	74.514	0.466	1228.901	0.403	24	0.115	-.RPGSVSLNQSPR.-
R5/RRR5-3/2	771.949	771.928	26.946	0.422	995.485	0.116	11	0.114	R.LGIEALR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1191.045	1191.402	-300.540	0.228	351.232	0.307	11	0.114	-.TLDVPIYITR.-
R5/RRR5-3/2	1563.782	1564.870	-1339.372	0.191	861.484	0.122	15	0.108	R.LAFLYLITGYM*DK.V
R5/RRR5-3/3	1298.434	1298.434	-0.162	0.481	1432.015	0.297	25	0.107	R.RPGSVSLNQSPR.T
R5/RRR5-1/3	1298.621	1298.434	144.513	0.484	1141.620	0.402	26	0.107	R.RPGSVSLNQSPR.T
R5/RRR5-3/3	1298.199	1298.434	-181.667	0.486	1275.079	0.343	23	0.105	R.RPGSVSLNQSPR.T
R5/RRR5-1/3	1298.456	1298.434	17.235	0.487	1361.027	0.306	25	0.104	-.RPGSVSLNQSPR.-
R5/RRR5-26/2	1837.876	1837.921	-24.223	0.478	1412.928	0.612	22	0.204	K.TSFWDAEPAPVEATAASS.-
R5/RRR5-26/2	1838.143	1837.921	121.121	0.428	1338.987	0.610	22	0.191	K.TSFWDAEPAPVEATAASS.-
R5/RRR5-26/2	1838.892	1837.921	-15.554	0.452	1327.963	0.583	22	0.183	K.TSFWDAEPAPVEATAASS.-
R5/RRR5-26/2	1430.356	1429.601	-171.763	0.528	977.522	0.517	21	0.161	K.GNVTPDAVLQTVSK.T
R5/RRR5-27/2	1428.618	1429.601	-1392.122	0.405	940.953	0.548	21	0.160	K.GNVTPDAVLQTVSK.T
R5/RRR5-27/2	1838.008	1837.921	47.522	0.447	1212.141	0.544	22	0.156	K.TSFWDAEPAPVEATAASS.-
R5/RRR5-27/2	1429.292	1429.601	-216.864	0.460	802.312	0.548	20	0.154	K.GNVTPDAVLQTVSK.T
R5/RRR5-26/2	1429.487	1429.601	-79.879	0.406	763.574	0.502	19	0.144	K.GNVTPDAVLQTVSK.T
R5/RRR5-27/2	1429.393	1429.601	-146.096	0.396	814.740	0.479	20	0.144	K.GNVTPDAVLQTVSK.T
R5/RRR5-27/2	1369.825	1370.542	-1257.463	0.390	1079.278	0.380	17	0.143	R.VGM*SCEGCVGAVK.R
R5/RRR5-27/2	1837.086	1837.921	-1001.947	0.336	1146.242	0.438	20	0.138	K.TSFWDAEPAPVEATAASS.-
R5/RRR5-26/2	1383.974	1384.537	-1133.123	0.357	759.573	0.362	16	0.128	K.M*QGVESFDVDIK.E
R5/RRR5-27/2	1383.772	1384.537	-1279.635	0.398	1025.229	0.249	17	0.126	K.M*QGVESFDVDIK.E
R5/RRR5-27/2	1370.122	1370.542	-307.811	0.346	547.679	0.351	14	0.121	R.VGM*SCEGCVGAVK.R
R5/RRR5-26/2	1370.022	1370.542	-1113.042	0.396	732.742	0.305	15	0.121	R.VGM*SCEGCVGAVK.R
R5/RRR5-26/3	1769.077	1769.955	-1064.225	0.505	1007.371	0.445	27	0.107	K.M*QGVESFDVDIKEQK.V
R5/RRR5-26/3	1771.284	1769.955	186.707	0.454	1180.858	0.382	29	0.106	K.M*QGVESFDVDIKEQK.V
R5/RRR5-26/3	1770.310	1769.955	201.368	0.455	1014.055	0.428	28	0.103	K.M*QGVESFDVDIKEQK.V
R5/RRR5-27/3	1526.834	1526.729	69.182	0.404	896.467	0.444	24	0.098	R.VGM*SCEGCVGAVKR.V
R5/RRR5-27/3	1525.650	1526.729	-1366.553	0.299	688.669	0.356	23	0.076	R.VGM*SCEGCVGAVKR.V
R5/RRR5-26/3	1526.735	1526.729	3.988	0.317	735.724	0.305	24	0.072	-.VGM*SCEGCVGAVKR.-
R5/RRR5-7/2	1471.240	1471.678	-298.228	0.403	2664.374	0.374	21	0.346	K.ESIVDVEGVVSLPK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1531.261	1531.652	-255.914	0.550	2342.603	0.538	25	0.335	R.VWTEVGGLDEAAAGR.S
R5/RRR5-7/2	1531.230	1531.652	-276.149	0.582	2060.594	0.529	24	0.283	R.VWTEVGGLDEAAAGR.S
R5/RRR5-7/2	1531.253	1531.652	-261.113	0.566	2027.454	0.522	24	0.276	R.VWTEVGGLDEAAAGR.S
R5/RRR5-8/2	1472.962	1471.678	193.459	0.482	1959.827	0.390	19	0.230	K.ESIVDVEGVVSLPK.E
R5/RRR5-7/2	1306.560	1307.477	-1472.227	0.334	1430.998	0.428	21	0.177	K.LIAGSSEGGAAVFK.L
R5/RRR5-7/2	1342.187	1341.556	-275.213	0.422	1072.842	0.441	17	0.154	K.LTYEEGIQM*LK.E
R5/RRR5-3/2	1532.853	1531.652	131.346	0.557	987.562	0.464	21	0.151	R.VWTEVGGLDEAAAGR.S
R5/RRR5-7/2	1050.017	1050.235	-208.093	0.476	1055.387	0.375	15	0.146	R.VFEVGPVFR.A
R5/RRR5-7/2	1306.786	1307.477	-1298.078	0.355	1019.401	0.386	19	0.141	K.LIAGSSEGGAAVFK.L
R5/RRR5-8/2	1049.984	1050.235	-239.817	0.427	711.826	0.433	12	0.136	R.VFEVGPVFR.A
R5/RRR5-7/2	1018.030	1018.151	-119.860	0.421	781.379	0.391	13	0.134	R.TPANQAIFR.I
R5/RRR5-8/2	1049.470	1050.235	-1687.166	0.421	871.514	0.331	13	0.131	R.VFEVGPVFR.A
R5/RRR5-8/2	1017.479	1018.151	-1648.036	0.389	545.398	0.391	13	0.130	R.TPANQAIFR.I
R5/RRR5-7/2	1018.015	1018.151	-134.415	0.413	635.538	0.370	13	0.129	R.TPANQAIFR.I
R5/RRR5-7/2	1306.514	1307.477	-1507.233	0.295	767.585	0.369	17	0.126	K.LIAGSSEGGAAVFK.L
R5/RRR5-7/2	1341.061	1341.556	-369.846	0.290	427.297	0.326	14	0.120	K.LTYEEGIQM*LK.E
R5/RRR5-7/2	1470.293	1471.678	-1626.633	0.283	1017.085	0.199	17	0.120	K.ESIVDVEGVVSLPK.E
R5/RRR5-7/2	1049.987	1050.235	-236.318	0.286	557.056	0.278	11	0.119	-.VFEVGPVFR.-
R5/RRR5-8/2	1049.916	1050.235	-304.204	0.250	371.794	0.308	9	0.113	-.VFEVGPVFR.-
R5/RRR5-7/3	1520.499	1519.593	-61.780	0.397	554.438	0.494	26	0.090	R.SEAEIEKAEQAGEK.L
R5/RRR5-7/3	1520.732	1519.593	91.363	0.345	576.830	0.473	26	0.085	R.SEAEIEKAEQAGEK.L
R5/RRR5-2/2	1593.691	1593.932	-151.970	0.535	1672.477	0.603	23	0.247	R.IVLNPISSLADLPLK.N
R5/RRR5-2/2	1594.269	1593.932	211.915	0.542	1428.306	0.611	21	0.217	R.IVLNPISSLADLPLK.N
R5/RRR5-2/2	1274.425	1274.484	-46.077	0.520	1477.317	0.447	16	0.188	K.VLDFLHELCK.F
R5/RRR5-2/2	1549.893	1548.726	108.177	0.430	1487.583	0.411	20	0.179	K.LGLEFGSNAVITNGR.V
R5/RRR5-2/2	1544.407	1543.794	-251.041	0.434	842.396	0.518	18	0.149	K.VSPGVWYLQLAPGR.S
R5/RRR5-2/2	1275.130	1275.479	-274.385	0.403	1138.012	0.378	16	0.147	K.VIFVDADQIVR.A
R5/RRR5-2/3	1886.629	1887.038	-217.387	0.546	1186.625	0.545	29	0.146	K.GVALEDPKTEDLSQEVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1544.500	1543.794	-190.620	0.398	939.788	0.440	19	0.144	K.VSPGVWYLQLAPGR.S
R5/RRR5-2/3	1886.331	1887.038	-907.839	0.517	1193.345	0.522	29	0.141	K.GVALEDPKTEDLSQEVR.G
R5/RRR5-2/2	1543.252	1543.794	-1002.071	0.363	802.538	0.461	18	0.139	K.VSPGVWYLQLAPGR.S
R5/RRR5-2/2	1359.467	1359.423	32.277	0.340	1034.433	0.358	18	0.138	K.WASSFISGDSSSK.K
R5/RRR5-2/2	1360.376	1359.423	-34.526	0.322	885.383	0.302	17	0.126	K.WASSFISGDSSSK.K
R5/RRR5-2/3	1888.142	1887.038	55.201	0.540	1041.535	0.520	26	0.125	K.GVALEDPKTEDLSQEVR.G
R5/RRR5-2/2	1123.129	1123.238	-97.525	0.280	1059.041	0.204	14	0.121	R.SADLYELPSK.F
R5/RRR5-2/2	1359.597	1359.423	128.451	0.243	688.970	0.251	16	0.116	K.WASSFISGDSSSK.K
R5/RRR5-3/3	1270.325	1270.420	-75.392	0.556	1625.323	0.446	27	0.169	R.RPGSVSLNQSPK.T
R5/RRR5-3/3	1269.516	1270.420	-1504.926	0.473	1586.228	0.440	25	0.163	R.RPGSVSLNQSPK.T
R5/RRR5-3/3	1269.999	1270.420	-333.107	0.534	1513.871	0.465	26	0.161	R.RPGSVSLNQSPK.T
R5/RRR5-5/3	1270.908	1270.420	385.041	0.526	1507.578	0.452	25	0.156	R.RPGSVSLNQSPK.T
R5/RRR5-1/3	1269.883	1270.420	-1214.376	0.538	1583.769	0.416	27	0.154	R.RPGSVSLNQSPK.T
R5/RRR5-3/2	1269.297	1268.527	-182.369	0.393	928.808	0.386	15	0.137	R.LILGELQAPSVK.Y
R5/RRR5-1/2	1268.109	1268.527	-330.744	0.288	964.273	0.334	15	0.131	R.LILGELQAPSVK.Y
R5/RRR5-1/3	1271.671	1270.420	197.882	0.530	1429.685	0.395	25	0.131	R.RPGSVSLNQSPK.T
R5/RRR5-1/2	1267.861	1268.527	-1317.940	0.239	1071.946	0.253	15	0.127	R.LILGELQAPSVK.Y
R5/RRR5-3/2	1267.877	1268.527	-1305.757	0.286	751.910	0.331	14	0.124	R.LILGELQAPSVK.Y
R5/RRR5-5/2	1267.658	1268.527	-1479.256	0.229	587.106	0.322	12	0.118	R.LILGELQAPSVK.Y
R5/RRR5-4/2	1268.595	1268.527	53.120	0.303	498.108	0.304	11	0.115	-.LILGELQAPSVK.-
R5/RRR5-5/2	1267.910	1268.527	-1279.650	0.266	277.539	0.397	12	0.113	-.LILGELQAPSVK.-
R5/RRR5-2/2	1268.006	1268.527	-1203.659	0.161	462.115	0.250	11	0.109	-.LILGELQAPSVK.-
R5/RRR5-5/3	1270.494	1270.420	58.041	0.487	1110.085	0.412	23	0.107	R.RPGSVSLNQSPK.T
R5/RRR5-5/3	1270.389	1270.420	-24.935	0.484	1192.514	0.365	23	0.103	R.RPGSVSLNQSPK.T
R5/RRR5-1/3	1270.570	1270.420	118.458	0.428	994.048	0.410	22	0.099	R.RPGSVSLNQSPK.T
R5/RRR5-16/2	1615.835	1616.797	-1217.717	0.488	1917.716	0.521	22	0.259	K.FPTLVTHQESLESK.V
R5/RRR5-16/2	1616.503	1616.797	-182.129	0.555	1914.773	0.507	22	0.255	K.FPTLVTHQESLESK.V
R5/RRR5-16/2	1616.363	1616.797	-269.104	0.552	1956.021	0.467	22	0.250	K.FPTLVTHQESLESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1363.220	1363.586	-269.408	0.377	1743.348	0.430	19	0.212	K.YHAFLASEAIIK.Q
R5/RRR5-16/2	1363.353	1363.586	-171.224	0.426	1647.131	0.384	19	0.193	K.YHAFLASEAIIK.Q
R5/RRR5-15/2	1248.097	1248.325	-183.406	0.472	1297.366	0.340	17	0.153	R.EAISQITNESR.E
R5/RRR5-16/2	1247.402	1248.325	-1546.464	0.367	1219.302	0.345	18	0.149	R.EAISQITNESR.E
R5/RRR5-16/2	1247.540	1248.325	-1435.589	0.377	1211.181	0.331	17	0.147	R.EAISQITNESR.E
R5/RRR5-16/3	1491.473	1491.759	-192.481	0.484	1711.221	0.321	28	0.145	K.KYHAFLASEAIIK.Q
R5/RRR5-15/2	1248.023	1248.325	-243.064	0.443	1192.777	0.333	16	0.145	R.EAISQITNESR.E
R5/RRR5-16/2	1248.079	1248.325	-198.222	0.506	1019.206	0.350	17	0.139	R.EAISQITNESR.E
R5/RRR5-17/3	1872.569	1873.099	-819.475	0.512	948.311	0.596	29	0.136	K.AGKFPTLVTHQESLESK.V
R5/RRR5-16/3	1872.613	1873.099	-260.499	0.485	1124.908	0.520	31	0.133	K.AGKFPTLVTHQESLESK.V
R5/RRR5-16/3	1872.977	1873.099	-65.515	0.502	989.480	0.556	30	0.130	K.AGKFPTLVTHQESLESK.V
R5/RRR5-16/2	1363.186	1363.586	-293.844	0.336	1007.600	0.262	17	0.127	K.YHAFLASEAIIK.Q
R5/RRR5-15/3	1491.481	1491.759	-186.938	0.519	1467.370	0.337	26	0.121	K.KYHAFLASEAIIK.Q
R5/RRR5-17/3	1873.336	1873.099	126.648	0.501	783.426	0.578	26	0.119	K.AGKFPTLVTHQESLESK.V
R5/RRR5-15/3	1873.435	1873.099	179.677	0.483	682.762	0.587	26	0.116	K.AGKFPTLVTHQESLESK.V
R5/RRR5-15/3	1873.184	1873.099	45.184	0.480	697.878	0.580	27	0.115	K.AGKFPTLVTHQESLESK.V
R5/RRR5-17/3	1616.793	1616.797	-2.213	0.396	1099.703	0.454	25	0.114	K.FPTLVTHQESLESK.V
R5/RRR5-17/3	1872.497	1873.099	-858.445	0.481	626.818	0.586	25	0.113	K.AGKFPTLVTHQESLESK.V
R5/RRR5-15/3	1872.267	1873.099	-981.754	0.469	786.355	0.535	27	0.111	K.AGKFPTLVTHQESLESK.V
R5/RRR5-16/3	1874.383	1873.099	152.020	0.475	862.179	0.505	28	0.110	K.AGKFPTLVTHQESLESK.V
R5/RRR5-15/3	1616.819	1616.797	13.917	0.414	1100.233	0.423	26	0.108	K.FPTLVTHQESLESK.V
R5/RRR5-16/3	1616.406	1616.797	-242.632	0.428	1259.021	0.359	26	0.107	K.FPTLVTHQESLESK.V
R5/RRR5-15/3	1491.335	1491.759	-284.736	0.491	1196.545	0.377	24	0.106	K.KYHAFLASEAIIK.Q
R5/RRR5-16/3	1491.755	1491.759	-2.603	0.526	1194.366	0.355	24	0.100	-.KYHAFLASEAIIK.-
R5/RRR5-15/3	1490.871	1491.759	-1270.109	0.460	1495.469	0.239	26	0.099	K.KYHAFLASEAIIK.Q
R5/RRR5-16/3	1732.629	1732.888	-149.971	0.418	871.472	0.410	28	0.093	K.VCM*LGDAQHVEEAEK.M
R5/RRR5-16/3	1615.956	1616.797	-1142.625	0.363	779.007	0.417	23	0.090	K.FPTLVTHQESLESK.V
R5/RRR5-15/3	1732.662	1732.888	-130.783	0.401	802.781	0.386	27	0.088	K.VCM*LGDAQHVEEAEK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/3	1491.240	1491.759	-1021.760	0.392	1248.328	0.263	24	0.087	K.KYHAFLASEAIIK.Q
R5/RRR5-16/3	1733.894	1732.888	3.582	0.401	899.672	0.354	28	0.086	K.VCM*LGDAQHVEEAEK.M
R5/RRR5-15/3	1732.333	1732.888	-899.988	0.374	817.323	0.374	26	0.086	K.VCM*LGDAQHVEEAEK.M
R5/RRR5-15/3	1733.132	1732.888	141.058	0.407	598.044	0.338	24	0.081	K.VCM*LGDAQHVEEAEK.M
R5/RRR5-15/3	1616.125	1616.797	-1037.730	0.346	1105.337	0.265	23	0.079	K.FPTLVTHQESLESK.V
R5/RRR5-16/3	1732.226	1732.888	-962.279	0.385	704.203	0.311	26	0.078	K.VCM*LGDAQHVEEAEK.M
R5/RRR5-17/3	1732.456	1732.888	-249.952	0.388	645.181	0.298	24	0.077	K.VCM*LGDAQHVEEAEK.M
R5/RRR5-15/3	1616.820	1616.797	14.485	0.343	1034.199	0.271	24	0.077	K.FPTLVTHQESLESK.V
R5/RRR5-16/3	1616.470	1616.797	-202.630	0.273	845.733	0.275	22	0.072	K.FPTLVTHQESLESK.V
R5/RRR5-12/2	1653.420	1652.751	-200.870	0.592	3163.845	0.565	28	1.000	K.AAAVVAGNGATNGATNGVH.-
R5/RRR5-12/2	1653.236	1652.751	294.560	0.578	2815.564	0.560	28	0.767	K.AAAVVAGNGATNGATNGVH.-
R5/RRR5-12/2	1653.414	1652.751	-204.129	0.580	2543.430	0.570	27	0.614	K.AAAVVAGNGATNGATNGVH.-
R5/RRR5-12/2	1169.459	1169.442	14.384	0.540	1880.841	0.474	18	0.242	R.ALVDVLAALKR.A
R5/RRR5-12/2	1168.745	1169.442	-1456.738	0.484	1668.595	0.429	17	0.204	R.ALVDVLAALKR.A
R5/RRR5-12/2	1012.912	1013.256	-340.399	0.493	1426.996	0.497	17	0.195	R.ALVDVLAALK.R
R5/RRR5-12/2	1169.019	1169.442	-362.759	0.475	1531.836	0.441	17	0.192	R.ALVDVLAALKR.A
R5/RRR5-11/2	1150.672	1150.310	316.275	0.407	1204.014	0.567	17	0.183	K.SPLTTVYAAAR.A
R5/RRR5-12/2	1013.172	1013.256	-83.155	0.544	1211.540	0.496	17	0.176	R.ALVDVLAALK.R
R5/RRR5-11/2	1150.523	1150.310	186.167	0.414	1239.039	0.493	17	0.174	K.SPLTTVYAAAR.A
R5/RRR5-12/2	1013.075	1013.256	-179.243	0.534	1193.860	0.491	17	0.174	R.ALVDVLAALK.R
R5/RRR5-11/2	1150.395	1150.310	74.223	0.480	1313.471	0.408	17	0.166	K.SPLTTVYAAAR.A
R5/RRR5-13/2	1150.925	1150.310	-334.952	0.346	934.938	0.483	15	0.149	K.SPLTTVYAAAR.A
R5/RRR5-12/2	1150.296	1150.310	-11.880	0.398	666.564	0.459	16	0.138	K.SPLTTVYAAAR.A
R5/RRR5-13/2	1150.097	1150.310	-185.621	0.343	702.745	0.470	14	0.137	K.SPLTTVYAAAR.A
R5/RRR5-12/2	1149.515	1150.310	-1565.997	0.304	615.946	0.476	16	0.134	K.SPLTTVYAAAR.A
R5/RRR5-12/2	1046.520	1047.145	-1557.086	0.279	944.271	0.291	17	0.125	R.SVTGLDDAIR.R
R5/RRR5-12/2	1151.319	1150.310	8.549	0.280	422.577	0.328	16	0.125	K.SPLTTVYAAAR.A
R5/RRR5-16/2	1150.385	1150.310	65.709	0.253	506.647	0.309	11	0.114	-.SPLTTVYAAAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/3	1524.667	1523.718	-33.183	0.389	881.907	0.414	22	0.092	R.EVVGDRDFFIVAR.T
R5/RRR5-12/3	1523.892	1523.718	114.835	0.396	686.315	0.421	20	0.086	R.EVVGDRDFFIVAR.T
R5/RRR5-12/3	1523.431	1523.718	-188.443	0.389	981.271	0.319	22	0.082	R.EVVGDRDFFIVAR.T
R5/RRR5-8/2	1217.997	1218.336	-278.610	0.472	1944.167	0.516	20	0.262	R.ALIAEGSCGSPR.S
R5/RRR5-8/2	1217.973	1218.336	-298.318	0.440	1690.555	0.467	19	0.215	R.ALIAEGSCGSPR.S
R5/RRR5-8/2	1264.036	1264.453	-330.260	0.492	1405.910	0.575	20	0.208	R.ILAFSQDVVSGK.I
R5/RRR5-8/2	1817.397	1816.951	246.126	0.532	1316.029	0.617	23	0.205	K.QGVAVTQENSLLDNTAR.I
R5/RRR5-8/2	1817.561	1816.951	-214.997	0.547	1264.098	0.633	23	0.204	K.QGVAVTQENSLLDNTAR.I
R5/RRR5-8/2	999.824	1000.174	-351.101	0.446	1610.662	0.438	16	0.200	K.AAGEVLALQK.R
R5/RRR5-7/2	1265.233	1264.453	-174.148	0.514	1333.537	0.548	20	0.196	R.ILAFSQDVVSGK.I
R5/RRR5-8/2	1217.421	1218.336	-1577.408	0.348	1660.125	0.345	20	0.185	R.ALIAEGSCGSPR.S
R5/RRR5-8/2	1263.862	1264.453	-1262.145	0.454	1207.034	0.539	18	0.180	R.ILAFSQDVVSGK.I
R5/RRR5-7/2	1816.346	1816.951	-886.121	0.502	1005.401	0.634	19	0.176	K.QGVAVTQENSLLDNTAR.I
R5/RRR5-7/2	1264.039	1264.453	-328.128	0.474	1182.918	0.512	19	0.175	R.ILAFSQDVVSGK.I
R5/RRR5-8/2	1265.148	1264.453	-241.710	0.529	1061.331	0.547	18	0.172	R.ILAFSQDVVSGK.I
R5/RRR5-7/2	1263.493	1264.453	-1555.744	0.392	961.523	0.480	17	0.152	R.ILAFSQDVVSGK.I
R5/RRR5-8/2	1162.119	1162.364	-211.304	0.444	893.979	0.452	14	0.144	R.AVGALVALYER.A
R5/RRR5-8/2	1187.221	1187.330	-92.260	0.370	949.604	0.361	18	0.137	R.DPGLAPNSFLR.T
R5/RRR5-8/2	1161.981	1162.364	-329.868	0.391	621.997	0.435	13	0.131	R.AVGALVALYER.A
R5/RRR5-8/2	1161.525	1162.364	-1587.963	0.388	636.605	0.413	14	0.130	R.AVGALVALYER.A
R5/RRR5-8/2	1186.827	1187.330	-1270.205	0.353	666.154	0.356	15	0.127	R.DPGLAPNSFLR.T
R5/RRR5-8/2	1146.028	1146.298	-236.638	0.292	794.080	0.347	14	0.125	R.M*GFTEEFLR.R
R5/RRR5-8/2	1187.442	1187.330	94.798	0.311	507.174	0.389	13	0.124	R.DPGLAPNSFLR.T
R5/RRR5-7/2	1187.140	1187.330	-160.852	0.250	393.011	0.329	12	0.116	-.DPGLAPNSFLR.-
R5/RRR5-17/2	1790.393	1791.081	-946.084	0.579	2556.368	0.561	24	0.387	K.KLQQVLNVYDEILSK.N
R5/RRR5-17/2	1662.471	1662.908	-264.144	0.587	2225.876	0.534	22	0.311	K.LQQVLNVYDEILSK.N
R5/RRR5-17/2	1791.411	1791.081	184.699	0.611	1960.522	0.572	21	0.278	K.KLQQVLNVYDEILSK.N
R5/RRR5-17/2	1662.463	1662.908	-268.712	0.588	2041.532	0.490	22	0.267	K.LQQVLNVYDEILSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1343.985	1343.460	-354.433	0.525	1840.416	0.535	18	0.253	R.YVCTQFPEGNK.T
R5/RRR5-17/2	1661.411	1662.908	-1507.683	0.451	2001.103	0.453	21	0.252	K.LQQVLNVYDEILSK.N
R5/RRR5-17/2	1344.134	1343.460	-243.173	0.534	1684.245	0.530	18	0.231	R.YVCTQFPEGNK.T
R5/RRR5-17/2	1344.068	1343.460	-292.923	0.507	1708.058	0.510	17	0.228	R.YVCTQFPEGNK.T
R5/RRR5-17/2	1274.678	1275.439	-1385.814	0.398	1430.983	0.445	17	0.182	K.LRDPNGQVTFK.H
R5/RRR5-17/2	1274.640	1275.439	-1415.440	0.450	1224.605	0.489	16	0.172	K.LRDPNGQVTFK.H
R5/RRR5-18/2	1663.251	1662.908	206.513	0.505	1143.781	0.398	20	0.151	K.LQQVLNVYDEILSK.N
R5/RRR5-17/2	1662.748	1662.908	-96.949	0.413	925.776	0.447	17	0.144	K.LQQVLNVYDEILSK.N
R5/RRR5-17/2	1276.135	1275.439	-238.573	0.436	897.277	0.433	15	0.143	K.LRDPNGQVTFK.H
R5/RRR5-17/2	1275.016	1275.439	-332.217	0.444	868.025	0.423	15	0.140	K.LRDPNGQVTFK.H
R5/RRR5-1/2	1664.189	1662.908	169.316	0.441	760.269	0.439	16	0.135	K.LQQVLNVYDEILSK.N
R5/RRR5-17/2	1096.012	1096.220	-190.424	0.442	614.210	0.403	13	0.135	R.WYDQISKR.E
R5/RRR5-17/2	1095.901	1096.220	-292.334	0.386	695.620	0.397	14	0.134	R.WYDQISKR.E
R5/RRR5-17/2	1096.897	1097.203	-280.125	0.357	743.224	0.389	15	0.133	K.TLYGTGSLER.A
R5/RRR5-17/2	1096.528	1097.203	-1532.915	0.262	827.335	0.371	15	0.130	K.TLYGTGSLER.A
R5/RRR5-16/2	1096.921	1097.203	-258.130	0.274	824.987	0.354	16	0.130	K.TLYGTGSLER.A
R5/RRR5-17/2	1096.075	1096.220	-133.443	0.380	597.022	0.355	13	0.129	R.WYDQISKR.E
R5/RRR5-17/2	1096.295	1097.203	-1746.218	0.254	605.907	0.397	15	0.126	K.TLYGTGSLER.A
R5/RRR5-15/2	1663.588	1662.908	-193.092	0.417	584.587	0.408	14	0.126	K.LQQVLNVYDEILSK.N
R5/RRR5-17/2	1096.479	1097.203	-1577.872	0.197	862.643	0.352	16	0.126	K.TLYGTGSLER.A
R5/RRR5-17/2	1096.885	1097.203	-291.513	0.282	481.613	0.341	14	0.124	K.TLYGTGSLER.A
R5/RRR5-16/2	1096.601	1097.203	-1465.486	0.236	658.510	0.336	15	0.123	K.TLYGTGSLER.A
R5/RRR5-15/2	1096.878	1097.203	-297.878	0.239	448.863	0.380	13	0.123	K.TLYGTGSLER.A
R5/RRR5-17/3	1275.558	1275.439	93.710	0.454	908.852	0.462	25	0.100	K.LRDPNGQVTFK.H
R5/RRR5-17/3	1275.339	1275.439	-78.360	0.352	523.808	0.348	21	0.078	K.LRDPNGQVTFK.H
R5/RRR5-16/3	1720.049	1719.920	75.330	0.605	2637.451	0.472	31	0.432	-.ILDVVYNASNNELVR.-
R5/RRR5-15/2	1605.953	1606.584	-1018.831	0.521	2654.227	0.597	24	0.419	K.DAAEGQEGEAATEEAK.K
R5/RRR5-15/2	1606.195	1606.584	-243.289	0.526	2536.210	0.590	24	0.391	K.DAAEGQEGEAATEEAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1606.157	1606.584	-267.078	0.567	2503.605	0.592	24	0.384	K.DAAEGQEGEAATEEAK.K
R5/RRR5-15/2	1606.132	1606.584	-282.710	0.510	2498.703	0.553	24	0.370	K.DAAEGQEGEAATEEAK.K
R5/RRR5-16/2	1720.467	1719.920	-264.278	0.590	2477.910	0.521	24	0.355	R.ILDVVYNASNNELVR.T
R5/RRR5-15/2	1720.352	1719.920	251.754	0.574	2409.440	0.506	24	0.337	R.ILDVVYNASNNELVR.T
R5/RRR5-15/2	1719.363	1719.920	-908.546	0.530	2227.199	0.503	23	0.303	R.ILDVVYNASNNELVR.T
R5/RRR5-16/2	1606.166	1606.584	-261.284	0.545	2046.608	0.568	23	0.291	K.DAAEGQEGEAATEEAK.K
R5/RRR5-16/2	1656.341	1656.735	-238.067	0.514	1928.042	0.519	23	0.259	R.LDTGNYSWGSEAVTR.K
R5/RRR5-16/2	1656.308	1656.735	-258.474	0.523	1873.841	0.533	23	0.256	R.LDTGNYSWGSEAVTR.K
R5/RRR5-15/2	1656.205	1656.735	-926.337	0.529	1853.702	0.530	22	0.251	R.LDTGNYSWGSEAVTR.K
R5/RRR5-16/3	1734.688	1734.757	-40.353	0.542	1902.705	0.513	31	0.251	K.KDAAEGQEGEAATEEAK.K
R5/RRR5-15/2	1656.290	1656.735	-269.122	0.523	1817.446	0.536	22	0.248	R.LDTGNYSWGSEAVTR.K
R5/RRR5-16/2	1657.172	1656.735	264.603	0.548	1768.073	0.560	22	0.247	R.LDTGNYSWGSEAVTR.K
R5/RRR5-15/2	1719.582	1719.920	-197.414	0.538	1852.934	0.494	22	0.245	-.ILDVVYNASNNELVR.-
R5/RRR5-15/2	1656.163	1656.735	-951.496	0.506	1796.175	0.502	22	0.236	R.LDTGNYSWGSEAVTR.K
R5/RRR5-15/3	1862.897	1862.930	-17.727	0.575	1573.611	0.581	37	0.213	K.KDAAEGQEGEAATEEAKK.S
R5/RRR5-16/3	1734.681	1734.757	-44.270	0.573	1645.251	0.524	30	0.205	K.KDAAEGQEGEAATEEAK.K
R5/RRR5-16/3	1863.955	1862.930	13.484	0.580	1367.377	0.600	35	0.186	K.KDAAEGQEGEAATEEAKK.S
R5/RRR5-15/3	1734.264	1734.757	-285.410	0.502	1753.696	0.407	30	0.183	K.KDAAEGQEGEAATEEAK.K
R5/RRR5-15/3	1735.659	1734.757	-57.084	0.597	1415.598	0.550	29	0.177	K.KDAAEGQEGEAATEEAK.K
R5/RRR5-15/3	1720.347	1719.920	249.114	0.480	1721.387	0.374	28	0.169	R.ILDVVYNASNNELVR.T
R5/RRR5-15/3	1863.783	1862.930	-79.141	0.607	1204.014	0.580	35	0.159	K.KDAAEGQEGEAATEEAKK.S
R5/RRR5-16/2	1245.625	1246.437	-1459.518	0.305	1346.942	0.353	16	0.157	K.SAIVQVDAAPFK.Q
R5/RRR5-16/2	1245.382	1246.437	-1654.854	0.261	1357.938	0.342	17	0.155	K.SAIVQVDAAPFK.Q
R5/RRR5-15/2	1246.132	1246.437	-245.595	0.347	1335.760	0.326	16	0.153	K.SAIVQVDAAPFK.Q
R5/RRR5-16/2	1246.058	1246.437	-305.056	0.274	856.377	0.309	16	0.125	K.SAIVQVDAAPFK.Q
R5/RRR5-15/2	1245.930	1246.437	-1213.094	0.250	924.160	0.203	16	0.119	K.SAIVQVDAAPFK.Q
R5/RRR5-25/2	1605.921	1606.584	-1038.597	0.229	564.300	0.308	15	0.116	K.DAAEGQEGEAATEEAK.K
R5/RRR5-6/2	1259.119	1259.434	-251.035	0.491	1771.196	0.590	19	0.257	R.VNLVQVLGSDSK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1258.767	1259.434	-1328.727	0.392	1574.152	0.546	18	0.217	R.VNLVQVLGSDSK.V
R5/RRR5-6/3	1453.681	1453.667	9.330	0.440	1933.296	0.395	28	0.211	K.APKPPAQAVDPFSK.F
R5/RRR5-6/2	1245.897	1246.520	-1307.075	0.552	1168.522	0.494	18	0.172	K.IVLDFLGLVEK.F
R5/RRR5-6/2	1206.775	1207.446	-1388.814	0.384	1050.557	0.569	15	0.167	K.FFLGIGLPGSAK.D
R5/RRR5-6/2	1246.053	1246.520	-376.197	0.421	1164.119	0.474	18	0.166	K.IVLDFLGLVEK.F
R5/RRR5-6/2	1299.385	1299.626	-186.155	0.432	1003.446	0.450	18	0.151	R.VFVPLVLSLPSK.V
R5/RRR5-6/2	1128.113	1128.258	-128.677	0.416	930.114	0.461	17	0.147	R.ALSYLSSTSAK.Q
R5/RRR5-6/2	1206.723	1207.446	-1432.198	0.262	966.180	0.440	16	0.139	K.FFLGIGLPGSAK.D
R5/RRR5-6/2	1245.719	1246.520	-1450.366	0.407	492.921	0.453	14	0.132	K.IVLDFLGLVEK.F
R5/RRR5-6/2	1299.257	1299.626	-285.309	0.377	822.398	0.350	18	0.131	R.VFVPLVLSLPSK.V
R5/RRR5-6/2	1487.011	1487.505	-333.270	0.322	899.299	0.361	16	0.130	K.SYDDGTFYFDEK.H
R5/RRR5-6/2	1298.627	1299.626	-1544.483	0.295	722.431	0.372	16	0.126	R.VFVPLVLSLPSK.V
R5/RRR5-6/3	1452.879	1453.667	-1234.936	0.393	1527.526	0.254	26	0.108	K.APKPPAQAVDPFSK.F
R5/RRR5-6/3	1453.562	1453.667	-72.921	0.444	1276.008	0.355	25	0.108	K.APKPPAQAVDPFSK.F
R5/RRR5-6/2	1235.270	1235.411	-114.937	0.444	764.837	0.500	15	0.143	K.VQEVVSEIFGK.A
R5/RRR5-17/2	1147.146	1147.261	-100.713	0.452	1266.337	0.492	17	0.177	K.EAISQVVGESK.E
R5/RRR5-16/2	1146.982	1147.261	-243.981	0.484	1251.580	0.491	16	0.175	K.EAISQVVGESK.E
R5/RRR5-15/2	1147.045	1147.261	-188.463	0.404	1174.590	0.457	16	0.163	K.EAISQVVGESK.E
R5/RRR5-17/2	1146.805	1147.261	-398.826	0.347	1132.732	0.444	17	0.157	K.EAISQVVGESK.E
R5/RRR5-16/2	1146.848	1147.261	-361.231	0.381	1181.480	0.407	16	0.155	K.EAISQVVGESK.E
R5/RRR5-16/2	1146.445	1147.261	-1589.094	0.312	1286.361	0.347	17	0.153	K.EAISQVVGESK.E
R5/RRR5-15/2	1146.953	1147.261	-269.607	0.296	1182.855	0.331	16	0.143	K.EAISQVVGESK.E
R5/RRR5-15/2	1146.457	1147.261	-1578.076	0.280	973.863	0.288	17	0.129	K.EAISQVVGESK.E
R5/RRR5-17/2	1146.851	1147.261	-358.668	0.234	487.383	0.279	13	0.119	K.EAISQVVGESK.E
R5/RRR5-7/2	1371.594	1372.553	-1432.147	0.482	4055.738	0.535	25	0.788	R.NVNSALAASGIGGIK.V
R5/RRR5-7/2	1372.177	1372.553	-274.609	0.538	3906.259	0.560	25	0.750	R.NVNSALAASGIGGIK.V
R5/RRR5-7/2	1372.278	1372.553	-200.892	0.552	3718.330	0.533	25	0.675	R.NVNSALAASGIGGIK.V
R5/RRR5-8/2	1372.134	1372.553	-305.937	0.549	3177.249	0.509	25	0.509	R.NVNSALAASGIGGIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1372.197	1372.553	-259.882	0.539	2701.873	0.517	24	0.400	R.NVNSALAASGIGGIK.V
R5/RRR5-8/2	1372.148	1372.553	-295.494	0.519	2686.519	0.524	24	0.399	R.NVNSALAASGIGGIK.V
R5/RRR5-15/2	1756.272	1755.949	184.420	0.565	1069.502	0.577	21	0.175	R.DISLNYATFQPGTTVK.D
R5/RRR5-15/2	1755.412	1755.949	-878.310	0.490	1179.219	0.530	21	0.175	R.DISLNYATFQPGTTVK.D
R5/RRR5-14/2	1755.613	1755.949	-192.107	0.501	1164.703	0.524	21	0.173	R.DISLNYATFQPGTTVK.D
R5/RRR5-7/2	1756.224	1755.949	156.713	0.530	1077.262	0.558	21	0.172	R.DISLNYATFQPGTTVK.D
R5/RRR5-7/2	1755.431	1755.949	-867.699	0.504	1130.213	0.529	21	0.171	R.DISLNYATFQPGTTVK.D
R5/RRR5-14/2	1756.273	1755.949	185.048	0.521	917.987	0.564	20	0.162	R.DISLNYATFQPGTTVK.D
R5/RRR5-8/2	1755.455	1755.949	-282.097	0.505	1010.667	0.503	20	0.157	R.DISLNYATFQPGTTVK.D
R5/RRR5-15/2	1755.586	1755.949	-207.732	0.500	873.026	0.553	19	0.156	R.DISLNYATFQPGTTVK.D
R5/RRR5-7/2	1799.454	1797.989	258.854	0.543	841.375	0.549	20	0.154	R.EISLNYATFQPGTTVR.D
R5/RRR5-8/2	1755.424	1755.949	-871.259	0.503	802.056	0.543	18	0.150	R.DISLNYATFQPGTTVK.D
R5/RRR5-9/2	1372.210	1372.553	-250.333	0.358	1132.601	0.397	20	0.149	R.NVNSALAASGIGGIK.V
R5/RRR5-7/2	1074.947	1075.201	-237.551	0.414	984.618	0.420	13	0.146	R.HFGLFNPDK.T
R5/RRR5-7/2	1076.023	1075.201	-166.652	0.423	926.236	0.427	13	0.145	R.HFGLFNPDK.T
R5/RRR5-8/2	1074.952	1075.201	-232.424	0.418	797.577	0.460	14	0.144	R.HFGLFNPDK.T
R5/RRR5-7/2	1074.971	1075.201	-214.652	0.398	756.412	0.440	13	0.140	R.HFGLFNPDK.T
R5/RRR5-14/2	1754.625	1755.949	-1328.711	0.341	918.458	0.394	20	0.137	R.DISLNYATFQPGTTVK.D
R5/RRR5-8/2	1075.040	1075.201	-150.405	0.415	714.709	0.414	13	0.136	R.HFGLFNPDK.T
R5/RRR5-7/2	1797.459	1797.989	-853.881	0.503	721.070	0.462	18	0.135	R.EISLNYATFQPGTTVR.D
R5/RRR5-14/2	1074.317	1075.201	-1759.604	0.318	748.081	0.372	13	0.131	R.HFGLFNPDK.T
R5/RRR5-9/2	1076.016	1075.201	-172.457	0.302	716.409	0.387	12	0.130	R.HFGLFNPDK.T
R5/RRR5-7/3	1373.077	1372.553	-347.468	0.400	1375.300	0.394	29	0.126	R.NVNSALAASGIGGIK.V
R5/RRR5-7/2	1611.354	1611.845	-305.925	0.367	953.527	0.276	20	0.125	R.SEVVQM*YVSLGINR.M
R5/RRR5-10/2	1075.805	1075.201	-369.836	0.333	582.953	0.239	12	0.121	R.HFGLFNPDK.T
R5/RRR5-8/2	1754.669	1755.949	-1303.208	0.280	462.350	0.371	14	0.120	R.DISLNYATFQPGTTVK.D
R5/RRR5-8/2	1074.392	1075.201	-1689.283	0.289	693.267	0.144	13	0.117	R.HFGLFNPDK.T
R5/RRR5-13/2	1074.127	1075.201	-1936.480	0.130	746.890	0.163	12	0.113	R.HFGLFNPDK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1075.264	1075.201	58.799	0.247	355.617	0.317	10	0.104	-.HFGLFNPDK.-
R5/RRR5-6/2	1075.341	1075.201	130.071	0.125	561.635	0.078	11	0.103	-.HFGLFNPDK.-
R5/RRR5-14/3	1231.700	1231.388	254.056	0.471	909.724	0.445	20	0.100	R.RHFGLFNPDK.T
R5/RRR5-7/3	1373.385	1372.553	-122.600	0.306	870.128	0.361	25	0.081	R.NVNSALAASGIGGIK.V
R5/RRR5-7/3	1372.931	1372.553	276.168	0.285	845.249	0.212	26	0.065	R.NVNSALAASGIGGIK.V
R5/RRR5-15/3	1230.922	1231.388	-379.142	0.293	633.375	0.240	19	0.061	-.RHFGLFNPDK.-
R5/RRR5-7/3	1231.287	1231.388	-81.909	0.358	557.053	0.229	20	0.051	-.RHFGLFNPDK.-
R5/RRR5-22/2	1748.986	1748.918	38.530	0.561	2447.955	0.536	25	0.354	K.ATDDKAGQEALLNVFR.A
R5/RRR5-23/2	1721.501	1721.929	-249.753	0.548	2478.022	0.489	25	0.345	R.AAEACEQFGGVLVTLR.M
R5/RRR5-23/2	1721.338	1721.929	-927.277	0.521	2345.234	0.438	25	0.304	R.AAEACEQFGGVLVTLR.M
R5/RRR5-23/2	1749.512	1748.918	-232.737	0.599	1969.157	0.550	24	0.274	K.ATDDKAGQEALLNVFR.A
R5/RRR5-23/2	1747.683	1748.918	-1283.128	0.526	1921.467	0.543	23	0.265	K.ATDDKAGQEALLNVFR.A
R5/RRR5-23/2	1748.509	1748.918	-234.831	0.563	1968.612	0.512	24	0.263	K.ATDDKAGQEALLNVFR.A
R5/RRR5-23/2	1721.162	1721.929	-1029.950	0.432	2097.526	0.380	24	0.248	R.AAEACEQFGGVLVTLR.M
R5/RRR5-23/2	1837.555	1838.095	-840.713	0.478	1548.161	0.622	23	0.243	K.ITLIGTSGISGSYVELRA.-
R5/RRR5-22/2	1767.451	1767.017	246.292	0.466	1553.953	0.500	22	0.204	K.ITLIGTSGISGSYVELR.-
R5/RRR5-23/2	1218.188	1218.387	-163.687	0.446	1517.053	0.432	16	0.188	K.AGQEALLNVFR.A
R5/RRR5-23/2	1617.550	1617.740	-117.824	0.537	1323.945	0.448	21	0.175	K.YLESFGPEENYLR.K
R5/RRR5-23/2	1618.142	1617.740	249.345	0.548	1073.249	0.480	19	0.160	K.YLESFGPEENYLR.K
R5/RRR5-23/2	1218.283	1218.387	-85.586	0.384	1233.689	0.388	15	0.155	K.AGQEALLNVFR.A
R5/RRR5-23/2	1617.256	1617.740	-299.995	0.495	1031.907	0.431	19	0.150	K.YLESFGPEENYLR.K
R5/RRR5-23/2	1218.167	1218.387	-181.279	0.471	795.729	0.379	13	0.130	K.AGQEALLNVFR.A
R5/RRR5-23/3	1748.806	1748.918	-64.391	0.408	1342.698	0.381	26	0.120	K.ATDDKAGQEALLNVFR.A
R5/RRR5-23/2	1618.171	1617.740	266.970	0.385	433.556	0.296	12	0.117	K.YLESFGPEENYLR.K
R5/RRR5-22/2	1617.095	1617.740	-1020.518	0.194	617.601	0.262	17	0.116	K.YLESFGPEENYLR.K
R5/RRR5-23/3	1748.861	1748.918	-32.885	0.437	911.403	0.332	23	0.079	K.ATDDKAGQEALLNVFR.A
R5/RRR5-8/1	1311.924	1312.580	-1266.340	0.258	847.958	0.114	13	0.413	K.AILSTINPELLK.S
R5/RRR5-8/2	1705.967	1705.914	31.463	0.546	1296.561	0.547	19	0.188	R.DNGMHALIIYDDLSK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1706.524	1705.914	-229.201	0.545	1368.158	0.513	19	0.187	R.DNGMHALIIYDDLSK.Q
R5/RRR5-8/2	1722.208	1721.913	171.907	0.576	1239.988	0.551	20	0.184	R.DNGM*HALIIYDDLSK.Q
R5/RRR5-8/2	1721.419	1721.913	-287.982	0.555	1071.521	0.556	20	0.172	R.DNGM*HALIIYDDLSK.Q
R5/RRR5-8/2	1722.278	1721.913	212.492	0.568	1024.195	0.556	19	0.167	R.DNGM*HALIIYDDLSK.Q
R5/RRR5-8/2	1312.304	1312.580	-211.379	0.413	1476.780	0.331	18	0.165	K.AILSTINPELLK.S
R5/RRR5-8/2	1312.235	1312.580	-264.013	0.393	1486.087	0.315	18	0.163	K.AILSTINPELLK.S
R5/RRR5-9/2	1312.256	1312.580	-248.241	0.425	1549.853	0.244	18	0.156	K.AILSTINPELLK.S
R5/RRR5-7/2	1302.320	1301.514	-150.104	0.390	1265.714	0.308	18	0.146	K.TAIAIDTILNQK.Q
R5/RRR5-8/2	1439.334	1439.689	-247.080	0.465	623.286	0.521	18	0.142	R.GIRPAINVGLSVSR.V
R5/RRR5-8/2	1439.301	1439.689	-270.309	0.504	659.418	0.501	18	0.141	R.GIRPAINVGLSVSR.V
R5/RRR5-9/2	1312.208	1312.580	-284.826	0.373	1120.964	0.336	16	0.141	K.AILSTINPELLK.S
R5/RRR5-2/2	1312.413	1312.580	-128.146	0.385	1262.015	0.268	17	0.140	K.AILSTINPELLK.S
R5/RRR5-8/2	1313.220	1312.580	-275.376	0.455	1331.682	0.243	17	0.139	K.AILSTINPELLK.S
R5/RRR5-2/2	1313.181	1312.580	-304.754	0.366	1296.375	0.241	17	0.138	K.AILSTINPELLK.S
R5/RRR5-8/2	1538.249	1538.688	-286.032	0.405	476.484	0.473	17	0.134	R.EAFPGDVFYLHSR.L
R5/RRR5-9/2	1721.474	1721.913	-255.683	0.471	494.882	0.482	17	0.134	R.DNGM*HALIIYDDLSK.Q
R5/RRR5-8/2	1439.238	1439.689	-313.791	0.454	522.259	0.455	16	0.131	R.GIRPAINVGLSVSR.V
R5/RRR5-9/2	1311.845	1312.580	-1327.045	0.335	1174.333	0.229	16	0.130	K.AILSTINPELLK.S
R5/RRR5-8/2	1077.083	1077.298	-201.045	0.460	921.189	0.279	14	0.128	R.KIELDAFLK.Q
R5/RRR5-8/2	1077.207	1077.298	-85.202	0.454	778.389	0.306	13	0.127	R.KIELDAFLK.Q
R5/RRR5-8/2	1538.240	1538.688	-291.845	0.332	422.026	0.373	17	0.126	R.EAFPGDVFYLHSR.L
R5/RRR5-8/2	1538.218	1538.688	-306.096	0.319	503.151	0.383	17	0.126	R.EAFPGDVFYLHSR.L
R5/RRR5-8/2	1538.308	1538.688	-247.579	0.327	524.601	0.358	18	0.126	R.EAFPGDVFYLHSR.L
R5/RRR5-9/2	1077.044	1077.298	-236.861	0.382	747.582	0.289	13	0.125	R.KIELDAFLK.Q
R5/RRR5-3/2	1312.433	1312.580	-112.938	0.384	967.229	0.258	15	0.125	K.AILSTINPELLK.S
R5/RRR5-8/2	1077.139	1077.298	-148.861	0.417	591.046	0.296	12	0.124	R.KIELDAFLK.Q
R5/RRR5-9/2	1076.424	1077.298	-1746.719	0.302	584.964	0.347	12	0.123	-.KIELDAFLK.-
R5/RRR5-8/2	1538.162	1538.688	-994.720	0.252	471.425	0.355	17	0.122	R.EAFPGDVFYLHSR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1077.109	1077.298	-176.715	0.331	584.078	0.298	11	0.122	R.KIELDAFLK.Q
R5/RRR5-8/2	1538.383	1538.688	-198.541	0.274	476.644	0.282	18	0.122	R.EAFPGDVFYLHSR.L
R5/RRR5-8/3	1440.614	1439.689	-52.117	0.467	1480.134	0.331	27	0.121	R.GIRPAINVGLSVSR.V
R5/RRR5-8/3	1721.828	1721.913	-49.352	0.449	1565.461	0.281	27	0.120	R.DNGM*HALIIYDDLSK.Q
R5/RRR5-8/3	1355.972	1355.589	283.594	0.458	1353.912	0.378	27	0.119	R.KSVHEPMQTGLK.A
R5/RRR5-8/2	1312.160	1312.580	-320.947	0.375	642.167	0.267	13	0.119	K.AILSTINPELLK.S
R5/RRR5-8/2	1704.480	1705.914	-1432.234	0.351	838.197	0.241	17	0.119	R.DNGMHALIIYDDLSK.Q
R5/RRR5-7/2	1312.420	1312.580	-122.641	0.294	688.267	0.181	15	0.117	K.AILSTINPELLK.S
R5/RRR5-2/2	1301.372	1301.514	-109.381	0.432	719.292	0.297	14	0.116	-.TAIAIDTILNQK.-
R5/RRR5-8/2	1301.555	1301.514	31.644	0.399	658.281	0.187	15	0.114	K.TAIAIDTILNQK.Q
R5/RRR5-8/3	1439.862	1439.689	120.474	0.482	1494.003	0.293	27	0.112	R.GIRPAINVGLSVSR.V
R5/RRR5-12/2	1301.679	1301.514	127.206	0.258	719.794	0.071	14	0.111	-.TAIAIDTILNQK.-
R5/RRR5-9/3	1440.760	1439.689	49.737	0.468	1355.867	0.336	26	0.110	R.GIRPAINVGLSVSR.V
R5/RRR5-1/2	1301.789	1301.514	211.843	0.256	465.478	0.236	13	0.105	-.TAIAIDTILNQK.-
R5/RRR5-9/3	1439.643	1439.689	-31.954	0.407	1420.238	0.271	24	0.101	R.GIRPAINVGLSVSR.V
R5/RRR5-8/3	1077.383	1077.298	78.388	0.469	1226.945	0.315	22	0.094	R.KIELDAFLK.Q
R5/RRR5-9/3	1439.335	1439.689	-246.451	0.435	1362.982	0.262	24	0.093	R.GIRPAINVGLSVSR.V
R5/RRR5-8/3	1077.345	1077.298	43.445	0.458	1255.974	0.296	22	0.092	R.KIELDAFLK.Q
R5/RRR5-8/3	1077.100	1077.298	-185.027	0.482	1176.172	0.312	22	0.090	R.KIELDAFLK.Q
R5/RRR5-8/3	1355.672	1355.589	61.484	0.458	1178.904	0.291	26	0.088	R.KSVHEPMQTGLK.A
R5/RRR5-8/3	1355.642	1355.589	39.539	0.426	549.341	0.291	21	0.080	R.KSVHEPMQTGLK.A
R5/RRR5-9/3	1077.506	1077.298	193.600	0.372	1140.578	0.275	21	0.080	R.KIELDAFLK.Q
R5/RRR5-7/3	1439.616	1439.689	-50.452	0.405	1242.599	0.193	24	0.073	R.GIRPAINVGLSVSR.V
R5/RRR5-7/3	1438.730	1439.689	-1365.711	0.286	807.542	0.248	22	0.070	R.GIRPAINVGLSVSR.V
R5/RRR5-8/3	1371.144	1371.588	-324.842	0.334	817.536	0.214	25	0.068	R.KSVHEPM*QTGLK.A
R5/RRR5-8/3	1721.486	1721.913	-248.754	0.370	829.474	0.210	24	0.064	R.DNGM*HALIIYDDLSK.Q
R5/RRR5-16/2	1532.906	1533.580	-1095.256	0.452	2816.722	0.533	24	0.432	R.AAGGASGGEELTVEER.N
R5/RRR5-16/2	1533.124	1533.580	-298.169	0.484	2583.314	0.554	24	0.388	R.AAGGASGGEELTVEER.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1533.996	1533.580	271.803	0.549	2529.339	0.574	24	0.383	R.AAGGASGGEELTVEER.N
R5/RRR5-15/2	1533.165	1533.580	-271.568	0.487	2227.605	0.559	23	0.320	R.AAGGASGGEELTVEER.N
R5/RRR5-15/2	1533.080	1533.580	-327.088	0.507	2147.545	0.537	23	0.299	R.AAGGASGGEELTVEER.N
R5/RRR5-16/2	1532.925	1533.580	-1083.022	0.454	2015.919	0.483	21	0.262	R.AAGGASGGEELTVEER.N
R5/RRR5-15/2	1389.210	1389.537	-235.900	0.490	1121.974	0.526	18	0.172	R.IISSIEQKEEGR.G
R5/RRR5-15/2	1389.146	1389.537	-282.095	0.458	1146.539	0.517	18	0.172	R.IISSIEQKEEGR.G
R5/RRR5-16/2	1389.091	1389.537	-322.123	0.394	774.783	0.489	19	0.145	R.IISSIEQKEEGR.G
R5/RRR5-15/2	1389.224	1389.537	-225.762	0.449	548.052	0.443	16	0.134	R.IISSIEQKEEGR.G
R5/RRR5-16/2	1390.009	1389.537	341.005	0.344	360.333	0.459	17	0.131	R.IISSIEQKEEGR.G
R5/RRR5-15/3	987.196	987.135	61.706	0.507	1199.743	0.083	20	0.052	-.GKIEAELAR.-
R5/RRR5-15/2	1108.126	1108.293	-151.065	0.458	1454.302	0.384	16	0.174	K.M*EGLLWGASK.L
R5/RRR5-15/2	1272.177	1272.480	-238.449	0.408	1262.513	0.451	16	0.169	R.WFTHIDALLR.L
R5/RRR5-15/2	1272.031	1272.480	-353.595	0.436	1119.061	0.487	16	0.165	R.WFTHIDALLR.L
R5/RRR5-16/2	1150.945	1151.338	-341.967	0.540	1156.983	0.444	15	0.163	K.KLDEYLLTR.S
R5/RRR5-16/2	1145.704	1146.276	-1376.710	0.486	1081.114	0.458	19	0.159	R.LSGVTADGQGIK.V
R5/RRR5-15/2	1145.973	1146.276	-265.137	0.445	1144.148	0.433	18	0.158	R.LSGVTADGQGIK.V
R5/RRR5-15/2	1108.101	1108.293	-173.277	0.410	1200.305	0.408	15	0.157	K.M*EGLLWGASK.L
R5/RRR5-15/2	1272.584	1272.480	82.298	0.426	968.264	0.477	17	0.155	R.WFTHIDALLR.L
R5/RRR5-14/2	1108.178	1108.293	-104.212	0.384	1220.048	0.383	15	0.155	K.M*EGLLWGASK.L
R5/RRR5-15/2	1271.491	1272.480	-1568.779	0.476	950.805	0.464	17	0.154	R.WFTHIDALLR.L
R5/RRR5-15/2	1150.401	1151.338	-1688.568	0.489	1071.491	0.404	15	0.151	K.KLDEYLLTR.S
R5/RRR5-15/2	1151.221	1151.338	-101.633	0.527	1062.645	0.398	15	0.150	K.KLDEYLLTR.S
R5/RRR5-15/2	1145.472	1146.276	-1579.326	0.372	1239.151	0.328	18	0.148	R.LSGVTADGQGIK.V
R5/RRR5-15/2	1108.212	1108.293	-73.606	0.462	991.673	0.426	14	0.148	K.M*EGLLWGASK.L
R5/RRR5-14/2	1152.008	1151.338	-287.023	0.534	1030.508	0.390	15	0.147	K.KLDEYLLTR.S
R5/RRR5-14/2	1108.941	1108.293	-318.112	0.422	929.791	0.431	14	0.145	K.M*EGLLWGASK.L
R5/RRR5-16/2	1745.568	1745.866	-171.679	0.440	601.886	0.551	23	0.144	K.VESTAVPSASTPDVADAK.A
R5/RRR5-15/2	1746.381	1745.866	-278.725	0.472	501.261	0.583	21	0.144	K.VESTAVPSASTPDVADAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1150.490	1151.338	-1610.324	0.503	886.530	0.418	14	0.144	K.KLDEYLLTR.S
R5/RRR5-14/2	1745.286	1745.866	-908.240	0.456	479.798	0.582	21	0.143	K.VESTAVPSASTPDVADAK.A
R5/RRR5-14/2	1746.395	1745.866	-270.941	0.456	612.209	0.530	23	0.143	K.VESTAVPSASTPDVADAK.A
R5/RRR5-15/2	1152.319	1151.338	-16.534	0.545	1007.313	0.361	15	0.141	K.KLDEYLLTR.S
R5/RRR5-16/2	1145.448	1146.276	-1600.845	0.420	896.115	0.415	17	0.141	R.LSGVTADGQGIK.V
R5/RRR5-15/2	1745.337	1745.866	-878.750	0.426	527.119	0.547	22	0.141	K.VESTAVPSASTPDVADAK.A
R5/RRR5-16/2	1745.261	1745.866	-922.634	0.409	524.955	0.554	22	0.141	K.VESTAVPSASTPDVADAK.A
R5/RRR5-16/2	1151.198	1151.338	-121.310	0.491	1022.100	0.337	15	0.139	K.KLDEYLLTR.S
R5/RRR5-16/2	1746.155	1745.866	166.066	0.456	493.278	0.534	21	0.139	K.VESTAVPSASTPDVADAK.A
R5/RRR5-15/2	1746.146	1745.866	160.388	0.446	394.003	0.576	19	0.139	K.VESTAVPSASTPDVADAK.A
R5/RRR5-16/2	1145.284	1146.276	-1744.968	0.299	1204.638	0.278	18	0.138	R.LSGVTADGQGIK.V
R5/RRR5-15/2	1145.440	1146.276	-1607.482	0.373	981.226	0.343	17	0.136	R.LSGVTADGQGIK.V
R5/RRR5-14/2	1151.158	1151.338	-156.839	0.454	851.790	0.324	14	0.132	K.KLDEYLLTR.S
R5/RRR5-14/2	1744.846	1745.866	-1161.433	0.379	419.774	0.484	20	0.131	K.VESTAVPSASTPDVADAK.A
R5/RRR5-14/2	1271.387	1272.480	-1651.246	0.373	720.180	0.367	15	0.131	R.WFTHIDALLR.L
R5/RRR5-15/2	1022.789	1023.165	-367.817	0.403	961.271	0.289	13	0.130	-.LDEYLLTR.-
R5/RRR5-15/2	1022.471	1023.165	-1661.545	0.352	1079.526	0.238	13	0.129	-.LDEYLLTR.-
R5/RRR5-24/2	1108.183	1108.293	-99.240	0.362	717.384	0.285	14	0.124	K.M*EGLLWGASK.L
R5/RRR5-15/2	1091.841	1092.294	-416.212	0.294	652.193	0.341	13	0.122	-.MEGLLWGASK.-
R5/RRR5-15/2	1092.012	1092.294	-258.393	0.241	666.980	0.260	13	0.119	K.MEGLLWGASK.L
R5/RRR5-15/2	1092.000	1092.294	-269.720	0.249	540.254	0.189	12	0.107	-.MEGLLWGASK.-
R5/RRR5-15/3	1272.695	1272.480	169.921	0.350	907.890	0.347	20	0.081	R.WFTHIDALLR.L
R5/RRR5-15/3	1271.708	1272.480	-1397.052	0.351	954.203	0.241	19	0.070	-.WFTHIDALLR.-
R5/RRR5-15/3	1272.235	1272.480	-193.218	0.279	913.655	0.277	19	0.070	-.WFTHIDALLR.-
R5/RRR5-20/2	1610.255	1610.741	-302.668	0.548	1574.800	0.535	20	0.217	K.DGTNVEEAFQCIVK.N
R5/RRR5-20/2	1610.203	1610.741	-957.744	0.515	1423.945	0.498	19	0.191	K.DGTNVEEAFQCIVK.N
R5/RRR5-20/2	1610.140	1610.741	-997.247	0.524	1282.555	0.532	19	0.185	K.DGTNVEEAFQCIVK.N
R5/RRR5-20/2	1036.890	1037.191	-291.731	0.416	1120.419	0.423	17	0.156	K.ATIGADFLTK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1057.930	1058.254	-306.703	0.404	1079.854	0.448	17	0.156	K.VIILGDSGVGK.T
R5/RRR5-20/2	1188.137	1188.359	-187.715	0.379	1157.108	0.378	17	0.151	R.FQSLGVAFYR.G
R5/RRR5-20/2	1037.063	1037.191	-124.508	0.409	952.143	0.451	16	0.149	K.ATIGADFLTK.E
R5/RRR5-20/2	1227.018	1227.348	-269.876	0.501	492.551	0.575	17	0.149	K.GNIPYFETSAK.D
R5/RRR5-20/2	1187.599	1188.359	-1486.808	0.426	1010.350	0.418	16	0.149	R.FQSLGVAFYR.G
R5/RRR5-19/2	1037.107	1037.191	-81.649	0.378	906.218	0.440	16	0.145	K.ATIGADFLTK.E
R5/RRR5-19/2	1187.796	1188.359	-1320.089	0.409	1156.095	0.335	16	0.145	R.FQSLGVAFYR.G
R5/RRR5-19/2	1036.439	1037.191	-1695.974	0.366	926.812	0.430	16	0.144	K.ATIGADFLTK.E
R5/RRR5-20/2	1036.450	1037.191	-1684.733	0.308	774.651	0.485	15	0.140	K.ATIGADFLTK.E
R5/RRR5-19/2	1227.141	1227.348	-168.778	0.359	408.486	0.464	16	0.132	K.GNIPYFETSAK.D
R5/RRR5-19/2	1188.040	1188.359	-269.765	0.403	831.726	0.344	15	0.132	R.FQSLGVAFYR.G
R5/RRR5-19/2	1036.512	1037.191	-1625.335	0.321	625.726	0.436	13	0.131	K.ATIGADFLTK.E
R5/RRR5-20/2	1187.913	1188.359	-377.397	0.438	758.032	0.340	15	0.130	R.FQSLGVAFYR.G
R5/RRR5-19/2	1187.499	1188.359	-1571.582	0.390	700.561	0.365	14	0.130	R.FQSLGVAFYR.G
R5/RRR5-19/2	1057.663	1058.254	-1508.210	0.345	823.437	0.298	15	0.126	K.VIILGDSGVGK.T
R5/RRR5-20/2	1226.420	1227.348	-1576.315	0.252	373.182	0.452	15	0.125	K.GNIPYFETSAK.D
R5/RRR5-20/2	1057.830	1058.254	-401.583	0.290	673.530	0.314	14	0.123	K.VIILGDSGVGK.T
R5/RRR5-18/2	1057.643	1058.254	-1526.992	0.310	484.367	0.388	12	0.123	-.VIILGDSGVGK.-
R5/RRR5-18/2	1058.417	1058.254	154.939	0.284	500.529	0.375	12	0.121	-.VIILGDSGVGK.-
R5/RRR5-19/2	1057.690	1058.254	-1482.473	0.228	604.520	0.241	13	0.117	K.VIILGDSGVGK.T
R5/RRR5-20/2	1226.414	1227.348	-1581.015	0.164	258.809	0.326	13	0.116	-.GNIPYFETSAK.-
R5/RRR5-27/2	1057.754	1058.254	-473.494	0.231	791.900	0.184	14	0.116	K.VIILGDSGVGK.T
R5/RRR5-20/3	1749.369	1747.936	248.446	0.345	908.985	0.310	23	0.073	R.GADCCVLVYDVNSM*K.S
R5/RRR5-4/2	1698.656	1698.943	-168.924	0.519	1783.837	0.505	21	0.236	R.LIWSTQFENFLATK.W
R5/RRR5-4/2	1698.349	1698.943	-940.910	0.507	1740.411	0.512	21	0.232	R.LIWSTQFENFLATK.W
R5/RRR5-4/2	1698.675	1698.943	-158.110	0.520	1703.973	0.493	21	0.223	R.LIWSTQFENFLATK.W
R5/RRR5-4/2	1373.685	1374.524	-1343.065	0.462	1342.863	0.443	17	0.175	R.DWLSAYWTGFK.S
R5/RRR5-4/2	1197.190	1197.416	-189.057	0.494	1143.673	0.464	17	0.162	R.GRLNVLGNVVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	983.570	984.178	-1640.186	0.468	967.771	0.356	14	0.139	R.LNVLGNVVR.K
R5/RRR5-1/2	983.949	984.178	-233.825	0.368	864.604	0.352	13	0.133	R.LNVLGNVVR.K
R5/RRR5-4/2	1374.197	1374.524	-238.923	0.380	983.277	0.318	15	0.132	R.DWLSAYWTGFK.S
R5/RRR5-4/2	984.274	984.178	97.635	0.461	848.777	0.313	13	0.129	R.LNVLGNVVR.K
R5/RRR5-4/2	984.062	984.178	-117.715	0.434	848.917	0.283	13	0.126	R.LNVLGNVVR.K
R5/RRR5-3/2	983.862	984.178	-321.828	0.400	873.539	0.271	13	0.126	R.LNVLGNVVR.K
R5/RRR5-4/2	1216.122	1216.278	-129.030	0.526	805.146	0.298	15	0.126	K.VYYELDEER.K
R5/RRR5-3/2	983.845	984.178	-339.381	0.390	773.358	0.303	12	0.126	R.LNVLGNVVR.K
R5/RRR5-4/2	1777.946	1779.023	-1171.626	0.448	602.849	0.385	17	0.125	-.VEQLCPFPYDLIQR.-
R5/RRR5-4/2	1778.174	1779.023	-1042.716	0.464	738.903	0.336	18	0.125	R.VEQLCPFPYDLIQR.E
R5/RRR5-4/2	1135.370	1134.260	96.342	0.505	936.712	0.272	14	0.123	-.VCELAAEWR.-
R5/RRR5-1/2	983.822	984.178	-362.412	0.335	717.183	0.287	12	0.122	-.LNVLGNVVR.-
R5/RRR5-3/2	984.511	984.178	338.875	0.448	875.964	0.227	13	0.121	R.LNVLGNVVR.K
R5/RRR5-4/2	1778.395	1779.023	-918.112	0.414	565.060	0.245	17	0.117	R.VEQLCPFPYDLIQR.E
R5/RRR5-4/2	1374.008	1374.524	-1106.343	0.230	409.123	0.335	11	0.117	R.DWLSAYWTGFK.S
R5/RRR5-23/2	1218.977	1218.386	-336.341	0.530	1578.714	0.444	16	0.198	K.AEIGLWFEPR.E
R5/RRR5-23/2	1219.030	1218.386	-292.737	0.450	1546.302	0.455	16	0.197	K.AEIGLWFEPR.E
R5/RRR5-23/2	1217.880	1218.386	-1240.130	0.396	1319.093	0.400	15	0.165	K.AEIGLWFEPR.E
R5/RRR5-23/2	1339.120	1339.436	-237.044	0.442	1286.574	0.414	19	0.164	R.NIIHGSDGPETAK.A
R5/RRR5-23/2	1218.244	1218.386	-116.544	0.416	1215.010	0.405	15	0.158	K.AEIGLWFEPR.E
R5/RRR5-23/2	987.679	988.163	-492.336	0.426	1256.722	0.359	14	0.154	R.GLISEILSR.F
R5/RRR5-23/2	988.026	988.163	-139.486	0.510	1238.336	0.370	14	0.154	R.GLISEILSR.F
R5/RRR5-23/2	1299.429	1299.366	48.468	0.439	930.162	0.461	16	0.148	R.ELVSYTSNEEK.W
R5/RRR5-23/2	1298.622	1299.366	-1347.063	0.357	1052.979	0.416	16	0.147	R.ELVSYTSNEEK.W
R5/RRR5-24/2	987.772	988.163	-397.714	0.464	1054.422	0.374	13	0.144	R.GLISEILSR.F
R5/RRR5-23/2	1217.474	1218.386	-1574.925	0.451	723.302	0.485	14	0.143	K.AEIGLWFEPR.E
R5/RRR5-24/2	987.810	988.163	-358.656	0.415	1007.206	0.362	13	0.140	R.GLISEILSR.F
R5/RRR5-23/2	987.631	988.163	-1556.146	0.425	1080.120	0.329	13	0.139	R.GLISEILSR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1298.964	1299.366	-310.069	0.369	857.141	0.396	15	0.135	R.ELVSYTSNEEK.W
R5/RRR5-23/2	1338.619	1339.436	-1361.418	0.406	940.799	0.366	17	0.135	R.NIIHGSDGPETAK.A
R5/RRR5-23/2	1339.163	1339.436	-204.579	0.445	861.733	0.396	16	0.135	R.NIIHGSDGPETAK.A
R5/RRR5-24/2	988.018	988.163	-147.790	0.487	1002.865	0.328	13	0.134	-.GLISEILSR.-
R5/RRR5-23/2	1070.887	1071.252	-341.808	0.349	817.909	0.378	16	0.133	R.KLIGATDPQK.S
R5/RRR5-23/2	1345.283	1345.572	-215.298	0.413	605.328	0.420	15	0.130	R.TFIAIKPDGVQR.G
R5/RRR5-23/2	1346.023	1345.572	336.048	0.447	573.075	0.403	14	0.126	-.TFIAIKPDGVQR.-
R5/RRR5-23/2	1071.134	1071.252	-110.489	0.348	830.904	0.272	16	0.124	R.KLIGATDPQK.S
R5/RRR5-23/2	1345.166	1345.572	-302.423	0.362	609.800	0.356	15	0.124	-.TFIAIKPDGVQR.-
R5/RRR5-23/2	987.643	988.163	-1544.475	0.191	684.808	0.302	12	0.119	-.GLISEILSR.-
R5/RRR5-23/2	987.564	988.163	-1623.943	0.161	726.091	0.227	12	0.116	-.GLISEILSR.-
R5/RRR5-13/1	1318.860	1319.488	-1238.421	0.260	796.957	0.188	15	0.368	R.DDLFNINAGIVK.G
R5/RRR5-13/1	1318.848	1319.488	-1247.716	0.239	820.815	0.077	15	0.363	R.DDLFNINAGIVK.G
R5/RRR5-13/2	1319.172	1319.488	-240.443	0.498	2075.759	0.394	19	0.247	R.DDLFNINAGIVK.G
R5/RRR5-12/2	1320.051	1319.488	-332.478	0.556	1929.104	0.416	19	0.231	R.DDLFNINAGIVK.G
R5/RRR5-12/2	1318.583	1319.488	-1449.239	0.412	1617.956	0.408	18	0.193	R.DDLFNINAGIVK.G
R5/RRR5-12/2	1319.152	1319.488	-255.575	0.481	1663.906	0.379	18	0.192	R.DDLFNINAGIVK.G
R5/RRR5-13/2	1319.204	1319.488	-216.492	0.436	1703.327	0.340	18	0.188	R.DDLFNINAGIVK.G
R5/RRR5-13/2	1390.090	1390.482	-282.344	0.480	1551.192	0.386	20	0.182	K.RTQDGGTEVVEAK.A
R5/RRR5-13/2	1848.276	1849.031	-952.889	0.442	1308.544	0.501	22	0.179	K.NGVEEVLGLGQLSEFEK.E
R5/RRR5-13/2	1848.253	1849.031	-965.156	0.442	1094.789	0.477	23	0.159	K.NGVEEVLGLGQLSEFEK.E
R5/RRR5-13/2	1233.977	1234.295	-258.631	0.547	964.828	0.482	19	0.156	R.TQDGGTEVVEAK.A
R5/RRR5-13/2	1233.909	1234.295	-313.815	0.503	875.278	0.469	18	0.149	R.TQDGGTEVVEAK.A
R5/RRR5-13/2	1233.514	1234.295	-1448.338	0.493	845.399	0.469	18	0.147	R.TQDGGTEVVEAK.A
R5/RRR5-13/2	1390.268	1390.482	-154.171	0.459	1100.517	0.350	18	0.141	K.RTQDGGTEVVEAK.A
R5/RRR5-13/2	1319.273	1319.488	-163.581	0.402	768.306	0.408	16	0.135	R.DDLFNINAGIVK.G
R5/RRR5-12/2	1234.946	1234.295	-283.511	0.386	668.590	0.356	16	0.127	R.TQDGGTEVVEAK.A
R5/RRR5-14/2	1319.276	1319.488	-161.353	0.464	820.212	0.355	15	0.124	-.DDLFNINAGIVK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1320.180	1319.488	-234.324	0.318	568.506	0.232	14	0.118	R.DDLFNINAGIVK.G
R5/RRR5-18/2	1609.486	1608.861	-233.891	0.603	2824.732	0.567	22	0.447	K.ALLTELQALEEHLK.A
R5/RRR5-18/2	1608.579	1608.861	-175.871	0.514	2449.065	0.446	21	0.326	K.ALLTELQALEEHLK.A
R5/RRR5-18/2	1608.136	1608.861	-1075.996	0.449	2360.176	0.383	19	0.290	K.ALLTELQALEEHLK.A
R5/RRR5-18/3	1828.426	1828.957	-839.762	0.531	1596.553	0.512	34	0.193	K.AAVGHPDTLGDCPFSQR.V
R5/RRR5-18/3	1828.788	1828.957	-92.706	0.570	1693.052	0.441	33	0.184	K.AAVGHPDTLGDCPFSQR.V
R5/RRR5-18/3	1829.163	1828.957	112.939	0.557	1398.584	0.452	32	0.146	K.AAVGHPDTLGDCPFSQR.V
R5/RRR5-18/2	989.521	990.095	-1595.553	0.346	649.120	0.527	14	0.141	K.VPVFNGGDGK.W
R5/RRR5-18/2	989.752	990.095	-347.375	0.349	676.587	0.513	14	0.140	K.VPVFNGGDGK.W
R5/RRR5-18/2	1616.522	1616.885	-225.072	0.490	1083.680	0.346	17	0.138	K.LIDVQNKPDWFLK.I
R5/RRR5-18/3	1498.806	1498.753	35.599	0.561	1436.106	0.412	28	0.138	K.LYHLQVALEHFK.G
R5/RRR5-18/2	990.484	990.095	394.435	0.281	753.672	0.469	13	0.135	K.VPVFNGGDGK.W
R5/RRR5-18/2	990.595	990.095	-506.152	0.315	779.177	0.432	13	0.134	K.VPVFNGGDGK.W
R5/RRR5-18/3	1498.331	1498.753	-282.589	0.525	1330.149	0.434	26	0.132	K.LYHLQVALEHFK.G
R5/RRR5-18/2	1122.169	1122.301	-118.339	0.370	313.041	0.470	13	0.131	K.EHLIAGWAPK.V
R5/RRR5-18/2	1122.046	1122.301	-228.016	0.322	275.873	0.548	12	0.131	K.EHLIAGWAPK.V
R5/RRR5-18/2	1122.320	1122.301	17.061	0.350	320.096	0.432	13	0.129	K.EHLIAGWAPK.V
R5/RRR5-18/2	1616.218	1616.885	-1034.177	0.452	914.278	0.282	16	0.122	K.LIDVQNKPDWFLK.I
R5/RRR5-18/3	1122.653	1122.301	314.559	0.524	1382.476	0.370	21	0.122	K.EHLIAGWAPK.V
R5/RRR5-18/2	990.249	990.095	156.023	0.211	483.558	0.378	11	0.119	K.VPVFNGGDGK.W
R5/RRR5-18/3	1121.788	1122.301	-1352.701	0.435	1254.783	0.382	20	0.111	K.EHLIAGWAPK.V
R5/RRR5-18/3	1498.328	1498.753	-284.551	0.462	1231.689	0.386	25	0.111	K.LYHLQVALEHFK.G
R5/RRR5-18/3	1122.454	1122.301	136.598	0.470	964.066	0.372	18	0.091	K.EHLIAGWAPK.V
R5/RRR5-17/2	1160.078	1160.303	-194.050	0.480	1513.039	0.496	19	0.202	K.AVDNSGTVVGIK.C
R5/RRR5-17/2	1160.116	1160.303	-161.749	0.443	1192.690	0.505	19	0.173	K.AVDNSGTVVGIK.C
R5/RRR5-16/2	1086.036	1085.234	-183.154	0.479	1241.791	0.455	14	0.169	R.VFQVEYATK.A
R5/RRR5-17/2	1085.065	1085.234	-156.124	0.494	1244.273	0.448	14	0.169	R.VFQVEYATK.A
R5/RRR5-17/2	1084.073	1084.248	-161.688	0.463	860.094	0.586	16	0.165	K.VPADLLEQAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1159.941	1160.303	-312.716	0.448	1051.918	0.498	19	0.162	K.AVDNSGTVVGIK.C
R5/RRR5-16/2	1159.445	1160.303	-1607.391	0.383	1084.036	0.500	18	0.162	K.AVDNSGTVVGIK.C
R5/RRR5-17/2	1083.731	1084.248	-1403.580	0.436	879.132	0.543	16	0.159	K.VPADLLEQAK.V
R5/RRR5-17/2	1083.996	1084.248	-233.083	0.487	858.145	0.514	16	0.156	K.VPADLLEQAK.V
R5/RRR5-16/2	1084.007	1084.248	-223.367	0.386	802.255	0.566	16	0.155	K.VPADLLEQAK.V
R5/RRR5-16/2	1084.260	1084.248	11.110	0.444	710.612	0.564	16	0.154	K.VPADLLEQAK.V
R5/RRR5-17/2	1085.171	1085.234	-58.965	0.427	1173.158	0.377	14	0.152	R.VFQVEYATK.A
R5/RRR5-16/2	1160.024	1160.303	-241.344	0.473	806.434	0.501	17	0.149	K.AVDNSGTVVGIK.C
R5/RRR5-15/2	1084.559	1084.248	287.238	0.413	673.572	0.536	15	0.147	K.VPADLLEQAK.V
R5/RRR5-16/2	1085.047	1085.234	-173.391	0.380	1020.321	0.399	14	0.145	R.VFQVEYATK.A
R5/RRR5-16/2	1083.971	1084.248	-256.131	0.409	633.390	0.496	16	0.143	K.VPADLLEQAK.V
R5/RRR5-17/2	1084.993	1085.234	-223.277	0.375	993.809	0.379	14	0.141	R.VFQVEYATK.A
R5/RRR5-17/2	991.990	992.150	-162.688	0.467	520.997	0.480	13	0.138	K.VYGEPISVK.E
R5/RRR5-17/2	1218.149	1218.419	-222.290	0.425	737.426	0.454	16	0.137	K.CKDGIVLGVEK.L
R5/RRR5-17/2	1159.278	1160.303	-1751.998	0.362	657.858	0.473	16	0.136	K.AVDNSGTVVGIK.C
R5/RRR5-15/2	1084.179	1084.248	-63.310	0.322	454.973	0.433	14	0.130	K.VPADLLEQAK.V
R5/RRR5-17/2	991.538	992.150	-1630.832	0.343	444.661	0.423	12	0.128	K.VYGEPISVK.E
R5/RRR5-17/2	1350.195	1350.435	-177.995	0.365	1103.641	0.513	18	0.126	K.VAAQAALEEM*DAD.-
R5/RRR5-17/2	991.306	992.150	-1866.007	0.283	466.240	0.370	12	0.123	K.VYGEPISVK.E
R5/RRR5-17/2	1349.919	1350.435	-1125.746	0.266	704.941	0.250	15	0.075	K.VAAQAALEEM*DAD.-
R5/RRR5-10/2	1858.285	1857.050	126.792	0.601	2299.954	0.521	23	0.318	K.LAYVALDYEQELETAK.N
R5/RRR5-10/2	1856.439	1857.050	-870.479	0.543	2249.183	0.466	23	0.294	K.LAYVALDYEQELETAK.N
R5/RRR5-11/2	1856.416	1857.050	-883.153	0.549	2127.693	0.493	23	0.282	K.LAYVALDYEQELETAK.N
R5/RRR5-10/2	1856.463	1857.050	-857.674	0.558	2122.768	0.476	23	0.276	K.LAYVALDYEQELETAK.N
R5/RRR5-11/2	1857.384	1857.050	180.314	0.595	2106.768	0.484	23	0.274	K.LAYVALDYEQELETAK.N
R5/RRR5-11/2	1857.289	1857.050	128.904	0.598	2130.696	0.470	23	0.273	K.LAYVALDYEQELETAK.N
R5/RRR5-10/2	1765.249	1764.915	189.864	0.489	1129.586	0.536	23	0.172	K.SYELPDGQVITIGSER.F
R5/RRR5-11/2	1118.826	1119.166	-304.947	0.417	614.415	0.517	14	0.142	R.GYSFTTSAER.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1118.810	1119.166	-319.397	0.405	523.710	0.490	14	0.138	R.GYSFTTSAER.E
R5/RRR5-10/2	1118.867	1119.166	-268.387	0.382	463.311	0.505	14	0.137	R.GYSFTTSAER.E
R5/RRR5-10/2	1118.986	1119.166	-161.129	0.369	505.032	0.492	14	0.136	R.GYSFTTSAER.E
R5/RRR5-11/2	1118.827	1119.166	-304.290	0.352	512.501	0.481	14	0.134	R.GYSFTTSAER.E
R5/RRR5-10/2	1118.904	1119.166	-234.456	0.342	419.877	0.516	13	0.134	R.GYSFTTSAER.E
R5/RRR5-14/2	1649.238	1649.845	-977.541	0.521	2444.901	0.572	24	0.368	K.LLSDLAAAM*EEGDVAK.F
R5/RRR5-14/2	1649.106	1649.845	-1057.951	0.457	2058.744	0.549	23	0.289	K.LLSDLAAAM*EEGDVAK.F
R5/RRR5-14/2	1492.304	1491.671	-246.432	0.509	1915.416	0.468	20	0.245	K.VAEIAAQLEQYQK.A
R5/RRR5-14/2	1134.131	1134.267	-120.437	0.440	1216.930	0.358	15	0.151	K.ANEIFEAIAR.Q
R5/RRR5-14/2	1400.081	1400.475	-282.341	0.429	1139.918	0.377	18	0.149	R.YQDIDPTFSGTR.E
R5/RRR5-14/2	1133.956	1134.267	-275.181	0.479	1119.721	0.378	15	0.148	K.ANEIFEAIAR.Q
R5/RRR5-14/2	1400.202	1400.475	-195.486	0.461	1174.318	0.335	18	0.144	R.YQDIDPTFSGTR.E
R5/RRR5-14/2	1488.459	1488.745	-192.532	0.447	948.731	0.440	17	0.143	R.GILLNAGICQLCR.G
R5/RRR5-14/2	1400.165	1400.475	-222.249	0.458	1074.837	0.371	17	0.143	R.YQDIDPTFSGTR.E
R5/RRR5-14/2	1308.252	1308.444	-147.173	0.457	937.918	0.370	16	0.134	R.GDVVAITNSM*ER.Y
R5/RRR5-14/2	1133.259	1134.267	-1776.772	0.293	727.538	0.306	13	0.122	K.ANEIFEAIAR.Q
R5/RRR5-16/2	1820.483	1820.945	-254.130	0.587	2304.406	0.609	28	0.350	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/2	1820.400	1820.945	-851.057	0.585	2264.324	0.578	27	0.332	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/3	1821.004	1820.945	32.628	0.582	2195.632	0.545	33	0.327	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-15/2	1820.337	1820.945	-885.591	0.590	2187.536	0.605	27	0.327	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-15/2	1820.313	1820.945	-899.257	0.561	2178.143	0.575	27	0.316	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/3	1821.179	1820.945	129.032	0.598	2058.583	0.546	33	0.294	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/2	1821.321	1820.945	207.211	0.581	1917.881	0.642	26	0.292	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-15/3	1820.979	1820.945	19.114	0.582	2034.221	0.553	34	0.292	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-15/2	1821.318	1820.945	205.665	0.571	1936.946	0.570	27	0.274	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/2	1310.034	1310.398	-278.663	0.511	2054.262	0.460	19	0.263	R.LPDATQGSDHLR.Q
R5/RRR5-16/3	1820.645	1820.945	-164.876	0.529	1899.402	0.522	34	0.250	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-15/2	1311.066	1310.398	-253.883	0.509	1996.239	0.441	20	0.249	R.LPDATQGSDHLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1821.639	1820.945	-168.348	0.554	1776.179	0.504	33	0.218	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-15/3	1821.714	1820.945	-126.906	0.576	1598.734	0.572	31	0.212	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/2	1310.075	1310.398	-247.159	0.493	1693.561	0.436	20	0.209	R.LPDATQGSDHLR.Q
R5/RRR5-15/2	1309.826	1310.398	-1203.740	0.465	1582.021	0.438	20	0.197	R.LPDATQGSDHLR.Q
R5/RRR5-16/2	1309.629	1310.398	-1355.093	0.488	1513.408	0.422	20	0.187	R.LPDATQGSDHLR.Q
R5/RRR5-15/2	1310.088	1310.398	-237.904	0.467	1461.582	0.432	20	0.184	R.LPDATQGSDHLR.Q
R5/RRR5-16/2	1534.206	1534.657	-295.325	0.488	1350.181	0.492	20	0.183	R.LAWHSAGTFDVSSR.T
R5/RRR5-16/2	1602.226	1600.751	297.214	0.532	592.132	0.596	22	0.154	K.SYPTVSDEYLAAVGK.A
R5/RRR5-16/2	1601.155	1600.751	253.138	0.463	757.592	0.545	21	0.152	K.SYPTVSDEYLAAVGK.A
R5/RRR5-16/2	1534.214	1534.657	-290.057	0.406	1118.523	0.404	20	0.150	R.LAWHSAGTFDVSSR.T
R5/RRR5-16/2	1600.253	1600.751	-311.828	0.425	598.209	0.538	22	0.145	K.SYPTVSDEYLAAVGK.A
R5/RRR5-15/2	1574.170	1574.870	-1083.133	0.420	662.651	0.383	19	0.130	K.ALM*ADPAFRPLVEK.Y
R5/RRR5-17/2	1600.168	1600.751	-991.908	0.346	370.297	0.483	17	0.130	K.SYPTVSDEYLAAVGK.A
R5/RRR5-17/2	1600.103	1600.751	-1032.655	0.335	415.488	0.445	19	0.129	K.SYPTVSDEYLAAVGK.A
R5/RRR5-16/2	1574.444	1574.870	-271.389	0.441	433.887	0.435	17	0.128	-.ALM*ADPAFRPLVEK.-
R5/RRR5-15/2	1574.308	1574.870	-994.767	0.433	582.896	0.394	18	0.127	-.ALM*ADPAFRPLVEK.-
R5/RRR5-17/2	1600.190	1600.751	-978.581	0.330	287.602	0.390	17	0.126	K.SYPTVSDEYLAAVGK.A
R5/RRR5-15/3	1534.966	1534.657	201.588	0.458	1256.369	0.430	26	0.123	R.LAWHSAGTFDVSSR.T
R5/RRR5-15/2	1600.037	1600.751	-1074.096	0.264	159.416	0.372	14	0.122	-.SYPTVSDEYLAAVGK.-
R5/RRR5-17/3	1534.499	1534.657	-103.664	0.437	1267.202	0.417	25	0.121	R.LAWHSAGTFDVSSR.T
R5/RRR5-17/3	1820.851	1820.945	-51.690	0.410	1042.197	0.499	28	0.120	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/2	1574.112	1574.870	-1119.574	0.367	520.470	0.278	18	0.120	-.ALM*ADPAFRPLVEK.-
R5/RRR5-16/2	1574.410	1574.870	-292.626	0.392	473.650	0.285	17	0.119	-.ALM*ADPAFRPLVEK.-
R5/RRR5-16/2	1558.135	1558.870	-1116.968	0.365	658.997	0.252	18	0.119	-.ALMADPAFRPLVEK.-
R5/RRR5-16/3	1533.904	1534.657	-1146.475	0.462	1192.099	0.425	26	0.116	R.LAWHSAGTFDVSSR.T
R5/RRR5-16/3	1534.269	1534.657	-254.145	0.481	1072.663	0.454	25	0.113	R.LAWHSAGTFDVSSR.T
R5/RRR5-17/3	1820.642	1820.945	-166.490	0.411	1011.969	0.470	28	0.112	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-15/3	1535.385	1534.657	-178.044	0.529	1048.461	0.438	25	0.108	R.LAWHSAGTFDVSSR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/3	1534.698	1534.657	26.549	0.475	973.632	0.459	23	0.107	-.LAWHSAGTFDVSSR.-
R5/RRR5-15/3	1534.456	1534.657	-131.793	0.484	944.929	0.450	23	0.101	-.LAWHSAGTFDVSSR.-
R5/RRR5-19/3	1310.809	1310.398	314.102	0.425	608.120	0.468	23	0.095	R.LPDATQGSDHLR.Q
R5/RRR5-16/3	1310.232	1310.398	-127.014	0.410	672.551	0.491	23	0.095	-.LPDATQGSDHLR.-
R5/RRR5-15/3	1310.453	1310.398	41.603	0.384	619.680	0.455	23	0.092	R.LPDATQGSDHLR.Q
R5/RRR5-15/3	1310.057	1310.398	-261.051	0.399	720.099	0.411	24	0.089	R.LPDATQGSDHLR.Q
R5/RRR5-19/3	1309.827	1310.398	-1202.954	0.373	515.105	0.385	22	0.087	R.LPDATQGSDHLR.Q
R5/RRR5-17/3	1821.147	1820.945	111.487	0.360	891.554	0.371	26	0.087	K.NPGEQSHAANAGLDIAVR.L
R5/RRR5-16/3	1310.241	1310.398	-120.285	0.326	537.941	0.402	22	0.082	-.LPDATQGSDHLR.-
R5/RRR5-17/3	1310.606	1310.398	159.167	0.436	826.755	0.312	25	0.081	R.LPDATQGSDHLR.Q
R5/RRR5-19/3	1310.702	1310.398	232.157	0.361	650.991	0.313	23	0.076	-.LPDATQGSDHLR.-
R5/RRR5-16/2	1668.330	1668.820	-294.700	0.472	2390.561	0.301	22	0.272	R.NDFDTCVDLLSQLK.V
R5/RRR5-15/2	1192.114	1192.390	-231.458	0.461	1527.368	0.485	17	0.202	K.LVEVTQLFSR.F
R5/RRR5-16/2	1192.115	1192.390	-231.252	0.545	1534.930	0.476	17	0.201	K.LVEVTQLFSR.F
R5/RRR5-16/2	1192.054	1192.390	-282.619	0.504	1443.198	0.469	17	0.190	K.LVEVTQLFSR.F
R5/RRR5-16/2	1832.233	1833.078	-1010.013	0.493	1270.130	0.561	24	0.190	K.EIPSLQVINQTLSYAR.E
R5/RRR5-16/2	1192.324	1192.390	-55.103	0.477	1438.215	0.464	17	0.189	K.LVEVTQLFSR.F
R5/RRR5-15/2	1832.935	1833.078	-78.395	0.514	1134.478	0.555	23	0.177	K.EIPSLQVINQTLSYAR.E
R5/RRR5-15/2	1191.910	1192.390	-403.764	0.522	1320.896	0.466	15	0.177	K.LVEVTQLFSR.F
R5/RRR5-15/2	1832.643	1833.078	-238.481	0.509	1177.052	0.529	23	0.176	K.EIPSLQVINQTLSYAR.E
R5/RRR5-16/2	1832.299	1833.078	-973.760	0.496	1108.174	0.555	23	0.175	K.EIPSLQVINQTLSYAR.E
R5/RRR5-16/2	1833.326	1833.078	135.397	0.556	1083.043	0.560	23	0.175	K.EIPSLQVINQTLSYAR.E
R5/RRR5-15/2	1191.656	1192.390	-1459.348	0.410	1155.546	0.473	15	0.164	K.LVEVTQLFSR.F
R5/RRR5-15/2	1832.202	1833.078	-1027.004	0.456	954.101	0.535	22	0.160	K.EIPSLQVINQTLSYAR.E
R5/RRR5-16/2	1373.293	1373.579	-209.124	0.352	948.742	0.391	15	0.135	R.DIYEHAVVLSVK.I
R5/RRR5-16/2	1122.892	1123.155	-234.823	0.498	806.661	0.323	15	0.130	K.IEDQDAFER.D
R5/RRR5-16/2	1123.005	1123.155	-133.405	0.389	787.545	0.289	15	0.126	K.IEDQDAFER.D
R5/RRR5-16/3	1366.027	1365.466	-322.149	0.453	1126.945	0.404	24	0.106	K.TVRDELAGCSEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/3	1366.666	1365.466	147.262	0.439	858.157	0.339	23	0.081	K.TVRDELAGCSEK.G
R5/RRR5-3/2	1688.266	1687.920	205.556	0.552	1846.796	0.569	23	0.261	R.AVSDEIKNVIIASATR.K
R5/RRR5-3/2	1687.459	1687.920	-273.728	0.528	1789.034	0.546	22	0.246	R.AVSDEIKNVIIASATR.K
R5/RRR5-3/2	1486.241	1486.653	-277.506	0.359	1449.561	0.347	21	0.165	R.LASSLSSPATPADLR.A
R5/RRR5-3/3	1235.682	1236.402	-1396.713	0.487	1622.436	0.392	24	0.156	K.LNNVITHPEAK.H
R5/RRR5-3/2	998.304	998.245	60.266	0.510	1139.919	0.383	15	0.151	K.LLVLLQNGK.Q
R5/RRR5-3/2	1236.077	1236.402	-264.035	0.490	840.117	0.473	16	0.147	K.LNNVITHPEAK.H
R5/RRR5-3/2	1711.048	1710.897	88.329	0.434	1079.365	0.420	16	0.146	R.IAICVFDDIAEQCR.E
R5/RRR5-3/2	998.315	998.245	71.058	0.504	939.303	0.401	14	0.143	K.LLVLLQNGK.Q
R5/RRR5-3/2	1236.077	1236.402	-264.234	0.425	948.682	0.404	15	0.141	K.LNNVITHPEAK.H
R5/RRR5-3/2	1417.229	1416.586	-252.725	0.335	755.637	0.493	17	0.138	K.VVHDQLSSM*VER.S
R5/RRR5-1/2	1236.572	1236.402	137.864	0.399	385.002	0.294	13	0.122	K.LNNVITHPEAK.H
R5/RRR5-3/2	1485.931	1486.653	-1162.180	0.255	783.451	0.239	18	0.117	R.LASSLSSPATPADLR.A
R5/RRR5-3/2	861.400	861.088	363.174	0.241	888.037	0.188	12	0.116	-.AM*AAVLLR.-
R5/RRR5-3/3	1236.358	1236.402	-36.415	0.424	1272.507	0.392	22	0.115	K.LNNVITHPEAK.H
R5/RRR5-3/2	1485.775	1486.653	-1267.204	0.230	821.465	0.160	18	0.113	R.LASSLSSPATPADLR.A
R5/RRR5-2/2	1487.635	1486.653	-11.655	0.356	778.298	0.184	15	0.111	-.LASSLSSPATPADLR.-
R5/RRR5-3/3	1236.306	1236.402	-78.457	0.420	1118.357	0.430	22	0.110	K.LNNVITHPEAK.H
R5/RRR5-17/2	1532.390	1531.776	-252.929	0.593	2414.576	0.644	24	0.384	K.AVASINSVLTDLVTK.G
R5/RRR5-18/2	1406.033	1406.551	-1082.598	0.558	2598.419	0.536	25	0.383	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-18/2	1406.098	1406.551	-323.425	0.565	2515.257	0.519	25	0.360	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-17/2	1406.096	1406.551	-324.383	0.563	2509.050	0.494	25	0.350	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-17/2	1531.590	1531.776	-122.198	0.558	2360.647	0.570	24	0.348	K.AVASINSVLTDLVTK.G
R5/RRR5-18/2	1390.044	1390.552	-1088.207	0.497	2457.240	0.475	25	0.335	K.AMAQVSQAGSGGLGR.V
R5/RRR5-17/2	1406.231	1406.551	-228.317	0.539	2335.443	0.534	25	0.331	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-18/2	1406.098	1406.551	-323.076	0.548	2363.244	0.517	25	0.331	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-17/2	1406.154	1406.551	-283.185	0.551	2284.906	0.553	25	0.328	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-18/2	1531.489	1531.776	-188.242	0.540	2224.703	0.577	24	0.325	K.AVASINSVLTDLVTK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1389.533	1390.552	-1456.833	0.406	2546.341	0.378	25	0.322	K.AMAQVSQAGSGGLGR.V
R5/RRR5-18/2	1390.010	1390.552	-1112.104	0.479	2365.358	0.442	24	0.308	K.AMAQVSQAGSGGLGR.V
R5/RRR5-18/2	1531.427	1531.776	-228.544	0.516	2162.236	0.547	23	0.304	K.AVASINSVLTDLVTK.G
R5/RRR5-18/2	1531.339	1531.776	-286.204	0.532	2077.411	0.589	23	0.303	K.AVASINSVLTDLVTK.G
R5/RRR5-18/2	1880.356	1880.077	148.484	0.584	1880.109	0.628	27	0.283	R.DLSPLTCAQCLSTAVSR.F
R5/RRR5-17/2	1532.243	1531.776	305.195	0.578	1815.983	0.579	22	0.258	K.AVASINSVLTDLVTK.G
R5/RRR5-18/2	1880.486	1880.077	217.815	0.613	1418.600	0.659	24	0.227	R.DLSPLTCAQCLSTAVSR.F
R5/RRR5-18/2	1394.109	1393.567	-329.306	0.553	1545.792	0.559	18	0.220	K.GNNVIYGLVQCR.G
R5/RRR5-18/2	1491.089	1490.547	-307.724	0.554	1658.105	0.464	18	0.210	R.FDQYCGAQQGCR.I
R5/RRR5-16/2	1530.739	1531.776	-1334.842	0.359	1566.830	0.504	20	0.205	K.AVASINSVLTDLVTK.G
R5/RRR5-18/2	1879.459	1880.077	-863.466	0.536	1330.170	0.591	24	0.202	R.DLSPLTCAQCLSTAVSR.F
R5/RRR5-17/2	1880.488	1880.077	219.052	0.602	1191.597	0.654	23	0.201	R.DLSPLTCAQCLSTAVSR.F
R5/RRR5-1/2	1531.600	1531.776	-115.802	0.468	1441.931	0.539	20	0.201	K.AVASINSVLTDLVTK.G
R5/RRR5-18/2	1490.009	1490.547	-1035.002	0.497	1652.313	0.387	18	0.193	R.FDQYCGAQQGCR.I
R5/RRR5-18/2	1240.470	1241.333	-1506.051	0.410	1351.764	0.540	21	0.192	K.GSTGVGFATSTAGK.G
R5/RRR5-18/2	1394.119	1393.567	-322.278	0.527	1271.643	0.564	17	0.191	K.GNNVIYGLVQCR.G
R5/RRR5-17/2	1879.447	1880.077	-869.725	0.498	1289.833	0.555	24	0.190	R.DLSPLTCAQCLSTAVSR.F
R5/RRR5-18/2	1489.920	1490.547	-1095.135	0.489	1503.669	0.438	17	0.188	R.FDQYCGAQQGCR.I
R5/RRR5-17/2	1393.473	1393.567	-67.621	0.476	1524.125	0.407	18	0.184	K.GNNVIYGLVQCR.G
R5/RRR5-17/2	1879.752	1880.077	-173.428	0.552	1112.348	0.597	23	0.183	R.DLSPLTCAQCLSTAVSR.F
R5/RRR5-18/2	1240.740	1241.333	-1287.245	0.425	1221.172	0.543	20	0.180	K.GSTGVGFATSTAGK.G
R5/RRR5-17/2	1241.204	1241.333	-103.833	0.429	1172.400	0.560	21	0.180	K.GSTGVGFATSTAGK.G
R5/RRR5-18/2	1392.982	1393.567	-1141.198	0.483	1354.605	0.445	17	0.175	K.GNNVIYGLVQCR.G
R5/RRR5-17/2	1241.126	1241.333	-166.778	0.443	1163.396	0.512	20	0.171	K.GSTGVGFATSTAGK.G
R5/RRR5-17/2	1240.418	1241.333	-1548.163	0.277	1265.304	0.441	21	0.162	K.GSTGVGFATSTAGK.G
R5/RRR5-18/2	1240.449	1241.333	-1522.856	0.336	1025.711	0.501	19	0.155	K.GSTGVGFATSTAGK.G
R5/RRR5-17/2	1392.508	1393.567	-1483.000	0.350	1127.126	0.354	16	0.143	K.GNNVIYGLVQCR.G
R5/RRR5-2/2	1531.168	1531.776	-1053.799	0.382	182.222	0.387	13	0.104	-.AVASINSVLTDLVTK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/3	1406.871	1406.551	227.802	0.432	1250.477	0.344	25	0.103	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-18/3	1489.947	1490.547	-1077.211	0.467	1228.003	0.338	22	0.100	R.FDQYCGAQQGCR.I
R5/RRR5-18/3	1406.633	1406.551	58.369	0.331	1264.866	0.291	26	0.092	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-18/3	1406.422	1406.551	-92.184	0.390	1075.140	0.316	25	0.085	K.AM*AQVSQAGSGGLGR.V
R5/RRR5-10/2	1572.638	1571.806	-106.630	0.473	1449.068	0.520	21	0.198	R.ISITGAGGFIASHIAR.R
R5/RRR5-10/2	1572.388	1571.806	-266.585	0.439	1385.183	0.546	19	0.195	R.ISITGAGGFIASHIAR.R
R5/RRR5-10/2	1572.539	1571.806	-170.092	0.496	1229.261	0.556	19	0.182	R.ISITGAGGFIASHIAR.R
R5/RRR5-1/2	1571.370	1571.806	-278.134	0.310	995.127	0.303	17	0.128	R.ISITGAGGFIASHIAR.R
R5/RRR5-12/2	1571.874	1571.806	43.806	0.305	588.917	0.294	17	0.119	R.ISITGAGGFIASHIAR.R
R5/RRR5-9/2	1572.064	1571.806	165.142	0.298	314.153	0.392	13	0.119	-.ISITGAGGFIASHIAR.-
R5/RRR5-9/2	1571.464	1571.806	-217.969	0.266	473.798	0.330	13	0.114	-.ISITGAGGFIASHIAR.-
R5/RRR5-2/2	1767.195	1767.020	99.656	0.606	3061.975	0.630	28	0.532	K.VAIIGSGPAGLAAADQLNK.M
R5/RRR5-2/2	1767.388	1767.020	208.685	0.593	2958.150	0.635	28	0.508	K.VAIIGSGPAGLAAADQLNK.M
R5/RRR5-2/2	1766.427	1767.020	-904.301	0.541	2343.799	0.610	26	0.359	K.VAIIGSGPAGLAAADQLNK.M
R5/RRR5-2/2	1471.186	1471.724	-1048.661	0.382	2556.809	0.376	24	0.326	K.LVSEAGVGVVASGVVK.G
R5/RRR5-2/2	1471.215	1471.724	-1028.750	0.459	2234.183	0.483	23	0.299	K.LVSEAGVGVVASGVVK.G
R5/RRR5-2/2	1948.592	1949.149	-801.540	0.539	2123.178	0.495	23	0.283	R.FGVSSYYLTNADELQIK.M
R5/RRR5-2/2	1170.128	1170.341	-182.129	0.482	1961.410	0.379	18	0.229	R.VGLLVESAEPR.E
R5/RRR5-2/2	1170.117	1170.341	-191.967	0.328	1801.711	0.335	18	0.199	R.VGLLVESAEPR.E
R5/RRR5-2/2	1169.626	1170.341	-1470.295	0.342	1860.713	0.250	18	0.188	R.VGLLVESAEPR.E
R5/RRR5-2/2	1432.184	1432.607	-295.931	0.473	1138.405	0.435	18	0.157	R.VFIETPIQNTNR.A
R5/RRR5-2/2	1432.904	1432.607	208.181	0.487	1060.904	0.389	17	0.145	R.VFIETPIQNTNR.A
R5/RRR5-2/2	949.195	949.126	73.123	0.420	706.490	0.354	13	0.131	K.VLDITYPK.K
R5/RRR5-2/2	948.784	949.126	-361.213	0.384	486.868	0.364	12	0.128	K.VLDITYPK.K
R5/RRR5-2/2	948.782	949.126	-363.408	0.366	513.152	0.354	12	0.127	K.VLDITYPK.K
R5/RRR5-2/2	1375.490	1376.580	-1523.868	0.282	895.975	0.179	15	0.115	-.DILSNFDTLLPK.-
R5/RRR5-11/2	1439.888	1439.619	187.383	0.483	2108.288	0.545	21	0.295	R.GGDLVSAFAELM*GR.Q
R5/RRR5-11/2	1423.323	1423.620	-209.257	0.513	1931.365	0.539	20	0.265	R.GGDLVSAFAELMGR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1439.384	1439.619	-164.196	0.431	1604.528	0.565	19	0.225	R.GGDLVSAFAELM*GR.Q
R5/RRR5-11/3	1596.633	1595.678	-28.275	0.473	1802.502	0.480	31	0.215	R.YHGHSMSDPGSTYR.T
R5/RRR5-11/2	1423.195	1423.620	-299.349	0.397	1621.206	0.491	19	0.210	R.GGDLVSAFAELMGR.Q
R5/RRR5-11/2	1438.430	1439.619	-1526.281	0.364	1312.963	0.472	17	0.173	R.GGDLVSAFAELM*GR.Q
R5/RRR5-11/3	1595.290	1595.678	-244.116	0.455	1681.090	0.407	29	0.170	R.YHGHSMSDPGSTYR.T
R5/RRR5-11/2	1270.170	1270.376	-162.097	0.432	1164.250	0.392	18	0.152	K.GFGVESFGADRK.E
R5/RRR5-11/2	1005.062	1005.152	-90.465	0.380	1056.003	0.335	15	0.138	K.RGDYVPGLK.V
R5/RRR5-11/2	1973.352	1974.178	-928.021	0.433	547.052	0.483	19	0.130	K.ESPM*PDTSELFTNVYVK.G
R5/RRR5-11/2	1269.486	1270.376	-1493.136	0.376	833.523	0.335	17	0.129	K.GFGVESFGADRK.E
R5/RRR5-11/2	1269.437	1270.376	-1531.483	0.401	617.286	0.369	16	0.127	K.GFGVESFGADRK.E
R5/RRR5-11/3	1930.446	1930.174	141.263	0.489	1312.593	0.416	27	0.126	K.EHAIANGPIVLEMDTYR.Y
R5/RRR5-11/3	1611.127	1611.677	-965.286	0.381	1125.389	0.405	28	0.105	R.YHGHSM*SDPGSTYR.T
R5/RRR5-11/3	1594.620	1595.678	-1294.622	0.295	1264.106	0.297	27	0.092	R.YHGHSMSDPGSTYR.T
R5/RRR5-11/3	1947.203	1946.174	14.862	0.350	1162.878	0.280	29	0.083	K.EHAIANGPIVLEM*DTYR.Y
R5/RRR5-9/2	1575.874	1575.815	38.101	0.562	1956.236	0.512	20	0.264	R.YFWTMVNQPNFK.K
R5/RRR5-9/2	1576.025	1575.815	134.040	0.561	1798.809	0.504	20	0.239	R.YFWTMVNQPNFK.K
R5/RRR5-9/2	1122.802	1122.296	-441.265	0.498	1734.727	0.510	17	0.231	K.ALIAAEYSGVK.V
R5/RRR5-9/2	1123.110	1122.296	-166.097	0.501	1426.229	0.464	16	0.186	K.ALIAAEYSGVK.V
R5/RRR5-9/2	1951.651	1952.155	-772.743	0.483	1065.967	0.570	24	0.172	K.VPVLETPDGPVSESNAIAR.Y
R5/RRR5-9/2	1122.038	1122.296	-231.073	0.432	1228.700	0.416	15	0.159	K.ALIAAEYSGVK.V
R5/RRR5-9/2	1951.498	1952.155	-851.793	0.520	650.215	0.611	20	0.150	K.VPVLETPDGPVSESNAIAR.Y
R5/RRR5-9/2	1093.984	1094.286	-276.954	0.365	902.037	0.502	16	0.150	K.NPLDLLPPSK.M
R5/RRR5-9/2	1952.434	1952.155	143.128	0.443	653.367	0.527	19	0.138	K.VPVLETPDGPVSESNAIAR.Y
R5/RRR5-9/2	1218.403	1218.490	-71.610	0.330	1090.965	0.310	15	0.135	K.MLVIGSEPPFK.V
R5/RRR5-2/2	1952.018	1952.155	-70.539	0.438	693.332	0.464	19	0.133	K.VPVLETPDGPVSESNAIAR.Y
R5/RRR5-9/2	1094.295	1094.286	7.988	0.314	679.757	0.438	15	0.132	K.NPLDLLPPSK.M
R5/RRR5-1/2	777.285	776.906	488.210	0.406	409.742	0.151	11	0.124	K.VGGFLQR.M
R5/RRR5-9/2	1217.988	1218.490	-1237.306	0.281	786.207	0.246	13	0.117	K.MLVIGSEPPFK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	777.063	776.906	201.742	0.397	892.891	0.181	11	0.117	-.VGGFLQR.-
R5/RRR5-9/2	777.137	776.906	297.197	0.422	947.169	0.187	11	0.116	-.VGGFLQR.-
R5/RRR5-9/2	1093.428	1094.286	-1703.990	0.189	343.280	0.378	10	0.116	K.NPLDLLPPSK.M
R5/RRR5-8/2	776.326	776.906	-2041.846	0.353	717.292	0.097	10	0.103	-.VGGFLQR.-
R5/RRR5-8/2	777.207	776.906	387.438	0.361	565.183	0.182	11	0.099	-.VGGFLQR.-
R5/RRR5-9/2	1493.994	1494.716	-1156.072	0.422	2746.225	0.481	22	0.399	K.VADFFDAAVNLALK.V
R5/RRR5-9/2	1494.320	1494.716	-265.928	0.478	2602.522	0.501	22	0.375	K.VADFFDAAVNLALK.V
R5/RRR5-9/2	1494.274	1494.716	-297.072	0.520	2389.920	0.537	21	0.344	K.VADFFDAAVNLALK.V
R5/RRR5-9/2	1092.050	1092.273	-204.680	0.536	1876.681	0.567	19	0.267	K.LIVAGASAYAR.L
R5/RRR5-8/2	1092.072	1092.273	-185.057	0.418	1926.265	0.535	19	0.263	K.LIVAGASAYAR.L
R5/RRR5-9/2	1208.002	1208.392	-323.687	0.503	1994.187	0.460	18	0.255	K.VLENVHIAANK.N
R5/RRR5-9/2	1091.784	1092.273	-448.979	0.451	1683.291	0.599	18	0.245	K.LIVAGASAYAR.L
R5/RRR5-9/2	1091.519	1092.273	-1611.850	0.481	1636.759	0.541	19	0.227	K.LIVAGASAYAR.L
R5/RRR5-8/2	1092.050	1092.273	-205.353	0.429	1420.612	0.501	18	0.193	K.LIVAGASAYAR.L
R5/RRR5-9/2	999.820	1000.046	-227.113	0.289	978.253	0.372	14	0.136	K.YSEGYPGAR.Y
R5/RRR5-8/2	918.070	918.118	-52.760	0.342	718.240	0.398	12	0.132	K.SAVLFRPK.L
R5/RRR5-8/2	1091.280	1092.273	-1832.106	0.306	527.011	0.477	12	0.129	K.LIVAGASAYAR.L
R5/RRR5-9/2	999.995	1000.046	-51.866	0.341	741.280	0.353	13	0.128	K.YSEGYPGAR.Y
R5/RRR5-9/2	917.894	918.118	-244.716	0.346	690.679	0.362	12	0.128	-.SAVLFRPK.-
R5/RRR5-9/2	999.871	1000.046	-176.284	0.315	715.268	0.365	12	0.127	K.YSEGYPGAR.Y
R5/RRR5-8/3	1259.939	1260.381	-351.606	0.468	1359.429	0.405	21	0.126	K.LRHDVEEYAK.Q
R5/RRR5-9/3	1260.409	1260.381	22.564	0.513	1277.375	0.432	21	0.125	K.LRHDVEEYAK.Q
R5/RRR5-9/2	917.761	918.118	-389.766	0.312	490.848	0.365	10	0.124	K.SAVLFRPK.L
R5/RRR5-9/3	1260.364	1260.381	-13.427	0.484	1480.646	0.325	22	0.118	K.LRHDVEEYAK.Q
R5/RRR5-9/2	917.798	918.118	-349.596	0.312	410.607	0.317	9	0.115	-.SAVLFRPK.-
R5/RRR5-9/3	1260.081	1260.381	-238.757	0.456	1035.241	0.389	19	0.098	K.LRHDVEEYAK.Q
R5/RRR5-8/3	1260.118	1260.381	-209.456	0.462	898.273	0.355	19	0.087	K.LRHDVEEYAK.Q
R5/RRR5-8/3	1260.474	1260.381	74.141	0.441	862.607	0.344	19	0.084	K.LRHDVEEYAK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1786.429	1786.919	-275.081	0.528	1623.346	0.513	25	0.219	-.AVFASGSPFDPVEYDGK.-
R5/RRR5-6/2	1786.792	1786.919	-71.169	0.565	1363.334	0.543	23	0.194	R.AVFASGSPFDPVEYDGK.I
R5/RRR5-7/2	1786.308	1786.919	-904.655	0.518	1485.348	0.461	24	0.191	-.AVFASGSPFDPVEYDGK.-
R5/RRR5-6/2	1786.159	1786.919	-988.290	0.485	1359.935	0.497	23	0.186	-.AVFASGSPFDPVEYDGK.-
R5/RRR5-7/2	1786.567	1786.919	-197.550	0.533	1360.768	0.493	23	0.185	-.AVFASGSPFDPVEYDGK.-
R5/RRR5-7/2	979.852	980.100	-253.546	0.486	1421.342	0.419	15	0.178	K.AYELGLASR.L
R5/RRR5-6/2	979.513	980.100	-1624.854	0.463	1518.222	0.366	15	0.177	K.AYELGLASR.L
R5/RRR5-7/2	979.981	980.100	-121.703	0.472	1398.828	0.406	15	0.174	K.AYELGLASR.L
R5/RRR5-3/2	980.236	980.100	139.006	0.431	1400.318	0.392	15	0.171	K.AYELGLASR.L
R5/RRR5-1/2	979.176	980.100	-1971.026	0.390	1503.628	0.333	15	0.169	K.AYELGLASR.L
R5/RRR5-7/2	979.406	980.100	-1734.416	0.449	1391.950	0.370	15	0.167	K.AYELGLASR.L
R5/RRR5-6/2	979.590	980.100	-1546.360	0.415	1472.685	0.331	15	0.166	K.AYELGLASR.L
R5/RRR5-6/2	1165.661	1166.355	-1458.281	0.434	1135.765	0.458	18	0.161	K.ISAHIAANVAAK.A
R5/RRR5-6/2	1166.095	1166.355	-224.023	0.425	1103.548	0.449	18	0.157	K.ISAHIAANVAAK.A
R5/RRR5-6/2	1315.270	1315.584	-239.294	0.444	651.918	0.586	20	0.153	K.TIKPTVLIGTSGK.G
R5/RRR5-7/2	1315.257	1315.584	-249.257	0.465	587.931	0.592	19	0.151	K.TIKPTVLIGTSGK.G
R5/RRR5-7/2	1165.954	1166.355	-344.916	0.439	1001.289	0.445	17	0.150	K.ISAHIAANVAAK.A
R5/RRR5-6/2	1316.220	1315.584	-277.725	0.462	622.515	0.535	20	0.147	K.TIKPTVLIGTSGK.G
R5/RRR5-6/2	1315.178	1315.584	-310.063	0.394	597.420	0.526	19	0.142	K.TIKPTVLIGTSGK.G
R5/RRR5-7/2	1314.619	1315.584	-1499.338	0.416	540.951	0.512	18	0.139	K.TIKPTVLIGTSGK.G
R5/RRR5-6/2	1540.463	1540.716	-164.414	0.376	872.877	0.285	16	0.122	K.YAESCMYSPLYR.N
R5/RRR5-6/3	1294.987	1294.528	355.427	0.490	1028.267	0.419	24	0.103	R.KISAHIAANVAAK.A
R5/RRR5-7/3	1294.750	1294.528	172.085	0.466	977.088	0.401	23	0.097	R.KISAHIAANVAAK.A
R5/RRR5-7/3	1294.758	1294.528	177.616	0.438	942.054	0.375	23	0.091	R.KISAHIAANVAAK.A
R5/RRR5-6/3	1294.427	1294.528	-78.292	0.441	942.123	0.368	22	0.089	-.KISAHIAANVAAK.-
R5/RRR5-6/3	1294.213	1294.528	-244.333	0.446	949.983	0.353	22	0.087	R.KISAHIAANVAAK.A
R5/RRR5-7/3	1295.311	1294.528	-168.035	0.424	662.276	0.336	20	0.080	R.KISAHIAANVAAK.A
R5/RRR5-8/2	1695.348	1695.849	-888.123	0.481	2179.130	0.469	22	0.285	K.LGYADLVEEVSVGESK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1446.370	1446.630	-180.612	0.548	1922.229	0.482	20	0.249	R.DAVTDLSLHYLAK.A
R5/RRR5-8/2	1446.590	1446.630	-27.474	0.521	1620.503	0.508	20	0.217	R.DAVTDLSLHYLAK.A
R5/RRR5-8/2	1446.294	1446.630	-233.362	0.507	1687.339	0.448	19	0.210	R.DAVTDLSLHYLAK.A
R5/RRR5-8/2	1331.020	1331.414	-297.082	0.474	1441.708	0.459	17	0.186	R.GSNQLVIDEAER.S
R5/RRR5-8/2	1330.948	1331.414	-351.281	0.449	1383.037	0.409	17	0.171	R.GSNQLVIDEAER.S
R5/RRR5-8/2	1289.211	1289.417	-160.368	0.468	1302.617	0.426	19	0.169	K.LGGTVDDTELIR.G
R5/RRR5-8/2	1330.475	1331.414	-1462.237	0.337	1095.321	0.383	17	0.145	R.GSNQLVIDEAER.S
R5/RRR5-8/2	1288.996	1289.417	-327.760	0.476	1080.803	0.365	18	0.144	K.LGGTVDDTELIR.G
R5/RRR5-8/2	1288.885	1289.417	-1192.424	0.397	979.119	0.369	19	0.140	K.LGGTVDDTELIR.G
R5/RRR5-8/2	1202.759	1203.407	-1374.415	0.384	1055.220	0.208	14	0.122	-.ASGCNVLLIQK.-
R5/RRR5-8/2	1202.326	1203.407	-1736.316	0.340	755.950	0.221	14	0.116	K.ASGCNVLLIQK.S
R5/RRR5-8/2	1327.687	1327.597	68.001	0.239	817.905	0.214	14	0.115	K.IAVIQFQVSPPK.T
R5/RRR5-8/2	1327.339	1327.597	-194.503	0.273	736.137	0.219	14	0.114	K.IAVIQFQVSPPK.T
R5/RRR5-9/2	1294.731	1295.420	-1308.557	0.436	2190.568	0.399	19	0.268	K.ADIEDYLASVAK.G
R5/RRR5-9/2	1295.597	1295.420	137.017	0.520	1885.839	0.465	19	0.241	K.ADIEDYLASVAK.G
R5/RRR5-9/2	1528.405	1528.733	-215.057	0.563	1387.219	0.458	20	0.179	R.KLAEDNNVPLSSIK.G
R5/RRR5-9/3	1650.283	1649.910	226.823	0.396	1776.591	0.359	27	0.172	R.ILKADIEDYLASVAK.G
R5/RRR5-9/2	1143.129	1143.402	-239.448	0.462	1037.737	0.333	16	0.137	K.KISINDLVIK.A
R5/RRR5-9/2	1014.669	1015.229	-1541.890	0.402	886.840	0.297	15	0.130	K.ISINDLVIK.A
R5/RRR5-9/2	1014.699	1015.229	-1511.678	0.403	919.303	0.233	15	0.124	K.ISINDLVIK.A
R5/RRR5-9/3	1649.952	1649.910	25.844	0.415	1329.716	0.396	26	0.123	R.ILKADIEDYLASVAK.G
R5/RRR5-9/2	1014.626	1015.229	-1584.673	0.427	775.649	0.242	14	0.122	K.ISINDLVIK.A
R5/RRR5-10/2	1015.388	1015.229	156.983	0.379	705.495	0.252	13	0.120	-.ISINDLVIK.-
R5/RRR5-9/3	1986.576	1987.203	-821.290	0.453	911.150	0.400	30	0.089	K.ETAAAPGLGYVDLPNTQIR.K
R5/RRR5-9/3	1143.079	1143.402	-283.172	0.417	1053.161	0.282	21	0.080	K.KISINDLVIK.A
R5/RRR5-9/3	1650.273	1649.910	221.038	0.270	749.410	0.233	20	0.063	-.ILKADIEDYLASVAK.-
R5/RRR5-9/3	1143.432	1143.402	26.585	0.411	767.599	0.203	18	0.060	-.KISINDLVIK.-
R5/RRR5-11/3	1492.834	1491.714	80.563	0.601	3430.412	0.440	31	0.662	K.KVSPEVIAEYTVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/3	1491.118	1491.714	-1073.408	0.565	3253.648	0.396	31	0.565	K.KVSPEVIAEYTVR.T
R5/RRR5-12/3	1491.590	1491.714	-83.334	0.560	3099.393	0.404	31	0.514	K.KVSPEVIAEYTVR.T
R5/RRR5-12/3	1491.963	1491.714	167.187	0.586	3013.724	0.432	30	0.502	K.KVSPEVIAEYTVR.T
R5/RRR5-11/3	1491.906	1491.714	129.033	0.568	2795.749	0.413	29	0.422	K.KVSPEVIAEYTVR.T
R5/RRR5-12/3	1491.310	1491.714	-271.523	0.531	2466.482	0.417	27	0.333	K.KVSPEVIAEYTVR.T
R5/RRR5-11/2	1570.182	1569.698	309.127	0.528	2061.922	0.530	25	0.284	K.GDAVLGEGASESLHVK.D
R5/RRR5-11/2	1569.281	1569.698	-266.567	0.545	2085.301	0.486	25	0.274	K.GDAVLGEGASESLHVK.D
R5/RRR5-12/2	1568.698	1569.698	-1278.971	0.522	2017.889	0.519	25	0.274	K.GDAVLGEGASESLHVK.D
R5/RRR5-10/3	1491.679	1491.714	-23.493	0.496	2279.633	0.372	27	0.266	K.KVSPEVIAEYTVR.T
R5/RRR5-11/2	1492.355	1491.714	-241.419	0.591	1738.707	0.595	21	0.254	K.KVSPEVIAEYTVR.T
R5/RRR5-11/2	1492.542	1491.714	-115.469	0.595	1726.987	0.600	21	0.254	K.KVSPEVIAEYTVR.T
R5/RRR5-11/2	1569.245	1569.698	-289.745	0.530	1873.581	0.509	24	0.249	K.GDAVLGEGASESLHVK.D
R5/RRR5-12/2	1491.419	1491.714	-197.979	0.574	1745.798	0.548	21	0.242	K.KVSPEVIAEYTVR.T
R5/RRR5-11/2	1492.310	1491.714	-271.537	0.605	1655.697	0.571	20	0.236	K.KVSPEVIAEYTVR.T
R5/RRR5-12/2	1491.284	1491.714	-288.883	0.528	1631.700	0.528	21	0.223	K.KVSPEVIAEYTVR.T
R5/RRR5-12/2	1568.758	1569.698	-1240.445	0.485	1566.012	0.482	23	0.203	K.GDAVLGEGASESLHVK.D
R5/RRR5-12/2	1492.425	1491.714	-194.318	0.569	1408.213	0.554	19	0.203	K.KVSPEVIAEYTVR.T
R5/RRR5-12/3	1312.805	1312.501	232.858	0.534	1595.411	0.423	24	0.160	K.KPWSLSFSFGR.A
R5/RRR5-12/2	1312.359	1312.501	-107.999	0.395	974.560	0.489	17	0.154	K.KPWSLSFSFGR.A
R5/RRR5-11/2	1364.145	1363.541	-290.855	0.493	769.855	0.480	18	0.146	K.VSPEVIAEYTVR.T
R5/RRR5-12/2	1312.271	1312.501	-175.557	0.370	751.703	0.500	18	0.144	K.KPWSLSFSFGR.A
R5/RRR5-11/2	1156.055	1155.240	-160.411	0.446	462.559	0.557	16	0.144	K.ANSEATLGTYK.G
R5/RRR5-12/3	1312.263	1312.501	-181.726	0.508	1430.894	0.430	22	0.142	K.KPWSLSFSFGR.A
R5/RRR5-11/2	1155.291	1155.240	44.129	0.468	545.466	0.493	16	0.140	K.ANSEATLGTYK.G
R5/RRR5-11/3	1312.211	1312.501	-221.061	0.499	1406.126	0.434	23	0.140	K.KPWSLSFSFGR.A
R5/RRR5-11/2	1363.059	1363.541	-354.683	0.404	770.657	0.418	17	0.136	K.VSPEVIAEYTVR.T
R5/RRR5-10/3	1491.586	1491.714	-85.797	0.413	1494.323	0.385	27	0.135	K.KVSPEVIAEYTVR.T
R5/RRR5-11/2	1363.176	1363.541	-268.788	0.429	694.478	0.385	17	0.132	K.VSPEVIAEYTVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1311.610	1312.501	-1445.555	0.280	675.780	0.398	17	0.128	K.KPWSLSFSFGR.A
R5/RRR5-11/2	1154.955	1155.240	-247.598	0.368	449.972	0.398	15	0.128	K.ANSEATLGTYK.G
R5/RRR5-11/2	1312.317	1312.501	-140.097	0.310	618.073	0.355	16	0.126	K.KPWSLSFSFGR.A
R5/RRR5-12/2	1363.245	1363.541	-217.940	0.341	616.571	0.321	16	0.124	K.VSPEVIAEYTVR.T
R5/RRR5-11/2	1311.558	1312.501	-1485.380	0.280	631.274	0.320	17	0.124	K.KPWSLSFSFGR.A
R5/RRR5-12/2	1363.182	1363.541	-264.296	0.262	690.820	0.332	16	0.123	K.VSPEVIAEYTVR.T
R5/RRR5-11/2	1154.909	1155.240	-287.151	0.356	229.908	0.367	14	0.122	-.ANSEATLGTYK.-
R5/RRR5-11/3	1312.307	1312.501	-147.992	0.494	1273.364	0.419	22	0.122	K.KPWSLSFSFGR.A
R5/RRR5-12/3	1312.491	1312.501	-7.204	0.435	1403.622	0.357	23	0.119	K.KPWSLSFSFGR.A
R5/RRR5-11/3	1312.072	1312.501	-327.884	0.325	973.924	0.256	21	0.073	K.KPWSLSFSFGR.A
R5/RRR5-10/3	1491.145	1491.714	-1055.161	0.341	952.507	0.159	23	0.064	K.KVSPEVIAEYTVR.T
R5/RRR5-10/2	1116.818	1117.278	-412.823	0.439	1777.125	0.553	19	0.247	K.ALESAGLALGSK.S
R5/RRR5-10/2	1117.252	1117.278	-23.080	0.514	1665.495	0.593	19	0.243	K.ALESAGLALGSK.S
R5/RRR5-10/2	1298.174	1298.471	-229.053	0.492	1660.953	0.587	21	0.241	R.LLAGESGIGPIDR.F
R5/RRR5-10/2	1118.291	1117.278	11.539	0.430	1497.761	0.595	19	0.220	K.ALESAGLALGSK.S
R5/RRR5-10/2	1297.503	1298.471	-1521.287	0.392	1432.562	0.585	20	0.208	R.LLAGESGIGPIDR.F
R5/RRR5-10/2	1298.334	1298.471	-105.394	0.501	1462.410	0.525	20	0.203	R.LLAGESGIGPIDR.F
R5/RRR5-10/2	1161.035	1160.215	-155.610	0.432	1330.398	0.504	17	0.184	R.GFSSEGYIDGK.N
R5/RRR5-10/2	1122.346	1123.233	-1685.722	0.356	1307.745	0.401	17	0.162	R.SDGLGVSSCIK.Q
R5/RRR5-10/2	1122.955	1123.233	-248.329	0.494	1119.319	0.429	17	0.156	R.SDGLGVSSCIK.Q
R5/RRR5-10/2	1545.176	1545.592	-270.487	0.394	936.050	0.364	16	0.131	R.GFSSEGYIDGKNDR.R
R5/RRR5-10/2	1055.200	1055.125	70.825	0.456	761.640	0.331	14	0.129	R.FDASNFPTR.F
R5/RRR5-10/2	1160.143	1160.215	-62.330	0.344	690.738	0.322	16	0.124	R.GFSSEGYIDGK.N
R5/RRR5-10/2	1055.045	1055.125	-76.083	0.402	970.578	0.183	14	0.119	R.FDASNFPTR.F
R5/RRR5-8/2	1240.261	1240.477	-175.187	0.567	2300.283	0.427	18	0.290	R.ALNILADILQR.S
R5/RRR5-7/2	1240.238	1240.477	-193.947	0.488	2294.375	0.408	18	0.285	R.ALNILADILQR.S
R5/RRR5-8/2	1239.711	1240.477	-1429.050	0.472	2243.748	0.404	18	0.276	R.ALNILADILQR.S
R5/RRR5-8/2	1240.275	1240.477	-164.030	0.569	2058.716	0.433	18	0.254	R.ALNILADILQR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1240.413	1240.477	-52.276	0.468	1987.583	0.432	16	0.244	R.ALNILADILQR.S
R5/RRR5-7/2	1240.273	1240.477	-165.708	0.465	1728.446	0.444	16	0.213	R.ALNILADILQR.S
R5/RRR5-2/2	1239.810	1240.477	-1348.648	0.469	1780.221	0.399	17	0.210	R.ALNILADILQR.S
R5/RRR5-8/2	1188.932	1189.344	-347.827	0.456	1597.568	0.405	19	0.192	R.IDAVDATTVKR.V
R5/RRR5-8/2	1251.014	1251.372	-287.699	0.447	1340.721	0.475	16	0.181	K.YIETHYTAPR.M
R5/RRR5-8/2	1212.568	1212.469	82.029	0.460	1386.292	0.413	17	0.174	R.RIPIPELFAR.I
R5/RRR5-8/2	1250.395	1251.372	-1586.042	0.457	1240.452	0.479	16	0.173	K.YIETHYTAPR.M
R5/RRR5-8/2	1188.536	1189.344	-1526.121	0.517	1154.338	0.469	17	0.165	R.IDAVDATTVKR.V
R5/RRR5-8/2	1189.033	1189.344	-262.640	0.490	1111.881	0.474	17	0.163	R.IDAVDATTVKR.V
R5/RRR5-8/2	1251.210	1251.372	-130.304	0.452	1134.897	0.460	16	0.162	K.YIETHYTAPR.M
R5/RRR5-8/2	1212.336	1212.469	-109.840	0.479	1181.115	0.407	16	0.157	R.RIPIPELFAR.I
R5/RRR5-7/2	1212.984	1212.469	-400.887	0.462	1051.390	0.407	15	0.149	R.RIPIPELFAR.I
R5/RRR5-8/2	1211.999	1212.469	-388.485	0.439	1027.032	0.407	15	0.147	R.RIPIPELFAR.I
R5/RRR5-7/2	1212.361	1212.469	-89.135	0.437	977.243	0.389	15	0.143	R.RIPIPELFAR.I
R5/RRR5-8/2	1056.173	1056.282	-104.171	0.362	460.091	0.496	14	0.133	-.IPIPELFAR.-
R5/RRR5-8/2	1056.128	1056.282	-146.490	0.345	504.928	0.414	14	0.130	R.IPIPELFAR.I
R5/RRR5-8/2	960.841	961.205	-379.107	0.400	744.788	0.354	15	0.128	R.MVITAAGAVK.H
R5/RRR5-7/2	1212.248	1212.469	-182.972	0.428	793.318	0.306	14	0.127	R.RIPIPELFAR.I
R5/RRR5-18/2	1212.961	1212.469	407.232	0.331	352.916	0.327	12	0.125	R.RIPIPELFAR.I
R5/RRR5-2/2	1240.206	1240.477	-219.323	0.403	492.075	0.341	13	0.125	R.ALNILADILQR.S
R5/RRR5-8/2	1055.700	1056.282	-1503.592	0.327	575.766	0.313	14	0.124	R.IPIPELFAR.I
R5/RRR5-5/2	1240.377	1240.477	-80.903	0.303	586.458	0.333	12	0.122	R.ALNILADILQR.S
R5/RRR5-8/3	1240.441	1240.477	-29.732	0.427	1497.361	0.288	25	0.113	R.ALNILADILQR.S
R5/RRR5-8/3	1212.379	1212.469	-74.047	0.376	1087.386	0.353	22	0.090	R.RIPIPELFAR.I
R5/RRR5-8/3	1212.694	1212.469	186.152	0.394	983.698	0.334	21	0.083	R.RIPIPELFAR.I
R5/RRR5-13/2	1245.445	1245.368	61.775	0.525	1911.906	0.441	20	0.237	K.SINDIAASQGIR.I
R5/RRR5-12/2	1245.024	1245.368	-276.889	0.547	1767.044	0.451	20	0.221	K.SINDIAASQGIR.I
R5/RRR5-13/2	1442.189	1441.565	-262.042	0.530	1623.727	0.522	20	0.221	R.SLETFVVDTSNTK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1245.072	1245.368	-238.429	0.548	1731.866	0.456	20	0.218	K.SINDIAASQGIR.I
R5/RRR5-12/2	1245.047	1245.368	-258.199	0.555	1579.523	0.477	19	0.205	K.SINDIAASQGIR.I
R5/RRR5-13/2	1245.117	1245.368	-202.332	0.488	1595.806	0.436	19	0.198	K.SINDIAASQGIR.I
R5/RRR5-12/2	1610.838	1610.883	-27.941	0.481	1408.599	0.451	22	0.181	R.VLNISGVQLIGINNR.S
R5/RRR5-12/2	1346.080	1346.515	-324.320	0.360	1101.010	0.528	17	0.165	R.DFYGALASAFKR.N
R5/RRR5-12/2	1610.096	1610.883	-1113.011	0.365	1400.123	0.320	21	0.157	R.VLNISGVQLIGINNR.S
R5/RRR5-12/2	1346.215	1346.515	-223.880	0.375	886.109	0.513	16	0.149	R.DFYGALASAFKR.N
R5/RRR5-12/2	1345.931	1346.515	-1180.455	0.270	990.016	0.481	16	0.146	R.DFYGALASAFKR.N
R5/RRR5-14/2	1610.818	1610.883	-40.559	0.408	904.516	0.378	18	0.134	R.VLNISGVQLIGINNR.S
R5/RRR5-12/3	1775.875	1776.073	-111.705	0.557	1309.595	0.445	33	0.134	K.KPLKEVIEAAGQAPPAR.D
R5/RRR5-13/2	1610.565	1610.883	-197.929	0.361	1137.403	0.257	19	0.131	R.VLNISGVQLIGINNR.S
R5/RRR5-12/3	1775.979	1776.073	-53.272	0.512	1239.298	0.460	32	0.130	K.KPLKEVIEAAGQAPPAR.D
R5/RRR5-13/2	1652.436	1652.786	-212.548	0.457	835.751	0.360	17	0.129	R.ENFNPVEIAQAYEK.N
R5/RRR5-13/2	1610.342	1610.883	-959.790	0.373	1165.331	0.221	20	0.128	R.VLNISGVQLIGINNR.S
R5/RRR5-12/2	1653.250	1652.786	281.672	0.468	865.171	0.322	18	0.126	R.ENFNPVEIAQAYEK.N
R5/RRR5-12/3	1776.261	1776.073	106.067	0.542	1226.562	0.442	33	0.124	K.KPLKEVIEAAGQAPPAR.D
R5/RRR5-11/2	1556.419	1556.788	-237.775	0.463	1670.629	0.500	21	0.219	R.GVLFATEALLAEHGK.G
R5/RRR5-11/2	1174.304	1173.385	-68.356	0.531	1355.595	0.551	20	0.199	K.VIAISDVTGAVK.N
R5/RRR5-11/2	1173.210	1173.385	-149.299	0.492	1343.182	0.504	20	0.188	K.VIAISDVTGAVK.N
R5/RRR5-11/2	1162.123	1162.320	-170.109	0.437	1420.123	0.453	20	0.184	K.TAVANIPYGGAK.G
R5/RRR5-11/2	1174.190	1173.385	-165.962	0.533	1152.522	0.554	19	0.181	K.VIAISDVTGAVK.N
R5/RRR5-11/2	1162.061	1162.320	-223.852	0.494	1380.486	0.430	19	0.176	K.TAVANIPYGGAK.G
R5/RRR5-11/2	1119.829	1120.154	-290.898	0.401	1334.605	0.388	18	0.164	K.GFDGGDAIDPR.S
R5/RRR5-11/2	1746.731	1747.879	-1233.288	0.496	1254.531	0.427	23	0.162	K.GGIGCSPGDLSISELER.L
R5/RRR5-11/2	1747.330	1747.879	-889.380	0.502	1211.908	0.411	23	0.156	K.GGIGCSPGDLSISELER.L
R5/RRR5-11/2	1557.981	1556.788	124.590	0.402	938.588	0.459	16	0.143	R.GVLFATEALLAEHGK.G
R5/RRR5-11/2	1119.818	1120.154	-300.960	0.428	908.072	0.427	15	0.142	K.GFDGGDAIDPR.S
R5/RRR5-11/2	1161.427	1162.320	-1634.691	0.359	921.751	0.393	16	0.137	K.TAVANIPYGGAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1558.262	1556.788	305.442	0.411	776.735	0.388	16	0.128	R.GVLFATEALLAEHGK.G
R5/RRR5-11/2	1081.327	1082.259	-1792.159	0.310	621.223	0.415	12	0.124	R.M*GAFTLGVNR.V
R5/RRR5-9/2	1124.101	1124.318	-194.488	0.540	1555.505	0.563	17	0.224	R.LPANLIQAQR.D
R5/RRR5-8/2	1257.244	1257.423	-142.923	0.488	2030.489	0.309	17	0.220	K.GWNLNLAELAR.I
R5/RRR5-9/2	1123.960	1124.318	-319.785	0.565	1545.442	0.544	17	0.218	R.LPANLIQAQR.D
R5/RRR5-9/2	1124.125	1124.318	-172.591	0.579	1485.240	0.528	17	0.208	R.LPANLIQAQR.D
R5/RRR5-8/2	1124.083	1124.318	-210.393	0.534	1472.407	0.532	17	0.207	R.LPANLIQAQR.D
R5/RRR5-8/2	1123.904	1124.318	-369.477	0.507	1424.434	0.518	17	0.199	R.LPANLIQAQR.D
R5/RRR5-9/2	1256.950	1257.423	-377.319	0.496	1348.157	0.398	17	0.167	K.GWNLNLAELAR.I
R5/RRR5-9/2	1056.127	1056.284	-149.620	0.389	1003.733	0.383	14	0.139	R.TVVLLVQAGR.A
R5/RRR5-9/2	1256.547	1257.423	-1497.597	0.418	1048.928	0.335	17	0.139	K.GWNLNLAELAR.I
R5/RRR5-9/2	1209.774	1209.292	399.095	0.377	666.486	0.314	14	0.124	R.DLFGAHTYER.I
R5/RRR5-9/2	1209.193	1209.292	-82.686	0.349	808.652	0.257	15	0.122	R.DLFGAHTYER.I
R5/RRR5-9/2	1209.650	1209.292	296.098	0.319	528.658	0.299	14	0.122	R.DLFGAHTYER.I
R5/RRR5-9/2	1132.136	1132.341	-181.211	0.318	772.692	0.187	13	0.103	-.GFVLSLSRPR.-
R5/RRR5-9/3	1574.029	1574.722	-1078.551	0.468	1061.043	0.380	24	0.097	R.IDRPGSFHTEWTK.L
R5/RRR5-9/3	1574.836	1574.722	72.597	0.424	802.705	0.441	23	0.094	R.IDRPGSFHTEWTK.L
R5/RRR5-9/3	1574.805	1574.722	53.356	0.486	883.306	0.400	24	0.092	R.IDRPGSFHTEWTK.L
R5/RRR5-24/2	1369.332	1369.592	-190.147	0.468	1966.406	0.384	19	0.231	R.LVVIVDVVDQNR.A
R5/RRR5-24/2	1355.080	1355.524	-328.310	0.420	1365.290	0.559	18	0.197	R.VALVNYGKDYGR.L
R5/RRR5-24/2	1355.150	1355.524	-276.885	0.496	1299.355	0.489	18	0.179	R.VALVNYGKDYGR.L
R5/RRR5-24/2	1356.183	1355.524	-251.847	0.447	1301.082	0.485	18	0.178	R.VALVNYGKDYGR.L
R5/RRR5-24/3	1369.556	1369.592	-26.571	0.482	1562.984	0.390	25	0.149	R.LVVIVDVVDQNR.A
R5/RRR5-24/2	1102.938	1103.275	-306.251	0.391	1016.958	0.389	16	0.144	R.ALVDAPDM*VR.C
R5/RRR5-23/2	864.108	864.024	97.255	0.405	540.537	0.515	12	0.141	R.VALVNYGK.D
R5/RRR5-24/2	1102.281	1103.275	-1813.951	0.313	1068.596	0.349	16	0.140	R.ALVDAPDM*VR.C
R5/RRR5-25/2	863.886	864.024	-160.097	0.378	564.522	0.480	13	0.139	R.VALVNYGK.D
R5/RRR5-24/2	863.876	864.024	-172.288	0.371	540.843	0.493	12	0.138	R.VALVNYGK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	863.962	864.024	-71.369	0.369	575.234	0.455	13	0.137	R.VALVNYGK.D
R5/RRR5-24/2	1102.909	1103.275	-332.680	0.419	686.111	0.420	14	0.135	R.ALVDAPDM*VR.C
R5/RRR5-24/2	863.555	864.024	-544.104	0.307	530.090	0.437	12	0.131	R.VALVNYGK.D
R5/RRR5-24/2	1086.948	1087.275	-301.613	0.360	731.720	0.371	13	0.129	R.ALVDAPDMVR.C
R5/RRR5-24/2	863.904	864.024	-139.402	0.313	459.443	0.418	11	0.129	R.VALVNYGK.D
R5/RRR5-24/2	1259.004	1259.517	-1205.749	0.430	746.562	0.324	16	0.126	-.LSLTDIKIDIK.-
R5/RRR5-25/2	863.376	864.024	-1914.966	0.297	547.680	0.349	11	0.125	R.VALVNYGK.D
R5/RRR5-23/2	1369.171	1369.592	-308.120	0.303	633.066	0.403	13	0.124	R.LVVIVDVVDQNR.A
R5/RRR5-24/2	1258.701	1259.517	-1447.664	0.396	854.484	0.248	17	0.122	-.LSLTDIKIDIK.-
R5/RRR5-24/2	1259.556	1259.517	31.047	0.361	792.382	0.244	17	0.121	-.LSLTDIKIDIK.-
R5/RRR5-24/2	1087.005	1087.275	-249.671	0.323	682.597	0.261	12	0.119	-.ALVDAPDMVR.-
R5/RRR5-24/3	1369.463	1369.592	-94.699	0.445	986.620	0.444	21	0.103	R.LVVIVDVVDQNR.A
R5/RRR5-10/2	1511.061	1511.657	-1059.557	0.314	1974.147	0.187	21	0.188	K.ELDYFAQALESPK.R
R5/RRR5-10/2	1399.382	1399.575	-138.205	0.459	1519.002	0.360	18	0.173	K.AADGDIVLLENLR.F
R5/RRR5-10/2	1399.216	1399.575	-257.402	0.397	1380.724	0.329	17	0.156	K.AADGDIVLLENLR.F
R5/RRR5-10/2	1232.489	1232.367	99.181	0.444	822.943	0.420	17	0.139	R.VDFNVPLDANK.N
R5/RRR5-10/3	1649.542	1649.788	-150.061	0.469	1138.234	0.536	27	0.137	K.LGDVYINDAFGTAHR.A
R5/RRR5-10/2	1399.526	1399.575	-34.872	0.361	1130.298	0.283	15	0.132	K.AADGDIVLLENLR.F
R5/RRR5-10/2	1143.459	1143.406	45.763	0.448	770.451	0.310	16	0.126	K.RPFLAILGGAK.V
R5/RRR5-10/2	1144.332	1143.406	-65.118	0.413	751.368	0.305	16	0.125	K.RPFLAILGGAK.V
R5/RRR5-10/2	1144.246	1143.406	-140.666	0.407	661.103	0.289	16	0.122	-.RPFLAILGGAK.-
R5/RRR5-10/2	1231.526	1232.367	-1499.491	0.349	468.147	0.290	13	0.119	R.VDFNVPLDANK.N
R5/RRR5-10/3	1649.366	1649.788	-256.638	0.379	907.553	0.532	26	0.112	K.LGDVYINDAFGTAHR.A
R5/RRR5-10/3	1385.630	1385.572	42.019	0.428	1103.009	0.248	25	0.077	-.AHSSM*VGVDLPQK.-
R5/RRR5-4/2	1760.379	1760.968	-904.904	0.523	3265.905	0.509	25	0.534	K.FTSAFQEIVDAYGIAK.Y
R5/RRR5-4/2	1760.448	1760.968	-865.782	0.560	2909.701	0.563	24	0.465	K.FTSAFQEIVDAYGIAK.Y
R5/RRR5-4/2	1760.344	1760.968	-925.162	0.512	2955.980	0.515	24	0.458	K.FTSAFQEIVDAYGIAK.Y
R5/RRR5-4/2	1695.067	1695.854	-1057.073	0.439	1748.108	0.350	19	0.195	K.NISSEFEQWNTLVK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1695.633	1695.854	-130.666	0.499	1477.573	0.388	18	0.173	K.NISSEFEQWNTLVK.K
R5/RRR5-4/3	1931.174	1931.146	14.980	0.468	1401.542	0.500	31	0.161	K.VRPAYSFGVDPVWHGSR.S
R5/RRR5-6/2	1760.599	1760.968	-209.922	0.449	1103.863	0.479	21	0.160	K.FTSAFQEIVDAYGIAK.Y
R5/RRR5-4/2	1302.193	1303.447	-1736.198	0.328	986.621	0.410	15	0.141	K.NAFVIFYSGER.A
R5/RRR5-4/2	971.643	971.176	481.911	0.393	735.932	0.462	16	0.140	K.LGSLSGLVPK.E
R5/RRR5-4/2	970.651	971.176	-1575.800	0.418	745.286	0.433	16	0.139	K.LGSLSGLVPK.E
R5/RRR5-6/2	1760.526	1760.968	-251.449	0.362	881.496	0.415	16	0.135	K.FTSAFQEIVDAYGIAK.Y
R5/RRR5-4/2	970.507	971.176	-1725.279	0.357	550.269	0.439	15	0.132	K.LGSLSGLVPK.E
R5/RRR5-5/2	1760.394	1760.968	-896.481	0.337	944.987	0.332	17	0.129	K.FTSAFQEIVDAYGIAK.Y
R5/RRR5-22/2	1613.954	1614.776	-1132.579	0.221	1176.954	0.329	16	0.125	K.FVPFAFASIIEEED.-
R5/RRR5-4/2	1302.168	1303.447	-1755.977	0.213	654.947	0.264	13	0.115	K.NAFVIFYSGER.A
R5/RRR5-4/3	1931.767	1931.146	-196.494	0.429	901.699	0.451	24	0.098	K.VRPAYSFGVDPVWHGSR.S
R5/RRR5-11/2	1637.728	1638.910	-1336.754	0.455	1695.638	0.563	25	0.238	R.TPMGGFLGALSSLSATK.L
R5/RRR5-11/2	1942.187	1942.207	-10.251	0.483	1642.336	0.576	23	0.233	R.NSGAFAWEIVPIEVPVGR.G
R5/RRR5-11/2	1639.412	1638.910	-304.678	0.544	1453.594	0.651	23	0.228	R.TPMGGFLGALSSLSATK.L
R5/RRR5-11/2	1656.145	1654.910	142.467	0.502	1590.623	0.566	24	0.225	R.TPM*GGFLGALSSLSATK.L
R5/RRR5-11/2	1637.791	1638.910	-1297.679	0.419	1564.939	0.563	24	0.220	R.TPMGGFLGALSSLSATK.L
R5/RRR5-11/2	1538.978	1539.543	-1020.049	0.439	1612.709	0.504	19	0.213	R.EDQDAYAIQSNER.G
R5/RRR5-11/2	1942.593	1942.207	199.632	0.535	1321.376	0.589	23	0.199	R.NSGAFAWEIVPIEVPVGR.G
R5/RRR5-10/2	1198.180	1198.397	-181.952	0.489	1511.985	0.447	17	0.192	K.AQELGLQVIAR.I
R5/RRR5-11/2	1089.022	1089.185	-149.710	0.486	1236.920	0.578	17	0.191	K.ALANAGLESSR.V
R5/RRR5-11/2	1088.584	1089.185	-1474.479	0.407	1369.573	0.517	17	0.190	K.ALANAGLESSR.V
R5/RRR5-11/2	1656.074	1654.910	99.667	0.479	1147.467	0.598	21	0.183	R.TPM*GGFLGALSSLSATK.L
R5/RRR5-11/3	1941.553	1942.207	-854.335	0.312	1790.769	0.379	33	0.181	R.NSGAFAWEIVPIEVPVGR.G
R5/RRR5-11/2	1088.924	1089.185	-240.349	0.497	1187.776	0.539	17	0.180	K.ALANAGLESSR.V
R5/RRR5-11/3	1960.191	1960.180	5.389	0.523	1339.958	0.525	36	0.160	K.INVHGGAVSLGHPLGCSGAR.I
R5/RRR5-11/2	1941.549	1942.207	-856.158	0.500	846.449	0.563	20	0.154	R.NSGAFAWEIVPIEVPVGR.G
R5/RRR5-11/3	1959.768	1960.180	-210.898	0.491	1298.705	0.491	33	0.145	K.INVHGGAVSLGHPLGCSGAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1198.419	1198.397	18.021	0.250	583.012	0.204	13	0.114	K.AQELGLQVIAR.I
R5/RRR5-11/3	1941.261	1942.207	-1004.981	0.328	1320.728	0.302	29	0.099	R.NSGAFAWEIVPIEVPVGR.G
R5/RRR5-11/3	1941.575	1942.207	-842.595	0.293	1040.805	0.286	27	0.077	R.NSGAFAWEIVPIEVPVGR.G
R5/RRR5-11/3	1959.809	1960.180	-189.996	0.393	589.906	0.343	26	0.075	K.INVHGGAVSLGHPLGCSGAR.I
R5/RRR5-8/2	1970.189	1970.240	-26.139	0.568	1453.938	0.520	22	0.197	R.EGNFDLVGNNMPVFFIR.D
R5/RRR5-8/2	1150.717	1151.384	-1452.960	0.440	946.377	0.554	17	0.163	R.APGVQTPIIVR.F
R5/RRR5-8/2	1151.004	1151.384	-330.993	0.455	901.743	0.528	17	0.158	R.APGVQTPIIVR.F
R5/RRR5-8/2	1986.766	1986.240	-239.277	0.565	1053.912	0.489	20	0.156	R.EGNFDLVGNNM*PVFFIR.D
R5/RRR5-8/2	1151.063	1151.384	-279.707	0.480	837.345	0.523	16	0.153	R.APGVQTPIIVR.F
R5/RRR5-9/2	1515.469	1515.802	-220.427	0.493	955.100	0.468	18	0.149	R.LGPNYLM*LPANAPK.C
R5/RRR5-9/2	1515.469	1515.802	-220.427	0.458	1008.915	0.442	17	0.147	R.LGPNYLM*LPANAPK.C
R5/RRR5-8/2	1970.462	1970.240	113.112	0.565	832.592	0.525	18	0.147	R.EGNFDLVGNNMPVFFIR.D
R5/RRR5-9/2	1515.359	1515.802	-293.484	0.409	911.765	0.436	17	0.141	R.LGPNYLM*LPANAPK.C
R5/RRR5-8/2	1986.437	1986.240	99.745	0.518	789.185	0.480	17	0.138	R.EGNFDLVGNNM*PVFFIR.D
R5/RRR5-8/2	1969.343	1970.240	-966.117	0.471	831.096	0.454	17	0.137	R.EGNFDLVGNNMPVFFIR.D
R5/RRR5-8/2	1985.129	1986.240	-1066.252	0.468	678.761	0.447	16	0.130	R.EGNFDLVGNNM*PVFFIR.D
R5/RRR5-1/2	1151.387	1151.384	3.125	0.361	585.329	0.427	14	0.130	R.APGVQTPIIVR.F
R5/RRR5-9/2	1969.512	1970.240	-880.245	0.420	697.268	0.373	16	0.124	R.EGNFDLVGNNMPVFFIR.D
R5/RRR5-8/2	1514.859	1515.802	-1286.338	0.237	653.875	0.264	14	0.115	R.LGPNYLM*LPANAPK.C
R5/RRR5-8/2	1680.396	1680.796	-238.812	0.334	922.547	0.197	17	0.115	K.DLTDSIAAGNYPEWK.L
R5/RRR5-8/2	1680.541	1680.796	-152.458	0.333	630.489	0.242	14	0.112	K.DLTDSIAAGNYPEWK.L
R5/RRR5-9/3	1144.722	1144.351	324.272	0.473	826.858	0.374	19	0.088	R.HAEKVPIPPR.V
R5/RRR5-9/3	1144.130	1144.351	-194.519	0.399	666.833	0.361	18	0.084	R.HAEKVPIPPR.V
R5/RRR5-9/3	1144.496	1144.351	126.318	0.385	874.635	0.343	19	0.083	R.HAEKVPIPPR.V
R5/RRR5-8/3	1144.739	1144.351	339.829	0.437	755.884	0.357	19	0.082	-.HAEKVPIPPR.-
R5/RRR5-8/3	1144.485	1144.351	116.691	0.380	654.647	0.299	17	0.078	R.HAEKVPIPPR.V
R5/RRR5-8/3	1144.372	1144.351	18.004	0.394	704.702	0.303	18	0.076	-.HAEKVPIPPR.-
R5/RRR5-8/3	1144.210	1144.351	-123.561	0.379	487.052	0.311	16	0.073	-.HAEKVPIPPR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1377.302	1377.480	-129.220	0.424	2391.470	0.511	22	0.337	R.DVADADSLVSSLGK.A
R5/RRR5-9/2	1192.145	1192.346	-169.830	0.490	1280.581	0.526	18	0.186	K.VGGIEVDSLFR.T
R5/RRR5-9/2	1819.644	1818.148	273.207	0.519	820.860	0.603	23	0.162	R.TSIPGIFAIGDVAAFPLK.M
R5/RRR5-9/2	1402.455	1402.536	-57.323	0.432	1050.143	0.472	19	0.155	K.GALIDKLEAGSDGR.V
R5/RRR5-8/2	1817.730	1818.148	-230.806	0.455	871.103	0.522	23	0.152	R.TSIPGIFAIGDVAAFPLK.M
R5/RRR5-9/2	1312.268	1311.425	-119.483	0.440	796.661	0.506	17	0.148	K.IATFWIDSDSR.L
R5/RRR5-9/2	1817.511	1818.148	-903.742	0.428	799.217	0.518	22	0.146	R.TSIPGIFAIGDVAAFPLK.M
R5/RRR5-9/2	1403.171	1402.536	-260.777	0.455	881.956	0.444	18	0.142	K.GALIDKLEAGSDGR.V
R5/RRR5-9/2	1817.480	1818.148	-920.801	0.422	671.976	0.518	20	0.139	R.TSIPGIFAIGDVAAFPLK.M
R5/RRR5-9/2	1362.202	1362.468	-195.996	0.434	959.536	0.366	17	0.136	K.SATSVEDALEIAR.S
R5/RRR5-9/2	1310.795	1311.425	-1246.751	0.344	457.628	0.429	13	0.126	K.IATFWIDSDSR.L
R5/RRR5-9/2	1362.109	1362.468	-264.863	0.422	1055.897	0.234	16	0.123	K.SATSVEDALEIAR.S
R5/RRR5-1/2	1192.373	1192.346	22.528	0.361	577.752	0.302	14	0.121	K.VGGIEVDSLFR.T
R5/RRR5-9/2	1362.039	1362.468	-316.115	0.347	888.454	0.172	16	0.114	K.SATSVEDALEIAR.S
R5/RRR5-5/2	1829.390	1829.987	-875.520	0.547	2716.070	0.529	25	0.411	R.VYLEQYGASEDAWIGK.G
R5/RRR5-5/2	1457.707	1458.513	-1242.469	0.527	2234.493	0.559	23	0.322	R.VYGSSSNDVSSVTR.Q
R5/RRR5-5/2	1458.166	1458.513	-238.431	0.489	2035.447	0.548	23	0.285	R.VYGSSSNDVSSVTR.Q
R5/RRR5-6/2	1458.098	1458.513	-285.381	0.525	1925.502	0.560	22	0.271	R.VYGSSSNDVSSVTR.Q
R5/RRR5-6/2	1457.716	1458.513	-1236.750	0.484	1956.896	0.526	22	0.266	R.VYGSSSNDVSSVTR.Q
R5/RRR5-6/2	1458.193	1458.513	-220.122	0.504	1878.896	0.538	22	0.258	R.VYGSSSNDVSSVTR.Q
R5/RRR5-5/2	1666.184	1666.821	-984.866	0.488	1133.830	0.509	21	0.167	R.NNLQAHGVTEQSVLR.A
R5/RRR5-6/2	1350.292	1349.519	-168.528	0.460	1029.955	0.417	14	0.145	R.GLAYIQDNLWR.L
R5/RRR5-6/2	1349.243	1349.519	-205.501	0.414	1167.943	0.336	14	0.142	R.GLAYIQDNLWR.L
R5/RRR5-5/3	1666.341	1666.821	-288.521	0.495	1226.323	0.444	27	0.124	R.NNLQAHGVTEQSVLR.A
R5/RRR5-6/2	1597.466	1597.798	-208.826	0.334	1009.590	0.255	17	0.122	R.AYFLAAANIFEPNR.A
R5/RRR5-5/3	1667.137	1666.821	190.380	0.525	1145.123	0.425	27	0.113	R.NNLQAHGVTEQSVLR.A
R5/RRR5-6/3	1366.306	1366.591	-209.128	0.408	1004.703	0.467	27	0.108	R.TAILAEAIASHLR.Q
R5/RRR5-6/3	1367.473	1366.591	-86.779	0.434	1074.607	0.423	28	0.105	R.TAILAEAIASHLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1666.686	1666.821	-80.860	0.464	946.266	0.461	26	0.105	R.NNLQAHGVTEQSVLR.A
R5/RRR5-5/3	1366.541	1366.591	-37.068	0.336	1134.885	0.402	29	0.101	R.TAILAEAIASHLR.Q
R5/RRR5-5/3	1366.475	1366.591	-85.588	0.320	867.435	0.454	26	0.095	R.TAILAEAIASHLR.Q
R5/RRR5-6/3	1366.535	1366.591	-41.503	0.332	896.491	0.436	26	0.094	R.TAILAEAIASHLR.Q
R5/RRR5-5/3	1366.736	1366.591	106.047	0.371	965.500	0.384	27	0.091	R.TAILAEAIASHLR.Q
R5/RRR5-7/2	1043.862	1044.187	-311.833	0.481	1270.936	0.465	17	0.174	K.VVNDGVTIAR.A
R5/RRR5-7/2	1168.044	1168.371	-281.091	0.437	1192.023	0.488	17	0.168	K.LANAVGVTLGPR.G
R5/RRR5-7/2	1043.737	1044.187	-432.461	0.511	1102.641	0.479	16	0.164	K.VVNDGVTIAR.A
R5/RRR5-7/2	1043.863	1044.187	-311.364	0.462	1116.290	0.456	17	0.161	K.VVNDGVTIAR.A
R5/RRR5-7/2	1555.463	1554.856	-253.900	0.508	978.183	0.474	20	0.153	K.EILPILEKTTQLR.A
R5/RRR5-3/2	1497.906	1497.725	121.413	0.520	2489.575	0.444	21	0.332	R.SALLQGQALQALQR.F
R5/RRR5-3/2	1497.169	1497.725	-1042.647	0.465	2489.980	0.416	21	0.324	R.SALLQGQALQALQR.F
R5/RRR5-3/2	1496.840	1497.725	-1263.072	0.406	1623.382	0.400	18	0.191	R.SALLQGQALQALQR.F
R5/RRR5-3/2	948.979	949.129	-158.514	0.446	926.001	0.425	13	0.146	K.IEALVFTR.L
R5/RRR5-3/2	948.938	949.129	-201.228	0.445	953.098	0.403	13	0.144	K.IEALVFTR.L
R5/RRR5-3/2	1056.925	1057.229	-288.634	0.392	1092.802	0.364	16	0.144	K.SIQNVGLAVR.Y
R5/RRR5-3/2	1148.258	1148.377	-103.494	0.393	963.942	0.375	15	0.138	K.ATFEVVQLLK.N
R5/RRR5-3/2	948.672	949.129	-482.508	0.351	896.700	0.339	13	0.133	K.IEALVFTR.L
R5/RRR5-3/2	1056.915	1057.229	-297.556	0.342	1069.826	0.268	16	0.131	K.SIQNVGLAVR.Y
R5/RRR5-3/2	1148.261	1148.377	-101.361	0.347	838.963	0.331	14	0.128	K.ATFEVVQLLK.N
R5/RRR5-1/2	829.780	828.986	-249.528	0.324	995.631	0.198	11	0.120	-.KANRALR.-
R5/RRR5-3/3	1102.483	1102.271	192.490	0.455	330.558	0.522	15	0.102	R.VLRPNFEAR.T
R5/RRR5-2/3	1102.208	1102.271	-58.065	0.447	296.614	0.520	14	0.101	R.VLRPNFEAR.T
R5/RRR5-1/3	1101.729	1102.271	-1403.723	0.464	295.289	0.466	14	0.099	R.VLRPNFEAR.T
R5/RRR5-1/3	1102.088	1102.271	-166.556	0.451	291.846	0.392	14	0.096	R.VLRPNFEAR.T
R5/RRR5-3/3	1102.263	1102.271	-7.411	0.410	314.532	0.404	15	0.095	R.VLRPNFEAR.T
R5/RRR5-3/3	1102.286	1102.271	13.249	0.450	339.814	0.437	15	0.091	-.VLRPNFEAR.-
R5/RRR5-1/3	1102.369	1102.271	89.218	0.437	304.121	0.394	14	0.081	-.VLRPNFEAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1514.227	1514.706	-317.091	0.532	1472.109	0.567	21	0.213	R.KLAEDNNVPLSSVK.G
R5/RRR5-9/2	1232.528	1233.438	-1554.795	0.386	1171.222	0.471	17	0.163	R.VIDGAIGAEFLK.A
R5/RRR5-9/2	1233.152	1233.438	-232.691	0.400	1249.904	0.413	17	0.160	R.VIDGAIGAEFLK.A
R5/RRR5-9/2	1986.496	1987.203	-861.810	0.451	863.951	0.518	21	0.146	K.EALAAPGLSYTDVPNAQIR.K
R5/RRR5-9/3	1585.812	1585.744	42.602	0.420	1410.587	0.409	29	0.135	K.LRGELNPLQESSGGK.K
R5/RRR5-9/3	1586.024	1585.744	177.150	0.321	984.819	0.241	25	0.070	K.LRGELNPLQESSGGK.K
R5/RRR5-9/3	1585.622	1585.744	-77.272	0.296	823.744	0.207	25	0.064	K.LRGELNPLQESSGGK.K
R5/RRR5-5/2	1124.010	1123.284	-244.502	0.588	1644.077	0.520	17	0.223	K.LSEGYLTLAR.D
R5/RRR5-4/2	1122.389	1123.284	-1693.840	0.405	1691.392	0.422	17	0.205	K.LSEGYLTLAR.D
R5/RRR5-5/2	1123.116	1123.284	-150.071	0.448	1589.215	0.461	17	0.203	K.LSEGYLTLAR.D
R5/RRR5-4/2	1123.018	1123.284	-237.413	0.505	1498.787	0.454	17	0.193	K.LSEGYLTLAR.D
R5/RRR5-4/2	1370.481	1370.748	-194.901	0.468	1230.155	0.555	21	0.186	R.LLPVALGLLYLGK.Q
R5/RRR5-4/2	1123.250	1123.284	-30.369	0.417	1510.494	0.339	17	0.171	K.LSEGYLTLAR.D
R5/RRR5-5/2	1370.132	1370.748	-1182.928	0.405	977.779	0.600	19	0.170	R.LLPVALGLLYLGK.Q
R5/RRR5-5/2	1348.457	1348.486	-21.665	0.523	1272.436	0.453	16	0.168	R.NLAGEIAQEFQK.R
R5/RRR5-5/2	1122.913	1123.284	-331.532	0.328	1360.856	0.364	16	0.161	K.LSEGYLTLAR.D
R5/RRR5-4/2	1348.209	1348.486	-206.658	0.445	1151.294	0.410	17	0.154	R.NLAGEIAQEFQK.R
R5/RRR5-2/2	1123.248	1123.284	-32.440	0.363	1350.427	0.293	15	0.150	K.LSEGYLTLAR.D
R5/RRR5-4/2	1052.156	1052.163	-6.122	0.334	1143.920	0.356	14	0.143	K.FEDLTSALR.I
R5/RRR5-5/2	1348.454	1348.486	-24.208	0.335	841.080	0.406	15	0.134	R.NLAGEIAQEFQK.R
R5/RRR5-4/2	899.983	900.098	-128.032	0.318	938.073	0.326	13	0.130	R.IALLLDNK.S
R5/RRR5-4/2	1370.249	1370.748	-365.064	0.261	574.142	0.436	14	0.124	R.LLPVALGLLYLGK.Q
R5/RRR5-4/2	1348.002	1348.486	-360.734	0.245	619.284	0.343	15	0.121	R.NLAGEIAQEFQK.R
R5/RRR5-1/2	1123.075	1123.284	-186.380	0.246	624.830	0.168	12	0.115	-.LSEGYLTLAR.-
R5/RRR5-4/2	1370.269	1370.748	-350.583	0.156	468.897	0.374	13	0.114	R.LLPVALGLLYLGK.Q
R5/RRR5-4/3	1232.525	1232.459	54.167	0.413	974.462	0.241	20	0.072	K.FLRPHYGTLK.S
R5/RRR5-4/3	1232.813	1232.459	288.190	0.375	1182.762	0.187	22	0.071	-.FLRPHYGTLK.-
R5/RRR5-7/2	1202.238	1202.419	-151.499	0.523	1909.575	0.512	20	0.256	R.LLAVEGCAALGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1202.255	1202.419	-137.443	0.478	1941.766	0.478	20	0.251	R.LLAVEGCAALGK.L
R5/RRR5-6/2	1203.169	1202.419	-208.979	0.430	1686.374	0.511	19	0.224	R.LLAVEGCAALGK.L
R5/RRR5-7/2	1201.387	1202.419	-1696.602	0.403	1837.962	0.382	19	0.213	R.LLAVEGCAALGK.L
R5/RRR5-7/2	1203.298	1202.419	-100.897	0.549	1516.034	0.519	19	0.208	R.LLAVEGCAALGK.L
R5/RRR5-6/2	1202.187	1202.419	-193.567	0.407	1718.435	0.382	19	0.199	R.LLAVEGCAALGK.L
R5/RRR5-7/2	1123.120	1122.258	-123.253	0.516	1299.499	0.498	17	0.183	R.LAAGEWFTAR.V
R5/RRR5-7/2	1284.222	1284.442	-172.145	0.498	1397.694	0.457	18	0.183	K.FAATVEQNYLK.T
R5/RRR5-7/2	1285.244	1284.442	-154.480	0.492	1324.457	0.485	18	0.182	K.FAATVEQNYLK.T
R5/RRR5-7/2	1122.195	1122.258	-56.255	0.396	1327.510	0.489	17	0.181	R.LAAGEWFTAR.V
R5/RRR5-7/2	1533.426	1533.749	-211.319	0.355	1579.662	0.338	19	0.175	K.ESDIVDWFVPVVK.R
R5/RRR5-6/2	1285.315	1284.442	-99.793	0.522	1307.888	0.424	18	0.169	K.FAATVEQNYLK.T
R5/RRR5-6/2	1766.544	1766.115	243.646	0.511	1006.660	0.535	24	0.165	K.VLQALIPILDQSVVEK.N
R5/RRR5-7/2	1121.362	1122.258	-1695.499	0.400	1286.831	0.415	16	0.165	R.LAAGEWFTAR.V
R5/RRR5-7/2	1284.140	1284.442	-236.228	0.481	1228.910	0.412	17	0.161	K.FAATVEQNYLK.T
R5/RRR5-6/2	1765.527	1766.115	-902.265	0.477	964.416	0.494	24	0.156	K.VLQALIPILDQSVVEK.N
R5/RRR5-6/2	1284.280	1284.442	-126.663	0.460	1210.568	0.374	17	0.153	K.FAATVEQNYLK.T
R5/RRR5-7/3	1766.308	1766.115	109.403	0.534	1248.297	0.528	29	0.149	K.VLQALIPILDQSVVEK.N
R5/RRR5-6/2	1765.684	1766.115	-244.751	0.461	774.205	0.471	21	0.142	K.VLQALIPILDQSVVEK.N
R5/RRR5-7/2	1765.911	1766.115	-115.829	0.466	815.830	0.422	22	0.138	K.VLQALIPILDQSVVEK.N
R5/RRR5-7/2	1190.180	1190.335	-131.225	0.445	921.039	0.380	14	0.138	K.INNPHYLYR.M
R5/RRR5-6/2	1283.426	1284.442	-1575.846	0.361	1071.579	0.319	17	0.138	K.FAATVEQNYLK.T
R5/RRR5-6/3	1766.828	1766.115	-163.107	0.466	1117.795	0.504	28	0.128	K.VLQALIPILDQSVVEK.N
R5/RRR5-5/2	1203.365	1202.419	-45.237	0.228	469.845	0.301	14	0.119	R.LLAVEGCAALGK.L
R5/RRR5-5/2	1766.024	1766.115	-51.762	0.390	529.591	0.275	18	0.119	K.VLQALIPILDQSVVEK.N
R5/RRR5-7/2	1766.872	1766.115	-138.079	0.383	287.245	0.416	13	0.118	-.VLQALIPILDQSVVEK.-
R5/RRR5-7/3	1765.395	1766.115	-977.069	0.341	736.160	0.414	23	0.085	K.VLQALIPILDQSVVEK.N
R5/RRR5-7/3	1765.596	1766.115	-862.641	0.367	886.693	0.277	25	0.073	K.VLQALIPILDQSVVEK.N
R5/RRR5-9/2	1504.403	1503.768	-243.229	0.560	2316.356	0.411	20	0.289	K.TVFIQELINNIAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1436.181	1436.595	-289.481	0.460	2033.790	0.495	21	0.269	R.FTQAGSEVSALLGR.I
R5/RRR5-9/2	1503.464	1503.768	-202.989	0.522	2253.622	0.378	20	0.269	K.TVFIQELINNIAK.A
R5/RRR5-9/2	1503.486	1503.768	-188.328	0.488	2200.095	0.337	20	0.250	K.TVFIQELINNIAK.A
R5/RRR5-9/2	1407.452	1406.609	-112.011	0.497	1685.798	0.578	19	0.241	R.VALTGLTVAEEFR.S
R5/RRR5-9/2	1435.946	1436.595	-1151.732	0.401	1250.989	0.390	17	0.155	R.FTQAGSEVSALLGR.I
R5/RRR5-9/2	1774.223	1774.992	-1000.390	0.428	896.040	0.508	18	0.146	R.GISELGIYPAVDPLDSK.S
R5/RRR5-9/2	1435.660	1436.595	-1352.290	0.355	1036.817	0.377	16	0.138	R.FTQAGSEVSALLGR.I
R5/RRR5-9/2	1149.062	1149.322	-226.704	0.378	843.599	0.319	13	0.127	R.VQQILQEYK.S
R5/RRR5-8/2	1504.018	1503.768	167.077	0.366	196.440	0.276	15	0.124	-.TVFIQELINNIAK.-
R5/RRR5-8/2	1504.025	1503.768	171.554	0.372	379.433	0.252	18	0.124	K.TVFIQELINNIAK.A
R5/RRR5-15/2	1969.606	1970.261	-842.719	0.586	4185.655	0.541	31	0.833	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-16/2	1970.060	1970.261	-102.272	0.600	4129.371	0.567	31	0.827	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-15/2	1969.878	1970.261	-195.016	0.609	3951.224	0.554	31	0.758	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-15/2	1969.516	1970.261	-888.698	0.545	3830.411	0.504	30	0.696	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-15/3	1970.864	1970.261	-202.256	0.588	3249.620	0.504	38	0.650	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-14/2	1969.924	1970.261	-171.829	0.590	3496.378	0.555	29	0.617	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-14/3	1970.831	1970.261	-219.033	0.565	3078.946	0.543	37	0.613	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-14/2	1969.073	1970.261	-1114.859	0.526	3423.947	0.528	30	0.585	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-15/3	1970.044	1970.261	-110.484	0.569	2862.482	0.590	38	0.562	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-16/2	1970.481	1970.261	111.619	0.615	3342.479	0.522	28	0.555	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-14/2	1969.499	1970.261	-897.720	0.591	3134.162	0.540	28	0.509	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-14/2	1663.311	1662.872	264.657	0.539	1793.750	0.415	23	0.214	K.AVVAQYNASQLITQR.E
R5/RRR5-15/2	1662.324	1662.872	-933.828	0.505	1703.926	0.443	22	0.210	K.AVVAQYNASQLITQR.E
R5/RRR5-15/2	1663.179	1662.872	185.467	0.552	1572.815	0.473	22	0.202	K.AVVAQYNASQLITQR.E
R5/RRR5-14/2	1663.232	1662.872	217.262	0.549	1542.491	0.469	22	0.197	K.AVVAQYNASQLITQR.E
R5/RRR5-14/2	1663.125	1662.872	152.492	0.539	1607.521	0.434	22	0.196	K.AVVAQYNASQLITQR.E
R5/RRR5-16/2	1662.295	1662.872	-951.448	0.418	1628.780	0.400	21	0.192	K.AVVAQYNASQLITQR.E
R5/RRR5-15/2	1662.280	1662.872	-960.221	0.472	1600.232	0.365	23	0.183	K.AVVAQYNASQLITQR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1374.229	1374.485	-187.064	0.521	1251.386	0.524	20	0.183	R.ARPNLVESTSGSR.D
R5/RRR5-14/2	1374.184	1374.485	-220.036	0.498	1254.900	0.491	20	0.176	R.ARPNLVESTSGSR.D
R5/RRR5-14/2	1375.024	1374.485	-336.549	0.528	1248.063	0.490	20	0.176	R.ARPNLVESTSGSR.D
R5/RRR5-15/3	1969.936	1970.261	-165.402	0.483	1648.086	0.433	30	0.174	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-15/2	1374.200	1374.485	-208.719	0.521	1209.208	0.482	20	0.171	R.ARPNLVESTSGSR.D
R5/RRR5-15/2	1374.144	1374.485	-249.446	0.504	1057.000	0.523	19	0.167	R.ARPNLVESTSGSR.D
R5/RRR5-14/2	1374.054	1374.485	-315.312	0.516	908.263	0.504	19	0.155	R.ARPNLVESTSGSR.D
R5/RRR5-14/2	1080.071	1080.133	-57.656	0.411	620.393	0.404	15	0.135	R.TLGENFNER.V
R5/RRR5-14/2	1080.107	1080.133	-23.987	0.401	511.795	0.377	14	0.131	R.TLGENFNER.V
R5/RRR5-15/2	1206.200	1206.459	-216.067	0.322	332.580	0.530	15	0.130	R.VPVPPAGAGTLVK.L
R5/RRR5-14/2	1079.979	1080.133	-142.915	0.409	495.864	0.351	14	0.130	R.TLGENFNER.V
R5/RRR5-16/2	1373.753	1374.485	-1265.014	0.420	626.726	0.364	18	0.129	R.ARPNLVESTSGSR.D
R5/RRR5-15/2	1079.724	1080.133	-380.173	0.454	619.671	0.319	15	0.129	R.TLGENFNER.V
R5/RRR5-15/2	1205.869	1206.459	-1322.743	0.265	302.361	0.498	14	0.124	R.VPVPPAGAGTLVK.L
R5/RRR5-15/2	1079.471	1080.133	-1544.774	0.308	453.451	0.279	13	0.124	R.TLGENFNER.V
R5/RRR5-14/2	1206.485	1206.459	21.148	0.305	245.970	0.499	13	0.123	-.VPVPPAGAGTLVK.-
R5/RRR5-15/2	1207.335	1206.459	-103.298	0.250	370.852	0.426	16	0.123	R.VPVPPAGAGTLVK.L
R5/RRR5-16/3	1970.110	1970.261	-77.294	0.531	1123.551	0.478	30	0.122	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-16/2	1373.804	1374.485	-1227.446	0.406	304.049	0.303	14	0.121	-.ARPNLVESTSGSR.-
R5/RRR5-15/2	1079.198	1080.133	-1798.842	0.251	650.215	0.252	15	0.120	R.TLGENFNER.V
R5/RRR5-14/3	1969.788	1970.261	-241.028	0.270	629.879	0.280	24	0.070	K.SAELIGQAIANNPAFLALR.Q
R5/RRR5-5/2	1324.284	1324.468	-139.756	0.462	2020.361	0.576	21	0.290	K.ILVAGSHADDLGR.Q
R5/RRR5-5/2	1324.030	1324.468	-331.941	0.488	2018.177	0.535	21	0.279	K.ILVAGSHADDLGR.Q
R5/RRR5-5/2	1324.070	1324.468	-301.693	0.475	1535.575	0.534	19	0.212	K.ILVAGSHADDLGR.Q
R5/RRR5-5/2	1059.063	1059.198	-128.627	0.527	1664.712	0.401	17	0.198	R.IGEATALEVR.A
R5/RRR5-5/2	1058.576	1059.198	-1537.328	0.446	1521.437	0.393	17	0.182	R.IGEATALEVR.A
R5/RRR5-5/2	1058.366	1059.198	-1736.842	0.438	1563.697	0.360	17	0.180	R.IGEATALEVR.A
R5/RRR5-5/2	1781.728	1782.063	-188.810	0.471	940.527	0.510	20	0.154	R.ATGIPYVFAPCVAVCR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1593.666	1593.835	-105.951	0.396	1562.781	0.390	25	0.149	K.M*HANHHLITDFLK.N
R5/RRR5-5/2	1454.181	1454.659	-329.427	0.388	891.731	0.500	20	0.149	K.ATIFPHNVGLGATR.D
R5/RRR5-5/2	1454.053	1454.659	-1107.582	0.406	717.184	0.509	19	0.142	K.ATIFPHNVGLGATR.D
R5/RRR5-5/2	1781.589	1782.063	-266.688	0.430	864.141	0.452	19	0.140	R.ATGIPYVFAPCVAVCR.D
R5/RRR5-5/2	1189.152	1188.398	-207.118	0.484	786.478	0.424	16	0.139	K.SSYSPVLPLPK.K
R5/RRR5-5/2	1187.653	1188.398	-1473.545	0.371	796.572	0.415	16	0.136	K.SSYSPVLPLPK.K
R5/RRR5-5/3	1454.879	1454.659	152.303	0.440	1075.054	0.561	28	0.135	K.ATIFPHNVGLGATR.D
R5/RRR5-5/2	1780.798	1782.063	-1275.836	0.347	779.593	0.417	18	0.131	R.ATGIPYVFAPCVAVCR.D
R5/RRR5-5/3	1454.301	1454.659	-246.567	0.408	1296.896	0.452	30	0.130	K.ATIFPHNVGLGATR.D
R5/RRR5-5/2	1187.689	1188.398	-1443.193	0.315	678.208	0.381	15	0.127	K.SSYSPVLPLPK.K
R5/RRR5-5/3	1454.537	1454.659	-83.521	0.380	856.184	0.491	26	0.102	K.ATIFPHNVGLGATR.D
R5/RRR5-1/2	1060.162	1059.198	-34.371	0.361	653.831	0.194	13	0.100	-.IGEATALEVR.-
R5/RRR5-5/3	1578.024	1577.835	119.974	0.436	560.670	0.525	19	0.095	K.MHANHHLITDFLK.N
R5/RRR5-3/2	1249.120	1249.441	-257.946	0.419	1357.751	0.459	17	0.177	R.AALNLAYQGLSK.V
R5/RRR5-3/2	1424.209	1424.586	-265.866	0.272	1046.154	0.317	17	0.131	K.AGWPVAGSPDPTLR.I
R5/RRR5-3/2	1248.859	1249.441	-1270.838	0.322	637.396	0.281	15	0.119	R.AALNLAYQGLSK.V
R5/RRR5-3/2	1424.064	1424.586	-1071.839	0.282	736.375	0.288	15	0.117	K.AGWPVAGSPDPTLR.I
R5/RRR5-3/2	1466.431	1465.720	-197.261	0.364	861.360	0.218	16	0.116	K.FGVKDEWVLPFK.I
R5/RRR5-24/2	1805.593	1806.035	-245.309	0.429	2187.476	0.456	25	0.282	R.VCCLSIIDPGDSDIIK.T
R5/RRR5-25/2	1806.469	1806.035	241.176	0.553	1866.158	0.497	26	0.245	R.VCCLSIIDPGDSDIIK.T
R5/RRR5-25/2	1805.423	1806.035	-895.551	0.498	1578.189	0.494	25	0.208	R.VCCLSIIDPGDSDIIK.T
R5/RRR5-25/2	1806.456	1806.035	233.654	0.545	1554.342	0.503	24	0.207	R.VCCLSIIDPGDSDIIK.T
R5/RRR5-24/2	1333.354	1334.520	-1629.518	0.364	1897.046	0.289	17	0.200	K.SEIEYYAM*LAK.T
R5/RRR5-24/2	1805.398	1806.035	-909.127	0.500	1393.281	0.476	24	0.185	R.VCCLSIIDPGDSDIIK.T
R5/RRR5-24/2	1396.260	1396.654	-283.201	0.347	1398.191	0.378	18	0.166	K.LVIISNNCPPLR.K
R5/RRR5-25/2	1462.145	1462.693	-1061.728	0.545	1019.940	0.477	20	0.159	R.KSEIEYYAM*LAK.T
R5/RRR5-24/2	1396.267	1396.654	-277.763	0.359	808.707	0.448	15	0.137	K.LVIISNNCPPLR.K
R5/RRR5-24/2	1396.409	1396.654	-176.202	0.337	955.246	0.379	16	0.136	K.LVIISNNCPPLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	1333.282	1334.520	-1683.694	0.254	805.983	0.361	15	0.126	-.SEIEYYAM*LAK.-
R5/RRR5-26/2	1807.806	1806.035	-126.893	0.368	797.693	0.318	17	0.123	R.VCCLSIIDPGDSDIIK.T
R5/RRR5-24/2	1333.953	1334.520	-1177.847	0.262	603.031	0.283	14	0.118	K.SEIEYYAM*LAK.T
R5/RRR5-25/2	1446.509	1446.693	-127.693	0.460	688.573	0.220	15	0.113	-.KSEIEYYAMLAK.-
R5/RRR5-24/3	1634.285	1634.880	-979.013	0.431	1178.142	0.364	27	0.102	K.STDNINNKLQLVM*K.S
R5/RRR5-24/3	1634.819	1634.880	-37.475	0.469	368.857	0.451	20	0.093	K.STDNINNKLQLVM*K.S
R5/RRR5-25/3	1463.453	1462.693	-164.593	0.404	1068.257	0.347	23	0.090	R.KSEIEYYAM*LAK.T
R5/RRR5-24/3	1634.337	1634.880	-947.293	0.423	519.625	0.423	22	0.088	K.STDNINNKLQLVM*K.S
R5/RRR5-25/3	1634.456	1634.880	-260.414	0.429	515.416	0.416	22	0.088	K.STDNINNKLQLVM*K.S
R5/RRR5-25/3	1634.535	1634.880	-211.750	0.450	612.536	0.402	23	0.087	K.STDNINNKLQLVM*K.S
R5/RRR5-25/3	1462.280	1462.693	-282.993	0.343	663.896	0.244	21	0.069	R.KSEIEYYAM*LAK.T
R5/RRR5-8/2	1104.299	1105.224	-1748.862	0.358	655.383	0.573	17	0.145	K.VVGVDTSGSGVK.L
R5/RRR5-8/2	1486.408	1486.736	-220.721	0.359	1154.405	0.356	20	0.144	K.IVSSTGALALSEIPK.K
R5/RRR5-8/2	1104.827	1105.224	-360.453	0.439	760.657	0.488	17	0.144	K.VVGVDTSGSGVK.L
R5/RRR5-8/2	1105.013	1105.224	-191.864	0.429	683.037	0.475	18	0.140	K.VVGVDTSGSGVK.L
R5/RRR5-8/2	1486.225	1486.736	-1019.596	0.315	532.961	0.347	14	0.117	-.IVSSTGALALSEIPK.-
R5/RRR5-19/3	1633.190	1632.831	220.426	0.523	2875.740	0.460	33	0.478	K.TIAECLADELINAAK.G
R5/RRR5-20/3	1632.587	1632.831	-149.820	0.574	2901.011	0.421	34	0.459	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1632.291	1632.831	-946.510	0.505	3067.313	0.433	23	0.448	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1633.338	1632.831	-302.588	0.560	2904.968	0.498	23	0.434	K.TIAECLADELINAAK.G
R5/RRR5-18/2	1633.224	1632.831	241.195	0.535	2763.471	0.472	22	0.393	K.TIAECLADELINAAK.G
R5/RRR5-21/2	1632.428	1632.831	-247.630	0.538	2731.706	0.477	22	0.387	K.TIAECLADELINAAK.G
R5/RRR5-19/3	1633.522	1632.831	-189.571	0.551	2678.067	0.401	33	0.381	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1421.205	1420.639	-306.574	0.507	2355.910	0.592	21	0.353	R.VNQAIYLLTTGAR.E
R5/RRR5-19/2	1633.259	1632.831	263.005	0.540	2579.066	0.463	22	0.351	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1632.282	1632.831	-952.141	0.508	2578.366	0.453	22	0.348	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1632.673	1632.831	-97.160	0.515	2531.908	0.476	22	0.347	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1421.200	1420.639	-309.676	0.530	2321.263	0.582	21	0.343	R.VNQAIYLLTTGAR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1632.261	1632.831	-964.829	0.517	2529.860	0.440	21	0.334	K.TIAECLADELINAAK.G
R5/RRR5-19/2	1633.206	1632.831	230.478	0.541	2462.237	0.474	21	0.332	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1633.232	1632.831	246.217	0.551	2327.588	0.502	20	0.315	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1421.272	1420.639	-258.834	0.554	2141.161	0.590	21	0.313	R.VNQAIYLLTTGAR.E
R5/RRR5-20/2	1421.157	1420.639	-339.925	0.548	2050.960	0.600	20	0.301	R.VNQAIYLLTTGAR.E
R5/RRR5-18/2	1632.414	1632.831	-256.182	0.466	2414.527	0.375	21	0.294	K.TIAECLADELINAAK.G
R5/RRR5-20/3	1632.381	1632.831	-276.522	0.558	2356.231	0.392	32	0.291	K.TIAECLADELINAAK.G
R5/RRR5-19/2	1421.159	1420.639	-338.460	0.548	1965.374	0.582	20	0.281	R.VNQAIYLLTTGAR.E
R5/RRR5-21/2	1631.980	1632.831	-1137.549	0.418	2319.910	0.356	21	0.273	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1632.181	1632.831	-1014.236	0.473	2171.316	0.407	20	0.262	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1420.098	1420.639	-1088.197	0.430	1893.251	0.504	20	0.249	R.VNQAIYLLTTGAR.E
R5/RRR5-19/2	1419.934	1420.639	-1204.470	0.426	1865.268	0.517	21	0.248	R.VNQAIYLLTTGAR.E
R5/RRR5-20/2	1421.495	1420.639	-101.602	0.469	1789.727	0.514	19	0.237	R.VNQAIYLLTTGAR.E
R5/RRR5-20/3	1632.557	1632.831	-168.272	0.552	2047.237	0.407	32	0.229	K.TIAECLADELINAAK.G
R5/RRR5-18/2	1632.442	1632.831	-239.002	0.445	1879.663	0.432	19	0.227	K.TIAECLADELINAAK.G
R5/RRR5-18/2	1420.405	1420.639	-165.209	0.427	1493.304	0.549	21	0.209	R.VNQAIYLLTTGAR.E
R5/RRR5-21/2	1420.052	1420.639	-1120.737	0.406	1540.282	0.449	19	0.193	R.VNQAIYLLTTGAR.E
R5/RRR5-20/2	1419.770	1420.639	-1319.994	0.384	1391.790	0.508	20	0.189	R.VNQAIYLLTTGAR.E
R5/RRR5-20/2	1420.332	1420.639	-217.025	0.400	1505.669	0.379	20	0.176	R.VNQAIYLLTTGAR.E
R5/RRR5-18/2	1420.311	1420.639	-231.855	0.400	1175.706	0.503	18	0.169	R.VNQAIYLLTTGAR.E
R5/RRR5-20/3	1632.339	1632.831	-302.181	0.558	1714.425	0.386	29	0.164	K.TIAECLADELINAAK.G
R5/RRR5-20/2	1224.094	1224.354	-212.408	0.406	837.327	0.585	19	0.161	K.HATYLPHTAGR.Y
R5/RRR5-20/2	1223.960	1224.354	-322.568	0.408	781.265	0.596	18	0.159	K.HATYLPHTAGR.Y
R5/RRR5-20/2	1575.554	1576.825	-1445.767	0.635	694.916	0.593	20	0.158	R.RVNQAIYLLTTGAR.E
R5/RRR5-20/2	1576.177	1576.825	-1048.719	0.594	556.818	0.603	20	0.154	R.RVNQAIYLLTTGAR.E
R5/RRR5-20/2	1576.745	1576.825	-51.220	0.594	610.253	0.574	20	0.152	R.RVNQAIYLLTTGAR.E
R5/RRR5-19/2	1419.581	1420.639	-1453.855	0.355	1088.141	0.439	15	0.151	R.VNQAIYLLTTGAR.E
R5/RRR5-20/2	1224.123	1224.354	-188.698	0.381	577.565	0.619	17	0.150	K.HATYLPHTAGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1223.944	1224.354	-335.276	0.408	515.578	0.617	16	0.149	K.HATYLPHTAGR.Y
R5/RRR5-21/2	1420.217	1420.639	-297.648	0.417	967.671	0.414	18	0.144	R.VNQAIYLLTTGAR.E
R5/RRR5-20/2	1224.025	1224.354	-269.136	0.300	567.856	0.553	16	0.138	K.HATYLPHTAGR.Y
R5/RRR5-21/2	998.996	999.146	-151.313	0.367	366.773	0.477	13	0.135	R.QAVDISPLR.R
R5/RRR5-19/2	998.598	999.146	-1554.872	0.373	389.237	0.429	14	0.134	R.QAVDISPLR.R
R5/RRR5-19/2	1576.336	1576.825	-311.433	0.501	407.475	0.476	17	0.133	R.RVNQAIYLLTTGAR.E
R5/RRR5-20/2	999.140	999.146	-6.569	0.352	296.251	0.445	13	0.133	R.QAVDISPLR.R
R5/RRR5-19/2	1224.209	1224.354	-118.076	0.279	346.789	0.494	14	0.128	K.HATYLPHTAGR.Y
R5/RRR5-20/2	1632.295	1632.831	-943.657	0.395	1171.818	0.227	17	0.128	-.TIAECLADELINAAK.-
R5/RRR5-20/2	999.014	999.146	-132.804	0.279	439.309	0.392	15	0.127	R.QAVDISPLR.R
R5/RRR5-20/2	999.711	999.146	-436.442	0.346	569.785	0.363	14	0.127	-.QAVDISPLR.-
R5/RRR5-20/2	1224.098	1224.354	-209.207	0.272	402.866	0.436	15	0.127	K.HATYLPHTAGR.Y
R5/RRR5-20/2	999.268	999.146	121.716	0.372	573.111	0.293	14	0.126	R.QAVDISPLR.R
R5/RRR5-21/2	1419.344	1420.639	-1621.965	0.310	545.574	0.347	15	0.124	R.VNQAIYLLTTGAR.E
R5/RRR5-20/2	998.544	999.146	-1609.152	0.244	350.633	0.507	14	0.121	-.QAVDISPLR.-
R5/RRR5-21/2	999.146	999.146	0.170	0.193	235.611	0.331	11	0.120	-.QAVDISPLR.-
R5/RRR5-20/2	1632.099	1632.831	-1064.549	0.373	904.379	0.192	16	0.114	-.TIAECLADELINAAK.-
R5/RRR5-20/3	1576.927	1576.825	64.892	0.357	1480.388	0.290	26	0.112	R.RVNQAIYLLTTGAR.E
R5/RRR5-20/3	1224.458	1224.354	85.372	0.577	593.100	0.553	21	0.112	K.HATYLPHTAGR.Y
R5/RRR5-20/2	1632.610	1632.831	-135.711	0.408	915.711	0.161	16	0.110	-.TIAECLADELINAAK.-
R5/RRR5-20/3	1224.124	1224.354	-188.259	0.543	539.868	0.536	20	0.109	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.633	1224.354	229.178	0.537	450.249	0.530	20	0.109	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.598	1224.354	200.390	0.538	774.879	0.500	23	0.107	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.491	1224.354	112.516	0.552	675.651	0.509	22	0.107	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.189	1224.354	-134.991	0.560	570.957	0.514	21	0.107	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.687	1224.354	273.406	0.546	583.515	0.515	21	0.107	K.HATYLPHTAGR.Y
R5/RRR5-21/3	1223.797	1224.354	-1276.065	0.508	526.114	0.520	20	0.106	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.334	1224.354	-15.872	0.525	644.011	0.511	21	0.106	K.HATYLPHTAGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/3	1224.510	1224.354	128.113	0.480	370.194	0.509	18	0.106	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.051	1224.354	-247.986	0.538	602.948	0.509	21	0.106	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.445	1224.354	75.173	0.549	639.723	0.503	22	0.106	K.HATYLPHTAGR.Y
R5/RRR5-19/2	1632.216	1632.831	-992.385	0.329	692.022	0.087	14	0.105	-.TIAECLADELINAAK.-
R5/RRR5-19/3	1224.555	1224.354	164.852	0.515	528.400	0.500	20	0.104	K.HATYLPHTAGR.Y
R5/RRR5-17/3	1224.410	1224.354	46.376	0.491	435.314	0.492	19	0.104	K.HATYLPHTAGR.Y
R5/RRR5-21/3	1224.922	1224.354	-353.711	0.472	488.724	0.503	19	0.104	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.390	1224.354	30.177	0.551	560.506	0.490	21	0.104	K.HATYLPHTAGR.Y
R5/RRR5-21/3	1224.529	1224.354	143.709	0.521	496.445	0.489	20	0.104	K.HATYLPHTAGR.Y
R5/RRR5-21/3	1224.677	1224.354	265.160	0.514	443.336	0.478	20	0.103	K.HATYLPHTAGR.Y
R5/RRR5-18/3	1224.706	1224.354	288.848	0.494	528.942	0.490	21	0.103	K.HATYLPHTAGR.Y
R5/RRR5-18/3	1224.239	1224.354	-93.732	0.528	691.662	0.482	23	0.103	K.HATYLPHTAGR.Y
R5/RRR5-21/3	1224.534	1224.354	148.207	0.531	543.432	0.480	22	0.103	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.546	1224.354	157.805	0.516	555.819	0.483	21	0.103	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.116	1224.354	-194.262	0.520	424.851	0.473	18	0.102	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1225.037	1224.354	-259.380	0.417	311.707	0.455	16	0.102	K.HATYLPHTAGR.Y
R5/RRR5-21/3	1224.614	1224.354	213.585	0.508	541.293	0.478	21	0.102	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.911	1224.354	-362.261	0.536	579.065	0.474	22	0.102	K.HATYLPHTAGR.Y
R5/RRR5-13/3	1224.931	1224.354	-346.062	0.394	282.506	0.217	17	0.102	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1223.997	1224.354	-292.410	0.524	471.333	0.464	19	0.101	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.643	1224.354	237.274	0.444	408.977	0.464	18	0.101	K.HATYLPHTAGR.Y
R5/RRR5-24/3	1223.788	1224.354	-1283.277	0.486	480.250	0.474	18	0.101	K.HATYLPHTAGR.Y
R5/RRR5-25/3	1224.292	1224.354	-50.675	0.455	273.263	0.392	15	0.101	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.671	1224.354	260.063	0.501	590.088	0.471	21	0.101	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.519	1224.354	135.761	0.418	363.715	0.449	17	0.100	K.HATYLPHTAGR.Y
R5/RRR5-17/3	1225.119	1224.354	-191.604	0.458	397.826	0.443	18	0.100	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.531	1224.354	145.658	0.544	514.774	0.453	20	0.100	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.037	1224.354	-259.091	0.408	332.715	0.430	16	0.100	K.HATYLPHTAGR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/3	1224.575	1224.354	181.797	0.406	480.179	0.471	20	0.099	K.HATYLPHTAGR.Y
R5/RRR5-22/3	1224.723	1224.354	302.190	0.417	477.521	0.466	19	0.099	K.HATYLPHTAGR.Y
R5/RRR5-22/3	1223.943	1224.354	-336.688	0.450	505.683	0.458	19	0.099	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.434	1224.354	65.874	0.476	530.282	0.450	21	0.099	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1224.011	1224.354	-281.003	0.492	438.075	0.435	18	0.099	K.HATYLPHTAGR.Y
R5/RRR5-11/3	1224.740	1224.354	316.131	0.374	306.996	0.294	17	0.098	K.HATYLPHTAGR.Y
R5/RRR5-19/2	1632.214	1632.831	-993.962	0.345	728.821	0.162	14	0.098	-.TIAECLADELINAAK.-
R5/RRR5-20/3	1224.168	1224.354	-152.097	0.448	420.659	0.424	18	0.098	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.156	1224.354	-161.850	0.445	457.356	0.419	20	0.097	K.HATYLPHTAGR.Y
R5/RRR5-21/3	1224.465	1224.354	91.371	0.492	466.232	0.405	19	0.096	K.HATYLPHTAGR.Y
R5/RRR5-25/3	1224.417	1224.354	52.226	0.358	568.749	0.466	21	0.096	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.612	1224.354	211.635	0.402	544.138	0.442	21	0.096	K.HATYLPHTAGR.Y
R5/RRR5-14/3	1224.946	1224.354	-333.914	0.436	459.540	0.398	20	0.096	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.427	1224.354	60.025	0.509	534.627	0.403	21	0.095	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.458	1224.354	85.821	0.452	415.662	0.360	18	0.095	K.HATYLPHTAGR.Y
R5/RRR5-14/3	1224.621	1224.354	218.982	0.329	358.045	0.332	18	0.095	K.HATYLPHTAGR.Y
R5/RRR5-17/3	1225.351	1224.354	-2.120	0.430	439.224	0.376	18	0.094	K.HATYLPHTAGR.Y
R5/RRR5-20/3	1224.074	1224.354	-228.776	0.287	403.246	0.407	17	0.093	K.HATYLPHTAGR.Y
R5/RRR5-18/3	1223.343	1224.354	-1648.398	0.401	531.949	0.384	19	0.091	K.HATYLPHTAGR.Y
R5/RRR5-19/3	1632.511	1632.831	-196.851	0.386	1127.049	0.275	26	0.082	K.TIAECLADELINAAK.G
R5/RRR5-19/3	1631.449	1632.831	-1464.460	0.323	752.398	0.231	26	0.071	K.TIAECLADELINAAK.G
R5/RRR5-25/3	1224.986	1224.354	-301.069	0.368	177.012	0.443	13	0.071	-.HATYLPHTAGR.-
R5/RRR5-21/3	1631.917	1632.831	-1176.615	0.314	761.337	0.200	26	0.069	K.TIAECLADELINAAK.G
R5/RRR5-14/2	1797.798	1798.032	-130.664	0.599	2811.646	0.585	26	0.448	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1797.391	1798.032	-916.243	0.591	2637.728	0.599	26	0.415	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1796.820	1798.032	-1234.887	0.572	2599.880	0.591	26	0.404	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1737.952	1738.962	-1159.699	0.565	2539.314	0.593	22	0.391	K.SPFQEYTDLLAKPTK.A
R5/RRR5-15/2	1797.273	1798.032	-981.701	0.570	2535.231	0.579	26	0.386	K.KVLQFAGIEDVFTSSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1669.608	1669.860	-150.963	0.550	2439.672	0.594	24	0.370	K.VLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1669.481	1669.860	-227.613	0.521	2490.703	0.550	24	0.366	K.VLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1670.318	1669.860	274.982	0.591	2436.829	0.574	24	0.362	K.VLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1671.081	1669.860	132.790	0.593	2328.995	0.610	23	0.353	K.VLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1669.630	1669.860	-137.761	0.524	2351.163	0.549	24	0.338	K.VLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1738.390	1738.962	-906.771	0.579	2226.025	0.570	21	0.321	K.SPFQEYTDLLAKPTK.A
R5/RRR5-14/2	1796.453	1798.032	-1998.334	0.501	2174.534	0.587	24	0.318	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1739.159	1738.962	113.582	0.574	2170.471	0.592	21	0.318	K.SPFQEYTDLLAKPTK.A
R5/RRR5-16/2	1797.555	1798.032	-266.499	0.592	2162.365	0.593	24	0.318	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1669.607	1669.860	-151.696	0.528	2184.804	0.548	23	0.307	K.VLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1737.751	1738.962	-1275.806	0.506	2092.960	0.527	21	0.286	K.SPFQEYTDLLAKPTK.A
R5/RRR5-15/2	1738.271	1738.962	-975.790	0.564	2101.365	0.524	21	0.285	K.SPFQEYTDLLAKPTK.A
R5/RRR5-15/2	1738.534	1738.962	-247.024	0.564	1940.655	0.567	20	0.272	K.SPFQEYTDLLAKPTK.A
R5/RRR5-16/2	1739.220	1738.962	148.707	0.563	2079.792	0.488	21	0.271	K.SPFQEYTDLLAKPTK.A
R5/RRR5-16/2	1797.036	1798.032	-1114.280	0.526	1885.410	0.572	23	0.266	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1798.715	1798.032	-177.089	0.602	1852.297	0.589	23	0.266	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-16/2	1738.386	1738.962	-909.239	0.510	1707.465	0.482	20	0.218	K.SPFQEYTDLLAKPTK.A
R5/RRR5-15/2	1404.214	1403.565	-250.992	0.502	974.688	0.557	16	0.167	K.TYGFLTPDFWR.E
R5/RRR5-11/2	1670.794	1669.860	-39.470	0.433	1117.273	0.447	19	0.156	K.VLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1403.106	1403.565	-328.067	0.468	920.277	0.492	15	0.153	K.TYGFLTPDFWR.E
R5/RRR5-16/2	1403.132	1403.565	-309.824	0.390	785.481	0.504	14	0.145	K.TYGFLTPDFWR.E
R5/RRR5-15/2	1402.369	1403.565	-1571.142	0.331	965.827	0.438	15	0.145	K.TYGFLTPDFWR.E
R5/RRR5-14/2	1403.156	1403.565	-292.978	0.346	888.992	0.473	14	0.145	K.TYGFLTPDFWR.E
R5/RRR5-16/2	1402.915	1403.565	-1179.634	0.397	763.422	0.503	13	0.143	K.TYGFLTPDFWR.E
R5/RRR5-15/3	1797.837	1798.032	-108.774	0.513	1376.794	0.451	29	0.142	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1403.067	1403.565	-356.001	0.422	744.875	0.461	14	0.140	K.TYGFLTPDFWR.E
R5/RRR5-15/2	1402.366	1403.565	-1573.065	0.396	749.226	0.446	14	0.138	K.TYGFLTPDFWR.E
R5/RRR5-15/3	1797.153	1798.032	-1048.812	0.424	1424.056	0.414	31	0.137	K.KVLQFAGIEDVFTSSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1671.025	1669.860	99.017	0.376	697.203	0.465	17	0.136	K.VLQFAGIEDVFTSSR.G
R5/RRR5-16/2	1403.895	1403.565	235.245	0.422	663.814	0.455	13	0.136	K.TYGFLTPDFWR.E
R5/RRR5-14/3	1798.729	1798.032	-169.097	0.438	1215.228	0.476	28	0.131	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-2/2	1670.727	1669.860	-79.411	0.324	610.600	0.421	16	0.128	K.VLQFAGIEDVFTSSR.G
R5/RRR5-14/2	1403.084	1403.565	-343.954	0.315	579.836	0.407	12	0.127	K.TYGFLTPDFWR.E
R5/RRR5-14/2	1402.964	1403.565	-1144.947	0.407	458.636	0.469	11	0.125	-.TYGFLTPDFWR.-
R5/RRR5-12/2	1671.304	1669.860	266.908	0.290	343.247	0.342	14	0.122	K.VLQFAGIEDVFTSSR.G
R5/RRR5-1/2	1670.040	1669.860	108.239	0.291	497.291	0.342	15	0.121	K.VLQFAGIEDVFTSSR.G
R5/RRR5-1/2	1670.481	1669.860	-227.257	0.315	431.329	0.343	14	0.121	K.VLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1402.700	1403.565	-1333.876	0.262	563.486	0.320	12	0.121	K.TYGFLTPDFWR.E
R5/RRR5-20/2	1403.036	1403.565	-1093.489	0.238	215.349	0.340	10	0.121	-.TYGFLTPDFWR.-
R5/RRR5-11/2	1671.314	1669.860	272.620	0.288	498.439	0.308	15	0.120	K.VLQFAGIEDVFTSSR.G
R5/RRR5-19/2	1740.129	1738.962	96.562	0.344	948.217	0.224	17	0.120	K.SPFQEYTDLLAKPTK.A
R5/RRR5-1/2	1670.147	1669.860	172.744	0.258	422.783	0.309	14	0.119	K.VLQFAGIEDVFTSSR.G
R5/RRR5-15/2	1798.985	1798.032	-26.312	0.348	395.394	0.313	13	0.118	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-14/3	1798.150	1798.032	65.590	0.407	1135.581	0.423	28	0.111	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-16/3	1738.962	1738.962	0.196	0.495	830.451	0.471	24	0.102	K.SPFQEYTDLLAKPTK.A
R5/RRR5-15/3	1738.977	1738.962	8.645	0.471	815.180	0.468	23	0.100	K.SPFQEYTDLLAKPTK.A
R5/RRR5-14/3	1739.139	1738.962	102.101	0.470	963.616	0.405	26	0.097	K.SPFQEYTDLLAKPTK.A
R5/RRR5-14/3	1738.987	1738.962	14.664	0.458	731.371	0.461	24	0.096	K.SPFQEYTDLLAKPTK.A
R5/RRR5-14/3	1797.786	1798.032	-137.381	0.441	868.844	0.414	26	0.094	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-16/3	1739.118	1738.962	90.063	0.458	610.532	0.464	21	0.093	K.SPFQEYTDLLAKPTK.A
R5/RRR5-15/2	1388.087	1388.569	-348.215	0.274	899.891	0.305	16	0.087	K.ALM*IDAPVENVEA.-
R5/RRR5-15/3	1738.938	1738.962	-13.851	0.427	702.681	0.394	23	0.086	K.SPFQEYTDLLAKPTK.A
R5/RRR5-16/3	1738.296	1738.962	-961.169	0.380	692.874	0.390	23	0.085	K.SPFQEYTDLLAKPTK.A
R5/RRR5-15/2	1387.812	1388.569	-1270.035	0.347	823.678	0.338	15	0.082	K.ALM*IDAPVENVEA.-
R5/RRR5-16/3	1797.765	1798.032	-149.028	0.316	805.609	0.249	25	0.070	K.KVLQFAGIEDVFTSSR.G
R5/RRR5-15/3	1797.855	1798.032	-99.171	0.349	968.218	0.179	25	0.063	K.KVLQFAGIEDVFTSSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1708.405	1708.894	-287.214	0.479	1914.802	0.514	21	0.257	R.DVWWQDVVTSFPTK.C
R5/RRR5-5/2	1709.829	1708.894	-38.569	0.531	1952.953	0.488	21	0.255	R.DVWWQDVVTSFPTK.C
R5/RRR5-5/2	1248.368	1247.334	27.108	0.453	1419.971	0.512	18	0.194	K.DIVDAGLAESEK.Q
R5/RRR5-5/2	1582.289	1582.785	-314.594	0.449	1021.569	0.578	22	0.171	R.VLGSVGEPINPSAWR.W
R5/RRR5-5/2	1062.244	1062.246	-1.799	0.456	1086.773	0.507	13	0.165	K.GPVQISWFK.G
R5/RRR5-5/2	1211.261	1211.310	-40.494	0.452	1114.307	0.402	18	0.151	R.VDDVINVSGHR.I
R5/RRR5-1/2	1582.213	1582.785	-996.509	0.349	1064.795	0.347	19	0.138	R.VLGSVGEPINPSAWR.W
R5/RRR5-5/2	1062.184	1062.246	-58.627	0.492	791.879	0.407	13	0.137	K.GPVQISWFK.G
R5/RRR5-1/2	1582.635	1582.785	-95.126	0.424	659.155	0.459	18	0.135	R.VLGSVGEPINPSAWR.W
R5/RRR5-5/2	1581.825	1582.785	-1242.582	0.287	811.979	0.412	19	0.132	R.VLGSVGEPINPSAWR.W
R5/RRR5-6/2	1581.935	1582.785	-1172.994	0.375	520.710	0.477	16	0.130	R.VLGSVGEPINPSAWR.W
R5/RRR5-4/2	1708.975	1708.894	47.527	0.252	585.871	0.198	13	0.112	R.DVWWQDVVTSFPTK.C
R5/RRR5-5/3	1538.932	1538.727	133.245	0.385	688.456	0.460	24	0.092	R.IGTAEVESALVSHPK.C
R5/RRR5-5/3	1538.561	1538.727	-108.443	0.407	503.830	0.462	22	0.087	-.IGTAEVESALVSHPK.-
R5/RRR5-1/3	1538.820	1538.727	60.452	0.328	513.506	0.430	19	0.082	-.IGTAEVESALVSHPK.-
R5/RRR5-6/3	1538.581	1538.727	-95.431	0.346	679.152	0.371	25	0.081	R.IGTAEVESALVSHPK.C
R5/RRR5-5/3	1538.924	1538.727	128.233	0.349	746.831	0.307	24	0.075	R.IGTAEVESALVSHPK.C
R5/RRR5-16/2	1936.350	1937.097	-905.058	0.585	3040.577	0.580	24	0.508	K.IEDLSSQLQTQAAEQFK.A
R5/RRR5-16/2	1521.750	1520.840	-59.346	0.547	2330.666	0.457	21	0.307	K.NILFVISKPDVFK.S
R5/RRR5-16/2	1519.968	1520.840	-1235.557	0.533	1811.625	0.468	19	0.230	K.NILFVISKPDVFK.S
R5/RRR5-16/2	1528.374	1528.645	-177.570	0.521	1382.665	0.577	20	0.204	K.SPNSDTYVIFGEAK.I
R5/RRR5-16/2	1528.151	1528.645	-324.217	0.519	1382.630	0.551	20	0.199	K.SPNSDTYVIFGEAK.I
R5/RRR5-15/2	1519.608	1520.840	-1472.970	0.406	1836.611	0.307	20	0.197	K.NILFVISKPDVFK.S
R5/RRR5-16/2	1519.903	1520.840	-1278.062	0.513	1705.311	0.376	19	0.195	K.NILFVISKPDVFK.S
R5/RRR5-16/2	1528.009	1528.645	-1073.445	0.475	1314.012	0.541	20	0.190	K.SPNSDTYVIFGEAK.I
R5/RRR5-20/2	1528.294	1528.645	-229.974	0.460	1325.531	0.520	20	0.186	K.SPNSDTYVIFGEAK.I
R5/RRR5-16/2	1043.980	1044.184	-195.927	0.485	862.774	0.510	15	0.153	K.APDLSNVISK.A
R5/RRR5-20/2	1528.375	1528.645	-176.769	0.504	936.321	0.487	18	0.151	K.SPNSDTYVIFGEAK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1043.449	1044.184	-1667.331	0.398	766.829	0.436	15	0.138	K.APDLSNVISK.A
R5/RRR5-16/2	1043.529	1044.184	-1590.470	0.361	635.076	0.503	14	0.138	K.APDLSNVISK.A
R5/RRR5-16/2	1534.133	1533.729	263.638	0.394	1204.828	0.412	18	0.131	K.AANGDIVTAIMELTN.-
R5/RRR5-19/2	1292.250	1292.509	-201.395	0.481	1624.845	0.525	20	0.221	K.FSGKDVVLVATR.R
R5/RRR5-19/2	1292.325	1292.509	-142.738	0.484	1469.836	0.534	18	0.205	K.FSGKDVVLVATR.R
R5/RRR5-19/2	1293.121	1292.509	-301.339	0.523	1379.543	0.551	19	0.200	K.FSGKDVVLVATR.R
R5/RRR5-19/2	1292.369	1292.509	-108.533	0.470	1334.304	0.516	18	0.187	K.FSGKDVVLVATR.R
R5/RRR5-19/2	1293.364	1292.509	-112.331	0.495	1358.516	0.493	19	0.186	K.FSGKDVVLVATR.R
R5/RRR5-19/2	1837.295	1837.967	-912.669	0.537	1202.321	0.581	19	0.186	R.NNTEYKLDTFSSVYR.R
R5/RRR5-19/2	1292.314	1292.509	-151.740	0.497	1300.768	0.508	18	0.183	K.FSGKDVVLVATR.R
R5/RRR5-19/2	1837.383	1837.967	-864.847	0.515	941.546	0.562	18	0.161	R.NNTEYKLDTFSSVYR.R
R5/RRR5-19/2	1837.421	1837.967	-843.773	0.533	940.799	0.548	18	0.159	R.NNTEYKLDTFSSVYR.R
R5/RRR5-19/2	1068.025	1068.297	-254.911	0.412	1005.525	0.311	15	0.135	K.AVIIHVPYR.L
R5/RRR5-19/2	1068.005	1068.297	-274.175	0.368	875.825	0.367	14	0.135	K.AVIIHVPYR.L
R5/RRR5-19/2	1028.630	1029.219	-1548.755	0.342	994.388	0.226	15	0.125	K.DVVLVATRR.I
R5/RRR5-19/2	1028.600	1029.219	-1578.320	0.350	831.133	0.226	14	0.121	K.DVVLVATRR.I
R5/RRR5-19/2	1068.264	1068.297	-30.213	0.380	606.468	0.274	12	0.121	K.AVIIHVPYR.L
R5/RRR5-19/2	1029.352	1029.219	129.459	0.420	669.806	0.202	13	0.117	K.DVVLVATRR.I
R5/RRR5-19/3	1838.614	1837.967	-192.864	0.526	758.082	0.551	27	0.108	R.NNTEYKLDTFSSVYR.R
R5/RRR5-19/3	1421.316	1420.682	-257.974	0.388	1377.359	0.282	25	0.100	K.KFSGKDVVLVATR.R
R5/RRR5-19/3	1421.128	1420.682	315.048	0.407	1014.407	0.266	23	0.076	K.KFSGKDVVLVATR.R
R5/RRR5-19/3	1292.801	1292.509	226.801	0.390	1019.716	0.269	21	0.076	-.FSGKDVVLVATR.-
R5/RRR5-19/3	1421.023	1420.682	240.887	0.400	861.173	0.271	23	0.073	K.KFSGKDVVLVATR.R
R5/RRR5-19/3	1292.748	1292.509	185.327	0.409	1377.960	0.119	23	0.070	-.FSGKDVVLVATR.-
R5/RRR5-19/3	1292.742	1292.509	180.782	0.416	956.236	0.240	20	0.068	-.FSGKDVVLVATR.-
R5/RRR5-19/3	1292.428	1292.509	-63.161	0.376	1066.773	0.184	21	0.066	-.FSGKDVVLVATR.-
R5/RRR5-19/3	1292.815	1292.509	237.453	0.397	1082.589	0.159	20	0.063	-.FSGKDVVLVATR.-
R5/RRR5-22/2	951.904	952.090	-195.649	0.473	1011.619	0.442	13	0.153	K.TSQIYAIR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	951.912	952.090	-186.901	0.502	999.032	0.435	13	0.152	K.TSQIYAIR.Q
R5/RRR5-23/2	1086.963	1087.297	-307.466	0.381	903.697	0.490	16	0.151	K.AFEPILLAGR.S
R5/RRR5-22/2	951.281	952.090	-1906.550	0.422	890.750	0.455	13	0.148	K.TSQIYAIR.Q
R5/RRR5-23/2	1086.980	1087.297	-292.255	0.456	651.018	0.507	14	0.144	K.AFEPILLAGR.S
R5/RRR5-23/2	951.445	952.090	-1733.269	0.410	830.197	0.442	13	0.144	K.TSQIYAIR.Q
R5/RRR5-22/2	1086.816	1087.297	-443.709	0.335	801.728	0.475	15	0.142	K.AFEPILLAGR.S
R5/RRR5-23/2	955.990	956.120	-136.668	0.436	902.873	0.394	13	0.142	K.ALVAYYQK.Y
R5/RRR5-23/2	951.905	952.090	-194.620	0.417	894.726	0.380	13	0.139	K.TSQIYAIR.Q
R5/RRR5-23/2	1087.133	1087.297	-150.533	0.371	873.277	0.409	15	0.139	K.AFEPILLAGR.S
R5/RRR5-23/2	952.076	952.090	-14.675	0.373	971.964	0.351	13	0.138	K.TSQIYAIR.Q
R5/RRR5-23/2	1308.376	1309.490	-1620.284	0.390	774.493	0.440	16	0.137	K.TAVAVSYCKPGR.G
R5/RRR5-22/2	1087.113	1087.297	-169.007	0.401	620.090	0.475	13	0.137	K.AFEPILLAGR.S
R5/RRR5-22/2	955.953	956.120	-174.584	0.371	830.829	0.389	13	0.137	K.ALVAYYQK.Y
R5/RRR5-22/2	1086.973	1087.297	-298.790	0.313	665.576	0.472	14	0.135	K.AFEPILLAGR.S
R5/RRR5-23/2	1309.111	1309.490	-289.989	0.413	778.125	0.405	16	0.134	K.TAVAVSYCKPGR.G
R5/RRR5-23/2	1309.040	1309.490	-344.721	0.386	665.732	0.453	15	0.134	K.TAVAVSYCKPGR.G
R5/RRR5-23/2	955.929	956.120	-199.821	0.412	729.937	0.364	13	0.133	K.ALVAYYQK.Y
R5/RRR5-22/2	955.935	956.120	-194.312	0.306	807.844	0.379	13	0.133	K.ALVAYYQK.Y
R5/RRR5-23/2	884.717	885.043	-370.003	0.334	897.487	0.342	11	0.131	R.TLLVADPR.R
R5/RRR5-22/2	884.793	885.043	-284.038	0.305	763.068	0.399	10	0.130	-.TLLVADPR.-
R5/RRR5-22/2	955.529	956.120	-1669.867	0.292	793.063	0.347	13	0.129	K.ALVAYYQK.Y
R5/RRR5-21/2	951.993	952.090	-101.617	0.400	654.575	0.312	12	0.127	K.TSQIYAIR.Q
R5/RRR5-23/2	955.504	956.120	-1695.922	0.291	762.157	0.317	13	0.126	K.ALVAYYQK.Y
R5/RRR5-17/2	1088.007	1087.297	-267.109	0.302	280.760	0.357	12	0.126	K.AFEPILLAGR.S
R5/RRR5-21/2	955.944	956.120	-184.961	0.249	480.694	0.357	10	0.122	K.ALVAYYQK.Y
R5/RRR5-22/2	1308.364	1309.490	-1629.469	0.280	312.154	0.311	13	0.121	K.TAVAVSYCKPGR.G
R5/RRR5-22/2	884.459	885.043	-1795.949	0.182	469.833	0.272	12	0.117	R.TLLVADPR.R
R5/RRR5-22/2	884.874	885.043	-191.998	0.137	807.580	0.040	12	0.110	R.TLLVADPR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/1	1558.713	1559.526	-1166.778	0.285	657.129	0.253	14	0.822	R.YFNIAENEGEEED.-
R5/RRR5-24/1	1559.545	1559.526	12.326	0.349	380.683	0.356	11	0.342	R.YFNIAENEGEEED.-
R5/RRR5-24/2	1558.793	1559.526	-1115.476	0.387	1689.461	0.400	20	0.235	R.YFNIAENEGEEED.-
R5/RRR5-24/2	1558.940	1559.526	-1020.653	0.352	1437.527	0.418	18	0.179	R.YFNIAENEGEEED.-
R5/RRR5-24/2	1111.462	1112.215	-1582.048	0.351	1082.235	0.520	17	0.163	K.VTVTSDGAFSK.R
R5/RRR5-24/2	1112.029	1112.215	-167.532	0.498	1019.037	0.508	17	0.162	K.VTVTSDGAFSK.R
R5/RRR5-24/2	1267.823	1268.401	-1248.883	0.381	975.261	0.477	16	0.150	K.VTVTSDGAFSKR.Y
R5/RRR5-24/2	1559.289	1559.526	-152.849	0.395	1266.106	0.460	18	0.149	R.YFNIAENEGEEED.-
R5/RRR5-24/2	1111.956	1112.215	-233.388	0.441	917.367	0.458	17	0.148	K.VTVTSDGAFSK.R
R5/RRR5-24/2	1189.901	1190.289	-326.656	0.455	977.162	0.422	18	0.146	K.AGNLGDSVTVTR.D
R5/RRR5-24/2	1269.029	1268.401	-294.324	0.404	787.887	0.443	15	0.137	K.VTVTSDGAFSKR.Y
R5/RRR5-24/2	1049.522	1050.252	-1652.762	0.359	836.449	0.272	14	0.125	K.IM*EIASLEK.F
R5/RRR5-24/2	1049.648	1050.252	-1531.952	0.410	847.069	0.245	14	0.123	K.IM*EIASLEK.F
R5/RRR5-24/2	1050.094	1050.252	-150.458	0.450	808.243	0.226	14	0.120	K.IM*EIASLEK.F
R5/RRR5-24/2	1190.114	1190.289	-147.590	0.315	703.390	0.182	16	0.114	K.AGNLGDSVTVTR.D
R5/RRR5-18/2	1663.368	1663.767	-240.889	0.538	2410.959	0.594	25	0.367	K.DLASAGADVGSATDWVK.N
R5/RRR5-17/2	1663.187	1663.767	-952.631	0.422	2529.283	0.392	27	0.324	K.DLASAGADVGSATDWVK.N
R5/RRR5-18/2	1663.140	1663.767	-981.221	0.459	2216.662	0.497	27	0.300	K.DLASAGADVGSATDWVK.N
R5/RRR5-18/2	1248.154	1248.478	-260.798	0.526	2137.363	0.505	18	0.287	K.LLNANSITM*VR.I
R5/RRR5-17/2	1248.297	1248.478	-145.423	0.511	1756.000	0.489	19	0.229	K.LLNANSITM*VR.I
R5/RRR5-17/2	1248.068	1248.478	-329.486	0.541	1556.008	0.506	18	0.209	K.LLNANSITM*VR.I
R5/RRR5-18/2	1534.354	1534.736	-249.334	0.508	1472.653	0.532	24	0.207	R.IYDTDPTVLNALAK.T
R5/RRR5-18/2	1248.066	1248.478	-330.958	0.507	1572.191	0.484	18	0.206	K.LLNANSITM*VR.I
R5/RRR5-17/2	1248.086	1248.478	-315.061	0.501	1585.745	0.475	18	0.205	K.LLNANSITM*VR.I
R5/RRR5-18/2	1248.067	1248.478	-330.566	0.520	1515.326	0.486	18	0.200	K.LLNANSITM*VR.I
R5/RRR5-18/2	1249.579	1248.478	81.163	0.491	1442.122	0.487	17	0.192	K.LLNANSITM*VR.I
R5/RRR5-17/2	1535.263	1534.736	-308.679	0.517	1205.989	0.552	22	0.184	R.IYDTDPTVLNALAK.T
R5/RRR5-18/2	1232.149	1232.479	-268.454	0.457	1470.471	0.432	17	0.184	K.LLNANSITMVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1248.002	1248.478	-382.383	0.380	1341.395	0.398	18	0.166	K.LLNANSITM*VR.I
R5/RRR5-18/2	1232.007	1232.479	-383.666	0.437	1165.788	0.451	17	0.162	K.LLNANSITMVR.I
R5/RRR5-18/2	1533.790	1534.736	-1272.318	0.353	1198.602	0.450	22	0.162	R.IYDTDPTVLNALAK.T
R5/RRR5-17/2	1232.204	1232.479	-224.027	0.456	1031.551	0.474	16	0.157	K.LLNANSITMVR.I
R5/RRR5-17/2	1232.232	1232.479	-201.169	0.479	1012.065	0.444	16	0.152	K.LLNANSITMVR.I
R5/RRR5-17/2	1232.301	1232.479	-144.723	0.446	966.245	0.460	16	0.151	K.LLNANSITMVR.I
R5/RRR5-18/2	1533.268	1534.736	-1614.523	0.332	930.815	0.465	19	0.145	R.IYDTDPTVLNALAK.T
R5/RRR5-17/2	1398.141	1397.556	-297.707	0.488	1248.748	0.313	19	0.144	R.DASNLIDPPEVVK.L
R5/RRR5-18/2	963.995	964.229	-243.424	0.455	725.346	0.360	13	0.131	-.VM*VM*LPNK.-
R5/RRR5-18/2	963.786	964.229	-461.092	0.490	735.169	0.343	13	0.129	-.VM*VM*LPNK.-
R5/RRR5-18/2	1398.142	1397.556	-297.006	0.497	924.468	0.324	17	0.129	R.DASNLIDPPEVVK.L
R5/RRR5-18/2	963.405	964.229	-1898.886	0.384	546.099	0.334	11	0.124	-.VM*VM*LPNK.-
R5/RRR5-17/2	1662.229	1663.767	-2135.023	0.291	1268.721	0.138	21	0.123	K.DLASAGADVGSATDWVK.N
R5/RRR5-18/2	1397.535	1397.556	-14.947	0.483	726.493	0.299	15	0.118	-.DASNLIDPPEVVK.-
R5/RRR5-16/2	1397.224	1397.556	-237.965	0.331	921.563	0.205	16	0.118	R.DASNLIDPPEVVK.L
R5/RRR5-16/2	1397.247	1397.556	-221.487	0.317	577.469	0.221	13	0.115	R.DASNLIDPPEVVK.L
R5/RRR5-5/3	1752.451	1751.922	-269.942	0.569	1949.268	0.494	34	0.254	K.IGGVPHGLSTDSEVVQR.E
R5/RRR5-5/3	1752.962	1751.922	22.859	0.557	1778.745	0.489	32	0.219	K.IGGVPHGLSTDSEVVQR.E
R5/RRR5-5/2	1552.921	1552.749	110.647	0.538	1493.507	0.447	20	0.189	R.VFISDEFDELLPK.Y
R5/RRR5-4/2	1579.068	1578.702	232.254	0.485	1369.362	0.416	18	0.170	K.ETTTEWELLNDVK.A
R5/RRR5-4/2	1486.062	1486.653	-1073.261	0.377	1381.125	0.394	21	0.167	K.GLVDSDTLPLNVSR.E
R5/RRR5-4/2	1552.406	1552.749	-222.064	0.253	656.960	0.178	15	0.113	-.VFISDEFDELLPK.-
R5/RRR5-7/2	1554.231	1552.749	310.488	0.321	623.659	0.191	14	0.113	R.VFISDEFDELLPK.Y
R5/RRR5-4/3	1701.195	1701.774	-930.851	0.446	949.879	0.349	23	0.083	K.APHDLYESYYNSNK.S
R5/RRR5-4/3	1808.812	1808.022	-116.541	0.345	1095.829	0.146	26	0.058	R.FLALTDKEVLGEGDTAK.L
R5/RRR5-2/2	1648.619	1648.802	-111.370	0.541	2670.307	0.512	24	0.393	K.YLAAEQGGGQTIVANR.V
R5/RRR5-2/2	1623.431	1623.746	-194.701	0.539	2043.082	0.532	22	0.280	R.LAGESNTELLDFASR.F
R5/RRR5-8/2	1267.599	1268.403	-1427.746	0.430	2028.843	0.487	18	0.266	R.FAQAQLDVYGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1624.273	1623.746	-291.914	0.547	1609.645	0.545	20	0.222	R.LAGESNTELLDFASR.F
R5/RRR5-3/2	1623.159	1623.746	-980.649	0.517	1675.585	0.495	20	0.218	R.LAGESNTELLDFASR.F
R5/RRR5-8/2	1269.065	1268.403	-266.820	0.465	1270.063	0.526	18	0.184	R.FAQAQLDVYGR.A
R5/RRR5-2/2	1263.600	1263.340	206.230	0.455	1327.265	0.482	16	0.180	K.YYQDAYNAVR.K
R5/RRR5-3/2	1624.428	1623.746	-196.390	0.514	1313.767	0.474	19	0.175	R.LAGESNTELLDFASR.F
R5/RRR5-3/2	1623.726	1623.746	-12.412	0.498	1205.509	0.518	19	0.174	R.LAGESNTELLDFASR.F
R5/RRR5-8/2	1268.438	1268.403	27.644	0.421	1253.365	0.417	18	0.163	R.FAQAQLDVYGR.A
R5/RRR5-2/2	1267.955	1268.403	-354.732	0.334	1014.850	0.453	15	0.148	R.FAQAQLDVYGR.A
R5/RRR5-3/2	1648.191	1648.802	-980.464	0.415	1062.943	0.406	22	0.146	K.YLAAEQGGGQTIVANR.V
R5/RRR5-1/2	1624.689	1623.746	-35.088	0.449	716.045	0.483	16	0.138	R.LAGESNTELLDFASR.F
R5/RRR5-2/2	1278.897	1278.436	361.154	0.348	946.765	0.285	15	0.126	K.DLLDGTQLQFK.S
R5/RRR5-3/2	1108.041	1108.229	-170.787	0.308	796.607	0.276	13	0.122	R.INETTFNLR.V
R5/RRR5-2/2	1107.178	1108.229	-1858.880	0.370	775.027	0.229	14	0.120	R.INETTFNLR.V
R5/RRR5-2/2	1277.364	1278.436	-1627.320	0.249	523.727	0.267	13	0.116	K.DLLDGTQLQFK.S
R5/RRR5-22/2	1878.183	1878.179	1.734	0.437	1504.385	0.441	20	0.186	K.GVDDILLVSVNDPFVM*K.A
R5/RRR5-23/2	1160.365	1161.379	-1740.966	0.396	1745.031	0.194	16	0.165	R.RFALLADNLK.V
R5/RRR5-23/2	1005.166	1005.192	-26.750	0.481	1270.300	0.327	16	0.151	-.FALLADNLK.-
R5/RRR5-22/2	1186.141	1186.339	-167.077	0.449	840.176	0.433	17	0.143	K.FLADGLGTYTK.A
R5/RRR5-23/2	1005.003	1005.192	-188.663	0.456	1166.522	0.305	15	0.142	-.FALLADNLK.-
R5/RRR5-23/2	1004.805	1005.192	-386.586	0.428	1160.897	0.305	15	0.141	-.FALLADNLK.-
R5/RRR5-23/2	1185.531	1186.339	-1529.163	0.438	839.427	0.410	17	0.140	K.FLADGLGTYTK.A
R5/RRR5-23/2	1185.545	1186.339	-1517.061	0.357	988.510	0.366	18	0.140	K.FLADGLGTYTK.A
R5/RRR5-23/2	1161.175	1161.379	-176.258	0.387	1527.209	0.145	16	0.139	R.RFALLADNLK.V
R5/RRR5-22/2	1004.835	1005.192	-356.600	0.388	1018.814	0.339	14	0.138	-.FALLADNLK.-
R5/RRR5-22/2	1188.256	1188.353	-82.082	0.349	814.508	0.437	15	0.138	K.ALGLELDLSEK.G
R5/RRR5-22/2	1187.114	1186.339	-189.424	0.424	834.363	0.391	17	0.137	K.FLADGLGTYTK.A
R5/RRR5-23/2	1188.047	1188.353	-258.427	0.344	884.937	0.403	16	0.137	K.ALGLELDLSEK.G
R5/RRR5-23/2	1185.982	1186.339	-301.926	0.417	957.725	0.345	18	0.137	K.FLADGLGTYTK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1186.120	1186.339	-184.938	0.330	1069.775	0.308	18	0.136	K.FLADGLGTYTK.A
R5/RRR5-23/2	1188.108	1188.353	-207.094	0.375	744.671	0.443	14	0.136	K.ALGLELDLSEK.G
R5/RRR5-22/2	1004.565	1005.192	-1625.103	0.410	1017.979	0.329	14	0.135	-.FALLADNLK.-
R5/RRR5-23/2	1187.975	1188.353	-319.147	0.348	821.050	0.374	15	0.132	K.ALGLELDLSEK.G
R5/RRR5-22/2	1160.964	1161.379	-358.210	0.281	1346.526	0.156	14	0.131	R.RFALLADNLK.V
R5/RRR5-23/2	1160.328	1161.379	-1772.888	0.353	1257.003	0.098	15	0.121	-.RFALLADNLK.-
R5/RRR5-22/2	1876.557	1878.179	-1936.246	0.302	259.708	0.431	14	0.119	K.GVDDILLVSVNDPFVM*K.A
R5/RRR5-17/2	1294.051	1294.482	-334.143	0.496	1700.760	0.505	19	0.226	K.SDLLLASNPVHK.S
R5/RRR5-17/2	1294.111	1294.482	-287.106	0.533	1594.209	0.510	19	0.215	K.SDLLLASNPVHK.S
R5/RRR5-17/2	1294.187	1294.482	-228.434	0.531	1389.120	0.523	18	0.195	K.SDLLLASNPVHK.S
R5/RRR5-17/2	1363.308	1362.601	-215.954	0.543	1194.149	0.506	19	0.175	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1362.131	1362.601	-346.206	0.457	1147.376	0.517	18	0.172	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1363.222	1362.601	-278.568	0.499	1170.904	0.491	19	0.170	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1363.200	1362.601	-295.189	0.486	983.445	0.522	18	0.162	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1363.266	1362.601	-246.317	0.428	908.737	0.523	16	0.155	K.LLGVWSSPYAIR.V
R5/RRR5-18/2	1363.147	1362.601	-334.451	0.480	906.693	0.466	17	0.149	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1363.244	1362.601	-262.847	0.482	839.024	0.488	17	0.149	K.LLGVWSSPYAIR.V
R5/RRR5-18/2	1363.097	1362.601	364.983	0.464	734.203	0.518	16	0.147	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1656.252	1656.771	-919.805	0.500	690.383	0.468	21	0.141	K.SLPYEYVEENLGDK.S
R5/RRR5-17/2	1657.162	1656.771	236.677	0.512	589.265	0.480	20	0.139	K.SLPYEYVEENLGDK.S
R5/RRR5-18/2	1362.301	1362.601	-220.877	0.394	795.277	0.408	17	0.137	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1362.329	1362.601	-200.112	0.301	429.805	0.518	13	0.130	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1361.909	1362.601	-1246.168	0.392	532.094	0.387	14	0.127	K.LLGVWSSPYAIR.V
R5/RRR5-17/2	1115.001	1115.219	-195.965	0.377	772.453	0.311	14	0.127	R.FWAAYVDDK.V
R5/RRR5-17/2	1115.011	1115.219	-187.289	0.331	961.907	0.265	14	0.127	R.FWAAYVDDK.V
R5/RRR5-17/2	1656.099	1656.771	-1012.748	0.417	544.911	0.353	19	0.126	K.SLPYEYVEENLGDK.S
R5/RRR5-17/2	1116.188	1115.219	-27.929	0.182	744.266	0.195	13	0.114	R.FWAAYVDDK.V
R5/RRR5-17/2	941.101	941.196	-101.817	0.471	877.433	0.170	12	0.112	-.VRVVLNLK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	941.327	941.196	139.224	0.431	886.427	0.114	12	0.111	-.VRVVLNLK.-
R5/RRR5-17/2	941.238	941.196	45.058	0.487	880.408	0.170	12	0.109	-.VRVVLNLK.-
R5/RRR5-13/2	1839.558	1840.028	-256.088	0.559	3504.042	0.495	29	0.592	R.AFIAGVADDNGYGWAIAK.A
R5/RRR5-14/2	1839.164	1840.028	-1016.259	0.544	3380.944	0.531	28	0.574	R.AFIAGVADDNGYGWAIAK.A
R5/RRR5-14/2	1839.674	1840.028	-192.846	0.534	3314.119	0.523	28	0.552	R.AFIAGVADDNGYGWAIAK.A
R5/RRR5-13/2	1839.418	1840.028	-878.135	0.559	3351.373	0.493	28	0.548	R.AFIAGVADDNGYGWAIAK.A
R5/RRR5-14/2	1838.903	1840.028	-1159.021	0.523	3039.802	0.533	27	0.485	R.AFIAGVADDNGYGWAIAK.A
R5/RRR5-13/2	1838.783	1840.028	-1224.350	0.396	2305.436	0.402	24	0.286	R.AFIAGVADDNGYGWAIAK.A
R5/RRR5-14/3	1442.459	1441.661	-140.920	0.523	1633.797	0.401	27	0.160	K.IRVNTISAGPLGSR.A
R5/RRR5-14/2	1171.590	1172.317	-1478.490	0.463	572.669	0.509	17	0.142	R.VNTISAGPLGSR.A
R5/RRR5-14/2	1556.333	1556.808	-306.231	0.417	886.103	0.450	17	0.141	K.MIEYSYVNAPLQK.E
R5/RRR5-13/2	1172.083	1172.317	-199.688	0.439	580.446	0.501	17	0.141	R.VNTISAGPLGSR.A
R5/RRR5-13/2	1172.015	1172.317	-257.887	0.448	475.089	0.517	16	0.139	R.VNTISAGPLGSR.A
R5/RRR5-13/2	1172.149	1172.317	-143.480	0.436	561.881	0.472	17	0.138	R.VNTISAGPLGSR.A
R5/RRR5-14/2	1171.642	1172.317	-1433.908	0.424	560.639	0.469	17	0.137	R.VNTISAGPLGSR.A
R5/RRR5-13/2	1113.842	1113.205	-326.538	0.436	632.952	0.435	15	0.137	R.YAGSSNWTVK.E
R5/RRR5-14/2	1112.535	1113.205	-1505.246	0.390	612.174	0.427	15	0.134	R.YAGSSNWTVK.E
R5/RRR5-14/2	1112.916	1113.205	-259.811	0.327	650.654	0.445	16	0.134	R.YAGSSNWTVK.E
R5/RRR5-13/2	1112.587	1113.205	-1458.186	0.377	777.934	0.379	16	0.134	R.YAGSSNWTVK.E
R5/RRR5-13/2	1113.096	1113.205	-97.524	0.466	677.682	0.350	16	0.131	R.YAGSSNWTVK.E
R5/RRR5-14/2	1112.464	1113.205	-1569.066	0.347	588.921	0.400	14	0.130	R.YAGSSNWTVK.E
R5/RRR5-14/2	1171.790	1172.317	-1306.984	0.413	424.069	0.392	16	0.129	R.VNTISAGPLGSR.A
R5/RRR5-14/2	1839.864	1840.028	-89.279	0.382	709.686	0.366	19	0.125	R.AFIAGVADDNGYGWAIAK.A
R5/RRR5-13/3	1441.577	1441.661	-58.919	0.389	1101.944	0.273	26	0.081	K.IRVNTISAGPLGSR.A
R5/RRR5-14/3	1441.678	1441.661	11.786	0.444	1112.500	0.272	24	0.080	K.IRVNTISAGPLGSR.A
R5/RRR5-14/3	1442.030	1441.661	256.312	0.386	947.540	0.311	22	0.080	K.IRVNTISAGPLGSR.A
R5/RRR5-13/3	1441.048	1441.661	-1123.024	0.397	1023.755	0.289	23	0.079	K.IRVNTISAGPLGSR.A
R5/RRR5-15/2	1695.372	1695.895	-901.254	0.449	853.700	0.517	21	0.151	K.LLESHLVPSSTAPESK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1696.462	1695.895	-255.965	0.517	697.473	0.554	19	0.148	K.LLESHLVPSSTAPESK.V
R5/RRR5-15/2	1695.391	1695.895	-889.905	0.474	676.130	0.561	19	0.147	K.LLESHLVPSSTAPESK.V
R5/RRR5-15/2	1695.373	1695.895	-900.820	0.475	672.310	0.527	19	0.143	K.LLESHLVPSSTAPESK.V
R5/RRR5-15/3	1695.821	1695.895	-43.985	0.407	692.054	0.454	26	0.090	-.LLESHLVPSSTAPESK.-
R5/RRR5-16/3	1695.462	1695.895	-256.196	0.364	633.184	0.428	25	0.084	-.LLESHLVPSSTAPESK.-
R5/RRR5-15/3	1695.902	1695.895	4.208	0.358	690.819	0.382	25	0.080	-.LLESHLVPSSTAPESK.-
R5/RRR5-16/3	1696.997	1695.895	59.796	0.309	592.787	0.278	23	0.070	-.LLESHLVPSSTAPESK.-
R5/RRR5-19/3	1967.801	1968.156	-181.012	0.473	1793.796	0.520	32	0.235	K.KAM*EDAIEGM*NGLDLDGR.A
R5/RRR5-19/2	1276.018	1275.434	-326.967	0.511	1487.733	0.495	17	0.199	R.GFGFVTFDEKK.A
R5/RRR5-19/2	1275.284	1275.434	-117.667	0.440	1322.515	0.455	16	0.174	R.GFGFVTFDEKK.A
R5/RRR5-19/2	1438.128	1438.614	-339.489	0.450	1265.647	0.448	19	0.166	R.AITVDKAQPQGPGR.D
R5/RRR5-19/2	1275.203	1275.434	-181.524	0.435	1212.267	0.386	16	0.154	R.GFGFVTFDEKK.A
R5/RRR5-19/2	1147.692	1147.261	376.304	0.396	1077.515	0.356	15	0.142	R.GFGFVTFDEK.K
R5/RRR5-19/2	879.811	879.980	-193.242	0.489	1081.510	0.318	14	0.140	K.FGNLTEAK.V
R5/RRR5-19/2	1274.931	1275.434	-1182.523	0.381	1122.197	0.318	16	0.139	R.GFGFVTFDEKK.A
R5/RRR5-19/2	879.916	879.980	-73.693	0.485	1044.018	0.310	14	0.137	K.FGNLTEAK.V
R5/RRR5-19/2	879.486	879.980	-563.761	0.453	1060.697	0.257	14	0.131	K.FGNLTEAK.V
R5/RRR5-18/2	879.209	879.980	-2020.852	0.351	487.960	0.273	12	0.124	K.FGNLTEAK.V
R5/RRR5-19/2	1146.496	1147.261	-1544.170	0.214	320.091	0.304	13	0.116	-.GFGFVTFDEK.-
R5/RRR5-19/2	1147.212	1147.261	-43.075	0.287	372.059	0.353	12	0.113	-.GFGFVTFDEK.-
R5/RRR5-19/3	1967.594	1968.156	-796.638	0.507	1000.996	0.424	27	0.100	K.KAM*EDAIEGM*NGLDLDGR.A
R5/RRR5-19/3	1439.481	1438.614	-93.028	0.320	721.512	0.458	24	0.090	R.AITVDKAQPQGPGR.D
R5/RRR5-19/3	1438.074	1438.614	-1074.689	0.284	388.169	0.371	19	0.080	R.AITVDKAQPQGPGR.D
R5/RRR5-18/3	1439.516	1438.614	-68.275	0.293	527.166	0.355	22	0.078	R.AITVDKAQPQGPGR.D
R5/RRR5-19/3	1438.439	1438.614	-122.546	0.282	594.596	0.328	22	0.075	R.AITVDKAQPQGPGR.D
R5/RRR5-25/2	1786.321	1786.939	-908.089	0.511	2474.684	0.488	24	0.346	K.FVSESVEEQTEQVM*K.N
R5/RRR5-25/2	1403.623	1404.596	-1410.021	0.421	1035.250	0.507	19	0.161	R.STYQVAALPLNAR.I
R5/RRR5-25/2	1403.637	1404.596	-1400.151	0.412	1069.727	0.476	19	0.158	R.STYQVAALPLNAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	1055.691	1056.151	-437.074	0.431	956.251	0.516	17	0.158	K.ASGASYSSVVK.T
R5/RRR5-26/2	1287.355	1287.489	-104.486	0.439	862.088	0.567	17	0.158	K.APAALGPYSQAIK.A
R5/RRR5-25/2	1404.064	1404.596	-1094.869	0.475	1060.219	0.459	19	0.156	R.STYQVAALPLNAR.I
R5/RRR5-25/2	1541.496	1540.807	-202.086	0.511	958.505	0.460	18	0.150	K.TTIM*LADLQDFKK.V
R5/RRR5-25/2	1288.307	1287.489	-142.233	0.479	612.380	0.567	16	0.147	K.APAALGPYSQAIK.A
R5/RRR5-26/2	1404.093	1404.596	-1073.918	0.413	1026.392	0.412	18	0.146	R.STYQVAALPLNAR.I
R5/RRR5-25/2	1540.255	1540.807	-1010.196	0.465	742.030	0.473	19	0.142	K.TTIM*LADLQDFKK.V
R5/RRR5-26/2	1286.963	1287.489	-1189.544	0.414	817.051	0.464	17	0.142	K.APAALGPYSQAIK.A
R5/RRR5-25/2	1286.659	1287.489	-1426.579	0.409	723.849	0.492	17	0.142	K.APAALGPYSQAIK.A
R5/RRR5-25/2	1286.567	1287.489	-1498.816	0.323	801.205	0.478	18	0.140	K.APAALGPYSQAIK.A
R5/RRR5-25/2	1055.895	1056.151	-243.229	0.391	677.635	0.475	15	0.138	K.ASGASYSSVVK.T
R5/RRR5-25/2	1540.202	1540.807	-1045.208	0.468	556.194	0.454	18	0.135	K.TTIM*LADLQDFKK.V
R5/RRR5-26/2	1286.573	1287.489	-1493.670	0.292	636.409	0.381	16	0.126	K.APAALGPYSQAIK.A
R5/RRR5-25/2	1055.342	1056.151	-1719.543	0.257	694.190	0.386	15	0.125	K.ASGASYSSVVK.T
R5/RRR5-3/2	1471.311	1471.596	-194.776	0.444	2387.104	0.500	20	0.332	K.TALSNFEAALDYR.N
R5/RRR5-3/2	1471.321	1471.596	-187.701	0.411	2139.393	0.441	19	0.271	K.TALSNFEAALDYR.N
R5/RRR5-3/2	1471.145	1471.596	-307.652	0.402	2174.273	0.382	19	0.261	K.TALSNFEAALDYR.N
R5/RRR5-3/2	1385.321	1384.562	-174.077	0.451	1471.054	0.542	17	0.206	K.YIDNLTNIYVR.F
R5/RRR5-3/2	1385.216	1384.562	-250.457	0.532	1291.750	0.496	16	0.180	K.YIDNLTNIYVR.F
R5/RRR5-3/2	1175.017	1174.417	-342.047	0.483	1435.619	0.326	16	0.161	R.LYLINSPVVR.A
R5/RRR5-3/2	1264.151	1264.370	-173.426	0.406	1414.252	0.328	17	0.159	R.ADQSLFEAGVAR.E
R5/RRR5-3/2	1323.162	1323.479	-239.903	0.410	1082.393	0.463	16	0.155	K.YVAEWEAVVTR.T
R5/RRR5-3/2	1264.048	1264.370	-255.190	0.459	1023.974	0.439	16	0.149	R.ADQSLFEAGVAR.E
R5/RRR5-3/2	1175.318	1174.417	-84.756	0.483	1205.962	0.330	15	0.145	R.LYLINSPVVR.A
R5/RRR5-3/2	1263.988	1264.370	-302.375	0.425	1221.336	0.307	17	0.142	R.ADQSLFEAGVAR.E
R5/RRR5-3/2	1175.181	1174.417	-201.975	0.455	1139.138	0.309	15	0.139	-.LYLINSPVVR.-
R5/RRR5-3/2	1196.266	1195.475	-175.079	0.304	326.764	0.496	14	0.126	R.LYTVVPYLVK.Y
R5/RRR5-17/2	1519.454	1518.782	-217.130	0.502	2324.578	0.477	21	0.313	K.ASILLLQDAAAYLR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1519.059	1518.782	182.672	0.494	2205.079	0.468	21	0.289	K.ASILLLQDAAAYLR.K
R5/RRR5-17/2	1146.920	1147.288	-321.668	0.397	1406.897	0.446	17	0.180	K.ALAAEM*GPNTR.V
R5/RRR5-18/2	1519.689	1518.782	-61.522	0.385	1404.544	0.402	17	0.169	K.ASILLLQDAAAYLR.K
R5/RRR5-17/2	1808.341	1808.026	174.912	0.530	989.785	0.547	19	0.162	R.FLTTNETIKNELIDR.S
R5/RRR5-17/2	1146.545	1147.288	-1524.627	0.391	1210.098	0.372	17	0.152	K.ALAAEM*GPNTR.V
R5/RRR5-17/2	1102.921	1102.180	-235.522	0.529	942.893	0.428	16	0.147	K.NVDEAVEGLR.A
R5/RRR5-17/2	1101.495	1102.180	-1534.895	0.403	1046.580	0.300	17	0.135	K.NVDEAVEGLR.A
R5/RRR5-17/2	816.532	817.009	-585.184	0.393	723.480	0.327	13	0.128	K.TALLGLTK.A
R5/RRR5-17/2	816.522	817.009	-597.788	0.325	796.306	0.248	12	0.117	-.TALLGLTK.-
R5/RRR5-23/3	1842.075	1842.027	25.874	0.494	1756.530	0.518	28	0.221	K.ERLEFLDVDKCECK.S
R5/RRR5-22/2	1017.647	1018.146	-492.456	0.392	1452.588	0.424	18	0.180	K.STLVEGGGIGK.A
R5/RRR5-22/2	1017.959	1018.146	-184.878	0.416	1460.423	0.415	18	0.180	K.STLVEGGGIGK.A
R5/RRR5-22/2	1017.554	1018.146	-1569.524	0.403	1448.136	0.419	18	0.179	K.STLVEGGGIGK.A
R5/RRR5-22/3	1842.545	1842.027	-262.723	0.538	1364.756	0.545	25	0.168	K.ERLEFLDVDKCECK.S
R5/RRR5-23/3	1841.713	1842.027	-171.167	0.512	1484.549	0.489	25	0.167	K.ERLEFLDVDKCECK.S
R5/RRR5-22/3	1842.046	1842.027	10.122	0.488	1431.542	0.477	25	0.157	K.ERLEFLDVDKCECK.S
R5/RRR5-23/2	1094.008	1094.286	-255.012	0.515	873.294	0.505	16	0.155	K.AKESLTGIFK.T
R5/RRR5-23/2	1442.367	1441.695	-227.800	0.446	765.086	0.545	20	0.153	K.LLPGVEVKDEITK.A
R5/RRR5-22/2	1442.186	1441.695	341.402	0.447	743.602	0.543	20	0.152	K.LLPGVEVKDEITK.A
R5/RRR5-22/2	1441.355	1441.695	-236.540	0.403	874.896	0.500	21	0.151	K.LLPGVEVKDEITK.A
R5/RRR5-23/2	1442.071	1441.695	261.705	0.425	748.674	0.520	20	0.148	K.LLPGVEVKDEITK.A
R5/RRR5-23/2	1441.097	1441.695	-1112.187	0.453	710.670	0.498	19	0.145	K.LLPGVEVKDEITK.A
R5/RRR5-22/3	1841.535	1842.027	-268.319	0.444	1371.154	0.456	24	0.143	K.ERLEFLDVDKCECK.S
R5/RRR5-23/2	1093.434	1094.286	-1698.494	0.382	910.469	0.420	16	0.143	K.AKESLTGIFK.T
R5/RRR5-22/2	1093.675	1094.286	-1476.907	0.457	711.654	0.435	15	0.139	K.AKESLTGIFK.T
R5/RRR5-22/2	1441.268	1441.695	-296.954	0.360	797.074	0.427	20	0.138	K.LLPGVEVKDEITK.A
R5/RRR5-22/2	1094.046	1094.286	-219.639	0.446	646.247	0.457	14	0.138	K.AKESLTGIFK.T
R5/RRR5-23/2	1017.242	1018.146	-1878.011	0.346	1021.261	0.345	16	0.137	K.STLVEGGGIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/3	1841.278	1842.027	-953.127	0.424	1217.668	0.486	24	0.133	K.ERLEFLDVDKCECK.S
R5/RRR5-22/2	1356.016	1356.575	-1153.331	0.373	1110.582	0.266	17	0.130	R.AAVM*DWHTLAPK.I
R5/RRR5-23/2	1017.242	1018.146	-1877.890	0.254	592.970	0.290	14	0.115	-.STLVEGGGIGK.-
R5/RRR5-23/3	1356.083	1356.575	-363.815	0.320	478.192	0.555	19	0.096	R.AAVM*DWHTLAPK.I
R5/RRR5-22/3	1356.585	1356.575	7.126	0.318	420.878	0.499	18	0.090	R.AAVM*DWHTLAPK.I
R5/RRR5-22/3	1356.179	1356.575	-293.371	0.295	518.479	0.456	20	0.086	R.AAVM*DWHTLAPK.I
R5/RRR5-23/3	1357.044	1356.575	346.542	0.305	539.407	0.445	21	0.085	R.AAVM*DWHTLAPK.I
R5/RRR5-23/3	1356.555	1356.575	-14.942	0.278	488.930	0.418	19	0.082	R.AAVM*DWHTLAPK.I
R5/RRR5-13/2	1204.144	1204.404	-216.029	0.582	2331.947	0.409	19	0.291	R.VVSNFVAQALR.K
R5/RRR5-13/2	1204.227	1204.404	-147.182	0.555	2143.468	0.457	19	0.276	R.VVSNFVAQALR.K
R5/RRR5-13/2	1432.264	1431.727	-324.124	0.500	1976.441	0.551	22	0.276	K.TNVVGTLNMLGLAK.R
R5/RRR5-13/2	1432.263	1431.727	-324.979	0.548	1893.050	0.555	23	0.265	K.TNVVGTLNMLGLAK.R
R5/RRR5-13/2	1447.596	1447.726	-89.952	0.484	2037.287	0.434	23	0.254	K.TNVVGTLNM*LGLAK.R
R5/RRR5-13/2	1204.272	1204.404	-109.254	0.500	1990.019	0.412	19	0.241	R.VVSNFVAQALR.K
R5/RRR5-13/2	1431.260	1431.727	-326.918	0.537	1688.498	0.492	22	0.221	K.TNVVGTLNMLGLAK.R
R5/RRR5-13/2	1447.487	1447.726	-165.916	0.442	1237.072	0.347	20	0.149	K.TNVVGTLNM*LGLAK.R
R5/RRR5-13/2	1333.291	1332.577	-214.663	0.392	835.398	0.331	16	0.126	R.VVSNFVAQALRK.E
R5/RRR5-14/2	1204.184	1204.404	-182.977	0.351	407.767	0.323	12	0.120	-.VVSNFVAQALR.-
R5/RRR5-13/3	1354.470	1354.471	-1.013	0.461	622.483	0.485	21	0.096	R.TAETLTM*DYHR.G
R5/RRR5-13/3	1354.549	1354.471	57.559	0.406	570.170	0.394	20	0.085	R.TAETLTM*DYHR.G
R5/RRR5-13/3	1354.063	1354.471	-302.253	0.377	639.893	0.362	21	0.081	R.TAETLTM*DYHR.G
R5/RRR5-13/3	1338.528	1338.472	41.919	0.402	574.735	0.307	21	0.080	R.TAETLTMDYHR.G
R5/RRR5-22/3	1639.832	1639.792	24.623	0.534	2376.650	0.400	32	0.304	K.HSGNISLDDVIEIAR.I
R5/RRR5-22/2	1344.075	1344.496	-314.328	0.425	2090.782	0.423	23	0.258	R.VTGGEVGAASSLAPK.I
R5/RRR5-21/3	1640.421	1639.792	-226.652	0.556	2142.999	0.389	30	0.245	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/3	1344.541	1344.496	33.673	0.412	2048.455	0.387	30	0.232	R.VTGGEVGAASSLAPK.I
R5/RRR5-21/2	1343.579	1344.496	-1431.025	0.370	1929.250	0.357	22	0.219	R.VTGGEVGAASSLAPK.I
R5/RRR5-22/2	1344.207	1344.496	-215.835	0.412	1672.184	0.411	20	0.199	R.VTGGEVGAASSLAPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1344.013	1344.496	-360.620	0.395	1661.273	0.401	20	0.196	R.VTGGEVGAASSLAPK.I
R5/RRR5-22/3	1639.876	1639.792	51.612	0.589	1808.723	0.425	29	0.194	K.HSGNISLDDVIEIAR.I
R5/RRR5-22/3	1344.150	1344.496	-258.096	0.461	1928.689	0.341	31	0.190	R.VTGGEVGAASSLAPK.I
R5/RRR5-21/2	1638.897	1639.792	-1159.867	0.554	1179.907	0.587	22	0.188	K.HSGNISLDDVIEIAR.I
R5/RRR5-22/2	1638.815	1639.792	-1210.130	0.559	1108.058	0.571	22	0.179	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	1343.817	1344.496	-1253.379	0.286	1659.915	0.301	21	0.176	R.VTGGEVGAASSLAPK.I
R5/RRR5-22/2	1639.529	1639.792	-160.678	0.570	1009.406	0.587	22	0.175	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	1255.177	1254.544	-292.988	0.504	902.089	0.588	22	0.169	K.VSVVPSAAALVIK.A
R5/RRR5-22/3	1639.155	1639.792	-1001.376	0.499	1789.906	0.357	28	0.169	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	1254.201	1254.544	-273.984	0.466	1133.309	0.494	22	0.168	K.VSVVPSAAALVIK.A
R5/RRR5-21/2	1638.747	1639.792	-1251.721	0.513	990.000	0.559	22	0.168	K.HSGNISLDDVIEIAR.I
R5/RRR5-22/2	1640.153	1639.792	220.544	0.600	941.275	0.571	22	0.168	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	1255.175	1254.544	-294.647	0.480	873.483	0.590	22	0.167	K.VSVVPSAAALVIK.A
R5/RRR5-21/2	1639.452	1639.792	-208.183	0.514	1130.471	0.488	22	0.166	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	1639.428	1639.792	-222.674	0.571	942.132	0.555	22	0.165	K.HSGNISLDDVIEIAR.I
R5/RRR5-22/2	1254.287	1254.544	-205.245	0.471	901.252	0.536	22	0.161	K.VSVVPSAAALVIK.A
R5/RRR5-22/2	1254.310	1254.544	-186.695	0.514	883.630	0.527	22	0.160	K.VSVVPSAAALVIK.A
R5/RRR5-22/2	1254.154	1254.544	-312.068	0.455	934.746	0.483	22	0.155	K.VSVVPSAAALVIK.A
R5/RRR5-21/3	1254.640	1254.544	77.023	0.471	1465.495	0.451	25	0.153	K.VSVVPSAAALVIK.A
R5/RRR5-21/2	1641.243	1639.792	275.676	0.483	626.239	0.534	19	0.144	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/3	1344.553	1344.496	42.688	0.410	1568.114	0.370	30	0.143	R.VTGGEVGAASSLAPK.I
R5/RRR5-21/2	1640.101	1639.792	188.824	0.457	737.198	0.485	20	0.143	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	881.970	882.082	-128.078	0.395	364.314	0.496	13	0.138	K.IGPLGLSPK.K
R5/RRR5-20/2	1639.714	1639.792	-47.759	0.471	555.079	0.476	19	0.137	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	882.003	882.082	-90.454	0.427	347.066	0.469	12	0.136	K.IGPLGLSPK.K
R5/RRR5-21/2	881.511	882.082	-1788.484	0.367	397.092	0.481	13	0.136	K.IGPLGLSPK.K
R5/RRR5-21/2	1732.228	1731.793	251.654	0.363	1284.625	0.312	23	0.134	K.DLQEEISDGEVEIPSA.-
R5/RRR5-22/2	881.889	882.082	-219.721	0.348	383.513	0.451	13	0.133	K.IGPLGLSPK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	881.562	882.082	-1730.187	0.338	309.958	0.413	12	0.131	K.IGPLGLSPK.K
R5/RRR5-21/2	881.976	882.082	-120.442	0.329	304.827	0.431	11	0.130	K.IGPLGLSPK.K
R5/RRR5-22/2	1640.841	1639.792	30.324	0.397	399.694	0.403	17	0.128	K.HSGNISLDDVIEIAR.I
R5/RRR5-22/2	881.778	882.082	-346.659	0.251	352.405	0.442	12	0.126	K.IGPLGLSPK.K
R5/RRR5-21/2	881.764	882.082	-362.077	0.276	360.713	0.370	12	0.126	K.IGPLGLSPK.K
R5/RRR5-22/2	1640.585	1639.792	-126.170	0.361	488.652	0.357	18	0.126	K.HSGNISLDDVIEIAR.I
R5/RRR5-22/2	881.887	882.082	-222.637	0.248	400.162	0.372	13	0.125	K.IGPLGLSPK.K
R5/RRR5-20/2	881.571	882.082	-1719.613	0.281	314.679	0.396	12	0.125	-.IGPLGLSPK.-
R5/RRR5-20/2	1343.840	1344.496	-1236.320	0.297	666.443	0.348	18	0.124	R.VTGGEVGAASSLAPK.I
R5/RRR5-21/2	1255.563	1254.544	15.348	0.241	436.432	0.348	15	0.121	K.VSVVPSAAALVIK.A
R5/RRR5-21/3	1639.949	1639.792	95.957	0.546	1308.024	0.392	25	0.119	-.HSGNISLDDVIEIAR.-
R5/RRR5-21/3	1639.309	1639.792	-295.669	0.468	1475.347	0.308	27	0.114	K.HSGNISLDDVIEIAR.I
R5/RRR5-21/2	1732.256	1731.793	267.765	0.384	1092.213	0.346	22	0.111	K.DLQEEISDGEVEIPSA.-
R5/RRR5-20/2	881.753	882.082	-374.301	0.200	202.662	0.348	10	0.103	-.IGPLGLSPK.-
R5/RRR5-21/2	1732.672	1731.793	-70.071	0.343	797.082	0.255	19	0.083	K.DLQEEISDGEVEIPSA.-
R5/RRR5-22/3	1253.943	1254.544	-1280.391	0.349	865.593	0.347	21	0.081	-.VSVVPSAAALVIK.-
R5/RRR5-22/3	1254.076	1254.544	-374.436	0.297	1019.885	0.318	25	0.081	K.VSVVPSAAALVIK.A
R5/RRR5-21/3	1254.319	1254.544	-180.067	0.370	700.420	0.365	21	0.077	-.VSVVPSAAALVIK.-
R5/RRR5-21/3	1254.584	1254.544	32.379	0.319	544.795	0.311	20	0.077	K.VSVVPSAAALVIK.A
R5/RRR5-15/2	1560.090	1560.650	-1003.028	0.485	1585.435	0.601	22	0.234	R.TLDAHIEEQFGSGR.L
R5/RRR5-16/2	1560.210	1560.650	-282.870	0.494	1312.960	0.568	20	0.195	R.TLDAHIEEQFGSGR.L
R5/RRR5-16/2	1560.166	1560.650	-311.365	0.518	1280.633	0.579	20	0.195	R.TLDAHIEEQFGSGR.L
R5/RRR5-16/2	1560.146	1560.650	-966.735	0.508	1291.470	0.519	20	0.184	R.TLDAHIEEQFGSGR.L
R5/RRR5-13/2	1566.372	1565.532	-102.757	0.380	1038.113	0.559	18	0.164	K.DAEGQDAEATTEEAK.K
R5/RRR5-16/3	1560.807	1560.650	100.823	0.447	1371.678	0.477	27	0.148	R.TLDAHIEEQFGSGR.L
R5/RRR5-16/3	1560.812	1560.650	104.235	0.419	1295.738	0.498	29	0.143	R.TLDAHIEEQFGSGR.L
R5/RRR5-15/3	1560.739	1560.650	57.171	0.431	1170.030	0.488	29	0.127	R.TLDAHIEEQFGSGR.L
R5/RRR5-16/3	1560.877	1560.650	146.000	0.460	1047.739	0.505	27	0.122	R.TLDAHIEEQFGSGR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1565.272	1565.532	-166.579	0.245	629.292	0.285	15	0.115	K.DAEGQDAEATTEEAK.K
R5/RRR5-15/2	1565.547	1565.532	9.337	0.240	540.299	0.294	14	0.114	K.DAEGQDAEATTEEAK.K
R5/RRR5-15/3	1560.338	1560.650	-200.699	0.379	971.621	0.432	26	0.100	R.TLDAHIEEQFGSGR.L
R5/RRR5-15/3	1560.761	1560.650	71.055	0.323	738.809	0.412	23	0.086	R.TLDAHIEEQFGSGR.L
R5/RRR5-14/2	1901.029	1902.181	-1135.055	0.534	2902.918	0.630	26	0.493	K.NPINYTQIAVLADDILK.N
R5/RRR5-14/2	1901.405	1902.181	-936.437	0.576	2796.359	0.615	25	0.460	K.NPINYTQIAVLADDILK.N
R5/RRR5-14/2	1613.164	1612.674	304.913	0.591	2758.286	0.603	25	0.447	K.VGDLDSYEIEGGETK.S
R5/RRR5-14/2	1612.303	1612.674	-230.445	0.563	2736.136	0.534	25	0.415	K.VGDLDSYEIEGGETK.S
R5/RRR5-14/2	1613.244	1612.674	-267.044	0.573	2596.012	0.573	25	0.399	K.VGDLDSYEIEGGETK.S
R5/RRR5-14/2	1901.722	1902.181	-241.729	0.596	2549.751	0.594	25	0.395	K.NPINYTQIAVLADDILK.N
R5/RRR5-14/3	1901.558	1902.181	-856.014	0.503	1953.209	0.429	32	0.229	K.NPINYTQIAVLADDILK.N
R5/RRR5-14/2	1737.309	1737.911	-924.672	0.523	1768.769	0.428	22	0.215	R.DSKDNIEMTVSELQK.N
R5/RRR5-14/2	1192.418	1193.326	-1605.247	0.368	1137.005	0.488	19	0.163	K.GLCGGINSTSVK.V
R5/RRR5-14/2	1192.920	1193.326	-341.327	0.470	1064.129	0.488	19	0.162	K.GLCGGINSTSVK.V
R5/RRR5-14/2	1192.894	1193.326	-363.197	0.480	1062.346	0.457	18	0.156	K.GLCGGINSTSVK.V
R5/RRR5-14/3	1901.957	1902.181	-118.173	0.448	1456.111	0.421	31	0.144	K.NPINYTQIAVLADDILK.N
R5/RRR5-14/2	1059.911	1060.226	-298.679	0.386	780.800	0.500	14	0.144	K.NVIVAITSDK.G
R5/RRR5-14/2	1059.367	1060.226	-1760.280	0.372	910.005	0.420	15	0.141	K.NVIVAITSDK.G
R5/RRR5-14/2	1753.471	1753.910	-251.073	0.472	488.457	0.492	16	0.131	R.DSKDNIEM*TVSELQK.N
R5/RRR5-14/2	1060.194	1060.226	-31.020	0.345	717.141	0.354	14	0.127	K.NVIVAITSDK.G
R5/RRR5-14/3	1900.863	1902.181	-1222.696	0.297	841.749	0.314	26	0.074	K.NPINYTQIAVLADDILK.N
R5/RRR5-19/2	1712.589	1712.926	-197.505	0.582	2159.508	0.538	26	0.301	R.NQDTGLAELPATVAALK.N
R5/RRR5-18/2	1714.362	1712.926	254.919	0.654	1863.493	0.577	25	0.264	R.NQDTGLAELPATVAALK.N
R5/RRR5-19/2	1777.176	1775.896	158.414	0.543	1965.260	0.497	21	0.257	R.TEDDIALANSVDVGSLR.H
R5/RRR5-18/2	1712.570	1712.926	-208.731	0.574	1853.081	0.514	25	0.246	R.NQDTGLAELPATVAALK.N
R5/RRR5-18/2	1712.576	1712.926	-205.013	0.566	1818.225	0.504	25	0.239	R.NQDTGLAELPATVAALK.N
R5/RRR5-19/2	1713.050	1712.926	72.644	0.594	1660.948	0.522	24	0.222	R.NQDTGLAELPATVAALK.N
R5/RRR5-18/2	1188.266	1188.359	-78.681	0.370	1626.178	0.357	17	0.184	R.AFAYFVLSGGR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1324.083	1324.380	-225.403	0.417	794.896	0.533	15	0.151	K.VVYDEYNHER.H
R5/RRR5-19/2	1324.020	1324.380	-272.945	0.443	789.823	0.508	14	0.148	K.VVYDEYNHER.H
R5/RRR5-18/2	1323.799	1324.380	-1198.249	0.426	563.557	0.554	13	0.143	K.VVYDEYNHER.H
R5/RRR5-19/2	1188.005	1188.359	-299.660	0.429	1005.550	0.395	14	0.142	R.AFAYFVLSGGR.F
R5/RRR5-19/2	1323.783	1324.380	-1210.009	0.392	617.893	0.503	14	0.140	K.VVYDEYNHER.H
R5/RRR5-19/2	986.029	986.168	-140.975	0.311	775.433	0.324	16	0.127	K.FVLSM*SASK.D
R5/RRR5-19/2	1187.461	1188.359	-1603.906	0.281	696.202	0.354	15	0.124	R.AFAYFVLSGGR.F
R5/RRR5-18/2	985.413	986.168	-1786.493	0.319	518.809	0.306	14	0.122	-.FVLSM*SASK.-
R5/RRR5-19/2	985.798	986.168	-376.617	0.362	557.932	0.247	14	0.120	-.FVLSM*SASK.-
R5/RRR5-6/2	1402.707	1403.608	-1359.356	0.524	2821.618	0.506	24	0.424	K.AIGIDKFGASAPAGK.I
R5/RRR5-6/2	1884.444	1885.107	-885.221	0.564	2625.227	0.620	27	0.423	K.IYQEYGITAENVIATAK.S
R5/RRR5-6/2	1885.330	1885.107	118.674	0.611	2569.633	0.619	26	0.409	K.IYQEYGITAENVIATAK.S
R5/RRR5-6/2	1884.412	1885.107	-901.999	0.555	2566.092	0.603	26	0.403	K.IYQEYGITAENVIATAK.S
R5/RRR5-6/3	1884.495	1885.107	-857.884	0.533	2417.063	0.489	33	0.367	K.IYQEYGITAENVIATAK.S
R5/RRR5-6/2	1403.277	1403.608	-236.851	0.532	2309.649	0.539	23	0.330	K.AIGIDKFGASAPAGK.I
R5/RRR5-6/3	1884.611	1885.107	-263.941	0.546	2256.094	0.478	32	0.318	K.IYQEYGITAENVIATAK.S
R5/RRR5-6/2	1376.039	1376.540	-1094.122	0.480	2264.882	0.405	21	0.281	R.VSLEAGSTLGWQK.Y
R5/RRR5-6/2	1376.166	1376.540	-272.478	0.500	1902.228	0.486	20	0.247	R.VSLEAGSTLGWQK.Y
R5/RRR5-6/2	1402.417	1403.608	-1567.596	0.500	1753.843	0.537	23	0.240	K.AIGIDKFGASAPAGK.I
R5/RRR5-5/2	1377.145	1376.540	-287.843	0.407	1608.633	0.452	19	0.201	R.VSLEAGSTLGWQK.Y
R5/RRR5-6/2	1376.182	1376.540	-260.998	0.467	1431.461	0.397	18	0.172	R.VSLEAGSTLGWQK.Y
R5/RRR5-6/2	1443.362	1442.640	-193.119	0.491	810.031	0.586	22	0.163	K.LAQLPGTSIEGVEK.G
R5/RRR5-6/2	1443.404	1442.640	-163.933	0.487	693.908	0.553	20	0.151	K.LAQLPGTSIEGVEK.G
R5/RRR5-1/2	1442.363	1442.640	-192.234	0.426	711.484	0.510	21	0.146	K.LAQLPGTSIEGVEK.G
R5/RRR5-5/2	1443.198	1442.640	-307.077	0.466	641.949	0.521	20	0.146	K.LAQLPGTSIEGVEK.G
R5/RRR5-1/2	1443.434	1442.640	-142.639	0.494	569.990	0.542	19	0.146	K.LAQLPGTSIEGVEK.G
R5/RRR5-2/2	1442.117	1442.640	-1059.016	0.456	740.839	0.486	21	0.145	K.LAQLPGTSIEGVEK.G
R5/RRR5-4/2	1442.359	1442.640	-195.290	0.447	784.906	0.462	21	0.144	K.LAQLPGTSIEGVEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1443.514	1442.640	-87.500	0.403	789.974	0.461	21	0.143	K.LAQLPGTSIEGVEK.G
R5/RRR5-6/2	1442.275	1442.640	-253.537	0.452	694.925	0.464	21	0.142	K.LAQLPGTSIEGVEK.G
R5/RRR5-5/2	1443.297	1442.640	-238.342	0.442	604.442	0.494	20	0.141	K.LAQLPGTSIEGVEK.G
R5/RRR5-5/2	1441.913	1442.640	-1201.055	0.447	555.378	0.505	19	0.141	K.LAQLPGTSIEGVEK.G
R5/RRR5-1/2	1442.215	1442.640	-295.316	0.432	584.017	0.484	19	0.139	K.LAQLPGTSIEGVEK.G
R5/RRR5-3/2	1443.521	1442.640	-82.664	0.455	425.726	0.525	17	0.139	K.LAQLPGTSIEGVEK.G
R5/RRR5-6/2	1172.475	1172.314	138.405	0.446	561.268	0.474	17	0.138	K.ESVLPEAVTAR.V
R5/RRR5-6/2	1442.965	1442.640	225.990	0.412	590.843	0.440	19	0.135	K.LAQLPGTSIEGVEK.G
R5/RRR5-4/2	1442.185	1442.640	-316.461	0.404	504.838	0.416	18	0.131	K.LAQLPGTSIEGVEK.G
R5/RRR5-6/2	1171.334	1172.314	-1694.976	0.294	504.441	0.386	15	0.123	K.ESVLPEAVTAR.V
R5/RRR5-2/2	1376.261	1376.540	-202.890	0.274	284.171	0.417	12	0.121	R.VSLEAGSTLGWQK.Y
R5/RRR5-6/3	1885.179	1885.107	38.337	0.356	590.109	0.347	23	0.074	-.IYQEYGITAENVIATAK.-
R5/RRR5-18/2	1431.287	1431.702	-290.556	0.465	1324.638	0.561	19	0.183	K.LGSQIDILAPIKY.-
R5/RRR5-18/2	1432.219	1431.702	-338.240	0.476	1252.732	0.604	19	0.176	K.LGSQIDILAPIKY.-
R5/RRR5-18/3	1538.450	1538.759	-201.791	0.478	1674.223	0.444	27	0.175	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/2	1431.249	1431.702	-317.425	0.440	1253.141	0.559	19	0.172	K.LGSQIDILAPIKY.-
R5/RRR5-18/2	1430.912	1431.702	-1254.698	0.423	1250.022	0.481	18	0.161	K.LGSQIDILAPIKY.-
R5/RRR5-19/2	1431.187	1431.702	-1061.800	0.368	1245.052	0.459	18	0.160	K.LGSQIDILAPIKY.-
R5/RRR5-18/3	1538.679	1538.759	-52.443	0.460	1541.063	0.435	27	0.153	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/3	1538.566	1538.759	-125.858	0.435	1485.004	0.430	27	0.145	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/3	1538.339	1538.759	-273.675	0.442	1514.889	0.416	28	0.144	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/3	1538.579	1538.759	-117.262	0.484	1407.864	0.445	27	0.140	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/3	1523.099	1522.760	223.778	0.486	1313.761	0.471	26	0.137	R.MNTKPSHGPIHFR.A
R5/RRR5-19/3	1538.630	1538.759	-84.434	0.455	1337.092	0.459	26	0.137	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/2	1411.780	1411.594	132.029	0.446	787.475	0.397	16	0.132	R.CEEMCISGGLVR.Q
R5/RRR5-18/3	1538.719	1538.759	-26.064	0.456	1323.501	0.439	26	0.130	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/2	1431.317	1431.702	-269.592	0.359	923.011	0.560	16	0.129	K.LGSQIDILAPIKY.-
R5/RRR5-18/2	887.131	887.016	129.649	0.364	806.347	0.357	12	0.128	R.GEAALANLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/3	1538.386	1538.759	-243.224	0.506	1270.826	0.449	27	0.127	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/3	1538.328	1538.759	-280.960	0.489	1218.774	0.466	26	0.127	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/3	1539.527	1538.759	-150.990	0.499	1297.705	0.433	26	0.126	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/3	1538.197	1538.759	-1018.533	0.447	1261.972	0.426	25	0.121	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/3	1538.189	1538.759	-1023.673	0.414	1122.113	0.461	25	0.117	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/3	1538.791	1538.759	21.081	0.473	1191.160	0.382	25	0.105	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/3	1522.999	1522.760	157.470	0.438	1196.092	0.377	24	0.105	R.MNTKPSHGPIHFR.A
R5/RRR5-19/3	1538.118	1538.759	-1070.406	0.388	523.231	0.440	22	0.094	R.M*NTKPSHGPIHFR.A
R5/RRR5-19/3	1538.677	1538.759	-53.756	0.383	757.517	0.407	23	0.091	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/3	1091.102	1091.279	-162.566	0.385	624.955	0.444	16	0.089	K.YCLLGHLSK.E
R5/RRR5-18/3	1091.085	1091.279	-177.718	0.345	809.398	0.415	18	0.087	K.YCLLGHLSK.E
R5/RRR5-19/3	1090.927	1091.279	-323.196	0.377	638.136	0.375	16	0.082	K.YCLLGHLSK.E
R5/RRR5-19/3	1523.916	1522.760	103.223	0.405	592.806	0.305	19	0.081	R.MNTKPSHGPIHFR.A
R5/RRR5-17/3	1538.703	1538.759	-36.687	0.327	625.831	0.284	21	0.079	R.M*NTKPSHGPIHFR.A
R5/RRR5-18/3	1091.423	1091.279	132.292	0.374	672.892	0.318	17	0.078	K.YCLLGHLSK.E
R5/RRR5-19/3	1522.545	1522.760	-141.630	0.396	878.448	0.200	23	0.069	R.MNTKPSHGPIHFR.A
R5/RRR5-16/3	1538.076	1538.759	-1097.421	0.246	733.034	0.136	20	0.065	-.M*NTKPSHGPIHFR.-
R5/RRR5-11/2	1847.250	1848.090	-999.019	0.521	1838.875	0.536	23	0.252	R.YFKGEDFPVQNYIVK.E
R5/RRR5-11/2	1847.672	1848.090	-226.999	0.553	1344.557	0.541	21	0.193	R.YFKGEDFPVQNYIVK.E
R5/RRR5-11/2	1339.979	1340.481	-1124.474	0.530	1464.983	0.468	18	0.192	K.YEEDLDAM*LPK.C
R5/RRR5-11/2	1083.547	1084.297	-1620.432	0.544	1375.082	0.430	17	0.176	K.KGVIIVNNAR.G
R5/RRR5-11/2	1083.720	1084.297	-1459.971	0.485	1472.906	0.364	17	0.172	K.KGVIIVNNAR.G
R5/RRR5-11/2	1340.050	1340.481	-322.851	0.469	1400.398	0.348	18	0.163	K.YEEDLDAM*LPK.C
R5/RRR5-11/2	1083.375	1084.297	-1779.926	0.452	1122.319	0.408	16	0.154	K.KGVIIVNNAR.G
R5/RRR5-11/2	1339.965	1340.481	-1134.719	0.405	1187.503	0.373	17	0.151	K.YEEDLDAM*LPK.C
R5/RRR5-16/2	1084.741	1084.297	409.881	0.457	496.423	0.337	15	0.128	K.KGVIIVNNAR.G
R5/RRR5-10/2	1341.331	1340.481	-112.234	0.382	1115.969	0.214	17	0.127	K.YEEDLDAM*LPK.C
R5/RRR5-11/2	957.022	956.125	-107.224	0.485	731.654	0.282	13	0.118	-.GVIIVNNAR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	957.011	956.125	-119.379	0.413	838.690	0.226	13	0.117	-.GVIIVNNAR.-
R5/RRR5-11/3	1848.811	1848.090	-151.172	0.494	691.373	0.496	25	0.095	R.YFKGEDFPVQNYIVK.E
R5/RRR5-11/3	1085.191	1085.276	-78.156	0.545	1541.178	0.179	23	0.091	R.LKIDPELEK.E
R5/RRR5-11/3	1085.036	1085.276	-221.701	0.494	1376.299	0.186	21	0.081	R.LKIDPELEK.E
R5/RRR5-11/3	1085.626	1085.276	323.822	0.474	1454.590	0.157	21	0.080	R.LKIDPELEK.E
R5/RRR5-11/2	1438.468	1438.656	-131.301	0.538	3412.072	0.568	25	0.603	K.YVILGGGVAAGYAAR.E
R5/RRR5-11/2	1438.131	1438.656	-1063.654	0.502	2800.415	0.525	25	0.427	K.YVILGGGVAAGYAAR.E
R5/RRR5-11/2	1438.181	1438.656	-331.134	0.474	2555.190	0.507	24	0.367	K.YVILGGGVAAGYAAR.E
R5/RRR5-11/2	1985.148	1985.143	2.121	0.568	1520.345	0.530	23	0.207	K.LSDFGTQGADSNNILYLR.E
R5/RRR5-11/2	1985.774	1985.143	-186.611	0.570	1368.341	0.519	21	0.186	K.LSDFGTQGADSNNILYLR.E
R5/RRR5-10/2	1984.444	1985.143	-859.061	0.518	1456.844	0.463	22	0.185	K.LSDFGTQGADSNNILYLR.E
R5/RRR5-10/2	1586.586	1586.769	-115.647	0.416	1208.304	0.397	21	0.155	R.EVDDADKLVAAIQAK.K
R5/RRR5-10/2	1586.598	1586.769	-108.161	0.486	1125.720	0.396	24	0.152	R.EVDDADKLVAAIQAK.K
R5/RRR5-10/2	1586.234	1586.769	-970.441	0.475	827.328	0.456	22	0.144	R.EVDDADKLVAAIQAK.K
R5/RRR5-11/2	1586.507	1586.769	-165.353	0.496	944.173	0.377	22	0.139	R.EVDDADKLVAAIQAK.K
R5/RRR5-11/2	1586.347	1586.769	-266.863	0.487	819.982	0.369	21	0.133	R.EVDDADKLVAAIQAK.K
R5/RRR5-11/2	1586.260	1586.769	-954.294	0.473	925.704	0.335	21	0.132	R.EVDDADKLVAAIQAK.K
R5/RRR5-11/2	1431.246	1431.619	-260.966	0.413	527.751	0.422	17	0.130	K.EAVAPYERPALSK.G
R5/RRR5-11/2	1431.153	1431.619	-325.916	0.403	686.929	0.381	18	0.130	K.EAVAPYERPALSK.G
R5/RRR5-11/2	1431.247	1431.619	-260.367	0.417	640.203	0.387	18	0.130	K.EAVAPYERPALSK.G
R5/RRR5-23/2	1964.387	1965.195	-923.367	0.544	2047.974	0.612	29	0.305	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-23/2	1964.514	1965.195	-858.552	0.548	2047.750	0.563	29	0.290	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-25/2	1964.789	1965.195	-207.299	0.538	2012.111	0.576	29	0.288	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-25/2	1964.939	1965.195	-131.015	0.494	1902.211	0.545	29	0.262	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-25/2	1964.582	1965.195	-823.809	0.549	1824.130	0.560	28	0.255	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-23/2	1964.485	1965.195	-873.211	0.538	1807.112	0.545	28	0.249	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-22/2	1964.467	1965.195	-882.256	0.509	1813.430	0.529	28	0.245	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-22/2	1964.221	1965.195	-1008.343	0.536	1404.850	0.566	25	0.203	R.IWVFSGDTDAVLPVTSTR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/3	1298.866	1298.479	299.409	0.526	1351.193	0.550	25	0.165	R.GAGHEVPLHRPK.Q
R5/RRR5-23/2	905.925	906.064	-153.952	0.452	1189.749	0.427	12	0.161	K.GLNFVTVR.G
R5/RRR5-22/2	1963.795	1965.195	-1226.028	0.395	980.141	0.506	21	0.154	R.IWVFSGDTDAVLPVTSTR.Y
R5/RRR5-22/2	1535.909	1536.713	-1178.331	0.541	721.158	0.567	18	0.153	K.HSTVYFNLAEVQK.A
R5/RRR5-23/2	905.857	906.064	-228.707	0.409	1206.428	0.366	12	0.152	K.GLNFVTVR.G
R5/RRR5-23/3	1298.648	1298.479	130.746	0.522	1607.363	0.397	27	0.152	R.GAGHEVPLHRPK.Q
R5/RRR5-23/2	1535.965	1536.713	-1141.620	0.548	732.459	0.533	19	0.150	K.HSTVYFNLAEVQK.A
R5/RRR5-25/2	905.925	906.064	-153.681	0.375	1096.244	0.399	12	0.149	K.GLNFVTVR.G
R5/RRR5-23/2	905.880	906.064	-203.427	0.448	1023.463	0.384	12	0.145	K.GLNFVTVR.G
R5/RRR5-22/2	905.889	906.064	-194.234	0.361	900.354	0.313	12	0.131	K.GLNFVTVR.G
R5/RRR5-23/2	1092.008	1092.316	-282.948	0.365	466.118	0.489	12	0.129	K.ALHVSPIINK.S
R5/RRR5-26/2	905.838	906.064	-249.798	0.334	754.977	0.314	12	0.127	K.GLNFVTVR.G
R5/RRR5-15/2	1966.918	1965.195	-141.465	0.390	313.921	0.527	13	0.119	-.IWVFSGDTDAVLPVTSTR.-
R5/RRR5-22/2	905.459	906.064	-1777.486	0.281	741.929	0.209	12	0.119	-.GLNFVTVR.-
R5/RRR5-25/3	1298.442	1298.479	-28.639	0.509	1155.485	0.434	24	0.115	R.GAGHEVPLHRPK.Q
R5/RRR5-22/2	905.520	906.064	-1709.896	0.249	639.106	0.169	11	0.115	-.GLNFVTVR.-
R5/RRR5-22/3	1298.430	1298.479	-37.833	0.504	1157.493	0.398	23	0.108	R.GAGHEVPLHRPK.Q
R5/RRR5-25/3	1298.244	1298.479	-181.142	0.484	1067.339	0.407	23	0.103	R.GAGHEVPLHRPK.Q
R5/RRR5-23/3	1298.883	1298.479	312.414	0.487	916.290	0.439	22	0.101	R.GAGHEVPLHRPK.Q
R5/RRR5-22/3	1298.760	1298.479	216.993	0.429	989.471	0.361	21	0.091	R.GAGHEVPLHRPK.Q
R5/RRR5-25/3	1298.604	1298.479	96.525	0.471	949.556	0.362	23	0.084	-.GAGHEVPLHRPK.-
R5/RRR5-24/3	1298.127	1298.479	-271.562	0.416	550.348	0.379	18	0.072	-.GAGHEVPLHRPK.-
R5/RRR5-20/2	1466.004	1465.633	253.841	0.483	1782.604	0.496	21	0.234	R.DSSVAVIVFDVASR.Q
R5/RRR5-19/2	1215.477	1214.437	33.079	0.423	1830.089	0.400	18	0.217	R.GSDVIIVLVGNK.T
R5/RRR5-20/2	1465.379	1465.633	-173.841	0.375	1731.880	0.433	20	0.211	R.DSSVAVIVFDVASR.Q
R5/RRR5-20/2	1510.460	1510.781	-212.830	0.419	1595.282	0.471	20	0.203	K.AKDLGVMFIETSAK.A
R5/RRR5-20/2	1465.821	1465.633	128.247	0.448	1553.534	0.485	20	0.203	R.DSSVAVIVFDVASR.Q
R5/RRR5-20/2	1213.872	1214.437	-1292.639	0.394	1229.121	0.355	17	0.150	R.GSDVIIVLVGNK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1477.487	1476.721	-158.803	0.441	611.234	0.535	21	0.145	K.IAAALPGM*ETLSSAK.Q
R5/RRR5-17/2	1317.200	1317.432	-176.666	0.443	985.962	0.375	16	0.140	-.LQLWDTAGQER.-
R5/RRR5-19/2	1318.062	1317.432	-281.889	0.480	937.683	0.381	16	0.140	R.LQLWDTAGQER.F
R5/RRR5-18/2	1316.533	1317.432	-1446.938	0.300	1029.205	0.301	16	0.133	R.LQLWDTAGQER.F
R5/RRR5-19/2	1461.708	1460.722	-9.516	0.402	375.651	0.486	17	0.132	K.IAAALPGMETLSSAK.Q
R5/RRR5-20/2	1461.514	1460.722	-142.634	0.389	524.484	0.441	19	0.131	K.IAAALPGMETLSSAK.Q
R5/RRR5-19/2	1476.231	1476.721	-333.110	0.333	436.657	0.444	18	0.128	K.IAAALPGM*ETLSSAK.Q
R5/RRR5-19/2	1316.860	1317.432	-1197.961	0.310	796.539	0.316	15	0.127	R.LQLWDTAGQER.F
R5/RRR5-20/2	1476.168	1476.721	-1054.969	0.283	505.089	0.420	20	0.127	K.IAAALPGM*ETLSSAK.Q
R5/RRR5-19/2	1316.530	1317.432	-1449.453	0.270	830.791	0.318	15	0.127	R.LQLWDTAGQER.F
R5/RRR5-20/2	1476.105	1476.721	-1098.146	0.270	529.902	0.402	20	0.125	K.IAAALPGM*ETLSSAK.Q
R5/RRR5-19/2	1316.392	1317.432	-1554.985	0.276	874.641	0.272	15	0.124	-.LQLWDTAGQER.-
R5/RRR5-17/2	1316.491	1317.432	-1478.977	0.312	806.829	0.289	14	0.124	R.LQLWDTAGQER.F
R5/RRR5-17/2	1318.178	1317.432	-193.439	0.358	910.539	0.244	15	0.124	R.LQLWDTAGQER.F
R5/RRR5-18/2	1316.590	1317.432	-1403.447	0.256	1005.042	0.216	16	0.123	R.LQLWDTAGQER.F
R5/RRR5-20/2	1460.448	1460.722	-187.674	0.302	442.590	0.351	18	0.123	K.IAAALPGMETLSSAK.Q
R5/RRR5-20/2	1316.408	1317.432	-1542.130	0.274	921.854	0.222	15	0.122	R.LQLWDTAGQER.F
R5/RRR5-20/2	1317.022	1317.432	-312.604	0.317	832.878	0.223	15	0.120	-.LQLWDTAGQER.-
R5/RRR5-20/2	1214.017	1214.437	-346.893	0.280	522.395	0.299	13	0.118	R.GSDVIIVLVGNK.T
R5/RRR5-20/2	1316.556	1317.432	-1429.243	0.276	903.804	0.103	15	0.114	-.LQLWDTAGQER.-
R5/RRR5-15/2	1116.365	1115.393	-24.853	0.544	1718.960	0.504	17	0.229	K.LLLAYVGIPR.Y
R5/RRR5-14/2	1074.992	1074.255	-245.058	0.509	1517.178	0.498	16	0.211	R.TFLLSLVGSH.-
R5/RRR5-15/2	1074.926	1074.255	-306.353	0.449	1354.287	0.580	16	0.193	R.TFLLSLVGSH.-
R5/RRR5-15/2	1372.033	1372.661	-1189.849	0.478	1389.138	0.384	17	0.166	K.AM*LLWILDPAGR.D
R5/RRR5-15/2	1115.652	1115.393	233.030	0.473	1017.342	0.487	14	0.157	K.LLLAYVGIPR.Y
R5/RRR5-14/2	1020.817	1021.152	-328.888	0.360	880.430	0.395	13	0.137	R.ALIQQEYR.T
R5/RRR5-14/2	1074.150	1074.255	-97.526	0.305	1031.078	0.461	13	0.133	R.TFLLSLVGSH.-
R5/RRR5-15/2	1115.415	1115.393	20.130	0.358	710.838	0.413	14	0.132	K.LLLAYVGIPR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1020.688	1021.152	-455.602	0.346	1105.266	0.229	13	0.128	R.ALIQQEYR.T
R5/RRR5-15/2	1074.154	1074.255	-93.651	0.318	887.417	0.465	14	0.124	R.TFLLSLVGSH.-
R5/RRR5-14/2	1073.324	1074.255	-1803.894	0.372	596.286	0.385	15	0.123	R.TFLLSLVGSH.-
R5/RRR5-15/2	1189.762	1190.286	-1284.360	0.253	1125.420	0.146	16	0.118	R.EALSGDTIDLR.A
R5/RRR5-15/2	1073.543	1074.255	-1599.265	0.332	735.737	0.369	13	0.112	R.TFLLSLVGSH.-
R5/RRR5-19/2	1678.567	1678.870	-180.865	0.427	959.571	0.372	19	0.138	R.LFTLQIWDTAGQER.F
R5/RRR5-20/2	1678.116	1678.870	-1048.490	0.388	1341.415	0.212	19	0.136	R.LFTLQIWDTAGQER.F
R5/RRR5-19/2	1678.401	1678.870	-280.093	0.389	355.383	0.378	14	0.123	R.LFTLQIWDTAGQER.F
R5/RRR5-19/2	1679.064	1678.870	116.116	0.383	412.190	0.322	14	0.120	R.LFTLQIWDTAGQER.F
R5/RRR5-20/2	1678.124	1678.870	-1043.451	0.394	739.481	0.195	16	0.113	R.LFTLQIWDTAGQER.F
R5/RRR5-17/2	1281.190	1281.503	-245.341	0.493	1417.785	0.467	17	0.186	K.NM*GLLLAEFEK.I
R5/RRR5-16/2	1250.625	1251.414	-1434.396	0.460	1420.250	0.421	17	0.179	R.TYLNTLQEIR.I
R5/RRR5-17/2	1370.666	1370.490	128.799	0.495	1063.816	0.494	20	0.163	K.ITIDPDDPAAVSR.Y
R5/RRR5-17/2	1280.990	1281.503	-1184.831	0.439	1187.167	0.444	16	0.162	K.NM*GLLLAEFEK.I
R5/RRR5-16/2	1071.397	1072.194	-1681.890	0.366	1035.071	0.516	15	0.160	R.TPVNGDDLLK.G
R5/RRR5-17/2	1369.502	1370.490	-1456.507	0.331	1165.752	0.444	21	0.158	K.ITIDPDDPAAVSR.Y
R5/RRR5-17/2	1071.992	1072.194	-189.208	0.452	1047.955	0.469	15	0.157	R.TPVNGDDLLK.G
R5/RRR5-17/2	1071.978	1072.194	-202.003	0.439	982.551	0.489	15	0.156	R.TPVNGDDLLK.G
R5/RRR5-16/2	1251.175	1251.414	-191.468	0.488	1075.519	0.428	16	0.154	R.TYLNTLQEIR.I
R5/RRR5-16/2	1072.301	1072.194	100.524	0.470	946.920	0.479	15	0.153	R.TPVNGDDLLK.G
R5/RRR5-17/2	1280.723	1281.503	-1394.442	0.393	1055.472	0.443	15	0.151	K.NM*GLLLAEFEK.I
R5/RRR5-17/2	1071.466	1072.194	-1617.105	0.404	939.328	0.470	15	0.150	R.TPVNGDDLLK.G
R5/RRR5-16/2	1369.981	1370.490	-1104.948	0.404	907.990	0.458	19	0.146	K.ITIDPDDPAAVSR.Y
R5/RRR5-16/2	1370.167	1370.490	-236.945	0.433	865.629	0.456	18	0.144	K.ITIDPDDPAAVSR.Y
R5/RRR5-16/2	1250.604	1251.414	-1451.357	0.355	850.564	0.406	15	0.138	R.TYLNTLQEIR.I
R5/RRR5-15/2	1251.111	1251.414	-242.562	0.385	640.920	0.478	13	0.138	R.TYLNTLQEIR.I
R5/RRR5-17/2	1251.362	1251.414	-41.741	0.360	768.291	0.385	14	0.133	R.TYLNTLQEIR.I
R5/RRR5-15/2	1251.282	1251.414	-106.030	0.336	681.071	0.362	14	0.129	R.TYLNTLQEIR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1281.161	1281.503	-268.378	0.338	630.529	0.392	15	0.128	K.NM*GLLLAEFEK.I
R5/RRR5-15/2	1250.563	1251.414	-1484.399	0.320	429.048	0.421	11	0.126	R.TYLNTLQEIR.I
R5/RRR5-15/2	1252.239	1251.414	-139.877	0.356	497.709	0.354	13	0.124	-.TYLNTLQEIR.-
R5/RRR5-17/3	1230.689	1230.435	207.059	0.415	971.816	0.347	20	0.086	R.IKYTIDTFTK.G
R5/RRR5-16/3	1230.524	1230.435	72.613	0.392	711.153	0.340	18	0.079	R.IKYTIDTFTK.G
R5/RRR5-17/3	1230.025	1230.435	-333.928	0.336	959.635	0.293	20	0.076	R.IKYTIDTFTK.G
R5/RRR5-16/2	1295.521	1295.430	70.161	0.498	1092.337	0.621	21	0.185	R.HSGLAVAGLAADGR.Q
R5/RRR5-16/2	1115.242	1114.231	10.143	0.473	652.587	0.516	16	0.145	K.VPDDLVEQAK.A
R5/RRR5-16/2	1040.857	1041.182	-312.969	0.354	1049.968	0.396	14	0.144	R.VFQVEYAGK.A
R5/RRR5-15/2	1706.345	1706.964	-951.928	0.511	2207.685	0.540	24	0.312	R.IQDNLALVYLSSITR.T
R5/RRR5-15/2	1706.502	1706.964	-272.037	0.503	1812.602	0.525	23	0.245	R.IQDNLALVYLSSITR.T
R5/RRR5-15/2	1296.169	1296.411	-187.372	0.440	1729.311	0.426	19	0.211	K.AYISSNLSLGDR.H
R5/RRR5-16/2	1707.504	1706.964	-270.228	0.530	1342.944	0.527	19	0.188	R.IQDNLALVYLSSITR.T
R5/RRR5-15/2	1295.446	1296.411	-1521.812	0.339	1598.142	0.293	19	0.170	K.AYISSNLSLGDR.H
R5/RRR5-15/2	1707.761	1706.964	-119.701	0.468	1099.486	0.516	18	0.165	R.IQDNLALVYLSSITR.T
R5/RRR5-15/2	1295.928	1296.411	-374.285	0.293	1460.927	0.290	18	0.156	K.AYISSNLSLGDR.H
R5/RRR5-15/2	1181.511	1182.372	-1579.944	0.376	1121.235	0.382	16	0.147	R.FISDAVASM*PK.L
R5/RRR5-15/2	1182.174	1182.372	-167.826	0.428	1072.814	0.364	16	0.143	R.FISDAVASM*PK.L
R5/RRR5-15/2	1833.442	1834.153	-935.556	0.458	841.144	0.489	21	0.142	R.VIGTLLGSVLPDGTVHVR.N
R5/RRR5-15/2	1052.041	1052.120	-75.136	0.419	697.162	0.470	13	0.140	K.YVDDVVEGR.V
R5/RRR5-15/2	1051.428	1052.120	-1613.689	0.302	820.216	0.389	14	0.132	K.YVDDVVEGR.V
R5/RRR5-15/2	1182.260	1182.372	-94.493	0.321	982.474	0.318	15	0.132	-.FISDAVASM*PK.-
R5/RRR5-15/2	1051.534	1052.120	-1512.576	0.324	832.862	0.356	14	0.131	K.YVDDVVEGR.V
R5/RRR5-15/3	1834.674	1834.153	-261.582	0.458	858.128	0.569	34	0.119	R.VIGTLLGSVLPDGTVHVR.N
R5/RRR5-15/3	1834.948	1834.153	-111.612	0.520	690.930	0.552	30	0.108	R.VIGTLLGSVLPDGTVHVR.N
R5/RRR5-15/3	1833.852	1834.153	-164.423	0.435	735.837	0.516	30	0.102	R.VIGTLLGSVLPDGTVHVR.N
R5/RRR5-13/2	1359.190	1359.509	-235.435	0.528	2074.777	0.552	21	0.385	R.IGEVISGEGVHYV.-
R5/RRR5-13/2	1358.867	1359.509	-1212.467	0.468	1931.285	0.516	20	0.330	R.IGEVISGEGVHYV.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1542.455	1542.671	-140.547	0.418	2443.771	0.426	23	0.320	K.EGEYDLSGFAVGAVK.K
R5/RRR5-13/2	1359.321	1359.509	-138.675	0.547	1744.549	0.539	21	0.263	R.IGEVISGEGVHYV.-
R5/RRR5-13/2	1200.117	1200.327	-175.129	0.463	1469.510	0.331	17	0.165	K.SGLSLNDQLPR.N
R5/RRR5-13/2	1199.527	1200.327	-1505.401	0.447	1339.379	0.379	17	0.163	K.SGLSLNDQLPR.N
R5/RRR5-13/2	1200.230	1200.327	-81.467	0.456	1453.464	0.310	17	0.160	K.SGLSLNDQLPR.N
R5/RRR5-13/2	1534.527	1533.797	-176.459	0.413	753.679	0.489	17	0.142	K.IFTAAWEVPPVFR.W
R5/RRR5-13/2	1534.922	1533.797	81.234	0.384	501.489	0.422	15	0.127	K.IFTAAWEVPPVFR.W
R5/RRR5-13/2	1534.955	1533.797	102.929	0.309	244.416	0.339	13	0.117	-.IFTAAWEVPPVFR.-
R5/RRR5-13/3	1626.138	1626.798	-1023.961	0.429	1048.766	0.392	26	0.098	K.GIAHITGGGFTDNIPR.V
R5/RRR5-13/3	1626.498	1626.798	-184.857	0.405	745.961	0.378	23	0.069	-.GIAHITGGGFTDNIPR.-
R5/RRR5-13/3	1626.279	1626.798	-936.804	0.306	714.469	0.271	22	0.068	-.GIAHITGGGFTDNIPR.-
R5/RRR5-6/2	1666.184	1665.740	267.654	0.563	2931.484	0.555	27	0.471	K.AEEAAAAAGDGLSEFQK.K
R5/RRR5-6/2	1851.635	1852.034	-215.867	0.502	1401.539	0.567	24	0.204	K.ANFLSADDFEPSLIPSK.T
R5/RRR5-6/2	1851.256	1852.034	-962.995	0.520	1448.813	0.521	24	0.199	K.ANFLSADDFEPSLIPSK.T
R5/RRR5-6/2	1851.610	1852.034	-229.426	0.527	1305.451	0.462	24	0.173	K.ANFLSADDFEPSLIPSK.T
R5/RRR5-6/2	1334.345	1334.632	-216.054	0.423	1089.034	0.531	21	0.169	K.KPAAPVKPVAEVK.K
R5/RRR5-6/2	1333.993	1334.632	-1232.872	0.438	949.922	0.481	20	0.153	K.KPAAPVKPVAEVK.K
R5/RRR5-6/2	1468.260	1468.641	-260.141	0.456	1062.570	0.376	18	0.144	K.WHAPLIDNPNYK.G
R5/RRR5-6/2	1334.232	1334.632	-300.955	0.412	788.511	0.454	19	0.141	K.KPAAPVKPVAEVK.K
R5/RRR5-6/2	1307.367	1306.531	-126.112	0.468	657.540	0.470	16	0.139	K.LADIPFLEPYK.T
R5/RRR5-6/2	1468.167	1468.641	-323.787	0.464	965.437	0.373	17	0.138	K.WHAPLIDNPNYK.G
R5/RRR5-1/2	1851.553	1852.034	-260.645	0.463	893.601	0.365	20	0.131	K.ANFLSADDFEPSLIPSK.T
R5/RRR5-4/2	1334.474	1334.632	-119.330	0.354	273.700	0.504	13	0.126	-.KPAAPVKPVAEVK.-
R5/RRR5-6/2	1306.051	1306.531	-368.852	0.364	425.393	0.372	14	0.124	K.LADIPFLEPYK.T
R5/RRR5-6/2	1467.533	1468.641	-1440.556	0.284	799.500	0.260	15	0.119	K.WHAPLIDNPNYK.G
R5/RRR5-1/2	1850.974	1852.034	-1116.008	0.334	611.010	0.282	17	0.117	K.ANFLSADDFEPSLIPSK.T
R5/RRR5-6/3	1469.189	1468.641	-308.570	0.507	1552.845	0.249	25	0.111	K.WHAPLIDNPNYK.G
R5/RRR5-2/2	1827.393	1827.071	176.975	0.544	2374.960	0.570	23	0.351	K.FAALQQSIQSYLDTIK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1827.499	1827.071	235.386	0.585	2085.027	0.567	22	0.297	K.FAALQQSIQSYLDTIK.G
R5/RRR5-1/2	1827.544	1827.071	260.101	0.506	1776.816	0.535	21	0.241	K.FAALQQSIQSYLDTIK.G
R5/RRR5-2/2	1600.261	1600.799	-963.924	0.404	2229.735	0.254	21	0.234	K.VSGGIDLDTVNIIQR.D
R5/RRR5-1/2	1600.132	1600.799	-1044.573	0.344	2245.998	0.231	21	0.232	K.VSGGIDLDTVNIIQR.D
R5/RRR5-2/2	1174.247	1173.345	-83.687	0.413	1439.255	0.500	17	0.193	K.ITLGDALSLNR.A
R5/RRR5-1/2	1827.244	1827.071	95.041	0.473	1474.118	0.473	20	0.190	K.FAALQQSIQSYLDTIK.G
R5/RRR5-2/2	1599.933	1600.799	-1169.441	0.359	1745.744	0.221	19	0.169	K.VSGGIDLDTVNIIQR.D
R5/RRR5-2/2	1599.953	1600.799	-1157.259	0.388	1478.407	0.283	19	0.156	K.VSGGIDLDTVNIIQR.D
R5/RRR5-2/2	1057.175	1057.229	-51.029	0.348	1183.455	0.396	16	0.153	K.VLLNAVASNR.F
R5/RRR5-2/2	1291.791	1292.335	-1199.031	0.417	1031.153	0.395	17	0.143	R.SLDSSDSPLSQR.A
R5/RRR5-3/2	1601.653	1600.799	-91.244	0.389	1277.456	0.252	19	0.137	K.VSGGIDLDTVNIIQR.D
R5/RRR5-2/2	1668.376	1666.943	260.258	0.429	869.500	0.348	17	0.128	R.VLEGTQAELVLQPLR.L
R5/RRR5-2/2	1668.402	1666.943	275.811	0.343	656.764	0.235	15	0.114	-.VLEGTQAELVLQPLR.-
R5/RRR5-1/2	1599.974	1600.799	-1144.082	0.289	1260.127	0.030	17	0.111	K.VSGGIDLDTVNIIQR.D
R5/RRR5-6/2	1058.257	1057.229	26.193	0.244	847.248	0.097	14	0.111	-.VLLNAVASNR.-
R5/RRR5-2/2	1668.548	1666.943	-237.646	0.343	528.725	0.223	13	0.108	-.VLEGTQAELVLQPLR.-
R5/RRR5-12/2	1441.919	1442.643	-1199.522	0.496	1963.956	0.609	21	0.290	R.VPTANVSVVDLTAR.I
R5/RRR5-12/2	1441.775	1442.643	-1299.253	0.484	1899.084	0.610	21	0.280	R.VPTANVSVVDLTAR.I
R5/RRR5-12/2	1442.297	1442.643	-240.545	0.529	1464.455	0.603	21	0.220	R.VPTANVSVVDLTAR.I
R5/RRR5-12/2	1277.144	1277.538	-308.752	0.432	1510.553	0.498	17	0.201	R.RVLDLLSYVAK.V
R5/RRR5-12/2	1121.947	1121.351	-361.282	0.536	1101.933	0.503	16	0.168	R.VLDLLSYVAK.V
R5/RRR5-12/2	1277.309	1277.538	-179.787	0.491	1009.136	0.516	14	0.159	R.RVLDLLSYVAK.V
R5/RRR5-12/2	1120.708	1121.351	-1470.999	0.377	792.443	0.449	15	0.139	R.VLDLLSYVAK.V
R5/RRR5-12/2	1385.254	1386.536	-1652.246	0.377	733.362	0.449	20	0.136	R.GAAQNIIPSSTGAAK.A
R5/RRR5-12/2	1386.137	1386.536	-288.714	0.418	746.354	0.411	21	0.135	R.GAAQNIIPSSTGAAK.A
R5/RRR5-12/2	1386.082	1386.536	-328.740	0.411	817.275	0.389	21	0.134	R.GAAQNIIPSSTGAAK.A
R5/RRR5-13/2	1386.221	1386.536	-228.018	0.445	633.069	0.366	18	0.126	R.GAAQNIIPSSTGAAK.A
R5/RRR5-12/2	1177.932	1178.320	-330.391	0.385	761.834	0.316	14	0.124	K.AGISLNDNFVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1178.226	1178.320	-79.871	0.273	733.822	0.280	14	0.120	K.AGISLNDNFVK.L
R5/RRR5-12/2	1177.477	1178.320	-1569.569	0.296	807.489	0.228	15	0.119	K.AGISLNDNFVK.L
R5/RRR5-13/2	1442.205	1442.643	-304.571	0.272	342.244	0.322	11	0.107	-.VPTANVSVVDLTAR.-
R5/RRR5-17/2	1582.462	1582.850	-245.932	0.581	4405.068	0.679	31	1.000	R.SPPVAGGAVAAGGAGALMK.G
R5/RRR5-17/2	1598.315	1598.849	-963.113	0.596	4205.786	0.680	31	0.924	R.SPPVAGGAVAAGGAGALM*K.G
R5/RRR5-17/2	1582.253	1582.850	-1012.270	0.546	4219.971	0.661	31	0.919	R.SPPVAGGAVAAGGAGALMK.G
R5/RRR5-17/2	1599.095	1598.849	154.074	0.615	3823.677	0.669	31	0.781	R.SPPVAGGAVAAGGAGALM*K.G
R5/RRR5-17/3	1598.762	1598.849	-54.818	0.474	1623.625	0.532	31	0.208	R.SPPVAGGAVAAGGAGALM*K.G
R5/RRR5-17/2	1023.535	1024.199	-1630.391	0.459	386.534	0.646	13	0.149	R.GPLPASQVVR.D
R5/RRR5-17/3	1295.615	1295.473	110.167	0.463	1446.567	0.439	24	0.147	R.DRGPLPASQVVR.D
R5/RRR5-16/2	1024.033	1024.199	-162.320	0.421	425.080	0.578	14	0.143	R.GPLPASQVVR.D
R5/RRR5-17/2	1023.590	1024.199	-1576.357	0.406	466.749	0.554	14	0.141	R.GPLPASQVVR.D
R5/RRR5-17/3	1295.740	1295.473	206.680	0.507	1310.707	0.470	23	0.140	R.DRGPLPASQVVR.D
R5/RRR5-17/2	1023.928	1024.199	-265.530	0.332	430.507	0.433	13	0.128	R.GPLPASQVVR.D
R5/RRR5-17/2	1294.726	1295.473	-1353.291	0.279	810.859	0.365	17	0.127	R.DRGPLPASQVVR.D
R5/RRR5-17/3	1295.723	1295.473	193.359	0.436	1331.265	0.396	24	0.122	R.DRGPLPASQVVR.D
R5/RRR5-17/2	1294.776	1295.473	-1314.942	0.270	541.684	0.327	15	0.119	R.DRGPLPASQVVR.D
R5/RRR5-17/2	1190.984	1191.234	-210.706	0.460	771.472	0.535	15	0.101	R.VGSAADWSNHF.-
R5/RRR5-17/2	1190.403	1191.234	-1542.549	0.318	556.536	0.475	16	0.098	R.VGSAADWSNHF.-
R5/RRR5-17/2	1190.285	1191.234	-1642.686	0.335	664.385	0.456	15	0.095	R.VGSAADWSNHF.-
R5/RRR5-17/3	1599.055	1598.849	128.611	0.333	851.240	0.236	29	0.065	R.SPPVAGGAVAAGGAGALM*K.G
R5/RRR5-15/2	1080.776	1081.244	-433.953	0.402	769.909	0.407	14	0.137	R.LENTISYIK.G
R5/RRR5-15/2	1080.991	1081.244	-235.090	0.447	809.708	0.382	14	0.136	R.LENTISYIK.G
R5/RRR5-16/2	1239.601	1239.449	123.008	0.356	1015.483	0.345	15	0.136	R.VNALENVVKPR.L
R5/RRR5-16/2	1081.180	1081.244	-58.956	0.365	608.971	0.313	14	0.126	R.LENTISYIK.G
R5/RRR5-15/2	1081.013	1081.244	-214.245	0.342	675.308	0.277	14	0.124	R.LENTISYIK.G
R5/RRR5-16/2	1080.838	1081.244	-377.176	0.331	508.147	0.288	13	0.124	R.LENTISYIK.G
R5/RRR5-15/3	1395.614	1395.636	-15.898	0.524	1257.526	0.395	26	0.115	R.RVNALENVVKPR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1240.062	1239.449	-313.640	0.305	568.577	0.217	12	0.110	-.VNALENVVKPR.-
R5/RRR5-15/3	1395.784	1395.636	106.208	0.558	1107.578	0.420	23	0.109	R.RVNALENVVKPR.L
R5/RRR5-15/3	1656.781	1655.747	20.676	0.403	575.047	0.496	25	0.093	K.GELDELEREDFFR.L
R5/RRR5-15/3	1395.641	1395.636	3.446	0.532	1085.246	0.341	24	0.093	R.RVNALENVVKPR.L
R5/RRR5-16/3	1395.157	1395.636	-344.075	0.487	942.308	0.348	22	0.087	R.RVNALENVVKPR.L
R5/RRR5-15/3	1761.413	1761.957	-879.078	0.456	1162.329	0.290	27	0.087	K.QFAEEQLAEEVALKR.G
R5/RRR5-16/3	1395.613	1395.636	-16.162	0.530	887.554	0.348	22	0.086	R.RVNALENVVKPR.L
R5/RRR5-15/3	1655.687	1655.747	-35.845	0.386	590.230	0.423	24	0.085	K.GELDELEREDFFR.L
R5/RRR5-16/3	1763.015	1761.957	33.215	0.407	637.719	0.311	26	0.077	K.QFAEEQLAEEVALKR.G
R5/RRR5-15/3	1656.738	1655.747	-5.374	0.305	545.863	0.356	21	0.077	K.GELDELEREDFFR.L
R5/RRR5-16/3	1761.407	1761.957	-882.418	0.331	960.721	0.151	28	0.061	K.QFAEEQLAEEVALKR.G
R5/RRR5-18/3	1787.525	1788.082	-873.874	0.493	2005.803	0.371	29	0.218	R.NKFDPLWNSLVIGGVK.K
R5/RRR5-17/2	1641.345	1641.889	-943.899	0.488	1236.544	0.538	24	0.184	R.TQYPYVTGSSIIALK.Y
R5/RRR5-18/2	1787.448	1788.082	-916.887	0.506	1169.049	0.548	22	0.178	R.NKFDPLWNSLVIGGVK.K
R5/RRR5-18/3	1787.865	1788.082	-121.742	0.443	1642.147	0.434	29	0.176	R.NKFDPLWNSLVIGGVK.K
R5/RRR5-18/2	1787.143	1788.082	-1088.317	0.449	1293.262	0.469	23	0.174	R.NKFDPLWNSLVIGGVK.K
R5/RRR5-17/2	1787.557	1788.082	-856.009	0.471	1235.701	0.493	23	0.174	R.NKFDPLWNSLVIGGVK.K
R5/RRR5-18/2	1787.503	1788.082	-886.310	0.510	1022.072	0.578	21	0.171	R.NKFDPLWNSLVIGGVK.K
R5/RRR5-17/2	1641.217	1641.889	-1021.707	0.399	1176.028	0.485	24	0.167	R.TQYPYVTGSSIIALK.Y
R5/RRR5-17/2	1640.814	1641.889	-1268.874	0.365	938.557	0.444	21	0.145	R.TQYPYVTGSSIIALK.Y
R5/RRR5-18/2	1643.495	1641.889	-240.598	0.422	800.738	0.477	20	0.143	R.TQYPYVTGSSIIALK.Y
R5/RRR5-18/2	1643.307	1641.889	255.064	0.402	828.460	0.471	20	0.143	R.TQYPYVTGSSIIALK.Y
R5/RRR5-18/2	1049.996	1050.313	-302.432	0.404	1081.243	0.317	12	0.137	K.CLLVLLYR.D
R5/RRR5-18/2	1654.382	1654.885	-910.854	0.452	742.047	0.399	19	0.132	K.ITTEGATIYPPYSLK.T
R5/RRR5-18/2	1050.002	1050.313	-296.833	0.316	952.245	0.312	12	0.130	K.CLLVLLYR.D
R5/RRR5-17/2	1655.322	1654.885	265.195	0.494	752.995	0.339	19	0.126	K.ITTEGATIYPPYSLK.T
R5/RRR5-18/2	1654.303	1654.885	-958.931	0.415	628.754	0.379	16	0.125	K.ITTEGATIYPPYSLK.T
R5/RRR5-18/2	1654.025	1654.885	-1128.014	0.317	790.679	0.307	19	0.124	K.ITTEGATIYPPYSLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1654.565	1654.885	-193.849	0.478	687.446	0.331	18	0.123	K.ITTEGATIYPPYSLK.T
R5/RRR5-17/2	1654.247	1654.885	-993.084	0.401	518.180	0.271	15	0.117	K.ITTEGATIYPPYSLK.T
R5/RRR5-18/3	1787.921	1787.928	-4.036	0.458	488.762	0.523	22	0.091	R.TEWREDM*TFEEAVK.L
R5/RRR5-12/2	1577.174	1577.807	-1038.353	0.475	2737.082	0.534	25	0.416	R.IAVLGASGYTGAEIVR.L
R5/RRR5-12/2	1577.334	1577.807	-300.369	0.512	2683.701	0.530	25	0.403	R.IAVLGASGYTGAEIVR.L
R5/RRR5-12/2	1577.382	1577.807	-270.243	0.509	2540.128	0.534	24	0.373	R.IAVLGASGYTGAEIVR.L
R5/RRR5-12/2	1298.158	1298.597	-339.122	0.397	1462.345	0.538	18	0.202	R.AIIISVIDNLVK.G
R5/RRR5-12/2	972.973	973.149	-180.905	0.447	1223.599	0.453	15	0.168	K.VSNIIIDAK.S
R5/RRR5-12/2	973.012	973.149	-140.380	0.415	940.021	0.446	13	0.147	K.VSNIIIDAK.S
R5/RRR5-12/2	1525.503	1524.844	-224.375	0.407	723.563	0.550	14	0.142	K.VTISFTPNLICMK.R
R5/RRR5-12/2	972.229	973.149	-1980.134	0.354	735.570	0.417	13	0.134	K.VSNIIIDAK.S
R5/RRR5-12/2	1991.425	1993.205	-1903.946	0.428	875.687	0.438	16	0.133	K.EANLYTEIAEGIHAYGIK.G
R5/RRR5-12/2	1298.314	1298.597	-218.843	0.303	746.671	0.336	13	0.121	R.AIIISVIDNLVK.G
R5/RRR5-16/2	1952.782	1951.208	-218.919	0.613	2138.016	0.600	29	0.316	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-16/2	1950.479	1951.208	-889.337	0.545	2134.749	0.598	29	0.315	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-15/2	1950.224	1951.208	-1020.791	0.484	2032.078	0.535	28	0.279	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-16/2	1951.069	1951.208	-71.515	0.568	1967.850	0.570	28	0.279	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-15/2	1950.724	1951.208	-248.963	0.504	2038.393	0.516	28	0.275	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-15/2	1950.472	1951.208	-892.918	0.512	1730.940	0.544	27	0.237	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-16/3	1922.077	1922.086	-4.569	0.460	1266.147	0.519	31	0.148	R.AEAAAVGEDERVISGTFAK.L
R5/RRR5-17/2	1949.654	1951.208	-1828.497	0.318	1167.742	0.308	22	0.138	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-16/2	1044.102	1044.227	-119.916	0.368	754.775	0.361	14	0.130	K.VQSLLQDIK.Q
R5/RRR5-16/2	1913.731	1913.162	-225.689	0.424	737.999	0.418	18	0.128	K.NNLELVLLTTPTTPTER.M
R5/RRR5-16/2	1328.985	1329.438	-341.850	0.324	655.239	0.369	18	0.126	R.QLGEAASPEEGLK.R
R5/RRR5-16/2	1329.203	1329.438	-177.465	0.311	685.819	0.366	18	0.126	R.QLGEAASPEEGLK.R
R5/RRR5-16/2	1329.093	1329.438	-260.388	0.323	755.575	0.299	19	0.124	R.QLGEAASPEEGLK.R
R5/RRR5-16/2	1044.142	1044.227	-82.037	0.329	594.284	0.276	12	0.120	K.VQSLLQDIK.Q
R5/RRR5-16/3	1921.903	1922.086	-95.350	0.377	989.420	0.478	28	0.108	R.AEAAAVGEDERVISGTFAK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1950.751	1951.208	-235.096	0.315	1182.947	0.316	27	0.088	K.TAFIPFITAGDPDLATTAK.A
R5/RRR5-11/2	1524.237	1524.699	-304.326	0.482	2113.930	0.412	20	0.259	R.FSFEETTATLHLK.L
R5/RRR5-11/2	1523.880	1524.699	-1197.515	0.437	1411.142	0.415	19	0.175	R.FSFEETTATLHLK.L
R5/RRR5-11/2	1524.327	1524.699	-245.111	0.479	1395.303	0.414	19	0.173	R.FSFEETTATLHLK.L
R5/RRR5-11/2	1307.736	1307.650	66.276	0.446	1079.737	0.465	17	0.158	R.VVLLIDVPIIGR.I
R5/RRR5-11/2	1306.986	1307.650	-1276.614	0.455	1011.747	0.489	17	0.157	R.VVLLIDVPIIGR.I
R5/RRR5-12/2	1290.100	1290.530	-334.312	0.351	1159.243	0.424	16	0.154	K.IPISLIYDDIK.S
R5/RRR5-13/2	1308.482	1307.650	-128.999	0.428	872.378	0.466	16	0.145	R.VVLLIDVPIIGR.I
R5/RRR5-12/2	1307.026	1307.650	-1246.318	0.466	605.979	0.503	14	0.139	R.VVLLIDVPIIGR.I
R5/RRR5-12/2	1289.853	1290.530	-1304.203	0.329	900.940	0.343	15	0.130	K.IPISLIYDDIK.S
R5/RRR5-12/2	1307.231	1307.650	-321.408	0.402	708.930	0.343	17	0.128	R.VVLLIDVPIIGR.I
R5/RRR5-12/2	1307.481	1307.650	-129.846	0.321	490.591	0.292	13	0.118	-.VVLLIDVPIIGR.-
R5/RRR5-11/3	1937.267	1937.228	20.305	0.408	889.411	0.366	26	0.081	K.STYNDIKPGSIIPYLVR.V
R5/RRR5-12/3	1300.301	1301.473	-1674.941	0.432	959.854	0.289	22	0.077	K.VKDFIHDIGEK.I
R5/RRR5-13/2	1645.030	1645.838	-1102.103	0.581	2580.396	0.542	24	0.385	K.IKDEEGNPAFALVNK.A
R5/RRR5-13/2	1646.188	1645.838	213.041	0.630	2535.262	0.524	23	0.367	K.IKDEEGNPAFALVNK.A
R5/RRR5-13/2	1723.460	1722.922	-269.360	0.609	1830.347	0.523	22	0.245	K.IRDEEGYPAFALVNK.V
R5/RRR5-13/2	1723.536	1722.922	-224.736	0.581	1770.632	0.473	22	0.225	K.IRDEEGYPAFALVNK.V
R5/RRR5-13/2	1846.297	1845.993	165.348	0.636	1204.141	0.691	27	0.213	K.ILPWGDEAYAGGSANAPR.G
R5/RRR5-13/2	1845.477	1845.993	-823.636	0.546	1224.406	0.672	26	0.209	K.ILPWGDEAYAGGSANAPR.G
R5/RRR5-13/2	1845.293	1845.993	-923.576	0.550	1241.079	0.649	27	0.207	K.ILPWGDEAYAGGSANAPR.G
R5/RRR5-13/2	1081.992	1081.161	-156.680	0.487	1509.115	0.448	17	0.193	K.ADEGFSVTVR.G
R5/RRR5-13/2	1722.320	1722.922	-932.933	0.564	1356.360	0.478	20	0.179	K.IRDEEGYPAFALVNK.V
R5/RRR5-13/2	1230.295	1229.362	-54.597	0.435	727.763	0.511	17	0.145	R.GGSVCLAPTNPR.D
R5/RRR5-13/2	1229.038	1229.362	-263.854	0.427	884.424	0.430	18	0.143	R.GGSVCLAPTNPR.D
R5/RRR5-13/3	1645.714	1645.838	-75.567	0.414	1326.030	0.399	30	0.122	K.IKDEEGNPAFALVNK.A
R5/RRR5-14/2	1081.917	1081.161	-226.515	0.344	543.943	0.329	14	0.122	-.ADEGFSVTVR.-
R5/RRR5-13/2	1228.254	1229.362	-1720.994	0.323	556.023	0.301	14	0.120	R.GGSVCLAPTNPR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/3	1846.047	1845.993	29.765	0.425	776.945	0.434	26	0.086	K.ILPWGDEAYAGGSANAPR.G
R5/RRR5-13/3	1646.059	1645.838	134.428	0.443	688.399	0.436	23	0.086	-.IKDEEGNPAFALVNK.-
R5/RRR5-16/3	1837.743	1837.934	-104.114	0.566	1698.731	0.517	35	0.211	K.HHSNTAVGAELSHSFSR.N
R5/RRR5-16/2	1263.160	1263.420	-206.420	0.500	1509.582	0.503	18	0.203	K.SLITISGEVDTK.A
R5/RRR5-15/3	1837.741	1837.934	-105.013	0.540	1572.780	0.530	35	0.194	K.HHSNTAVGAELSHSFSR.N
R5/RRR5-15/3	1837.450	1837.934	-264.252	0.543	1443.791	0.552	33	0.182	K.HHSNTAVGAELSHSFSR.N
R5/RRR5-16/2	1998.331	1998.217	57.188	0.550	1101.506	0.597	23	0.178	K.FTLTTCTPEGVTITAAGTR.K
R5/RRR5-15/2	1264.242	1263.420	-141.357	0.530	1035.208	0.567	16	0.171	K.SLITISGEVDTK.A
R5/RRR5-15/2	1263.264	1263.420	-123.924	0.378	958.469	0.462	17	0.148	K.SLITISGEVDTK.A
R5/RRR5-15/3	1837.782	1837.934	-82.926	0.524	1240.837	0.525	31	0.147	K.HHSNTAVGAELSHSFSR.N
R5/RRR5-15/2	1227.432	1227.435	-2.654	0.471	826.122	0.396	16	0.137	K.SILSLVVPDQR.S
R5/RRR5-15/2	1227.288	1227.435	-120.274	0.424	755.595	0.410	16	0.136	K.SILSLVVPDQR.S
R5/RRR5-16/2	1227.072	1227.435	-297.104	0.386	795.706	0.398	16	0.135	K.SILSLVVPDQR.S
R5/RRR5-15/2	1262.918	1263.420	-1192.802	0.407	746.006	0.372	15	0.129	K.SLITISGEVDTK.A
R5/RRR5-16/2	1226.688	1227.435	-1428.551	0.311	567.930	0.304	13	0.117	-.SILSLVVPDQR.-
R5/RRR5-15/3	1622.576	1621.816	-148.782	0.397	1204.593	0.294	24	0.091	-.KNESVFGELQTQLK.-
R5/RRR5-8/2	945.090	945.055	36.713	0.458	976.757	0.383	15	0.143	R.LDAANTLAR.A
R5/RRR5-8/2	944.993	945.055	-65.768	0.436	834.807	0.408	14	0.140	R.LDAANTLAR.A
R5/RRR5-7/2	1370.116	1369.629	356.769	0.375	1068.690	0.364	17	0.138	K.VGPALACGNAVVLK.T
R5/RRR5-7/2	945.836	945.055	-232.956	0.435	742.775	0.305	13	0.126	R.LDAANTLAR.A
R5/RRR5-8/3	1356.397	1356.593	-145.077	0.478	1338.154	0.382	26	0.121	R.SNLKPVTLELGGK.S
R5/RRR5-8/2	945.530	945.055	503.507	0.409	671.411	0.235	13	0.120	R.LDAANTLAR.A
R5/RRR5-9/2	1136.160	1136.323	-144.038	0.414	1405.334	0.409	16	0.173	K.ALIAAEYTGVK.V
R5/RRR5-9/2	1337.042	1336.434	-294.096	0.503	862.461	0.554	15	0.158	K.SFTSEFPHVER.Y
R5/RRR5-9/2	1335.926	1336.434	-1132.382	0.500	954.226	0.474	16	0.152	K.SFTSEFPHVER.Y
R5/RRR5-9/2	1135.660	1136.323	-1468.234	0.300	897.383	0.346	14	0.129	K.ALIAAEYTGVK.V
R5/RRR5-9/2	1135.977	1136.323	-305.085	0.239	1006.305	0.317	14	0.129	K.ALIAAEYTGVK.V
R5/RRR5-10/2	1782.896	1784.047	-1210.195	0.547	1657.124	0.477	21	0.211	R.LINSDEVQSVVKPINK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1784.437	1784.047	218.904	0.596	1550.804	0.499	21	0.203	R.LINSDEVQSVVKPINK.E
R5/RRR5-10/2	1783.483	1784.047	-879.932	0.577	1577.826	0.464	21	0.198	R.LINSDEVQSVVKPINK.E
R5/RRR5-10/2	1795.330	1795.160	95.366	0.447	1260.960	0.494	23	0.173	R.IAVASALAATAVPSLVLAR.G
R5/RRR5-10/2	1794.732	1795.160	-239.016	0.209	860.280	0.134	18	0.108	R.IAVASALAATAVPSLVLAR.G
R5/RRR5-15/2	1353.787	1354.536	-1295.699	0.485	1798.006	0.527	20	0.243	R.IPSGEVWVGNPAK.F
R5/RRR5-16/2	1354.121	1354.536	-307.566	0.492	1714.852	0.545	21	0.237	R.IPSGEVWVGNPAK.F
R5/RRR5-15/2	1354.249	1354.536	-212.607	0.490	1682.488	0.534	20	0.230	R.IPSGEVWVGNPAK.F
R5/RRR5-16/2	1353.982	1354.536	-1150.738	0.483	1702.733	0.514	21	0.228	R.IPSGEVWVGNPAK.F
R5/RRR5-16/2	1353.858	1354.536	-1242.635	0.482	1488.634	0.564	20	0.214	R.IPSGEVWVGNPAK.F
R5/RRR5-15/2	1353.814	1354.536	-1275.686	0.483	1561.731	0.524	20	0.213	R.IPSGEVWVGNPAK.F
R5/RRR5-15/2	1001.560	1002.150	-1592.265	0.441	891.543	0.414	17	0.143	R.LGSTIQGGLR.V
R5/RRR5-16/2	1001.877	1002.150	-273.269	0.470	740.414	0.388	16	0.135	R.LGSTIQGGLR.V
R5/RRR5-15/2	1125.077	1124.223	-129.350	0.467	581.397	0.410	14	0.135	K.TFDEIELEK.M
R5/RRR5-15/2	1001.517	1002.150	-1635.611	0.464	704.817	0.370	16	0.133	R.LGSTIQGGLR.V
R5/RRR5-16/2	1001.887	1002.150	-263.489	0.496	761.211	0.352	16	0.132	R.LGSTIQGGLR.V
R5/RRR5-15/2	1817.899	1816.131	-127.738	0.445	273.245	0.470	18	0.132	R.EIPPELILPDNILPNK.A
R5/RRR5-15/2	1816.023	1816.131	-59.775	0.415	306.880	0.548	17	0.131	-.EIPPELILPDNILPNK.-
R5/RRR5-16/2	1123.898	1124.223	-290.063	0.407	608.649	0.379	14	0.131	K.TFDEIELEK.M
R5/RRR5-15/2	1815.500	1816.131	-901.236	0.374	314.052	0.514	17	0.131	R.EIPPELILPDNILPNK.A
R5/RRR5-16/2	1815.584	1816.131	-854.731	0.409	233.017	0.497	16	0.131	R.EIPPELILPDNILPNK.A
R5/RRR5-16/2	1815.272	1816.131	-1027.140	0.352	359.379	0.470	20	0.130	R.EIPPELILPDNILPNK.A
R5/RRR5-15/2	1123.941	1124.223	-250.944	0.427	486.150	0.320	13	0.126	K.TFDEIELEK.M
R5/RRR5-16/2	1815.449	1816.131	-929.115	0.397	241.399	0.505	15	0.123	-.EIPPELILPDNILPNK.-
R5/RRR5-15/2	1123.311	1124.223	-1706.509	0.190	520.175	0.260	13	0.117	K.TFDEIELEK.M
R5/RRR5-15/3	1102.453	1102.290	148.628	0.421	922.879	0.229	21	0.071	K.HSM*VGAGSLVK.Q
R5/RRR5-15/3	1102.571	1102.290	255.633	0.337	1085.592	0.144	22	0.062	K.HSM*VGAGSLVK.Q
R5/RRR5-16/3	1102.232	1102.290	-53.120	0.347	1262.595	0.082	21	0.059	K.HSM*VGAGSLVK.Q
R5/RRR5-8/2	1133.217	1133.320	-91.363	0.494	1813.890	0.498	20	0.238	K.ALVSAGLSSSIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1133.145	1133.320	-155.442	0.508	1783.426	0.506	20	0.236	K.ALVSAGLSSSIK.V
R5/RRR5-7/2	1132.424	1133.320	-1679.586	0.438	1720.499	0.535	19	0.233	K.ALVSAGLSSSIK.V
R5/RRR5-15/2	1134.058	1133.320	-232.079	0.528	1615.312	0.564	19	0.229	K.ALVSAGLSSSIK.V
R5/RRR5-15/2	1132.507	1133.320	-1605.731	0.438	1778.454	0.469	19	0.225	K.ALVSAGLSSSIK.V
R5/RRR5-7/2	1784.325	1783.963	203.753	0.547	1485.403	0.538	23	0.207	R.DISLNYATFQPGTTVR.D
R5/RRR5-7/2	1132.948	1133.320	-329.676	0.481	1591.606	0.471	19	0.204	K.ALVSAGLSSSIK.V
R5/RRR5-7/2	1133.137	1133.320	-162.683	0.480	1550.871	0.486	19	0.203	K.ALVSAGLSSSIK.V
R5/RRR5-7/2	1783.350	1783.963	-906.979	0.508	1461.196	0.523	23	0.201	R.DISLNYATFQPGTTVR.D
R5/RRR5-15/2	1133.098	1133.320	-197.050	0.471	1423.574	0.522	18	0.197	K.ALVSAGLSSSIK.V
R5/RRR5-14/2	1132.468	1133.320	-1640.275	0.407	1445.414	0.517	18	0.197	K.ALVSAGLSSSIK.V
R5/RRR5-9/2	1132.993	1133.320	-290.004	0.377	1591.083	0.429	18	0.194	K.ALVSAGLSSSIK.V
R5/RRR5-8/2	1132.929	1133.320	-346.325	0.444	1304.915	0.525	17	0.185	K.ALVSAGLSSSIK.V
R5/RRR5-15/2	1783.348	1783.963	-908.079	0.501	1281.977	0.526	22	0.183	R.DISLNYATFQPGTTVR.D
R5/RRR5-15/2	1783.408	1783.963	-874.202	0.518	1208.612	0.545	22	0.181	R.DISLNYATFQPGTTVR.D
R5/RRR5-8/2	1783.482	1783.963	-270.112	0.519	1263.258	0.516	22	0.180	R.DISLNYATFQPGTTVR.D
R5/RRR5-8/2	1132.435	1133.320	-1669.731	0.396	1338.641	0.472	18	0.178	K.ALVSAGLSSSIK.V
R5/RRR5-15/2	1783.138	1783.963	-1026.424	0.462	1339.152	0.466	22	0.177	R.DISLNYATFQPGTTVR.D
R5/RRR5-14/2	1133.151	1133.320	-149.715	0.379	1271.748	0.504	17	0.177	K.ALVSAGLSSSIK.V
R5/RRR5-7/2	1561.783	1562.751	-1263.388	0.392	1439.091	0.374	19	0.169	R.DNVEAYWPSVIIR.Y
R5/RRR5-14/2	1563.075	1562.751	208.155	0.533	1256.364	0.445	19	0.167	R.DNVEAYWPSVIIR.Y
R5/RRR5-16/2	1132.839	1133.320	-426.223	0.417	1020.373	0.537	16	0.163	K.ALVSAGLSSSIK.V
R5/RRR5-7/2	1782.622	1783.963	-1317.115	0.372	1194.820	0.413	21	0.155	R.DISLNYATFQPGTTVR.D
R5/RRR5-8/2	1562.461	1562.751	-185.764	0.434	1289.528	0.351	19	0.154	R.DNVEAYWPSVIIR.Y
R5/RRR5-7/2	1567.555	1567.767	-135.485	0.429	876.863	0.499	19	0.151	R.IYYPDKEALDALR.G
R5/RRR5-7/2	1562.214	1562.751	-986.852	0.412	1273.461	0.331	19	0.150	R.DNVEAYWPSVIIR.Y
R5/RRR5-14/2	1561.811	1562.751	-1245.885	0.425	1188.494	0.360	19	0.149	R.DNVEAYWPSVIIR.Y
R5/RRR5-15/2	1562.406	1562.751	-221.505	0.424	1268.914	0.311	19	0.147	R.DNVEAYWPSVIIR.Y
R5/RRR5-7/2	1567.320	1567.767	-285.961	0.428	826.286	0.469	18	0.145	R.IYYPDKEALDALR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1568.351	1567.767	-266.178	0.469	726.014	0.489	18	0.144	R.IYYPDKEALDALR.G
R5/RRR5-7/2	1566.972	1567.767	-1148.799	0.409	829.519	0.444	18	0.142	R.IYYPDKEALDALR.G
R5/RRR5-7/2	1562.319	1562.751	-277.080	0.403	1174.583	0.306	19	0.141	R.DNVEAYWPSVIIR.Y
R5/RRR5-15/2	1567.376	1567.767	-250.564	0.351	881.448	0.417	19	0.140	R.IYYPDKEALDALR.G
R5/RRR5-8/2	916.039	916.097	-63.235	0.433	792.977	0.407	13	0.140	R.SEVVQLLK.S
R5/RRR5-14/2	1566.837	1567.767	-1235.558	0.412	832.826	0.423	18	0.139	R.IYYPDKEALDALR.G
R5/RRR5-8/2	915.762	916.097	-366.484	0.463	742.400	0.402	13	0.139	R.SEVVQLLK.S
R5/RRR5-8/2	1566.583	1567.767	-1398.634	0.396	805.533	0.425	18	0.138	R.IYYPDKEALDALR.G
R5/RRR5-15/2	915.492	916.097	-1758.274	0.413	594.225	0.442	12	0.137	R.SEVVQLLK.S
R5/RRR5-15/2	1566.964	1567.767	-1154.510	0.406	680.303	0.451	17	0.137	R.IYYPDKEALDALR.G
R5/RRR5-14/2	916.043	916.097	-59.225	0.506	734.090	0.384	13	0.137	R.SEVVQLLK.S
R5/RRR5-14/2	1561.898	1562.751	-1189.688	0.325	1111.610	0.300	19	0.136	R.DNVEAYWPSVIIR.Y
R5/RRR5-7/2	915.944	916.097	-167.907	0.483	735.254	0.381	13	0.136	R.SEVVQLLK.S
R5/RRR5-7/2	915.974	916.097	-134.351	0.455	747.424	0.380	13	0.136	R.SEVVQLLK.S
R5/RRR5-14/2	915.967	916.097	-141.971	0.467	778.445	0.355	13	0.134	R.SEVVQLLK.S
R5/RRR5-8/2	915.773	916.097	-355.115	0.372	758.629	0.373	13	0.134	R.SEVVQLLK.S
R5/RRR5-15/2	915.481	916.097	-1770.734	0.424	782.833	0.378	13	0.134	-.SEVVQLLK.-
R5/RRR5-15/2	1567.265	1567.767	-961.172	0.370	669.153	0.426	17	0.133	R.IYYPDKEALDALR.G
R5/RRR5-8/2	1562.021	1562.751	-1110.819	0.338	1249.017	0.216	18	0.133	R.DNVEAYWPSVIIR.Y
R5/RRR5-14/2	915.982	916.097	-125.929	0.378	740.186	0.365	13	0.131	-.SEVVQLLK.-
R5/RRR5-14/2	1567.397	1567.767	-236.813	0.360	617.708	0.397	16	0.129	R.IYYPDKEALDALR.G
R5/RRR5-9/2	1567.251	1567.767	-970.555	0.344	546.614	0.401	16	0.128	R.IYYPDKEALDALR.G
R5/RRR5-14/2	1567.651	1567.767	-74.244	0.307	575.212	0.387	17	0.127	R.IYYPDKEALDALR.G
R5/RRR5-7/2	915.842	916.097	-279.555	0.349	609.945	0.338	12	0.126	-.SEVVQLLK.-
R5/RRR5-16/2	915.899	916.097	-216.575	0.314	690.464	0.272	12	0.124	R.SEVVQLLK.S
R5/RRR5-15/2	916.267	916.097	186.393	0.426	724.803	0.301	13	0.123	-.SEVVQLLK.-
R5/RRR5-14/2	915.527	916.097	-1720.629	0.349	836.181	0.224	12	0.122	R.SEVVQLLK.S
R5/RRR5-15/2	1561.558	1562.751	-1408.231	0.333	941.382	0.208	16	0.120	R.DNVEAYWPSVIIR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	915.900	916.097	-216.040	0.282	743.097	0.206	12	0.117	-.SEVVQLLK.-
R5/RRR5-15/3	1567.769	1567.767	1.349	0.432	931.786	0.432	29	0.099	R.IYYPDKEALDALR.G
R5/RRR5-7/3	1567.868	1567.767	64.603	0.384	394.357	0.434	22	0.096	R.IYYPDKEALDALR.G
R5/RRR5-8/3	1568.901	1567.767	85.358	0.425	495.465	0.444	23	0.096	R.IYYPDKEALDALR.G
R5/RRR5-8/3	1567.530	1567.767	-151.547	0.430	588.732	0.447	25	0.095	R.IYYPDKEALDALR.G
R5/RRR5-7/3	1567.964	1567.767	125.741	0.397	852.009	0.418	26	0.094	R.IYYPDKEALDALR.G
R5/RRR5-15/3	1567.655	1567.767	-71.754	0.412	425.276	0.413	21	0.094	R.IYYPDKEALDALR.G
R5/RRR5-15/3	1567.600	1567.767	-107.020	0.447	595.727	0.426	26	0.094	R.IYYPDKEALDALR.G
R5/RRR5-7/3	1567.414	1567.767	-226.078	0.371	528.932	0.449	24	0.094	R.IYYPDKEALDALR.G
R5/RRR5-14/3	1567.919	1567.767	97.047	0.402	646.776	0.420	27	0.091	R.IYYPDKEALDALR.G
R5/RRR5-8/3	1567.821	1567.767	34.149	0.378	561.989	0.398	23	0.089	R.IYYPDKEALDALR.G
R5/RRR5-9/3	1567.618	1567.767	-95.186	0.361	400.309	0.404	20	0.088	-.IYYPDKEALDALR.-
R5/RRR5-14/3	1567.427	1567.767	-217.406	0.326	458.568	0.351	23	0.088	R.IYYPDKEALDALR.G
R5/RRR5-14/3	1566.471	1567.767	-1469.947	0.296	419.531	0.340	21	0.087	R.IYYPDKEALDALR.G
R5/RRR5-14/3	1567.618	1567.767	-95.421	0.348	524.346	0.361	23	0.087	R.IYYPDKEALDALR.G
R5/RRR5-14/3	1567.094	1567.767	-1070.784	0.307	569.254	0.357	25	0.084	R.IYYPDKEALDALR.G
R5/RRR5-14/3	1567.061	1567.767	-1092.019	0.256	594.923	0.339	26	0.079	R.IYYPDKEALDALR.G
R5/RRR5-10/2	1654.693	1654.974	-170.452	0.514	2327.463	0.527	24	0.329	K.ETLIAGGPFVLPLAQK.H
R5/RRR5-10/2	1655.671	1654.974	-183.515	0.575	2185.339	0.526	23	0.302	K.ETLIAGGPFVLPLAQK.H
R5/RRR5-10/2	1655.538	1654.974	-264.141	0.578	2228.750	0.489	23	0.298	K.ETLIAGGPFVLPLAQK.H
R5/RRR5-10/2	1422.594	1423.575	-1396.996	0.411	1392.731	0.431	21	0.175	R.AGGTM*TGVLSAANEK.A
R5/RRR5-10/2	1106.193	1106.300	-96.915	0.338	1393.677	0.425	17	0.173	R.IILTASGGAFR.D
R5/RRR5-10/3	1771.156	1770.064	52.418	0.515	1494.417	0.488	29	0.171	R.VVALAAGSNVTLLADQVK.T
R5/RRR5-10/2	1423.184	1423.575	-275.360	0.455	1076.005	0.539	19	0.167	R.AGGTM*TGVLSAANEK.A
R5/RRR5-10/2	1422.650	1423.575	-1356.922	0.419	1115.840	0.487	19	0.161	R.AGGTM*TGVLSAANEK.A
R5/RRR5-10/2	1106.222	1106.300	-70.460	0.359	1133.759	0.303	15	0.136	R.IILTASGGAFR.D
R5/RRR5-10/2	1210.335	1209.374	-32.028	0.377	723.268	0.467	14	0.136	K.ITVDSATLFNK.G
R5/RRR5-10/2	1209.434	1209.374	49.644	0.340	881.343	0.368	15	0.132	K.ITVDSATLFNK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/3	1769.201	1770.064	-1056.283	0.397	832.561	0.385	25	0.083	R.VVALAAGSNVTLLADQVK.T
R5/RRR5-9/2	1859.374	1859.065	166.753	0.548	2414.149	0.539	24	0.348	K.ELAITSDEALSLEELPK.R
R5/RRR5-9/2	1858.269	1859.065	-969.178	0.480	2185.817	0.462	23	0.283	K.ELAITSDEALSLEELPK.R
R5/RRR5-8/2	1858.655	1859.065	-221.112	0.438	2081.197	0.449	22	0.263	K.ELAITSDEALSLEELPK.R
R5/RRR5-8/2	1728.155	1726.953	117.494	0.582	1323.143	0.561	23	0.194	R.LNLEAAGVEVDNIGAIK.V
R5/RRR5-9/2	1630.269	1629.799	289.472	0.514	1162.539	0.527	23	0.175	R.TSVPNIWAVGDVTNR.M
R5/RRR5-9/2	1629.221	1629.799	-971.289	0.490	1108.439	0.533	22	0.171	R.TSVPNIWAVGDVTNR.M
R5/RRR5-8/2	1727.742	1726.953	-122.002	0.514	1020.971	0.520	24	0.162	R.LNLEAAGVEVDNIGAIK.V
R5/RRR5-8/2	1045.981	1046.160	-171.556	0.395	1056.111	0.427	17	0.152	R.TVVASNLEGR.G
R5/RRR5-9/2	1045.924	1046.160	-225.881	0.361	868.882	0.450	15	0.143	R.TVVASNLEGR.G
R5/RRR5-8/2	1628.696	1629.799	-1294.627	0.339	687.497	0.461	18	0.133	R.TSVPNIWAVGDVTNR.M
R5/RRR5-9/2	1045.959	1046.160	-192.864	0.402	730.530	0.382	14	0.132	R.TVVASNLEGR.G
R5/RRR5-8/2	1045.256	1046.160	-1826.681	0.335	735.321	0.381	14	0.131	R.TVVASNLEGR.G
R5/RRR5-7/2	1858.557	1859.065	-813.558	0.358	924.645	0.353	18	0.130	K.ELAITSDEALSLEELPK.R
R5/RRR5-8/2	1045.746	1046.160	-396.857	0.324	891.319	0.224	15	0.122	R.TVVASNLEGR.G
R5/RRR5-8/2	1857.767	1859.065	-1240.640	0.322	784.088	0.282	17	0.119	K.ELAITSDEALSLEELPK.R
R5/RRR5-9/2	1045.891	1046.160	-257.496	0.224	673.505	0.210	15	0.117	R.TVVASNLEGR.G
R5/RRR5-9/3	1295.418	1296.455	-1576.910	0.444	1327.033	0.261	24	0.092	R.LHPGTNLSELSK.T
R5/RRR5-9/3	1296.052	1296.455	-311.532	0.441	904.107	0.250	21	0.071	-.LHPGTNLSELSK.-
R5/RRR5-9/3	1296.605	1296.455	116.079	0.472	815.613	0.210	21	0.067	-.LHPGTNLSELSK.-
R5/RRR5-13/2	1766.636	1767.022	-218.976	0.539	1890.170	0.517	23	0.253	R.VLDTHVEGGNLFIVPR.F
R5/RRR5-13/2	1766.318	1767.022	-967.644	0.513	1693.285	0.508	22	0.224	R.VLDTHVEGGNLFIVPR.F
R5/RRR5-13/2	1204.975	1205.299	-269.936	0.513	1512.049	0.467	17	0.196	R.AWDLAESDAVK.L
R5/RRR5-13/2	1204.377	1205.299	-1600.286	0.377	1575.040	0.393	17	0.186	R.AWDLAESDAVK.L
R5/RRR5-13/2	1766.365	1767.022	-940.793	0.499	1322.636	0.526	20	0.186	R.VLDTHVEGGNLFIVPR.F
R5/RRR5-14/2	1734.513	1734.932	-241.950	0.483	1122.955	0.589	24	0.181	K.LSLNAGGLALPSFSDSGK.V
R5/RRR5-13/2	1204.963	1205.299	-279.287	0.486	1477.147	0.396	17	0.178	R.AWDLAESDAVK.L
R5/RRR5-13/2	1734.314	1734.932	-935.659	0.437	1144.100	0.565	24	0.177	K.LSLNAGGLALPSFSDSGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1398.444	1398.740	-212.192	0.426	1000.609	0.499	19	0.157	R.VVVLNTANLPMVK.E
R5/RRR5-13/2	1186.214	1186.383	-143.017	0.522	1021.095	0.444	19	0.153	K.LVSSQPASGIVK.I
R5/RRR5-13/2	1186.052	1186.383	-279.817	0.470	908.308	0.477	18	0.151	K.LVSSQPASGIVK.I
R5/RRR5-13/2	1186.184	1186.383	-168.310	0.485	854.305	0.492	18	0.150	K.LVSSQPASGIVK.I
R5/RRR5-13/2	1398.359	1398.740	-273.495	0.390	744.375	0.467	16	0.138	R.VVVLNTANLPMVK.E
R5/RRR5-13/2	1398.310	1398.740	-308.529	0.331	669.568	0.439	16	0.131	R.VVVLNTANLPMVK.E
R5/RRR5-14/2	1734.314	1734.932	-935.235	0.396	582.311	0.430	18	0.127	K.LSLNAGGLALPSFSDSGK.V
R5/RRR5-13/2	1734.508	1734.932	-244.915	0.369	510.016	0.382	17	0.121	K.LSLNAGGLALPSFSDSGK.V
R5/RRR5-13/2	1414.205	1414.739	-1087.936	0.300	487.545	0.361	13	0.120	R.VVVLNTANLPM*VK.E
R5/RRR5-13/3	1767.924	1767.022	-55.107	0.510	934.765	0.349	26	0.082	-.VLDTHVEGGNLFIVPR.-
R5/RRR5-13/3	1766.500	1767.022	-863.794	0.452	730.328	0.343	24	0.070	-.VLDTHVEGGNLFIVPR.-
R5/RRR5-13/2	1425.177	1424.628	-316.801	0.519	1719.179	0.520	21	0.232	R.IHNAILQTISEGK.F
R5/RRR5-13/2	1425.463	1424.628	-115.835	0.501	1601.898	0.516	21	0.217	R.IHNAILQTISEGK.F
R5/RRR5-12/2	1424.449	1424.628	-125.889	0.533	1513.346	0.479	20	0.198	R.IHNAILQTISEGK.F
R5/RRR5-12/2	1684.895	1684.828	39.777	0.466	1375.187	0.481	18	0.182	R.TESFLTWESLESVR.R
R5/RRR5-13/2	1424.345	1424.628	-198.792	0.455	1407.677	0.449	19	0.181	R.IHNAILQTISEGK.F
R5/RRR5-12/2	1802.711	1802.018	-170.719	0.548	1252.396	0.526	24	0.180	R.ATLFPGDGIGPEIAESVK.Q
R5/RRR5-12/2	1802.046	1802.018	15.789	0.449	1231.255	0.494	25	0.173	R.ATLFPGDGIGPEIAESVK.Q
R5/RRR5-13/2	1800.994	1802.018	-1127.400	0.388	1257.943	0.482	25	0.172	R.ATLFPGDGIGPEIAESVK.Q
R5/RRR5-13/2	1801.219	1802.018	-1001.778	0.405	1284.075	0.453	25	0.169	R.ATLFPGDGIGPEIAESVK.Q
R5/RRR5-13/2	1243.065	1243.314	-200.203	0.461	1131.413	0.462	17	0.163	R.HLQFNNQADR.I
R5/RRR5-12/2	1802.125	1802.018	59.678	0.442	1153.459	0.465	24	0.161	R.ATLFPGDGIGPEIAESVK.Q
R5/RRR5-12/2	1425.105	1424.628	335.786	0.489	1239.613	0.415	19	0.161	R.IHNAILQTISEGK.F
R5/RRR5-13/2	1801.349	1802.018	-929.387	0.408	1064.416	0.466	23	0.155	R.ATLFPGDGIGPEIAESVK.Q
R5/RRR5-12/2	1684.486	1684.828	-203.271	0.340	729.049	0.476	15	0.134	R.TESFLTWESLESVR.R
R5/RRR5-13/2	1880.505	1879.302	108.131	0.395	647.890	0.493	19	0.133	K.NLANPTALMLSAVM*M*LR.H
R5/RRR5-13/2	1242.993	1243.314	-259.020	0.415	802.805	0.370	15	0.133	R.HLQFNNQADR.I
R5/RRR5-12/2	1684.427	1684.828	-238.968	0.260	562.348	0.211	14	0.113	R.TESFLTWESLESVR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/3	1426.016	1426.640	-1142.160	0.478	2128.666	0.453	28	0.272	K.DGKPVQIELIDAK.T
R5/RRR5-8/2	1414.155	1413.605	-318.751	0.540	1488.547	0.566	18	0.214	K.GLGLENINVVTQR.G
R5/RRR5-8/2	1379.032	1379.500	-340.986	0.416	840.421	0.543	16	0.152	K.SLGLQVSSPGYDR.Q
R5/RRR5-9/3	1426.926	1426.640	200.763	0.492	1557.386	0.383	25	0.145	K.DGKPVQIELIDAK.T
R5/RRR5-9/2	1379.022	1379.500	-348.269	0.464	734.661	0.496	16	0.142	K.SLGLQVSSPGYDR.Q
R5/RRR5-9/2	1412.744	1413.605	-1321.186	0.416	827.535	0.393	15	0.131	K.GLGLENINVVTQR.G
R5/RRR5-8/2	1378.981	1379.500	-1104.839	0.276	536.482	0.386	14	0.122	K.SLGLQVSSPGYDR.Q
R5/RRR5-9/2	1378.420	1379.500	-1514.145	0.287	542.294	0.342	13	0.120	K.SLGLQVSSPGYDR.Q
R5/RRR5-9/2	1378.538	1379.500	-1427.508	0.294	546.861	0.308	14	0.118	-.SLGLQVSSPGYDR.-
R5/RRR5-9/2	1456.447	1456.754	-211.559	0.277	927.851	0.203	18	0.116	R.NIIIATGSVPFVPK.G
R5/RRR5-9/2	1467.971	1467.566	276.938	0.353	750.527	0.471	18	0.101	K.VNSGVSHSVNEPVAA.-
R5/RRR5-9/2	1467.123	1467.566	-303.071	0.340	699.962	0.509	17	0.100	K.VNSGVSHSVNEPVAA.-
R5/RRR5-9/2	1467.072	1467.566	-337.882	0.314	637.098	0.442	17	0.096	K.VNSGVSHSVNEPVAA.-
R5/RRR5-8/2	1466.563	1467.566	-1369.711	0.175	601.785	0.241	16	0.090	K.VNSGVSHSVNEPVAA.-
R5/RRR5-8/3	1426.533	1426.640	-75.462	0.438	1208.156	0.283	23	0.088	K.DGKPVQIELIDAK.T
R5/RRR5-9/3	1426.287	1426.640	-248.534	0.439	795.232	0.307	23	0.078	K.DGKPVQIELIDAK.T
R5/RRR5-5/2	1611.506	1610.835	-204.803	0.573	3162.358	0.559	23	0.529	R.NGILEAYSGILQGFK.S
R5/RRR5-5/2	1514.412	1513.764	-233.295	0.567	1940.572	0.600	22	0.285	K.GLLLQTLSSPVASAR.S
R5/RRR5-5/2	1514.447	1513.764	-210.329	0.534	1821.803	0.643	22	0.278	K.GLLLQTLSSPVASAR.S
R5/RRR5-5/2	1337.336	1337.452	-86.848	0.500	1929.403	0.411	20	0.233	R.VVCEATQSTDVK.I
R5/RRR5-5/2	1337.029	1337.452	-317.358	0.458	1604.547	0.426	19	0.197	R.VVCEATQSTDVK.I
R5/RRR5-5/2	1366.432	1366.502	-51.039	0.454	1080.237	0.406	16	0.148	R.TAAYETLNEVVR.C
R5/RRR5-5/2	1366.294	1366.502	-152.575	0.446	1027.802	0.375	17	0.142	R.TAAYETLNEVVR.C
R5/RRR5-1/2	1514.107	1513.764	227.097	0.362	657.276	0.419	16	0.128	K.GLLLQTLSSPVASAR.S
R5/RRR5-5/2	1365.384	1366.502	-1555.862	0.338	851.267	0.305	16	0.126	R.TAAYETLNEVVR.C
R5/RRR5-4/2	1366.489	1366.502	-9.194	0.350	522.554	0.401	14	0.126	R.TAAYETLNEVVR.C
R5/RRR5-5/2	955.031	955.133	-107.447	0.312	762.596	0.274	13	0.117	-.VAGIEIPQK.-
R5/RRR5-5/2	1610.383	1610.835	-281.964	0.356	486.515	0.306	14	0.116	-.NGILEAYSGILQGFK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1609.940	1610.835	-1180.652	0.257	481.277	0.296	14	0.115	R.NGILEAYSGILQGFK.S
R5/RRR5-14/2	1420.130	1419.606	-336.119	0.487	1629.953	0.512	18	0.216	R.AFQLYSSGIFTGK.C
R5/RRR5-13/2	1420.246	1419.606	-254.194	0.464	1418.504	0.584	18	0.208	R.AFQLYSSGIFTGK.C
R5/RRR5-13/2	1540.339	1539.719	-247.491	0.554	1183.957	0.635	22	0.196	K.AVANQPVSVAIEAGGR.A
R5/RRR5-24/2	1540.151	1539.719	281.448	0.548	1259.168	0.589	23	0.194	K.AVANQPVSVAIEAGGR.A
R5/RRR5-16/2	1540.344	1539.719	-243.834	0.557	1161.582	0.608	22	0.188	K.AVANQPVSVAIEAGGR.A
R5/RRR5-12/2	1539.117	1539.719	-1043.504	0.493	1164.651	0.564	23	0.181	K.AVANQPVSVAIEAGGR.A
R5/RRR5-25/2	1539.190	1539.719	-996.125	0.546	1089.119	0.574	22	0.176	K.AVANQPVSVAIEAGGR.A
R5/RRR5-11/2	1539.496	1539.719	-144.953	0.492	1086.258	0.569	22	0.175	K.AVANQPVSVAIEAGGR.A
R5/RRR5-14/2	1539.300	1539.719	-272.952	0.497	1083.028	0.557	23	0.173	K.AVANQPVSVAIEAGGR.A
R5/RRR5-16/2	1539.142	1539.719	-1027.418	0.547	962.539	0.610	21	0.173	K.AVANQPVSVAIEAGGR.A
R5/RRR5-25/2	1539.262	1539.719	-297.696	0.499	1007.059	0.595	21	0.173	K.AVANQPVSVAIEAGGR.A
R5/RRR5-11/2	1539.138	1539.719	-1029.966	0.513	1087.210	0.551	22	0.172	K.AVANQPVSVAIEAGGR.A
R5/RRR5-15/2	1539.375	1539.719	-223.626	0.514	1026.253	0.574	22	0.171	K.AVANQPVSVAIEAGGR.A
R5/RRR5-15/2	1539.318	1539.719	-261.177	0.545	997.851	0.578	22	0.170	K.AVANQPVSVAIEAGGR.A
R5/RRR5-12/2	1539.289	1539.719	-279.874	0.513	1063.765	0.536	22	0.168	K.AVANQPVSVAIEAGGR.A
R5/RRR5-16/2	1539.194	1539.719	-993.815	0.499	928.808	0.586	21	0.166	K.AVANQPVSVAIEAGGR.A
R5/RRR5-15/2	1539.205	1539.719	-986.171	0.516	940.767	0.574	21	0.165	K.AVANQPVSVAIEAGGR.A
R5/RRR5-25/2	1539.248	1539.719	-306.767	0.516	875.558	0.586	21	0.163	K.AVANQPVSVAIEAGGR.A
R5/RRR5-24/2	1539.240	1539.719	-311.939	0.528	954.489	0.537	21	0.160	K.AVANQPVSVAIEAGGR.A
R5/RRR5-18/2	1539.311	1539.719	-265.552	0.514	856.865	0.566	21	0.159	K.AVANQPVSVAIEAGGR.A
R5/RRR5-12/2	1335.685	1334.536	111.410	0.471	1270.007	0.382	17	0.157	K.CGIAVEPSYPLK.K
R5/RRR5-15/2	1420.426	1419.606	-127.279	0.449	1087.501	0.459	18	0.157	R.AFQLYSSGIFTGK.C
R5/RRR5-2/2	1539.338	1539.719	-248.129	0.499	846.365	0.552	21	0.156	K.AVANQPVSVAIEAGGR.A
R5/RRR5-24/2	1539.294	1539.719	-276.452	0.531	751.201	0.588	20	0.156	K.AVANQPVSVAIEAGGR.A
R5/RRR5-18/2	1539.102	1539.719	-1053.697	0.481	1074.595	0.458	22	0.156	K.AVANQPVSVAIEAGGR.A
R5/RRR5-11/2	1539.103	1539.719	-1053.060	0.480	839.269	0.548	21	0.155	K.AVANQPVSVAIEAGGR.A
R5/RRR5-14/2	1540.168	1539.719	292.416	0.456	917.932	0.522	20	0.155	K.AVANQPVSVAIEAGGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1419.156	1419.606	-317.887	0.419	1102.566	0.447	16	0.154	R.AFQLYSSGIFTGK.C
R5/RRR5-14/2	1539.395	1539.719	-210.897	0.466	915.585	0.484	19	0.148	K.AVANQPVSVAIEAGGR.A
R5/RRR5-14/2	1334.151	1334.536	-289.869	0.387	1168.279	0.369	17	0.148	K.CGIAVEPSYPLK.K
R5/RRR5-12/2	1538.792	1539.719	-1255.849	0.381	787.423	0.501	20	0.144	K.AVANQPVSVAIEAGGR.A
R5/RRR5-1/2	1539.112	1539.719	-1047.167	0.396	693.091	0.482	19	0.139	K.AVANQPVSVAIEAGGR.A
R5/RRR5-25/2	1420.278	1419.606	-231.688	0.352	940.773	0.382	17	0.137	-.AFQLYSSGIFTGK.-
R5/RRR5-12/2	1419.139	1419.606	-330.314	0.354	781.950	0.433	14	0.134	R.AFQLYSSGIFTGK.C
R5/RRR5-15/2	1419.535	1419.606	-50.510	0.382	770.757	0.398	15	0.132	R.AFQLYSSGIFTGK.C
R5/RRR5-12/2	1419.159	1419.606	-315.815	0.360	864.316	0.328	15	0.128	R.AFQLYSSGIFTGK.C
R5/RRR5-14/2	1040.960	1041.099	-133.216	0.307	879.536	0.284	15	0.127	K.SWGESGYVR.M
R5/RRR5-13/2	1418.921	1419.606	-1191.351	0.348	383.219	0.395	13	0.125	R.AFQLYSSGIFTGK.C
R5/RRR5-14/2	1041.023	1041.099	-73.109	0.358	900.621	0.228	15	0.124	K.SWGESGYVR.M
R5/RRR5-14/2	1333.975	1334.536	-1173.872	0.369	985.604	0.252	15	0.124	K.CGIAVEPSYPLK.K
R5/RRR5-12/2	1040.775	1041.099	-311.699	0.327	772.438	0.255	14	0.123	K.SWGESGYVR.M
R5/RRR5-13/2	1419.133	1419.606	-334.629	0.340	550.512	0.331	14	0.123	R.AFQLYSSGIFTGK.C
R5/RRR5-24/2	1418.954	1419.606	-1168.199	0.291	625.042	0.315	15	0.122	R.AFQLYSSGIFTGK.C
R5/RRR5-11/2	1419.094	1419.606	-1068.778	0.241	577.267	0.363	14	0.122	R.AFQLYSSGIFTGK.C
R5/RRR5-15/2	1419.316	1419.606	-205.190	0.301	642.033	0.273	16	0.121	R.AFQLYSSGIFTGK.C
R5/RRR5-13/2	1040.955	1041.099	-138.627	0.291	820.196	0.220	14	0.121	K.SWGESGYVR.M
R5/RRR5-13/2	1041.043	1041.099	-53.702	0.291	855.172	0.210	14	0.121	K.SWGESGYVR.M
R5/RRR5-12/2	1040.892	1041.099	-198.743	0.274	952.444	0.167	15	0.119	K.SWGESGYVR.M
R5/RRR5-14/2	1040.841	1041.099	-248.394	0.255	718.755	0.216	14	0.119	K.SWGESGYVR.M
R5/RRR5-14/2	1419.229	1419.606	-266.626	0.264	635.645	0.269	14	0.119	R.AFQLYSSGIFTGK.C
R5/RRR5-11/2	1041.030	1041.099	-65.816	0.291	771.621	0.183	14	0.119	K.SWGESGYVR.M
R5/RRR5-14/3	1463.142	1462.709	297.006	0.469	769.468	0.382	23	0.087	K.CGIAVEPSYPLKK.G
R5/RRR5-14/3	1462.333	1462.709	-257.939	0.467	795.782	0.362	24	0.086	K.CGIAVEPSYPLKK.G
R5/RRR5-14/3	1462.684	1462.709	-17.053	0.395	809.654	0.316	24	0.079	K.CGIAVEPSYPLKK.G
R5/RRR5-13/3	1463.628	1462.709	-55.606	0.479	654.537	0.325	20	0.076	-.CGIAVEPSYPLKK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/3	1462.679	1462.709	-20.820	0.379	812.196	0.255	24	0.073	K.CGIAVEPSYPLKK.G
R5/RRR5-12/3	1461.964	1462.709	-1197.070	0.245	1068.500	0.044	24	0.053	-.CGIAVEPSYPLKK.-
R5/RRR5-9/2	1522.234	1522.642	-268.371	0.517	1496.225	0.474	21	0.195	R.ELGEAALANYTQNK.S
R5/RRR5-9/2	1820.506	1821.131	-895.126	0.483	1277.026	0.557	23	0.189	K.TAEQTPLSGLVMAQFVK.E
R5/RRR5-9/2	1820.312	1821.131	-1002.301	0.466	1200.086	0.588	22	0.186	K.TAEQTPLSGLVMAQFVK.E
R5/RRR5-8/2	1819.929	1821.131	-1213.353	0.430	1160.242	0.554	22	0.176	K.TAEQTPLSGLVMAQFVK.E
R5/RRR5-8/2	1664.701	1663.898	-119.047	0.472	944.128	0.585	21	0.165	K.EAGFPAGVLNVISGFGK.I
R5/RRR5-9/2	1663.516	1663.898	-230.711	0.450	876.819	0.612	20	0.164	K.EAGFPAGVLNVISGFGK.I
R5/RRR5-8/2	1663.472	1663.898	-256.772	0.413	912.379	0.563	21	0.158	K.EAGFPAGVLNVISGFGK.I
R5/RRR5-8/2	1354.255	1354.620	-270.920	0.426	924.453	0.483	17	0.149	K.IGPALATGNTVVLK.T
R5/RRR5-8/2	1663.026	1663.898	-1128.976	0.345	883.525	0.494	20	0.145	K.EAGFPAGVLNVISGFGK.I
R5/RRR5-9/2	1354.325	1354.620	-219.104	0.467	831.047	0.486	17	0.145	K.IGPALATGNTVVLK.T
R5/RRR5-8/2	1354.232	1354.620	-287.379	0.423	706.882	0.484	16	0.138	K.IGPALATGNTVVLK.T
R5/RRR5-9/2	1353.800	1354.620	-1348.865	0.358	908.863	0.411	17	0.138	K.IGPALATGNTVVLK.T
R5/RRR5-9/2	1354.256	1354.620	-270.196	0.445	792.162	0.440	17	0.138	K.IGPALATGNTVVLK.T
R5/RRR5-9/2	1662.451	1663.898	-1476.249	0.266	639.819	0.493	17	0.130	K.EAGFPAGVLNVISGFGK.I
R5/RRR5-8/2	1557.008	1556.789	141.182	0.328	629.163	0.416	16	0.125	K.GYFIQPTIFTNVR.N
R5/RRR5-8/2	1353.930	1354.620	-1252.246	0.375	572.710	0.340	14	0.120	-.IGPALATGNTVVLK.-
R5/RRR5-9/2	1662.454	1663.898	-1474.479	0.197	632.846	0.381	17	0.119	K.EAGFPAGVLNVISGFGK.I
R5/RRR5-1/2	1664.419	1663.898	-288.699	0.250	534.562	0.323	16	0.118	K.EAGFPAGVLNVISGFGK.I
R5/RRR5-4/2	1761.424	1762.000	-897.555	0.480	3246.046	0.565	26	0.559	R.FLVLNAAELAVDGSSVR.F
R5/RRR5-4/2	1754.631	1754.916	-162.977	0.547	1891.725	0.527	23	0.256	R.ETALLYDELLSSASNK.Q
R5/RRR5-4/2	1755.493	1754.916	-242.127	0.584	1903.373	0.498	22	0.248	R.ETALLYDELLSSASNK.Q
R5/RRR5-5/2	1754.067	1754.916	-1057.745	0.406	1132.822	0.437	19	0.153	R.ETALLYDELLSSASNK.Q
R5/RRR5-4/2	1213.115	1213.324	-173.152	0.488	1171.727	0.317	16	0.141	K.LNVDQTGFYR.V
R5/RRR5-4/2	1461.644	1461.604	27.913	0.421	688.567	0.447	17	0.135	K.M*DFTGTLNDQM*R.G
R5/RRR5-4/2	1739.030	1739.910	-1084.492	0.287	974.599	0.295	17	0.123	R.NQDAFYVLGGISLEGR.E
R5/RRR5-8/2	1555.400	1554.729	-212.112	0.539	1866.120	0.597	20	0.272	R.LAIGDLATQYFADR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1403.172	1403.521	-249.434	0.515	1677.986	0.479	19	0.217	K.TFSYAGFEQQPK.T
R5/RRR5-8/2	1174.889	1175.318	-366.262	0.330	844.934	0.448	14	0.138	K.SQFFVNSFAK.A
R5/RRR5-8/2	1175.335	1175.318	14.833	0.311	1033.430	0.330	15	0.135	K.SQFFVNSFAK.A
R5/RRR5-8/2	1325.678	1325.538	106.063	0.402	648.089	0.423	14	0.130	R.DSFLVNGVAFKK.T
R5/RRR5-8/2	1323.233	1322.363	-98.044	0.421	913.264	0.330	16	0.128	R.GGADQFIEEAER.S
R5/RRR5-8/2	1326.065	1325.538	-357.191	0.311	600.120	0.327	14	0.121	R.DSFLVNGVAFKK.T
R5/RRR5-8/2	1326.248	1325.538	-218.850	0.341	497.603	0.321	13	0.120	R.DSFLVNGVAFKK.T
R5/RRR5-10/2	1102.996	1103.299	-275.801	0.506	1105.016	0.507	18	0.169	K.RPFAAIVGGSK.V
R5/RRR5-10/2	1103.013	1103.299	-259.923	0.447	864.894	0.474	17	0.148	K.RPFAAIVGGSK.V
R5/RRR5-10/2	1000.459	1000.219	240.586	0.424	571.160	0.431	13	0.127	-.FSLAPLVPR.-
R5/RRR5-10/2	1852.003	1853.153	-1164.442	0.340	556.692	0.455	16	0.125	K.LVSELPNGSVLLLENVR.F
R5/RRR5-10/2	1852.850	1853.153	-163.853	0.370	601.411	0.403	17	0.123	K.LVSELPNGSVLLLENVR.F
R5/RRR5-13/2	1991.502	1991.298	103.187	0.603	1593.842	0.643	26	0.243	R.AFSGLGGLGVDEPAMVSALAK.W
R5/RRR5-13/2	1990.045	1991.298	-1135.411	0.514	1414.627	0.579	24	0.204	R.AFSGLGGLGVDEPAMVSALAK.W
R5/RRR5-13/2	959.910	960.067	-164.171	0.384	1574.915	0.287	15	0.166	R.TAEELLGAR.K
R5/RRR5-13/2	1173.146	1173.338	-164.127	0.374	1398.525	0.280	17	0.151	R.EAALCLATPAR.Y
R5/RRR5-12/2	1173.124	1173.338	-183.438	0.409	1333.842	0.304	18	0.151	R.EAALCLATPAR.Y
R5/RRR5-13/3	1578.850	1578.665	117.468	0.510	1178.986	0.558	25	0.148	R.HIEEDLGHEETLR.E
R5/RRR5-12/3	1579.402	1578.665	-167.501	0.536	1214.621	0.520	26	0.142	R.HIEEDLGHEETLR.E
R5/RRR5-12/2	1058.364	1059.155	-1697.512	0.401	697.417	0.432	15	0.138	K.LVENDDVVR.I
R5/RRR5-13/2	1059.040	1059.155	-109.323	0.525	700.216	0.403	15	0.138	K.LVENDDVVR.I
R5/RRR5-13/2	1058.948	1059.155	-196.511	0.535	696.014	0.400	15	0.137	K.LVENDDVVR.I
R5/RRR5-13/2	1058.948	1059.155	-196.048	0.508	685.726	0.385	15	0.136	K.LVENDDVVR.I
R5/RRR5-12/2	1058.986	1059.155	-160.778	0.475	717.031	0.376	15	0.135	K.LVENDDVVR.I
R5/RRR5-13/3	1579.503	1578.665	-102.958	0.510	1059.891	0.541	24	0.132	R.HIEEDLGHEETLR.E
R5/RRR5-13/3	1578.716	1578.665	32.207	0.502	1183.027	0.492	25	0.132	R.HIEEDLGHEETLR.E
R5/RRR5-12/2	1058.506	1059.155	-1562.993	0.354	645.944	0.268	14	0.124	K.LVENDDVVR.I
R5/RRR5-12/3	1578.630	1578.665	-22.470	0.462	1145.086	0.476	26	0.123	R.HIEEDLGHEETLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1679.108	1679.898	-1068.733	0.385	922.498	0.463	28	0.102	K.TPFQEYTDLLARPK.G
R5/RRR5-14/3	1678.340	1679.898	-2125.989	0.401	657.704	0.495	25	0.097	K.TPFQEYTDLLARPK.G
R5/RRR5-14/3	1679.147	1679.898	-1045.630	0.396	1027.866	0.388	29	0.095	K.TPFQEYTDLLARPK.G
R5/RRR5-14/3	1679.265	1679.898	-975.015	0.315	366.420	0.467	22	0.089	K.TPFQEYTDLLARPK.G
R5/RRR5-15/3	1679.879	1679.898	-11.350	0.406	472.931	0.384	21	0.085	K.TPFQEYTDLLARPK.G
R5/RRR5-2/2	1346.478	1346.509	-22.970	0.451	1364.047	0.476	19	0.181	R.VVELTGETAADLK.L
R5/RRR5-2/2	1159.402	1158.373	24.752	0.391	965.385	0.456	17	0.146	R.IVALSASLANAK.D
R5/RRR5-2/2	1688.097	1686.844	150.672	0.416	1115.977	0.357	19	0.142	R.YYDLSSQEIGELIR.F
R5/RRR5-2/2	1257.002	1257.377	-299.576	0.360	878.622	0.348	14	0.128	K.TGYFQVTDLGR.I
R5/RRR5-2/2	1687.443	1686.844	-238.033	0.343	953.453	0.266	19	0.124	R.YYDLSSQEIGELIR.F
R5/RRR5-1/2	1287.775	1287.572	157.483	0.369	571.806	0.398	13	0.124	R.VVYIAPIEALAK.E
R5/RRR5-2/2	1397.633	1398.632	-1434.286	0.335	665.686	0.376	13	0.123	R.DSVLLQLPHFTK.E
R5/RRR5-2/2	1287.596	1287.572	18.579	0.300	649.256	0.389	13	0.123	R.VVYIAPIEALAK.E
R5/RRR5-1/2	1398.316	1398.632	-226.396	0.329	683.485	0.245	14	0.116	-.DSVLLQLPHFTK.-
R5/RRR5-8/2	1614.790	1615.850	-1279.314	0.438	1984.239	0.442	22	0.248	R.TQNVVACQAVANIVK.S
R5/RRR5-8/2	973.368	974.137	-1822.912	0.394	1045.720	0.539	16	0.166	K.AGANVVLTTK.G
R5/RRR5-7/2	974.136	974.137	-0.265	0.496	1099.930	0.483	16	0.164	K.AGANVVLTTK.G
R5/RRR5-8/2	973.995	974.137	-145.706	0.460	988.781	0.529	15	0.163	K.AGANVVLTTK.G
R5/RRR5-8/2	974.138	974.137	1.369	0.444	1031.273	0.508	16	0.163	K.AGANVVLTTK.G
R5/RRR5-7/2	973.965	974.137	-177.138	0.451	1017.332	0.482	16	0.158	K.AGANVVLTTK.G
R5/RRR5-7/2	1561.500	1560.863	-232.611	0.343	1512.314	0.235	18	0.150	K.IIQFATEAAITILR.I
R5/RRR5-7/2	1101.305	1101.275	26.947	0.527	889.877	0.403	16	0.141	R.IADDDVILVK.G
R5/RRR5-7/2	1102.131	1101.275	-131.266	0.360	1021.686	0.373	15	0.141	R.IADDDVILVK.G
R5/RRR5-8/2	1285.302	1285.472	-132.182	0.536	881.308	0.426	15	0.139	K.VLVELAELQDR.E
R5/RRR5-8/2	1101.281	1101.275	5.602	0.337	772.607	0.351	14	0.128	-.IADDDVILVK.-
R5/RRR5-7/2	1221.241	1221.346	-86.883	0.431	1432.577	0.501	17	0.194	R.HFEVDLSAFR.N
R5/RRR5-6/2	1221.471	1221.346	102.481	0.482	1349.320	0.474	17	0.183	R.HFEVDLSAFR.N
R5/RRR5-7/2	1221.149	1221.346	-161.987	0.367	1253.145	0.487	16	0.173	R.HFEVDLSAFR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1222.286	1221.346	-49.645	0.418	1150.488	0.442	16	0.160	R.HFEVDLSAFR.N
R5/RRR5-7/2	1221.177	1221.346	-139.324	0.440	1062.331	0.470	16	0.159	R.HFEVDLSAFR.N
R5/RRR5-6/2	1222.019	1221.346	-268.676	0.365	1060.653	0.464	15	0.155	R.HFEVDLSAFR.N
R5/RRR5-7/2	1116.248	1115.264	-13.668	0.417	1008.306	0.467	14	0.152	-.VGDALEFVHK.-
R5/RRR5-6/2	1210.959	1211.348	-322.189	0.297	1139.326	0.360	14	0.143	K.GEFVEYIPTR.E
R5/RRR5-7/2	1372.916	1373.604	-1233.263	0.388	704.841	0.475	19	0.140	K.VEPLVNM*GQITR.A
R5/RRR5-7/2	1373.261	1373.604	-250.705	0.394	587.971	0.430	18	0.133	K.VEPLVNM*GQITR.A
R5/RRR5-7/2	1372.877	1373.604	-1262.015	0.392	607.545	0.426	18	0.133	K.VEPLVNM*GQITR.A
R5/RRR5-1/2	1116.248	1115.264	-13.668	0.371	552.689	0.331	13	0.119	-.VGDALEFVHK.-
R5/RRR5-6/2	1211.135	1211.348	-176.872	0.228	645.621	0.179	12	0.113	-.GEFVEYIPTR.-
R5/RRR5-6/3	1448.472	1448.611	-96.169	0.489	1155.639	0.412	23	0.111	R.ARHFEVDLSAFR.N
R5/RRR5-6/3	1448.093	1448.611	-1051.612	0.470	920.475	0.446	21	0.100	R.ARHFEVDLSAFR.N
R5/RRR5-11/2	1356.291	1356.467	-129.868	0.526	1531.109	0.507	20	0.206	K.TLEAEAAHGTVTR.H
R5/RRR5-10/2	1356.120	1356.467	-256.643	0.468	1226.359	0.483	19	0.172	K.TLEAEAAHGTVTR.H
R5/RRR5-10/2	1356.106	1356.467	-267.210	0.515	1056.757	0.532	19	0.168	K.TLEAEAAHGTVTR.H
R5/RRR5-11/2	1774.624	1775.079	-257.179	0.541	1215.946	0.462	19	0.164	R.NILNGTVFREPILCK.N
R5/RRR5-11/2	1356.223	1356.467	-180.339	0.551	940.324	0.554	18	0.164	K.TLEAEAAHGTVTR.H
R5/RRR5-11/2	1356.079	1356.467	-287.078	0.513	1015.556	0.520	19	0.164	K.TLEAEAAHGTVTR.H
R5/RRR5-10/2	1355.690	1356.467	-1314.381	0.515	881.443	0.519	18	0.155	K.TLEAEAAHGTVTR.H
R5/RRR5-10/2	1078.327	1077.302	23.094	0.375	1429.121	0.284	16	0.153	K.DLALLIHGPK.V
R5/RRR5-10/2	1775.856	1775.079	-125.453	0.468	1174.637	0.378	19	0.148	R.NILNGTVFREPILCK.N
R5/RRR5-11/2	1774.515	1775.079	-883.620	0.528	1070.096	0.424	18	0.147	R.NILNGTVFREPILCK.N
R5/RRR5-11/2	1774.612	1775.079	-263.528	0.499	1090.133	0.398	18	0.145	R.NILNGTVFREPILCK.N
R5/RRR5-11/2	1775.653	1775.079	-240.481	0.488	664.855	0.382	18	0.128	R.NILNGTVFREPILCK.N
R5/RRR5-1/2	1774.546	1775.079	-866.494	0.366	600.956	0.300	16	0.119	R.NILNGTVFREPILCK.N
R5/RRR5-4/2	1548.401	1548.762	-233.946	0.416	2580.554	0.505	22	0.373	R.EVVEIATNALDVFK.S
R5/RRR5-4/2	1645.807	1645.881	-44.979	0.510	1420.158	0.432	22	0.177	R.GYVEAVLNSLAANVPK.A
R5/RRR5-4/2	1937.589	1936.194	204.761	0.484	1355.982	0.428	21	0.169	R.IVLEADGYQPYLISPEK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1937.117	1936.194	-39.921	0.500	1276.725	0.452	20	0.166	R.IVLEADGYQPYLISPEK.G
R5/RRR5-4/2	1782.364	1782.035	185.636	0.409	1239.338	0.459	24	0.166	R.VLLDIVNASANATPGLGR.Y
R5/RRR5-4/3	1781.130	1782.035	-1072.580	0.331	1590.848	0.417	30	0.162	R.VLLDIVNASANATPGLGR.Y
R5/RRR5-4/2	1781.626	1782.035	-230.054	0.369	886.103	0.386	20	0.131	R.VLLDIVNASANATPGLGR.Y
R5/RRR5-4/2	1140.538	1140.358	158.275	0.353	793.733	0.375	14	0.128	R.LPNLLSGLQGK.S
R5/RRR5-4/3	1781.484	1782.035	-873.195	0.395	1186.369	0.442	27	0.119	R.VLLDIVNASANATPGLGR.Y
R5/RRR5-4/3	1781.737	1782.035	-167.686	0.328	597.756	0.273	25	0.069	-.VLLDIVNASANATPGLGR.-
R5/RRR5-7/2	1577.302	1577.721	-266.298	0.539	1720.160	0.485	25	0.223	K.FAGAISDGGDIVLEGR.V
R5/RRR5-7/2	1029.785	1029.215	-419.535	0.453	1986.788	0.317	17	0.218	K.LSEAGLAVLR.G
R5/RRR5-6/2	1549.242	1548.722	-310.873	0.570	1490.906	0.476	22	0.193	R.AIGAELVSFDEAIGR.A
R5/RRR5-7/2	1549.271	1548.722	-291.979	0.469	1569.691	0.405	22	0.187	R.AIGAELVSFDEAIGR.A
R5/RRR5-6/2	1548.826	1548.722	66.987	0.494	1458.455	0.432	22	0.182	R.AIGAELVSFDEAIGR.A
R5/RRR5-6/2	1548.318	1548.722	-261.952	0.441	1310.807	0.447	21	0.171	R.AIGAELVSFDEAIGR.A
R5/RRR5-7/2	1548.112	1548.722	-1043.214	0.350	1461.308	0.368	22	0.170	R.AIGAELVSFDEAIGR.A
R5/RRR5-7/2	1548.337	1548.722	-249.454	0.440	1068.710	0.468	19	0.156	R.AIGAELVSFDEAIGR.A
R5/RRR5-6/2	1131.954	1132.337	-339.917	0.462	957.854	0.437	14	0.146	K.VAQFDALIVR.S
R5/RRR5-6/2	1131.978	1132.337	-318.061	0.474	817.571	0.329	13	0.126	-.VAQFDALIVR.-
R5/RRR5-7/2	1029.552	1029.215	327.796	0.245	656.131	0.091	14	0.112	-.LSEAGLAVLR.-
R5/RRR5-6/2	1678.252	1678.891	-979.973	0.543	2277.253	0.534	23	0.321	K.NQVAM*NPINTVFDAK.R
R5/RRR5-6/2	1678.383	1678.891	-901.184	0.556	2337.588	0.495	23	0.319	K.NQVAM*NPINTVFDAK.R
R5/RRR5-6/2	1662.050	1662.892	-1111.369	0.490	1926.363	0.557	23	0.270	K.NQVAMNPINTVFDAK.R
R5/RRR5-6/2	1678.440	1678.891	-269.946	0.568	1927.959	0.533	22	0.262	K.NQVAM*NPINTVFDAK.R
R5/RRR5-6/2	1229.012	1229.325	-255.292	0.483	2007.522	0.441	19	0.252	R.VEIIANDQGNR.I
R5/RRR5-6/2	1228.931	1229.325	-322.060	0.496	2038.071	0.364	19	0.236	R.VEIIANDQGNR.I
R5/RRR5-6/2	1229.080	1229.325	-200.489	0.493	1713.039	0.408	19	0.206	R.VEIIANDQGNR.I
R5/RRR5-6/2	1834.592	1835.078	-265.630	0.588	1309.669	0.558	24	0.194	K.NQVAM*NPINTVFDAKR.L
R5/RRR5-6/2	1834.356	1835.078	-941.404	0.516	1337.189	0.517	24	0.188	K.NQVAM*NPINTVFDAKR.L
R5/RRR5-6/2	1662.043	1662.892	-1115.647	0.525	1349.941	0.480	21	0.181	K.NQVAMNPINTVFDAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1834.515	1835.078	-854.360	0.516	983.252	0.473	22	0.152	K.NQVAM*NPINTVFDAKR.L
R5/RRR5-1/2	1678.037	1678.891	-1108.442	0.438	1151.864	0.402	19	0.151	K.NQVAM*NPINTVFDAK.R
R5/RRR5-6/2	1474.186	1474.554	-250.208	0.272	547.436	0.519	19	0.131	R.TTPSYVGFTDTER.L
R5/RRR5-6/2	1473.996	1474.554	-1060.118	0.283	581.634	0.398	19	0.126	R.TTPSYVGFTDTER.L
R5/RRR5-6/2	1473.392	1474.554	-1472.056	0.244	460.544	0.458	18	0.124	R.TTPSYVGFTDTER.L
R5/RRR5-6/2	1660.864	1660.958	-56.359	0.491	2381.984	0.375	23	0.291	R.GIAM*EGATDALIQLIK.D
R5/RRR5-6/2	1492.414	1492.720	-206.215	0.381	2296.848	0.347	21	0.272	R.DGSVLMSVSLDQLK.A
R5/RRR5-6/2	1819.791	1820.101	-171.103	0.466	1679.191	0.569	23	0.236	K.SAIGIGTLLM*DGLGDTIR.V
R5/RRR5-6/2	1644.397	1644.958	-952.124	0.466	2046.438	0.340	22	0.229	R.GIAMEGATDALIQLIK.D
R5/RRR5-6/2	1350.029	1349.584	330.244	0.416	1684.692	0.487	18	0.218	K.ASNPVIMVQAYR.L
R5/RRR5-6/2	1519.648	1520.712	-1362.148	0.369	1832.979	0.351	20	0.206	R.TLFDLQEVSAQIR.E
R5/RRR5-6/2	1644.424	1644.958	-935.729	0.421	1989.172	0.206	22	0.191	R.GIAMEGATDALIQLIK.D
R5/RRR5-6/2	1804.467	1804.102	203.175	0.512	1316.087	0.547	20	0.187	K.SAIGIGTLLMDGLGDTIR.V
R5/RRR5-6/2	1820.205	1820.101	56.965	0.466	855.591	0.525	19	0.148	K.SAIGIGTLLM*DGLGDTIR.V
R5/RRR5-6/2	1819.535	1820.101	-863.407	0.405	890.870	0.508	20	0.148	K.SAIGIGTLLM*DGLGDTIR.V
R5/RRR5-5/2	1803.881	1804.102	-122.961	0.335	361.636	0.404	12	0.118	K.SAIGIGTLLMDGLGDTIR.V
R5/RRR5-6/3	1520.076	1520.712	-1079.701	0.396	1270.484	0.308	25	0.096	R.TLFDLQEVSAQIR.E
R5/RRR5-3/2	1201.163	1200.453	-242.660	0.546	1885.426	0.459	19	0.239	K.LLDSIVALLSR.T
R5/RRR5-3/2	1200.470	1200.453	14.216	0.434	1654.572	0.376	18	0.192	K.LLDSIVALLSR.T
R5/RRR5-3/2	1085.204	1085.367	-150.237	0.543	1253.939	0.449	14	0.169	R.LPNILVIFR.S
R5/RRR5-3/2	1541.885	1542.718	-1192.107	0.478	1308.463	0.408	20	0.164	R.FGPIIEQNVDPANK.G
R5/RRR5-3/2	1541.382	1542.718	-1520.237	0.376	1427.161	0.296	20	0.155	R.FGPIIEQNVDPANK.G
R5/RRR5-3/2	1102.494	1103.210	-1560.600	0.390	822.785	0.548	15	0.153	R.TSGYSVSFVR.L
R5/RRR5-3/2	1200.044	1200.453	-341.852	0.479	1164.223	0.370	17	0.150	K.LLDSIVALLSR.T
R5/RRR5-3/2	1102.823	1103.210	-351.560	0.392	733.094	0.504	14	0.143	R.TSGYSVSFVR.L
R5/RRR5-1/2	1224.881	1225.506	-1330.901	0.366	604.921	0.428	14	0.126	K.ATALALLPSVIR.F
R5/RRR5-3/2	1102.963	1103.210	-224.524	0.278	458.107	0.362	12	0.121	R.TSGYSVSFVR.L
R5/RRR5-6/2	1106.080	1106.300	-198.985	0.443	1551.593	0.546	16	0.216	K.TALLQSFLGR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1434.757	1434.662	65.998	0.561	1496.756	0.493	20	0.198	R.NVLGGLSLEGFLSK.W
R5/RRR5-6/3	1902.484	1903.125	-865.443	0.457	1695.149	0.431	30	0.184	K.SSLVVSVATEAFPENVPR.V
R5/RRR5-6/2	1435.265	1434.662	-277.637	0.390	1299.488	0.540	17	0.184	R.NVLGGLSLEGFLSK.W
R5/RRR5-6/2	1888.765	1889.099	-177.332	0.503	1222.090	0.541	19	0.177	R.APDQTLELTGQAIDFLR.G
R5/RRR5-6/2	1105.590	1106.300	-1551.358	0.340	924.791	0.510	14	0.150	K.TALLQSFLGR.Q
R5/RRR5-6/2	1888.458	1889.099	-871.410	0.469	938.633	0.506	17	0.149	R.APDQTLELTGQAIDFLR.G
R5/RRR5-6/2	1888.659	1889.099	-233.612	0.432	850.053	0.505	16	0.143	R.APDQTLELTGQAIDFLR.G
R5/RRR5-6/2	1331.519	1332.533	-1517.180	0.420	855.623	0.430	15	0.139	K.GRLETTWTVLR.K
R5/RRR5-6/2	1331.595	1332.533	-1459.995	0.293	666.835	0.310	14	0.120	K.GRLETTWTVLR.K
R5/RRR5-6/3	1902.208	1903.125	-1010.970	0.354	1141.732	0.335	27	0.091	K.SSLVVSVATEAFPENVPR.V
R5/RRR5-6/2	1018.099	1018.213	-111.855	0.448	1650.287	0.379	15	0.192	K.VAEAMEVLR.N
R5/RRR5-6/2	1018.127	1018.213	-84.313	0.432	1247.548	0.343	15	0.151	K.VAEAMEVLR.N
R5/RRR5-6/3	1831.585	1831.172	226.304	0.430	1296.132	0.467	27	0.137	R.ALEM*LNFTPINGKPIR.I
R5/RRR5-6/2	1183.281	1182.418	-116.469	0.326	567.080	0.291	15	0.120	K.FGTITSAVVMR.E
R5/RRR5-6/2	1198.233	1198.418	-154.866	0.236	912.336	0.086	17	0.111	K.FGTITSAVVM*R.E
R5/RRR5-6/3	1550.033	1549.863	109.860	0.430	1221.685	0.354	24	0.105	-.M*VGSKPLYVALAQR.-
R5/RRR5-6/3	1444.098	1443.588	-339.960	0.470	737.667	0.481	21	0.095	K.KFDDKEWYVGR.A
R5/RRR5-6/3	1831.601	1831.172	234.825	0.355	907.212	0.439	24	0.095	R.ALEM*LNFTPINGKPIR.I
R5/RRR5-6/3	1534.148	1533.864	185.854	0.407	993.078	0.282	25	0.078	K.MVGSKPLYVALAQR.K
R5/RRR5-6/3	1534.346	1533.864	315.221	0.432	885.250	0.292	25	0.077	K.MVGSKPLYVALAQR.K
R5/RRR5-6/3	1549.084	1549.863	-1152.270	0.320	906.092	0.133	23	0.054	-.M*VGSKPLYVALAQR.-
R5/RRR5-3/2	1763.023	1762.040	-9.765	0.594	2713.335	0.485	24	0.389	K.LVENYAELLASQGLLK.T
R5/RRR5-3/2	1762.566	1762.040	-269.983	0.560	2057.319	0.451	22	0.258	K.LVENYAELLASQGLLK.T
R5/RRR5-3/2	1485.982	1484.697	192.821	0.531	1717.625	0.542	17	0.236	K.TYVDLLQDLM*EK.T
R5/RRR5-3/2	1469.935	1468.697	162.289	0.606	1820.925	0.491	18	0.236	K.TYVDLLQDLMEK.T
R5/RRR5-4/2	1761.498	1762.040	-878.195	0.490	1958.567	0.419	21	0.236	K.LVENYAELLASQGLLK.T
R5/RRR5-4/2	1761.445	1762.040	-908.388	0.431	1673.860	0.365	20	0.189	K.LVENYAELLASQGLLK.T
R5/RRR5-3/2	1720.700	1721.886	-1274.716	0.475	1400.382	0.477	19	0.184	R.KEEWNVLCDTLASR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1318.265	1318.416	-114.481	0.383	960.638	0.374	17	0.135	K.LNSGDISPNVSSK.L
R5/RRR5-3/3	1761.283	1762.040	-1000.865	0.382	1028.554	0.236	26	0.070	K.LVENYAELLASQGLLK.T
R5/RRR5-2/3	1498.890	1498.793	65.207	0.336	975.613	0.230	23	0.066	K.VSAELKPVIATLTR.L
R5/RRR5-3/3	1761.330	1762.040	-973.832	0.388	665.727	0.242	22	0.065	-.LVENYAELLASQGLLK.-
R5/RRR5-24/3	1721.688	1721.810	-70.845	0.593	2502.419	0.539	30	0.407	K.HGYIGEFEFVDDHR.S
R5/RRR5-24/3	1721.558	1721.810	-146.913	0.609	2198.261	0.545	30	0.326	K.HGYIGEFEFVDDHR.S
R5/RRR5-25/3	1721.148	1721.810	-968.504	0.529	2098.989	0.513	29	0.289	K.HGYIGEFEFVDDHR.S
R5/RRR5-24/3	1721.393	1721.810	-242.735	0.583	2138.341	0.480	29	0.282	K.HGYIGEFEFVDDHR.S
R5/RRR5-25/3	1721.860	1721.810	29.423	0.580	1999.148	0.497	29	0.259	K.HGYIGEFEFVDDHR.S
R5/RRR5-24/3	1637.591	1637.818	-138.970	0.469	2005.481	0.481	33	0.251	R.FDVGVKEIESWTAR.L
R5/RRR5-24/3	1637.824	1637.818	3.684	0.540	1928.886	0.464	32	0.230	R.FDVGVKEIESWTAR.L
R5/RRR5-24/3	1638.945	1637.818	78.050	0.556	1800.714	0.474	33	0.209	R.FDVGVKEIESWTAR.L
R5/RRR5-25/3	1721.662	1721.810	-86.421	0.527	1794.830	0.451	28	0.202	K.HGYIGEFEFVDDHR.S
R5/RRR5-25/3	1637.796	1637.818	-13.248	0.494	1949.222	0.375	32	0.200	R.FDVGVKEIESWTAR.L
R5/RRR5-25/3	1638.011	1637.818	118.495	0.534	1584.025	0.497	31	0.182	R.FDVGVKEIESWTAR.L
R5/RRR5-25/3	1639.019	1637.818	123.091	0.533	1534.687	0.494	30	0.174	R.FDVGVKEIESWTAR.L
R5/RRR5-24/2	1638.557	1637.818	-159.428	0.522	927.255	0.582	22	0.169	R.FDVGVKEIESWTAR.L
R5/RRR5-25/2	1636.749	1637.818	-1267.836	0.424	1092.263	0.444	22	0.156	R.FDVGVKEIESWTAR.L
R5/RRR5-25/2	1638.452	1637.818	-224.077	0.543	787.602	0.524	21	0.153	R.FDVGVKEIESWTAR.L
R5/RRR5-24/2	1637.505	1637.818	-191.308	0.465	880.994	0.471	21	0.149	R.FDVGVKEIESWTAR.L
R5/RRR5-25/2	1637.312	1637.818	-922.370	0.520	843.881	0.469	21	0.147	R.FDVGVKEIESWTAR.L
R5/RRR5-24/2	1637.443	1637.818	-229.748	0.530	643.216	0.509	18	0.142	R.FDVGVKEIESWTAR.L
R5/RRR5-24/2	958.443	959.122	-1757.406	0.417	957.324	0.338	15	0.137	R.VSVLNDALK.T
R5/RRR5-25/2	958.917	959.122	-214.775	0.405	875.284	0.357	15	0.136	R.VSVLNDALK.T
R5/RRR5-25/2	788.869	788.909	-50.769	0.360	675.681	0.424	11	0.134	K.CGVISPR.F
R5/RRR5-24/2	958.501	959.122	-1696.624	0.357	939.644	0.322	15	0.134	R.VSVLNDALK.T
R5/RRR5-25/2	788.539	788.909	-470.330	0.337	552.263	0.424	10	0.130	K.CGVISPR.F
R5/RRR5-25/2	958.435	959.122	-1765.084	0.276	916.677	0.311	15	0.129	R.VSVLNDALK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	959.799	959.122	-337.678	0.374	863.649	0.288	15	0.129	R.VSVLNDALK.T
R5/RRR5-24/2	958.381	959.122	-1822.290	0.280	795.023	0.327	14	0.127	R.VSVLNDALK.T
R5/RRR5-25/2	958.901	959.122	-231.250	0.364	751.590	0.302	14	0.127	R.VSVLNDALK.T
R5/RRR5-25/2	788.722	788.909	-238.146	0.340	645.762	0.303	11	0.125	K.CGVISPR.F
R5/RRR5-25/2	958.939	959.122	-191.916	0.238	719.044	0.191	12	0.117	R.VSVLNDALK.T
R5/RRR5-25/2	958.960	959.122	-169.313	0.336	474.847	0.274	11	0.113	-.VSVLNDALK.-
R5/RRR5-25/3	1722.930	1721.810	70.088	0.505	739.531	0.471	22	0.098	K.HGYIGEFEFVDDHR.S
R5/RRR5-18/2	1700.020	1699.882	81.267	0.524	2927.093	0.578	25	0.476	K.AITEIFAEAGFSDVTK.N
R5/RRR5-18/2	1699.314	1699.882	-926.038	0.451	2786.680	0.561	24	0.436	K.AITEIFAEAGFSDVTK.N
R5/RRR5-18/2	1699.170	1699.882	-1011.071	0.411	2558.907	0.508	24	0.367	K.AITEIFAEAGFSDVTK.N
R5/RRR5-18/2	1190.901	1190.334	-364.833	0.624	2064.021	0.437	18	0.255	K.NFLAVLADNGR.L
R5/RRR5-18/2	1190.206	1190.334	-107.973	0.575	1956.638	0.411	18	0.235	K.NFLAVLADNGR.L
R5/RRR5-18/2	1190.022	1190.334	-262.422	0.572	1863.916	0.433	18	0.228	K.NFLAVLADNGR.L
R5/RRR5-18/3	1700.875	1699.882	-4.119	0.583	1661.218	0.552	28	0.222	K.AITEIFAEAGFSDVTK.N
R5/RRR5-19/2	1700.288	1699.882	238.955	0.460	605.764	0.564	21	0.147	K.AITEIFAEAGFSDVTK.N
R5/RRR5-19/2	1700.170	1699.882	169.622	0.424	782.120	0.480	22	0.143	K.AITEIFAEAGFSDVTK.N
R5/RRR5-18/2	1196.377	1195.435	-48.776	0.509	652.454	0.459	14	0.137	K.KSPLFSQFIK.D
R5/RRR5-18/2	1707.709	1707.006	-174.696	0.414	939.989	0.394	17	0.136	K.SPLFSQFIKDLSVPK.E
R5/RRR5-19/2	1699.559	1699.882	-191.167	0.284	492.640	0.366	19	0.123	K.AITEIFAEAGFSDVTK.N
R5/RRR5-18/2	1707.062	1707.006	33.093	0.367	581.149	0.246	15	0.113	K.SPLFSQFIKDLSVPK.E
R5/RRR5-25/2	1797.488	1798.924	-1359.419	0.430	2436.378	0.550	24	0.356	K.CANGGLDLDWDTVFSK.I
R5/RRR5-25/2	1799.287	1798.924	202.263	0.568	2385.346	0.571	23	0.352	K.CANGGLDLDWDTVFSK.I
R5/RRR5-25/2	1798.198	1798.924	-962.812	0.565	2218.042	0.612	23	0.334	K.CANGGLDLDWDTVFSK.I
R5/RRR5-25/2	1799.270	1798.924	192.398	0.603	2213.941	0.606	23	0.331	K.CANGGLDLDWDTVFSK.I
R5/RRR5-26/2	1798.094	1798.924	-1020.883	0.516	2043.501	0.602	22	0.300	K.CANGGLDLDWDTVFSK.I
R5/RRR5-26/2	1798.431	1798.924	-275.288	0.536	1989.774	0.565	23	0.281	K.CANGGLDLDWDTVFSK.I
R5/RRR5-26/2	1627.064	1626.790	168.740	0.494	1823.063	0.542	22	0.249	K.YGWTAFCGPVGPTGR.D
R5/RRR5-26/2	1626.280	1626.790	-931.111	0.446	1588.423	0.532	21	0.216	K.YGWTAFCGPVGPTGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	1626.321	1626.790	-289.063	0.495	1573.133	0.513	21	0.210	K.YGWTAFCGPVGPTGR.D
R5/RRR5-25/2	1626.238	1626.790	-957.336	0.485	1538.682	0.512	20	0.205	K.YGWTAFCGPVGPTGR.D
R5/RRR5-26/2	1626.514	1626.790	-170.093	0.454	1476.520	0.516	20	0.200	K.YGWTAFCGPVGPTGR.D
R5/RRR5-25/2	1626.028	1626.790	-1086.519	0.473	1088.242	0.507	18	0.162	K.YGWTAFCGPVGPTGR.D
R5/RRR5-26/2	1800.384	1798.924	256.204	0.477	1093.780	0.470	20	0.157	K.CANGGLDLDWDTVFSK.I
R5/RRR5-26/2	1626.210	1626.790	-974.367	0.424	1019.031	0.460	18	0.151	K.YGWTAFCGPVGPTGR.D
R5/RRR5-25/2	1626.323	1626.790	-287.858	0.431	870.754	0.489	16	0.145	K.YGWTAFCGPVGPTGR.D
R5/RRR5-26/2	1626.182	1626.790	-992.002	0.435	796.921	0.485	18	0.143	K.YGWTAFCGPVGPTGR.D
R5/RRR5-25/2	1136.921	1137.185	-232.679	0.513	903.556	0.390	17	0.142	K.IDTDGQGFQR.G
R5/RRR5-26/2	1136.743	1137.185	-389.323	0.516	726.650	0.432	16	0.141	K.IDTDGQGFQR.G
R5/RRR5-25/2	1136.952	1137.185	-204.889	0.484	846.914	0.391	17	0.140	K.IDTDGQGFQR.G
R5/RRR5-26/2	1626.090	1626.790	-1048.680	0.380	975.756	0.387	17	0.138	K.YGWTAFCGPVGPTGR.D
R5/RRR5-26/2	1136.375	1137.185	-1597.249	0.442	787.021	0.369	17	0.136	K.IDTDGQGFQR.G
R5/RRR5-24/2	1136.813	1137.185	-328.017	0.482	728.897	0.360	16	0.133	K.IDTDGQGFQR.G
R5/RRR5-25/2	1136.959	1137.185	-198.750	0.478	576.027	0.385	15	0.133	K.IDTDGQGFQR.G
R5/RRR5-26/2	1136.316	1137.185	-1649.590	0.361	682.565	0.381	16	0.133	K.IDTDGQGFQR.G
R5/RRR5-24/2	1136.981	1137.185	-179.793	0.455	597.836	0.381	15	0.133	K.IDTDGQGFQR.G
R5/RRR5-26/2	1137.458	1137.185	241.479	0.418	588.630	0.365	15	0.131	K.IDTDGQGFQR.G
R5/RRR5-25/3	1842.922	1842.041	-64.258	0.561	1056.994	0.537	27	0.130	R.SKYGWTAFCGPVGPTGR.D
R5/RRR5-25/2	1137.078	1137.185	-93.637	0.450	656.160	0.332	16	0.130	K.IDTDGQGFQR.G
R5/RRR5-24/2	1136.350	1137.185	-1619.372	0.433	541.250	0.349	15	0.130	K.IDTDGQGFQR.G
R5/RRR5-25/2	1136.142	1137.185	-1803.084	0.380	507.429	0.318	15	0.128	K.IDTDGQGFQR.G
R5/RRR5-26/2	1137.843	1137.185	-301.357	0.391	432.054	0.276	14	0.126	K.IDTDGQGFQR.G
R5/RRR5-25/2	1626.002	1626.790	-1102.575	0.328	647.822	0.360	15	0.123	K.YGWTAFCGPVGPTGR.D
R5/RRR5-24/2	1800.136	1798.924	117.829	0.331	447.595	0.374	16	0.123	K.CANGGLDLDWDTVFSK.I
R5/RRR5-26/3	1841.311	1842.041	-942.338	0.420	732.667	0.433	26	0.088	R.SKYGWTAFCGPVGPTGR.D
R5/RRR5-3/2	1118.077	1118.351	-245.690	0.528	1288.457	0.445	18	0.172	K.LGFGVVDAVIK.A
R5/RRR5-3/2	1117.539	1118.351	-1625.923	0.450	1275.777	0.452	18	0.172	K.LGFGVVDAVIK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1011.848	1012.183	-332.106	0.479	1192.364	0.455	15	0.166	R.LSDFLAFAK.G
R5/RRR5-4/2	1119.034	1118.351	-284.102	0.532	1263.964	0.418	18	0.165	K.LGFGVVDAVIK.A
R5/RRR5-3/2	1012.049	1012.183	-132.667	0.451	1146.188	0.467	14	0.164	R.LSDFLAFAK.G
R5/RRR5-4/2	1118.080	1118.351	-242.623	0.483	1235.343	0.421	18	0.163	K.LGFGVVDAVIK.A
R5/RRR5-3/2	1163.363	1163.351	9.829	0.496	1291.996	0.362	17	0.158	K.VNLVQSLFSR.V
R5/RRR5-4/2	1117.437	1118.351	-1717.233	0.407	1200.331	0.386	17	0.154	K.LGFGVVDAVIK.A
R5/RRR5-3/2	1698.292	1698.861	-926.595	0.402	1058.667	0.432	18	0.145	K.GAGVDGIITDFPATAHR.Y
R5/RRR5-3/2	1212.293	1212.421	-105.703	0.408	692.063	0.524	17	0.145	K.TLSGNPPTIIAK.G
R5/RRR5-4/2	1211.910	1212.421	-1250.583	0.397	772.592	0.490	16	0.143	K.TLSGNPPTIIAK.G
R5/RRR5-3/2	1117.480	1118.351	-1678.819	0.417	1076.804	0.336	17	0.141	K.LGFGVVDAVIK.A
R5/RRR5-3/2	1213.225	1212.421	-161.632	0.435	660.948	0.490	16	0.140	K.TLSGNPPTIIAK.G
R5/RRR5-3/2	1163.206	1163.351	-125.637	0.428	969.549	0.364	15	0.139	K.VNLVQSLFSR.V
R5/RRR5-4/2	1163.033	1163.351	-274.617	0.491	625.284	0.447	12	0.134	K.VNLVQSLFSR.V
R5/RRR5-3/2	1211.670	1212.421	-1449.390	0.367	555.763	0.482	15	0.133	K.TLSGNPPTIIAK.G
R5/RRR5-3/2	1162.801	1163.351	-1337.515	0.441	649.096	0.375	12	0.126	-.VNLVQSLFSR.-
R5/RRR5-3/3	1698.348	1698.861	-893.699	0.355	894.373	0.371	26	0.085	K.GAGVDGIITDFPATAHR.Y
R5/RRR5-3/3	1699.285	1698.861	250.508	0.386	746.167	0.390	26	0.084	K.GAGVDGIITDFPATAHR.Y
R5/RRR5-4/3	1699.871	1698.861	6.214	0.335	830.012	0.346	27	0.080	K.GAGVDGIITDFPATAHR.Y
R5/RRR5-3/3	1698.804	1698.861	-33.529	0.362	743.968	0.282	25	0.072	K.GAGVDGIITDFPATAHR.Y
R5/RRR5-3/2	1669.605	1668.955	-209.923	0.407	764.875	0.559	22	0.152	R.FDPLPIVPVEDVLSK.Y
R5/RRR5-4/2	1085.923	1086.219	-273.710	0.381	809.878	0.462	14	0.142	R.LSDFLDFTK.G
R5/RRR5-3/2	1202.379	1201.395	-13.504	0.409	804.113	0.463	17	0.141	K.TLSGDSPLVIAK.G
R5/RRR5-3/2	1668.398	1668.955	-935.639	0.343	573.699	0.501	19	0.135	R.FDPLPIVPVEDVLSK.Y
R5/RRR5-4/2	1668.462	1668.955	-295.924	0.385	577.664	0.477	19	0.135	R.FDPLPIVPVEDVLSK.Y
R5/RRR5-4/2	1085.796	1086.219	-390.789	0.411	686.653	0.391	13	0.131	R.LSDFLDFTK.G
R5/RRR5-3/2	1668.415	1668.955	-925.649	0.319	497.353	0.482	18	0.130	R.FDPLPIVPVEDVLSK.Y
R5/RRR5-4/2	1668.957	1668.955	1.496	0.296	527.196	0.426	18	0.126	R.FDPLPIVPVEDVLSK.Y
R5/RRR5-4/2	1737.558	1737.849	-168.313	0.364	570.002	0.442	18	0.126	K.GGFSGLFPDSSEFAYR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1201.932	1201.395	-386.136	0.278	670.842	0.351	17	0.123	K.TLSGDSPLVIAK.G
R5/RRR5-4/2	1668.209	1668.955	-1049.579	0.250	417.904	0.391	17	0.122	R.FDPLPIVPVEDVLSK.Y
R5/RRR5-18/2	1897.292	1898.104	-957.891	0.588	2679.989	0.546	26	0.406	K.LGWAIDEDFGSFEALVK.K
R5/RRR5-18/2	1898.486	1898.104	201.755	0.637	2622.669	0.567	26	0.400	K.LGWAIDEDFGSFEALVK.K
R5/RRR5-18/2	1897.346	1898.104	-929.213	0.584	2470.730	0.575	26	0.373	K.LGWAIDEDFGSFEALVK.K
R5/RRR5-18/2	1745.429	1744.968	265.113	0.605	1666.142	0.587	25	0.242	K.KLSVETTANQDPLVTK.G
R5/RRR5-18/2	1743.941	1744.968	-1165.827	0.573	1603.990	0.556	25	0.226	K.KLSVETTANQDPLVTK.G
R5/RRR5-18/2	1616.284	1616.795	-937.703	0.496	1547.228	0.523	19	0.209	K.LSVETTANQDPLVTK.G
R5/RRR5-18/2	1744.531	1744.968	-251.088	0.589	1266.057	0.569	22	0.191	K.KLSVETTANQDPLVTK.G
R5/RRR5-18/2	1616.385	1616.795	-254.481	0.472	1117.638	0.557	17	0.172	K.LSVETTANQDPLVTK.G
R5/RRR5-18/2	1615.889	1616.795	-1183.277	0.438	1165.780	0.506	17	0.167	K.LSVETTANQDPLVTK.G
R5/RRR5-18/2	1504.713	1505.702	-1326.360	0.408	1094.997	0.394	17	0.147	K.NVRPDYLSNIWK.V
R5/RRR5-18/2	1505.540	1505.702	-108.048	0.457	951.431	0.391	16	0.139	K.NVRPDYLSNIWK.V
R5/RRR5-18/2	1504.567	1505.702	-1423.815	0.348	854.882	0.347	15	0.129	K.NVRPDYLSNIWK.V
R5/RRR5-19/2	1616.401	1616.795	-244.404	0.318	378.123	0.372	15	0.120	-.LSVETTANQDPLVTK.-
R5/RRR5-18/3	1505.863	1505.702	107.225	0.572	869.036	0.396	25	0.094	K.NVRPDYLSNIWK.V
R5/RRR5-18/3	1505.569	1505.702	-89.025	0.582	896.745	0.385	26	0.093	K.NVRPDYLSNIWK.V
R5/RRR5-18/3	1505.694	1505.702	-5.588	0.578	726.012	0.399	24	0.091	K.NVRPDYLSNIWK.V
R5/RRR5-6/2	1790.512	1789.966	-254.008	0.588	1445.516	0.502	20	0.190	R.ASSGDLDNTNIISQILK.L
R5/RRR5-6/2	1788.486	1789.966	-1390.290	0.364	1526.525	0.348	19	0.170	R.ASSGDLDNTNIISQILK.L
R5/RRR5-6/2	1123.953	1124.226	-243.316	0.428	1142.407	0.380	15	0.148	K.FSENVLDATK.K
R5/RRR5-6/2	1788.460	1789.966	-1965.984	0.363	1073.416	0.300	19	0.131	R.ASSGDLDNTNIISQILK.L
R5/RRR5-6/2	1708.558	1706.969	-241.612	0.491	658.014	0.416	20	0.130	R.LGQSKPIYQAFNAIR.N
R5/RRR5-6/2	1116.466	1117.232	-1585.813	0.264	1109.514	0.113	15	0.115	R.LEGELADLEK.G
R5/RRR5-6/3	1983.952	1984.197	-123.903	0.312	886.213	0.309	24	0.071	K.YDINEEDLRPYFALPK.V
R5/RRR5-3/2	1293.812	1293.320	381.406	0.460	1924.873	0.448	21	0.242	K.DSSQDEAGTAAIK.T
R5/RRR5-5/2	1293.059	1293.320	-201.837	0.412	1319.459	0.363	19	0.158	K.DSSQDEAGTAAIK.T
R5/RRR5-3/2	1587.526	1587.714	-118.510	0.398	879.576	0.381	17	0.131	K.EGTESSAFWFALGGK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1650.320	1650.815	-300.884	0.366	696.841	0.397	17	0.125	R.ASALAALSSAFNPSSQK.N
R5/RRR5-3/2	1650.586	1650.815	-138.906	0.314	822.068	0.332	18	0.123	R.ASALAALSSAFNPSSQK.N
R5/RRR5-5/2	1587.917	1587.714	128.102	0.333	796.769	0.324	16	0.122	K.EGTESSAFWFALGGK.Q
R5/RRR5-3/3	1282.988	1282.556	337.470	0.470	1318.853	0.343	22	0.109	R.IQDFKPVPLPK.A
R5/RRR5-3/3	1863.140	1862.030	59.063	0.396	1427.493	0.288	28	0.107	R.SSLNHDDVFILDTEKK.I
R5/RRR5-3/3	1282.568	1282.556	9.239	0.400	1266.960	0.257	22	0.087	R.IQDFKPVPLPK.A
R5/RRR5-3/3	1282.981	1282.556	332.605	0.457	1206.428	0.270	23	0.086	R.IQDFKPVPLPK.A
R5/RRR5-17/3	1672.384	1672.857	-283.378	0.582	2070.676	0.486	29	0.270	R.AKDVALVYNECYAR.L
R5/RRR5-17/2	1672.400	1672.857	-273.997	0.584	1821.202	0.588	21	0.263	R.AKDVALVYNECYAR.L
R5/RRR5-17/2	1672.463	1672.857	-236.358	0.600	1759.929	0.590	21	0.255	R.AKDVALVYNECYAR.L
R5/RRR5-17/2	1673.238	1672.857	228.403	0.640	1757.216	0.586	21	0.253	R.AKDVALVYNECYAR.L
R5/RRR5-17/2	1445.920	1446.534	-1119.739	0.444	1883.007	0.471	18	0.240	R.AACYDCGTSVWR.D
R5/RRR5-16/3	1672.199	1672.857	-994.475	0.547	1819.847	0.506	29	0.227	R.AKDVALVYNECYAR.L
R5/RRR5-17/3	1672.910	1672.857	31.564	0.591	1947.696	0.442	29	0.226	R.AKDVALVYNECYAR.L
R5/RRR5-16/2	1446.132	1446.534	-278.853	0.433	1771.757	0.450	18	0.220	R.AACYDCGTSVWR.D
R5/RRR5-16/2	1446.022	1446.534	-1048.621	0.426	1925.418	0.360	18	0.219	R.AACYDCGTSVWR.D
R5/RRR5-17/2	1445.912	1446.534	-1124.910	0.494	1691.948	0.484	18	0.219	R.AACYDCGTSVWR.D
R5/RRR5-16/3	1673.178	1672.857	192.473	0.551	1984.937	0.404	30	0.218	R.AKDVALVYNECYAR.L
R5/RRR5-17/2	1447.141	1446.534	-272.059	0.506	1605.832	0.502	18	0.213	R.AACYDCGTSVWR.D
R5/RRR5-16/2	1475.010	1473.606	274.786	0.597	1390.391	0.517	19	0.193	K.DVALVYNECYAR.L
R5/RRR5-16/2	1474.962	1473.606	242.338	0.584	1289.864	0.533	19	0.188	K.DVALVYNECYAR.L
R5/RRR5-17/2	1473.238	1473.606	-250.203	0.490	1328.004	0.495	19	0.184	K.DVALVYNECYAR.L
R5/RRR5-16/2	1473.574	1473.606	-21.654	0.544	1287.138	0.500	19	0.181	K.DVALVYNECYAR.L
R5/RRR5-17/2	1473.233	1473.606	-253.611	0.436	1258.207	0.484	19	0.175	K.DVALVYNECYAR.L
R5/RRR5-16/3	1671.985	1672.857	-1123.228	0.543	1560.618	0.475	27	0.173	R.AKDVALVYNECYAR.L
R5/RRR5-17/2	1473.166	1473.606	-299.583	0.439	1285.495	0.451	19	0.171	K.DVALVYNECYAR.L
R5/RRR5-16/2	1445.728	1446.534	-1252.764	0.391	1327.476	0.423	17	0.168	R.AACYDCGTSVWR.D
R5/RRR5-15/2	1474.497	1473.606	-73.870	0.526	1110.109	0.498	18	0.167	K.DVALVYNECYAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1267.127	1267.367	-189.541	0.509	1349.032	0.355	18	0.160	R.LSDKDDFLADK.V
R5/RRR5-15/2	1474.583	1473.606	-15.328	0.504	1034.375	0.470	17	0.156	K.DVALVYNECYAR.L
R5/RRR5-15/2	1473.170	1473.606	-296.757	0.363	1194.552	0.393	18	0.154	K.DVALVYNECYAR.L
R5/RRR5-17/2	1267.095	1267.367	-215.636	0.508	1208.260	0.371	18	0.153	R.LSDKDDFLADK.V
R5/RRR5-16/2	1266.716	1267.367	-1307.147	0.478	1182.433	0.356	17	0.149	R.LSDKDDFLADK.V
R5/RRR5-17/2	1266.552	1267.367	-1437.336	0.436	1159.309	0.363	17	0.149	R.LSDKDDFLADK.V
R5/RRR5-15/2	1445.893	1446.534	-1138.305	0.416	1165.579	0.371	15	0.147	R.AACYDCGTSVWR.D
R5/RRR5-16/2	1266.655	1267.367	-1355.637	0.481	1120.231	0.323	18	0.141	R.LSDKDDFLADK.V
R5/RRR5-18/2	1472.885	1473.606	-1171.726	0.357	1211.403	0.270	18	0.138	K.DVALVYNECYAR.L
R5/RRR5-16/2	1266.822	1267.367	-1223.050	0.429	1028.092	0.325	17	0.137	R.LSDKDDFLADK.V
R5/RRR5-15/2	1446.027	1446.534	-1045.400	0.396	1135.236	0.301	15	0.137	-.AACYDCGTSVWR.-
R5/RRR5-15/2	1266.977	1267.367	-308.330	0.437	987.793	0.338	17	0.137	R.LSDKDDFLADK.V
R5/RRR5-15/2	1446.077	1446.534	-317.134	0.389	1226.092	0.250	15	0.135	-.AACYDCGTSVWR.-
R5/RRR5-17/3	1672.625	1672.857	-139.170	0.585	1310.858	0.451	26	0.134	R.AKDVALVYNECYAR.L
R5/RRR5-19/2	1474.650	1473.606	30.337	0.251	169.506	0.499	15	0.125	-.DVALVYNECYAR.-
R5/RRR5-19/2	1474.859	1473.606	172.207	0.065	126.593	0.463	14	0.106	-.DVALVYNECYAR.-
R5/RRR5-16/3	1268.410	1267.367	34.343	0.528	1066.414	0.339	23	0.092	R.LSDKDDFLADK.V
R5/RRR5-16/3	1268.307	1267.367	-47.758	0.484	906.337	0.367	23	0.088	R.LSDKDDFLADK.V
R5/RRR5-4/2	1479.846	1478.672	117.848	0.352	800.245	0.390	17	0.128	R.EVIAIASNALDSFK.N
R5/RRR5-19/2	1551.447	1551.685	-153.938	0.538	2681.862	0.546	21	0.406	K.LQIWDTAGQESFR.S
R5/RRR5-19/2	1551.143	1551.685	-997.289	0.532	2483.186	0.553	21	0.367	K.LQIWDTAGQESFR.S
R5/RRR5-19/2	1550.482	1551.685	-1424.687	0.392	2527.791	0.455	20	0.343	K.LQIWDTAGQESFR.S
R5/RRR5-19/2	1359.075	1358.435	-265.725	0.474	1108.650	0.484	16	0.162	R.AVSYEEGEQFAK.E
R5/RRR5-18/2	1550.849	1551.685	-1187.506	0.351	1290.218	0.402	20	0.162	K.LQIWDTAGQESFR.S
R5/RRR5-19/2	1358.957	1358.435	-352.600	0.478	1024.609	0.514	16	0.161	R.AVSYEEGEQFAK.E
R5/RRR5-18/2	1551.292	1551.685	-253.873	0.391	1276.970	0.386	21	0.159	K.LQIWDTAGQESFR.S
R5/RRR5-19/2	1358.993	1358.435	-326.284	0.463	1040.219	0.459	16	0.154	R.AVSYEEGEQFAK.E
R5/RRR5-18/2	1357.981	1358.435	-335.092	0.417	1011.320	0.466	16	0.152	R.AVSYEEGEQFAK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1551.244	1551.685	-284.978	0.425	1005.600	0.430	19	0.149	K.LQIWDTAGQESFR.S
R5/RRR5-18/2	1358.045	1358.435	-287.744	0.415	884.708	0.444	15	0.142	R.AVSYEEGEQFAK.E
R5/RRR5-18/2	1358.149	1358.435	-211.456	0.395	855.802	0.442	15	0.140	R.AVSYEEGEQFAK.E
R5/RRR5-19/2	1320.513	1320.519	-4.971	0.304	999.607	0.351	16	0.134	R.GAAGALLVYDITR.R
R5/RRR5-19/2	1320.322	1320.519	-149.634	0.373	850.513	0.317	14	0.125	R.GAAGALLVYDITR.R
R5/RRR5-21/2	1320.950	1320.519	326.855	0.356	407.293	0.355	14	0.123	R.GAAGALLVYDITR.R
R5/RRR5-19/2	1320.217	1320.519	-229.587	0.333	531.243	0.287	14	0.119	R.GAAGALLVYDITR.R
R5/RRR5-18/2	1320.145	1320.519	-284.505	0.306	754.184	0.253	13	0.117	-.GAAGALLVYDITR.-
R5/RRR5-18/3	1690.422	1689.809	-229.799	0.397	1083.452	0.345	25	0.091	R.ETFNHLASWLEDAR.Q
R5/RRR5-19/3	1689.557	1689.809	-149.768	0.369	855.460	0.272	23	0.072	-.ETFNHLASWLEDAR.-
R5/RRR5-19/3	1689.315	1689.809	-293.512	0.342	897.898	0.244	23	0.069	R.ETFNHLASWLEDAR.Q
R5/RRR5-24/2	1891.536	1892.096	-827.595	0.555	2588.088	0.608	25	0.410	R.FAIYDFDFLTAEDVPK.S
R5/RRR5-24/2	1891.288	1892.096	-959.249	0.552	2456.334	0.628	25	0.389	R.FAIYDFDFLTAEDVPK.S
R5/RRR5-24/2	1891.940	1892.096	-83.133	0.589	2266.994	0.621	24	0.348	R.FAIYDFDFLTAEDVPK.S
R5/RRR5-24/2	1965.390	1965.999	-821.477	0.531	1289.066	0.642	25	0.209	R.TTSYEDFTSSLPEGDCR.F
R5/RRR5-24/2	1966.441	1965.999	225.292	0.533	1234.202	0.636	25	0.202	R.TTSYEDFTSSLPEGDCR.F
R5/RRR5-24/2	1466.796	1467.693	-1296.790	0.381	1662.209	0.395	19	0.196	R.IFYILWSPDNAK.V
R5/RRR5-24/2	1467.343	1467.693	-238.776	0.476	1449.208	0.441	18	0.183	R.IFYILWSPDNAK.V
R5/RRR5-25/2	1965.766	1965.999	-119.001	0.536	1093.407	0.595	22	0.180	R.TTSYEDFTSSLPEGDCR.F
R5/RRR5-24/2	1467.264	1467.693	-292.861	0.461	1454.402	0.388	18	0.174	R.IFYILWSPDNAK.V
R5/RRR5-24/2	1467.111	1467.693	-1081.116	0.400	1390.108	0.417	18	0.173	R.IFYILWSPDNAK.V
R5/RRR5-24/2	1467.253	1467.693	-300.206	0.437	1305.651	0.445	18	0.171	R.IFYILWSPDNAK.V
R5/RRR5-24/2	1466.991	1467.693	-1163.664	0.346	1467.964	0.346	18	0.167	R.IFYILWSPDNAK.V
R5/RRR5-24/2	1965.380	1965.999	-826.153	0.473	799.782	0.613	21	0.160	R.TTSYEDFTSSLPEGDCR.F
R5/RRR5-24/2	1071.294	1071.190	98.218	0.316	726.374	0.349	14	0.127	K.MLYASSNER.F
R5/RRR5-24/2	1467.496	1467.693	-134.627	0.420	741.205	0.343	14	0.126	R.IFYILWSPDNAK.V
R5/RRR5-24/2	1070.874	1071.190	-295.850	0.339	657.939	0.320	13	0.125	K.MLYASSNER.F
R5/RRR5-24/2	1070.676	1071.190	-1418.065	0.266	639.583	0.329	13	0.122	K.MLYASSNER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1745.561	1746.001	-252.412	0.492	2170.171	0.447	22	0.276	K.GVDVILDNIGGLYLQR.N
R5/RRR5-14/2	1745.925	1746.001	-43.241	0.504	1955.399	0.449	22	0.244	K.GVDVILDNIGGLYLQR.N
R5/RRR5-14/2	1745.512	1746.001	-280.968	0.475	1922.364	0.433	21	0.235	K.GVDVILDNIGGLYLQR.N
R5/RRR5-14/2	942.370	943.126	-1868.712	0.278	872.043	0.290	14	0.125	R.LTIQAAGLR.N
R5/RRR5-14/2	1067.151	1067.174	-22.213	0.362	831.507	0.286	14	0.124	K.VFVTAGSEEK.L
R5/RRR5-14/2	942.454	943.126	-1778.775	0.342	700.778	0.254	13	0.121	R.LTIQAAGLR.N
R5/RRR5-14/2	942.395	943.126	-1842.028	0.302	747.331	0.251	13	0.120	-.LTIQAAGLR.-
R5/RRR5-14/2	1100.393	1099.312	73.702	0.407	910.574	0.195	16	0.119	R.RLTIQAAGLR.N
R5/RRR5-14/2	1066.842	1067.174	-312.002	0.321	898.905	0.172	15	0.117	K.VFVTAGSEEK.L
R5/RRR5-14/2	1099.253	1099.312	-54.088	0.399	750.400	0.213	14	0.107	-.RLTIQAAGLR.-
R5/RRR5-3/2	1219.207	1218.296	-73.169	0.406	2025.924	0.285	18	0.215	R.EGETAAEILER.I
R5/RRR5-3/2	1565.274	1565.711	-280.155	0.504	1695.176	0.423	19	0.206	K.IENINDQYWTLR.A
R5/RRR5-3/2	1565.394	1565.711	-203.093	0.497	1598.669	0.466	19	0.205	K.IENINDQYWTLR.A
R5/RRR5-3/2	1240.318	1240.473	-124.736	0.516	981.779	0.448	15	0.151	K.SKEDILLFFK.L
R5/RRR5-3/2	1240.132	1240.473	-275.316	0.505	1054.537	0.399	14	0.146	K.SKEDILLFFK.L
R5/RRR5-3/2	1218.164	1218.296	-108.812	0.346	1408.839	0.234	17	0.145	R.EGETAAEILER.I
R5/RRR5-3/2	1219.294	1218.296	-1.568	0.463	1226.809	0.280	16	0.139	R.EGETAAEILER.I
R5/RRR5-3/2	1159.590	1159.360	199.071	0.406	761.251	0.374	14	0.131	K.AEAHLYTIIK.V
R5/RRR5-1/2	1160.247	1159.360	-97.782	0.279	563.437	0.220	13	0.114	-.AEAHLYTIIK.-
R5/RRR5-2/3	1736.751	1736.908	-90.640	0.331	939.768	0.354	22	0.083	-.YPDVPSFLEYVHNR.-
R5/RRR5-3/3	1737.234	1736.908	188.266	0.355	630.472	0.274	20	0.069	R.YPDVPSFLEYVHNR.Q
R5/RRR5-15/2	1617.213	1617.743	-949.202	0.503	2882.073	0.496	24	0.435	R.ELTAEVQQSGVTGAAR.V
R5/RRR5-15/2	1618.541	1617.743	-125.089	0.579	2609.171	0.570	24	0.400	R.ELTAEVQQSGVTGAAR.V
R5/RRR5-15/2	1617.050	1617.743	-1049.924	0.508	2587.779	0.463	24	0.358	R.ELTAEVQQSGVTGAAR.V
R5/RRR5-15/2	1363.273	1363.455	-133.603	0.492	1453.275	0.512	19	0.198	K.VFGESSPEAQPSK.S
R5/RRR5-14/2	1639.218	1637.818	245.168	0.434	658.238	0.490	17	0.134	K.GYTGAQYLPAIPTER.I
R5/RRR5-15/3	1865.904	1865.976	-38.631	0.331	611.771	0.434	33	0.087	K.VFGESSPEAQPSKSESAK.T
R5/RRR5-16/3	1865.843	1865.976	-71.507	0.292	414.159	0.384	28	0.084	K.VFGESSPEAQPSKSESAK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/3	1866.956	1865.976	-10.409	0.278	414.919	0.347	28	0.083	K.VFGESSPEAQPSKSESAK.T
R5/RRR5-16/3	1865.912	1865.976	-34.300	0.318	879.647	0.358	38	0.082	K.VFGESSPEAQPSKSESAK.T
R5/RRR5-15/3	1865.543	1865.976	-232.478	0.271	440.560	0.347	28	0.081	K.VFGESSPEAQPSKSESAK.T
R5/RRR5-16/3	1865.865	1865.976	-59.597	0.254	535.876	0.325	31	0.077	K.VFGESSPEAQPSKSESAK.T
R5/RRR5-15/3	1865.732	1865.976	-131.164	0.268	641.860	0.311	33	0.075	K.VFGESSPEAQPSKSESAK.T
R5/RRR5-16/2	1398.202	1397.561	-256.975	0.524	1700.146	0.487	19	0.221	K.LYGSTLSWNVTR.C
R5/RRR5-17/2	1396.842	1397.561	-1233.760	0.503	1595.570	0.472	19	0.206	K.LYGSTLSWNVTR.C
R5/RRR5-17/2	1397.306	1397.561	-182.923	0.491	1652.340	0.432	19	0.203	K.LYGSTLSWNVTR.C
R5/RRR5-16/2	1397.167	1397.561	-282.667	0.429	1440.121	0.388	18	0.173	K.LYGSTLSWNVTR.C
R5/RRR5-17/2	1397.061	1397.561	-1076.957	0.490	1467.495	0.360	18	0.171	-.LYGSTLSWNVTR.-
R5/RRR5-15/2	1397.403	1397.561	-113.255	0.340	1342.077	0.405	17	0.166	K.LYGSTLSWNVTR.C
R5/RRR5-17/2	1107.105	1107.285	-162.416	0.499	1236.083	0.388	15	0.158	K.KVLEVYEAR.L
R5/RRR5-17/2	1106.428	1107.285	-1682.863	0.398	1273.792	0.375	15	0.158	K.KVLEVYEAR.L
R5/RRR5-18/2	931.060	930.147	-94.031	0.475	490.916	0.490	14	0.142	K.VASLM*KPPA.-
R5/RRR5-16/2	978.931	979.112	-185.370	0.458	854.643	0.406	13	0.142	K.VLEVYEAR.L
R5/RRR5-18/2	929.319	930.147	-1973.074	0.326	447.809	0.489	14	0.141	K.VASLM*KPPA.-
R5/RRR5-17/2	978.423	979.112	-1731.028	0.422	785.897	0.421	13	0.141	K.VLEVYEAR.L
R5/RRR5-17/2	1106.504	1107.285	-1614.033	0.400	995.346	0.358	14	0.139	K.KVLEVYEAR.L
R5/RRR5-17/2	978.871	979.112	-246.920	0.518	753.275	0.401	13	0.139	K.VLEVYEAR.L
R5/RRR5-17/2	929.908	930.147	-258.465	0.439	535.013	0.443	14	0.138	K.VASLM*KPPA.-
R5/RRR5-17/2	978.409	979.112	-1745.193	0.412	781.743	0.395	13	0.138	K.VLEVYEAR.L
R5/RRR5-18/2	929.950	930.147	-213.295	0.444	584.381	0.514	14	0.137	K.VASLM*KPPA.-
R5/RRR5-17/2	978.874	979.112	-243.542	0.510	901.084	0.348	13	0.136	K.VLEVYEAR.L
R5/RRR5-17/2	930.075	930.147	-78.202	0.399	556.072	0.430	14	0.136	K.VASLM*KPPA.-
R5/RRR5-17/2	929.969	930.147	-192.752	0.416	558.882	0.409	14	0.136	K.VASLM*KPPA.-
R5/RRR5-16/2	978.936	979.112	-180.491	0.482	722.015	0.378	13	0.136	K.VLEVYEAR.L
R5/RRR5-17/2	978.935	979.112	-180.867	0.475	714.307	0.377	13	0.135	K.VLEVYEAR.L
R5/RRR5-16/2	929.752	930.147	-426.805	0.445	629.076	0.509	14	0.135	K.VASLM*KPPA.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	929.923	930.147	-241.608	0.406	501.252	0.445	13	0.135	K.VASLM*KPPA.-
R5/RRR5-17/2	929.931	930.147	-233.048	0.405	596.521	0.469	14	0.135	K.VASLM*KPPA.-
R5/RRR5-16/2	978.889	979.112	-228.655	0.437	812.312	0.352	13	0.135	K.VLEVYEAR.L
R5/RRR5-16/2	929.959	930.147	-203.023	0.397	606.871	0.470	14	0.134	K.VASLM*KPPA.-
R5/RRR5-17/2	929.937	930.147	-227.122	0.446	555.081	0.460	13	0.132	K.VASLM*KPPA.-
R5/RRR5-10/2	978.924	979.112	-192.500	0.375	848.300	0.300	13	0.130	K.VLEVYEAR.L
R5/RRR5-17/2	929.861	930.147	-309.172	0.457	752.977	0.403	14	0.128	K.VASLM*KPPA.-
R5/RRR5-17/2	978.312	979.112	-1845.112	0.358	756.990	0.268	13	0.126	K.VLEVYEAR.L
R5/RRR5-17/2	913.897	914.148	-275.595	0.286	755.541	0.305	13	0.121	K.VASLMKPPA.-
R5/RRR5-2/2	978.934	979.112	-181.742	0.319	872.792	0.161	13	0.119	K.VLEVYEAR.L
R5/RRR5-19/2	1375.558	1376.528	-1436.832	0.450	1602.216	0.423	18	0.194	K.CCDSIVQLPQR.I
R5/RRR5-19/2	1376.184	1376.528	-250.499	0.472	1559.631	0.437	18	0.193	K.CCDSIVQLPQR.I
R5/RRR5-24/2	1376.008	1376.528	-1108.294	0.469	1580.107	0.410	18	0.189	K.CCDSIVQLPQR.I
R5/RRR5-19/2	1376.066	1376.528	-336.561	0.491	1415.854	0.451	17	0.182	K.CCDSIVQLPQR.I
R5/RRR5-23/2	1376.058	1376.528	-342.880	0.488	1415.735	0.434	17	0.178	K.CCDSIVQLPQR.I
R5/RRR5-23/2	1376.078	1376.528	-328.105	0.492	1395.689	0.436	17	0.177	K.CCDSIVQLPQR.I
R5/RRR5-1/2	1376.017	1376.528	-1101.881	0.472	1385.803	0.438	17	0.177	K.CCDSIVQLPQR.I
R5/RRR5-27/2	1376.325	1376.528	-147.993	0.411	1528.667	0.346	18	0.172	K.CCDSIVQLPQR.I
R5/RRR5-20/2	1376.088	1376.528	-321.074	0.464	1396.679	0.410	17	0.172	K.CCDSIVQLPQR.I
R5/RRR5-23/2	1376.115	1376.528	-301.227	0.483	1412.006	0.403	17	0.172	K.CCDSIVQLPQR.I
R5/RRR5-21/2	1377.103	1376.528	-309.990	0.479	1321.496	0.439	17	0.172	K.CCDSIVQLPQR.I
R5/RRR5-21/2	1377.439	1376.528	-65.208	0.483	1428.796	0.385	17	0.170	K.CCDSIVQLPQR.I
R5/RRR5-27/2	1376.093	1376.528	-317.247	0.459	1457.113	0.359	17	0.168	K.CCDSIVQLPQR.I
R5/RRR5-1/2	1376.000	1376.528	-1113.995	0.460	1315.189	0.412	17	0.166	K.CCDSIVQLPQR.I
R5/RRR5-22/2	1376.123	1376.528	-295.442	0.442	1408.081	0.368	17	0.166	K.CCDSIVQLPQR.I
R5/RRR5-24/2	1375.543	1376.528	-1447.439	0.391	1347.102	0.397	17	0.166	K.CCDSIVQLPQR.I
R5/RRR5-17/2	1377.181	1376.528	-252.985	0.443	1550.423	0.300	17	0.165	K.CCDSIVQLPQR.I
R5/RRR5-1/2	1375.960	1376.528	-1143.036	0.442	1334.449	0.370	17	0.160	K.CCDSIVQLPQR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1375.538	1376.528	-1450.826	0.393	1377.163	0.347	17	0.160	K.CCDSIVQLPQR.I
R5/RRR5-19/2	1754.103	1754.855	-1001.673	0.511	1003.863	0.477	24	0.157	R.CDDELEPGKCTAACK.S
R5/RRR5-19/2	1754.406	1754.855	-257.002	0.510	1011.947	0.443	23	0.151	R.CDDELEPGKCTAACK.S
R5/RRR5-20/2	1376.066	1376.528	-336.650	0.416	1393.141	0.289	17	0.151	K.CCDSIVQLPQR.I
R5/RRR5-24/2	1376.160	1376.528	-268.476	0.419	1308.592	0.320	17	0.151	K.CCDSIVQLPQR.I
R5/RRR5-16/2	1376.216	1376.528	-227.807	0.443	1112.060	0.382	15	0.147	K.CCDSIVQLPQR.I
R5/RRR5-16/2	1375.994	1376.528	-1118.182	0.440	1006.577	0.419	15	0.147	K.CCDSIVQLPQR.I
R5/RRR5-19/2	1377.047	1376.528	-350.814	0.410	1208.182	0.327	16	0.145	K.CCDSIVQLPQR.I
R5/RRR5-20/2	1375.621	1376.528	-1390.572	0.410	1180.931	0.325	16	0.143	K.CCDSIVQLPQR.I
R5/RRR5-22/2	1375.460	1376.528	-1508.413	0.349	1117.442	0.319	16	0.139	K.CCDSIVQLPQR.I
R5/RRR5-18/2	1062.896	1063.091	-184.146	0.448	1000.109	0.347	14	0.139	R.CDDELEPGK.C
R5/RRR5-18/2	1376.184	1376.528	-251.033	0.395	1305.140	0.245	16	0.139	K.CCDSIVQLPQR.I
R5/RRR5-19/2	1277.921	1277.359	-343.343	0.295	883.264	0.416	16	0.138	K.ECVEAPGDFPR.G
R5/RRR5-19/2	1277.958	1277.359	-314.208	0.356	788.393	0.423	16	0.138	K.ECVEAPGDFPR.G
R5/RRR5-17/2	1277.945	1277.359	-324.845	0.352	696.898	0.455	15	0.137	K.ECVEAPGDFPR.G
R5/RRR5-18/2	1277.982	1277.359	-295.424	0.342	679.376	0.449	15	0.136	K.ECVEAPGDFPR.G
R5/RRR5-1/2	1278.001	1277.359	-280.283	0.297	866.794	0.392	17	0.135	K.ECVEAPGDFPR.G
R5/RRR5-20/2	1277.858	1277.359	391.725	0.342	698.685	0.440	15	0.135	K.ECVEAPGDFPR.G
R5/RRR5-19/2	1754.103	1754.855	-1002.023	0.487	719.790	0.414	21	0.134	R.CDDELEPGKCTAACK.S
R5/RRR5-22/2	1062.978	1063.091	-106.845	0.413	838.150	0.337	14	0.133	R.CDDELEPGK.C
R5/RRR5-28/2	1277.915	1277.359	-348.422	0.363	769.986	0.372	16	0.133	K.ECVEAPGDFPR.G
R5/RRR5-22/2	1062.747	1063.091	-324.610	0.374	937.340	0.299	14	0.131	R.CDDELEPGK.C
R5/RRR5-18/2	1062.564	1063.091	-1441.277	0.430	953.848	0.290	14	0.131	R.CDDELEPGK.C
R5/RRR5-19/2	1062.715	1063.091	-355.151	0.421	1002.314	0.283	14	0.131	-.CDDELEPGK.-
R5/RRR5-27/2	1062.931	1063.091	-151.312	0.298	956.286	0.293	14	0.130	R.CDDELEPGK.C
R5/RRR5-19/2	1376.247	1376.528	-204.850	0.399	1041.127	0.256	16	0.129	K.CCDSIVQLPQR.I
R5/RRR5-23/2	1062.966	1063.091	-117.673	0.335	927.630	0.278	14	0.129	R.CDDELEPGK.C
R5/RRR5-19/2	1062.965	1063.091	-119.286	0.363	983.063	0.255	14	0.128	R.CDDELEPGK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-28/2	1276.950	1277.359	-320.496	0.279	701.169	0.348	15	0.126	K.ECVEAPGDFPR.G
R5/RRR5-20/2	1062.968	1063.091	-115.830	0.370	901.912	0.256	14	0.126	R.CDDELEPGK.C
R5/RRR5-22/2	1062.925	1063.091	-157.072	0.348	924.095	0.249	14	0.126	R.CDDELEPGK.C
R5/RRR5-1/2	1063.035	1063.091	-52.706	0.409	949.786	0.243	14	0.126	R.CDDELEPGK.C
R5/RRR5-1/2	1277.023	1277.359	-263.431	0.253	948.346	0.252	17	0.125	K.ECVEAPGDFPR.G
R5/RRR5-27/2	1277.156	1277.359	-159.293	0.259	673.165	0.313	15	0.123	K.ECVEAPGDFPR.G
R5/RRR5-3/2	1376.110	1376.528	-304.609	0.358	820.564	0.244	15	0.122	K.CCDSIVQLPQR.I
R5/RRR5-20/2	1277.081	1277.359	-218.072	0.270	673.674	0.280	15	0.122	K.ECVEAPGDFPR.G
R5/RRR5-19/2	1063.144	1063.091	49.566	0.353	951.516	0.178	14	0.121	R.CDDELEPGK.C
R5/RRR5-22/2	1276.950	1277.359	-321.263	0.282	700.541	0.227	15	0.120	K.ECVEAPGDFPR.G
R5/RRR5-1/2	1277.015	1277.359	-269.761	0.237	824.428	0.206	16	0.119	K.ECVEAPGDFPR.G
R5/RRR5-19/2	1062.341	1063.091	-1652.087	0.309	1002.548	0.145	14	0.119	R.CDDELEPGK.C
R5/RRR5-19/2	1062.636	1063.091	-429.379	0.343	996.687	0.149	14	0.119	R.CDDELEPGK.C
R5/RRR5-22/2	1277.048	1277.359	-243.676	0.190	665.210	0.246	15	0.118	K.ECVEAPGDFPR.G
R5/RRR5-16/2	1277.088	1277.359	-212.127	0.182	617.451	0.270	14	0.118	K.ECVEAPGDFPR.G
R5/RRR5-23/2	1062.221	1063.091	-1766.271	0.314	966.958	0.121	14	0.117	R.CDDELEPGK.C
R5/RRR5-23/2	1062.397	1063.091	-1599.333	0.286	973.580	0.115	14	0.117	R.CDDELEPGK.C
R5/RRR5-15/2	1277.174	1277.359	-144.911	0.229	900.731	0.112	15	0.115	K.ECVEAPGDFPR.G
R5/RRR5-19/3	1753.591	1754.855	-1294.870	0.401	1100.237	0.385	29	0.100	R.CDDELEPGKCTAACK.S
R5/RRR5-15/3	1755.620	1754.855	-134.613	0.392	484.559	0.427	22	0.092	R.CDDELEPGKCTAACK.S
R5/RRR5-18/3	1754.470	1754.855	-220.293	0.397	573.799	0.421	25	0.091	R.CDDELEPGKCTAACK.S
R5/RRR5-13/3	1754.461	1754.855	-225.110	0.403	509.402	0.369	23	0.087	R.CDDELEPGKCTAACK.S
R5/RRR5-20/3	1754.232	1754.855	-928.184	0.407	667.679	0.383	25	0.087	R.CDDELEPGKCTAACK.S
R5/RRR5-19/3	1753.829	1754.855	-1158.983	0.367	751.585	0.378	26	0.086	R.CDDELEPGKCTAACK.S
R5/RRR5-18/3	1754.095	1754.855	-1006.467	0.392	553.948	0.373	22	0.086	R.CDDELEPGKCTAACK.S
R5/RRR5-20/3	1754.380	1754.855	-271.599	0.383	573.427	0.374	22	0.086	R.CDDELEPGKCTAACK.S
R5/RRR5-23/3	1754.126	1754.855	-988.546	0.387	649.681	0.365	26	0.085	R.CDDELEPGKCTAACK.S
R5/RRR5-1/3	1754.677	1754.855	-101.995	0.387	613.108	0.343	25	0.084	R.CDDELEPGKCTAACK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/3	1753.894	1754.855	-1121.557	0.351	608.161	0.358	23	0.084	R.CDDELEPGKCTAACK.S
R5/RRR5-23/3	1754.704	1754.855	-86.294	0.393	806.939	0.342	28	0.084	R.CDDELEPGKCTAACK.S
R5/RRR5-20/3	1754.505	1754.855	-199.982	0.370	551.419	0.327	23	0.083	R.CDDELEPGKCTAACK.S
R5/RRR5-1/3	1754.163	1754.855	-967.376	0.356	619.284	0.340	24	0.083	R.CDDELEPGKCTAACK.S
R5/RRR5-20/2	1888.756	1888.973	-114.907	0.578	2444.416	0.667	25	0.401	K.GQIQSDGGTYNLYQSTR.Y
R5/RRR5-20/2	1888.280	1888.973	-899.244	0.555	2373.669	0.644	25	0.378	K.GQIQSDGGTYNLYQSTR.Y
R5/RRR5-20/2	1719.048	1719.902	-1081.888	0.459	1342.525	0.553	19	0.193	R.TGGTITM*SNFFNAWR.N
R5/RRR5-20/2	1719.393	1719.902	-880.648	0.487	1448.802	0.495	19	0.192	R.TGGTITM*SNFFNAWR.N
R5/RRR5-21/2	1703.317	1703.903	-933.709	0.462	1374.796	0.522	18	0.189	R.TGGTITMSNFFNAWR.N
R5/RRR5-20/2	1719.109	1719.902	-1046.096	0.464	1116.037	0.538	18	0.169	R.TGGTITM*SNFFNAWR.N
R5/RRR5-21/2	1719.991	1719.902	51.747	0.504	1034.281	0.492	17	0.155	R.TGGTITM*SNFFNAWR.N
R5/RRR5-21/2	1199.982	1199.342	-301.159	0.422	1009.378	0.314	14	0.135	K.TFNQYWAIR.T
R5/RRR5-20/2	1199.443	1199.342	84.254	0.413	1147.971	0.247	15	0.133	K.TFNQYWAIR.T
R5/RRR5-21/2	1199.713	1199.342	309.878	0.318	565.025	0.447	12	0.132	K.TFNQYWAIR.T
R5/RRR5-21/2	1199.549	1199.342	172.740	0.285	851.865	0.358	13	0.131	K.TFNQYWAIR.T
R5/RRR5-21/2	1079.910	1080.173	-243.829	0.336	804.173	0.347	15	0.130	R.YNAPSIEGTK.T
R5/RRR5-20/2	1199.230	1199.342	-93.786	0.395	803.281	0.308	13	0.128	K.TFNQYWAIR.T
R5/RRR5-20/2	1199.553	1199.342	175.802	0.431	519.436	0.348	12	0.128	K.TFNQYWAIR.T
R5/RRR5-21/2	1199.817	1199.342	397.101	0.293	602.215	0.376	12	0.127	K.TFNQYWAIR.T
R5/RRR5-20/2	1199.782	1199.342	367.824	0.354	432.630	0.331	12	0.127	K.TFNQYWAIR.T
R5/RRR5-21/2	1080.201	1080.173	26.454	0.399	602.893	0.351	13	0.127	R.YNAPSIEGTK.T
R5/RRR5-20/2	1199.329	1199.342	-11.088	0.412	717.622	0.302	13	0.126	K.TFNQYWAIR.T
R5/RRR5-20/2	1079.821	1080.173	-327.301	0.351	596.251	0.372	13	0.126	-.YNAPSIEGTK.-
R5/RRR5-21/2	1079.412	1080.173	-1636.054	0.254	682.872	0.323	13	0.122	R.YNAPSIEGTK.T
R5/RRR5-21/2	1199.438	1199.342	79.967	0.342	678.843	0.202	13	0.120	K.TFNQYWAIR.T
R5/RRR5-20/2	1079.890	1080.173	-262.654	0.236	801.952	0.204	14	0.118	R.YNAPSIEGTK.T
R5/RRR5-20/2	1079.499	1080.173	-1555.281	0.191	774.394	0.205	14	0.116	R.YNAPSIEGTK.T
R5/RRR5-21/2	1199.507	1199.342	137.531	0.313	441.409	0.287	10	0.107	-.TFNQYWAIR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1318.058	1318.416	-272.229	0.488	2355.067	0.479	21	0.316	R.LANDTQGTVEAAK.W
R5/RRR5-10/2	1319.160	1318.416	-194.316	0.524	1881.661	0.578	21	0.268	R.LANDTQGTVEAAK.W
R5/RRR5-11/2	1319.075	1318.416	-258.746	0.522	1906.340	0.531	21	0.259	R.LANDTQGTVEAAK.W
R5/RRR5-11/2	1460.895	1460.527	252.215	0.518	1718.417	0.583	20	0.247	K.AISTSNAYDDQFK.Q
R5/RRR5-11/2	1459.992	1460.527	-1054.772	0.452	1683.019	0.539	20	0.231	K.AISTSNAYDDQFK.Q
R5/RRR5-10/2	1461.028	1460.527	-342.381	0.505	1585.889	0.543	19	0.220	K.AISTSNAYDDQFK.Q
R5/RRR5-10/2	1460.027	1460.527	-343.370	0.460	1547.058	0.514	20	0.209	K.AISTSNAYDDQFK.Q
R5/RRR5-10/2	1317.601	1318.416	-1381.183	0.396	1627.619	0.461	21	0.205	R.LANDTQGTVEAAK.W
R5/RRR5-10/2	1317.638	1318.416	-1352.710	0.395	1615.930	0.464	21	0.204	R.LANDTQGTVEAAK.W
R5/RRR5-11/2	1318.421	1318.416	4.122	0.465	1402.528	0.568	20	0.204	R.LANDTQGTVEAAK.W
R5/RRR5-11/2	1319.122	1318.416	-223.095	0.437	1396.594	0.521	20	0.194	R.LANDTQGTVEAAK.W
R5/RRR5-10/2	1460.112	1460.527	-285.072	0.486	1221.388	0.589	18	0.190	K.AISTSNAYDDQFK.Q
R5/RRR5-13/2	1317.353	1318.416	-1570.673	0.351	1571.259	0.399	20	0.186	R.LANDTQGTVEAAK.W
R5/RRR5-13/2	1319.083	1318.416	-253.082	0.504	1260.698	0.537	19	0.185	R.LANDTQGTVEAAK.W
R5/RRR5-11/2	1286.217	1286.493	-215.285	0.465	1313.894	0.497	19	0.183	K.IPATAECVPSIK.E
R5/RRR5-11/2	1460.122	1460.527	-278.361	0.468	1197.624	0.531	19	0.178	K.AISTSNAYDDQFK.Q
R5/RRR5-11/2	1285.549	1286.493	-1516.670	0.400	1123.228	0.520	19	0.169	K.IPATAECVPSIK.E
R5/RRR5-11/2	1286.109	1286.493	-299.936	0.483	1008.121	0.532	18	0.165	K.IPATAECVPSIK.E
R5/RRR5-10/2	1285.497	1286.493	-1557.687	0.384	1118.314	0.470	18	0.160	K.IPATAECVPSIK.E
R5/RRR5-10/2	1319.278	1318.416	-104.370	0.446	1108.041	0.464	18	0.159	R.LANDTQGTVEAAK.W
R5/RRR5-13/2	1318.091	1318.416	-246.585	0.468	1112.995	0.448	18	0.157	R.LANDTQGTVEAAK.W
R5/RRR5-1/2	1318.080	1318.416	-255.690	0.426	1203.345	0.394	20	0.156	R.LANDTQGTVEAAK.W
R5/RRR5-7/2	1318.330	1318.416	-65.439	0.478	957.807	0.474	18	0.152	R.LANDTQGTVEAAK.W
R5/RRR5-11/2	1177.972	1178.320	-296.496	0.503	969.942	0.418	16	0.146	R.GVTSNPSIFQK.A
R5/RRR5-11/2	1317.922	1318.416	-375.749	0.383	952.246	0.423	21	0.146	R.LANDTQGTVEAAK.W
R5/RRR5-10/2	1177.959	1178.320	-307.517	0.428	667.615	0.418	15	0.134	R.GVTSNPSIFQK.A
R5/RRR5-10/2	1178.029	1178.320	-247.425	0.476	665.699	0.412	15	0.134	R.GVTSNPSIFQK.A
R5/RRR5-11/2	1177.910	1178.320	-349.315	0.445	648.146	0.404	15	0.133	R.GVTSNPSIFQK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1178.070	1178.320	-212.912	0.385	651.514	0.363	15	0.128	R.GVTSNPSIFQK.A
R5/RRR5-11/2	1178.091	1178.320	-194.824	0.463	659.992	0.343	15	0.127	R.GVTSNPSIFQK.A
R5/RRR5-11/2	1317.246	1318.416	-1651.758	0.227	456.861	0.317	20	0.123	R.LANDTQGTVEAAK.W
R5/RRR5-18/2	1624.202	1624.726	-941.198	0.466	1897.170	0.562	22	0.267	K.GCVFTYDAVGSYER.T
R5/RRR5-18/2	1687.049	1687.870	-1082.346	0.416	1361.648	0.519	24	0.189	R.DAVTPLSETEAVDLVK.D
R5/RRR5-18/2	1687.209	1687.870	-987.470	0.465	1221.182	0.563	23	0.185	R.DAVTPLSETEAVDLVK.D
R5/RRR5-18/2	1688.322	1687.870	268.496	0.533	1270.380	0.528	23	0.184	R.DAVTPLSETEAVDLVK.D
R5/RRR5-17/2	1687.301	1687.870	-932.921	0.476	1211.682	0.536	23	0.180	R.DAVTPLSETEAVDLVK.D
R5/RRR5-17/2	1687.482	1687.870	-230.481	0.482	1260.125	0.512	23	0.179	R.DAVTPLSETEAVDLVK.D
R5/RRR5-17/2	1686.791	1687.870	-1235.957	0.339	1187.503	0.471	23	0.163	R.DAVTPLSETEAVDLVK.D
R5/RRR5-18/2	1050.968	1051.264	-282.697	0.492	1147.239	0.436	16	0.160	K.SPSPLLLPAR.D
R5/RRR5-17/2	1051.163	1051.264	-97.097	0.456	909.676	0.432	15	0.145	K.SPSPLLLPAR.D
R5/RRR5-18/2	995.785	996.056	-273.281	0.382	996.096	0.394	15	0.144	K.DVFASATER.D
R5/RRR5-18/2	1051.047	1051.264	-207.540	0.515	820.905	0.447	14	0.143	K.SPSPLLLPAR.D
R5/RRR5-18/2	1050.537	1051.264	-1648.972	0.378	871.405	0.431	14	0.141	K.SPSPLLLPAR.D
R5/RRR5-17/2	1050.496	1051.264	-1688.315	0.363	760.818	0.424	13	0.135	K.SPSPLLLPAR.D
R5/RRR5-18/2	995.939	996.056	-117.479	0.300	834.727	0.403	14	0.135	K.DVFASATER.D
R5/RRR5-17/2	996.022	996.056	-34.617	0.356	836.549	0.357	13	0.132	K.DVFASATER.D
R5/RRR5-17/2	995.261	996.056	-1808.584	0.278	853.074	0.313	14	0.127	K.DVFASATER.D
R5/RRR5-18/2	995.271	996.056	-1798.848	0.324	752.550	0.287	13	0.124	K.DVFASATER.D
R5/RRR5-17/2	995.299	996.056	-1770.874	0.251	646.137	0.335	13	0.123	K.DVFASATER.D
R5/RRR5-17/2	1050.330	1051.264	-1846.649	0.256	672.069	0.268	13	0.120	K.SPSPLLLPAR.D
R5/RRR5-16/2	1687.570	1687.870	-178.232	0.349	547.315	0.310	16	0.119	R.DAVTPLSETEAVDLVK.D
R5/RRR5-22/2	1316.009	1316.443	-330.242	0.383	2387.928	0.409	24	0.303	R.ATGGEVGASSALAPK.I
R5/RRR5-22/2	1316.100	1316.443	-261.471	0.382	1935.472	0.389	23	0.227	R.ATGGEVGASSALAPK.I
R5/RRR5-21/2	1315.486	1316.443	-1491.648	0.381	1933.852	0.385	23	0.226	R.ATGGEVGASSALAPK.I
R5/RRR5-21/2	1316.127	1316.443	-240.627	0.381	1734.907	0.414	22	0.207	R.ATGGEVGASSALAPK.I
R5/RRR5-21/2	1315.539	1316.443	-1451.289	0.334	1748.825	0.404	22	0.206	R.ATGGEVGASSALAPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1315.884	1316.443	-1188.429	0.332	1720.672	0.338	22	0.190	R.ATGGEVGASSALAPK.I
R5/RRR5-22/2	1584.716	1584.882	-105.354	0.412	1275.172	0.467	22	0.170	R.QAAVSVVPTASSLIIK.A
R5/RRR5-22/2	1358.935	1359.551	-1192.765	0.373	528.104	0.379	13	0.122	K.SITIDEVIEIAR.T
R5/RRR5-22/2	1358.477	1359.551	-1531.056	0.221	933.990	0.206	16	0.117	K.SITIDEVIEIAR.T
R5/RRR5-14/2	1564.506	1564.680	-111.723	0.504	2224.719	0.494	22	0.302	K.SADWSHFLTGSLDK.S
R5/RRR5-14/2	1261.985	1261.279	-233.778	0.484	1295.300	0.521	19	0.186	R.SFSSGGEDGYVR.L
R5/RRR5-14/2	1261.015	1261.407	-312.021	0.381	1384.172	0.489	18	0.185	R.TIITAGEDATIR.I
R5/RRR5-14/2	1262.384	1261.279	82.866	0.477	1060.446	0.511	18	0.165	R.SFSSGGEDGYVR.L
R5/RRR5-13/2	1261.084	1261.407	-257.246	0.405	1151.166	0.480	17	0.164	R.TIITAGEDATIR.I
R5/RRR5-13/2	1260.728	1261.407	-1335.886	0.327	1280.288	0.365	19	0.155	R.TIITAGEDATIR.I
R5/RRR5-14/2	1260.403	1261.279	-1493.307	0.389	986.915	0.451	17	0.149	R.SFSSGGEDGYVR.L
R5/RRR5-13/2	1260.964	1261.279	-251.251	0.423	859.499	0.490	16	0.148	R.SFSSGGEDGYVR.L
R5/RRR5-14/2	1260.495	1261.407	-1521.853	0.300	1060.599	0.413	16	0.145	R.TIITAGEDATIR.I
R5/RRR5-14/2	1260.483	1261.407	-1530.900	0.304	1005.903	0.425	17	0.144	R.TIITAGEDATIR.I
R5/RRR5-13/2	1086.177	1086.264	-80.102	0.377	1078.553	0.345	16	0.141	K.ILQEEIGGVK.G
R5/RRR5-13/2	1261.055	1261.279	-178.415	0.394	811.241	0.437	15	0.138	R.SFSSGGEDGYVR.L
R5/RRR5-14/2	1085.988	1086.264	-254.528	0.388	1079.291	0.305	16	0.136	K.ILQEEIGGVK.G
R5/RRR5-13/2	1260.261	1261.279	-1606.074	0.267	728.180	0.398	15	0.128	R.SFSSGGEDGYVR.L
R5/RRR5-6/2	1376.143	1375.492	-254.778	0.546	1747.771	0.500	18	0.231	K.NSLENYAYNMR.N
R5/RRR5-6/2	1390.911	1391.492	-1139.954	0.499	1274.611	0.445	17	0.170	K.NSLENYAYNM*R.N
R5/RRR5-6/2	1390.938	1391.492	-1120.478	0.487	1243.724	0.423	18	0.165	K.NSLENYAYNM*R.N
R5/RRR5-6/2	1390.925	1391.492	-1129.731	0.484	1159.089	0.461	17	0.164	K.NSLENYAYNM*R.N
R5/RRR5-6/2	1375.097	1375.492	-288.183	0.453	1163.633	0.441	16	0.160	K.NSLENYAYNMR.N
R5/RRR5-15/2	1595.428	1595.779	-220.680	0.546	2259.547	0.593	24	0.340	K.VPGVDDVTGEPLIQR.K
R5/RRR5-15/2	1635.254	1634.812	270.995	0.606	2439.583	0.382	22	0.298	K.VLNFAIDDSILEER.I
R5/RRR5-15/2	1635.209	1634.812	243.748	0.598	2452.831	0.372	22	0.297	K.VLNFAIDDSILEER.I
R5/RRR5-16/2	1633.421	1634.812	-1468.306	0.421	2493.969	0.268	22	0.280	K.VLNFAIDDSILEER.I
R5/RRR5-15/2	1634.502	1634.812	-190.161	0.597	2275.710	0.395	22	0.275	K.VLNFAIDDSILEER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1633.905	1634.812	-1170.679	0.403	2085.748	0.255	21	0.215	K.VLNFAIDDSILEER.I
R5/RRR5-15/2	1021.543	1022.181	-1609.180	0.453	1247.742	0.491	14	0.176	K.GFILDGFPR.T
R5/RRR5-15/2	1021.901	1022.181	-275.103	0.482	1211.023	0.449	14	0.166	K.GFILDGFPR.T
R5/RRR5-16/2	1021.685	1022.181	-486.914	0.456	1232.335	0.428	14	0.164	K.GFILDGFPR.T
R5/RRR5-15/2	1021.801	1022.181	-373.625	0.473	1190.990	0.434	14	0.162	K.GFILDGFPR.T
R5/RRR5-16/2	1022.057	1022.181	-122.443	0.483	1182.664	0.436	14	0.162	K.GFILDGFPR.T
R5/RRR5-16/2	1022.011	1022.181	-166.894	0.529	1166.721	0.434	14	0.161	K.GFILDGFPR.T
R5/RRR5-15/2	1038.356	1038.266	87.184	0.396	753.885	0.364	15	0.130	R.LILVGPPGSGK.G
R5/RRR5-15/2	1037.629	1038.266	-1582.169	0.310	658.136	0.318	14	0.121	-.LILVGPPGSGK.-
R5/RRR5-16/2	1038.966	1038.266	-289.616	0.363	504.933	0.312	12	0.118	-.LILVGPPGSGK.-
R5/RRR5-17/2	1639.544	1638.849	-186.216	0.581	2156.681	0.544	22	0.302	K.TNLNVEQVFFSIAR.D
R5/RRR5-18/2	1638.184	1638.849	-1019.413	0.538	2120.003	0.531	22	0.293	K.TNLNVEQVFFSIAR.D
R5/RRR5-18/2	1638.418	1638.849	-263.987	0.540	2058.140	0.551	22	0.289	K.TNLNVEQVFFSIAR.D
R5/RRR5-18/2	1639.363	1638.849	-297.368	0.583	2075.508	0.541	22	0.288	K.TNLNVEQVFFSIAR.D
R5/RRR5-19/2	1637.805	1638.849	-1251.843	0.385	2196.650	0.413	22	0.272	K.TNLNVEQVFFSIAR.D
R5/RRR5-17/2	1637.881	1638.849	-1204.989	0.427	2073.417	0.481	22	0.271	K.TNLNVEQVFFSIAR.D
R5/RRR5-18/2	1164.141	1165.278	-1841.123	0.373	1913.845	0.396	18	0.226	K.GQALADEYGIK.F
R5/RRR5-17/2	1637.392	1638.849	-1504.899	0.358	1808.681	0.410	19	0.215	K.TNLNVEQVFFSIAR.D
R5/RRR5-17/2	1165.540	1165.278	225.892	0.412	1667.119	0.326	17	0.183	K.GQALADEYGIK.F
R5/RRR5-18/2	1164.356	1165.278	-1655.185	0.304	1421.859	0.286	16	0.153	K.GQALADEYGIK.F
R5/RRR5-18/2	1165.086	1165.278	-164.842	0.383	1238.006	0.339	16	0.149	K.GQALADEYGIK.F
R5/RRR5-17/2	1073.115	1072.280	-154.554	0.456	1061.179	0.389	17	0.147	K.LLLIGDSGVGK.S
R5/RRR5-17/2	1072.303	1072.280	20.825	0.389	1077.485	0.338	17	0.140	K.LLLIGDSGVGK.S
R5/RRR5-17/2	1071.674	1072.280	-1502.886	0.332	932.556	0.346	16	0.133	K.LLLIGDSGVGK.S
R5/RRR5-18/2	1072.242	1072.280	-36.267	0.365	908.272	0.322	15	0.130	K.LLLIGDSGVGK.S
R5/RRR5-20/2	1071.977	1072.280	-283.667	0.265	612.980	0.228	13	0.113	-.LLLIGDSGVGK.-
R5/RRR5-18/3	1558.381	1558.764	-246.480	0.389	1204.579	0.318	25	0.093	R.IKLQIWDTAGQER.F
R5/RRR5-15/2	1619.451	1618.813	-224.060	0.610	2374.193	0.480	22	0.318	K.VLNFAIDDAILEER.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1618.379	1618.813	-268.995	0.555	2413.922	0.434	22	0.312	K.VLNFAIDDAILEER.I
R5/RRR5-16/2	1619.319	1618.813	-305.737	0.587	2384.834	0.431	22	0.305	K.VLNFAIDDAILEER.I
R5/RRR5-16/2	1619.195	1618.813	236.555	0.589	2412.417	0.404	22	0.300	K.VLNFAIDDAILEER.I
R5/RRR5-16/2	1618.435	1618.813	-233.808	0.566	2343.750	0.391	22	0.286	K.VLNFAIDDAILEER.I
R5/RRR5-15/2	1618.549	1618.813	-163.214	0.541	2305.755	0.379	22	0.277	K.VLNFAIDDAILEER.I
R5/RRR5-16/2	1611.081	1611.778	-1056.930	0.487	1486.253	0.503	22	0.200	K.TPGLDDVTGEPLIQR.K
R5/RRR5-16/2	1611.748	1611.778	-18.886	0.530	1354.028	0.548	21	0.195	K.TPGLDDVTGEPLIQR.K
R5/RRR5-16/2	1611.254	1611.778	-949.065	0.498	1447.396	0.466	22	0.188	K.TPGLDDVTGEPLIQR.K
R5/RRR5-15/2	1610.803	1611.778	-1230.186	0.463	1428.459	0.441	22	0.181	K.TPGLDDVTGEPLIQR.K
R5/RRR5-15/2	1611.216	1611.778	-972.796	0.527	1294.823	0.490	21	0.178	K.TPGLDDVTGEPLIQR.K
R5/RRR5-15/2	1096.505	1097.326	-1665.934	0.326	968.733	0.298	16	0.129	R.VILVGPPGCGK.G
R5/RRR5-15/2	1096.904	1097.326	-385.827	0.330	589.558	0.315	13	0.121	R.VILVGPPGCGK.G
R5/RRR5-15/2	1097.034	1097.326	-266.920	0.285	659.520	0.314	13	0.120	R.VILVGPPGCGK.G
R5/RRR5-6/2	1620.131	1618.813	197.046	0.400	928.082	0.243	15	0.119	K.VLNFAIDDAILEER.I
R5/RRR5-6/2	1619.768	1618.813	-27.485	0.334	876.215	0.230	16	0.119	K.VLNFAIDDAILEER.I
R5/RRR5-25/2	1772.270	1772.912	-929.209	0.532	1792.417	0.474	22	0.229	K.FVSESVEDQTEQVM*K.N
R5/RRR5-25/2	1772.173	1772.912	-984.116	0.546	1672.030	0.509	21	0.222	K.FVSESVEDQTEQVM*K.N
R5/RRR5-25/3	1772.353	1772.912	-882.163	0.352	951.139	0.269	26	0.070	K.FVSESVEDQTEQVM*K.N
R5/RRR5-20/2	1771.367	1769.934	245.126	0.582	1526.489	0.548	23	0.213	K.DGATDPTFLYFSHGLK.E
R5/RRR5-19/2	1503.195	1502.650	-304.187	0.507	1284.201	0.582	19	0.196	R.EIENGILWEVDGK.W
R5/RRR5-19/2	1770.571	1769.934	-205.974	0.534	1387.407	0.519	23	0.192	K.DGATDPTFLYFSHGLK.E
R5/RRR5-19/2	1769.305	1769.934	-923.867	0.478	1455.060	0.468	23	0.189	K.DGATDPTFLYFSHGLK.E
R5/RRR5-19/2	1502.330	1502.650	-214.063	0.464	1220.769	0.534	19	0.180	R.EIENGILWEVDGK.W
R5/RRR5-20/2	1503.253	1502.650	-265.406	0.543	982.290	0.620	17	0.176	R.EIENGILWEVDGK.W
R5/RRR5-19/2	1503.502	1502.650	-99.237	0.518	1069.410	0.568	18	0.174	R.EIENGILWEVDGK.W
R5/RRR5-20/2	1770.391	1769.934	258.470	0.521	1156.820	0.502	22	0.169	K.DGATDPTFLYFSHGLK.E
R5/RRR5-19/2	1502.401	1502.650	-166.786	0.472	1077.245	0.507	18	0.164	R.EIENGILWEVDGK.W
R5/RRR5-19/2	1769.198	1769.934	-984.269	0.491	1036.266	0.504	21	0.160	K.DGATDPTFLYFSHGLK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1502.429	1502.650	-147.632	0.483	966.881	0.509	17	0.157	R.EIENGILWEVDGK.W
R5/RRR5-20/2	1769.319	1769.934	-915.763	0.476	966.950	0.502	21	0.155	K.DGATDPTFLYFSHGLK.E
R5/RRR5-20/2	1502.147	1502.650	-1003.817	0.415	936.913	0.505	17	0.153	R.EIENGILWEVDGK.W
R5/RRR5-20/2	1769.112	1769.934	-1033.386	0.470	921.026	0.510	20	0.153	K.DGATDPTFLYFSHGLK.E
R5/RRR5-19/2	1063.939	1064.217	-262.219	0.467	814.614	0.388	14	0.137	K.VVDIVDTFR.L
R5/RRR5-20/2	1064.033	1064.217	-173.363	0.455	931.847	0.347	14	0.136	K.VVDIVDTFR.L
R5/RRR5-20/2	1063.595	1064.217	-1529.614	0.376	1009.114	0.303	15	0.134	K.VVDIVDTFR.L
R5/RRR5-19/2	1063.716	1064.217	-1415.258	0.382	1019.025	0.273	15	0.131	K.VVDIVDTFR.L
R5/RRR5-19/2	1063.536	1064.217	-1584.841	0.393	970.889	0.271	15	0.130	K.VVDIVDTFR.L
R5/RRR5-20/2	1063.983	1064.217	-219.976	0.341	801.774	0.309	14	0.128	K.VVDIVDTFR.L
R5/RRR5-19/2	1230.107	1230.395	-234.461	0.488	891.458	0.262	15	0.124	R.LQEQPPFDKK.Q
R5/RRR5-19/2	1230.100	1230.395	-240.435	0.508	813.576	0.255	14	0.120	R.LQEQPPFDKK.Q
R5/RRR5-20/2	1230.102	1230.395	-238.543	0.486	774.005	0.238	14	0.119	R.LQEQPPFDKK.Q
R5/RRR5-20/2	1230.033	1230.395	-294.896	0.459	876.908	0.196	15	0.118	R.LQEQPPFDKK.Q
R5/RRR5-20/2	1229.949	1230.395	-363.802	0.498	764.783	0.244	14	0.115	-.LQEQPPFDKK.-
R5/RRR5-26/3	1934.700	1934.877	-91.460	0.495	2493.636	0.542	39	0.422	R.GGGGYGGGGGYGNQGGYGDGNR.G
R5/RRR5-26/3	1934.881	1934.877	2.232	0.535	2428.923	0.554	38	0.408	R.GGGGYGGGGGYGNQGGYGDGNR.G
R5/RRR5-26/3	1934.204	1934.877	-867.646	0.484	2302.368	0.470	38	0.330	R.GGGGYGGGGGYGNQGGYGDGNR.G
R5/RRR5-26/2	1431.641	1432.519	-1315.891	0.450	1841.015	0.484	23	0.239	R.GFGFVSFANGDDAK.S
R5/RRR5-26/2	1432.199	1432.519	-223.861	0.478	1735.220	0.502	22	0.229	R.GFGFVSFANGDDAK.S
R5/RRR5-26/2	1934.116	1934.877	-912.940	0.551	1482.533	0.639	23	0.225	R.GGGGYGGGGGYGNQGGYGDGNR.G
R5/RRR5-26/2	1431.913	1432.519	-1124.707	0.468	1795.551	0.452	22	0.225	R.GFGFVSFANGDDAK.S
R5/RRR5-26/2	1934.255	1934.877	-840.777	0.558	1352.545	0.623	22	0.205	R.GGGGYGGGGGYGNQGGYGDGNR.G
R5/RRR5-26/2	1934.086	1934.877	-928.464	0.532	1291.332	0.635	23	0.202	R.GGGGYGGGGGYGNQGGYGDGNR.G
R5/RRR5-26/2	1431.550	1430.501	33.902	0.434	992.807	0.391	18	0.141	R.EAFTSFGDVTEAR.V
R5/RRR5-26/2	1431.312	1430.501	-132.299	0.449	834.044	0.445	18	0.141	R.EAFTSFGDVTEAR.V
R5/RRR5-26/2	1431.304	1430.501	-138.288	0.421	840.888	0.448	17	0.141	R.EAFTSFGDVTEAR.V
R5/RRR5-26/2	1541.801	1542.675	-1219.428	0.379	281.996	0.509	17	0.129	K.SAM*DAM*DGKELEGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/3	1542.740	1542.675	41.908	0.416	753.568	0.615	27	0.120	K.SAM*DAM*DGKELEGR.S
R5/RRR5-26/3	1542.484	1542.675	-124.180	0.382	758.612	0.607	28	0.116	K.SAM*DAM*DGKELEGR.S
R5/RRR5-26/3	1542.541	1542.675	-87.267	0.414	440.139	0.562	21	0.098	-.SAM*DAM*DGKELEGR.-
R5/RRR5-25/3	1542.327	1542.675	-226.122	0.419	458.149	0.501	23	0.096	K.SAM*DAM*DGKELEGR.S
R5/RRR5-25/3	1542.192	1542.675	-314.147	0.399	348.981	0.559	20	0.096	-.SAM*DAM*DGKELEGR.-
R5/RRR5-25/3	1541.247	1542.675	-1579.976	0.304	611.295	0.505	24	0.093	K.SAM*DAM*DGKELEGR.S
R5/RRR5-24/2	1655.408	1653.905	-300.699	0.512	1425.737	0.520	22	0.195	R.TLLGATNPLASAPGTIR.G
R5/RRR5-24/2	1390.957	1391.468	-1089.341	0.501	1391.102	0.474	19	0.184	K.AGEVVNWSSENAK.W
R5/RRR5-24/2	1653.284	1653.905	-983.368	0.441	1347.080	0.493	22	0.181	R.TLLGATNPLASAPGTIR.G
R5/RRR5-24/2	1390.973	1391.468	-357.336	0.515	1276.814	0.507	18	0.180	K.AGEVVNWSSENAK.W
R5/RRR5-24/2	1391.038	1391.468	-310.494	0.521	1236.658	0.477	18	0.171	K.AGEVVNWSSENAK.W
R5/RRR5-24/2	949.878	950.031	-160.684	0.479	1148.253	0.359	14	0.147	R.GDFAIDVGR.N
R5/RRR5-24/2	949.449	950.031	-1671.212	0.403	1092.205	0.360	14	0.144	R.GDFAIDVGR.N
R5/RRR5-24/2	911.416	912.112	-1866.421	0.384	959.327	0.411	14	0.143	R.GLVGPIISR.F
R5/RRR5-24/2	911.933	912.112	-196.102	0.344	1054.235	0.336	14	0.138	R.GLVGPIISR.F
R5/RRR5-24/2	949.357	950.031	-1767.582	0.411	1038.465	0.319	14	0.137	R.GDFAIDVGR.N
R5/RRR5-24/2	911.447	912.112	-1831.564	0.308	680.489	0.336	12	0.124	R.GLVGPIISR.F
R5/RRR5-23/2	950.054	950.031	24.407	0.330	611.193	0.286	11	0.095	-.GDFAIDVGR.-
R5/RRR5-17/3	1491.515	1491.760	-164.647	0.579	1624.936	0.473	29	0.181	R.KTDLLLAANPVHAK.V
R5/RRR5-17/2	1389.129	1389.582	-326.521	0.478	1255.994	0.507	20	0.179	K.LLGSTNPSPFVTR.V
R5/RRR5-17/3	1491.365	1491.760	-265.766	0.520	1730.891	0.416	30	0.179	R.KTDLLLAANPVHAK.V
R5/RRR5-17/2	1447.521	1446.630	-75.246	0.405	1209.363	0.495	19	0.171	R.GLPYDLVAVDLDR.K
R5/RRR5-17/2	1390.196	1389.582	-277.919	0.461	771.868	0.554	18	0.152	K.LLGSTNPSPFVTR.V
R5/RRR5-17/2	1447.757	1446.630	87.816	0.290	918.445	0.463	18	0.142	R.GLPYDLVAVDLDR.K
R5/RRR5-17/2	1389.204	1389.582	-272.829	0.477	688.359	0.479	16	0.138	K.LLGSTNPSPFVTR.V
R5/RRR5-17/2	885.056	885.086	-33.770	0.440	788.427	0.344	13	0.132	R.VELALALR.G
R5/RRR5-17/3	1491.902	1491.760	95.262	0.595	1282.174	0.408	27	0.120	R.KTDLLLAANPVHAK.V
R5/RRR5-16/2	1445.843	1446.630	-1239.962	0.267	733.235	0.249	15	0.117	R.GLPYDLVAVDLDR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	885.723	885.086	-411.398	0.323	915.352	0.144	13	0.116	-.VELALALR.-
R5/RRR5-17/2	1447.389	1446.630	-167.289	0.236	528.264	0.280	13	0.116	R.GLPYDLVAVDLDR.K
R5/RRR5-16/3	1491.946	1491.760	124.926	0.538	1124.885	0.420	26	0.110	R.KTDLLLAANPVHAK.V
R5/RRR5-16/3	1492.882	1491.760	81.872	0.527	1040.888	0.436	23	0.107	R.KTDLLLAANPVHAK.V
R5/RRR5-16/3	1491.429	1491.760	-223.025	0.506	683.870	0.400	20	0.086	R.KTDLLLAANPVHAK.V
R5/RRR5-15/2	1686.505	1686.932	-253.701	0.474	2621.237	0.429	26	0.353	R.LISEATAAAGTGLIELR.R
R5/RRR5-16/2	1686.420	1686.932	-899.286	0.372	2714.885	0.353	25	0.348	R.LISEATAAAGTGLIELR.R
R5/RRR5-16/2	1686.371	1686.932	-928.208	0.372	2766.751	0.316	25	0.347	R.LISEATAAAGTGLIELR.R
R5/RRR5-15/2	1237.121	1236.469	-281.982	0.536	2150.053	0.539	20	0.301	R.M*LLGLNAAGFGR.-
R5/RRR5-15/2	1685.813	1686.932	-1260.641	0.344	2349.982	0.307	24	0.268	R.LISEATAAAGTGLIELR.R
R5/RRR5-15/2	1236.127	1236.469	-277.653	0.488	1662.399	0.559	19	0.234	R.M*LLGLNAAGFGR.-
R5/RRR5-15/2	1686.658	1686.932	-162.794	0.473	1826.535	0.401	22	0.214	R.LISEATAAAGTGLIELR.R
R5/RRR5-16/2	1237.169	1236.469	-243.177	0.501	1544.075	0.520	19	0.211	R.M*LLGLNAAGFGR.-
R5/RRR5-15/2	1236.270	1236.469	-161.847	0.568	1484.027	0.538	19	0.208	R.M*LLGLNAAGFGR.-
R5/RRR5-15/2	1416.912	1417.509	-1130.739	0.518	1266.504	0.610	22	0.201	R.SPNVAYVPAGDNGR.M
R5/RRR5-15/2	1220.076	1220.470	-323.595	0.444	1355.823	0.518	19	0.190	R.MLLGLNAAGFGR.-
R5/RRR5-15/2	1417.129	1417.509	-269.008	0.495	1115.949	0.577	21	0.180	R.SPNVAYVPAGDNGR.M
R5/RRR5-15/2	1219.087	1219.437	-287.438	0.386	1738.985	0.210	17	0.168	K.DLQM*VNLTLR.L
R5/RRR5-15/2	1416.657	1417.509	-1310.881	0.417	899.077	0.494	19	0.149	R.SPNVAYVPAGDNGR.M
R5/RRR5-15/2	1218.988	1219.437	-368.919	0.462	1260.683	0.260	15	0.138	K.DLQM*VNLTLR.L
R5/RRR5-16/2	1236.043	1236.469	-345.822	0.337	510.058	0.411	14	0.120	-.M*LLGLNAAGFGR.-
R5/RRR5-16/2	1236.776	1236.469	249.253	0.282	586.516	0.271	13	0.114	-.M*LLGLNAAGFGR.-
R5/RRR5-17/2	1389.228	1389.573	-249.558	0.514	1859.315	0.451	19	0.233	K.VIACIGETLEQR.E
R5/RRR5-17/2	1452.117	1452.613	-342.571	0.475	1689.516	0.493	20	0.220	R.EAGTTM*EVVAAQTK.A
R5/RRR5-17/2	1452.054	1452.613	-1077.347	0.476	1654.077	0.476	20	0.212	R.EAGTTM*EVVAAQTK.A
R5/RRR5-17/2	1389.223	1389.573	-253.260	0.538	1583.564	0.479	19	0.206	K.VIACIGETLEQR.E
R5/RRR5-17/2	1049.656	1050.233	-1507.117	0.395	1724.357	0.405	17	0.205	K.VAYALSQGIK.V
R5/RRR5-17/2	1603.232	1602.773	287.099	0.580	1202.229	0.608	22	0.194	K.WLATNVSPAVAESTR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1602.446	1602.773	-204.662	0.486	1216.804	0.592	23	0.191	K.WLATNVSPAVAESTR.I
R5/RRR5-17/2	1389.171	1389.573	-290.728	0.517	1502.484	0.428	19	0.187	K.VIACIGETLEQR.E
R5/RRR5-17/2	1452.163	1452.613	-310.774	0.482	1427.936	0.467	20	0.186	R.EAGTTM*EVVAAQTK.A
R5/RRR5-17/2	1049.483	1050.233	-1672.912	0.410	1475.630	0.418	17	0.182	K.VAYALSQGIK.V
R5/RRR5-17/2	1602.348	1602.773	-265.956	0.516	1077.519	0.575	21	0.176	K.WLATNVSPAVAESTR.I
R5/RRR5-17/2	1049.998	1050.233	-224.305	0.439	1559.644	0.341	16	0.175	K.VAYALSQGIK.V
R5/RRR5-16/2	1453.133	1452.613	-331.631	0.519	1204.299	0.502	18	0.171	R.EAGTTM*EVVAAQTK.A
R5/RRR5-17/2	1388.839	1389.573	-1252.418	0.460	1245.478	0.375	19	0.156	K.VIACIGETLEQR.E
R5/RRR5-16/2	1451.609	1452.613	-1384.525	0.387	1085.514	0.462	17	0.154	R.EAGTTM*EVVAAQTK.A
R5/RRR5-18/2	1049.874	1050.233	-343.051	0.389	1285.185	0.336	16	0.153	K.VAYALSQGIK.V
R5/RRR5-17/2	1388.703	1389.573	-1351.111	0.376	1257.027	0.338	18	0.150	K.VIACIGETLEQR.E
R5/RRR5-18/2	1049.616	1050.233	-1545.552	0.416	1317.408	0.300	16	0.149	K.VAYALSQGIK.V
R5/RRR5-18/2	1049.594	1050.233	-1566.348	0.342	1168.916	0.368	15	0.148	K.VAYALSQGIK.V
R5/RRR5-5/2	1611.259	1610.812	277.941	0.506	1748.799	0.606	22	0.256	K.ASNTLSIIDSGVGM*TK.S
R5/RRR5-5/2	1610.205	1610.812	-1001.137	0.459	1729.307	0.577	23	0.245	K.ASNTLSIIDSGVGM*TK.S
R5/RRR5-5/3	1951.158	1951.255	-49.932	0.579	1772.713	0.547	32	0.238	K.SKLDAQPELFIHIVPDK.A
R5/RRR5-5/2	1595.471	1594.813	-214.689	0.540	1440.729	0.610	21	0.217	K.ASNTLSIIDSGVGMTK.S
R5/RRR5-5/2	1594.255	1594.813	-980.227	0.465	1664.017	0.495	22	0.217	K.ASNTLSIIDSGVGMTK.S
R5/RRR5-5/3	1951.821	1951.255	-222.891	0.590	1626.333	0.550	32	0.212	K.SKLDAQPELFIHIVPDK.A
R5/RRR5-5/2	1594.221	1594.813	-1001.599	0.428	1445.730	0.511	21	0.195	K.ASNTLSIIDSGVGMTK.S
R5/RRR5-5/2	1736.326	1736.004	185.975	0.570	1124.620	0.533	21	0.172	K.LDAQPELFIHIVPDK.A
R5/RRR5-5/2	1735.392	1736.004	-931.903	0.508	1107.929	0.541	21	0.172	K.LDAQPELFIHIVPDK.A
R5/RRR5-5/2	1735.499	1736.004	-869.904	0.533	1068.646	0.545	20	0.169	K.LDAQPELFIHIVPDK.A
R5/RRR5-5/2	1609.815	1610.812	-1244.151	0.345	1250.214	0.481	21	0.169	K.ASNTLSIIDSGVGM*TK.S
R5/RRR5-5/3	1951.063	1951.255	-98.506	0.550	1415.602	0.520	31	0.168	K.SKLDAQPELFIHIVPDK.A
R5/RRR5-4/2	1735.112	1736.004	-1093.998	0.444	915.398	0.424	19	0.141	K.LDAQPELFIHIVPDK.A
R5/RRR5-3/3	1908.007	1909.022	-1059.286	0.509	2651.914	0.498	35	0.440	K.TQEKDADAM*QVDNAVEK.K
R5/RRR5-3/2	1419.329	1418.645	-223.331	0.549	2519.347	0.548	24	0.373	K.M*GAILASGILDAGGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1418.349	1418.645	-209.155	0.561	2190.267	0.549	23	0.311	K.M*GAILASGILDAGGR.N
R5/RRR5-3/3	1909.819	1909.022	-106.744	0.544	2133.666	0.508	31	0.301	K.TQEKDADAM*QVDNAVEK.K
R5/RRR5-3/3	1909.765	1909.022	-135.020	0.540	2030.781	0.540	33	0.290	K.TQEKDADAM*QVDNAVEK.K
R5/RRR5-3/2	1417.877	1418.645	-1250.717	0.556	1630.948	0.536	20	0.222	K.M*GAILASGILDAGGR.N
R5/RRR5-3/2	1402.141	1402.645	-1075.937	0.470	1557.428	0.510	19	0.207	K.MGAILASGILDAGGR.N
R5/RRR5-3/2	1178.476	1178.403	62.065	0.470	1261.654	0.464	16	0.171	K.LPTAILSTYAK.A
R5/RRR5-3/2	1177.408	1178.403	-1699.439	0.371	1154.644	0.435	17	0.157	K.LPTAILSTYAK.A
R5/RRR5-3/2	1178.187	1178.403	-183.793	0.368	1248.766	0.363	16	0.153	K.LPTAILSTYAK.A
R5/RRR5-3/2	1402.046	1402.645	-1144.037	0.352	953.448	0.375	18	0.135	K.MGAILASGILDAGGR.N
R5/RRR5-4/2	1177.941	1178.403	-392.857	0.287	434.618	0.450	13	0.126	K.LPTAILSTYAK.A
R5/RRR5-3/3	1910.359	1910.163	102.948	0.443	1272.068	0.384	29	0.114	K.KAPEPEPTFQILTNPAR.V
R5/RRR5-3/3	1910.276	1910.163	59.305	0.453	1361.693	0.323	28	0.107	K.KAPEPEPTFQILTNPAR.V
R5/RRR5-3/3	1908.831	1910.163	-1225.033	0.348	896.069	0.346	24	0.082	-.KAPEPEPTFQILTNPAR.-
R5/RRR5-2/3	1909.132	1909.022	57.844	0.368	934.164	0.325	25	0.080	K.TQEKDADAM*QVDNAVEK.K
R5/RRR5-4/3	1910.777	1910.163	-202.273	0.328	760.301	0.210	21	0.057	-.KAPEPEPTFQILTNPAR.-
R5/RRR5-16/2	1031.029	1031.145	-112.649	0.488	1834.420	0.593	20	0.267	K.VAAATAAAGEAK.G
R5/RRR5-16/2	1140.607	1141.303	-1490.742	0.476	1458.566	0.538	19	0.205	R.VPSPVTAGSAVR.L
R5/RRR5-17/2	1141.009	1141.303	-257.706	0.397	1203.408	0.608	18	0.189	R.VPSPVTAGSAVR.L
R5/RRR5-16/2	1210.892	1211.308	-345.260	0.483	1637.883	0.371	19	0.189	R.VSFGENFSPAR.A
R5/RRR5-15/2	1141.225	1141.303	-68.406	0.425	1082.682	0.628	18	0.184	R.VPSPVTAGSAVR.L
R5/RRR5-17/2	1140.516	1141.303	-1571.375	0.372	1225.415	0.559	18	0.182	R.VPSPVTAGSAVR.L
R5/RRR5-17/2	1030.570	1031.145	-1533.366	0.397	1335.123	0.481	20	0.180	K.VAAATAAAGEAK.G
R5/RRR5-17/2	1140.968	1141.303	-294.200	0.448	1181.031	0.537	18	0.177	R.VPSPVTAGSAVR.L
R5/RRR5-15/2	1141.091	1141.303	-186.227	0.419	1118.294	0.570	18	0.177	R.VPSPVTAGSAVR.L
R5/RRR5-16/2	1141.174	1141.303	-112.613	0.460	1023.519	0.561	18	0.170	R.VPSPVTAGSAVR.L
R5/RRR5-16/2	1141.101	1141.303	-177.320	0.401	1001.957	0.591	17	0.170	R.VPSPVTAGSAVR.L
R5/RRR5-17/2	1210.908	1211.308	-331.505	0.507	1354.571	0.384	18	0.166	R.VSFGENFSPAR.A
R5/RRR5-17/2	1030.232	1031.145	-1862.709	0.382	1179.334	0.442	20	0.161	K.VAAATAAAGEAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1211.291	1211.308	-14.415	0.443	1228.286	0.393	18	0.158	R.VSFGENFSPAR.A
R5/RRR5-16/2	1210.960	1211.308	-288.419	0.464	1440.239	0.279	19	0.154	R.VSFGENFSPAR.A
R5/RRR5-17/2	1210.733	1211.308	-1304.991	0.372	1271.041	0.315	18	0.148	R.VSFGENFSPAR.A
R5/RRR5-15/3	1643.784	1643.829	-26.943	0.424	981.441	0.565	28	0.125	R.SPAAEALGPTHVLHSR.Y
R5/RRR5-10/3	1797.922	1797.946	-13.430	0.554	2639.884	0.452	36	0.408	K.YFRPAEVDSLQGDATK.A
R5/RRR5-10/3	1797.216	1797.946	-965.662	0.564	2265.146	0.459	35	0.308	K.YFRPAEVDSLQGDATK.A
R5/RRR5-10/2	1720.557	1719.857	-175.132	0.529	2349.661	0.442	22	0.307	R.DWGFAGDYVEAM*WR.M
R5/RRR5-10/3	1798.223	1797.946	154.169	0.574	1991.143	0.431	34	0.234	K.YFRPAEVDSLQGDATK.A
R5/RRR5-10/2	1721.403	1719.857	-265.091	0.598	1467.133	0.571	22	0.214	R.DWGFAGDYVEAM*WR.M
R5/RRR5-10/2	1048.097	1048.220	-118.525	0.506	1152.390	0.391	16	0.153	K.VFLGNLSAAR.D
R5/RRR5-10/2	1048.990	1048.220	-220.319	0.523	1144.880	0.380	16	0.150	K.VFLGNLSAAR.D
R5/RRR5-10/2	1047.975	1048.220	-234.552	0.490	1131.706	0.341	16	0.144	K.VFLGNLSAAR.D
R5/RRR5-10/2	1044.378	1044.189	181.407	0.355	814.966	0.342	13	0.127	K.GYEVHGLIR.R
R5/RRR5-18/2	1080.491	1081.204	-1590.568	0.396	1345.072	0.509	17	0.186	K.STIGVEFATR.S
R5/RRR5-17/2	1275.028	1275.352	-255.009	0.457	1341.347	0.460	17	0.178	K.AQIWDTAGQER.F
R5/RRR5-17/2	1274.849	1275.352	-1182.503	0.469	1279.042	0.483	17	0.177	K.AQIWDTAGQER.F
R5/RRR5-18/2	1274.449	1275.352	-1498.081	0.393	1389.047	0.416	17	0.173	K.AQIWDTAGQER.F
R5/RRR5-18/2	1081.048	1081.204	-145.265	0.447	1257.153	0.460	17	0.172	K.STIGVEFATR.S
R5/RRR5-18/2	1081.011	1081.204	-179.022	0.432	1251.418	0.465	16	0.171	K.STIGVEFATR.S
R5/RRR5-18/2	1306.540	1306.533	5.847	0.337	1527.358	0.342	19	0.171	R.GAVGALLVYDISK.H
R5/RRR5-18/2	1306.048	1306.533	-372.322	0.396	1426.379	0.386	17	0.169	R.GAVGALLVYDISK.H
R5/RRR5-17/2	1274.972	1275.352	-299.290	0.435	1325.055	0.396	17	0.165	K.AQIWDTAGQER.F
R5/RRR5-20/2	1274.753	1275.352	-1258.374	0.339	1320.848	0.401	17	0.164	K.AQIWDTAGQER.F
R5/RRR5-20/2	1081.746	1081.204	-424.963	0.378	1138.467	0.463	15	0.160	K.STIGVEFATR.S
R5/RRR5-17/2	1043.591	1044.227	-1572.073	0.363	1106.047	0.442	17	0.154	K.VVLIGDSGVGK.S
R5/RRR5-18/2	1274.974	1275.352	-297.657	0.424	1042.684	0.421	16	0.149	K.AQIWDTAGQER.F
R5/RRR5-17/2	1080.934	1081.204	-250.960	0.377	956.832	0.406	15	0.143	K.STIGVEFATR.S
R5/RRR5-17/2	1045.052	1044.227	-167.608	0.403	848.813	0.424	15	0.139	K.VVLIGDSGVGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1043.481	1044.227	-1677.722	0.199	416.544	0.391	11	0.116	K.VVLIGDSGVGK.S
R5/RRR5-26/2	1367.438	1366.552	-83.324	0.412	1197.770	0.447	17	0.161	K.LQAFWNHPAGPK.T
R5/RRR5-26/2	954.682	955.154	-495.404	0.390	1109.794	0.462	13	0.160	R.YSM*VITPK.N
R5/RRR5-26/2	954.822	955.154	-348.252	0.396	1035.939	0.468	13	0.156	R.YSM*VITPK.N
R5/RRR5-25/2	954.761	955.154	-412.009	0.396	983.519	0.475	13	0.154	R.YSM*VITPK.N
R5/RRR5-26/2	955.954	955.154	-209.644	0.456	870.738	0.484	13	0.152	R.YSM*VITPK.N
R5/RRR5-26/2	954.288	955.154	-1960.940	0.282	940.567	0.430	13	0.141	R.YSM*VITPK.N
R5/RRR5-25/2	954.482	955.154	-1756.069	0.309	894.263	0.372	12	0.134	R.YSM*VITPK.N
R5/RRR5-26/2	1689.160	1689.715	-923.486	0.388	795.016	0.449	19	0.102	K.DYFSDQKDDVASLEG.-
R5/RRR5-26/2	1690.351	1689.715	-216.183	0.444	646.724	0.496	18	0.099	K.DYFSDQKDDVASLEG.-
R5/RRR5-26/2	1689.358	1689.715	-211.889	0.396	621.701	0.449	18	0.098	K.DYFSDQKDDVASLEG.-
R5/RRR5-25/2	1688.775	1689.715	-1151.927	0.294	571.224	0.390	17	0.095	K.DYFSDQKDDVASLEG.-
R5/RRR5-25/3	1844.174	1844.103	38.857	0.356	948.701	0.289	28	0.072	K.WGISIANVADFAKPPEK.I
R5/RRR5-26/2	1618.702	1618.637	40.421	0.412	1015.668	0.507	20	0.123	K.DYFSDEKDAAASLEG.-
R5/RRR5-26/2	1617.977	1618.637	-1029.042	0.276	833.023	0.393	19	0.101	K.DYFSDEKDAAASLEG.-
R5/RRR5-25/2	1617.433	1618.637	-1366.396	0.267	615.121	0.347	16	0.092	K.DYFSDEKDAAASLEG.-
R5/RRR5-26/2	1617.803	1618.637	-1137.149	0.227	722.319	0.244	18	0.092	K.DYFSDEKDAAASLEG.-
R5/RRR5-5/2	1624.402	1623.811	-252.821	0.414	975.976	0.470	18	0.148	K.ANGTLTIQDSGIGM*TK.A
R5/RRR5-5/2	1624.228	1623.811	257.634	0.358	919.828	0.406	17	0.135	K.ANGTLTIQDSGIGM*TK.A
R5/RRR5-5/2	1292.145	1292.375	-178.481	0.422	821.524	0.382	16	0.133	R.EIISNSSDALDK.I
R5/RRR5-5/2	1560.749	1561.719	-1266.187	0.467	822.142	0.360	20	0.132	R.EIISNSSDALDKIR.Y
R5/RRR5-5/2	1292.107	1292.375	-208.050	0.465	794.952	0.375	16	0.132	R.EIISNSSDALDK.I
R5/RRR5-5/2	1561.341	1561.719	-243.064	0.468	766.080	0.364	20	0.131	R.EIISNSSDALDKIR.Y
R5/RRR5-5/2	1561.228	1561.719	-315.858	0.411	813.317	0.339	20	0.130	R.EIISNSSDALDKIR.Y
R5/RRR5-3/2	1562.634	1561.719	-54.973	0.509	653.364	0.318	20	0.124	R.EIISNSSDALDKIR.Y
R5/RRR5-5/2	1624.438	1623.811	-230.355	0.370	681.035	0.381	16	0.124	K.ANGTLTIQDSGIGM*TK.A
R5/RRR5-5/2	1291.498	1292.375	-1457.163	0.340	681.238	0.271	15	0.119	R.EIISNSSDALDK.I
R5/RRR5-13/2	1615.202	1614.744	284.138	0.534	1499.951	0.409	20	0.180	K.TWQGRPENVEAAQK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1614.442	1614.744	-187.443	0.488	1417.252	0.425	19	0.176	K.TWQGRPENVEAAQK.A
R5/RRR5-13/2	1614.242	1614.744	-933.428	0.483	1523.074	0.371	20	0.176	K.TWQGRPENVEAAQK.A
R5/RRR5-13/2	1614.216	1614.744	-949.295	0.467	1442.097	0.376	20	0.170	K.TWQGRPENVEAAQK.A
R5/RRR5-13/2	1129.633	1129.295	299.947	0.411	1349.229	0.368	18	0.162	R.AKANSLAQLGR.Y
R5/RRR5-12/2	1614.128	1614.744	-1004.493	0.488	1320.876	0.390	19	0.161	K.TWQGRPENVEAAQK.A
R5/RRR5-13/2	1129.193	1129.295	-90.821	0.443	1244.197	0.352	18	0.152	R.AKANSLAQLGR.Y
R5/RRR5-13/2	929.991	930.044	-57.284	0.460	745.673	0.418	15	0.140	K.ANSLAQLGR.Y
R5/RRR5-13/2	929.848	930.044	-211.087	0.457	740.288	0.370	15	0.135	K.ANSLAQLGR.Y
R5/RRR5-13/2	929.899	930.044	-156.171	0.470	709.091	0.361	15	0.133	K.ANSLAQLGR.Y
R5/RRR5-12/2	929.786	930.044	-278.391	0.429	749.839	0.354	15	0.133	K.ANSLAQLGR.Y
R5/RRR5-12/2	1500.318	1499.771	-303.138	0.369	607.298	0.448	19	0.132	R.TVVSIPCGPSALAVK.E
R5/RRR5-12/2	929.752	930.044	-315.537	0.411	711.230	0.299	14	0.126	K.ANSLAQLGR.Y
R5/RRR5-13/3	1129.331	1129.295	31.796	0.419	1634.511	0.279	22	0.126	R.AKANSLAQLGR.Y
R5/RRR5-12/2	1499.801	1499.771	20.359	0.323	802.900	0.319	21	0.126	R.TVVSIPCGPSALAVK.E
R5/RRR5-13/3	1129.709	1129.295	367.651	0.465	1494.453	0.332	21	0.124	R.AKANSLAQLGR.Y
R5/RRR5-12/2	1500.631	1499.771	-93.634	0.259	483.211	0.299	15	0.117	R.TVVSIPCGPSALAVK.E
R5/RRR5-13/2	1498.755	1499.771	-1349.114	0.197	602.860	0.288	19	0.116	R.TVVSIPCGPSALAVK.E
R5/RRR5-13/3	1129.477	1129.295	161.710	0.463	1268.145	0.246	21	0.085	R.AKANSLAQLGR.Y
R5/RRR5-18/2	1241.028	1241.401	-301.879	0.403	1888.909	0.391	19	0.222	K.AFM*DATGGLWR.T
R5/RRR5-19/2	1745.570	1744.966	-227.792	0.613	1115.984	0.596	24	0.186	K.LWQVPETLSDDVLTK.M
R5/RRR5-18/2	1744.497	1744.966	-269.762	0.515	959.388	0.566	23	0.168	K.LWQVPETLSDDVLTK.M
R5/RRR5-18/2	1473.233	1473.486	-172.249	0.423	1026.403	0.550	22	0.165	K.GGSPYGSGTFAGDGSR.V
R5/RRR5-19/2	1744.028	1744.966	-1114.661	0.494	925.046	0.549	23	0.163	K.LWQVPETLSDDVLTK.M
R5/RRR5-18/2	1062.873	1063.276	-379.508	0.503	1171.469	0.435	14	0.161	R.FGM*M*AAQFK.A
R5/RRR5-18/2	1473.002	1473.486	-329.540	0.364	842.565	0.609	21	0.158	K.GGSPYGSGTFAGDGSR.V
R5/RRR5-18/2	1743.480	1744.966	-1430.112	0.365	1138.565	0.434	24	0.156	K.LWQVPETLSDDVLTK.M
R5/RRR5-18/2	1744.420	1744.966	-888.968	0.508	811.841	0.547	22	0.156	K.LWQVPETLSDDVLTK.M
R5/RRR5-18/2	1473.088	1473.486	-271.257	0.400	878.830	0.564	21	0.156	K.GGSPYGSGTFAGDGSR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1744.478	1744.966	-280.643	0.455	968.175	0.481	23	0.154	K.LWQVPETLSDDVLTK.M
R5/RRR5-18/2	1063.982	1063.276	-276.582	0.519	1007.848	0.414	14	0.148	R.FGM*M*AAQFK.A
R5/RRR5-18/2	1241.825	1241.401	342.035	0.346	664.004	0.411	13	0.129	K.AFM*DATGGLWR.T
R5/RRR5-19/2	1062.708	1063.276	-1479.841	0.335	841.409	0.278	14	0.125	R.FGM*M*AAQFK.A
R5/RRR5-18/2	1241.062	1241.401	-273.853	0.266	870.057	0.296	15	0.125	K.AFM*DATGGLWR.T
R5/RRR5-18/2	1240.469	1241.401	-1562.141	0.284	752.540	0.270	15	0.121	K.AFM*DATGGLWR.T
R5/RRR5-18/2	1225.000	1225.402	-328.491	0.287	483.600	0.263	15	0.121	K.AFMDATGGLWR.T
R5/RRR5-18/2	1030.871	1031.277	-395.220	0.240	457.406	0.267	12	0.116	-.FGMMAAQFK.-
R5/RRR5-4/2	1262.057	1261.514	-362.695	0.421	2248.996	0.595	19	0.335	R.ALLDEMAVVATK.E
R5/RRR5-4/2	1513.276	1513.760	-320.284	0.356	1243.279	0.404	18	0.156	K.LLVSEELWPLGEK.L
R5/RRR5-3/2	1260.772	1261.514	-1385.853	0.308	442.685	0.340	13	0.119	R.ALLDEMAVVATK.E
R5/RRR5-18/2	1772.600	1772.978	-214.234	0.554	1559.288	0.563	24	0.221	R.NQDVSLTELPATVSAVK.N
R5/RRR5-18/2	1772.433	1772.978	-874.642	0.538	1482.304	0.568	24	0.213	R.NQDVSLTELPATVSAVK.N
R5/RRR5-18/2	1772.488	1772.978	-277.244	0.546	1471.061	0.530	24	0.203	R.NQDVSLTELPATVSAVK.N
R5/RRR5-19/2	1772.321	1772.978	-937.631	0.458	1109.317	0.478	21	0.159	R.NQDVSLTELPATVSAVK.N
R5/RRR5-18/2	1338.109	1338.407	-223.132	0.430	837.611	0.408	15	0.139	K.IVYDEYNHER.Y
R5/RRR5-18/2	1338.032	1338.407	-281.067	0.395	795.504	0.393	15	0.135	K.IVYDEYNHER.Y
R5/RRR5-18/2	1337.542	1338.407	-1398.489	0.404	758.225	0.381	14	0.132	K.IVYDEYNHER.Y
R5/RRR5-18/3	1471.632	1471.598	23.277	0.475	1567.441	0.427	33	0.162	K.KPVASDEGGAGAAGGVK.E
R5/RRR5-18/3	1472.362	1471.598	-160.510	0.520	1445.740	0.458	32	0.154	K.KPVASDEGGAGAAGGVK.E
R5/RRR5-18/2	1057.706	1058.254	-1467.054	0.306	981.107	0.396	17	0.138	K.IVLIGDSGVGK.S
R5/RRR5-9/2	1931.521	1931.043	248.065	0.629	2275.371	0.594	24	0.340	R.YYGGNDVIDEIENLCR.D
R5/RRR5-9/2	1816.427	1816.986	-860.737	0.557	2360.797	0.543	23	0.340	K.VSAATGYIDYEKLEEK.A
R5/RRR5-9/2	1931.458	1931.043	215.363	0.628	2101.458	0.620	23	0.317	R.YYGGNDVIDEIENLCR.D
R5/RRR5-8/2	1619.323	1619.839	-938.892	0.377	2125.697	0.410	21	0.260	K.ISATSIYFESLPYK.V
R5/RRR5-9/2	1620.404	1619.839	-269.490	0.526	1777.309	0.520	21	0.239	K.ISATSIYFESLPYK.V
R5/RRR5-9/2	1929.830	1931.043	-1149.965	0.522	1659.532	0.579	22	0.237	R.YYGGNDVIDEIENLCR.D
R5/RRR5-9/3	1930.535	1931.043	-783.613	0.459	2194.615	0.311	30	0.232	R.YYGGNDVIDEIENLCR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1207.410	1207.398	10.180	0.457	1658.358	0.518	19	0.224	K.LIICGGSAYPR.D
R5/RRR5-9/2	1620.263	1619.839	262.696	0.498	1813.929	0.387	21	0.211	K.ISATSIYFESLPYK.V
R5/RRR5-9/2	1817.253	1816.986	147.240	0.546	1558.057	0.530	19	0.210	K.VSAATGYIDYEKLEEK.A
R5/RRR5-9/2	1206.798	1207.398	-1329.740	0.440	1624.880	0.452	19	0.205	K.LIICGGSAYPR.D
R5/RRR5-9/2	1816.458	1816.986	-844.074	0.575	1461.280	0.534	20	0.201	K.VSAATGYIDYEKLEEK.A
R5/RRR5-8/2	1207.137	1207.398	-216.406	0.401	1735.792	0.374	19	0.200	K.LIICGGSAYPR.D
R5/RRR5-8/2	1206.499	1207.398	-1578.800	0.405	1494.044	0.438	18	0.187	K.LIICGGSAYPR.D
R5/RRR5-9/2	1619.288	1619.839	-960.688	0.377	1574.683	0.355	20	0.178	K.ISATSIYFESLPYK.V
R5/RRR5-9/2	1207.065	1207.398	-276.163	0.486	1245.216	0.484	17	0.175	K.LIICGGSAYPR.D
R5/RRR5-8/2	1619.412	1619.839	-264.212	0.362	1546.749	0.329	19	0.170	K.ISATSIYFESLPYK.V
R5/RRR5-8/2	1206.532	1207.398	-1551.358	0.379	1432.673	0.329	17	0.162	K.LIICGGSAYPR.D
R5/RRR5-9/3	1931.206	1931.043	84.655	0.488	1465.419	0.378	27	0.133	R.YYGGNDVIDEIENLCR.D
R5/RRR5-9/3	1931.657	1931.043	-200.245	0.297	1235.570	0.313	26	0.094	R.YYGGNDVIDEIENLCR.D
R5/RRR5-16/3	1964.024	1963.098	-37.698	0.532	2292.130	0.516	33	0.345	K.VAHATYAFNDFYQTTGR.A
R5/RRR5-20/2	1908.174	1909.040	-981.110	0.508	1680.439	0.569	23	0.235	R.ASGSCDFAGAASIVNQQPK.I
R5/RRR5-16/3	1962.944	1963.098	-78.761	0.510	1766.707	0.481	30	0.212	K.VAHATYAFNDFYQTTGR.A
R5/RRR5-16/3	1962.395	1963.098	-870.467	0.514	1222.980	0.537	27	0.148	K.VAHATYAFNDFYQTTGR.A
R5/RRR5-20/3	1962.529	1963.098	-802.094	0.412	1363.837	0.441	27	0.138	K.VAHATYAFNDFYQTTGR.A
R5/RRR5-15/2	928.009	928.023	-14.989	0.435	716.169	0.444	11	0.138	-.VYEVDFR.-
R5/RRR5-15/2	1286.104	1285.432	-255.669	0.435	894.299	0.377	15	0.136	R.NFGLFYPNGQK.V
R5/RRR5-16/2	1285.909	1285.432	372.324	0.451	869.167	0.378	15	0.135	R.NFGLFYPNGQK.V
R5/RRR5-17/2	928.015	928.023	-9.448	0.394	594.592	0.417	11	0.134	K.VYEVDFR.G
R5/RRR5-16/2	1285.792	1285.432	280.754	0.390	1019.784	0.300	15	0.132	R.NFGLFYPNGQK.V
R5/RRR5-16/2	927.740	928.023	-305.994	0.398	569.865	0.384	11	0.129	-.VYEVDFR.-
R5/RRR5-16/2	1285.068	1285.432	-284.077	0.433	689.616	0.402	13	0.129	-.NFGLFYPNGQK.-
R5/RRR5-16/2	927.507	928.023	-1640.124	0.368	613.764	0.339	11	0.126	-.VYEVDFR.-
R5/RRR5-16/2	1286.592	1285.432	124.892	0.353	741.977	0.185	12	0.113	-.NFGLFYPNGQK.-
R5/RRR5-12/2	1677.089	1677.832	-1042.342	0.431	1618.824	0.427	24	0.198	K.ILQSLEESVTDTDVK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1278.081	1278.439	-280.840	0.447	1636.008	0.306	18	0.176	R.LAYDTQGIIQR.V
R5/RRR5-12/2	1329.210	1329.486	-208.414	0.453	1259.649	0.444	19	0.168	K.IPATWQGIEASR.L
R5/RRR5-12/2	1328.900	1329.486	-1197.426	0.461	976.002	0.554	18	0.165	K.IPATWQGIEASR.L
R5/RRR5-12/2	978.056	978.127	-72.620	0.407	1400.558	0.309	14	0.156	R.RVEELFGK.I
R5/RRR5-12/2	1328.867	1329.486	-1222.333	0.424	1299.618	0.328	20	0.153	K.IPATWQGIEASR.L
R5/RRR5-12/2	1277.434	1278.439	-1574.131	0.350	1166.018	0.321	16	0.141	R.LAYDTQGIIQR.V
R5/RRR5-4/2	1820.724	1821.066	-188.599	0.533	1559.603	0.609	21	0.231	R.QAVALLQDNYPEFIAK.K
R5/RRR5-10/2	1820.460	1821.066	-884.791	0.483	1187.007	0.602	20	0.188	R.QAVALLQDNYPEFIAK.K
R5/RRR5-4/2	1171.260	1170.384	-106.375	0.528	1000.990	0.508	16	0.160	K.IVLTINNPASK.K
R5/RRR5-4/2	1171.139	1170.384	-209.362	0.474	1048.077	0.463	16	0.156	K.IVLTINNPASK.K
R5/RRR5-4/2	1142.938	1143.362	-371.979	0.417	934.009	0.382	14	0.139	K.M*M*SPFLTQR.T
R5/RRR5-4/2	1143.112	1143.362	-219.829	0.453	908.435	0.361	14	0.136	K.M*M*SPFLTQR.T
R5/RRR5-3/2	1821.625	1821.066	-242.814	0.398	613.397	0.515	17	0.136	R.QAVALLQDNYPEFIAK.K
R5/RRR5-8/2	1822.228	1821.066	88.919	0.459	266.172	0.475	14	0.124	-.QAVALLQDNYPEFIAK.-
R5/RRR5-3/3	1272.759	1272.496	206.688	0.497	1340.265	0.272	24	0.094	R.KVPANEEPIM*K.G
R5/RRR5-4/3	1272.715	1272.496	172.496	0.464	998.551	0.291	22	0.081	R.KVPANEEPIM*K.G
R5/RRR5-10/3	1271.977	1272.496	-1197.812	0.392	828.298	0.357	20	0.068	-.KVPANEEPIM*K.-
R5/RRR5-4/3	1272.291	1272.496	-162.049	0.420	996.890	0.167	22	0.066	R.KVPANEEPIM*K.G
R5/RRR5-4/3	1272.259	1272.496	-187.170	0.348	906.153	0.168	20	0.064	-.KVPANEEPIM*K.-
R5/RRR5-3/3	1272.616	1272.496	94.581	0.430	737.236	0.205	20	0.049	-.KVPANEEPIM*K.-
R5/RRR5-15/2	1197.551	1198.305	-1468.317	0.517	1522.948	0.402	17	0.184	R.TCYAQASQIR.Q
R5/RRR5-15/2	1198.106	1198.305	-166.124	0.543	1496.096	0.399	17	0.180	R.TCYAQASQIR.Q
R5/RRR5-15/2	1197.999	1198.305	-255.667	0.552	1357.117	0.447	16	0.177	R.TCYAQASQIR.Q
R5/RRR5-16/2	1197.777	1198.305	-1279.548	0.486	1372.911	0.426	16	0.175	R.TCYAQASQIR.Q
R5/RRR5-16/2	1199.025	1198.305	-234.208	0.541	1356.414	0.399	16	0.168	R.TCYAQASQIR.Q
R5/RRR5-16/2	1198.019	1198.305	-238.697	0.515	1313.717	0.386	16	0.163	R.TCYAQASQIR.Q
R5/RRR5-15/2	1580.430	1579.824	-249.967	0.478	913.225	0.541	20	0.160	K.ATSSIFPLQNVFVR.K
R5/RRR5-16/2	1580.299	1579.824	301.260	0.425	939.082	0.495	20	0.154	K.ATSSIFPLQNVFVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1580.319	1579.824	313.730	0.439	903.697	0.501	20	0.153	K.ATSSIFPLQNVFVR.K
R5/RRR5-15/2	1762.186	1761.979	117.796	0.482	842.330	0.549	17	0.152	K.NVLTNFWGMSFTTDK.L
R5/RRR5-15/2	1580.235	1579.824	260.363	0.490	953.008	0.442	20	0.148	K.ATSSIFPLQNVFVR.K
R5/RRR5-13/2	1580.200	1579.824	238.751	0.508	613.073	0.539	17	0.144	K.ATSSIFPLQNVFVR.K
R5/RRR5-14/2	1579.439	1579.824	-244.775	0.375	894.160	0.440	19	0.143	K.ATSSIFPLQNVFVR.K
R5/RRR5-14/2	1579.993	1579.824	106.969	0.475	811.354	0.453	19	0.142	K.ATSSIFPLQNVFVR.K
R5/RRR5-15/2	889.465	890.021	-1755.283	0.351	790.794	0.464	13	0.142	K.APSVFNVR.N
R5/RRR5-14/2	1579.419	1579.824	-257.569	0.433	823.600	0.414	19	0.138	K.ATSSIFPLQNVFVR.K
R5/RRR5-16/2	1579.296	1579.824	-970.518	0.319	923.826	0.393	20	0.138	K.ATSSIFPLQNVFVR.K
R5/RRR5-17/2	1579.572	1579.824	-160.188	0.379	790.369	0.427	19	0.138	K.ATSSIFPLQNVFVR.K
R5/RRR5-12/2	1579.787	1579.824	-23.840	0.405	854.090	0.386	19	0.136	K.ATSSIFPLQNVFVR.K
R5/RRR5-16/2	889.916	890.021	-118.542	0.350	563.420	0.472	11	0.135	K.APSVFNVR.N
R5/RRR5-27/2	889.981	890.021	-45.345	0.367	680.068	0.407	12	0.134	K.APSVFNVR.N
R5/RRR5-14/2	889.955	890.021	-74.925	0.319	704.010	0.419	12	0.134	K.APSVFNVR.N
R5/RRR5-15/2	890.126	890.021	118.071	0.313	604.061	0.451	12	0.134	K.APSVFNVR.N
R5/RRR5-17/2	1579.634	1579.824	-120.884	0.427	671.741	0.409	17	0.132	K.ATSSIFPLQNVFVR.K
R5/RRR5-15/2	889.520	890.021	-1692.684	0.295	658.274	0.421	12	0.132	K.APSVFNVR.N
R5/RRR5-14/2	890.160	890.021	156.304	0.366	556.025	0.389	11	0.130	K.APSVFNVR.N
R5/RRR5-14/2	889.928	890.021	-105.058	0.363	490.107	0.412	10	0.130	K.APSVFNVR.N
R5/RRR5-20/2	1579.179	1579.824	-1044.788	0.368	608.460	0.389	17	0.129	K.ATSSIFPLQNVFVR.K
R5/RRR5-15/2	1578.990	1579.824	-1165.412	0.333	657.203	0.368	17	0.127	K.ATSSIFPLQNVFVR.K
R5/RRR5-12/2	1580.457	1579.824	-233.152	0.360	606.646	0.367	16	0.126	K.ATSSIFPLQNVFVR.K
R5/RRR5-17/2	890.761	890.021	-293.268	0.268	640.151	0.354	12	0.126	K.APSVFNVR.N
R5/RRR5-10/2	1199.434	1198.305	108.243	0.253	287.613	0.361	13	0.125	R.TCYAQASQIR.Q
R5/RRR5-17/2	1579.189	1579.824	-1038.501	0.350	589.205	0.338	16	0.124	K.ATSSIFPLQNVFVR.K
R5/RRR5-18/2	1779.305	1777.978	184.176	0.382	320.404	0.438	14	0.124	K.NVLTNFWGM*SFTTDK.L
R5/RRR5-27/2	889.969	890.021	-59.241	0.242	605.290	0.333	11	0.123	K.APSVFNVR.N
R5/RRR5-18/2	1579.245	1579.824	-1002.956	0.326	562.735	0.288	16	0.121	K.ATSSIFPLQNVFVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1776.730	1777.978	-1269.445	0.312	447.903	0.357	15	0.119	K.NVLTNFWGM*SFTTDK.L
R5/RRR5-16/2	889.884	890.021	-155.007	0.224	461.897	0.300	10	0.119	-.APSVFNVR.-
R5/RRR5-16/2	889.309	890.021	-1931.955	0.241	456.330	0.457	10	0.119	-.APSVFNVR.-
R5/RRR5-3/2	1579.877	1579.824	33.122	0.226	496.193	0.284	14	0.118	K.ATSSIFPLQNVFVR.K
R5/RRR5-15/2	1347.267	1346.517	-186.264	0.409	1380.885	0.594	18	0.205	R.TLTGIQIWGSGGR.G
R5/RRR5-15/2	1042.809	1043.202	-378.250	0.472	1492.369	0.486	16	0.198	R.GLVAQAQSLR.S
R5/RRR5-15/2	1043.119	1043.202	-79.770	0.452	1585.457	0.425	16	0.195	R.GLVAQAQSLR.S
R5/RRR5-15/2	1346.783	1346.517	198.402	0.470	1144.480	0.576	17	0.180	R.TLTGIQIWGSGGR.G
R5/RRR5-15/2	1073.024	1073.228	-190.966	0.456	1348.254	0.409	18	0.170	R.SLATAAQAAIR.A
R5/RRR5-14/2	1347.849	1346.517	247.116	0.375	1059.943	0.556	19	0.168	R.TLTGIQIWGSGGR.G
R5/RRR5-15/2	1072.957	1073.228	-253.397	0.438	1218.332	0.353	17	0.150	R.SLATAAQAAIR.A
R5/RRR5-15/2	1346.120	1346.517	-295.842	0.377	840.700	0.541	15	0.149	R.TLTGIQIWGSGGR.G
R5/RRR5-15/2	1072.598	1073.228	-1524.193	0.384	1233.740	0.295	16	0.142	R.SLATAAQAAIR.A
R5/RRR5-14/2	1043.062	1043.202	-134.474	0.316	640.449	0.265	14	0.120	R.GLVAQAQSLR.S
R5/RRR5-16/2	1345.296	1346.517	-1655.907	0.240	538.342	0.257	15	0.117	-.TLTGIQIWGSGGR.-
R5/RRR5-14/2	1347.339	1346.517	-132.639	0.211	299.149	0.347	11	0.112	-.TLTGIQIWGSGGR.-
R5/RRR5-15/3	1544.291	1543.798	319.653	0.449	788.452	0.449	26	0.094	R.GSKPAIVIHGTVHAR.E
R5/RRR5-15/3	1543.166	1543.798	-1061.285	0.399	471.640	0.411	24	0.083	R.GSKPAIVIHGTVHAR.E
R5/RRR5-12/2	1568.811	1569.657	-1180.075	0.441	2012.490	0.507	25	0.270	K.NFGDEALIGEGSFGR.V
R5/RRR5-12/2	1569.085	1569.657	-1004.612	0.482	1900.978	0.517	25	0.256	K.NFGDEALIGEGSFGR.V
R5/RRR5-12/2	1569.298	1569.657	-229.426	0.551	1898.118	0.513	25	0.255	K.NFGDEALIGEGSFGR.V
R5/RRR5-12/2	1366.997	1367.538	-1130.737	0.387	571.676	0.521	17	0.137	K.GAQPGPVLSWAQR.V
R5/RRR5-12/2	995.401	996.189	-1801.196	0.393	563.056	0.460	14	0.136	K.ALQPLLNAR.A
R5/RRR5-12/2	1367.303	1367.538	-172.520	0.340	683.580	0.485	18	0.136	K.GAQPGPVLSWAQR.V
R5/RRR5-6/2	1181.990	1181.372	-323.870	0.405	953.481	0.343	15	0.135	R.VYFGVLRNGR.S
R5/RRR5-12/2	996.112	996.189	-77.511	0.389	412.361	0.457	13	0.133	K.ALQPLLNAR.A
R5/RRR5-12/2	996.264	996.189	76.243	0.405	518.412	0.389	14	0.131	K.ALQPLLNAR.A
R5/RRR5-6/2	1181.197	1181.372	-148.497	0.367	980.490	0.231	15	0.124	R.VYFGVLRNGR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1182.143	1181.372	-193.742	0.382	827.275	0.214	14	0.118	-.VYFGVLRNGR.-
R5/RRR5-13/2	1657.187	1657.850	-1006.911	0.528	2017.008	0.668	31	0.318	K.GLPLGSGLGSSAASAAAAAK.A
R5/RRR5-13/2	1656.978	1657.850	-1133.244	0.511	1944.899	0.635	31	0.295	K.GLPLGSGLGSSAASAAAAAK.A
R5/RRR5-13/2	1658.512	1657.850	-204.683	0.605	1774.003	0.701	30	0.288	K.GLPLGSGLGSSAASAAAAAK.A
R5/RRR5-13/2	1162.166	1162.364	-170.418	0.429	2040.716	0.260	17	0.211	K.AVDALFGSLLR.Q
R5/RRR5-13/2	1161.725	1162.364	-1414.741	0.474	1546.042	0.319	16	0.168	K.AVDALFGSLLR.Q
R5/RRR5-13/3	1911.006	1911.192	-97.623	0.439	789.149	0.432	26	0.090	R.SYDPFHLIPLSSPPALR.L
R5/RRR5-13/3	1093.337	1093.261	69.182	0.418	902.363	0.380	19	0.086	K.SHAVSIHLTK.G
R5/RRR5-13/3	1910.413	1911.192	-933.951	0.313	582.365	0.416	23	0.078	R.SYDPFHLIPLSSPPALR.L
R5/RRR5-8/3	1981.126	1981.204	-39.628	0.528	2783.416	0.555	36	0.526	K.QIGVIGWGSQGPAQAQNLR.D
R5/RRR5-8/2	1789.334	1789.021	175.265	0.565	2975.211	0.570	25	0.486	R.FDYILTQQAFVTVDK.N
R5/RRR5-8/2	1788.262	1789.021	-986.442	0.422	2902.214	0.494	24	0.439	R.FDYILTQQAFVTVDK.N
R5/RRR5-8/2	1789.031	1789.021	5.844	0.551	2460.616	0.585	26	0.376	R.FDYILTQQAFVTVDK.N
R5/RRR5-8/2	1980.680	1981.204	-771.741	0.528	2206.083	0.651	26	0.346	K.QIGVIGWGSQGPAQAQNLR.D
R5/RRR5-8/2	1980.584	1981.204	-820.801	0.539	2054.581	0.609	25	0.305	K.QIGVIGWGSQGPAQAQNLR.D
R5/RRR5-8/2	1980.531	1981.204	-847.467	0.534	1724.601	0.650	25	0.264	K.QIGVIGWGSQGPAQAQNLR.D
R5/RRR5-8/3	1980.501	1981.204	-862.756	0.417	1413.753	0.470	29	0.153	K.QIGVIGWGSQGPAQAQNLR.D
R5/RRR5-8/2	1662.283	1662.849	-944.772	0.399	699.276	0.513	20	0.140	K.EGLPAFPM*GNIDQTR.M
R5/RRR5-8/3	1616.429	1616.800	-230.244	0.355	911.667	0.481	24	0.103	K.EKVSLAGHDEYIVR.G
R5/RRR5-8/3	1617.160	1616.800	223.330	0.461	813.357	0.440	24	0.095	K.EKVSLAGHDEYIVR.G
R5/RRR5-8/3	1616.868	1616.800	42.200	0.337	562.289	0.445	19	0.084	K.EKVSLAGHDEYIVR.G
R5/RRR5-8/2	1345.178	1345.506	-244.834	0.467	1496.741	0.548	22	0.210	K.FDM*GGSAAVFGAAK.A
R5/RRR5-8/2	1192.050	1191.271	-185.353	0.453	1112.628	0.572	17	0.177	K.EVAAASEISGEK.F
R5/RRR5-8/2	1192.112	1191.271	-132.964	0.455	1021.912	0.516	17	0.162	K.EVAAASEISGEK.F
R5/RRR5-8/2	1272.267	1272.388	-95.524	0.410	1175.617	0.422	18	0.157	K.GLTFDSGGYNIK.T
R5/RRR5-8/2	1851.600	1852.072	-255.546	0.468	1027.628	0.499	19	0.155	R.LTLADALVYACNQGVDK.I
R5/RRR5-8/2	1272.224	1272.388	-129.980	0.423	1071.538	0.446	18	0.154	K.GLTFDSGGYNIK.T
R5/RRR5-8/2	1272.224	1272.388	-129.595	0.399	994.137	0.413	18	0.145	K.GLTFDSGGYNIK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1190.451	1191.271	-1533.025	0.259	780.656	0.368	15	0.126	K.EVAAASEISGEK.F
R5/RRR5-8/2	1851.023	1852.072	-1110.157	0.268	309.454	0.350	13	0.115	R.LTLADALVYACNQGVDK.I
R5/RRR5-8/2	962.943	963.112	-176.496	0.519	1257.849	0.386	13	0.158	R.IGDLELFR.A
R5/RRR5-8/2	1626.099	1624.819	172.680	0.512	781.885	0.511	20	0.149	K.EALTPYFELTNAVR.I
R5/RRR5-8/2	1002.146	1002.062	83.920	0.458	638.045	0.404	14	0.134	K.FASTFSADR.T
R5/RRR5-9/2	1625.633	1624.819	-114.376	0.439	629.631	0.435	18	0.133	K.EALTPYFELTNAVR.I
R5/RRR5-8/2	1625.190	1624.819	229.354	0.450	540.319	0.462	17	0.133	K.EALTPYFELTNAVR.I
R5/RRR5-8/2	1002.008	1002.062	-54.022	0.408	642.843	0.406	13	0.132	K.FASTFSADR.T
R5/RRR5-8/3	1424.430	1424.497	-46.907	0.499	643.281	0.487	19	0.099	R.FEAHSNQQFCR.Y
R5/RRR5-9/3	1424.606	1424.497	76.987	0.446	791.074	0.396	20	0.090	R.FEAHSNQQFCR.Y
R5/RRR5-8/3	1424.712	1424.497	151.360	0.455	494.505	0.397	20	0.085	-.FEAHSNQQFCR.-
R5/RRR5-8/3	1424.030	1424.497	-328.845	0.424	603.195	0.358	19	0.084	R.FEAHSNQQFCR.Y
R5/RRR5-9/3	1424.680	1424.497	128.934	0.432	581.692	0.338	20	0.084	R.FEAHSNQQFCR.Y
R5/RRR5-9/3	1423.972	1424.497	-1074.111	0.454	592.436	0.402	18	0.081	-.FEAHSNQQFCR.-
R5/RRR5-17/2	1418.518	1419.648	-1505.696	0.359	1489.336	0.437	17	0.184	K.GANEVLLVIEAYK.T
R5/RRR5-17/2	1141.032	1141.299	-235.382	0.371	1319.702	0.437	18	0.149	K.VEGSTILTALH.-
R5/RRR5-17/3	1850.678	1851.084	-220.121	0.485	1198.245	0.520	31	0.140	K.VTAVPAKEEEICGATFK.V
R5/RRR5-17/2	1140.919	1141.299	-334.885	0.396	1128.509	0.480	18	0.123	K.VEGSTILTALH.-
R5/RRR5-17/2	1405.197	1405.533	-240.100	0.316	932.455	0.252	16	0.120	-.STSTLLVASDPEGK.-
R5/RRR5-17/2	1419.467	1419.648	-127.969	0.301	637.425	0.254	14	0.115	K.GANEVLLVIEAYK.T
R5/RRR5-17/3	1850.655	1851.084	-232.330	0.393	580.181	0.421	27	0.083	K.VTAVPAKEEEICGATFK.V
R5/RRR5-15/2	1879.644	1880.095	-240.660	0.545	1307.129	0.672	30	0.216	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/2	1410.189	1410.578	-277.022	0.494	1775.576	0.411	20	0.212	R.SVQM*EGLTWGASK.L
R5/RRR5-16/2	1410.034	1410.578	-1098.399	0.498	1736.695	0.405	20	0.206	R.SVQM*EGLTWGASK.L
R5/RRR5-15/2	1511.240	1511.659	-278.020	0.517	1379.903	0.553	21	0.200	K.TYVSGNAISKDDIK.V
R5/RRR5-16/2	1880.395	1880.095	160.006	0.593	1136.729	0.673	29	0.199	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/2	1410.393	1410.578	-131.401	0.485	1612.072	0.417	20	0.195	R.SVQM*EGLTWGASK.L
R5/RRR5-16/2	1511.211	1511.659	-297.389	0.460	1367.054	0.508	21	0.189	K.TYVSGNAISKDDIK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1879.699	1880.095	-211.211	0.518	1104.321	0.633	29	0.187	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/2	1878.971	1880.095	-1133.980	0.510	1111.395	0.626	29	0.186	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-16/2	1879.608	1880.095	-260.141	0.549	1043.830	0.656	28	0.186	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/2	1510.764	1511.659	-1257.752	0.482	1253.272	0.496	20	0.176	K.TYVSGNAISKDDIK.V
R5/RRR5-15/2	1879.527	1880.095	-836.596	0.541	934.426	0.633	27	0.173	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/2	1511.229	1511.659	-285.313	0.470	1182.650	0.493	20	0.170	K.TYVSGNAISKDDIK.V
R5/RRR5-15/3	1880.161	1880.095	35.053	0.419	1380.968	0.523	37	0.164	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-16/2	1510.620	1511.659	-1353.512	0.472	1124.451	0.485	19	0.163	K.TYVSGNAISKDDIK.V
R5/RRR5-16/2	1324.132	1324.467	-253.042	0.425	996.503	0.372	16	0.139	R.WYDTVAAALASR.F
R5/RRR5-16/2	1324.606	1324.467	105.224	0.346	970.814	0.341	16	0.133	R.WYDTVAAALASR.F
R5/RRR5-16/3	1879.437	1880.095	-884.785	0.411	1324.046	0.435	35	0.132	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/3	1881.036	1880.095	-31.388	0.423	982.734	0.542	34	0.124	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/3	1880.196	1880.095	53.611	0.425	1240.209	0.435	35	0.123	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-15/2	1323.757	1324.467	-1295.310	0.284	673.773	0.197	14	0.114	R.WYDTVAAALASR.F
R5/RRR5-16/3	1879.108	1880.095	-1060.472	0.345	528.441	0.401	29	0.081	K.AVGVNLPGGGAASSAAAAAPAAK.D
R5/RRR5-11/2	1427.165	1427.688	-1070.820	0.521	1839.640	0.495	19	0.242	K.LSISDVEYLLM*K.S
R5/RRR5-11/2	1656.935	1656.966	-18.254	0.446	1413.781	0.453	21	0.182	R.TKLSISDVEYLLM*K.S
R5/RRR5-11/2	1427.004	1427.688	-1183.767	0.458	1281.525	0.482	16	0.174	K.LSISDVEYLLM*K.S
R5/RRR5-11/2	1089.140	1089.309	-156.327	0.398	834.481	0.336	14	0.131	R.INEPILYVK.M
R5/RRR5-11/2	1088.998	1089.309	-287.104	0.390	957.150	0.264	14	0.127	R.INEPILYVK.M
R5/RRR5-11/2	1088.495	1089.309	-1671.782	0.274	743.633	0.267	13	0.120	R.INEPILYVK.M
R5/RRR5-11/3	1819.264	1819.015	137.445	0.334	820.969	0.369	25	0.079	R.VHNAALSAQPALVQNER.K
R5/RRR5-11/3	1820.039	1819.015	13.036	0.286	466.062	0.386	26	0.076	R.VHNAALSAQPALVQNER.K
R5/RRR5-5/2	1651.008	1650.881	77.228	0.533	2791.119	0.488	25	0.409	R.FASEVAGVQDLGMLGR.G
R5/RRR5-5/2	1650.568	1650.881	-190.684	0.481	2674.397	0.486	25	0.384	R.FASEVAGVQDLGMLGR.G
R5/RRR5-5/2	1666.333	1666.881	-931.484	0.472	2192.625	0.454	23	0.282	R.FASEVAGVQDLGM*LGR.G
R5/RRR5-5/2	1666.315	1666.881	-942.149	0.446	1874.795	0.444	22	0.232	R.FASEVAGVQDLGM*LGR.G
R5/RRR5-5/2	1933.190	1934.140	-1011.228	0.502	1330.827	0.567	25	0.195	R.ALSEVAGAQLPYDSLSGVR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1933.440	1934.140	-881.596	0.520	1259.781	0.566	25	0.188	R.ALSEVAGAQLPYDSLSGVR.D
R5/RRR5-5/2	1665.259	1666.881	-2181.405	0.332	1494.540	0.313	20	0.162	R.FASEVAGVQDLGM*LGR.G
R5/RRR5-5/2	1363.099	1363.541	-325.211	0.411	855.383	0.395	17	0.135	R.ANVILPSSAFSEK.E
R5/RRR5-5/2	1268.966	1269.340	-295.014	0.389	742.062	0.402	15	0.131	R.GSGEEIGTYVEK.L
R5/RRR5-5/2	1269.188	1269.340	-120.066	0.418	723.987	0.373	16	0.129	R.GSGEEIGTYVEK.L
R5/RRR5-5/2	1363.215	1363.541	-239.949	0.376	862.482	0.335	17	0.129	R.ANVILPSSAFSEK.E
R5/RRR5-5/2	1269.112	1269.340	-179.983	0.428	666.936	0.382	15	0.128	R.GSGEEIGTYVEK.L
R5/RRR5-5/2	1362.810	1363.541	-1274.093	0.234	712.780	0.151	15	0.112	R.ANVILPSSAFSEK.E
R5/RRR5-5/3	1933.875	1934.140	-137.400	0.323	896.193	0.284	26	0.067	R.ALSEVAGAQLPYDSLSGVR.D
R5/RRR5-15/2	1454.317	1454.561	-168.007	0.558	1697.290	0.613	21	0.253	R.DLVGVAYTEEETK.A
R5/RRR5-14/2	1454.136	1454.561	-293.147	0.489	1748.919	0.564	21	0.246	R.DLVGVAYTEEETK.A
R5/RRR5-15/2	1454.217	1454.561	-237.310	0.519	1659.922	0.609	21	0.246	R.DLVGVAYTEEETK.A
R5/RRR5-15/2	1454.144	1454.561	-287.252	0.539	1631.552	0.568	21	0.233	R.DLVGVAYTEEETK.A
R5/RRR5-14/2	1455.256	1454.561	-210.471	0.530	1562.256	0.524	20	0.213	R.DLVGVAYTEEETK.A
R5/RRR5-14/2	1453.935	1454.561	-1121.482	0.461	1436.803	0.525	20	0.199	R.DLVGVAYTEEETK.A
R5/RRR5-16/2	1454.132	1454.561	-296.011	0.414	1181.224	0.498	19	0.170	R.DLVGVAYTEEETK.A
R5/RRR5-15/2	1664.274	1664.883	-969.886	0.430	760.970	0.506	22	0.145	R.FANGGAYPPDLSLITK.A
R5/RRR5-15/2	1889.681	1890.049	-195.064	0.526	865.828	0.467	19	0.141	K.LSDRFPQPYPNEQAAR.F
R5/RRR5-15/2	1666.207	1664.883	195.271	0.459	571.338	0.515	21	0.140	R.FANGGAYPPDLSLITK.A
R5/RRR5-15/2	1665.128	1664.883	147.824	0.477	550.880	0.513	20	0.139	R.FANGGAYPPDLSLITK.A
R5/RRR5-15/2	1664.762	1664.883	-73.002	0.450	560.637	0.483	21	0.137	R.FANGGAYPPDLSLITK.A
R5/RRR5-16/2	1665.257	1664.883	225.159	0.415	615.945	0.464	20	0.135	R.FANGGAYPPDLSLITK.A
R5/RRR5-14/3	1889.894	1890.049	-81.919	0.470	961.054	0.349	27	0.086	K.LSDRFPQPYPNEQAAR.F
R5/RRR5-14/3	1889.069	1890.049	-1050.927	0.407	811.908	0.351	24	0.079	K.LSDRFPQPYPNEQAAR.F
R5/RRR5-15/3	1978.957	1979.247	-146.845	0.241	964.106	0.134	23	0.050	R.EGLHYNPYFPGGAIAM*PK.M
R5/RRR5-8/2	1607.328	1607.833	-939.348	0.469	2510.759	0.450	23	0.340	R.SPPIEEVINTGVVPR.F
R5/RRR5-8/2	1607.211	1607.833	-1011.862	0.491	2248.306	0.494	22	0.305	R.SPPIEEVINTGVVPR.F
R5/RRR5-8/2	1345.016	1344.624	292.059	0.540	1621.219	0.634	20	0.248	K.VVVESGAVPIFVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1601.531	1601.903	-232.912	0.506	1826.029	0.508	22	0.243	R.IVTVCLEGLENILK.V
R5/RRR5-8/2	1601.205	1601.903	-1064.061	0.437	1985.365	0.414	20	0.240	R.IVTVCLEGLENILK.V
R5/RRR5-8/2	1601.255	1601.903	-1032.219	0.481	1784.535	0.430	20	0.217	R.IVTVCLEGLENILK.V
R5/RRR5-8/2	1602.894	1601.903	-5.546	0.569	1757.849	0.450	20	0.217	R.IVTVCLEGLENILK.V
R5/RRR5-8/3	1975.826	1976.416	-806.994	0.386	1537.105	0.421	29	0.156	R.LVELLM*HPSASVLIPALR.T
R5/RRR5-8/2	1344.108	1344.624	-1131.136	0.345	1131.897	0.385	17	0.146	K.VVVESGAVPIFVK.L
R5/RRR5-8/3	1977.489	1976.416	37.433	0.469	1495.157	0.395	31	0.141	R.LVELLM*HPSASVLIPALR.T
R5/RRR5-8/2	1975.997	1976.416	-212.610	0.404	774.789	0.471	19	0.136	R.LVELLM*HPSASVLIPALR.T
R5/RRR5-7/3	1976.446	1976.416	15.276	0.495	1363.758	0.393	29	0.125	R.LVELLM*HPSASVLIPALR.T
R5/RRR5-8/2	1961.187	1960.416	-117.219	0.326	446.418	0.291	15	0.113	R.LVELLMHPSASVLIPALR.T
R5/RRR5-2/3	1975.304	1976.416	-1072.280	0.271	724.493	0.233	24	0.065	R.LVELLM*HPSASVLIPALR.T
R5/RRR5-12/3	1753.203	1752.910	167.626	0.547	1903.360	0.390	31	0.202	K.VNTLHDGVALAQETQR.S
R5/RRR5-12/2	1099.034	1099.266	-211.512	0.470	1604.892	0.390	17	0.190	K.VLQDVLAGQR.G
R5/RRR5-12/2	1216.116	1216.323	-170.913	0.501	1379.639	0.412	17	0.173	R.LLLEEENEAR.I
R5/RRR5-12/2	1449.248	1448.603	-245.390	0.491	1158.493	0.482	18	0.166	R.SGEAINTLESWIK.I
R5/RRR5-12/2	1099.014	1099.266	-229.675	0.435	1362.724	0.364	15	0.162	K.VLQDVLAGQR.G
R5/RRR5-12/2	1217.493	1216.323	140.125	0.471	1443.731	0.298	17	0.158	R.LLLEEENEAR.I
R5/RRR5-12/2	1448.387	1448.603	-149.252	0.404	1371.135	0.293	18	0.150	R.SGEAINTLESWIK.I
R5/RRR5-11/2	1447.814	1448.603	-1239.543	0.447	1067.541	0.379	17	0.143	R.SGEAINTLESWIK.I
R5/RRR5-12/2	1099.007	1099.266	-235.693	0.302	1154.338	0.324	15	0.140	K.VLQDVLAGQR.G
R5/RRR5-12/2	1447.921	1448.603	-1165.207	0.369	1017.908	0.306	16	0.131	R.SGEAINTLESWIK.I
R5/RRR5-11/2	1448.548	1448.603	-38.003	0.434	633.560	0.404	15	0.129	R.SGEAINTLESWIK.I
R5/RRR5-12/3	1752.356	1752.910	-889.281	0.524	1427.710	0.340	26	0.120	-.VNTLHDGVALAQETQR.-
R5/RRR5-12/3	1752.804	1752.910	-60.542	0.516	1414.717	0.322	26	0.114	-.VNTLHDGVALAQETQR.-
R5/RRR5-9/2	1025.758	1026.215	-447.084	0.440	1236.076	0.464	19	0.170	K.IGGIGTVPVGR.V
R5/RRR5-15/2	1026.063	1026.215	-148.276	0.475	1208.996	0.472	19	0.170	K.IGGIGTVPVGR.V
R5/RRR5-9/2	1025.585	1026.215	-1593.465	0.413	1233.755	0.462	19	0.168	K.IGGIGTVPVGR.V
R5/RRR5-4/2	1026.063	1026.215	-148.873	0.447	1220.489	0.458	19	0.168	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1025.574	1026.215	-1604.347	0.407	1221.254	0.455	18	0.166	K.IGGIGTVPVGR.V
R5/RRR5-5/2	1025.598	1026.215	-1581.628	0.404	1189.931	0.451	18	0.163	K.IGGIGTVPVGR.V
R5/RRR5-3/2	1026.066	1026.215	-145.770	0.486	1060.466	0.495	18	0.163	K.IGGIGTVPVGR.V
R5/RRR5-9/2	1026.005	1026.215	-205.565	0.463	1092.014	0.477	18	0.162	K.IGGIGTVPVGR.V
R5/RRR5-4/2	1026.180	1026.215	-33.719	0.503	1038.050	0.488	18	0.161	K.IGGIGTVPVGR.V
R5/RRR5-1/2	1025.947	1026.215	-262.024	0.498	1071.995	0.472	18	0.160	K.IGGIGTVPVGR.V
R5/RRR5-6/2	1026.407	1026.215	187.684	0.458	1050.615	0.472	18	0.159	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1026.106	1026.215	-105.911	0.548	1051.598	0.460	18	0.157	K.IGGIGTVPVGR.V
R5/RRR5-6/2	1026.290	1026.215	73.535	0.510	898.822	0.516	17	0.157	K.IGGIGTVPVGR.V
R5/RRR5-13/2	1026.040	1026.215	-170.475	0.497	1040.999	0.459	18	0.157	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1026.114	1026.215	-98.393	0.432	1071.227	0.453	18	0.157	K.IGGIGTVPVGR.V
R5/RRR5-3/2	1025.660	1026.215	-1520.651	0.432	1056.945	0.456	18	0.156	K.IGGIGTVPVGR.V
R5/RRR5-5/2	1025.967	1026.215	-242.090	0.524	1065.073	0.446	18	0.156	K.IGGIGTVPVGR.V
R5/RRR5-15/2	1026.091	1026.215	-120.709	0.441	953.265	0.484	17	0.154	K.IGGIGTVPVGR.V
R5/RRR5-2/2	1026.017	1026.215	-193.390	0.468	1005.948	0.451	17	0.153	K.IGGIGTVPVGR.V
R5/RRR5-10/2	1026.173	1026.215	-41.236	0.485	946.352	0.470	17	0.153	K.IGGIGTVPVGR.V
R5/RRR5-1/2	1026.075	1026.215	-136.461	0.451	879.745	0.494	17	0.152	K.IGGIGTVPVGR.V
R5/RRR5-10/2	1026.116	1026.215	-96.603	0.432	1065.602	0.427	17	0.152	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1026.039	1026.215	-171.430	0.448	927.906	0.475	17	0.152	K.IGGIGTVPVGR.V
R5/RRR5-15/2	1025.737	1026.215	-467.624	0.383	1035.492	0.432	18	0.151	K.IGGIGTVPVGR.V
R5/RRR5-10/2	1025.957	1026.215	-252.236	0.476	896.035	0.471	17	0.150	K.IGGIGTVPVGR.V
R5/RRR5-12/2	1026.040	1026.215	-170.714	0.425	852.214	0.490	17	0.150	K.IGGIGTVPVGR.V
R5/RRR5-14/2	1026.188	1026.215	-26.321	0.438	1004.153	0.424	17	0.149	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1752.552	1752.026	-270.897	0.515	881.471	0.498	20	0.148	K.AGMVVTFAPSNVTTEVK.S
R5/RRR5-11/2	1026.084	1026.215	-127.869	0.507	903.737	0.447	17	0.148	K.IGGIGTVPVGR.V
R5/RRR5-12/2	1026.043	1026.215	-167.730	0.401	824.485	0.490	16	0.147	K.IGGIGTVPVGR.V
R5/RRR5-11/2	1025.473	1026.215	-1703.962	0.382	833.976	0.492	16	0.147	K.IGGIGTVPVGR.V
R5/RRR5-2/2	1026.068	1026.215	-143.503	0.482	910.598	0.434	17	0.146	K.IGGIGTVPVGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1025.579	1026.215	-1600.161	0.378	870.285	0.465	16	0.146	K.IGGIGTVPVGR.V
R5/RRR5-5/2	1026.185	1026.215	-29.304	0.472	835.870	0.459	16	0.145	K.IGGIGTVPVGR.V
R5/RRR5-11/2	1025.872	1026.215	-335.443	0.442	932.709	0.420	17	0.145	K.IGGIGTVPVGR.V
R5/RRR5-16/2	1025.621	1026.215	-1559.149	0.359	839.067	0.470	17	0.145	K.IGGIGTVPVGR.V
R5/RRR5-9/2	1025.316	1026.215	-1857.549	0.384	792.537	0.480	16	0.144	K.IGGIGTVPVGR.V
R5/RRR5-2/2	1025.425	1026.215	-1750.368	0.397	850.793	0.446	17	0.144	K.IGGIGTVPVGR.V
R5/RRR5-12/2	1027.200	1026.215	-14.376	0.496	962.382	0.399	17	0.143	K.IGGIGTVPVGR.V
R5/RRR5-13/2	1025.653	1026.215	-1527.705	0.365	890.900	0.436	16	0.143	K.IGGIGTVPVGR.V
R5/RRR5-6/2	1025.573	1026.215	-1605.303	0.362	853.749	0.449	16	0.143	K.IGGIGTVPVGR.V
R5/RRR5-14/2	1026.049	1026.215	-162.359	0.422	779.535	0.423	16	0.139	K.IGGIGTVPVGR.V
R5/RRR5-14/2	1026.112	1026.215	-100.541	0.427	676.276	0.454	15	0.139	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1261.196	1261.411	-170.628	0.454	729.582	0.453	14	0.138	K.ANISPNAPWYK.G
R5/RRR5-3/2	1025.908	1026.215	-300.463	0.390	590.774	0.474	14	0.137	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1752.272	1752.026	141.310	0.457	794.555	0.438	20	0.136	K.AGMVVTFAPSNVTTEVK.S
R5/RRR5-9/2	1752.231	1752.026	117.487	0.504	710.910	0.465	19	0.136	K.AGMVVTFAPSNVTTEVK.S
R5/RRR5-4/2	1025.768	1026.215	-436.695	0.426	830.588	0.372	16	0.135	K.IGGIGTVPVGR.V
R5/RRR5-13/2	1025.890	1026.215	-317.415	0.336	811.399	0.372	17	0.134	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1262.270	1261.411	-111.509	0.408	876.426	0.345	15	0.131	K.ANISPNAPWYK.G
R5/RRR5-9/2	1026.765	1026.215	-439.490	0.394	382.190	0.388	14	0.131	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1260.429	1261.411	-1577.108	0.400	638.319	0.413	14	0.130	K.ANISPNAPWYK.G
R5/RRR5-16/2	1025.347	1026.215	-1827.402	0.260	389.520	0.390	13	0.126	K.IGGIGTVPVGR.V
R5/RRR5-22/2	1025.710	1026.215	-1471.637	0.286	489.738	0.359	12	0.124	K.IGGIGTVPVGR.V
R5/RRR5-8/2	1750.696	1752.026	-1334.350	0.296	798.099	0.326	20	0.124	K.AGMVVTFAPSNVTTEVK.S
R5/RRR5-16/2	1025.582	1026.215	-1596.933	0.316	543.803	0.420	12	0.121	-.IGGIGTVPVGR.-
R5/RRR5-8/2	750.889	750.862	35.284	0.325	975.159	0.139	10	0.117	R.FDEIVK.E
R5/RRR5-8/2	751.020	750.862	209.879	0.409	851.358	0.145	10	0.115	-.FDEIVK.-
R5/RRR5-11/2	1736.956	1736.813	82.218	0.542	2000.495	0.542	21	0.278	K.GQEDLCESFFAYNR.A
R5/RRR5-11/2	1737.612	1736.813	-116.024	0.570	1608.980	0.566	20	0.228	K.GQEDLCESFFAYNR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1049.616	1050.190	-1504.376	0.437	803.771	0.449	14	0.140	K.LAESGAFNLK.N
R5/RRR5-11/2	1664.293	1663.850	266.782	0.444	1111.193	0.355	21	0.140	K.AFGASEVIAVDVLDEK.L
R5/RRR5-11/2	1050.159	1050.190	-29.918	0.353	850.821	0.435	14	0.138	K.LAESGAFNLK.N
R5/RRR5-10/3	1855.253	1856.027	-959.113	0.480	882.928	0.584	32	0.126	R.TLGATHTVNAAKEDAVEK.I
R5/RRR5-11/3	1856.203	1856.027	94.936	0.487	819.174	0.558	33	0.117	R.TLGATHTVNAAKEDAVEK.I
R5/RRR5-11/3	1855.536	1856.027	-265.701	0.480	840.776	0.534	32	0.114	R.TLGATHTVNAAKEDAVEK.I
R5/RRR5-10/3	1855.297	1856.027	-935.630	0.454	751.469	0.544	30	0.110	R.TLGATHTVNAAKEDAVEK.I
R5/RRR5-10/3	1855.344	1856.027	-910.166	0.501	669.603	0.556	30	0.109	R.TLGATHTVNAAKEDAVEK.I
R5/RRR5-11/3	1855.427	1856.027	-864.890	0.426	811.922	0.488	32	0.103	R.TLGATHTVNAAKEDAVEK.I
R5/RRR5-25/3	1365.599	1365.565	24.726	0.608	3369.201	0.468	33	0.659	R.HHVIGQYVVGQK.G
R5/RRR5-25/3	1365.287	1365.565	-204.486	0.510	2465.452	0.434	29	0.343	R.HHVIGQYVVGQK.G
R5/RRR5-26/3	1365.339	1365.565	-166.277	0.537	1929.951	0.390	27	0.204	R.HHVIGQYVVGQK.G
R5/RRR5-25/2	1270.029	1270.374	-272.112	0.413	643.279	0.587	19	0.152	K.VPPNSASLEEAR.H
R5/RRR5-25/2	1269.632	1270.374	-1376.568	0.400	651.482	0.573	18	0.149	K.VPPNSASLEEAR.H
R5/RRR5-26/2	1270.139	1270.374	-185.525	0.435	589.771	0.579	17	0.149	K.VPPNSASLEEAR.H
R5/RRR5-25/2	1269.813	1270.374	-1232.703	0.436	726.953	0.503	19	0.147	K.VPPNSASLEEAR.H
R5/RRR5-25/2	1270.143	1270.374	-182.825	0.374	684.573	0.545	18	0.146	K.VPPNSASLEEAR.H
R5/RRR5-25/2	1270.087	1270.374	-226.792	0.408	598.122	0.540	18	0.145	K.VPPNSASLEEAR.H
R5/RRR5-25/2	1269.854	1270.374	-1200.460	0.357	578.202	0.525	17	0.140	K.VPPNSASLEEAR.H
R5/RRR5-26/2	1269.682	1270.374	-1336.301	0.319	533.673	0.499	16	0.134	K.VPPNSASLEEAR.H
R5/RRR5-26/2	1269.970	1270.374	-318.980	0.331	519.495	0.470	17	0.133	K.VPPNSASLEEAR.H
R5/RRR5-25/3	1649.532	1649.881	-212.263	0.474	902.503	0.457	24	0.102	K.QRHHVIGQYVVGQK.G
R5/RRR5-25/3	1650.170	1649.881	175.569	0.461	945.336	0.379	24	0.091	K.QRHHVIGQYVVGQK.G
R5/RRR5-25/3	1649.755	1649.881	-76.866	0.451	758.673	0.406	22	0.087	K.QRHHVIGQYVVGQK.G
R5/RRR5-25/3	1365.577	1365.565	8.857	0.343	1075.421	0.155	23	0.064	R.HHVIGQYVVGQK.G
R5/RRR5-10/2	1599.475	1598.730	-160.108	0.483	2072.647	0.515	21	0.281	R.SSICYIDGDEGILR.Y
R5/RRR5-10/2	1118.206	1118.311	-93.684	0.507	1982.541	0.531	19	0.273	K.APTIAAAAYLR.L
R5/RRR5-10/2	1598.597	1598.730	-83.147	0.444	2002.140	0.420	21	0.245	R.SSICYIDGDEGILR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1479.219	1479.662	-300.427	0.452	1770.557	0.535	21	0.242	K.IYDPGYLNTAPVR.S
R5/RRR5-10/2	1118.163	1118.311	-132.121	0.485	1791.942	0.518	18	0.241	K.APTIAAAAYLR.L
R5/RRR5-10/2	1479.325	1479.662	-228.400	0.480	1745.919	0.514	21	0.234	K.IYDPGYLNTAPVR.S
R5/RRR5-10/2	1118.155	1118.311	-139.568	0.474	1750.796	0.506	18	0.233	K.APTIAAAAYLR.L
R5/RRR5-10/2	1479.292	1479.662	-250.586	0.448	1525.465	0.486	20	0.201	K.IYDPGYLNTAPVR.S
R5/RRR5-9/2	1598.111	1598.730	-1016.245	0.352	1422.217	0.326	19	0.159	R.SSICYIDGDEGILR.Y
R5/RRR5-10/2	915.171	915.029	155.778	0.462	967.464	0.442	15	0.149	R.GGALAVVDGR.T
R5/RRR5-10/2	915.029	915.029	-0.349	0.445	969.807	0.426	15	0.147	R.GGALAVVDGR.T
R5/RRR5-10/2	915.104	915.029	82.202	0.449	797.461	0.457	14	0.142	R.GGALAVVDGR.T
R5/RRR5-9/2	915.345	915.029	345.955	0.273	651.621	0.303	14	0.122	R.GGALAVVDGR.T
R5/RRR5-9/2	1118.027	1118.311	-254.352	0.261	781.499	0.205	14	0.116	K.APTIAAAAYLR.L
R5/RRR5-15/2	1318.200	1318.538	-257.617	0.334	645.661	0.412	13	0.126	K.LGLDVASCLITR.A
R5/RRR5-16/2	1317.404	1318.538	-1624.794	0.284	465.565	0.333	13	0.119	K.LGLDVASCLITR.A
R5/RRR5-15/2	1317.659	1318.538	-1430.742	0.336	429.488	0.336	12	0.116	-.LGLDVASCLITR.-
R5/RRR5-16/3	1260.274	1260.384	-87.311	0.398	627.783	0.510	20	0.098	K.ATVSHNSQLFR.F
R5/RRR5-15/3	1460.484	1460.702	-149.283	0.412	546.450	0.472	24	0.091	K.VALNPDKWLEFK.L
R5/RRR5-15/3	1460.427	1460.702	-188.650	0.360	505.715	0.441	23	0.085	K.VALNPDKWLEFK.L
R5/RRR5-15/3	1460.596	1460.702	-72.444	0.361	332.734	0.475	20	0.085	-.VALNPDKWLEFK.-
R5/RRR5-16/3	1260.585	1260.384	159.946	0.332	927.407	0.343	22	0.082	K.ATVSHNSQLFR.F
R5/RRR5-16/3	1260.700	1260.384	251.562	0.295	502.197	0.343	19	0.080	K.ATVSHNSQLFR.F
R5/RRR5-15/3	1260.176	1260.384	-166.016	0.364	670.291	0.337	21	0.080	K.ATVSHNSQLFR.F
R5/RRR5-15/3	1260.482	1260.384	78.221	0.367	712.786	0.327	21	0.074	-.ATVSHNSQLFR.-
R5/RRR5-15/3	1260.995	1260.384	-309.561	0.327	896.003	0.274	23	0.073	K.ATVSHNSQLFR.F
R5/RRR5-15/3	1317.044	1317.474	-327.018	0.403	1004.877	0.208	22	0.067	-.DRSQGELTGILK.-
R5/RRR5-14/2	1824.955	1826.237	-1254.410	0.313	1814.804	0.385	23	0.209	K.VAILGASGGIGQPLALLM*K.M
R5/RRR5-13/2	1185.644	1186.427	-1507.537	0.417	1324.922	0.443	19	0.174	R.LLGVTTLDVVR.A
R5/RRR5-13/2	1185.506	1186.427	-1624.934	0.460	1192.233	0.472	17	0.168	R.LLGVTTLDVVR.A
R5/RRR5-13/2	1503.275	1502.697	-281.692	0.436	1202.164	0.451	19	0.163	R.ANTFVAEVLGLDPR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/3	1826.285	1826.237	26.516	0.422	1471.466	0.456	31	0.158	K.VAILGASGGIGQPLALLM*K.M
R5/RRR5-13/2	1809.568	1810.238	-925.504	0.391	1094.679	0.427	20	0.148	K.VAILGASGGIGQPLALLMK.M
R5/RRR5-13/2	1244.934	1245.365	-346.441	0.494	812.233	0.460	19	0.146	R.IQNGGTEVVEAK.A
R5/RRR5-14/2	1245.026	1245.365	-272.660	0.461	765.519	0.439	18	0.140	R.IQNGGTEVVEAK.A
R5/RRR5-14/2	1245.994	1245.365	-297.898	0.478	633.003	0.442	17	0.136	R.IQNGGTEVVEAK.A
R5/RRR5-14/2	1185.520	1186.427	-1613.038	0.400	744.849	0.425	14	0.135	R.LLGVTTLDVVR.A
R5/RRR5-14/2	1245.965	1245.365	-321.391	0.434	540.623	0.409	16	0.130	R.IQNGGTEVVEAK.A
R5/RRR5-13/2	1186.130	1186.427	-250.690	0.328	781.594	0.273	15	0.122	R.LLGVTTLDVVR.A
R5/RRR5-14/2	1825.166	1826.237	-1138.078	0.321	610.983	0.366	18	0.120	K.VAILGASGGIGQPLALLM*K.M
R5/RRR5-13/2	1502.245	1502.697	-301.772	0.256	773.020	0.234	14	0.116	-.ANTFVAEVLGLDPR.-
R5/RRR5-14/2	1502.251	1502.697	-297.940	0.290	540.869	0.269	13	0.115	-.ANTFVAEVLGLDPR.-
R5/RRR5-14/2	1502.244	1502.697	-302.424	0.260	601.140	0.245	13	0.114	R.ANTFVAEVLGLDPR.D
R5/RRR5-1/2	1555.382	1555.758	-242.657	0.472	1409.125	0.450	21	0.181	K.LLDVLNTPSEAVQR.A
R5/RRR5-1/2	1555.428	1555.758	-213.131	0.471	1369.792	0.461	21	0.180	K.LLDVLNTPSEAVQR.A
R5/RRR5-2/2	1555.355	1555.758	-259.979	0.480	1216.869	0.480	21	0.171	K.LLDVLNTPSEAVQR.A
R5/RRR5-2/2	1696.977	1696.970	4.213	0.508	1227.212	0.449	23	0.165	K.SAGLQAIDEIVPTLLR.A
R5/RRR5-2/2	1696.528	1696.970	-260.790	0.462	1172.897	0.404	23	0.154	K.SAGLQAIDEIVPTLLR.A
R5/RRR5-2/2	1555.520	1555.758	-153.220	0.493	1034.726	0.447	20	0.153	K.LLDVLNTPSEAVQR.A
R5/RRR5-5/2	1458.131	1458.725	-1096.675	0.409	1368.299	0.310	16	0.151	K.VTSLLDQLIQLSK.T
R5/RRR5-2/2	1555.362	1555.758	-255.491	0.444	1029.156	0.445	18	0.150	K.LLDVLNTPSEAVQR.A
R5/RRR5-2/2	876.852	877.066	-244.022	0.405	579.254	0.517	12	0.139	K.YGIAAILR.Q
R5/RRR5-1/2	1458.437	1458.725	-198.594	0.434	1136.426	0.325	16	0.138	K.VTSLLDQLIQLSK.T
R5/RRR5-2/2	1458.582	1458.725	-98.683	0.394	1080.824	0.341	16	0.138	K.VTSLLDQLIQLSK.T
R5/RRR5-1/2	1458.824	1458.725	68.099	0.450	882.606	0.402	16	0.137	K.VTSLLDQLIQLSK.T
R5/RRR5-1/2	1554.523	1555.758	-1442.092	0.320	932.091	0.382	18	0.136	K.LLDVLNTPSEAVQR.A
R5/RRR5-1/2	1639.572	1639.852	-171.053	0.475	904.996	0.329	17	0.124	K.SSDPDTLLSMFNAIK.A
R5/RRR5-1/2	1458.360	1458.725	-250.992	0.343	597.955	0.257	13	0.116	K.VTSLLDQLIQLSK.T
R5/RRR5-5/2	1457.406	1458.725	-1596.071	0.265	804.642	0.179	14	0.114	K.VTSLLDQLIQLSK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1495.190	1495.616	-285.917	0.471	1173.723	0.435	19	0.159	K.VSTILNDEFQNSK.E
R5/RRR5-4/2	1496.071	1495.616	305.127	0.432	812.763	0.386	17	0.132	K.VSTILNDEFQNSK.E
R5/RRR5-11/3	1505.815	1504.756	39.295	0.528	3111.322	0.429	31	0.529	K.KVSPQLIAEYTVR.A
R5/RRR5-12/3	1505.629	1504.756	-84.631	0.620	2920.450	0.455	29	0.477	K.KVSPQLIAEYTVR.A
R5/RRR5-10/3	1504.689	1504.756	-44.487	0.517	2753.236	0.422	28	0.411	K.KVSPQLIAEYTVR.A
R5/RRR5-12/3	1504.996	1504.756	160.045	0.597	2719.131	0.438	31	0.402	K.KVSPQLIAEYTVR.A
R5/RRR5-12/3	1504.240	1504.756	-1010.528	0.580	2450.596	0.434	29	0.328	K.KVSPQLIAEYTVR.A
R5/RRR5-11/2	1504.493	1504.756	-175.181	0.527	1857.319	0.477	21	0.239	K.KVSPQLIAEYTVR.A
R5/RRR5-1/3	1504.620	1504.756	-90.872	0.494	2165.049	0.371	27	0.236	K.KVSPQLIAEYTVR.A
R5/RRR5-11/2	1503.751	1504.756	-1337.141	0.495	1792.210	0.475	21	0.230	K.KVSPQLIAEYTVR.A
R5/RRR5-11/3	1504.493	1504.756	-175.230	0.550	2004.394	0.427	30	0.223	K.KVSPQLIAEYTVR.A
R5/RRR5-2/3	1504.517	1504.756	-159.237	0.496	2046.773	0.398	28	0.223	K.KVSPQLIAEYTVR.A
R5/RRR5-12/2	1504.355	1504.756	-267.002	0.506	1729.861	0.473	20	0.221	K.KVSPQLIAEYTVR.A
R5/RRR5-12/2	1504.259	1504.756	-331.320	0.542	1512.460	0.535	20	0.210	K.KVSPQLIAEYTVR.A
R5/RRR5-12/2	1503.901	1504.756	-1237.359	0.493	1631.744	0.469	20	0.208	K.KVSPQLIAEYTVR.A
R5/RRR5-11/2	1504.283	1504.756	-315.525	0.522	1503.288	0.484	20	0.198	K.KVSPQLIAEYTVR.A
R5/RRR5-11/3	1504.523	1504.756	-155.330	0.456	1848.195	0.400	27	0.189	K.KVSPQLIAEYTVR.A
R5/RRR5-1/2	1504.319	1504.756	-291.507	0.474	1399.925	0.442	19	0.179	K.KVSPQLIAEYTVR.A
R5/RRR5-11/2	1296.216	1296.501	-221.087	0.432	1175.422	0.507	18	0.172	K.KPWALSFSFGR.A
R5/RRR5-11/3	1296.739	1296.501	184.049	0.576	1603.480	0.421	24	0.161	K.KPWALSFSFGR.A
R5/RRR5-11/2	1505.536	1504.756	-146.759	0.508	1098.725	0.460	18	0.158	K.KVSPQLIAEYTVR.A
R5/RRR5-12/2	1377.216	1376.583	-266.847	0.476	677.845	0.560	18	0.152	K.VSPQLIAEYTVR.A
R5/RRR5-11/3	1296.704	1296.501	156.860	0.568	1447.835	0.447	24	0.148	K.KPWALSFSFGR.A
R5/RRR5-12/2	1376.993	1376.583	298.703	0.408	664.976	0.533	18	0.146	K.VSPQLIAEYTVR.A
R5/RRR5-11/2	1376.168	1376.583	-302.461	0.428	628.219	0.540	17	0.146	K.VSPQLIAEYTVR.A
R5/RRR5-12/3	1296.285	1296.501	-167.248	0.556	1412.038	0.452	24	0.145	K.KPWALSFSFGR.A
R5/RRR5-1/3	1504.994	1504.756	158.703	0.401	1808.819	0.282	26	0.145	K.KVSPQLIAEYTVR.A
R5/RRR5-11/2	1376.017	1376.583	-1141.565	0.399	701.867	0.486	18	0.142	K.VSPQLIAEYTVR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/3	1504.051	1504.756	-1137.158	0.452	1617.283	0.358	24	0.142	K.KVSPQLIAEYTVR.A
R5/RRR5-12/2	1297.041	1296.501	-355.556	0.467	699.174	0.447	18	0.141	K.KPWALSFSFGR.A
R5/RRR5-12/3	1296.055	1296.501	-345.540	0.542	1461.868	0.414	22	0.141	K.KPWALSFSFGR.A
R5/RRR5-12/2	1376.168	1376.583	-302.461	0.410	657.178	0.483	18	0.141	K.VSPQLIAEYTVR.A
R5/RRR5-13/2	1375.744	1376.583	-1340.966	0.345	772.669	0.449	15	0.137	K.VSPQLIAEYTVR.A
R5/RRR5-11/2	1297.352	1296.501	-115.383	0.416	599.515	0.407	17	0.134	K.KPWALSFSFGR.A
R5/RRR5-12/2	1297.334	1296.501	-129.069	0.420	494.013	0.408	16	0.132	K.KPWALSFSFGR.A
R5/RRR5-11/2	1295.453	1296.501	-1586.167	0.296	646.974	0.427	16	0.131	K.KPWALSFSFGR.A
R5/RRR5-12/2	1296.198	1296.501	-234.692	0.320	622.726	0.369	17	0.128	K.KPWALSFSFGR.A
R5/RRR5-8/3	1505.296	1504.756	-306.700	0.487	1382.848	0.403	25	0.127	K.KVSPQLIAEYTVR.A
R5/RRR5-4/2	1295.754	1296.501	-1352.312	0.309	241.735	0.266	12	0.125	K.KPWALSFSFGR.A
R5/RRR5-10/3	1504.655	1504.756	-67.312	0.456	1292.871	0.427	26	0.124	K.KVSPQLIAEYTVR.A
R5/RRR5-13/2	1376.001	1376.583	-1153.146	0.312	535.373	0.373	13	0.124	K.VSPQLIAEYTVR.A
R5/RRR5-2/2	1377.139	1376.583	-323.140	0.353	279.755	0.331	12	0.122	-.VSPQLIAEYTVR.-
R5/RRR5-1/2	1376.217	1376.583	-266.418	0.268	370.809	0.341	12	0.121	K.VSPQLIAEYTVR.A
R5/RRR5-10/2	1376.430	1376.583	-111.334	0.217	291.707	0.329	12	0.121	K.VSPQLIAEYTVR.A
R5/RRR5-10/2	1376.141	1376.583	-322.129	0.170	336.370	0.378	12	0.118	K.VSPQLIAEYTVR.A
R5/RRR5-2/3	1504.035	1504.756	-1147.426	0.371	1212.276	0.305	27	0.091	K.KVSPQLIAEYTVR.A
R5/RRR5-11/3	1504.911	1504.756	103.307	0.365	807.436	0.408	27	0.090	K.KVSPQLIAEYTVR.A
R5/RRR5-11/3	1296.419	1296.501	-63.958	0.440	1081.845	0.330	21	0.090	K.KPWALSFSFGR.A
R5/RRR5-1/3	1504.354	1504.756	-267.663	0.403	1434.852	0.223	26	0.089	K.KVSPQLIAEYTVR.A
R5/RRR5-8/2	1420.575	1420.639	-44.957	0.464	1871.116	0.466	20	0.238	R.AYAQSVATLNLLR.A
R5/RRR5-8/2	1421.295	1420.639	-242.980	0.526	1767.839	0.480	21	0.229	R.AYAQSVATLNLLR.A
R5/RRR5-8/2	1419.978	1420.639	-1172.874	0.404	1757.877	0.452	20	0.219	R.AYAQSVATLNLLR.A
R5/RRR5-8/2	1259.953	1260.404	-359.262	0.503	1534.308	0.493	19	0.204	R.AFATGGYAAM*QR.V
R5/RRR5-8/2	1260.062	1260.404	-272.850	0.512	1474.768	0.512	19	0.202	R.AFATGGYAAM*QR.V
R5/RRR5-8/2	1404.373	1404.596	-159.510	0.496	849.053	0.408	16	0.137	K.TRPFDSILAEVR.A
R5/RRR5-8/2	1404.369	1404.596	-162.562	0.449	716.474	0.350	15	0.125	-.TRPFDSILAEVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1404.254	1404.596	-244.446	0.398	608.062	0.371	14	0.124	-.TRPFDSILAEVR.-
R5/RRR5-8/3	975.905	976.244	-348.303	0.400	816.132	0.366	16	0.083	R.VKLPHLIR.A
R5/RRR5-8/3	976.405	976.244	165.745	0.441	807.481	0.297	16	0.078	R.VKLPHLIR.A
R5/RRR5-8/3	976.534	976.244	298.405	0.386	1007.820	0.276	17	0.077	R.VKLPHLIR.A
R5/RRR5-8/3	1404.580	1404.596	-11.482	0.430	1201.209	0.127	21	0.058	-.TRPFDSILAEVR.-
R5/RRR5-8/3	1404.375	1404.596	-158.211	0.331	778.837	0.067	20	0.045	-.TRPFDSILAEVR.-
R5/RRR5-6/2	1163.047	1163.348	-259.560	0.482	1667.324	0.509	17	0.224	R.VLETEVAVFR.A
R5/RRR5-6/2	1352.259	1352.479	-162.488	0.508	1489.322	0.561	16	0.213	R.VAEDGWWSVFR.V
R5/RRR5-5/2	1353.260	1352.479	-162.096	0.447	1549.972	0.433	17	0.192	R.VAEDGWWSVFR.V
R5/RRR5-6/2	1352.344	1352.479	-100.098	0.421	1425.488	0.493	16	0.191	R.VAEDGWWSVFR.V
R5/RRR5-6/2	1586.118	1586.683	-989.115	0.427	1412.080	0.427	22	0.177	R.VDVSPETLEPTGGER.R
R5/RRR5-5/2	1353.134	1352.479	-255.491	0.445	1198.984	0.494	15	0.170	R.VAEDGWWSVFR.V
R5/RRR5-6/2	1163.070	1163.348	-240.080	0.499	1466.788	0.349	17	0.169	R.VLETEVAVFR.A
R5/RRR5-6/2	1586.271	1586.683	-260.315	0.432	1184.027	0.444	20	0.160	R.VDVSPETLEPTGGER.R
R5/RRR5-6/2	856.536	857.033	-581.511	0.336	588.969	0.471	11	0.133	K.TPGVTILR.S
R5/RRR5-6/2	856.534	857.033	-583.656	0.332	652.833	0.422	12	0.132	K.TPGVTILR.S
R5/RRR5-6/2	856.265	857.033	-2070.640	0.233	523.796	0.385	11	0.121	K.TPGVTILR.S
R5/RRR5-10/2	1372.903	1373.494	-1162.883	0.444	1630.868	0.455	21	0.206	R.VLQDPSSSAEALR.T
R5/RRR5-10/2	1791.547	1792.023	-266.504	0.499	1411.598	0.568	25	0.205	K.TEAIFPATLETISNVGK.V
R5/RRR5-10/2	1374.052	1373.494	-322.975	0.491	1354.460	0.493	21	0.186	R.VLQDPSSSAEALR.T
R5/RRR5-10/2	1492.555	1491.706	-101.277	0.531	1242.126	0.548	20	0.186	K.ELAITNLTNCLTK.E
R5/RRR5-10/2	1445.595	1446.665	-1436.077	0.396	833.887	0.545	19	0.152	K.IPGTSELQISLCK.E
R5/RRR5-10/2	1445.636	1446.665	-1407.749	0.398	802.938	0.455	19	0.140	K.IPGTSELQISLCK.E
R5/RRR5-7/2	1612.421	1612.810	-241.666	0.470	1300.214	0.486	20	0.179	K.VLEPLFSYWNSTR.Q
R5/RRR5-7/2	1612.594	1612.810	-134.358	0.432	1111.120	0.507	19	0.166	K.VLEPLFSYWNSTR.Q
R5/RRR5-6/3	1338.442	1338.538	-71.784	0.587	1249.002	0.502	23	0.142	K.VGIKDHESVVVR.I
R5/RRR5-6/2	1612.372	1612.810	-272.200	0.410	844.812	0.429	17	0.139	K.VLEPLFSYWNSTR.Q
R5/RRR5-7/2	1171.997	1171.374	-322.662	0.431	493.869	0.517	14	0.137	R.NVLAPAAPYVR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1612.353	1612.810	-284.277	0.439	947.244	0.366	17	0.136	K.VLEPLFSYWNSTR.Q
R5/RRR5-6/3	1338.486	1338.538	-38.988	0.558	1089.711	0.509	24	0.127	K.VGIKDHESVVVR.I
R5/RRR5-6/2	1611.854	1612.810	-1216.774	0.299	917.459	0.237	17	0.122	K.VLEPLFSYWNSTR.Q
R5/RRR5-7/2	1170.513	1171.374	-1594.179	0.283	473.820	0.348	13	0.120	R.NVLAPAAPYVR.K
R5/RRR5-7/3	1245.620	1244.385	189.488	0.519	938.705	0.520	21	0.117	R.THRVETTFPR.L
R5/RRR5-7/3	1338.364	1338.538	-130.108	0.551	1131.542	0.445	25	0.117	K.VGIKDHESVVVR.I
R5/RRR5-6/3	1244.971	1244.385	-333.067	0.552	1006.717	0.479	21	0.114	R.THRVETTFPR.L
R5/RRR5-6/3	1244.783	1244.385	320.828	0.485	1035.733	0.461	22	0.111	R.THRVETTFPR.L
R5/RRR5-6/3	1244.621	1244.385	190.723	0.562	910.207	0.476	20	0.108	R.THRVETTFPR.L
R5/RRR5-6/3	1338.699	1338.538	120.981	0.584	865.047	0.488	22	0.108	K.VGIKDHESVVVR.I
R5/RRR5-7/3	1244.483	1244.385	79.177	0.502	772.389	0.363	21	0.087	R.THRVETTFPR.L
R5/RRR5-4/2	1519.923	1520.624	-1122.575	0.498	2762.812	0.520	24	0.415	R.VEQGSLTGETASVNK.T
R5/RRR5-4/2	1520.705	1520.624	53.170	0.529	2368.806	0.551	23	0.344	R.VEQGSLTGETASVNK.T
R5/RRR5-1/2	1519.718	1520.624	-1258.238	0.407	2263.244	0.382	23	0.274	R.VEQGSLTGETASVNK.T
R5/RRR5-3/2	1979.063	1978.232	-85.784	0.532	1999.439	0.474	23	0.255	R.SGYIQLLDGSVVLLDEGAK.A
R5/RRR5-4/2	1519.400	1520.624	-1468.175	0.371	1982.916	0.418	22	0.241	R.VEQGSLTGETASVNK.T
R5/RRR5-3/2	1520.190	1520.624	-286.531	0.505	1564.131	0.464	21	0.199	R.VEQGSLTGETASVNK.T
R5/RRR5-2/2	1979.441	1978.232	105.671	0.434	913.903	0.426	21	0.139	R.SGYIQLLDGSVVLLDEGAK.A
R5/RRR5-1/2	895.987	896.028	-45.724	0.346	811.636	0.427	12	0.137	R.HAAPSVWK.L
R5/RRR5-4/2	1000.985	1001.119	-134.561	0.427	1182.044	0.213	14	0.129	K.GAVENLLER.S
R5/RRR5-1/2	896.031	896.028	3.469	0.310	521.837	0.354	11	0.123	R.HAAPSVWK.L
R5/RRR5-4/2	1001.009	1001.119	-109.851	0.418	982.890	0.191	13	0.119	-.GAVENLLER.-
R5/RRR5-4/2	1978.551	1978.232	161.722	0.383	597.306	0.323	18	0.118	R.SGYIQLLDGSVVLLDEGAK.A
R5/RRR5-2/2	1979.933	1978.232	-151.790	0.365	207.881	0.324	16	0.116	-.SGYIQLLDGSVVLLDEGAK.-
R5/RRR5-1/2	1001.167	1001.119	47.681	0.445	820.498	0.185	12	0.114	-.GAVENLLER.-
R5/RRR5-1/2	1000.636	1001.119	-484.064	0.265	641.222	0.121	12	0.112	-.GAVENLLER.-
R5/RRR5-6/2	1505.340	1505.742	-267.885	0.503	1990.866	0.457	21	0.252	K.IAGIQGGFFELQPK.E
R5/RRR5-2/2	1506.411	1505.742	-220.473	0.553	1698.666	0.549	20	0.235	K.IAGIQGGFFELQPK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1335.270	1335.534	-198.482	0.497	1401.804	0.446	20	0.182	R.INTLLQGYSGIR.F
R5/RRR5-6/2	1335.139	1335.534	-296.808	0.488	1194.937	0.445	19	0.164	R.INTLLQGYSGIR.F
R5/RRR5-1/2	1505.586	1505.742	-103.897	0.440	1207.252	0.456	18	0.164	K.IAGIQGGFFELQPK.E
R5/RRR5-6/2	1334.426	1335.534	-1584.341	0.420	1020.480	0.451	18	0.152	R.INTLLQGYSGIR.F
R5/RRR5-2/2	1335.289	1335.534	-183.717	0.458	920.881	0.457	18	0.149	R.INTLLQGYSGIR.F
R5/RRR5-2/2	1685.605	1685.817	-126.577	0.420	923.145	0.437	19	0.141	R.EINSVNDNPLIDVSR.G
R5/RRR5-7/2	1507.186	1505.742	295.240	0.403	592.965	0.492	18	0.137	K.IAGIQGGFFELQPK.E
R5/RRR5-2/2	1335.235	1335.534	-224.346	0.503	896.631	0.373	17	0.136	R.INTLLQGYSGIR.F
R5/RRR5-6/2	1505.228	1505.742	-1009.164	0.423	639.783	0.391	18	0.130	K.IAGIQGGFFELQPK.E
R5/RRR5-7/2	1506.911	1505.742	111.994	0.397	523.293	0.383	18	0.128	K.IAGIQGGFFELQPK.E
R5/RRR5-1/2	1505.479	1505.742	-175.717	0.303	724.077	0.296	14	0.119	K.IAGIQGGFFELQPK.E
R5/RRR5-6/2	1642.377	1642.792	-253.510	0.539	1814.495	0.586	24	0.261	K.LAGLSAGGGEEPQQLSK.N
R5/RRR5-6/2	1642.426	1642.792	-223.833	0.532	1781.743	0.543	23	0.244	K.LAGLSAGGGEEPQQLSK.N
R5/RRR5-6/2	1643.269	1642.792	291.057	0.559	1619.931	0.577	22	0.231	K.LAGLSAGGGEEPQQLSK.N
R5/RRR5-6/2	1497.449	1497.717	-179.357	0.453	1414.728	0.400	21	0.173	K.FLANITVADYIEK.Y
R5/RRR5-6/2	1376.178	1375.550	-271.052	0.489	1217.825	0.482	19	0.172	K.LLFYDLYGGGEK.V
R5/RRR5-6/2	1375.034	1375.550	-1105.873	0.404	1109.607	0.395	17	0.149	K.LLFYDLYGGGEK.V
R5/RRR5-2/2	1375.122	1375.550	-312.574	0.379	1009.547	0.331	16	0.134	K.LLFYDLYGGGEK.V
R5/RRR5-6/2	1324.793	1325.403	-1219.438	0.382	1098.339	0.268	15	0.130	R.TSELEDNEFIK.F
R5/RRR5-6/2	1324.820	1325.403	-1198.711	0.332	501.756	0.256	13	0.116	-.TSELEDNEFIK.-
R5/RRR5-6/2	1374.350	1375.550	-1605.577	0.216	643.137	0.275	13	0.116	K.LLFYDLYGGGEK.V
R5/RRR5-8/2	1355.219	1355.560	-252.387	0.525	1414.973	0.499	17	0.193	R.TFLDQLVEVYK.Q
R5/RRR5-1/2	1355.423	1355.560	-101.858	0.415	1319.757	0.506	16	0.183	R.TFLDQLVEVYK.Q
R5/RRR5-8/2	1355.132	1355.560	-317.456	0.478	1051.906	0.504	16	0.163	R.TFLDQLVEVYK.Q
R5/RRR5-8/3	1609.648	1609.854	-128.261	0.483	1488.345	0.413	27	0.147	R.KEHQFLAELGLAPR.N
R5/RRR5-8/2	1151.299	1150.349	-43.561	0.405	812.577	0.488	17	0.146	R.IPLVSFTGSTK.V
R5/RRR5-8/2	1425.255	1425.717	-325.632	0.390	850.435	0.391	16	0.134	R.EELFGPVLYVMK.V
R5/RRR5-8/2	1150.228	1150.349	-106.191	0.317	880.268	0.374	17	0.134	R.IPLVSFTGSTK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1150.523	1150.349	151.368	0.331	764.655	0.370	16	0.130	R.IPLVSFTGSTK.V
R5/RRR5-8/2	1354.862	1355.560	-1257.168	0.284	754.145	0.359	15	0.127	R.TFLDQLVEVYK.Q
R5/RRR5-8/2	1425.795	1425.717	54.562	0.299	570.876	0.400	13	0.122	R.EELFGPVLYVMK.V
R5/RRR5-24/3	1774.191	1774.911	-972.328	0.524	2642.524	0.456	34	0.411	R.HGTHAEFTTCLWTGR.V
R5/RRR5-24/3	1774.663	1774.911	-139.895	0.564	2593.632	0.451	33	0.394	R.HGTHAEFTTCLWTGR.V
R5/RRR5-24/3	1775.745	1774.911	-94.028	0.605	2345.472	0.451	32	0.324	R.HGTHAEFTTCLWTGR.V
R5/RRR5-24/2	1116.062	1116.296	-210.808	0.462	1320.457	0.499	17	0.184	R.KVTIQNLSGR.D
R5/RRR5-25/2	987.686	988.123	-444.607	0.452	1107.732	0.470	14	0.162	K.VTIQNLSGR.D
R5/RRR5-24/2	987.729	988.123	-400.583	0.406	1113.373	0.436	14	0.156	K.VTIQNLSGR.D
R5/RRR5-24/2	987.955	988.123	-171.470	0.420	1113.306	0.400	14	0.151	K.VTIQNLSGR.D
R5/RRR5-24/2	1116.895	1116.296	-360.505	0.490	900.841	0.457	16	0.150	R.KVTIQNLSGR.D
R5/RRR5-25/2	988.077	988.123	-47.287	0.380	1022.611	0.429	14	0.149	K.VTIQNLSGR.D
R5/RRR5-24/2	987.512	988.123	-1636.427	0.410	1092.969	0.390	14	0.149	K.VTIQNLSGR.D
R5/RRR5-25/2	1116.199	1116.296	-87.161	0.450	828.933	0.465	15	0.146	R.KVTIQNLSGR.D
R5/RRR5-25/2	1116.126	1116.296	-153.424	0.418	799.165	0.474	15	0.145	R.KVTIQNLSGR.D
R5/RRR5-24/2	1115.989	1116.296	-276.320	0.491	754.775	0.454	15	0.143	R.KVTIQNLSGR.D
R5/RRR5-23/2	1115.590	1116.296	-1534.379	0.302	483.112	0.320	12	0.122	R.KVTIQNLSGR.D
R5/RRR5-24/3	1116.088	1116.296	-187.394	0.368	1028.318	0.280	20	0.078	R.KVTIQNLSGR.D
R5/RRR5-25/3	1115.572	1116.296	-1550.494	0.347	732.307	0.332	18	0.078	R.KVTIQNLSGR.D
R5/RRR5-25/3	1115.765	1116.296	-1376.408	0.322	814.594	0.327	17	0.077	R.KVTIQNLSGR.D
R5/RRR5-24/3	1116.379	1116.296	73.895	0.392	944.459	0.257	19	0.074	R.KVTIQNLSGR.D
R5/RRR5-5/2	1612.661	1611.818	-98.138	0.493	935.650	0.619	19	0.171	R.VPEPTVDETIEILR.G
R5/RRR5-9/2	1531.254	1530.662	-267.429	0.439	1552.271	0.492	22	0.203	R.EVDAVISSGVTPAER.L
R5/RRR5-8/2	1259.424	1259.431	-6.087	0.460	1732.191	0.340	17	0.192	R.DLAEEILQLSK.N
R5/RRR5-9/2	1930.051	1931.267	-1151.229	0.506	1059.967	0.614	25	0.179	R.AGLALQPIATAIFANSPFK.E
R5/RRR5-9/2	1259.212	1259.431	-174.397	0.483	1580.163	0.315	17	0.171	R.DLAEEILQLSK.N
R5/RRR5-9/3	1930.540	1931.267	-897.166	0.478	1503.905	0.454	30	0.162	R.AGLALQPIATAIFANSPFK.E
R5/RRR5-9/2	1259.097	1259.431	-266.501	0.419	1523.921	0.256	17	0.156	R.DLAEEILQLSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1259.031	1259.431	-318.834	0.391	1403.050	0.299	15	0.154	R.DLAEEILQLSK.N
R5/RRR5-8/2	1286.621	1287.553	-1506.285	0.289	720.116	0.336	14	0.122	-.WALSDIPIM*PK.-
R5/RRR5-8/2	1286.700	1287.553	-1444.341	0.232	633.081	0.275	13	0.116	K.WALSDIPIM*PK.G
R5/RRR5-8/2	1258.419	1259.431	-1603.853	0.362	831.132	0.180	14	0.115	R.DLAEEILQLSK.N
R5/RRR5-5/2	1617.245	1616.883	224.500	0.495	2315.100	0.514	22	0.322	K.SQPDLAILAVNTFVK.D
R5/RRR5-3/2	1616.618	1616.883	-164.318	0.489	2212.219	0.533	21	0.309	K.SQPDLAILAVNTFVK.D
R5/RRR5-3/2	1617.911	1616.883	17.662	0.453	1504.491	0.568	19	0.213	K.SQPDLAILAVNTFVK.D
R5/RRR5-1/2	1616.866	1616.883	-10.496	0.308	1561.864	0.398	19	0.183	K.SQPDLAILAVNTFVK.D
R5/RRR5-3/2	1011.903	1012.140	-234.867	0.368	1173.693	0.228	13	0.132	K.YNDPIYVK.M
R5/RRR5-3/2	1011.970	1012.140	-168.671	0.405	866.235	0.265	12	0.125	-.YNDPIYVK.-
R5/RRR5-3/2	1011.786	1012.140	-351.064	0.416	797.452	0.245	12	0.121	-.YNDPIYVK.-
R5/RRR5-3/2	981.619	982.114	-506.352	0.248	783.186	0.311	13	0.121	R.TSFLEAWK.S
R5/RRR5-5/2	1011.682	1012.140	-454.091	0.311	896.021	0.095	12	0.113	K.YNDPIYVK.M
R5/RRR5-3/3	1179.237	1178.409	-146.782	0.513	1150.569	0.295	22	0.089	K.RPTILAHEIK.V
R5/RRR5-3/3	1178.438	1178.409	24.445	0.516	791.834	0.241	20	0.071	-.RPTILAHEIK.-
R5/RRR5-10/2	1208.005	1208.300	-244.528	0.356	1438.802	0.394	18	0.172	K.VDFGDIDGLEK.I
R5/RRR5-10/2	1740.347	1740.938	-917.008	0.457	1269.018	0.346	19	0.148	K.AFSDVLEHDLPQLQK.Q
R5/RRR5-10/3	1596.963	1596.813	93.749	0.468	1077.989	0.417	26	0.106	R.SAHNYHPIPVVFSK.G
R5/RRR5-10/3	1598.016	1596.813	127.322	0.434	654.388	0.467	23	0.092	R.SAHNYHPIPVVFSK.G
R5/RRR5-10/3	1596.896	1596.813	51.890	0.401	752.346	0.348	23	0.080	R.SAHNYHPIPVVFSK.G
R5/RRR5-10/3	1420.674	1421.670	-1408.879	0.339	813.998	0.374	24	0.078	R.GVLAKPTHDTIIR.L
R5/RRR5-5/2	1242.597	1241.459	111.873	0.522	1882.550	0.555	20	0.264	K.SPGLDDILVALK.T
R5/RRR5-5/2	1241.155	1241.459	-245.199	0.412	1515.006	0.445	19	0.191	K.SPGLDDILVALK.T
R5/RRR5-5/2	1240.733	1241.459	-1395.111	0.392	969.475	0.420	17	0.144	K.SPGLDDILVALK.T
R5/RRR5-5/2	1589.538	1589.774	-149.016	0.410	353.597	0.558	18	0.136	K.VIPIFNENDAISTR.K
R5/RRR5-5/2	1589.195	1589.774	-996.831	0.384	409.612	0.449	19	0.130	K.VIPIFNENDAISTR.K
R5/RRR5-5/2	1617.991	1618.808	-1126.120	0.302	894.664	0.183	17	0.113	R.EQLTETVESLLDLK.V
R5/RRR5-6/3	1532.489	1531.658	-110.870	0.421	870.273	0.366	24	0.082	R.RVDSAAVFHNASTR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/3	1955.836	1955.204	-188.629	0.501	1940.997	0.379	29	0.211	R.FKNPPDWQEILTYFR.G
R5/RRR5-6/2	1892.315	1891.160	82.585	0.407	560.469	0.466	16	0.126	R.EGINIFLAGFVPTENLR.F
R5/RRR5-6/3	1522.415	1522.816	-264.327	0.404	608.929	0.483	22	0.092	K.AIIKPQYVDHIPK.A
R5/RRR5-6/3	1143.685	1143.274	360.161	0.496	1142.431	0.285	21	0.086	R.FRDESLTFK.I
R5/RRR5-7/3	1143.845	1143.274	-376.428	0.457	899.149	0.354	21	0.085	R.FRDESLTFK.I
R5/RRR5-6/3	1522.750	1522.816	-43.436	0.331	447.198	0.425	22	0.083	K.AIIKPQYVDHIPK.A
R5/RRR5-6/3	1522.494	1522.816	-211.840	0.339	826.653	0.362	23	0.081	K.AIIKPQYVDHIPK.A
R5/RRR5-6/3	1143.723	1143.274	394.031	0.529	918.203	0.279	19	0.079	R.FRDESLTFK.I
R5/RRR5-8/2	1422.327	1422.565	-167.998	0.505	1527.893	0.506	23	0.207	R.YGTAGLLSPNTEAK.I
R5/RRR5-8/2	1421.634	1422.565	-1362.359	0.438	1321.040	0.451	21	0.173	R.YGTAGLLSPNTEAK.I
R5/RRR5-8/2	1367.360	1367.536	-129.354	0.490	781.655	0.656	20	0.167	R.HSGVVALIDAATGR.R
R5/RRR5-8/2	990.027	990.178	-152.622	0.421	943.394	0.401	14	0.141	K.VAFVTDIPK.N
R5/RRR5-8/2	1421.478	1422.565	-1472.845	0.354	863.884	0.375	18	0.132	R.YGTAGLLSPNTEAK.I
R5/RRR5-8/3	1562.496	1562.799	-194.192	0.381	914.187	0.408	30	0.092	R.AVAGAASALAAHPVSLR.K
R5/RRR5-8/3	1563.801	1562.799	1.588	0.385	694.519	0.455	29	0.090	R.AVAGAASALAAHPVSLR.K
R5/RRR5-8/3	1562.484	1562.799	-202.069	0.345	595.889	0.428	28	0.084	R.AVAGAASALAAHPVSLR.K
R5/RRR5-6/2	1108.373	1109.214	-1666.544	0.380	1388.024	0.262	16	0.147	R.IAEGYELASR.I
R5/RRR5-7/2	1368.788	1369.635	-1353.774	0.381	592.056	0.559	18	0.143	K.QQQILLATQVVK.M
R5/RRR5-7/2	1057.271	1057.226	42.545	0.384	950.379	0.409	14	0.141	K.AVLAVADLER.K
R5/RRR5-7/2	1370.334	1369.635	-220.387	0.417	611.420	0.489	19	0.140	K.QQQILLATQVVK.M
R5/RRR5-7/2	1057.084	1057.226	-134.427	0.322	966.233	0.373	14	0.136	K.AVLAVADLER.K
R5/RRR5-7/2	1368.585	1369.635	-1502.482	0.330	392.752	0.490	17	0.131	K.QQQILLATQVVK.M
R5/RRR5-7/2	977.410	978.081	-1714.659	0.329	1036.223	0.128	14	0.116	R.FQELSPEK.L
R5/RRR5-4/2	1388.353	1387.518	-119.108	0.581	1814.687	0.556	22	0.255	K.VVNADEDVGDLLK.V
R5/RRR5-4/2	1387.158	1387.518	-259.904	0.499	1700.153	0.481	21	0.220	K.VVNADEDVGDLLK.V
R5/RRR5-4/2	1387.013	1387.518	-1088.378	0.417	1385.485	0.428	18	0.174	K.VVNADEDVGDLLK.V
R5/RRR5-4/2	1313.237	1313.480	-185.590	0.459	1277.172	0.440	17	0.169	K.VVFLEDYNVSK.A
R5/RRR5-4/2	1791.722	1791.940	-121.951	0.398	745.692	0.503	19	0.139	R.AETISAVLYPNDNLDR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1313.183	1313.480	-227.181	0.335	781.513	0.264	15	0.120	K.VVFLEDYNVSK.A
R5/RRR5-4/3	1823.200	1823.984	-981.448	0.417	362.354	0.561	24	0.098	K.LVDEAYRDQEGWITK.T
R5/RRR5-4/3	1823.814	1823.984	-93.127	0.317	235.497	0.325	20	0.086	K.LVDEAYRDQEGWITK.T
R5/RRR5-4/3	1824.093	1823.984	60.227	0.356	209.437	0.354	19	0.072	-.LVDEAYRDQEGWITK.-
R5/RRR5-6/2	1520.785	1519.724	40.447	0.512	1736.169	0.441	18	0.213	K.SQFGIIILDDIER.L
R5/RRR5-6/2	1598.127	1596.809	199.912	0.533	1098.471	0.616	20	0.185	K.LGIGGLSAEFTDIFR.R
R5/RRR5-6/2	1519.071	1519.724	-1091.529	0.351	1546.987	0.305	18	0.166	K.SQFGIIILDDIER.L
R5/RRR5-6/2	1598.284	1596.809	298.330	0.495	1007.180	0.538	18	0.162	K.LGIGGLSAEFTDIFR.R
R5/RRR5-5/2	1520.970	1519.724	162.076	0.377	1328.335	0.371	17	0.159	K.SQFGIIILDDIER.L
R5/RRR5-5/2	1521.245	1519.724	-315.870	0.433	1039.478	0.487	16	0.156	K.SQFGIIILDDIER.L
R5/RRR5-6/2	1173.369	1173.386	-14.881	0.406	988.779	0.508	16	0.155	K.GILLYGPPGTGK.T
R5/RRR5-6/2	1598.299	1596.809	307.749	0.483	840.300	0.557	17	0.154	K.LGIGGLSAEFTDIFR.R
R5/RRR5-6/2	1876.196	1877.045	-988.435	0.363	314.552	0.538	17	0.128	K.ESSFLSPDVNLQELAAR.T
R5/RRR5-6/2	1173.552	1173.386	141.512	0.391	726.210	0.360	14	0.125	K.GILLYGPPGTGK.T
R5/RRR5-5/2	1597.656	1596.809	-95.764	0.344	340.143	0.479	13	0.124	K.LGIGGLSAEFTDIFR.R
R5/RRR5-6/2	1875.715	1877.045	-1246.001	0.295	114.978	0.422	12	0.119	K.ESSFLSPDVNLQELAAR.T
R5/RRR5-4/2	1729.464	1729.912	-259.788	0.459	1956.372	0.402	21	0.232	R.ISEAFSGSSLISDFIR.S
R5/RRR5-4/2	1299.283	1299.414	-100.699	0.431	1022.880	0.428	14	0.146	K.EAEISQFFATR.T
R5/RRR5-4/2	1228.131	1228.336	-167.346	0.380	1160.990	0.311	15	0.141	K.LNIDETGFYR.V
R5/RRR5-4/2	1227.738	1228.336	-1305.265	0.363	1096.040	0.295	14	0.135	K.LNIDETGFYR.V
R5/RRR5-4/2	1228.380	1228.336	36.519	0.330	1144.119	0.256	15	0.133	K.LNIDETGFYR.V
R5/RRR5-4/2	1429.177	1429.598	-295.011	0.321	711.226	0.365	17	0.123	K.ISIDATPDLAGDIK.Q
R5/RRR5-12/2	1229.211	1228.336	-101.958	0.304	660.209	0.231	12	0.117	K.LNIDETGFYR.V
R5/RRR5-4/2	1728.994	1729.912	-1112.314	0.272	1024.754	0.183	17	0.116	R.ISEAFSGSSLISDFIR.S
R5/RRR5-4/2	1298.426	1299.414	-1535.575	0.231	806.382	0.221	14	0.115	K.EAEISQFFATR.T
R5/RRR5-6/3	1507.016	1506.729	191.150	0.483	1003.811	0.567	27	0.132	R.GPAEASVDAVHLVLK.E
R5/RRR5-6/3	1506.892	1506.729	108.899	0.485	1031.346	0.530	28	0.126	R.GPAEASVDAVHLVLK.E
R5/RRR5-6/3	1506.391	1506.729	-224.996	0.435	511.470	0.531	21	0.096	R.GPAEASVDAVHLVLK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/3	1706.259	1705.809	264.804	0.433	574.728	0.517	27	0.095	K.TEGGQEYAEFLHAPR.K
R5/RRR5-6/3	1706.015	1705.809	121.235	0.388	612.217	0.526	28	0.094	K.TEGGQEYAEFLHAPR.K
R5/RRR5-6/3	1104.434	1104.374	54.851	0.543	864.967	0.371	19	0.090	R.RPLVLQLHK.T
R5/RRR5-6/3	1104.286	1104.374	-79.272	0.579	655.162	0.350	19	0.087	R.RPLVLQLHK.T
R5/RRR5-6/3	1104.825	1104.374	409.566	0.578	725.285	0.356	19	0.087	R.RPLVLQLHK.T
R5/RRR5-6/3	1320.515	1319.540	-18.750	0.541	1007.750	0.313	21	0.083	-.LQHPWVGIVNR.-
R5/RRR5-6/3	1320.029	1319.540	371.826	0.512	829.701	0.323	19	0.079	R.LQHPWVGIVNR.S
R5/RRR5-9/1	418.981	419.368	-927.667	-2.529	1.327	0.000	1	1.000	R.GGGDGG.-
R5/RRR5-18/1	418.966	419.368	-962.037	-1.999	1.067	0.000	1	0.619	R.GGGDGG.-
R5/RRR5-11/1	418.951	419.368	-999.041	-1.953	10.000	0.000	1	0.584	-.GGGDGG.-
R5/RRR5-15/1	418.959	419.368	-980.319	-1.777	1.131	0.000	1	0.491	R.GGGDGG.-
R5/RRR5-15/1	418.975	419.368	-940.976	-1.641	23.231	0.072	2	0.408	R.GGGDGG.-
R5/RRR5-15/1	418.984	419.368	-918.600	-1.299	10.000	0.000	1	0.271	-.GGGDGG.-
R5/RRR5-27/1	418.983	419.368	-921.525	-1.460	4.997	0.379	1	0.266	-.GGGDGG.-
R5/RRR5-2/1	419.080	419.368	-690.949	-0.734	22.801	0.933	2	0.225	-.GGGDGG.-
R5/RRR5-12/1	418.980	419.368	-929.715	-1.131	10.000	0.000	1	0.216	-.GGGDGG.-
R5/RRR5-6/2	1063.840	1064.257	-392.755	0.323	853.135	0.381	14	0.134	-.FEILEAITK.-
R5/RRR5-6/2	1064.149	1064.257	-100.974	0.469	786.838	0.377	14	0.129	-.FEILEAITK.-
R5/RRR5-6/2	1064.193	1064.257	-59.897	0.504	844.940	0.324	14	0.127	-.FEILEAITK.-
R5/RRR5-2/2	1064.973	1064.257	-267.253	0.413	847.511	0.298	14	0.125	-.FEILEAITK.-
R5/RRR5-1/2	1064.156	1064.257	-95.106	0.320	602.186	0.194	12	0.111	-.FEILEAITK.-
R5/RRR5-2/2	1064.104	1064.257	-144.241	0.158	569.915	0.188	12	0.107	-.FEILEAITK.-
R5/RRR5-5/2	1391.565	1390.615	-35.776	0.526	1313.048	0.572	18	0.196	K.LPFAAAQIGQAFR.N
R5/RRR5-6/2	976.829	977.144	-323.832	0.475	925.726	0.483	12	0.152	K.ANVLAFWR.Q
R5/RRR5-6/2	1606.407	1606.847	-274.201	0.390	1063.698	0.398	19	0.144	R.VFTPSVIEPSFGIGR.I
R5/RRR5-6/2	1116.093	1116.290	-176.795	0.426	1001.281	0.337	17	0.136	R.VGIDEVASVVK.Q
R5/RRR5-6/2	1606.319	1606.847	-953.962	0.389	645.923	0.474	16	0.133	R.VFTPSVIEPSFGIGR.I
R5/RRR5-6/2	1115.428	1116.290	-1674.334	0.288	791.629	0.341	17	0.126	R.VGIDEVASVVK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1606.299	1606.847	-966.475	0.285	508.803	0.247	14	0.114	R.VFTPSVIEPSFGIGR.I
R5/RRR5-5/2	1390.405	1390.615	-151.162	0.248	508.641	0.268	12	0.113	K.LPFAAAQIGQAFR.N
R5/RRR5-5/2	1458.465	1458.599	-92.395	0.499	1507.414	0.517	17	0.206	K.YNVESWLDYLR.S
R5/RRR5-5/2	1358.376	1358.520	-106.233	0.427	1548.628	0.343	17	0.173	K.VSLSENEPILEK.M
R5/RRR5-5/2	1458.159	1458.599	-303.086	0.489	1125.944	0.455	15	0.159	K.YNVESWLDYLR.S
R5/RRR5-5/3	1758.950	1758.869	46.517	0.434	1457.978	0.446	25	0.153	K.TSHVFYSQADGFSSPK.E
R5/RRR5-5/2	1249.384	1250.343	-1572.233	0.431	947.896	0.420	16	0.145	R.LQNDIQSFER.E
R5/RRR5-5/2	1250.057	1250.343	-229.055	0.523	842.574	0.425	15	0.141	R.LQNDIQSFER.E
R5/RRR5-5/2	1358.017	1358.520	-1109.814	0.380	1030.301	0.368	17	0.140	K.VSLSENEPILEK.M
R5/RRR5-5/2	1358.023	1358.520	-366.908	0.355	1362.927	0.215	18	0.139	K.VSLSENEPILEK.M
R5/RRR5-5/2	1250.092	1250.343	-201.527	0.368	723.653	0.306	14	0.124	R.LQNDIQSFER.E
R5/RRR5-2/2	1459.719	1458.599	82.316	0.327	312.374	0.316	12	0.117	-.YNVESWLDYLR.-
R5/RRR5-6/2	1188.964	1188.313	-294.578	0.527	1392.134	0.421	16	0.175	R.LTEEEANLLR.L
R5/RRR5-6/2	1188.118	1188.313	-164.429	0.513	1281.232	0.358	17	0.156	R.LTEEEANLLR.L
R5/RRR5-6/2	1368.885	1369.635	-1282.123	0.364	919.500	0.438	18	0.141	R.LFPLLASAYAFR.F
R5/RRR5-6/2	1129.041	1129.249	-184.636	0.399	624.798	0.467	17	0.138	R.QGALANEQLGK.L
R5/RRR5-6/2	1187.497	1188.313	-1533.435	0.420	965.102	0.313	16	0.133	R.LTEEEANLLR.L
R5/RRR5-18/2	1129.149	1129.249	-88.872	0.277	581.598	0.069	12	0.102	-.QGALANEQLGK.-
R5/RRR5-6/3	1894.052	1893.087	-18.599	0.469	965.462	0.408	26	0.093	R.SLEDHSPLPGVTLGDIGGK.F
R5/RRR5-18/2	1130.081	1129.249	-148.496	0.343	571.556	0.074	11	0.082	-.QGALANEQLGK.-
R5/RRR5-6/3	1894.207	1893.087	63.233	0.297	706.562	0.252	23	0.058	-.SLEDHSPLPGVTLGDIGGK.-
R5/RRR5-6/2	1187.132	1187.370	-200.457	0.438	1243.262	0.350	15	0.150	K.TVELKPDWAK.G
R5/RRR5-6/2	1312.313	1311.469	-119.292	0.493	652.371	0.452	16	0.138	R.QVLVDLQENPR.A
R5/RRR5-6/2	1312.488	1311.469	14.029	0.468	573.085	0.440	15	0.133	R.QVLVDLQENPR.A
R5/RRR5-6/3	1887.647	1886.098	-239.971	0.342	871.937	0.475	24	0.094	R.LGAAHLGLGDAASAVAAYEK.G
R5/RRR5-6/3	1659.514	1659.740	-136.396	0.412	979.564	0.313	23	0.078	K.ANRGDLTQEEIQER.Q
R5/RRR5-15/2	1817.419	1818.019	-882.971	0.575	3013.562	0.679	28	0.542	K.ALAVGADVSLDTATGNLTK.Y
R5/RRR5-15/2	1817.519	1818.019	-275.630	0.534	2655.269	0.659	27	0.444	K.ALAVGADVSLDTATGNLTK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1817.450	1818.019	-865.710	0.574	2598.833	0.692	27	0.443	K.ALAVGADVSLDTATGNLTK.Y
R5/RRR5-16/2	1591.353	1590.845	-310.494	0.649	1915.358	0.516	23	0.256	K.KADLIFGEIQSQIK.N
R5/RRR5-16/2	1461.759	1462.673	-1312.817	0.421	1922.495	0.424	19	0.234	K.ADLIFGEIQSQIK.N
R5/RRR5-15/2	1590.038	1590.845	-1139.950	0.600	1707.188	0.512	22	0.227	K.KADLIFGEIQSQIK.N
R5/RRR5-16/2	1590.362	1590.845	-304.683	0.588	1619.452	0.501	22	0.214	K.KADLIFGEIQSQIK.N
R5/RRR5-16/2	1590.423	1590.845	-266.333	0.596	1502.838	0.549	21	0.212	K.KADLIFGEIQSQIK.N
R5/RRR5-16/3	1590.850	1590.845	2.715	0.497	1950.372	0.377	28	0.212	K.KADLIFGEIQSQIK.N
R5/RRR5-15/2	1463.311	1462.673	-247.717	0.539	1624.139	0.471	19	0.207	K.ADLIFGEIQSQIK.N
R5/RRR5-15/2	1590.484	1590.845	-228.218	0.579	1554.387	0.497	22	0.206	K.KADLIFGEIQSQIK.N
R5/RRR5-16/2	1462.130	1462.673	-1058.170	0.431	1718.945	0.392	19	0.201	K.ADLIFGEIQSQIK.N
R5/RRR5-16/2	1462.164	1462.673	-1034.532	0.395	1648.734	0.367	19	0.188	K.ADLIFGEIQSQIK.N
R5/RRR5-15/2	1462.099	1462.673	-1079.379	0.360	1664.816	0.354	19	0.187	K.ADLIFGEIQSQIK.N
R5/RRR5-15/2	1462.471	1462.673	-138.187	0.383	1454.317	0.285	18	0.155	K.ADLIFGEIQSQIK.N
R5/RRR5-23/2	1830.825	1832.006	-1194.496	0.389	3002.141	0.525	29	0.473	K.GGTDSVIGVTLLGADGSGVR.I
R5/RRR5-23/2	1831.351	1832.006	-906.138	0.486	2766.839	0.573	29	0.435	K.GGTDSVIGVTLLGADGSGVR.I
R5/RRR5-24/2	1831.221	1832.006	-977.342	0.491	2714.964	0.516	30	0.402	K.GGTDSVIGVTLLGADGSGVR.I
R5/RRR5-24/2	1831.557	1832.006	-245.909	0.519	2553.263	0.567	29	0.385	K.GGTDSVIGVTLLGADGSGVR.I
R5/RRR5-24/2	1832.424	1832.006	228.940	0.568	2455.236	0.578	29	0.368	K.GGTDSVIGVTLLGADGSGVR.I
R5/RRR5-23/2	1830.566	1832.006	-1336.661	0.339	2277.660	0.466	27	0.299	K.GGTDSVIGVTLLGADGSGVR.I
R5/RRR5-26/2	978.991	979.072	-82.931	0.452	1230.104	0.523	15	0.180	R.GNLDIFSGR.G
R5/RRR5-27/2	978.713	979.072	-367.681	0.449	1074.436	0.526	14	0.168	R.GNLDIFSGR.G
R5/RRR5-24/2	978.458	979.072	-1653.884	0.436	1033.923	0.541	14	0.168	R.GNLDIFSGR.G
R5/RRR5-24/2	978.445	979.072	-1667.546	0.442	1035.367	0.503	14	0.162	R.GNLDIFSGR.G
R5/RRR5-23/2	978.769	979.072	-310.368	0.428	1021.627	0.494	14	0.160	R.GNLDIFSGR.G
R5/RRR5-27/2	978.897	979.072	-179.623	0.430	1058.078	0.477	14	0.160	R.GNLDIFSGR.G
R5/RRR5-27/2	978.438	979.072	-1674.440	0.430	1057.423	0.474	14	0.159	R.GNLDIFSGR.G
R5/RRR5-23/2	978.818	979.072	-259.818	0.455	1043.981	0.467	14	0.158	R.GNLDIFSGR.G
R5/RRR5-28/2	978.691	979.072	-389.832	0.449	1041.670	0.461	14	0.157	R.GNLDIFSGR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	978.803	979.072	-275.833	0.451	1011.757	0.472	14	0.156	R.GNLDIFSGR.G
R5/RRR5-25/2	978.942	979.072	-132.838	0.456	1055.907	0.452	14	0.156	R.GNLDIFSGR.G
R5/RRR5-22/2	978.844	979.072	-233.543	0.435	926.639	0.495	13	0.154	R.GNLDIFSGR.G
R5/RRR5-25/2	978.846	979.072	-231.542	0.414	1014.659	0.449	14	0.153	R.GNLDIFSGR.G
R5/RRR5-28/2	978.384	979.072	-1730.096	0.406	873.418	0.474	13	0.148	R.GNLDIFSGR.G
R5/RRR5-22/2	978.832	979.072	-245.679	0.430	843.412	0.474	13	0.147	R.GNLDIFSGR.G
R5/RRR5-24/2	978.301	979.072	-1815.722	0.401	815.419	0.478	13	0.146	R.GNLDIFSGR.G
R5/RRR5-1/2	979.051	979.072	-21.023	0.404	870.006	0.432	13	0.143	R.GNLDIFSGR.G
R5/RRR5-26/2	978.853	979.072	-224.535	0.422	836.956	0.425	13	0.141	R.GNLDIFSGR.G
R5/RRR5-24/2	1073.877	1074.248	-346.443	0.305	909.710	0.349	13	0.132	K.CVYTIYVR.T
R5/RRR5-22/2	1832.226	1832.006	120.777	0.347	341.065	0.401	19	0.123	K.GGTDSVIGVTLLGADGSGVR.I
R5/RRR5-24/2	1073.691	1074.248	-1454.793	0.252	638.090	0.303	12	0.121	K.CVYTIYVR.T
R5/RRR5-24/2	1073.351	1074.248	-1773.165	0.215	813.526	0.248	14	0.118	K.CVYTIYVR.T
R5/RRR5-12/2	1510.585	1510.781	-129.639	0.531	3351.611	0.561	24	0.580	K.M*VGYALQAAEILSK.E
R5/RRR5-12/2	1494.305	1494.781	-319.762	0.507	2998.026	0.504	24	0.464	K.MVGYALQAAEILSK.E
R5/RRR5-12/2	1494.381	1494.781	-268.621	0.546	2668.827	0.549	23	0.404	K.MVGYALQAAEILSK.E
R5/RRR5-12/2	1510.420	1510.781	-239.411	0.462	2381.908	0.480	23	0.324	K.M*VGYALQAAEILSK.E
R5/RRR5-12/2	1201.254	1201.355	-83.946	0.477	1730.201	0.385	19	0.202	K.EGISAEVINLR.S
R5/RRR5-11/2	1200.962	1201.355	-328.031	0.390	1549.586	0.305	17	0.167	K.EGISAEVINLR.S
R5/RRR5-12/2	1494.595	1494.781	-125.059	0.444	1228.878	0.443	18	0.163	K.MVGYALQAAEILSK.E
R5/RRR5-12/2	1202.177	1201.355	-148.248	0.495	1278.954	0.373	17	0.157	K.EGISAEVINLR.S
R5/RRR5-12/2	1202.386	1201.355	25.700	0.499	1046.807	0.369	17	0.143	K.EGISAEVINLR.S
R5/RRR5-12/2	1704.339	1704.929	-935.435	0.449	905.818	0.439	21	0.143	R.IAGADVPM*PYAANLER.M
R5/RRR5-12/2	1704.483	1704.929	-262.361	0.412	793.966	0.387	20	0.132	R.IAGADVPM*PYAANLER.M
R5/RRR5-12/2	1688.452	1688.930	-283.429	0.357	636.440	0.429	19	0.130	R.IAGADVPMPYAANLER.M
R5/RRR5-12/2	1704.295	1704.929	-961.753	0.420	671.504	0.364	19	0.126	R.IAGADVPM*PYAANLER.M
R5/RRR5-12/2	1688.450	1688.930	-284.662	0.364	706.161	0.344	19	0.125	R.IAGADVPMPYAANLER.M
R5/RRR5-13/2	1509.942	1510.781	-1221.124	0.298	435.330	0.372	14	0.121	K.M*VGYALQAAEILSK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1201.234	1201.355	-101.274	0.302	671.579	0.218	13	0.117	K.EGISAEVINLR.S
R5/RRR5-22/2	1139.114	1138.292	-156.562	0.471	762.098	0.428	16	0.141	K.CPFTGTVSIR.G
R5/RRR5-21/2	1267.932	1267.410	-378.300	0.486	350.785	0.461	16	0.137	R.EAIEGTYIDKK.C
R5/RRR5-21/2	1138.939	1139.237	-262.259	0.368	767.367	0.409	15	0.135	R.EAIEGTYIDK.K
R5/RRR5-22/2	1266.993	1267.410	-330.456	0.491	412.436	0.429	16	0.134	R.EAIEGTYIDKK.C
R5/RRR5-21/2	1139.237	1138.292	-48.213	0.403	535.111	0.439	14	0.134	K.CPFTGTVSIR.G
R5/RRR5-22/2	1137.288	1138.292	-1767.679	0.400	550.462	0.408	15	0.133	K.CPFTGTVSIR.G
R5/RRR5-20/2	1138.183	1138.292	-96.665	0.459	486.485	0.384	14	0.130	K.CPFTGTVSIR.G
R5/RRR5-21/2	1267.033	1267.410	-298.653	0.383	388.176	0.340	16	0.128	R.EAIEGTYIDKK.C
R5/RRR5-21/2	1267.169	1267.410	-191.081	0.429	416.082	0.309	16	0.126	R.EAIEGTYIDKK.C
R5/RRR5-21/2	1138.941	1139.237	-260.431	0.313	546.611	0.345	13	0.123	R.EAIEGTYIDK.K
R5/RRR5-20/2	1138.190	1138.292	-90.426	0.353	370.115	0.402	13	0.118	-.CPFTGTVSIR.-
R5/RRR5-21/2	1138.466	1139.237	-1560.223	0.171	531.478	0.250	13	0.114	R.EAIEGTYIDK.K
R5/RRR5-18/2	1137.627	1138.292	-1467.848	0.314	258.442	0.343	11	0.110	-.CPFTGTVSIR.-
R5/RRR5-28/1	467.464	467.454	19.644	-2.292	1.976	0.000	2	0.823	R.GYGGGG.G
R5/RRR5-22/1	467.251	467.454	-436.945	-1.894	2.181	0.000	2	0.558	R.GYGGGG.G
R5/RRR5-26/1	467.279	467.454	-377.702	-1.856	2.148	0.000	2	0.536	R.GYGGGG.G
R5/RRR5-24/1	467.474	467.454	42.430	-1.777	1.707	0.000	2	0.491	R.GYGGGG.G
R5/RRR5-21/2	1924.170	1924.960	-933.312	0.542	2872.734	0.633	29	0.485	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-22/1	467.417	467.454	-80.154	-1.759	1.864	0.000	2	0.481	R.GYGGGG.G
R5/RRR5-23/1	467.459	467.454	9.298	-1.852	2.029	0.301	2	0.468	R.GYGGGG.G
R5/RRR5-27/1	467.415	467.454	-83.691	-1.764	51.688	0.466	4	0.467	R.GYGGGG.G
R5/RRR5-28/1	467.393	467.454	-132.681	-1.680	1.767	0.000	2	0.440	R.GYGGGG.G
R5/RRR5-25/1	467.245	467.454	-450.315	-1.612	5.627	0.034	3	0.401	R.GYGGGG.G
R5/RRR5-21/1	467.348	467.454	-228.841	-1.583	2.403	0.000	2	0.393	R.GYGGGG.G
R5/RRR5-27/1	467.323	467.454	-282.955	-1.516	1.757	0.000	2	0.361	R.GYGGGG.G
R5/RRR5-21/2	1925.192	1924.960	121.050	0.587	2243.052	0.639	25	0.347	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-29/1	467.712	467.454	552.874	-1.491	23.777	0.000	2	0.346	-.GYGGGG.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/1	467.921	467.454	1000.851	-1.433	39.049	0.000	3	0.336	R.GYGGGG.G
R5/RRR5-18/1	467.899	467.454	952.621	-1.472	8.993	0.000	1	0.327	-.GYGGGG.-
R5/RRR5-13/1	467.890	467.454	933.014	-1.278	52.738	0.790	4	0.325	R.GYGGGG.G
R5/RRR5-18/1	467.407	467.454	-101.374	-1.581	8.565	0.233	1	0.321	-.GYGGGG.-
R5/RRR5-22/2	1925.108	1924.960	77.299	0.595	1979.890	0.678	24	0.311	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-22/2	1924.425	1924.960	-799.899	0.572	1869.845	0.697	24	0.299	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-22/2	1924.377	1924.960	-825.306	0.526	1915.561	0.663	24	0.296	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-29/1	467.234	467.454	-474.041	-1.344	1.581	0.000	2	0.289	R.GYGGGG.G
R5/RRR5-21/2	1924.397	1924.960	-814.672	0.512	1798.371	0.646	24	0.272	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-3/1	467.875	467.454	902.425	-1.253	20.713	0.000	2	0.261	R.GYGGGG.G
R5/RRR5-3/1	467.799	467.454	739.514	-0.958	67.285	0.832	4	0.257	R.GYGGGG.G
R5/RRR5-23/1	467.437	467.454	-36.801	-1.280	1.779	0.000	2	0.254	-.GYGGGG.-
R5/RRR5-27/1	467.785	467.454	709.437	-1.342	24.604	0.553	2	0.245	-.GYGGGG.-
R5/RRR5-23/1	467.904	467.454	963.078	-1.024	52.850	0.796	3	0.239	R.GYGGGG.G
R5/RRR5-28/1	467.354	467.454	-216.263	-0.564	69.910	0.909	4	0.236	R.GYGGGG.G
R5/RRR5-22/1	467.906	467.454	967.130	-1.193	27.516	0.706	2	0.235	R.GYGGGG.G
R5/RRR5-13/1	467.694	467.454	513.889	-0.673	27.716	0.919	3	0.227	R.GYGGGG.G
R5/RRR5-12/1	467.866	467.454	882.031	-0.495	40.837	0.922	3	0.221	R.GYGGGG.G
R5/RRR5-29/1	467.741	467.454	615.400	-0.825	33.810	0.858	3	0.219	R.GYGGGG.G
R5/RRR5-22/3	1924.918	1924.960	-21.735	0.379	832.961	0.363	25	0.079	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-21/3	1924.850	1924.960	-57.230	0.302	789.976	0.295	27	0.069	R.SLNDGDVVEFSVGSGNDGR.T
R5/RRR5-2/2	1910.554	1911.144	-834.801	0.606	1926.566	0.602	28	0.284	R.YEAVGVDPSTTLLEFLR.T
R5/RRR5-2/2	1910.037	1911.144	-1106.754	0.577	1911.729	0.595	28	0.280	R.YEAVGVDPSTTLLEFLR.T
R5/RRR5-2/2	1910.416	1911.144	-907.218	0.578	1765.770	0.596	27	0.258	R.YEAVGVDPSTTLLEFLR.T
R5/RRR5-3/2	1266.761	1267.543	-1410.422	0.335	876.156	0.523	17	0.149	K.LVSAPVILEAVR.L
R5/RRR5-2/2	1267.214	1267.543	-260.060	0.369	759.088	0.515	17	0.145	K.LVSAPVILEAVR.L
R5/RRR5-2/2	1155.393	1155.371	18.692	0.482	953.129	0.420	14	0.144	R.VSLAVSYLFR.F
R5/RRR5-2/2	1266.717	1267.543	-1445.461	0.326	793.091	0.502	17	0.143	K.LVSAPVILEAVR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1155.353	1155.371	-15.643	0.423	951.771	0.396	13	0.139	R.VSLAVSYLFR.F
R5/RRR5-2/2	1267.544	1267.543	0.907	0.335	698.488	0.505	16	0.139	K.LVSAPVILEAVR.L
R5/RRR5-2/2	1266.934	1267.543	-1273.775	0.303	524.382	0.496	15	0.131	K.LVSAPVILEAVR.L
R5/RRR5-2/2	1311.988	1312.411	-323.135	0.430	634.525	0.428	15	0.130	K.HSNVDSSDLPIK.S
R5/RRR5-3/2	1348.698	1349.583	-1401.264	0.339	1160.966	0.228	15	0.128	R.YGGMYALALAYR.G
R5/RRR5-3/2	1349.468	1349.583	-84.887	0.218	761.943	0.288	12	0.116	R.YGGMYALALAYR.G
R5/RRR5-3/3	1614.582	1614.827	-152.135	0.402	662.631	0.585	28	0.106	R.IVSLLSESYNPHVR.Y
R5/RRR5-3/3	1614.711	1614.827	-72.392	0.444	681.781	0.554	26	0.105	R.IVSLLSESYNPHVR.Y
R5/RRR5-3/3	1614.709	1614.827	-73.644	0.371	698.437	0.416	26	0.085	R.IVSLLSESYNPHVR.Y
R5/RRR5-4/2	1222.262	1221.388	-103.138	0.574	1465.552	0.438	17	0.184	R.AVAYLLTNAER.V
R5/RRR5-4/2	1221.153	1221.388	-192.867	0.545	1438.859	0.405	17	0.175	R.AVAYLLTNAER.V
R5/RRR5-4/2	1202.209	1202.388	-149.160	0.513	1080.423	0.559	17	0.175	R.HALSAISAIYR.L
R5/RRR5-4/2	1169.028	1169.354	-280.226	0.411	812.660	0.301	14	0.127	R.LIDTFYQIR.A
R5/RRR5-3/2	1201.847	1202.388	-1285.707	0.287	578.052	0.414	15	0.125	R.HALSAISAIYR.L
R5/RRR5-4/2	1169.089	1169.354	-228.162	0.305	659.887	0.122	13	0.114	R.LIDTFYQIR.A
R5/RRR5-4/3	1818.720	1819.009	-159.362	0.441	935.547	0.435	25	0.100	K.LVDRPQNYTLAPESSK.Q
R5/RRR5-4/3	1819.418	1819.009	225.993	0.432	1081.050	0.338	25	0.090	K.LVDRPQNYTLAPESSK.Q
R5/RRR5-3/3	1818.693	1819.009	-174.006	0.374	495.738	0.402	21	0.083	K.LVDRPQNYTLAPESSK.Q
R5/RRR5-3/3	1818.332	1819.009	-925.023	0.431	661.873	0.386	23	0.081	-.LVDRPQNYTLAPESSK.-
R5/RRR5-2/3	1819.145	1819.009	75.097	0.333	475.218	0.371	22	0.081	K.LVDRPQNYTLAPESSK.Q
R5/RRR5-18/2	1202.171	1202.383	-176.460	0.459	1411.180	0.387	17	0.170	K.INIKDDVSAVK.K
R5/RRR5-18/2	1197.031	1197.323	-244.418	0.520	1155.271	0.466	18	0.166	R.HLVAVQTDEGK.A
R5/RRR5-18/2	1197.012	1197.323	-260.480	0.512	1119.779	0.457	18	0.162	R.HLVAVQTDEGK.A
R5/RRR5-18/2	1197.058	1197.323	-222.217	0.516	1112.905	0.445	18	0.159	R.HLVAVQTDEGK.A
R5/RRR5-18/3	1330.357	1330.556	-149.666	0.408	980.257	0.313	21	0.081	-.INIKDDVSAVKK.-
R5/RRR5-18/3	1330.242	1330.556	-236.519	0.380	894.986	0.312	21	0.077	-.INIKDDVSAVKK.-
R5/RRR5-3/2	1316.130	1315.458	-250.208	0.443	1029.166	0.476	15	0.156	R.FTWTIENFTR.I
R5/RRR5-3/2	1315.242	1315.458	-165.199	0.411	1067.029	0.432	15	0.152	R.FTWTIENFTR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1267.173	1267.415	-191.757	0.430	1079.885	0.414	16	0.150	R.FTWTIENLSR.V
R5/RRR5-3/2	1861.720	1859.971	-135.451	0.455	791.351	0.506	18	0.141	R.AEEVPEEEKNLGPFDR.L
R5/RRR5-19/2	1851.537	1850.066	255.078	0.608	2805.349	0.608	25	0.456	R.NVQAILDSYTTIVNAAR.S
R5/RRR5-18/2	1849.318	1850.066	-947.916	0.400	1984.578	0.432	23	0.244	R.NVQAILDSYTTIVNAAR.S
R5/RRR5-18/2	1375.072	1375.515	-322.914	0.340	1761.498	0.400	20	0.207	K.VWSQLSSAGLGNR.V
R5/RRR5-18/2	1848.936	1850.066	-1155.248	0.339	1650.849	0.393	22	0.192	R.NVQAILDSYTTIVNAAR.S
R5/RRR5-18/2	1376.508	1375.515	-5.124	0.354	1527.134	0.373	20	0.177	K.VWSQLSSAGLGNR.V
R5/RRR5-19/2	1381.055	1381.578	-1105.920	0.481	1170.062	0.482	20	0.168	R.VDLVGSM*TSLQSK.C
R5/RRR5-19/2	1380.590	1381.578	-1444.179	0.402	1180.090	0.453	20	0.163	R.VDLVGSM*TSLQSK.C
R5/RRR5-19/2	1380.955	1381.578	-1179.234	0.444	1121.315	0.384	19	0.148	R.VDLVGSM*TSLQSK.C
R5/RRR5-18/2	1381.204	1381.578	-271.831	0.461	1014.846	0.399	19	0.145	R.VDLVGSM*TSLQSK.C
R5/RRR5-19/2	1849.933	1850.066	-72.181	0.447	778.764	0.485	17	0.139	R.NVQAILDSYTTIVNAAR.S
R5/RRR5-19/2	1374.510	1375.515	-1463.492	0.255	1309.951	0.177	18	0.131	K.VWSQLSSAGLGNR.V
R5/RRR5-19/2	1849.220	1850.066	-1000.934	0.279	915.594	0.320	18	0.126	R.NVQAILDSYTTIVNAAR.S
R5/RRR5-18/2	1851.329	1850.066	142.479	0.443	782.815	0.359	18	0.126	R.NVQAILDSYTTIVNAAR.S
R5/RRR5-18/2	1375.201	1375.515	-229.133	0.309	1135.996	0.196	18	0.125	K.VWSQLSSAGLGNR.V
R5/RRR5-12/2	1651.320	1651.932	-979.274	0.515	3091.528	0.582	26	0.522	R.VPQVGSIAINDGVILR.N
R5/RRR5-12/2	1651.512	1651.932	-254.777	0.483	2118.642	0.539	23	0.296	R.VPQVGSIAINDGVILR.N
R5/RRR5-12/2	1107.205	1107.281	-69.513	0.518	1352.322	0.485	16	0.185	K.YGAVEDILVK.M
R5/RRR5-12/2	1921.403	1922.258	-968.174	0.516	1041.269	0.563	24	0.170	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-12/2	1922.477	1922.258	113.961	0.551	907.846	0.599	22	0.166	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-12/2	1921.685	1922.258	-821.301	0.521	774.789	0.595	21	0.157	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-12/2	1106.925	1107.281	-322.716	0.410	1018.315	0.450	15	0.152	K.YGAVEDILVK.M
R5/RRR5-12/2	1922.719	1922.258	240.476	0.506	742.095	0.566	21	0.151	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-12/2	1921.725	1922.258	-800.450	0.552	790.523	0.539	21	0.149	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-12/2	1923.254	1922.258	-2.267	0.553	717.350	0.550	20	0.147	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-12/3	1922.508	1922.258	130.510	0.409	1266.623	0.444	30	0.128	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-11/2	1922.034	1922.258	-117.122	0.438	502.978	0.452	17	0.128	K.LIANIEAQPSIAVQNVLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1106.338	1107.281	-1761.574	0.212	487.393	0.254	15	0.118	K.YGAVEDILVK.M
R5/RRR5-12/3	1921.677	1922.258	-825.453	0.418	1038.574	0.403	25	0.098	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-12/3	1922.125	1922.258	-69.254	0.250	715.265	0.336	23	0.071	K.LIANIEAQPSIAVQNVLK.S
R5/RRR5-20/2	1631.276	1630.999	170.030	0.589	2288.603	0.543	21	0.325	R.IKQVLLSLQAFTLR.L
R5/RRR5-19/2	1464.064	1464.562	-341.420	0.513	1572.837	0.395	22	0.187	K.FDSDGNLIDAQIR.E
R5/RRR5-19/2	1464.346	1464.562	-148.378	0.569	1405.168	0.448	21	0.181	K.FDSDGNLIDAQIR.E
R5/RRR5-20/2	1465.012	1464.562	307.835	0.561	1359.369	0.411	21	0.170	K.FDSDGNLIDAQIR.E
R5/RRR5-20/2	1464.133	1464.562	-294.240	0.553	1395.134	0.379	21	0.167	K.FDSDGNLIDAQIR.E
R5/RRR5-19/2	1631.149	1630.999	91.867	0.478	1014.588	0.514	20	0.162	R.IKQVLLSLQAFTLR.L
R5/RRR5-19/2	1632.556	1630.999	-272.359	0.499	945.869	0.504	18	0.154	R.IKQVLLSLQAFTLR.L
R5/RRR5-19/2	1464.224	1464.562	-231.842	0.516	1068.382	0.441	19	0.154	K.FDSDGNLIDAQIR.E
R5/RRR5-20/2	1463.724	1464.562	-1259.779	0.486	1250.896	0.348	20	0.151	K.FDSDGNLIDAQIR.E
R5/RRR5-21/2	932.903	933.003	-107.961	0.428	838.649	0.411	13	0.141	K.NALDWASR.G
R5/RRR5-19/2	1630.152	1630.999	-1136.346	0.376	1141.644	0.309	20	0.139	R.IKQVLLSLQAFTLR.L
R5/RRR5-19/2	932.320	933.003	-1810.915	0.391	886.951	0.357	13	0.136	K.NALDWASR.G
R5/RRR5-21/2	932.330	933.003	-1799.995	0.383	901.919	0.351	13	0.136	K.NALDWASR.G
R5/RRR5-19/2	932.895	933.003	-116.493	0.381	822.145	0.366	13	0.135	K.NALDWASR.G
R5/RRR5-20/2	932.944	933.003	-63.992	0.388	816.312	0.348	13	0.133	K.NALDWASR.G
R5/RRR5-19/2	1631.739	1630.999	-159.719	0.395	540.964	0.425	17	0.130	R.IKQVLLSLQAFTLR.L
R5/RRR5-20/2	932.845	933.003	-169.787	0.407	867.569	0.293	13	0.130	K.NALDWASR.G
R5/RRR5-20/2	932.456	933.003	-1664.640	0.392	831.256	0.295	13	0.129	K.NALDWASR.G
R5/RRR5-19/2	932.989	933.003	-15.565	0.407	834.520	0.272	13	0.127	K.NALDWASR.G
R5/RRR5-19/2	1632.540	1630.999	-282.262	0.333	222.782	0.302	13	0.121	-.IKQVLLSLQAFTLR.-
R5/RRR5-19/2	1631.252	1630.999	155.322	0.333	448.348	0.270	16	0.120	R.IKQVLLSLQAFTLR.L
R5/RRR5-11/2	1303.338	1303.447	-84.322	0.433	1308.319	0.420	18	0.165	R.SVGTLGEADLRGK.K
R5/RRR5-11/2	1117.999	1118.223	-200.916	0.493	1133.899	0.417	17	0.155	R.SVGTLGEADLR.G
R5/RRR5-10/2	1118.029	1118.223	-173.861	0.409	1013.639	0.363	16	0.140	R.SVGTLGEADLR.G
R5/RRR5-11/2	1300.055	1299.412	-275.528	0.392	582.896	0.441	18	0.134	R.ADLNVPLDDAQK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1298.524	1299.412	-1458.142	0.265	643.208	0.355	19	0.124	R.ADLNVPLDDAQK.I
R5/RRR5-11/2	1299.091	1299.412	-248.118	0.292	570.351	0.324	16	0.121	R.ADLNVPLDDAQK.I
R5/RRR5-10/2	1117.426	1118.223	-1612.391	0.329	671.061	0.299	14	0.121	-.SVGTLGEADLR.-
R5/RRR5-12/2	1118.141	1118.223	-73.541	0.359	676.658	0.205	14	0.116	-.SVGTLGEADLR.-
R5/RRR5-13/2	1117.954	1118.223	-241.555	0.389	337.285	0.332	12	0.088	-.SVGTLGEADLR.-
R5/RRR5-23/2	1494.669	1495.659	-1335.436	0.394	2129.634	0.529	23	0.293	K.ITLISDFGEISGSR.G
R5/RRR5-23/2	1495.304	1495.659	-238.487	0.549	1936.038	0.606	22	0.286	K.ITLISDFGEISGSR.G
R5/RRR5-23/2	1495.376	1495.659	-190.168	0.539	1850.057	0.565	22	0.261	K.ITLISDFGEISGSR.G
R5/RRR5-22/2	1495.836	1495.659	118.144	0.450	1469.826	0.529	20	0.203	K.ITLISDFGEISGSR.G
R5/RRR5-23/3	1495.317	1495.659	-229.405	0.384	1779.146	0.428	28	0.195	K.ITLISDFGEISGSR.G
R5/RRR5-23/3	1623.615	1623.832	-134.058	0.366	1296.965	0.474	25	0.137	R.KITLISDFGEISGSR.G
R5/RRR5-23/2	1496.107	1495.659	300.209	0.333	741.676	0.398	15	0.129	K.ITLISDFGEISGSR.G
R5/RRR5-23/2	1495.402	1495.659	-172.479	0.289	394.708	0.327	13	0.119	K.ITLISDFGEISGSR.G
R5/RRR5-23/3	1495.248	1495.659	-275.721	0.369	1103.865	0.349	23	0.094	-.ITLISDFGEISGSR.-
R5/RRR5-23/2	1536.434	1535.837	-262.619	0.448	868.708	0.423	20	0.090	K.IM*LTHVLHGQGSII.-
R5/RRR5-23/2	1535.208	1535.837	-1063.862	0.361	911.756	0.227	20	0.080	K.IM*LTHVLHGQGSII.-
R5/RRR5-13/3	1960.019	1959.187	-86.000	0.487	2540.236	0.589	36	0.470	R.DADVVISTLGALQIADQTK.L
R5/RRR5-13/2	1205.059	1205.432	-310.457	0.487	1832.226	0.487	21	0.240	R.ILVVGGTGYIGR.H
R5/RRR5-14/3	1065.493	1065.251	227.383	0.494	954.821	0.346	19	0.088	R.LGHPTTALVR.D
R5/RRR5-13/3	1065.385	1065.251	126.303	0.504	785.115	0.349	19	0.085	R.LGHPTTALVR.D
R5/RRR5-13/3	1065.660	1065.251	384.521	0.494	724.889	0.341	18	0.074	-.LGHPTTALVR.-
R5/RRR5-14/3	1065.389	1065.251	130.354	0.471	723.954	0.332	18	0.073	-.LGHPTTALVR.-
R5/RRR5-14/3	1065.212	1065.251	-36.950	0.454	603.146	0.334	17	0.073	-.LGHPTTALVR.-
R5/RRR5-13/3	1065.268	1065.251	16.238	0.472	703.661	0.314	17	0.071	-.LGHPTTALVR.-
R5/RRR5-6/2	1536.178	1536.755	-1029.560	0.495	1916.157	0.530	20	0.262	R.SKFESLVQSLIER.T
R5/RRR5-6/2	1536.942	1536.755	122.472	0.442	1425.655	0.452	17	0.181	R.SKFESLVQSLIER.T
R5/RRR5-6/2	1291.234	1291.478	-189.890	0.420	763.811	0.385	14	0.129	K.VQDIVSQIFNK.T
R5/RRR5-17/2	1582.211	1582.734	-965.480	0.451	2900.577	0.412	22	0.408	R.SNVGELLEYSLETK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1582.345	1582.734	-246.414	0.494	2449.613	0.482	21	0.338	R.SNVGELLEYSLETK.K
R5/RRR5-17/2	1471.334	1471.679	-235.465	0.497	1746.281	0.478	20	0.225	R.KYDAFIASDSLIK.Q
R5/RRR5-17/3	1490.562	1490.622	-39.819	0.531	1288.392	0.525	28	0.152	K.HGGIDSM*SADDLKK.L
R5/RRR5-17/2	1581.467	1582.734	-1437.419	0.325	1418.711	0.217	19	0.142	R.SNVGELLEYSLETK.K
R5/RRR5-17/3	1490.368	1490.622	-170.323	0.526	1142.459	0.533	28	0.138	K.HGGIDSM*SADDLKK.L
R5/RRR5-17/3	1490.783	1490.622	108.635	0.535	1249.732	0.467	29	0.132	K.HGGIDSM*SADDLKK.L
R5/RRR5-4/2	1561.106	1560.692	265.985	0.479	925.437	0.589	21	0.168	R.TYINPYATFADAGR.K
R5/RRR5-4/2	1561.763	1560.692	45.971	0.451	435.126	0.555	19	0.141	R.TYINPYATFADAGR.K
R5/RRR5-4/2	1587.519	1587.888	-233.040	0.413	727.742	0.487	19	0.139	K.LLVFQSTLPSLGVGR.L
R5/RRR5-4/2	1587.456	1587.888	-272.847	0.387	900.192	0.411	20	0.138	K.LLVFQSTLPSLGVGR.L
R5/RRR5-3/2	1561.169	1560.692	306.991	0.388	875.878	0.403	17	0.135	R.TYINPYATFADAGR.K
R5/RRR5-1/2	1332.542	1331.500	31.276	0.361	480.932	0.509	16	0.133	R.QADTGAIVSLLSR.I
R5/RRR5-3/2	1332.672	1331.500	128.842	0.367	464.360	0.500	16	0.133	R.QADTGAIVSLLSR.I
R5/RRR5-3/2	1330.451	1331.500	-1545.086	0.367	416.254	0.401	15	0.126	R.QADTGAIVSLLSR.I
R5/RRR5-4/2	1331.709	1331.500	157.068	0.290	267.940	0.333	13	0.120	-.QADTGAIVSLLSR.-
R5/RRR5-4/3	1582.119	1581.799	202.893	0.433	1273.592	0.337	27	0.103	R.LTTHAIPASQSLVSR.W
R5/RRR5-26/2	1631.214	1631.683	-288.496	0.545	1801.408	0.553	24	0.250	K.GSPAADEEQSTAAAAVR.F
R5/RRR5-26/2	1494.207	1494.718	-1013.985	0.349	871.701	0.409	19	0.112	R.SEPRPSLAQLLSPV.-
R5/RRR5-27/2	1494.177	1494.718	-1034.082	0.327	784.174	0.381	18	0.106	R.SEPRPSLAQLLSPV.-
R5/RRR5-27/2	1494.772	1494.718	36.154	0.350	772.192	0.382	18	0.105	R.SEPRPSLAQLLSPV.-
R5/RRR5-27/3	1760.768	1759.856	-50.429	0.447	938.210	0.448	32	0.103	R.KGSPAADEEQSTAAAAVR.F
R5/RRR5-26/2	1494.194	1494.718	-1022.680	0.323	663.849	0.384	17	0.103	R.SEPRPSLAQLLSPV.-
R5/RRR5-27/2	1494.040	1494.718	-1126.370	0.273	806.118	0.265	18	0.102	R.SEPRPSLAQLLSPV.-
R5/RRR5-26/3	1759.115	1759.856	-992.911	0.439	642.096	0.425	27	0.089	R.KGSPAADEEQSTAAAAVR.F
R5/RRR5-27/3	1759.678	1759.856	-101.461	0.411	642.406	0.411	28	0.087	R.KGSPAADEEQSTAAAAVR.F
R5/RRR5-27/3	1758.890	1759.856	-1121.156	0.392	880.888	0.347	29	0.083	R.KGSPAADEEQSTAAAAVR.F
R5/RRR5-26/3	1759.813	1759.856	-24.749	0.422	787.575	0.297	29	0.076	R.KGSPAADEEQSTAAAAVR.F
R5/RRR5-26/3	1759.909	1759.856	30.248	0.386	578.423	0.293	25	0.073	-.KGSPAADEEQSTAAAAVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-27/3	1828.227	1828.001	124.110	0.482	1745.773	0.418	29	0.188	R.RVTSGEQQVVSGM*NYR.L
R5/RRR5-27/2	1671.199	1671.814	-969.600	0.467	1377.188	0.484	21	0.184	R.VTSGEQQVVSGM*NYR.L
R5/RRR5-27/3	1671.347	1671.814	-280.181	0.389	1772.373	0.347	30	0.166	R.VTSGEQQVVSGM*NYR.L
R5/RRR5-27/3	1671.662	1671.814	-91.602	0.475	1724.878	0.345	31	0.158	R.VTSGEQQVVSGM*NYR.L
R5/RRR5-27/2	1042.303	1043.116	-1744.696	0.358	763.603	0.572	16	0.151	R.HASLSSDGLR.F
R5/RRR5-27/2	1042.972	1043.116	-138.477	0.430	734.919	0.542	16	0.151	R.HASLSSDGLR.F
R5/RRR5-27/2	1042.422	1043.116	-1630.332	0.384	770.476	0.517	16	0.147	R.HASLSSDGLR.F
R5/RRR5-27/2	1671.014	1671.814	-1080.786	0.461	905.664	0.444	18	0.141	R.VTSGEQQVVSGM*NYR.L
R5/RRR5-27/3	1827.403	1828.001	-876.852	0.440	1072.178	0.397	25	0.100	R.RVTSGEQQVVSGM*NYR.L
R5/RRR5-27/3	1671.119	1671.814	-1017.570	0.394	1205.046	0.290	27	0.089	R.VTSGEQQVVSGM*NYR.L
R5/RRR5-25/2	1744.287	1744.825	-884.660	0.509	1721.190	0.605	26	0.251	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-24/2	1744.231	1744.825	-917.049	0.516	1643.219	0.579	25	0.233	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-25/2	1745.153	1744.825	188.495	0.570	1487.877	0.591	24	0.216	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-24/2	1744.288	1744.825	-884.168	0.499	1507.406	0.538	24	0.206	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-24/3	1900.460	1901.012	-818.676	0.455	1881.287	0.399	36	0.204	R.RASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-24/2	1745.152	1744.825	187.934	0.561	1365.384	0.588	22	0.200	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-25/3	1900.961	1901.012	-26.600	0.508	1702.034	0.434	36	0.184	R.RASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-25/2	1744.311	1744.825	-870.820	0.484	1151.720	0.553	23	0.174	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-25/2	1168.911	1169.268	-306.231	0.439	699.315	0.424	16	0.138	R.FYTDEAPGLR.L
R5/RRR5-25/2	1169.005	1169.268	-225.769	0.427	621.591	0.399	15	0.133	R.FYTDEAPGLR.L
R5/RRR5-25/2	1168.969	1169.268	-256.674	0.413	543.908	0.366	15	0.130	R.FYTDEAPGLR.L
R5/RRR5-26/2	1170.021	1169.268	-211.969	0.354	487.848	0.306	14	0.124	R.FYTDEAPGLR.L
R5/RRR5-25/2	1170.295	1169.268	22.743	0.335	369.536	0.329	13	0.123	-.FYTDEAPGLR.-
R5/RRR5-25/3	1900.813	1901.012	-104.574	0.449	1345.796	0.374	32	0.118	R.RASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-25/3	1900.121	1901.012	-998.116	0.461	1425.242	0.320	34	0.113	R.RASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-24/3	1744.361	1744.825	-266.959	0.396	956.597	0.435	35	0.098	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-25/3	1744.331	1744.825	-284.231	0.410	344.602	0.465	29	0.087	R.ASTAGGSGGFSGGGGSNM*LR.F
R5/RRR5-8/3	1170.561	1170.303	221.251	0.491	1749.847	0.539	23	0.227	K.FGAAVVSPEHR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/3	1170.336	1170.303	28.747	0.492	1517.038	0.533	22	0.185	K.FGAAVVSPEHR.Y
R5/RRR5-8/2	1481.032	1481.590	-1055.082	0.431	1120.107	0.379	19	0.147	K.SSPFESLTTENLR.F
R5/RRR5-8/3	1170.255	1170.303	-40.774	0.474	1157.083	0.515	19	0.135	K.FGAAVVSPEHR.Y
R5/RRR5-8/2	1481.045	1481.590	-1046.144	0.383	972.104	0.343	18	0.134	K.SSPFESLTTENLR.F
R5/RRR5-17/3	1298.291	1298.475	-142.659	0.515	1350.757	0.421	23	0.131	K.KFGAAVVSPEHR.Y
R5/RRR5-8/2	1481.117	1481.590	-320.295	0.395	665.615	0.289	17	0.121	K.SSPFESLTTENLR.F
R5/RRR5-17/3	1170.064	1170.303	-204.334	0.429	1196.272	0.428	20	0.117	K.FGAAVVSPEHR.Y
R5/RRR5-8/3	1298.386	1298.475	-68.953	0.536	923.991	0.420	20	0.096	-.KFGAAVVSPEHR.-
R5/RRR5-8/3	1298.447	1298.475	-22.133	0.521	968.920	0.383	21	0.094	K.KFGAAVVSPEHR.Y
R5/RRR5-17/3	1170.697	1170.303	337.471	0.394	765.561	0.358	18	0.082	K.FGAAVVSPEHR.Y
R5/RRR5-17/3	1298.410	1298.475	-50.564	0.447	879.443	0.321	20	0.080	K.KFGAAVVSPEHR.Y
R5/RRR5-8/3	1298.711	1298.475	182.072	0.479	937.611	0.311	21	0.078	-.KFGAAVVSPEHR.-
R5/RRR5-10/2	1870.748	1871.037	-154.890	0.537	2805.709	0.442	24	0.395	K.LAYVALDYEQELDTAR.S
R5/RRR5-11/2	1870.722	1871.037	-168.767	0.556	2527.422	0.555	24	0.377	K.LAYVALDYEQELDTAR.S
R5/RRR5-10/2	1870.096	1871.037	-1041.221	0.483	2660.363	0.438	24	0.364	K.LAYVALDYEQELDTAR.S
R5/RRR5-10/2	1870.371	1871.037	-893.453	0.472	2556.705	0.485	24	0.360	K.LAYVALDYEQELDTAR.S
R5/RRR5-6/2	1540.349	1540.647	-194.313	0.514	2339.513	0.524	23	0.332	K.ACWSGGGCSTAGQLK.A
R5/RRR5-5/2	966.950	967.058	-111.631	0.475	697.696	0.382	13	0.132	K.SAGQFSEIK.L
R5/RRR5-5/2	967.263	967.058	213.084	0.455	739.304	0.358	13	0.131	K.SAGQFSEIK.L
R5/RRR5-5/2	966.970	967.058	-90.736	0.483	819.516	0.338	13	0.130	K.SAGQFSEIK.L
R5/RRR5-6/2	967.045	967.058	-13.245	0.375	804.193	0.325	13	0.128	K.SAGQFSEIK.L
R5/RRR5-6/2	1403.578	1404.593	-1440.075	0.365	739.573	0.405	16	0.128	R.SFPVVITLGNNDK.F
R5/RRR5-24/2	1866.291	1867.118	-982.007	0.507	2322.688	0.542	26	0.333	K.DM*PVLQDGPPPGGFAPVR.Y
R5/RRR5-24/2	1866.365	1867.118	-942.017	0.497	2200.238	0.545	26	0.311	K.DM*PVLQDGPPPGGFAPVR.Y
R5/RRR5-24/2	1867.367	1867.118	133.384	0.594	1838.358	0.543	25	0.251	K.DM*PVLQDGPPPGGFAPVR.Y
R5/RRR5-24/2	1570.200	1570.726	-975.048	0.463	815.944	0.564	22	0.158	R.TALVPVLQAEEDER.F
R5/RRR5-24/2	1944.636	1945.205	-809.341	0.498	912.410	0.524	22	0.153	R.TALVPVLQAEEDERFVK.E
R5/RRR5-24/2	1570.353	1570.726	-238.238	0.467	826.594	0.523	22	0.153	R.TALVPVLQAEEDER.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1570.052	1570.726	-1069.499	0.384	720.086	0.466	21	0.139	R.TALVPVLQAEEDER.F
R5/RRR5-2/2	1716.349	1714.987	211.537	0.483	1489.234	0.335	21	0.165	K.VQLVQFGILSPDEIR.Q
R5/RRR5-1/2	1715.487	1714.987	-292.023	0.425	1274.482	0.408	19	0.160	K.VQLVQFGILSPDEIR.Q
R5/RRR5-2/2	1565.243	1565.708	-297.917	0.414	1325.116	0.222	18	0.135	K.EAFEWVIGEIESR.F
R5/RRR5-2/2	1086.124	1085.194	-65.113	0.416	878.634	0.366	13	0.133	R.GFVENSYLR.G
R5/RRR5-2/2	1576.016	1575.831	117.727	0.457	1010.896	0.342	17	0.132	K.TPSLSVYLKPEVNK.K
R5/RRR5-18/3	1403.662	1403.520	101.164	0.543	2364.827	0.382	30	0.295	K.IKSEGEAEAAAAQK.S
R5/RRR5-18/3	1404.093	1403.520	-305.175	0.551	2226.870	0.411	29	0.276	K.IKSEGEAEAAAAQK.S
R5/RRR5-17/3	1403.593	1403.520	52.101	0.560	1881.832	0.419	29	0.207	K.IKSEGEAEAAAAQK.S
R5/RRR5-18/3	1403.439	1403.520	-58.470	0.552	1995.852	0.361	30	0.206	K.IKSEGEAEAAAAQK.S
R5/RRR5-6/2	1506.296	1506.598	-200.575	0.568	2694.389	0.624	24	0.442	R.TKNEAALEAATDSGK.Q
R5/RRR5-6/2	1498.234	1497.679	-297.513	0.451	1317.694	0.447	17	0.170	R.SFASVSAAQFPWAK.M
R5/RRR5-6/2	1099.192	1099.306	-103.770	0.470	1335.728	0.334	14	0.155	R.DLVLQLLER.I
R5/RRR5-6/2	1498.691	1497.679	8.365	0.380	1098.901	0.390	17	0.144	R.SFASVSAAQFPWAK.M
R5/RRR5-6/2	1099.020	1099.306	-260.868	0.411	729.135	0.374	13	0.131	R.DLVLQLLER.I
R5/RRR5-6/2	1098.927	1099.306	-346.010	0.383	550.145	0.344	12	0.125	R.DLVLQLLER.I
R5/RRR5-2/2	1586.348	1585.658	-195.933	0.422	617.675	0.466	20	0.135	K.TSPIPQDDAQGQATR.Y
R5/RRR5-3/2	1157.298	1157.430	-114.747	0.372	667.977	0.427	14	0.133	R.ADIPIIIVFR.A
R5/RRR5-3/2	1809.050	1809.909	-1030.740	0.416	629.044	0.473	21	0.133	K.EGDATPFTDVTVDNISK.A
R5/RRR5-3/2	1586.381	1585.658	-175.400	0.413	494.902	0.450	18	0.129	K.TSPIPQDDAQGQATR.Y
R5/RRR5-3/2	1156.881	1157.430	-1343.195	0.336	518.919	0.360	13	0.124	R.ADIPIIIVFR.A
R5/RRR5-3/2	1157.278	1157.430	-131.888	0.326	495.167	0.321	13	0.122	R.ADIPIIIVFR.A
R5/RRR5-1/3	1916.715	1915.010	-154.440	0.508	1033.879	0.443	29	0.107	R.HGSYDKLDDDGLAPPGTR.V
R5/RRR5-3/3	1914.271	1915.010	-911.090	0.425	651.043	0.446	27	0.087	R.HGSYDKLDDDGLAPPGTR.V
R5/RRR5-21/2	1687.467	1687.985	-902.082	0.562	2344.869	0.658	25	0.377	R.HVVFGQVIEGM*DIVK.M
R5/RRR5-21/2	1688.581	1687.985	-239.484	0.580	2253.772	0.649	25	0.356	R.HVVFGQVIEGM*DIVK.M
R5/RRR5-21/2	1687.493	1687.985	-291.951	0.506	2046.383	0.668	24	0.323	R.HVVFGQVIEGM*DIVK.M
R5/RRR5-21/2	1409.132	1409.611	-341.175	0.471	2011.624	0.524	21	0.275	K.VYFDISIGNPVGK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1995.795	1994.193	-200.029	0.644	1504.447	0.668	27	0.242	R.VVIGLYGDDVPQTAENFR.A
R5/RRR5-21/2	1993.583	1994.193	-810.413	0.553	1553.874	0.599	28	0.231	R.VVIGLYGDDVPQTAENFR.A
R5/RRR5-21/2	1409.279	1409.611	-236.277	0.434	1674.672	0.506	20	0.222	K.VYFDISIGNPVGK.N
R5/RRR5-21/2	1408.572	1409.611	-1452.179	0.384	1693.745	0.410	19	0.202	K.VYFDISIGNPVGK.N
R5/RRR5-21/2	1993.488	1994.193	-858.173	0.557	1165.306	0.607	25	0.189	R.VVIGLYGDDVPQTAENFR.A
R5/RRR5-21/3	1994.780	1994.193	-207.872	0.400	1298.915	0.405	32	0.121	R.VVIGLYGDDVPQTAENFR.A
R5/RRR5-21/3	1994.512	1994.193	159.991	0.335	1100.270	0.357	30	0.092	R.VVIGLYGDDVPQTAENFR.A
R5/RRR5-26/2	1220.239	1220.400	-132.207	0.434	1903.674	0.368	17	0.219	K.SDFVVQIGVQK.V
R5/RRR5-26/2	1544.358	1544.730	-242.169	0.489	1227.993	0.528	21	0.180	K.AGQTVTIEYTGYLK.D
R5/RRR5-26/2	1544.401	1544.730	-213.781	0.479	1223.823	0.491	21	0.173	K.AGQTVTIEYTGYLK.D
R5/RRR5-26/2	1167.204	1167.274	-60.103	0.414	1152.187	0.381	14	0.149	K.GWDEGVTQM*K.V
R5/RRR5-26/2	1166.813	1167.274	-396.641	0.452	1087.530	0.395	14	0.148	K.GWDEGVTQM*K.V
R5/RRR5-26/2	1166.843	1167.274	-370.189	0.435	1036.476	0.404	14	0.146	K.GWDEGVTQM*K.V
R5/RRR5-26/2	1219.977	1220.400	-347.205	0.378	1278.309	0.216	16	0.133	K.SDFVVQIGVQK.V
R5/RRR5-17/2	1451.249	1450.619	-255.513	0.577	2131.187	0.606	22	0.319	K.GPDFATIINSVTSK.K
R5/RRR5-17/2	1451.435	1450.619	-127.175	0.581	1869.921	0.609	22	0.277	K.GPDFATIINSVTSK.K
R5/RRR5-17/2	1751.379	1751.956	-902.703	0.535	2130.896	0.467	25	0.276	R.IIYGGSVNAANCAELAK.K
R5/RRR5-17/2	1451.141	1450.619	-330.117	0.596	1825.479	0.572	22	0.260	K.GPDFATIINSVTSK.K
R5/RRR5-17/2	1751.311	1751.956	-941.748	0.515	1980.435	0.467	24	0.253	R.IIYGGSVNAANCAELAK.K
R5/RRR5-17/2	1229.959	1230.353	-321.592	0.511	1475.298	0.456	21	0.191	K.TNVSPEVASGIR.I
R5/RRR5-17/2	1230.040	1230.353	-255.178	0.499	1338.364	0.486	20	0.184	K.TNVSPEVASGIR.I
R5/RRR5-17/2	1230.016	1230.353	-274.793	0.469	1383.846	0.444	20	0.179	K.TNVSPEVASGIR.I
R5/RRR5-24/2	1320.045	1320.493	-340.603	0.481	1760.264	0.495	17	0.231	K.SEIEYYAM*LGK.V
R5/RRR5-24/2	1320.174	1320.493	-242.355	0.492	1608.184	0.478	17	0.209	K.SEIEYYAM*LGK.V
R5/RRR5-24/2	1319.467	1320.493	-1540.280	0.373	1586.734	0.365	16	0.182	K.SEIEYYAM*LGK.V
R5/RRR5-24/3	1394.960	1394.681	200.142	0.335	1130.502	0.374	24	0.095	K.LIILANNCPPLR.K
R5/RRR5-12/2	1720.610	1720.910	-174.881	0.524	2393.142	0.462	22	0.320	K.NLSLGTEAFWLGQQR.K
R5/RRR5-12/2	1719.901	1720.910	-1171.658	0.424	2248.397	0.377	21	0.271	K.NLSLGTEAFWLGQQR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1719.635	1720.910	-1326.768	0.353	1784.461	0.365	20	0.202	K.NLSLGTEAFWLGQQR.K
R5/RRR5-12/2	1516.451	1516.679	-150.789	0.511	1404.194	0.486	19	0.187	K.IDTNGVVSALLEER.L
R5/RRR5-12/2	1515.649	1516.679	-1342.881	0.360	1419.312	0.393	20	0.170	K.IDTNGVVSALLEER.L
R5/RRR5-12/2	1516.147	1516.679	-1013.445	0.400	1088.009	0.380	19	0.144	K.IDTNGVVSALLEER.L
R5/RRR5-12/2	792.772	792.906	-169.516	0.389	926.990	0.328	13	0.132	K.SGVGFVAR.Y
R5/RRR5-12/3	1720.058	1720.910	-1080.055	0.302	1050.902	0.228	24	0.067	K.NLSLGTEAFWLGQQR.K
R5/RRR5-22/1	998.373	999.102	-1736.281	0.271	738.891	0.487	12	0.999	R.LNAYIQGGY.-
R5/RRR5-22/1	998.346	999.102	-1763.370	0.292	601.016	0.326	11	0.627	R.LNAYIQGGY.-
R5/RRR5-22/1	998.380	999.102	-1729.893	0.262	506.429	0.305	10	0.455	R.LNAYIQGGY.-
R5/RRR5-22/2	1325.107	1324.593	-368.100	0.530	1554.878	0.520	17	0.212	R.VLQAM*QLM*TEK.R
R5/RRR5-22/2	1324.299	1324.593	-223.080	0.506	1706.010	0.399	17	0.202	R.VLQAM*QLM*TEK.R
R5/RRR5-22/2	1323.602	1324.593	-1509.075	0.414	1648.756	0.290	17	0.174	R.VLQAM*QLM*TEK.R
R5/RRR5-22/2	945.430	946.083	-1753.491	0.422	980.428	0.367	15	0.141	K.SIAGIVTER.D
R5/RRR5-22/2	946.089	946.083	5.680	0.511	960.840	0.367	15	0.140	K.SIAGIVTER.D
R5/RRR5-22/2	945.938	946.083	-153.782	0.452	859.151	0.327	14	0.131	K.SIAGIVTER.D
R5/RRR5-22/2	998.959	999.102	-143.475	0.332	1028.464	0.539	15	0.124	R.LNAYIQGGY.-
R5/RRR5-22/2	998.846	999.102	-256.753	0.320	769.122	0.487	13	0.100	R.LNAYIQGGY.-
R5/RRR5-22/2	998.875	999.102	-227.573	0.278	680.607	0.544	12	0.098	R.LNAYIQGGY.-
R5/RRR5-9/2	1421.080	1421.624	-1089.858	0.492	1837.591	0.570	21	0.261	R.VLISGSLDLFSNR.F
R5/RRR5-9/2	1421.207	1421.624	-294.168	0.418	1369.798	0.551	18	0.195	R.VLISGSLDLFSNR.F
R5/RRR5-9/2	1311.017	1311.380	-277.707	0.566	1486.913	0.450	18	0.188	K.AGNEQFVTETSK.W
R5/RRR5-9/2	1299.791	1299.499	225.450	0.249	647.213	0.436	12	0.124	K.VPDVYGVFQFK.V
R5/RRR5-9/2	1300.385	1299.499	-87.903	0.270	352.726	0.387	12	0.119	-.VPDVYGVFQFK.-
R5/RRR5-9/2	1421.109	1421.624	-1069.330	0.227	348.822	0.356	14	0.118	R.VLISGSLDLFSNR.F
R5/RRR5-5/2	1040.179	1040.285	-102.359	0.492	1091.239	0.372	15	0.148	R.IRPVLTVNK.M
R5/RRR5-1/2	1039.486	1040.285	-1735.172	0.455	857.302	0.465	13	0.147	R.IRPVLTVNK.M
R5/RRR5-4/2	1307.942	1308.492	-1188.718	0.484	801.823	0.478	18	0.146	R.NMSVIAHVDHGK.S
R5/RRR5-4/2	1039.701	1040.285	-1527.789	0.487	805.106	0.450	13	0.144	R.IRPVLTVNK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1307.958	1308.492	-1176.253	0.471	712.364	0.473	18	0.142	R.NMSVIAHVDHGK.S
R5/RRR5-3/2	1039.528	1040.285	-1694.703	0.441	738.474	0.437	13	0.139	R.IRPVLTVNK.M
R5/RRR5-3/2	1039.683	1040.285	-1545.362	0.469	671.050	0.423	12	0.135	R.IRPVLTVNK.M
R5/RRR5-2/2	1040.030	1040.285	-245.880	0.337	758.951	0.387	12	0.132	R.IRPVLTVNK.M
R5/RRR5-5/2	1039.727	1040.285	-1502.786	0.441	749.069	0.348	12	0.129	R.IRPVLTVNK.M
R5/RRR5-4/2	1041.038	1040.285	-237.644	0.439	746.742	0.335	12	0.128	R.IRPVLTVNK.M
R5/RRR5-2/2	1041.126	1040.285	-152.481	0.495	725.546	0.329	12	0.113	-.IRPVLTVNK.-
R5/RRR5-4/3	1458.169	1458.755	-1090.904	0.533	891.535	0.388	24	0.093	R.IRPVLTVNKM*DR.C
R5/RRR5-4/3	1458.901	1458.755	100.060	0.545	1015.705	0.356	25	0.092	R.IRPVLTVNKM*DR.C
R5/RRR5-4/3	1458.644	1458.755	-76.319	0.540	775.201	0.373	23	0.088	R.IRPVLTVNKM*DR.C
R5/RRR5-3/3	1457.794	1458.755	-1349.573	0.492	567.587	0.343	21	0.085	R.IRPVLTVNKM*DR.C
R5/RRR5-3/3	1458.847	1458.755	63.052	0.479	573.679	0.294	22	0.083	R.IRPVLTVNKM*DR.C
R5/RRR5-1/3	1458.079	1458.755	-1152.816	0.412	581.739	0.308	22	0.081	R.IRPVLTVNKM*DR.C
R5/RRR5-21/3	1772.492	1772.935	-250.726	0.480	1179.157	0.503	29	0.133	K.TSQKPVSPEDGEEIKK.K
R5/RRR5-21/2	1081.262	1081.324	-57.366	0.392	945.353	0.276	14	0.126	K.TCLLIVFSK.G
R5/RRR5-21/3	1644.642	1644.762	-73.383	0.439	694.195	0.488	22	0.091	K.TSQKPVSPEDGEEIK.K
R5/RRR5-10/3	1977.827	1978.192	-185.449	0.537	3877.814	0.567	42	1.000	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-9/3	1978.594	1978.192	203.728	0.533	3747.245	0.550	40	0.923	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-9/2	1977.487	1978.192	-865.117	0.596	4131.532	0.548	30	0.815	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-9/2	1978.447	1978.192	129.178	0.615	4077.308	0.573	30	0.809	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-9/2	1978.879	1978.192	-158.677	0.632	3801.381	0.587	30	0.723	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-10/2	1977.645	1978.192	-784.936	0.566	3903.052	0.515	30	0.721	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-10/2	1978.489	1978.192	150.464	0.607	3006.531	0.574	27	0.488	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-10/2	1977.425	1978.192	-896.536	0.488	2814.829	0.483	26	0.410	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-10/3	1977.317	1978.192	-951.330	0.500	2570.311	0.466	36	0.402	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-8/2	1977.541	1978.192	-837.480	0.402	1730.538	0.421	24	0.206	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-5/2	1979.428	1978.192	119.465	0.429	1115.281	0.460	19	0.153	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-5/2	1979.156	1978.192	-18.225	0.451	1043.296	0.484	19	0.152	R.SNFGALLDTVELQLASGGGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1978.300	1978.192	54.735	0.367	1034.811	0.431	21	0.145	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-5/2	1978.987	1978.192	-103.915	0.367	1175.852	0.364	21	0.145	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-10/2	1978.759	1978.192	-219.819	0.327	599.994	0.418	17	0.125	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-10/2	1979.508	1978.192	159.788	0.368	572.640	0.395	19	0.125	R.SNFGALLDTVELQLASGGGK.S
R5/RRR5-9/3	1601.706	1601.736	-18.592	0.453	924.724	0.336	24	0.083	R.VCAYLDPSEPNHAK.I
R5/RRR5-9/3	1601.246	1601.736	-306.941	0.365	745.275	0.344	24	0.078	R.VCAYLDPSEPNHAK.I
R5/RRR5-10/3	1601.558	1601.736	-111.135	0.367	607.435	0.344	22	0.077	R.VCAYLDPSEPNHAK.I
R5/RRR5-26/2	1079.871	1080.176	-283.408	0.492	1683.043	0.580	19	0.242	R.LAGSSAAAFER.C
R5/RRR5-25/2	1079.929	1080.176	-229.653	0.535	1665.117	0.577	19	0.240	R.LAGSSAAAFER.C
R5/RRR5-26/2	1079.926	1080.176	-232.148	0.512	1662.600	0.563	19	0.236	R.LAGSSAAAFER.C
R5/RRR5-25/2	1080.858	1080.176	-294.816	0.557	1635.537	0.563	19	0.233	R.LAGSSAAAFER.C
R5/RRR5-25/2	1079.438	1080.176	-1614.690	0.442	1484.878	0.570	18	0.214	R.LAGSSAAAFER.C
R5/RRR5-26/2	1079.887	1080.176	-268.551	0.505	1426.193	0.542	18	0.203	R.LAGSSAAAFER.C
R5/RRR5-25/2	1734.261	1734.963	-984.330	0.480	1336.124	0.431	20	0.170	R.VGGPCGYGVCYLYLR.R
R5/RRR5-25/2	1734.257	1734.963	-986.591	0.487	1146.864	0.432	19	0.155	R.VGGPCGYGVCYLYLR.R
R5/RRR5-25/2	1734.133	1734.963	-1058.395	0.474	1082.587	0.443	19	0.153	R.VGGPCGYGVCYLYLR.R
R5/RRR5-25/2	1200.176	1199.374	-165.327	0.535	860.798	0.466	14	0.149	R.TCWYTVQIK.T
R5/RRR5-25/2	1199.127	1199.374	-206.824	0.408	759.642	0.358	13	0.131	R.TCWYTVQIK.T
R5/RRR5-25/2	1734.222	1734.963	-1007.015	0.442	716.020	0.361	15	0.123	R.VGGPCGYGVCYLYLR.R
R5/RRR5-25/2	1198.388	1199.374	-1661.921	0.339	526.524	0.212	11	0.116	-.TCWYTVQIK.-
R5/RRR5-22/2	1737.271	1737.720	-258.973	0.559	2195.973	0.580	24	0.321	K.DATDDFEDVGHSTTAR.A
R5/RRR5-23/2	1737.208	1737.720	-872.572	0.578	2035.159	0.570	24	0.290	K.DATDDFEDVGHSTTAR.A
R5/RRR5-22/2	1737.171	1737.720	-894.440	0.549	2028.861	0.564	23	0.287	K.DATDDFEDVGHSTTAR.A
R5/RRR5-23/2	1737.376	1737.720	-198.210	0.578	2051.276	0.538	23	0.282	K.DATDDFEDVGHSTTAR.A
R5/RRR5-23/2	1737.231	1737.720	-282.096	0.567	1924.802	0.563	23	0.270	K.DATDDFEDVGHSTTAR.A
R5/RRR5-22/2	1887.358	1888.025	-885.671	0.584	1756.863	0.631	28	0.265	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-23/2	1888.460	1888.025	231.353	0.573	1770.720	0.591	28	0.257	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-23/2	1887.435	1888.025	-844.637	0.565	1718.249	0.617	28	0.256	K.FLEDHPGGDDVLLSSTGK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1737.104	1737.720	-932.746	0.566	1816.820	0.537	23	0.247	K.DATDDFEDVGHSTTAR.A
R5/RRR5-22/2	1887.178	1888.025	-981.191	0.550	1662.899	0.595	27	0.242	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-22/2	1887.581	1888.025	-235.432	0.551	1574.661	0.621	27	0.238	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-23/2	1888.475	1888.025	239.067	0.549	1569.760	0.605	27	0.233	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-23/3	1887.850	1888.025	-92.854	0.507	1713.106	0.430	34	0.182	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-23/3	1644.882	1643.819	38.504	0.559	1603.431	0.465	28	0.178	K.HNSKDDCWLIIGGK.V
R5/RRR5-23/3	1645.343	1643.819	-290.268	0.554	1373.265	0.505	26	0.158	K.HNSKDDCWLIIGGK.V
R5/RRR5-22/3	1889.091	1888.025	35.114	0.497	1317.025	0.436	31	0.131	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-23/3	1887.430	1888.025	-847.112	0.471	1363.829	0.378	31	0.121	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-23/3	1737.437	1737.720	-163.082	0.365	929.394	0.555	29	0.121	K.DATDDFEDVGHSTTAR.A
R5/RRR5-23/3	1644.653	1643.819	-101.411	0.539	891.701	0.501	24	0.110	K.HNSKDDCWLIIGGK.V
R5/RRR5-22/3	1737.180	1737.720	-889.016	0.335	589.017	0.530	24	0.099	K.DATDDFEDVGHSTTAR.A
R5/RRR5-23/3	1737.818	1737.720	56.665	0.358	595.571	0.499	24	0.096	K.DATDDFEDVGHSTTAR.A
R5/RRR5-22/3	1737.831	1737.720	64.379	0.359	515.749	0.505	23	0.095	K.DATDDFEDVGHSTTAR.A
R5/RRR5-24/3	1737.525	1737.720	-112.656	0.334	543.266	0.499	23	0.094	K.DATDDFEDVGHSTTAR.A
R5/RRR5-24/3	1737.420	1737.720	-173.126	0.333	394.534	0.460	19	0.089	K.DATDDFEDVGHSTTAR.A
R5/RRR5-23/3	1737.882	1737.720	93.650	0.346	595.969	0.438	25	0.089	K.DATDDFEDVGHSTTAR.A
R5/RRR5-24/3	1738.789	1737.720	39.910	0.362	523.900	0.433	23	0.088	K.DATDDFEDVGHSTTAR.A
R5/RRR5-23/3	1887.491	1888.025	-815.170	0.401	863.597	0.361	26	0.084	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-22/3	1887.374	1888.025	-877.205	0.403	1081.848	0.301	29	0.084	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-22/3	1887.256	1888.025	-939.735	0.315	1053.410	0.185	28	0.065	K.FLEDHPGGDDVLLSSTGK.D
R5/RRR5-21/3	1887.017	1888.025	-1067.253	0.180	786.437	0.053	23	0.056	-.FLEDHPGGDDVLLSSTGK.-
R5/RRR5-24/2	1901.334	1902.051	-905.756	0.553	1323.742	0.613	26	0.206	K.FLEDHPGGDDVLLSSTAK.D
R5/RRR5-24/3	1657.425	1657.845	-254.171	0.463	1109.629	0.495	24	0.124	K.HNTKDDCWLIIGGK.V
R5/RRR5-24/3	1902.105	1902.051	28.630	0.434	1051.519	0.365	30	0.093	K.FLEDHPGGDDVLLSSTAK.D
R5/RRR5-23/3	1902.715	1902.051	-177.101	0.423	789.041	0.359	26	0.080	K.FLEDHPGGDDVLLSSTAK.D
R5/RRR5-24/3	1901.821	1902.051	-121.142	0.408	588.825	0.368	23	0.073	-.FLEDHPGGDDVLLSSTAK.-
R5/RRR5-10/2	1636.370	1636.825	-278.608	0.479	1512.937	0.491	19	0.200	K.ELILNYANQLCER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1636.494	1636.825	-202.873	0.417	1103.519	0.477	18	0.159	K.ELILNYANQLCER.L
R5/RRR5-9/3	1867.562	1866.102	246.981	0.406	886.832	0.437	21	0.094	K.TKELILNYANQLCER.L
R5/RRR5-9/3	1560.588	1559.710	-78.512	0.459	722.673	0.435	25	0.093	K.HYKGDHTYVPVSR.K
R5/RRR5-10/3	1560.404	1559.710	-196.689	0.463	678.251	0.432	25	0.093	K.HYKGDHTYVPVSR.K
R5/RRR5-9/3	1558.999	1559.710	-1101.122	0.438	657.595	0.435	24	0.092	K.HYKGDHTYVPVSR.K
R5/RRR5-10/3	1559.739	1559.710	18.861	0.469	880.821	0.382	26	0.091	K.HYKGDHTYVPVSR.K
R5/RRR5-9/3	1560.339	1559.710	-238.363	0.393	470.496	0.418	21	0.089	K.HYKGDHTYVPVSR.K
R5/RRR5-10/3	1560.041	1559.710	212.750	0.382	575.470	0.385	23	0.085	K.HYKGDHTYVPVSR.K
R5/RRR5-10/3	1866.299	1866.102	106.067	0.372	931.353	0.245	23	0.068	K.TKELILNYANQLCER.L
R5/RRR5-18/2	1502.396	1501.750	-236.464	0.595	2049.242	0.631	23	0.311	K.AVASINSVLTDLVAK.G
R5/RRR5-17/2	1501.485	1501.750	-177.489	0.557	2084.877	0.547	23	0.292	K.AVASINSVLTDLVAK.G
R5/RRR5-18/2	1501.375	1501.750	-250.570	0.523	1977.056	0.569	23	0.281	K.AVASINSVLTDLVAK.G
R5/RRR5-17/2	1501.280	1501.750	-314.362	0.487	1958.843	0.571	23	0.278	K.AVASINSVLTDLVAK.G
R5/RRR5-18/2	1501.381	1501.750	-246.492	0.485	1975.414	0.525	23	0.268	K.AVASINSVLTDLVAK.G
R5/RRR5-17/2	1501.373	1501.750	-251.712	0.522	1768.374	0.547	22	0.244	K.AVASINSVLTDLVAK.G
R5/RRR5-18/2	1380.289	1379.540	-182.606	0.511	1623.268	0.577	18	0.233	K.ANNVIYGLAQCR.G
R5/RRR5-18/2	1380.097	1379.540	-322.093	0.506	1641.812	0.552	18	0.229	K.ANNVIYGLAQCR.G
R5/RRR5-18/2	1378.980	1379.540	-1135.295	0.450	1474.985	0.448	18	0.187	K.ANNVIYGLAQCR.G
R5/RRR5-18/2	1379.012	1379.540	-1111.740	0.433	1286.401	0.422	17	0.165	K.ANNVIYGLAQCR.G
R5/RRR5-18/2	1185.253	1185.226	23.076	0.394	655.911	0.544	18	0.140	K.GSTGGGFATSSAGK.A
R5/RRR5-17/2	1379.288	1379.540	-183.715	0.335	738.541	0.387	13	0.128	K.ANNVIYGLAQCR.G
R5/RRR5-3/2	1502.194	1501.750	296.140	0.348	534.132	0.281	15	0.118	K.AVASINSVLTDLVAK.G
R5/RRR5-25/2	1229.058	1229.385	-267.499	0.512	1143.800	0.497	15	0.168	R.ISAM*IYEETR.G
R5/RRR5-25/2	1326.419	1326.527	-81.747	0.456	1425.363	0.365	19	0.167	R.DNIQGITKPAIR.R
R5/RRR5-25/2	1326.097	1326.527	-325.422	0.482	1187.198	0.452	18	0.164	R.DNIQGITKPAIR.R
R5/RRR5-25/2	1465.449	1465.720	-184.944	0.433	1235.745	0.434	18	0.162	K.TVTSLDVVYALKR.Q
R5/RRR5-25/2	1326.143	1326.527	-290.327	0.469	1105.697	0.452	18	0.158	R.DNIQGITKPAIR.R
R5/RRR5-25/2	1327.043	1326.527	-365.693	0.490	1163.421	0.377	18	0.150	R.DNIQGITKPAIR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/2	1326.320	1326.527	-156.896	0.449	1135.469	0.385	18	0.150	R.DNIQGITKPAIR.R
R5/RRR5-26/2	1325.813	1326.527	-1296.811	0.442	973.306	0.450	17	0.150	R.DNIQGITKPAIR.R
R5/RRR5-26/2	1326.113	1326.527	-312.861	0.468	1006.370	0.430	17	0.149	R.DNIQGITKPAIR.R
R5/RRR5-25/2	1326.254	1326.527	-206.386	0.480	976.611	0.403	17	0.144	R.DNIQGITKPAIR.R
R5/RRR5-25/2	1326.526	1326.527	-0.795	0.419	961.195	0.374	16	0.138	R.DNIQGITKPAIR.R
R5/RRR5-27/2	1326.094	1326.527	-327.823	0.288	337.495	0.356	11	0.120	-.DNIQGITKPAIR.-
R5/RRR5-5/2	1572.260	1571.718	-292.071	0.522	2234.210	0.560	21	0.320	R.GLEGLTVQQAIDGNR.L
R5/RRR5-4/2	1572.314	1571.718	-257.331	0.515	2298.521	0.495	21	0.311	R.GLEGLTVQQAIDGNR.L
R5/RRR5-4/2	1649.221	1649.744	-926.251	0.471	1914.760	0.525	21	0.259	R.YGDQTSTITAAHVER.G
R5/RRR5-4/2	1571.094	1571.718	-1036.448	0.396	1901.223	0.498	21	0.248	R.GLEGLTVQQAIDGNR.L
R5/RRR5-5/3	1649.975	1649.744	140.676	0.541	1564.670	0.659	29	0.237	R.YGDQTSTITAAHVER.G
R5/RRR5-4/2	1571.179	1571.718	-982.078	0.384	1823.912	0.456	20	0.227	R.GLEGLTVQQAIDGNR.L
R5/RRR5-5/2	1572.249	1571.718	-298.770	0.507	1674.054	0.525	19	0.224	R.GLEGLTVQQAIDGNR.L
R5/RRR5-7/3	1649.370	1649.744	-227.501	0.508	1449.533	0.642	28	0.211	R.YGDQTSTITAAHVER.G
R5/RRR5-5/2	1649.126	1649.744	-983.917	0.468	1476.464	0.562	19	0.209	R.YGDQTSTITAAHVER.G
R5/RRR5-5/2	1571.199	1571.718	-969.597	0.460	1555.539	0.517	19	0.208	R.GLEGLTVQQAIDGNR.L
R5/RRR5-4/3	1649.713	1649.744	-18.385	0.518	1290.861	0.688	27	0.202	R.YGDQTSTITAAHVER.G
R5/RRR5-5/2	1649.338	1649.744	-246.501	0.498	1430.945	0.547	20	0.202	R.YGDQTSTITAAHVER.G
R5/RRR5-5/3	1650.065	1649.744	195.429	0.530	1439.161	0.593	28	0.192	R.YGDQTSTITAAHVER.G
R5/RRR5-5/2	1650.200	1649.744	277.444	0.516	1360.938	0.533	20	0.192	R.YGDQTSTITAAHVER.G
R5/RRR5-5/3	1649.325	1649.744	-254.343	0.520	1320.571	0.637	27	0.190	R.YGDQTSTITAAHVER.G
R5/RRR5-4/3	1649.825	1649.744	49.520	0.526	1337.034	0.612	28	0.184	R.YGDQTSTITAAHVER.G
R5/RRR5-5/2	1400.195	1399.685	-350.482	0.488	1206.678	0.518	18	0.176	R.EILAGVNPM*VIAR.L
R5/RRR5-5/2	1399.406	1399.685	-199.669	0.458	1352.189	0.439	19	0.174	R.EILAGVNPM*VIAR.L
R5/RRR5-5/2	1384.320	1383.685	-264.771	0.527	1234.473	0.465	18	0.168	R.EILAGVNPMVIAR.L
R5/RRR5-2/3	1649.371	1649.744	-226.388	0.502	1171.809	0.627	26	0.167	R.YGDQTSTITAAHVER.G
R5/RRR5-5/2	1384.407	1383.685	-201.608	0.517	1330.309	0.412	18	0.166	R.EILAGVNPMVIAR.L
R5/RRR5-3/3	1649.886	1649.744	86.252	0.534	1185.758	0.601	27	0.161	R.YGDQTSTITAAHVER.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1649.773	1649.744	17.572	0.515	1115.377	0.623	26	0.159	R.YGDQTSTITAAHVER.G
R5/RRR5-4/3	1650.079	1649.744	203.664	0.496	1063.096	0.637	25	0.157	R.YGDQTSTITAAHVER.G
R5/RRR5-3/3	1650.123	1649.744	230.704	0.516	1190.599	0.556	26	0.149	R.YGDQTSTITAAHVER.G
R5/RRR5-4/2	1398.797	1399.685	-1353.399	0.381	943.957	0.404	17	0.140	R.EILAGVNPM*VIAR.L
R5/RRR5-5/2	1383.135	1383.685	-1124.005	0.400	876.940	0.416	16	0.138	-.EILAGVNPMVIAR.-
R5/RRR5-5/2	1571.715	1571.718	-1.450	0.323	810.013	0.448	15	0.135	R.GLEGLTVQQAIDGNR.L
R5/RRR5-1/2	1570.740	1571.718	-1262.498	0.336	1049.908	0.328	17	0.134	R.GLEGLTVQQAIDGNR.L
R5/RRR5-7/3	1651.073	1649.744	200.278	0.448	991.457	0.565	25	0.132	R.YGDQTSTITAAHVER.G
R5/RRR5-4/2	1398.887	1399.685	-1288.895	0.391	779.044	0.367	17	0.131	R.EILAGVNPM*VIAR.L
R5/RRR5-5/2	1399.181	1399.685	-1077.647	0.362	824.267	0.332	17	0.128	R.EILAGVNPM*VIAR.L
R5/RRR5-3/3	1649.587	1649.744	-95.429	0.459	953.547	0.553	23	0.126	R.YGDQTSTITAAHVER.G
R5/RRR5-4/2	1399.138	1399.685	-1108.571	0.360	857.682	0.292	16	0.125	R.EILAGVNPM*VIAR.L
R5/RRR5-7/3	1651.065	1649.744	194.940	0.379	834.550	0.533	23	0.113	R.YGDQTSTITAAHVER.G
R5/RRR5-22/2	1421.866	1421.619	174.234	0.513	1233.439	0.581	18	0.192	K.CHFVAIDIFNGK.K
R5/RRR5-22/2	1300.205	1300.483	-214.476	0.444	1487.254	0.403	20	0.181	R.LPTDDSLLGQIK.T
R5/RRR5-22/2	1420.951	1421.619	-1177.500	0.461	1081.419	0.578	17	0.176	K.CHFVAIDIFNGK.K
R5/RRR5-22/2	1301.320	1300.483	-125.475	0.499	1253.574	0.455	20	0.171	R.LPTDDSLLGQIK.T
R5/RRR5-22/2	1300.228	1300.483	-196.581	0.455	1180.452	0.398	19	0.155	R.LPTDDSLLGQIK.T
R5/RRR5-22/2	1420.525	1421.619	-1478.229	0.388	862.406	0.543	15	0.152	K.CHFVAIDIFNGK.K
R5/RRR5-22/2	1134.892	1135.255	-320.697	0.295	221.534	0.491	14	0.132	K.TYPQQAGTIR.K
R5/RRR5-23/2	1135.904	1135.255	-310.063	0.289	239.234	0.516	14	0.132	K.TYPQQAGTIR.K
R5/RRR5-21/2	1134.776	1135.255	-423.769	0.306	240.291	0.422	14	0.131	K.TYPQQAGTIR.K
R5/RRR5-22/2	1135.949	1135.255	-270.063	0.290	258.419	0.439	13	0.129	K.TYPQQAGTIR.K
R5/RRR5-22/2	1134.522	1135.255	-1531.868	0.233	240.534	0.485	14	0.127	K.TYPQQAGTIR.K
R5/RRR5-21/2	1134.845	1135.255	-362.787	0.287	219.172	0.373	14	0.127	-.TYPQQAGTIR.-
R5/RRR5-21/2	1134.832	1135.255	-374.119	0.221	295.788	0.440	15	0.125	K.TYPQQAGTIR.K
R5/RRR5-22/2	1135.967	1135.255	-253.892	0.214	369.173	0.381	15	0.123	K.TYPQQAGTIR.K
R5/RRR5-22/2	1134.496	1135.255	-1554.891	0.188	252.767	0.377	15	0.123	K.TYPQQAGTIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1135.008	1135.255	-218.077	0.286	167.148	0.430	12	0.123	-.TYPQQAGTIR.-
R5/RRR5-23/2	1135.913	1135.255	-301.653	0.216	226.359	0.462	14	0.122	-.TYPQQAGTIR.-
R5/RRR5-22/2	1300.896	1300.483	317.964	0.285	531.240	0.349	15	0.122	R.LPTDDSLLGQIK.T
R5/RRR5-22/2	1134.420	1135.255	-1622.343	0.160	251.890	0.320	15	0.122	K.TYPQQAGTIR.K
R5/RRR5-22/3	1422.327	1421.619	-206.013	0.382	1203.372	0.301	23	0.090	K.CHFVAIDIFNGK.K
R5/RRR5-22/3	1422.739	1421.619	84.747	0.419	1173.064	0.230	24	0.077	K.CHFVAIDIFNGK.K
R5/RRR5-19/2	1298.765	1299.585	-1405.268	0.487	1974.542	0.497	19	0.261	R.TLINNLIIGVTK.G
R5/RRR5-19/2	1299.221	1299.585	-280.982	0.509	1755.809	0.532	19	0.240	R.TLINNLIIGVTK.G
R5/RRR5-19/2	1299.173	1299.585	-318.124	0.517	1846.893	0.457	19	0.233	R.TLINNLIIGVTK.G
R5/RRR5-18/3	1501.842	1501.669	115.339	0.541	1735.286	0.477	29	0.204	K.SLSHVAVNFSQPSK.N
R5/RRR5-18/2	1299.100	1299.585	-374.407	0.440	849.725	0.463	15	0.143	R.TLINNLIIGVTK.G
R5/RRR5-18/3	1500.696	1501.669	-1318.415	0.508	1428.636	0.406	26	0.137	K.SLSHVAVNFSQPSK.N
R5/RRR5-18/3	1501.306	1501.669	-242.435	0.545	1284.033	0.409	25	0.121	K.SLSHVAVNFSQPSK.N
R5/RRR5-19/3	1715.234	1715.885	-965.598	0.454	1006.539	0.278	24	0.075	-.YIHSSEQLEIPDGVK.-
R5/RRR5-19/3	1715.861	1715.885	-14.323	0.455	1141.757	0.215	26	0.073	-.YIHSSEQLEIPDGVK.-
R5/RRR5-19/3	1715.502	1715.885	-224.048	0.432	717.252	0.200	20	0.032	-.YIHSSEQLEIPDGVK.-
R5/RRR5-1/2	951.334	951.236	102.599	0.200	902.848	0.060	12	0.108	-.M*GKALMKR.V
R5/RRR5-14/2	1897.631	1898.214	-836.420	0.529	1729.807	0.576	29	0.246	K.VM*VGLPTTGGVTPVPGAAEK.A
R5/RRR5-14/2	1594.475	1594.853	-237.594	0.472	1715.662	0.406	18	0.202	K.FASFETIVEM*IYK.H
R5/RRR5-14/2	1898.432	1898.214	115.405	0.551	1248.199	0.619	26	0.198	K.VM*VGLPTTGGVTPVPGAAEK.A
R5/RRR5-14/2	1595.034	1594.853	114.208	0.520	1556.993	0.466	18	0.197	K.FASFETIVEM*IYK.H
R5/RRR5-14/2	1897.605	1898.214	-850.240	0.522	1340.137	0.565	27	0.196	K.VM*VGLPTTGGVTPVPGAAEK.A
R5/RRR5-14/2	1881.784	1882.214	-229.195	0.540	1287.246	0.569	25	0.191	K.VMVGLPTTGGVTPVPGAAEK.A
R5/RRR5-14/2	1881.374	1882.214	-981.290	0.504	1118.250	0.587	24	0.178	K.VMVGLPTTGGVTPVPGAAEK.A
R5/RRR5-14/2	1595.463	1594.853	-245.121	0.537	1378.419	0.427	18	0.172	K.FASFETIVEM*IYK.H
R5/RRR5-14/2	1883.951	1882.214	-140.156	0.504	1003.204	0.536	23	0.161	K.VMVGLPTTGGVTPVPGAAEK.A
R5/RRR5-14/2	1594.408	1594.853	-279.609	0.486	1264.020	0.408	18	0.160	K.FASFETIVEM*IYK.H
R5/RRR5-14/2	1594.159	1594.853	-1065.887	0.453	1253.108	0.390	19	0.158	K.FASFETIVEM*IYK.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1579.741	1578.853	-71.274	0.370	994.934	0.400	16	0.142	K.FASFETIVEMIYK.H
R5/RRR5-16/2	1882.592	1882.214	201.377	0.451	693.891	0.510	18	0.137	K.VMVGLPTTGGVTPVPGAAEK.A
R5/RRR5-14/2	1594.315	1594.853	-967.408	0.322	325.234	0.339	15	0.126	K.FASFETIVEM*IYK.H
R5/RRR5-14/2	1594.068	1594.853	-1122.785	0.356	845.434	0.286	16	0.124	K.FASFETIVEM*IYK.H
R5/RRR5-15/2	1593.736	1594.853	-1332.210	0.300	457.041	0.360	15	0.124	K.FASFETIVEM*IYK.H
R5/RRR5-15/2	1593.994	1594.853	-1169.462	0.320	359.632	0.315	14	0.124	K.FASFETIVEM*IYK.H
R5/RRR5-14/2	1594.412	1594.853	-277.151	0.268	160.288	0.303	12	0.123	-.FASFETIVEM*IYK.-
R5/RRR5-1/2	1594.903	1594.853	31.232	0.282	320.288	0.308	13	0.122	K.FASFETIVEM*IYK.H
R5/RRR5-15/2	1579.974	1578.853	76.593	0.245	670.439	0.320	16	0.122	K.FASFETIVEMIYK.H
R5/RRR5-14/2	1594.614	1594.853	-150.120	0.351	465.427	0.308	14	0.122	K.FASFETIVEM*IYK.H
R5/RRR5-16/2	1882.339	1882.214	66.631	0.342	426.889	0.354	16	0.119	K.VMVGLPTTGGVTPVPGAAEK.A
R5/RRR5-5/2	1554.216	1554.724	-972.708	0.446	1541.284	0.425	21	0.189	K.LSTSAQSEVEYVLK.F
R5/RRR5-5/2	1279.007	1279.424	-327.160	0.451	1003.328	0.350	17	0.138	R.NIEQFKVEGSK.V
R5/RRR5-5/2	1278.554	1279.424	-1467.032	0.421	557.496	0.393	14	0.127	R.NIEQFKVEGSK.V
R5/RRR5-5/2	1086.074	1086.226	-140.309	0.295	850.603	0.239	14	0.121	K.FPLHSTLDR.L
R5/RRR5-5/2	1553.628	1554.724	-1353.004	0.255	903.641	0.244	18	0.119	K.LSTSAQSEVEYVLK.F
R5/RRR5-4/2	1087.305	1086.226	73.688	0.299	541.607	0.236	11	0.097	-.FPLHSTLDR.-
R5/RRR5-13/2	1347.083	1347.414	-246.186	0.531	2204.069	0.606	20	0.332	K.APVTSAEVSQDSR.F
R5/RRR5-13/2	1346.538	1347.414	-1396.783	0.484	2189.565	0.565	20	0.316	K.APVTSAEVSQDSR.F
R5/RRR5-13/2	1347.052	1347.414	-269.460	0.511	2132.398	0.575	20	0.310	K.APVTSAEVSQDSR.F
R5/RRR5-13/2	1126.010	1126.242	-206.010	0.405	832.142	0.359	18	0.134	R.FITTADGSSVK.F
R5/RRR5-13/2	1125.441	1126.242	-1604.825	0.301	621.746	0.341	15	0.123	R.FITTADGSSVK.F
R5/RRR5-13/2	1125.910	1126.242	-295.743	0.335	570.678	0.289	15	0.121	R.FITTADGSSVK.F
R5/RRR5-13/3	1949.245	1949.144	51.869	0.442	361.641	0.547	24	0.089	R.ACAFSEDTHLLLTGGVEK.I
R5/RRR5-14/2	1608.547	1608.814	-166.969	0.526	2269.688	0.427	23	0.289	K.FKDLVEEISESLAK.T
R5/RRR5-14/2	1894.471	1894.969	-263.465	0.587	1970.713	0.585	26	0.285	K.TEGKETEEDSSAAGLLEK.L
R5/RRR5-14/2	1608.432	1608.814	-238.536	0.540	1967.944	0.464	22	0.251	K.FKDLVEEISESLAK.T
R5/RRR5-14/3	1766.006	1765.898	61.411	0.487	675.830	0.501	26	0.095	K.KSEEVATKEESTEAVK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/3	1894.019	1894.969	-1032.763	0.346	1132.457	0.285	29	0.082	K.TEGKETEEDSSAAGLLEK.L
R5/RRR5-16/3	1894.490	1894.969	-253.840	0.418	1032.582	0.228	29	0.069	K.TEGKETEEDSSAAGLLEK.L
R5/RRR5-14/3	1608.637	1608.814	-110.760	0.423	1068.413	0.194	27	0.068	K.FKDLVEEISESLAK.T
R5/RRR5-19/3	1824.520	1825.078	-856.386	0.569	2144.328	0.507	33	0.292	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-18/2	1808.310	1809.079	-981.194	0.509	2034.938	0.481	21	0.263	K.AFMIDKDQVDWIQAK.F
R5/RRR5-19/3	1824.291	1825.078	-982.534	0.553	1767.891	0.509	30	0.217	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-18/2	1341.103	1341.574	-351.908	0.426	1517.117	0.553	18	0.213	K.LSAVFVNGFVCK.N
R5/RRR5-18/2	1342.838	1341.574	197.708	0.568	1402.686	0.578	18	0.208	K.LSAVFVNGFVCK.N
R5/RRR5-18/3	1825.113	1825.078	19.276	0.579	1673.557	0.518	30	0.203	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-19/2	1798.407	1798.942	-856.427	0.499	1163.933	0.632	22	0.193	R.IDFAPNGQNPPHTHPR.A
R5/RRR5-19/2	1798.568	1798.942	-208.826	0.494	1097.942	0.647	21	0.189	R.IDFAPNGQNPPHTHPR.A
R5/RRR5-19/3	1824.893	1825.078	-101.991	0.562	1573.377	0.516	29	0.187	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-18/2	1799.175	1798.942	129.597	0.530	1053.149	0.637	21	0.185	R.IDFAPNGQNPPHTHPR.A
R5/RRR5-19/2	1824.439	1825.078	-901.145	0.569	1115.376	0.581	23	0.182	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-19/2	1799.435	1798.942	274.847	0.491	1069.177	0.626	19	0.181	R.IDFAPNGQNPPHTHPR.A
R5/RRR5-19/2	1798.474	1798.942	-261.053	0.472	1006.322	0.629	20	0.177	R.IDFAPNGQNPPHTHPR.A
R5/RRR5-18/3	1808.651	1809.079	-237.320	0.518	1454.442	0.536	30	0.175	K.AFMIDKDQVDWIQAK.F
R5/RRR5-18/2	1798.331	1798.942	-898.947	0.469	976.539	0.626	20	0.174	R.IDFAPNGQNPPHTHPR.A
R5/RRR5-19/2	1824.389	1825.078	-928.483	0.561	993.008	0.590	22	0.174	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-18/2	1798.413	1798.942	-853.088	0.501	913.379	0.616	20	0.169	R.IDFAPNGQNPPHTHPR.A
R5/RRR5-18/2	1825.365	1825.078	157.489	0.587	968.209	0.558	22	0.167	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-18/2	1825.276	1825.078	108.932	0.577	742.659	0.606	20	0.160	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-18/3	1810.017	1809.079	-34.344	0.590	1269.502	0.560	30	0.158	K.AFMIDKDQVDWIQAK.F
R5/RRR5-18/2	1825.444	1825.078	201.146	0.576	699.873	0.575	20	0.154	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-19/2	1807.619	1809.079	-1364.670	0.406	1365.813	0.300	20	0.150	K.AFMIDKDQVDWIQAK.F
R5/RRR5-19/2	1824.365	1825.078	-941.649	0.531	791.676	0.505	21	0.149	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-19/3	1808.653	1809.079	-235.898	0.490	1266.694	0.511	28	0.145	K.AFMIDKDQVDWIQAK.F
R5/RRR5-19/2	1340.398	1341.574	-1628.161	0.347	875.770	0.412	15	0.136	K.LSAVFVNGFVCK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/3	1825.064	1825.078	-7.994	0.555	1254.203	0.477	27	0.134	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-19/2	1807.970	1809.079	-1169.709	0.465	977.042	0.348	17	0.132	K.AFMIDKDQVDWIQAK.F
R5/RRR5-19/2	1341.497	1341.574	-57.099	0.386	345.675	0.442	12	0.124	-.LSAVFVNGFVCK.-
R5/RRR5-18/3	1824.844	1825.078	-128.966	0.561	1066.036	0.484	26	0.119	K.AFM*IDKDQVDWIQAK.F
R5/RRR5-19/3	1809.031	1809.079	-26.207	0.382	800.291	0.440	24	0.095	K.AFMIDKDQVDWIQAK.F
R5/RRR5-19/3	1808.711	1809.079	-204.108	0.348	858.467	0.355	22	0.084	K.AFMIDKDQVDWIQAK.F
R5/RRR5-17/2	1669.961	1669.904	34.048	0.550	1207.935	0.515	21	0.177	R.RVEPYVAYGYPNLK.S
R5/RRR5-16/2	1513.415	1513.718	-200.683	0.423	1228.593	0.484	21	0.172	R.VEPYVAYGYPNLK.S
R5/RRR5-17/2	1669.451	1669.904	-272.574	0.540	1092.395	0.541	20	0.172	R.RVEPYVAYGYPNLK.S
R5/RRR5-17/2	1670.343	1669.904	263.323	0.550	1000.703	0.514	19	0.160	R.RVEPYVAYGYPNLK.S
R5/RRR5-16/2	1669.583	1669.904	-193.205	0.544	989.184	0.459	19	0.150	R.RVEPYVAYGYPNLK.S
R5/RRR5-17/2	1513.148	1513.718	-1040.455	0.377	1186.183	0.367	21	0.150	R.VEPYVAYGYPNLK.S
R5/RRR5-16/2	1513.091	1513.718	-1078.526	0.314	973.584	0.414	21	0.142	R.VEPYVAYGYPNLK.S
R5/RRR5-17/2	1512.649	1513.718	-1372.094	0.319	1051.810	0.362	20	0.140	R.VEPYVAYGYPNLK.S
R5/RRR5-16/2	1513.202	1513.718	-1004.817	0.350	850.897	0.405	20	0.137	R.VEPYVAYGYPNLK.S
R5/RRR5-16/2	1669.387	1669.904	-911.468	0.500	653.468	0.411	16	0.129	R.RVEPYVAYGYPNLK.S
R5/RRR5-16/2	1265.630	1266.429	-1425.517	0.276	889.145	0.295	14	0.126	K.EANNFLWPFK.L
R5/RRR5-16/2	1266.275	1266.429	-121.889	0.382	740.123	0.305	13	0.125	K.EANNFLWPFK.L
R5/RRR5-17/2	1266.024	1266.429	-320.361	0.281	683.969	0.298	12	0.121	K.EANNFLWPFK.L
R5/RRR5-17/2	1513.176	1513.718	-1022.312	0.298	784.332	0.251	18	0.121	R.VEPYVAYGYPNLK.S
R5/RRR5-17/2	1266.627	1266.429	156.729	0.291	633.913	0.236	13	0.119	K.EANNFLWPFK.L
R5/RRR5-16/2	1265.832	1266.429	-1265.405	0.269	559.090	0.263	12	0.119	K.EANNFLWPFK.L
R5/RRR5-17/2	1266.119	1266.429	-245.393	0.320	669.791	0.197	12	0.116	K.EANNFLWPFK.L
R5/RRR5-16/2	1294.353	1294.485	-102.029	0.518	1290.845	0.559	18	0.192	K.VIQDHVATVVGR.W
R5/RRR5-15/2	1878.504	1879.019	-809.286	0.503	1495.740	0.448	21	0.187	R.AWDVLNEIFNEDGSLR.Q
R5/RRR5-15/2	1877.996	1879.019	-1080.522	0.476	1026.795	0.516	21	0.160	R.AWDVLNEIFNEDGSLR.Q
R5/RRR5-15/2	935.140	935.059	86.398	0.497	514.393	0.417	13	0.136	R.VLGEDFVR.I
R5/RRR5-16/2	935.093	935.059	35.993	0.468	541.732	0.417	13	0.136	R.VLGEDFVR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	935.030	935.059	-30.655	0.458	463.091	0.380	13	0.133	R.VLGEDFVR.I
R5/RRR5-15/2	1101.958	1102.263	-277.505	0.479	2010.153	0.480	18	0.262	R.ALLEVVESGGK.N
R5/RRR5-15/2	1101.980	1102.263	-257.389	0.502	1823.760	0.510	18	0.243	R.ALLEVVESGGK.N
R5/RRR5-16/2	1102.162	1102.263	-92.271	0.485	1848.724	0.489	18	0.241	R.ALLEVVESGGK.N
R5/RRR5-15/2	1102.055	1102.263	-189.491	0.450	1683.573	0.526	17	0.228	R.ALLEVVESGGK.N
R5/RRR5-16/2	1102.902	1102.263	-328.666	0.493	1564.187	0.530	17	0.215	R.ALLEVVESGGK.N
R5/RRR5-14/2	1102.029	1102.263	-212.937	0.323	1262.309	0.335	17	0.149	R.ALLEVVESGGK.N
R5/RRR5-15/2	920.548	921.075	-1663.827	0.306	770.296	0.370	13	0.130	R.YIAGLQQK.Y
R5/RRR5-15/2	921.095	921.075	21.054	0.383	764.530	0.333	13	0.130	R.YIAGLQQK.Y
R5/RRR5-15/2	921.214	921.075	150.769	0.341	761.325	0.324	13	0.128	R.YIAGLQQK.Y
R5/RRR5-15/3	1782.808	1783.099	-163.774	0.353	1126.386	0.380	28	0.098	R.KIASLDTHIALACAGLK.A
R5/RRR5-7/2	1761.393	1761.957	-890.481	0.559	2583.586	0.543	26	0.385	K.YGLAADNVVDAVLVDAR.G
R5/RRR5-7/2	1761.518	1761.957	-249.709	0.541	2594.032	0.509	23	0.374	K.YGLAADNVVDAVLVDAR.G
R5/RRR5-7/2	1762.323	1761.957	208.103	0.580	2506.598	0.540	24	0.366	K.YGLAADNVVDAVLVDAR.G
R5/RRR5-7/2	1729.437	1728.972	269.617	0.508	1020.904	0.510	22	0.162	R.WQAVAPSLPDDLFIR.V
R5/RRR5-7/2	1829.232	1830.078	-1012.273	0.457	1127.441	0.349	23	0.142	R.SERPEAFAVLDLVNIR.A
R5/RRR5-7/2	1727.621	1728.972	-1365.000	0.346	846.158	0.445	20	0.139	R.WQAVAPSLPDDLFIR.V
R5/RRR5-7/2	1728.521	1728.972	-261.347	0.427	678.482	0.458	19	0.136	R.WQAVAPSLPDDLFIR.V
R5/RRR5-7/2	1829.775	1830.078	-165.986	0.459	781.953	0.409	19	0.132	R.SERPEAFAVLDLVNIR.A
R5/RRR5-1/2	1729.248	1728.972	160.468	0.359	663.092	0.390	18	0.127	R.WQAVAPSLPDDLFIR.V
R5/RRR5-7/3	1830.963	1830.078	-62.806	0.507	857.700	0.374	24	0.084	-.SERPEAFAVLDLVNIR.-
R5/RRR5-7/3	1830.173	1830.078	51.999	0.496	886.738	0.335	24	0.079	-.SERPEAFAVLDLVNIR.-
R5/RRR5-7/3	1829.744	1830.078	-182.959	0.378	764.951	0.177	22	0.058	-.SERPEAFAVLDLVNIR.-
R5/RRR5-22/2	1964.515	1965.230	-875.566	0.509	1796.478	0.568	24	0.253	R.IAECLVGDETGIIVFTAR.N
R5/RRR5-22/2	1964.548	1965.230	-858.662	0.515	1780.994	0.576	24	0.252	R.IAECLVGDETGIIVFTAR.N
R5/RRR5-22/2	1964.173	1965.230	-1050.319	0.478	1452.822	0.556	22	0.205	R.IAECLVGDETGIIVFTAR.N
R5/RRR5-22/2	1137.005	1136.237	-204.126	0.447	887.591	0.487	15	0.149	K.AAESPADFTVK.E
R5/RRR5-22/3	1798.400	1799.070	-931.326	0.510	1202.608	0.497	27	0.135	K.VDQLRPGTHGHNLLLK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1136.096	1136.237	-124.432	0.364	617.132	0.442	15	0.132	K.AAESPADFTVK.E
R5/RRR5-22/3	1964.034	1965.230	-1121.560	0.308	1258.415	0.349	29	0.103	R.IAECLVGDETGIIVFTAR.N
R5/RRR5-22/3	1964.404	1965.230	-932.497	0.332	1123.283	0.394	26	0.101	R.IAECLVGDETGIIVFTAR.N
R5/RRR5-22/3	1798.287	1799.070	-994.500	0.422	832.738	0.367	23	0.082	K.VDQLRPGTHGHNLLLK.V
R5/RRR5-22/3	1798.726	1799.070	-191.798	0.404	707.232	0.227	23	0.062	-.VDQLRPGTHGHNLLLK.-
R5/RRR5-10/2	1791.417	1791.940	-852.934	0.525	1918.055	0.513	26	0.257	K.SYELPDGQVITIGNER.-
R5/RRR5-10/2	1791.395	1791.940	-865.042	0.500	1395.596	0.590	23	0.208	K.SYELPDGQVITIGNER.-
R5/RRR5-10/2	1792.446	1791.940	-276.548	0.552	1313.641	0.562	23	0.195	K.SYELPDGQVITIGNER.-
R5/RRR5-11/2	1955.338	1955.244	48.239	0.508	1157.453	0.598	24	0.186	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-11/2	1791.431	1791.940	-845.068	0.462	1423.048	0.468	23	0.186	K.SYELPDGQVITIGNER.-
R5/RRR5-10/2	1954.931	1955.244	-160.433	0.528	1176.084	0.566	23	0.181	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-11/2	1954.787	1955.244	-234.102	0.538	1031.434	0.596	22	0.174	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-11/2	1955.704	1955.244	235.919	0.521	908.455	0.625	21	0.169	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-10/2	1954.670	1955.244	-807.504	0.508	870.110	0.602	21	0.163	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-10/2	1955.668	1955.244	217.643	0.517	878.503	0.589	21	0.162	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-13/3	1955.176	1955.244	-34.738	0.403	840.130	0.421	28	0.094	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-11/3	1954.528	1955.244	-880.360	0.445	619.343	0.456	25	0.093	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-10/3	1956.013	1955.244	-118.224	0.492	842.405	0.405	29	0.092	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-13/3	1955.393	1955.244	76.846	0.415	682.869	0.423	27	0.090	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-10/3	1955.322	1955.244	40.499	0.405	648.744	0.430	26	0.090	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-11/3	1955.652	1955.244	209.624	0.454	775.892	0.398	28	0.089	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-10/3	1956.203	1955.244	-20.950	0.463	518.802	0.358	25	0.084	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-10/3	1954.726	1955.244	-778.424	0.414	644.439	0.373	25	0.083	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-12/3	1955.341	1955.244	49.985	0.379	553.757	0.353	24	0.082	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-12/3	1954.854	1955.244	-199.998	0.400	568.016	0.327	25	0.080	R.VAPEEHPVLLTEAPINPK.S
R5/RRR5-3/2	1441.696	1441.652	30.946	0.498	1777.054	0.488	21	0.232	K.LLVSEDLQPLGEK.L
R5/RRR5-3/2	1441.073	1441.652	-1098.866	0.474	1791.895	0.456	20	0.225	K.LLVSEDLQPLGEK.L
R5/RRR5-4/2	1440.693	1441.652	-1363.798	0.410	1552.770	0.435	20	0.192	K.LLVSEDLQPLGEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-3/2	1440.744	1441.652	-1328.057	0.398	1597.693	0.366	19	0.183	K.LLVSEDLQPLGEK.L
R5/RRR5-4/3	1948.236	1948.218	9.287	0.533	1080.182	0.606	26	0.149	R.IRDPDYHVTLRPHLSK.E
R5/RRR5-4/3	1490.455	1490.705	-167.669	0.327	969.104	0.376	24	0.088	K.EVM*DGSKPAAELVK.L
R5/RRR5-3/3	1490.464	1490.705	-161.999	0.260	881.443	0.256	23	0.068	K.EVM*DGSKPAAELVK.L
R5/RRR5-4/3	1490.665	1490.705	-26.454	0.307	524.045	0.294	18	0.059	-.EVM*DGSKPAAELVK.-
R5/RRR5-16/2	1479.660	1479.660	0.198	0.402	1527.582	0.398	17	0.181	R.STNEALLVIEAYR.T
R5/RRR5-16/2	1479.031	1479.660	-1104.936	0.302	1584.930	0.218	18	0.155	R.STNEALLVIEAYR.T
R5/RRR5-16/2	1030.827	1031.188	-351.884	0.477	1145.073	0.348	15	0.147	R.LDNLSSLIR.Q
R5/RRR5-17/2	1479.501	1479.660	-107.881	0.325	1148.478	0.375	17	0.146	R.STNEALLVIEAYR.T
R5/RRR5-16/2	1031.018	1031.188	-165.495	0.472	1057.703	0.327	15	0.139	R.LDNLSSLIR.Q
R5/RRR5-15/2	1031.073	1031.188	-112.169	0.422	1134.651	0.297	15	0.139	R.LDNLSSLIR.Q
R5/RRR5-16/2	1031.012	1031.188	-171.553	0.399	1104.282	0.274	15	0.135	R.LDNLSSLIR.Q
R5/RRR5-15/2	1031.031	1031.188	-152.549	0.402	848.172	0.247	14	0.124	R.LDNLSSLIR.Q
R5/RRR5-16/3	1345.560	1345.486	55.531	0.423	1027.584	0.363	22	0.090	R.DRGPYPADQVVK.D
R5/RRR5-21/3	1866.901	1867.012	-59.367	0.519	1707.679	0.511	28	0.213	R.HDVESAIPYHAELTQR.G
R5/RRR5-21/3	1867.060	1867.012	26.118	0.507	1424.828	0.537	26	0.176	R.HDVESAIPYHAELTQR.G
R5/RRR5-22/2	1464.145	1464.604	-314.391	0.406	825.256	0.409	15	0.135	R.LSYLWADDPEVR.A
R5/RRR5-22/2	1463.844	1464.604	-1205.811	0.328	833.912	0.380	15	0.131	R.LSYLWADDPEVR.A
R5/RRR5-22/2	977.993	978.164	-175.094	0.392	893.918	0.230	14	0.123	R.CTALPLFR.H
R5/RRR5-22/2	1463.142	1464.604	-1687.804	0.289	816.553	0.297	15	0.122	R.LSYLWADDPEVR.A
R5/RRR5-22/2	977.922	978.164	-247.598	0.460	754.581	0.231	13	0.121	R.CTALPLFR.H
R5/RRR5-23/3	1867.647	1867.012	-195.668	0.431	881.340	0.472	25	0.102	R.HDVESAIPYHAELTQR.G
R5/RRR5-18/2	956.909	957.149	-252.204	0.518	1345.453	0.440	15	0.176	R.AAVLLLDNK.K
R5/RRR5-18/2	956.604	957.149	-1619.737	0.535	1323.399	0.446	15	0.175	R.AAVLLLDNK.K
R5/RRR5-18/2	957.040	957.149	-114.898	0.569	1301.300	0.427	15	0.169	R.AAVLLLDNK.K
R5/RRR5-18/2	1348.104	1348.533	-318.838	0.484	1160.863	0.402	17	0.154	K.SREPVVQLYTR.D
R5/RRR5-18/2	1196.882	1197.323	-369.556	0.484	920.263	0.499	16	0.154	R.RDDADLPPVAK.R
R5/RRR5-18/2	1197.208	1197.323	-96.604	0.462	1071.071	0.429	16	0.152	R.RDDADLPPVAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1197.128	1197.323	-163.805	0.470	1020.705	0.421	17	0.149	R.RDDADLPPVAK.R
R5/RRR5-18/2	1349.388	1348.533	-107.939	0.463	1091.151	0.367	17	0.145	K.SREPVVQLYTR.D
R5/RRR5-18/2	1348.131	1348.533	-298.761	0.479	1142.118	0.340	17	0.144	K.SREPVVQLYTR.D
R5/RRR5-25/2	1242.023	1242.366	-276.375	0.499	1193.399	0.516	17	0.176	K.HQYLPADAQAK.Q
R5/RRR5-25/2	1242.082	1242.366	-229.244	0.499	1019.018	0.509	16	0.161	K.HQYLPADAQAK.Q
R5/RRR5-25/2	1232.300	1231.426	-102.099	0.508	710.276	0.373	17	0.132	R.EALGALPLYQR.T
R5/RRR5-25/2	1232.125	1231.426	-245.207	0.516	631.926	0.382	16	0.131	R.EALGALPLYQR.T
R5/RRR5-25/2	1490.416	1490.753	-226.582	0.307	890.918	0.379	16	0.130	K.M*LSSLSAWLVNPR.R
R5/RRR5-25/2	1230.423	1231.426	-1632.284	0.362	607.887	0.360	16	0.127	R.EALGALPLYQR.T
R5/RRR5-17/2	1289.263	1289.467	-159.032	0.492	1405.931	0.588	19	0.210	R.VVGGWASPFVNR.V
R5/RRR5-17/2	1288.534	1289.467	-1504.890	0.363	1396.001	0.549	18	0.196	R.VVGGWASPFVNR.V
R5/RRR5-17/2	1289.128	1289.467	-264.092	0.423	1328.162	0.528	18	0.188	R.VVGGWASPFVNR.V
R5/RRR5-17/2	1113.134	1113.251	-105.000	0.471	1342.100	0.470	17	0.181	K.VPNLAAWADR.F
R5/RRR5-17/2	1113.330	1113.251	71.416	0.501	1291.075	0.490	17	0.181	K.VPNLAAWADR.F
R5/RRR5-17/2	1113.138	1113.251	-101.370	0.444	1190.326	0.482	17	0.170	K.VPNLAAWADR.F
R5/RRR5-17/2	1157.745	1158.327	-1370.005	0.458	1228.075	0.439	17	0.165	K.IAGVELLDEAK.V
R5/RRR5-17/2	1157.857	1158.327	-407.074	0.434	1148.882	0.475	17	0.165	K.IAGVELLDEAK.V
R5/RRR5-17/2	1157.637	1158.327	-1463.629	0.390	1187.606	0.401	17	0.155	K.IAGVELLDEAK.V
R5/RRR5-14/2	1390.223	1390.610	-278.970	0.493	1375.406	0.508	19	0.191	K.KLSAILSWENTK.K
R5/RRR5-14/2	1389.300	1390.610	-1667.175	0.353	1088.390	0.419	15	0.147	K.KLSAILSWENTK.K
R5/RRR5-14/3	1561.250	1561.786	-986.881	0.480	1460.295	0.436	28	0.147	K.RGEEVLKAEEMAAK.Y
R5/RRR5-14/3	1561.409	1561.786	-241.964	0.442	1303.076	0.422	28	0.125	K.RGEEVLKAEEMAAK.Y
R5/RRR5-14/2	865.869	866.033	-189.920	0.404	1204.077	0.343	13	0.110	K.KLIGCFGA.-
R5/RRR5-14/3	1577.694	1577.785	-58.257	0.387	972.582	0.389	29	0.093	K.RGEEVLKAEEM*AAK.Y
R5/RRR5-14/3	1578.077	1577.785	185.338	0.434	1052.539	0.352	29	0.092	K.RGEEVLKAEEM*AAK.Y
R5/RRR5-14/3	1577.706	1577.785	-50.690	0.418	927.042	0.376	27	0.090	K.RGEEVLKAEEM*AAK.Y
R5/RRR5-25/3	1577.337	1577.785	-284.849	0.338	673.310	0.338	23	0.079	K.RGEEVLKAEEM*AAK.Y
R5/RRR5-14/3	1561.760	1561.786	-16.951	0.397	843.022	0.281	23	0.075	K.RGEEVLKAEEMAAK.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/3	1968.109	1968.415	-155.601	0.448	2677.006	0.409	40	0.399	R.LVELLLHPSPSVLIPALR.T
R5/RRR5-8/3	1968.322	1968.415	-47.071	0.446	2332.448	0.368	38	0.286	R.LVELLLHPSPSVLIPALR.T
R5/RRR5-8/2	1607.407	1607.833	-265.500	0.444	1601.710	0.348	21	0.179	R.SPPIEEVIQSGVVPR.F
R5/RRR5-8/2	1607.739	1607.833	-58.762	0.466	1324.849	0.347	20	0.154	R.SPPIEEVIQSGVVPR.F
R5/RRR5-8/2	1606.600	1607.833	-1393.899	0.310	891.651	0.225	17	0.117	R.SPPIEEVIQSGVVPR.F
R5/RRR5-8/3	1968.105	1968.415	-157.935	0.252	1151.874	0.194	26	0.067	R.LVELLLHPSPSVLIPALR.T
R5/RRR5-11/2	1706.341	1706.877	-902.923	0.433	1954.664	0.490	20	0.255	K.LAADVIEFAEDQWAK.-
R5/RRR5-11/3	1744.057	1744.845	-1028.301	0.511	1721.445	0.527	32	0.223	R.THDVGGHFAAYEQPSK.L
R5/RRR5-11/2	1707.879	1706.877	1.247	0.496	1503.376	0.538	20	0.208	K.LAADVIEFAEDQWAK.-
R5/RRR5-11/2	1446.177	1445.642	-322.784	0.497	1054.013	0.448	18	0.153	R.ENIDPSVIGPIYK.Y
R5/RRR5-10/2	1706.229	1706.877	-968.784	0.305	785.044	0.438	19	0.134	K.LAADVIEFAEDQWAK.-
R5/RRR5-11/2	1707.002	1706.877	73.547	0.287	437.777	0.298	16	0.119	K.LAADVIEFAEDQWAK.-
R5/RRR5-11/2	1445.663	1445.642	14.939	0.270	341.520	0.351	12	0.116	-.ENIDPSVIGPIYK.-
R5/RRR5-11/3	1706.301	1706.877	-926.200	0.434	1046.772	0.374	24	0.092	K.LAADVIEFAEDQWAK.-
R5/RRR5-18/2	1204.977	1205.297	-266.481	0.330	1204.008	0.340	17	0.146	K.EALESVTAEQK.Y
R5/RRR5-18/2	1204.744	1205.297	-1293.389	0.384	886.763	0.397	15	0.136	K.EALESVTAEQK.Y
R5/RRR5-19/3	1179.967	1180.292	-277.017	0.390	1643.690	0.300	24	0.128	K.DEHLDPINVK.I
R5/RRR5-18/3	1180.026	1180.292	-226.577	0.519	1037.552	0.370	21	0.095	K.DEHLDPINVK.I
R5/RRR5-18/3	1759.821	1759.979	-90.391	0.520	757.173	0.453	28	0.093	K.IAELKEALESVTAEQK.Y
R5/RRR5-18/3	1180.478	1180.292	157.473	0.480	1121.673	0.282	21	0.084	K.DEHLDPINVK.I
R5/RRR5-18/3	1179.747	1180.292	-1313.591	0.431	962.748	0.317	20	0.083	K.DEHLDPINVK.I
R5/RRR5-7/2	1346.405	1346.600	-145.189	0.580	2460.481	0.388	20	0.308	R.KFDLGALVDLVR.K
R5/RRR5-7/2	1346.019	1346.600	-1177.922	0.414	1486.195	0.403	17	0.179	R.KFDLGALVDLVR.K
R5/RRR5-7/2	1200.928	1201.312	-320.802	0.407	1085.417	0.500	20	0.164	K.IVDPDTGASLGR.N
R5/RRR5-7/2	1006.226	1006.202	23.420	0.372	1174.436	0.281	14	0.136	K.GDVVM*SLLR.N
R5/RRR5-7/2	1200.295	1201.312	-1685.088	0.270	743.021	0.452	16	0.132	K.IVDPDTGASLGR.N
R5/RRR5-7/2	1200.337	1201.312	-1649.941	0.276	685.674	0.415	16	0.128	K.IVDPDTGASLGR.N
R5/RRR5-7/3	1346.473	1346.600	-94.861	0.432	1216.326	0.269	24	0.084	-.KFDLGALVDLVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/3	1347.685	1346.600	63.529	0.515	1189.521	0.246	24	0.081	-.KFDLGALVDLVR.-
R5/RRR5-15/2	1828.454	1827.067	212.161	0.581	1886.458	0.586	23	0.271	R.SLGLGDLDFSAVYEVLK.G
R5/RRR5-15/2	1828.792	1827.067	-150.811	0.562	1867.494	0.584	23	0.267	R.SLGLGDLDFSAVYEVLK.G
R5/RRR5-15/2	1240.210	1240.390	-145.281	0.444	1358.456	0.448	19	0.177	K.SFFLGEIGNGAK.M
R5/RRR5-16/2	1206.242	1206.330	-72.839	0.491	1083.821	0.458	17	0.156	K.GGAFVEAPVSGSK.K
R5/RRR5-16/2	1206.178	1206.330	-126.541	0.457	1037.211	0.437	17	0.150	K.GGAFVEAPVSGSK.K
R5/RRR5-15/2	1206.140	1206.330	-157.709	0.441	1095.174	0.399	17	0.147	K.GGAFVEAPVSGSK.K
R5/RRR5-15/2	1206.088	1206.330	-200.961	0.425	893.757	0.387	16	0.135	K.GGAFVEAPVSGSK.K
R5/RRR5-15/2	1240.008	1240.390	-308.816	0.335	487.066	0.343	12	0.116	-.SFFLGEIGNGAK.-
R5/RRR5-16/2	1828.387	1827.067	175.205	0.294	378.994	0.324	12	0.112	-.SLGLGDLDFSAVYEVLK.-
R5/RRR5-11/2	1524.339	1523.668	-216.755	0.591	2353.520	0.459	20	0.313	K.INDDEVEYWIVK.A
R5/RRR5-11/2	1690.227	1689.883	204.665	0.529	1665.406	0.526	21	0.225	R.SQDEALQIAELICAK.L
R5/RRR5-11/2	1689.508	1689.883	-222.306	0.453	1691.643	0.472	22	0.216	R.SQDEALQIAELICAK.L
R5/RRR5-11/2	1690.261	1689.883	224.654	0.461	1334.337	0.491	19	0.180	R.SQDEALQIAELICAK.L
R5/RRR5-11/2	1415.258	1415.578	-226.627	0.489	1237.257	0.421	20	0.160	R.GNIASAINTIQANK.V
R5/RRR5-15/2	1017.075	1017.188	-111.968	0.474	1630.198	0.397	17	0.193	R.AMIGQVAGGGR.T
R5/RRR5-17/2	1254.259	1254.504	-196.171	0.376	1216.190	0.428	19	0.161	R.ATLSIGNVLPIR.S
R5/RRR5-17/3	1974.921	1975.066	-73.231	0.438	1246.880	0.549	31	0.154	R.ASGDYAIVISHNPDNGTSR.I
R5/RRR5-17/2	1254.698	1254.504	155.097	0.445	976.138	0.434	17	0.148	R.ATLSIGNVLPIR.S
R5/RRR5-17/3	1974.489	1975.066	-800.646	0.399	1229.763	0.492	31	0.136	R.ASGDYAIVISHNPDNGTSR.I
R5/RRR5-15/3	1974.787	1975.066	-141.497	0.468	989.141	0.582	27	0.135	R.ASGDYAIVISHNPDNGTSR.I
R5/RRR5-14/3	1975.037	1975.066	-14.365	0.429	1165.021	0.505	31	0.133	R.ASGDYAIVISHNPDNGTSR.I
R5/RRR5-14/2	1254.959	1254.504	363.750	0.265	945.322	0.335	17	0.131	R.ATLSIGNVLPIR.S
R5/RRR5-14/2	1254.277	1254.504	-181.917	0.336	853.281	0.348	16	0.131	R.ATLSIGNVLPIR.S
R5/RRR5-1/2	1254.320	1254.504	-147.551	0.349	852.093	0.273	16	0.124	R.ATLSIGNVLPIR.S
R5/RRR5-16/2	1033.218	1033.188	29.855	0.302	788.328	0.288	14	0.120	-.AM*IGQVAGGGR.-
R5/RRR5-14/2	1254.325	1254.504	-143.060	0.225	764.384	0.241	15	0.119	R.ATLSIGNVLPIR.S
R5/RRR5-17/3	1975.075	1975.066	4.791	0.444	1048.125	0.482	29	0.117	R.ASGDYAIVISHNPDNGTSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1254.169	1254.504	-267.743	0.193	522.443	0.186	12	0.115	-.ATLSIGNVLPIR.-
R5/RRR5-17/2	1254.285	1254.504	-175.278	0.189	563.919	0.158	12	0.114	-.ATLSIGNVLPIR.-
R5/RRR5-20/2	1254.018	1254.504	-388.746	0.209	483.711	0.245	12	0.114	-.ATLSIGNVLPIR.-
R5/RRR5-13/2	1254.196	1254.504	-245.968	0.265	472.032	0.226	11	0.112	-.ATLSIGNVLPIR.-
R5/RRR5-1/3	1974.684	1975.066	-193.866	0.379	445.878	0.458	22	0.088	R.ASGDYAIVISHNPDNGTSR.I
R5/RRR5-20/3	1974.435	1975.066	-828.387	0.294	1017.597	0.208	29	0.067	R.ASGDYAIVISHNPDNGTSR.I
R5/RRR5-22/2	1335.144	1334.500	-267.186	0.488	906.866	0.386	18	0.139	R.IEVTEPASFNVK.E
R5/RRR5-21/2	945.105	945.100	4.585	0.361	953.344	0.347	13	0.135	R.LAVDKWGR.I
R5/RRR5-21/2	944.664	945.100	-462.652	0.378	777.721	0.320	13	0.128	R.LAVDKWGR.I
R5/RRR5-22/2	1334.000	1334.500	-375.350	0.364	873.002	0.289	18	0.126	R.IEVTEPASFNVK.E
R5/RRR5-22/2	1936.392	1937.051	-859.070	0.352	1097.520	0.449	18	0.123	K.EDNNLSLVEYELVNVEG.-
R5/RRR5-22/2	1333.586	1334.500	-1439.086	0.289	709.537	0.216	16	0.117	R.IEVTEPASFNVK.E
R5/RRR5-18/2	1014.982	1015.299	-313.830	0.431	1500.785	0.456	15	0.192	R.FGMMAAQMK.A
R5/RRR5-18/2	1014.477	1015.299	-1801.240	0.353	1308.937	0.450	15	0.171	R.FGMMAAQMK.A
R5/RRR5-18/2	1014.906	1015.299	-388.408	0.371	1292.179	0.448	14	0.170	R.FGMMAAQMK.A
R5/RRR5-18/2	1778.497	1779.029	-864.362	0.551	1110.166	0.511	24	0.170	K.IWQVPETLHEEVLGK.M
R5/RRR5-18/2	1778.587	1779.029	-249.309	0.546	1127.024	0.497	24	0.168	K.IWQVPETLHEEVLGK.M
R5/RRR5-18/2	1046.815	1047.298	-463.266	0.443	1247.776	0.401	16	0.162	R.FGM*M*AAQMK.A
R5/RRR5-18/2	1778.549	1779.029	-271.068	0.508	1120.466	0.450	24	0.160	K.IWQVPETLHEEVLGK.M
R5/RRR5-18/2	1046.814	1047.298	-463.851	0.447	758.575	0.474	13	0.144	R.FGM*M*AAQMK.A
R5/RRR5-18/2	1046.539	1047.298	-1685.601	0.384	705.515	0.444	13	0.137	R.FGM*M*AAQMK.A
R5/RRR5-18/2	1778.425	1779.029	-904.603	0.402	443.580	0.356	16	0.122	K.IWQVPETLHEEVLGK.M
R5/RRR5-18/3	1856.756	1857.039	-152.835	0.482	831.769	0.532	29	0.111	R.WPTEM*ELEHAFHQGK.Y
R5/RRR5-18/3	1779.978	1779.029	-28.664	0.390	1080.210	0.407	30	0.101	K.IWQVPETLHEEVLGK.M
R5/RRR5-18/3	1855.998	1857.039	-1102.771	0.429	846.799	0.426	26	0.093	R.WPTEM*ELEHAFHQGK.Y
R5/RRR5-18/3	1841.325	1841.039	155.680	0.329	429.622	0.403	22	0.081	R.WPTEMELEHAFHQGK.Y
R5/RRR5-18/3	1778.835	1779.029	-109.489	0.352	567.622	0.308	23	0.073	K.IWQVPETLHEEVLGK.M
R5/RRR5-13/2	1449.315	1449.588	-188.862	0.448	1373.321	0.508	18	0.188	K.DGTTLLWDLTEGK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1449.200	1449.588	-268.293	0.541	1414.140	0.476	19	0.187	K.DGTTLLWDLTEGK.M
R5/RRR5-13/2	1443.218	1443.576	-249.045	0.438	1350.225	0.439	19	0.174	R.YWLCAATEDSVK.I
R5/RRR5-13/2	1443.280	1443.576	-206.194	0.407	1301.322	0.444	18	0.170	R.YWLCAATEDSVK.I
R5/RRR5-13/2	1449.386	1449.588	-139.181	0.501	1225.709	0.467	18	0.168	K.DGTTLLWDLTEGK.M
R5/RRR5-13/2	1771.452	1771.992	-871.670	0.498	896.668	0.498	18	0.147	K.LDAGAIIHSLCFSPNR.Y
R5/RRR5-13/3	1772.122	1771.992	73.531	0.588	926.386	0.647	28	0.146	K.LDAGAIIHSLCFSPNR.Y
R5/RRR5-13/3	1772.117	1771.992	71.044	0.557	1045.547	0.597	28	0.145	K.LDAGAIIHSLCFSPNR.Y
R5/RRR5-13/3	1771.590	1771.992	-227.494	0.532	908.626	0.624	27	0.138	K.LDAGAIIHSLCFSPNR.Y
R5/RRR5-13/2	1771.071	1771.992	-1087.893	0.420	746.666	0.470	17	0.135	K.LDAGAIIHSLCFSPNR.Y
R5/RRR5-12/2	1449.240	1449.588	-240.406	0.356	445.811	0.401	12	0.122	K.DGTTLLWDLTEGK.M
R5/RRR5-11/2	1184.598	1185.304	-1444.995	0.408	1649.896	0.405	16	0.197	K.FGCTDFVNPK.D
R5/RRR5-10/2	1185.132	1185.304	-145.524	0.456	1606.987	0.385	16	0.188	K.FGCTDFVNPK.D
R5/RRR5-11/2	1185.310	1185.304	4.689	0.501	1470.954	0.443	16	0.187	K.FGCTDFVNPK.D
R5/RRR5-10/2	1184.934	1185.304	-313.146	0.423	1527.748	0.411	16	0.186	K.FGCTDFVNPK.D
R5/RRR5-11/2	1184.505	1185.304	-1523.665	0.412	1339.862	0.405	15	0.167	K.FGCTDFVNPK.D
R5/RRR5-2/2	1186.244	1185.304	-50.947	0.460	834.005	0.504	15	0.151	K.FGCTDFVNPK.D
R5/RRR5-2/2	1186.136	1185.304	-142.098	0.433	763.604	0.447	15	0.142	K.FGCTDFVNPK.D
R5/RRR5-1/2	1643.487	1643.908	-257.064	0.436	745.798	0.499	16	0.140	R.IIGVDLNPAKFEQAK.K
R5/RRR5-2/2	1185.972	1185.304	-280.662	0.418	691.803	0.439	14	0.137	K.FGCTDFVNPK.D
R5/RRR5-10/2	1039.748	1040.238	-472.509	0.443	643.034	0.420	16	0.137	R.IIGVDLNPAK.F
R5/RRR5-10/2	1643.260	1643.908	-1005.982	0.447	819.453	0.437	17	0.136	R.IIGVDLNPAKFEQAK.K
R5/RRR5-10/2	1039.553	1040.238	-1626.352	0.404	644.022	0.418	16	0.136	R.IIGVDLNPAK.F
R5/RRR5-10/2	1040.154	1040.238	-81.527	0.472	595.246	0.399	15	0.134	R.IIGVDLNPAK.F
R5/RRR5-8/2	1040.043	1040.238	-188.663	0.403	499.915	0.419	15	0.134	R.IIGVDLNPAK.F
R5/RRR5-7/2	1040.040	1040.238	-191.607	0.400	460.055	0.416	14	0.132	R.IIGVDLNPAK.F
R5/RRR5-6/2	1040.910	1040.238	-316.364	0.399	533.965	0.404	14	0.132	R.IIGVDLNPAK.F
R5/RRR5-3/2	1039.943	1040.238	-284.988	0.366	594.445	0.396	15	0.132	R.IIGVDLNPAK.F
R5/RRR5-2/2	1041.145	1040.238	-89.917	0.532	485.155	0.433	14	0.131	-.IIGVDLNPAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1041.068	1040.238	-163.663	0.502	588.854	0.355	15	0.130	R.IIGVDLNPAK.F
R5/RRR5-1/2	1185.201	1185.304	-87.562	0.395	707.853	0.317	15	0.128	K.FGCTDFVNPK.D
R5/RRR5-3/2	1040.118	1040.238	-115.667	0.349	447.314	0.298	13	0.125	R.IIGVDLNPAK.F
R5/RRR5-3/2	1185.415	1185.304	93.720	0.288	551.216	0.228	14	0.121	K.FGCTDFVNPK.D
R5/RRR5-10/2	1644.353	1643.908	271.357	0.440	479.549	0.242	15	0.098	-.IIGVDLNPAKFEQAK.-
R5/RRR5-15/2	1860.189	1859.285	-52.038	0.530	1379.180	0.610	23	0.209	R.LPLVGPLLTPPVSVASVAK.V
R5/RRR5-15/2	1859.661	1859.285	202.807	0.529	1140.343	0.610	22	0.184	R.LPLVGPLLTPPVSVASVAK.V
R5/RRR5-16/2	1858.808	1859.285	-257.717	0.540	1017.088	0.639	22	0.180	R.LPLVGPLLTPPVSVASVAK.V
R5/RRR5-16/2	1858.638	1859.285	-889.080	0.491	1015.631	0.587	21	0.169	R.LPLVGPLLTPPVSVASVAK.V
R5/RRR5-15/2	1858.563	1859.285	-929.367	0.496	769.812	0.564	19	0.149	R.LPLVGPLLTPPVSVASVAK.V
R5/RRR5-15/2	1585.865	1586.772	-1206.064	0.412	865.685	0.490	19	0.143	K.INGTANINAISVAAEK.G
R5/RRR5-15/2	961.921	962.080	-165.100	0.387	859.281	0.417	15	0.139	R.ATEAELLSK.F
R5/RRR5-11/2	1424.202	1424.542	-239.045	0.457	1839.775	0.495	17	0.241	K.YAFEYAYLNNR.K
R5/RRR5-11/2	1282.183	1281.433	-196.101	0.497	1555.992	0.571	18	0.224	K.LADGLFLESCR.E
R5/RRR5-11/2	1281.055	1281.433	-296.340	0.490	1617.055	0.529	18	0.222	K.LADGLFLESCR.E
R5/RRR5-11/2	1281.248	1281.433	-145.215	0.496	1313.595	0.528	18	0.190	K.LADGLFLESCR.E
R5/RRR5-11/2	1424.158	1424.542	-270.346	0.459	1371.204	0.444	16	0.177	K.YAFEYAYLNNR.K
R5/RRR5-11/2	1194.143	1194.366	-186.874	0.461	911.708	0.443	16	0.147	R.HQDVDIVVIR.E
R5/RRR5-11/2	1423.724	1424.542	-1280.640	0.384	815.601	0.385	13	0.131	K.YAFEYAYLNNR.K
R5/RRR5-11/2	1194.231	1194.366	-112.736	0.212	435.412	0.367	12	0.117	R.HQDVDIVVIR.E
R5/RRR5-17/2	1406.001	1405.487	-346.637	0.511	1428.166	0.509	18	0.197	R.FYCWDTAGQEK.F
R5/RRR5-17/2	1404.524	1405.487	-1401.795	0.418	1534.804	0.458	18	0.196	R.FYCWDTAGQEK.F
R5/RRR5-17/3	1761.996	1762.988	-1134.154	0.463	1480.079	0.565	28	0.189	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1404.791	1405.487	-1211.004	0.464	1594.822	0.380	18	0.186	R.FYCWDTAGQEK.F
R5/RRR5-17/3	1763.066	1762.988	44.187	0.483	1420.243	0.515	30	0.163	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1763.401	1762.988	234.777	0.554	1129.902	0.481	19	0.163	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1762.422	1762.988	-891.628	0.532	988.928	0.542	17	0.162	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1516.358	1516.752	-260.771	0.542	980.401	0.461	20	0.153	R.VCENIPIVLCGNK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1516.321	1516.752	-285.243	0.533	1025.586	0.436	20	0.152	R.VCENIPIVLCGNK.V
R5/RRR5-17/2	1762.484	1762.988	-856.168	0.508	890.572	0.502	16	0.149	K.SNYNFEKPFLYLAR.K
R5/RRR5-18/2	1516.032	1516.752	-1138.136	0.500	1123.129	0.378	19	0.147	R.VCENIPIVLCGNK.V
R5/RRR5-17/3	1762.779	1762.988	-119.168	0.445	1272.111	0.512	26	0.146	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1762.451	1762.988	-874.802	0.545	806.265	0.502	16	0.145	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/3	1762.792	1762.988	-111.770	0.531	1163.862	0.549	27	0.144	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1515.512	1516.752	-1482.121	0.406	1021.866	0.379	20	0.143	R.VCENIPIVLCGNK.V
R5/RRR5-16/2	1762.458	1762.988	-871.047	0.486	878.893	0.437	17	0.141	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1762.251	1762.988	-989.053	0.512	830.198	0.462	16	0.141	K.SNYNFEKPFLYLAR.K
R5/RRR5-18/2	1516.035	1516.752	-1135.549	0.476	908.999	0.366	19	0.136	R.VCENIPIVLCGNK.V
R5/RRR5-16/3	1762.660	1762.988	-186.797	0.487	1188.273	0.503	27	0.134	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/3	1763.059	1762.988	40.437	0.549	1014.872	0.566	27	0.134	K.SNYNFEKPFLYLAR.K
R5/RRR5-17/2	1762.332	1762.988	-942.529	0.457	744.721	0.409	15	0.131	K.SNYNFEKPFLYLAR.K
R5/RRR5-16/3	1763.018	1762.988	16.895	0.470	973.418	0.554	24	0.127	K.SNYNFEKPFLYLAR.K
R5/RRR5-15/2	1762.317	1762.988	-951.291	0.404	450.384	0.378	14	0.124	K.SNYNFEKPFLYLAR.K
R5/RRR5-18/2	1763.114	1762.988	71.345	0.324	383.325	0.303	14	0.121	K.SNYNFEKPFLYLAR.K
R5/RRR5-19/2	1763.809	1762.988	-101.806	0.381	120.484	0.419	11	0.094	-.SNYNFEKPFLYLAR.-
R5/RRR5-18/3	1762.938	1762.988	-28.525	0.266	707.938	0.385	22	0.082	K.SNYNFEKPFLYLAR.K
R5/RRR5-4/2	1623.452	1623.833	-235.197	0.492	1642.687	0.507	19	0.218	R.VINTALFSEYYFR.V
R5/RRR5-5/2	1623.916	1623.833	51.299	0.471	1466.491	0.495	18	0.195	R.VINTALFSEYYFR.V
R5/RRR5-4/2	1327.320	1326.541	-166.851	0.568	1345.748	0.369	17	0.160	R.M*VEESFILDVK.H
R5/RRR5-4/2	974.926	975.083	-161.517	0.403	869.019	0.429	13	0.143	K.HGESYLLR.V
R5/RRR5-4/2	974.922	975.083	-165.787	0.425	770.686	0.420	13	0.139	K.HGESYLLR.V
R5/RRR5-4/2	974.511	975.083	-1617.992	0.397	850.588	0.403	13	0.139	K.HGESYLLR.V
R5/RRR5-5/2	975.045	975.083	-39.443	0.417	623.837	0.362	12	0.130	K.HGESYLLR.V
R5/RRR5-4/2	1326.205	1326.541	-254.235	0.277	554.122	0.212	12	0.114	-.M*VEESFILDVK.-
R5/RRR5-5/2	1326.975	1326.541	328.120	0.354	736.638	0.183	14	0.114	R.M*VEESFILDVK.H
R5/RRR5-20/2	1450.378	1450.663	-197.334	0.418	1146.923	0.365	18	0.146	K.VRVELPDAYPYK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1421.764	1422.567	-1271.899	0.434	828.140	0.480	16	0.141	R.GPTESIYQGGVWK.V
R5/RRR5-20/2	948.698	949.086	-409.449	0.445	849.050	0.349	14	0.133	K.SPSIGFVNK.I
R5/RRR5-20/2	948.592	949.086	-521.658	0.401	857.320	0.344	13	0.131	K.SPSIGFVNK.I
R5/RRR5-14/2	1264.068	1264.326	-205.013	0.558	1772.713	0.475	20	0.228	K.FGDAVQEDVGAR.L
R5/RRR5-14/2	1359.269	1359.421	-112.379	0.476	1655.989	0.512	22	0.222	K.AEEPSASGDPLASK.S
R5/RRR5-14/2	1263.991	1264.326	-266.244	0.549	1709.509	0.443	20	0.212	K.FGDAVQEDVGAR.L
R5/RRR5-14/2	1358.920	1359.421	-1108.085	0.446	1599.125	0.464	22	0.204	K.AEEPSASGDPLASK.S
R5/RRR5-14/2	1264.162	1264.326	-130.228	0.591	1443.049	0.490	20	0.194	K.FGDAVQEDVGAR.L
R5/RRR5-14/2	1358.932	1359.421	-360.896	0.429	1366.688	0.488	20	0.184	K.AEEPSASGDPLASK.S
R5/RRR5-21/2	1264.259	1264.326	-53.808	0.507	904.507	0.392	18	0.139	K.FGDAVQEDVGAR.L
R5/RRR5-14/2	1411.179	1411.587	-290.271	0.460	621.834	0.406	16	0.129	K.LNGYGYDNLILR.V
R5/RRR5-13/2	856.001	856.005	-4.950	0.498	1119.960	0.401	13	0.153	K.TPAQVALR.W
R5/RRR5-13/2	1009.991	1010.126	-133.786	0.377	627.186	0.403	15	0.131	R.AIGVSNFSSK.K
R5/RRR5-13/2	855.460	856.005	-1811.316	0.339	621.790	0.362	12	0.127	K.TPAQVALR.W
R5/RRR5-13/2	1342.624	1342.525	73.719	0.329	1129.682	0.142	16	0.119	-.WGLEQGQSVLPK.-
R5/RRR5-13/2	1009.277	1010.126	-1837.452	0.302	638.636	0.221	15	0.118	R.AIGVSNFSSK.K
R5/RRR5-22/2	1342.964	1343.485	-1136.365	0.401	1287.953	0.361	19	0.156	K.EAFELVSGEM*SK.T
R5/RRR5-23/2	1685.310	1685.902	-947.536	0.432	734.401	0.505	25	0.146	R.LDPGVTASHAFVLETK.V
R5/RRR5-23/2	1685.303	1685.902	-951.899	0.459	664.289	0.518	24	0.145	R.LDPGVTASHAFVLETK.V
R5/RRR5-23/2	1685.314	1685.902	-944.918	0.445	594.525	0.544	23	0.144	R.LDPGVTASHAFVLETK.V
R5/RRR5-22/2	1239.064	1239.405	-275.948	0.425	845.317	0.446	17	0.144	R.FQGSPAVITYR.V
R5/RRR5-23/2	1240.122	1239.405	-228.816	0.414	782.784	0.469	16	0.143	R.FQGSPAVITYR.V
R5/RRR5-23/2	1239.141	1239.405	-213.781	0.416	806.702	0.436	16	0.140	R.FQGSPAVITYR.V
R5/RRR5-23/2	1240.352	1239.405	-42.506	0.397	579.256	0.407	15	0.131	R.FQGSPAVITYR.V
R5/RRR5-22/2	1238.619	1239.405	-1446.126	0.417	648.674	0.387	15	0.131	R.FQGSPAVITYR.V
R5/RRR5-22/2	1239.089	1239.405	-255.884	0.432	647.290	0.383	15	0.131	R.FQGSPAVITYR.V
R5/RRR5-23/2	1327.001	1327.486	-366.720	0.272	512.766	0.270	15	0.118	K.EAFELVSGEMSK.T
R5/RRR5-22/2	1343.240	1343.485	-183.157	0.320	425.116	0.247	12	0.089	-.EAFELVSGEM*SK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1215.891	1216.282	-322.695	0.473	747.708	0.450	16	0.141	R.AQGSYTFADQK.T
R5/RRR5-21/2	1216.061	1216.282	-182.297	0.472	658.102	0.475	15	0.140	R.AQGSYTFADQK.T
R5/RRR5-21/2	1215.867	1216.282	-341.934	0.470	708.140	0.460	15	0.139	R.AQGSYTFADQK.T
R5/RRR5-20/2	1215.434	1216.282	-1524.683	0.426	709.995	0.403	15	0.133	R.AQGSYTFADQK.T
R5/RRR5-21/2	887.976	888.004	-31.452	0.392	1118.762	0.200	13	0.127	R.NEVLSAVR.E
R5/RRR5-20/2	887.387	888.004	-1827.898	0.364	1243.729	0.149	13	0.126	R.NEVLSAVR.E
R5/RRR5-20/2	887.501	888.004	-1698.398	0.293	1236.637	0.147	13	0.126	R.NEVLSAVR.E
R5/RRR5-21/2	887.438	888.004	-1770.261	0.301	1176.057	0.136	13	0.123	-.NEVLSAVR.-
R5/RRR5-20/2	887.770	888.004	-264.674	0.410	1152.259	0.150	13	0.122	R.NEVLSAVR.E
R5/RRR5-21/3	1761.016	1761.017	-0.884	0.462	922.984	0.547	28	0.121	K.VYFHDVVGGTKPTAIR.V
R5/RRR5-21/2	887.824	888.004	-203.703	0.354	1124.408	0.126	13	0.119	R.NEVLSAVR.E
R5/RRR5-21/3	1760.633	1761.017	-218.688	0.428	942.058	0.484	28	0.109	K.VYFHDVVGGTKPTAIR.V
R5/RRR5-21/3	1760.900	1761.017	-66.695	0.425	702.394	0.523	25	0.102	K.VYFHDVVGGTKPTAIR.V
R5/RRR5-20/3	1760.771	1761.017	-140.443	0.329	607.184	0.304	23	0.074	K.VYFHDVVGGTKPTAIR.V
R5/RRR5-22/2	1412.279	1412.617	-239.676	0.499	1625.167	0.428	19	0.199	K.IFFIAWSPSTSR.I
R5/RRR5-22/2	1908.650	1910.072	-1272.612	0.425	1555.950	0.428	25	0.191	R.YALYDFDFVTGENVQK.S
R5/RRR5-22/2	1412.406	1412.617	-149.847	0.457	1435.300	0.386	18	0.172	K.IFFIAWSPSTSR.I
R5/RRR5-22/2	1413.228	1412.617	-276.075	0.420	1133.691	0.397	16	0.150	K.IFFIAWSPSTSR.I
R5/RRR5-22/2	1411.530	1412.617	-1482.791	0.324	1417.624	0.204	18	0.141	K.IFFIAWSPSTSR.I
R5/RRR5-22/3	1602.545	1602.712	-104.451	0.451	1439.902	0.350	31	0.123	R.SHSNASSGM*GVAPDIR.D
R5/RRR5-22/3	1601.934	1602.712	-1113.067	0.398	1444.921	0.335	31	0.119	R.SHSNASSGM*GVAPDIR.D
R5/RRR5-22/2	1412.249	1412.617	-261.528	0.274	771.886	0.266	13	0.119	K.IFFIAWSPSTSR.I
R5/RRR5-22/3	1602.641	1602.712	-44.626	0.426	1463.250	0.293	31	0.111	R.SHSNASSGM*GVAPDIR.D
R5/RRR5-14/2	1217.278	1217.442	-135.646	0.493	1962.345	0.466	18	0.252	R.EALFVLAQLGR.K
R5/RRR5-14/2	1289.611	1290.493	-1463.853	0.413	1293.375	0.463	15	0.172	R.YQILAGVIEQR.M
R5/RRR5-14/2	1291.338	1290.493	-120.471	0.530	1342.717	0.426	16	0.170	R.YQILAGVIEQR.M
R5/RRR5-14/2	1289.713	1290.493	-1384.468	0.436	1235.961	0.408	15	0.159	R.YQILAGVIEQR.M
R5/RRR5-14/2	1216.527	1217.442	-1579.070	0.456	1053.664	0.457	15	0.154	R.EALFVLAQLGR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1217.059	1217.442	-315.544	0.430	1114.679	0.350	16	0.143	R.EALFVLAQLGR.K
R5/RRR5-14/2	1118.936	1119.335	-357.549	0.415	666.448	0.383	16	0.132	R.LLADDLFLAK.L
R5/RRR5-14/2	1119.343	1119.335	6.606	0.411	604.707	0.315	15	0.125	R.LLADDLFLAK.L
R5/RRR5-13/2	1922.294	1923.114	-949.127	0.512	1211.465	0.580	20	0.184	R.GLLTSDQTLFESPETKR.L
R5/RRR5-14/2	1304.755	1305.420	-1280.393	0.491	979.543	0.453	16	0.151	R.TSNVFDGVYFR.E
R5/RRR5-14/2	1305.375	1305.420	-34.386	0.339	844.665	0.355	15	0.131	R.TSNVFDGVYFR.E
R5/RRR5-13/2	1305.453	1305.420	25.359	0.439	678.700	0.330	15	0.125	-.TSNVFDGVYFR.-
R5/RRR5-13/2	1305.240	1305.420	-138.512	0.375	631.634	0.317	14	0.124	R.TSNVFDGVYFR.E
R5/RRR5-14/2	1304.755	1305.420	-1280.111	0.321	658.752	0.302	13	0.121	R.TSNVFDGVYFR.E
R5/RRR5-13/3	1634.488	1634.794	-187.915	0.436	1095.119	0.442	26	0.110	K.M*GQLDLKEGDAGEVR.T
R5/RRR5-6/2	886.509	885.988	-542.239	0.392	894.951	0.429	13	0.142	R.TPVDNALR.D
R5/RRR5-6/2	982.506	983.187	-1715.610	0.455	499.423	0.457	15	0.136	R.IPAVQDLVK.K
R5/RRR5-6/2	1848.730	1850.106	-1288.958	0.469	804.724	0.337	18	0.121	K.LSFKDIDEVILVGGSTR.I
R5/RRR5-21/2	1423.175	1423.550	-264.252	0.465	1151.802	0.323	17	0.139	R.DYQDDKADVILK.Y
R5/RRR5-21/2	1135.278	1135.252	23.014	0.380	800.159	0.404	15	0.135	K.AYGELPDTLR.L
R5/RRR5-21/2	1135.361	1135.252	96.127	0.394	846.026	0.361	15	0.133	K.AYGELPDTLR.L
R5/RRR5-21/3	1911.899	1913.077	-1142.634	0.387	1073.800	0.371	25	0.092	R.ELVFKEDGQEYAQVTR.M
R5/RRR5-12/3	1997.286	1998.189	-955.427	0.455	1979.295	0.591	35	0.304	R.AHAPAAVASGAVVVDNSSAFR.M
R5/RRR5-12/2	1559.557	1558.868	-200.561	0.602	1805.816	0.558	22	0.252	K.GAALNAVQIAEM*LLK.-
R5/RRR5-12/2	1559.435	1558.868	-278.540	0.577	1492.705	0.535	21	0.206	K.GAALNAVQIAEM*LLK.-
R5/RRR5-12/2	1558.110	1558.868	-1131.843	0.407	1473.154	0.426	19	0.181	K.GAALNAVQIAEM*LLK.-
R5/RRR5-12/2	1160.941	1160.260	-275.218	0.567	1130.819	0.483	17	0.166	R.AAEGVTIIDDR.A
R5/RRR5-12/2	1160.261	1160.260	1.202	0.490	1107.297	0.481	17	0.163	R.AAEGVTIIDDR.A
R5/RRR5-12/3	1997.584	1998.189	-805.517	0.391	984.610	0.462	26	0.106	R.AHAPAAVASGAVVVDNSSAFR.M
R5/RRR5-20/3	1998.431	1998.189	121.570	0.316	601.640	0.378	25	0.078	R.AHAPAAVASGAVVVDNSSAFR.M
R5/RRR5-11/3	1998.005	1998.189	-92.208	0.299	804.925	0.204	26	0.062	R.AHAPAAVASGAVVVDNSSAFR.M
R5/RRR5-12/3	1997.086	1998.189	-1056.037	0.328	937.217	0.176	26	0.058	R.AHAPAAVASGAVVVDNSSAFR.M
R5/RRR5-24/3	1464.793	1464.605	128.161	0.492	1412.386	0.522	32	0.162	K.VVAKQEGLEDGYR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1787.515	1786.963	-251.557	0.502	409.341	0.520	17	0.130	K.EAALAAVPNDNPTIFDK.I
R5/RRR5-24/2	1656.407	1656.950	-934.281	0.469	919.526	0.318	18	0.126	R.DINPQAPTHIVIIPK.V
R5/RRR5-24/2	1656.586	1656.950	-220.663	0.463	1004.736	0.275	19	0.125	R.DINPQAPTHIVIIPK.V
R5/RRR5-24/2	1656.184	1656.950	-1069.989	0.436	862.399	0.231	18	0.116	R.DINPQAPTHIVIIPK.V
R5/RRR5-24/3	1464.380	1464.605	-154.613	0.459	1043.821	0.489	29	0.115	K.VVAKQEGLEDGYR.I
R5/RRR5-24/3	1464.122	1464.605	-331.130	0.416	893.942	0.511	28	0.107	K.VVAKQEGLEDGYR.I
R5/RRR5-10/2	1729.403	1729.822	-243.443	0.545	2037.237	0.604	23	0.301	K.EAFVSSSEEPFTVDGK.E
R5/RRR5-10/2	1729.114	1729.822	-991.155	0.499	2128.013	0.534	23	0.295	K.EAFVSSSEEPFTVDGK.E
R5/RRR5-10/2	1729.090	1729.822	-1004.834	0.510	1532.035	0.564	21	0.217	K.EAFVSSSEEPFTVDGK.E
R5/RRR5-10/2	1666.409	1665.871	-277.847	0.571	1328.014	0.581	21	0.198	K.GFAIGNGLTDPAIQYK.A
R5/RRR5-10/2	1666.331	1665.871	276.889	0.547	1371.380	0.551	21	0.196	K.GFAIGNGLTDPAIQYK.A
R5/RRR5-10/2	1665.256	1665.871	-972.769	0.512	1146.033	0.558	20	0.176	K.GFAIGNGLTDPAIQYK.A
R5/RRR5-10/2	1696.537	1696.923	-228.457	0.499	805.453	0.509	21	0.149	R.NLEVGIPELLENDIK.V
R5/RRR5-10/2	1696.549	1696.923	-221.528	0.454	649.353	0.504	19	0.140	R.NLEVGIPELLENDIK.V
R5/RRR5-16/2	1665.771	1665.871	-60.390	0.445	778.654	0.465	16	0.136	K.GFAIGNGLTDPAIQYK.A
R5/RRR5-17/2	1696.120	1696.923	-1066.090	0.379	726.006	0.358	19	0.127	R.NLEVGIPELLENDIK.V
R5/RRR5-10/2	1696.165	1696.923	-1039.426	0.349	589.523	0.316	18	0.121	R.NLEVGIPELLENDIK.V
R5/RRR5-10/3	1697.000	1696.923	45.618	0.489	843.525	0.370	22	0.080	-.NLEVGIPELLENDIK.-
R5/RRR5-7/2	1316.976	1316.486	373.117	0.540	2253.444	0.517	19	0.312	K.SIQVIVVTDGER.I
R5/RRR5-6/2	1316.217	1316.486	-205.076	0.442	2349.198	0.428	19	0.302	K.SIQVIVVTDGER.I
R5/RRR5-6/2	1316.152	1316.486	-254.390	0.424	2222.750	0.439	19	0.284	K.SIQVIVVTDGER.I
R5/RRR5-7/2	1316.320	1316.486	-125.998	0.439	2153.219	0.437	19	0.272	K.SIQVIVVTDGER.I
R5/RRR5-7/2	1786.414	1785.934	269.654	0.532	1378.337	0.513	23	0.189	R.AVFASGSPFDPVEYNGK.I
R5/RRR5-6/2	1315.543	1316.486	-1481.439	0.388	1408.769	0.478	17	0.185	K.SIQVIVVTDGER.I
R5/RRR5-7/2	1801.282	1802.123	-1024.766	0.421	872.743	0.548	21	0.154	R.ILGLGDLGCQGM*GIPVGK.L
R5/RRR5-7/2	1801.463	1802.123	-924.143	0.450	583.787	0.516	18	0.136	R.ILGLGDLGCQGM*GIPVGK.L
R5/RRR5-6/2	1801.998	1802.123	-69.258	0.428	539.027	0.527	18	0.136	R.ILGLGDLGCQGM*GIPVGK.L
R5/RRR5-7/2	1785.431	1786.123	-950.770	0.415	703.768	0.456	19	0.134	R.ILGLGDLGCQGMGIPVGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1801.453	1802.123	-929.722	0.403	471.338	0.465	17	0.128	R.ILGLGDLGCQGM*GIPVGK.L
R5/RRR5-7/2	1785.399	1786.123	-968.411	0.338	670.788	0.412	19	0.128	R.ILGLGDLGCQGMGIPVGK.L
R5/RRR5-6/2	1801.622	1802.123	-835.579	0.441	412.937	0.457	16	0.127	R.ILGLGDLGCQGM*GIPVGK.L
R5/RRR5-7/2	1785.289	1786.123	-1030.743	0.410	524.705	0.406	17	0.124	R.ILGLGDLGCQGMGIPVGK.L
R5/RRR5-21/2	1366.044	1365.620	311.372	0.528	1368.316	0.497	18	0.187	R.VVM*ELFADTVPK.T
R5/RRR5-21/2	1366.270	1365.620	-257.010	0.479	1357.477	0.497	18	0.186	R.VVM*ELFADTVPK.T
R5/RRR5-21/2	1365.124	1365.620	-364.583	0.311	1078.947	0.374	17	0.142	R.VVM*ELFADTVPK.T
R5/RRR5-22/2	1658.200	1656.881	192.965	0.525	335.388	0.544	18	0.138	-.IIPNFMCQGGDFTR.-
R5/RRR5-23/2	1657.292	1656.881	248.774	0.413	401.112	0.468	19	0.136	R.IIPNFMCQGGDFTR.X
R5/RRR5-23/2	1673.250	1672.880	221.661	0.313	397.311	0.563	18	0.135	R.IIPNFM*CQGGDFTR.X
R5/RRR5-22/2	1657.089	1656.881	125.710	0.461	410.529	0.453	18	0.134	R.IIPNFMCQGGDFTR.X
R5/RRR5-22/2	1673.224	1672.880	206.078	0.350	369.898	0.490	18	0.134	R.IIPNFM*CQGGDFTR.X
R5/RRR5-23/2	1658.038	1656.881	95.140	0.432	315.372	0.455	17	0.134	R.IIPNFMCQGGDFTR.X
R5/RRR5-22/2	1656.415	1656.881	-281.889	0.367	335.991	0.452	19	0.133	R.IIPNFMCQGGDFTR.X
R5/RRR5-22/2	1673.204	1672.880	193.933	0.401	372.974	0.440	18	0.133	R.IIPNFM*CQGGDFTR.X
R5/RRR5-23/2	1672.981	1672.880	60.617	0.361	444.857	0.461	18	0.133	R.IIPNFM*CQGGDFTR.X
R5/RRR5-21/2	1052.584	1052.291	279.678	0.370	785.687	0.365	14	0.133	R.VFFDILIGK.A
R5/RRR5-22/2	1673.271	1672.880	233.878	0.358	308.101	0.469	17	0.132	R.IIPNFM*CQGGDFTR.X
R5/RRR5-21/2	1052.143	1052.291	-140.644	0.412	569.823	0.405	13	0.132	R.VFFDILIGK.A
R5/RRR5-22/2	1673.271	1672.880	234.097	0.316	315.320	0.485	17	0.131	R.IIPNFM*CQGGDFTR.X
R5/RRR5-21/2	1052.043	1052.291	-235.973	0.400	591.881	0.385	13	0.131	R.VFFDILIGK.A
R5/RRR5-21/2	1052.058	1052.291	-222.121	0.358	464.028	0.452	11	0.130	R.VFFDILIGK.A
R5/RRR5-23/2	1672.728	1672.880	-91.402	0.287	335.078	0.472	17	0.129	R.IIPNFM*CQGGDFTR.X
R5/RRR5-22/2	1657.260	1656.881	229.201	0.378	283.555	0.403	15	0.129	R.IIPNFMCQGGDFTR.X
R5/RRR5-23/2	1656.973	1656.881	55.743	0.374	257.792	0.391	16	0.126	-.IIPNFMCQGGDFTR.-
R5/RRR5-22/2	1673.128	1672.880	148.279	0.267	387.063	0.368	19	0.126	R.IIPNFM*CQGGDFTR.X
R5/RRR5-21/2	1672.102	1672.880	-1066.914	0.204	211.712	0.344	17	0.125	R.IIPNFM*CQGGDFTR.X
R5/RRR5-21/2	1051.777	1052.291	-1443.429	0.296	618.022	0.258	13	0.121	R.VFFDILIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1672.250	1672.880	-978.081	0.129	163.478	0.377	16	0.120	R.IIPNFM*CQGGDFTR.X
R5/RRR5-21/2	1672.147	1672.880	-1040.014	0.093	197.317	0.315	17	0.118	R.IIPNFM*CQGGDFTR.X
R5/RRR5-19/2	1763.619	1764.013	-223.794	0.496	1634.559	0.547	22	0.225	K.SGGLGDLKYPLISDVTK.S
R5/RRR5-18/2	1212.513	1213.323	-1496.649	0.473	1569.661	0.507	18	0.209	R.AGGVDDAPLVGNK.A
R5/RRR5-19/2	1213.021	1213.323	-249.170	0.518	1543.349	0.514	19	0.208	R.AGGVDDAPLVGNK.A
R5/RRR5-19/3	1763.336	1764.013	-953.873	0.423	1706.989	0.442	33	0.188	K.SGGLGDLKYPLISDVTK.S
R5/RRR5-18/2	1213.135	1213.323	-155.285	0.512	1392.941	0.486	20	0.188	R.AGGVDDAPLVGNK.A
R5/RRR5-18/2	1213.160	1213.323	-134.593	0.499	1277.105	0.530	17	0.183	R.AGGVDDAPLVGNK.A
R5/RRR5-19/2	1763.304	1764.013	-971.936	0.509	1067.368	0.564	21	0.171	K.SGGLGDLKYPLISDVTK.S
R5/RRR5-19/2	1763.756	1764.013	-145.820	0.540	1074.817	0.564	20	0.171	K.SGGLGDLKYPLISDVTK.S
R5/RRR5-19/2	1213.006	1213.323	-261.386	0.489	1145.311	0.509	18	0.169	R.AGGVDDAPLVGNK.A
R5/RRR5-19/2	1213.024	1213.323	-246.949	0.529	1076.982	0.527	17	0.167	R.AGGVDDAPLVGNK.A
R5/RRR5-19/2	1486.425	1486.740	-212.729	0.457	1046.319	0.464	22	0.157	K.SFGVLIPDQGIALR.G
R5/RRR5-19/2	1487.711	1486.740	-19.884	0.499	1082.472	0.401	22	0.150	K.SFGVLIPDQGIALR.G
R5/RRR5-19/2	1486.441	1486.740	-201.854	0.417	993.049	0.364	22	0.140	K.SFGVLIPDQGIALR.G
R5/RRR5-18/2	1764.335	1764.013	183.369	0.459	774.663	0.467	19	0.138	K.SGGLGDLKYPLISDVTK.S
R5/RRR5-19/3	1763.829	1764.013	-104.555	0.419	1378.899	0.421	31	0.134	K.SGGLGDLKYPLISDVTK.S
R5/RRR5-18/2	1486.255	1486.740	-327.920	0.394	403.138	0.448	16	0.127	-.SFGVLIPDQGIALR.-
R5/RRR5-21/2	1487.902	1486.740	109.064	0.343	309.741	0.337	13	0.104	-.SFGVLIPDQGIALR.-
R5/RRR5-18/3	1763.282	1764.013	-984.524	0.370	973.255	0.343	26	0.084	K.SGGLGDLKYPLISDVTK.S
R5/RRR5-10/2	1224.209	1224.262	-43.467	0.502	1462.814	0.376	17	0.172	R.GDSVDQFSNVR.H
R5/RRR5-10/2	1223.995	1224.262	-218.727	0.455	1561.544	0.320	17	0.171	R.GDSVDQFSNVR.H
R5/RRR5-10/2	1224.978	1224.262	-232.345	0.541	1399.803	0.399	17	0.171	R.GDSVDQFSNVR.H
R5/RRR5-10/2	1273.136	1273.503	-288.855	0.391	965.071	0.380	15	0.137	K.FKDEIVPVPTK.I
R5/RRR5-10/2	971.771	972.209	-451.384	0.411	480.177	0.441	14	0.135	K.GLPILGVFR.S
R5/RRR5-10/2	972.142	972.209	-69.221	0.386	356.015	0.466	12	0.133	K.GLPILGVFR.S
R5/RRR5-11/2	971.992	972.209	-224.042	0.388	346.868	0.420	13	0.132	K.GLPILGVFR.S
R5/RRR5-11/2	972.082	972.209	-130.312	0.321	321.677	0.521	12	0.132	K.GLPILGVFR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/2	1154.199	1154.340	-122.692	0.391	1175.117	0.401	16	0.155	K.LFEQLGATFK.A
R5/RRR5-27/2	1542.448	1541.814	-238.024	0.452	737.174	0.549	20	0.149	K.LVPLLTEAGAIASSAK.T
R5/RRR5-26/2	1154.024	1154.340	-274.852	0.413	1027.680	0.418	15	0.148	K.LFEQLGATFK.A
R5/RRR5-27/2	1154.282	1154.340	-50.024	0.348	1114.593	0.345	15	0.142	K.LFEQLGATFK.A
R5/RRR5-26/2	1153.931	1154.340	-355.725	0.368	896.452	0.398	14	0.138	K.LFEQLGATFK.A
R5/RRR5-27/2	1541.409	1541.814	-263.523	0.359	803.157	0.422	20	0.135	K.LVPLLTEAGAIASSAK.T
R5/RRR5-26/2	1541.343	1541.814	-306.826	0.321	852.217	0.382	21	0.133	K.LVPLLTEAGAIASSAK.T
R5/RRR5-27/3	1549.262	1549.793	-991.317	0.446	1609.782	0.307	31	0.129	K.AKETVASAPVVVYSK.S
R5/RRR5-27/2	1153.869	1154.340	-409.435	0.416	1064.320	0.238	15	0.127	K.LFEQLGATFK.A
R5/RRR5-26/2	1541.413	1541.814	-261.378	0.346	550.210	0.432	18	0.127	-.LVPLLTEAGAIASSAK.-
R5/RRR5-27/2	1540.811	1541.814	-1304.265	0.275	661.789	0.311	19	0.121	K.LVPLLTEAGAIASSAK.T
R5/RRR5-26/2	1541.162	1541.814	-1075.168	0.280	477.274	0.343	17	0.120	K.LVPLLTEAGAIASSAK.T
R5/RRR5-27/3	1549.993	1549.793	129.489	0.490	1022.652	0.420	28	0.103	K.AKETVASAPVVVYSK.S
R5/RRR5-27/3	1549.550	1549.793	-157.532	0.468	1163.049	0.362	29	0.101	K.AKETVASAPVVVYSK.S
R5/RRR5-26/3	1549.213	1549.793	-1023.119	0.408	1100.523	0.204	28	0.071	K.AKETVASAPVVVYSK.S
R5/RRR5-26/3	1549.338	1549.793	-294.465	0.357	814.200	0.205	26	0.068	K.AKETVASAPVVVYSK.S
R5/RRR5-11/2	1806.788	1807.127	-188.427	0.411	825.212	0.462	24	0.141	R.AVTLIPGDGIGPLVTGAVR.Q
R5/RRR5-11/2	1807.065	1807.127	-34.461	0.440	662.190	0.443	22	0.132	R.AVTLIPGDGIGPLVTGAVR.Q
R5/RRR5-11/2	1807.654	1807.127	-262.707	0.434	660.910	0.429	21	0.130	R.AVTLIPGDGIGPLVTGAVR.Q
R5/RRR5-9/2	1978.388	1979.049	-842.506	0.574	1967.383	0.681	26	0.311	K.TVGGGDDAFNTFFSETGAGK.H
R5/RRR5-9/2	1977.692	1979.049	-1195.682	0.530	1952.463	0.672	26	0.305	K.TVGGGDDAFNTFFSETGAGK.H
R5/RRR5-9/2	1978.424	1979.049	-823.863	0.541	1620.256	0.703	25	0.262	K.TVGGGDDAFNTFFSETGAGK.H
R5/RRR5-9/2	1702.364	1702.929	-922.437	0.479	1594.262	0.480	24	0.206	R.AVFVDLEPTVIDEVR.T
R5/RRR5-9/2	1702.454	1702.929	-280.235	0.502	1499.145	0.514	23	0.203	R.AVFVDLEPTVIDEVR.T
R5/RRR5-9/2	1703.401	1702.929	277.620	0.577	1415.848	0.540	24	0.200	R.AVFVDLEPTVIDEVR.T
R5/RRR5-10/2	1978.300	1979.049	-886.856	0.500	1137.639	0.652	21	0.190	K.TVGGGDDAFNTFFSETGAGK.H
R5/RRR5-10/2	1703.299	1702.929	217.543	0.573	1245.464	0.566	23	0.189	R.AVFVDLEPTVIDEVR.T
R5/RRR5-10/2	1702.393	1702.929	-905.088	0.455	1330.230	0.514	23	0.186	R.AVFVDLEPTVIDEVR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1703.061	1702.929	77.312	0.570	1142.482	0.575	22	0.182	R.AVFVDLEPTVIDEVR.T
R5/RRR5-1/2	1703.166	1702.929	139.346	0.534	1128.551	0.526	22	0.172	R.AVFVDLEPTVIDEVR.T
R5/RRR5-9/3	1702.934	1702.929	2.537	0.507	1481.795	0.489	30	0.169	R.AVFVDLEPTVIDEVR.T
R5/RRR5-1/2	1703.290	1702.929	212.584	0.531	1054.365	0.533	21	0.167	R.AVFVDLEPTVIDEVR.T
R5/RRR5-7/2	1702.630	1702.929	-176.152	0.497	1014.699	0.522	19	0.161	R.AVFVDLEPTVIDEVR.T
R5/RRR5-5/2	1703.126	1702.929	115.698	0.469	1090.843	0.470	21	0.159	R.AVFVDLEPTVIDEVR.T
R5/RRR5-8/2	1702.525	1702.929	-238.081	0.488	1038.157	0.484	21	0.158	R.AVFVDLEPTVIDEVR.T
R5/RRR5-15/2	1702.623	1702.929	-180.252	0.465	975.809	0.497	19	0.155	R.AVFVDLEPTVIDEVR.T
R5/RRR5-3/2	1703.402	1702.929	278.266	0.521	959.358	0.486	20	0.153	R.AVFVDLEPTVIDEVR.T
R5/RRR5-6/2	1702.661	1702.929	-157.956	0.501	989.383	0.461	20	0.151	R.AVFVDLEPTVIDEVR.T
R5/RRR5-2/2	1702.300	1702.929	-960.160	0.494	909.318	0.483	20	0.150	R.AVFVDLEPTVIDEVR.T
R5/RRR5-4/2	1703.188	1702.929	152.212	0.440	903.105	0.457	19	0.145	R.AVFVDLEPTVIDEVR.T
R5/RRR5-10/2	1701.876	1702.929	-1210.398	0.395	894.572	0.431	20	0.142	R.AVFVDLEPTVIDEVR.T
R5/RRR5-20/2	1702.324	1702.929	-945.689	0.408	836.778	0.442	18	0.140	R.AVFVDLEPTVIDEVR.T
R5/RRR5-3/2	1702.304	1702.929	-957.784	0.400	731.031	0.413	18	0.133	R.AVFVDLEPTVIDEVR.T
R5/RRR5-15/2	1704.614	1702.929	-185.500	0.429	805.884	0.335	18	0.127	R.AVFVDLEPTVIDEVR.T
R5/RRR5-2/2	1701.795	1702.929	-1258.227	0.333	659.863	0.332	16	0.123	R.AVFVDLEPTVIDEVR.T
R5/RRR5-3/2	1702.296	1702.929	-962.248	0.421	702.198	0.314	17	0.123	R.AVFVDLEPTVIDEVR.T
R5/RRR5-11/2	1702.172	1702.929	-1035.398	0.317	653.281	0.268	17	0.120	R.AVFVDLEPTVIDEVR.T
R5/RRR5-1/2	1701.991	1702.929	-1142.623	0.344	517.387	0.292	15	0.120	R.AVFVDLEPTVIDEVR.T
R5/RRR5-2/2	1702.367	1702.929	-920.781	0.384	883.061	0.194	18	0.116	R.AVFVDLEPTVIDEVR.T
R5/RRR5-1/2	1978.747	1979.049	-153.428	0.407	247.268	0.494	12	0.108	-.TVGGGDDAFNTFFSETGAGK.-
R5/RRR5-1/2	1978.010	1979.049	-1034.244	0.339	285.346	0.375	13	0.107	-.TVGGGDDAFNTFFSETGAGK.-
R5/RRR5-9/3	1978.982	1979.049	-34.412	0.367	802.283	0.379	27	0.077	K.TVGGGDDAFNTFFSETGAGK.H
R5/RRR5-18/2	1777.014	1777.874	-1049.805	0.503	1125.692	0.484	19	0.162	K.DGAPDSFHFVEDWVR.T
R5/RRR5-18/2	1777.360	1777.874	-854.169	0.496	1183.801	0.451	20	0.161	K.DGAPDSFHFVEDWVR.T
R5/RRR5-18/2	1777.232	1777.874	-926.636	0.497	1147.362	0.444	19	0.157	K.DGAPDSFHFVEDWVR.T
R5/RRR5-18/2	1245.034	1245.365	-266.069	0.431	901.159	0.417	16	0.141	K.EAVNQSLENLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1245.214	1245.365	-121.394	0.385	941.792	0.388	16	0.139	K.EAVNQSLENLK.T
R5/RRR5-18/2	1245.048	1245.365	-255.249	0.357	871.294	0.366	16	0.133	K.EAVNQSLENLK.T
R5/RRR5-18/3	1078.457	1078.199	239.976	0.377	975.609	0.276	17	0.073	K.FKTEFYDK.K
R5/RRR5-6/2	1687.392	1687.870	-284.260	0.504	2582.087	0.440	25	0.349	R.VVDSLDDLSLDIPSAK.S
R5/RRR5-6/2	1687.453	1687.870	-247.972	0.457	2430.292	0.410	24	0.312	R.VVDSLDDLSLDIPSAK.S
R5/RRR5-5/2	1687.377	1687.870	-293.115	0.390	2008.263	0.311	23	0.219	R.VVDSLDDLSLDIPSAK.S
R5/RRR5-6/2	1755.348	1755.946	-913.147	0.491	1065.191	0.570	21	0.171	K.SVAPIIEEYFSTGDVK.L
R5/RRR5-6/2	1882.965	1883.132	-89.317	0.486	492.600	0.517	19	0.132	R.AVIDDVLAPLNLDEISGK.L
R5/RRR5-9/2	1423.140	1423.550	-289.122	0.491	2094.855	0.516	22	0.285	K.FIASEGDTVTPGTK.V
R5/RRR5-9/2	1795.384	1795.885	-838.979	0.496	1864.661	0.646	24	0.283	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-10/2	1422.986	1423.550	-1102.767	0.475	2100.150	0.506	22	0.283	K.FIASEGDTVTPGTK.V
R5/RRR5-10/2	1795.205	1795.885	-939.115	0.491	1862.727	0.642	23	0.281	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-9/2	1423.093	1423.550	-322.428	0.503	2006.675	0.529	22	0.274	K.FIASEGDTVTPGTK.V
R5/RRR5-10/2	1423.062	1423.550	-343.686	0.510	2000.822	0.462	22	0.255	K.FIASEGDTVTPGTK.V
R5/RRR5-10/2	1423.136	1423.550	-291.704	0.455	1948.534	0.458	21	0.246	K.FIASEGDTVTPGTK.V
R5/RRR5-9/2	1423.154	1423.550	-278.882	0.508	1858.797	0.467	21	0.236	K.FIASEGDTVTPGTK.V
R5/RRR5-9/2	1795.235	1795.885	-922.390	0.497	1420.784	0.659	22	0.224	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-9/2	1795.257	1795.885	-910.103	0.516	1329.892	0.678	21	0.217	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-10/2	1795.247	1795.885	-915.359	0.500	1256.564	0.647	21	0.203	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-9/2	1399.008	1399.466	-328.078	0.456	1047.858	0.383	17	0.142	R.DADNM*NFADIEK.G
R5/RRR5-10/3	1796.336	1795.885	251.662	0.351	649.145	0.515	26	0.096	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-10/3	1796.456	1795.885	-239.817	0.374	467.188	0.449	24	0.086	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-10/3	1796.936	1795.885	28.330	0.328	436.147	0.447	24	0.085	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-9/3	1796.912	1795.885	15.043	0.296	511.545	0.415	26	0.081	K.SAAPAETHVAPSEDSTPK.E
R5/RRR5-12/1	963.596	964.183	-1651.870	0.228	769.641	0.376	12	0.400	R.TALAFVTLK.S
R5/RRR5-13/1	963.566	964.183	-1683.943	0.207	734.475	0.284	12	0.333	R.TALAFVTLK.S
R5/RRR5-13/1	963.562	964.183	-1687.507	0.190	715.891	0.312	12	0.328	R.TALAFVTLK.S
R5/RRR5-13/1	963.522	964.183	-1729.830	0.236	631.594	0.300	12	0.252	R.TALAFVTLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1689.121	1689.761	-973.957	0.507	1379.814	0.498	20	0.186	K.NGVNAEGCLFDEHAR.T
R5/RRR5-12/1	963.634	964.183	-1612.736	0.246	494.810	0.339	11	0.183	R.TALAFVTLK.S
R5/RRR5-13/2	1689.266	1689.761	-294.020	0.527	1306.950	0.504	20	0.181	K.NGVNAEGCLFDEHAR.T
R5/RRR5-12/2	964.008	964.183	-182.651	0.441	977.424	0.493	15	0.158	R.TALAFVTLK.S
R5/RRR5-13/2	964.086	964.183	-101.485	0.474	970.833	0.465	15	0.155	R.TALAFVTLK.S
R5/RRR5-13/2	963.541	964.183	-1709.350	0.414	1038.359	0.425	15	0.151	R.TALAFVTLK.S
R5/RRR5-12/2	965.018	964.183	-171.422	0.501	982.275	0.417	15	0.149	R.TALAFVTLK.S
R5/RRR5-12/2	963.669	964.183	-1576.609	0.449	972.448	0.421	15	0.148	R.TALAFVTLK.S
R5/RRR5-13/2	963.591	964.183	-1657.039	0.427	1009.929	0.407	15	0.148	R.TALAFVTLK.S
R5/RRR5-13/2	1795.249	1794.037	118.422	0.350	896.724	0.138	20	0.110	K.IFHYGSISLITEPCR.-
R5/RRR5-9/2	1847.734	1848.048	-170.668	0.514	1498.904	0.527	22	0.205	R.ELDHLANFLQAAVDYK.K
R5/RRR5-9/2	1846.675	1848.048	-1289.132	0.454	1369.519	0.569	20	0.199	R.ELDHLANFLQAAVDYK.K
R5/RRR5-9/3	1932.815	1932.162	-179.822	0.496	1567.863	0.484	32	0.180	K.TLTETNKNLDEIVELAK.K
R5/RRR5-9/2	1069.974	1070.223	-233.506	0.392	1097.850	0.424	16	0.153	K.VYAYGAAQVK.K
R5/RRR5-9/2	1069.355	1070.223	-1751.968	0.335	824.285	0.466	15	0.141	K.VYAYGAAQVK.K
R5/RRR5-9/2	1847.686	1848.048	-196.582	0.256	862.267	0.424	18	0.132	R.ELDHLANFLQAAVDYK.K
R5/RRR5-9/2	1070.002	1070.223	-207.411	0.314	725.578	0.373	14	0.128	K.VYAYGAAQVK.K
R5/RRR5-9/3	1848.337	1848.048	156.878	0.439	1166.594	0.360	24	0.099	R.ELDHLANFLQAAVDYK.K
R5/RRR5-9/3	1932.982	1932.162	-93.157	0.349	866.428	0.276	24	0.070	K.TLTETNKNLDEIVELAK.K
R5/RRR5-9/3	1847.528	1848.048	-825.314	0.273	734.973	0.244	22	0.063	R.ELDHLANFLQAAVDYK.K
R5/RRR5-9/3	1931.547	1932.162	-838.571	0.287	832.189	0.139	24	0.057	K.TLTETNKNLDEIVELAK.K
R5/RRR5-10/2	1828.430	1827.097	182.633	0.474	1908.750	0.495	21	0.250	K.IISYAQGFQLMQEAAR.E
R5/RRR5-10/2	1970.753	1970.170	-212.263	0.468	778.592	0.459	17	0.135	R.KNPDLENLLFDDFFNK.A
R5/RRR5-10/2	1970.712	1970.170	-233.142	0.419	491.194	0.407	14	0.121	R.KNPDLENLLFDDFFNK.A
R5/RRR5-10/3	1672.330	1672.782	-271.234	0.406	987.298	0.435	25	0.102	K.YPEGQDIHVNWTGR.G
R5/RRR5-10/3	1672.679	1672.782	-61.905	0.383	1011.874	0.358	26	0.089	K.YPEGQDIHVNWTGR.G
R5/RRR5-10/3	1672.519	1672.782	-157.773	0.350	739.745	0.304	23	0.074	K.YPEGQDIHVNWTGR.G
R5/RRR5-17/1	1015.549	1016.174	-1604.800	0.253	716.171	0.468	16	0.376	K.LVLVGDGGTGK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/1	1015.575	1016.174	-1579.020	0.250	581.248	0.468	14	0.282	K.LVLVGDGGTGK.T
R5/RRR5-17/1	1015.542	1016.174	-1611.864	0.271	586.906	0.424	14	0.267	K.LVLVGDGGTGK.T
R5/RRR5-18/2	1214.910	1215.337	-352.584	0.374	1053.521	0.297	16	0.133	K.NLQYYDISAK.S
R5/RRR5-18/2	1016.053	1016.174	-118.708	0.405	848.801	0.342	17	0.132	K.LVLVGDGGTGK.T
R5/RRR5-18/2	1015.974	1016.174	-196.688	0.397	774.819	0.251	16	0.121	K.LVLVGDGGTGK.T
R5/RRR5-18/2	1015.888	1016.174	-281.431	0.370	619.983	0.255	15	0.120	K.LVLVGDGGTGK.T
R5/RRR5-14/3	1632.407	1632.755	-213.740	0.463	437.726	0.538	24	0.098	K.IVASEDRDLTVEER.N
R5/RRR5-14/3	1632.835	1632.755	49.173	0.446	476.954	0.504	25	0.095	K.IVASEDRDLTVEER.N
R5/RRR5-14/3	1632.195	1632.755	-958.463	0.427	352.750	0.444	23	0.091	K.IVASEDRDLTVEER.N
R5/RRR5-18/2	1455.467	1455.595	-88.463	0.515	2139.663	0.474	22	0.280	K.GVISLDTSGSSYLR.A
R5/RRR5-18/2	1455.458	1455.595	-94.352	0.502	2056.373	0.516	22	0.279	K.GVISLDTSGSSYLR.A
R5/RRR5-18/2	1454.692	1455.595	-1312.462	0.420	1365.913	0.457	19	0.177	K.GVISLDTSGSSYLR.A
R5/RRR5-18/2	1002.523	1003.180	-1657.724	0.315	1350.098	0.288	14	0.148	K.AIQAFSPLR.I
R5/RRR5-18/2	1004.031	1003.180	-148.359	0.465	1005.748	0.331	13	0.135	K.AIQAFSPLR.I
R5/RRR5-18/3	1519.812	1519.769	28.662	0.505	1129.869	0.455	29	0.118	R.KPLVVAPGGFYDQK.W
R5/RRR5-18/3	1519.490	1519.769	-184.298	0.392	492.651	0.356	19	0.074	-.KPLVVAPGGFYDQK.-
R5/RRR5-9/2	1585.586	1585.824	-150.778	0.498	2134.905	0.343	21	0.243	R.FELTFYALNPELK.V
R5/RRR5-9/2	1586.331	1585.824	-311.709	0.544	2098.221	0.341	20	0.235	R.FELTFYALNPELK.V
R5/RRR5-9/2	1586.580	1585.824	-154.233	0.529	1793.116	0.329	20	0.194	R.FELTFYALNPELK.V
R5/RRR5-10/2	1041.698	1042.170	-454.111	0.468	1370.030	0.467	15	0.183	K.YAELVYAGR.W
R5/RRR5-10/2	1041.905	1042.170	-255.073	0.489	1263.434	0.473	15	0.175	K.YAELVYAGR.W
R5/RRR5-9/2	1042.155	1042.170	-13.582	0.548	1298.510	0.421	15	0.168	K.YAELVYAGR.W
R5/RRR5-9/2	1041.394	1042.170	-1709.772	0.408	1369.419	0.386	15	0.167	K.YAELVYAGR.W
R5/RRR5-9/2	1132.855	1133.369	-1339.907	0.360	449.705	0.528	14	0.135	K.KHNVPIPVTK.K
R5/RRR5-10/2	1042.050	1042.170	-114.748	0.304	1087.473	0.182	15	0.124	K.YAELVYAGR.W
R5/RRR5-9/2	1133.728	1133.369	318.086	0.384	527.392	0.296	13	0.121	K.KHNVPIPVTK.K
R5/RRR5-7/2	1494.223	1494.628	-272.173	0.411	1880.997	0.434	21	0.231	R.ELGEGGIDNYLSVK.Q
R5/RRR5-7/2	1462.355	1462.626	-186.341	0.510	1622.360	0.537	21	0.224	K.SPIVVFDDVDVEK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1463.539	1462.626	-59.950	0.533	1545.641	0.545	20	0.216	K.SPIVVFDDVDVEK.A
R5/RRR5-7/2	1463.229	1462.626	-272.164	0.549	1505.767	0.558	20	0.215	K.SPIVVFDDVDVEK.A
R5/RRR5-7/2	1495.356	1494.628	-182.883	0.478	1549.978	0.540	20	0.214	R.ELGEGGIDNYLSVK.Q
R5/RRR5-7/2	1306.178	1306.446	-206.090	0.440	1315.097	0.538	19	0.190	R.LGPVVSEGQYEK.I
R5/RRR5-8/2	1463.321	1462.626	-209.394	0.479	1335.207	0.510	19	0.186	K.SPIVVFDDVDVEK.A
R5/RRR5-7/2	1306.000	1306.446	-342.429	0.442	1322.032	0.512	19	0.185	R.LGPVVSEGQYEK.I
R5/RRR5-7/2	1494.274	1494.628	-237.750	0.457	1367.600	0.451	19	0.177	R.ELGEGGIDNYLSVK.Q
R5/RRR5-8/2	1462.237	1462.626	-266.906	0.380	1355.154	0.435	19	0.173	K.SPIVVFDDVDVEK.A
R5/RRR5-7/2	1305.639	1306.446	-1388.117	0.404	1102.106	0.531	18	0.168	R.LGPVVSEGQYEK.I
R5/RRR5-8/2	1462.264	1462.626	-248.397	0.459	1133.901	0.493	18	0.166	K.SPIVVFDDVDVEK.A
R5/RRR5-21/2	1413.236	1412.610	-265.504	0.542	1191.335	0.543	20	0.181	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1413.195	1412.610	-294.622	0.516	1056.297	0.583	19	0.177	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1412.286	1412.610	-230.659	0.433	1111.381	0.557	19	0.174	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1660.470	1659.948	-288.869	0.468	1112.878	0.551	23	0.174	K.SGTTPLSPAIVFILDK.V
R5/RRR5-15/2	1412.269	1412.610	-242.105	0.407	1283.432	0.471	20	0.174	K.VVEVVESSPPEIK.A
R5/RRR5-21/2	1412.526	1412.610	-59.688	0.469	1212.906	0.489	20	0.172	K.VVEVVESSPPEIK.A
R5/RRR5-20/2	1412.165	1412.610	-315.992	0.489	1062.585	0.545	19	0.170	K.VVEVVESSPPEIK.A
R5/RRR5-15/2	1412.116	1412.610	-351.119	0.435	1087.820	0.527	19	0.168	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1412.191	1412.610	-298.127	0.408	1096.627	0.522	19	0.167	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1660.421	1659.948	285.691	0.437	1041.186	0.546	22	0.167	K.SGTTPLSPAIVFILDK.V
R5/RRR5-15/2	1412.309	1412.610	-214.010	0.508	967.158	0.540	18	0.163	K.VVEVVESSPPEIK.A
R5/RRR5-21/2	1412.040	1412.610	-1115.303	0.382	1132.062	0.479	19	0.162	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1659.281	1659.948	-1007.706	0.429	1065.318	0.499	22	0.161	K.SGTTPLSPAIVFILDK.V
R5/RRR5-20/2	1412.225	1412.610	-274.017	0.408	1085.691	0.473	19	0.159	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1783.241	1782.844	223.308	0.431	707.552	0.622	26	0.159	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-22/2	1659.394	1659.948	-939.019	0.414	1004.178	0.507	22	0.158	K.SGTTPLSPAIVFILDK.V
R5/RRR5-22/2	1659.467	1659.948	-290.372	0.430	977.201	0.520	21	0.158	K.SGTTPLSPAIVFILDK.V
R5/RRR5-21/2	1659.585	1659.948	-219.084	0.391	1018.904	0.480	22	0.155	K.SGTTPLSPAIVFILDK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1659.692	1659.948	-154.668	0.396	1009.405	0.469	22	0.153	K.SGTTPLSPAIVFILDK.V
R5/RRR5-15/2	1659.978	1659.948	18.394	0.414	891.866	0.502	21	0.151	K.SGTTPLSPAIVFILDK.V
R5/RRR5-15/2	1659.215	1659.948	-1047.594	0.415	919.469	0.489	21	0.150	K.SGTTPLSPAIVFILDK.V
R5/RRR5-15/2	1658.901	1659.948	-1237.473	0.370	1037.112	0.436	22	0.149	K.SGTTPLSPAIVFILDK.V
R5/RRR5-21/2	1659.758	1659.948	-114.606	0.437	878.331	0.478	21	0.147	K.SGTTPLSPAIVFILDK.V
R5/RRR5-21/2	1782.223	1782.844	-911.949	0.361	685.322	0.557	25	0.146	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-20/2	1411.621	1412.610	-1413.568	0.355	863.648	0.484	17	0.145	K.VVEVVESSPPEIK.A
R5/RRR5-15/2	1783.072	1782.844	128.570	0.346	577.509	0.581	24	0.143	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-12/2	1660.658	1659.948	-174.927	0.424	817.433	0.478	19	0.143	K.SGTTPLSPAIVFILDK.V
R5/RRR5-16/2	1782.221	1782.844	-913.256	0.302	831.751	0.488	27	0.143	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-22/2	1783.203	1782.844	201.959	0.333	510.932	0.599	23	0.141	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-1/2	1411.879	1412.610	-1229.900	0.333	1143.708	0.331	18	0.141	K.VVEVVESSPPEIK.A
R5/RRR5-16/2	1783.228	1782.844	216.169	0.331	587.952	0.550	24	0.140	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-21/2	1659.271	1659.948	-1013.320	0.360	798.752	0.437	20	0.137	K.SGTTPLSPAIVFILDK.V
R5/RRR5-15/2	1782.323	1782.844	-855.499	0.308	634.060	0.512	24	0.137	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-20/2	1782.212	1782.844	-918.207	0.268	739.637	0.466	26	0.135	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-21/2	1782.377	1782.844	-262.655	0.262	752.650	0.466	25	0.135	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-13/2	1660.776	1659.948	-103.920	0.404	663.867	0.436	18	0.133	K.SGTTPLSPAIVFILDK.V
R5/RRR5-15/2	1782.171	1782.844	-941.586	0.253	691.310	0.456	25	0.132	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-12/2	1660.620	1659.948	-198.082	0.404	598.008	0.444	17	0.131	K.SGTTPLSPAIVFILDK.V
R5/RRR5-22/2	1412.276	1412.610	-237.596	0.329	500.050	0.410	17	0.129	K.VVEVVESSPPEIK.A
R5/RRR5-22/2	1782.221	1782.844	-913.324	0.242	595.146	0.457	24	0.128	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-22/2	1782.193	1782.844	-929.002	0.214	573.628	0.401	23	0.123	K.AEPEPEPEAPAAETTSR.E
R5/RRR5-12/2	1660.957	1659.948	5.631	0.319	386.425	0.375	13	0.121	K.SGTTPLSPAIVFILDK.V
R5/RRR5-22/2	1360.467	1360.541	-54.322	0.509	1548.224	0.464	18	0.200	K.FVAYTSAWTWK.K
R5/RRR5-13/2	1591.798	1590.846	-29.891	0.468	1074.653	0.421	20	0.152	K.EVFWLPVDSAWLK.I
R5/RRR5-13/2	1292.418	1291.481	-49.320	0.443	995.505	0.419	16	0.146	R.GVNVIYALTGQR.R
R5/RRR5-22/2	1291.240	1291.481	-187.234	0.308	1081.597	0.377	16	0.142	R.GVNVIYALTGQR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1292.210	1291.481	-210.592	0.334	895.342	0.364	16	0.133	R.GVNVIYALTGQR.R
R5/RRR5-14/2	1292.187	1291.481	-228.030	0.404	837.677	0.362	15	0.131	R.GVNVIYALTGQR.R
R5/RRR5-13/2	1590.962	1590.846	73.294	0.442	692.837	0.356	18	0.129	K.EVFWLPVDSAWLK.I
R5/RRR5-13/2	1590.557	1590.846	-182.329	0.373	808.177	0.322	18	0.128	K.EVFWLPVDSAWLK.I
R5/RRR5-13/2	1291.083	1291.481	-309.306	0.273	858.979	0.343	15	0.128	R.GVNVIYALTGQR.R
R5/RRR5-14/2	1591.333	1590.846	307.250	0.445	625.008	0.354	17	0.127	K.EVFWLPVDSAWLK.I
R5/RRR5-21/2	1591.838	1590.846	-4.970	0.382	359.003	0.363	16	0.127	K.EVFWLPVDSAWLK.I
R5/RRR5-14/2	1590.363	1590.846	-304.298	0.395	607.942	0.317	17	0.124	K.EVFWLPVDSAWLK.I
R5/RRR5-22/2	1291.084	1291.481	-308.642	0.290	496.766	0.372	14	0.123	R.GVNVIYALTGQR.R
R5/RRR5-14/2	1590.401	1590.846	-280.348	0.347	509.913	0.289	16	0.122	K.EVFWLPVDSAWLK.I
R5/RRR5-13/2	1291.196	1291.481	-221.757	0.253	718.836	0.260	15	0.119	R.GVNVIYALTGQR.R
R5/RRR5-22/2	1589.859	1590.846	-1253.246	0.251	631.451	0.222	15	0.117	K.EVFWLPVDSAWLK.I
R5/RRR5-6/2	1420.614	1421.581	-1388.676	0.452	1140.919	0.506	20	0.169	R.IVTNVGQDNAVYK.A
R5/RRR5-5/2	1422.554	1421.581	-18.815	0.514	904.979	0.542	18	0.159	R.IVTNVGQDNAVYK.A
R5/RRR5-6/2	1421.153	1421.581	-301.760	0.451	994.122	0.502	19	0.158	R.IVTNVGQDNAVYK.A
R5/RRR5-5/2	1422.038	1421.581	322.303	0.499	940.480	0.516	18	0.157	R.IVTNVGQDNAVYK.A
R5/RRR5-6/2	1823.524	1823.127	218.375	0.496	888.172	0.527	20	0.153	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-6/2	1421.192	1421.581	-274.098	0.475	870.145	0.513	18	0.153	R.IVTNVGQDNAVYK.A
R5/RRR5-6/2	1824.024	1823.127	-56.493	0.515	859.963	0.534	20	0.152	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-6/2	1824.419	1823.127	160.553	0.393	862.385	0.514	20	0.148	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-5/2	1822.602	1823.127	-839.146	0.486	791.156	0.522	19	0.146	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-5/2	1822.147	1823.127	-1089.719	0.382	812.378	0.459	19	0.139	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-4/2	1422.323	1421.581	-181.341	0.443	743.501	0.445	16	0.136	-.IVTNVGQDNAVYK.-
R5/RRR5-1/2	1822.948	1823.127	-98.436	0.380	549.323	0.429	16	0.126	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-5/2	1821.631	1823.127	-1373.933	0.270	678.761	0.346	17	0.121	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-15/2	1824.859	1823.127	-147.312	0.276	568.320	0.364	15	0.120	K.GSLVDLNLPSITIPNLR.M
R5/RRR5-6/3	1739.425	1739.877	-260.596	0.468	727.459	0.500	21	0.095	R.FGSLAWHDGGNHWVR.I
R5/RRR5-8/2	1707.595	1706.840	-143.733	0.563	1530.993	0.531	20	0.209	R.TGFDLQHVQDGLYGR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1712.410	1712.969	-913.379	0.454	1388.384	0.516	23	0.192	K.QTLDLGSTGLLPLEVR.F
R5/RRR5-3/2	1713.913	1712.969	-32.476	0.414	1539.307	0.422	22	0.187	K.QTLDLGSTGLLPLEVR.F
R5/RRR5-8/2	1713.570	1712.969	-233.760	0.535	1176.596	0.531	22	0.176	K.QTLDLGSTGLLPLEVR.F
R5/RRR5-8/2	1530.096	1528.646	294.741	0.471	1230.691	0.467	18	0.169	R.WDEQFYGQDLVK.K
R5/RRR5-8/2	1712.662	1712.969	-179.624	0.497	1053.823	0.541	21	0.167	K.QTLDLGSTGLLPLEVR.F
R5/RRR5-7/2	1708.183	1706.840	201.654	0.317	202.171	0.429	17	0.125	R.TGFDLQHVQDGLYGR.H
R5/RRR5-7/2	1713.535	1712.969	-254.129	0.321	606.441	0.417	15	0.124	K.QTLDLGSTGLLPLEVR.F
R5/RRR5-8/3	1707.245	1706.840	237.830	0.454	961.830	0.482	27	0.110	R.TGFDLQHVQDGLYGR.H
R5/RRR5-8/3	1706.661	1706.840	-105.367	0.456	801.927	0.493	24	0.102	R.TGFDLQHVQDGLYGR.H
R5/RRR5-8/3	1706.294	1706.840	-908.696	0.425	765.427	0.459	23	0.094	R.TGFDLQHVQDGLYGR.H
R5/RRR5-10/2	1306.080	1306.406	-250.540	0.421	1421.600	0.456	18	0.183	K.LGVSYNQPDGQK.L
R5/RRR5-10/2	1171.428	1170.381	40.594	0.461	1168.720	0.548	16	0.178	K.LDVLSGLPEVK.L
R5/RRR5-10/2	1305.769	1306.406	-1257.551	0.420	1260.281	0.437	18	0.166	K.LGVSYNQPDGQK.L
R5/RRR5-10/2	1170.491	1170.381	94.602	0.417	1078.224	0.423	15	0.150	K.LDVLSGLPEVK.L
R5/RRR5-9/3	1891.920	1892.191	-143.294	0.418	1138.614	0.448	32	0.116	R.IEELVGVPVHYIGVGPGR.D
R5/RRR5-10/3	1891.651	1892.191	-816.549	0.358	1034.215	0.408	30	0.099	R.IEELVGVPVHYIGVGPGR.D
R5/RRR5-10/3	1891.617	1892.191	-834.428	0.262	699.178	0.317	25	0.072	R.IEELVGVPVHYIGVGPGR.D
R5/RRR5-10/3	1891.976	1892.191	-113.587	0.195	1103.826	0.063	28	0.051	R.IEELVGVPVHYIGVGPGR.D
R5/RRR5-18/2	1131.047	1131.348	-267.339	0.486	984.326	0.396	15	0.144	K.AFM*TM*AGEIK.N
R5/RRR5-18/2	1131.073	1131.348	-244.060	0.438	749.317	0.441	14	0.139	K.AFM*TM*AGEIK.N
R5/RRR5-18/2	1131.880	1131.348	-414.688	0.457	722.996	0.413	14	0.135	K.AFM*TM*AGEIK.N
R5/RRR5-19/2	1130.841	1131.348	-1336.882	0.243	470.728	0.291	13	0.119	K.AFM*TM*AGEIK.N
R5/RRR5-18/3	1923.265	1922.177	45.715	0.459	966.766	0.484	33	0.112	R.M*ASQPATNASKPATVQM*R.G
R5/RRR5-18/3	1906.050	1906.178	-67.050	0.370	1066.057	0.404	31	0.102	R.M*ASQPATNASKPATVQMR.G
R5/RRR5-19/3	1922.050	1922.177	-66.497	0.405	692.726	0.471	29	0.097	R.M*ASQPATNASKPATVQM*R.G
R5/RRR5-18/3	1923.531	1922.177	184.343	0.412	770.820	0.446	30	0.096	R.M*ASQPATNASKPATVQM*R.G
R5/RRR5-18/3	1921.466	1922.177	-893.034	0.375	928.054	0.403	31	0.094	R.M*ASQPATNASKPATVQM*R.G
R5/RRR5-18/3	1922.054	1922.177	-64.204	0.381	800.956	0.431	31	0.094	R.M*ASQPATNASKPATVQM*R.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/3	1906.250	1906.178	37.875	0.356	360.158	0.464	25	0.093	R.MASQPATNASKPATVQM*R.G
R5/RRR5-18/3	1923.739	1922.177	-228.606	0.410	808.522	0.416	31	0.093	R.M*ASQPATNASKPATVQM*R.G
R5/RRR5-18/3	1922.547	1922.177	192.875	0.422	722.583	0.416	29	0.090	R.M*ASQPATNASKPATVQM*R.G
R5/RRR5-18/3	1906.653	1906.178	250.163	0.372	925.686	0.365	30	0.088	R.M*ASQPATNASKPATVQMR.G
R5/RRR5-13/2	1188.044	1187.368	-273.577	0.484	1623.181	0.429	18	0.200	K.VLEVKGEDAVK.M
R5/RRR5-13/2	1187.021	1187.368	-293.204	0.519	1617.551	0.406	18	0.194	K.VLEVKGEDAVK.M
R5/RRR5-13/2	1216.196	1216.373	-145.633	0.442	1568.434	0.401	18	0.188	K.IRDSASQLIGR.T
R5/RRR5-13/2	1187.269	1187.368	-83.594	0.479	1322.913	0.462	17	0.177	K.VLEVKGEDAVK.M
R5/RRR5-13/2	1296.752	1297.569	-1405.467	0.409	1182.797	0.523	19	0.174	K.LIVTVLPSLGER.Y
R5/RRR5-13/2	1216.121	1216.373	-207.760	0.487	1318.950	0.434	18	0.172	K.IRDSASQLIGR.T
R5/RRR5-13/2	1296.654	1297.569	-1481.397	0.390	800.227	0.494	17	0.145	K.LIVTVLPSLGER.Y
R5/RRR5-13/2	1215.645	1216.373	-1425.816	0.415	872.637	0.327	16	0.130	K.IRDSASQLIGR.T
R5/RRR5-12/2	1296.868	1297.569	-1315.275	0.400	628.207	0.400	14	0.128	K.LIVTVLPSLGER.Y
R5/RRR5-12/2	1297.791	1297.569	171.457	0.436	442.210	0.296	14	0.121	K.LIVTVLPSLGER.Y
R5/RRR5-13/2	1296.738	1297.569	-1415.963	0.243	663.816	0.281	13	0.117	K.LIVTVLPSLGER.Y
R5/RRR5-13/3	1216.689	1216.373	260.914	0.448	1002.589	0.291	20	0.075	-.IRDSASQLIGR.-
R5/RRR5-13/3	1216.573	1216.373	164.928	0.481	900.858	0.288	19	0.063	-.IRDSASQLIGR.-
R5/RRR5-11/2	1694.535	1694.909	-221.141	0.542	1664.462	0.512	20	0.222	R.IVTFNSDWQLLTEK.E
R5/RRR5-11/2	1607.370	1607.786	-259.793	0.390	947.048	0.390	20	0.139	R.DLPDSTFTISELIR.N
R5/RRR5-11/2	1455.420	1455.683	-181.171	0.407	482.986	0.493	16	0.134	R.LTAPPEQILPGYR.S
R5/RRR5-10/2	1607.231	1607.786	-970.485	0.370	1018.008	0.268	21	0.129	R.DLPDSTFTISELIR.N
R5/RRR5-11/2	1607.062	1607.786	-1076.410	0.292	804.495	0.316	20	0.125	R.DLPDSTFTISELIR.N
R5/RRR5-10/2	1455.804	1455.683	82.874	0.315	395.358	0.409	15	0.124	R.LTAPPEQILPGYR.S
R5/RRR5-10/2	1606.656	1607.786	-1329.761	0.294	904.443	0.238	21	0.122	R.DLPDSTFTISELIR.N
R5/RRR5-11/2	1455.147	1455.683	-1059.126	0.388	321.513	0.447	14	0.122	-.LTAPPEQILPGYR.-
R5/RRR5-10/2	1694.545	1694.909	-215.720	0.416	525.968	0.356	12	0.116	-.IVTFNSDWQLLTEK.-
R5/RRR5-10/2	1418.144	1418.534	-275.550	0.511	1702.188	0.570	20	0.242	R.GPLLDEDGPSYVR.V
R5/RRR5-10/2	1418.158	1418.534	-265.964	0.535	1465.262	0.610	19	0.222	R.GPLLDEDGPSYVR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1895.385	1896.007	-858.084	0.530	1642.514	0.463	20	0.206	R.ENINNFEENDFQILR.V
R5/RRR5-10/2	1418.174	1418.534	-254.220	0.510	1374.937	0.585	19	0.206	R.GPLLDEDGPSYVR.V
R5/RRR5-10/2	1896.275	1896.007	141.943	0.562	1662.557	0.450	20	0.205	R.ENINNFEENDFQILR.V
R5/RRR5-10/2	1275.265	1274.529	-207.053	0.452	780.272	0.362	16	0.131	K.LISGTCLQLLR.R
R5/RRR5-10/2	1274.275	1274.529	-200.008	0.306	609.078	0.179	14	0.110	-.LISGTCLQLLR.-
R5/RRR5-3/2	1174.953	1175.274	-274.437	0.466	2506.751	0.447	21	0.339	R.LAGEEASGITAR.H
R5/RRR5-3/2	1878.163	1877.130	18.083	0.492	1307.314	0.411	21	0.162	R.SVAEALFLPYDLVPDAR.G
R5/RRR5-3/2	1878.613	1877.130	258.244	0.465	1082.879	0.355	20	0.137	R.SVAEALFLPYDLVPDAR.G
R5/RRR5-3/2	1283.413	1284.447	-1589.599	0.345	784.034	0.414	17	0.131	R.KSPALAALADGNR.L
R5/RRR5-8/2	1144.929	1144.303	-327.617	0.538	2002.762	0.376	17	0.232	R.AEVSDIAIAVR.E
R5/RRR5-8/2	1395.185	1395.540	-255.337	0.398	1362.197	0.359	19	0.161	K.EGDYVTLVQSGVK.S
R5/RRR5-8/2	1394.834	1395.540	-1227.023	0.341	1414.746	0.295	18	0.154	K.EGDYVTLVQSGVK.S
R5/RRR5-8/2	1511.867	1511.853	9.049	0.360	769.338	0.386	15	0.128	R.LALYQGVVPIYM*K.F
R5/RRR5-8/2	1395.195	1395.540	-247.876	0.358	849.015	0.319	18	0.127	K.EGDYVTLVQSGVK.S
R5/RRR5-8/2	1511.688	1511.853	-109.767	0.300	737.856	0.378	15	0.125	R.LALYQGVVPIYM*K.F
R5/RRR5-7/2	1145.276	1144.303	-24.226	0.347	912.075	0.263	16	0.124	R.AEVSDIAIAVR.E
R5/RRR5-13/2	1591.302	1590.797	-312.274	0.530	739.547	0.556	17	0.151	K.VVTIFSAPNYCYR.C
R5/RRR5-13/2	952.322	952.048	288.424	0.451	1248.185	0.305	13	0.146	K.YGNANVWK.T
R5/RRR5-13/2	951.431	952.048	-1705.049	0.366	1023.859	0.281	13	0.132	K.YGNANVWK.T
R5/RRR5-13/2	951.599	952.048	-473.691	0.446	767.644	0.340	12	0.130	K.YGNANVWK.T
R5/RRR5-13/2	1589.897	1590.797	-1199.156	0.291	527.874	0.384	14	0.120	K.VVTIFSAPNYCYR.C
R5/RRR5-13/3	1731.792	1731.993	-115.916	0.417	1000.182	0.410	24	0.097	K.AKEILM*EESNVQPVK.S
R5/RRR5-13/3	1731.580	1731.993	-238.856	0.440	786.704	0.307	23	0.074	K.AKEILM*EESNVQPVK.S
R5/RRR5-6/2	1949.667	1950.184	-780.563	0.569	756.756	0.631	19	0.162	K.VSFGNYTYPIAWDFLR.A
R5/RRR5-6/2	1949.131	1950.184	-1056.540	0.539	773.462	0.616	19	0.160	K.VSFGNYTYPIAWDFLR.A
R5/RRR5-6/2	1949.681	1950.184	-773.022	0.516	596.425	0.620	18	0.152	K.VSFGNYTYPIAWDFLR.A
R5/RRR5-6/2	1857.454	1858.166	-924.385	0.453	917.077	0.451	23	0.145	K.QIVVSCGTLSSPLVLQR.S
R5/RRR5-4/2	1950.886	1950.184	-153.234	0.331	473.958	0.471	15	0.127	K.VSFGNYTYPIAWDFLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1951.756	1950.184	-220.163	0.425	528.114	0.421	16	0.127	K.VSFGNYTYPIAWDFLR.A
R5/RRR5-6/2	1949.276	1950.184	-981.967	0.382	432.957	0.465	14	0.127	K.VSFGNYTYPIAWDFLR.A
R5/RRR5-1/2	1949.288	1950.184	-975.680	0.389	310.461	0.491	12	0.125	K.VSFGNYTYPIAWDFLR.A
R5/RRR5-6/2	1858.350	1858.166	99.314	0.417	458.047	0.392	20	0.125	K.QIVVSCGTLSSPLVLQR.S
R5/RRR5-5/2	1949.535	1950.184	-848.443	0.300	224.299	0.376	11	0.120	K.VSFGNYTYPIAWDFLR.A
R5/RRR5-5/3	1113.277	1113.248	26.481	0.442	1192.597	0.216	23	0.076	R.DLHGFEGPIK.V
R5/RRR5-5/3	1113.663	1113.248	373.938	0.447	887.170	0.218	19	0.058	-.DLHGFEGPIK.-
R5/RRR5-15/2	1515.662	1515.737	-49.487	0.388	1140.990	0.367	18	0.143	R.AGDGVFHFVVEIPK.E
R5/RRR5-15/2	1049.015	1049.205	-182.031	0.359	676.184	0.396	15	0.129	R.FGLGNKPTSK.E
R5/RRR5-15/2	1070.860	1071.249	-364.798	0.297	731.650	0.358	14	0.124	K.IVAISLDDPK.A
R5/RRR5-15/3	1515.934	1515.737	130.218	0.407	1220.535	0.403	28	0.112	R.AGDGVFHFVVEIPK.E
R5/RRR5-15/3	1515.530	1515.737	-137.196	0.379	1008.609	0.300	25	0.079	R.AGDGVFHFVVEIPK.E
R5/RRR5-20/2	1877.484	1878.113	-870.113	0.610	3289.110	0.583	26	0.570	R.IVNAGGECLTFDQLALR.A
R5/RRR5-20/2	1878.151	1878.113	20.691	0.639	3109.935	0.582	25	0.520	R.IVNAGGECLTFDQLALR.A
R5/RRR5-19/2	1877.381	1878.113	-924.942	0.573	2938.926	0.567	26	0.473	R.IVNAGGECLTFDQLALR.A
R5/RRR5-20/2	1877.471	1878.113	-877.031	0.570	2876.727	0.593	25	0.468	R.IVNAGGECLTFDQLALR.A
R5/RRR5-19/2	1877.306	1878.113	-965.350	0.590	2882.955	0.582	26	0.465	R.IVNAGGECLTFDQLALR.A
R5/RRR5-19/2	1877.512	1878.113	-855.166	0.605	2723.505	0.600	25	0.434	R.IVNAGGECLTFDQLALR.A
R5/RRR5-19/3	1878.082	1878.113	-16.312	0.442	1837.295	0.463	29	0.221	R.IVNAGGECLTFDQLALR.A
R5/RRR5-19/2	1183.184	1182.398	-180.947	0.463	1651.899	0.496	19	0.217	R.APLGQNTVLLR.G
R5/RRR5-19/2	1182.151	1182.398	-209.898	0.537	1504.013	0.519	19	0.206	R.APLGQNTVLLR.G
R5/RRR5-21/2	1183.411	1182.398	11.214	0.460	1537.204	0.478	19	0.200	R.APLGQNTVLLR.G
R5/RRR5-22/2	1182.014	1182.398	-326.039	0.489	1514.548	0.483	19	0.199	R.APLGQNTVLLR.G
R5/RRR5-20/2	1183.026	1182.398	-315.307	0.507	1373.050	0.497	18	0.188	R.APLGQNTVLLR.G
R5/RRR5-20/2	1183.047	1182.398	-297.915	0.543	1256.107	0.551	17	0.188	R.APLGQNTVLLR.G
R5/RRR5-20/2	1183.329	1182.398	-58.419	0.489	1337.052	0.508	18	0.187	R.APLGQNTVLLR.G
R5/RRR5-20/2	1182.090	1182.398	-261.697	0.484	1306.387	0.521	18	0.187	R.APLGQNTVLLR.G
R5/RRR5-19/2	1183.212	1182.398	-157.350	0.410	1401.841	0.413	18	0.174	R.APLGQNTVLLR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/3	1879.128	1878.113	8.098	0.524	1558.480	0.467	31	0.173	R.IVNAGGECLTFDQLALR.A
R5/RRR5-19/2	1182.595	1182.398	167.038	0.449	1123.032	0.521	17	0.171	R.APLGQNTVLLR.G
R5/RRR5-20/2	1182.775	1182.398	319.595	0.453	1209.712	0.455	18	0.167	R.APLGQNTVLLR.G
R5/RRR5-21/2	1182.289	1182.398	-92.541	0.382	1205.006	0.467	17	0.166	R.APLGQNTVLLR.G
R5/RRR5-18/2	1183.236	1182.398	-137.583	0.413	1275.378	0.423	18	0.166	R.APLGQNTVLLR.G
R5/RRR5-21/2	1183.246	1182.398	-128.683	0.439	1214.962	0.439	18	0.164	R.APLGQNTVLLR.G
R5/RRR5-19/2	1183.167	1182.398	-195.955	0.436	1193.016	0.434	18	0.162	R.APLGQNTVLLR.G
R5/RRR5-21/2	1182.264	1182.398	-113.566	0.396	1042.179	0.505	17	0.161	R.APLGQNTVLLR.G
R5/RRR5-18/2	1182.227	1182.398	-144.846	0.380	859.058	0.483	16	0.147	R.APLGQNTVLLR.G
R5/RRR5-18/2	1181.488	1182.398	-1621.444	0.391	846.782	0.419	16	0.140	R.APLGQNTVLLR.G
R5/RRR5-18/2	1181.708	1182.398	-1434.645	0.345	709.044	0.484	14	0.139	R.APLGQNTVLLR.G
R5/RRR5-20/3	1879.039	1878.113	-39.403	0.478	1143.579	0.516	27	0.134	R.IVNAGGECLTFDQLALR.A
R5/RRR5-20/2	1183.531	1182.398	112.698	0.385	475.819	0.414	15	0.132	R.APLGQNTVLLR.G
R5/RRR5-21/2	1183.039	1182.398	-304.023	0.336	478.602	0.445	12	0.129	R.APLGQNTVLLR.G
R5/RRR5-7/2	1503.823	1502.632	127.298	0.513	1080.185	0.545	19	0.171	K.M*KDAEENPEGPIR.I
R5/RRR5-8/2	1060.077	1060.226	-141.209	0.318	800.335	0.431	15	0.135	K.ALSLVDSQVK.N
R5/RRR5-8/2	1154.409	1153.352	49.783	0.490	851.209	0.369	14	0.134	R.YPQVELYLK.S
R5/RRR5-8/2	1060.036	1060.226	-179.676	0.265	676.652	0.281	15	0.119	K.ALSLVDSQVK.N
R5/RRR5-8/2	1537.007	1536.756	163.730	0.486	756.550	0.471	19	0.141	K.AALAPYFELTNAVR.V
R5/RRR5-8/2	1535.411	1536.756	-1531.889	0.334	909.036	0.404	18	0.136	K.AALAPYFELTNAVR.V
R5/RRR5-8/2	1399.696	1399.660	26.101	0.577	1504.544	0.475	18	0.195	K.VLWLIENVDAVK.N
R5/RRR5-9/2	1398.796	1399.660	-1336.198	0.414	1504.952	0.428	18	0.186	K.VLWLIENVDAVK.N
R5/RRR5-8/2	1463.328	1463.613	-194.751	0.401	1729.824	0.204	20	0.164	R.DSLGIISTASEIEK.L
R5/RRR5-8/2	1400.180	1399.660	-343.706	0.462	1100.312	0.444	15	0.154	K.VLWLIENVDAVK.N
R5/RRR5-8/2	1022.126	1022.137	-10.315	0.459	1369.062	0.305	15	0.153	K.SAEGEFLLR.V
R5/RRR5-8/2	1021.651	1022.137	-476.864	0.324	1349.979	0.202	15	0.137	K.SAEGEFLLR.V
R5/RRR5-8/2	1463.247	1463.613	-250.573	0.382	1092.299	0.254	19	0.128	R.DSLGIISTASEIEK.L
R5/RRR5-8/2	1399.412	1399.660	-177.398	0.250	587.322	0.313	12	0.117	K.VLWLIENVDAVK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1292.734	1293.408	-1299.024	0.360	1052.465	0.380	17	0.144	K.FYFNPGDTGFK.A
R5/RRR5-14/2	1292.970	1293.408	-339.725	0.321	773.501	0.359	15	0.129	K.FYFNPGDTGFK.A
R5/RRR5-18/2	1292.863	1293.408	-1198.699	0.351	506.032	0.319	13	0.121	-.FYFNPGDTGFK.-
R5/RRR5-14/2	1292.181	1293.408	-1728.616	0.250	662.153	0.211	13	0.116	K.FYFNPGDTGFK.A
R5/RRR5-13/2	1292.507	1293.408	-1475.351	0.176	770.406	0.145	15	0.113	K.FYFNPGDTGFK.A
R5/RRR5-14/3	1328.538	1328.412	94.903	0.323	949.421	0.370	23	0.082	K.SHIPDGPGYQEK.F
R5/RRR5-14/2	1075.072	1075.238	-154.500	0.315	700.743	0.364	13	0.075	K.VLLTLDGEKS.-
R5/RRR5-16/2	1885.114	1886.138	-1076.831	0.475	946.116	0.578	22	0.162	K.SGATVLPDLVAAQEWLSK.N
R5/RRR5-16/2	1428.269	1427.542	-191.388	0.577	1273.807	0.600	19	0.155	K.NLKDEPVAAEQNV.-
R5/RRR5-16/2	1481.123	1481.499	-254.162	0.432	1071.037	0.409	16	0.148	K.AGYEYDEETFEK.I
R5/RRR5-16/2	1481.026	1481.499	-320.314	0.395	895.374	0.284	15	0.124	K.AGYEYDEETFEK.I
R5/RRR5-16/2	1480.924	1481.499	-1066.320	0.348	746.960	0.292	15	0.122	K.AGYEYDEETFEK.I
R5/RRR5-17/2	1427.398	1427.542	-101.011	0.422	624.507	0.548	20	0.094	K.NLKDEPVAAEQNV.-
R5/RRR5-10/2	1458.137	1458.596	-315.602	0.413	1478.271	0.507	20	0.198	R.EADPLDSQVVTVGK.F
R5/RRR5-10/2	1458.206	1458.596	-268.316	0.430	1479.552	0.487	20	0.195	R.EADPLDSQVVTVGK.F
R5/RRR5-10/2	1458.215	1458.596	-262.017	0.375	1098.896	0.513	18	0.163	R.EADPLDSQVVTVGK.F
R5/RRR5-10/3	1744.141	1742.958	105.002	0.504	1646.651	0.390	28	0.162	K.QRIEEVIVSQASVQR.C
R5/RRR5-10/2	1716.622	1716.916	-171.935	0.443	904.987	0.499	21	0.147	K.GTVVLVFQPAEEGGGGAK.K
R5/RRR5-10/3	1744.234	1742.958	158.695	0.466	1487.007	0.314	26	0.119	K.QRIEEVIVSQASVQR.C
R5/RRR5-10/3	1802.380	1803.052	-930.493	0.508	1771.079	0.342	29	0.167	R.KEDGENFILVLQQLR.D
R5/RRR5-10/2	1081.007	1081.161	-142.779	0.484	795.478	0.515	15	0.152	R.VVDTYDNVR.S
R5/RRR5-10/2	1080.856	1081.161	-282.696	0.401	831.347	0.445	15	0.142	R.VVDTYDNVR.S
R5/RRR5-10/3	1839.547	1839.990	-241.520	0.347	871.834	0.411	24	0.084	R.GFANTDGIGKPAQGGSPHK.S
R5/RRR5-7/2	1754.414	1754.961	-884.462	0.473	1475.581	0.576	22	0.213	K.EGVAFYNSLIDDVIAK.G
R5/RRR5-7/2	1754.698	1754.961	-150.690	0.494	1494.257	0.563	22	0.213	K.EGVAFYNSLIDDVIAK.G
R5/RRR5-8/2	1754.212	1754.961	-1000.006	0.450	1514.383	0.543	22	0.210	K.EGVAFYNSLIDDVIAK.G
R5/RRR5-7/2	1753.754	1754.961	-1262.628	0.424	1087.848	0.522	20	0.165	K.EGVAFYNSLIDDVIAK.G
R5/RRR5-7/2	1493.152	1493.707	-1044.640	0.375	745.107	0.327	18	0.124	R.LPEFTPEQSAM*VK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1755.082	1754.961	68.951	0.321	338.694	0.341	14	0.118	-.EGVAFYNSLIDDVIAK.-
R5/RRR5-7/3	1878.012	1877.952	32.127	0.471	571.878	0.518	30	0.099	K.ILNNDNGDVANDFYHR.Y
R5/RRR5-7/3	1877.361	1877.952	-849.601	0.405	419.492	0.489	27	0.091	K.ILNNDNGDVANDFYHR.Y
R5/RRR5-7/3	1877.846	1877.952	-56.282	0.332	259.570	0.428	22	0.087	K.ILNNDNGDVANDFYHR.Y
R5/RRR5-1/2	1900.419	1900.130	152.908	0.474	817.172	0.502	18	0.140	K.NTGDGAGILVALPHNFFR.E
R5/RRR5-2/2	958.146	958.184	-39.052	0.441	1173.582	0.248	14	0.135	R.RLSILSIR.A
R5/RRR5-2/2	958.204	958.184	21.516	0.574	874.914	0.267	14	0.125	R.RLSILSIR.A
R5/RRR5-2/2	957.343	958.184	-1928.434	0.456	804.972	0.271	12	0.124	R.RLSILSIR.A
R5/RRR5-2/3	1437.677	1437.671	3.771	0.499	830.062	0.470	25	0.100	K.VAESLGHVILGWR.W
R5/RRR5-2/3	1437.292	1437.671	-264.563	0.487	669.854	0.433	23	0.089	K.VAESLGHVILGWR.W
R5/RRR5-11/2	1760.621	1761.095	-270.281	0.517	1557.831	0.533	24	0.215	R.VLVVTNTTVAPLYLEK.V
R5/RRR5-11/2	1760.464	1761.095	-929.620	0.487	1130.692	0.483	21	0.162	R.VLVVTNTTVAPLYLEK.V
R5/RRR5-11/2	1060.889	1061.213	-305.790	0.428	994.851	0.382	14	0.141	R.LGWIDESIK.K
R5/RRR5-11/2	1275.190	1275.391	-157.810	0.371	774.085	0.397	17	0.133	R.VSTVVDVDLGDR.S
R5/RRR5-11/2	1274.746	1275.391	-1294.014	0.279	1106.909	0.258	17	0.130	R.VSTVVDVDLGDR.S
R5/RRR5-11/2	1274.420	1275.391	-1550.858	0.305	594.326	0.398	15	0.125	R.VSTVVDVDLGDR.S
R5/RRR5-9/2	1554.254	1552.749	-319.560	0.601	894.805	0.558	21	0.165	R.FIDIPEEVAEVYK.L
R5/RRR5-10/2	1259.112	1258.440	-261.150	0.397	670.882	0.554	17	0.147	K.AVEPAACPTLTK.G
R5/RRR5-8/2	1553.961	1552.749	136.574	0.530	846.176	0.456	20	0.146	R.FIDIPEEVAEVYK.L
R5/RRR5-10/2	1258.100	1258.440	-271.189	0.409	589.850	0.527	16	0.141	K.AVEPAACPTLTK.G
R5/RRR5-9/2	1258.001	1258.440	-349.850	0.407	631.475	0.487	16	0.138	K.AVEPAACPTLTK.G
R5/RRR5-9/2	1552.378	1552.749	-240.050	0.426	897.830	0.335	21	0.134	R.FIDIPEEVAEVYK.L
R5/RRR5-9/2	1258.014	1258.440	-339.627	0.353	555.872	0.468	15	0.132	K.AVEPAACPTLTK.G
R5/RRR5-10/2	1552.362	1552.749	-249.991	0.394	857.663	0.315	20	0.130	R.FIDIPEEVAEVYK.L
R5/RRR5-1/2	1554.046	1552.749	191.716	0.487	602.281	0.390	17	0.130	R.FIDIPEEVAEVYK.L
R5/RRR5-8/2	1552.487	1552.749	-169.213	0.384	784.206	0.331	20	0.130	R.FIDIPEEVAEVYK.L
R5/RRR5-10/2	1551.960	1552.749	-1156.361	0.296	981.311	0.269	21	0.128	R.FIDIPEEVAEVYK.L
R5/RRR5-8/2	1553.312	1552.749	-282.155	0.412	794.260	0.282	20	0.126	R.FIDIPEEVAEVYK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1000.210	1000.131	79.737	0.255	992.895	0.272	14	0.126	R.ASSNPVSIPK.Q
R5/RRR5-10/2	1257.499	1258.440	-1548.067	0.253	470.296	0.422	14	0.123	K.AVEPAACPTLTK.G
R5/RRR5-9/2	1552.289	1552.749	-297.643	0.300	682.090	0.273	19	0.123	R.FIDIPEEVAEVYK.L
R5/RRR5-9/2	1001.106	1000.131	-25.024	0.310	654.227	0.280	15	0.119	-.ASSNPVSIPK.-
R5/RRR5-10/2	1552.344	1552.749	-261.982	0.278	703.227	0.200	18	0.118	R.FIDIPEEVAEVYK.L
R5/RRR5-9/3	1552.706	1552.749	-28.168	0.470	1299.564	0.376	23	0.115	R.FIDIPEEVAEVYK.L
R5/RRR5-10/2	1001.091	1000.131	-40.190	0.268	551.177	0.150	14	0.100	-.ASSNPVSIPK.-
R5/RRR5-11/2	1775.370	1776.068	-959.814	0.440	810.075	0.493	25	0.147	R.YGLPPSFLSAVLAPSQK.G
R5/RRR5-11/2	1776.637	1776.068	-243.794	0.452	712.351	0.506	23	0.144	R.YGLPPSFLSAVLAPSQK.G
R5/RRR5-11/2	1775.532	1776.068	-868.012	0.434	702.607	0.483	23	0.141	R.YGLPPSFLSAVLAPSQK.G
R5/RRR5-11/2	1274.365	1275.434	-1628.363	0.368	865.530	0.421	17	0.138	K.EIVGSIQSQVSK.I
R5/RRR5-11/2	1274.881	1275.434	-1221.657	0.315	992.198	0.364	17	0.136	K.EIVGSIQSQVSK.I
R5/RRR5-11/2	1775.442	1776.068	-918.811	0.367	642.652	0.485	21	0.136	R.YGLPPSFLSAVLAPSQK.G
R5/RRR5-11/2	1948.198	1949.189	-1025.120	0.457	569.079	0.489	19	0.136	R.SILEELCGNVHSIYWK.S
R5/RRR5-11/2	1947.557	1949.189	-1870.890	0.411	400.241	0.395	16	0.123	R.SILEELCGNVHSIYWK.S
R5/RRR5-11/2	1948.672	1949.189	-780.773	0.322	156.937	0.311	14	0.123	R.SILEELCGNVHSIYWK.S
R5/RRR5-11/2	1947.711	1949.189	-1276.006	0.375	266.595	0.375	15	0.123	R.SILEELCGNVHSIYWK.S
R5/RRR5-11/2	1775.536	1776.068	-865.597	0.258	306.188	0.334	15	0.118	R.YGLPPSFLSAVLAPSQK.G
R5/RRR5-14/2	991.699	992.150	-456.574	0.379	1557.171	0.265	15	0.164	-.GFEVIDAIK.-
R5/RRR5-14/2	992.993	992.150	-158.578	0.467	1363.645	0.347	14	0.161	-.GFEVIDAIK.-
R5/RRR5-15/2	991.506	992.150	-1663.114	0.402	1310.824	0.324	14	0.153	-.GFEVIDAIK.-
R5/RRR5-15/2	991.493	992.150	-1676.597	0.402	1289.181	0.321	14	0.151	R.GFEVIDAIK.T
R5/RRR5-14/2	991.815	992.150	-339.369	0.463	1346.404	0.284	14	0.148	-.GFEVIDAIK.-
R5/RRR5-15/2	992.005	992.150	-146.764	0.424	1204.538	0.321	14	0.146	-.GFEVIDAIK.-
R5/RRR5-14/2	1549.220	1549.732	-978.883	0.463	698.050	0.454	22	0.138	K.M*GNLLPSSGTATEVR.L
R5/RRR5-15/2	1549.204	1549.732	-989.642	0.454	656.907	0.363	21	0.127	K.M*GNLLPSSGTATEVR.L
R5/RRR5-15/3	1346.197	1346.496	-222.397	0.363	561.495	0.496	23	0.094	R.DM*TALSGAHTIGR.A
R5/RRR5-15/3	1346.238	1346.496	-192.105	0.342	559.287	0.469	23	0.090	R.DM*TALSGAHTIGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1346.229	1346.496	-198.654	0.323	460.055	0.406	21	0.085	R.DM*TALSGAHTIGR.A
R5/RRR5-14/3	1346.725	1346.496	170.576	0.339	449.844	0.421	20	0.083	-.DM*TALSGAHTIGR.-
R5/RRR5-14/3	1346.539	1346.496	32.300	0.346	459.717	0.344	20	0.083	R.DM*TALSGAHTIGR.A
R5/RRR5-16/3	1346.470	1346.496	-19.120	0.271	527.804	0.336	22	0.078	R.DM*TALSGAHTIGR.A
R5/RRR5-13/2	1751.710	1752.092	-218.676	0.536	1887.514	0.496	26	0.246	K.AVVAGASGGIGQPLSLLLK.L
R5/RRR5-13/2	1751.181	1752.092	-1094.377	0.420	1089.678	0.451	21	0.152	K.AVVAGASGGIGQPLSLLLK.L
R5/RRR5-14/2	1235.256	1234.470	-173.220	0.431	958.977	0.397	17	0.141	R.LFGVTTLDIVR.A
R5/RRR5-14/2	1753.164	1752.092	41.581	0.259	1004.189	0.223	19	0.119	K.AVVAGASGGIGQPLSLLLK.L
R5/RRR5-12/1	829.345	829.961	-1954.405	0.295	592.630	0.452	10	0.629	K.LLVAVADE.-
R5/RRR5-12/2	1001.058	1001.202	-144.152	0.439	1048.495	0.463	15	0.157	K.VTVLQDVVK.G
R5/RRR5-12/2	1001.162	1001.202	-40.554	0.487	909.070	0.487	15	0.154	K.VTVLQDVVK.G
R5/RRR5-12/2	1000.913	1001.202	-289.740	0.442	874.139	0.462	15	0.148	K.VTVLQDVVK.G
R5/RRR5-12/3	1374.140	1374.527	-282.602	0.370	1112.148	0.200	24	0.069	K.FGFHDAFNYKK.E
R5/RRR5-10/2	1249.690	1250.384	-1360.325	0.356	1053.747	0.269	16	0.128	R.AFDEGWGGVIAK.T
R5/RRR5-11/2	1249.419	1250.384	-1577.677	0.356	492.711	0.242	13	0.115	-.AFDEGWGGVIAK.-
R5/RRR5-10/3	1125.545	1125.262	252.399	0.458	304.206	0.482	17	0.099	K.AAWHELIER.V
R5/RRR5-10/3	1124.996	1125.262	-236.735	0.473	330.253	0.281	17	0.096	K.AAWHELIER.V
R5/RRR5-10/3	920.947	920.134	-203.637	0.499	822.120	0.410	19	0.093	R.AVHPIALAK.V
R5/RRR5-10/3	1125.263	1125.262	1.119	0.397	259.366	0.347	15	0.081	-.AAWHELIER.-
R5/RRR5-11/3	1125.555	1125.262	261.371	0.439	227.819	0.331	14	0.074	-.AAWHELIER.-
R5/RRR5-10/3	920.580	920.134	485.718	0.434	819.583	0.279	18	0.067	-.AVHPIALAK.-
R5/RRR5-11/3	1125.168	1125.262	-83.432	0.462	207.679	0.452	14	0.064	-.AAWHELIER.-
R5/RRR5-10/3	920.322	920.134	204.781	0.462	638.642	0.359	17	0.062	-.AVHPIALAK.-
R5/RRR5-11/3	920.206	920.134	78.672	0.441	575.318	0.290	16	0.054	-.AVHPIALAK.-
R5/RRR5-10/2	1834.517	1835.050	-837.901	0.424	946.938	0.524	18	0.151	R.ISFAGFDGKPEDVLNPK.K
R5/RRR5-10/3	1305.441	1305.594	-117.961	0.503	1147.898	0.502	21	0.131	R.HVVLITNVKPGK.L
R5/RRR5-10/3	1305.788	1305.594	148.455	0.484	1172.545	0.419	21	0.113	R.HVVLITNVKPGK.L
R5/RRR5-10/2	1238.353	1238.374	-16.671	0.215	933.702	0.146	15	0.112	K.FFSPEELVNR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/3	1834.822	1835.050	-124.665	0.378	666.166	0.498	26	0.089	R.ISFAGFDGKPEDVLNPK.K
R5/RRR5-8/2	1259.179	1258.488	-246.453	0.377	1287.577	0.330	16	0.150	R.EIIYDIGPLPK.N
R5/RRR5-8/2	1023.174	1023.125	48.630	0.497	956.383	0.386	15	0.143	K.SGNFELVTR.E
R5/RRR5-8/2	1022.951	1023.125	-170.391	0.492	965.821	0.336	14	0.135	K.SGNFELVTR.E
R5/RRR5-8/2	1022.967	1023.125	-154.470	0.485	908.023	0.352	14	0.135	K.SGNFELVTR.E
R5/RRR5-8/2	1258.352	1258.488	-108.256	0.294	1068.800	0.305	13	0.132	R.EIIYDIGPLPK.N
R5/RRR5-8/2	1257.456	1258.488	-1620.367	0.355	925.672	0.277	14	0.125	R.EIIYDIGPLPK.N
R5/RRR5-8/3	1322.510	1322.491	14.839	0.450	937.097	0.371	24	0.087	K.IKLEDAGFDWK.I
R5/RRR5-11/2	1995.651	1995.288	182.422	0.403	1030.832	0.539	21	0.159	K.GYINAGFAGIMLEDQVAPK.A
R5/RRR5-11/2	1254.085	1254.458	-298.124	0.396	608.158	0.484	17	0.137	K.INEGIPAGILEK.I
R5/RRR5-11/2	1990.713	1992.243	-1778.545	0.411	741.983	0.449	24	0.136	R.LGLPDAGLISYGEMVDQGR.L
R5/RRR5-11/2	1990.721	1992.243	-1774.109	0.414	801.970	0.389	23	0.131	R.LGLPDAGLISYGEMVDQGR.L
R5/RRR5-11/2	1254.965	1254.458	-394.111	0.460	448.195	0.461	15	0.130	-.INEGIPAGILEK.-
R5/RRR5-11/2	1254.255	1254.458	-161.811	0.383	540.305	0.435	15	0.128	-.INEGIPAGILEK.-
R5/RRR5-11/2	1990.715	1992.243	-1777.436	0.367	377.767	0.372	19	0.121	R.LGLPDAGLISYGEMVDQGR.L
R5/RRR5-4/2	1412.140	1412.614	-336.460	0.417	1865.270	0.450	20	0.233	K.LVQIENPLAEGTK.Y
R5/RRR5-4/2	1934.762	1935.166	-209.440	0.527	1163.173	0.531	22	0.172	K.GVPSLFSDLSPLYEQPGK.A
R5/RRR5-4/2	1934.370	1935.166	-931.049	0.496	1080.085	0.536	20	0.165	K.GVPSLFSDLSPLYEQPGK.A
R5/RRR5-4/2	1412.007	1412.614	-1141.343	0.413	1294.115	0.374	18	0.157	K.LVQIENPLAEGTK.Y
R5/RRR5-4/2	1003.073	1003.263	-190.063	0.413	756.683	0.377	15	0.134	K.ILLAFQAVK.Q
R5/RRR5-4/2	1002.526	1003.263	-1737.651	0.314	692.440	0.307	14	0.124	K.ILLAFQAVK.Q
R5/RRR5-4/2	1002.477	1003.263	-1786.956	0.272	783.270	0.298	14	0.123	K.ILLAFQAVK.Q
R5/RRR5-6/2	1769.347	1769.034	177.383	0.445	453.515	0.489	16	0.130	K.QLLQWPIEEIETLR.R
R5/RRR5-12/3	1309.498	1309.455	32.844	0.317	1000.343	0.229	21	0.068	R.RLDYGHVYASK.S
R5/RRR5-24/3	1477.032	1476.488	-309.999	0.421	1222.992	0.148	27	0.067	-.GEDGLDTSANGAGGVR.-
R5/RRR5-22/3	1309.738	1309.455	216.390	0.338	768.798	0.181	20	0.065	R.RLDYGHVYASK.S
R5/RRR5-24/3	1476.142	1476.488	-235.371	0.369	805.933	0.102	24	0.055	-.GEDGLDTSANGAGGVR.-
R5/RRR5-9/2	1168.289	1168.368	-68.079	0.397	1446.386	0.355	16	0.168	K.AEEIVLQPIR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1168.030	1168.368	-290.319	0.394	1589.445	0.273	16	0.166	K.AEEIVLQPIR.E
R5/RRR5-9/2	1168.050	1168.368	-272.914	0.439	1625.585	0.258	16	0.165	K.AEEIVLQPIR.E
R5/RRR5-9/2	1185.930	1186.340	-346.643	0.341	1177.921	0.372	16	0.147	R.EISGAVQLPGSK.S
R5/RRR5-9/2	1186.055	1186.340	-241.312	0.373	1218.666	0.303	16	0.141	R.EISGAVQLPGSK.S
R5/RRR5-9/2	1002.818	1003.132	-313.303	0.375	659.801	0.403	15	0.130	K.ALGLSVEADK.V
R5/RRR5-1/2	1322.105	1322.449	-260.931	0.450	1881.188	0.412	17	0.226	K.GVADFLQEVTSR.K
R5/RRR5-2/2	1451.491	1450.622	-90.730	0.562	1495.965	0.553	19	0.212	R.KGVADFLQEVTSR.K
R5/RRR5-2/2	1322.268	1322.449	-137.191	0.419	1457.752	0.323	16	0.161	K.GVADFLQEVTSR.K
R5/RRR5-1/2	1321.678	1322.449	-1344.222	0.387	1004.169	0.398	16	0.142	K.GVADFLQEVTSR.K
R5/RRR5-1/2	1922.518	1922.169	182.102	0.461	801.297	0.472	16	0.134	-.AISVGGQETNIITDYVLK.-
R5/RRR5-1/2	1322.147	1322.449	-229.437	0.312	565.675	0.437	13	0.126	K.GVADFLQEVTSR.K
R5/RRR5-9/2	1589.488	1589.821	-210.028	0.604	2903.427	0.598	24	0.476	K.THINIVVIGHVDSGK.S
R5/RRR5-9/2	1589.404	1589.821	-263.038	0.585	2816.330	0.643	24	0.474	K.THINIVVIGHVDSGK.S
R5/RRR5-9/2	1589.405	1589.821	-262.421	0.614	2735.544	0.663	24	0.463	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1588.940	1589.821	-1187.365	0.560	2678.849	0.560	34	0.461	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.682	1589.821	-87.280	0.538	2218.598	0.549	33	0.325	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1590.125	1589.821	191.670	0.547	2197.682	0.552	32	0.322	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.679	1589.821	-89.360	0.568	2246.353	0.523	34	0.318	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.462	1589.821	-226.409	0.542	1958.438	0.571	30	0.277	K.THINIVVIGHVDSGK.S
R5/RRR5-2/3	1589.834	1589.821	8.608	0.505	2080.794	0.499	30	0.273	K.THINIVVIGHVDSGK.S
R5/RRR5-10/3	1589.389	1589.821	-272.755	0.458	2032.827	0.511	32	0.267	K.THINIVVIGHVDSGK.S
R5/RRR5-9/2	1590.594	1589.821	-143.067	0.493	1532.316	0.648	21	0.237	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.678	1589.821	-90.400	0.544	1731.819	0.581	31	0.234	K.THINIVVIGHVDSGK.S
R5/RRR5-10/3	1589.130	1589.821	-1067.378	0.502	1734.820	0.576	30	0.234	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.745	1589.821	-48.114	0.534	1814.024	0.537	30	0.233	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.394	1589.821	-269.287	0.552	1762.874	0.552	31	0.228	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.385	1589.821	-275.182	0.516	1874.285	0.495	31	0.227	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.169	1589.821	-1042.504	0.512	1714.859	0.563	29	0.226	K.THINIVVIGHVDSGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/3	1589.709	1589.821	-70.412	0.534	1714.682	0.548	30	0.219	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1589.878	1589.821	36.332	0.546	1571.164	0.586	30	0.208	K.THINIVVIGHVDSGK.S
R5/RRR5-10/3	1589.175	1589.821	-1038.918	0.491	1435.804	0.576	28	0.185	K.THINIVVIGHVDSGK.S
R5/RRR5-9/3	1590.009	1589.821	118.684	0.534	1515.651	0.524	30	0.178	K.THINIVVIGHVDSGK.S
R5/RRR5-1/2	1121.049	1121.268	-196.546	0.429	854.409	0.525	13	0.152	K.STTTGHLIYK.L
R5/RRR5-8/2	1121.083	1121.268	-165.305	0.489	819.840	0.511	14	0.151	K.STTTGHLIYK.L
R5/RRR5-2/2	1120.532	1121.268	-1554.382	0.423	883.673	0.463	14	0.147	K.STTTGHLIYK.L
R5/RRR5-2/2	1120.427	1121.268	-1648.177	0.355	909.738	0.452	15	0.146	K.STTTGHLIYK.L
R5/RRR5-8/2	1120.941	1121.268	-292.575	0.399	773.892	0.460	14	0.142	K.STTTGHLIYK.L
R5/RRR5-1/2	1121.014	1121.268	-227.680	0.396	746.434	0.477	13	0.141	K.STTTGHLIYK.L
R5/RRR5-6/2	1121.019	1121.268	-222.764	0.404	803.396	0.434	14	0.140	K.STTTGHLIYK.L
R5/RRR5-5/2	1120.373	1121.268	-1696.559	0.338	778.842	0.458	14	0.140	K.STTTGHLIYK.L
R5/RRR5-9/2	1589.441	1589.821	-239.845	0.417	663.848	0.508	16	0.138	K.THINIVVIGHVDSGK.S
R5/RRR5-3/2	1121.023	1121.268	-219.050	0.368	849.469	0.408	14	0.138	K.STTTGHLIYK.L
R5/RRR5-8/2	1121.084	1121.268	-164.978	0.400	777.135	0.430	13	0.138	K.STTTGHLIYK.L
R5/RRR5-1/2	1120.618	1121.268	-1476.579	0.347	823.564	0.419	14	0.138	K.STTTGHLIYK.L
R5/RRR5-2/2	1121.047	1121.268	-198.294	0.392	773.427	0.418	13	0.136	K.STTTGHLIYK.L
R5/RRR5-3/2	1121.063	1121.268	-183.438	0.387	780.201	0.402	14	0.136	K.STTTGHLIYK.L
R5/RRR5-3/2	1120.546	1121.268	-1541.250	0.364	722.962	0.392	13	0.132	K.STTTGHLIYK.L
R5/RRR5-9/2	1589.214	1589.821	-1014.231	0.373	653.359	0.449	15	0.131	K.THINIVVIGHVDSGK.S
R5/RRR5-10/2	1120.996	1121.268	-243.958	0.277	394.719	0.386	11	0.125	K.STTTGHLIYK.L
R5/RRR5-9/2	1590.937	1589.821	73.064	0.311	466.431	0.390	16	0.124	K.THINIVVIGHVDSGK.S
R5/RRR5-4/2	1120.418	1121.268	-1656.168	0.257	320.538	0.410	10	0.122	-.STTTGHLIYK.-
R5/RRR5-3/3	1589.680	1589.821	-88.898	0.424	1174.608	0.413	25	0.111	K.THINIVVIGHVDSGK.S
R5/RRR5-8/3	1588.385	1589.821	-1538.003	0.383	947.677	0.482	27	0.110	K.THINIVVIGHVDSGK.S
R5/RRR5-8/3	1589.432	1589.821	-245.594	0.431	607.371	0.475	24	0.099	K.THINIVVIGHVDSGK.S
R5/RRR5-8/3	1588.386	1589.821	-1537.193	0.335	560.115	0.495	24	0.098	K.THINIVVIGHVDSGK.S
R5/RRR5-4/3	1589.538	1589.821	-178.449	0.339	920.089	0.373	25	0.090	K.THINIVVIGHVDSGK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1263.481	1263.468	10.697	0.452	1680.906	0.443	18	0.209	K.SYGVNVVVAINK.F
R5/RRR5-6/2	1346.203	1345.483	-208.148	0.535	1218.253	0.456	18	0.168	R.LDIDPESITWR.R
R5/RRR5-6/2	1345.233	1345.483	-185.726	0.450	1102.776	0.446	16	0.157	R.LDIDPESITWR.R
R5/RRR5-6/2	1262.777	1263.468	-1343.318	0.355	1113.209	0.367	16	0.143	K.SYGVNVVVAINK.F
R5/RRR5-6/2	1485.902	1486.587	-1136.880	0.399	907.830	0.422	18	0.141	K.FASDTEAEM*DVVR.N
R5/RRR5-6/2	1485.717	1486.587	-1261.871	0.325	901.286	0.436	19	0.140	K.FASDTEAEM*DVVR.N
R5/RRR5-6/2	1345.083	1345.483	-297.981	0.425	693.518	0.407	15	0.133	R.LDIDPESITWR.R
R5/RRR5-6/2	1485.783	1486.587	-1217.316	0.266	421.213	0.368	16	0.121	K.FASDTEAEM*DVVR.N
R5/RRR5-9/2	1560.106	1558.759	223.462	0.495	1819.807	0.492	21	0.236	K.TFGSSADIFAGIFPK.N
R5/RRR5-6/2	1558.495	1558.759	-169.739	0.393	1422.432	0.442	19	0.179	K.TFGSSADIFAGIFPK.N
R5/RRR5-5/2	1559.129	1558.759	238.208	0.388	1320.020	0.481	18	0.176	K.TFGSSADIFAGIFPK.N
R5/RRR5-10/2	1560.001	1558.759	155.823	0.443	1376.494	0.445	19	0.175	K.TFGSSADIFAGIFPK.N
R5/RRR5-6/2	1558.057	1558.759	-1095.335	0.341	1421.145	0.402	19	0.171	K.TFGSSADIFAGIFPK.N
R5/RRR5-6/2	1192.165	1191.363	-167.157	0.423	1003.673	0.579	14	0.167	K.HAENVPWPLK.T
R5/RRR5-5/2	1560.077	1558.759	204.317	0.491	1096.923	0.498	18	0.162	K.TFGSSADIFAGIFPK.N
R5/RRR5-9/2	1559.730	1558.759	-18.731	0.474	1115.655	0.477	18	0.159	K.TFGSSADIFAGIFPK.N
R5/RRR5-6/2	1557.798	1558.759	-1262.298	0.296	1062.011	0.399	18	0.143	K.TFGSSADIFAGIFPK.N
R5/RRR5-3/2	1559.392	1558.759	-235.909	0.398	856.322	0.434	16	0.137	K.TFGSSADIFAGIFPK.N
R5/RRR5-2/2	1558.832	1558.759	47.314	0.396	944.300	0.354	18	0.133	K.TFGSSADIFAGIFPK.N
R5/RRR5-6/3	1364.580	1364.574	4.197	0.486	1138.983	0.342	24	0.095	R.FIKEEFGQIPR.I
R5/RRR5-6/3	1364.611	1364.574	26.942	0.476	1094.637	0.354	22	0.095	R.FIKEEFGQIPR.I
R5/RRR5-10/3	1364.680	1364.574	78.214	0.447	1016.460	0.372	23	0.093	R.FIKEEFGQIPR.I
R5/RRR5-5/3	1364.530	1364.574	-31.873	0.353	1154.833	0.345	24	0.093	R.FIKEEFGQIPR.I
R5/RRR5-6/3	1364.257	1364.574	-232.596	0.440	808.616	0.367	20	0.086	R.FIKEEFGQIPR.I
R5/RRR5-4/2	1177.277	1177.332	-46.655	0.407	1669.124	0.440	16	0.207	K.SFEVTELPVR.S
R5/RRR5-4/2	1558.145	1557.799	222.957	0.502	1221.080	0.376	20	0.153	R.QMYLLGYLANQSR.V
R5/RRR5-4/2	1177.197	1177.332	-114.783	0.328	1113.507	0.317	15	0.137	K.SFEVTELPVR.S
R5/RRR5-4/3	1652.611	1652.899	-174.558	0.406	1480.594	0.370	25	0.134	R.KQWVVAGADDM*FIR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1830.609	1829.045	-238.880	0.503	1135.793	0.555	21	0.173	R.AATGTPLVQLLSLSDGER.I
R5/RRR5-4/2	1416.570	1416.607	-25.982	0.267	1132.836	0.385	16	0.142	R.GADPAIVLNNLYR.H
R5/RRR5-1/2	1828.460	1829.045	-869.202	0.288	421.424	0.339	16	0.116	R.AATGTPLVQLLSLSDGER.I
R5/RRR5-18/2	1146.989	1147.307	-278.352	0.320	991.396	0.124	13	0.114	R.CSVIERRAR.F
R5/RRR5-17/2	1146.926	1147.307	-333.451	0.296	938.867	0.107	13	0.112	R.CSVIERRAR.F
R5/RRR5-7/2	1055.078	1055.250	-163.578	0.410	1168.115	0.387	14	0.150	K.APSSEILPIK.F
R5/RRR5-7/3	1836.721	1837.026	-166.232	0.446	1030.551	0.547	27	0.128	R.SFLQSHGLQDTQIYAK.V
R5/RRR5-7/3	1922.252	1922.069	95.561	0.362	471.384	0.571	27	0.094	K.HVGDPM*PHEESVASSAVR.T
R5/RRR5-7/3	1837.652	1837.026	-203.659	0.476	650.853	0.483	25	0.094	R.SFLQSHGLQDTQIYAK.V
R5/RRR5-7/3	1922.199	1922.069	67.569	0.398	317.008	0.559	22	0.092	K.HVGDPM*PHEESVASSAVR.T
R5/RRR5-4/2	1844.869	1844.098	-124.278	0.528	1518.690	0.502	20	0.199	K.NSPAIIFIDEIDSIAPK.R
R5/RRR5-4/2	1577.772	1577.760	7.558	0.445	1103.177	0.574	19	0.173	K.TPVSGDVDLQFIASK.T
R5/RRR5-2/2	1845.067	1844.098	-16.763	0.359	721.642	0.278	16	0.115	K.NSPAIIFIDEIDSIAPK.R
R5/RRR5-1/3	1726.668	1726.870	-117.016	0.471	603.525	0.552	27	0.099	K.HANLTGEVVEGQKDTK.S
R5/RRR5-6/2	1824.707	1826.092	-1310.892	0.334	1292.256	0.348	20	0.150	K.NILITGAAGFIASHVANR.L
R5/RRR5-14/2	1233.292	1233.377	-69.565	0.375	1003.616	0.420	17	0.146	R.M*PISSDLSNPR.N
R5/RRR5-14/2	1233.071	1233.377	-249.101	0.375	751.009	0.349	15	0.127	R.M*PISSDLSNPR.N
R5/RRR5-6/2	1824.711	1826.092	-1309.011	0.311	559.552	0.398	16	0.119	K.NILITGAAGFIASHVANR.L
R5/RRR5-14/3	1489.034	1488.695	228.110	0.402	1086.282	0.208	24	0.070	-.VRM*PISSDLSNPR.-
R5/RRR5-5/2	1630.228	1630.780	-955.067	0.449	809.077	0.514	19	0.144	R.IGTNFSISGFGSSLDK.S
R5/RRR5-5/2	1416.505	1416.562	-40.850	0.363	1046.156	0.315	18	0.133	R.GVGAQGIELSETVR.R
R5/RRR5-5/2	1343.267	1343.468	-150.542	0.299	939.724	0.322	18	0.127	R.VNLATGDAVPETR.S
R5/RRR5-5/2	1417.140	1416.562	-298.986	0.349	704.651	0.259	16	0.116	R.GVGAQGIELSETVR.R
R5/RRR5-4/2	1393.045	1392.625	301.765	0.427	1810.012	0.392	17	0.212	R.SVEQLGYITLLR.Q
R5/RRR5-4/2	1525.394	1525.642	-163.550	0.457	1470.961	0.481	21	0.193	R.SSPESSVLTDVFTR.L
R5/RRR5-4/2	1525.190	1525.642	-297.794	0.409	1346.047	0.423	20	0.170	R.SSPESSVLTDVFTR.L
R5/RRR5-4/2	1392.517	1392.625	-78.482	0.427	1495.039	0.296	17	0.160	R.SVEQLGYITLLR.Q
R5/RRR5-4/2	1392.402	1392.625	-160.705	0.422	1458.268	0.242	17	0.148	R.SVEQLGYITLLR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1503.440	1503.637	-131.490	0.356	812.906	0.401	15	0.129	K.ESLDNLQTLVENK.F
R5/RRR5-2/2	1859.965	1861.044	-1121.343	0.260	704.698	0.369	16	0.119	R.LDIDFAEVYANSALYR.S
R5/RRR5-8/2	1999.545	1999.124	211.336	0.599	2956.011	0.601	27	0.493	K.AFDNEATEEALGFAISNAK.A
R5/RRR5-8/2	1998.749	1999.124	-188.279	0.531	2119.331	0.540	24	0.295	K.AFDNEATEEALGFAISNAK.A
R5/RRR5-8/2	1073.888	1074.250	-337.774	0.460	998.059	0.337	16	0.138	K.IVCTLGPASR.S
R5/RRR5-8/2	1074.063	1074.250	-174.138	0.361	836.201	0.344	15	0.131	K.IVCTLGPASR.S
R5/RRR5-8/2	1074.056	1074.250	-180.865	0.385	839.226	0.335	15	0.131	K.IVCTLGPASR.S
R5/RRR5-8/2	1074.776	1074.250	-442.300	0.291	455.778	0.248	13	0.092	-.IVCTLGPASR.-
R5/RRR5-8/2	1101.667	1101.315	320.008	0.385	1160.677	0.481	15	0.165	K.NISVIAVCPK.G
R5/RRR5-8/2	1101.991	1101.315	-294.607	0.335	1045.931	0.334	14	0.136	K.NISVIAVCPK.G
R5/RRR5-8/2	1101.157	1101.315	-143.613	0.336	905.465	0.360	14	0.133	K.NISVIAVCPK.G
R5/RRR5-6/2	1048.985	1048.217	-222.304	0.402	1407.953	0.466	16	0.184	R.VNDFVAAALK.Q
R5/RRR5-6/2	1049.019	1048.217	-189.500	0.366	1604.040	0.333	16	0.178	R.VNDFVAAALK.Q
R5/RRR5-6/2	1181.949	1182.395	-378.576	0.460	527.775	0.532	15	0.141	R.VPVNDANLIVK.T
R5/RRR5-6/2	1182.332	1182.395	-53.394	0.398	550.199	0.475	15	0.134	R.VPVNDANLIVK.T
R5/RRR5-6/2	1044.098	1044.227	-123.786	0.287	874.195	0.302	13	0.124	R.LAIGVSQVEK.G
R5/RRR5-6/2	1044.189	1044.227	-36.421	0.320	590.128	0.323	14	0.122	R.LAIGVSQVEK.G
R5/RRR5-16/2	1867.697	1868.124	-229.482	0.555	2726.704	0.655	30	0.459	R.LQAQSALAEAAAASGVALPK.G
R5/RRR5-16/3	1867.779	1868.124	-185.494	0.441	2646.481	0.498	38	0.445	R.LQAQSALAEAAAASGVALPK.G
R5/RRR5-16/2	1868.695	1868.124	-230.539	0.590	2609.727	0.636	29	0.425	R.LQAQSALAEAAAASGVALPK.G
R5/RRR5-16/2	1868.405	1868.124	150.876	0.537	2469.724	0.627	29	0.391	R.LQAQSALAEAAAASGVALPK.G
R5/RRR5-16/3	1868.020	1868.124	-55.989	0.334	1994.168	0.344	34	0.207	R.LQAQSALAEAAAASGVALPK.G
R5/RRR5-16/2	1480.077	1480.565	-330.364	0.480	721.692	0.512	19	0.146	K.QYLAGGQDTSNLGR.G
R5/RRR5-15/2	1480.227	1480.565	-228.674	0.468	788.680	0.474	21	0.145	K.QYLAGGQDTSNLGR.G
R5/RRR5-16/2	1480.065	1480.565	-338.639	0.433	851.412	0.436	21	0.142	K.QYLAGGQDTSNLGR.G
R5/RRR5-16/2	1480.141	1480.565	-287.253	0.477	694.218	0.487	19	0.142	K.QYLAGGQDTSNLGR.G
R5/RRR5-15/2	1480.140	1480.565	-287.915	0.454	672.597	0.449	19	0.137	K.QYLAGGQDTSNLGR.G
R5/RRR5-15/3	1867.798	1868.124	-175.167	0.301	818.033	0.220	27	0.063	R.LQAQSALAEAAAASGVALPK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1314.183	1314.513	-252.163	0.325	739.114	0.356	15	0.123	R.KGADILVEALER.C
R5/RRR5-7/3	1705.077	1705.035	24.973	0.457	1248.292	0.356	25	0.105	R.LPKPPATELLEQVLR.L
R5/RRR5-7/3	1184.710	1184.372	285.577	0.405	600.182	0.507	19	0.093	R.SPVITNHLFR.H
R5/RRR5-7/3	1184.619	1184.372	209.168	0.256	497.037	0.316	17	0.071	R.SPVITNHLFR.H
R5/RRR5-6/2	1598.289	1596.812	299.708	0.465	753.075	0.478	18	0.138	R.VLGSVGEPINPTAWR.W
R5/RRR5-3/2	1553.955	1553.678	179.194	0.483	1033.392	0.464	18	0.152	R.TNVDM*VTGQLSDTR.S
R5/RRR5-2/2	984.270	985.206	-1972.953	0.404	1156.445	0.348	16	0.146	R.LLAGVGSVLR.L
R5/RRR5-1/2	1264.659	1263.469	150.390	0.396	924.673	0.458	16	0.145	R.NLSAGFIHIYK.F
R5/RRR5-2/2	985.242	985.206	36.708	0.449	972.975	0.292	15	0.130	R.LLAGVGSVLR.L
R5/RRR5-3/2	984.363	985.206	-1877.863	0.328	930.443	0.278	15	0.127	R.LLAGVGSVLR.L
R5/RRR5-1/2	985.283	985.206	78.336	0.392	761.270	0.282	15	0.125	R.LLAGVGSVLR.L
R5/RRR5-3/2	1512.508	1512.776	-177.571	0.546	1734.544	0.595	22	0.253	R.LPLITISDSGNLLR.D
R5/RRR5-1/2	1512.489	1512.776	-190.526	0.469	1771.681	0.562	22	0.248	R.LPLITISDSGNLLR.D
R5/RRR5-3/2	1513.266	1512.776	324.557	0.557	1623.046	0.561	21	0.229	R.LPLITISDSGNLLR.D
R5/RRR5-2/2	1513.656	1512.776	-79.886	0.533	1457.500	0.569	21	0.211	R.LPLITISDSGNLLR.D
R5/RRR5-2/2	1512.195	1512.776	-1048.965	0.474	1497.490	0.510	20	0.202	R.LPLITISDSGNLLR.D
R5/RRR5-3/2	1511.444	1512.776	-1547.513	0.346	1459.151	0.447	20	0.183	R.LPLITISDSGNLLR.D
R5/RRR5-1/2	1512.959	1512.776	121.419	0.420	1056.398	0.415	18	0.147	R.LPLITISDSGNLLR.D
R5/RRR5-3/2	1365.163	1365.603	-323.733	0.310	1057.509	0.395	17	0.141	R.LLLVNPTDINPR.Q
R5/RRR5-3/2	1057.752	1058.214	-437.843	0.364	854.381	0.363	14	0.132	R.SVLLGALNDR.L
R5/RRR5-1/2	1057.877	1058.214	-319.392	0.244	716.013	0.216	13	0.115	-.SVLLGALNDR.-
R5/RRR5-4/2	1193.091	1193.334	-204.689	0.390	1368.342	0.262	17	0.145	R.AVAYLLSNADR.V
R5/RRR5-5/2	1329.315	1329.569	-192.003	0.456	1124.156	0.432	17	0.155	R.ALVEGPFLDVLR.S
R5/RRR5-5/2	1329.137	1329.569	-326.151	0.352	989.331	0.413	16	0.142	R.ALVEGPFLDVLR.S
R5/RRR5-5/2	1501.523	1501.664	-94.393	0.430	837.547	0.428	17	0.136	K.LPADTPYSQFAYK.F
R5/RRR5-5/2	1329.335	1329.569	-176.895	0.360	662.414	0.427	14	0.127	-.ALVEGPFLDVLR.-
R5/RRR5-5/3	1447.157	1447.573	-288.140	0.523	1518.359	0.239	25	0.105	-.SKDREEIAEIEK.-
R5/RRR5-5/3	1447.655	1447.573	56.520	0.517	1203.441	0.344	24	0.101	K.SKDREEIAEIEK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1447.617	1447.573	30.387	0.530	1220.719	0.294	25	0.092	K.SKDREEIAEIEK.M
R5/RRR5-27/2	1116.081	1116.290	-187.438	0.553	2655.572	0.605	21	0.417	R.VVGAGGAVVACR.G
R5/RRR5-13/2	1117.154	1116.290	-121.719	0.533	2420.000	0.638	21	0.379	R.VVGAGGAVVACR.G
R5/RRR5-18/2	1115.377	1116.290	-1719.746	0.483	2358.025	0.623	21	0.361	R.VVGAGGAVVACR.G
R5/RRR5-19/2	1116.039	1116.290	-225.623	0.558	2290.947	0.637	21	0.354	R.VVGAGGAVVACR.G
R5/RRR5-20/2	1116.070	1116.290	-197.972	0.571	2269.532	0.643	21	0.351	R.VVGAGGAVVACR.G
R5/RRR5-19/2	1115.511	1116.290	-1599.684	0.493	2312.402	0.618	21	0.350	R.VVGAGGAVVACR.G
R5/RRR5-19/2	1115.502	1116.290	-1607.819	0.487	2332.734	0.594	21	0.346	R.VVGAGGAVVACR.G
R5/RRR5-20/2	1116.011	1116.290	-250.204	0.553	2280.477	0.608	21	0.342	R.VVGAGGAVVACR.G
R5/RRR5-21/2	1115.897	1116.290	-353.147	0.535	2175.031	0.658	21	0.339	R.VVGAGGAVVACR.G
R5/RRR5-21/2	1115.905	1116.290	-345.683	0.534	2238.993	0.613	21	0.336	R.VVGAGGAVVACR.G
R5/RRR5-26/2	1116.004	1116.290	-256.568	0.549	2135.042	0.671	20	0.336	R.VVGAGGAVVACR.G
R5/RRR5-20/2	1115.987	1116.290	-271.822	0.553	2212.052	0.613	21	0.331	R.VVGAGGAVVACR.G
R5/RRR5-14/2	1116.024	1116.290	-238.572	0.484	2153.888	0.637	21	0.327	R.VVGAGGAVVACR.G
R5/RRR5-22/2	1115.854	1116.290	-392.003	0.484	2201.592	0.608	21	0.327	R.VVGAGGAVVACR.G
R5/RRR5-27/2	1115.931	1116.290	-322.854	0.553	2192.967	0.604	21	0.325	R.VVGAGGAVVACR.G
R5/RRR5-18/2	1116.056	1116.290	-209.822	0.534	2166.808	0.617	21	0.324	R.VVGAGGAVVACR.G
R5/RRR5-28/2	1115.430	1116.290	-1671.915	0.436	2196.947	0.569	20	0.313	R.VVGAGGAVVACR.G
R5/RRR5-27/2	1115.468	1116.290	-1638.382	0.467	2096.370	0.589	21	0.302	R.VVGAGGAVVACR.G
R5/RRR5-17/2	1115.845	1116.290	-399.467	0.473	2020.840	0.617	20	0.298	R.VVGAGGAVVACR.G
R5/RRR5-20/2	1115.940	1116.290	-314.733	0.447	2034.805	0.592	20	0.292	R.VVGAGGAVVACR.G
R5/RRR5-18/2	1115.899	1116.290	-351.391	0.530	1954.533	0.616	20	0.288	R.VVGAGGAVVACR.G
R5/RRR5-26/2	1115.961	1116.290	-295.417	0.531	1936.510	0.624	20	0.288	R.VVGAGGAVVACR.G
R5/RRR5-28/2	1115.435	1116.290	-1667.737	0.460	1925.936	0.616	20	0.282	R.VVGAGGAVVACR.G
R5/RRR5-14/2	1117.036	1116.290	-227.614	0.531	1895.093	0.623	19	0.281	R.VVGAGGAVVACR.G
R5/RRR5-1/2	1116.190	1116.290	-90.014	0.464	1868.689	0.627	21	0.277	R.VVGAGGAVVACR.G
R5/RRR5-28/2	1115.302	1116.290	-1787.265	0.430	1897.954	0.574	19	0.266	R.VVGAGGAVVACR.G
R5/RRR5-21/2	1116.053	1116.290	-213.224	0.512	1780.151	0.631	19	0.266	R.VVGAGGAVVACR.G

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Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1673.296	1673.852	-932.534	0.495	1876.982	0.557	22	0.259	R.GLVSYDFPASFWAGR.V
R5/RRR5-20/2	1116.116	1116.290	-155.839	0.354	1903.917	0.514	20	0.249	R.VVGAGGAVVACR.G
R5/RRR5-20/2	1674.155	1673.852	181.619	0.542	1617.876	0.596	22	0.234	R.GLVSYDFPASFWAGR.V
R5/RRR5-20/2	1673.134	1673.852	-1029.658	0.527	1636.879	0.577	21	0.231	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1674.583	1673.852	-160.751	0.569	1520.230	0.593	22	0.221	R.GLVSYDFPASFWAGR.V
R5/RRR5-13/2	1116.106	1116.290	-165.275	0.380	1774.293	0.457	20	0.220	R.VVGAGGAVVACR.G
R5/RRR5-20/2	1674.382	1673.852	-281.350	0.573	1481.596	0.589	21	0.215	R.GLVSYDFPASFWAGR.V
R5/RRR5-20/2	1674.215	1673.852	217.885	0.571	1476.846	0.591	21	0.215	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1674.127	1673.852	165.020	0.603	1445.240	0.592	21	0.212	R.GLVSYDFPASFWAGR.V
R5/RRR5-14/2	1116.891	1116.290	-357.765	0.473	1397.578	0.602	18	0.210	R.VVGAGGAVVACR.G
R5/RRR5-20/2	1673.924	1673.852	43.622	0.566	1369.711	0.603	21	0.207	R.GLVSYDFPASFWAGR.V
R5/RRR5-20/2	1673.405	1673.852	-267.540	0.532	1420.725	0.566	21	0.204	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1675.282	1673.852	257.431	0.581	1313.480	0.602	20	0.200	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1672.817	1673.852	-1220.006	0.453	1415.261	0.546	21	0.198	R.GLVSYDFPASFWAGR.V
R5/RRR5-20/2	1673.282	1673.852	-940.737	0.489	1333.981	0.557	20	0.193	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1674.338	1673.852	291.506	0.580	1247.679	0.593	20	0.192	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1673.297	1673.852	-931.875	0.527	1224.609	0.576	20	0.187	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1674.163	1673.852	186.298	0.537	1274.691	0.524	20	0.181	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1674.202	1673.852	210.135	0.507	1081.429	0.556	19	0.171	R.GLVSYDFPASFWAGR.V
R5/RRR5-17/2	1115.934	1116.290	-319.781	0.395	1046.364	0.534	20	0.166	R.VVGAGGAVVACR.G
R5/RRR5-18/2	1674.336	1673.852	290.483	0.508	1149.128	0.486	19	0.163	R.GLVSYDFPASFWAGR.V
R5/RRR5-20/2	1673.168	1673.852	-1009.441	0.488	1037.396	0.535	18	0.163	R.GLVSYDFPASFWAGR.V
R5/RRR5-22/2	1674.945	1673.852	55.949	0.486	993.316	0.499	18	0.155	R.GLVSYDFPASFWAGR.V
R5/RRR5-18/2	1674.346	1673.852	295.892	0.483	952.334	0.470	18	0.148	R.GLVSYDFPASFWAGR.V
R5/RRR5-18/2	1674.834	1673.852	-10.645	0.498	750.503	0.530	18	0.148	R.GLVSYDFPASFWAGR.V
R5/RRR5-21/2	1674.888	1673.852	21.959	0.542	744.574	0.541	17	0.147	R.GLVSYDFPASFWAGR.V
R5/RRR5-2/2	1674.560	1673.852	-174.791	0.457	797.780	0.516	17	0.146	R.GLVSYDFPASFWAGR.V
R5/RRR5-2/2	1675.103	1673.852	150.525	0.417	903.672	0.429	18	0.141	R.GLVSYDFPASFWAGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1116.102	1116.290	-169.005	0.363	804.615	0.436	18	0.140	R.VVGAGGAVVACR.G
R5/RRR5-21/2	1674.556	1673.852	-176.985	0.503	615.563	0.530	15	0.140	R.GLVSYDFPASFWAGR.V
R5/RRR5-2/2	1673.697	1673.852	-92.803	0.407	833.692	0.436	17	0.138	R.GLVSYDFPASFWAGR.V
R5/RRR5-1/2	1674.551	1673.852	-179.764	0.475	703.594	0.475	16	0.137	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/3	1673.550	1673.852	-180.684	0.458	1352.059	0.439	28	0.137	R.GLVSYDFPASFWAGR.V
R5/RRR5-20/2	1116.389	1116.290	89.206	0.318	534.970	0.460	17	0.133	R.VVGAGGAVVACR.G
R5/RRR5-17/2	1673.954	1673.852	61.322	0.409	572.824	0.472	15	0.133	R.GLVSYDFPASFWAGR.V
R5/RRR5-16/2	1115.904	1116.290	-346.781	0.313	740.075	0.387	19	0.133	R.VVGAGGAVVACR.G
R5/RRR5-6/2	1115.790	1116.290	-448.866	0.310	487.963	0.471	14	0.131	R.VVGAGGAVVACR.G
R5/RRR5-17/2	1673.850	1673.852	-1.215	0.374	412.204	0.471	15	0.130	R.GLVSYDFPASFWAGR.V
R5/RRR5-15/2	1675.212	1673.852	215.563	0.344	287.889	0.491	14	0.130	R.GLVSYDFPASFWAGR.V
R5/RRR5-14/2	1673.296	1673.852	-932.241	0.370	689.280	0.398	15	0.128	R.GLVSYDFPASFWAGR.V
R5/RRR5-17/2	1674.276	1673.852	254.075	0.356	528.636	0.396	17	0.128	R.GLVSYDFPASFWAGR.V
R5/RRR5-16/2	1673.515	1673.852	-201.604	0.357	413.688	0.429	15	0.128	R.GLVSYDFPASFWAGR.V
R5/RRR5-16/2	1673.842	1673.852	-5.458	0.321	368.924	0.424	15	0.127	R.GLVSYDFPASFWAGR.V
R5/RRR5-22/2	1674.465	1673.852	-231.688	0.410	486.788	0.428	13	0.126	R.GLVSYDFPASFWAGR.V
R5/RRR5-13/2	1673.569	1673.852	-169.481	0.410	622.984	0.317	17	0.123	R.GLVSYDFPASFWAGR.V
R5/RRR5-15/2	1674.175	1673.852	193.610	0.270	407.981	0.348	15	0.123	R.GLVSYDFPASFWAGR.V
R5/RRR5-1/2	1673.648	1673.852	-121.702	0.317	410.715	0.320	13	0.121	R.GLVSYDFPASFWAGR.V
R5/RRR5-1/2	1673.225	1673.852	-975.088	0.316	604.625	0.282	14	0.119	R.GLVSYDFPASFWAGR.V
R5/RRR5-21/2	1672.825	1673.852	-1215.023	0.265	583.481	0.243	14	0.117	R.GLVSYDFPASFWAGR.V
R5/RRR5-19/2	1116.821	1116.290	-421.264	0.235	219.708	0.389	12	0.114	-.VVGAGGAVVACR.-
R5/RRR5-20/2	1116.431	1116.290	126.709	0.203	206.798	0.385	13	0.109	-.VVGAGGAVVACR.-
R5/RRR5-16/2	1674.328	1673.852	285.585	0.250	136.630	0.415	11	0.103	-.GLVSYDFPASFWAGR.-
R5/RRR5-19/2	1116.831	1116.290	-411.832	0.251	202.500	0.366	10	0.094	-.VVGAGGAVVACR.-
R5/RRR5-19/3	1673.615	1673.852	-141.611	0.306	957.741	0.257	29	0.070	R.GLVSYDFPASFWAGR.V
R5/RRR5-25/3	1717.686	1717.776	-52.941	0.572	2582.517	0.485	31	0.408	K.HGYIGEFEELDDHR.S
R5/RRR5-25/3	1717.895	1717.776	68.939	0.544	2274.767	0.448	30	0.306	K.HGYIGEFEELDDHR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/3	1717.513	1717.776	-153.782	0.542	1615.725	0.471	28	0.182	K.HGYIGEFEELDDHR.S
R5/RRR5-25/2	898.502	899.073	-1753.435	0.425	731.139	0.398	12	0.134	K.IVVQLNGR.L
R5/RRR5-25/2	898.314	899.073	-1963.834	0.383	862.682	0.354	13	0.133	K.IVVQLNGR.L
R5/RRR5-15/2	1706.391	1705.894	292.416	0.609	3401.737	0.552	25	0.591	R.YVFTGASWVTNAFNK.V
R5/RRR5-15/2	1706.738	1705.894	-91.580	0.611	2882.380	0.571	24	0.462	R.YVFTGASWVTNAFNK.V
R5/RRR5-14/2	1706.557	1705.894	-197.701	0.443	793.383	0.409	17	0.132	R.YVFTGASWVTNAFNK.V
R5/RRR5-4/2	1352.712	1351.484	169.293	0.403	739.637	0.397	15	0.129	R.LGDTDLFAEIEK.D
R5/RRR5-4/2	1002.271	1003.178	-1908.199	0.348	795.215	0.332	14	0.125	K.TVTLVSIGGR.K
R5/RRR5-4/2	1283.387	1283.504	-91.452	0.387	791.842	0.334	14	0.124	K.LALHNAGFLAQK.R
R5/RRR5-4/2	1284.177	1283.504	-255.004	0.301	691.903	0.138	15	0.112	-.LALHNAGFLAQK.-
R5/RRR5-22/3	1756.989	1756.896	53.433	0.531	2685.362	0.495	34	0.444	K.KGDNDLPGLTDTEKPR.M
R5/RRR5-15/2	1374.136	1373.537	-292.928	0.570	1206.169	0.359	18	0.149	K.KLEIDDDQKLR.A
R5/RRR5-13/3	1757.183	1756.896	164.006	0.528	1375.076	0.434	30	0.137	K.KGDNDLPGLTDTEKPR.M
R5/RRR5-22/3	1756.343	1756.896	-886.845	0.478	1197.748	0.449	28	0.123	K.KGDNDLPGLTDTEKPR.M
R5/RRR5-15/2	1373.185	1373.537	-257.377	0.483	905.463	0.237	17	0.121	K.KLEIDDDQKLR.A
R5/RRR5-16/3	1372.538	1373.537	-1460.966	0.466	961.621	0.434	23	0.102	K.KLEIDDDQKLR.A
R5/RRR5-14/3	1373.564	1373.537	19.368	0.509	1153.645	0.364	24	0.100	K.KLEIDDDQKLR.A
R5/RRR5-16/3	1372.846	1373.537	-1235.625	0.463	950.417	0.405	22	0.097	K.KLEIDDDQKLR.A
R5/RRR5-12/3	1756.230	1756.896	-951.005	0.423	981.499	0.383	27	0.093	K.KGDNDLPGLTDTEKPR.M
R5/RRR5-16/3	1373.367	1373.537	-124.518	0.472	904.690	0.387	21	0.093	K.KLEIDDDQKLR.A
R5/RRR5-13/3	1373.220	1373.537	-231.524	0.421	1008.168	0.365	21	0.092	K.KLEIDDDQKLR.A
R5/RRR5-15/3	1373.699	1373.537	117.764	0.502	716.120	0.384	20	0.089	K.KLEIDDDQKLR.A
R5/RRR5-14/3	1374.040	1373.537	-363.220	0.448	796.120	0.383	21	0.089	K.KLEIDDDQKLR.A
R5/RRR5-15/3	1373.635	1373.537	71.510	0.468	724.854	0.372	20	0.088	K.KLEIDDDQKLR.A
R5/RRR5-14/3	1373.367	1373.537	-124.786	0.402	653.173	0.370	18	0.086	K.KLEIDDDQKLR.A
R5/RRR5-13/3	1373.265	1373.537	-199.019	0.332	683.323	0.372	18	0.084	K.KLEIDDDQKLR.A
R5/RRR5-21/3	1373.282	1373.537	-186.713	0.403	890.062	0.335	21	0.084	K.KLEIDDDQKLR.A
R5/RRR5-15/3	1373.556	1373.537	13.619	0.434	743.697	0.320	20	0.082	K.KLEIDDDQKLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/3	1373.498	1373.537	-29.169	0.381	776.451	0.288	19	0.075	-.KLEIDDDQKLR.-
R5/RRR5-12/3	1756.380	1756.896	-865.704	0.382	912.379	0.265	28	0.074	K.KGDNDLPGLTDTEKPR.M
R5/RRR5-3/2	1603.147	1601.716	269.549	0.524	740.595	0.501	18	0.141	K.ALTSSSTSNSEM*LEK.L
R5/RRR5-3/2	1474.087	1474.643	-1059.139	0.290	772.205	0.262	16	0.115	R.AVQGVEFSDPVAVR.H
R5/RRR5-3/3	1313.566	1312.505	46.165	0.461	640.504	0.505	19	0.093	R.SFSRPVLHAAAR.V
R5/RRR5-11/2	1562.266	1562.774	-968.305	0.504	2401.544	0.470	24	0.325	K.M*GQIGVLSGTQGEIR.L
R5/RRR5-12/2	1562.164	1562.774	-1033.499	0.502	2165.678	0.442	23	0.275	K.M*GQIGVLSGTQGEIR.L
R5/RRR5-12/2	1562.214	1562.774	-1001.882	0.494	2019.925	0.436	23	0.251	K.M*GQIGVLSGTQGEIR.L
R5/RRR5-11/2	894.048	894.010	42.096	0.406	913.550	0.393	13	0.141	K.ATVNSFVR.S
R5/RRR5-12/2	893.835	894.010	-196.511	0.353	855.380	0.412	13	0.139	K.ATVNSFVR.S
R5/RRR5-11/2	894.001	894.010	-10.355	0.385	774.049	0.411	12	0.137	K.ATVNSFVR.S
R5/RRR5-12/2	893.531	894.010	-537.772	0.311	692.360	0.377	12	0.129	K.ATVNSFVR.S
R5/RRR5-12/2	893.561	894.010	-504.046	0.274	550.232	0.329	11	0.123	K.ATVNSFVR.S
R5/RRR5-11/2	893.776	894.010	-262.552	0.264	628.044	0.211	12	0.119	K.ATVNSFVR.S
R5/RRR5-5/2	1209.083	1209.379	-245.526	0.544	2600.344	0.624	21	0.419	R.VPAGAAALYYGR.G
R5/RRR5-5/2	1208.798	1209.379	-1311.739	0.444	2087.501	0.597	20	0.307	R.VPAGAAALYYGR.G
R5/RRR5-5/2	1208.349	1209.379	-1684.902	0.427	1518.015	0.610	19	0.226	R.VPAGAAALYYGR.G
R5/RRR5-5/2	1730.690	1730.948	-149.526	0.468	1040.026	0.512	19	0.157	R.TPAFLGLSAGAGAWPASR.Y
R5/RRR5-5/2	1732.559	1730.948	-225.121	0.339	594.856	0.388	20	0.123	R.TPAFLGLSAGAGAWPASR.Y
R5/RRR5-10/2	1470.333	1469.712	-258.109	0.544	2611.370	0.550	21	0.393	K.SGLVALNLDLAQVR.Q
R5/RRR5-10/2	1469.214	1469.712	-339.640	0.386	2463.871	0.324	20	0.292	K.SGLVALNLDLAQVR.Q
R5/RRR5-10/2	1469.293	1469.712	-285.874	0.397	2301.687	0.419	20	0.292	K.SGLVALNLDLAQVR.Q
R5/RRR5-10/2	1431.918	1432.653	-1215.253	0.512	1379.326	0.555	18	0.200	K.WGNIQFPLPFGR.V
R5/RRR5-9/2	1432.485	1432.653	-117.917	0.514	1277.438	0.483	19	0.177	K.WGNIQFPLPFGR.V
R5/RRR5-10/2	1432.339	1432.653	-219.736	0.500	1250.577	0.411	18	0.161	K.WGNIQFPLPFGR.V
R5/RRR5-9/2	1469.481	1469.712	-157.025	0.440	1149.753	0.425	19	0.155	K.SGLVALNLDLAQVR.Q
R5/RRR5-10/2	1432.290	1432.653	-254.535	0.442	955.770	0.454	16	0.148	K.WGNIQFPLPFGR.V
R5/RRR5-9/2	1432.281	1432.653	-260.777	0.463	866.516	0.441	15	0.142	K.WGNIQFPLPFGR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1432.203	1432.653	-315.076	0.438	822.690	0.354	15	0.130	K.WGNIQFPLPFGR.V
R5/RRR5-10/2	1432.170	1432.653	-338.251	0.427	545.610	0.415	13	0.128	K.WGNIQFPLPFGR.V
R5/RRR5-17/2	1660.012	1659.866	88.094	0.521	1671.060	0.523	23	0.226	R.FDPATTPLLAAWAER.F
R5/RRR5-17/2	1659.210	1659.866	-1001.034	0.447	1123.613	0.485	20	0.163	R.FDPATTPLLAAWAER.F
R5/RRR5-17/3	1815.462	1816.053	-878.568	0.451	1580.348	0.420	29	0.162	K.RFDPATTPLLAAWAER.F
R5/RRR5-17/2	1659.036	1659.866	-1106.821	0.384	1256.870	0.417	20	0.161	R.FDPATTPLLAAWAER.F
R5/RRR5-17/2	1658.644	1659.866	-1344.036	0.272	1123.914	0.317	19	0.136	R.FDPATTPLLAAWAER.F
R5/RRR5-17/3	1815.411	1816.053	-907.223	0.333	997.032	0.257	27	0.072	K.RFDPATTPLLAAWAER.F
R5/RRR5-2/2	1513.705	1513.764	-39.360	0.462	1458.706	0.597	23	0.216	K.VPTGVSGTALAASLLR.D
R5/RRR5-2/2	1514.522	1513.764	-160.763	0.513	1374.968	0.579	23	0.204	K.VPTGVSGTALAASLLR.D
R5/RRR5-1/2	1529.796	1528.776	13.237	0.415	1560.283	0.336	17	0.172	K.ELSSLQQEIIVLR.Q
R5/RRR5-2/2	1514.458	1513.764	-203.051	0.418	1062.014	0.480	21	0.157	K.VPTGVSGTALAASLLR.D
R5/RRR5-1/2	1514.253	1513.764	323.860	0.342	1100.067	0.397	19	0.145	K.VPTGVSGTALAASLLR.D
R5/RRR5-2/2	1221.431	1220.308	100.881	0.423	941.341	0.381	16	0.137	K.LAGCQSELDAR.E
R5/RRR5-20/2	1259.159	1258.490	-262.987	0.575	1915.879	0.583	19	0.277	R.SIVGATLEVIQK.K
R5/RRR5-20/2	1258.386	1258.490	-82.567	0.488	1912.947	0.551	19	0.267	R.SIVGATLEVIQK.K
R5/RRR5-20/2	1257.557	1258.490	-1541.668	0.417	1792.971	0.525	19	0.241	R.SIVGATLEVIQK.K
R5/RRR5-20/2	1386.328	1386.662	-242.220	0.437	608.481	0.415	16	0.128	R.SIVGATLEVIQKK.R
R5/RRR5-12/2	1616.300	1616.868	-973.145	0.573	2503.369	0.547	23	0.369	K.MGQIQVLTGSQGQIR.A
R5/RRR5-12/2	1616.369	1616.868	-309.628	0.575	2470.406	0.542	23	0.361	K.MGQIQVLTGSQGQIR.A
R5/RRR5-12/2	1633.056	1632.867	115.608	0.585	2509.326	0.517	23	0.359	K.M*GQIQVLTGSQGQIR.A
R5/RRR5-12/2	1616.295	1616.868	-976.254	0.557	2352.487	0.516	23	0.329	K.MGQIQVLTGSQGQIR.A
R5/RRR5-12/3	1988.467	1987.161	154.320	0.526	1576.517	0.565	30	0.209	R.TPNVFDNKYYVDLQNR.Q
R5/RRR5-12/3	1987.364	1987.161	102.224	0.473	1119.453	0.497	26	0.126	R.TPNVFDNKYYVDLQNR.Q
R5/RRR5-12/3	1987.134	1987.161	-13.754	0.449	1037.377	0.530	25	0.126	R.TPNVFDNKYYVDLQNR.Q
R5/RRR5-9/2	1556.189	1556.786	-1029.854	0.579	2683.163	0.482	22	0.381	K.MFVLDEADEMLSR.G
R5/RRR5-9/2	1556.211	1556.786	-1015.441	0.524	2488.105	0.436	22	0.328	K.MFVLDEADEMLSR.G
R5/RRR5-9/2	1555.638	1556.786	-1385.178	0.440	1966.290	0.348	20	0.221	K.MFVLDEADEMLSR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1572.336	1572.786	-286.800	0.444	1737.502	0.289	19	0.181	K.MFVLDEADEM*LSR.G
R5/RRR5-9/2	1571.958	1572.786	-1166.457	0.408	1316.302	0.342	18	0.154	K.MFVLDEADEM*LSR.G
R5/RRR5-10/2	1571.831	1572.786	-1247.327	0.387	1256.048	0.314	19	0.146	K.M*FVLDEADEMLSR.G
R5/RRR5-9/2	1573.033	1572.786	157.607	0.322	807.302	0.227	14	0.117	K.M*FVLDEADEMLSR.G
R5/RRR5-10/2	1589.469	1588.785	-199.676	0.336	751.977	0.112	14	0.108	-.M*FVLDEADEM*LSR.-
R5/RRR5-10/3	1369.525	1369.466	43.474	0.445	824.712	0.443	23	0.095	K.GHDVIAQAQSGTGK.T
R5/RRR5-10/3	1369.407	1369.466	-42.891	0.438	779.088	0.432	22	0.091	K.GHDVIAQAQSGTGK.T
R5/RRR5-10/3	1369.318	1369.466	-108.345	0.403	878.782	0.258	23	0.071	K.GHDVIAQAQSGTGK.T
R5/RRR5-9/2	1806.937	1806.050	-62.854	0.572	1497.899	0.617	21	0.226	K.ALSFYDVVFDAVYAPK.V
R5/RRR5-9/2	1807.629	1806.050	-233.314	0.591	1368.652	0.631	20	0.213	K.ALSFYDVVFDAVYAPK.V
R5/RRR5-9/2	1807.421	1806.050	206.027	0.527	1088.274	0.545	19	0.168	K.ALSFYDVVFDAVYAPK.V
R5/RRR5-9/2	1935.119	1934.223	-53.945	0.457	320.841	0.549	16	0.131	K.KALSFYDVVFDAVYAPK.V
R5/RRR5-9/2	1936.111	1934.223	-57.712	0.435	164.005	0.544	14	0.128	K.KALSFYDVVFDAVYAPK.V
R5/RRR5-15/2	1858.798	1858.206	-220.305	0.595	3276.152	0.507	26	0.534	R.GCIVSQDLSVLNLVIVK.Q
R5/RRR5-15/2	1857.747	1858.206	-247.912	0.533	3253.159	0.493	26	0.525	R.GCIVSQDLSVLNLVIVK.Q
R5/RRR5-15/2	1857.447	1858.206	-949.766	0.529	2656.996	0.518	25	0.391	R.GCIVSQDLSVLNLVIVK.Q
R5/RRR5-12/2	1859.406	1858.206	107.949	0.383	668.478	0.272	15	0.114	R.GCIVSQDLSVLNLVIVK.Q
R5/RRR5-18/3	1980.950	1981.147	-99.307	0.584	2328.806	0.621	37	0.412	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-17/3	1980.458	1981.147	-855.326	0.526	2039.357	0.612	34	0.330	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-18/2	1981.455	1981.147	156.356	0.580	1839.416	0.596	23	0.265	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-17/2	1980.441	1981.147	-864.012	0.545	1845.569	0.591	23	0.265	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-17/2	1980.381	1981.147	-894.085	0.525	1709.697	0.608	23	0.250	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-17/2	1980.418	1981.147	-875.645	0.545	1747.899	0.557	23	0.242	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-18/2	1980.489	1981.147	-839.263	0.533	1748.383	0.556	23	0.242	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-18/2	1980.348	1981.147	-910.793	0.514	1576.302	0.518	22	0.210	K.DLSVIATEVGEEGQEYLK.L
R5/RRR5-18/2	1245.257	1245.408	-121.193	0.469	892.951	0.398	16	0.139	R.AREVLLEASEK.L
R5/RRR5-17/2	1244.948	1245.408	-370.237	0.433	806.570	0.374	16	0.133	R.AREVLLEASEK.L
R5/RRR5-17/3	1245.377	1245.408	-25.042	0.488	1198.202	0.385	21	0.108	R.AREVLLEASEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/3	1245.722	1245.408	253.309	0.439	1414.928	0.216	23	0.090	R.AREVLLEASEK.L
R5/RRR5-2/2	1613.821	1613.834	-8.392	0.470	1062.061	0.448	20	0.151	K.LELQLSPGDSVIDVK.Q
R5/RRR5-2/2	1305.253	1305.545	-224.340	0.383	1079.196	0.368	16	0.140	K.VGSYLLDTVIPK.F
R5/RRR5-2/2	1540.182	1538.814	240.026	0.424	636.819	0.410	16	0.125	R.VVAQSIIPGILQGDK.S
R5/RRR5-9/2	1172.337	1171.372	-29.515	0.488	2585.530	0.497	18	0.371	R.VSQLELALAAR.A
R5/RRR5-9/2	1171.055	1171.372	-271.795	0.277	1117.896	0.210	15	0.125	R.VSQLELALAAR.A
R5/RRR5-9/3	1702.753	1702.890	-80.406	0.375	1131.330	0.287	25	0.083	R.RKFDLPEGGPITDEK.M
R5/RRR5-9/3	1702.018	1702.890	-1102.976	0.397	886.251	0.300	24	0.075	-.RKFDLPEGGPITDEK.-
R5/RRR5-23/2	1647.277	1647.917	-998.656	0.496	1467.529	0.503	21	0.198	R.SGKM*ELPEWVDIVK.T
R5/RRR5-23/2	1649.086	1647.917	102.603	0.575	1405.158	0.523	22	0.197	R.SGKM*ELPEWVDIVK.T
R5/RRR5-23/2	1647.333	1647.917	-964.805	0.489	1123.251	0.491	20	0.165	R.SGKM*ELPEWVDIVK.T
R5/RRR5-23/2	1646.635	1647.917	-1390.379	0.470	1006.279	0.510	20	0.160	R.SGKM*ELPEWVDIVK.T
R5/RRR5-23/2	1359.192	1359.616	-312.814	0.449	887.940	0.405	18	0.142	K.MELPEWVDIVK.T
R5/RRR5-23/2	1375.108	1375.615	-1099.089	0.460	791.354	0.417	18	0.141	K.M*ELPEWVDIVK.T
R5/RRR5-23/2	1374.958	1375.615	-1209.005	0.445	805.442	0.411	18	0.140	K.M*ELPEWVDIVK.T
R5/RRR5-23/2	1358.950	1359.616	-1229.781	0.437	881.222	0.349	18	0.135	K.MELPEWVDIVK.T
R5/RRR5-24/2	1375.007	1375.615	-1173.076	0.423	743.898	0.398	16	0.135	K.M*ELPEWVDIVK.T
R5/RRR5-23/2	1375.362	1375.615	-184.637	0.331	579.642	0.277	15	0.122	K.M*ELPEWVDIVK.T
R5/RRR5-23/2	1358.844	1359.616	-1307.997	0.333	572.708	0.304	14	0.121	-.MELPEWVDIVK.-
R5/RRR5-23/2	1358.486	1359.616	-1572.143	0.256	773.115	0.149	17	0.116	K.MELPEWVDIVK.T
R5/RRR5-23/3	1647.258	1647.917	-1010.122	0.380	1038.446	0.227	25	0.071	R.SGKM*ELPEWVDIVK.T
R5/RRR5-23/3	1647.541	1647.917	-229.384	0.301	898.482	0.098	24	0.056	R.SGKM*ELPEWVDIVK.T
R5/RRR5-16/2	1616.735	1616.795	-36.927	0.511	2306.964	0.579	23	0.344	R.IALTDNSIVEENLGK.Y
R5/RRR5-16/2	1274.075	1273.509	-342.073	0.464	1235.654	0.455	16	0.167	R.LLQINNGVFVR.V
R5/RRR5-21/2	1792.570	1793.055	-271.021	0.608	3160.646	0.577	24	0.526	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-21/2	1793.234	1793.055	100.438	0.632	2782.067	0.598	23	0.441	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-20/2	1794.469	1793.055	231.780	0.614	2769.439	0.570	23	0.427	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1793.469	1793.055	231.909	0.615	2568.547	0.567	22	0.382	K.AM*SIM*NSFINDIFEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1791.864	1793.055	-1226.095	0.566	2391.479	0.573	23	0.350	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1792.416	1793.055	-917.239	0.540	2451.473	0.514	21	0.341	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1792.676	1793.055	-211.653	0.597	2327.819	0.577	22	0.338	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-19/2	1792.552	1793.055	-840.670	0.555	2273.484	0.555	22	0.322	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-16/2	1791.552	1793.055	-1961.044	0.447	2409.848	0.450	22	0.315	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-21/2	1792.364	1793.055	-946.160	0.558	2267.753	0.533	22	0.314	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-21/2	1792.236	1793.055	-1018.095	0.577	2252.464	0.538	23	0.313	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1792.392	1793.055	-930.708	0.569	2217.183	0.529	21	0.303	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-21/2	1776.388	1777.055	-941.499	0.573	2192.543	0.503	22	0.291	K.AM*SIMNSFINDIFEK.L
R5/RRR5-22/2	1760.394	1761.056	-946.905	0.568	2253.002	0.448	21	0.283	K.AMSIMNSFINDIFEK.L
R5/RRR5-21/2	1775.795	1777.055	-1276.622	0.547	2047.701	0.525	21	0.275	K.AM*SIMNSFINDIFEK.L
R5/RRR5-21/2	1792.299	1793.055	-982.810	0.549	1968.860	0.565	21	0.274	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1792.445	1793.055	-900.625	0.553	1948.423	0.539	20	0.263	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-16/2	1792.476	1793.055	-883.396	0.558	1966.008	0.517	21	0.260	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1761.327	1761.056	154.139	0.583	2048.314	0.450	21	0.251	K.AMSIMNSFINDIFEK.L
R5/RRR5-22/2	1792.611	1793.055	-248.339	0.563	1806.479	0.559	19	0.247	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-20/2	1791.915	1793.055	-1197.705	0.552	1843.148	0.518	22	0.243	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1777.790	1777.055	-149.715	0.638	1676.631	0.579	20	0.234	K.AM*SIMNSFINDIFEK.L
R5/RRR5-22/2	1759.841	1761.056	-1262.644	0.502	1894.422	0.434	21	0.228	K.AMSIMNSFINDIFEK.L
R5/RRR5-21/2	1775.471	1777.055	-2024.796	0.503	1757.471	0.475	21	0.221	K.AM*SIMNSFINDIFEK.L
R5/RRR5-22/2	1777.200	1777.055	81.578	0.616	1627.970	0.529	20	0.216	K.AM*SIMNSFINDIFEK.L
R5/RRR5-22/2	1791.997	1793.055	-1151.463	0.573	1584.211	0.532	19	0.212	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1778.614	1777.055	-248.635	0.624	1463.103	0.546	20	0.201	K.AM*SIMNSFINDIFEK.L
R5/RRR5-22/2	1778.204	1777.055	83.735	0.556	1132.785	0.456	19	0.156	K.AMSIM*NSFINDIFEK.L
R5/RRR5-20/2	1794.099	1793.055	24.570	0.511	688.866	0.570	17	0.149	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-2/2	1793.759	1793.055	-165.179	0.448	919.398	0.472	16	0.145	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-3/2	1793.985	1793.055	-38.762	0.457	622.497	0.505	14	0.136	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-15/2	1794.454	1793.055	222.912	0.381	743.531	0.438	15	0.133	K.AM*SIM*NSFINDIFEK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1794.295	1793.055	134.224	0.442	574.834	0.436	17	0.132	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-22/2	1776.075	1777.055	-1118.488	0.380	650.125	0.340	15	0.123	K.AMSIM*NSFINDIFEK.L
R5/RRR5-18/2	1794.090	1793.055	19.725	0.351	299.540	0.369	12	0.123	K.AM*SIM*NSFINDIFEK.L
R5/RRR5-23/2	1626.058	1625.757	185.485	0.606	2092.418	0.649	22	0.324	R.YVCQDQFTGQPGPK.C
R5/RRR5-22/2	1625.063	1625.757	-1045.651	0.531	1926.426	0.634	22	0.291	R.YVCQDQFTGQPGPK.C
R5/RRR5-21/2	1625.224	1625.757	-946.256	0.524	1927.777	0.622	22	0.288	R.YVCQDQFTGQPGPK.C
R5/RRR5-23/2	1626.330	1625.757	-263.540	0.570	1820.182	0.644	22	0.278	R.YVCQDQFTGQPGPK.C
R5/RRR5-21/2	1625.302	1625.757	-280.882	0.541	1840.575	0.630	22	0.277	R.YVCQDQFTGQPGPK.C
R5/RRR5-21/2	1625.123	1625.757	-1008.319	0.539	1875.447	0.595	22	0.272	R.YVCQDQFTGQPGPK.C
R5/RRR5-22/2	1626.085	1625.757	202.047	0.549	1802.753	0.625	22	0.270	R.YVCQDQFTGQPGPK.C
R5/RRR5-22/2	1626.174	1625.757	256.998	0.570	1720.377	0.642	22	0.263	R.YVCQDQFTGQPGPK.C
R5/RRR5-20/2	1625.057	1625.757	-1049.271	0.529	1714.845	0.611	21	0.253	R.YVCQDQFTGQPGPK.C
R5/RRR5-23/2	1625.163	1625.757	-983.508	0.527	1686.266	0.623	21	0.252	R.YVCQDQFTGQPGPK.C
R5/RRR5-23/2	1624.607	1625.757	-1327.126	0.452	1693.538	0.583	22	0.242	R.YVCQDQFTGQPGPK.C
R5/RRR5-23/3	1405.658	1406.554	-1353.246	0.405	1293.185	0.323	24	0.102	-.CCDNIERLPTK.-
R5/RRR5-23/3	1406.284	1406.554	-192.909	0.486	735.758	0.345	21	0.077	-.CCDNIERLPTK.-
R5/RRR5-23/3	1406.631	1406.554	54.818	0.402	713.716	0.300	21	0.076	K.CCDNIERLPTK.T
R5/RRR5-11/2	1506.237	1506.601	-242.202	0.491	2438.706	0.591	25	0.374	K.LASLSQGAAGESSTAR.E
R5/RRR5-11/2	1356.410	1356.553	-105.575	0.372	861.179	0.496	15	0.141	R.GVAIGVGQSEILGR.I
R5/RRR5-18/2	1576.011	1576.603	-1013.482	0.559	2125.085	0.480	21	0.281	R.LNADDWENDENLK.K
R5/RRR5-18/2	1174.067	1174.374	-262.338	0.512	1727.828	0.494	17	0.228	K.LSELGILSWR.L
R5/RRR5-18/2	1174.191	1174.374	-156.369	0.456	1560.860	0.454	17	0.199	K.LSELGILSWR.L
R5/RRR5-18/2	1174.183	1174.374	-163.148	0.432	1279.052	0.424	16	0.166	K.LSELGILSWR.L
R5/RRR5-21/2	1734.646	1735.790	-1240.045	0.452	2170.985	0.547	21	0.307	R.WSEYDFDQVFADGR.D
R5/RRR5-20/2	1734.947	1735.790	-1065.803	0.527	2193.019	0.523	21	0.304	R.WSEYDFDQVFADGR.D
R5/RRR5-20/2	1735.656	1735.790	-77.498	0.570	1946.952	0.596	20	0.284	R.WSEYDFDQVFADGR.D
R5/RRR5-21/3	1517.429	1517.668	-158.406	0.449	725.087	0.527	24	0.106	K.VSDTEVIGYHQLR.V
R5/RRR5-21/3	1517.546	1517.668	-80.940	0.449	677.004	0.523	24	0.103	K.VSDTEVIGYHQLR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/3	1517.818	1517.668	98.879	0.390	639.925	0.515	23	0.099	K.VSDTEVIGYHQLR.V
R5/RRR5-21/3	1517.498	1517.668	-112.894	0.417	585.442	0.515	24	0.099	K.VSDTEVIGYHQLR.V
R5/RRR5-20/3	1517.280	1517.668	-256.708	0.371	594.853	0.442	24	0.089	K.VSDTEVIGYHQLR.V
R5/RRR5-20/3	1517.335	1517.668	-220.145	0.347	538.081	0.450	22	0.089	K.VSDTEVIGYHQLR.V
R5/RRR5-1/2	1630.812	1630.910	-60.107	0.398	1662.498	0.358	21	0.187	R.LDQPIILTGFSALNK.L
R5/RRR5-2/2	1631.793	1630.910	-71.776	0.452	1433.740	0.374	22	0.169	R.LDQPIILTGFSALNK.L
R5/RRR5-2/2	1631.098	1630.910	115.703	0.396	1281.650	0.392	20	0.159	R.LDQPIILTGFSALNK.L
R5/RRR5-1/2	1018.284	1018.148	133.932	0.434	1136.339	0.444	15	0.158	R.GGAWVVVDSK.I
R5/RRR5-2/2	1017.930	1018.148	-214.713	0.399	1214.459	0.393	14	0.154	R.GGAWVVVDSK.I
R5/RRR5-2/2	1631.305	1630.910	242.980	0.430	1184.959	0.342	19	0.144	R.LDQPIILTGFSALNK.L
R5/RRR5-2/2	1747.044	1746.064	-11.473	0.369	926.977	0.361	20	0.129	K.GIIFLGPPSAAM*AALGDK.I
R5/RRR5-5/2	1602.877	1601.871	3.238	0.508	2518.272	0.603	23	0.395	R.IPALFVVNISSGEVR.A
R5/RRR5-3/2	1632.231	1631.898	205.186	0.304	978.554	0.243	17	0.121	K.VSTPTLFLLGAQDLR.V
R5/RRR5-4/2	1631.649	1631.898	-152.899	0.391	806.105	0.284	17	0.119	K.VSTPTLFLLGAQDLR.V
R5/RRR5-14/2	1772.285	1772.962	-949.119	0.545	1976.840	0.668	27	0.310	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-14/2	1756.463	1756.962	-285.002	0.522	2058.936	0.584	24	0.297	R.GMGDAADLVALSGGHTVGK.-
R5/RRR5-14/2	1772.372	1772.962	-899.887	0.539	1984.150	0.599	29	0.291	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-14/2	1771.754	1772.962	-1249.524	0.491	1151.135	0.636	24	0.191	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-14/3	1772.434	1772.962	-864.287	0.434	1369.907	0.575	35	0.177	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-13/3	1772.806	1772.962	-87.934	0.446	1044.761	0.569	32	0.137	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-13/3	1774.321	1772.962	203.376	0.402	714.623	0.576	30	0.114	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-14/3	1772.925	1772.962	-20.906	0.387	936.409	0.506	34	0.113	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-15/3	1772.647	1772.962	-177.767	0.435	878.352	0.496	31	0.109	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-13/3	1772.603	1772.962	-202.741	0.420	629.884	0.556	29	0.108	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-14/3	1772.120	1772.962	-1042.175	0.399	892.747	0.482	33	0.107	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-16/3	1772.773	1772.962	-106.790	0.383	698.574	0.508	30	0.102	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-16/3	1771.819	1772.962	-1212.862	0.366	729.584	0.488	28	0.100	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-14/3	1756.961	1756.962	-0.921	0.309	333.102	0.497	25	0.095	R.GMGDAADLVALSGGHTVGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1772.423	1772.962	-870.613	0.302	879.162	0.393	31	0.090	R.GM*GDAADLVALSGGHTVGK.-
R5/RRR5-14/3	1757.818	1756.962	-82.240	0.220	279.877	0.380	26	0.089	R.GMGDAADLVALSGGHTVGK.-
R5/RRR5-14/3	1756.479	1756.962	-275.806	0.232	291.626	0.391	25	0.089	R.GMGDAADLVALSGGHTVGK.-
R5/RRR5-27/2	1189.099	1189.384	-240.591	0.450	1495.386	0.449	19	0.190	K.LSAGIASILESK.L
R5/RRR5-26/2	1189.047	1189.384	-284.364	0.533	1336.829	0.500	19	0.186	K.LSAGIASILESK.L
R5/RRR5-26/2	1188.998	1189.384	-325.771	0.510	1192.030	0.468	18	0.167	K.LSAGIASILESK.L
R5/RRR5-26/2	1189.002	1189.384	-321.960	0.473	1202.992	0.431	19	0.162	K.LSAGIASILESK.L
R5/RRR5-27/2	1189.223	1189.384	-136.066	0.532	1114.818	0.465	18	0.161	K.LSAGIASILESK.L
R5/RRR5-26/2	1317.293	1317.557	-201.284	0.444	1022.995	0.511	18	0.159	K.KLSAGIASILESK.L
R5/RRR5-27/2	1189.200	1189.384	-155.322	0.328	1054.354	0.375	16	0.141	K.LSAGIASILESK.L
R5/RRR5-5/3	1748.040	1746.986	30.978	0.465	2131.049	0.515	30	0.304	R.FLEKPELFYDAFAR.A
R5/RRR5-5/2	1128.912	1129.250	-301.138	0.515	1548.646	0.438	18	0.194	K.SPAGANQWVAK.N
R5/RRR5-5/2	1128.971	1129.250	-248.524	0.526	1248.473	0.446	17	0.168	K.SPAGANQWVAK.N
R5/RRR5-5/2	1128.417	1129.250	-1629.671	0.396	1174.873	0.468	16	0.164	K.SPAGANQWVAK.N
R5/RRR5-5/2	1746.477	1746.986	-866.118	0.453	853.288	0.460	20	0.143	R.FLEKPELFYDAFAR.A
R5/RRR5-5/3	1746.606	1746.986	-218.061	0.361	1015.498	0.280	23	0.076	R.FLEKPELFYDAFAR.A
R5/RRR5-22/2	1351.188	1351.449	-193.697	0.515	2166.792	0.507	20	0.296	K.YGVGDAHFEVTR.F
R5/RRR5-22/2	1350.993	1351.449	-338.366	0.515	2032.306	0.526	20	0.279	K.YGVGDAHFEVTR.F
R5/RRR5-21/2	1651.163	1651.844	-1021.559	0.371	2172.032	0.404	23	0.266	K.SAWSEAYNQLVAAIK.Q
R5/RRR5-22/2	1350.947	1351.449	-1114.897	0.454	1987.894	0.482	20	0.260	K.YGVGDAHFEVTR.F
R5/RRR5-22/2	1651.447	1651.844	-241.145	0.509	1931.884	0.472	22	0.247	K.SAWSEAYNQLVAAIK.Q
R5/RRR5-22/2	1650.615	1651.844	-1354.802	0.369	1967.220	0.396	22	0.233	K.SAWSEAYNQLVAAIK.Q
R5/RRR5-22/2	1651.281	1651.844	-949.416	0.470	1843.590	0.441	22	0.228	K.SAWSEAYNQLVAAIK.Q
R5/RRR5-22/3	1651.444	1651.844	-242.785	0.510	1526.982	0.465	26	0.168	K.SAWSEAYNQLVAAIK.Q
R5/RRR5-22/2	1652.531	1651.844	-190.087	0.345	786.386	0.323	18	0.125	K.SAWSEAYNQLVAAIK.Q
R5/RRR5-21/3	1351.479	1351.449	22.719	0.454	770.297	0.551	21	0.111	K.YGVGDAHFEVTR.F
R5/RRR5-22/3	1350.403	1351.449	-1519.412	0.450	615.505	0.593	19	0.110	K.YGVGDAHFEVTR.F
R5/RRR5-21/3	1352.575	1351.449	93.262	0.391	795.916	0.507	21	0.103	K.YGVGDAHFEVTR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/3	1352.640	1351.449	141.865	0.436	671.039	0.469	20	0.094	K.YGVGDAHFEVTR.F
R5/RRR5-22/3	1650.924	1651.844	-1166.443	0.371	465.606	0.405	21	0.080	K.SAWSEAYNQLVAAIK.Q
R5/RRR5-13/2	1576.590	1576.843	-160.802	0.458	2045.312	0.524	23	0.278	R.MFYGPGGPYALFAGK.D
R5/RRR5-13/2	1576.503	1576.843	-216.029	0.499	1939.221	0.567	24	0.274	R.MFYGPGGPYALFAGK.D
R5/RRR5-13/2	1576.399	1576.843	-282.295	0.497	2043.093	0.494	23	0.269	R.MFYGPGGPYALFAGK.D
R5/RRR5-13/2	1577.815	1576.843	-17.274	0.561	1808.546	0.594	23	0.262	R.MFYGPGGPYALFAGK.D
R5/RRR5-13/2	1576.001	1576.843	-1171.972	0.371	1855.503	0.501	22	0.242	R.MFYGPGGPYALFAGK.D
R5/RRR5-13/2	1593.528	1592.842	-197.637	0.544	1337.914	0.643	21	0.214	R.M*FYGPGGPYALFAGK.D
R5/RRR5-13/2	1592.002	1592.842	-1159.322	0.452	1415.607	0.532	21	0.197	R.M*FYGPGGPYALFAGK.D
R5/RRR5-13/2	1592.162	1592.842	-1058.082	0.457	1334.024	0.522	21	0.187	R.M*FYGPGGPYALFAGK.D
R5/RRR5-13/2	1166.927	1167.254	-280.836	0.476	1241.696	0.448	16	0.168	K.GQIYDVTQSR.M
R5/RRR5-13/2	1167.972	1167.254	-242.008	0.468	1278.599	0.403	16	0.163	K.GQIYDVTQSR.M
R5/RRR5-13/2	1167.975	1167.254	-239.281	0.497	1132.281	0.449	15	0.160	K.GQIYDVTQSR.M
R5/RRR5-14/2	1167.204	1167.254	-42.652	0.322	1021.967	0.225	15	0.125	K.GQIYDVTQSR.M
R5/RRR5-12/2	1594.234	1592.842	246.582	0.281	244.018	0.361	14	0.121	-.M*FYGPGGPYALFAGK.-
R5/RRR5-14/2	1166.188	1167.254	-1776.682	0.240	622.432	0.066	13	0.107	-.GQIYDVTQSR.-
R5/RRR5-26/2	1260.922	1260.466	362.904	0.616	2003.933	0.573	18	0.288	R.FTTFALSGFIR.A
R5/RRR5-26/2	1260.005	1260.466	-366.396	0.531	1345.305	0.555	18	0.199	R.FTTFALSGFIR.A
R5/RRR5-26/2	1260.109	1260.466	-283.874	0.485	1450.292	0.483	19	0.194	R.FTTFALSGFIR.A
R5/RRR5-26/2	1674.244	1674.796	-929.666	0.523	1261.398	0.478	19	0.171	R.AQGDADSALDRLWQK.R
R5/RRR5-26/2	1674.326	1674.796	-281.945	0.531	1089.124	0.494	18	0.160	R.AQGDADSALDRLWQK.R
R5/RRR5-26/2	1674.314	1674.796	-289.040	0.511	1064.450	0.470	18	0.154	R.AQGDADSALDRLWQK.R
R5/RRR5-25/2	1260.074	1260.466	-311.671	0.283	387.795	0.414	14	0.125	R.FTTFALSGFIR.A
R5/RRR5-16/3	1949.526	1949.071	233.708	0.545	2522.443	0.480	32	0.383	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-15/3	1948.254	1949.071	-935.828	0.479	2417.034	0.460	31	0.347	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-15/2	1909.416	1910.068	-868.130	0.522	2358.818	0.561	26	0.344	R.ASGSCDFAGAATIVTQQPK.I
R5/RRR5-16/2	1910.384	1910.068	165.570	0.563	2274.798	0.573	25	0.331	R.ASGSCDFAGAATIVTQQPK.I
R5/RRR5-16/2	1910.460	1910.068	205.874	0.574	2262.346	0.580	25	0.330	R.ASGSCDFAGAATIVTQQPK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/3	1948.985	1949.071	-44.397	0.526	2245.870	0.489	29	0.316	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-16/2	1909.315	1910.068	-921.143	0.507	2137.792	0.566	25	0.305	R.ASGSCDFAGAATIVTQQPK.I
R5/RRR5-17/3	1948.472	1949.071	-823.275	0.493	2215.266	0.473	30	0.302	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-15/2	1909.361	1910.068	-896.754	0.499	2006.571	0.573	24	0.284	R.ASGSCDFAGAATIVTQQPK.I
R5/RRR5-15/3	1948.754	1949.071	-163.336	0.492	2147.482	0.456	31	0.277	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-15/2	1909.465	1910.068	-842.331	0.498	1986.431	0.524	24	0.267	R.ASGSCDFAGAATIVTQQPK.I
R5/RRR5-16/3	1948.159	1949.071	-984.611	0.479	2035.245	0.459	30	0.254	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-16/3	1949.316	1949.071	126.046	0.514	1875.683	0.527	29	0.248	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-17/2	1909.662	1910.068	-213.411	0.286	661.616	0.235	19	0.115	R.ASGSCDFAGAATIVTQQPK.I
R5/RRR5-17/3	1948.151	1949.071	-988.574	0.426	1124.543	0.392	26	0.103	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-15/3	1947.790	1949.071	-1174.506	0.399	1138.143	0.360	27	0.098	K.VAHATYAFNDYYQTAGR.A
R5/RRR5-22/2	1499.395	1499.734	-227.139	0.563	1820.438	0.565	20	0.257	K.APLLDVTQFGYFK.V
R5/RRR5-22/2	1498.621	1499.734	-1414.676	0.430	1710.294	0.553	20	0.237	K.APLLDVTQFGYFK.V
R5/RRR5-22/2	1499.110	1499.734	-1087.033	0.530	1600.376	0.574	20	0.230	K.APLLDVTQFGYFK.V
R5/RRR5-22/3	969.207	969.077	133.878	0.491	780.724	0.463	16	0.099	K.YHPGYFGK.V
R5/RRR5-22/3	969.163	969.077	88.594	0.485	837.417	0.446	17	0.097	K.YHPGYFGK.V
R5/RRR5-22/3	969.085	969.077	8.627	0.484	681.011	0.445	16	0.094	K.YHPGYFGK.V
R5/RRR5-23/3	969.009	969.077	-70.975	0.323	876.392	0.228	15	0.068	-.YHPGYFGK.-
R5/RRR5-8/2	1852.343	1852.017	176.566	0.580	2536.580	0.526	23	0.367	R.M*TNFYTNFQVDEIGR.V
R5/RRR5-8/2	1851.435	1852.017	-857.167	0.547	2404.044	0.549	22	0.349	R.M*TNFYTNFQVDEIGR.V
R5/RRR5-8/2	1836.361	1836.018	187.245	0.609	2381.191	0.508	23	0.330	R.MTNFYTNFQVDEIGR.V
R5/RRR5-8/2	1851.359	1852.017	-898.536	0.519	2324.731	0.527	22	0.327	R.M*TNFYTNFQVDEIGR.V
R5/RRR5-8/2	1835.901	1836.018	-64.130	0.546	2166.711	0.504	22	0.292	R.MTNFYTNFQVDEIGR.V
R5/RRR5-8/2	1836.417	1836.018	217.975	0.604	2108.038	0.536	22	0.290	R.MTNFYTNFQVDEIGR.V
R5/RRR5-8/2	1204.308	1204.356	-39.407	0.510	1607.811	0.395	17	0.189	R.AAELTTLLESR.M
R5/RRR5-9/2	1204.224	1204.356	-109.563	0.401	1649.993	0.335	16	0.185	-.AAELTTLLESR.-
R5/RRR5-8/2	1203.453	1204.356	-1586.051	0.402	1656.635	0.321	17	0.180	R.AAELTTLLESR.M
R5/RRR5-8/2	1203.437	1204.356	-1598.789	0.381	1677.255	0.282	17	0.175	R.AAELTTLLESR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1204.124	1204.356	-193.154	0.473	1281.009	0.453	16	0.171	R.AAELTTLLESR.M
R5/RRR5-1/2	1203.971	1204.356	-320.703	0.503	1348.260	0.395	15	0.164	R.AAELTTLLESR.M
R5/RRR5-9/2	1204.212	1204.356	-119.732	0.401	1240.814	0.412	16	0.160	R.AAELTTLLESR.M
R5/RRR5-9/2	1203.951	1204.356	-337.285	0.466	886.362	0.389	14	0.136	R.AAELTTLLESR.M
R5/RRR5-8/3	1204.600	1204.356	203.615	0.420	937.969	0.301	22	0.077	R.AAELTTLLESR.M
R5/RRR5-11/2	1602.427	1602.815	-242.715	0.505	2336.763	0.497	23	0.321	R.AVNITINSIGTELTR.D
R5/RRR5-11/2	1602.409	1602.815	-253.873	0.506	2161.800	0.479	23	0.285	R.AVNITINSIGTELTR.D
R5/RRR5-12/2	1602.403	1602.815	-257.465	0.476	2019.093	0.441	22	0.252	R.AVNITINSIGTELTR.D
R5/RRR5-11/2	1602.406	1602.815	-255.708	0.472	1841.657	0.465	21	0.233	R.AVNITINSIGTELTR.D
R5/RRR5-11/2	1286.947	1287.422	-370.248	0.412	725.502	0.415	15	0.132	K.ISYGESQM*LDK.A
R5/RRR5-10/2	1174.192	1174.329	-117.371	0.431	1214.661	0.359	16	0.152	K.RDELTLEGLK.Q
R5/RRR5-10/2	1174.067	1174.329	-224.274	0.435	1256.811	0.321	16	0.149	K.RDELTLEGLK.Q
R5/RRR5-9/2	1173.705	1174.329	-1387.991	0.457	1306.184	0.299	16	0.148	K.RDELTLEGLK.Q
R5/RRR5-9/2	1175.244	1174.329	-72.885	0.452	1275.009	0.273	16	0.142	K.RDELTLEGLK.Q
R5/RRR5-10/2	1173.643	1174.329	-1440.851	0.410	1232.359	0.265	16	0.139	K.RDELTLEGLK.Q
R5/RRR5-9/2	1175.299	1174.329	-26.003	0.471	1114.108	0.290	15	0.135	K.RDELTLEGLK.Q
R5/RRR5-10/2	1019.056	1018.143	-86.099	0.421	916.318	0.272	14	0.126	-.DELTLEGLK.-
R5/RRR5-10/2	1018.920	1018.143	-219.611	0.431	944.599	0.277	14	0.126	-.DELTLEGLK.-
R5/RRR5-17/2	1974.389	1974.204	93.911	0.558	1403.822	0.559	23	0.200	R.IYDADPTVLNALANQNIK.V
R5/RRR5-17/2	1532.293	1532.672	-247.831	0.508	1322.682	0.562	19	0.194	R.ATEGPIVADKNCEK.I
R5/RRR5-17/2	1532.154	1532.672	-993.267	0.434	1097.392	0.491	19	0.162	R.ATEGPIVADKNCEK.I
R5/RRR5-17/2	1532.104	1532.672	-1026.064	0.438	790.857	0.503	16	0.144	R.ATEGPIVADKNCEK.I
R5/RRR5-17/2	1001.098	1001.116	-17.319	0.433	605.835	0.516	15	0.143	R.ATEGPIVADK.N
R5/RRR5-17/2	1000.961	1001.116	-154.563	0.379	680.678	0.498	15	0.141	R.ATEGPIVADK.N
R5/RRR5-17/2	1000.850	1001.116	-266.026	0.351	716.451	0.453	16	0.137	R.ATEGPIVADK.N
R5/RRR5-16/2	1532.753	1532.672	53.631	0.357	354.687	0.517	13	0.128	R.ATEGPIVADKNCEK.I
R5/RRR5-16/2	1001.080	1001.116	-35.298	0.339	370.636	0.321	12	0.096	-.ATEGPIVADK.-
R5/RRR5-18/2	1199.271	1199.425	-128.903	0.459	2109.175	0.425	18	0.260	R.VDIGQVLLSVR.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	1199.061	1199.425	-304.862	0.523	2041.935	0.461	19	0.260	R.VDIGQVLLSVR.C
R5/RRR5-25/2	1199.044	1199.425	-319.060	0.504	2123.128	0.412	19	0.258	R.VDIGQVLLSVR.C
R5/RRR5-15/2	1200.485	1199.425	49.709	0.483	1882.217	0.506	18	0.249	R.VDIGQVLLSVR.C
R5/RRR5-18/2	1200.156	1199.425	-224.704	0.559	1892.837	0.456	19	0.237	R.VDIGQVLLSVR.C
R5/RRR5-25/2	1199.278	1199.425	-123.593	0.478	1947.853	0.411	19	0.234	R.VDIGQVLLSVR.C
R5/RRR5-19/2	1199.455	1199.425	24.844	0.410	1674.355	0.469	17	0.212	R.VDIGQVLLSVR.C
R5/RRR5-19/2	1199.125	1199.425	-251.240	0.406	1160.366	0.465	17	0.163	R.VDIGQVLLSVR.C
R5/RRR5-1/2	1199.466	1199.425	34.439	0.416	1036.273	0.345	15	0.138	R.VDIGQVLLSVR.C
R5/RRR5-26/2	1198.764	1199.425	-1390.333	0.434	671.801	0.428	15	0.136	R.VDIGQVLLSVR.C
R5/RRR5-16/2	1199.432	1199.425	5.246	0.309	787.060	0.376	15	0.131	R.VDIGQVLLSVR.C
R5/RRR5-20/2	1199.341	1199.425	-70.706	0.329	593.805	0.371	14	0.127	R.VDIGQVLLSVR.C
R5/RRR5-19/2	1199.360	1199.425	-54.474	0.307	762.702	0.319	15	0.126	R.VDIGQVLLSVR.C
R5/RRR5-14/2	1199.299	1199.425	-105.317	0.429	736.617	0.325	14	0.126	R.VDIGQVLLSVR.C
R5/RRR5-16/2	1198.616	1199.425	-1514.308	0.285	433.373	0.426	12	0.126	R.VDIGQVLLSVR.C
R5/RRR5-17/3	1567.428	1567.726	-190.300	0.436	922.757	0.418	27	0.096	R.CKPNNAVHASEALR.R
R5/RRR5-17/3	1567.666	1567.726	-37.974	0.403	990.828	0.399	28	0.095	R.CKPNNAVHASEALR.R
R5/RRR5-17/3	1567.688	1567.726	-24.150	0.430	769.277	0.416	25	0.089	R.CKPNNAVHASEALR.R
R5/RRR5-7/2	1752.389	1752.904	-867.249	0.549	2386.117	0.496	23	0.330	R.SFGTDLDTATNELVIR.V
R5/RRR5-7/2	1752.501	1752.904	-230.314	0.536	2441.935	0.460	24	0.329	R.SFGTDLDTATNELVIR.V
R5/RRR5-7/2	1495.302	1495.706	-270.830	0.407	1210.624	0.398	18	0.156	R.FSNLVFEPLWSR.N
R5/RRR5-7/2	1495.216	1495.706	-328.984	0.235	882.700	0.124	15	0.111	R.FSNLVFEPLWSR.N
R5/RRR5-18/2	1141.021	1141.346	-285.495	0.482	1959.276	0.489	18	0.257	R.LVNILNAANAK.A
R5/RRR5-18/2	1266.161	1266.470	-244.611	0.501	1766.331	0.550	17	0.246	R.LEQAFVNIFGK.K
R5/RRR5-18/2	1141.231	1141.346	-101.235	0.498	1602.679	0.548	18	0.225	R.LVNILNAANAK.A
R5/RRR5-18/2	1141.205	1141.346	-123.553	0.496	1490.032	0.468	18	0.194	R.LVNILNAANAK.A
R5/RRR5-18/2	1266.240	1266.470	-182.325	0.354	784.322	0.492	14	0.140	R.LEQAFVNIFGK.K
R5/RRR5-15/2	1421.345	1421.622	-195.679	0.496	1884.777	0.597	22	0.274	K.LPGLFIWSADSSK.V
R5/RRR5-15/2	1420.893	1421.622	-1220.460	0.524	1640.574	0.629	21	0.248	K.LPGLFIWSADSSK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1422.275	1421.622	-244.534	0.489	1526.450	0.625	20	0.231	K.LPGLFIWSADSSK.V
R5/RRR5-16/2	1421.226	1421.622	-279.346	0.503	1630.713	0.547	21	0.227	K.LPGLFIWSADSSK.V
R5/RRR5-16/2	1421.259	1421.622	-256.338	0.517	1550.604	0.577	21	0.224	K.LPGLFIWSADSSK.V
R5/RRR5-15/2	1421.253	1421.622	-260.647	0.510	1546.645	0.554	20	0.218	K.LPGLFIWSADSSK.V
R5/RRR5-15/2	1338.080	1338.404	-242.261	0.481	1374.490	0.533	17	0.195	K.VSSYGFEYETR.G
R5/RRR5-15/2	1338.954	1338.404	-337.111	0.521	1211.219	0.584	17	0.191	K.VSSYGFEYETR.G
R5/RRR5-16/2	1420.637	1421.622	-1401.236	0.479	1114.898	0.606	17	0.183	K.LPGLFIWSADSSK.V
R5/RRR5-16/2	1338.256	1338.404	-110.667	0.430	1386.172	0.461	17	0.182	K.VSSYGFEYETR.G
R5/RRR5-14/2	1421.248	1421.622	-263.835	0.512	1028.357	0.609	17	0.177	K.LPGLFIWSADSSK.V
R5/RRR5-16/2	1338.012	1338.404	-293.608	0.471	1142.616	0.522	17	0.173	K.VSSYGFEYETR.G
R5/RRR5-15/2	1338.017	1338.404	-289.855	0.459	1118.201	0.522	17	0.171	K.VSSYGFEYETR.G
R5/RRR5-15/2	1421.852	1421.622	162.094	0.389	1025.619	0.508	17	0.158	K.LPGLFIWSADSSK.V
R5/RRR5-15/2	1421.522	1421.622	-70.766	0.422	949.909	0.528	16	0.157	K.LPGLFIWSADSSK.V
R5/RRR5-14/2	1421.577	1421.622	-31.834	0.449	897.203	0.538	16	0.156	K.LPGLFIWSADSSK.V
R5/RRR5-16/2	1337.434	1338.404	-1476.781	0.361	1037.986	0.418	17	0.148	K.VSSYGFEYETR.G
R5/RRR5-9/2	1544.370	1544.735	-237.252	0.456	2373.932	0.501	24	0.330	K.VTALVNDTVGTLAGGR.Y
R5/RRR5-9/2	1544.304	1544.735	-279.916	0.426	2037.077	0.514	23	0.274	K.VTALVNDTVGTLAGGR.Y
R5/RRR5-9/2	1544.400	1544.735	-217.745	0.492	1718.306	0.551	22	0.238	K.VTALVNDTVGTLAGGR.Y
R5/RRR5-9/2	1601.788	1601.827	-24.124	0.477	1545.224	0.464	21	0.197	K.LKDILGVADTSLEAR.Y
R5/RRR5-27/2	1123.052	1123.284	-207.098	0.466	1114.576	0.448	16	0.159	R.VCGNPHGLIR.K
R5/RRR5-27/2	1123.039	1123.284	-218.766	0.475	1111.442	0.437	16	0.158	R.VCGNPHGLIR.K
R5/RRR5-28/2	1122.970	1123.284	-280.490	0.466	1051.031	0.442	16	0.155	R.VCGNPHGLIR.K
R5/RRR5-27/2	1123.106	1123.284	-159.448	0.471	1065.736	0.434	16	0.155	R.VCGNPHGLIR.K
R5/RRR5-28/2	1123.020	1123.284	-236.104	0.440	1098.822	0.407	16	0.152	R.VCGNPHGLIR.K
R5/RRR5-28/2	1122.799	1123.284	-433.306	0.430	877.609	0.435	15	0.144	R.VCGNPHGLIR.K
R5/RRR5-28/2	975.796	976.120	-332.379	0.291	1116.639	0.330	11	0.140	K.YGLM*CCR.Q
R5/RRR5-28/2	975.752	976.120	-377.817	0.361	1157.101	0.280	11	0.138	K.YGLM*CCR.Q
R5/RRR5-27/2	975.829	976.120	-299.244	0.333	1151.250	0.282	11	0.137	K.YGLM*CCR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-28/2	1122.782	1123.284	-1342.223	0.381	1083.451	0.295	16	0.136	R.VCGNPHGLIR.K
R5/RRR5-28/2	959.846	960.120	-286.383	0.333	1049.145	0.313	11	0.136	K.YGLMCCR.Q
R5/RRR5-27/2	975.678	976.120	-454.645	0.312	1081.069	0.301	11	0.136	K.YGLM*CCR.Q
R5/RRR5-28/2	975.795	976.120	-333.634	0.367	1016.099	0.290	11	0.133	K.YGLM*CCR.Q
R5/RRR5-28/2	1122.836	1123.284	-400.251	0.322	519.965	0.306	14	0.124	R.VCGNPHGLIR.K
R5/RRR5-27/2	975.352	976.120	-1817.431	0.284	798.539	0.269	10	0.123	K.YGLM*CCR.Q
R5/RRR5-28/2	1122.989	1123.284	-263.149	0.286	771.328	0.239	16	0.122	R.VCGNPHGLIR.K
R5/RRR5-23/2	1206.087	1206.380	-243.395	0.498	1173.536	0.511	19	0.174	R.KGHAVGDIPGVR.F
R5/RRR5-23/2	1206.041	1206.380	-281.271	0.507	1002.689	0.518	18	0.163	R.KGHAVGDIPGVR.F
R5/RRR5-23/2	1205.962	1206.380	-346.976	0.489	982.381	0.509	18	0.160	R.KGHAVGDIPGVR.F
R5/RRR5-23/2	1078.104	1078.207	-95.806	0.455	681.951	0.562	16	0.150	K.GHAVGDIPGVR.F
R5/RRR5-23/2	1077.974	1078.207	-216.326	0.391	577.729	0.537	15	0.140	K.GHAVGDIPGVR.F
R5/RRR5-28/2	1077.815	1078.207	-364.034	0.324	534.052	0.569	15	0.138	K.GHAVGDIPGVR.F
R5/RRR5-28/3	1206.233	1206.380	-122.334	0.497	1127.275	0.420	25	0.109	R.KGHAVGDIPGVR.F
R5/RRR5-22/3	1206.412	1206.380	26.872	0.517	887.817	0.459	24	0.104	R.KGHAVGDIPGVR.F
R5/RRR5-22/3	1206.331	1206.380	-40.570	0.490	925.952	0.450	23	0.104	R.KGHAVGDIPGVR.F
R5/RRR5-23/3	1206.693	1206.380	260.640	0.499	806.942	0.449	23	0.100	R.KGHAVGDIPGVR.F
R5/RRR5-23/3	1206.529	1206.380	124.136	0.448	1187.158	0.354	26	0.098	R.KGHAVGDIPGVR.F
R5/RRR5-27/3	1206.552	1206.380	143.465	0.457	1000.670	0.389	24	0.096	R.KGHAVGDIPGVR.F
R5/RRR5-26/3	1205.888	1206.380	-408.994	0.445	931.664	0.382	23	0.093	R.KGHAVGDIPGVR.F
R5/RRR5-26/3	1206.371	1206.380	-7.228	0.430	876.015	0.393	23	0.092	R.KGHAVGDIPGVR.F
R5/RRR5-27/3	1206.120	1206.380	-216.143	0.460	896.961	0.382	23	0.092	R.KGHAVGDIPGVR.F
R5/RRR5-23/3	1206.872	1206.380	409.428	0.482	619.491	0.392	20	0.091	R.KGHAVGDIPGVR.F
R5/RRR5-24/3	1206.292	1206.380	-72.543	0.461	816.062	0.398	21	0.089	-.KGHAVGDIPGVR.-
R5/RRR5-20/3	1206.217	1206.380	-135.277	0.452	663.328	0.375	20	0.088	R.KGHAVGDIPGVR.F
R5/RRR5-20/3	1206.019	1206.380	-300.221	0.439	833.555	0.362	22	0.087	R.KGHAVGDIPGVR.F
R5/RRR5-24/3	1206.538	1206.380	131.290	0.421	855.061	0.356	22	0.087	R.KGHAVGDIPGVR.F
R5/RRR5-21/3	1206.237	1206.380	-118.375	0.413	686.069	0.361	20	0.086	R.KGHAVGDIPGVR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-28/3	1207.103	1206.380	-230.167	0.481	639.728	0.336	22	0.086	R.KGHAVGDIPGVR.F
R5/RRR5-19/3	1206.190	1206.380	-157.815	0.368	674.503	0.388	21	0.085	-.KGHAVGDIPGVR.-
R5/RRR5-21/3	1205.608	1206.380	-1473.648	0.380	772.368	0.339	22	0.084	R.KGHAVGDIPGVR.F
R5/RRR5-21/3	1206.929	1206.380	-374.302	0.409	776.276	0.359	22	0.083	-.KGHAVGDIPGVR.-
R5/RRR5-20/3	1206.163	1206.380	-180.201	0.394	898.808	0.325	23	0.083	R.KGHAVGDIPGVR.F
R5/RRR5-22/3	1206.289	1206.380	-75.131	0.417	788.857	0.327	22	0.080	-.KGHAVGDIPGVR.-
R5/RRR5-27/3	1205.659	1206.380	-1431.544	0.338	604.914	0.260	20	0.076	-.KGHAVGDIPGVR.-
R5/RRR5-24/3	1205.878	1206.380	-1249.133	0.375	852.126	0.231	23	0.073	R.KGHAVGDIPGVR.F
R5/RRR5-28/3	1205.181	1206.380	-1829.843	0.258	666.143	0.237	20	0.070	-.KGHAVGDIPGVR.-
R5/RRR5-8/2	1746.937	1746.901	21.053	0.550	2250.860	0.528	24	0.315	R.VTGSLADGAATIQSALDR.M
R5/RRR5-8/2	1903.469	1904.153	-887.566	0.459	1419.626	0.436	23	0.178	R.SALDYLELQPDLSALVR.G
R5/RRR5-9/2	1905.284	1904.153	68.849	0.453	1165.735	0.484	22	0.165	R.SALDYLELQPDLSALVR.G
R5/RRR5-8/2	1905.160	1904.153	3.303	0.420	894.267	0.488	19	0.146	R.SALDYLELQPDLSALVR.G
R5/RRR5-8/2	1905.096	1904.153	-30.309	0.438	801.571	0.413	18	0.132	R.SALDYLELQPDLSALVR.G
R5/RRR5-22/2	1071.570	1072.240	-1563.247	0.442	1547.912	0.557	19	0.219	R.VLVVDGGGSLR.C
R5/RRR5-22/2	1072.167	1072.240	-68.701	0.469	1566.535	0.535	19	0.217	R.VLVVDGGGSLR.C
R5/RRR5-22/2	1071.670	1072.240	-1469.760	0.439	1600.896	0.516	19	0.216	R.VLVVDGGGSLR.C
R5/RRR5-22/2	1278.226	1278.484	-202.263	0.417	549.397	0.458	16	0.135	R.ALQPVFQVYGR.R
R5/RRR5-22/2	1278.376	1278.484	-84.532	0.341	542.631	0.419	16	0.129	R.ALQPVFQVYGR.R
R5/RRR5-22/2	1278.485	1278.484	0.708	0.271	473.748	0.303	14	0.120	R.ALQPVFQVYGR.R
R5/RRR5-23/2	1072.209	1072.240	-28.960	0.240	406.898	0.273	11	0.107	-.VLVVDGGGSLR.-
R5/RRR5-13/2	943.811	944.071	-275.616	0.497	1592.407	0.454	15	0.202	R.SAVQAALQR.E
R5/RRR5-1/2	943.971	944.071	-106.436	0.490	1616.151	0.429	15	0.199	R.SAVQAALQR.E
R5/RRR5-13/2	943.968	944.071	-109.290	0.491	1516.363	0.426	15	0.188	R.SAVQAALQR.E
R5/RRR5-16/2	944.054	944.071	-17.458	0.468	1518.080	0.404	15	0.184	R.SAVQAALQR.E
R5/RRR5-16/2	943.902	944.071	-179.083	0.460	1502.724	0.388	15	0.179	R.SAVQAALQR.E
R5/RRR5-15/2	943.234	944.071	-1953.516	0.456	1489.082	0.383	15	0.177	R.SAVQAALQR.E
R5/RRR5-13/2	943.398	944.071	-1778.619	0.443	1373.426	0.412	14	0.172	R.SAVQAALQR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	943.493	944.071	-1676.959	0.431	1379.295	0.390	15	0.169	R.SAVQAALQR.E
R5/RRR5-14/2	1027.047	1027.243	-191.289	0.459	1295.721	0.317	15	0.149	R.EIALAAGLIR.I
R5/RRR5-13/2	1027.074	1027.243	-164.462	0.373	914.930	0.366	14	0.135	-.EIALAAGLIR.-
R5/RRR5-14/2	944.152	944.071	86.806	0.381	1141.933	0.222	15	0.130	R.SAVQAALQR.E
R5/RRR5-14/2	944.261	944.071	202.326	0.314	939.443	0.191	14	0.121	R.SAVQAALQR.E
R5/RRR5-13/2	1026.545	1027.243	-1659.006	0.259	675.556	0.227	13	0.117	R.EIALAAGLIR.I
R5/RRR5-16/2	1027.150	1027.243	-90.665	0.227	691.859	0.256	11	0.116	-.EIALAAGLIR.-
R5/RRR5-14/2	1985.637	1986.259	-819.637	0.590	2052.492	0.502	23	0.272	R.AYALILENNPFDQIVHK.R
R5/RRR5-14/2	1034.059	1034.230	-166.311	0.415	1017.005	0.410	15	0.147	R.LEALLFEAK.G
R5/RRR5-14/2	1034.020	1034.230	-204.327	0.391	825.338	0.402	14	0.137	R.LEALLFEAK.G
R5/RRR5-19/2	1567.424	1567.727	-194.237	0.495	1966.209	0.493	21	0.259	K.LQLNDFTGAVFEGR.L
R5/RRR5-19/2	1567.614	1567.727	-72.762	0.521	1873.134	0.526	20	0.253	K.LQLNDFTGAVFEGR.L
R5/RRR5-19/2	1133.095	1132.209	-100.989	0.499	1331.251	0.465	20	0.179	K.NSDVAAAVAGTR.W
R5/RRR5-19/2	1566.384	1567.727	-1500.505	0.298	987.653	0.398	17	0.138	K.LQLNDFTGAVFEGR.L
R5/RRR5-11/2	1344.257	1344.539	-210.362	0.534	1690.263	0.572	21	0.242	R.LVDIGTVTAQQAK.D
R5/RRR5-11/2	1344.258	1344.539	-209.633	0.524	1563.536	0.528	21	0.215	R.LVDIGTVTAQQAK.D
R5/RRR5-11/2	1343.646	1344.539	-1413.459	0.423	1419.097	0.510	21	0.194	R.LVDIGTVTAQQAK.D
R5/RRR5-11/2	1168.251	1168.350	-84.745	0.470	856.266	0.344	14	0.130	K.DWGFSGVMLR.-
R5/RRR5-11/2	1184.206	1184.349	-121.130	0.353	793.322	0.238	14	0.119	K.DWGFSGVM*LR.-
R5/RRR5-12/2	1743.134	1743.895	-1013.315	0.563	1907.780	0.584	22	0.275	K.AYYAVEEVKENATQK.S
R5/RRR5-12/2	1087.444	1088.283	-1695.916	0.444	1676.526	0.586	19	0.242	R.VVGVLLGTSSR.G
R5/RRR5-12/2	1088.129	1088.283	-141.844	0.557	1670.589	0.518	19	0.227	R.VVGVLLGTSSR.G
R5/RRR5-12/2	1087.521	1088.283	-1625.432	0.418	1306.851	0.545	17	0.189	R.VVGVLLGTSSR.G
R5/RRR5-15/3	1771.132	1770.922	118.990	0.585	1958.584	0.574	32	0.286	K.KGENDLPGLTDTEKPR.M
R5/RRR5-15/3	1770.814	1770.922	-61.136	0.567	1994.798	0.535	32	0.278	K.KGENDLPGLTDTEKPR.M
R5/RRR5-15/3	1769.829	1770.922	-1186.277	0.556	1807.637	0.536	30	0.239	K.KGENDLPGLTDTEKPR.M
R5/RRR5-16/3	1770.910	1770.922	-6.894	0.519	1490.371	0.538	29	0.185	K.KGENDLPGLTDTEKPR.M
R5/RRR5-14/3	1770.387	1770.922	-869.920	0.470	678.038	0.486	25	0.098	K.KGENDLPGLTDTEKPR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1660.470	1660.893	-255.467	0.526	1826.434	0.564	26	0.258	R.IINEPTAAAIAYGIDK.K
R5/RRR5-5/2	1660.331	1660.893	-943.503	0.470	1606.637	0.553	24	0.224	R.IINEPTAAAIAYGIDK.K
R5/RRR5-5/2	1660.287	1660.893	-969.855	0.487	1504.883	0.522	24	0.206	R.IINEPTAAAIAYGIDK.K
R5/RRR5-1/2	1660.842	1660.893	-30.565	0.463	1342.107	0.565	23	0.197	R.IINEPTAAAIAYGIDK.K
R5/RRR5-6/2	1788.552	1789.066	-848.961	0.560	1225.929	0.590	24	0.192	R.IINEPTAAAIAYGIDKK.A
R5/RRR5-5/2	1660.514	1660.893	-228.916	0.495	1330.811	0.542	22	0.191	R.IINEPTAAAIAYGIDK.K
R5/RRR5-6/2	1789.366	1789.066	168.214	0.535	1168.722	0.543	23	0.177	R.IINEPTAAAIAYGIDKK.A
R5/RRR5-6/2	1788.775	1789.066	-163.014	0.563	912.697	0.559	21	0.160	R.IINEPTAAAIAYGIDKK.A
R5/RRR5-6/2	1661.629	1660.893	-159.056	0.380	1075.152	0.355	20	0.140	-.IINEPTAAAIAYGIDK.-
R5/RRR5-13/2	1844.385	1843.932	246.640	0.535	1859.347	0.555	23	0.259	R.GFLNSDQTLFSDNAGTR.L
R5/RRR5-12/2	988.827	989.102	-278.856	0.274	940.267	0.247	13	0.123	R.AGLDSLCPR.G
R5/RRR5-12/2	989.022	989.102	-80.605	0.354	698.764	0.278	13	0.122	R.AGLDSLCPR.G
R5/RRR5-12/2	989.286	989.102	186.868	0.198	511.588	0.242	11	0.115	R.AGLDSLCPR.G
R5/RRR5-13/2	1861.499	1859.933	-233.732	0.572	1976.980	0.602	23	0.290	R.DAGVNFFDNAEVYANGR.A
R5/RRR5-13/2	1860.242	1859.933	166.807	0.540	1737.962	0.562	22	0.243	R.DAGVNFFDNAEVYANGR.A
R5/RRR5-13/2	1218.914	1219.330	-342.285	0.343	909.714	0.238	16	0.122	K.LFWGGQGPNDK.G
R5/RRR5-13/2	1219.538	1219.330	170.311	0.357	926.432	0.227	16	0.121	K.LFWGGQGPNDK.G
R5/RRR5-17/2	1008.779	1008.107	-326.016	0.513	1988.156	0.369	16	0.230	R.FGELDVAEK.V
R5/RRR5-17/2	1007.495	1008.107	-1604.517	0.414	2037.567	0.309	16	0.222	R.FGELDVAEK.V
R5/RRR5-17/2	1007.827	1008.107	-278.702	0.469	1858.689	0.298	16	0.197	R.FGELDVAEK.V
R5/RRR5-16/2	1007.964	1008.107	-142.011	0.393	1477.315	0.268	14	0.155	R.FGELDVAEK.V
R5/RRR5-15/2	1007.969	1008.107	-136.908	0.325	1166.299	0.193	14	0.128	-.FGELDVAEK.-
R5/RRR5-17/3	1844.207	1845.091	-1024.575	0.462	1215.488	0.363	27	0.104	K.VFDEEKAPLLAAWAQR.F
R5/RRR5-9/2	1828.577	1829.048	-258.295	0.584	1592.735	0.634	23	0.243	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-10/2	1828.659	1829.048	-213.424	0.555	1488.821	0.622	23	0.227	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-9/2	1829.342	1829.048	161.259	0.573	1417.222	0.599	25	0.215	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-9/2	1828.426	1829.048	-889.708	0.558	1215.906	0.613	23	0.196	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-10/2	1828.495	1829.048	-852.110	0.583	1187.857	0.601	23	0.191	R.GIYAYGFEKPSAIQQR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/3	1829.226	1829.048	97.474	0.486	1510.187	0.538	30	0.187	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-9/3	1829.254	1829.048	112.833	0.445	1332.549	0.518	28	0.156	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-9/3	1829.244	1829.048	107.312	0.484	1293.064	0.479	29	0.140	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-10/3	1829.678	1829.048	-202.807	0.430	1238.561	0.470	26	0.132	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-10/2	925.822	926.138	-342.797	0.213	787.542	0.397	14	0.126	R.AVLPIISGR.-
R5/RRR5-10/2	925.354	926.138	-1934.169	0.202	678.374	0.373	13	0.121	R.AVLPIISGR.-
R5/RRR5-10/2	925.934	926.138	-221.500	0.218	559.332	0.368	13	0.120	R.AVLPIISGR.-
R5/RRR5-10/3	1829.218	1829.048	93.057	0.443	985.728	0.477	25	0.111	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-10/3	1828.423	1829.048	-891.391	0.345	1004.116	0.435	24	0.103	R.GIYAYGFEKPSAIQQR.A
R5/RRR5-19/2	1312.986	1313.502	-1158.445	0.474	1863.511	0.391	20	0.219	K.FM*EVISGTGDIK.A
R5/RRR5-19/2	1312.615	1313.502	-1442.334	0.411	1748.390	0.443	19	0.216	K.FM*EVISGTGDIK.A
R5/RRR5-19/2	1312.990	1313.502	-1155.457	0.453	1606.726	0.434	19	0.199	K.FM*EVISGTGDIK.A
R5/RRR5-19/2	1256.955	1257.484	-1219.589	0.552	1258.864	0.456	15	0.169	R.AM*DFLVELFR.N
R5/RRR5-19/2	1296.911	1297.503	-1231.304	0.451	986.202	0.517	16	0.159	K.FMEVISGTGDIK.A
R5/RRR5-19/2	1296.924	1297.503	-1221.002	0.234	847.994	0.273	16	0.122	K.FMEVISGTGDIK.A
R5/RRR5-18/2	1296.893	1297.503	-1245.010	0.205	646.953	0.094	14	0.113	K.FMEVISGTGDIK.A
R5/RRR5-12/2	1157.961	1158.244	-244.629	0.490	1783.121	0.482	19	0.231	K.VASDDLDPAVR.E
R5/RRR5-13/2	1158.211	1158.244	-28.184	0.499	1506.029	0.457	19	0.194	K.VASDDLDPAVR.E
R5/RRR5-12/2	1159.038	1158.244	-178.273	0.541	1357.977	0.502	19	0.189	K.VASDDLDPAVR.E
R5/RRR5-13/2	1157.946	1158.244	-257.955	0.446	1395.474	0.431	19	0.178	K.VASDDLDPAVR.E
R5/RRR5-12/2	1157.459	1158.244	-1546.575	0.349	1427.869	0.350	19	0.165	K.VASDDLDPAVR.E
R5/RRR5-13/2	1564.657	1563.888	-148.412	0.413	680.313	0.506	17	0.137	R.GLVMIHPYFLGTSK.V
R5/RRR5-13/2	1157.151	1158.244	-1814.259	0.326	1036.974	0.326	18	0.136	K.VASDDLDPAVR.E
R5/RRR5-8/3	1952.260	1952.120	71.827	0.453	2254.771	0.479	33	0.323	K.GLHSSLNHLANEFDQIR.S
R5/RRR5-9/2	1951.782	1952.120	-173.802	0.588	1594.626	0.586	23	0.230	K.GLHSSLNHLANEFDQIR.S
R5/RRR5-8/3	1952.241	1952.120	62.232	0.442	1794.655	0.487	31	0.222	K.GLHSSLNHLANEFDQIR.S
R5/RRR5-9/2	1426.320	1426.561	-168.987	0.541	1084.180	0.478	18	0.160	R.SSGGFWTWLTGAR.S
R5/RRR5-8/2	1426.208	1426.561	-248.238	0.455	1050.590	0.422	16	0.147	R.SSGGFWTWLTGAR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1951.305	1952.120	-932.757	0.392	572.709	0.397	18	0.124	K.GLHSSLNHLANEFDQIR.S
R5/RRR5-8/2	1426.148	1426.561	-290.144	0.274	591.711	0.241	14	0.115	-.SSGGFWTWLTGAR.-
R5/RRR5-13/2	1543.068	1543.651	-1029.009	0.504	1862.311	0.492	23	0.244	K.ITGCYVVGSAGSDEK.V
R5/RRR5-12/2	1543.353	1543.651	-193.459	0.491	1765.701	0.494	23	0.231	K.ITGCYVVGSAGSDEK.V
R5/RRR5-12/2	1353.539	1352.475	47.163	0.485	831.466	0.531	15	0.152	K.FGFDDAFNYKK.E
R5/RRR5-12/2	1353.410	1352.475	-48.635	0.352	531.728	0.375	11	0.121	K.FGFDDAFNYKK.E
R5/RRR5-13/3	1352.695	1352.475	162.768	0.484	867.415	0.412	23	0.093	K.FGFDDAFNYKK.E
R5/RRR5-13/3	1352.736	1352.475	193.717	0.425	580.260	0.384	20	0.083	K.FGFDDAFNYKK.E
R5/RRR5-3/3	1281.139	1281.443	-237.939	0.511	1501.785	0.470	23	0.164	K.HVVDDGLELRK.A
R5/RRR5-3/3	1281.539	1281.443	75.263	0.574	1264.140	0.530	23	0.151	K.HVVDDGLELRK.A
R5/RRR5-3/3	1281.018	1281.443	-332.726	0.526	1274.470	0.511	22	0.147	K.HVVDDGLELRK.A
R5/RRR5-3/2	1154.266	1153.270	-3.671	0.316	958.890	0.339	15	0.131	K.HVVDDGLELR.K
R5/RRR5-17/2	1203.995	1204.357	-301.477	0.475	1677.086	0.503	18	0.222	R.YVDIGIPANNK.G
R5/RRR5-17/2	1203.862	1204.357	-412.570	0.468	1490.090	0.543	18	0.210	R.YVDIGIPANNK.G
R5/RRR5-11/2	1203.468	1204.357	-1574.127	0.374	1554.569	0.414	18	0.188	R.YVDIGIPANNK.G
R5/RRR5-11/2	1204.194	1204.357	-135.798	0.477	1393.762	0.448	18	0.181	R.YVDIGIPANNK.G
R5/RRR5-17/2	1204.129	1204.357	-190.205	0.440	1254.668	0.462	17	0.171	R.YVDIGIPANNK.G
R5/RRR5-11/2	1203.572	1204.357	-1487.523	0.395	1362.884	0.382	17	0.165	R.YVDIGIPANNK.G
R5/RRR5-11/2	1465.968	1464.730	162.645	0.473	721.577	0.519	15	0.145	K.QSIGCLFWLLAR.M
R5/RRR5-12/2	1203.514	1204.357	-1536.020	0.322	1142.697	0.350	17	0.144	R.YVDIGIPANNK.G
R5/RRR5-11/2	1465.475	1464.730	-174.498	0.486	699.740	0.464	17	0.141	K.QSIGCLFWLLAR.M
R5/RRR5-18/2	1464.972	1464.730	165.764	0.442	477.437	0.472	15	0.134	K.QSIGCLFWLLAR.M
R5/RRR5-17/2	1465.891	1464.730	110.367	0.382	495.332	0.423	14	0.128	K.QSIGCLFWLLAR.M
R5/RRR5-18/2	1465.734	1464.730	2.539	0.370	232.524	0.285	12	0.118	-.QSIGCLFWLLAR.-
R5/RRR5-10/3	1187.308	1187.328	-16.935	0.428	2476.143	0.235	27	0.255	R.AKEEAEAVALR.A
R5/RRR5-9/2	1490.077	1489.696	256.067	0.504	1555.356	0.537	19	0.214	K.IASLQSEITSLQAK.G
R5/RRR5-10/2	1187.075	1187.328	-213.875	0.425	1429.375	0.237	17	0.145	R.AKEEAEAVALR.A
R5/RRR5-10/2	1490.193	1489.696	334.347	0.379	728.246	0.540	16	0.142	K.IASLQSEITSLQAK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/3	1187.357	1187.328	24.364	0.363	2069.086	0.120	25	0.138	R.AKEEAEAVALR.A
R5/RRR5-10/3	1187.374	1187.328	38.594	0.411	2088.248	0.102	26	0.134	R.AKEEAEAVALR.A
R5/RRR5-15/3	1469.704	1468.556	100.866	0.561	2085.857	0.350	27	0.214	R.HYNDISELSPHR.L
R5/RRR5-17/3	1468.356	1468.556	-136.892	0.523	2063.873	0.335	28	0.204	R.HYNDISELSPHR.L
R5/RRR5-15/3	1468.384	1468.556	-117.503	0.565	1945.092	0.365	27	0.194	R.HYNDISELSPHR.L
R5/RRR5-15/3	1468.455	1468.556	-69.097	0.620	1928.770	0.356	27	0.186	R.HYNDISELSPHR.L
R5/RRR5-16/3	1468.105	1468.556	-308.298	0.533	1536.050	0.371	25	0.137	R.HYNDISELSPHR.L
R5/RRR5-16/2	1423.872	1422.559	220.594	0.382	1048.162	0.338	17	0.136	K.IIAVCADDPEYR.H
R5/RRR5-16/3	1468.321	1468.556	-160.285	0.451	1117.844	0.342	23	0.094	R.HYNDISELSPHR.L
R5/RRR5-18/3	1468.169	1468.556	-264.252	0.387	949.918	0.289	21	0.078	R.HYNDISELSPHR.L
R5/RRR5-26/3	1544.665	1544.740	-48.844	0.469	1299.053	0.386	31	0.117	R.LRHGGSGGPADPVPVK.L
R5/RRR5-26/3	1544.855	1544.740	74.323	0.426	1004.559	0.416	28	0.100	R.LRHGGSGGPADPVPVK.L
R5/RRR5-26/3	1275.086	1275.396	-243.149	0.397	917.668	0.395	23	0.091	R.HGGSGGPADPVPVK.L
R5/RRR5-26/3	1275.347	1275.396	-38.470	0.328	801.175	0.263	20	0.068	-.HGGSGGPADPVPVK.-
R5/RRR5-26/3	1543.986	1544.740	-1139.782	0.360	617.333	0.262	23	0.067	-.LRHGGSGGPADPVPVK.-
R5/RRR5-25/3	1275.165	1275.396	-181.492	0.299	874.100	0.226	22	0.066	R.HGGSGGPADPVPVK.L
R5/RRR5-26/3	1275.311	1275.396	-66.265	0.291	869.692	0.218	21	0.065	R.HGGSGGPADPVPVK.L
R5/RRR5-21/2	1175.154	1174.286	-113.107	0.485	1484.316	0.474	15	0.194	R.DNFFFAGIDK.V
R5/RRR5-21/2	1175.117	1174.286	-144.472	0.485	1469.419	0.439	16	0.186	R.DNFFFAGIDK.V
R5/RRR5-21/2	1175.121	1174.286	-141.138	0.522	1280.868	0.475	15	0.176	R.DNFFFAGIDK.V
R5/RRR5-20/2	1173.578	1174.286	-1460.128	0.494	1042.336	0.498	14	0.161	R.DNFFFAGIDK.V
R5/RRR5-21/2	893.376	894.007	-1831.131	0.380	1035.998	0.365	13	0.139	K.GGEYAVGIK.N
R5/RRR5-20/2	1173.767	1174.286	-1298.733	0.305	635.710	0.262	13	0.120	R.DNFFFAGIDK.V
R5/RRR5-13/2	1826.571	1826.237	183.237	0.630	2816.800	0.602	28	0.452	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-12/2	1825.430	1826.237	-992.701	0.552	2778.261	0.529	28	0.417	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-13/3	1825.698	1826.237	-845.561	0.496	2250.355	0.578	35	0.366	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-12/2	1825.400	1826.237	-1009.486	0.549	2333.332	0.546	26	0.331	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-13/2	1810.666	1810.238	237.506	0.605	2144.838	0.605	25	0.315	K.VAILGAAGGIGQPLSLLMK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1809.321	1810.238	-1062.661	0.540	2284.507	0.520	26	0.314	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-13/2	1826.466	1826.237	125.598	0.600	2108.759	0.591	26	0.305	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-13/2	1810.645	1810.238	225.743	0.632	2140.307	0.564	26	0.300	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-12/2	1825.489	1826.237	-960.206	0.548	2106.493	0.553	25	0.293	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-12/2	1809.824	1810.238	-229.446	0.567	1929.149	0.556	24	0.265	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-13/2	1810.353	1810.238	63.667	0.547	1779.793	0.519	24	0.234	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-13/3	1825.783	1826.237	-249.193	0.473	1682.847	0.517	34	0.210	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-13/2	1809.734	1810.238	-833.409	0.442	1582.667	0.412	23	0.187	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-2/2	1811.787	1810.238	-249.606	0.401	1443.198	0.435	20	0.177	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-13/2	1810.423	1810.238	102.619	0.458	1351.136	0.426	21	0.167	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-13/2	1809.646	1810.238	-882.230	0.449	1321.508	0.416	21	0.163	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-12/2	1809.430	1810.238	-1002.104	0.380	1192.665	0.364	20	0.146	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-12/2	1809.799	1810.238	-243.183	0.383	1208.179	0.310	19	0.138	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-12/2	1808.816	1810.238	-1342.783	0.265	1316.563	0.181	20	0.130	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-2/2	1825.649	1826.237	-872.536	0.333	576.989	0.342	17	0.121	K.VAILGAAGGIGQPLSLLM*K.L
R5/RRR5-12/3	1809.235	1810.238	-1110.395	0.341	1198.106	0.379	31	0.106	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-13/3	1810.017	1810.238	-122.214	0.335	1133.308	0.359	27	0.096	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-13/3	1809.495	1810.238	-965.808	0.249	679.103	0.311	24	0.071	K.VAILGAAGGIGQPLSLLMK.L
R5/RRR5-22/2	1306.160	1306.450	-222.122	0.551	1688.305	0.567	19	0.240	R.TGEIVVFNVDGR.E
R5/RRR5-22/2	1306.103	1306.450	-266.190	0.510	1555.254	0.530	18	0.214	R.TGEIVVFNVDGR.E
R5/RRR5-22/2	1306.091	1306.450	-275.192	0.480	1511.626	0.477	17	0.197	R.TGEIVVFNVDGR.E
R5/RRR5-22/3	1755.749	1754.923	-99.387	0.419	735.531	0.477	24	0.091	K.VHERQESAEVDILTK.G
R5/RRR5-22/2	1147.059	1147.304	-213.758	0.513	995.028	0.506	18	0.162	K.IGSLVDVQTSK.D
R5/RRR5-22/2	1146.929	1147.304	-328.006	0.455	1037.481	0.479	18	0.159	K.IGSLVDVQTSK.D
R5/RRR5-22/2	1146.665	1147.304	-1433.856	0.455	980.776	0.477	18	0.155	K.IGSLVDVQTSK.D
R5/RRR5-22/3	1814.680	1815.018	-187.076	0.425	986.828	0.466	27	0.107	K.IGSLVDVQTSKDPEGLR.I
R5/RRR5-22/3	1815.323	1815.018	168.398	0.378	1000.910	0.446	29	0.103	K.IGSLVDVQTSKDPEGLR.I
R5/RRR5-12/2	1325.281	1325.538	-194.435	0.538	1559.556	0.592	18	0.229	R.YSGNFLVNLLGK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1325.307	1325.538	-174.476	0.498	1546.042	0.575	20	0.224	R.YSGNFLVNLLGK.W
R5/RRR5-12/2	1325.357	1325.538	-136.964	0.526	1601.092	0.543	19	0.223	R.YSGNFLVNLLGK.W
R5/RRR5-12/2	1325.467	1325.538	-53.540	0.548	1538.865	0.537	19	0.214	R.YSGNFLVNLLGK.W
R5/RRR5-12/2	1325.457	1325.538	-60.653	0.524	1381.193	0.562	18	0.202	R.YSGNFLVNLLGK.W
R5/RRR5-12/2	1325.038	1325.538	-378.166	0.514	1223.647	0.509	18	0.177	R.YSGNFLVNLLGK.W
R5/RRR5-12/2	1165.036	1165.278	-208.568	0.379	1150.471	0.294	17	0.138	K.TWIEVSGSSAK.D
R5/RRR5-12/2	1164.339	1165.278	-1670.563	0.326	1065.008	0.303	17	0.134	K.TWIEVSGSSAK.D
R5/RRR5-12/2	1164.594	1165.278	-1449.839	0.294	973.234	0.181	17	0.119	K.TWIEVSGSSAK.D
R5/RRR5-16/2	1263.740	1264.453	-1359.346	0.459	1613.385	0.464	18	0.205	K.DIGNAVYALISK.E
R5/RRR5-16/2	1264.551	1264.453	77.980	0.433	1482.377	0.512	18	0.201	K.DIGNAVYALISK.E
R5/RRR5-15/2	1263.993	1264.453	-364.368	0.516	1328.585	0.522	18	0.189	K.DIGNAVYALISK.E
R5/RRR5-16/2	1273.157	1273.420	-207.012	0.303	739.250	0.277	14	0.118	-.EGEWINGQVIK.-
R5/RRR5-8/2	1239.751	1240.388	-1324.616	0.489	1933.526	0.584	19	0.278	K.YGVTESTLLTR.N
R5/RRR5-7/2	1240.301	1240.388	-69.951	0.548	1868.354	0.589	19	0.271	K.YGVTESTLLTR.N
R5/RRR5-8/2	1241.204	1240.388	-148.913	0.592	1581.060	0.615	19	0.239	K.YGVTESTLLTR.N
R5/RRR5-7/2	1240.043	1240.388	-278.791	0.524	1568.196	0.590	18	0.230	K.YGVTESTLLTR.N
R5/RRR5-7/2	1240.032	1240.388	-288.075	0.513	1648.913	0.546	19	0.230	K.YGVTESTLLTR.N
R5/RRR5-8/2	1240.033	1240.388	-287.285	0.554	1475.159	0.569	19	0.216	K.YGVTESTLLTR.N
R5/RRR5-9/2	1240.085	1240.388	-244.818	0.441	1371.512	0.555	18	0.199	K.YGVTESTLLTR.N
R5/RRR5-7/2	1868.561	1869.154	-855.200	0.523	1397.902	0.515	25	0.193	R.LPIYVVQPQDGLDAIAR.N
R5/RRR5-8/2	1869.124	1869.154	-15.892	0.587	1273.144	0.545	24	0.187	R.LPIYVVQPQDGLDAIAR.N
R5/RRR5-8/2	1868.677	1869.154	-255.766	0.557	1215.604	0.500	24	0.173	R.LPIYVVQPQDGLDAIAR.N
R5/RRR5-7/2	1869.356	1869.154	108.422	0.566	1093.427	0.533	23	0.169	R.LPIYVVQPQDGLDAIAR.N
R5/RRR5-7/2	1868.673	1869.154	-257.929	0.547	1090.039	0.510	23	0.165	R.LPIYVVQPQDGLDAIAR.N
R5/RRR5-8/2	1868.490	1869.154	-892.911	0.528	1028.414	0.517	23	0.162	R.LPIYVVQPQDGLDAIAR.N
R5/RRR5-13/2	1241.216	1240.388	-139.047	0.350	495.444	0.450	16	0.133	K.YGVTESTLLTR.N
R5/RRR5-13/2	1241.368	1240.388	-16.137	0.291	660.737	0.391	17	0.129	K.YGVTESTLLTR.N
R5/RRR5-17/2	902.057	902.074	-18.881	0.438	1130.766	0.237	13	0.129	R.LSVQIVSR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1081.891	1082.191	-277.899	0.423	1040.557	0.138	12	0.114	R.LYQFEPER.L
R5/RRR5-14/2	1828.493	1828.059	238.070	0.483	1725.157	0.572	24	0.244	R.ELGDFPLPIALVENSGR.C
R5/RRR5-14/2	1828.320	1828.059	143.670	0.501	1544.966	0.562	23	0.218	R.ELGDFPLPIALVENSGR.C
R5/RRR5-14/2	1828.605	1828.059	-248.716	0.502	1508.860	0.567	23	0.215	R.ELGDFPLPIALVENSGR.C
R5/RRR5-14/2	1149.014	1149.237	-194.213	0.450	934.091	0.328	16	0.132	K.SSTVNSIVGER.V
R5/RRR5-14/2	1148.862	1149.237	-327.028	0.368	804.616	0.311	16	0.127	K.SSTVNSIVGER.V
R5/RRR5-6/2	1149.874	1149.237	-316.092	0.271	679.395	0.090	14	0.101	-.SSTVNSIVGER.-
R5/RRR5-21/2	1320.276	1320.430	-116.996	0.418	1529.205	0.497	18	0.202	R.DLSIGEEVGWSK.N
R5/RRR5-21/2	1183.918	1184.371	-383.428	0.431	721.817	0.489	17	0.143	K.NNPTLAAINKK.F
R5/RRR5-21/2	1185.005	1184.371	-309.511	0.431	714.273	0.418	17	0.136	K.NNPTLAAINKK.F
R5/RRR5-22/2	1403.768	1402.446	229.510	0.418	1189.116	0.418	15	0.157	R.VYEDEEEWFR.Q
R5/RRR5-22/2	1197.250	1197.325	-62.546	0.523	793.670	0.333	13	0.127	R.NQYEFLVQR.M
R5/RRR5-10/2	1983.663	1984.152	-247.113	0.548	2084.726	0.560	25	0.296	R.ELQDEGFDVQTAGYGLLK.T
R5/RRR5-10/2	1758.866	1759.984	-1208.003	0.444	766.187	0.496	18	0.139	R.DAVGGLDRDPFVSLLGK.L
R5/RRR5-10/2	1759.340	1759.984	-937.242	0.435	738.746	0.419	18	0.129	R.DAVGGLDRDPFVSLLGK.L
R5/RRR5-12/2	1551.124	1550.783	220.730	0.586	1851.754	0.461	20	0.233	K.TLFVINFDPINTR.T
R5/RRR5-12/2	1550.362	1550.783	-272.426	0.463	1546.498	0.318	19	0.168	K.TLFVINFDPINTR.T
R5/RRR5-12/2	1550.167	1550.783	-1045.464	0.356	1059.006	0.267	15	0.127	K.TLFVINFDPINTR.T
R5/RRR5-12/3	1332.765	1332.490	207.047	0.468	916.033	0.340	18	0.082	-.LRVEWTKEDR.-
R5/RRR5-24/2	1170.194	1170.256	-53.215	0.398	1001.601	0.440	17	0.150	K.LQGFAEDYAR.Q
R5/RRR5-24/2	1169.981	1170.256	-235.627	0.414	1020.700	0.413	17	0.148	K.LQGFAEDYAR.Q
R5/RRR5-24/2	1169.464	1170.256	-1537.294	0.435	729.018	0.428	16	0.138	K.LQGFAEDYAR.Q
R5/RRR5-21/2	1370.349	1369.546	-144.082	0.565	1460.572	0.550	20	0.210	K.HLLDETISDVVK.S
R5/RRR5-21/2	1369.323	1369.546	-163.146	0.541	1542.616	0.505	20	0.208	K.HLLDETISDVVK.S
R5/RRR5-21/2	1369.361	1369.546	-135.513	0.511	1443.516	0.498	20	0.196	K.HLLDETISDVVK.S
R5/RRR5-20/2	1368.929	1369.546	-1184.146	0.450	858.481	0.473	16	0.146	K.HLLDETISDVVK.S
R5/RRR5-21/2	1138.981	1139.197	-190.765	0.458	640.917	0.408	15	0.136	R.LIDDYNTER.K
R5/RRR5-21/2	1138.796	1139.197	-353.572	0.481	604.997	0.365	15	0.132	R.LIDDYNTER.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1138.474	1139.197	-1518.593	0.404	599.380	0.333	14	0.128	R.LIDDYNTER.K
R5/RRR5-20/2	1139.200	1139.197	2.406	0.337	646.979	0.323	15	0.127	R.LIDDYNTER.K
R5/RRR5-20/2	1184.204	1184.411	-174.795	0.422	2044.479	0.320	17	0.226	R.AALDVVELVVR.E
R5/RRR5-20/2	1184.261	1184.411	-126.608	0.489	1930.717	0.347	17	0.216	R.AALDVVELVVR.E
R5/RRR5-20/2	1183.706	1184.411	-1444.428	0.473	1138.327	0.419	17	0.156	R.AALDVVELVVR.E
R5/RRR5-20/2	1288.030	1288.474	-345.876	0.417	836.513	0.326	15	0.126	R.VQVDYTQPIPK.D
R5/RRR5-17/3	1888.271	1888.964	-899.710	0.518	1947.484	0.548	33	0.272	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-17/3	1888.179	1888.964	-948.581	0.535	1710.420	0.504	30	0.208	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-16/3	1889.802	1888.964	-85.956	0.531	1578.295	0.514	30	0.189	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-17/3	1889.645	1888.964	-169.352	0.531	1435.997	0.562	30	0.183	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-16/3	1888.444	1888.964	-807.335	0.553	1502.747	0.508	30	0.175	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-16/3	1888.963	1888.964	-0.889	0.518	1278.069	0.533	29	0.153	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-15/3	1888.941	1888.964	-12.168	0.538	1084.937	0.570	28	0.142	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-17/2	1831.184	1831.063	66.621	0.362	745.952	0.473	19	0.133	K.NAGVLALFDVDGTLTAPR.K
R5/RRR5-15/3	1888.643	1888.964	-170.868	0.494	1013.779	0.540	26	0.128	R.TIGHTVTSPDDTAEQCR.S
R5/RRR5-18/2	973.907	974.094	-192.549	0.402	1888.657	0.367	19	0.217	R.LSADAGAGALK.L
R5/RRR5-18/2	974.018	974.094	-77.635	0.446	1592.653	0.389	19	0.189	R.LSADAGAGALK.L
R5/RRR5-19/2	973.904	974.094	-195.441	0.336	1711.771	0.285	19	0.179	R.LSADAGAGALK.L
R5/RRR5-18/3	1256.457	1256.417	31.647	0.435	740.808	0.446	22	0.092	R.M*LGGGGVDGAIHR.A
R5/RRR5-18/3	1256.788	1256.417	295.988	0.386	648.106	0.364	22	0.080	R.M*LGGGGVDGAIHR.A
R5/RRR5-18/3	1256.374	1256.417	-34.716	0.296	429.604	0.358	19	0.078	R.M*LGGGGVDGAIHR.A
R5/RRR5-9/2	1261.060	1260.374	-250.261	0.529	1068.018	0.566	16	0.177	K.SKFDNLYGCR.H
R5/RRR5-8/2	1260.145	1260.374	-182.624	0.500	990.628	0.526	15	0.164	K.SKFDNLYGCR.H
R5/RRR5-9/2	1261.023	1260.374	-279.202	0.517	861.557	0.570	15	0.163	K.SKFDNLYGCR.H
R5/RRR5-8/2	1260.023	1260.374	-279.812	0.499	1028.077	0.504	15	0.162	K.SKFDNLYGCR.H
R5/RRR5-9/2	1261.023	1260.374	-279.590	0.496	942.837	0.494	15	0.156	K.SKFDNLYGCR.H
R5/RRR5-8/2	1259.869	1260.374	-1198.118	0.489	1087.809	0.410	16	0.152	K.SKFDNLYGCR.H
R5/RRR5-9/2	905.258	906.083	-2021.332	0.441	938.924	0.230	15	0.124	R.ATDVMLAGK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	905.533	906.083	-1716.633	0.392	895.432	0.196	15	0.121	R.ATDVMLAGK.V
R5/RRR5-9/2	921.544	922.082	-1674.355	0.249	640.092	0.217	13	0.118	R.ATDVM*LAGK.V
R5/RRR5-9/2	905.562	906.083	-1684.264	0.323	554.238	0.194	13	0.113	-.ATDVMLAGK.-
R5/RRR5-17/2	905.868	906.083	-238.031	0.177	657.552	0.190	11	0.111	-.ATDVMLAGK.-
R5/RRR5-7/2	1646.708	1647.806	-1277.566	0.347	2740.345	0.468	25	0.390	R.TEEELIEAIATATGAK.K
R5/RRR5-8/2	1647.769	1647.806	-22.188	0.444	1736.202	0.502	21	0.227	R.TEEELIEAIATATGAK.K
R5/RRR5-2/2	1649.039	1647.806	141.767	0.472	1717.797	0.502	21	0.224	R.TEEELIEAIATATGAK.K
R5/RRR5-7/2	1646.637	1647.806	-1321.417	0.337	1736.953	0.384	21	0.200	R.TEEELIEAIATATGAK.K
R5/RRR5-7/2	1646.784	1647.806	-1231.486	0.327	1710.080	0.364	22	0.193	R.TEEELIEAIATATGAK.K
R5/RRR5-8/2	1647.205	1647.806	-974.807	0.322	1521.437	0.414	19	0.182	R.TEEELIEAIATATGAK.K
R5/RRR5-8/2	1647.480	1647.806	-198.324	0.379	1521.615	0.384	21	0.178	R.TEEELIEAIATATGAK.K
R5/RRR5-7/3	1647.803	1647.806	-1.614	0.478	1594.130	0.443	29	0.170	R.TEEELIEAIATATGAK.K
R5/RRR5-7/3	1647.837	1647.806	19.116	0.496	1537.761	0.388	28	0.144	R.TEEELIEAIATATGAK.K
R5/RRR5-8/3	1647.071	1647.806	-1056.590	0.409	1368.493	0.419	26	0.133	R.TEEELIEAIATATGAK.K
R5/RRR5-1/2	1646.961	1647.806	-1123.708	0.316	930.687	0.298	17	0.125	R.TEEELIEAIATATGAK.K
R5/RRR5-7/3	1647.410	1647.806	-240.852	0.456	1289.900	0.408	30	0.122	R.TEEELIEAIATATGAK.K
R5/RRR5-13/2	1456.343	1456.625	-194.340	0.506	1853.655	0.537	21	0.255	R.NDVFQYLASSLAK.L
R5/RRR5-13/2	1456.519	1456.625	-72.596	0.560	1878.903	0.501	20	0.248	R.NDVFQYLASSLAK.L
R5/RRR5-13/2	1456.267	1456.625	-246.477	0.430	1114.722	0.493	17	0.163	R.NDVFQYLASSLAK.L
R5/RRR5-13/2	1153.094	1153.267	-150.842	0.469	900.707	0.390	15	0.139	K.YVVNDSTNIK.S
R5/RRR5-13/2	1153.112	1153.267	-134.488	0.394	1012.764	0.346	15	0.138	K.YVVNDSTNIK.S
R5/RRR5-13/2	1152.391	1153.267	-1633.274	0.334	1111.063	0.289	16	0.135	K.YVVNDSTNIK.S
R5/RRR5-6/2	1153.762	1153.267	430.355	0.259	576.643	0.184	11	0.114	K.YVVNDSTNIK.S
R5/RRR5-1/2	1879.028	1878.030	-0.952	0.499	728.539	0.568	20	0.148	R.ELPAGNFSPFFSDSYAK.S
R5/RRR5-1/2	1452.880	1452.638	167.396	0.415	686.770	0.452	16	0.133	R.AIISGTSSIYNLGR.K
R5/RRR5-2/2	1674.672	1675.736	-1236.567	0.362	550.279	0.506	17	0.129	K.NDDTVGHSVTNLSTSK.T
R5/RRR5-2/2	1453.720	1452.638	56.378	0.356	683.655	0.389	16	0.126	R.AIISGTSSIYNLGR.K
R5/RRR5-18/2	1650.216	1649.825	237.376	0.519	1811.028	0.594	25	0.262	R.CSYTVWPGALPGGGAR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1649.230	1649.825	-970.195	0.458	1691.385	0.580	24	0.241	R.CSYTVWPGALPGGGAR.L
R5/RRR5-16/2	1885.452	1885.070	203.020	0.554	1637.869	0.541	23	0.222	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-18/2	1649.318	1649.825	-916.769	0.417	1600.064	0.532	25	0.218	R.CSYTVWPGALPGGGAR.L
R5/RRR5-18/2	1649.375	1649.825	-273.516	0.432	1562.148	0.525	25	0.212	R.CSYTVWPGALPGGGAR.L
R5/RRR5-17/2	1649.373	1649.825	-274.704	0.451	1327.247	0.542	23	0.191	R.CSYTVWPGALPGGGAR.L
R5/RRR5-17/2	1885.625	1885.070	-236.975	0.564	1225.146	0.583	25	0.189	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-18/2	1884.518	1885.070	-825.869	0.535	1242.442	0.556	25	0.185	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-27/2	1884.488	1885.070	-841.995	0.482	1137.061	0.591	24	0.181	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-18/2	1884.449	1885.070	-862.803	0.500	1235.963	0.519	24	0.177	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-17/2	1884.462	1885.070	-855.911	0.492	1189.556	0.526	24	0.174	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-18/2	1885.386	1885.070	168.154	0.590	1008.673	0.604	23	0.173	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-17/2	1884.529	1885.070	-820.147	0.499	1159.393	0.534	24	0.173	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-17/2	1649.397	1649.825	-260.299	0.395	1116.071	0.495	22	0.163	R.CSYTVWPGALPGGGAR.L
R5/RRR5-18/2	1648.806	1649.825	-1228.491	0.301	1176.565	0.462	22	0.159	R.CSYTVWPGALPGGGAR.L
R5/RRR5-19/2	1884.465	1885.070	-854.220	0.473	946.890	0.504	22	0.152	R.LDPGQSWSISVAAGTPAAR.I
R5/RRR5-16/2	1649.230	1649.825	-970.047	0.381	412.137	0.405	16	0.123	-.CSYTVWPGALPGGGAR.-
R5/RRR5-15/2	1601.257	1601.767	-946.209	0.504	1634.697	0.516	24	0.220	K.NQGNPDLIGM*GALER.S
R5/RRR5-15/2	1036.137	1036.163	-25.714	0.416	743.116	0.333	13	0.128	K.VLDIYEQR.L
R5/RRR5-16/2	1215.062	1215.342	-230.714	0.570	1818.062	0.396	18	0.212	R.SLEGLQANVQR.L
R5/RRR5-21/2	1214.501	1215.342	-1519.906	0.470	1711.569	0.387	18	0.200	R.SLEGLQANVQR.L
R5/RRR5-16/2	1216.097	1215.342	-201.723	0.565	1648.003	0.408	18	0.196	R.SLEGLQANVQR.L
R5/RRR5-16/2	1215.022	1215.342	-263.673	0.532	1751.637	0.352	18	0.195	R.SLEGLQANVQR.L
R5/RRR5-15/2	1215.137	1215.342	-169.237	0.472	1696.534	0.368	18	0.194	R.SLEGLQANVQR.L
R5/RRR5-21/2	1214.893	1215.342	-370.326	0.558	1658.775	0.387	18	0.192	R.SLEGLQANVQR.L
R5/RRR5-15/2	1215.015	1215.342	-269.620	0.477	1622.928	0.378	18	0.188	R.SLEGLQANVQR.L
R5/RRR5-21/2	1215.039	1215.342	-249.562	0.537	1586.453	0.398	17	0.187	R.SLEGLQANVQR.L
R5/RRR5-15/2	1214.553	1215.342	-1476.897	0.414	1418.019	0.324	18	0.160	R.SLEGLQANVQR.L
R5/RRR5-20/2	1214.257	1215.342	-1722.078	0.431	708.124	0.320	18	0.127	-.SLEGLQANVQR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1215.028	1215.342	-258.533	0.480	736.010	0.293	18	0.125	-.SLEGLQANVQR.-
R5/RRR5-16/3	1456.996	1457.659	-1145.270	0.418	967.807	0.343	24	0.083	K.KYAPTIGISVDHR.R
R5/RRR5-18/2	1522.961	1522.773	124.159	0.419	2006.582	0.366	21	0.232	K.FVNDLHALISPPAK.G
R5/RRR5-18/2	1522.473	1522.773	-197.479	0.439	1544.589	0.434	18	0.190	K.FVNDLHALISPPAK.G
R5/RRR5-18/2	1559.381	1558.677	-190.842	0.502	864.448	0.519	21	0.153	K.FVSNGQPGPAQNVDK.S
R5/RRR5-18/2	1558.230	1558.677	-288.179	0.545	823.031	0.499	22	0.150	K.FVSNGQPGPAQNVDK.S
R5/RRR5-18/2	1559.135	1558.677	294.591	0.556	722.835	0.525	21	0.149	K.FVSNGQPGPAQNVDK.S
R5/RRR5-18/2	1558.122	1558.677	-1000.915	0.513	802.034	0.468	22	0.145	K.FVSNGQPGPAQNVDK.S
R5/RRR5-18/2	1522.084	1522.773	-1113.179	0.261	1029.844	0.337	16	0.132	K.FVNDLHALISPPAK.G
R5/RRR5-18/3	1522.567	1522.773	-135.717	0.500	712.562	0.493	27	0.100	K.FVNDLHALISPPAK.G
R5/RRR5-18/3	1521.899	1522.773	-1234.923	0.434	859.612	0.469	29	0.100	K.FVNDLHALISPPAK.G
R5/RRR5-18/3	1522.416	1522.773	-234.771	0.431	664.434	0.451	26	0.091	K.FVNDLHALISPPAK.G
R5/RRR5-15/2	1986.788	1987.198	-206.852	0.555	2693.273	0.590	28	0.427	K.GDVSDEAVAALDKIEAALAK.F
R5/RRR5-15/2	1986.484	1987.198	-865.267	0.536	2178.440	0.613	26	0.328	K.GDVSDEAVAALDKIEAALAK.F
R5/RRR5-15/3	1986.812	1987.198	-194.408	0.366	1060.527	0.365	36	0.092	K.GDVSDEAVAALDKIEAALAK.F
R5/RRR5-15/3	1986.962	1987.198	-118.786	0.277	939.705	0.267	32	0.069	K.GDVSDEAVAALDKIEAALAK.F
R5/RRR5-17/2	1489.317	1488.710	-264.684	0.497	1628.246	0.524	21	0.220	K.AQDTFTPISAVIPK.S
R5/RRR5-15/2	1488.710	1488.710	-0.379	0.474	1680.348	0.492	21	0.219	K.AQDTFTPISAVIPK.S
R5/RRR5-16/2	1488.533	1488.710	-119.153	0.436	1579.675	0.495	21	0.208	K.AQDTFTPISAVIPK.S
R5/RRR5-17/2	1488.394	1488.710	-213.023	0.449	1497.902	0.511	20	0.202	K.AQDTFTPISAVIPK.S
R5/RRR5-17/2	1488.454	1488.710	-172.791	0.412	1566.215	0.366	20	0.179	K.AQDTFTPISAVIPK.S
R5/RRR5-16/2	1488.202	1488.710	-1016.185	0.419	1395.382	0.443	19	0.177	K.AQDTFTPISAVIPK.S
R5/RRR5-16/2	1488.322	1488.710	-261.323	0.396	1284.146	0.475	19	0.173	K.AQDTFTPISAVIPK.S
R5/RRR5-15/2	1489.031	1488.710	216.203	0.429	877.753	0.456	18	0.144	K.AQDTFTPISAVIPK.S
R5/RRR5-15/2	1488.261	1488.710	-302.715	0.334	1112.452	0.314	18	0.137	K.AQDTFTPISAVIPK.S
R5/RRR5-16/2	1029.968	1030.202	-227.716	0.331	417.633	0.492	14	0.129	K.SAGLPWTLGK.A
R5/RRR5-26/2	1343.147	1343.513	-273.069	0.440	1356.086	0.507	19	0.188	R.LDEALATGLFHR.I
R5/RRR5-26/2	1342.942	1343.513	-1173.510	0.445	1093.493	0.483	17	0.161	R.LDEALATGLFHR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/2	1342.796	1343.513	-1282.506	0.420	973.633	0.472	17	0.151	R.LDEALATGLFHR.I
R5/RRR5-26/2	1209.161	1209.399	-197.198	0.449	882.118	0.496	18	0.151	R.GTVGVM*VTATTR.C
R5/RRR5-16/2	1208.735	1209.399	-1380.777	0.418	845.486	0.503	17	0.149	R.GTVGVM*VTATTR.C
R5/RRR5-26/2	1208.925	1209.399	-392.904	0.366	814.233	0.463	18	0.141	R.GTVGVM*VTATTR.C
R5/RRR5-26/3	1343.372	1343.513	-105.653	0.460	839.723	0.478	23	0.104	R.LDEALATGLFHR.I
R5/RRR5-15/3	1343.612	1343.513	73.837	0.462	688.399	0.478	22	0.100	R.LDEALATGLFHR.I
R5/RRR5-16/3	1343.861	1343.513	259.547	0.490	914.975	0.428	24	0.100	R.LDEALATGLFHR.I
R5/RRR5-25/3	1343.576	1343.513	47.321	0.498	779.252	0.451	23	0.099	R.LDEALATGLFHR.I
R5/RRR5-15/3	1343.356	1343.513	-117.275	0.443	587.036	0.460	21	0.096	R.LDEALATGLFHR.I
R5/RRR5-25/3	1343.654	1343.513	104.998	0.460	610.651	0.488	21	0.095	-.LDEALATGLFHR.-
R5/RRR5-16/3	1343.392	1343.513	-90.750	0.447	707.942	0.444	23	0.095	R.LDEALATGLFHR.I
R5/RRR5-16/3	1342.589	1343.513	-1437.425	0.439	618.618	0.451	22	0.095	R.LDEALATGLFHR.I
R5/RRR5-26/3	1343.413	1343.513	-74.617	0.435	929.400	0.383	25	0.092	R.LDEALATGLFHR.I
R5/RRR5-26/3	1343.686	1343.513	128.778	0.477	799.057	0.396	23	0.091	R.LDEALATGLFHR.I
R5/RRR5-25/3	1343.940	1343.513	318.293	0.395	710.495	0.354	21	0.084	R.LDEALATGLFHR.I
R5/RRR5-10/2	1230.242	1230.436	-158.003	0.493	1159.407	0.473	17	0.166	K.TLNDQIVVLSK.R
R5/RRR5-10/2	1295.330	1295.500	-131.348	0.304	1449.218	0.353	16	0.165	K.AAIDIVELCYK.A
R5/RRR5-10/2	1230.134	1230.436	-246.599	0.524	865.865	0.429	16	0.142	K.TLNDQIVVLSK.R
R5/RRR5-10/2	1295.226	1295.500	-211.803	0.159	984.024	0.199	14	0.116	K.AAIDIVELCYK.A
R5/RRR5-14/2	1580.304	1580.723	-265.947	0.503	1726.959	0.548	23	0.240	R.QSDVEAFFAAELPR.Y
R5/RRR5-14/2	1580.293	1580.723	-272.999	0.478	1465.041	0.528	21	0.203	R.QSDVEAFFAAELPR.Y
R5/RRR5-14/2	885.882	886.074	-217.970	0.448	1062.906	0.388	14	0.147	R.GLVGSAILR.H
R5/RRR5-14/2	885.478	886.074	-1808.194	0.416	1054.698	0.377	14	0.145	R.GLVGSAILR.H
R5/RRR5-14/2	886.025	886.074	-55.428	0.410	1054.995	0.352	14	0.141	R.GLVGSAILR.H
R5/RRR5-13/2	1725.341	1725.878	-893.973	0.475	1696.922	0.626	24	0.253	K.ATGTVVVSDSGDFATIGK.Y
R5/RRR5-13/2	1406.257	1405.664	-290.330	0.510	1579.461	0.447	19	0.198	K.FAADAVTLKDILK.K
R5/RRR5-13/2	1405.167	1405.664	-355.033	0.423	1526.320	0.440	19	0.190	K.FAADAVTLKDILK.K
R5/RRR5-7/2	1697.437	1697.953	-895.541	0.453	1928.478	0.570	22	0.273	R.VIEVGEVDPAAYPLPK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1697.427	1697.953	-901.605	0.470	1763.535	0.561	22	0.246	R.VIEVGEVDPAAYPLPK.T
R5/RRR5-7/2	1696.646	1697.953	-1363.508	0.314	1681.992	0.483	21	0.213	R.VIEVGEVDPAAYPLPK.T
R5/RRR5-7/2	1001.982	1002.107	-124.774	0.488	912.717	0.383	15	0.138	K.VGELVGGSQR.E
R5/RRR5-7/2	1001.997	1002.107	-110.476	0.484	843.578	0.361	14	0.132	K.VGELVGGSQR.E
R5/RRR5-16/2	1263.465	1263.514	-39.112	0.338	813.465	0.395	15	0.132	K.LVAPWFQVFR.G
R5/RRR5-16/2	1172.209	1172.314	-89.472	0.331	799.270	0.301	13	0.123	R.FWVSYIDNK.L
R5/RRR5-6/2	1929.806	1929.204	-206.933	0.566	2646.863	0.617	28	0.425	R.NLADPSSLAVATTNLISLK.G
R5/RRR5-6/2	1929.376	1929.204	89.058	0.568	2516.304	0.600	28	0.391	R.NLADPSSLAVATTNLISLK.G
R5/RRR5-6/2	1928.090	1929.204	-1099.757	0.324	1073.294	0.430	18	0.145	R.NLADPSSLAVATTNLISLK.G
R5/RRR5-5/2	1929.186	1929.204	-9.495	0.320	338.752	0.321	17	0.118	R.NLADPSSLAVATTNLISLK.G
R5/RRR5-12/2	1273.007	1273.418	-323.701	0.443	1456.728	0.439	17	0.183	K.GLIDINQDSLGK.A
R5/RRR5-12/2	1072.372	1072.283	83.277	0.437	1169.753	0.419	17	0.158	K.ISQATLALVR.N
R5/RRR5-12/2	1273.189	1273.418	-180.176	0.358	1242.738	0.387	17	0.155	K.GLIDINQDSLGK.A
R5/RRR5-12/2	1073.108	1072.283	-163.568	0.474	987.414	0.333	16	0.136	K.ISQATLALVR.N
R5/RRR5-12/2	1272.665	1273.418	-1381.560	0.247	860.344	0.358	14	0.126	K.GLIDINQDSLGK.A
R5/RRR5-26/2	1246.736	1247.385	-1326.916	0.401	1032.194	0.466	16	0.154	R.HLAHLEELER.Q
R5/RRR5-26/3	1314.335	1314.561	-172.962	0.529	1502.017	0.341	24	0.127	K.VREVPGYLKPR.L
R5/RRR5-25/3	1247.823	1247.385	351.396	0.554	1459.382	0.371	22	0.125	R.HLAHLEELER.Q
R5/RRR5-26/3	1314.458	1314.561	-78.775	0.504	1103.485	0.371	23	0.099	K.VREVPGYLKPR.L
R5/RRR5-26/3	1314.422	1314.561	-106.303	0.455	1189.665	0.322	22	0.095	-.VREVPGYLKPR.-
R5/RRR5-25/3	1247.633	1247.385	198.947	0.535	1194.313	0.310	23	0.091	R.HLAHLEELER.Q
R5/RRR5-25/3	1247.024	1247.385	-290.349	0.493	660.941	0.347	22	0.087	R.HLAHLEELER.Q
R5/RRR5-27/3	1247.046	1247.385	-273.113	0.332	275.812	0.322	20	0.086	-.HLAHLEELER.-
R5/RRR5-27/3	1247.153	1247.385	-186.574	0.537	483.063	0.304	20	0.085	-.HLAHLEELER.-
R5/RRR5-26/3	1247.361	1247.385	-19.800	0.543	801.230	0.323	22	0.085	R.HLAHLEELER.Q
R5/RRR5-27/3	1247.301	1247.385	-67.655	0.477	489.917	0.350	19	0.081	-.HLAHLEELER.-
R5/RRR5-26/3	1246.941	1247.385	-357.530	0.435	622.114	0.365	19	0.079	-.HLAHLEELER.-
R5/RRR5-26/3	1247.156	1247.385	-184.733	0.522	881.613	0.322	21	0.077	-.HLAHLEELER.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/3	1246.691	1247.385	-1363.509	0.451	1089.014	0.243	21	0.076	R.HLAHLEELER.Q
R5/RRR5-26/3	1247.519	1247.385	107.544	0.484	646.951	0.294	19	0.074	-.HLAHLEELER.-
R5/RRR5-27/3	1246.796	1247.385	-1278.844	0.430	472.272	0.363	19	0.069	-.HLAHLEELER.-
R5/RRR5-26/3	1247.287	1247.385	-79.140	0.417	613.455	0.293	19	0.066	-.HLAHLEELER.-
R5/RRR5-27/3	1247.159	1247.385	-182.230	0.461	447.129	0.342	18	0.063	-.HLAHLEELER.-
R5/RRR5-18/2	1728.548	1728.967	-243.210	0.509	1093.601	0.557	24	0.176	K.IWQVPETLSEEVLGK.M
R5/RRR5-18/2	1728.481	1728.967	-282.107	0.497	1052.461	0.547	24	0.171	K.IWQVPETLSEEVLGK.M
R5/RRR5-18/2	1729.398	1728.967	250.083	0.563	879.642	0.574	22	0.164	K.IWQVPETLSEEVLGK.M
R5/RRR5-18/2	1730.518	1728.967	-260.054	0.475	805.771	0.416	20	0.137	K.IWQVPETLSEEVLGK.M
R5/RRR5-4/2	1395.458	1395.690	-166.723	0.452	2023.124	0.441	18	0.252	R.VTIDLLEM*VFAK.G
R5/RRR5-4/2	1396.473	1395.690	-155.291	0.475	1748.653	0.443	19	0.216	R.VTIDLLEM*VFAK.G
R5/RRR5-4/2	1395.153	1395.690	-1104.546	0.439	1795.228	0.385	18	0.208	R.VTIDLLEM*VFAK.G
R5/RRR5-4/2	1395.642	1395.690	-34.319	0.460	1766.285	0.372	18	0.202	R.VTIDLLEM*VFAK.G
R5/RRR5-3/2	1395.269	1395.690	-302.321	0.424	1691.432	0.376	17	0.194	R.VTIDLLEM*VFAK.G
R5/RRR5-3/2	1396.263	1395.690	-306.227	0.447	1287.934	0.457	18	0.172	R.VTIDLLEM*VFAK.G
R5/RRR5-4/2	1395.049	1395.690	-1179.141	0.332	1609.367	0.282	17	0.168	R.VTIDLLEM*VFAK.G
R5/RRR5-3/2	1395.050	1395.690	-1179.053	0.492	1099.566	0.375	15	0.143	R.VTIDLLEM*VFAK.G
R5/RRR5-4/2	1394.784	1395.690	-1370.027	0.409	783.545	0.432	14	0.136	R.VTIDLLEM*VFAK.G
R5/RRR5-2/2	1380.484	1379.690	-149.765	0.369	489.086	0.282	13	0.120	R.VTIDLLEMVFAK.G
R5/RRR5-24/2	1225.123	1225.420	-243.011	0.426	1344.100	0.490	18	0.183	R.VLLINEGPNAGK.L
R5/RRR5-23/2	1131.768	1132.206	-388.763	0.389	1382.704	0.443	18	0.178	R.VLVDGPSSDSR.L
R5/RRR5-24/2	1133.163	1132.206	-38.747	0.416	1520.930	0.361	18	0.176	R.VLVDGPSSDSR.L
R5/RRR5-24/2	1132.124	1132.206	-73.066	0.393	1298.491	0.427	17	0.168	R.VLVDGPSSDSR.L
R5/RRR5-23/2	1225.146	1225.420	-223.618	0.467	1037.088	0.494	17	0.160	R.VLLINEGPNAGK.L
R5/RRR5-23/2	1225.237	1225.420	-149.055	0.482	1101.766	0.448	17	0.157	R.VLLINEGPNAGK.L
R5/RRR5-23/2	1225.313	1225.420	-87.194	0.445	1064.030	0.464	17	0.157	R.VLLINEGPNAGK.L
R5/RRR5-24/2	1225.326	1225.420	-76.201	0.438	986.354	0.451	16	0.149	R.VLLINEGPNAGK.L
R5/RRR5-23/2	1131.907	1132.206	-264.970	0.403	964.181	0.374	15	0.138	R.VLVDGPSSDSR.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1131.339	1132.206	-1655.440	0.271	1000.040	0.316	15	0.131	R.VLVDGPSSDSR.L
R5/RRR5-24/2	1224.978	1225.420	-361.380	0.360	577.593	0.398	14	0.127	R.VLLINEGPNAGK.L
R5/RRR5-24/2	1131.324	1132.206	-1668.882	0.262	905.888	0.234	15	0.121	R.VLVDGPSSDSR.L
R5/RRR5-11/2	1200.966	1201.398	-360.450	0.481	1695.512	0.569	20	0.241	K.VIALGDVTGSIR.N
R5/RRR5-11/2	1200.586	1201.398	-1513.659	0.423	1573.476	0.481	21	0.205	K.VIALGDVTGSIR.N
R5/RRR5-11/2	1119.030	1119.295	-237.931	0.441	914.943	0.319	15	0.126	K.TAVAAIPYGGAK.G
R5/RRR5-25/2	1100.368	1101.322	-1780.590	0.332	746.927	0.402	15	0.131	R.LVTIATLVDR.L
R5/RRR5-25/2	1100.913	1101.322	-371.966	0.377	406.766	0.437	12	0.125	-.LVTIATLVDR.-
R5/RRR5-25/3	995.590	995.158	435.994	0.450	1037.252	0.189	19	0.057	-.AQHAVLLDK.-
R5/RRR5-25/3	995.705	995.158	-455.457	0.383	668.693	0.176	17	0.030	-.AQHAVLLDK.-
R5/RRR5-26/3	996.133	995.158	-24.671	0.464	723.000	0.161	18	0.023	-.AQHAVLLDK.-
R5/RRR5-22/2	1187.081	1187.411	-278.853	0.474	1387.773	0.520	19	0.194	K.AVVVLGSSEVVK.G
R5/RRR5-22/2	1187.108	1187.411	-255.846	0.491	1352.131	0.521	19	0.191	K.AVVVLGSSEVVK.G
R5/RRR5-22/2	1336.223	1336.476	-189.819	0.487	1168.001	0.532	18	0.175	R.AVVVHADPDDLGK.G
R5/RRR5-22/2	1336.285	1336.476	-143.448	0.481	1180.551	0.503	18	0.170	R.AVVVHADPDDLGK.G
R5/RRR5-22/2	1187.065	1187.411	-292.574	0.484	1273.848	0.408	19	0.163	K.AVVVLGSSEVVK.G
R5/RRR5-21/2	1187.269	1187.411	-120.409	0.405	970.780	0.418	17	0.144	K.AVVVLGSSEVVK.G
R5/RRR5-21/2	1117.181	1117.275	-84.016	0.516	823.683	0.502	16	0.152	K.LEVSDVVVEK.A
R5/RRR5-21/2	1116.571	1117.275	-1530.179	0.385	741.656	0.461	16	0.140	K.LEVSDVVVEK.A
R5/RRR5-21/2	927.288	927.080	225.109	0.487	678.532	0.395	12	0.134	R.HLDTIISK.T
R5/RRR5-21/2	1116.510	1117.275	-1585.642	0.391	843.641	0.337	16	0.132	K.LEVSDVVVEK.A
R5/RRR5-21/2	926.601	927.080	-519.042	0.489	698.989	0.330	12	0.128	R.HLDTIISK.T
R5/RRR5-21/2	926.807	927.080	-295.932	0.448	627.496	0.314	12	0.126	R.HLDTIISK.T
R5/RRR5-16/2	843.982	843.994	-14.813	0.375	1430.056	0.394	15	0.172	K.VALVTGAGR.G
R5/RRR5-16/3	1440.744	1439.556	131.150	0.446	1084.852	0.324	24	0.088	-.RGADVVVNYGSSSK.-
R5/RRR5-14/2	1212.921	1212.424	411.182	0.533	1693.149	0.529	22	0.231	K.VLVIGGGDGGVLR.E
R5/RRR5-14/2	1212.968	1212.424	-376.970	0.542	1676.285	0.503	22	0.223	K.VLVIGGGDGGVLR.E
R5/RRR5-13/2	1212.251	1212.424	-143.279	0.454	1244.862	0.489	18	0.173	K.VLVIGGGDGGVLR.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1212.058	1212.424	-302.704	0.353	477.440	0.442	18	0.131	K.VLVIGGGDGGVLR.E
R5/RRR5-12/2	1212.041	1212.424	-317.255	0.271	474.003	0.416	13	0.123	K.VLVIGGGDGGVLR.E
R5/RRR5-11/2	1212.836	1212.424	340.849	0.272	700.102	0.272	16	0.120	K.VLVIGGGDGGVLR.E
R5/RRR5-11/2	1211.717	1212.424	-1412.654	0.238	790.401	0.219	16	0.117	K.VLVIGGGDGGVLR.E
R5/RRR5-14/3	1356.580	1356.595	-11.076	0.439	1013.572	0.410	26	0.099	R.VSLHIGDGVAFLK.N
R5/RRR5-14/3	1356.834	1356.595	176.529	0.510	805.449	0.424	23	0.092	R.VSLHIGDGVAFLK.N
R5/RRR5-26/2	1500.153	1499.673	321.088	0.520	1163.754	0.532	21	0.178	R.LM*GFFPNDSEVAR.Y
R5/RRR5-26/2	1500.289	1499.673	-257.057	0.509	882.949	0.557	19	0.161	R.LM*GFFPNDSEVAR.Y
R5/RRR5-26/2	1499.172	1499.673	-1004.360	0.462	1000.728	0.455	20	0.153	R.LM*GFFPNDSEVAR.Y
R5/RRR5-26/2	1354.148	1354.536	-287.487	0.477	765.175	0.528	15	0.148	K.VVGNFSALDYLR.L
R5/RRR5-27/2	1498.860	1499.673	-1213.196	0.399	719.719	0.497	18	0.142	R.LM*GFFPNDSEVAR.Y
R5/RRR5-26/2	1353.692	1354.536	-1365.885	0.428	779.743	0.450	15	0.138	K.VVGNFSALDYLR.L
R5/RRR5-26/2	1353.991	1354.536	-1144.220	0.336	810.439	0.439	15	0.136	K.VVGNFSALDYLR.L
R5/RRR5-26/2	1483.304	1483.674	-249.826	0.368	484.115	0.364	15	0.125	R.LMGFFPNDSEVAR.Y
R5/RRR5-27/2	1353.883	1354.536	-1224.074	0.204	236.712	0.395	12	0.119	K.VVGNFSALDYLR.L
R5/RRR5-26/2	1482.995	1483.674	-1135.585	0.345	564.523	0.218	16	0.118	R.LMGFFPNDSEVAR.Y
R5/RRR5-15/2	1609.613	1609.850	-147.994	0.433	827.349	0.462	19	0.143	K.STSSIFPLQNVFIR.K
R5/RRR5-15/2	1610.076	1609.850	140.407	0.457	669.511	0.491	18	0.140	K.STSSIFPLQNVFIR.K
R5/RRR5-16/2	1609.293	1609.850	-970.535	0.367	832.024	0.368	19	0.132	K.STSSIFPLQNVFIR.K
R5/RRR5-15/2	1609.768	1609.850	-51.158	0.423	572.720	0.442	16	0.130	K.STSSIFPLQNVFIR.K
R5/RRR5-10/3	1756.545	1755.873	-187.203	0.524	1798.353	0.558	31	0.248	R.TAVHQGIGHQTYAESR.G
R5/RRR5-10/3	1755.363	1755.873	-862.578	0.520	1848.450	0.507	31	0.238	R.TAVHQGIGHQTYAESR.G
R5/RRR5-10/3	1755.731	1755.873	-80.664	0.514	1721.431	0.518	29	0.218	R.TAVHQGIGHQTYAESR.G
R5/RRR5-10/2	1757.621	1755.873	-143.613	0.393	1092.982	0.576	19	0.171	R.TAVHQGIGHQTYAESR.G
R5/RRR5-10/2	1755.283	1755.873	-908.228	0.288	576.678	0.359	16	0.118	R.TAVHQGIGHQTYAESR.G
R5/RRR5-10/3	1773.629	1774.094	-263.095	0.404	997.263	0.509	28	0.116	R.APEYLALNDKVISLVK.G
R5/RRR5-10/3	1774.163	1774.094	38.890	0.419	832.885	0.550	26	0.112	R.APEYLALNDKVISLVK.G
R5/RRR5-24/2	1307.038	1307.502	-356.224	0.456	1242.909	0.473	19	0.172	R.LM*GSLTNTQGLR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1306.936	1307.502	-1202.014	0.452	996.161	0.492	18	0.157	R.LM*GSLTNTQGLR.F
R5/RRR5-24/2	1307.196	1307.502	-234.793	0.446	1048.895	0.468	18	0.157	R.LM*GSLTNTQGLR.F
R5/RRR5-24/2	747.655	747.908	-339.822	0.424	819.133	0.355	11	0.132	-.FGVVVAR.-
R5/RRR5-24/2	748.016	747.908	144.840	0.414	769.020	0.356	11	0.132	R.FGVVVAR.F
R5/RRR5-24/2	747.887	747.908	-28.504	0.432	750.470	0.352	11	0.132	R.FGVVVAR.F
R5/RRR5-23/2	1220.046	1220.357	-255.763	0.472	881.188	0.519	20	0.157	K.LNPAADAGSIYK.T
R5/RRR5-22/2	1220.009	1220.357	-286.079	0.476	867.818	0.518	20	0.157	K.LNPAADAGSIYK.T
R5/RRR5-22/2	1219.968	1220.357	-319.408	0.473	789.591	0.522	19	0.153	K.LNPAADAGSIYK.T
R5/RRR5-20/2	1220.996	1220.357	-296.678	0.500	697.106	0.536	18	0.151	K.LNPAADAGSIYK.T
R5/RRR5-22/2	1221.016	1220.357	-280.027	0.442	736.607	0.512	19	0.149	K.LNPAADAGSIYK.T
R5/RRR5-23/2	1220.137	1220.357	-180.986	0.416	715.582	0.480	19	0.144	K.LNPAADAGSIYK.T
R5/RRR5-21/2	1220.015	1220.357	-280.658	0.431	711.563	0.445	19	0.141	K.LNPAADAGSIYK.T
R5/RRR5-21/2	1219.503	1220.357	-1524.716	0.361	564.726	0.532	17	0.140	K.LNPAADAGSIYK.T
R5/RRR5-20/2	1219.823	1220.357	-1261.039	0.380	721.737	0.459	18	0.140	K.LNPAADAGSIYK.T
R5/RRR5-21/2	1219.727	1220.357	-1340.238	0.409	615.772	0.441	18	0.137	K.LNPAADAGSIYK.T
R5/RRR5-23/2	1219.332	1220.357	-1665.810	0.308	611.409	0.449	18	0.133	K.LNPAADAGSIYK.T
R5/RRR5-19/2	1220.227	1220.357	-106.521	0.329	436.617	0.424	16	0.130	K.LNPAADAGSIYK.T
R5/RRR5-20/2	1219.884	1220.357	-388.684	0.293	451.166	0.305	15	0.123	K.LNPAADAGSIYK.T
R5/RRR5-9/2	1093.050	1093.215	-151.287	0.495	1896.861	0.492	18	0.249	K.IGYDNAAAVAK.K
R5/RRR5-10/2	1092.306	1093.215	-1752.707	0.339	1817.518	0.419	18	0.218	K.IGYDNAAAVAK.K
R5/RRR5-10/2	1093.135	1093.215	-72.872	0.474	1596.959	0.469	17	0.205	K.IGYDNAAAVAK.K
R5/RRR5-10/2	1237.418	1236.316	82.658	0.479	1632.694	0.447	18	0.205	R.SLQNFDIGGER.E
R5/RRR5-9/2	1092.750	1093.215	-426.958	0.427	1528.321	0.486	17	0.201	K.IGYDNAAAVAK.K
R5/RRR5-10/2	1093.023	1093.215	-176.158	0.262	969.484	0.147	16	0.117	K.IGYDNAAAVAK.K
R5/RRR5-14/2	1545.322	1545.639	-205.334	0.507	1207.090	0.443	20	0.164	K.FNDLSTNHNNQLK.T
R5/RRR5-14/2	1545.322	1545.639	-205.334	0.529	1249.696	0.416	21	0.163	K.FNDLSTNHNNQLK.T
R5/RRR5-14/2	1545.134	1545.639	-976.603	0.509	1255.656	0.397	19	0.159	K.FNDLSTNHNNQLK.T
R5/RRR5-14/3	1673.408	1673.812	-241.866	0.468	1154.974	0.492	27	0.128	K.KFNDLSTNHNNQLK.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/3	1674.730	1673.812	-48.597	0.490	899.748	0.421	26	0.096	K.KFNDLSTNHNNQLK.T
R5/RRR5-14/3	1673.909	1673.812	58.389	0.472	805.383	0.424	25	0.092	K.KFNDLSTNHNNQLK.T
R5/RRR5-25/2	1208.337	1207.361	-19.719	0.366	610.007	0.512	15	0.136	K.IVNAGSFTIER.E
R5/RRR5-25/2	1123.950	1124.271	-286.454	0.325	678.609	0.369	14	0.126	R.DPNVLFAGYK.L
R5/RRR5-25/2	1123.881	1124.271	-348.024	0.250	425.814	0.274	12	0.105	-.DPNVLFAGYK.-
R5/RRR5-12/3	1513.733	1513.812	-52.431	0.508	2717.735	0.473	34	0.443	K.HLGVVGLGGLGHLGVK.F
R5/RRR5-12/3	1513.369	1513.812	-293.575	0.565	2507.165	0.519	34	0.401	K.HLGVVGLGGLGHLGVK.F
R5/RRR5-12/3	1513.400	1513.812	-273.182	0.544	2115.037	0.501	32	0.290	K.HLGVVGLGGLGHLGVK.F
R5/RRR5-11/3	1513.958	1513.812	96.179	0.564	1916.994	0.524	32	0.255	K.HLGVVGLGGLGHLGVK.F
R5/RRR5-11/3	1513.607	1513.812	-135.793	0.478	1673.551	0.424	29	0.175	K.HLGVVGLGGLGHLGVK.F
R5/RRR5-14/2	1558.138	1558.804	-1072.491	0.468	1425.338	0.521	21	0.196	R.LFYGPGGPYALFAGK.D
R5/RRR5-14/2	1558.301	1558.804	-967.330	0.457	1304.769	0.479	20	0.176	R.LFYGPGGPYALFAGK.D
R5/RRR5-16/2	1560.060	1558.804	164.686	0.465	1065.609	0.498	19	0.160	R.LFYGPGGPYALFAGK.D
R5/RRR5-14/2	1557.425	1558.804	-1531.934	0.337	1384.055	0.314	21	0.154	R.LFYGPGGPYALFAGK.D
R5/RRR5-16/2	1560.177	1558.804	240.246	0.465	1049.720	0.455	18	0.152	R.LFYGPGGPYALFAGK.D
R5/RRR5-14/2	1152.899	1153.227	-285.740	0.418	827.274	0.373	14	0.131	K.GQIYDVSQSR.L
R5/RRR5-14/2	1501.546	1501.744	-132.064	0.449	1956.988	0.332	19	0.216	R.VQVCVAEQDVLLK.E
R5/RRR5-14/2	1480.210	1480.603	-266.147	0.212	934.624	0.378	17	0.127	R.FVFPETSGLDDPR.V
R5/RRR5-18/2	1298.123	1298.427	-234.815	0.441	1176.952	0.555	21	0.179	K.EAAAASAPLPSQGK.T
R5/RRR5-18/2	1298.049	1298.427	-291.989	0.352	872.665	0.512	19	0.147	K.EAAAASAPLPSQGK.T
R5/RRR5-10/2	1232.030	1231.381	-285.573	0.502	1272.011	0.547	17	0.189	R.SIVQELLGDTR.I
R5/RRR5-10/2	1759.683	1760.067	-218.937	0.504	1216.905	0.362	22	0.148	R.ISQAITNVVIPTFDIK.L
R5/RRR5-10/2	1231.031	1231.381	-285.407	0.368	1056.422	0.399	17	0.146	R.SIVQELLGDTR.I
R5/RRR5-9/2	1230.544	1231.381	-1497.205	0.411	495.443	0.437	14	0.131	R.SIVQELLGDTR.I
R5/RRR5-10/2	1230.450	1231.381	-1573.939	0.292	550.796	0.408	15	0.126	R.SIVQELLGDTR.I
R5/RRR5-20/2	1333.810	1334.500	-1270.217	0.429	795.884	0.364	15	0.129	R.IEVTDPASFQVK.E
R5/RRR5-20/2	1334.025	1334.500	-357.171	0.404	764.290	0.376	14	0.128	R.IEVTDPASFQVK.E
R5/RRR5-14/2	1785.251	1786.020	-994.142	0.504	1427.704	0.531	21	0.198	R.TGNTFLGSLLWVDYAK.W

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1785.915	1786.020	-59.206	0.497	1227.772	0.503	20	0.173	R.TGNTFLGSLLWVDYAK.W
R5/RRR5-22/2	1382.218	1381.475	-186.337	0.549	1494.200	0.532	21	0.209	R.WVGAAVDFSEGSR.A
R5/RRR5-22/2	1381.163	1381.475	-226.903	0.479	1492.845	0.529	21	0.207	R.WVGAAVDFSEGSR.A
R5/RRR5-22/2	1381.055	1381.475	-305.291	0.544	1482.122	0.531	21	0.207	R.WVGAAVDFSEGSR.A
R5/RRR5-22/3	1982.134	1982.204	-35.623	0.475	1678.139	0.370	29	0.160	K.YGAKPDAETLDM*LNTVAR.Q
R5/RRR5-22/3	1981.992	1982.204	-107.716	0.446	1496.122	0.414	28	0.148	K.YGAKPDAETLDM*LNTVAR.Q
R5/RRR5-22/3	1981.531	1982.204	-847.107	0.413	1011.016	0.334	27	0.084	K.YGAKPDAETLDM*LNTVAR.Q
R5/RRR5-24/2	1432.134	1432.567	-302.866	0.460	1537.606	0.488	20	0.201	R.VTGGGHTSQVYAVR.Q
R5/RRR5-24/2	1432.209	1432.567	-250.532	0.473	868.920	0.487	20	0.149	R.VTGGGHTSQVYAVR.Q
R5/RRR5-24/3	1433.543	1432.567	-16.460	0.485	652.672	0.495	27	0.099	R.VTGGGHTSQVYAVR.Q
R5/RRR5-24/3	1432.921	1432.567	247.730	0.430	541.039	0.469	25	0.092	R.VTGGGHTSQVYAVR.Q
R5/RRR5-24/3	1432.789	1432.567	155.976	0.429	679.719	0.444	27	0.092	R.VTGGGHTSQVYAVR.Q
R5/RRR5-23/3	1432.703	1432.567	95.481	0.416	494.084	0.422	22	0.087	R.VTGGGHTSQVYAVR.Q
R5/RRR5-24/3	1622.967	1622.894	45.285	0.401	1046.101	0.299	27	0.081	K.VNGRPLSLVEPATLR.Y
R5/RRR5-24/3	1622.784	1622.894	-67.769	0.336	731.089	0.281	23	0.069	-.VNGRPLSLVEPATLR.-
R5/RRR5-17/2	926.054	926.138	-91.242	0.454	980.096	0.386	12	0.142	R.SQLIVLPR.N
R5/RRR5-17/2	925.543	926.138	-1729.260	0.403	1067.071	0.356	12	0.142	R.SQLIVLPR.N
R5/RRR5-16/2	925.838	926.138	-325.070	0.374	1061.558	0.355	12	0.141	R.SQLIVLPR.N
R5/RRR5-17/3	1501.619	1501.626	-4.502	0.406	684.988	0.489	21	0.095	K.NTAETVPFEHVTR.I
R5/RRR5-17/3	1501.419	1501.626	-138.077	0.425	703.785	0.419	21	0.087	K.NTAETVPFEHVTR.I
R5/RRR5-17/3	1501.488	1501.626	-92.203	0.434	715.971	0.414	21	0.087	K.NTAETVPFEHVTR.I
R5/RRR5-13/2	1279.204	1279.421	-170.428	0.528	1026.421	0.558	20	0.173	R.LVGDVDFAEVSK.V
R5/RRR5-13/2	1280.174	1279.421	-193.061	0.569	883.071	0.594	19	0.169	R.LVGDVDFAEVSK.V
R5/RRR5-13/2	1466.467	1466.834	-250.690	0.393	1160.379	0.501	21	0.168	R.SNIVGLPVSLLLLK.A
R5/RRR5-13/2	1466.425	1466.834	-279.586	0.378	887.706	0.494	19	0.148	R.SNIVGLPVSLLLLK.A
R5/RRR5-13/2	1465.525	1466.834	-1580.379	0.351	806.843	0.444	18	0.138	R.SNIVGLPVSLLLLK.A
R5/RRR5-13/2	1466.625	1466.834	-142.638	0.342	704.091	0.398	16	0.129	R.SNIVGLPVSLLLLK.A
R5/RRR5-14/2	1466.199	1466.834	-1118.030	0.313	658.242	0.386	16	0.126	R.SNIVGLPVSLLLLK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1279.109	1279.421	-244.623	0.301	564.376	0.271	15	0.119	R.LVGDVDFAEVSK.V
R5/RRR5-2/2	1466.322	1466.834	-1034.187	0.222	646.484	0.191	14	0.114	-.SNIVGLPVSLLLLK.-
R5/RRR5-26/2	1031.773	1032.173	-389.060	0.354	1228.355	0.378	17	0.154	K.AVQASELVSK.H
R5/RRR5-25/2	1032.140	1032.173	-32.457	0.450	893.708	0.511	14	0.153	K.AVQASELVSK.H
R5/RRR5-25/2	1031.507	1032.173	-1620.165	0.317	775.028	0.323	14	0.125	K.AVQASELVSK.H
R5/RRR5-26/3	1505.386	1504.716	-219.696	0.466	1030.137	0.399	26	0.100	K.NKQHVVQPPTVEK.C
R5/RRR5-26/3	1504.293	1504.716	-282.324	0.474	729.919	0.375	23	0.086	K.NKQHVVQPPTVEK.C
R5/RRR5-25/3	1504.823	1504.716	71.581	0.472	775.911	0.361	24	0.083	-.NKQHVVQPPTVEK.-
R5/RRR5-26/3	1503.687	1504.716	-1353.614	0.431	575.552	0.368	21	0.081	-.NKQHVVQPPTVEK.-
R5/RRR5-25/3	1504.373	1504.716	-228.349	0.430	648.955	0.295	22	0.078	K.NKQHVVQPPTVEK.C
R5/RRR5-25/3	1503.319	1504.716	-1599.133	0.463	431.422	0.400	18	0.077	-.NKQHVVQPPTVEK.-
R5/RRR5-23/2	1648.244	1648.713	-285.292	0.556	1115.928	0.495	22	0.164	K.DATADFNDIGHTATAK.E
R5/RRR5-23/2	1647.778	1648.713	-1177.839	0.505	1135.468	0.490	21	0.164	K.DATADFNDIGHTATAK.E
R5/RRR5-23/2	1158.887	1158.285	-344.801	0.432	931.646	0.420	15	0.142	K.AVYSFQEVSK.H
R5/RRR5-17/2	1518.580	1518.721	-93.333	0.523	2538.205	0.575	24	0.385	K.AAAVGANSQAAQSMLK.Q
R5/RRR5-17/2	1535.699	1534.721	-14.300	0.541	1741.447	0.554	22	0.241	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-17/2	1518.202	1518.721	-1003.928	0.519	1628.113	0.566	22	0.229	K.AAAVGANSQAAQSMLK.Q
R5/RRR5-17/3	1534.008	1534.721	-1119.599	0.473	1750.335	0.527	29	0.229	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-17/3	1535.602	1534.721	-77.696	0.576	1554.068	0.598	28	0.218	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-17/2	1535.784	1534.721	41.427	0.542	1405.223	0.578	20	0.205	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-16/2	1535.857	1534.721	89.256	0.434	837.748	0.533	20	0.151	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-15/2	1535.948	1534.721	148.399	0.428	560.192	0.520	17	0.137	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-16/2	1535.865	1534.721	94.039	0.374	382.165	0.550	17	0.134	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-19/2	1536.112	1534.721	255.667	0.204	184.190	0.463	16	0.121	K.AAAVGANSQAAQSM*LK.Q
R5/RRR5-5/2	1240.276	1240.434	-128.294	0.374	1324.487	0.515	18	0.182	R.VPATNILLGEGR.G
R5/RRR5-5/2	1356.172	1356.550	-279.475	0.265	945.347	0.250	17	0.121	R.LLVLEAADQLDR.H
R5/RRR5-26/2	1486.197	1486.719	-1027.301	0.424	1213.454	0.422	19	0.159	R.GIM*QPVPVSDALSR.F
R5/RRR5-26/2	1471.600	1470.720	-81.670	0.429	770.670	0.478	19	0.142	R.GIMQPVPVSDALSR.F

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/2	1486.180	1486.719	-1038.434	0.396	1072.974	0.358	19	0.141	R.GIM*QPVPVSDALSR.F
R5/RRR5-26/2	1486.080	1486.719	-1106.476	0.362	1091.952	0.328	19	0.138	R.GIM*QPVPVSDALSR.F
R5/RRR5-26/2	1038.907	1039.148	-231.967	0.299	855.900	0.289	16	0.125	R.FAGGAPEM*SR.A
R5/RRR5-26/2	1038.618	1039.148	-1476.651	0.318	633.834	0.307	15	0.123	R.FAGGAPEM*SR.A
R5/RRR5-26/2	1038.886	1039.148	-252.714	0.310	583.168	0.311	15	0.122	-.FAGGAPEM*SR.-
R5/RRR5-7/2	1298.190	1297.526	-259.608	0.404	757.727	0.562	20	0.152	K.VVGVPVSLNGDLK.N
R5/RRR5-7/2	1298.058	1297.526	-361.691	0.430	791.354	0.519	22	0.151	K.VVGVPVSLNGDLK.N
R5/RRR5-7/2	820.416	820.959	-1886.598	0.413	864.221	0.478	13	0.149	R.VGVVFSGR.Q
R5/RRR5-7/2	1298.324	1297.526	-156.130	0.444	629.269	0.539	20	0.146	K.VVGVPVSLNGDLK.N
R5/RRR5-7/2	820.615	820.959	-421.136	0.398	784.995	0.468	13	0.143	R.VGVVFSGR.Q
R5/RRR5-6/2	820.946	820.959	-16.049	0.418	615.736	0.518	11	0.142	R.VGVVFSGR.Q
R5/RRR5-14/2	1218.241	1217.266	-21.368	0.483	1217.651	0.475	16	0.171	R.DLGYLDDSYR.A
R5/RRR5-14/2	1217.052	1217.266	-176.515	0.380	910.002	0.399	15	0.139	R.DLGYLDDSYR.A
R5/RRR5-14/3	1630.648	1629.885	-145.493	0.469	888.657	0.497	25	0.105	K.AAVIGLLYEVGRPDR.F
R5/RRR5-18/2	1790.630	1791.083	-253.854	0.553	1102.483	0.593	23	0.182	K.LLAVPLFELYDNVQR.Y
R5/RRR5-18/2	1559.316	1559.792	-306.117	0.446	974.865	0.399	20	0.142	R.YGPVISTIPQQLSR.F
R5/RRR5-18/2	1559.355	1559.792	-281.062	0.458	840.668	0.381	19	0.134	R.YGPVISTIPQQLSR.F
R5/RRR5-18/2	1559.059	1559.792	-1114.736	0.448	869.487	0.364	19	0.133	R.YGPVISTIPQQLSR.F
R5/RRR5-16/3	1819.107	1819.141	-18.827	0.545	1159.488	0.572	28	0.151	K.LPNNAVAPSLFFFRPK.N
R5/RRR5-16/3	1819.295	1819.141	84.647	0.535	1226.512	0.544	29	0.150	K.LPNNAVAPSLFFFRPK.N
R5/RRR5-15/3	1818.950	1819.141	-105.459	0.514	1068.049	0.506	30	0.125	K.LPNNAVAPSLFFFRPK.N
R5/RRR5-16/2	1436.495	1437.690	-1532.197	0.294	1099.716	0.203	17	0.122	R.YLMIVEAIGSQGR.Y
R5/RRR5-15/3	1818.943	1819.141	-109.397	0.521	977.817	0.507	27	0.118	K.LPNNAVAPSLFFFRPK.N
R5/RRR5-15/3	1818.718	1819.141	-233.616	0.468	998.403	0.497	28	0.117	K.LPNNAVAPSLFFFRPK.N
R5/RRR5-16/3	1819.230	1819.141	48.812	0.542	889.141	0.493	28	0.110	K.LPNNAVAPSLFFFRPK.N
R5/RRR5-14/3	1296.766	1296.548	168.891	0.458	1388.047	0.474	26	0.149	K.HITGGMMGGHAVK.L
R5/RRR5-14/3	1296.040	1296.548	-1167.478	0.507	971.897	0.564	22	0.130	K.HITGGMMGGHAVK.L
R5/RRR5-15/3	1296.384	1296.548	-127.143	0.466	1046.229	0.480	23	0.117	K.HITGGMMGGHAVK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/3	1296.337	1296.548	-163.699	0.456	749.176	0.486	21	0.101	K.HITGGMMGGHAVK.L
R5/RRR5-15/3	1295.886	1296.548	-1286.521	0.412	949.985	0.417	23	0.098	K.HITGGMMGGHAVK.L
R5/RRR5-25/3	1122.162	1122.261	-88.565	0.530	481.829	0.392	16	0.094	K.KHFSVNAYR.V
R5/RRR5-14/3	1121.689	1122.261	-1406.033	0.531	764.962	0.414	17	0.094	K.KHFSVNAYR.V
R5/RRR5-25/3	1121.997	1122.261	-236.059	0.471	669.331	0.404	17	0.092	K.KHFSVNAYR.V
R5/RRR5-24/3	1122.551	1122.261	258.799	0.562	580.237	0.375	16	0.090	K.KHFSVNAYR.V
R5/RRR5-15/3	1122.027	1122.261	-209.209	0.575	467.352	0.403	15	0.089	-.KHFSVNAYR.-
R5/RRR5-15/3	1122.314	1122.261	47.104	0.518	566.084	0.335	16	0.088	K.KHFSVNAYR.V
R5/RRR5-14/3	1121.638	1122.261	-1451.289	0.505	338.784	0.428	13	0.087	-.KHFSVNAYR.-
R5/RRR5-24/3	1122.445	1122.261	164.578	0.510	586.239	0.401	15	0.087	-.KHFSVNAYR.-
R5/RRR5-25/3	1121.189	1122.261	-1853.680	0.539	677.405	0.391	17	0.086	-.KHFSVNAYR.-
R5/RRR5-25/3	1122.757	1122.261	442.937	0.555	546.988	0.380	15	0.085	-.KHFSVNAYR.-
R5/RRR5-15/3	1296.507	1296.548	-31.515	0.427	870.235	0.336	22	0.082	K.HITGGMMGGHAVK.L
R5/RRR5-14/3	1122.384	1122.261	109.771	0.550	450.106	0.384	15	0.079	-.KHFSVNAYR.-
R5/RRR5-15/3	1122.411	1122.261	133.658	0.546	554.899	0.330	16	0.078	-.KHFSVNAYR.-
R5/RRR5-24/3	1122.406	1122.261	129.404	0.496	350.343	0.401	13	0.073	-.KHFSVNAYR.-
R5/RRR5-25/3	1122.658	1122.261	354.474	0.500	664.705	0.326	16	0.073	-.KHFSVNAYR.-
R5/RRR5-16/2	1138.924	1138.169	-216.252	0.455	712.430	0.459	14	0.139	R.AVSAEDNFER.A
R5/RRR5-16/2	1137.914	1138.169	-224.621	0.349	777.855	0.265	15	0.123	R.AVSAEDNFER.A
R5/RRR5-16/2	1137.790	1138.169	-334.622	0.308	806.942	0.265	15	0.122	R.AVSAEDNFER.A
R5/RRR5-16/3	1145.517	1145.336	158.591	0.448	922.706	0.427	20	0.098	K.LSHPDHVLVK.R
R5/RRR5-16/3	1145.590	1145.336	221.905	0.473	708.430	0.424	18	0.092	K.LSHPDHVLVK.R
R5/RRR5-15/3	1145.386	1145.336	43.643	0.447	713.951	0.427	18	0.091	K.LSHPDHVLVK.R
R5/RRR5-16/3	1144.849	1145.336	-426.843	0.428	780.153	0.442	19	0.089	-.LSHPDHVLVK.-
R5/RRR5-15/3	1145.132	1145.336	-178.632	0.412	523.070	0.392	17	0.064	-.LSHPDHVLVK.-
R5/RRR5-10/2	1692.306	1691.903	238.346	0.546	1522.716	0.531	24	0.210	K.FVAPDVSILESDSAIK.S
R5/RRR5-10/2	1690.596	1691.903	-1368.822	0.375	1668.632	0.454	24	0.208	K.FVAPDVSILESDSAIK.S
R5/RRR5-10/2	1690.575	1691.903	-1381.513	0.357	1442.669	0.429	23	0.178	K.FVAPDVSILESDSAIK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1644.262	1644.762	-915.195	0.364	594.299	0.500	18	0.134	K.QWDEFVETFDISK.S
R5/RRR5-19/2	947.880	948.058	-188.019	0.442	1349.638	0.470	15	0.181	R.SPAAEAVFR.N
R5/RRR5-19/2	947.685	948.058	-394.900	0.397	851.563	0.415	15	0.140	R.SPAAEAVFR.N
R5/RRR5-19/2	947.755	948.058	-320.718	0.451	748.569	0.395	12	0.133	R.SPAAEAVFR.N
R5/RRR5-19/3	1233.334	1233.359	-20.224	0.464	1224.657	0.383	23	0.109	R.HREPLPDSGPK.K
R5/RRR5-19/3	1233.477	1233.359	96.510	0.491	1210.299	0.359	23	0.103	R.HREPLPDSGPK.K
R5/RRR5-19/3	1233.690	1233.359	269.624	0.511	1039.073	0.411	22	0.103	R.HREPLPDSGPK.K
R5/RRR5-20/3	1233.239	1233.359	-96.920	0.478	1005.317	0.353	21	0.091	R.HREPLPDSGPK.K
R5/RRR5-20/3	1233.354	1233.359	-3.397	0.446	792.431	0.379	20	0.087	R.HREPLPDSGPK.K
R5/RRR5-5/2	1488.363	1488.622	-174.694	0.517	1830.146	0.579	24	0.263	K.IDSPSGVDVTVSPSK.L
R5/RRR5-6/2	1337.041	1337.421	-284.756	0.479	1653.437	0.546	21	0.230	R.NVGSNANAVYEAK.I
R5/RRR5-6/2	1337.554	1337.421	99.995	0.519	1493.814	0.570	21	0.217	R.NVGSNANAVYEAK.I
R5/RRR5-5/2	1336.957	1337.421	-347.413	0.426	1593.656	0.492	21	0.209	R.NVGSNANAVYEAK.I
R5/RRR5-6/2	1337.137	1337.421	-212.581	0.468	1308.083	0.519	20	0.186	R.NVGSNANAVYEAK.I
R5/RRR5-5/2	1488.270	1488.622	-236.981	0.413	1290.007	0.519	21	0.181	K.IDSPSGVDVTVSPSK.L
R5/RRR5-18/2	1334.306	1334.546	-180.641	0.321	962.270	0.382	16	0.134	R.GAVGALLVYDISR.R
R5/RRR5-17/2	1365.870	1366.613	-1280.142	0.424	999.113	0.535	17	0.162	R.VLGSWASPFVM*R.V
R5/RRR5-17/2	1308.138	1308.509	-284.121	0.454	721.195	0.510	16	0.144	K.SELLLASNPVHK.K
R5/RRR5-17/2	1366.287	1366.613	-239.259	0.407	714.780	0.434	15	0.135	R.VLGSWASPFVM*R.V
R5/RRR5-16/2	1365.686	1366.613	-1415.151	0.375	497.380	0.398	13	0.125	R.VLGSWASPFVM*R.V
R5/RRR5-17/2	1308.119	1308.509	-298.820	0.387	375.367	0.394	12	0.123	K.SELLLASNPVHK.K
R5/RRR5-17/2	1366.196	1366.613	-306.489	0.336	482.626	0.295	13	0.118	-.VLGSWASPFVM*R.-
R5/RRR5-16/2	1351.553	1350.614	-44.806	0.287	544.255	0.282	12	0.117	R.VLGSWASPFVMR.V
R5/RRR5-15/2	1307.801	1308.509	-1309.803	0.176	154.068	0.381	12	0.116	-.SELLLASNPVHK.-
R5/RRR5-9/2	1404.244	1404.550	-218.465	0.450	1143.558	0.515	19	0.169	R.TLAIDFAPDADVR.L
R5/RRR5-9/2	1286.389	1287.488	-1636.366	0.288	1105.583	0.404	15	0.144	K.DASLVEIVTAIR.E
R5/RRR5-9/2	1286.618	1287.488	-1457.838	0.187	608.462	0.204	14	0.112	K.DASLVEIVTAIR.E
R5/RRR5-2/2	1822.152	1821.965	102.899	0.409	947.666	0.364	18	0.131	R.AQAYAEDVDIPEVWSK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	950.434	950.097	355.891	0.385	874.782	0.230	11	0.121	R.VM*DYIHR.L
R5/RRR5-22/2	1332.324	1331.497	-130.734	0.438	515.387	0.474	17	0.136	R.QALTLQSVVEDK.T
R5/RRR5-22/2	1331.301	1331.497	-148.124	0.381	567.916	0.473	17	0.135	R.QALTLQSVVEDK.T
R5/RRR5-22/2	1174.886	1175.318	-368.555	0.375	830.150	0.331	16	0.128	K.FFDSVGSIFR.G
R5/RRR5-22/2	1331.107	1331.497	-293.843	0.301	263.495	0.399	12	0.122	R.QALTLQSVVEDK.T
R5/RRR5-19/2	1571.739	1571.759	-12.823	0.501	1156.794	0.493	18	0.166	K.TAINVNDVFHEIAK.R
R5/RRR5-20/2	1572.474	1571.759	-181.778	0.454	884.146	0.529	17	0.153	K.TAINVNDVFHEIAK.R
R5/RRR5-19/2	1571.160	1571.759	-1021.053	0.420	922.768	0.431	17	0.141	K.TAINVNDVFHEIAK.R
R5/RRR5-19/2	1072.133	1072.280	-137.908	0.340	787.637	0.410	15	0.133	K.LVLLGDVGTGK.S
R5/RRR5-20/2	1572.584	1571.759	-111.772	0.350	359.609	0.380	15	0.124	K.TAINVNDVFHEIAK.R
R5/RRR5-19/2	1072.866	1072.280	-387.510	0.318	611.715	0.361	13	0.123	K.LVLLGDVGTGK.S
R5/RRR5-19/2	1071.735	1072.280	-1446.366	0.209	610.078	0.179	13	0.113	K.LVLLGDVGTGK.S
R5/RRR5-10/2	1401.591	1402.532	-1389.441	0.486	2449.631	0.594	22	0.377	K.TPEGAQASLVDSVK.V
R5/RRR5-11/3	1486.141	1485.651	330.776	0.538	1531.226	0.415	28	0.148	K.SM*GHHVTVISSSAR.K
R5/RRR5-10/2	1130.942	1131.333	-346.340	0.261	1055.122	0.336	15	0.133	K.HFGLM*SPGLR.G
R5/RRR5-10/3	1484.901	1485.651	-1182.108	0.513	1433.992	0.388	28	0.129	K.SM*GHHVTVISSSAR.K
R5/RRR5-10/3	1485.512	1485.651	-94.003	0.510	1219.524	0.464	26	0.128	K.SM*GHHVTVISSSAR.K
R5/RRR5-10/3	1485.659	1485.651	5.149	0.562	1269.364	0.439	27	0.126	K.SM*GHHVTVISSSAR.K
R5/RRR5-11/3	1469.577	1469.652	-51.298	0.547	1297.298	0.394	27	0.117	-.SMGHHVTVISSSAR.-
R5/RRR5-11/3	1484.577	1485.651	-1401.331	0.483	1265.051	0.385	27	0.113	K.SM*GHHVTVISSSAR.K
R5/RRR5-11/3	1485.555	1485.651	-65.071	0.498	1208.526	0.372	26	0.105	K.SM*GHHVTVISSSAR.K
R5/RRR5-10/3	1469.854	1469.652	138.007	0.521	1045.842	0.411	26	0.102	-.SMGHHVTVISSSAR.-
R5/RRR5-10/3	1469.860	1469.652	141.630	0.553	1134.897	0.386	27	0.100	-.SMGHHVTVISSSAR.-
R5/RRR5-11/3	1469.445	1469.652	-141.290	0.546	956.410	0.347	25	0.085	-.SMGHHVTVISSSAR.-
R5/RRR5-11/3	1468.911	1469.652	-1188.491	0.471	962.881	0.296	25	0.080	K.SMGHHVTVISSSAR.K
R5/RRR5-10/2	1253.982	1254.504	-1217.119	0.512	1636.189	0.564	19	0.232	K.INNAVAQVLLAK.R
R5/RRR5-10/2	1253.987	1254.504	-1213.404	0.533	1476.182	0.562	18	0.212	K.INNAVAQVLLAK.R
R5/RRR5-10/2	1253.454	1254.504	-1640.193	0.447	1518.860	0.528	18	0.208	K.INNAVAQVLLAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/3	1984.010	1984.197	-94.525	0.528	1464.835	0.526	35	0.178	R.IIAETGAGQHGVATATVCAR.F
R5/RRR5-10/3	1983.988	1984.197	-105.495	0.492	1117.491	0.499	32	0.126	R.IIAETGAGQHGVATATVCAR.F
R5/RRR5-20/2	1590.256	1590.716	-289.921	0.458	1465.814	0.408	23	0.179	R.EYVAEGSAPALPETR.R
R5/RRR5-20/2	1590.187	1590.716	-964.564	0.445	1461.777	0.388	23	0.175	R.EYVAEGSAPALPETR.R
R5/RRR5-20/2	1590.275	1590.716	-278.061	0.504	1117.215	0.492	22	0.165	R.EYVAEGSAPALPETR.R
R5/RRR5-19/2	1590.401	1590.716	-198.667	0.501	1102.214	0.497	22	0.165	R.EYVAEGSAPALPETR.R
R5/RRR5-20/2	1543.059	1542.890	109.450	0.475	975.770	0.483	18	0.153	R.LLELGVKPVFLTGR.T
R5/RRR5-19/2	1590.190	1590.716	-962.406	0.427	1105.014	0.405	22	0.150	R.EYVAEGSAPALPETR.R
R5/RRR5-19/2	1589.699	1590.716	-1272.935	0.353	1170.709	0.382	22	0.150	R.EYVAEGSAPALPETR.R
R5/RRR5-20/3	1542.160	1542.890	-1125.292	0.435	1323.314	0.441	27	0.132	R.LLELGVKPVFLTGR.T
R5/RRR5-23/2	1541.789	1542.890	-1366.728	0.392	648.780	0.414	16	0.129	R.LLELGVKPVFLTGR.T
R5/RRR5-20/3	1542.053	1542.890	-1195.043	0.387	1248.160	0.443	27	0.124	R.LLELGVKPVFLTGR.T
R5/RRR5-20/2	1541.487	1542.890	-1563.659	0.368	755.068	0.333	16	0.124	R.LLELGVKPVFLTGR.T
R5/RRR5-20/3	1542.829	1542.890	-39.974	0.523	1278.738	0.425	27	0.124	R.LLELGVKPVFLTGR.T
R5/RRR5-19/2	1541.391	1542.890	-1626.588	0.363	674.926	0.282	16	0.119	R.LLELGVKPVFLTGR.T
R5/RRR5-19/3	1542.073	1542.890	-1182.165	0.356	1135.149	0.357	25	0.097	R.LLELGVKPVFLTGR.T
R5/RRR5-18/3	1541.513	1542.890	-1547.161	0.327	538.117	0.343	20	0.080	R.LLELGVKPVFLTGR.T
R5/RRR5-18/3	1542.118	1542.890	-1152.714	0.379	708.081	0.314	22	0.078	R.LLELGVKPVFLTGR.T
R5/RRR5-19/3	1541.999	1542.890	-1230.219	0.299	909.489	0.271	24	0.073	R.LLELGVKPVFLTGR.T
R5/RRR5-24/2	1213.132	1212.339	-171.535	0.371	668.875	0.460	14	0.132	K.NNSSIVGFFAR.T
R5/RRR5-24/3	1149.858	1149.287	-374.193	0.437	1136.918	0.324	21	0.091	K.LPHTAGPWGGR.G
R5/RRR5-24/3	1149.564	1149.287	241.960	0.406	884.482	0.290	19	0.074	-.LPHTAGPWGGR.-
R5/RRR5-17/2	1058.075	1058.254	-169.479	0.481	883.090	0.507	16	0.153	K.LSGIVGVPTSK.R
R5/RRR5-17/2	1085.559	1085.279	258.889	0.431	754.902	0.481	16	0.141	K.TPIKDALAAGK.E
R5/RRR5-17/2	1058.091	1058.254	-153.624	0.475	778.503	0.436	15	0.139	K.LSGIVGVPTSK.R
R5/RRR5-17/2	1057.751	1058.254	-1424.627	0.391	577.751	0.454	13	0.130	-.LSGIVGVPTSK.-
R5/RRR5-17/3	1085.360	1085.279	75.161	0.418	519.270	0.433	18	0.087	K.TPIKDALAAGK.E
R5/RRR5-17/3	1085.397	1085.279	108.830	0.397	679.424	0.422	19	0.087	K.TPIKDALAAGK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/3	1085.678	1085.279	368.803	0.472	768.686	0.394	21	0.085	-.TPIKDALAAGK.-
R5/RRR5-25/2	1562.101	1562.620	-975.244	0.382	747.515	0.481	21	0.140	R.QSGTTPGYSYSTANK.N
R5/RRR5-25/2	1562.117	1562.620	-964.575	0.360	705.434	0.438	21	0.134	R.QSGTTPGYSYSTANK.N
R5/RRR5-24/2	922.934	923.088	-167.763	0.354	954.457	0.311	13	0.132	R.ADLISYLK.E
R5/RRR5-25/2	923.135	923.088	50.717	0.344	823.116	0.338	13	0.130	R.ADLISYLK.E
R5/RRR5-25/2	1563.079	1562.620	294.944	0.374	435.049	0.474	18	0.130	R.QSGTTPGYSYSTANK.N
R5/RRR5-24/2	922.999	923.088	-97.049	0.332	867.083	0.310	13	0.129	R.ADLISYLK.E
R5/RRR5-24/2	943.900	944.111	-223.511	0.500	1192.981	0.414	14	0.159	R.GLVGEIISR.F
R5/RRR5-24/2	944.062	944.111	-51.631	0.431	1114.152	0.392	14	0.150	R.GLVGEIISR.F
R5/RRR5-24/2	944.235	944.111	132.635	0.526	1135.424	0.383	14	0.150	R.GLVGEIISR.F
R5/RRR5-23/2	943.973	944.111	-146.060	0.415	1238.516	0.327	14	0.148	R.GLVGEIISR.F
R5/RRR5-24/3	1780.733	1780.062	-185.313	0.425	1233.895	0.364	32	0.106	R.KLIGATNPLQAEPGTIR.G
R5/RRR5-24/3	1779.695	1780.062	-206.955	0.324	658.318	0.312	22	0.069	-.KLIGATNPLQAEPGTIR.-
R5/RRR5-16/2	1589.481	1588.791	-195.855	0.564	1479.521	0.455	20	0.187	R.DNVQAYWPNVIIR.Y
R5/RRR5-16/2	1589.458	1588.791	-210.494	0.543	1436.154	0.461	20	0.185	R.DNVQAYWPNVIIR.Y
R5/RRR5-15/2	1588.397	1588.791	-248.790	0.491	1489.097	0.427	20	0.184	R.DNVQAYWPNVIIR.Y
R5/RRR5-16/2	1588.294	1588.791	-314.330	0.486	1489.655	0.425	20	0.183	R.DNVQAYWPNVIIR.Y
R5/RRR5-15/2	1588.375	1588.791	-262.823	0.480	1412.304	0.436	20	0.179	R.DNVQAYWPNVIIR.Y
R5/RRR5-16/2	1588.458	1588.791	-210.549	0.518	1275.996	0.435	19	0.166	R.DNVQAYWPNVIIR.Y
R5/RRR5-15/2	1808.160	1808.027	73.495	0.479	916.715	0.567	21	0.162	R.EIPLNYATFQPGTTVR.D
R5/RRR5-15/2	1588.246	1588.791	-976.073	0.483	1300.520	0.400	19	0.162	R.DNVQAYWPNVIIR.Y
R5/RRR5-14/2	1588.321	1588.791	-297.057	0.440	1284.940	0.404	19	0.162	R.DNVQAYWPNVIIR.Y
R5/RRR5-14/2	1588.474	1588.791	-200.681	0.476	1181.846	0.443	18	0.160	R.DNVQAYWPNVIIR.Y
R5/RRR5-12/2	1589.539	1588.791	-159.030	0.498	1102.855	0.443	17	0.154	R.DNVQAYWPNVIIR.Y
R5/RRR5-13/2	1589.628	1588.791	-103.026	0.525	1038.565	0.432	17	0.148	R.DNVQAYWPNVIIR.Y
R5/RRR5-15/2	1807.572	1808.027	-252.762	0.460	876.135	0.482	21	0.148	R.EIPLNYATFQPGTTVR.D
R5/RRR5-15/2	1808.433	1808.027	225.139	0.476	813.840	0.494	21	0.147	R.EIPLNYATFQPGTTVR.D
R5/RRR5-15/2	1808.674	1808.027	-196.016	0.491	647.336	0.556	19	0.147	R.EIPLNYATFQPGTTVR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1807.185	1808.027	-1022.454	0.416	757.158	0.497	21	0.144	R.EIPLNYATFQPGTTVR.D
R5/RRR5-1/2	1589.496	1588.791	-186.148	0.507	969.240	0.421	16	0.143	R.DNVQAYWPNVIIR.Y
R5/RRR5-14/2	1588.304	1588.791	-307.776	0.462	1022.566	0.375	17	0.140	R.DNVQAYWPNVIIR.Y
R5/RRR5-14/2	1807.356	1808.027	-927.517	0.424	688.767	0.483	20	0.140	R.EIPLNYATFQPGTTVR.D
R5/RRR5-15/2	1809.404	1808.027	208.643	0.476	577.078	0.493	19	0.138	R.EIPLNYATFQPGTTVR.D
R5/RRR5-13/2	1588.550	1588.791	-152.346	0.408	1028.331	0.342	17	0.137	R.DNVQAYWPNVIIR.Y
R5/RRR5-16/2	1807.487	1808.027	-854.766	0.404	705.743	0.453	20	0.137	R.EIPLNYATFQPGTTVR.D
R5/RRR5-2/2	1589.767	1588.791	-15.450	0.477	940.515	0.370	16	0.135	R.DNVQAYWPNVIIR.Y
R5/RRR5-16/2	1807.243	1808.027	-990.174	0.429	571.265	0.480	18	0.135	R.EIPLNYATFQPGTTVR.D
R5/RRR5-16/2	1807.642	1808.027	-214.009	0.449	563.589	0.477	18	0.135	R.EIPLNYATFQPGTTVR.D
R5/RRR5-13/2	1807.677	1808.027	-194.160	0.432	573.402	0.457	18	0.133	R.EIPLNYATFQPGTTVR.D
R5/RRR5-14/2	1807.305	1808.027	-955.793	0.374	693.340	0.419	20	0.133	R.EIPLNYATFQPGTTVR.D
R5/RRR5-13/2	1807.546	1808.027	-267.193	0.419	482.092	0.473	17	0.132	R.EIPLNYATFQPGTTVR.D
R5/RRR5-17/2	1588.616	1588.791	-110.721	0.414	950.065	0.315	16	0.130	R.DNVQAYWPNVIIR.Y
R5/RRR5-12/2	1588.883	1588.791	57.670	0.444	948.509	0.312	16	0.129	R.DNVQAYWPNVIIR.Y
R5/RRR5-17/2	1588.998	1588.791	130.480	0.442	790.744	0.354	15	0.128	R.DNVQAYWPNVIIR.Y
R5/RRR5-13/2	1588.304	1588.791	-307.776	0.365	913.494	0.290	16	0.127	R.DNVQAYWPNVIIR.Y
R5/RRR5-1/2	1588.345	1588.791	-281.790	0.322	827.002	0.282	15	0.123	R.DNVQAYWPNVIIR.Y
R5/RRR5-14/2	1806.917	1808.027	-1171.407	0.272	486.839	0.326	18	0.122	R.EIPLNYATFQPGTTVR.D
R5/RRR5-13/2	1806.816	1808.027	-1227.784	0.291	444.075	0.284	16	0.120	R.EIPLNYATFQPGTTVR.D
R5/RRR5-19/2	1589.308	1588.791	-305.193	0.255	190.142	0.339	13	0.115	-.DNVQAYWPNVIIR.-
R5/RRR5-15/3	1808.164	1808.027	75.756	0.426	925.411	0.368	27	0.087	R.EIPLNYATFQPGTTVR.D
R5/RRR5-14/3	1808.757	1808.027	-150.120	0.434	793.584	0.357	26	0.082	R.EIPLNYATFQPGTTVR.D
R5/RRR5-14/3	1808.197	1808.027	94.342	0.388	744.860	0.369	23	0.080	R.EIPLNYATFQPGTTVR.D
R5/RRR5-17/2	1859.906	1859.111	-110.765	0.536	614.299	0.545	19	0.141	K.VFVESSLPVIEYYNAK.D
R5/RRR5-17/2	1074.935	1075.155	-205.320	0.506	986.723	0.364	15	0.141	R.VDDNIETIR.K
R5/RRR5-17/2	1074.360	1075.155	-1675.201	0.450	948.495	0.337	15	0.136	R.VDDNIETIR.K
R5/RRR5-17/2	1074.397	1075.155	-1640.842	0.416	1000.122	0.306	15	0.134	R.VDDNIETIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	1307.976	1307.434	-351.741	0.487	1805.189	0.458	19	0.228	R.VDAAEVFDTIAR.R
R5/RRR5-7/2	1307.431	1307.434	-2.586	0.412	1594.399	0.423	19	0.195	R.VDAAEVFDTIAR.R
R5/RRR5-7/2	1466.505	1466.835	-226.055	0.459	1198.766	0.498	19	0.172	K.LIFVDPALLPVLR.D
R5/RRR5-7/2	1466.254	1466.835	-1082.082	0.406	1099.296	0.517	18	0.166	K.LIFVDPALLPVLR.D
R5/RRR5-1/2	1466.275	1466.835	-1067.119	0.436	1015.266	0.402	16	0.143	K.LIFVDPALLPVLR.D
R5/RRR5-7/2	1466.502	1466.835	-227.808	0.383	872.569	0.389	16	0.135	K.LIFVDPALLPVLR.D
R5/RRR5-7/2	1466.227	1466.835	-1100.139	0.355	917.150	0.362	15	0.133	K.LIFVDPALLPVLR.D
R5/RRR5-7/2	1466.309	1466.835	-1044.049	0.325	816.695	0.390	15	0.132	K.LIFVDPALLPVLR.D
R5/RRR5-1/2	1466.236	1466.835	-1093.953	0.335	897.119	0.332	15	0.129	K.LIFVDPALLPVLR.D
R5/RRR5-2/2	1466.647	1466.835	-128.861	0.400	787.570	0.338	15	0.127	K.LIFVDPALLPVLR.D
R5/RRR5-6/2	1467.091	1466.835	174.704	0.327	662.322	0.292	14	0.120	K.LIFVDPALLPVLR.D
R5/RRR5-7/2	1306.741	1307.434	-1299.809	0.269	739.194	0.286	15	0.120	R.VDAAEVFDTIAR.R
R5/RRR5-10/2	1466.710	1466.835	-85.949	0.359	485.676	0.311	12	0.118	-.LIFVDPALLPVLR.-
R5/RRR5-3/2	1466.329	1466.835	-1030.759	0.266	576.806	0.233	14	0.117	-.LIFVDPALLPVLR.-
R5/RRR5-8/2	1466.061	1466.835	-1213.675	0.222	568.034	0.227	13	0.114	-.LIFVDPALLPVLR.-
R5/RRR5-20/2	1292.998	1292.420	-326.745	0.442	1357.063	0.467	18	0.179	K.AVDVTGPDGSFVK.G
R5/RRR5-20/2	1293.185	1292.420	-181.840	0.429	1154.573	0.454	19	0.161	K.AVDVTGPDGSFVK.G
R5/RRR5-20/2	1293.017	1292.420	-312.537	0.387	907.365	0.461	17	0.144	K.AVDVTGPDGSFVK.G
R5/RRR5-20/3	1495.501	1495.567	-44.146	0.386	927.861	0.497	25	0.107	R.SCYNCGEAGHIAR.D
R5/RRR5-20/3	1494.808	1495.567	-1179.819	0.377	752.224	0.506	25	0.098	R.SCYNCGEAGHIAR.D
R5/RRR5-20/3	1494.763	1495.567	-1210.202	0.370	617.598	0.487	23	0.091	R.SCYNCGEAGHIAR.D
R5/RRR5-12/2	1191.955	1192.303	-292.709	0.511	1067.232	0.563	19	0.177	K.VLAPYSAEDAR.G
R5/RRR5-12/2	1191.888	1192.303	-349.430	0.453	1105.113	0.457	19	0.161	K.VLAPYSAEDAR.G
R5/RRR5-12/2	1191.898	1192.303	-341.004	0.418	1039.433	0.473	19	0.158	K.VLAPYSAEDAR.G
R5/RRR5-12/2	1769.233	1770.046	-1027.501	0.447	896.470	0.520	20	0.152	K.SNYMSAGQISVPIVFR.G
R5/RRR5-11/2	1192.102	1192.303	-169.734	0.377	708.034	0.435	16	0.136	K.VLAPYSAEDAR.G
R5/RRR5-12/2	1770.085	1770.046	22.023	0.472	666.431	0.467	18	0.135	K.SNYMSAGQISVPIVFR.G
R5/RRR5-12/2	1769.184	1770.046	-1055.420	0.373	851.089	0.389	20	0.133	K.SNYMSAGQISVPIVFR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1787.392	1786.045	194.627	0.370	739.661	0.414	18	0.131	K.SNYM*SAGQISVPIVFR.G
R5/RRR5-10/2	959.979	959.082	-108.169	0.472	1510.233	0.488	16	0.200	R.AVVSAIGADR.V
R5/RRR5-11/2	958.964	959.082	-123.604	0.438	1145.034	0.381	15	0.149	R.AVVSAIGADR.V
R5/RRR5-10/2	1303.199	1303.489	-223.096	0.345	910.121	0.363	14	0.132	R.LFISNPDLVER.F
R5/RRR5-10/2	1303.295	1303.489	-149.428	0.375	698.392	0.249	14	0.118	R.LFISNPDLVER.F
R5/RRR5-14/2	1610.788	1610.883	-59.334	0.469	1569.738	0.495	21	0.206	K.IAIVGFGNFGQFLAR.T
R5/RRR5-14/2	1611.123	1610.883	149.359	0.412	566.286	0.402	15	0.124	K.IAIVGFGNFGQFLAR.T
R5/RRR5-14/2	1396.084	1396.528	-318.755	0.390	932.230	0.267	15	0.123	-.DGWDGLPFVFDK.-
R5/RRR5-14/2	1397.272	1396.528	-184.067	0.285	864.441	0.283	15	0.122	-.DGWDGLPFVFDK.-
R5/RRR5-14/2	1611.575	1610.883	-191.651	0.350	490.066	0.326	14	0.117	-.IAIVGFGNFGQFLAR.-
R5/RRR5-5/2	1481.165	1480.645	-324.913	0.516	1928.620	0.450	21	0.241	R.DGSDFSAAIIGSLVK.A
R5/RRR5-5/2	1698.559	1696.947	-229.083	0.393	483.719	0.483	17	0.128	K.M*ASTPGVSATLFDALAK.A
R5/RRR5-1/2	1697.786	1696.947	-95.125	0.279	432.171	0.308	15	0.114	K.M*ASTPGVSATLFDALAK.A
R5/RRR5-23/2	1215.685	1216.366	-1387.196	0.434	1571.775	0.317	16	0.171	R.LLEELERGEK.G
R5/RRR5-23/3	1805.736	1806.930	-1218.578	0.544	1274.727	0.507	28	0.146	R.INM*SCVNHETGAVDSR.K
R5/RRR5-23/3	1806.561	1806.930	-204.744	0.505	1208.857	0.474	28	0.130	R.INM*SCVNHETGAVDSR.K
R5/RRR5-23/3	1806.761	1806.930	-93.721	0.472	935.953	0.483	25	0.108	R.INM*SCVNHETGAVDSR.K
R5/RRR5-8/2	1466.426	1465.678	-172.130	0.531	1610.549	0.476	21	0.209	K.FLGNSLEVYPLGR.T
R5/RRR5-8/2	1465.491	1465.678	-128.128	0.412	1413.371	0.443	20	0.180	K.FLGNSLEVYPLGR.T
R5/RRR5-8/2	1465.516	1465.678	-110.665	0.507	1204.804	0.496	19	0.173	K.FLGNSLEVYPLGR.T
R5/RRR5-8/2	932.885	933.089	-220.309	0.564	990.961	0.405	13	0.146	K.VNNLIFGR.T
R5/RRR5-8/2	932.946	933.089	-154.283	0.524	955.857	0.356	13	0.138	K.VNNLIFGR.T
R5/RRR5-8/2	933.148	933.089	62.375	0.508	800.452	0.361	12	0.133	K.VNNLIFGR.T
R5/RRR5-11/3	1851.236	1851.180	30.277	0.462	1613.089	0.523	29	0.203	K.LLVDKDPGLVGNLLVER.L
R5/RRR5-11/2	1721.081	1720.945	79.348	0.451	1181.462	0.565	22	0.179	K.DIATATGIVLDPVYSGK.A
R5/RRR5-1/2	1060.973	1061.133	-151.476	0.393	1122.279	0.308	15	0.139	R.EAQWATAQR.T
R5/RRR5-1/2	1117.964	1118.219	-229.177	0.475	1029.020	0.329	16	0.137	R.ELSEIAEQAK.R
R5/RRR5-2/2	1118.063	1118.219	-140.018	0.436	885.189	0.348	15	0.133	R.ELSEIAEQAK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1060.559	1061.133	-1488.969	0.271	839.915	0.178	13	0.116	R.EAQWATAQR.T
R5/RRR5-17/2	1199.429	1198.310	99.669	0.434	1116.633	0.315	15	0.137	R.ADNLYLEGFR.X
R5/RRR5-17/2	1203.118	1203.371	-210.820	0.432	870.537	0.362	18	0.134	R.ASPTTALTLATR.A
R5/RRR5-17/2	1202.362	1203.371	-1675.471	0.350	736.602	0.344	18	0.128	R.ASPTTALTLATR.A
R5/RRR5-17/2	1202.422	1203.371	-1625.493	0.341	584.359	0.249	15	0.118	R.ASPTTALTLATR.A
R5/RRR5-21/2	1265.236	1264.371	-107.570	0.507	366.597	0.541	15	0.141	K.GGAPAEFQPSFR.G
R5/RRR5-21/2	1674.570	1674.919	-209.520	0.458	810.368	0.456	20	0.140	R.SYLNLPSEVVPNTLK.K
R5/RRR5-21/2	1264.293	1264.371	-62.328	0.416	417.350	0.554	15	0.140	K.GGAPAEFQPSFR.G
R5/RRR5-21/2	1264.393	1264.371	17.177	0.421	481.609	0.535	15	0.140	K.GGAPAEFQPSFR.G
R5/RRR5-21/2	1264.170	1264.371	-159.767	0.410	487.303	0.524	16	0.140	K.GGAPAEFQPSFR.G
R5/RRR5-21/2	1264.447	1264.371	60.266	0.388	362.847	0.564	14	0.138	K.GGAPAEFQPSFR.G
R5/RRR5-21/2	1263.476	1264.371	-1504.308	0.358	429.154	0.527	15	0.136	K.GGAPAEFQPSFR.G
R5/RRR5-21/2	1264.048	1264.371	-256.449	0.426	437.729	0.476	15	0.135	K.GGAPAEFQPSFR.G
R5/RRR5-21/2	1674.490	1674.919	-256.911	0.499	571.291	0.474	17	0.132	R.SYLNLPSEVVPNTLK.K
R5/RRR5-22/2	1263.975	1264.371	-314.729	0.322	403.451	0.427	15	0.129	K.GGAPAEFQPSFR.G
R5/RRR5-22/2	1263.855	1264.371	-1203.155	0.362	444.918	0.399	15	0.129	K.GGAPAEFQPSFR.G
R5/RRR5-22/2	1265.082	1264.371	-228.947	0.302	234.630	0.332	12	0.120	-.GGAPAEFQPSFR.-
R5/RRR5-22/2	1265.083	1264.371	-228.754	0.257	424.510	0.341	13	0.118	-.GGAPAEFQPSFR.-
R5/RRR5-15/3	1413.630	1413.606	16.610	0.504	1181.631	0.588	27	0.156	R.LPAAGPPSPAEHLR.E
R5/RRR5-16/3	1413.742	1413.606	96.502	0.494	655.219	0.601	23	0.116	R.LPAAGPPSPAEHLR.E
R5/RRR5-15/3	1413.521	1413.606	-60.955	0.481	761.371	0.541	22	0.110	R.LPAAGPPSPAEHLR.E
R5/RRR5-16/3	1414.683	1413.606	54.332	0.463	695.133	0.561	22	0.110	R.LPAAGPPSPAEHLR.E
R5/RRR5-16/3	1413.287	1413.606	-226.780	0.479	780.931	0.521	25	0.108	R.LPAAGPPSPAEHLR.E
R5/RRR5-15/3	1954.988	1956.257	-1163.825	0.447	863.717	0.447	32	0.096	R.MGLSDKEIVALSGAHTLGR.S
R5/RRR5-15/3	1955.391	1956.257	-956.863	0.323	175.350	0.447	24	0.062	-.MGLSDKEIVALSGAHTLGR.-
R5/RRR5-12/2	1166.050	1166.349	-257.317	0.468	1096.398	0.549	18	0.174	R.LPTSVYSALSK.A
R5/RRR5-12/2	1165.405	1166.349	-1672.606	0.418	1107.885	0.532	18	0.171	R.LPTSVYSALSK.A
R5/RRR5-12/2	1166.038	1166.349	-266.979	0.372	829.927	0.475	17	0.144	R.LPTSVYSALSK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	857.867	858.021	-180.202	0.390	987.809	0.354	14	0.139	R.SAGLIGLAR.N
R5/RRR5-12/2	857.429	858.021	-1861.704	0.288	961.204	0.215	14	0.123	R.SAGLIGLAR.N
R5/RRR5-13/2	858.036	858.021	17.464	0.231	560.481	0.349	13	0.122	R.SAGLIGLAR.N
R5/RRR5-12/2	857.406	858.021	-1888.886	0.276	605.273	0.238	11	0.117	-.SAGLIGLAR.-
R5/RRR5-13/2	857.845	858.021	-205.612	0.173	591.320	0.269	13	0.116	R.SAGLIGLAR.N
R5/RRR5-15/2	1603.786	1603.839	-33.255	0.513	1204.034	0.426	19	0.158	K.LNSSLSQVLVNCLR.Y
R5/RRR5-15/2	1295.180	1295.379	-153.767	0.480	1176.930	0.432	18	0.157	K.GSVSTESAVTQTK.F
R5/RRR5-16/2	1605.402	1603.839	-273.305	0.509	1038.402	0.427	17	0.146	K.LNSSLSQVLVNCLR.Y
R5/RRR5-18/2	915.830	916.099	-293.997	0.389	920.961	0.396	13	0.139	K.AADVLLWK.D
R5/RRR5-18/2	983.086	982.112	-26.853	0.415	902.876	0.285	14	0.128	K.SPPDIPEVK.I
R5/RRR5-18/2	981.988	982.112	-127.003	0.414	792.741	0.275	14	0.125	K.SPPDIPEVK.I
R5/RRR5-18/2	981.332	982.112	-1819.283	0.349	755.373	0.271	14	0.124	K.SPPDIPEVK.I
R5/RRR5-21/2	982.291	982.112	182.403	0.345	665.278	0.172	13	0.117	K.SPPDIPEVK.I
R5/RRR5-10/2	1308.594	1307.517	59.169	0.464	1202.362	0.430	15	0.159	R.VLACFSNNLLR.R
R5/RRR5-10/3	1901.663	1902.181	-800.532	0.471	1062.433	0.426	25	0.104	K.TPLKDLLETTLTYQHK.T
R5/RRR5-7/2	957.913	958.054	-147.450	0.458	1379.039	0.280	15	0.150	K.DLAGGLQQR.R
R5/RRR5-7/2	957.932	958.054	-128.019	0.459	1161.091	0.267	14	0.134	K.DLAGGLQQR.R
R5/RRR5-15/1	1129.581	1130.320	-1544.248	0.205	831.087	0.491	16	0.540	K.VAVITGGASGIGK.A
R5/RRR5-16/2	1129.845	1130.320	-421.175	0.409	2425.669	0.538	22	0.348	K.VAVITGGASGIGK.A
R5/RRR5-16/2	1130.961	1130.320	-317.914	0.561	2221.842	0.610	22	0.334	K.VAVITGGASGIGK.A
R5/RRR5-16/2	1129.501	1130.320	-1614.991	0.458	2267.901	0.539	22	0.319	K.VAVITGGASGIGK.A
R5/RRR5-15/2	1130.004	1130.320	-279.935	0.519	2245.692	0.526	22	0.312	K.VAVITGGASGIGK.A
R5/RRR5-15/1	1129.599	1130.320	-1528.291	0.168	638.355	0.388	15	0.311	K.VAVITGGASGIGK.A
R5/RRR5-17/2	1129.963	1130.320	-316.461	0.411	2311.515	0.471	22	0.306	K.VAVITGGASGIGK.A
R5/RRR5-14/2	1130.109	1130.320	-186.953	0.524	2196.953	0.529	22	0.304	K.VAVITGGASGIGK.A
R5/RRR5-15/2	1130.005	1130.320	-279.394	0.508	2141.096	0.545	22	0.300	K.VAVITGGASGIGK.A
R5/RRR5-14/2	1130.216	1130.320	-92.472	0.506	2163.487	0.521	22	0.296	K.VAVITGGASGIGK.A
R5/RRR5-17/2	1130.110	1130.320	-186.628	0.482	2111.345	0.534	22	0.291	K.VAVITGGASGIGK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/1	1129.699	1130.320	-1439.284	0.175	586.222	0.443	15	0.290	K.VAVITGGASGIGK.A
R5/RRR5-13/2	1130.017	1130.320	-268.989	0.474	1930.914	0.558	21	0.270	K.VAVITGGASGIGK.A
R5/RRR5-17/2	1129.951	1130.320	-326.975	0.443	1888.884	0.580	21	0.268	K.VAVITGGASGIGK.A
R5/RRR5-14/2	1129.343	1130.320	-1755.722	0.359	1517.111	0.496	19	0.198	K.VAVITGGASGIGK.A
R5/RRR5-1/2	1130.069	1130.320	-223.039	0.347	1193.588	0.420	18	0.157	K.VAVITGGASGIGK.A
R5/RRR5-16/2	1327.688	1328.497	-1366.263	0.414	1021.606	0.482	16	0.155	K.VIIADVQDELGR.S
R5/RRR5-16/2	1327.453	1328.497	-1544.518	0.386	979.812	0.487	16	0.153	K.VIIADVQDELGR.S
R5/RRR5-15/2	1328.022	1328.497	-358.325	0.291	840.206	0.346	15	0.128	K.VIIADVQDELGR.S
R5/RRR5-15/2	1329.416	1328.497	-60.749	0.306	774.713	0.316	15	0.124	-.VIIADVQDELGR.-
R5/RRR5-16/2	1329.306	1328.497	-143.649	0.434	666.962	0.363	13	0.119	-.VIIADVQDELGR.-
R5/RRR5-15/2	1327.825	1328.497	-1262.757	0.251	582.264	0.207	14	0.116	-.VIIADVQDELGR.-
R5/RRR5-16/2	1327.691	1328.497	-1363.955	0.220	631.588	0.280	13	0.116	-.VIIADVQDELGR.-
R5/RRR5-14/2	1130.761	1130.320	391.467	0.232	425.174	0.404	13	0.111	-.VAVITGGASGIGK.-
R5/RRR5-25/2	1213.157	1213.369	-175.467	0.468	1386.222	0.339	19	0.161	K.VTLSGNQQPIR.V
R5/RRR5-25/2	1213.149	1213.369	-182.130	0.449	1096.065	0.320	17	0.138	K.VTLSGNQQPIR.V
R5/RRR5-25/3	1759.625	1759.901	-157.234	0.395	1062.569	0.294	24	0.079	K.LSELVNDAYKDAHQR.S
R5/RRR5-14/2	1229.007	1228.463	-372.648	0.407	689.955	0.420	18	0.135	R.VTPTVTDIIIR.A
R5/RRR5-14/2	1228.247	1228.463	-176.501	0.337	563.876	0.310	15	0.122	R.VTPTVTDIIIR.A
R5/RRR5-14/3	1582.727	1582.704	14.604	0.425	519.082	0.563	23	0.100	R.ATHTQEVLGEQGRR.I
R5/RRR5-14/3	1582.579	1582.704	-79.046	0.308	427.410	0.463	21	0.084	R.ATHTQEVLGEQGRR.I
R5/RRR5-14/3	1582.728	1582.704	15.532	0.317	439.865	0.398	21	0.081	R.ATHTQEVLGEQGRR.I
R5/RRR5-13/2	1788.660	1788.978	-178.016	0.469	1167.451	0.480	19	0.163	K.TPSLIFEYVNNTDFK.V
R5/RRR5-13/2	1427.825	1426.680	101.733	0.376	845.151	0.448	15	0.136	K.ILQNLCGGPNIVK.L
R5/RRR5-25/2	1334.126	1333.535	-307.947	0.369	1329.643	0.164	16	0.128	K.SQIEYYAM*LAK.T
R5/RRR5-12/3	1404.254	1404.704	-321.793	0.301	990.523	0.173	22	0.061	-.ASLGMKESLKALR.-
R5/RRR5-4/2	1503.123	1502.740	255.311	0.558	1460.406	0.550	22	0.209	K.FSVSPVVQQGVQVK.N
R5/RRR5-4/2	1502.527	1502.740	-142.326	0.570	1454.271	0.509	22	0.199	K.FSVSPVVQQGVQVK.N
R5/RRR5-4/2	1502.252	1502.740	-325.732	0.516	1477.424	0.458	22	0.190	K.FSVSPVVQQGVQVK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1481.266	1481.722	-309.186	0.323	1213.557	0.281	16	0.136	R.AFNQFILDPIFR.I
R5/RRR5-18/2	1636.214	1634.686	-289.485	0.570	2472.650	0.550	27	0.365	R.ASDFDSLGSDGGPGPVR.S
R5/RRR5-18/2	1636.158	1634.686	289.703	0.571	2019.327	0.582	25	0.292	R.ASDFDSLGSDGGPGPVR.S
R5/RRR5-19/2	1635.969	1634.686	173.883	0.577	1895.202	0.555	25	0.264	R.ASDFDSLGSDGGPGPVR.S
R5/RRR5-15/2	1315.250	1315.536	-218.166	0.384	853.145	0.454	15	0.142	R.YVTVGAYCLLR.S
R5/RRR5-15/2	1314.623	1315.536	-1459.658	0.195	1168.030	0.279	16	0.132	R.YVTVGAYCLLR.S
R5/RRR5-15/3	1461.793	1461.706	59.317	0.466	1772.745	0.213	25	0.126	R.KLTNEEIM*EIPK.L
R5/RRR5-16/2	1315.463	1315.536	-56.088	0.269	389.121	0.389	11	0.120	R.YVTVGAYCLLR.S
R5/RRR5-15/3	1461.883	1461.706	121.249	0.424	1478.908	0.176	23	0.087	R.KLTNEEIM*EIPK.L
R5/RRR5-6/2	1212.932	1212.424	-406.961	0.540	1851.735	0.437	20	0.228	K.DAGIIAGLNVLR.I
R5/RRR5-6/2	1212.366	1212.424	-47.931	0.489	1677.861	0.401	19	0.199	K.DAGIIAGLNVLR.I
R5/RRR5-6/2	1213.528	1212.424	86.101	0.376	1232.721	0.372	16	0.152	K.DAGIIAGLNVLR.I
R5/RRR5-6/2	1213.592	1212.424	139.163	0.157	476.751	0.275	14	0.114	K.DAGIIAGLNVLR.I
R5/RRR5-6/3	1442.525	1442.603	-54.127	0.489	1262.608	0.336	23	0.103	K.GKVEILVNDQGNR.I
R5/RRR5-6/3	1441.510	1442.603	-1456.294	0.421	707.805	0.324	22	0.074	-.GKVEILVNDQGNR.-
R5/RRR5-14/2	1098.076	1098.304	-209.069	0.457	1225.842	0.520	18	0.178	K.HGM*VAAGALVR.Q
R5/RRR5-14/3	1899.856	1900.082	-119.238	0.479	776.354	0.570	28	0.111	K.AHAAENAKPVEKTEFEK.L
R5/RRR5-14/3	1098.358	1098.304	48.808	0.463	1367.345	0.167	20	0.077	K.HGM*VAAGALVR.Q
R5/RRR5-5/2	1416.135	1416.601	-330.064	0.373	1196.825	0.403	18	0.153	K.AIDPGLVYDIDPK.D
R5/RRR5-5/2	1220.698	1221.343	-1352.011	0.369	1118.143	0.308	17	0.137	K.SAIVTTASVTDR.F
R5/RRR5-7/2	1221.677	1221.343	273.941	0.198	566.178	0.233	14	0.113	K.SAIVTTASVTDR.F
R5/RRR5-7/2	1517.382	1516.639	-169.739	0.462	1386.557	0.442	21	0.178	K.DNQTVQSVLGTPTR.D
R5/RRR5-7/2	1280.034	1280.538	-1178.670	0.382	797.245	0.568	16	0.150	R.GLPTLVLIGPDGK.T
R5/RRR5-6/2	1280.108	1280.538	-336.922	0.291	1007.801	0.358	16	0.134	R.GLPTLVLIGPDGK.T
R5/RRR5-6/2	1516.486	1516.639	-100.890	0.418	841.762	0.375	17	0.132	K.DNQTVQSVLGTPTR.D
R5/RRR5-7/2	1516.227	1516.639	-272.583	0.345	1010.660	0.269	18	0.128	-.DNQTVQSVLGTPTR.-
R5/RRR5-7/2	1516.207	1516.639	-285.345	0.330	888.638	0.282	18	0.124	K.DNQTVQSVLGTPTR.D
R5/RRR5-8/1	994.455	995.113	-1671.897	0.264	852.317	0.301	12	0.452	R.DSAAVFAWK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/1	994.427	995.113	-1700.632	0.304	802.686	0.257	12	0.380	R.DSAAVFAWK.G
R5/RRR5-9/1	994.482	995.113	-1645.013	0.302	634.107	0.297	11	0.258	R.DSAAVFAWK.G
R5/RRR5-9/1	994.470	995.113	-1656.543	0.285	626.944	0.285	11	0.251	-.DSAAVFAWK.-
R5/RRR5-8/1	994.458	995.113	-1669.061	0.297	575.846	0.390	11	0.248	-.DSAAVFAWK.-
R5/RRR5-9/2	995.026	995.113	-88.055	0.477	1413.924	0.482	15	0.190	R.DSAAVFAWK.G
R5/RRR5-8/2	994.847	995.113	-267.877	0.475	1252.102	0.468	14	0.172	R.DSAAVFAWK.G
R5/RRR5-8/2	995.082	995.113	-31.082	0.512	1265.035	0.436	14	0.168	R.DSAAVFAWK.G
R5/RRR5-9/2	994.519	995.113	-1607.909	0.403	1267.888	0.440	14	0.168	R.DSAAVFAWK.G
R5/RRR5-9/2	994.564	995.113	-1562.410	0.394	1269.652	0.432	14	0.166	R.DSAAVFAWK.G
R5/RRR5-8/2	994.539	995.113	-1586.947	0.468	1177.581	0.459	14	0.165	R.DSAAVFAWK.G
R5/RRR5-1/2	994.924	995.113	-190.943	0.418	1269.499	0.419	15	0.165	R.DSAAVFAWK.G
R5/RRR5-2/2	995.137	995.113	24.163	0.452	1100.940	0.444	14	0.158	R.DSAAVFAWK.G
R5/RRR5-1/2	994.862	995.113	-252.489	0.427	1142.844	0.417	14	0.156	R.DSAAVFAWK.G
R5/RRR5-8/2	1762.263	1762.917	-941.254	0.393	937.249	0.277	15	0.123	K.GM*SLQEYWWCTER.A
R5/RRR5-1/2	994.782	995.113	-333.495	0.261	397.989	0.337	10	0.118	-.DSAAVFAWK.-
R5/RRR5-9/2	1763.555	1762.917	-205.899	0.323	614.396	0.133	14	0.110	K.GM*SLQEYWWCTER.A
R5/RRR5-14/2	1500.349	1499.693	-229.932	0.551	1163.146	0.442	19	0.160	R.SIGISNYDIFLTR.D
R5/RRR5-13/2	1499.170	1499.693	-1018.632	0.451	1113.575	0.417	19	0.153	R.SIGISNYDIFLTR.D
R5/RRR5-14/2	898.034	898.085	-56.868	0.526	1104.607	0.360	13	0.146	K.TPAQLVLR.W
R5/RRR5-13/2	898.076	898.085	-10.513	0.566	1061.338	0.331	13	0.138	K.TPAQLVLR.W
R5/RRR5-14/2	897.963	898.085	-136.637	0.495	996.336	0.328	13	0.137	K.TPAQLVLR.W
R5/RRR5-13/2	898.026	898.085	-66.276	0.552	1067.457	0.309	13	0.136	K.TPAQLVLR.W
R5/RRR5-14/2	1498.479	1499.693	-1482.055	0.380	971.473	0.355	17	0.135	R.SIGISNYDIFLTR.D
R5/RRR5-14/2	897.953	898.085	-147.956	0.551	1057.531	0.300	13	0.134	K.TPAQLVLR.W
R5/RRR5-13/2	897.456	898.085	-1820.213	0.505	1008.597	0.299	13	0.133	K.TPAQLVLR.W
R5/RRR5-14/2	1499.074	1499.693	-1083.302	0.401	1017.938	0.297	18	0.131	R.SIGISNYDIFLTR.D
R5/RRR5-19/2	1596.091	1595.847	153.450	0.413	536.689	0.531	21	0.143	R.VIPNFMLQGGDFTR.G
R5/RRR5-20/2	1612.256	1611.847	254.399	0.377	445.310	0.565	21	0.142	R.VIPNFM*LQGGDFTR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1595.265	1595.847	-995.110	0.427	646.871	0.443	22	0.138	R.VIPNFMLQGGDFTR.G
R5/RRR5-20/2	1612.113	1611.847	165.790	0.428	332.957	0.480	21	0.138	R.VIPNFM*LQGGDFTR.G
R5/RRR5-22/2	1269.757	1269.300	361.343	0.347	785.348	0.445	17	0.138	R.GNGTGGESIYGEK.-
R5/RRR5-20/2	1595.254	1595.847	-1001.641	0.435	598.452	0.444	22	0.138	R.VIPNFMLQGGDFTR.G
R5/RRR5-20/2	1595.121	1595.847	-1085.773	0.406	509.313	0.480	20	0.137	R.VIPNFMLQGGDFTR.G
R5/RRR5-22/2	1269.844	1269.300	-359.989	0.368	669.177	0.447	17	0.135	R.GNGTGGESIYGEK.-
R5/RRR5-19/2	1611.011	1611.847	-1143.117	0.332	348.566	0.527	20	0.135	R.VIPNFM*LQGGDFTR.G
R5/RRR5-20/2	1610.596	1611.847	-1401.878	0.326	352.873	0.422	20	0.130	R.VIPNFM*LQGGDFTR.G
R5/RRR5-19/2	1611.252	1611.847	-992.869	0.308	420.493	0.434	21	0.130	R.VIPNFM*LQGGDFTR.G
R5/RRR5-23/2	1268.936	1269.300	-287.495	0.402	536.373	0.390	17	0.130	R.GNGTGGESIYGEK.-
R5/RRR5-22/2	1269.857	1269.300	-349.862	0.366	475.606	0.438	14	0.129	R.GNGTGGESIYGEK.-
R5/RRR5-22/2	1268.927	1269.300	-294.927	0.349	448.713	0.395	16	0.128	R.GNGTGGESIYGEK.-
R5/RRR5-22/2	1268.841	1269.300	-362.976	0.316	311.152	0.438	14	0.128	R.GNGTGGESIYGEK.-
R5/RRR5-21/2	1268.903	1269.300	-313.459	0.363	385.580	0.389	15	0.127	R.GNGTGGESIYGEK.-
R5/RRR5-21/2	1269.049	1269.300	-197.841	0.350	344.273	0.373	14	0.126	R.GNGTGGESIYGEK.-
R5/RRR5-23/2	1268.582	1269.300	-1358.211	0.296	430.516	0.378	15	0.125	R.GNGTGGESIYGEK.-
R5/RRR5-19/2	1595.382	1595.847	-292.366	0.306	355.199	0.332	17	0.125	R.VIPNFMLQGGDFTR.G
R5/RRR5-23/2	1269.400	1269.300	79.514	0.272	701.828	0.333	17	0.125	R.GNGTGGESIYGEK.-
R5/RRR5-19/2	1610.532	1611.847	-1441.541	0.204	236.257	0.307	18	0.124	R.VIPNFM*LQGGDFTR.G
R5/RRR5-22/2	1268.900	1269.300	-316.354	0.341	418.208	0.314	15	0.124	R.GNGTGGESIYGEK.-
R5/RRR5-22/2	1268.365	1269.300	-1529.882	0.257	315.441	0.326	14	0.123	R.GNGTGGESIYGEK.-
R5/RRR5-22/2	1268.266	1269.300	-1608.101	0.231	399.335	0.333	16	0.122	R.GNGTGGESIYGEK.-
R5/RRR5-23/2	1268.369	1269.300	-1527.175	0.203	255.684	0.342	13	0.121	R.GNGTGGESIYGEK.-
R5/RRR5-20/3	1611.189	1611.847	-1031.899	0.217	961.675	0.209	24	0.059	R.VIPNFM*LQGGDFTR.G
R5/RRR5-19/2	1048.216	1047.189	25.159	0.445	1012.006	0.285	14	0.131	R.LYVGNLDPR.V
R5/RRR5-19/2	1046.946	1047.189	-233.028	0.360	874.486	0.299	13	0.127	R.LYVGNLDPR.V
R5/RRR5-19/3	1456.343	1457.517	-1497.159	0.450	969.873	0.464	22	0.104	K.CYECGEAGHFAR.E
R5/RRR5-13/2	1610.260	1608.731	-293.390	0.606	2468.586	0.543	24	0.363	R.VEEEGDVATAFTLAR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1187.765	1187.411	298.770	0.463	1221.064	0.462	18	0.168	K.KVDAIESLIAK.L
R5/RRR5-14/3	1661.918	1661.796	73.656	0.500	792.207	0.450	26	0.094	K.TKVDELEKDNLSNR.Q
R5/RRR5-18/2	1563.579	1562.733	-98.654	0.348	229.126	0.554	15	0.126	K.QQAPGPAM*EVGSFAR.A
R5/RRR5-18/2	1363.847	1364.526	-1234.252	0.247	618.264	0.436	16	0.122	R.IAASFDELEAVAK.Q
R5/RRR5-17/2	1533.078	1532.721	233.072	0.487	1473.586	0.473	19	0.191	K.GIALSQYYPAYSAK.K
R5/RRR5-17/2	1533.305	1532.721	-272.502	0.551	1406.258	0.485	19	0.186	K.GIALSQYYPAYSAK.K
R5/RRR5-17/2	1647.015	1647.834	-1107.995	0.445	1226.983	0.444	24	0.164	K.M*DGAAWVPASNEAALK.Q
R5/RRR5-17/2	1531.872	1532.721	-1210.929	0.296	829.773	0.307	15	0.122	K.GIALSQYYPAYSAK.K
R5/RRR5-19/2	1353.045	1353.500	-336.948	0.438	1132.444	0.412	18	0.152	K.FLGTLQDVSCGR.D
R5/RRR5-19/2	1197.067	1197.234	-139.880	0.390	880.998	0.328	17	0.131	R.FEDGSISDQAK.R
R5/RRR5-19/2	1197.976	1197.234	-215.301	0.404	883.548	0.318	17	0.130	R.FEDGSISDQAK.R
R5/RRR5-19/2	1198.020	1197.234	-178.604	0.384	775.799	0.271	16	0.122	-.FEDGSISDQAK.-
R5/RRR5-28/2	1303.852	1304.437	-1219.115	0.466	2346.339	0.564	23	0.344	K.NVAAGAAGGPYISR.A
R5/RRR5-28/2	1303.514	1304.437	-1479.424	0.445	2312.807	0.535	24	0.328	K.NVAAGAAGGPYISR.A
R5/RRR5-28/2	1304.147	1304.437	-222.653	0.516	2003.785	0.543	23	0.278	K.NVAAGAAGGPYISR.A
R5/RRR5-27/2	1303.542	1304.437	-1458.071	0.436	1856.140	0.536	22	0.253	K.NVAAGAAGGPYISR.A
R5/RRR5-27/2	1303.396	1304.437	-1570.771	0.460	1905.588	0.499	22	0.251	K.NVAAGAAGGPYISR.A
R5/RRR5-27/2	1303.420	1304.437	-1552.331	0.416	1810.562	0.486	22	0.234	K.NVAAGAAGGPYISR.A
R5/RRR5-9/2	1689.545	1688.943	-235.997	0.521	1374.044	0.460	23	0.180	R.ALFVDLEPTVIDEVK.T
R5/RRR5-9/2	1689.454	1688.943	-290.146	0.532	1279.339	0.477	22	0.175	R.ALFVDLEPTVIDEVK.T
R5/RRR5-9/2	1689.515	1688.943	-254.191	0.548	1075.519	0.491	21	0.162	R.ALFVDLEPTVIDEVK.T
R5/RRR5-8/2	1689.558	1688.943	-228.242	0.522	830.278	0.467	18	0.142	R.ALFVDLEPTVIDEVK.T
R5/RRR5-8/2	1688.305	1688.943	-972.760	0.435	842.808	0.295	19	0.124	R.ALFVDLEPTVIDEVK.T
R5/RRR5-3/2	1688.773	1688.943	-100.602	0.378	577.139	0.242	16	0.115	-.ALFVDLEPTVIDEVK.-
R5/RRR5-26/2	1570.256	1570.753	-317.707	0.500	2391.550	0.540	23	0.344	K.AGGAYTMNTASAVTVR.S
R5/RRR5-26/2	1586.159	1586.752	-1007.616	0.490	2061.535	0.514	22	0.277	K.AGGAYTM*NTASAVTVR.S
R5/RRR5-26/2	1586.274	1586.752	-302.613	0.488	1940.769	0.508	21	0.257	K.AGGAYTM*NTASAVTVR.S
R5/RRR5-25/2	1586.309	1586.752	-280.609	0.517	1873.825	0.530	22	0.253	K.AGGAYTM*NTASAVTVR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/2	1586.188	1586.752	-989.304	0.495	1846.584	0.509	21	0.243	K.AGGAYTM*NTASAVTVR.S
R5/RRR5-25/2	1586.402	1586.752	-221.474	0.500	1596.614	0.471	21	0.203	K.AGGAYTM*NTASAVTVR.S
R5/RRR5-25/2	1586.363	1586.752	-246.254	0.514	1369.943	0.497	21	0.185	K.AGGAYTM*NTASAVTVR.S
R5/RRR5-25/2	1463.772	1464.562	-1226.614	0.431	2588.942	0.355	22	0.324	R.FEALDANGDGVLSR.A
R5/RRR5-25/2	1463.941	1464.562	-1110.722	0.490	2451.248	0.421	23	0.319	R.FEALDANGDGVLSR.A
R5/RRR5-25/2	1464.270	1464.562	-200.061	0.526	2320.972	0.470	22	0.310	R.FEALDANGDGVLSR.A
R5/RRR5-18/2	1176.236	1175.317	-69.285	0.557	1044.074	0.374	18	0.143	K.AADSNTTILLR.L
R5/RRR5-17/3	1810.053	1809.143	-50.104	0.292	902.795	0.294	23	0.069	K.LIQNIVIEAIQSLPTR.A
R5/RRR5-17/2	1594.270	1594.746	-299.558	0.477	1071.356	0.540	22	0.170	K.LAEAPYLDSVDWSK.W
R5/RRR5-16/2	1348.720	1349.601	-1398.882	0.390	1480.227	0.284	19	0.156	R.GAFTVVLSGGSLIK.N
R5/RRR5-16/2	1595.277	1594.746	-294.841	0.524	833.997	0.546	20	0.156	K.LAEAPYLDSVDWSK.W
R5/RRR5-16/2	1349.152	1349.601	-333.746	0.343	1079.361	0.306	17	0.132	R.GAFTVVLSGGSLIK.N
R5/RRR5-3/3	1822.522	1822.938	-228.972	0.552	1328.048	0.485	32	0.147	K.SSLAGEHAAAGNFDTAM*R.L
R5/RRR5-3/2	1189.968	1190.248	-235.579	0.440	1191.512	0.267	16	0.135	K.GWSESASPNVR.G
R5/RRR5-3/2	1190.159	1190.248	-74.749	0.435	811.264	0.325	16	0.128	-.GWSESASPNVR.-
R5/RRR5-3/2	1190.020	1190.248	-191.637	0.388	846.750	0.203	17	0.119	-.GWSESASPNVR.-
R5/RRR5-11/3	1823.811	1822.938	-69.741	0.427	906.827	0.335	30	0.081	K.SSLAGEHAAAGNFDTAM*R.L
R5/RRR5-15/2	1441.276	1441.620	-239.271	0.493	1361.418	0.403	19	0.169	R.IYNQNLINHVGR.G
R5/RRR5-16/2	1441.208	1441.620	-286.857	0.515	1162.875	0.480	19	0.168	R.IYNQNLINHVGR.G
R5/RRR5-16/2	1396.180	1396.533	-253.226	0.449	1163.905	0.458	17	0.162	R.NNIQAYPSVSFR.Y
R5/RRR5-16/2	1397.163	1396.533	-265.141	0.497	1039.169	0.500	17	0.161	R.NNIQAYPSVSFR.Y
R5/RRR5-15/2	1396.106	1396.533	-306.385	0.434	1126.168	0.460	17	0.160	R.NNIQAYPSVSFR.Y
R5/RRR5-15/2	1396.012	1396.533	-1092.325	0.407	1008.148	0.398	16	0.143	R.NNIQAYPSVSFR.Y
R5/RRR5-16/2	1395.511	1396.533	-1453.225	0.310	1104.038	0.221	16	0.126	R.NNIQAYPSVSFR.Y
R5/RRR5-13/2	1220.438	1221.345	-1567.188	0.395	1310.425	0.443	19	0.171	K.VFGSPTSAEVAR.V
R5/RRR5-12/2	1222.083	1221.345	-214.561	0.397	1127.966	0.425	19	0.155	K.VFGSPTSAEVAR.V
R5/RRR5-12/2	1442.006	1441.572	301.623	0.430	981.236	0.468	21	0.153	R.QGNPDLIGTGALER.A
R5/RRR5-13/2	1220.487	1221.345	-1526.195	0.345	1262.870	0.348	19	0.152	K.VFGSPTSAEVAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1441.195	1441.572	-262.053	0.455	641.056	0.577	19	0.150	R.QGNPDLIGTGALER.A
R5/RRR5-13/2	1441.150	1441.572	-293.920	0.441	624.139	0.514	18	0.141	R.QGNPDLIGTGALER.A
R5/RRR5-13/2	1221.070	1221.345	-225.368	0.413	946.885	0.396	17	0.141	K.VFGSPTSAEVAR.V
R5/RRR5-12/2	1221.203	1221.345	-116.061	0.420	833.021	0.358	18	0.133	K.VFGSPTSAEVAR.V
R5/RRR5-12/2	1221.251	1221.345	-76.756	0.371	881.868	0.347	18	0.133	K.VFGSPTSAEVAR.V
R5/RRR5-12/2	1440.577	1441.572	-1388.980	0.326	506.771	0.499	17	0.132	R.QGNPDLIGTGALER.A
R5/RRR5-13/2	1440.549	1441.572	-1408.640	0.339	459.499	0.411	17	0.127	R.QGNPDLIGTGALER.A
R5/RRR5-13/2	1441.069	1441.572	-1046.108	0.355	447.575	0.371	17	0.125	R.QGNPDLIGTGALER.A
R5/RRR5-15/2	1930.726	1930.151	-220.722	0.481	1990.378	0.557	25	0.375	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-15/2	1932.054	1930.151	-50.482	0.579	1797.111	0.656	27	0.316	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-16/2	1731.372	1730.852	-277.959	0.574	2153.054	0.552	23	0.303	R.SGTALCSYIASTAQSGR.I
R5/RRR5-15/2	1730.221	1730.852	-945.515	0.513	2044.582	0.585	23	0.295	R.SGTALCSYIASTAQSGR.I
R5/RRR5-16/2	1730.461	1730.852	-226.455	0.530	2095.160	0.540	23	0.290	R.SGTALCSYIASTAQSGR.I
R5/RRR5-15/2	1931.531	1930.151	197.543	0.478	1681.794	0.592	25	0.277	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-16/2	1731.269	1730.852	241.892	0.583	1866.123	0.615	22	0.274	R.SGTALCSYIASTAQSGR.I
R5/RRR5-16/2	1930.410	1930.151	134.676	0.422	1629.018	0.580	24	0.264	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-16/2	1930.474	1930.151	167.779	0.486	1546.266	0.593	25	0.239	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-15/2	1730.344	1730.852	-874.123	0.502	1714.153	0.563	21	0.238	R.SGTALCSYIASTAQSGR.I
R5/RRR5-15/2	1930.345	1930.151	100.811	0.414	1575.751	0.485	24	0.234	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-16/2	1931.351	1930.151	104.055	0.469	1458.085	0.593	24	0.218	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-15/2	1729.629	1730.852	-1288.734	0.433	1531.460	0.521	20	0.205	R.SGTALCSYIASTAQSGR.I
R5/RRR5-16/2	1930.526	1930.151	194.918	0.491	1377.440	0.558	24	0.193	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-16/2	1929.504	1930.151	-856.173	0.381	1328.402	0.512	24	0.184	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-16/2	1930.241	1930.151	46.646	0.464	1277.104	0.610	22	0.182	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-15/2	1930.199	1930.151	24.827	0.470	1202.539	0.570	23	0.163	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-15/2	1928.889	1930.151	-1175.979	0.376	1162.496	0.537	22	0.157	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-15/2	1929.178	1930.151	-1025.834	0.274	688.483	0.380	18	0.104	R.ISGIPSGTVNLLAFNGNPSA.-
R5/RRR5-24/2	1324.069	1324.511	-335.075	0.362	495.553	0.539	16	0.137	K.QIPLSGPNSVVGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1325.201	1324.511	-235.007	0.350	552.167	0.504	17	0.135	K.QIPLSGPNSVVGR.A
R5/RRR5-23/2	1324.223	1324.511	-218.445	0.337	535.878	0.464	16	0.131	K.QIPLSGPNSVVGR.A
R5/RRR5-23/2	1323.667	1324.511	-1397.701	0.299	470.337	0.506	16	0.130	K.QIPLSGPNSVVGR.A
R5/RRR5-23/2	1324.127	1324.511	-291.046	0.334	462.128	0.441	15	0.128	K.QIPLSGPNSVVGR.A
R5/RRR5-24/2	1323.771	1324.511	-1318.604	0.212	467.934	0.356	16	0.119	K.QIPLSGPNSVVGR.A
R5/RRR5-23/3	1414.216	1413.479	-186.286	0.317	299.757	0.567	23	0.095	K.GGHELSLSTGNAGGR.L
R5/RRR5-24/3	1413.855	1413.479	267.048	0.291	247.272	0.311	22	0.089	K.GGHELSLSTGNAGGR.L
R5/RRR5-23/3	1413.588	1413.479	77.414	0.358	276.219	0.422	23	0.087	-.GGHELSLSTGNAGGR.-
R5/RRR5-24/3	1413.684	1413.479	145.613	0.320	244.605	0.412	21	0.086	-.GGHELSLSTGNAGGR.-
R5/RRR5-24/3	1413.538	1413.479	42.467	0.349	276.161	0.352	23	0.082	-.GGHELSLSTGNAGGR.-
R5/RRR5-9/2	1446.850	1447.533	-1167.085	0.527	1512.467	0.495	24	0.202	R.EVEAIGGNVSASASR.E
R5/RRR5-9/2	1447.248	1447.533	-198.015	0.546	1459.473	0.507	24	0.199	R.EVEAIGGNVSASASR.E
R5/RRR5-9/2	1721.401	1721.011	226.778	0.486	1332.977	0.455	21	0.174	K.AYVPEMVEVLIDSVR.N
R5/RRR5-17/2	1606.371	1606.798	-266.738	0.470	2623.790	0.338	23	0.326	R.FQAQADAVNLICGAK.T
R5/RRR5-12/2	1558.136	1558.671	-988.020	0.447	520.105	0.487	18	0.133	R.GCSANVFLDNAAYR.Q
R5/RRR5-12/2	1314.226	1314.477	-190.853	0.271	251.265	0.566	13	0.127	R.QHAFWVPVSSR.Y
R5/RRR5-12/2	1314.146	1314.477	-252.356	0.216	225.234	0.512	12	0.120	R.QHAFWVPVSSR.Y
R5/RRR5-12/2	1315.171	1314.477	-232.982	0.208	259.760	0.441	14	0.120	R.QHAFWVPVSSR.Y
R5/RRR5-27/2	1333.549	1333.497	39.093	0.442	1100.656	0.429	19	0.154	R.NLNM*GNAASIPSK.C
R5/RRR5-27/2	1334.056	1333.497	-331.061	0.485	1099.057	0.413	19	0.152	R.NLNM*GNAASIPSK.C
R5/RRR5-27/2	1334.165	1333.497	-249.451	0.496	966.852	0.439	19	0.148	R.NLNM*GNAASIPSK.C
R5/RRR5-27/2	1814.820	1815.002	-100.361	0.500	761.779	0.531	21	0.146	K.CGVSVAFPISTSVDCSK.I
R5/RRR5-26/2	1334.007	1333.497	-368.061	0.441	811.242	0.461	18	0.143	R.NLNM*GNAASIPSK.C
R5/RRR5-26/2	1332.904	1333.497	-1198.201	0.433	981.241	0.369	19	0.140	R.NLNM*GNAASIPSK.C
R5/RRR5-27/2	1333.089	1333.497	-306.779	0.412	883.785	0.402	19	0.140	R.NLNM*GNAASIPSK.C
R5/RRR5-27/2	1332.999	1333.497	-374.218	0.382	930.299	0.381	19	0.139	R.NLNM*GNAASIPSK.C
R5/RRR5-27/2	1333.985	1333.497	367.203	0.465	813.944	0.403	18	0.137	R.NLNM*GNAASIPSK.C
R5/RRR5-26/2	1333.025	1333.497	-355.106	0.436	824.208	0.353	18	0.132	R.NLNM*GNAASIPSK.C

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-28/2	1333.046	1333.497	-339.211	0.352	485.836	0.326	15	0.123	R.NLNM*GNAASIPSK.C
R5/RRR5-12/2	1234.359	1235.371	-1635.313	0.395	827.216	0.222	13	0.116	K.IDYINEALQR.L
R5/RRR5-12/3	1148.337	1148.300	32.283	0.375	1001.662	0.196	21	0.061	-.VHPANLNLGGR.-
R5/RRR5-3/2	1010.543	1011.243	-1687.457	0.372	734.428	0.403	15	0.133	R.LIGASLPAIR.A
R5/RRR5-3/2	1010.666	1011.243	-1564.895	0.316	686.939	0.417	15	0.131	R.LIGASLPAIR.A
R5/RRR5-3/2	1490.251	1490.749	-335.265	0.424	623.425	0.450	16	0.131	R.TYIGPM*TPPLVER.I
R5/RRR5-3/2	1011.078	1011.243	-163.915	0.429	555.701	0.384	14	0.129	R.LIGASLPAIR.A
R5/RRR5-12/2	1615.118	1615.641	-945.809	0.464	2429.484	0.472	25	0.332	R.LDFSSGQSTGTASNSR.L
R5/RRR5-11/2	1615.083	1615.641	-967.283	0.436	2045.160	0.457	23	0.261	R.LDFSSGQSTGTASNSR.L
R5/RRR5-14/2	1994.154	1995.261	-1059.762	0.553	1053.847	0.588	24	0.174	R.VQIANFLCPGNYAVSGGVK.G
R5/RRR5-13/2	1204.034	1204.352	-265.266	0.390	1227.717	0.388	17	0.156	R.LESALAETEIK.T
R5/RRR5-14/2	1204.456	1204.352	86.241	0.382	1229.746	0.287	17	0.142	R.LESALAETEIK.T
R5/RRR5-13/2	1203.527	1204.352	-1521.150	0.324	693.100	0.285	15	0.122	R.LESALAETEIK.T
R5/RRR5-14/2	1204.324	1204.352	-23.648	0.240	975.024	0.127	16	0.115	R.LESALAETEIK.T
R5/RRR5-21/2	1282.917	1283.330	-322.537	0.410	512.347	0.470	15	0.129	K.GDGTGGKSIYGDR.F
R5/RRR5-21/2	1637.366	1637.770	-247.406	0.403	769.841	0.441	19	0.093	K.SGELEVPEEGIHVEL.-
R5/RRR5-21/2	1637.050	1637.770	-1053.326	0.355	551.807	0.447	18	0.092	K.SGELEVPEEGIHVEL.-
R5/RRR5-21/2	1637.261	1637.770	-924.193	0.377	713.175	0.394	18	0.088	K.SGELEVPEEGIHVEL.-
R5/RRR5-6/2	1787.523	1785.871	-195.302	0.566	2285.807	0.608	25	0.350	R.AYLQATGQDGDVDM*ER.L
R5/RRR5-5/2	1258.211	1257.422	-167.919	0.533	1157.463	0.531	17	0.175	K.ADLVNNLGTIAR.S
R5/RRR5-5/2	1256.456	1257.422	-1569.231	0.317	837.699	0.305	15	0.124	K.ADLVNNLGTIAR.S
R5/RRR5-5/2	1257.349	1257.422	-57.901	0.334	570.659	0.408	13	0.124	-.ADLVNNLGTIAR.-
R5/RRR5-5/3	1847.564	1847.148	225.665	0.444	1068.060	0.371	26	0.096	K.HSEFISYPIYLHVLK.E
R5/RRR5-5/3	1847.804	1847.148	-186.770	0.426	1026.509	0.300	27	0.081	K.HSEFISYPIYLHVLK.E
R5/RRR5-5/3	1846.312	1847.148	-997.710	0.365	685.860	0.328	21	0.073	-.HSEFISYPIYLHVLK.-
R5/RRR5-8/2	1258.704	1257.455	198.278	0.462	1536.022	0.485	18	0.201	K.AAIDVVCNPLGK.S
R5/RRR5-9/2	1257.224	1257.455	-184.509	0.479	1318.981	0.471	17	0.177	K.AAIDVVCNPLGK.S
R5/RRR5-1/2	1130.963	1130.318	-315.424	0.360	1033.473	0.456	15	0.151	K.FVLNDPSLPK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1257.263	1257.455	-153.146	0.287	1315.559	0.291	16	0.145	K.AAIDVVCNPLGK.S
R5/RRR5-9/2	1130.566	1130.318	219.560	0.324	743.275	0.236	13	0.117	K.FVLNDPSLPK.S
R5/RRR5-14/2	1229.248	1228.377	-105.241	0.540	853.038	0.388	14	0.133	R.AILENPNDITK.V
R5/RRR5-15/2	1229.031	1228.377	-282.285	0.344	839.251	0.366	15	0.131	R.AILENPNDITK.V
R5/RRR5-15/2	1227.194	1228.377	-1784.239	0.231	167.462	0.392	12	0.114	-.AILENPNDITK.-
R5/RRR5-15/3	1436.528	1436.615	-60.862	0.425	620.148	0.479	21	0.095	K.AM*AAHLDELGYTK.E
R5/RRR5-15/3	1436.176	1436.615	-306.914	0.464	799.435	0.405	24	0.091	K.AM*AAHLDELGYTK.E
R5/RRR5-14/3	1436.472	1436.615	-100.243	0.422	602.407	0.392	21	0.085	K.AM*AAHLDELGYTK.E
R5/RRR5-14/3	1436.477	1436.615	-96.535	0.408	709.587	0.373	21	0.083	K.AM*AAHLDELGYTK.E
R5/RRR5-15/3	1435.442	1436.615	-1518.990	0.386	920.078	0.294	24	0.078	K.AM*AAHLDELGYTK.E
R5/RRR5-10/2	1753.120	1754.018	-1086.113	0.401	1306.404	0.488	24	0.176	K.IQLLDLPGIIEGASEGK.G
R5/RRR5-10/2	1088.072	1088.324	-232.998	0.459	616.246	0.470	14	0.135	R.VALIGFPSVGK.S
R5/RRR5-10/2	1087.907	1088.324	-384.516	0.428	599.186	0.381	14	0.127	R.VALIGFPSVGK.S
R5/RRR5-16/2	1617.202	1617.659	-283.046	0.466	1325.469	0.427	20	0.169	K.NSWGADWGDNGYFK.M
R5/RRR5-17/2	1616.813	1617.659	-1144.736	0.423	994.165	0.422	17	0.144	K.NSWGADWGDNGYFK.M
R5/RRR5-17/2	1617.284	1617.659	-232.082	0.406	1053.328	0.357	19	0.140	K.NSWGADWGDNGYFK.M
R5/RRR5-17/2	1617.282	1617.659	-233.672	0.462	661.523	0.430	16	0.131	K.NSWGADWGDNGYFK.M
R5/RRR5-17/3	1401.210	1401.549	-242.627	0.475	1327.122	0.262	27	0.091	K.DWREDGIVSPVK.D
R5/RRR5-17/3	1401.522	1401.549	-19.544	0.522	1161.229	0.309	26	0.091	K.DWREDGIVSPVK.D
R5/RRR5-17/3	1401.111	1401.549	-313.951	0.476	908.648	0.249	24	0.075	K.DWREDGIVSPVK.D
R5/RRR5-16/3	1401.981	1401.549	309.133	0.476	858.310	0.293	24	0.074	-.DWREDGIVSPVK.-
R5/RRR5-16/3	1401.751	1401.549	144.101	0.424	721.297	0.245	20	0.073	K.DWREDGIVSPVK.D
R5/RRR5-15/3	1401.707	1401.549	112.791	0.409	746.706	0.212	22	0.072	K.DWREDGIVSPVK.D
R5/RRR5-16/3	1401.460	1401.549	-63.838	0.473	815.360	0.248	24	0.069	-.DWREDGIVSPVK.-
R5/RRR5-14/2	1114.982	1115.267	-256.035	0.334	822.053	0.545	18	0.147	R.AHAYAAAVAAAK.G
R5/RRR5-14/2	1441.797	1442.646	-1286.751	0.414	719.296	0.497	15	0.137	R.WVLSAADPWVAAR.G
R5/RRR5-14/3	1115.104	1115.267	-146.715	0.486	1004.660	0.369	23	0.092	R.AHAYAAAVAAAK.G
R5/RRR5-14/3	1114.929	1115.267	-303.884	0.373	626.225	0.289	18	0.066	-.AHAYAAAVAAAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1883.559	1884.165	-855.346	0.563	2207.583	0.642	26	0.344	K.GPDVVGSFGLLQPLADGLK.L
R5/RRR5-1/2	1883.474	1884.165	-900.498	0.494	1915.142	0.596	25	0.278	K.GPDVVGSFGLLQPLADGLK.L
R5/RRR5-6/2	1650.509	1650.856	-210.942	0.552	1495.912	0.391	22	0.177	R.QFLTLNALNEFDPK.I
R5/RRR5-6/2	1650.440	1650.856	-252.865	0.499	1187.218	0.403	19	0.154	R.QFLTLNALNEFDPK.I
R5/RRR5-6/2	1650.088	1650.856	-1074.684	0.475	1185.325	0.367	20	0.149	R.QFLTLNALNEFDPK.I
R5/RRR5-6/3	1439.412	1439.510	-68.194	0.428	935.895	0.447	26	0.101	R.CEVHAVNADPGGGR.Q
R5/RRR5-6/3	1439.498	1439.510	-8.227	0.451	958.915	0.408	26	0.096	R.CEVHAVNADPGGGR.Q
R5/RRR5-6/3	1438.976	1439.510	-1068.740	0.452	691.994	0.424	23	0.088	R.CEVHAVNADPGGGR.Q
R5/RRR5-9/2	1426.915	1427.584	-1172.664	0.358	1628.700	0.232	17	0.160	R.ASYIDFLLEAER.S
R5/RRR5-8/3	1573.782	1573.820	-24.251	0.415	811.291	0.466	25	0.098	R.LPYLNAVFHETLR.R
R5/RRR5-9/3	1573.238	1573.820	-1008.740	0.411	796.161	0.436	23	0.091	-.LPYLNAVFHETLR.-
R5/RRR5-8/3	1574.193	1573.820	238.020	0.339	461.579	0.419	19	0.084	R.LPYLNAVFHETLR.R
R5/RRR5-8/3	1573.441	1573.820	-241.242	0.295	814.926	0.294	23	0.073	R.LPYLNAVFHETLR.R
R5/RRR5-8/2	1503.650	1503.597	35.452	0.434	1435.710	0.495	22	0.191	R.ASQPTDTTTSPLAGR.L
R5/RRR5-7/2	1333.285	1332.525	-180.779	0.472	705.332	0.548	19	0.150	K.IATTATEIVDVAK.M
R5/RRR5-7/2	1332.109	1332.525	-313.199	0.404	808.910	0.425	19	0.138	K.IATTATEIVDVAK.M
R5/RRR5-7/2	1332.524	1332.525	-0.791	0.297	394.253	0.342	15	0.121	K.IATTATEIVDVAK.M
R5/RRR5-14/2	1795.447	1794.039	227.791	0.467	1288.994	0.548	21	0.185	R.LATSGLSVVEATSFVSPK.W
R5/RRR5-14/2	1593.851	1594.877	-1275.150	0.289	818.374	0.323	16	0.120	R.NIEGVSLPVLTPNLK.G
R5/RRR5-9/2	1740.936	1741.879	-1119.383	0.407	1289.953	0.475	22	0.172	R.EVAAFAQFGSDLDAATK.Q
R5/RRR5-7/2	1587.245	1587.754	-953.547	0.468	1147.580	0.293	21	0.136	R.NCPEFAFSFLGAAR.L
R5/RRR5-7/2	1586.721	1587.754	-1285.047	0.356	1050.998	0.192	20	0.121	R.NCPEFAFSFLGAAR.L
R5/RRR5-1/2	1258.254	1257.470	-171.708	0.328	874.823	0.321	14	0.125	R.EAARVKVWAAR.A
R5/RRR5-12/3	1128.719	1129.295	-1400.421	0.342	1078.375	0.096	21	0.057	-.RGGVKAAAAAEK.-
R5/RRR5-4/2	1732.373	1731.934	254.106	0.519	1563.530	0.514	21	0.210	K.LNSELLNNLGNFINR.V
R5/RRR5-5/2	1203.440	1202.301	115.411	0.465	1022.500	0.570	19	0.171	K.SHGIGVFGNDAK.D
R5/RRR5-4/2	1731.727	1731.934	-120.095	0.532	1124.314	0.475	19	0.160	K.LNSELLNNLGNFINR.V
R5/RRR5-5/2	1202.731	1202.301	357.862	0.351	649.262	0.555	15	0.140	K.SHGIGVFGNDAK.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1731.949	1731.934	8.581	0.373	1047.483	0.335	17	0.134	K.LNSELLNNLGNFINR.V
R5/RRR5-6/2	1732.645	1731.934	-167.447	0.406	600.601	0.375	16	0.124	K.LNSELLNNLGNFINR.V
R5/RRR5-5/3	1732.155	1731.934	127.711	0.425	723.333	0.483	21	0.091	K.LNSELLNNLGNFINR.V
R5/RRR5-16/2	1711.744	1711.896	-89.524	0.479	961.286	0.465	21	0.148	K.TEGVFSFLPASQATGAK.F
R5/RRR5-16/2	1131.899	1132.249	-310.187	0.360	713.890	0.357	17	0.126	K.AGNSVGLEVASK.Y
R5/RRR5-16/2	1711.075	1711.896	-1067.936	0.420	645.115	0.403	18	0.126	K.TEGVFSFLPASQATGAK.F
R5/RRR5-8/2	1040.096	1039.210	-110.490	0.514	868.476	0.447	15	0.146	K.SPELAGPVLR.L
R5/RRR5-8/2	1039.961	1039.210	-240.598	0.473	825.607	0.436	15	0.142	K.SPELAGPVLR.L
R5/RRR5-8/2	1040.211	1039.210	0.517	0.513	870.422	0.420	15	0.142	K.SPELAGPVLR.L
R5/RRR5-7/2	1039.298	1039.210	84.631	0.355	673.450	0.277	13	0.121	K.SPELAGPVLR.L
R5/RRR5-8/3	1319.288	1319.495	-157.557	0.443	767.574	0.479	22	0.098	K.IGVLTHSHGEIR.H
R5/RRR5-8/3	1319.628	1319.495	100.925	0.435	519.569	0.519	20	0.096	K.IGVLTHSHGEIR.H
R5/RRR5-8/3	1319.206	1319.495	-219.239	0.338	573.850	0.351	20	0.078	K.IGVLTHSHGEIR.H
R5/RRR5-13/2	1542.270	1540.848	274.197	0.516	943.157	0.423	17	0.142	K.VM*DVVLPFFESLK.L
R5/RRR5-12/2	1060.156	1059.243	-82.876	0.464	453.798	0.478	15	0.139	K.LGPQNAIFAK.A
R5/RRR5-13/2	1059.198	1059.243	-42.840	0.318	388.193	0.481	14	0.132	K.LGPQNAIFAK.A
R5/RRR5-12/2	1059.068	1059.243	-166.083	0.353	431.649	0.425	14	0.131	K.LGPQNAIFAK.A
R5/RRR5-13/2	1058.802	1059.243	-417.751	0.362	346.648	0.415	13	0.130	K.LGPQNAIFAK.A
R5/RRR5-12/2	1059.141	1059.243	-96.712	0.295	470.830	0.412	15	0.128	K.LGPQNAIFAK.A
R5/RRR5-12/2	1058.519	1059.243	-1634.109	0.270	516.760	0.289	15	0.123	K.LGPQNAIFAK.A
R5/RRR5-13/2	1058.415	1059.243	-1732.249	0.181	356.551	0.323	14	0.120	K.LGPQNAIFAK.A
R5/RRR5-12/2	1524.099	1524.849	-1151.391	0.234	691.711	0.214	15	0.113	K.VMDVVLPFFESLK.L
R5/RRR5-17/2	1328.176	1328.493	-239.827	0.416	1023.093	0.425	17	0.148	R.NCLPDQVVVQR.I
R5/RRR5-17/2	1328.115	1328.493	-285.932	0.462	877.125	0.349	17	0.133	R.NCLPDQVVVQR.I
R5/RRR5-17/3	1950.247	1952.195	-2030.288	0.346	1048.196	0.321	28	0.081	R.QTIAGNILVGSYCAITNR.G
R5/RRR5-14/2	1365.295	1365.514	-161.026	0.321	1034.123	0.454	16	0.149	K.EPYTATIVSVER.L
R5/RRR5-14/2	1366.513	1365.514	-0.771	0.366	987.309	0.436	15	0.145	K.EPYTATIVSVER.L
R5/RRR5-14/2	1365.090	1365.514	-311.193	0.259	1105.462	0.408	16	0.145	K.EPYTATIVSVER.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	910.801	911.037	-260.669	0.195	839.463	0.313	13	0.122	R.LYSIASTR.Y
R5/RRR5-14/2	910.356	911.037	-1852.656	0.273	730.583	0.215	12	0.119	R.LYSIASTR.Y
R5/RRR5-14/2	910.198	911.037	-2027.446	0.245	677.688	0.229	12	0.118	R.LYSIASTR.Y
R5/RRR5-13/2	911.090	911.037	57.771	0.189	718.727	0.169	12	0.114	R.LYSIASTR.Y
R5/RRR5-9/2	1058.960	1059.155	-185.293	0.505	1156.396	0.315	15	0.142	R.IEEELGNVR.Y
R5/RRR5-9/2	1058.953	1059.155	-191.769	0.496	1008.493	0.326	15	0.137	R.IEEELGNVR.Y
R5/RRR5-9/2	1331.044	1331.604	-1175.445	0.307	719.073	0.393	14	0.124	R.EGLVLLMDAIEK.A
R5/RRR5-9/2	1058.936	1059.155	-207.844	0.347	784.775	0.289	14	0.124	-.IEEELGNVR.-
R5/RRR5-9/2	1754.992	1754.918	42.374	0.562	2272.135	0.566	23	0.331	K.IPFSSFDILTDDEVR.Q
R5/RRR5-8/2	1755.284	1754.918	209.008	0.540	2108.609	0.522	23	0.289	K.IPFSSFDILTDDEVR.Q
R5/RRR5-9/2	1753.468	1754.918	-1401.577	0.390	1389.442	0.394	19	0.167	K.IPFSSFDILTDDEVR.Q
R5/RRR5-11/2	1554.258	1554.770	-975.439	0.433	984.381	0.430	20	0.145	R.VLTDVGDVPIQEIR.D
R5/RRR5-11/2	1101.275	1101.322	-42.093	0.380	1000.488	0.368	16	0.140	R.VIDASLTLIR.E
R5/RRR5-11/2	1101.587	1101.322	241.896	0.148	600.015	0.212	13	0.111	R.VIDASLTLIR.E
R5/RRR5-11/2	1397.114	1397.473	-257.175	0.364	616.463	0.452	16	0.129	K.DGTGTLTVFTNDR.G
R5/RRR5-11/3	1884.760	1885.236	-253.461	0.407	1456.177	0.336	30	0.122	R.QAIPFLESLVVADVAALK.D
R5/RRR5-12/2	1125.846	1125.280	-386.522	0.364	949.219	0.338	14	0.131	K.GLAEM*FGDLR.V
R5/RRR5-12/2	1176.955	1177.289	-284.581	0.252	921.069	0.364	15	0.130	K.GYDPEVIDIR.S
R5/RRR5-12/2	1176.659	1177.289	-1388.773	0.133	654.103	0.176	12	0.110	-.GYDPEVIDIR.-
R5/RRR5-4/2	1675.342	1675.862	-909.982	0.394	1533.556	0.525	20	0.205	K.AAVAVLGDLADTLGSSSK.D
R5/RRR5-4/2	1675.376	1675.862	-290.976	0.381	1519.479	0.442	22	0.188	K.AAVAVLGDLADTLGSSSK.D
R5/RRR5-5/2	1674.671	1675.862	-1312.456	0.325	1370.775	0.479	20	0.178	K.AAVAVLGDLADTLGSSSK.D
R5/RRR5-1/2	1675.754	1675.862	-64.852	0.334	786.517	0.516	19	0.141	K.AAVAVLGDLADTLGSSSK.D
R5/RRR5-4/2	1337.087	1336.476	-291.430	0.335	742.422	0.350	14	0.125	R.ASAYEALNEIVR.V
R5/RRR5-5/2	1336.351	1336.476	-93.600	0.325	850.524	0.236	14	0.118	R.ASAYEALNEIVR.V
R5/RRR5-5/2	1674.578	1675.862	-1368.536	0.286	525.306	0.343	16	0.118	K.AAVAVLGDLADTLGSSSK.D
R5/RRR5-5/2	1335.420	1336.476	-1544.105	0.250	540.870	0.168	12	0.110	-.ASAYEALNEIVR.-
R5/RRR5-9/2	1066.884	1066.269	-361.681	0.404	611.071	0.468	14	0.137	R.LVFQVCTAK.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1066.122	1066.269	-138.226	0.217	627.843	0.354	12	0.119	R.LVFQVCTAK.M
R5/RRR5-4/2	1324.179	1323.439	-197.093	0.519	1639.347	0.462	17	0.209	R.INFVTWSQDGR.H
R5/RRR5-4/2	1474.208	1474.602	-268.144	0.490	1407.885	0.396	19	0.170	K.IQSNETSNVVQVR.T
R5/RRR5-4/2	1322.376	1323.439	-1564.706	0.425	1161.583	0.445	16	0.160	R.INFVTWSQDGR.H
R5/RRR5-4/2	1322.718	1323.439	-1304.658	0.444	916.007	0.433	15	0.143	R.INFVTWSQDGR.H
R5/RRR5-17/2	1348.973	1349.510	-1142.214	0.465	850.908	0.302	13	0.124	-.VEWCVLDWNK.-
R5/RRR5-17/2	1349.202	1349.510	-228.376	0.227	737.577	0.122	12	0.106	-.VEWCVLDWNK.-
R5/RRR5-23/3	1695.109	1694.081	16.886	0.396	938.347	0.258	25	0.068	-.MMLSAVAGKAAELGMGR.-
R5/RRR5-11/2	1758.425	1756.854	-244.926	0.434	1493.318	0.482	23	0.194	R.LGFTEAAGNFQTSNNGK.G
R5/RRR5-11/2	1586.339	1586.689	-221.096	0.496	1187.443	0.528	22	0.176	K.GGLGNDAVILNSQDGR.S
R5/RRR5-11/2	1586.014	1586.689	-1059.508	0.485	861.037	0.595	19	0.161	K.GGLGNDAVILNSQDGR.S
R5/RRR5-11/2	1585.719	1586.689	-1246.326	0.431	805.134	0.524	19	0.147	K.GGLGNDAVILNSQDGR.S
R5/RRR5-7/2	1225.702	1226.408	-1395.937	0.433	1301.172	0.491	20	0.179	R.GIPSLVAIGADGR.T
R5/RRR5-6/2	1226.306	1226.408	-83.229	0.331	898.667	0.431	16	0.139	R.GIPSLVAIGADGR.T
R5/RRR5-7/3	1861.303	1861.004	161.081	0.444	1388.894	0.404	31	0.131	K.TPLTAHGADAFPFTEER.-
R5/RRR5-7/2	1225.495	1226.408	-1565.517	0.305	724.968	0.414	15	0.129	R.GIPSLVAIGADGR.T
R5/RRR5-6/2	1226.038	1226.408	-302.148	0.274	751.199	0.372	14	0.125	R.GIPSLVAIGADGR.T
R5/RRR5-6/2	1225.897	1226.408	-1236.315	0.338	759.614	0.284	16	0.122	R.GIPSLVAIGADGR.T
R5/RRR5-7/3	1862.392	1861.004	209.175	0.449	1266.188	0.380	30	0.112	K.TPLTAHGADAFPFTEER.-
R5/RRR5-6/3	1860.273	1861.004	-933.324	0.406	1016.534	0.388	28	0.096	K.TPLTAHGADAFPFTEER.-
R5/RRR5-6/3	1860.560	1861.004	-239.319	0.430	807.479	0.372	27	0.085	K.TPLTAHGADAFPFTEER.-
R5/RRR5-6/3	1860.925	1861.004	-42.583	0.425	818.743	0.357	26	0.083	K.TPLTAHGADAFPFTEER.-
R5/RRR5-7/3	1861.399	1861.004	212.674	0.435	630.527	0.295	24	0.068	-.TPLTAHGADAFPFTEER.-
R5/RRR5-9/2	1659.699	1659.861	-97.938	0.473	1419.509	0.446	21	0.181	K.ELQGVVFDDVPEALK.H
R5/RRR5-9/2	1659.667	1659.861	-117.490	0.453	1028.399	0.466	18	0.152	K.ELQGVVFDDVPEALK.H
R5/RRR5-8/2	1659.377	1659.861	-292.527	0.462	1102.253	0.423	19	0.151	K.ELQGVVFDDVPEALK.H
R5/RRR5-8/2	1659.292	1659.861	-948.890	0.328	927.380	0.316	18	0.128	K.ELQGVVFDDVPEALK.H
R5/RRR5-8/3	1854.465	1854.950	-262.421	0.557	1103.720	0.485	34	0.123	K.HLTSTYSSDETKEDIK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/3	1854.714	1854.950	-127.520	0.577	793.336	0.507	30	0.109	K.HLTSTYSSDETKEDIK.L
R5/RRR5-7/3	1854.310	1854.950	-886.738	0.547	606.157	0.493	27	0.100	K.HLTSTYSSDETKEDIK.L
R5/RRR5-8/3	1854.908	1854.950	-22.556	0.500	662.677	0.477	28	0.099	K.HLTSTYSSDETKEDIK.L
R5/RRR5-16/3	1854.822	1854.950	-69.094	0.519	731.287	0.456	31	0.098	K.HLTSTYSSDETKEDIK.L
R5/RRR5-7/3	1854.491	1854.950	-248.355	0.513	547.037	0.433	26	0.092	K.HLTSTYSSDETKEDIK.L
R5/RRR5-1/3	1854.125	1854.950	-987.068	0.395	286.230	0.330	21	0.085	-.HLTSTYSSDETKEDIK.-
R5/RRR5-14/2	1192.344	1193.288	-1635.022	0.356	755.709	0.371	13	0.127	-.LNLDDAFEQK.-
R5/RRR5-14/2	1329.340	1329.398	-44.082	0.320	894.775	0.361	17	0.085	R.DGLLQGQATTTSH.-
R5/RRR5-15/1	1151.676	1152.279	-1396.297	0.411	926.038	0.365	14	0.559	R.AALYLASDEAK.Y
R5/RRR5-14/3	1845.625	1845.008	-207.987	0.587	2299.356	0.505	37	0.326	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-15/3	1844.563	1845.008	-241.726	0.569	2173.438	0.502	36	0.295	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-15/3	1845.808	1845.008	-108.667	0.553	2109.537	0.466	38	0.263	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/3	1844.376	1845.008	-887.332	0.514	1996.200	0.488	33	0.253	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-15/3	1845.076	1845.008	37.246	0.564	1794.450	0.490	34	0.212	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/3	1845.065	1845.008	30.875	0.535	1784.867	0.485	33	0.210	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/2	1151.404	1152.279	-1632.971	0.403	1793.353	0.364	17	0.204	R.AALYLASDEAK.Y
R5/RRR5-14/2	1152.985	1152.279	-256.197	0.580	1584.731	0.463	17	0.201	R.AALYLASDEAK.Y
R5/RRR5-15/2	1151.953	1152.279	-284.168	0.497	1525.769	0.431	17	0.189	R.AALYLASDEAK.Y
R5/RRR5-16/2	1153.143	1152.279	-118.239	0.512	1526.427	0.424	17	0.187	R.AALYLASDEAK.Y
R5/RRR5-16/3	1844.834	1845.008	-94.754	0.539	1752.091	0.435	33	0.185	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-15/2	1152.082	1152.279	-171.804	0.542	1559.654	0.398	17	0.185	R.AALYLASDEAK.Y
R5/RRR5-16/2	1152.015	1152.279	-229.843	0.505	1500.590	0.409	17	0.182	R.AALYLASDEAK.Y
R5/RRR5-16/2	1152.050	1152.279	-199.228	0.508	1468.347	0.419	17	0.181	R.AALYLASDEAK.Y
R5/RRR5-14/2	1151.993	1152.279	-248.765	0.510	1433.110	0.432	16	0.179	R.AALYLASDEAK.Y
R5/RRR5-15/2	1152.127	1152.279	-132.371	0.502	1363.732	0.451	16	0.177	R.AALYLASDEAK.Y
R5/RRR5-15/2	1845.446	1845.008	238.272	0.527	1104.727	0.550	23	0.173	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-16/3	1845.035	1845.008	14.850	0.550	1470.761	0.515	33	0.170	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-15/2	1846.636	1845.008	-202.064	0.531	975.909	0.540	22	0.161	K.YVNGHNLVVDGGFTSHK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/3	1845.289	1845.008	152.592	0.543	1434.497	0.472	30	0.152	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-15/3	1845.699	1845.008	-168.077	0.530	1254.830	0.459	33	0.129	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/3	1845.198	1845.008	103.133	0.475	1054.266	0.485	35	0.118	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/3	1845.383	1845.008	203.938	0.481	922.555	0.463	35	0.106	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/3	1845.309	1845.008	163.937	0.534	650.314	0.507	31	0.105	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/3	1846.213	1845.008	111.598	0.472	926.358	0.455	26	0.104	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-14/3	1845.707	1845.008	-163.698	0.429	1220.185	0.344	29	0.100	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-15/3	1846.562	1845.008	-242.128	0.396	473.167	0.408	27	0.092	K.YVNGHNLVVDGGFTSHK.G
R5/RRR5-9/2	1182.198	1182.396	-168.463	0.463	934.613	0.425	17	0.144	R.LAFLGSSLFAR.A
R5/RRR5-9/2	1200.290	1200.410	-100.436	0.362	920.835	0.237	17	0.121	R.LLAAELTEIAR.A
R5/RRR5-6/2	1859.871	1858.166	-158.955	0.514	1351.146	0.526	21	0.187	K.GVLISNASIICLVAGVDR.L
R5/RRR5-6/2	1857.458	1858.166	-922.273	0.369	707.046	0.415	15	0.124	K.GVLISNASIICLVAGVDR.L
R5/RRR5-6/3	1418.426	1418.540	-80.684	0.386	721.572	0.533	28	0.101	R.AAADGRPSVGPTYR.S
R5/RRR5-6/3	1418.331	1418.540	-147.893	0.344	490.663	0.529	23	0.092	R.AAADGRPSVGPTYR.S
R5/RRR5-6/3	1418.821	1418.540	198.933	0.334	463.558	0.499	24	0.088	R.AAADGRPSVGPTYR.S
R5/RRR5-14/2	1828.547	1828.016	-256.960	0.431	568.228	0.462	19	0.129	R.AGAEEVLPLGPLNDFER.A
R5/RRR5-9/2	1310.365	1310.445	-61.352	0.501	859.065	0.542	17	0.159	R.RGPEWFASFGR.K
R5/RRR5-8/2	1310.850	1310.445	309.852	0.449	541.231	0.539	13	0.140	R.RGPEWFASFGR.K
R5/RRR5-9/2	1561.603	1560.841	-153.172	0.347	313.238	0.580	20	0.136	K.AVQSGLGTAAVIVMDK.S
R5/RRR5-9/2	1309.671	1310.445	-1358.415	0.474	627.109	0.401	16	0.133	R.RGPEWFASFGR.K
R5/RRR5-8/2	1311.024	1310.445	-321.785	0.366	573.434	0.360	15	0.127	R.RGPEWFASFGR.K
R5/RRR5-9/2	1561.040	1560.841	127.484	0.353	249.815	0.529	19	0.126	-.AVQSGLGTAAVIVMDK.-
R5/RRR5-9/2	1577.247	1576.841	258.743	0.265	241.406	0.376	17	0.124	K.AVQSGLGTAAVIVM*DK.S
R5/RRR5-8/2	1577.499	1576.841	-217.074	0.217	138.663	0.470	17	0.123	K.AVQSGLGTAAVIVM*DK.S
R5/RRR5-8/2	1560.865	1560.841	15.562	0.308	172.550	0.365	14	0.121	-.AVQSGLGTAAVIVMDK.-
R5/RRR5-9/2	1577.746	1576.841	-60.283	0.193	124.157	0.392	16	0.117	-.AVQSGLGTAAVIVM*DK.-
R5/RRR5-9/2	1577.799	1576.841	-26.681	0.111	119.418	0.358	16	0.115	-.AVQSGLGTAAVIVM*DK.-
R5/RRR5-1/2	1542.298	1541.620	-209.462	0.505	1145.096	0.509	19	0.169	R.ISAEDETSGM*DLTR.H

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1678.712	1677.802	-53.652	0.510	763.444	0.577	21	0.152	K.TYGPAGGINGQWSGVGR.T
R5/RRR5-2/2	1543.019	1541.620	258.794	0.487	437.368	0.538	20	0.143	R.ISAEDETSGM*DLTR.H
R5/RRR5-2/2	1542.714	1541.620	60.513	0.502	493.336	0.511	18	0.139	R.ISAEDETSGM*DLTR.H
R5/RRR5-1/2	1542.947	1541.620	212.226	0.515	619.002	0.473	18	0.138	R.ISAEDETSGM*DLTR.H
R5/RRR5-12/2	1542.345	1541.620	-179.131	0.423	882.321	0.389	17	0.135	R.ISAEDETSGM*DLTR.H
R5/RRR5-1/2	1542.231	1541.620	-253.055	0.486	553.783	0.481	16	0.135	R.ISAEDETSGM*DLTR.H
R5/RRR5-3/2	1542.830	1541.620	136.058	0.479	369.700	0.472	17	0.134	R.ISAEDETSGM*DLTR.H
R5/RRR5-16/2	1144.034	1144.346	-273.613	0.461	2017.256	0.659	22	0.313	K.VAVITGAASGIGK.A
R5/RRR5-16/2	1144.083	1144.346	-230.580	0.476	2059.744	0.615	22	0.308	K.VAVITGAASGIGK.A
R5/RRR5-16/2	1144.107	1144.346	-210.243	0.473	2094.342	0.580	22	0.303	K.VAVITGAASGIGK.A
R5/RRR5-15/2	1144.204	1144.346	-125.048	0.508	1834.524	0.602	21	0.269	K.VAVITGAASGIGK.A
R5/RRR5-15/2	1143.344	1144.346	-1756.388	0.316	1800.793	0.456	20	0.223	K.VAVITGAASGIGK.A
R5/RRR5-15/2	1144.098	1144.346	-217.521	0.406	1487.282	0.517	20	0.202	K.VAVITGAASGIGK.A
R5/RRR5-10/2	1441.307	1441.720	-287.524	0.458	1126.877	0.459	16	0.158	R.VLDAM*LPFYLSR.Y
R5/RRR5-10/3	1561.810	1560.718	58.806	0.536	1074.942	0.503	26	0.124	R.IRVEPQM*SGGGQER.G
R5/RRR5-10/2	1441.111	1441.720	-1120.085	0.357	558.940	0.192	13	0.110	-.VLDAM*LPFYLSR.-
R5/RRR5-10/3	1559.561	1560.718	-1387.562	0.362	950.333	0.279	26	0.074	R.IRVEPQM*SGGGQER.G
R5/RRR5-7/2	1196.804	1197.453	-1381.151	0.418	1477.281	0.357	16	0.171	K.ELVQNLLVLR.F
R5/RRR5-8/2	1197.315	1197.453	-114.899	0.380	1504.103	0.297	16	0.162	K.ELVQNLLVLR.F
R5/RRR5-8/2	1198.097	1197.453	-297.545	0.514	1431.696	0.332	16	0.162	K.ELVQNLLVLR.F
R5/RRR5-8/2	1198.225	1197.453	-190.222	0.505	1472.183	0.292	16	0.157	K.ELVQNLLVLR.F
R5/RRR5-7/2	1196.808	1197.453	-1378.283	0.431	1333.295	0.285	15	0.147	K.ELVQNLLVLR.F
R5/RRR5-7/2	1196.668	1197.453	-1495.491	0.366	1090.311	0.278	14	0.133	K.ELVQNLLVLR.F
R5/RRR5-8/3	1954.740	1955.202	-236.965	0.321	863.701	0.408	25	0.086	K.AAWQIFTPLLHDIDEGK.V
R5/RRR5-8/3	1953.645	1955.202	-1825.959	0.269	582.248	0.392	22	0.074	K.AAWQIFTPLLHDIDEGK.V
R5/RRR5-25/3	1810.879	1810.988	-60.358	0.457	1148.889	0.315	28	0.090	R.VFDKDQNGFISAAELR.H
R5/RRR5-25/3	1905.054	1905.045	4.388	0.335	985.434	0.375	28	0.086	K.EAFSLFDKDGDGCITTK.E
R5/RRR5-24/3	1811.134	1810.988	81.006	0.404	716.694	0.249	23	0.061	-.VFDKDQNGFISAAELR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1870.430	1870.006	227.234	0.538	948.781	0.519	22	0.156	K.TYEPSEEPFDISLVSR.E
R5/RRR5-8/2	1734.476	1735.016	-890.747	0.386	392.666	0.575	20	0.134	K.APPPPALPSAPLFTTEK.S
R5/RRR5-8/2	1035.398	1035.219	174.348	0.179	908.388	0.234	15	0.115	K.VLAEAFAVSK.D
R5/RRR5-22/2	1780.359	1780.973	-909.469	0.376	880.493	0.191	15	0.066	-.M*M*EEVDNCANQM*LF.-
R5/RRR5-5/2	1486.448	1485.625	-119.073	0.534	1326.646	0.483	22	0.181	R.GVVDSNDLPLNVSR.E
R5/RRR5-5/2	1485.701	1485.625	51.703	0.521	1235.181	0.436	21	0.164	R.GVVDSNDLPLNVSR.E
R5/RRR5-4/2	1485.687	1485.625	42.144	0.456	1154.140	0.414	19	0.154	R.GVVDSNDLPLNVSR.E
R5/RRR5-4/2	1486.100	1485.625	320.850	0.498	1043.810	0.420	19	0.148	R.GVVDSNDLPLNVSR.E
R5/RRR5-5/2	1485.143	1485.625	-325.445	0.420	1170.437	0.354	21	0.147	R.GVVDSNDLPLNVSR.E
R5/RRR5-1/2	1486.387	1485.625	-160.593	0.360	619.257	0.363	15	0.124	R.GVVDSNDLPLNVSR.E
R5/RRR5-1/2	1486.292	1485.625	-224.281	0.363	691.071	0.289	15	0.120	R.GVVDSNDLPLNVSR.E
R5/RRR5-2/2	1486.273	1485.625	-237.217	0.299	592.182	0.288	14	0.118	R.GVVDSNDLPLNVSR.E
R5/RRR5-5/3	1597.712	1596.852	-87.569	0.371	1116.597	0.297	24	0.083	R.KVFEINPEHEIIK.G
R5/RRR5-10/2	1471.435	1471.768	-227.211	0.535	2238.580	0.520	21	0.309	K.TNMVMVFGEITTK.A
R5/RRR5-10/2	1487.228	1487.767	-1038.332	0.497	2187.458	0.495	21	0.293	K.TNMVM*VFGEITTK.A
R5/RRR5-10/2	1470.818	1471.768	-1329.538	0.432	2242.530	0.428	21	0.283	K.TNMVMVFGEITTK.A
R5/RRR5-10/2	1503.095	1503.767	-1115.432	0.503	2127.635	0.441	21	0.268	K.TNM*VM*VFGEITTK.A
R5/RRR5-10/2	1503.092	1503.767	-1117.389	0.516	2201.536	0.375	21	0.260	K.TNM*VM*VFGEITTK.A
R5/RRR5-10/2	1471.099	1471.768	-1137.693	0.452	2002.040	0.451	20	0.252	K.TNMVMVFGEITTK.A
R5/RRR5-10/2	1503.253	1503.767	-1009.921	0.505	2107.858	0.373	20	0.245	K.TNM*VM*VFGEITTK.A
R5/RRR5-11/2	1503.632	1503.767	-89.702	0.466	1771.029	0.360	19	0.199	K.TNM*VM*VFGEITTK.A
R5/RRR5-11/2	1504.463	1503.767	-202.286	0.503	1243.364	0.431	18	0.163	K.TNM*VM*VFGEITTK.A
R5/RRR5-10/2	1486.978	1487.767	-1206.972	0.388	1044.216	0.235	17	0.125	K.TNMVM*VFGEITTK.A
R5/RRR5-13/2	1364.140	1364.534	-289.331	0.481	869.011	0.386	15	0.136	K.FNWNTVINSLR.R
R5/RRR5-13/2	1364.165	1364.534	-271.465	0.419	1029.607	0.316	16	0.134	K.FNWNTVINSLR.R
R5/RRR5-13/2	1364.303	1364.534	-170.028	0.334	568.382	0.310	13	0.120	K.FNWNTVINSLR.R
R5/RRR5-13/2	1872.449	1873.056	-861.140	0.479	846.906	0.566	20	0.103	R.GWIPLDQSIRDTVGSDI.-
R5/RRR5-13/2	1872.453	1873.056	-858.654	0.433	733.494	0.527	18	0.093	R.GWIPLDQSIRDTVGSDI.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1873.608	1873.056	-239.736	0.468	736.769	0.479	19	0.089	R.GWIPLDQSIRDTVGSDI.-
R5/RRR5-3/2	1340.244	1339.543	-223.416	0.512	1616.427	0.450	17	0.202	R.TAAMDFVSELVR.K
R5/RRR5-3/2	1711.901	1711.041	-82.006	0.493	707.728	0.521	19	0.143	R.ENILGFVTQLPPLLR.A
R5/RRR5-7/2	1824.397	1825.012	-887.848	0.477	1183.339	0.502	23	0.169	K.IIFASGSPFSDVDLGNGK.I
R5/RRR5-7/2	1824.445	1825.012	-861.115	0.475	1185.537	0.484	22	0.165	K.IIFASGSPFSDVDLGNGK.I
R5/RRR5-7/2	1739.074	1737.936	80.076	0.448	1101.881	0.415	18	0.148	R.WPNVIVQFEDFQSK.W
R5/RRR5-7/2	1826.600	1825.012	-226.132	0.272	436.248	0.306	15	0.115	K.IIFASGSPFSDVDLGNGK.I
R5/RRR5-6/2	1787.578	1787.993	-232.849	0.412	939.737	0.406	20	0.136	K.LSVDNLDEVILVGGSTR.I
R5/RRR5-6/2	1013.229	1013.213	16.421	0.443	558.217	0.411	15	0.135	R.IPSVQELVK.K
R5/RRR5-6/2	1012.906	1013.213	-303.776	0.301	359.077	0.298	13	0.124	R.IPSVQELVK.K
R5/RRR5-6/2	1013.002	1013.213	-208.868	0.251	373.333	0.350	13	0.122	R.IPSVQELVK.K
R5/RRR5-6/2	1209.098	1209.420	-267.395	0.424	1221.154	0.542	21	0.182	K.VPGATDLGLIPR.K
R5/RRR5-6/2	1208.964	1209.420	-378.219	0.408	1224.521	0.508	20	0.176	K.VPGATDLGLIPR.K
R5/RRR5-5/2	1209.005	1209.420	-344.584	0.381	823.278	0.510	17	0.148	K.VPGATDLGLIPR.K
R5/RRR5-6/2	1208.959	1209.420	-382.271	0.335	744.772	0.396	16	0.131	K.VPGATDLGLIPR.K
R5/RRR5-5/2	1209.036	1209.420	-318.752	0.332	764.242	0.361	17	0.130	K.VPGATDLGLIPR.K
R5/RRR5-2/2	1210.599	1209.420	148.408	0.296	552.818	0.353	13	0.122	K.VPGATDLGLIPR.K
R5/RRR5-6/3	1838.806	1837.067	-142.140	0.419	1513.261	0.216	25	0.097	R.TQHTSPQVVVDLLDVGK.K
R5/RRR5-24/2	1258.580	1259.439	-1482.046	0.458	2247.224	0.479	22	0.301	R.FPGVNGLGISAAR.V
R5/RRR5-24/2	1259.321	1259.439	-93.978	0.485	2177.196	0.493	22	0.293	R.FPGVNGLGISAAR.V
R5/RRR5-24/2	1259.171	1259.439	-213.395	0.461	2114.568	0.485	22	0.280	R.FPGVNGLGISAAR.V
R5/RRR5-4/2	1198.288	1197.406	-99.173	0.473	1452.195	0.427	18	0.182	K.IPADLIINAEK.A
R5/RRR5-4/2	1198.272	1197.406	-112.458	0.476	1048.028	0.480	18	0.160	K.IPADLIINAEK.A
R5/RRR5-4/2	1134.146	1134.265	-105.106	0.388	1274.181	0.330	18	0.150	K.LSSAIEASISR.G
R5/RRR5-4/2	1197.041	1197.406	-305.581	0.394	1044.541	0.387	16	0.144	K.IPADLIINAEK.A
R5/RRR5-22/2	1154.249	1154.297	-41.646	0.308	729.048	0.338	13	0.126	K.YYNLPEVQK.A
R5/RRR5-22/2	1154.026	1154.297	-235.172	0.267	503.471	0.292	11	0.119	K.YYNLPEVQK.A
R5/RRR5-21/2	1153.959	1154.297	-293.116	0.256	650.375	0.265	11	0.118	K.YYNLPEVQK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/3	1326.668	1326.492	132.875	0.424	766.394	0.443	23	0.093	R.GAGHEVPLHRPR.Q
R5/RRR5-22/3	1326.182	1326.492	-234.751	0.374	919.347	0.375	22	0.088	R.GAGHEVPLHRPR.Q
R5/RRR5-21/3	1326.861	1326.492	279.020	0.398	625.282	0.411	19	0.086	R.GAGHEVPLHRPR.Q
R5/RRR5-22/3	1326.111	1326.492	-287.944	0.416	410.473	0.384	17	0.081	-.GAGHEVPLHRPR.-
R5/RRR5-8/2	989.919	989.153	-237.115	0.406	505.791	0.526	15	0.140	K.LAPAYAVAGR.I
R5/RRR5-8/2	989.753	989.153	-405.268	0.450	557.300	0.480	16	0.140	K.LAPAYAVAGR.I
R5/RRR5-8/2	989.382	989.153	232.637	0.380	534.846	0.455	15	0.134	K.LAPAYAVAGR.I
R5/RRR5-8/2	1433.803	1433.502	210.441	0.348	741.515	0.382	16	0.127	R.EVEEFDPPSEVR.A
R5/RRR5-5/2	1628.367	1627.864	-306.444	0.515	1425.487	0.421	20	0.174	R.SNIISELKPLAAENK.Q
R5/RRR5-5/2	1932.745	1933.143	-206.618	0.499	814.629	0.505	18	0.141	R.AQGAGLCSSIEELDQLIK.S
R5/RRR5-12/2	1853.536	1855.084	-1920.014	0.363	622.668	0.478	22	0.134	R.HVAETLGIDLEPLYQR.I
R5/RRR5-12/2	1772.542	1773.106	-884.741	0.443	390.112	0.503	17	0.129	K.LVAPPLYVLTTQTLDK.D
R5/RRR5-12/2	1855.010	1855.084	-39.774	0.355	561.872	0.368	15	0.119	R.HVAETLGIDLEPLYQR.I
R5/RRR5-13/2	1693.435	1692.976	271.806	0.383	834.293	0.443	18	0.136	R.DFVPAIYDTTVIIPK.D
R5/RRR5-13/3	1565.492	1565.740	-158.670	0.492	816.163	0.382	26	0.088	K.AM*GNEHALVISNHR.S
R5/RRR5-13/3	1565.215	1565.740	-976.797	0.422	1044.463	0.320	29	0.086	K.AM*GNEHALVISNHR.S
R5/RRR5-13/3	1565.961	1565.740	141.965	0.395	718.085	0.298	26	0.076	K.AM*GNEHALVISNHR.S
R5/RRR5-6/2	1970.357	1971.268	-972.828	0.486	1035.639	0.508	23	0.157	K.MNDIAPNLTSLIGEVVGAR.L
R5/RRR5-7/2	1389.068	1388.585	348.640	0.338	788.399	0.355	17	0.126	K.CPASTLQILGAEK.A
R5/RRR5-10/2	1791.538	1791.894	-198.779	0.454	972.786	0.477	22	0.152	K.VVSIDGFEDVPQNDEK.S
R5/RRR5-10/2	1791.227	1791.894	-933.134	0.425	881.021	0.507	21	0.149	K.VVSIDGFEDVPQNDEK.S
R5/RRR5-11/3	1563.001	1562.755	157.591	0.382	1279.415	0.247	31	0.085	K.AVAHQPVSVAIEAGGR.E
R5/RRR5-21/2	1662.526	1662.860	-201.685	0.501	2233.610	0.485	24	0.298	K.AITSGVLAGCSDAIAQK.I
R5/RRR5-21/2	1662.240	1662.860	-977.775	0.444	2121.604	0.458	24	0.273	K.AITSGVLAGCSDAIAQK.I
R5/RRR5-21/2	1662.280	1662.860	-953.666	0.482	1995.044	0.477	23	0.258	K.AITSGVLAGCSDAIAQK.I
R5/RRR5-5/2	1219.850	1220.317	-383.776	0.349	955.938	0.375	16	0.135	R.DVVASNPTNFR.L
R5/RRR5-5/2	1254.983	1254.461	-382.106	0.309	1041.709	0.302	17	0.132	K.GNIDTPLALAIR.N
R5/RRR5-5/2	1254.114	1254.461	-277.323	0.278	770.964	0.291	16	0.121	K.GNIDTPLALAIR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/2	1253.661	1254.461	-1440.005	0.216	542.446	0.287	14	0.116	K.GNIDTPLALAIR.N
R5/RRR5-27/2	1374.980	1375.507	-1113.575	0.499	2162.516	0.513	19	0.295	R.EGDILTLLESER.E
R5/RRR5-27/2	1375.085	1375.507	-307.863	0.434	1913.385	0.461	18	0.242	R.EGDILTLLESER.E
R5/RRR5-28/2	1375.113	1375.507	-287.378	0.479	1777.905	0.506	19	0.236	R.EGDILTLLESER.E
R5/RRR5-27/2	1376.129	1375.507	-275.422	0.554	1707.863	0.512	18	0.227	R.EGDILTLLESER.E
R5/RRR5-28/2	1375.154	1375.507	-257.632	0.475	1740.405	0.466	19	0.221	R.EGDILTLLESER.E
R5/RRR5-28/2	1374.378	1375.507	-1553.519	0.328	1609.690	0.439	19	0.197	R.EGDILTLLESER.E
R5/RRR5-6/2	1000.226	1001.162	-1941.234	0.455	1229.998	0.438	17	0.165	R.IGAATALEVR.A
R5/RRR5-6/2	1231.199	1231.464	-215.757	0.446	841.315	0.491	17	0.148	R.ITVGTTILDAVK.A
R5/RRR5-6/2	1231.181	1231.464	-230.876	0.380	936.782	0.444	18	0.145	R.ITVGTTILDAVK.A
R5/RRR5-6/2	1231.226	1231.464	-193.477	0.353	820.005	0.397	17	0.134	R.ITVGTTILDAVK.A
R5/RRR5-25/2	1523.204	1523.713	-993.235	0.417	2281.504	0.402	22	0.283	R.LSYGAISDLSGIQAK.K
R5/RRR5-24/2	1523.353	1523.713	-237.069	0.501	1829.784	0.432	21	0.222	R.LSYGAISDLSGIQAK.K
R5/RRR5-24/2	1523.097	1523.713	-1063.804	0.464	1770.154	0.409	21	0.210	R.LSYGAISDLSGIQAK.K
R5/RRR5-25/2	1523.276	1523.713	-287.880	0.436	1862.496	0.359	21	0.210	R.LSYGAISDLSGIQAK.K
R5/RRR5-25/2	1523.361	1523.713	-231.924	0.374	1811.198	0.361	21	0.205	R.LSYGAISDLSGIQAK.K
R5/RRR5-24/2	1523.166	1523.713	-1018.420	0.418	1701.491	0.342	20	0.188	R.LSYGAISDLSGIQAK.K
R5/RRR5-15/2	1487.612	1487.725	-76.346	0.403	723.916	0.347	17	0.124	R.VDVLSEALPFIQR.F
R5/RRR5-15/3	1509.876	1509.693	122.145	0.383	804.577	0.424	24	0.085	-.ALAQGVHTASIIDGR.-
R5/RRR5-2/2	1875.499	1875.067	230.732	0.474	2213.462	0.482	23	0.294	K.ILLLDEATSALDVESER.I
R5/RRR5-1/2	1875.302	1875.067	125.576	0.501	1474.598	0.528	21	0.201	K.ILLLDEATSALDVESER.I
R5/RRR5-20/2	1587.382	1587.755	-236.223	0.506	2083.987	0.567	26	0.298	K.LAFGSLGDSFSATSVK.A
R5/RRR5-20/2	1587.515	1587.755	-151.828	0.504	2064.400	0.568	26	0.295	K.LAFGSLGDSFSATSVK.A
R5/RRR5-20/2	1588.346	1587.755	-258.279	0.548	1955.883	0.579	25	0.281	K.LAFGSLGDSFSATSVK.A
R5/RRR5-19/2	1587.212	1587.755	-975.320	0.468	1943.356	0.539	25	0.267	K.LAFGSLGDSFSATSVK.A
R5/RRR5-19/2	1586.768	1587.755	-1256.305	0.332	1893.366	0.437	25	0.232	K.LAFGSLGDSFSATSVK.A
R5/RRR5-19/2	1587.046	1587.755	-1080.420	0.428	1594.848	0.546	23	0.220	K.LAFGSLGDSFSATSVK.A
R5/RRR5-6/2	1121.215	1121.271	-50.954	0.428	692.703	0.497	14	0.140	R.HADAIPVLER.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/3	1557.629	1557.688	-38.023	0.417	744.819	0.444	25	0.093	K.LGTANPDVEDEKLR.L
R5/RRR5-7/3	1557.446	1557.688	-155.712	0.424	565.701	0.398	22	0.085	K.LGTANPDVEDEKLR.L
R5/RRR5-6/3	1557.760	1557.688	46.395	0.379	648.774	0.358	23	0.080	K.LGTANPDVEDEKLR.L
R5/RRR5-7/3	1557.239	1557.688	-288.764	0.372	486.437	0.377	21	0.079	-.LGTANPDVEDEKLR.-
R5/RRR5-22/2	1869.896	1869.018	-65.452	0.594	2085.239	0.574	24	0.301	K.LPDATLSYFDSPDGELK.T
R5/RRR5-20/2	1110.139	1109.147	-6.795	0.284	898.193	0.315	14	0.129	K.EGEAADEEMK.K
R5/RRR5-29/2	1110.005	1109.147	-128.129	0.354	851.723	0.276	14	0.126	K.EGEAADEEMK.K
R5/RRR5-22/2	963.849	964.165	-329.052	0.410	1145.931	0.187	13	0.125	-.M*ITKIEGR.-
R5/RRR5-30/2	1109.330	1109.147	165.487	0.272	310.178	0.305	11	0.124	K.EGEAADEEMK.K
R5/RRR5-27/2	1109.900	1109.147	-223.120	0.286	711.528	0.282	12	0.122	K.EGEAADEEMK.K
R5/RRR5-28/2	1109.944	1109.147	-182.849	0.306	555.960	0.272	12	0.122	K.EGEAADEEMK.K
R5/RRR5-26/2	1109.795	1109.147	-317.910	0.281	519.363	0.252	12	0.121	K.EGEAADEEMK.K
R5/RRR5-22/2	1109.755	1109.147	-353.667	0.254	574.244	0.254	12	0.120	K.EGEAADEEMK.K
R5/RRR5-27/2	1109.801	1109.147	-312.171	0.356	579.185	0.234	12	0.118	-.EGEAADEEMK.-
R5/RRR5-29/2	1109.817	1109.147	-298.266	0.226	589.318	0.191	12	0.118	K.EGEAADEEMK.K
R5/RRR5-21/2	1109.910	1109.147	-213.521	0.303	654.467	0.157	13	0.117	K.EGEAADEEMK.K
R5/RRR5-29/2	1109.890	1109.147	-232.168	0.313	653.055	0.179	12	0.117	K.EGEAADEEMK.K
R5/RRR5-28/2	1109.865	1109.147	-254.788	0.329	617.914	0.195	12	0.117	-.EGEAADEEMK.-
R5/RRR5-26/2	1109.661	1109.147	-438.767	0.244	841.835	0.122	13	0.115	K.EGEAADEEMK.K
R5/RRR5-29/2	1110.071	1109.147	-68.230	0.303	671.259	0.129	12	0.112	-.EGEAADEEMK.-
R5/RRR5-3/2	1110.118	1109.147	-25.986	0.261	547.222	0.199	12	0.111	-.EGEAADEEMK.-
R5/RRR5-30/2	1109.315	1109.147	152.024	0.249	563.168	0.103	11	0.110	-.EGEAADEEMK.-
R5/RRR5-12/2	1110.025	1109.147	-109.706	0.243	595.603	0.188	11	0.109	-.EGEAADEEMK.-
R5/RRR5-20/2	1110.101	1109.147	-40.986	0.290	428.179	0.279	10	0.105	-.EGEAADEEMK.-
R5/RRR5-5/2	1203.476	1203.416	50.501	0.385	1763.114	0.392	17	0.207	K.ILLENAGAVFR.T
R5/RRR5-2/2	1204.201	1203.416	-179.009	0.412	1586.837	0.436	18	0.197	K.ILLENAGAVFR.T
R5/RRR5-1/2	1204.314	1203.416	-84.851	0.361	955.710	0.470	15	0.148	K.ILLENAGAVFR.T
R5/RRR5-2/2	1390.129	1390.563	-312.986	0.311	755.083	0.345	16	0.122	K.VGESPEEIAAFLK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-10/2	1928.591	1929.161	-816.455	0.509	2113.549	0.531	25	0.294	R.FQIGPEQIETLYQYAK.F
R5/RRR5-4/2	1034.265	1033.246	18.513	0.487	881.304	0.479	15	0.149	K.TFASGIIVPK.K
R5/RRR5-8/2	1200.421	1199.334	72.558	0.316	870.974	0.398	14	0.135	K.YEELGELFAK.S
R5/RRR5-7/2	1199.683	1199.334	291.414	0.246	1081.536	0.279	15	0.130	K.YEELGELFAK.S
R5/RRR5-8/2	1199.955	1199.334	-317.389	0.297	797.231	0.340	15	0.128	K.YEELGELFAK.S
R5/RRR5-8/2	1199.768	1199.334	362.930	0.287	570.980	0.397	14	0.126	K.YEELGELFAK.S
R5/RRR5-8/2	1193.030	1193.414	-323.131	0.311	722.191	0.333	13	0.125	R.TIEDLITFIK.E
R5/RRR5-7/2	1194.221	1193.414	-162.256	0.358	494.663	0.340	12	0.123	R.TIEDLITFIK.E
R5/RRR5-7/2	1192.677	1193.414	-1461.179	0.286	642.418	0.340	13	0.123	R.TIEDLITFIK.E
R5/RRR5-8/2	1193.220	1193.414	-163.726	0.218	309.999	0.325	10	0.107	-.TIEDLITFIK.-
R5/RRR5-15/2	1526.414	1526.674	-170.579	0.502	1923.600	0.622	23	0.288	R.LIAATYSGSTPTTSR.C
R5/RRR5-15/2	1526.385	1526.674	-189.513	0.444	1563.337	0.608	22	0.231	R.LIAATYSGSTPTTSR.C
R5/RRR5-3/2	1042.014	1042.209	-188.071	0.427	1233.517	0.408	14	0.160	R.LSDFLTFAK.D
R5/RRR5-3/2	1042.282	1042.209	69.470	0.415	998.593	0.453	14	0.152	R.LSDFLTFAK.D
R5/RRR5-3/2	1426.518	1427.549	-1428.075	0.343	1071.658	0.426	17	0.148	R.NPVYQNAGNFFR.L
R5/RRR5-3/2	1042.107	1042.209	-98.880	0.402	1084.508	0.362	15	0.145	R.LSDFLTFAK.D
R5/RRR5-3/2	1427.174	1427.549	-263.340	0.425	867.627	0.470	16	0.144	R.NPVYQNAGNFFR.L
R5/RRR5-8/2	1394.896	1394.558	242.819	0.436	957.467	0.352	17	0.137	R.WEFSNPTPFIR.S
R5/RRR5-8/2	1536.248	1536.926	-1095.424	0.247	1156.825	0.297	18	0.134	R.VAPLQVIVIPVPYK.D
R5/RRR5-8/2	1394.202	1394.558	-256.659	0.439	704.703	0.397	15	0.132	R.WEFSNPTPFIR.S
R5/RRR5-8/2	1394.110	1394.558	-322.632	0.460	722.609	0.314	15	0.124	R.WEFSNPTPFIR.S
R5/RRR5-8/2	1536.598	1536.926	-214.150	0.220	963.806	0.245	16	0.119	R.VAPLQVIVIPVPYK.D
R5/RRR5-2/2	1327.150	1327.555	-305.882	0.430	1311.473	0.502	17	0.181	R.VGQIIAQLLSER.L
R5/RRR5-1/2	1327.611	1327.555	42.459	0.423	1191.592	0.500	16	0.170	R.VGQIIAQLLSER.L
R5/RRR5-1/2	1481.447	1481.634	-126.748	0.379	853.819	0.481	19	0.144	R.ALDLPVYFGDAGSR.E
R5/RRR5-2/2	1481.270	1481.634	-246.532	0.387	799.064	0.473	19	0.141	R.ALDLPVYFGDAGSR.E
R5/RRR5-2/2	1327.393	1327.555	-122.549	0.276	1120.413	0.267	16	0.131	R.VGQIIAQLLSER.L
R5/RRR5-7/1	949.481	950.070	-1679.394	0.225	819.324	0.135	11	0.381	-.GFEVIDAAK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1393.310	1393.607	-213.765	0.547	2591.767	0.511	22	0.371	R.VVSCADILAFAAR.D
R5/RRR5-7/1	949.407	950.070	-1757.094	0.246	795.070	0.186	11	0.366	R.GFEVIDAAK.A
R5/RRR5-7/1	949.428	950.070	-1734.680	0.261	785.629	0.232	12	0.359	R.GFEVIDAAK.A
R5/RRR5-10/1	949.457	950.070	-1704.065	0.239	764.322	0.188	11	0.345	-.GFEVIDAAK.-
R5/RRR5-9/2	1393.138	1393.607	-337.622	0.546	2358.411	0.490	21	0.319	R.VVSCADILAFAAR.D
R5/RRR5-10/2	1394.096	1393.607	351.774	0.553	2308.142	0.493	21	0.311	R.VVSCADILAFAAR.D
R5/RRR5-8/2	1393.265	1393.607	-246.374	0.477	2206.731	0.468	21	0.287	R.VVSCADILAFAAR.D
R5/RRR5-8/1	949.467	950.070	-1693.473	0.296	673.786	0.246	11	0.276	-.GFEVIDAAK.-
R5/RRR5-9/1	949.434	950.070	-1728.480	0.249	695.395	0.172	11	0.273	R.GFEVIDAAK.A
R5/RRR5-8/2	1393.052	1393.607	-1119.431	0.435	2155.703	0.444	20	0.272	R.VVSCADILAFAAR.D
R5/RRR5-10/1	949.698	950.070	-393.340	0.278	668.329	0.218	11	0.264	-.GFEVIDAAK.-
R5/RRR5-8/2	1393.285	1393.607	-231.519	0.485	2039.117	0.472	20	0.261	R.VVSCADILAFAAR.D
R5/RRR5-8/1	949.442	950.070	-1720.664	0.267	627.567	0.217	10	0.243	-.GFEVIDAAK.-
R5/RRR5-10/2	1393.593	1393.607	-9.718	0.464	1710.861	0.470	19	0.216	R.VVSCADILAFAAR.D
R5/RRR5-7/2	1394.176	1393.607	-309.707	0.476	1704.818	0.450	19	0.211	R.VVSCADILAFAAR.D
R5/RRR5-10/2	1394.207	1393.607	-287.482	0.502	1586.851	0.503	18	0.209	R.VVSCADILAFAAR.D
R5/RRR5-7/2	1393.074	1393.607	-1103.594	0.410	1505.384	0.451	18	0.189	R.VVSCADILAFAAR.D
R5/RRR5-10/2	1392.962	1393.607	-1184.371	0.427	1389.673	0.449	17	0.177	R.VVSCADILAFAAR.D
R5/RRR5-11/2	1392.976	1393.607	-1174.515	0.448	1198.259	0.488	17	0.168	R.VVSCADILAFAAR.D
R5/RRR5-8/2	1394.715	1393.607	77.549	0.345	1323.048	0.416	18	0.165	R.VVSCADILAFAAR.D
R5/RRR5-1/2	950.261	950.070	201.178	0.423	1222.050	0.411	15	0.160	R.GFEVIDAAK.A
R5/RRR5-9/1	949.490	950.070	-1669.836	0.247	524.588	0.133	10	0.159	-.GFEVIDAAK.-
R5/RRR5-9/1	949.465	950.070	-1695.605	0.264	507.653	0.179	10	0.158	-.GFEVIDAAK.-
R5/RRR5-8/1	949.458	950.070	-1703.032	0.251	518.131	0.131	10	0.156	-.GFEVIDAAK.-
R5/RRR5-10/1	949.475	950.070	-1685.207	0.195	523.649	0.080	10	0.154	-.GFEVIDAAK.-
R5/RRR5-8/2	949.359	950.070	-1808.592	0.354	1176.979	0.399	14	0.154	R.GFEVIDAAK.A
R5/RRR5-10/2	949.505	950.070	-1653.446	0.365	1093.463	0.427	14	0.153	R.GFEVIDAAK.A
R5/RRR5-8/2	949.932	950.070	-146.240	0.424	1164.027	0.387	14	0.153	R.GFEVIDAAK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/2	949.558	950.070	-1597.136	0.418	1146.880	0.390	14	0.152	R.GFEVIDAAK.A
R5/RRR5-8/2	949.244	950.070	-1929.667	0.339	1234.055	0.351	15	0.151	R.GFEVIDAAK.A
R5/RRR5-10/2	950.061	950.070	-9.744	0.419	1094.318	0.401	14	0.150	R.GFEVIDAAK.A
R5/RRR5-10/2	950.108	950.070	39.612	0.444	1063.999	0.395	14	0.148	R.GFEVIDAAK.A
R5/RRR5-13/2	949.206	950.070	-1969.859	0.409	1174.807	0.351	14	0.148	R.GFEVIDAAK.A
R5/RRR5-2/2	949.724	950.070	-366.206	0.354	1049.676	0.406	14	0.147	R.GFEVIDAAK.A
R5/RRR5-7/2	1395.000	1393.607	282.691	0.343	1126.284	0.387	17	0.147	R.VVSCADILAFAAR.D
R5/RRR5-11/2	950.056	950.070	-15.028	0.290	1201.743	0.350	14	0.147	R.GFEVIDAAK.A
R5/RRR5-8/2	1394.540	1393.607	-47.991	0.308	1148.367	0.381	16	0.147	R.VVSCADILAFAAR.D
R5/RRR5-13/2	949.480	950.070	-1680.442	0.335	1131.575	0.361	14	0.146	R.GFEVIDAAK.A
R5/RRR5-7/2	949.469	950.070	-1691.679	0.354	1016.080	0.399	14	0.145	R.GFEVIDAAK.A
R5/RRR5-7/2	1394.991	1393.607	275.891	0.364	1103.228	0.371	16	0.144	R.VVSCADILAFAAR.D
R5/RRR5-5/2	950.009	950.070	-65.163	0.345	1152.391	0.306	14	0.140	R.GFEVIDAAK.A
R5/RRR5-2/2	950.958	950.070	-118.272	0.479	1000.029	0.356	14	0.140	R.GFEVIDAAK.A
R5/RRR5-7/2	949.213	950.070	-1962.622	0.389	962.807	0.378	13	0.140	R.GFEVIDAAK.A
R5/RRR5-5/2	950.031	950.070	-41.835	0.350	1085.836	0.308	14	0.137	R.GFEVIDAAK.A
R5/RRR5-11/2	949.427	950.070	-1736.374	0.257	916.091	0.370	13	0.133	R.GFEVIDAAK.A
R5/RRR5-11/2	1394.949	1393.607	246.145	0.330	1014.836	0.316	16	0.133	R.VVSCADILAFAAR.D
R5/RRR5-9/2	1394.570	1393.607	-26.392	0.329	709.413	0.411	15	0.131	R.VVSCADILAFAAR.D
R5/RRR5-7/2	1393.258	1393.607	-251.472	0.298	840.323	0.273	15	0.123	R.VVSCADILAFAAR.D
R5/RRR5-11/2	1394.485	1393.607	-87.415	0.233	812.638	0.289	13	0.121	R.VVSCADILAFAAR.D
R5/RRR5-1/2	1394.481	1393.607	-90.927	0.255	499.899	0.299	12	0.119	R.VVSCADILAFAAR.D
R5/RRR5-9/2	951.013	950.070	-60.202	0.124	574.878	0.141	12	0.115	-.GFEVIDAAK.-
R5/RRR5-6/2	1394.985	1393.607	271.592	0.267	589.409	0.174	13	0.113	-.VVSCADILAFAAR.-
R5/RRR5-9/3	1394.807	1393.607	143.853	0.443	1339.695	0.285	25	0.101	-.VVSCADILAFAAR.-
R5/RRR5-9/3	1393.546	1393.607	-43.510	0.436	717.983	0.240	21	0.067	-.VVSCADILAFAAR.-
R5/RRR5-2/2	1109.063	1109.218	-139.829	0.331	1580.729	0.458	19	0.197	K.NAVTSVAFSGR.A
R5/RRR5-2/2	1109.126	1109.218	-82.529	0.357	1160.043	0.425	17	0.155	K.NAVTSVAFSGR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-1/2	1797.914	1798.029	-64.191	0.379	596.437	0.421	14	0.121	K.ATLSPALETALDYYLR.V
R5/RRR5-10/3	1926.171	1926.157	7.105	0.495	2217.775	0.428	35	0.286	K.SIALDVEELADNLQLGPK.F
R5/RRR5-10/3	1925.148	1926.157	-1046.877	0.462	1448.744	0.455	34	0.153	K.SIALDVEELADNLQLGPK.F
R5/RRR5-10/3	1924.724	1926.157	-1267.907	0.453	1336.593	0.418	33	0.129	K.SIALDVEELADNLQLGPK.F
R5/RRR5-21/3	1582.948	1582.651	188.594	0.518	2012.096	0.556	28	0.296	R.SGAEVHTGHELCER.K
R5/RRR5-21/3	1582.764	1582.651	72.002	0.496	1819.441	0.557	30	0.251	R.SGAEVHTGHELCER.K
R5/RRR5-12/2	1701.103	1700.920	107.990	0.613	1984.176	0.589	27	0.286	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-16/2	1700.228	1700.920	-998.056	0.543	1860.665	0.521	25	0.248	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-12/2	1701.532	1700.920	-228.866	0.654	1720.253	0.589	25	0.246	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-16/2	1700.454	1700.920	-274.949	0.569	1551.496	0.612	25	0.232	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-17/2	1700.357	1700.920	-921.869	0.558	1553.251	0.583	24	0.224	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-17/2	1701.362	1700.920	260.825	0.555	1694.389	0.496	25	0.220	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-17/2	1700.780	1700.920	-82.615	0.569	1484.614	0.570	24	0.213	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-16/2	1700.380	1700.920	-908.176	0.596	1447.291	0.587	24	0.212	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-17/2	1701.200	1700.920	164.913	0.606	1386.609	0.571	23	0.201	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-12/2	1700.257	1700.920	-980.828	0.566	1328.650	0.558	22	0.193	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-15/2	1700.392	1700.920	-901.473	0.547	1211.104	0.547	22	0.180	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-21/2	1701.197	1700.920	163.546	0.498	1094.958	0.524	19	0.165	R.NLAGNSAIFVAPNGLNK.G
R5/RRR5-11/2	1702.599	1700.920	-189.099	0.361	206.429	0.383	12	0.107	-.NLAGNSAIFVAPNGLNK.-
R5/RRR5-6/2	1145.163	1145.288	-109.654	0.481	732.927	0.306	14	0.124	K.VLELDSQNVK.A
R5/RRR5-6/2	1145.059	1145.288	-200.765	0.458	683.881	0.293	14	0.123	K.VLELDSQNVK.A
R5/RRR5-6/2	1144.622	1145.288	-1459.948	0.375	803.108	0.269	14	0.123	K.VLELDSQNVK.A
R5/RRR5-6/2	1126.002	1126.280	-247.875	0.289	773.614	0.313	13	0.121	K.DGFFCPALAK.A
R5/RRR5-5/2	1697.801	1697.954	-90.764	0.447	613.290	0.424	18	0.131	R.LFLSPGYPYEEILR.T
R5/RRR5-4/2	1413.201	1413.557	-252.342	0.359	772.775	0.436	16	0.131	K.SLVGGFYDAGDAIK.F
R5/RRR5-5/2	1699.180	1697.954	133.260	0.448	713.164	0.366	19	0.129	R.LFLSPGYPYEEILR.T
R5/RRR5-5/2	1697.003	1697.954	-1153.485	0.341	807.949	0.332	18	0.126	R.LFLSPGYPYEEILR.T
R5/RRR5-2/2	1503.757	1502.649	72.170	0.496	1292.312	0.524	20	0.184	R.NPIDSSTIDLLEGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/2	1130.252	1129.292	-35.164	0.460	809.759	0.314	14	0.125	-.LVQTLGNDLR.-
R5/RRR5-2/2	1130.027	1129.292	-234.857	0.397	643.831	0.283	14	0.120	-.LVQTLGNDLR.-
R5/RRR5-8/2	1459.751	1459.629	83.908	0.463	867.253	0.319	19	0.129	R.QFIEGLDLPEAAR.S
R5/RRR5-9/2	1459.435	1459.629	-132.938	0.466	737.987	0.338	18	0.127	R.QFIEGLDLPEAAR.S
R5/RRR5-9/2	1460.612	1459.629	-11.368	0.377	508.338	0.376	16	0.126	R.QFIEGLDLPEAAR.S
R5/RRR5-8/2	1459.290	1459.629	-233.046	0.339	650.381	0.289	17	0.121	R.QFIEGLDLPEAAR.S
R5/RRR5-9/3	1704.312	1704.907	-938.847	0.409	891.940	0.367	22	0.083	K.LTPHSYIGEAEFLAR.N
R5/RRR5-9/3	1704.178	1704.907	-1017.807	0.373	665.380	0.330	20	0.071	-.LTPHSYIGEAEFLAR.-
R5/RRR5-22/2	1356.049	1355.542	-365.089	0.571	1975.092	0.565	20	0.280	R.FSQVVSNALDM*K.L
R5/RRR5-22/2	1354.613	1355.542	-1428.583	0.456	2165.543	0.457	20	0.279	R.FSQVVSNALDM*K.L
R5/RRR5-22/2	1354.440	1355.542	-1556.585	0.438	2124.392	0.464	20	0.274	R.FSQVVSNALDM*K.L
R5/RRR5-23/2	1355.171	1355.542	-275.159	0.541	2064.240	0.492	19	0.272	R.FSQVVSNALDM*K.L
R5/RRR5-23/2	1340.146	1339.543	-297.343	0.543	1801.568	0.564	19	0.253	R.FSQVVSNALDMK.L
R5/RRR5-23/2	1355.209	1355.542	-246.783	0.509	1674.210	0.506	19	0.222	R.FSQVVSNALDM*K.L
R5/RRR5-23/2	1355.147	1355.542	-292.330	0.532	1709.147	0.484	19	0.221	R.FSQVVSNALDM*K.L
R5/RRR5-23/2	1355.889	1355.542	256.763	0.458	1221.972	0.498	17	0.174	R.FSQVVSNALDM*K.L
R5/RRR5-23/2	1354.703	1355.542	-1362.150	0.438	1256.740	0.438	18	0.166	R.FSQVVSNALDM*K.L
R5/RRR5-23/2	1355.498	1355.542	-32.838	0.448	1108.434	0.478	17	0.162	R.FSQVVSNALDM*K.L
R5/RRR5-23/3	1355.591	1355.542	36.203	0.405	1214.634	0.340	24	0.099	R.FSQVVSNALDM*K.L
R5/RRR5-23/3	1355.433	1355.542	-80.996	0.461	982.310	0.363	21	0.090	R.FSQVVSNALDM*K.L
R5/RRR5-23/3	1354.608	1355.542	-1432.259	0.316	744.743	0.208	21	0.065	-.FSQVVSNALDM*K.-
R5/RRR5-5/2	1929.643	1930.292	-857.238	0.431	930.126	0.521	19	0.150	R.IIALLGGPCTEGPGM*IVSK.D
R5/RRR5-1/2	1929.581	1930.292	-889.690	0.366	378.518	0.438	16	0.122	R.IIALLGGPCTEGPGM*IVSK.D
R5/RRR5-1/2	1930.521	1930.292	118.764	0.366	117.543	0.497	14	0.118	-.IIALLGGPCTEGPGM*IVSK.-
R5/RRR5-5/3	1765.560	1765.002	-251.225	0.367	655.283	0.536	26	0.093	R.TGGLVVLSESFGHSVFK.D
R5/RRR5-4/2	1243.903	1244.423	-1225.801	0.482	802.152	0.492	18	0.146	R.QSALALLGDLSR.V
R5/RRR5-4/2	1273.199	1274.449	-1772.755	0.302	991.972	0.396	14	0.136	K.SLLENSAITLGR.L
R5/RRR5-1/2	1226.212	1225.375	-133.560	0.340	700.687	0.331	15	0.122	-.YATGINVFDPK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/2	1840.588	1841.056	-255.080	0.519	2147.188	0.455	26	0.275	R.SIALSDAGALGDPAAELLR.T
R5/RRR5-3/2	1485.245	1485.753	-1018.208	0.336	1294.334	0.428	20	0.163	R.LAVGEALTNLVWAK.V
R5/RRR5-3/2	1254.076	1254.418	-273.621	0.359	777.269	0.426	17	0.133	R.SPNSVIVEVGPR.M
R5/RRR5-13/2	1492.844	1492.742	68.761	0.565	2171.246	0.441	21	0.276	K.LQFLSLLDNTVTK.Q
R5/RRR5-12/2	1493.997	1492.742	171.394	0.614	2135.531	0.452	21	0.272	K.LQFLSLLDNTVTK.Q
R5/RRR5-6/3	1335.302	1335.579	-207.748	0.491	903.952	0.376	23	0.091	K.SLHPKWSPAALK.S
R5/RRR5-6/3	1335.236	1335.579	-257.688	0.439	847.411	0.385	23	0.089	K.SLHPKWSPAALK.S
R5/RRR5-6/3	1335.728	1335.579	112.267	0.444	1099.642	0.306	24	0.087	K.SLHPKWSPAALK.S
R5/RRR5-5/3	1334.539	1335.579	-1533.437	0.391	894.096	0.331	22	0.082	K.SLHPKWSPAALK.S
R5/RRR5-6/3	1335.245	1335.579	-250.809	0.463	940.903	0.242	24	0.074	K.SLHPKWSPAALK.S
R5/RRR5-1/2	1638.656	1637.902	-150.751	0.532	846.471	0.529	22	0.154	R.IPGTELLPGDIVSIGR.S
R5/RRR5-3/2	1636.896	1637.902	-1229.051	0.433	670.496	0.532	19	0.142	R.IPGTELLPGDIVSIGR.S
R5/RRR5-1/2	1638.031	1637.902	79.111	0.486	534.603	0.458	18	0.131	R.IPGTELLPGDIVSIGR.S
R5/RRR5-3/2	1327.706	1327.421	215.730	0.393	768.479	0.350	14	0.125	K.GIDWIYTSDEK.A
R5/RRR5-3/2	1824.514	1825.076	-858.773	0.514	1938.965	0.564	22	0.272	R.LTQM*NTDLFGGVDAVVK.Y
R5/RRR5-1/2	1825.659	1825.076	-229.305	0.563	1737.691	0.536	23	0.236	R.LTQM*NTDLFGGVDAVVK.Y
R5/RRR5-3/2	1824.340	1825.076	-954.490	0.534	1616.310	0.542	21	0.221	R.LTQM*NTDLFGGVDAVVK.Y
R5/RRR5-1/2	1824.329	1825.076	-960.603	0.495	1617.783	0.536	21	0.220	R.LTQM*NTDLFGGVDAVVK.Y
R5/RRR5-10/3	1101.382	1101.278	94.745	0.534	2208.951	0.374	25	0.255	R.AKGEAEAILAK.S
R5/RRR5-10/3	1101.248	1101.278	-27.986	0.540	1820.858	0.276	24	0.149	R.AKGEAEAILAK.S
R5/RRR5-10/2	1100.715	1101.278	-1424.860	0.372	856.235	0.396	16	0.134	R.AKGEAEAILAK.S
R5/RRR5-10/3	1100.724	1101.278	-1416.072	0.509	1335.948	0.367	22	0.116	R.AKGEAEAILAK.S
R5/RRR5-1/2	1162.908	1162.319	-354.769	0.450	856.588	0.371	15	0.134	K.WADLFEPGVK.H
R5/RRR5-5/2	1742.780	1742.029	-143.166	0.312	734.044	0.470	16	0.129	K.GM*PLEVITEFFSVGAK.Q
R5/RRR5-17/2	1643.151	1643.908	-1073.037	0.458	1829.389	0.572	26	0.259	K.NLVAPVIGEANLAAYK.A
R5/RRR5-17/2	1644.347	1643.908	267.486	0.538	1632.528	0.611	25	0.243	K.NLVAPVIGEANLAAYK.A
R5/RRR5-17/2	1643.211	1643.908	-1035.891	0.452	1743.622	0.538	26	0.239	K.NLVAPVIGEANLAAYK.A
R5/RRR5-17/2	1645.189	1643.908	171.123	0.359	328.449	0.407	14	0.122	K.NLVAPVIGEANLAAYK.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/3	1429.056	1429.511	-319.378	0.523	1998.677	0.482	29	0.249	K.DCRPVESSEPPR.Y
R5/RRR5-23/3	1429.595	1429.511	58.562	0.574	1635.224	0.514	28	0.194	K.DCRPVESSEPPR.Y
R5/RRR5-22/3	1429.356	1429.511	-108.848	0.531	1292.374	0.445	26	0.130	K.DCRPVESSEPPR.Y
R5/RRR5-22/3	1428.906	1429.511	-1127.126	0.496	1272.630	0.449	26	0.128	K.DCRPVESSEPPR.Y
R5/RRR5-23/3	1429.254	1429.511	-180.814	0.515	1294.510	0.431	26	0.127	K.DCRPVESSEPPR.Y
R5/RRR5-23/3	1428.946	1429.511	-1098.690	0.492	1193.845	0.448	24	0.122	K.DCRPVESSEPPR.Y
R5/RRR5-19/2	1752.759	1751.022	-150.368	0.557	2123.737	0.405	21	0.256	R.IIFIGQYINSQVAQR.V
R5/RRR5-13/2	1677.445	1677.873	-256.312	0.570	1821.583	0.588	23	0.264	K.VPNDVCADVVYNAIK.V
R5/RRR5-13/2	1677.403	1677.873	-281.063	0.544	1357.811	0.599	21	0.207	K.VPNDVCADVVYNAIK.V
R5/RRR5-3/2	1403.076	1403.480	-288.893	0.437	964.192	0.340	17	0.131	K.AGASQDQILNETR.L
R5/RRR5-3/2	998.618	998.205	415.682	0.428	916.284	0.229	13	0.123	R.NLQLQLIR.D
R5/RRR5-3/2	998.839	998.205	-367.076	0.410	579.736	0.231	11	0.119	R.NLQLQLIR.D
R5/RRR5-3/2	999.125	998.205	-79.973	0.383	676.495	0.126	12	0.113	-.NLQLQLIR.-
R5/RRR5-6/2	1614.234	1614.734	-932.219	0.501	2059.246	0.434	20	0.256	K.AVFDELQYSADDIK.A
R5/RRR5-6/2	1614.317	1614.734	-259.130	0.508	1763.867	0.440	19	0.216	K.AVFDELQYSADDIK.A
R5/RRR5-5/2	1459.086	1458.752	229.787	0.310	769.187	0.283	15	0.119	-.MQAKAIADAAVAVAK.-
R5/RRR5-5/2	1459.323	1458.752	-294.622	0.357	677.630	0.273	16	0.118	R.MQAKAIADAAVAVAK.E
R5/RRR5-5/2	1459.044	1458.752	200.927	0.272	661.971	0.248	14	0.115	R.MQAKAIADAAVAVAK.E
R5/RRR5-4/2	1459.291	1458.752	-317.115	0.299	641.060	0.225	14	0.114	R.MQAKAIADAAVAVAK.E
R5/RRR5-5/2	1460.148	1458.752	272.217	0.386	773.326	0.201	17	0.114	-.MQAKAIADAAVAVAK.-
R5/RRR5-5/2	1458.699	1458.752	-36.731	0.323	587.047	0.125	13	0.104	-.MQAKAIADAAVAVAK.-
R5/RRR5-3/2	1479.817	1479.750	45.621	0.421	574.649	0.468	17	0.134	R.AQVQIPLEVVNLR.A
R5/RRR5-3/2	1478.450	1479.750	-1560.186	0.331	542.137	0.379	15	0.122	R.AQVQIPLEVVNLR.A
R5/RRR5-3/3	1936.403	1936.202	103.998	0.417	767.766	0.403	24	0.083	-.HQAQIITSLKDPDISIR.-
R5/RRR5-3/3	1935.236	1936.202	-1018.834	0.404	582.533	0.447	24	0.083	-.HQAQIITSLKDPDISIR.-
R5/RRR5-23/2	1389.120	1389.625	-1086.375	0.582	1903.204	0.519	20	0.257	K.NVSNFLVQAGIVK.K
R5/RRR5-24/2	1550.077	1549.706	240.547	0.508	1766.469	0.586	22	0.254	R.TLSDPLFFGYSSSK.N
R5/RRR5-23/2	1550.201	1549.706	320.457	0.513	1371.915	0.534	20	0.194	R.TLSDPLFFGYSSSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-24/2	1549.176	1549.706	-990.178	0.477	1404.262	0.519	20	0.194	R.TLSDPLFFGYSSSK.N
R5/RRR5-23/2	1549.267	1549.706	-284.077	0.455	1455.900	0.483	21	0.192	R.TLSDPLFFGYSSSK.N
R5/RRR5-24/2	1550.226	1549.706	-310.123	0.523	1427.731	0.494	20	0.191	R.TLSDPLFFGYSSSK.N
R5/RRR5-23/2	1550.211	1549.706	-319.919	0.491	1290.482	0.517	19	0.182	R.TLSDPLFFGYSSSK.N
R5/RRR5-23/2	1549.304	1549.706	-259.651	0.465	1304.063	0.508	20	0.182	R.TLSDPLFFGYSSSK.N
R5/RRR5-23/2	1550.021	1549.706	203.905	0.499	1265.258	0.471	19	0.171	R.TLSDPLFFGYSSSK.N
R5/RRR5-23/2	1549.234	1549.706	-305.263	0.435	1052.992	0.513	18	0.162	R.TLSDPLFFGYSSSK.N
R5/RRR5-22/2	1548.871	1549.706	-1187.837	0.319	1068.156	0.383	18	0.143	R.TLSDPLFFGYSSSK.N
R5/RRR5-21/2	1549.238	1549.706	-302.418	0.305	686.316	0.454	16	0.132	R.TLSDPLFFGYSSSK.N
R5/RRR5-22/2	1548.496	1549.706	-1431.338	0.216	882.720	0.221	16	0.118	R.TLSDPLFFGYSSSK.N
R5/RRR5-14/2	1794.571	1794.001	-240.334	0.539	1811.031	0.567	26	0.256	R.DIPLNYATFQPGTTVR.D
R5/RRR5-15/2	1793.422	1794.001	-883.043	0.464	1607.698	0.501	24	0.212	R.DIPLNYATFQPGTTVR.D
R5/RRR5-14/2	1793.454	1794.001	-865.141	0.476	1546.446	0.508	24	0.207	R.DIPLNYATFQPGTTVR.D
R5/RRR5-15/2	1793.401	1794.001	-894.728	0.439	1548.115	0.480	24	0.201	R.DIPLNYATFQPGTTVR.D
R5/RRR5-15/2	1793.541	1794.001	-257.265	0.492	1251.683	0.508	22	0.177	R.DIPLNYATFQPGTTVR.D
R5/RRR5-16/2	1793.430	1794.001	-878.328	0.456	972.097	0.524	20	0.158	R.DIPLNYATFQPGTTVR.D
R5/RRR5-16/2	1793.384	1794.001	-904.226	0.439	807.675	0.506	17	0.144	R.DIPLNYATFQPGTTVR.D
R5/RRR5-13/2	1793.385	1794.001	-903.542	0.429	559.562	0.454	17	0.131	R.DIPLNYATFQPGTTVR.D
R5/RRR5-14/2	1792.568	1794.001	-1361.307	0.279	539.564	0.287	16	0.118	R.DIPLNYATFQPGTTVR.D
R5/RRR5-16/2	1792.604	1794.001	-1341.267	0.269	553.036	0.209	15	0.115	R.DIPLNYATFQPGTTVR.D
R5/RRR5-13/2	1269.034	1268.491	-361.087	0.526	1785.973	0.566	19	0.252	R.IVVAGNQIAVQR.T
R5/RRR5-14/2	1268.184	1268.491	-242.579	0.452	1433.286	0.463	17	0.186	R.IVVAGNQIAVQR.T
R5/RRR5-13/2	1267.601	1268.491	-1494.969	0.412	1358.485	0.471	17	0.180	R.IVVAGNQIAVQR.T
R5/RRR5-13/2	1267.724	1268.491	-1398.052	0.411	1482.386	0.398	17	0.178	R.IVVAGNQIAVQR.T
R5/RRR5-14/2	1267.970	1268.491	-1202.727	0.385	1497.202	0.358	18	0.172	R.IVVAGNQIAVQR.T
R5/RRR5-14/2	1267.530	1268.491	-1551.271	0.330	1344.621	0.403	17	0.165	R.IVVAGNQIAVQR.T
R5/RRR5-26/2	1268.151	1268.491	-268.943	0.388	1204.582	0.383	17	0.153	R.IVVAGNQIAVQR.T
R5/RRR5-25/2	1377.248	1377.546	-217.369	0.534	1862.843	0.536	22	0.256	K.GTDPVAIDLGSM*GK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-25/2	1377.223	1377.546	-235.153	0.484	1642.451	0.537	19	0.224	K.GTDPVAIDLGSM*GK.G
R5/RRR5-3/2	1001.262	1001.205	56.359	0.422	999.130	0.390	15	0.141	K.VSILAGTLAR.L
R5/RRR5-3/2	1336.478	1336.691	-159.918	0.301	676.246	0.421	15	0.125	-.ALALVVPSVVVLR.-
R5/RRR5-23/2	1581.348	1581.685	-213.277	0.512	1824.200	0.538	20	0.248	K.VSDSGELNSLMDDAK.Y
R5/RRR5-23/2	1597.040	1597.684	-1032.688	0.535	1495.495	0.497	21	0.198	K.VSDSGELNSLM*DDAK.Y
R5/RRR5-23/2	1597.101	1597.684	-994.471	0.504	1385.740	0.473	20	0.182	K.VSDSGELNSLM*DDAK.Y
R5/RRR5-23/2	1597.166	1597.684	-953.495	0.475	1176.127	0.447	19	0.160	K.VSDSGELNSLM*DDAK.Y
R5/RRR5-22/2	1597.403	1597.684	-176.304	0.434	1090.583	0.419	19	0.149	K.VSDSGELNSLM*DDAK.Y
R5/RRR5-21/2	1944.735	1945.166	-222.091	0.516	1720.257	0.596	23	0.248	K.VQASIAANTWVVSGSPQTK.K
R5/RRR5-21/2	1944.461	1945.166	-878.992	0.511	1580.565	0.525	23	0.212	K.VQASIAANTWVVSGSPQTK.K
R5/RRR5-10/2	1389.041	1389.487	-321.870	0.460	1937.296	0.466	20	0.247	R.VVLDCATADPDGR.K
R5/RRR5-9/2	1389.078	1389.487	-295.771	0.456	1909.985	0.450	20	0.239	R.VVLDCATADPDGR.K
R5/RRR5-10/2	1388.609	1389.487	-1356.493	0.392	1997.224	0.400	20	0.239	R.VVLDCATADPDGR.K
R5/RRR5-9/2	1388.945	1389.487	-1113.750	0.492	1892.784	0.387	20	0.221	R.VVLDCATADPDGR.K
R5/RRR5-9/2	1388.437	1389.487	-1481.352	0.351	1790.481	0.396	20	0.210	R.VVLDCATADPDGR.K
R5/RRR5-12/2	1932.584	1933.152	-813.565	0.471	1837.692	0.524	25	0.247	R.SFLQAVSTVTEEAPSPLR.V
R5/RRR5-12/2	1932.663	1933.152	-253.443	0.469	1673.535	0.526	24	0.225	R.SFLQAVSTVTEEAPSPLR.V
R5/RRR5-12/2	1933.107	1933.152	-22.903	0.527	1469.251	0.608	23	0.219	R.SFLQAVSTVTEEAPSPLR.V
R5/RRR5-3/2	1212.653	1212.426	187.735	0.383	756.553	0.409	15	0.131	-.HGFGAQLLQLK.-
R5/RRR5-3/2	1491.283	1490.689	-273.448	0.342	735.286	0.442	16	0.128	K.AVSVFNASAVGAGLAR.S
R5/RRR5-14/2	1210.065	1210.365	-248.969	0.551	1600.017	0.630	21	0.244	K.APSAAVAQPAAAGK.V
R5/RRR5-14/2	1210.202	1210.365	-134.821	0.503	1373.624	0.651	20	0.219	K.APSAAVAQPAAAGK.V
R5/RRR5-14/2	1211.176	1210.365	-156.750	0.562	1419.087	0.620	20	0.219	K.APSAAVAQPAAAGK.V
R5/RRR5-9/2	1432.130	1432.514	-269.097	0.524	1707.813	0.566	19	0.243	R.VNVYYNEASCGR.F
R5/RRR5-9/2	1431.980	1432.514	-1074.294	0.517	1675.393	0.551	19	0.234	R.VNVYYNEASCGR.F
R5/RRR5-14/2	1261.124	1261.452	-260.927	0.481	1669.496	0.592	23	0.243	R.AFTVGIGGPVGTGK.T
R5/RRR5-14/2	1260.934	1261.452	-1207.788	0.469	1410.392	0.569	22	0.206	R.AFTVGIGGPVGTGK.T
R5/RRR5-14/2	1277.140	1276.485	-270.981	0.315	911.972	0.350	16	0.128	R.SMPTSGAVDLVAK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-30/2	1534.093	1533.797	193.571	0.391	1219.600	0.158	16	0.121	K.TFKLVQQLEASLR.G
R5/RRR5-28/2	1534.258	1533.797	301.283	0.388	1169.501	0.140	16	0.117	K.TFKLVQQLEASLR.G
R5/RRR5-18/2	1535.019	1533.797	144.959	0.298	765.039	0.029	15	0.106	K.TFKLVQQLEASLR.G
R5/RRR5-17/3	1581.797	1581.717	50.798	0.516	1827.122	0.507	29	0.232	K.NHAVHISQIGEGYR.A
R5/RRR5-17/3	1581.891	1581.717	109.889	0.497	1275.160	0.497	26	0.143	K.NHAVHISQIGEGYR.A
R5/RRR5-17/3	1581.660	1581.717	-36.400	0.510	1108.736	0.535	27	0.135	K.NHAVHISQIGEGYR.A
R5/RRR5-2/2	1788.701	1788.938	-132.903	0.452	1944.338	0.413	22	0.233	R.SGGAAASAQIIDLLEDTR.I
R5/RRR5-1/2	1789.881	1788.938	-31.987	0.450	1008.654	0.419	18	0.140	R.SGGAAASAQIIDLLEDTR.I
R5/RRR5-1/2	1788.488	1788.938	-251.968	0.292	532.185	0.281	14	0.111	-.SGGAAASAQIIDLLEDTR.-
R5/RRR5-14/2	1656.556	1655.788	-140.327	0.494	1718.347	0.555	21	0.238	R.GLFSSDASLLTDATTR.D
R5/RRR5-10/2	1594.404	1594.836	-271.735	0.459	1789.811	0.509	23	0.238	R.LPGYLGEYLALTGAR.L
R5/RRR5-10/2	1596.026	1594.836	119.243	0.503	1615.851	0.520	23	0.219	R.LPGYLGEYLALTGAR.L
R5/RRR5-11/2	1594.596	1594.836	-151.001	0.547	1512.035	0.528	22	0.208	R.LPGYLGEYLALTGAR.L
R5/RRR5-11/2	1594.842	1594.836	3.792	0.552	1547.014	0.488	22	0.202	R.LPGYLGEYLALTGAR.L
R5/RRR5-19/2	1189.270	1188.268	1.790	0.468	1695.867	0.553	18	0.236	R.FDDSFSAASLK.A
R5/RRR5-21/2	1188.148	1188.268	-101.771	0.494	1717.944	0.516	18	0.230	R.FDDSFSAASLK.A
R5/RRR5-2/2	1187.977	1188.268	-246.177	0.424	1606.547	0.521	18	0.216	R.FDDSFSAASLK.A
R5/RRR5-8/2	1189.398	1188.268	109.774	0.407	1611.311	0.453	18	0.202	R.FDDSFSAASLK.A
R5/RRR5-21/2	1187.974	1188.268	-248.549	0.420	1464.098	0.464	17	0.189	R.FDDSFSAASLK.A
R5/RRR5-21/2	1187.163	1188.268	-1779.017	0.335	1307.224	0.441	17	0.169	R.FDDSFSAASLK.A
R5/RRR5-18/2	1188.309	1188.268	34.557	0.368	1235.845	0.397	17	0.158	R.FDDSFSAASLK.A
R5/RRR5-2/2	1187.311	1188.268	-1653.193	0.343	1133.943	0.439	16	0.155	R.FDDSFSAASLK.A
R5/RRR5-20/2	1187.966	1188.268	-254.837	0.436	1309.439	0.306	17	0.149	R.FDDSFSAASLK.A
R5/RRR5-20/2	1188.028	1188.268	-202.985	0.419	1319.752	0.253	18	0.142	R.FDDSFSAASLK.A
R5/RRR5-2/2	1187.990	1188.268	-235.250	0.334	633.535	0.467	15	0.135	R.FDDSFSAASLK.A
R5/RRR5-3/2	1187.984	1188.268	-239.786	0.267	551.559	0.295	14	0.122	R.FDDSFSAASLK.A
R5/RRR5-15/2	1536.455	1536.841	-251.941	0.408	1774.836	0.494	20	0.230	R.ALALQENPGLVILGK.Q
R5/RRR5-16/2	1790.281	1791.093	-1015.225	0.492	1907.733	0.438	22	0.235	K.VDLSDCGPM*VLDVLLK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-16/2	1790.493	1791.093	-896.668	0.495	1330.989	0.432	19	0.167	K.VDLSDCGPM*VLDVLLK.I
R5/RRR5-15/2	1790.687	1791.093	-227.668	0.450	819.475	0.376	16	0.127	K.VDLSDCGPM*VLDVLLK.I
R5/RRR5-10/2	1533.157	1532.720	285.927	0.473	1802.684	0.495	21	0.235	K.APDSDLVLADFGIAK.M
R5/RRR5-17/2	1532.987	1532.720	174.702	0.316	261.241	0.334	13	0.108	-.APDSDLVLADFGIAK.-
R5/RRR5-27/2	1539.267	1539.711	-289.025	0.491	1681.404	0.560	20	0.236	R.FLFCQSSPASAPAR.E
R5/RRR5-27/2	1539.448	1539.711	-171.283	0.522	1339.305	0.561	20	0.197	R.FLFCQSSPASAPAR.E
R5/RRR5-26/2	1540.644	1539.711	-43.519	0.259	453.297	0.383	15	0.120	R.FLFCQSSPASAPAR.E
R5/RRR5-4/2	1417.263	1417.575	-220.970	0.335	1284.740	0.284	18	0.142	-.M*AAVANGGAAPEWR.V
R5/RRR5-4/2	1417.285	1417.575	-205.503	0.336	947.402	0.261	16	0.123	-.M*AAVANGGAAPEWR.-
R5/RRR5-4/2	1416.673	1417.575	-1346.839	0.234	715.205	0.166	14	0.112	-.M*AAVANGGAAPEWR.-
R5/RRR5-8/2	1485.132	1485.663	-1033.619	0.437	1989.590	0.355	20	0.228	K.YYNDLINELLSK.G
R5/RRR5-7/2	1439.499	1438.605	-73.880	0.536	1788.917	0.499	20	0.236	R.TTDVLDGFTDLLK.A
R5/RRR5-8/2	1438.391	1438.605	-148.672	0.411	1287.007	0.426	17	0.165	R.TTDVLDGFTDLLK.A
R5/RRR5-7/2	1439.222	1438.605	-266.495	0.432	976.883	0.519	16	0.156	R.TTDVLDGFTDLLK.A
R5/RRR5-17/2	1524.160	1524.703	-1015.025	0.419	1770.543	0.476	22	0.226	K.GVNPWIEVDGGVGPK.N
R5/RRR5-19/2	1893.082	1892.182	-53.074	0.581	1732.184	0.519	22	0.230	R.IVKAGGECLTFDQLALR.S
R5/RRR5-6/2	1892.582	1892.187	209.242	0.607	1541.388	0.585	28	0.226	R.FIVSGGAPLSVAVEEFLR.V
R5/RRR5-6/2	1891.288	1892.187	-1007.155	0.563	1598.217	0.554	28	0.225	R.FIVSGGAPLSVAVEEFLR.V
R5/RRR5-6/2	1891.339	1892.187	-980.457	0.523	1433.735	0.541	27	0.203	R.FIVSGGAPLSVAVEEFLR.V
R5/RRR5-10/2	1566.989	1565.622	235.295	0.530	1642.964	0.541	20	0.225	R.SVDTASGQLSSQEQK.T
R5/RRR5-1/2	1567.035	1565.622	264.197	0.300	227.295	0.339	13	0.119	R.SVDTASGQLSSQEQK.T
R5/RRR5-11/2	1603.911	1603.708	126.519	0.542	1405.548	0.640	22	0.222	K.AGDTVGVGYFVDSCR.A
R5/RRR5-11/2	1603.373	1603.708	-209.736	0.510	1377.502	0.562	22	0.201	K.AGDTVGVGYFVDSCR.A
R5/RRR5-12/2	1603.433	1603.708	-172.007	0.507	1366.575	0.540	22	0.195	K.AGDTVGVGYFVDSCR.A
R5/RRR5-12/2	1603.237	1603.708	-294.676	0.485	1230.393	0.568	21	0.187	K.AGDTVGVGYFVDSCR.A
R5/RRR5-12/2	1602.521	1603.708	-1369.179	0.336	1222.462	0.337	20	0.146	K.AGDTVGVGYFVDSCR.A
R5/RRR5-16/3	1659.870	1659.735	81.602	0.514	1696.856	0.508	27	0.205	K.SGGLESEKDYPYTGR.D
R5/RRR5-15/3	1659.601	1659.735	-81.058	0.477	1592.884	0.502	29	0.185	K.SGGLESEKDYPYTGR.D

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1659.274	1659.735	-278.525	0.522	941.389	0.547	19	0.160	K.SGGLESEKDYPYTGR.D
R5/RRR5-22/3	1659.234	1659.735	-907.609	0.495	1406.639	0.467	28	0.149	K.SGGLESEKDYPYTGR.D
R5/RRR5-14/3	1659.957	1659.735	133.819	0.524	1332.679	0.496	28	0.148	K.SGGLESEKDYPYTGR.D
R5/RRR5-15/2	1659.195	1659.735	-930.940	0.452	844.352	0.480	18	0.143	K.SGGLESEKDYPYTGR.D
R5/RRR5-22/3	1659.510	1659.735	-136.175	0.499	1296.563	0.451	28	0.132	K.SGGLESEKDYPYTGR.D
R5/RRR5-15/3	1659.473	1659.735	-158.201	0.459	1070.652	0.498	25	0.123	K.SGGLESEKDYPYTGR.D
R5/RRR5-15/3	1659.773	1659.735	22.962	0.479	1015.330	0.514	26	0.122	K.SGGLESEKDYPYTGR.D
R5/RRR5-14/3	1659.264	1659.735	-284.734	0.466	1140.335	0.468	26	0.122	K.SGGLESEKDYPYTGR.D
R5/RRR5-22/3	1659.666	1659.735	-41.882	0.445	1018.240	0.485	25	0.116	K.SGGLESEKDYPYTGR.D
R5/RRR5-14/3	1659.033	1659.735	-1028.824	0.461	977.766	0.485	26	0.113	K.SGGLESEKDYPYTGR.D
R5/RRR5-16/3	1659.308	1659.735	-258.163	0.439	1171.788	0.405	26	0.110	K.SGGLESEKDYPYTGR.D
R5/RRR5-16/3	1659.760	1659.735	15.217	0.403	878.427	0.376	25	0.089	K.SGGLESEKDYPYTGR.D
R5/RRR5-28/2	1484.197	1484.624	-288.447	0.439	1885.149	0.376	20	0.218	R.SPCSLYACEAGLR.A
R5/RRR5-28/2	1484.122	1484.624	-1014.771	0.398	1782.677	0.391	20	0.209	R.SPCSLYACEAGLR.A
R5/RRR5-28/2	1484.419	1484.624	-138.041	0.456	1779.964	0.356	20	0.200	R.SPCSLYACEAGLR.A
R5/RRR5-26/2	1485.426	1484.624	-133.332	0.393	994.211	0.307	17	0.131	R.SPCSLYACEAGLR.A
R5/RRR5-3/2	1818.067	1818.019	26.223	0.491	1616.196	0.544	23	0.222	R.GIAFVGGFSYADVLDSAK.G
R5/RRR5-3/2	1819.082	1818.019	34.757	0.477	1492.276	0.482	23	0.194	R.GIAFVGGFSYADVLDSAK.G
R5/RRR5-24/2	1344.609	1343.551	43.288	0.507	1565.297	0.558	19	0.222	R.TPEGTIIELTIR.G
R5/RRR5-24/2	1343.335	1343.551	-161.106	0.516	1398.509	0.503	19	0.192	R.TPEGTIIELTIR.G
R5/RRR5-25/2	1343.370	1343.551	-135.492	0.483	1335.898	0.522	19	0.190	R.TPEGTIIELTIR.G
R5/RRR5-25/2	1343.211	1343.551	-254.005	0.469	1286.171	0.544	19	0.189	R.TPEGTIIELTIR.G
R5/RRR5-25/2	1343.225	1343.551	-243.338	0.453	1255.750	0.558	18	0.188	R.TPEGTIIELTIR.G
R5/RRR5-25/2	1343.220	1343.551	-247.714	0.437	1270.566	0.496	19	0.178	R.TPEGTIIELTIR.G
R5/RRR5-24/2	1343.200	1343.551	-262.667	0.476	1167.521	0.468	19	0.166	R.TPEGTIIELTIR.G
R5/RRR5-25/2	1342.361	1343.551	-1636.725	0.417	993.164	0.489	17	0.155	R.TPEGTIIELTIR.G
R5/RRR5-17/3	1568.030	1567.772	164.738	0.522	1868.874	0.411	30	0.200	R.LPLRDVLDDAGVGAR.V
R5/RRR5-16/2	1567.183	1567.772	-1017.082	0.383	762.290	0.312	17	0.121	R.LPLRDVLDDAGVGAR.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-20/2	1567.921	1567.772	95.064	0.342	525.961	0.236	15	0.113	R.LPLRDVLDDAGVGAR.V
R5/RRR5-16/3	1567.819	1567.772	30.400	0.295	690.290	0.349	25	0.079	R.LPLRDVLDDAGVGAR.V
R5/RRR5-16/3	1567.626	1567.772	-93.311	0.405	898.436	0.293	24	0.077	R.LPLRDVLDDAGVGAR.V
R5/RRR5-16/3	1568.148	1567.772	240.734	0.444	982.554	0.255	24	0.073	R.LPLRDVLDDAGVGAR.V
R5/RRR5-13/3	1568.530	1567.772	-154.533	0.340	1015.864	0.237	24	0.071	R.LPLRDVLDDAGVGAR.V
R5/RRR5-17/3	1566.486	1567.772	-1463.602	0.296	651.811	0.237	22	0.067	-.LPLRDVLDDAGVGAR.-
R5/RRR5-17/3	1568.442	1567.772	-211.215	0.316	906.976	0.193	24	0.065	R.LPLRDVLDDAGVGAR.V
R5/RRR5-13/2	1798.212	1798.971	-981.121	0.533	1533.308	0.582	23	0.223	R.VGFYQSSCPNAEALVR.Q
R5/RRR5-10/2	1385.690	1386.490	-1302.713	0.446	1725.666	0.472	21	0.220	K.TYGASTSGNSLSLK.F
R5/RRR5-10/2	1386.006	1386.490	-350.136	0.471	1599.692	0.493	21	0.210	K.TYGASTSGNSLSLK.F
R5/RRR5-10/2	1386.193	1386.490	-214.950	0.442	1311.782	0.558	19	0.191	K.TYGASTSGNSLSLK.F
R5/RRR5-6/2	1191.786	1191.362	357.245	0.385	1860.725	0.380	19	0.216	R.FAATLGELVGGR.V
R5/RRR5-6/2	1191.948	1191.362	-348.282	0.175	479.511	0.377	13	0.114	R.FAATLGELVGGR.V
R5/RRR5-4/2	1421.106	1420.636	331.647	0.533	1805.554	0.444	19	0.224	R.VNDQYITNVLLK.I
R5/RRR5-3/2	1421.210	1420.636	-300.714	0.374	591.757	0.362	13	0.121	-.VNDQYITNVLLK.-
R5/RRR5-13/2	1819.202	1818.021	99.768	0.551	1437.977	0.604	24	0.216	K.AAANNIGLDGFDVIDAIK.S
R5/RRR5-13/2	1818.702	1818.021	-175.546	0.535	1306.847	0.552	23	0.190	K.AAANNIGLDGFDVIDAIK.S
R5/RRR5-12/2	1818.518	1818.021	274.588	0.544	1290.705	0.550	22	0.187	K.AAANNIGLDGFDVIDAIK.S
R5/RRR5-12/2	1816.810	1818.021	-1220.356	0.417	908.355	0.459	21	0.143	K.AAANNIGLDGFDVIDAIK.S
R5/RRR5-13/2	1816.682	1818.021	-1291.073	0.417	807.279	0.484	20	0.141	K.AAANNIGLDGFDVIDAIK.S
R5/RRR5-22/2	1513.142	1513.545	-267.151	0.462	1503.402	0.571	23	0.217	K.FTTDPSSTSEDAVR.E
R5/RRR5-22/2	1513.161	1513.545	-254.687	0.476	1359.907	0.587	22	0.205	K.FTTDPSSTSEDAVR.E
R5/RRR5-22/2	1513.038	1513.545	-999.100	0.448	1366.247	0.552	22	0.197	K.FTTDPSSTSEDAVR.E
R5/RRR5-8/2	1450.413	1449.677	-182.219	0.491	1477.596	0.585	21	0.215	R.ASASAVAFGLGLLSGK.G
R5/RRR5-8/2	1449.190	1449.677	-336.898	0.447	1406.858	0.481	19	0.184	R.ASASAVAFGLGLLSGK.G
R5/RRR5-8/2	1449.367	1449.677	-214.620	0.242	630.883	0.302	15	0.115	R.ASASAVAFGLGLLSGK.G
R5/RRR5-18/2	1851.436	1852.078	-889.827	0.481	1715.032	0.471	22	0.216	K.GVSYGALSNAIQTILSEK.S
R5/RRR5-8/2	1852.444	1852.078	198.111	0.497	1453.750	0.448	21	0.181	K.GVSYGALSNAIQTILSEK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	1540.450	1539.800	-227.682	0.442	1690.643	0.475	19	0.216	R.AFQTLLTYIGNVAK.N
R5/RRR5-15/3	1570.405	1570.729	-207.521	0.428	1580.934	0.524	30	0.194	R.SPSGVIHLTDTSVTR.F
R5/RRR5-15/3	1570.142	1570.729	-1014.316	0.406	981.864	0.460	25	0.105	R.SPSGVIHLTDTSVTR.F
R5/RRR5-14/3	1607.613	1606.808	-122.102	0.426	1718.444	0.449	28	0.196	K.ALAHQPVSVAIEASGR.N
R5/RRR5-7/2	1755.466	1755.137	188.132	0.526	1505.336	0.562	24	0.214	R.AKLGVQAFADALLVIPK.V
R5/RRR5-13/2	1115.119	1115.310	-171.570	0.529	1671.332	0.481	19	0.218	K.IQGIGAGFVPR.N
R5/RRR5-13/2	1115.043	1115.310	-239.880	0.516	1577.771	0.446	19	0.199	K.IQGIGAGFVPR.N
R5/RRR5-13/2	1115.204	1115.310	-95.363	0.469	1430.970	0.422	18	0.179	K.IQGIGAGFVPR.N
R5/RRR5-2/2	1615.745	1615.767	-13.535	0.450	1863.702	0.353	20	0.209	K.GTNIVQEELDDIIR.H
R5/RRR5-3/2	1616.640	1615.767	-78.811	0.477	1294.600	0.430	17	0.164	K.GTNIVQEELDDIIR.H
R5/RRR5-8/2	1591.925	1590.764	101.322	0.453	1372.625	0.599	19	0.206	K.YQTSFFPFGWGPR.I
R5/RRR5-15/2	1633.504	1633.912	-250.315	0.484	1545.798	0.531	23	0.212	K.VGPALLSGPVFATFEK.V
R5/RRR5-14/2	1633.412	1633.912	-921.349	0.495	1514.084	0.504	22	0.202	K.VGPALLSGPVFATFEK.V
R5/RRR5-15/2	1633.718	1633.912	-118.831	0.496	1470.864	0.513	22	0.199	K.VGPALLSGPVFATFEK.V
R5/RRR5-14/2	1633.383	1633.912	-939.131	0.491	1305.763	0.518	21	0.183	K.VGPALLSGPVFATFEK.V
R5/RRR5-14/2	1633.417	1633.912	-303.848	0.472	1281.267	0.472	21	0.173	K.VGPALLSGPVFATFEK.V
R5/RRR5-16/2	1633.488	1633.912	-260.436	0.465	1130.213	0.509	20	0.166	K.VGPALLSGPVFATFEK.V
R5/RRR5-15/2	1633.537	1633.912	-230.223	0.467	1096.368	0.462	20	0.156	K.VGPALLSGPVFATFEK.V
R5/RRR5-10/3	1468.597	1468.637	-27.697	0.491	1668.225	0.462	26	0.189	R.VTSHSLQELQPTK.S
R5/RRR5-10/3	1468.605	1468.637	-21.694	0.515	1523.162	0.456	25	0.164	R.VTSHSLQELQPTK.S
R5/RRR5-9/2	1470.006	1468.637	251.901	0.415	999.675	0.469	19	0.151	R.VTSHSLQELQPTK.S
R5/RRR5-1/2	1746.463	1746.982	-872.364	0.510	1860.209	0.364	24	0.210	K.NEILAESEFAAPTIIK.L
R5/RRR5-1/2	1746.349	1746.982	-938.325	0.459	1850.485	0.346	24	0.206	K.NEILAESEFAAPTIIK.L
R5/RRR5-1/2	1746.217	1746.982	-1013.840	0.435	1791.427	0.304	23	0.190	K.NEILAESEFAAPTIIK.L
R5/RRR5-21/2	1239.013	1238.372	-290.288	0.439	1516.445	0.528	20	0.209	K.YSGNDLLGVTAK.V
R5/RRR5-21/2	1238.618	1238.372	199.121	0.413	1108.151	0.486	18	0.163	K.YSGNDLLGVTAK.V
R5/RRR5-20/2	1237.588	1238.372	-1445.450	0.341	669.404	0.481	15	0.135	K.YSGNDLLGVTAK.V
R5/RRR5-21/2	1237.498	1238.372	-1518.869	0.264	444.807	0.399	13	0.121	K.YSGNDLLGVTAK.V

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1551.463	1552.713	-1454.169	0.437	1579.370	0.492	20	0.207	K.DFNLAEHPDIPGVK.N
R5/RRR5-22/2	1552.112	1552.713	-1034.215	0.519	1427.428	0.513	19	0.195	K.DFNLAEHPDIPGVK.N
R5/RRR5-22/2	1552.228	1552.713	-313.351	0.488	1315.157	0.488	18	0.178	K.DFNLAEHPDIPGVK.N
R5/RRR5-23/3	1441.668	1440.590	53.952	0.286	2043.532	0.086	32	0.131	K.AAAGTNKAAAGAAAPAR.K
R5/RRR5-19/2	1535.118	1533.831	187.779	0.550	1563.017	0.509	20	0.208	K.ALLYCGLAPTVLGGK.I
R5/RRR5-19/2	1534.095	1533.831	172.741	0.475	1500.399	0.484	20	0.196	K.ALLYCGLAPTVLGGK.I
R5/RRR5-5/2	1899.822	1899.178	-187.965	0.529	1353.810	0.587	21	0.199	K.LALGTLALEDALSTGSPIR.T
R5/RRR5-5/2	1898.942	1899.178	-124.994	0.449	1253.118	0.475	22	0.168	K.LALGTLALEDALSTGSPIR.T
R5/RRR5-5/2	1898.439	1899.178	-918.875	0.398	1050.093	0.430	21	0.146	K.LALGTLALEDALSTGSPIR.T
R5/RRR5-3/2	1308.120	1307.346	-173.399	0.523	1591.222	0.494	20	0.210	K.DTSQDEAGTAAIK.T
R5/RRR5-9/2	1484.142	1483.607	-314.610	0.505	1722.787	0.430	21	0.210	R.NPYYGGEAASVNLK.T
R5/RRR5-9/3	1598.806	1598.869	-39.762	0.527	1500.247	0.533	26	0.184	R.TPFYLYSKPQVVR.N
R5/RRR5-9/3	1599.074	1598.869	128.501	0.495	1383.444	0.530	26	0.165	R.TPFYLYSKPQVVR.N
R5/RRR5-9/3	1598.927	1598.869	36.279	0.497	1330.332	0.454	25	0.138	R.TPFYLYSKPQVVR.N
R5/RRR5-10/3	1599.966	1598.869	60.897	0.353	700.542	0.405	21	0.084	R.TPFYLYSKPQVVR.N
R5/RRR5-24/2	1631.197	1631.963	-1085.403	0.474	1537.943	0.499	23	0.206	R.CCVIPVLGQALLCK.T
R5/RRR5-18/2	1631.574	1631.963	-238.604	0.436	1413.664	0.383	22	0.170	R.CCVIPVLGQALLCK.T
R5/RRR5-24/2	1631.804	1631.963	-97.136	0.475	1188.368	0.378	21	0.151	R.CCVIPVLGQALLCK.T
R5/RRR5-6/2	1361.133	1360.535	-296.536	0.539	1622.452	0.468	19	0.208	R.NLSQQCLNALAK.A
R5/RRR5-6/2	1359.631	1360.535	-1404.675	0.462	1613.374	0.396	19	0.191	R.NLSQQCLNALAK.A
R5/RRR5-6/2	1359.601	1360.535	-1426.859	0.427	1236.431	0.360	18	0.152	R.NLSQQCLNALAK.A
R5/RRR5-2/2	1360.266	1360.535	-198.615	0.466	1057.649	0.396	18	0.147	R.NLSQQCLNALAK.A
R5/RRR5-1/2	1360.394	1360.535	-104.096	0.344	536.143	0.384	15	0.126	R.NLSQQCLNALAK.A
R5/RRR5-22/2	1830.559	1831.128	-859.577	0.597	1466.905	0.530	27	0.205	K.IFEVAPSASQMFSFLR.N
R5/RRR5-22/2	1831.604	1831.128	260.661	0.634	1383.843	0.536	27	0.198	K.IFEVAPSASQMFSFLR.N
R5/RRR5-22/3	1831.750	1831.128	-206.588	0.523	1731.591	0.429	32	0.190	K.IFEVAPSASQMFSFLR.N
R5/RRR5-22/2	1846.253	1847.127	-1018.010	0.571	1292.541	0.537	25	0.189	K.IFEVAPSASQM*FSFLR.N
R5/RRR5-22/2	1846.505	1847.127	-880.881	0.526	1168.867	0.505	24	0.172	K.IFEVAPSASQM*FSFLR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-22/2	1846.177	1847.127	-1059.568	0.547	1129.576	0.519	24	0.171	K.IFEVAPSASQM*FSFLR.N
R5/RRR5-22/2	1831.023	1831.128	-57.347	0.574	1074.349	0.528	24	0.169	K.IFEVAPSASQMFSFLR.N
R5/RRR5-21/2	1830.523	1831.128	-879.259	0.542	1192.013	0.467	25	0.167	K.IFEVAPSASQMFSFLR.N
R5/RRR5-22/2	1847.549	1847.127	229.104	0.517	817.047	0.447	21	0.141	K.IFEVAPSASQM*FSFLR.N
R5/RRR5-7/2	1649.205	1647.897	186.965	0.450	1698.069	0.418	21	0.202	R.GLVDSLGGFSQALAIAK.Q
R5/RRR5-14/2	1386.715	1385.593	88.062	0.480	1237.291	0.609	20	0.196	R.DVGVSPAIVGAFPR.K
R5/RRR5-14/2	1385.274	1385.593	-230.649	0.339	1517.950	0.370	20	0.175	R.DVGVSPAIVGAFPR.K
R5/RRR5-13/2	1386.665	1385.593	52.041	0.410	1182.293	0.530	19	0.174	R.DVGVSPAIVGAFPR.K
R5/RRR5-13/2	1386.854	1385.593	189.050	0.278	547.649	0.381	14	0.121	R.DVGVSPAIVGAFPR.K
R5/RRR5-7/2	1376.163	1376.536	-272.390	0.477	1505.392	0.506	20	0.203	R.YGALEGLDVVDPK.T
R5/RRR5-7/2	1375.951	1376.536	-1155.857	0.391	1146.843	0.367	16	0.144	R.YGALEGLDVVDPK.T
R5/RRR5-11/2	1934.603	1934.179	219.696	0.547	1393.483	0.552	24	0.199	K.LITELIGSPDDSSLGFLR.S
R5/RRR5-11/2	1933.876	1934.179	-157.368	0.499	1048.998	0.487	22	0.156	K.LITELIGSPDDSSLGFLR.S
R5/RRR5-16/2	1103.283	1102.266	14.914	0.391	1685.339	0.383	17	0.196	R.ATETALVLAGR.V
R5/RRR5-15/2	1103.238	1102.266	-25.704	0.431	1808.229	0.312	17	0.195	R.ATETALVLAGR.V
R5/RRR5-5/2	1394.069	1393.529	-330.721	0.580	1534.851	0.483	19	0.201	R.GFVISDWQGLDR.I
R5/RRR5-5/2	1393.341	1393.529	-135.290	0.486	1593.038	0.413	19	0.193	R.GFVISDWQGLDR.I
R5/RRR5-5/2	1392.511	1393.529	-1453.190	0.360	1762.572	0.254	19	0.178	R.GFVISDWQGLDR.I
R5/RRR5-2/2	1392.995	1393.529	-1104.711	0.400	725.752	0.338	13	0.123	R.GFVISDWQGLDR.I
R5/RRR5-2/2	1557.880	1557.665	138.706	0.487	1321.107	0.570	21	0.194	R.VM*GTGDATDGFPSTGK.D
R5/RRR5-10/2	1486.898	1486.779	79.823	0.333	1605.808	0.409	20	0.191	K.SEMIMVFGEITTK.A
R5/RRR5-16/2	1100.328	1099.288	36.873	0.391	1682.140	0.396	15	0.198	K.YGGIM*LWSR.Y
R5/RRR5-4/2	1859.513	1860.061	-835.000	0.551	980.711	0.627	24	0.178	R.GVVPASGFSFSSQQFWK.V
R5/RRR5-4/2	1860.263	1860.061	109.216	0.584	842.527	0.611	23	0.166	R.GVVPASGFSFSSQQFWK.V
R5/RRR5-4/2	1859.275	1860.061	-963.386	0.539	925.651	0.578	23	0.165	R.GVVPASGFSFSSQQFWK.V
R5/RRR5-11/2	1520.916	1520.674	159.586	0.525	924.733	0.648	21	0.176	K.HGGVAASSAYPYLAR.Q
R5/RRR5-12/2	1836.069	1835.005	35.102	0.473	1451.511	0.521	23	0.198	K.NGVEEVLGLGQLSDFEK.E
R5/RRR5-13/2	1834.458	1835.005	-845.736	0.330	593.485	0.339	20	0.122	K.NGVEEVLGLGQLSDFEK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1835.512	1835.005	-269.192	0.288	455.367	0.419	17	0.122	K.NGVEEVLGLGQLSDFEK.E
R5/RRR5-13/2	1836.561	1835.005	-242.106	0.298	580.731	0.343	17	0.119	K.NGVEEVLGLGQLSDFEK.E
R5/RRR5-18/2	1586.558	1586.726	-106.312	0.497	1243.664	0.591	26	0.195	K.DLALPVSGVSAEENGK.A
R5/RRR5-17/2	1586.081	1586.726	-1039.932	0.437	1244.548	0.502	25	0.177	K.DLALPVSGVSAEENGK.A
R5/RRR5-17/2	1586.082	1586.726	-1039.160	0.432	1026.750	0.518	23	0.162	K.DLALPVSGVSAEENGK.A
R5/RRR5-18/2	1587.334	1586.726	-247.414	0.514	936.129	0.525	23	0.159	K.DLALPVSGVSAEENGK.A
R5/RRR5-18/2	1586.157	1586.726	-992.179	0.418	945.985	0.536	23	0.159	K.DLALPVSGVSAEENGK.A
R5/RRR5-17/2	1164.053	1164.336	-244.085	0.443	1646.208	0.422	17	0.200	R.SIGAAVIYNQK.K
R5/RRR5-17/2	1164.475	1164.336	119.694	0.304	1061.345	0.248	15	0.126	R.SIGAAVIYNQK.K
R5/RRR5-7/3	1584.483	1584.675	-121.644	0.475	1517.828	0.489	27	0.169	K.HQLDDKWDGVNTR.L
R5/RRR5-1/3	1584.862	1584.675	118.606	0.456	1567.202	0.467	27	0.169	K.HQLDDKWDGVNTR.L
R5/RRR5-8/3	1585.804	1584.675	81.785	0.471	1512.625	0.453	26	0.158	K.HQLDDKWDGVNTR.L
R5/RRR5-8/3	1585.286	1584.675	-245.811	0.475	1432.617	0.484	26	0.157	K.HQLDDKWDGVNTR.L
R5/RRR5-8/3	1585.162	1584.675	308.360	0.414	1324.385	0.463	25	0.138	K.HQLDDKWDGVNTR.L
R5/RRR5-7/3	1585.623	1584.675	-32.525	0.439	1488.205	0.386	25	0.136	K.HQLDDKWDGVNTR.L
R5/RRR5-1/3	1585.908	1584.675	147.440	0.465	916.616	0.471	23	0.107	K.HQLDDKWDGVNTR.L
R5/RRR5-7/3	1585.561	1584.675	-71.793	0.440	1063.352	0.392	23	0.100	K.HQLDDKWDGVNTR.L
R5/RRR5-1/3	1585.956	1584.675	177.891	0.420	886.380	0.377	22	0.089	K.HQLDDKWDGVNTR.L
R5/RRR5-6/2	1869.933	1869.023	-48.362	0.440	1407.684	0.527	22	0.193	K.SQSVTDAVVSILGSFDSR.L
R5/RRR5-10/2	1445.385	1445.685	-208.520	0.500	1705.707	0.398	19	0.200	R.LPDFSLDVAQIVK.V
R5/RRR5-10/2	1445.040	1445.685	-1141.603	0.420	1237.550	0.357	16	0.149	R.LPDFSLDVAQIVK.V
R5/RRR5-11/2	1445.208	1445.685	-331.218	0.376	1034.506	0.365	16	0.139	R.LPDFSLDVAQIVK.V
R5/RRR5-10/2	1444.637	1445.685	-1421.689	0.451	895.546	0.382	18	0.136	R.LPDFSLDVAQIVK.V
R5/RRR5-13/2	1089.911	1089.181	-248.781	0.550	1685.604	0.382	17	0.196	K.LGGELTVDER.N
R5/RRR5-13/2	1089.874	1089.181	-282.828	0.539	1323.524	0.358	16	0.158	K.LGGELTVDER.N
R5/RRR5-12/2	1470.848	1469.793	37.408	0.418	1223.709	0.586	20	0.188	K.VLDPVPLIGFLTGK.L
R5/RRR5-12/2	1469.209	1469.793	-1081.239	0.270	969.889	0.279	18	0.126	K.VLDPVPLIGFLTGK.L
R5/RRR5-12/2	1470.108	1469.793	215.155	0.261	639.354	0.397	16	0.124	K.VLDPVPLIGFLTGK.L

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-21/2	1469.184	1469.793	-1098.091	0.259	295.048	0.360	12	0.119	K.VLDPVPLIGFLTGK.L
R5/RRR5-21/2	1468.800	1469.793	-1360.873	0.172	485.345	0.349	14	0.115	K.VLDPVPLIGFLTGK.L
R5/RRR5-12/2	1549.192	1548.766	276.328	0.530	1566.921	0.446	21	0.197	R.IPSFTKEQSELIR.G
R5/RRR5-20/2	1259.410	1260.376	-1565.356	0.442	1459.544	0.486	18	0.193	R.LGGGQQEVCGVR.E
R5/RRR5-20/2	1260.045	1260.376	-263.483	0.438	1311.189	0.457	18	0.174	R.LGGGQQEVCGVR.E
R5/RRR5-26/2	1315.015	1314.473	-349.299	0.486	1558.623	0.448	18	0.195	K.AIADILSNVNGAR.D
R5/RRR5-17/2	1295.126	1295.467	-263.909	0.458	1349.699	0.534	18	0.192	R.VNQSFVIATSTK.L
R5/RRR5-17/2	1295.243	1295.467	-173.138	0.468	1346.337	0.535	18	0.192	R.VNQSFVIATSTK.L
R5/RRR5-17/2	1294.379	1295.467	-1617.468	0.371	927.450	0.494	16	0.150	R.VNQSFVIATSTK.L
R5/RRR5-16/2	1294.456	1295.467	-1557.688	0.275	580.970	0.236	15	0.117	R.VNQSFVIATSTK.L
R5/RRR5-1/3	1913.630	1914.066	-228.181	0.464	1599.628	0.429	35	0.167	R.LGM*EKGEGM*SAVADSGEGR.G
R5/RRR5-1/2	1912.307	1914.066	-1971.235	0.400	568.262	0.568	23	0.139	R.LGM*EKGEGM*SAVADSGEGR.G
R5/RRR5-1/3	1913.667	1914.066	-208.887	0.464	1092.884	0.492	31	0.123	R.LGM*EKGEGM*SAVADSGEGR.G
R5/RRR5-1/3	1913.276	1914.066	-938.003	0.448	1056.326	0.463	30	0.113	R.LGM*EKGEGM*SAVADSGEGR.G
R5/RRR5-28/2	1108.934	1109.257	-292.541	0.430	1476.898	0.470	17	0.193	R.YIEATGIVSR.A
R5/RRR5-27/2	1108.371	1109.257	-1707.087	0.467	1311.496	0.405	17	0.167	R.YIEATGIVSR.A
R5/RRR5-28/2	1108.854	1109.257	-364.554	0.348	1167.378	0.450	17	0.160	R.YIEATGIVSR.A
R5/RRR5-28/2	1109.198	1109.257	-54.155	0.444	1148.531	0.369	17	0.150	R.YIEATGIVSR.A
R5/RRR5-27/2	1108.419	1109.257	-1663.160	0.319	1146.655	0.394	17	0.150	R.YIEATGIVSR.A
R5/RRR5-27/2	1108.775	1109.257	-436.357	0.336	1156.288	0.342	16	0.145	R.YIEATGIVSR.A
R5/RRR5-14/2	1523.702	1523.630	47.441	0.532	1426.504	0.502	20	0.194	K.VLSDNFEQLNTSR.A
R5/RRR5-14/2	1522.954	1523.630	-1103.538	0.477	1289.482	0.441	19	0.169	K.VLSDNFEQLNTSR.A
R5/RRR5-14/2	1522.549	1523.630	-1370.490	0.355	1159.661	0.342	18	0.143	K.VLSDNFEQLNTSR.A
R5/RRR5-17/2	1374.230	1374.524	-214.238	0.542	1757.114	0.332	18	0.191	R.DNWQELIQSIK.A
R5/RRR5-18/2	967.162	967.190	-29.384	0.519	1346.747	0.504	15	0.189	K.AILLQGVPR.N
R5/RRR5-18/2	966.639	967.190	-1609.382	0.448	1267.335	0.470	14	0.174	K.AILLQGVPR.N
R5/RRR5-18/2	966.546	967.190	-1706.189	0.449	1232.369	0.461	14	0.169	K.AILLQGVPR.N
R5/RRR5-20/2	966.414	967.190	-1843.249	0.385	761.101	0.281	13	0.124	K.AILLQGVPR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1388.096	1388.509	-298.097	0.453	1615.768	0.413	20	0.195	K.LADQIDQSAGITR.L
R5/RRR5-12/2	1672.565	1672.819	-152.014	0.448	368.482	0.556	21	0.137	K.LIGLAGDTNVQGEEQK.K
R5/RRR5-6/2	1674.755	1673.958	-121.402	0.342	950.663	0.119	17	0.107	K.SALPSMDVTWTVLPR.I
R5/RRR5-12/2	1415.144	1415.531	-274.577	0.501	1335.636	0.522	20	0.188	R.SPNELLNSEGGLGK.Q
R5/RRR5-11/2	1795.541	1795.885	-192.403	0.465	1404.956	0.496	23	0.180	R.LQDDDADLGELGAHLVGG.-
R5/RRR5-5/2	1364.257	1364.569	-229.625	0.440	1612.037	0.399	18	0.191	R.NLGFVSCIANIR.G
R5/RRR5-5/2	1363.726	1364.569	-1355.747	0.328	410.721	0.436	12	0.123	R.NLGFVSCIANIR.G
R5/RRR5-6/3	1954.603	1955.302	-871.745	0.423	1467.363	0.460	27	0.158	K.LMSTTYLVALCQAVDLR.H
R5/RRR5-6/2	1971.380	1971.301	39.937	0.452	705.546	0.348	19	0.123	K.LM*STTYLVALCQAVDLR.H
R5/RRR5-6/2	1970.623	1971.301	-853.987	0.426	654.255	0.360	18	0.123	K.LM*STTYLVALCQAVDLR.H
R5/RRR5-6/2	1971.919	1971.301	-194.464	0.453	494.972	0.357	16	0.119	K.LM*STTYLVALCQAVDLR.H
R5/RRR5-6/3	1954.589	1955.302	-878.986	0.301	1297.144	0.067	26	0.055	K.LMSTTYLVALCQAVDLR.H
R5/RRR5-5/2	1495.062	1494.678	257.998	0.509	1101.440	0.573	22	0.177	R.LPATGEPIGQLQGGR.E
R5/RRR5-8/2	1924.876	1923.026	-77.767	0.454	705.156	0.617	19	0.150	K.STGSSNTDIDLLETIAER.V
R5/RRR5-20/2	1828.523	1828.960	-240.157	0.510	1237.793	0.546	22	0.182	R.VVGNSVSEFQSGFSDIR.T
R5/RRR5-20/2	1828.313	1828.960	-903.894	0.511	1078.123	0.565	20	0.171	R.VVGNSVSEFQSGFSDIR.T
R5/RRR5-20/2	1828.565	1828.960	-217.118	0.507	998.403	0.546	20	0.162	R.VVGNSVSEFQSGFSDIR.T
R5/RRR5-19/2	1827.910	1828.960	-1124.864	0.344	299.354	0.295	16	0.120	R.VVGNSVSEFQSGFSDIR.T
R5/RRR5-22/2	1585.417	1585.739	-204.003	0.490	1310.182	0.525	22	0.187	K.STGFGLIYDNLDAAK.K
R5/RRR5-23/2	1586.225	1585.739	306.850	0.537	1150.553	0.542	21	0.176	K.STGFGLIYDNLDAAK.K
R5/RRR5-22/2	1585.220	1585.739	-961.175	0.504	1177.747	0.531	21	0.176	K.STGFGLIYDNLDAAK.K
R5/RRR5-23/2	1585.237	1585.739	-950.352	0.495	980.849	0.524	20	0.160	K.STGFGLIYDNLDAAK.K
R5/RRR5-22/2	1584.666	1585.739	-1312.519	0.341	1159.879	0.433	21	0.156	K.STGFGLIYDNLDAAK.K
R5/RRR5-23/2	1585.887	1585.739	93.678	0.409	711.638	0.456	17	0.135	K.STGFGLIYDNLDAAK.K
R5/RRR5-2/2	1594.232	1592.754	300.641	0.557	999.414	0.582	25	0.174	-.M*DGAASVPSSNEVALK.Q
R5/RRR5-17/2	1593.259	1592.754	-311.181	0.506	960.611	0.501	25	0.158	-.M*DGAASVPSSNEVALK.Q
R5/RRR5-16/2	1593.203	1592.754	282.622	0.488	808.916	0.564	23	0.158	-.M*DGAASVPSSNEVALK.Q
R5/RRR5-17/2	1592.217	1592.754	-967.776	0.454	960.110	0.475	25	0.154	-.M*DGAASVPSSNEVALK.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1593.039	1592.754	179.355	0.499	841.426	0.496	23	0.150	-.M*DGAASVPSSNEVALK.Q
R5/RRR5-15/2	1592.305	1592.754	-282.764	0.420	607.701	0.461	21	0.136	-.M*DGAASVPSSNEVALK.Q
R5/RRR5-17/2	1576.137	1576.754	-1029.015	0.311	356.626	0.311	19	0.124	-.MDGAASVPSSNEVALK.Q
R5/RRR5-17/2	1576.179	1576.754	-1002.732	0.257	435.286	0.276	20	0.121	-.MDGAASVPSSNEVALK.Q
R5/RRR5-11/2	1080.114	1080.259	-134.848	0.379	1230.852	0.524	16	0.177	K.AILQSYLSGK.H
R5/RRR5-11/2	1079.896	1080.259	-337.823	0.348	855.157	0.544	13	0.150	K.AILQSYLSGK.H
R5/RRR5-10/2	1081.210	1080.259	-45.478	0.351	786.636	0.405	13	0.133	K.AILQSYLSGK.H
R5/RRR5-10/2	1080.263	1080.259	3.671	0.203	866.249	0.199	15	0.117	K.AILQSYLSGK.H
R5/RRR5-23/2	1258.159	1258.472	-249.431	0.522	1543.900	0.413	16	0.188	K.FNLFM*QQVSK.S
R5/RRR5-23/2	1258.309	1258.472	-129.136	0.456	1381.542	0.383	16	0.168	K.FNLFM*QQVSK.S
R5/RRR5-23/2	1258.145	1258.472	-259.944	0.444	1325.527	0.379	16	0.163	K.FNLFM*QQVSK.S
R5/RRR5-23/2	1242.089	1242.472	-309.580	0.496	1300.093	0.327	16	0.152	K.FNLFMQQVSK.S
R5/RRR5-23/2	1242.207	1242.472	-213.845	0.475	1189.049	0.235	16	0.132	K.FNLFMQQVSK.S
R5/RRR5-23/2	1241.977	1242.472	-399.810	0.387	861.049	0.188	14	0.116	-.FNLFMQQVSK.-
R5/RRR5-25/2	1458.461	1458.599	-94.830	0.472	1280.260	0.527	17	0.182	R.FGLYGVDFASPER.T
R5/RRR5-9/3	1836.144	1836.186	-22.853	0.394	1834.200	0.229	31	0.140	K.GMTPISTFILEKGALEK.K
R5/RRR5-9/3	1837.959	1836.186	-123.620	0.426	1464.268	0.134	29	0.075	K.GMTPISTFILEKGALEK.K
R5/RRR5-8/2	1712.150	1710.867	165.789	0.494	1570.413	0.409	20	0.185	K.SNFATLDESTGIIVSR.R
R5/RRR5-9/3	1626.985	1626.883	63.196	0.372	1532.645	0.404	32	0.149	K.VAQGVVGAVADKGSVLR.F
R5/RRR5-17/2	1050.078	1050.233	-148.150	0.533	1144.944	0.547	16	0.179	R.SLGAAIIYNK.D
R5/RRR5-17/2	1050.216	1050.233	-16.626	0.505	1291.208	0.484	15	0.178	R.SLGAAIIYNK.D
R5/RRR5-18/2	1050.166	1050.233	-64.311	0.447	1053.345	0.549	15	0.170	R.SLGAAIIYNK.D
R5/RRR5-17/2	1050.046	1050.233	-178.821	0.519	1031.591	0.492	15	0.161	R.SLGAAIIYNK.D
R5/RRR5-1/2	1049.607	1050.233	-1553.847	0.311	885.108	0.252	14	0.123	R.SLGAAIIYNK.D
R5/RRR5-17/2	1548.070	1546.697	241.966	0.496	1454.495	0.455	21	0.187	R.FGTICVFCGSNAGR.R
R5/RRR5-18/2	1547.915	1546.697	141.695	0.445	315.308	0.414	15	0.126	R.FGTICVFCGSNAGR.R
R5/RRR5-17/2	1548.147	1546.697	292.095	0.403	434.876	0.320	13	0.117	R.FGTICVFCGSNAGR.R
R5/RRR5-3/2	1667.374	1666.710	-202.107	0.383	386.346	0.560	16	0.129	K.EGGGGGAGGEGGM*SDSVIR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-4/2	1666.588	1666.710	-73.270	0.259	407.776	0.419	15	0.116	K.EGGGGGAGGEGGM*SDSVIR.K
R5/RRR5-14/2	1079.177	1078.203	-24.689	0.480	1579.388	0.399	16	0.188	R.LFVANVGDSR.A
R5/RRR5-22/2	1544.462	1544.817	-230.182	0.405	1416.324	0.461	18	0.181	K.VIGEVLDIFNPTVK.M
R5/RRR5-7/2	1102.243	1102.266	-21.284	0.433	1433.437	0.462	17	0.186	K.AALLSSLGVDR.V
R5/RRR5-17/2	1938.368	1938.130	123.070	0.526	1292.281	0.510	21	0.179	K.YNVGQINSTQLTDAVWK.N
R5/RRR5-13/3	1719.017	1718.851	97.206	0.509	1611.471	0.385	34	0.154	K.RLTSSDADVQAEAAKR.W
R5/RRR5-13/3	1718.660	1718.851	-110.936	0.468	810.798	0.386	27	0.086	K.RLTSSDADVQAEAAKR.W
R5/RRR5-28/3	1707.715	1707.819	-60.880	0.393	1338.582	0.491	28	0.146	K.CM*SYCSGHSGPCCK.W
R5/RRR5-28/3	1707.961	1707.819	83.647	0.433	904.816	0.547	25	0.117	K.CM*SYCSGHSGPCCK.W
R5/RRR5-14/3	1596.081	1596.764	-1057.321	0.481	1149.187	0.548	26	0.142	K.TAGKDLASDKTTYPK.L
R5/RRR5-14/3	1596.264	1596.764	-314.150	0.417	1116.528	0.447	25	0.114	K.TAGKDLASDKTTYPK.L
R5/RRR5-14/3	1596.029	1596.764	-1090.265	0.450	955.471	0.506	27	0.114	K.TAGKDLASDKTTYPK.L
R5/RRR5-23/3	1774.321	1774.999	-948.243	0.469	1438.837	0.452	29	0.151	R.IIKDFIVQGGDPTGTGR.G
R5/RRR5-23/3	1774.969	1774.999	-16.950	0.444	1207.210	0.359	26	0.102	R.IIKDFIVQGGDPTGTGR.G
R5/RRR5-23/3	1774.946	1774.999	-29.780	0.443	1284.143	0.312	26	0.098	R.IIKDFIVQGGDPTGTGR.G
R5/RRR5-20/3	1464.250	1464.645	-270.771	0.524	1302.139	0.498	28	0.146	K.KGEEVPLSEYKGK.V
R5/RRR5-20/3	1464.907	1464.645	179.177	0.430	609.256	0.337	23	0.079	K.KGEEVPLSEYKGK.V
R5/RRR5-14/2	1240.238	1240.476	-192.268	0.398	1247.879	0.518	18	0.178	R.DVAWAPVLGLAK.A
R5/RRR5-14/2	1240.256	1240.476	-177.754	0.410	1317.655	0.400	18	0.164	R.DVAWAPVLGLAK.A
R5/RRR5-14/2	1240.188	1240.476	-232.852	0.348	971.623	0.447	15	0.144	R.DVAWAPVLGLAK.A
R5/RRR5-17/2	1827.676	1828.100	-232.899	0.505	1078.052	0.555	24	0.172	K.GLLTDQTLPLLTDSALR.D
R5/RRR5-17/2	1827.588	1828.100	-829.956	0.507	915.177	0.562	22	0.161	K.GLLTDQTLPLLTDSALR.D
R5/RRR5-17/2	1827.056	1828.100	-1122.308	0.459	997.328	0.525	22	0.160	K.GLLTDQTLPLLTDSALR.D
R5/RRR5-6/3	1673.190	1673.851	-995.788	0.555	743.388	0.537	26	0.106	R.KYGLLGKEEAHDNAK.R
R5/RRR5-13/2	1353.100	1353.465	-270.156	0.475	1341.657	0.486	19	0.183	R.DNVQAYPGVSFR.Y
R5/RRR5-13/2	1353.141	1353.465	-240.288	0.448	1073.283	0.516	18	0.166	R.DNVQAYPGVSFR.Y
R5/RRR5-13/2	1352.521	1353.465	-1441.752	0.347	1105.542	0.383	18	0.146	R.DNVQAYPGVSFR.Y
R5/RRR5-12/3	1773.932	1774.121	-106.692	0.407	1205.181	0.126	26	0.063	-.M*PITIETIRLAWQGK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/3	1774.142	1774.121	12.159	0.418	904.772	0.127	24	0.054	-.M*PITIETIRLAWQGK.-
R5/RRR5-11/3	1773.589	1774.121	-866.285	0.368	892.001	0.067	23	0.051	-.M*PITIETIRLAWQGK.-
R5/RRR5-12/2	1336.321	1336.645	-243.496	0.412	425.635	0.539	17	0.137	K.AIPLIDISPLVGK.I
R5/RRR5-12/2	1336.038	1336.645	-1206.333	0.328	340.519	0.501	16	0.129	K.AIPLIDISPLVGK.I
R5/RRR5-12/2	1336.366	1336.645	-209.130	0.324	470.346	0.466	16	0.128	K.AIPLIDISPLVGK.I
R5/RRR5-22/2	1660.175	1658.854	194.092	0.433	433.885	0.532	19	0.136	R.VIPNFM*CQGGDFTR.G
R5/RRR5-11/3	1300.304	1299.420	-89.520	0.554	747.469	0.530	20	0.109	R.HLSTLTGYHNR.T
R5/RRR5-11/3	1299.251	1299.420	-130.538	0.485	850.271	0.508	21	0.108	R.HLSTLTGYHNR.T
R5/RRR5-10/3	1298.624	1299.420	-1387.188	0.407	441.889	0.396	16	0.084	R.HLSTLTGYHNR.T
R5/RRR5-7/2	1064.985	1065.334	-328.756	0.373	452.714	0.566	15	0.140	K.AVKPVLVGGPK.M
R5/RRR5-7/2	1065.016	1065.334	-299.662	0.320	530.864	0.530	16	0.136	K.AVKPVLVGGPK.M
R5/RRR5-6/2	1064.981	1065.334	-332.322	0.303	519.193	0.551	16	0.136	K.AVKPVLVGGPK.M
R5/RRR5-6/2	1065.015	1065.334	-300.811	0.366	467.959	0.500	15	0.135	K.AVKPVLVGGPK.M
R5/RRR5-6/2	1065.061	1065.334	-256.885	0.239	442.238	0.438	15	0.124	K.AVKPVLVGGPK.M
R5/RRR5-6/3	1065.461	1065.334	119.313	0.401	916.126	0.368	21	0.089	K.AVKPVLVGGPK.M
R5/RRR5-6/3	1065.667	1065.334	313.342	0.408	891.398	0.365	20	0.088	K.AVKPVLVGGPK.M
R5/RRR5-6/3	1065.472	1065.334	129.568	0.423	862.837	0.353	20	0.086	K.AVKPVLVGGPK.M
R5/RRR5-4/3	1064.994	1065.334	-320.546	0.345	873.501	0.293	20	0.077	K.AVKPVLVGGPK.M
R5/RRR5-1/3	1065.531	1065.334	185.319	0.392	679.256	0.292	19	0.076	-.AVKPVLVGGPK.-
R5/RRR5-7/3	1065.364	1065.334	28.304	0.357	868.734	0.212	20	0.069	K.AVKPVLVGGPK.M
R5/RRR5-1/3	1064.777	1065.334	-1466.898	0.334	552.601	0.307	17	0.069	-.AVKPVLVGGPK.-
R5/RRR5-2/3	1065.587	1065.334	238.393	0.333	629.960	0.243	18	0.067	-.AVKPVLVGGPK.-
R5/RRR5-3/3	1065.197	1065.334	-129.365	0.371	602.039	0.312	18	0.056	-.AVKPVLVGGPK.-
R5/RRR5-12/2	1368.033	1368.518	-355.452	0.406	1657.945	0.317	20	0.180	K.YIGLSEASASTIR.R
R5/RRR5-12/2	1368.275	1368.518	-178.214	0.426	1465.804	0.313	19	0.161	K.YIGLSEASASTIR.R
R5/RRR5-11/2	1624.583	1623.832	-153.866	0.496	1066.415	0.549	22	0.168	K.AGSGVATLGLPDSPGVPK.G
R5/RRR5-11/2	1623.093	1623.832	-1074.755	0.382	1026.548	0.497	21	0.154	K.AGSGVATLGLPDSPGVPK.G
R5/RRR5-11/2	1623.319	1623.832	-934.997	0.394	779.319	0.508	19	0.141	K.AGSGVATLGLPDSPGVPK.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1374.480	1374.569	-65.082	0.478	1265.384	0.503	17	0.178	R.YATNAVTAFIFR.E
R5/RRR5-9/2	1375.003	1374.569	317.122	0.466	1035.941	0.455	18	0.154	R.YATNAVTAFIFR.E
R5/RRR5-9/2	1374.478	1374.569	-66.418	0.418	1044.220	0.419	18	0.149	R.YATNAVTAFIFR.E
R5/RRR5-21/2	1447.599	1447.616	-11.977	0.393	1455.188	0.419	21	0.179	K.TVTLQSELVGNASK.V
R5/RRR5-21/2	1447.544	1447.616	-50.378	0.354	535.812	0.373	15	0.121	K.TVTLQSELVGNASK.V
R5/RRR5-8/3	1514.133	1513.593	-305.112	0.497	1330.051	0.479	24	0.144	K.VLYHEDPNSPDAR.I
R5/RRR5-8/3	1513.283	1513.593	-205.726	0.442	1239.987	0.444	24	0.125	K.VLYHEDPNSPDAR.I
R5/RRR5-1/3	1513.678	1513.593	56.158	0.491	1105.590	0.450	22	0.115	K.VLYHEDPNSPDAR.I
R5/RRR5-8/3	1513.288	1513.593	-202.206	0.470	1079.548	0.436	23	0.110	K.VLYHEDPNSPDAR.I
R5/RRR5-1/3	1513.809	1513.593	143.018	0.427	1367.882	0.313	24	0.108	-.VLYHEDPNSPDAR.-
R5/RRR5-1/3	1513.658	1513.593	43.055	0.460	1199.345	0.375	23	0.106	K.VLYHEDPNSPDAR.I
R5/RRR5-13/2	1245.366	1245.408	-33.487	0.463	1315.365	0.483	18	0.178	K.NSLSGTIPASLGK.I
R5/RRR5-12/2	1245.076	1245.408	-266.945	0.346	743.191	0.396	18	0.130	K.NSLSGTIPASLGK.I
R5/RRR5-30/2	1533.353	1531.843	-320.451	0.350	1938.982	0.046	20	0.155	K.VM*LKSAAINPLETK.Q
R5/RRR5-13/2	1810.602	1811.069	-258.966	0.450	1384.757	0.458	21	0.179	R.IEALAEEIQPLLSEVR.D
R5/RRR5-13/2	1809.995	1811.069	-1149.730	0.285	1127.208	0.318	20	0.136	R.IEALAEEIQPLLSEVR.D
R5/RRR5-8/2	1502.340	1503.547	-1473.519	0.403	900.231	0.577	17	0.158	R.VHCAESGEESLER.E
R5/RRR5-8/3	1503.097	1503.547	-300.347	0.462	1483.163	0.366	26	0.132	R.VHCAESGEESLER.E
R5/RRR5-8/3	1503.283	1503.547	-176.064	0.470	1064.759	0.386	23	0.099	-.VHCAESGEESLER.-
R5/RRR5-21/3	1773.350	1772.938	232.727	0.444	1470.494	0.415	30	0.145	R.KENLSKPDDVLSAAER.Y
R5/RRR5-21/3	1772.919	1772.938	-10.754	0.402	800.747	0.320	23	0.074	R.KENLSKPDDVLSAAER.Y
R5/RRR5-1/3	1430.913	1430.632	197.166	0.510	1726.782	0.296	28	0.142	R.VTGKDEGLTLLQR.Q
R5/RRR5-1/3	1430.143	1430.632	-342.850	0.370	1229.134	0.297	24	0.091	R.VTGKDEGLTLLQR.Q
R5/RRR5-1/3	1430.454	1430.632	-124.899	0.433	1238.673	0.283	24	0.090	R.VTGKDEGLTLLQR.Q
R5/RRR5-17/2	1607.554	1607.786	-145.214	0.436	1450.791	0.426	22	0.180	R.YAVGPGQCSSLLAQR.I
R5/RRR5-17/2	1607.237	1607.786	-967.053	0.459	1198.064	0.452	21	0.163	R.YAVGPGQCSSLLAQR.I
R5/RRR5-9/2	1762.458	1762.985	-869.033	0.446	903.586	0.570	23	0.159	K.LLEATGISTVPGSGFGQK.E
R5/RRR5-9/2	1764.309	1762.985	184.135	0.488	870.520	0.562	24	0.158	K.LLEATGISTVPGSGFGQK.E

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	1380.068	1380.532	-337.004	0.466	801.094	0.572	21	0.155	R.HGEAVGIIGPSGTGK.S
R5/RRR5-9/2	1097.169	1097.242	-66.243	0.362	383.497	0.523	11	0.134	R.SHCASFLFK.N
R5/RRR5-8/2	1096.890	1097.242	-321.873	0.299	491.541	0.455	11	0.128	R.SHCASFLFK.N
R5/RRR5-8/2	1096.579	1097.242	-1520.896	0.315	448.969	0.361	12	0.125	R.SHCASFLFK.N
R5/RRR5-9/2	1096.457	1097.242	-1632.395	0.248	379.230	0.410	11	0.123	R.SHCASFLFK.N
R5/RRR5-8/2	1097.046	1097.242	-179.195	0.229	477.787	0.438	11	0.123	R.SHCASFLFK.N
R5/RRR5-7/3	1096.973	1097.242	-246.104	0.469	737.009	0.343	18	0.077	-.SHCASFLFK.-
R5/RRR5-7/3	1096.652	1097.242	-1454.266	0.394	747.517	0.318	17	0.077	-.SHCASFLFK.-
R5/RRR5-10/3	1097.462	1097.242	201.403	0.450	931.411	0.300	19	0.076	-.SHCASFLFK.-
R5/RRR5-8/3	1097.446	1097.242	186.345	0.449	640.779	0.277	17	0.073	-.SHCASFLFK.-
R5/RRR5-10/3	1096.858	1097.242	-350.526	0.452	627.184	0.261	16	0.072	-.SHCASFLFK.-
R5/RRR5-9/3	1096.983	1097.242	-236.810	0.345	717.349	0.263	18	0.072	-.SHCASFLFK.-
R5/RRR5-9/3	1096.755	1097.242	-445.505	0.430	995.431	0.205	18	0.069	-.SHCASFLFK.-
R5/RRR5-24/2	934.495	935.102	-1725.141	0.416	1453.659	0.407	15	0.178	K.SGLFVGINK.X
R5/RRR5-23/2	934.952	935.102	-160.958	0.492	1314.056	0.428	15	0.171	K.SGLFVGINK.X
R5/RRR5-23/2	935.139	935.102	39.657	0.522	1287.517	0.433	15	0.170	-.SGLFVGINK.-
R5/RRR5-24/2	935.109	935.102	7.449	0.486	1315.981	0.407	15	0.167	K.SGLFVGINK.X
R5/RRR5-23/2	935.891	935.102	-226.339	0.534	1260.953	0.428	15	0.167	K.SGLFVGINK.X
R5/RRR5-24/2	935.166	935.102	68.328	0.404	988.607	0.371	13	0.140	K.SGLFVGINK.X
R5/RRR5-20/2	935.367	935.102	284.162	0.174	793.672	0.138	12	0.114	K.SGLFVGINK.X
R5/RRR5-20/2	936.018	935.102	-90.009	0.239	416.420	0.341	10	0.107	-.SGLFVGINK.-
R5/RRR5-5/2	1359.903	1360.580	-1237.293	0.429	1302.396	0.479	20	0.178	K.FTEQALPVDLVK.R
R5/RRR5-5/2	1360.222	1360.580	-264.421	0.486	914.732	0.524	18	0.158	K.FTEQALPVDLVK.R
R5/RRR5-4/2	1360.345	1360.580	-173.493	0.440	721.590	0.292	17	0.123	K.FTEQALPVDLVK.R
R5/RRR5-10/2	1655.394	1655.984	-963.402	0.513	863.061	0.560	17	0.155	K.TPLQQLMNDALIVAK.Q
R5/RRR5-8/2	1672.073	1671.984	53.919	0.305	512.109	0.329	14	0.116	K.TPLQQLM*NDALIVAK.Q
R5/RRR5-1/2	1712.244	1710.953	170.142	0.510	765.079	0.531	19	0.145	R.AILAEQPDISAIAELR.E
R5/RRR5-25/3	1914.582	1914.959	-197.618	0.533	1131.193	0.515	30	0.132	K.KDGEEESSGVVDYDKEK.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/2	1205.987	1206.288	-250.928	0.463	1116.494	0.529	21	0.173	R.VIGSGTNLDSSR.F
R5/RRR5-12/2	1205.985	1206.288	-252.045	0.439	988.632	0.533	20	0.164	R.VIGSGTNLDSSR.F
R5/RRR5-12/2	1206.328	1206.288	33.229	0.433	1016.303	0.503	20	0.161	R.VIGSGTNLDSSR.F
R5/RRR5-12/2	1205.472	1206.288	-1511.587	0.384	882.327	0.553	19	0.157	R.VIGSGTNLDSSR.F
R5/RRR5-13/2	1206.141	1206.288	-122.687	0.449	893.492	0.487	19	0.152	R.VIGSGTNLDSSR.F
R5/RRR5-13/2	1205.960	1206.288	-272.863	0.422	864.591	0.467	19	0.147	R.VIGSGTNLDSSR.F
R5/RRR5-12/2	1603.906	1602.858	29.877	0.472	1284.158	0.483	19	0.174	R.LALYALEAGPEWIR.E
R5/RRR5-10/2	1488.235	1487.722	-328.553	0.434	1351.294	0.453	18	0.175	K.TTFINTLFSTTIK.N
R5/RRR5-10/2	1487.998	1487.722	186.238	0.279	876.433	0.334	16	0.126	K.TTFINTLFSTTIK.N
R5/RRR5-10/2	1579.174	1577.852	204.560	0.477	772.775	0.565	17	0.150	R.HALWLSNLDLAVPK.T
R5/RRR5-8/2	1472.390	1472.671	-191.390	0.331	382.490	0.521	18	0.127	R.VAPAPPAGEPALPER.A
R5/RRR5-9/2	1171.244	1170.301	-48.464	0.530	1073.756	0.505	15	0.167	K.SPNYTWFVR.L
R5/RRR5-9/2	1171.309	1170.301	6.626	0.504	1030.368	0.473	15	0.159	K.SPNYTWFVR.L
R5/RRR5-9/2	1171.139	1170.301	-138.690	0.450	914.072	0.467	14	0.150	K.SPNYTWFVR.L
R5/RRR5-13/2	1476.017	1475.580	296.498	0.484	1250.933	0.484	20	0.174	K.IEDLQVVDEGETK.S
R5/RRR5-13/2	1475.798	1475.580	148.038	0.361	703.849	0.384	17	0.128	K.IEDLQVVDEGETK.S
R5/RRR5-11/3	1071.487	1071.299	176.204	0.450	1859.973	0.163	22	0.121	R.KVRAVQLEK.A
R5/RRR5-11/3	1071.203	1071.299	-89.149	0.453	1757.255	0.095	22	0.092	R.KVRAVQLEK.A
R5/RRR5-10/2	1271.285	1270.500	-170.141	0.522	1500.562	0.393	18	0.179	R.LANNLEELILK.E
R5/RRR5-10/2	1269.738	1270.500	-1391.687	0.420	1411.659	0.376	17	0.168	R.LANNLEELILK.E
R5/RRR5-10/2	1270.392	1270.500	-85.256	0.483	1247.728	0.401	17	0.160	R.LANNLEELILK.E
R5/RRR5-9/2	1270.135	1270.500	-288.284	0.444	1321.348	0.333	18	0.155	R.LANNLEELILK.E
R5/RRR5-9/2	1270.279	1270.500	-174.517	0.535	1054.977	0.356	16	0.140	R.LANNLEELILK.E
R5/RRR5-9/2	1270.273	1270.500	-179.048	0.437	761.251	0.351	15	0.130	R.LANNLEELILK.E
R5/RRR5-3/2	1480.102	1480.520	-283.289	0.448	1164.307	0.502	21	0.167	R.SVQEALGSGSSSASGR.T
R5/RRR5-17/2	1571.540	1570.861	-204.480	0.484	1216.799	0.498	20	0.173	R.AVLVLQQNLTPFAR.S
R5/RRR5-17/2	1569.897	1570.861	-1254.597	0.246	985.045	0.301	17	0.126	R.AVLVLQQNLTPFAR.S
R5/RRR5-19/2	1987.541	1986.170	187.294	0.509	1057.170	0.524	21	0.161	K.DPSTLEGYDGFLFGIPTR.Y

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1278.899	1279.427	-1198.959	0.437	893.899	0.556	17	0.160	K.GVVTDIIHDPGR.G
R5/RRR5-15/2	1279.048	1279.427	-297.284	0.458	941.666	0.511	18	0.157	K.GVVTDIIHDPGR.G
R5/RRR5-16/2	1279.386	1279.427	-32.213	0.452	988.747	0.493	18	0.157	K.GVVTDIIHDPGR.G
R5/RRR5-16/2	1280.097	1279.427	-258.686	0.460	925.963	0.472	18	0.151	K.GVVTDIIHDPGR.G
R5/RRR5-15/2	1279.105	1279.427	-252.473	0.426	871.990	0.465	17	0.146	K.GVVTDIIHDPGR.G
R5/RRR5-15/2	1279.095	1279.427	-260.899	0.422	913.798	0.436	18	0.145	K.GVVTDIIHDPGR.G
R5/RRR5-16/2	1279.391	1279.427	-28.290	0.387	809.004	0.462	17	0.142	K.GVVTDIIHDPGR.G
R5/RRR5-17/2	1279.079	1279.427	-273.154	0.372	858.200	0.422	17	0.140	K.GVVTDIIHDPGR.G
R5/RRR5-17/2	1279.638	1279.427	164.991	0.366	814.432	0.363	16	0.132	K.GVVTDIIHDPGR.G
R5/RRR5-24/2	1195.734	1195.503	193.833	0.279	1549.752	0.267	16	0.160	R.FM*KIKVVGTR.-
R5/RRR5-30/2	1195.693	1195.503	159.229	0.355	1191.647	0.325	14	0.143	R.FM*KIKVVGTR.-
R5/RRR5-29/2	1196.154	1195.503	-292.643	0.407	704.227	0.325	13	0.125	R.FM*KIKVVGTR.-
R5/RRR5-14/2	1455.127	1455.680	-1070.415	0.446	713.437	0.549	14	0.141	R.FAFASLGDTVSLVK.K
R5/RRR5-19/2	1160.956	1161.204	-214.890	0.384	1596.144	0.313	19	0.173	R.GGEGEEVGSLAR.R
R5/RRR5-4/2	1205.613	1206.413	-1497.395	0.414	1598.077	0.326	17	0.175	R.FLSLAIGDIEK.A
R5/RRR5-9/2	1724.359	1724.038	186.342	0.501	1113.664	0.503	19	0.164	R.IAWEEPFGPVLPVIR.I
R5/RRR5-8/2	1723.471	1724.038	-912.063	0.453	942.471	0.498	20	0.153	R.IAWEEPFGPVLPVIR.I
R5/RRR5-9/2	1723.530	1724.038	-877.507	0.368	881.654	0.385	19	0.134	R.IAWEEPFGPVLPVIR.I
R5/RRR5-9/2	1723.524	1724.038	-881.347	0.397	738.518	0.399	18	0.131	R.IAWEEPFGPVLPVIR.I
R5/RRR5-4/2	1645.358	1645.790	-263.394	0.392	1251.226	0.462	21	0.166	K.TVGAVAEVIEEEAEAK.L
R5/RRR5-4/2	1678.460	1678.828	-220.195	0.439	1124.988	0.499	18	0.161	R.ASGISIAQNFTQVEGR.V
R5/RRR5-3/2	972.681	972.164	-497.662	0.408	1337.253	0.425	15	0.170	R.VAILETVAR.Y
R5/RRR5-7/3	1980.080	1979.202	-61.941	0.481	632.577	0.497	27	0.092	K.ILVFDEADHMLAEDGFR.S
R5/RRR5-18/3	1811.772	1811.887	-63.437	0.434	1415.413	0.410	29	0.136	K.HKEAEENGDQYYLSK.L
R5/RRR5-23/3	1717.656	1716.868	-123.795	0.460	822.378	0.545	26	0.115	R.VPDEVIDKVQEETSK.S
R5/RRR5-24/3	1716.831	1716.868	-21.874	0.396	913.406	0.513	29	0.112	R.VPDEVIDKVQEETSK.S
R5/RRR5-23/3	1718.200	1716.868	193.487	0.414	858.611	0.496	26	0.107	R.VPDEVIDKVQEETSK.S
R5/RRR5-24/3	1716.210	1716.868	-969.186	0.476	699.144	0.494	24	0.101	R.VPDEVIDKVQEETSK.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/3	1715.732	1716.868	-1248.942	0.410	568.971	0.527	24	0.100	R.VPDEVIDKVQEETSK.S
R5/RRR5-24/3	1716.103	1716.868	-1031.853	0.395	648.977	0.508	25	0.099	R.VPDEVIDKVQEETSK.S
R5/RRR5-23/3	1716.097	1716.868	-1035.067	0.430	675.418	0.492	26	0.099	R.VPDEVIDKVQEETSK.S
R5/RRR5-26/2	1338.132	1338.535	-302.091	0.462	1229.605	0.475	21	0.172	K.VSGVEIVPDPVAR.G
R5/RRR5-25/2	1338.149	1338.535	-289.278	0.466	1141.527	0.457	20	0.162	K.VSGVEIVPDPVAR.G
R5/RRR5-25/2	1337.783	1338.535	-1312.938	0.444	977.588	0.473	19	0.153	K.VSGVEIVPDPVAR.G
R5/RRR5-26/2	1337.697	1338.535	-1378.099	0.393	965.691	0.420	19	0.145	K.VSGVEIVPDPVAR.G
R5/RRR5-25/2	1337.908	1338.535	-1219.839	0.414	846.455	0.412	18	0.139	K.VSGVEIVPDPVAR.G
R5/RRR5-22/2	1338.000	1338.535	-1150.483	0.427	662.735	0.469	15	0.136	K.VSGVEIVPDPVAR.G
R5/RRR5-24/2	1338.450	1338.535	-63.083	0.453	816.859	0.391	18	0.136	K.VSGVEIVPDPVAR.G
R5/RRR5-26/2	1337.649	1338.535	-1414.212	0.378	830.211	0.370	18	0.133	K.VSGVEIVPDPVAR.G
R5/RRR5-24/2	1338.167	1338.535	-275.732	0.370	609.381	0.409	16	0.130	K.VSGVEIVPDPVAR.G
R5/RRR5-23/2	1337.939	1338.535	-1196.566	0.285	857.899	0.335	16	0.128	K.VSGVEIVPDPVAR.G
R5/RRR5-24/2	1337.932	1338.535	-1201.606	0.315	651.620	0.334	16	0.125	K.VSGVEIVPDPVAR.G
R5/RRR5-23/2	1337.442	1338.535	-1569.509	0.280	734.453	0.315	16	0.124	K.VSGVEIVPDPVAR.G
R5/RRR5-18/3	1858.915	1859.081	-89.524	0.390	1057.147	0.523	29	0.125	R.AAHGGPAFEPHATVVGAIR.L
R5/RRR5-18/3	1858.859	1859.081	-119.661	0.403	1043.855	0.455	29	0.109	R.AAHGGPAFEPHATVVGAIR.L
R5/RRR5-18/3	1859.304	1859.081	120.196	0.378	1046.302	0.412	30	0.101	R.AAHGGPAFEPHATVVGAIR.L
R5/RRR5-3/3	1929.047	1929.118	-37.017	0.493	1015.716	0.505	26	0.118	-.LKEGNLDPNELSIATEGK.-
R5/RRR5-3/3	1928.996	1929.118	-63.200	0.358	639.053	0.264	22	0.065	-.LKEGNLDPNELSIATEGK.-
R5/RRR5-7/2	1990.875	1991.145	-135.765	0.467	1101.029	0.509	20	0.162	K.GSYDFIGLNYYTTNYAK.S
R5/RRR5-6/2	1145.699	1146.366	-1459.324	0.460	685.580	0.510	13	0.143	K.IPANLIYWR.V
R5/RRR5-16/2	1712.767	1711.895	-74.817	0.533	892.079	0.508	20	0.152	R.QVVSTLYSLEDTISR.R
R5/RRR5-15/2	1712.593	1711.895	-176.915	0.461	845.868	0.444	18	0.139	R.QVVSTLYSLEDTISR.R
R5/RRR5-10/2	1089.125	1088.280	-142.501	0.466	976.166	0.518	16	0.160	R.LGGSLDALTIK.E
R5/RRR5-10/2	1088.308	1088.280	26.144	0.367	1029.340	0.335	16	0.136	R.LGGSLDALTIK.E
R5/RRR5-10/2	1088.303	1088.280	21.194	0.323	651.850	0.303	15	0.122	R.LGGSLDALTIK.E
R5/RRR5-13/3	1076.480	1076.234	229.612	0.528	1515.605	0.352	25	0.131	K.HVGHLGGALSK.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-13/3	1076.452	1076.234	203.002	0.512	1287.918	0.335	24	0.105	K.HVGHLGGALSK.N
R5/RRR5-13/3	1076.560	1076.234	304.144	0.422	1354.514	0.224	24	0.086	K.HVGHLGGALSK.N
R5/RRR5-13/2	1365.180	1365.557	-277.182	0.417	1450.855	0.381	17	0.171	R.TVEGYSDIIVLR.H
R5/RRR5-3/2	1413.373	1412.527	-109.550	0.440	511.674	0.487	17	0.135	K.IVASYQTTNGETK.S
R5/RRR5-2/2	1413.465	1412.527	-44.143	0.423	481.025	0.436	14	0.126	K.IVASYQTTNGETK.S
R5/RRR5-22/2	828.849	828.978	-155.786	0.383	362.350	0.432	11	0.133	R.TPPSWLK.I
R5/RRR5-22/2	828.931	828.978	-56.661	0.382	282.212	0.378	10	0.131	R.TPPSWLK.I
R5/RRR5-22/2	828.835	828.978	-172.776	0.305	346.894	0.323	11	0.126	R.TPPSWLK.I
R5/RRR5-26/2	1670.520	1669.947	-256.642	0.430	1104.945	0.507	24	0.164	K.AAAVATIASAVPTLASVR.M
R5/RRR5-26/2	1669.440	1669.947	-905.866	0.270	685.724	0.503	18	0.130	K.AAAVATIASAVPTLASVR.M
R5/RRR5-25/2	1832.684	1833.121	-239.678	0.433	1007.953	0.525	20	0.156	K.DAPSAVNVVVVPNVNLPK.E
R5/RRR5-6/2	1455.045	1453.621	292.273	0.353	1128.781	0.490	16	0.159	R.IWLDYADASAISK.G
R5/RRR5-21/2	1440.003	1440.710	-1189.044	0.506	678.594	0.492	18	0.140	K.QALVDQLGLELIK.D
R5/RRR5-5/2	1238.366	1238.458	-74.509	0.379	426.817	0.487	14	0.131	K.LPSIPALEELR.K
R5/RRR5-5/2	1238.220	1238.458	-193.373	0.334	364.406	0.485	13	0.128	K.LPSIPALEELR.K
R5/RRR5-2/2	1244.214	1244.456	-195.492	0.403	543.707	0.459	12	0.128	R.APNLDILTCVK.D
R5/RRR5-21/3	1447.230	1447.791	-1081.341	0.433	654.835	0.530	23	0.100	K.TPVALAPIAKPLAGK.K
R5/RRR5-21/3	1447.482	1447.791	-213.894	0.441	452.809	0.557	20	0.098	K.TPVALAPIAKPLAGK.K
R5/RRR5-21/3	1448.083	1447.791	202.438	0.390	357.037	0.520	17	0.084	-.TPVALAPIAKPLAGK.-
R5/RRR5-25/2	1308.189	1308.470	-215.413	0.463	1293.327	0.449	17	0.170	K.GVAFVNNFNIGR.F
R5/RRR5-6/2	1144.056	1144.305	-218.064	0.408	1010.709	0.517	19	0.161	R.FDLSGIAPAPR.G
R5/RRR5-5/2	1145.046	1144.305	-226.644	0.385	858.387	0.543	18	0.154	R.FDLSGIAPAPR.G
R5/RRR5-15/2	1441.351	1441.698	-241.807	0.462	1191.908	0.475	22	0.168	K.VTPTVLQSAGLNLK.Q
R5/RRR5-15/2	1441.349	1441.698	-243.082	0.404	1128.290	0.425	21	0.154	K.VTPTVLQSAGLNLK.Q
R5/RRR5-15/2	1441.297	1441.698	-279.194	0.395	1131.968	0.379	21	0.148	K.VTPTVLQSAGLNLK.Q
R5/RRR5-10/3	1879.370	1880.122	-934.756	0.369	627.395	0.530	26	0.094	K.VNVNGGAM*ALGHPLGATGAR.S
R5/RRR5-10/3	1879.993	1880.122	-68.498	0.368	569.609	0.425	26	0.080	K.VNVNGGAM*ALGHPLGATGAR.S
R5/RRR5-14/2	1498.850	1497.679	114.720	0.408	595.393	0.519	13	0.134	K.IDWSGAPFVVSYR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1497.196	1497.679	-323.233	0.277	408.520	0.346	11	0.115	K.IDWSGAPFVVSYR.G
R5/RRR5-17/2	1077.018	1077.171	-142.171	0.500	1060.928	0.494	18	0.161	K.TAESGTAALAGK.G
R5/RRR5-19/2	1198.002	1197.371	-309.219	0.435	1012.381	0.504	14	0.158	R.SLPNNHVFLR.C
R5/RRR5-19/2	1197.723	1197.371	294.548	0.386	1017.019	0.447	14	0.149	R.SLPNNHVFLR.C
R5/RRR5-6/2	1741.141	1741.021	69.292	0.383	551.239	0.500	18	0.130	K.QIEPEIGEIPVAFVAK.T
R5/RRR5-23/2	1083.303	1082.232	66.049	0.395	868.538	0.532	17	0.154	R.YGSLTGLSGVK.V
R5/RRR5-21/2	1082.079	1082.232	-141.506	0.349	965.337	0.372	17	0.139	R.YGSLTGLSGVK.V
R5/RRR5-24/2	1082.346	1082.232	106.039	0.369	855.263	0.408	16	0.138	R.YGSLTGLSGVK.V
R5/RRR5-21/2	1081.951	1082.232	-260.456	0.286	794.864	0.447	15	0.135	R.YGSLTGLSGVK.V
R5/RRR5-21/2	1082.051	1082.232	-167.421	0.431	542.730	0.395	14	0.129	R.YGSLTGLSGVK.V
R5/RRR5-22/2	1081.996	1082.232	-219.256	0.255	648.415	0.330	14	0.122	R.YGSLTGLSGVK.V
R5/RRR5-15/2	1441.152	1441.698	-1076.122	0.431	1010.237	0.512	20	0.160	K.ITPTVLQSAGLNVK.Q
R5/RRR5-15/2	1441.203	1441.698	-344.542	0.477	1018.900	0.477	22	0.157	K.ITPTVLQSAGLNVK.Q
R5/RRR5-15/2	1442.290	1441.698	-283.670	0.513	1068.997	0.447	22	0.156	K.ITPTVLQSAGLNVK.Q
R5/RRR5-16/2	1441.152	1441.698	-1075.782	0.281	636.323	0.349	16	0.122	K.ITPTVLQSAGLNVK.Q
R5/RRR5-4/3	1881.604	1881.080	-253.431	0.419	676.495	0.491	28	0.095	K.IAVSPGTEGTSSPLTLHGR.D
R5/RRR5-4/3	1881.063	1881.080	-8.997	0.386	592.782	0.495	26	0.091	K.IAVSPGTEGTSSPLTLHGR.D
R5/RRR5-4/3	1880.553	1881.080	-814.434	0.346	707.402	0.467	29	0.090	K.IAVSPGTEGTSSPLTLHGR.D
R5/RRR5-20/2	1679.380	1679.861	-287.002	0.442	736.821	0.514	20	0.144	R.EALGIHQGTVPSWQR.C
R5/RRR5-20/2	1679.133	1679.861	-1031.886	0.447	830.297	0.436	22	0.140	R.EALGIHQGTVPSWQR.C
R5/RRR5-22/2	1898.838	1898.064	-119.262	0.463	570.307	0.477	22	0.135	K.IFTQFWDEEGIANAQK.S
R5/RRR5-10/2	1142.047	1142.292	-215.446	0.375	899.525	0.519	15	0.153	K.TIFHLNPSGR.F
R5/RRR5-10/2	1142.058	1142.292	-205.795	0.407	852.988	0.522	15	0.152	K.TIFHLNPSGR.F
R5/RRR5-10/2	1142.165	1142.292	-112.086	0.363	878.820	0.428	15	0.141	K.TIFHLNPSGR.F
R5/RRR5-9/2	1141.515	1142.292	-1561.741	0.182	383.998	0.340	11	0.114	-.TIFHLNPSGR.-
R5/RRR5-13/2	1141.989	1142.292	-266.598	0.244	590.513	0.239	12	0.113	-.TIFHLNPSGR.-
R5/RRR5-23/2	943.663	943.061	-423.635	0.183	507.066	0.501	10	0.121	K.MGYHGSYK.I
R5/RRR5-13/2	943.631	943.061	-457.644	0.112	313.165	0.425	9	0.107	-.MGYHGSYK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-8/2	943.733	943.061	-348.616	0.028	459.833	0.317	10	0.103	K.MGYHGSYK.I
R5/RRR5-5/2	1474.486	1474.639	-103.930	0.378	1410.629	0.379	18	0.167	K.EISDLEGELLSIR.N
R5/RRR5-5/2	1474.752	1474.639	76.911	0.341	656.593	0.312	13	0.118	K.EISDLEGELLSIR.N
R5/RRR5-10/2	1614.091	1612.870	137.806	0.441	774.434	0.504	15	0.140	R.EVFSAVLM*SSDILGK.S
R5/RRR5-10/2	1612.561	1612.870	-192.041	0.350	787.075	0.262	17	0.118	R.EVFSAVLM*SSDILGK.S
R5/RRR5-9/2	1291.105	1291.438	-258.946	0.402	779.962	0.530	20	0.147	R.GIAAAPVTNSYAR.R
R5/RRR5-4/2	1600.535	1599.853	-198.863	0.352	477.405	0.473	17	0.129	R.YSLLPYYYTLFR.E
R5/RRR5-7/2	1864.828	1864.177	-188.012	0.427	802.305	0.525	18	0.145	R.LLVNLATTPEVIYFGGR.D
R5/RRR5-7/2	1864.792	1864.177	-207.450	0.403	552.557	0.426	17	0.126	R.LLVNLATTPEVIYFGGR.D
R5/RRR5-7/2	1865.301	1864.177	66.715	0.341	337.193	0.366	13	0.114	-.LLVNLATTPEVIYFGGR.-
R5/RRR5-6/3	1662.167	1662.907	-1050.014	0.433	1358.142	0.322	24	0.108	K.HIHPLLECLSEWK.G
R5/RRR5-6/3	1662.840	1662.907	-40.292	0.451	926.129	0.455	20	0.102	K.HIHPLLECLSEWK.G
R5/RRR5-6/3	1661.936	1662.907	-1189.398	0.432	1155.736	0.270	22	0.082	K.HIHPLLECLSEWK.G
R5/RRR5-8/2	1330.287	1330.600	-236.685	0.501	732.813	0.480	16	0.141	K.VYTLGPLQLVAR.K
R5/RRR5-8/2	1331.913	1330.600	235.181	0.416	477.775	0.538	15	0.137	K.VYTLGPLQLVAR.K
R5/RRR5-8/3	1727.882	1727.927	-26.618	0.412	1154.816	0.476	27	0.122	R.RVQEHM*TLASNPTAR.R
R5/RRR5-4/2	1889.199	1888.182	8.774	0.344	289.363	0.326	16	0.120	-.MNVLADALKSINNAEKR.-
R5/RRR5-3/2	1888.744	1888.182	-232.629	0.353	942.976	0.225	19	0.119	R.MNVLADALKSINNAEKR.A
R5/RRR5-11/2	1888.735	1888.182	-237.298	0.383	789.355	0.198	17	0.112	R.MNVLADALKSINNAEKR.A
R5/RRR5-10/2	1887.884	1888.182	-158.348	0.268	622.954	0.174	16	0.111	-.MNVLADALKSINNAEKR.-
R5/RRR5-11/2	1888.466	1888.182	150.440	0.335	654.867	0.126	17	0.109	-.MNVLADALKSINNAEKR.-
R5/RRR5-9/2	1888.137	1888.182	-23.838	0.339	497.713	0.262	15	0.108	-.MNVLADALKSINNAEKR.-
R5/RRR5-10/2	1454.884	1453.581	208.823	0.455	651.134	0.484	16	0.137	R.NTVNSFNTWIEK.M
R5/RRR5-9/2	1261.276	1260.464	-149.747	0.421	533.649	0.491	18	0.137	K.DNGVPLVAFSLK.D
R5/RRR5-9/2	1260.342	1260.464	-97.010	0.306	473.265	0.379	15	0.122	K.DNGVPLVAFSLK.D
R5/RRR5-11/3	1619.230	1617.805	263.265	0.432	624.636	0.499	22	0.091	R.HQADVCHAYQIM*K.K
R5/RRR5-10/2	1128.339	1128.387	-42.928	0.321	572.104	0.527	14	0.134	K.VPILTIGSLSK.R
R5/RRR5-10/2	1127.622	1128.387	-1570.125	0.287	718.571	0.420	14	0.128	K.VPILTIGSLSK.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-5/3	1581.800	1580.764	22.391	0.391	653.067	0.518	26	0.092	K.LTEVSVSDKLEGFR.A
R5/RRR5-25/3	1233.599	1233.424	142.557	0.484	671.144	0.468	20	0.095	K.LLRPNM*ESTR.D
R5/RRR5-25/3	1233.158	1233.424	-215.719	0.423	368.817	0.484	15	0.092	K.LLRPNM*ESTR.D
R5/RRR5-25/3	1233.206	1233.424	-176.841	0.456	384.657	0.432	15	0.089	K.LLRPNM*ESTR.D
R5/RRR5-7/2	1550.240	1550.781	-997.475	0.472	830.519	0.503	18	0.146	R.LLSSTNQPSFLSKK.D
R5/RRR5-2/2	1357.411	1357.580	-124.349	0.429	813.080	0.483	15	0.141	K.IPSVNDIPLNFK.V
R5/RRR5-19/2	1161.402	1161.375	22.918	0.525	1299.858	0.414	18	0.167	K.LLFLGLDNAGK.T
R5/RRR5-19/2	1161.105	1161.375	-233.632	0.530	1273.664	0.399	18	0.162	K.LLFLGLDNAGK.T
R5/RRR5-19/2	1160.542	1161.375	-1584.455	0.443	1321.860	0.374	18	0.162	K.LLFLGLDNAGK.T
R5/RRR5-19/2	1161.199	1161.375	-152.636	0.367	860.397	0.398	15	0.136	K.LLFLGLDNAGK.T
R5/RRR5-7/2	928.116	928.108	8.230	0.391	565.866	0.498	13	0.138	K.VPVSELVGK.T
R5/RRR5-7/2	927.684	928.108	-458.846	0.336	606.698	0.448	14	0.133	K.VPVSELVGK.T
R5/RRR5-7/2	927.989	928.108	-128.983	0.357	522.798	0.457	13	0.132	K.VPVSELVGK.T
R5/RRR5-25/2	1370.285	1370.577	-213.336	0.446	1101.070	0.477	18	0.161	K.TPIQNLKDAIEK.L
R5/RRR5-25/2	1370.167	1370.577	-300.122	0.475	1058.381	0.495	17	0.161	K.TPIQNLKDAIEK.L
R5/RRR5-25/2	1371.253	1370.577	-236.400	0.480	983.576	0.481	17	0.154	K.TPIQNLKDAIEK.L
R5/RRR5-8/2	1442.215	1442.600	-267.895	0.439	692.191	0.502	16	0.138	K.GLDFEFLPFGSGR.R
R5/RRR5-5/2	1531.163	1530.709	297.574	0.551	888.413	0.462	20	0.149	R.SPQFPEAIDWIAR.N
R5/RRR5-6/2	1530.255	1530.709	-297.128	0.489	869.576	0.465	20	0.148	R.SPQFPEAIDWIAR.N
R5/RRR5-5/2	1530.440	1530.709	-176.451	0.500	862.417	0.454	20	0.147	R.SPQFPEAIDWIAR.N
R5/RRR5-6/2	1530.340	1530.709	-241.507	0.514	903.566	0.429	20	0.145	R.SPQFPEAIDWIAR.N
R5/RRR5-6/2	1530.018	1530.709	-1108.527	0.487	867.157	0.419	20	0.142	R.SPQFPEAIDWIAR.N
R5/RRR5-5/2	1529.828	1530.709	-1233.356	0.374	568.045	0.347	17	0.126	R.SPQFPEAIDWIAR.N
R5/RRR5-12/3	1504.255	1504.676	-280.744	0.440	760.798	0.509	26	0.104	R.LAAALSSPAHPAGGAGR.N
R5/RRR5-13/3	1504.830	1504.676	102.824	0.390	884.093	0.455	27	0.100	R.LAAALSSPAHPAGGAGR.N
R5/RRR5-12/3	1504.726	1504.676	33.384	0.379	897.396	0.446	27	0.099	R.LAAALSSPAHPAGGAGR.N
R5/RRR5-13/3	1504.891	1504.676	143.581	0.377	696.727	0.444	24	0.090	R.LAAALSSPAHPAGGAGR.N
R5/RRR5-13/3	1504.115	1504.676	-1041.260	0.370	628.286	0.374	24	0.081	R.LAAALSSPAHPAGGAGR.N

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-12/3	1504.349	1504.676	-217.854	0.350	763.391	0.351	22	0.079	R.LAAALSSPAHPAGGAGR.N
R5/RRR5-9/2	1656.185	1655.962	134.724	0.394	730.782	0.483	17	0.135	R.SPPLPFLLSSLLQSR.A
R5/RRR5-21/2	1353.843	1354.446	-1187.664	0.386	1283.905	0.420	17	0.163	K.AFNVEEAPSDFK.V
R5/RRR5-21/2	1503.329	1503.685	-237.376	0.422	1348.898	0.397	20	0.166	R.ALEWITANGGITTR.D
R5/RRR5-16/2	1503.462	1503.685	-148.345	0.383	1463.901	0.316	18	0.160	R.ALEWITANGGITTR.D
R5/RRR5-21/2	1503.163	1503.685	-1015.764	0.358	958.625	0.313	19	0.131	R.ALEWITANGGITTR.D
R5/RRR5-21/2	1503.148	1503.685	-1025.711	0.305	1155.596	0.212	21	0.128	R.ALEWITANGGITTR.D
R5/RRR5-16/2	1503.126	1503.685	-1039.899	0.321	589.688	0.294	14	0.118	R.ALEWITANGGITTR.D
R5/RRR5-17/2	1325.223	1324.508	-215.878	0.530	1170.297	0.435	17	0.158	K.SELLLSSNPVHK.K
R5/RRR5-17/2	1324.323	1324.508	-140.399	0.479	954.876	0.462	16	0.149	K.SELLLSSNPVHK.K
R5/RRR5-6/2	1774.645	1775.041	-223.784	0.408	1111.060	0.469	18	0.157	K.IPIDYSWAQELGLIR.K
R5/RRR5-1/2	1775.260	1775.041	123.825	0.362	441.672	0.419	13	0.119	-.IPIDYSWAQELGLIR.-
R5/RRR5-8/2	1671.544	1672.116	-943.248	0.290	835.301	0.134	15	0.109	-.M*LYFLHIHLVKLK.H
R5/RRR5-6/3	1717.938	1717.908	17.837	0.443	776.172	0.487	26	0.099	R.IFSEAHEFYHPIAR.S
R5/RRR5-6/3	1718.063	1717.908	90.526	0.454	662.329	0.362	24	0.081	R.IFSEAHEFYHPIAR.S
R5/RRR5-23/3	1647.856	1647.860	-2.654	0.474	1195.254	0.448	29	0.122	R.TVNRPYGGVLSGTAVR.E
R5/RRR5-23/3	1648.803	1647.860	-34.992	0.530	1084.441	0.429	29	0.109	R.TVNRPYGGVLSGTAVR.E
R5/RRR5-23/3	1647.325	1647.860	-935.055	0.431	996.213	0.328	26	0.084	R.TVNRPYGGVLSGTAVR.E
R5/RRR5-17/2	1471.325	1471.638	-213.498	0.395	926.312	0.506	20	0.152	R.SSAPDLPSLLLDSR.I
R5/RRR5-17/2	1471.462	1471.638	-119.869	0.358	826.319	0.468	19	0.141	R.SSAPDLPSLLLDSR.I
R5/RRR5-17/2	1471.161	1471.638	-325.292	0.292	724.868	0.347	17	0.124	R.SSAPDLPSLLLDSR.I
R5/RRR5-19/3	1538.469	1538.734	-172.713	0.468	1183.410	0.448	27	0.121	R.KIENVATGPNNRPK.L
R5/RRR5-19/3	1538.414	1538.734	-208.772	0.454	1056.181	0.441	27	0.109	R.KIENVATGPNNRPK.L
R5/RRR5-18/3	1538.314	1538.734	-273.852	0.460	964.038	0.432	25	0.102	R.KIENVATGPNNRPK.L
R5/RRR5-18/3	1539.324	1538.734	-267.030	0.439	961.824	0.420	27	0.099	R.KIENVATGPNNRPK.L
R5/RRR5-19/3	1538.434	1538.734	-195.757	0.434	725.644	0.423	24	0.091	R.KIENVATGPNNRPK.L
R5/RRR5-18/3	1538.974	1538.734	156.472	0.405	890.735	0.384	25	0.090	R.KIENVATGPNNRPK.L
R5/RRR5-2/3	1996.291	1996.057	117.371	0.468	1180.732	0.415	31	0.113	R.QSKPDEVTEDDM*PSTSGR.Q

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-2/3	1997.772	1996.057	-143.123	0.495	747.298	0.466	26	0.093	R.QSKPDEVTEDDM*PSTSGR.Q
R5/RRR5-4/2	1787.476	1787.050	239.560	0.498	844.072	0.491	20	0.148	R.LDQLIYIPLPDDKSR.M
R5/RRR5-3/2	1786.649	1787.050	-224.610	0.443	748.083	0.408	19	0.133	R.LDQLIYIPLPDDKSR.M
R5/RRR5-4/2	1785.940	1787.050	-1184.480	0.403	843.770	0.296	20	0.125	R.LDQLIYIPLPDDKSR.M
R5/RRR5-4/2	1785.830	1787.050	-1246.600	0.369	591.740	0.330	16	0.121	R.LDQLIYIPLPDDKSR.M
R5/RRR5-19/2	1361.622	1360.414	153.438	0.551	711.756	0.412	16	0.131	R.YQQNGAPPAEER.N
R5/RRR5-4/2	1972.964	1971.206	-123.221	0.444	675.516	0.466	17	0.132	R.GVWLNDFQYAIFGLGNR.Q
R5/RRR5-4/2	1972.426	1971.206	111.509	0.383	393.171	0.392	14	0.118	R.GVWLNDFQYAIFGLGNR.Q
R5/RRR5-6/2	1993.623	1994.278	-832.444	0.403	559.877	0.447	20	0.127	R.AVIDEVLIPLNLDEIGNR.L
R5/RRR5-5/2	1484.749	1483.647	68.806	0.487	1408.524	0.366	19	0.164	K.FGYELEALVGQEK.D
R5/RRR5-14/2	1383.305	1383.615	-225.224	0.469	875.350	0.488	16	0.145	K.VIVIDVNDPLASK.L
R5/RRR5-28/2	1479.229	1477.752	323.189	0.498	755.793	0.294	14	0.118	K.DKM*VTGVKPEKTK.S
R5/RRR5-25/2	1477.203	1477.752	-1052.160	0.335	1140.776	0.085	16	0.115	-.DKM*VTGVKPEKTK.-
R5/RRR5-20/2	1477.261	1477.752	-333.377	0.327	1202.995	0.065	16	0.113	K.DKM*VTGVKPEKTK.S
R5/RRR5-2/2	1477.149	1477.752	-1088.669	0.340	1219.474	0.053	16	0.112	K.DKM*VTGVKPEKTK.S
R5/RRR5-26/2	1477.238	1477.752	-1027.933	0.330	1026.830	0.070	14	0.109	-.DKM*VTGVKPEKTK.-
R5/RRR5-23/2	1477.224	1477.752	-1037.558	0.344	1041.776	0.053	15	0.108	-.DKM*VTGVKPEKTK.-
R5/RRR5-3/2	1477.141	1477.752	-1093.814	0.372	946.474	0.078	15	0.108	-.DKM*VTGVKPEKTK.-
R5/RRR5-8/2	1477.172	1477.752	-1072.738	0.343	795.446	0.074	14	0.108	-.DKM*VTGVKPEKTK.-
R5/RRR5-2/2	1477.226	1477.752	-1036.230	0.342	839.182	0.060	14	0.107	-.DKM*VTGVKPEKTK.-
R5/RRR5-21/2	1477.242	1477.752	-1025.278	0.347	882.465	0.077	14	0.107	-.DKM*VTGVKPEKTK.-
R5/RRR5-1/2	1477.098	1477.752	-1123.355	0.324	850.969	0.050	14	0.106	-.DKM*VTGVKPEKTK.-
R5/RRR5-15/2	1477.184	1477.752	-1065.021	0.337	841.249	0.055	14	0.104	-.DKM*VTGVKPEKTK.-
R5/RRR5-3/2	1477.040	1477.752	-1162.358	0.333	765.328	0.050	13	0.103	-.DKM*VTGVKPEKTK.-
R5/RRR5-4/2	1477.247	1477.752	-1021.877	0.356	779.189	0.081	14	0.103	-.DKM*VTGVKPEKTK.-
R5/RRR5-14/2	1477.499	1477.752	-171.732	0.387	666.654	0.117	13	0.098	-.DKM*VTGVKPEKTK.-
R5/RRR5-15/2	1186.020	1186.345	-275.179	0.381	659.266	0.498	17	0.141	R.HSGIIDIQFR.R
R5/RRR5-15/2	1186.062	1186.345	-239.039	0.392	459.218	0.525	15	0.138	R.HSGIIDIQFR.R

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-18/2	1211.100	1211.393	-242.690	0.323	531.587	0.493	17	0.132	R.VPIVPSDGAISR.T
R5/RRR5-18/2	1210.495	1211.393	-1572.576	0.301	527.367	0.523	16	0.131	R.VPIVPSDGAISR.T
R5/RRR5-27/2	976.115	976.070	47.023	0.420	680.058	0.430	11	0.137	R.FYQAQYR.N
R5/RRR5-27/2	975.985	976.070	-87.076	0.398	744.559	0.395	12	0.136	R.FYQAQYR.N
R5/RRR5-27/2	975.867	976.070	-207.908	0.412	674.254	0.324	11	0.128	R.FYQAQYR.N
R5/RRR5-8/2	1324.199	1324.637	-331.806	0.420	616.946	0.459	16	0.131	R.LVPALTAILSGIR.E
R5/RRR5-26/2	1428.528	1429.560	-1426.408	0.495	1174.512	0.436	21	0.161	K.YSPAAHDVVEVNK.A
R5/RRR5-26/2	1429.240	1429.560	-224.325	0.503	1225.641	0.384	21	0.156	K.YSPAAHDVVEVNK.A
R5/RRR5-15/3	1510.214	1510.769	-1032.352	0.429	666.221	0.482	26	0.093	K.VKPVHVVDVPGHAR.L
R5/RRR5-15/3	1510.297	1510.769	-313.345	0.433	484.364	0.456	23	0.088	K.VKPVHVVDVPGHAR.L
R5/RRR5-8/2	1616.676	1615.918	-150.453	0.427	730.428	0.488	20	0.143	R.DFPLGDLPMLEVLR.C
R5/RRR5-8/2	1616.940	1615.918	13.432	0.489	703.108	0.445	20	0.139	R.DFPLGDLPMLEVLR.C
R5/RRR5-8/2	1617.025	1615.918	65.979	0.463	689.491	0.408	20	0.134	R.DFPLGDLPMLEVLR.C
R5/RRR5-9/2	1617.168	1615.918	154.555	0.393	298.762	0.458	14	0.128	R.DFPLGDLPMLEVLR.C
R5/RRR5-9/2	1616.966	1615.918	29.787	0.409	434.929	0.470	15	0.125	-.DFPLGDLPMLEVLR.-
R5/RRR5-9/2	1616.957	1615.918	23.957	0.362	517.805	0.330	16	0.122	R.DFPLGDLPMLEVLR.C
R5/RRR5-13/3	1730.332	1730.946	-935.874	0.475	867.105	0.477	30	0.104	R.VLSIQSHTVQGYVGNK.S
R5/RRR5-13/3	1730.210	1730.946	-1006.314	0.442	561.733	0.486	28	0.094	R.VLSIQSHTVQGYVGNK.S
R5/RRR5-13/3	1730.823	1730.946	-71.320	0.417	564.640	0.372	27	0.082	R.VLSIQSHTVQGYVGNK.S
R5/RRR5-9/2	1653.397	1651.836	-266.408	0.496	719.268	0.436	17	0.136	R.ELILQYADQLCER.L
R5/RRR5-9/2	1652.402	1651.836	-263.531	0.423	642.852	0.384	16	0.128	R.ELILQYADQLCER.L
R5/RRR5-21/2	1650.947	1651.836	-1147.693	0.255	807.863	0.181	16	0.115	R.ELILQYADQLCER.L
R5/RRR5-9/2	1652.999	1651.836	99.060	0.372	264.916	0.344	12	0.112	-.ELILQYADQLCER.-
R5/RRR5-25/3	1926.521	1925.291	119.943	0.471	1618.534	0.247	27	0.114	R.RYLQMIQKNSIFNLR.S
R5/RRR5-24/3	1926.681	1925.291	203.244	0.437	1413.724	0.262	27	0.098	R.RYLQMIQKNSIFNLR.S
R5/RRR5-24/3	1926.928	1925.291	-188.632	0.453	1339.591	0.232	26	0.085	R.RYLQMIQKNSIFNLR.S
R5/RRR5-25/3	1926.140	1925.291	-78.359	0.423	1103.834	0.182	25	0.067	-.RYLQMIQKNSIFNLR.-
R5/RRR5-25/3	1926.484	1925.291	100.688	0.435	1195.729	0.169	25	0.066	R.RYLQMIQKNSIFNLR.S

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-15/2	1600.313	1598.786	-296.744	0.402	802.563	0.496	18	0.140	R.RLDADDGVAAVVLAGR.G
R5/RRR5-23/2	1123.794	1124.229	-388.362	0.329	924.510	0.491	17	0.148	K.GISSSAVPYSR.N
R5/RRR5-23/2	1123.285	1124.229	-1735.542	0.417	776.607	0.417	16	0.137	K.GISSSAVPYSR.N
R5/RRR5-23/2	1123.830	1124.229	-356.101	0.339	457.555	0.515	13	0.131	K.GISSSAVPYSR.N
R5/RRR5-14/2	1299.171	1299.565	-304.271	0.327	514.996	0.476	15	0.127	R.HVSMISISLSPK.E
R5/RRR5-17/2	922.852	923.048	-213.417	0.376	772.406	0.479	11	0.085	K.ISEYGVRV.-
R5/RRR5-3/2	1720.479	1720.822	-199.944	0.400	1018.708	0.476	21	0.150	R.TLSFAIADGSQPGNEGR.E
R5/RRR5-7/2	1978.357	1978.234	62.469	0.337	612.267	0.471	17	0.125	R.ELTAPFVDDGLIEVVGFR.D
R5/RRR5-18/2	1578.044	1577.910	85.066	0.361	705.764	0.374	14	0.124	K.LYVICQHMKLSGK.E
R5/RRR5-18/2	1578.095	1577.910	117.494	0.332	620.718	0.300	13	0.112	-.LYVICQHMKLSGK.-
R5/RRR5-16/2	941.024	941.151	-135.524	0.323	547.435	0.449	12	0.131	K.IPFPLTPR.F
R5/RRR5-16/2	941.141	941.151	-11.267	0.311	555.888	0.412	12	0.128	K.IPFPLTPR.F
R5/RRR5-16/2	941.019	941.151	-140.859	0.307	466.022	0.427	11	0.127	K.IPFPLTPR.F
R5/RRR5-2/2	1618.835	1618.859	-14.568	0.377	738.759	0.420	15	0.126	R.FGALVAQLESVVASAR.Q
R5/RRR5-5/3	1310.213	1310.401	-144.304	0.376	1286.677	0.390	28	0.114	R.HGVPSAVGSANASR.G
R5/RRR5-20/2	1346.927	1347.366	-327.116	0.493	1267.386	0.403	18	0.163	K.YEDQIDSYGEK.G
R5/RRR5-15/2	1347.103	1347.366	-195.375	0.375	1231.246	0.387	18	0.156	K.YEDQIDSYGEK.G
R5/RRR5-15/2	1346.386	1347.366	-1474.601	0.319	1244.012	0.317	18	0.146	K.YEDQIDSYGEK.G
R5/RRR5-15/2	1348.176	1347.366	-141.093	0.394	723.985	0.371	16	0.131	K.YEDQIDSYGEK.G
R5/RRR5-12/2	1368.371	1368.584	-156.215	0.422	965.420	0.477	18	0.152	R.VLSGYNDIIM*AR.V
R5/RRR5-12/2	1368.216	1368.584	-269.612	0.399	978.895	0.326	17	0.133	R.VLSGYNDIIM*AR.V
R5/RRR5-4/2	1812.373	1813.046	-925.895	0.448	1134.477	0.445	21	0.155	K.AYLPVLESFGFNADLR.A
R5/RRR5-12/2	1629.817	1628.847	-18.526	0.396	1064.784	0.463	18	0.152	R.YNLLEYADVVTSLK.R
R5/RRR5-6/2	1251.095	1250.408	-251.028	0.484	1316.903	0.384	19	0.162	K.DAGTISGLNVM*R.I
R5/RRR5-9/2	1263.222	1263.465	-192.841	0.406	1176.923	0.434	18	0.159	K.IFGLSSVSDIPK.L
R5/RRR5-9/2	1263.328	1263.465	-108.314	0.380	1110.990	0.351	18	0.143	K.IFGLSSVSDIPK.L
R5/RRR5-9/2	1263.275	1263.465	-150.285	0.366	835.268	0.370	15	0.131	K.IFGLSSVSDIPK.L
R5/RRR5-15/2	1857.356	1857.057	161.331	0.419	578.051	0.436	20	0.126	K.GITPADAPETSALASWLR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-11/2	1685.913	1684.831	48.759	0.328	743.319	0.491	16	0.132	K.ALNLGSFFTSGADEVR.Q
R5/RRR5-25/2	1274.048	1274.446	-313.538	0.514	1299.894	0.372	17	0.158	K.LNNETVTIELK.N
R5/RRR5-25/2	1274.064	1274.446	-300.561	0.517	1210.895	0.359	17	0.150	K.LNNETVTIELK.N
R5/RRR5-25/2	1273.564	1274.446	-1481.913	0.393	966.104	0.230	15	0.122	K.LNNETVTIELK.N
R5/RRR5-9/3	1453.245	1452.704	-317.384	0.263	1607.672	0.124	24	0.086	K.EATM*NIVFLNRK.G
R5/RRR5-22/2	1148.334	1147.261	63.588	0.481	1255.843	0.381	15	0.157	K.KEEVAKEGEK.K
R5/RRR5-22/2	1148.201	1147.261	-51.995	0.398	897.829	0.366	13	0.132	-.KEEVAKEGEK.-
R5/RRR5-9/2	1894.728	1894.192	-245.335	0.324	827.213	0.477	19	0.137	-.MAEVEVAAAAAAAGVLHRR.I
R5/RRR5-8/2	1896.012	1894.192	-94.966	0.370	755.480	0.460	19	0.133	-.MAEVEVAAAAAAAGVLHRR.I
R5/RRR5-8/2	1895.670	1894.192	253.273	0.288	673.490	0.359	18	0.120	-.MAEVEVAAAAAAAGVLHRR.I
R5/RRR5-8/2	1247.119	1246.480	-290.856	0.352	689.548	0.488	15	0.136	R.ALLVGINYPGTK.A
R5/RRR5-8/2	1246.660	1246.480	144.606	0.311	850.743	0.366	16	0.129	R.ALLVGINYPGTK.A
R5/RRR5-7/2	1417.422	1417.675	-178.772	0.461	683.050	0.426	16	0.130	K.LGSILNVPESFLK.R
R5/RRR5-25/2	1603.164	1603.755	-995.324	0.401	789.773	0.483	21	0.141	K.NDIPIYEAEVGSAPK.K
R5/RRR5-15/2	940.420	941.150	-1844.986	0.390	1103.381	0.392	13	0.150	R.ILLITDPR.T
R5/RRR5-11/2	941.162	941.150	12.995	0.505	1071.773	0.382	13	0.148	R.ILLITDPR.T
R5/RRR5-16/2	941.101	941.150	-52.054	0.503	1051.916	0.387	13	0.147	R.ILLITDPR.T
R5/RRR5-12/2	940.934	941.150	-229.680	0.430	1037.547	0.385	12	0.145	R.ILLITDPR.T
R5/RRR5-13/2	941.196	941.150	49.679	0.517	1091.006	0.360	13	0.145	R.ILLITDPR.T
R5/RRR5-11/2	940.582	941.150	-1671.540	0.444	1032.359	0.375	13	0.145	R.ILLITDPR.T
R5/RRR5-17/2	941.157	941.150	7.141	0.490	1097.380	0.350	13	0.144	R.ILLITDPR.T
R5/RRR5-18/2	940.335	941.150	-1935.906	0.427	1024.991	0.370	13	0.144	R.ILLITDPR.T
R5/RRR5-11/2	941.074	941.150	-80.678	0.473	936.921	0.403	12	0.143	R.ILLITDPR.T
R5/RRR5-12/2	940.517	941.150	-1741.041	0.460	1083.810	0.347	13	0.143	R.ILLITDPR.T
R5/RRR5-12/2	940.601	941.150	-1651.591	0.426	1068.496	0.351	13	0.143	R.ILLITDPR.T
R5/RRR5-13/2	940.879	941.150	-289.163	0.459	1092.355	0.341	13	0.143	R.ILLITDPR.T
R5/RRR5-17/2	940.490	941.150	-1770.123	0.447	1056.379	0.344	13	0.142	R.ILLITDPR.T
R5/RRR5-18/2	940.521	941.150	-1736.608	0.375	936.505	0.396	12	0.141	R.ILLITDPR.T

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-14/2	940.641	941.150	-1608.436	0.469	1086.070	0.326	13	0.140	R.ILLITDPR.T
R5/RRR5-14/2	940.493	941.150	-1767.123	0.422	1081.125	0.326	13	0.140	R.ILLITDPR.T
R5/RRR5-14/2	941.209	941.150	63.207	0.512	1031.933	0.341	13	0.140	R.ILLITDPR.T
R5/RRR5-17/2	940.446	941.150	-1816.943	0.410	906.189	0.380	12	0.139	R.ILLITDPR.T
R5/RRR5-16/2	941.648	941.150	530.742	0.403	1089.928	0.313	13	0.139	R.ILLITDPR.T
R5/RRR5-18/2	940.901	941.150	-265.473	0.375	922.926	0.363	12	0.137	R.ILLITDPR.T
R5/RRR5-15/2	940.594	941.150	-1659.023	0.434	898.518	0.353	12	0.136	R.ILLITDPR.T
R5/RRR5-13/2	940.972	941.150	-189.855	0.474	1000.510	0.324	12	0.136	R.ILLITDPR.T
R5/RRR5-15/2	940.628	941.150	-1623.168	0.480	914.721	0.342	12	0.135	R.ILLITDPR.T
R5/RRR5-16/2	1712.159	1710.696	271.265	0.369	1322.138	0.370	21	0.154	R.SSSAADAASASAASSPSER.S
R5/RRR5-23/3	1171.072	1171.334	-223.814	0.452	717.516	0.449	20	0.094	R.KAHFGAPSSIR.R
R5/RRR5-23/3	1171.536	1171.334	173.201	0.510	744.681	0.374	22	0.087	R.KAHFGAPSSIR.R
R5/RRR5-23/3	1171.293	1171.334	-34.989	0.413	657.665	0.302	19	0.078	R.KAHFGAPSSIR.R
R5/RRR5-23/3	1171.161	1171.334	-148.056	0.399	742.361	0.270	20	0.074	R.KAHFGAPSSIR.R
R5/RRR5-13/2	1138.208	1138.259	-44.492	0.406	780.899	0.474	18	0.142	R.IGSQSPPPAAGR.T
R5/RRR5-14/2	1138.165	1138.259	-82.359	0.293	567.458	0.281	14	0.117	-.IGSQSPPPAAGR.-
R5/RRR5-7/2	1280.069	1280.449	-297.429	0.448	1198.234	0.417	16	0.157	R.TAEEIIDFITK.N
R5/RRR5-23/3	1224.016	1224.309	-240.141	0.407	702.215	0.464	24	0.091	K.QVHPDTGISNR.A
R5/RRR5-23/3	1224.157	1224.309	-124.143	0.385	396.605	0.436	20	0.083	-.QVHPDTGISNR.-
R5/RRR5-23/3	1224.236	1224.309	-59.478	0.328	408.688	0.370	20	0.071	-.QVHPDTGISNR.-
R5/RRR5-9/2	1498.923	1498.619	203.749	0.433	743.123	0.456	20	0.139	R.DLPSFFTDLADTR.L
R5/RRR5-11/2	1084.817	1085.234	-385.950	0.389	780.080	0.469	15	0.141	K.YGVSGYPTLK.F
R5/RRR5-11/2	1084.318	1085.234	-1773.072	0.337	632.878	0.444	13	0.130	K.YGVSGYPTLK.F
R5/RRR5-16/2	1213.139	1213.319	-149.229	0.437	1012.556	0.455	16	0.149	K.SAAAVDPVEPEK.V
R5/RRR5-5/2	1591.599	1591.790	-120.437	0.482	789.253	0.443	21	0.139	K.LISGDLQPTSGTVFR.S
R5/RRR5-5/2	1591.872	1591.790	51.101	0.468	587.594	0.349	18	0.122	K.LISGDLQPTSGTVFR.S
R5/RRR5-5/2	1994.044	1994.147	-52.106	0.369	603.731	0.449	21	0.126	K.DGGAVTALPGAEFFPDTEAK.V
R5/RRR5-5/2	1265.548	1264.413	107.039	0.352	945.249	0.457	19	0.144	R.FGLGAEVGISTGR.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/3	1442.064	1442.517	-315.054	0.420	983.203	0.460	25	0.105	R.ALAADHDASASAVSR.R
R5/RRR5-23/3	1442.093	1442.517	-294.671	0.387	479.272	0.435	19	0.079	-.ALAADHDASASAVSR.-
R5/RRR5-7/2	1464.494	1464.645	-103.635	0.446	1338.326	0.366	19	0.160	R.SVGLQLTLDDFQK.V
R5/RRR5-7/2	1463.923	1464.645	-1180.237	0.318	829.501	0.322	18	0.126	R.SVGLQLTLDDFQK.V
R5/RRR5-7/2	1464.123	1464.645	-1043.016	0.329	390.560	0.311	13	0.119	R.SVGLQLTLDDFQK.V
R5/RRR5-9/2	1434.587	1434.623	-24.973	0.443	1005.347	0.452	16	0.150	R.HWGIFTYDGLPK.Y
R5/RRR5-9/2	1434.838	1434.623	150.899	0.432	836.168	0.489	15	0.144	R.HWGIFTYDGLPK.Y
R5/RRR5-5/2	1321.011	1321.547	-1166.391	0.492	865.532	0.431	18	0.142	K.VYTAGSIIDLLR.F
R5/RRR5-5/2	1321.235	1321.547	-237.195	0.378	472.056	0.399	14	0.125	K.VYTAGSIIDLLR.F
R5/RRR5-19/2	1237.203	1237.518	-255.482	0.369	688.760	0.472	17	0.139	K.LPFAPVPLVQR.M
R5/RRR5-19/2	1237.392	1237.518	-102.273	0.310	587.563	0.473	16	0.133	K.LPFAPVPLVQR.M
R5/RRR5-18/2	1237.028	1237.518	-397.747	0.334	450.352	0.453	14	0.130	K.LPFAPVPLVQR.M
R5/RRR5-18/2	1237.189	1237.518	-266.767	0.308	603.844	0.414	16	0.129	K.LPFAPVPLVQR.M
R5/RRR5-19/2	1236.743	1237.518	-1440.103	0.298	482.025	0.431	15	0.126	-.LPFAPVPLVQR.-
R5/RRR5-18/2	1237.054	1237.518	-376.460	0.290	442.401	0.382	14	0.125	K.LPFAPVPLVQR.M
R5/RRR5-4/2	1641.794	1641.808	-8.547	0.380	714.435	0.469	16	0.136	R.WLDHPQELADAFAK.A
R5/RRR5-4/2	1642.576	1641.808	-141.670	0.395	482.391	0.429	13	0.125	R.WLDHPQELADAFAK.A
R5/RRR5-5/2	1641.302	1641.808	-920.351	0.274	648.694	0.327	15	0.120	R.WLDHPQELADAFAK.A
R5/RRR5-5/2	1641.784	1641.808	-14.588	0.266	577.833	0.298	14	0.117	R.WLDHPQELADAFAK.A
R5/RRR5-12/2	1470.761	1469.713	32.749	0.419	1110.518	0.427	15	0.150	R.IALNELNWLINR.Y
R5/RRR5-6/2	1038.959	1039.254	-283.961	0.328	786.912	0.475	15	0.140	R.LGVEPVIGVR.A
R5/RRR5-7/2	1039.109	1039.254	-139.816	0.332	817.726	0.395	15	0.134	R.LGVEPVIGVR.A
R5/RRR5-7/2	1038.341	1039.254	-1846.982	0.272	648.651	0.323	14	0.123	R.LGVEPVIGVR.A
R5/RRR5-6/2	1039.136	1039.254	-113.891	0.257	457.901	0.294	12	0.120	R.LGVEPVIGVR.A
R5/RRR5-7/2	1038.648	1039.254	-1550.675	0.360	457.948	0.274	12	0.117	-.LGVEPVIGVR.-
R5/RRR5-8/3	1305.939	1305.487	347.715	0.346	1472.474	0.273	24	0.106	R.KKM*AADPAAETR.R
R5/RRR5-8/3	1305.856	1305.487	283.606	0.267	1186.445	0.126	24	0.060	R.KKM*AADPAAETR.R
R5/RRR5-23/3	1402.490	1401.571	-57.949	0.423	957.755	0.454	25	0.103	R.IGVAM*DYSASSKR.A

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/3	1401.356	1401.571	-153.885	0.403	658.169	0.436	24	0.088	R.IGVAM*DYSASSKR.A
R5/RRR5-23/3	1400.574	1401.571	-1430.154	0.338	534.537	0.431	22	0.083	R.IGVAM*DYSASSKR.A
R5/RRR5-9/2	1733.436	1733.902	-269.858	0.410	598.172	0.426	17	0.125	R.AAPDLDALFPDGFVER.T
R5/RRR5-2/2	1907.453	1905.958	259.924	0.382	632.578	0.409	16	0.120	R.STSSAVHSEEAIQATSSGR.T
R5/RRR5-11/2	1481.417	1480.774	-241.879	0.510	1244.332	0.383	18	0.152	K.IQLLDLPGIIEGAK.D
R5/RRR5-9/2	1374.535	1375.529	-1455.244	0.368	1233.153	0.391	17	0.154	K.LSDGYYVM*DPAK.A
R5/RRR5-10/2	1281.629	1281.442	146.870	0.399	614.926	0.427	13	0.128	R.HWVLDPIDGTK.G
R5/RRR5-11/2	1144.652	1145.331	-1471.140	0.409	762.770	0.454	15	0.137	R.VVVDGNLITSK.A
R5/RRR5-8/2	1158.871	1159.230	-311.103	0.475	1171.987	0.384	15	0.152	R.SAVDYFEATR.A
R5/RRR5-8/2	1159.049	1159.230	-157.039	0.326	1070.525	0.346	15	0.139	R.SAVDYFEATR.A
R5/RRR5-8/2	1158.887	1159.230	-297.047	0.192	668.455	0.154	13	0.113	R.SAVDYFEATR.A
R5/RRR5-5/2	1638.204	1636.826	231.269	0.448	715.236	0.372	18	0.126	R.LGEEFPEELANFLK.E
R5/RRR5-21/2	1285.995	1285.409	-322.943	0.315	609.723	0.460	15	0.128	R.AQGLYM*GSDQAK.L
R5/RRR5-22/2	1345.283	1345.529	-183.717	0.374	652.354	0.450	19	0.135	R.NSPVPSFSGLLAR.A
R5/RRR5-22/2	1345.265	1345.529	-196.643	0.250	430.370	0.414	16	0.122	R.NSPVPSFSGLLAR.A
R5/RRR5-22/2	1344.899	1345.529	-1215.865	0.190	660.870	0.375	18	0.120	R.NSPVPSFSGLLAR.A
R5/RRR5-11/2	1210.015	1210.363	-288.442	0.409	1077.776	0.430	16	0.152	R.FDGILGLGFDR.L
R5/RRR5-11/2	1210.004	1210.363	-298.057	0.368	896.331	0.464	16	0.145	R.FDGILGLGFDR.L
R5/RRR5-11/2	1209.874	1210.363	-405.966	0.352	1022.913	0.303	16	0.132	R.FDGILGLGFDR.L
R5/RRR5-12/3	1773.285	1771.998	161.999	0.472	1249.099	0.383	28	0.112	R.RLDTDYIDLLQIHR.F
R5/RRR5-11/3	1773.540	1771.998	-259.104	0.476	1155.621	0.352	25	0.098	R.RLDTDYIDLLQIHR.F
R5/RRR5-13/2	1322.222	1322.404	-138.492	0.401	950.201	0.443	16	0.145	K.FDSGYYSNLQK.K
R5/RRR5-15/2	1456.332	1455.640	-212.080	0.473	1057.837	0.424	17	0.150	K.SQIQSYVFDVIR.A
R5/RRR5-15/2	1455.254	1455.640	-265.831	0.409	1207.061	0.342	17	0.146	K.SQIQSYVFDVIR.A
R5/RRR5-18/3	1389.647	1389.582	46.941	0.446	1055.532	0.429	23	0.105	R.LGQIVFSDPEKR.Q
R5/RRR5-18/3	1389.509	1389.582	-52.316	0.483	944.611	0.432	21	0.099	R.LGQIVFSDPEKR.Q
R5/RRR5-23/2	1100.840	1101.240	-364.984	0.399	1355.749	0.300	15	0.152	K.LGWDLNVQR.G
R5/RRR5-23/2	1100.772	1101.240	-426.849	0.399	997.481	0.236	14	0.125	K.LGWDLNVQR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-23/2	1100.818	1101.240	-384.566	0.318	1057.023	0.107	14	0.116	-.LGWDLNVQR.-
R5/RRR5-7/2	1706.824	1706.108	-166.753	0.400	751.086	0.433	17	0.132	K.VIFIEGHQIPLIVVK.R
R5/RRR5-7/2	1706.683	1706.108	-249.554	0.436	729.286	0.376	15	0.124	K.VIFIEGHQIPLIVVK.R
R5/RRR5-28/2	1299.119	1299.502	-295.141	0.418	801.649	0.450	16	0.138	R.LLAQAALTVGADR.A
R5/RRR5-27/2	1298.955	1299.502	-1194.303	0.298	777.505	0.325	18	0.124	R.LLAQAALTVGADR.A
R5/RRR5-4/2	1200.523	1199.425	81.527	0.450	1302.609	0.363	16	0.158	R.LLNLQTLDIR.N
R5/RRR5-4/2	1200.584	1199.425	132.717	0.401	779.716	0.249	14	0.121	R.LLNLQTLDIR.N
R5/RRR5-5/2	1200.365	1199.425	-50.654	0.397	729.080	0.195	13	0.115	R.LLNLQTLDIR.N
R5/RRR5-6/2	1552.078	1550.697	246.548	0.408	625.440	0.414	15	0.125	K.DNVNGFLVQPGDFK.A
R5/RRR5-6/2	964.468	965.088	-1684.730	0.439	1164.291	0.369	14	0.150	R.AGVANYTLR.A
R5/RRR5-6/2	964.892	965.088	-204.055	0.445	765.459	0.456	13	0.141	R.AGVANYTLR.A
R5/RRR5-6/2	964.135	965.088	-2032.252	0.342	1190.053	0.243	14	0.134	R.AGVANYTLR.A
R5/RRR5-22/2	1093.245	1092.184	56.264	0.523	1149.452	0.392	15	0.150	R.ATNLDPFADK.D
R5/RRR5-23/2	1358.887	1359.616	-1276.252	0.482	1070.612	0.411	16	0.149	R.LM*FSLIDNVYK.Q
R5/RRR5-23/2	1358.984	1359.616	-1204.627	0.476	932.747	0.395	15	0.139	R.LM*FSLIDNVYK.Q
R5/RRR5-23/2	1359.424	1359.616	-141.830	0.464	648.404	0.410	16	0.134	R.LM*FSLIDNVYK.Q
R5/RRR5-23/2	955.858	956.083	-236.662	0.336	584.819	0.425	14	0.132	K.HIWSSGIR.S
R5/RRR5-23/2	955.424	956.083	-1741.878	0.296	324.136	0.421	11	0.127	K.HIWSSGIR.S
R5/RRR5-23/2	955.567	956.083	-1591.706	0.315	275.587	0.249	10	0.122	-.HIWSSGIR.-
R5/RRR5-13/2	1502.106	1501.734	248.274	0.252	654.321	0.293	13	0.111	-.M*APALGKSVPSSSPR.-
R5/RRR5-4/2	1231.049	1231.335	-232.691	0.452	985.891	0.430	18	0.148	K.TTAGIEPEDVAK.R
R5/RRR5-4/2	1230.886	1231.335	-365.216	0.469	927.894	0.409	18	0.142	K.TTAGIEPEDVAK.R
R5/RRR5-4/2	1230.370	1231.335	-1601.307	0.378	778.843	0.321	16	0.126	K.TTAGIEPEDVAK.R
R5/RRR5-10/2	1609.175	1608.861	195.952	0.365	824.998	0.458	18	0.136	K.GAGSVLSFLTGSLALSK.H
R5/RRR5-10/2	1609.396	1608.861	-289.440	0.295	170.629	0.454	11	0.090	-.GAGSVLSFLTGSLALSK.-
R5/RRR5-9/2	1439.364	1438.693	-229.126	0.388	875.938	0.453	16	0.140	K.TFVLTPEQYIVK.L
R5/RRR5-8/2	1257.380	1257.379	0.914	0.483	1089.379	0.406	18	0.149	R.LDQSVLNASGPR.G
R5/RRR5-3/2	1224.714	1224.430	232.373	0.472	1080.430	0.390	17	0.147	R.FLAAGDEFLIK.I

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-26/2	956.267	956.035	242.742	0.371	768.525	0.450	13	0.083	R.GPAAAEGIVGN.-
R5/RRR5-7/2	1176.148	1176.347	-170.058	0.509	1490.292	0.276	16	0.156	R.GLDDLINIFR.R
R5/RRR5-7/2	1175.987	1176.347	-307.095	0.513	942.493	0.344	14	0.133	R.GLDDLINIFR.R
R5/RRR5-20/2	1437.185	1437.661	-332.215	0.442	1104.181	0.409	18	0.151	R.VVFELYDDIVPK.T
R5/RRR5-19/2	1437.023	1437.661	-1143.883	0.310	1136.475	0.388	16	0.147	R.VVFELYDDIVPK.T
R5/RRR5-20/2	1437.308	1437.661	-247.002	0.414	1133.348	0.351	18	0.145	R.VVFELYDDIVPK.T
R5/RRR5-19/2	1437.400	1437.661	-182.761	0.426	728.623	0.381	14	0.129	R.VVFELYDDIVPK.T
R5/RRR5-27/2	1193.114	1192.262	-123.821	0.349	734.748	0.457	14	0.132	R.TLNSAAATTADR.Q
R5/RRR5-6/2	1732.263	1732.916	-957.123	0.353	688.911	0.450	20	0.130	K.DGAPGLWPFGPVDFEK.M
R5/RRR5-7/3	1373.666	1373.542	90.270	0.495	1500.841	0.276	25	0.110	K.IYAHSSIGQLQR.A
R5/RRR5-7/3	1373.491	1373.542	-37.816	0.459	1184.426	0.234	22	0.078	K.IYAHSSIGQLQR.A
R5/RRR5-7/3	1372.351	1373.542	-1601.503	0.420	816.151	0.286	21	0.075	K.IYAHSSIGQLQR.A
R5/RRR5-14/2	1713.220	1712.840	222.787	0.444	872.844	0.435	19	0.139	R.SANTLATFDESTSVLR.K
R5/RRR5-14/2	1713.011	1712.840	100.235	0.457	1065.115	0.355	18	0.136	R.SANTLATFDESTSVLR.K
R5/RRR5-14/2	1713.344	1712.840	-290.245	0.355	674.800	0.361	16	0.122	R.SANTLATFDESTSVLR.K
R5/RRR5-13/2	1542.375	1542.673	-193.502	0.387	854.547	0.449	21	0.139	R.SLVAATPSDPDLEAR.G
R5/RRR5-10/2	1170.029	1170.427	-340.785	0.374	1021.897	0.433	14	0.145	R.LVAVLSELVAR.H
R5/RRR5-23/2	1245.484	1246.392	-1536.655	0.396	1450.406	0.281	17	0.157	-.SGDVTELQIGVK.-
R5/RRR5-22/2	1246.089	1246.392	-244.424	0.369	1211.881	0.244	17	0.134	K.SGDVTELQIGVK.H
R5/RRR5-23/2	1245.995	1246.392	-319.909	0.391	1268.510	0.201	17	0.131	K.SGDVTELQIGVK.H
R5/RRR5-6/2	1292.956	1293.444	-378.554	0.474	709.907	0.393	16	0.131	K.GICQVGPSFEAK.S
R5/RRR5-6/2	1293.302	1293.444	-109.969	0.480	623.555	0.397	15	0.128	K.GICQVGPSFEAK.S
R5/RRR5-7/2	1091.937	1091.222	-261.925	0.311	734.370	0.441	13	0.131	-.M*GFSYNSLR.N
R5/RRR5-10/2	1339.311	1339.519	-155.923	0.393	818.590	0.420	16	0.132	K.IGLSASTIASSFGK.T
R5/RRR5-7/2	1543.255	1541.731	-309.858	0.418	1362.487	0.325	18	0.154	-.ESDLAAAVAVAPVATR.-
R5/RRR5-7/2	1542.166	1541.731	282.986	0.302	1390.216	0.274	18	0.147	R.ESDLAAAVAVAPVATR.K
R5/RRR5-6/2	1541.946	1541.731	139.782	0.301	1260.187	0.303	17	0.141	R.ESDLAAAVAVAPVATR.K
R5/RRR5-6/2	1543.090	1541.731	233.147	0.360	1200.579	0.323	17	0.140	R.ESDLAAAVAVAPVATR.K

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-6/2	1542.253	1541.731	-311.329	0.323	983.017	0.375	16	0.135	-.ESDLAAAVAVAPVATR.-
R5/RRR5-16/2	1258.314	1258.408	-75.371	0.408	684.397	0.425	13	0.131	R.QDDLVNVIWR.N
R5/RRR5-11/3	1120.086	1119.252	-148.631	0.401	804.851	0.437	22	0.089	R.ILHDTSGTFK.Y
R5/RRR5-11/3	1119.259	1119.252	6.211	0.459	687.975	0.426	20	0.089	R.ILHDTSGTFK.Y
R5/RRR5-7/2	1141.065	1141.346	-246.534	0.395	630.138	0.434	16	0.135	R.AQPTLGLITAR.A
R5/RRR5-6/2	1141.137	1141.346	-183.108	0.416	513.829	0.420	16	0.133	R.AQPTLGLITAR.A
R5/RRR5-7/2	1141.188	1141.346	-139.112	0.369	573.385	0.385	16	0.130	R.AQPTLGLITAR.A
R5/RRR5-6/2	1142.129	1141.346	-190.560	0.400	418.906	0.377	15	0.129	R.AQPTLGLITAR.A
R5/RRR5-7/2	1141.112	1141.346	-205.108	0.345	388.542	0.403	14	0.127	R.AQPTLGLITAR.A
R5/RRR5-24/2	1210.615	1211.370	-1453.798	0.396	754.995	0.440	15	0.135	R.SFAGPAPSTM*TK.E
R5/RRR5-24/2	1210.237	1211.370	-1767.364	0.219	721.411	0.359	14	0.120	R.SFAGPAPSTM*TK.E
R5/RRR5-2/2	1254.226	1253.387	-128.136	0.295	1190.911	0.322	18	0.141	K.ALAAEVTSTFSR.R
R5/RRR5-2/2	1253.905	1253.387	-385.364	0.280	1061.859	0.331	17	0.134	K.ALAAEVTSTFSR.R
R5/RRR5-15/2	1678.645	1677.840	-116.672	0.435	852.290	0.433	14	0.136	K.EFTSVFYSLQNWR.S
R5/RRR5-14/2	1676.926	1677.840	-1145.099	0.325	963.067	0.264	16	0.124	K.EFTSVFYSLQNWR.S
R5/RRR5-14/2	1676.873	1677.840	-1176.751	0.304	813.654	0.257	15	0.119	K.EFTSVFYSLQNWR.S
R5/RRR5-12/3	1230.790	1231.381	-1297.017	0.422	808.294	0.408	19	0.091	R.LHFHDCFVR.-
R5/RRR5-11/3	1231.206	1231.381	-142.575	0.388	846.922	0.403	19	0.090	R.LHFHDCFVR.-
R5/RRR5-12/3	1231.745	1231.381	296.590	0.316	505.218	0.383	16	0.086	R.LHFHDCFVR.-
R5/RRR5-8/3	1231.343	1231.381	-31.294	0.415	830.597	0.366	20	0.086	R.LHFHDCFVR.-
R5/RRR5-9/3	1231.141	1231.381	-195.689	0.385	810.453	0.368	20	0.084	R.LHFHDCFVR.-
R5/RRR5-9/3	1230.462	1231.381	-1564.083	0.342	569.842	0.345	18	0.084	R.LHFHDCFVR.-
R5/RRR5-9/3	1231.149	1231.381	-189.273	0.422	910.536	0.325	20	0.083	R.LHFHDCFVR.-
R5/RRR5-8/3	1231.753	1231.381	302.552	0.450	874.617	0.301	20	0.080	R.LHFHDCFVR.-
R5/RRR5-11/3	1231.719	1231.381	274.976	0.397	624.526	0.225	18	0.079	R.LHFHDCFVR.-
R5/RRR5-11/3	1231.036	1231.381	-281.041	0.378	896.164	0.306	20	0.079	R.LHFHDCFVR.-
R5/RRR5-12/3	1231.341	1231.381	-32.934	0.281	764.145	0.358	19	0.079	R.LHFHDCFVR.-
R5/RRR5-8/3	1231.401	1231.381	16.583	0.351	910.675	0.277	20	0.075	R.LHFHDCFVR.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-7/3	1231.114	1231.381	-217.921	0.353	830.177	0.178	19	0.066	-.LHFHDCFVR.-
R5/RRR5-16/2	1726.298	1726.997	-987.594	0.392	1024.578	0.425	19	0.142	K.QGPGTAILLGPNFLAEK.G
R5/RRR5-24/2	1565.033	1563.629	258.819	0.375	637.726	0.355	15	0.122	-.M*AAAAADSCDDHRR.R
R5/RRR5-24/2	1564.374	1563.629	-163.863	0.322	556.289	0.318	13	0.115	-.M*AAAAADSCDDHRR.-
R5/RRR5-19/2	1565.022	1563.629	251.467	0.181	1050.798	0.048	15	0.109	-.M*AAAAADSCDDHRR.R
R5/RRR5-14/2	970.142	970.191	-50.685	0.490	1090.695	0.398	15	0.151	R.ALLDVGLIR.T
R5/RRR5-14/2	970.198	970.191	6.990	0.478	1082.521	0.372	15	0.147	R.ALLDVGLIR.T
R5/RRR5-14/2	970.087	970.191	-107.988	0.472	978.891	0.384	14	0.142	R.ALLDVGLIR.T
R5/RRR5-21/2	1032.283	1032.200	80.840	0.396	1435.758	0.259	16	0.150	-.M*GKQPAAGQK.S
R5/RRR5-22/2	1712.043	1710.869	102.008	0.425	804.543	0.434	21	0.139	K.DYGAELFVNGEIVQR.S
R5/RRR5-22/2	1712.012	1710.869	84.274	0.381	397.244	0.413	17	0.126	K.DYGAELFVNGEIVQR.S
R5/RRR5-22/2	1711.985	1710.869	68.255	0.332	287.831	0.313	14	0.119	K.DYGAELFVNGEIVQR.S
R5/RRR5-28/3	1476.710	1476.739	-20.000	0.363	1531.777	0.203	26	0.093	K.WVCAEIKNSKIK.L
R5/RRR5-28/3	1476.708	1476.739	-20.871	0.410	1464.668	0.218	25	0.091	K.WVCAEIKNSKIK.L
R5/RRR5-30/3	1476.680	1476.739	-40.273	0.386	1369.909	0.177	25	0.076	K.WVCAEIKNSKIK.L
R5/RRR5-30/3	1476.247	1476.739	-334.506	0.358	777.203	0.181	21	0.062	-.WVCAEIKNSKIK.-
R5/RRR5-28/3	1476.508	1476.739	-157.199	0.288	883.324	0.115	22	0.062	K.WVCAEIKNSKIK.L
R5/RRR5-29/3	1477.563	1476.739	-119.342	0.359	935.619	0.135	21	0.061	-.WVCAEIKNSKIK.-
R5/RRR5-26/3	1477.644	1476.739	-64.524	0.328	789.251	0.098	22	0.061	-.WVCAEIKNSKIK.-
R5/RRR5-27/3	1477.054	1476.739	213.637	0.397	908.553	0.147	21	0.060	-.WVCAEIKNSKIK.-
R5/RRR5-29/3	1476.883	1476.739	98.013	0.373	1089.896	0.119	22	0.060	-.WVCAEIKNSKIK.-
R5/RRR5-30/3	1476.561	1476.739	-121.247	0.366	1051.581	0.095	22	0.057	-.WVCAEIKNSKIK.-
R5/RRR5-29/3	1476.262	1476.739	-324.053	0.320	967.266	0.103	21	0.056	-.WVCAEIKNSKIK.-
R5/RRR5-27/3	1476.709	1476.739	-20.622	0.340	837.048	0.100	20	0.055	-.WVCAEIKNSKIK.-
R5/RRR5-1/2	1668.777	1667.839	-36.876	0.415	670.528	0.412	16	0.127	K.GTITEDDIAQLSYLK.M
R5/RRR5-1/2	1668.402	1667.839	-262.398	0.369	740.128	0.187	15	0.110	-.GTITEDDIAQLSYLK.-
R5/RRR5-14/2	1564.165	1562.834	212.628	0.524	1202.297	0.363	19	0.146	K.LFNIIEPDVAVFGK.K
R5/RRR5-17/2	1425.059	1424.691	258.987	0.486	843.564	0.402	16	0.136	R.SINTLFLTEMVR.G

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-17/2	1424.518	1424.691	-121.757	0.325	744.299	0.450	14	0.133	R.SINTLFLTEMVR.G
R5/RRR5-17/2	1424.765	1424.691	52.196	0.336	669.261	0.327	14	0.122	R.SINTLFLTEMVR.G
R5/RRR5-20/2	1661.713	1661.949	-142.637	0.450	942.711	0.422	18	0.141	R.FPPFPAVM*DINQIR.D
R5/RRR5-21/2	1663.568	1661.949	-229.619	0.388	678.013	0.290	15	0.117	R.FPPFPAVM*DINQIR.D
R5/RRR5-7/2	1104.350	1104.155	177.542	0.326	712.083	0.436	12	0.129	-.HSVEAEEFR.-
R5/RRR5-3/2	1104.852	1104.155	-274.783	0.157	739.682	0.186	13	0.111	R.HSVEAEEFR.K
R5/RRR5-14/2	1701.271	1701.905	-963.475	0.412	1351.045	0.325	21	0.153	R.GWAPTFLGYSAQGAFK.Y
R5/RRR5-14/2	1701.575	1701.905	-194.322	0.436	1200.313	0.389	21	0.152	R.GWAPTFLGYSAQGAFK.Y
R5/RRR5-14/2	1701.810	1701.905	-55.801	0.375	681.220	0.265	19	0.117	-.GWAPTFLGYSAQGAFK.-
R5/RRR5-27/3	1415.121	1415.579	-324.470	0.479	994.377	0.406	23	0.098	-.WADGKQEKPTVR.-
R5/RRR5-26/3	1415.290	1415.579	-204.788	0.466	636.454	0.382	21	0.087	K.WADGKQEKPTVR.T
R5/RRR5-26/3	1415.500	1415.579	-56.458	0.475	713.200	0.378	21	0.084	-.WADGKQEKPTVR.-
R5/RRR5-27/3	1415.395	1415.579	-130.812	0.448	522.189	0.373	20	0.079	-.WADGKQEKPTVR.-
R5/RRR5-27/3	1415.536	1415.579	-30.638	0.460	534.941	0.349	20	0.078	-.WADGKQEKPTVR.-
R5/RRR5-26/3	1415.282	1415.579	-210.369	0.452	497.235	0.348	19	0.075	-.WADGKQEKPTVR.-
R5/RRR5-27/3	1415.771	1415.579	136.188	0.417	578.822	0.319	20	0.072	-.WADGKQEKPTVR.-
R5/RRR5-8/2	1230.398	1230.393	4.119	0.502	867.806	0.392	17	0.137	K.LIDENVGTQLK.E
R5/RRR5-10/2	1405.247	1404.550	-216.044	0.393	802.065	0.431	15	0.137	R.FFDAFFDLEPR.Y
R5/RRR5-10/2	1404.499	1404.550	-36.754	0.324	519.460	0.299	13	0.119	R.FFDAFFDLEPR.Y
R5/RRR5-3/2	1178.835	1178.320	-412.916	0.297	659.624	0.387	13	0.124	K.YTSDPGLVLGR.Q
R5/RRR5-8/2	1178.259	1178.320	-51.604	0.279	588.401	0.403	12	0.122	K.YTSDPGLVLGR.Q
R5/RRR5-28/2	1087.026	1087.210	-170.485	0.448	918.343	0.402	14	0.142	R.GYISYQSLR.R
R5/RRR5-28/2	1086.307	1087.210	-1757.653	0.352	956.889	0.393	14	0.140	R.GYISYQSLR.R
R5/RRR5-28/2	1086.329	1087.210	-1737.104	0.346	754.803	0.321	13	0.126	R.GYISYQSLR.R
R5/RRR5-10/2	1020.965	1021.152	-183.854	0.451	1344.018	0.330	15	0.155	R.AVQIAYEAR.K
R5/RRR5-20/2	1080.061	1079.273	-196.977	0.322	1167.756	0.377	14	0.132	R.SPIAYTWKI.-
R5/RRR5-20/2	1079.874	1079.273	-370.256	0.311	986.934	0.212	12	0.100	R.SPIAYTWKI.-
R5/RRR5-20/2	1079.939	1079.273	-309.919	0.308	932.243	0.225	12	0.098	R.SPIAYTWKI.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-19/2	1079.947	1079.273	-302.548	0.240	643.467	0.131	11	0.093	R.SPIAYTWKI.-
R5/RRR5-14/2	1428.034	1426.647	272.165	0.506	853.541	0.384	16	0.133	K.VWVLDGGLPQWR.A
R5/RRR5-14/2	1427.932	1426.647	200.331	0.269	1048.634	0.193	16	0.120	K.VWVLDGGLPQWR.A
R5/RRR5-10/3	1382.181	1382.508	-237.375	0.456	1147.125	0.386	20	0.103	R.TRQEHDLLVDR.S
R5/RRR5-20/3	1918.320	1918.142	93.043	0.266	1077.875	0.361	26	0.087	K.QHLGEAGALAAGAFALYEK.H
R5/RRR5-22/2	1252.417	1253.432	-1613.396	0.343	879.736	0.434	16	0.139	-.FQGSPAIITYR.-
R5/RRR5-22/2	1253.502	1253.432	56.690	0.355	743.736	0.368	16	0.128	-.FQGSPAIITYR.-
R5/RRR5-19/2	1271.989	1272.390	-316.163	0.353	790.043	0.435	17	0.138	K.VLTPISQDDQR.Q
R5/RRR5-19/2	1272.260	1272.390	-102.742	0.312	675.452	0.384	16	0.128	K.VLTPISQDDQR.Q
R5/RRR5-19/2	1271.982	1272.390	-321.844	0.315	583.803	0.379	15	0.126	K.VLTPISQDDQR.Q
R5/RRR5-20/2	1271.633	1272.390	-1385.955	0.250	535.480	0.354	14	0.121	K.VLTPISQDDQR.Q
R5/RRR5-9/3	1960.410	1959.259	77.055	0.440	1112.356	0.391	28	0.101	R.TADLMLANHYANELLLR.L
R5/RRR5-20/2	1707.295	1707.842	-908.554	0.401	725.365	0.418	20	0.082	K.AM*GEEVPTQVKPSSGSS.-
R5/RRR5-20/2	1707.372	1707.842	-275.811	0.305	622.969	0.254	18	0.073	K.AM*GEEVPTQVKPSSGSS.-
R5/RRR5-1/2	1147.257	1146.321	-55.880	0.361	807.271	0.433	13	0.134	R.ITEGVNLPFR.V
R5/RRR5-12/3	1848.923	1848.201	-150.758	0.310	1178.629	0.102	27	0.057	-.M*QTDLINIGKKTISLR.R
R5/RRR5-12/3	1847.960	1848.201	-130.828	0.298	994.360	0.080	26	0.054	-.M*QTDLINIGKKTISLR.-
R5/RRR5-14/2	1137.994	1138.194	-176.552	0.301	1072.661	0.317	16	0.134	R.M*GTVGSAGGGGDR.G
R5/RRR5-14/2	1137.988	1138.194	-181.717	0.307	983.741	0.268	15	0.125	R.M*GTVGSAGGGGDR.G
R5/RRR5-16/2	1138.937	1138.194	-226.716	0.332	863.670	0.282	15	0.123	R.M*GTVGSAGGGGDR.G
R5/RRR5-16/2	1137.765	1138.194	-378.467	0.285	744.622	0.212	17	0.117	R.M*GTVGSAGGGGDR.G
R5/RRR5-14/2	1138.031	1138.194	-144.055	0.265	908.854	0.166	15	0.115	R.M*GTVGSAGGGGDR.G
R5/RRR5-14/2	1567.402	1567.769	-234.547	0.454	897.865	0.413	21	0.138	R.SRPSELALPVSDPAK.A
R5/RRR5-16/2	1106.371	1105.297	67.184	0.382	1136.978	0.377	17	0.147	R.AM*GASARVGLR.G
R5/RRR5-21/2	1739.884	1739.952	-38.817	0.381	675.431	0.395	16	0.074	K.IWELNSAYIRPYVD.-
R5/RRR5-10/2	1485.415	1484.640	-151.796	0.336	821.176	0.429	20	0.133	K.NGAAPATTDGLLGLGR.G
R5/RRR5-13/3	1554.773	1553.788	-9.703	0.428	924.152	0.414	24	0.092	R.LPLRDVLADTGIGGR.A
R5/RRR5-18/3	1723.722	1723.012	-169.068	0.262	715.720	0.426	23	0.077	-.NQMQSVVQSAMAAKTK.-

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-27/2	1197.777	1197.347	360.671	0.146	634.647	0.411	15	0.114	-.EFGGGLMDKSR.-
R5/RRR5-13/2	1390.225	1390.523	-214.943	0.357	997.005	0.416	17	0.143	K.IVETSDEWIAAR.T
R5/RRR5-13/2	1390.355	1390.523	-121.666	0.316	635.578	0.297	14	0.118	K.IVETSDEWIAAR.T
R5/RRR5-2/2	1824.443	1824.967	-837.762	0.372	829.763	0.402	17	0.128	K.EGSSLASELQQLEASFK.N
R5/RRR5-24/2	1604.327	1603.756	-268.222	0.325	1107.401	0.311	17	0.132	R.LESRDGLAVETVGEK.G
R5/RRR5-17/2	1130.741	1131.331	-1410.483	0.427	1069.283	0.398	17	0.147	R.VAGM*VTPAAAAR.S
R5/RRR5-10/2	1132.293	1131.331	-33.550	0.322	769.486	0.336	18	0.127	R.VAGM*VTPAAAAR.S
R5/RRR5-17/2	1130.352	1131.331	-1756.284	0.291	736.366	0.273	15	0.120	-.VAGM*VTPAAAAR.-
R5/RRR5-17/2	1130.348	1131.331	-1759.648	0.293	623.208	0.304	14	0.118	-.VAGM*VTPAAAAR.-
R5/RRR5-10/3	1451.519	1451.656	-94.871	0.344	1107.112	0.391	27	0.099	R.IVVGPAGGSVREGPR.V
R5/RRR5-10/3	1451.913	1451.656	177.618	0.293	775.459	0.289	25	0.069	R.IVVGPAGGSVREGPR.V
R5/RRR5-4/2	1265.126	1264.645	380.956	0.405	674.061	0.413	14	0.130	R.TVVVTIIFMIK.L
R5/RRR5-4/2	1265.023	1264.645	299.784	0.416	602.313	0.419	13	0.129	R.TVVVTIIFMIK.L
R5/RRR5-12/2	1384.543	1384.476	48.495	0.409	874.851	0.425	18	0.139	R.QDTAEALDFFAR.G
R5/RRR5-23/2	927.066	927.080	-15.070	0.473	1264.444	0.298	13	0.145	R.DPLNLINK.H
R5/RRR5-18/2	991.877	992.111	-236.400	0.532	1056.224	0.355	13	0.142	K.FAEEVLQR.E
R5/RRR5-18/2	991.315	992.111	-1816.834	0.434	1200.125	0.289	13	0.141	K.FAEEVLQR.E
R5/RRR5-5/3	1420.993	1420.599	278.416	0.480	1159.439	0.364	22	0.101	R.DRDLIISPHPTR.N
R5/RRR5-6/3	1419.181	1420.599	-1708.865	0.395	780.271	0.440	17	0.092	R.DRDLIISPHPTR.N
R5/RRR5-5/3	1421.098	1420.599	352.188	0.452	838.153	0.343	20	0.083	R.DRDLIISPHPTR.N
R5/RRR5-5/3	1420.986	1420.599	272.860	0.370	594.275	0.312	17	0.076	R.DRDLIISPHPTR.N
R5/RRR5-6/3	1420.662	1420.599	44.236	0.447	703.631	0.304	17	0.075	R.DRDLIISPHPTR.N
R5/RRR5-20/2	1031.900	1031.185	-276.649	0.421	821.806	0.402	14	0.136	K.DVVAEIGSIK.L
R5/RRR5-19/2	1030.411	1031.185	-1726.689	0.263	657.486	0.277	13	0.118	K.DVVAEIGSIK.L
R5/RRR5-18/2	1440.281	1440.630	-243.262	0.449	1038.391	0.391	16	0.139	R.VAGLDNQGIVGLQR.Q
R5/RRR5-8/2	1517.144	1517.665	-1005.919	0.345	1259.660	0.330	19	0.148	R.EVAIEDPFNVDIR.Q
R5/RRR5-8/2	1517.056	1517.665	-1063.844	0.285	1132.791	0.241	17	0.128	R.EVAIEDPFNVDIR.Q
R5/RRR5-1/2	1394.283	1394.601	-229.334	0.298	810.754	0.363	16	0.126	R.HDSIEQLLLLGR.M

Table S16: List of SePro filtered MS/MS spectra containing the SEQUEST scores and proposed peptide sequences detected in roots of *Oryza longistaminata.*

Rep/File/Charge	Measured MH	Theoretical MH	PPM	Primary Score	Secondary Score	Delta CN	Peaks Matched	Bayesian Score	Peptide Sequence
R5/RRR5-9/2	1192.505	1192.386	99.529	0.445	1045.534	0.387	16	0.146	R.ILVQEGIYEK.F
R5/RRR5-8/2	1192.132	1192.386	-214.200	0.460	964.760	0.361	16	0.138	R.ILVQEGIYEK.F
R5/RRR5-3/2	1236.107	1235.371	-214.603	0.444	782.813	0.370	18	0.129	R.LADFGAAISGANK.F